
BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME Thomas Leitner	POSITION TITLE Staff Scientist		
eRA COMMONS USER NAME TKLEITNER			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Royal Institute of Technology, Stockholm, Sweden	B.S.	1991	Biochemical Engineering
Karolinska Institute, Stockholm, Sweden	Ph.D.	1996	Virology
Los Alamos National Laboratory, Los Alamos, NM	Postdoc	1996-1998	Theoretical Biology

A. Personal Statement

My expertise rests on that I have studied HIV molecular evolution and molecular epidemiology for 20 years, during which time I've been PI on many projects investigating HIV molecular evolution. I am currently also co-PI on the Los Alamos HIV database, where my main responsibility is bioinformatics tool development and scientific content in the sequence database component. I have experience from running a Genomics core facility servicing a broad range of pathogen projects. I have published >100 scientific publications, mostly related to computational analyses of HIV evolution and molecular epidemiology, but also other pathogens and the molecular history of the domestic dog. I am currently collaborating with experimental, clinical, and theoretical scientists across the globe. All together making me particularly well-suited for study design and analyzing questions related to genetic evolution.

B. Positions and Honors

Positions

- 1998-2003 Assistant Professor and Head of the HIV & Retrovirus Section at the Swedish Institute for Infectious Disease Control, Sweden.
- 2001-2003 Head of the Genomics Core facility at the Swedish Institute for Infectious Disease Control, Sweden.
- 2003-present Staff Scientist at the Los Alamos National Laboratory, Theoretical Biology and Biophysics.

Honors

- 1996-1998 Postdoctoral fellowship, Swedish Research Council for Engineering Sciences (TFR)
- 1998-2002 Research fellowship, Swedish Medical Research Council (MFR)
- 2005 Women's Career Development Mentoring Award, LANL
- 2006 Outstanding Innovation Technology Transfer Award, LANL
- 2010 Outstanding Innovation Technology Transfer Award, LANL

Other Experience

- 1998-present Advisor for 13 PhD students, 4 postdocs, and other students
- 2003-2007 Chief editor of the HIV sequence database
- 2005-2008 Team leader HIV databases team, T-10, Los Alamos National Laboratory
- 2004-present Organizing committee, HIV Dynamics & Evolution conference
- 2009-present Affiliate at Center of Nonlinear Studies (CNLS), Los Alamos National Laboratory
- 2010-present Guest Associate Editor PLoS Computational Biology
- 2010, 2012 NIH study section reviewer
- 1998-present Regular reviewer for many journals including Nature, Science, PNAS, PLoS (Pathogens, Computational Biology, One), J Virol, Retrovirology, ARHR, Bioinformatics, Genetics, JAMA, MBE, MEEGID.

C. Selected peer-reviewed publications (in chronological order)

- Scarlatti G, **Leitner T**, Halapi E, Wahlberg J, Marchisio P, Clerici-Schoeller MA, Wigzell H, Fenyö EM, Albert J, Uhlén M, Rossi P. 1993. Comparison of variable region 3 sequences of human immunodeficiency virus type 1 from infected children with the RNA and DNA sequences of the virus populations of their mothers. *PNAS USA* 90:1721-1725
- Leitner T**, Halapi E, Scarlatti G, Rossi P, Albert J, Fenyö EM, Uhlén M. 1993. Analysis of heterogeneous viral populations by direct DNA sequencing. *BioTechniques* 15:120-126.
- Pettersson B, **Leitner T**, Ronaghi M, Bölske G, Uhlén M, Johansson KE. 1996. The phylogeny of the *Mycoplasma mycoides* cluster as determined by sequence analysis of the 16S rRNA genes from two rRNA operons. *J Bact* 178: 4131-4142.
- Leitner T**, Escanilla D, Franzén C, Uhlén M, Albert J. 1996. Accurate reconstruction of a known HIV-1 transmission history by phylogenetic tree analysis. *PNAS USA* 93:10864-10869.
- Leitner T**, Kumar S, Albert J. 1997. Tempo and mode of nucleotide substitutions in gag and env gene fragments in human immunodeficiency virus type 1 populations with a known transmission history. *J Virol* 71:4761-4770
- Halapi E, **Leitner T**, Jansson M, Scarlatti G, Orlandi P, Plebani A, Romiti L, Albert J, Wigzell H, Rossi P. 1997. Correlation between HIV sequence evolution, specific immune response and clinical outcome in vertically infected infants. *AIDS* 11:1709-1717.
- Alaeus A, **Leitner T**, Lidman K, Albert J. 1997. Most genetic subtypes of HIV-1 have entered Sweden. *AIDS* 11:199-202.
- Nijhuis M, Boucher CAB, Schipper P, **Leitner T**, Schuurman R, Albert J. 1998. Stochastic processes strongly influence HIV-1 evolution during suboptimal protease-inhibitor therapy. *PNAS USA* 95:14441-14446.
- Leitner T**, Albert J. 1999. The molecular clock of HIV-1 unveiled through analysis of a known transmission history. *PNAS USA* 96:10752-10757.
- Robertson DL, Anderson JP, Bradac JA, Carr JK, Foley B, Gao F, Hahn BH, Kuiken C, Learn GH, **Leitner T**, McCutchan F, Osmanov S, Peeters M, Pieniazek D, Salminen M, Wolinsky S, Korber B. 2000. HIV-1 nomenclature proposal. *Science* 288:55-57.
- Leitner T**, Albert J. 2000. Reconstruction of HIV-1 transmission chains for forensic purposes. *AIDS Rev.* 2:241-251.
- Savolainen P, Zhang Y-P, Luo J, Lundeberg J, **Leitner T**. 2002. Genetic evidence for an East Asian origin of domestic dogs. *Science* 298:1610-1613.
- Wilbe K, Salminen MO, Laukkanen T, McCutchan F, Ray SC, Albert J, **Leitner T**. 2003. Investigation of novel HIV-1 recombinant forms using the branching index. *Virology* 316:116-125.
- Savolainen P, **Leitner T**, Wilton AN, Matisoo-Smith E, Lundeberg J. 2004. A detailed picture of the origin of the Australian dingo, obtained from the study of mitochondrial DNA. *PNAS USA* 101:12387-12390.
- Zuniga R, Lucchetti A, Galvan P, Sanchez S, Sanchez C, Hernandez A, Sanchez H, Frahm N, Linde CH, Hewitt HS, Hildebrand W, Altfeld M, Allen TM, Walker BD, Korber TM, **Leitner T**, Brander C. 2006. Relative dominance of gag p24-specific cytotoxic T lymphocytes is associated with human immunodeficiency virus control. *J Virol* 80: 3122-3125.
- Schultz A-K, Zhang M, **Leitner T**, Kuiken C, Korber B, Morgenstern B, Stanke M. 2006. Jumping profile Hidden Markov Models for database searching and applications to recombination sites in HIV and HCV genomes. *BMC Bioinf* 7: 265-280.
- Zhang M, Schultz A-K, Calef C, **Leitner T**, Korber B, Morgenstern B, Stanke M. 2006. jpHMM at GOBICS: a web server to detect genomic recombination in HIV. *Nucleic Acids Res* 34: W463-W465.
- Leitner T**, Dazza M-C, Ekwilanga M, Apetrei C, Saragosti S. 2007. Sequence diversity among chimpanzee simian immunodeficiency viruses (SIVcpz) suggests that SIVcpzPtt was derived from SIVcpzPtt through additional recombination events. *AIDS Res Hum Retrovirus* 23: 1114-1118.
- Maljkovic Berry I, Ribeiro R, Kothari M, Athreya G, Daniels M, Lee HY, Bruno W, **Leitner T**. 2007. Unequal evolutionary rates in the HIV-1 pandemic: The evolutionary rate of HIV-1 slows down when the epidemic rate increases. *J Virol* 81: 10625-10635.

- Ripamonti C, **Leitner T**, Lauren A, Karlsson I, Pastore A, Cavarelli M, Antonsson L, Plebani A, Fenyö EM, Scarlatti G. 2007. Biological and genetic evolution of HIV type 1 in two siblings with different patterns of disease progression. *AIDS Res Hum Retroviruses* 23:1531-1540.
- Skar H, Sylvan S, Hansson H-B, Gustavsson O, Boman H, Albert J, **Leitner T**. 2008. Multiple HIV-1 introductions into the Swedish intravenous drug user population in the years of 2001-2002. *Genetics, Infection and Evolution* 8: 545-552.
- Hraber P, Kuiken C, Waugh M, Geer S, Bruno WJ, **Leitner T**. 2008. Automatic classification of HCV and HIV-1 sequences with the branching index. *J Gen Virol* 89: 2098-2107
- Lee HY, Park S, Perelson AS, **Leitner T**. 2008. Dynamic correlation between intrahost HIV-1 quasispecies evolution and disease progression. *PLoS Comput Biol* 4: e1000240.
- Schultz A-K, Zhang M, Bulla I, **Leitner T**, Korber B, Morgenstern B, Stanke M. 2009. jpHMM: Improving the reliability of recombination prediction in HIV-1. *Nucleic Acids Res* 37: W647-651.
- Tsibris AMN, Korber B, Arnaout R, Russ C, Lo C-C, **Leitner T**, Gaschen B, Theiler J, Paredes R, Su Z, Hughes MD, Gulick R, Greaves, Coakley E, Flexner C, Nusbaum C, Kuritzkes DR. 2009. Quantitative deep sequencing reveals dynamic HIV-1 escape and large population shifts during CCR5 antagonist therapy *in vivo*. *PLoS One* 4: e5683.
- Pang J, Kluetsch C, Zou X-J, Zhang A-B, Lou L-Y, Angleby H, Ardalan A, Ekstrom C, Skollermo A, Lundeberg J, Matsumura A, **Leitner T**, Zhang Y-P, Savolainen P. 2009. The dog originated south of Yangtze River less than 16,000 years ago, from numerous wolves. *Mol Biol Evol* 26: 2849-2864.
- Majkovic Berry I, Athreya G, Kothari M, Daniels M, Korber B, Kuiken C, **Leitner T**. 2009. The evolutionary rate dynamically tracks changes in HIV-1 epidemics: application of a simple method for optimizing the evolutionary rate in phylogenetic trees with longitudinal data. *Epidemics* 1: 230-239.
- Neher RA, **Leitner T**. 2010. Recombination rate and selection strength in HIV intra-patient evolution. *PLoS Comput Biol* 6: e1000660.
- Zhang M, Macke J, Foley B, Schultz A-K, Morgenstern B, Korber B, **Leitner T**. 2010. The role of recombination in the emergence of a complex and dynamic HIV epidemic. *Retrovirology* 7:25.
- Bulla I, Schultz A-K, Schreiber F, Zhang M, **Leitner T**, Korber B, Morgenstern B, Stanke M. 2010. HIV classification using coalescent theory. *Bioinformatics* 26: 1409-1415.
- Hedskog C, Mild M, Jernberg J, Sherwood E, Bratt G, **Leitner T**, Lundeberg J, Andersson B, Albert J. 2010. Dynamics of HIV-1 quasispecies during antiviral treatment dissected using ultra-deep pyrosequencing. *PLoS One* 5(7): e11345.
- Skar H, Borrego P, Wallstrom TC, Mild M, Marcelino J, Barroso H, Taveira N, **Leitner T**, Albert J. 2010. HIV-2 genetic evolution in patients with advanced disease is faster than in matched HIV-1 patients. *J Virol* 84: 7412-7415.
- Fischer W, Bhattacharya T, Keele B, Giorgi E, Hraber P, Gantsov V, Lo C-C, **Leitner T**, Nag A, Wallstrom T, Han C, Gleasner C, Green L, Wang S, McMichael A, Haynes B, Hahn B, Perelson A, Borrow P, Shaw G, Korber B. 2010. Rapid mutational escape from cytotoxic T-cell responses in acute HIV-1 infection – an ultra-deep view. *PLoS One* 5(8): e12303.
- Skar H, Axelsson M, Liitsola K, Brummer-Korvenkontio H, Thalme A, Gyllensten K, Berggren I, **Leitner T**, Albert J. 2011. The dynamics of two separate but linked CRF01_AE outbreaks among IDUs in Stockholm and Helsinki. *J Virol* 85: 510-518.
- Cale EM, Hraber P, Giorgi EE, Fischer W, Bhattacharya T, **Leitner T**, Yeh WW, Gleasner C, Green LD, Han CS, Korber B, Letvin NL. 2011. CD8+ T lymphocytes recognize but fail to contain the accumulation of SIV epitope escape mutations. *J Virol* 85:3746-3757.
- Skar H, Gutenkunst RN, Wilbe K, Alaeus A, Albert J, **Leitner T**. 2011. Daily sampling of an HIV-1 patient with slowly progressing disease displays persistence of multiple env subpopulations consistent with neutrality. *PLoS One* 6(8): e21747.
- Desmarais SM, **Leitner T**, Barron AE. 2012. Quantitative experimental determination of primer-dimer formation risk by free-solution conjugate electrophoresis. *Electrophoresis* 33(3): 483-491.
- Graw F, **Leitner T**, Ribeiro RM. 2012. Agent-based and phylogenetic analyses reveal how HIV-1 moves between risk groups: injecting drug users sustain the heterosexual epidemic in Latvia.. *Epidemics* 4(2):104-116.
- Immonen T, Gibson R, **Leitner T**, Arts EJ, Somersalo E, Calvetti D. 2012. A hybrid stochastic-deterministic computational model accurately describes spatial dynamics and virus diffusion in HIV-1 growth competition assay. *J Theor Biol* 17(312C): 120-132.

D. Research Support

Ongoing Research Support

236617 (Leitner) 07/01/2012 – 06/30/2015
UC Lab Research Program
Accurate evolutionary rates for precise pathogen sourcing
The overall goal with this project is to create more realistic molecular clocks to understand virus evolution.
Role: PI, phylogenetics, modeling

R01AI097265 (Luzuriaga, Janoff) 04/01/2012 – 03/31/2017
NIH/NIAID
HIV-1 Evolution and Functional Correlates of MTCT
The overall goal with this project is to understand biological and genetic determinants of HIV mother-to-child transmission.
Role: Co-investigator, study design, phylogenetics, modeling

R01AI087520 (Leitner) 06/15/2010 – 05/31/2014
NIH/NIAID
Reconstructing HIV Epidemics from HIV Phylogenetics
The overall goal with this project is to create realistic models connecting HIV sequence evolution to how HIV spread among hosts, ie the epidemic dynamics in the host population.
Role: PI, study design, phylogenetics, modeling

NIH-DOE contract Y1-AI-8309 (Korber, Kuiken, Leitner) 12/14/2007 – 12/16/2014
NIH/NIAID
HIV/SIV Database and analysis unit
The overall goal with this project is to provide the international scientific community with a richly annotated HIV database of DNA sequences and immunological information as well as creating user-friendly bioinformatics tools.
Role: Co-PI, bioinformatics development, sequence database scientific content

Completed Research Support in last 3 years

LDRD-DR, X9R8 (Korber, Swanson) 10/01/2008 – 09/30/2011
LANL
Understanding Drug Resistance and Co-infectivity in HIV and TB Infections to Guide Development of Advanced Diagnostics
The overall goal of this project is to investigate acute HIV infection, applying next-gen sequencing (454) technology to HIV and TB molecular analyses, to develop novel TB detection systems, and to investigate HIV-TB coinfection.
Role: Co-investigator, deep sequencing design and phylogenetics

N01-AI-15442 (Walker) 07/01/2003 – 06/30/2009
NIH
HLA Typing and epitope mapping relative to HIV vaccine design-contract #2
The overall goal of this project was to describe the underlying immune response to HIV in different human populations
Role: Co-investigator, subcontract, phylogenetics, statistics