

## Scientific publications by Thomas Leitner

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### Peer-reviewed papers

- Lundgren E, Locke M, Romero-Severson E, Dimitrijevic M, Axelsson M, Andersson E, Carlander C, Brännström J, Norrgren H, Mansson F, Elvstam O, Gisslen M, Fohlin L, Sönnernborg A, Albert J, **Leitner T**. 2024. Sweden surpasses the UNAIDS 95-95-95 Target: Estimating HIV-1 incidence between 2003-2022. *Eurosurveillance* 29(42):pii=2400058.
- Mbisa JL, Lapp Z, Bibby DF, Phillips L, Manso CF, Packer S, Simmons R, Harris K, Mohan J, **Leitner T**, Bradshaw D. 2024. Identification of two subtypes of hepatitis C virus genotype 8 and a potential new genotype successfully treated with direct acting antivirals. *J Inf Dis* *accepted*.
- Lin Q, Goldberg EE, **Leitner T**, Molina-Paris C, King AA, Romero-Severson EO. 2024. The number and pattern of viral genomic reassortments are not necessarily identifiable from segment trees. *Mol Biol Evol* April 22:msae078.
- Goldberg EE, Lundgren EJ, Romero-Severson EO, **Leitner T**. 2024. Inferring viral transmission time from phylogenies for known transmission pairs. *Mol Biol Evol* 41(1):msad282.
- Di Stefano M, Mona I, **Leitner T**, Giuseppina F, Marwan Jabr A, Mbisa T, Fiore J, Santantonio T. 2023. A novel Hepatitis C virus genotype 4 subtype identified by next generation sequencing full-genome characterization in a patient from Saudi-Arabia. *Front Microbiol* 14:1285367.
- Nchinda N, Elangovan R, Yun J, Dickson-Tetteh L, Kirtley S, Hemelaar J, WHO–UNAIDS Network for HIV Isolation Characterisation. 2023. Global associations of key populations with HIV-1 recombinants: a systematic review, global survey, and participant data meta-analysis. *Front Public Health* Jul 27;11:1153638.
- Castro LA, **Leitner T**, Romero-Severson E. 2023. Recombination smooths the time-signal disrupted by latency in within-host HIV phylogenies. *Virus Evol* 9(1):vead032.
- Fray EJ, Wu F, Simonetti FR, Zitzmann C, Sambaturu N, Molina-Paris C, Bender AM, Liu P-T, Ventura JD, Wiseman RW, O'Connor DH, Geleziunas R, **Leitner T**, Ribeiro RM, Perelson AS, Barouch DH, Siliciano JD, Siliciano RF. 2023. Antiretroviral therapy reveals triphasic decay of intact SIV genomes and persistence of ancestral variants: implications for HIV cure. *Cell Host & Microbe* *accepted*.
- Di Stefano M, Faleo G, **Leitner T**, Zheng W, Zhang Y, Hassan A, Arzallah M, Fiore JR, Ismail M, Santantonio TA. 2023. Molecular and genetic characterization of Hepatitis B virus (HBV) among Saudi chronically HBV-infected individuals. *Viruses* 15(2):458.
- Martin F, Marcelino J, Palladino C, Bartolo I, Tracana S, Moranguinho I, Goncalves P, Mateus R, Calado R, Borrego P, **Leitner T**, Clemente SV, Taveira N. 2022. Long-term and low-level envelope C2V3 stimulation from highly diverse virus isolates leads to frequent development of broad and elite antibody neutralization in HIV-1 infected individuals. *Microbiology Spectrum* Nov 29:e0163422.
- Kupperman MD, **Leitner T**, Ke R. 2022. A deep learning approach to real-time HIV outbreak detection using genetic data. *PLOS Comput Biol* 18(10):e1010598.
- Lundgren E, Romero-Severson E, Albert J, **Leitner T**. 2022. Combining biomarker and virus phylogenetic models improves epidemiological source identification. *PLOS Comput Biol* 18(8):e1009741.

- Linchangco G, Foley B, **Leitner T**. 2022. Updated HIV-1 consensus sequences change but stay within similar distance from worldwide samples. *Front Microbiol* 12:828765.
- Nasir A, Dimitrijevic M, Romero-Severson E, **Leitner T**. 2021. Large evolutionary rate heterogeneity among and within HIV-1 subtypes and CRFs. *Viruses* 13:1689.
- Di Stefano M, Ismail M, **Leitner T**, Faleo G, Adem SAE, Elamin MOME, Eltreifi O, Alwazzeah MJ, Fiore JR, Santantonio TA. 2021. Genetic subtypes and natural resistance mutations in HCV genotype 4 infected Saudi Arabian patients. *Viruses* 13:1832.
- Elangovan R, Jenks M, Yun J, Dickson-Tetteh L, Kirtley S, Hemelaar J, WHO–UNAIDS Network for HIV Isolation Characterisation. 2021. Global and regional estimates for subtype-specific therapeutic and prophylactic HIV-1 vaccines: a modeling study. *Front Microbiol* 12:690647.
- Hemelaar J, Elangovan R, Yun J, Dickson-Tetteh L, Kirtley S, Williams B, Gouws-Williams E, Ghys PD, WHO–UNAIDS Network for HIV Isolation Characterisation. 2020. Global and regional molecular epidemiology of HIV-1 recombinants in 1990-2015: a systematic review and global survey. *Lancet HIV* 7(11):e772-e781.
- Romero-Severson E, Nasir A, **Leitner T**. 2020. What should health departments do with HIV sequence data? *Viruses* 12(9):E1018.
- Rich SN, Richards VL, Mavian CN, Switzer W, Rife Magalis B, Poschman K, Geary S, Broadway SE, Bennett SB, Blanton J, **Leitner T**, Boatwright JL, Stetten NE, Cook RL, Spencer EC, Salemi M, Prosperi M. 2020. Employing molecular phylodynamic methods to identify and forecast HIV transmission clusters in public health settings: a qualitative study. *Viruses* 12(9):E921.
- Zhang Y, **Leitner T**, Albert J, Britton T. 2020. Inferring transmission heterogeneity using virus genealogies: estimation and targeted prevention. *PLOS Comput Biol* 16(9):e1008122.
- Leitner T**, Kumar S. 2020. Where did SARS-CoV-2 come from? *Mol Biol Evol* 37(9):2463-2564.
- Mavian C, Kosakovsky Pond S, Marini S, Rife Magalis B, Vandamme A-M, Dellicour S, Scarpino SV, Houldcroft C, Villabona-Arenas J, Paisie TK, Trovão NS, Boucher C, Zhang Y, Scheuermann RH, Gascuel O, Lam TT, Suchard MA, Abecasis A, Wilkinson E, de Oliveira T, Bento AI, Schmidt HA, Martin D, Hadfield J, Faria N, Grubaugh ND, Neher RA, Baele G, Lemey P, Stadler T, Albert J, Crandall KA, **Leitner T**, Stamatakis A, Prosperi M, Salemi M. 2020. Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. *PNAS USA* 117(23):12522-12523.
- Dawson L, Benbow N, Fletcher F, Kassaye S, Killelea A, Latham SR, Lee LL, **Leitner T**, Little S, Metha S, Martinez O, Minalga B, Poon A, Rennie S, Sugarman S, Sweeney P, Torian L, Wertheim JO, NIH working group on ethical issues in HIV phylogenetic research. 2020. Addressing ethical challenges in US-based HIV phylogenetic research. *J Inf Dis* 222(12):1997-2006.
- Giardina F, Romero-Severson E, Axelsson M, Svedhem V, **Leitner T**, Britton T, Albert J. 2019. Getting more from heterogeneous HIV-1 surveillance data in a high immigration country: estimation of incidence and undiagnosed population size using multiple biomarkers. *Int J Epidemiol* 48(6):1795-1803.
- Leitner T**. 2019. Phylogenetics in HIV transmission: taking within-host diversity into account. *Curr Opin HIV AIDS* 14(3):181-187.
- Hemelaar J, Elangovan R, Yun J, Dickson-Tetteh L, Fleminger I, Kirtley S, Williams B, Gouws-Williams E, Ghys PD, WHO–UNAIDS Network for HIV Isolation Characterisation. 2019. Global and regional molecular epidemiology of HIV-1, 1990-2015: a systematic review, global survey, and trend analysis. *Lancet Infect Dis* 19(2):143-155.
- Ezeonwumelu I, Bártolo I, Martin F, Abecasis A, Campos T, Romero-Severson EO, **Leitner T**, Taveira N. 2018. Accidental father-to-son HIV-1 transmission during the seroconversion period. *AIDS Res Hum Retrovir* 34(10):857-862.

- Leitner T**, Romero-Severson E. 2018. Phylogenetic patterns recover known HIV epidemiologic relationships and reveal common transmission of multiple variants. *Nature Microbiology* 3(9):983-988.
- Leitner T**. 2018. The puzzle of HIV neutral and selective evolution. *Mol Biol Evol* 35(6):1355-1358.
- Fun A, **Leitner T**, Vandekerckhove L, Däumer M, Thielen A, Buchholz B, Hoepelman A, Gisolf J, Schipper P, Wensing A, Nijhuis M. 2018. Impact of the HIV-1 genetic background and HIV-1 population size on the evolution of Raltegravir resistance. *Retrovirology* 15(1):1.
- Romero-Severson EO, Bulla I, Hengartner N, Bártolo I, Abecasis A, Azevedo-Pereira JM, Taveira N, **Leitner T**. 2017. Donor-recipient identification in para- and poly-phyletic trees under alternative HIV-1 transmission hypotheses using approximate Bayesian computation. *Genetics* 207(3):1089-1101.
- Volz EM, Romero-Severson E, **Leitner T**. 2017. Phylodynamic inference across epidemic scales. *Mol Biol Evol* 34(5):1276-1288.
- Giardina F, Romero-Severson EO, Albert J, Britton T, **Leitner T**. 2017. Inference of transmission network structure from HIV phylogenetic trees. *PLOS Comput Biol* 13(1):e1005316.
- Foley BT, **Leitner T**, Paraskevis D, Peeters M. 2016. Primate Immunodeficiency Virus Classification and Nomenclature: Review. *Infection, Genetics and Evolution* 46:150-158.
- Pineda-Peña A-C, Varanda J, de Sousa JD, Theys K, Bártolo I, **Leitner T**, Taveira N, Vandamme A-M, Abecasis AB. 2016. On the contribution of Angola to the initial spread of HIV-1. *Infection, Genetics and Evolution* 46:219-222.
- Bartolo I, Calado R, Borrego P, **Leitner T**, Taveira N. 2016. Rare HIV-1 subtype J genomes and a new H/U/CRF02\_AG recombinant genome suggests an ancient origin of HIV-1 in Angola. *AIDS Res Hum Retrovir* 32(8):822-8.
- Romero-Severson EO, Bulla I, **Leitner T**. 2016. Phylogenetically resolving epidemiologic linkage. *Proceedings of the National Academy of Sciences USA* 113(10):2690-2695.
- Sanborn KB, Somasundaran M, Luzuriaga K, **Leitner T**. 2015. Recombination elevates the effective evolutionary rate and facilitates the establishment of HIV-1 infection in infants after mother-to-child transmission. *Retrovirology* 12:96.
- Immonen TT, Conway JM, Romero-Severson EO, Perelson AS, **Leitner T**. 2015. Recombination enhances HIV-1 envelope diversity by facilitating survival of latent genomic fragments in the plasma virus population. *PLoS Comput Biol* 11(12):e1004625.
- Romero-Severson EO, Petrie CL, Ionides E, Albert J, **Leitner T**. 2015. Trends of HIV-1 incidence with credible intervals in Sweden 2002-2009 reconstructed using a dynamic model of within-patient IgG growth. *Int J Epidemiol* 44:998-1006.
- Romero-Severson EO, Volz E, Koopman JS, **Leitner T**, Ionides EL. 2015. Dynamic variation in sexual contact rates for a cohort of HIV-negative gay men. *Am J Epidemiol* 182:255-262.
- Yoon H, **Leitner T**. 2015. PrimerDesign-M: a multiple-alignment based multiple-primer design tool for walking across variable genomes. *Bioinformatics* 31(9):1472-1474.
- Immonen TT, **Leitner T**. 2014. Reduced evolutionary rates in HIV-1 reveal extensive latency periods among replicating lineages. *Retrovirology* 11(1):81.
- Romero-Severson E, Skar H, Bulla I, Albert J, **Leitner T**. 2014. Timing and order of transmission events is not directly reflected in a pathogen phylogeny. *Mol Biol Evol* 31(9): 2472-2482.
- Kilpelainen A, Axelsson Robertson R, **Leitner T**, Sandström E, Maeurer M, Wahren B. 2014. HIV-1 Nef protein carries multiple epitopes suitable for induction of cellular immunity for an HIV vaccine in Africa. *AIDS Res Hum Retroviruses* 30(11):1065-71.

- Angleby H, Oskarsson M, Pang J, Zhang Y-P, **Leitner T**, Braham C, Arvestad L, Lundeberg J, Webb KM, Savolainen P. 2014. Forensic informativity of ~3,000 bp of coding sequence of domestic dog mtDNA. *J Forensic Sci* 59(4): 898-908.
- Palaia JM, McConnell M, Gustafson CE, Stoermer KA, Nolan M, Guay LA, **Leitner T**, Taylor AW, Glenn Fowler M, Janoff EN. 2013. Neutralization of HIV subtypes A and D by breast milk IgG from women with HIV infection in Uganda. *J Infect* 68:264-272.
- Rocha C, Calado R, Borrego P, Marcelino JM, Bartolo I, Rosado L, Silva CS, Gomes P, Familia C, Quintas A, Skar H, **Leitner T**, Barroso H, Taveira N. 2013. Evolution of the human immunodeficiency virus type 2 *envelope* in the first years of infection is associated with the dynamics of the neutralizing antibody response. *Retrovirology* 10(1): 110.
- Brodin J, Krishnamoorthy M, Atherya G, Fischer W, Hrabec P, Gleasner C, Green L, Korber B, **Leitner T**. 2013. A multiple-alignment based primer design algorithm for genetically variable DNA targets. *BMC Bioinformatics* 14:255.
- Brodin J, Mild M, Hedskog C, Sherwood E, **Leitner T**, Andersson B, Albert J. 2013. PCR-induced transitions are the major source of error in cleaned ultra-deep pyrosequencing data. *PLoS One* 8(7): e70388.
- Skar H, Albert J, **Leitner T**. 2013. Towards estimation of HIV-1 date of infection: A time-continuous IgG-model shows that seroconversion does not occur at the midpoint between negative and positive tests. *PLoS One* 8(4): e60906.
- 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.
- 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.
- Desmarais SM, **Leitner T**, Barron AE. 2012. Quantitative experimental determination of primer-dimer formation risk by free-solution conjugate electrophoresis. *Electrophoresis* 33: 483-491.
- Balode D, Skar H, Mild M, Kolupajeva T, Ferdats A, Rozentale B, **Leitner T**, Albert J. 2012. Phylogenetic analysis of Latvian HIV-1 epidemic. *AIDS Res Hum Retroviruses* 28: 928-932.
- 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.
- Hemelaar J, Gouws E, Ghys PD, Osmanov S, WHO-UNAIDS Network for HIV Isolation and Characterization. 2011. Global trends in molecular epidemiology of HIV-1 during 2000-2007. *AIDS* 25: 679-689.
- Cale EM, Hrabec 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.
- Campbell MS, Mullins JI, Hughes JP, Celum C, Wong KG, Raugi DN, Sorensen S, Stoddard JN, Zhao H, Deng W, Kahle E, Panteleeff D, Baeten JM, McCutchan FE, Albert J, **Leitner T**, Wald A, Corey L, Lingappa JR. 2011. Viral linkage in HIV-1 seroconverters and their partners in an HIV-1 prevention clinical trial. *PLoS One* 6(3): e16986.
- 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.
- Fischer W, Bhattacharya T, Keele B, Giorgi E, Hrabec P, Ganusov 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.
- 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.
- 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.
- 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.
- Neher RA, **Leitner T**. 2009. Recombination rate and selection strength in HIV intra-patient evolution. *PLoS Comput Biol* 6: e1000660.
- Maljkovic 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.
- 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.
- Paraskevis D, Pybus O, Magiorkinnis G, Hatzakis A, Wensing AMJ, van de Vijver DA, Albert J, Angarano G, Asjo B, Balotta C, Boeri E, Camacho R, Chaix M-L, Costagliola D, De Luca A, de Mendoza C, Horban A, Korn K, Kucherer C, **Leitner T**, Loveday C, MacRae E, Maljkovic I, Meyer L, Nielsen C, Op de Coul ELM, Ormaasen V, Perrin L, Puchhammer-Stockl E, Roman F, Ruiz L, Salminen M, Schmit J-C, Schuurman R, Soriano V, Stanczak J, Stanojevic M, Van Laethem K, Violin M, Yerly S, Zazzi M, Boucher CA, Vandamme A-M, the SPREAD Programme. 2009. Tracing the HIV-1 subtype B mobility in Europe: a phylogenetic approach. *Retrovirology* 6:49.
- Pang J, Kluetsch C, Zou X-J, Zhang A-B, Lou L-Y, Angleby H, Ardalan A, Ekstrom C, Skolleremo A, Lundeberg J, Matsumura A, **Leitner T**, Zhang Y-P, Savolainen P. 2009. mtDNA Data Indicates a Single Origin for Dogs South of Yangtze River, less than 16,300 Years Ago, from Numerous Wolves. *Mol Biol Evol* 26:2849-2864.
- 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.
- 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.
- 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.
- 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.
- Johansen K, Mannerqvist K, Allard A, Andersson Y, Burman LG, Dillner L, Hedlund KO, Jönsson K, Kumlin U, **Leitner T**, Lysen M, Thorhagen M, Tiveljung-Lindell A, Wahlström C, Zwegberg-Wigart B, Widell A. 2008. Norovirus strains belonging to the GII.4 genotype dominate as a cause of nosocomial outbreaks of viral gastroenteritis in Sweden 1997-2005 arrival of new variants is associated with large nation-wide epidemics. *J Clin Virol* 42: 129-134.

- 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.
- 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.
- Leitner T**, Dazza M-C, Ekwilanga M, Apetrei C, Saragosti S. 2007. Sequence diversity among chimpanzee simian immunodeficiency viruses (SIVcpz) suggests that SIVcpzPts was derived from SIVcpzPtt through additional recombination events. *AIDS Res Hum Retrovirus* 23: 1114-1118.
- Madsen TV, **Leitner T**, Lohse N, Obel N, Ladefoged K, Gerstoft J, Petersen AB, Nielsen C, Joergensen LB. 2007. Introduction of HIV-1 into an isolated population: Molecular epidemiology study from Greenland. *AIDS Res Hum Retrovirus* 23: 675-681.
- Hraber PT, Fischer WM, Bruno WJ, **Leitner T**, Kuiken C. 2006. Comparative analysis of hepatitis C virus phylogenies from coding and non-coding regions: the 5' untranslated region (UTR) fails to classify subtypes. *Virology Journal* 3: 103-112.
- Clevestig P, Pramanik L, **Leitner T**, Ehrnst A. 2006. CCR5 use by human immunodeficiency virus type 1 is associated closely with the gp120 V3 loop N-linked glycosylation site. *J Gen Virol* 87: 607-612.
- 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. *NAR* 34: W463-W465.
- 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.
- 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.
- van de Vijver DAMC, Wensing AMJ, Angarano G, Asjo B, Balotta C, Boeri E, Camacho R, Chaix M-L, Costagliola D, Op de Coul E, de Luca A, Maljkovic I, de Mendoza C, Derdelinckx I, Grossman Z, Hamouda O, Hatzakis A, Hoepelman IM, Hemmer R, Horban A, Korn K, Kucherer C, **Leitner T**, Loveday C, MacRae E, Meyer L, Nielsen C, Ormaasen V, Perrin L, Paraskevis D, Puchhammer-Stockl E, Ruiz L, Salminen MO, Schmit JCC, Schneider F, Schuurman R, Soriano V, Stanczak G, Stanojevic M, Vandamme A-M, Van Laethem K, Violin M, Wilbe K, Yerly S, Zazzi M, Boucher CAB. 2006. The calculated genetic barrier for drug resistance mutations in six different non-B subtypes and two CRF's in a large European dataset is largely similar to subtype B. *J Acquir Immune Defic Syndr* 41: 352-360.
- Zhang M, Wilbe K, Wolfe ND, Gaschen B, Carr JK, **Leitner T**. 2005. HIV-1 CRF13\_cpx revisited: identification of a new sequence from Cameroon and signal for sub-subtype J2. *AIDS Res Hum Retroviruses* 21: 955-960.
- Clevestig P, Maljkovic I, Casper C, Carlenor E, Lindgren S, Naver L, Bohlin A-B, Fenyö EM, **Leitner T**, Ehrnst A. 2005. The X4 phenotype of HIV type 1 evolves from R5 in two children of mothers, carrying X4, and is not linked to transmission. *AIDS Res Hum Retroviruses* 21:371-378.
- Malmsten A, Shao X-W, Sjudahl S, Fredriksson E-L, Pettersson I, **Leitner T**, Kallander CFR, Sandström E, Gronowitz JS. 2005. Improved HIV-1 viral load

- determination based on reverse transcriptase activity recovered from human plasma. *J Med Virol.* Jul;76(3):291-6.
- Wensing AMJ, van de Vijver DAMC, Angarano G, Asjo B, Balotta C, Boeri E, Camacho R, Chaix M-L, Costagliola D, de Luca A, Derdelinckx I, Grossman Z, Hamouda O, Hatzakis A, Hemmer R, Hoepelman IM, Horban A, Korn K, Kucherer C, **Leitner T**, Loveday C, MacRae E, Maljkovic I, de Mendoza C, Meyer L, Nielsen C, Op de Coul E, Ormaasen V, Paraskevis D, Perrin L, Puchhammer-Stockl E, Ruiz L, Salminen MO, Schmit JCC, Schneider F, Schuurman R, Soriano V, Stanczak G, Stanojevic M, Vandamme AM, Van Laethem K, Violin M, Wilbe K, Yerly S, Zazzi M, Boucher CAB. 2005. Prevalence of drug-resistant HIV-1 variants in untreated individuals in Europe: implications for clinical management. *Journal of Infectious Diseases* 192:958-966.
- Aleman S, **Leitner T**, Liu MA, Wahren B. 2004. Minor nef gene alterations after human HIV-DNA immunisation. *AIDS* 18:817-819.
- 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. *Proceedings of the National Academy of Sciences USA* 101:12387-12390.
- Koivula T, Ekman M, **Leitner T**, Löfdahl S, Svensson SB, Källenius G. 2004. Genetic characterization of the Guinea Bissau family of *Mycobacterium tuberculosis* complex strains. *Microbes and Infection* 6:272-278.
- Balode D, Ferdats A, Dievberna I, Viksna L, Rozentale B, Kolupajeva T, Konicheva V, **Leitner T**. 2004. Rapid epidemic spread of HIV-1 subtype A1 among intravenous drug users in Latvia and slower spread of subtype B among other risk groups. *AIDS Res. Hum. Retrovirus.* 20:245-249.
- Tran Thi Thanh H, Maljkovic I, Swartling S, Phung Dac C, Chiodi F, **Leitner T**. 2004. HIV-1 CRF01\_AE in intravenous drug users in Hanoi, Vietnam. *AIDS Res. Hum. Retrovirus.* 20:341-345.
- Maljkovic I, Wilbe K, Sölver E, Alaeus A, **Leitner T**. 2003. Limited transmission of HIV-1 drug resistance in 100 Swedish drug-naive patients infected with subtypes A, B, C, D, G, U and CRF01\_AE. *AIDS Res. Hum. Retrovirus.* 19:989-997.
- Malmsten A, Shao X-W, Aperia K, Sandström E, Källander CFR, **Leitner T**, Gronowitz JS. 2003. HIV-1 viral load determination based on reverse transcriptase activity recovered from human plasma. *J. Med. Virol.* 71:347-359.
- Eriksson LE, Falk KI, Bratt G, Leandersson A-C, Wahren B, **Leitner T**. 2003. HIV-1 DNA development during long-term supervised therapy interruption. *AIDS Res. Hum. Retrovirus.* 19:259-265.
- Eriksson LE, **Leitner T**, Wahren B, Leandersson A-C, Falk KI. 2003. A multiplex real-time PCR for quantification of HIV-1 DNA and the human albumin gene in CD4+ cells. *APMIS* 111:625-633.
- Karlsson I, Antonsson L, Shi Y, Karlsson A, Albert J, **Leitner T**, Olde B, Owman C, Fenyö EM. 2003. HIV biological variability unveiled: frequent isolations and chimeric receptors reveal unprecedented variation of co-receptor use. *AIDS* 17:2561-2569.
- 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, Zhang Y-P, Luo J, Lundeberg J, **Leitner T**. 2002. Genetic evidence for an East Asian origin of domestic dogs. *Science* 298:1610-1613.

- Rollman E, Lund LH, Sjöstrand DE, **Leitner T**, Wahren B. 2002. A unique amino acid deletion in the chimpanzee Cyclin T1 does not affect Tat trans-activation of human immunodeficiency virus (HIV). *AIDS* 16:2335-2337.
- Wilbe K, Tscherning-Casper C, Albert J, **Leitner T**. 2002. Identification of two CRF11-cpx genomes and two preliminary representatives of a new circulating recombinant form (CRF13-cpx) of HIV type 1 in Cameroon. *AIDS Res. Hum. Retrovirus*. 18:849-856.
- Casper C, Navér L, Clevestig P, Belfrage E, **Leitner T**, Albert J, Lindgren S, Ottenblad C, Bohlin AB, Fenyö EM, Ehrnst A. 2002. Co-receptor change appears after the immune deficiency is established in children infected with different HIV-1 subtypes. *AIDS Res. Hum. Retrovirus*. 18:343-352.
- Casper CHE, Clevestig P, Carlenor E, **Leitner T**, Anzén B, Lidman K, Belfrage E, Albert J, Bohlin A-B, Navér L, Lindgren S, Fenyö EM, Ehrnst AC. 2002. Appearance of the X4 phenotype is linked in HIV-1 infected mother and child pairs despite the early presence of R5 virus in the child. *J Inf Disease* 186: 914-921.
- Ljungberg K, Hassan MS, Islam MN, Siddiqui MA, Aziz MM, Wahren B, Islam KB, **Leitner T**. 2002. Subtypes A, C, G and recombinant HIV-1 are circulating in Bangladesh. *AIDS Res. Hum. Retrovirus*. 18:667-670.
- Leitner T**, Albert J. 2000. Reconstruction of HIV-1 transmission chains for forensic purposes. *AIDS Rev*. 2:241-251.
- 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.
- O'Meara D, Wilbe K, **Leitner T**, Hejdeman B, Albert J, Lundeberg J. 2001. Monitoring resistance to HIV-1 protease inhibitors by pyrosequencing. *J Clin Microbiol* 39:464-473.
- Laukkanen T, Albert J, Liitsola K, Green SD, Carr J, **Leitner T**, McCutchan FE, Salminen KO. 1999. Virtually full-length sequences of HIV type 1 J reference strains. *AIDS Res. Hum. Retrovirus*. 15:293-297.
- Leitner T**, Albert J. 1999. The molecular clock of HIV-1 unveiled through analysis of a known transmission history. *Proceedings of the National Academy of Sciences USA* 96:10752-10757.
- 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. *Proceedings of the National Academy of Sciences USA* 95:14441-14446.
- Alaeus A, **Leitner T**, Lidman K, Albert J. 1997. Most genetic subtypes of HIV-1 have entered Sweden. *AIDS* 11:199-202.
- Colognesi C, Halapi E, Jansson M, Hodara V, Steuer G, Tresholdi E, **Leitner T**, Scarlatti G. 1997. The role of virologic and immunologic factors in mother-to-child transmission of HIV-1. *American J. Repr. Imm.* 38:197-200.
- 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.
- Di Stefano M, Gray F, **Leitner T**, Chiodi F. 1996. Analysis of env V3 sequences from HIV-1-infected brain indicates restrained virus expression throughout the disease. *Journal of Medical Virology* 49:41-48.
- 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. *Journal of Virology* 71:4761-4770 (see also correction 1998: 72:2565).
- Norrgren H, Marquina S, **Leitner T**, Aaby P, Melbye M, Poulsen AG, Larsen O, Dias F, Escanilla D, Biberfeldt G, Albert J, Naucler A. 1997. HIV-2 genetic variation and DNA load in asymptomatic carriers and AIDS cases in Guinea-Bissau. *J. Acquir. Immune Defic. Syndr.* 16:31-38.
- Pettersson B, Andersson AL, **Leitner T**, Olsvik O, Uhlen M, Storey C, Black CM. 1997. Evolutionary relationships among the members of the genus *Chlamydia* based on 16S rDNA analysis. *Journal of Bacteriology* 179:4195-4205.
- Savolainen P, Rosen B, Holmberg A, **Leitner T**, Uhlen M, Lundeberg J. 1997. Sequence analysis of domestic dog mitochondrial DNA for forensic use. *Journal of Forensic Sciences* 42:593-600.
- Leitner T**, Escanilla D, Franzén C, Uhlén M, Albert J. 1996. Accurate reconstruction of a known HIV-1 transmission history by phylogenetic tree analysis. *Proceedings of the National Academy of Sciences USA* 93:10864-10869.
- Leitner T**, Korovina G, Marquina S, Smolskaya T, Albert J. 1996. Molecular epidemiology and MT-2 cell tropism of Russian HIV-1 variants. *AIDS Res. Hum. Retrovirus.* 12:1595-1603.
- Marquina S, **Leitner T**, Rabinovich RD, Benetucci J, Libonatti O, Albert J. 1996. Co-existence of subtypes B, F and a B/F env recombinant of HIV-1 in Buenos Aires, Argentina. *AIDS Res. Hum. Retrovirus.* 12:1651-1654.
- Myers G, Lu H, Calef C, **Leitner T**. 1996. Heterogeneity of papilloma viruses. *Seminars in Cancer Biology* 7:349-358.
- 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. *Journal of Bacteriology* 178: 4131-4142.
- Scarlatti G, **Leitner T**, Hodara V, Jansson M, Karlsson A, Wahlberg J, Rossi P, Uhlén M, Fenyö EM, Albert J. 1996. Interplay of HIV-1 phenotype and neutralizing antibody response in pathogenesis of AIDS. *Immunology Letters* 51: 23-28.
- Di Stefano M, Sabri F, **Leitner T**, Svennerholm B, Hagberg L, Norkrans G, Chiodi F. 1995. Reverse transcriptase sequence of paired cerebrospinal fluid and blood HIV-1 isolates during AZT-treatment. *J Clin Microbiol.* 33:352-355.
- Leitner T**, Alaeus A, Marquina S, Lilja E, Lidman K, Albert J. 1995. Yet another subtype of HIV type 1? *AIDS Res. Hum. Retrovirus* 11:995-997.
- Leitner T**, Escanilla D, Marquina S, Wahlberg J, Broström C, Hansson HB, Uhlén M, Albert J. 1995. Biological and molecular characterization of subtype D, G and A/D recombinant HIV-1 transmissions in Sweden. *Virology* 209:136-146.
- Albert J, Wahlberg J, **Leitner T**, Escanilla D, Uhlén M. 1994. Analysis of a rape case by direct sequencing of the HIV-1 *pol* and *gag* genes. *Journal of Virology* 68:5918-5924.
- Rübsamen-Waigmann H, von Briesen H, Scheuermann EH, Albert J, **Leitner T**, Schoeppe W. 1994. HIV infection by a blood-clotting preparation in a surgical patient. *Münchener Medizinisches Wochenschrift* 136:41-45.
- 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.
- Scarlatti G, **Leitner T**, Halapi E, Wahlberg J, Jansson M, Wigzell H, Fenyö EM, Albert J, Uhlen M, Rossi P. 1993. Analysis of the HIV-1 envelope V3-loop

- sequences from ten mother-child pairs. *Ann. N. Y. Acad. Sci.* 693:277-280.
- 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. *Proceedings of the National Academy of Sciences USA* 90:1721-1725.
- Scarlatti G, **Leitner T**, Hodara V, Halapi E, Rossi P, Albert J, Fenyö EM. 1993. Neutralizing antibodies and viral characteristics in mother-to-child transmission of HIV-1. *AIDS* 7:45-48.
- Hultquist G, Seo M, **Leitner T**, Leygraf C, Sato N. 1987. The dissolution behaviour of iron, chromium, molybdenum and copper from pure metals and from ferritic stainless steels. *Corros. Sci.* 27:937-946.

## Books, book chapters, reviews

- Foley B, **Leitner T**, Apetrei C, Hahn B, Mizrahi I, Mullins J, Rambaut A, Wolinsky S, Korber B. 2018. HIV sequence compendium 2017. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Foley B, **Leitner T**, Apetrei C, Hahn B, Mizrahi I, Mullins J, Rambaut A, Wolinsky S, Korber B. 2017. HIV sequence compendium 2017. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Foley B, **Leitner T**, Apetrei C, Hahn B, Mizrahi I, Mullins J, Rambaut A, Wolinsky S, Korber B. 2016. HIV sequence compendium 2016. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Foley B, **Leitner T**, Apetrei C, Hahn B, Mizrahi I, Mullins J, Rambaut A, Wolinsky S, Korber B. 2015. HIV sequence compendium 2015. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Foley B, **Leitner T**, Apetrei C, Hahn B, Mizrahi I, Mullins J, Rambaut A, Wolinsky S, Korber B. 2014. HIV sequence compendium 2014. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Foley B, **Leitner T**, Apetrei C, Hahn B, Mizrahi I, Mullins J, Rambaut A, Wolinsky S, Korber B. 2013. HIV sequence compendium 2013. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Kuiken C, Foley B, **Leitner T**, Apetrei C, Hahn B, Mizrahi I, Mullins J, Rambaut A, Wolinsky S, Korber B. 2012. HIV sequence compendium 2012. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Kuiken C, Foley B, **Leitner T**, Apetrei C, Hahn B, Mizrahi I, Mullins J, Rambaut A, Wolinsky S, Korber B. 2011. HIV sequence compendium 2011. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Kuiken C, Foley B, **Leitner T**, Apetrei C, Hahn B, Mizrahi I, Mullins J, Rambaut A, Wolinsky S, Korber B. 2010. HIV sequence compendium 2010. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Kuiken C, **Leitner T**, Foley B, Hahn B, Marx P, McCutchan F, Wolinsky S, Korber B. 2009. HIV sequence compendium 2009. *Theoretical Biology and Biophysics*, Los Alamos National Laboratory, Los Alamos, NM.
- Schultz A, Zhang M, **Leitner T**, Korber B, Morgenstern B, Stanke M. 2008. JpHMM: Erkennung von Rekombinationen bei HIV. *BIOforum*. 2, 44-46. (In German).
- Kuiken C, **Leitner T**, Foley B, Hahn B, Marx P, McCutchan F, Wolinsky S, Korber B. 2008.

- HIV sequence compendium 2008. Theoretical Biology and Biophysics, Los Alamos National Laboratory, Los Alamos, NM.
- Korber BT, Miller CC, **Leitner T**. 2007. HIV subtypes, antigenic diversity, and vaccine design. Pp 65-75. *in* Kahn P, Gust I and Koff W. AIDS Vaccine Development: Challenges and Opportunities. Caister Academic Press, UK.
- Leitner T**, Foley B, Hahn B, Marx P, McCutchan F, Mellors J, Wolinsky S, Korber B. HIV sequence compendium 2006/2007. Theoretical Biology and Biophysics, Los Alamos National Laboratory.
- Leitner T**, Foley B, Hahn B, Marx P, McCutchan F, Mellors J, Wolinsky S, Korber B. 2005. HIV Sequence Compendium 2005. Theoretical Biology and Biophysics, Los Alamos National Laboratory, Los Alamos, NM.
- Leitner T**, Korber B, Daniels M, Calef C, Foley B. HIV-1 subtype and circulating recombinant form (CRF) reference sequences, 2005. Pp. XX *in* T. Leitner *et al.* HIV Sequence Compendium 2005. Theoretical Biology and Biophysics, Los Alamos National Laboratory, Los Alamos, NM.
- Leitner T**, Foley B, Hahn B, Marx P, McCutchan F, Mellors J, Wolinsky S, Korber B. 2004. HIV Sequence Compendium 2003. Theoretical Biology and Biophysics, Los Alamos National Laboratory, Los Alamos, NM.
- Leitner T**. 2002. The molecular epidemiology of human viruses. Kluwer Academic Publishers, Boston.
- Kuiken CL, **Leitner T**. 2001. HIV-1 subtyping. Pp. 27-53 *in* A. Rodrigues and G. Learn. Computational analysis of HIV molecular sequences. Kluwer Academic Publishers, Boston.
- Robertson DL, Anderson JP, Bradac JA, Carr JK, Funkhouser RK, 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: a reference guide to HIV-1 classification. *In* B. Korber *et al.* Human Retroviruses and AIDS 1999: a compilation and analysis of nucleic acid and amino acid sequences. Los Alamos National Laboratory, Los Alamos, NM.
- Carr J, Foley BT, **Leitner T**, Salminen M, Korber B, McCutchan F. 1999. Reference sequences representing the principal genetic diversity of HIV-1 in the pandemic. Pp. III19-III26 *in* B. Korber *et al.* Human retroviruses and AIDS 1998: a compilation and analysis of nucleic acid and amino acid sequences. Los Alamos National Laboratory, Los Alamos, NM.
- Leitner T**, Fitch WM. 1999. The phylogenetics of known transmission histories. Pp. 315-345 *in* K. A. Crandall. Molecular Evolution of HIV. Johns Hopkins, Baltimore, MD.
- Korber B, Foley B, **Leitner T**, Mellors JW, McCutchan F, Hahn B, Myers G, Kuiken C. 1998. Human Retroviruses and AIDS 1997: a compilation and analysis of nucleic acid and amino acid sequences. Los Alamos National Laboratory, Los Alamos, NM.
- Leitner T**. 1998. Phylogenetic methods and HIV evolution. Pp. 439-473 *in* N. Saksena. Human Immunodeficiency Virus: Biology, Immunology and Molecular Biology. Medical Systems, Sasson, Italy.
- Leitner T**, Korber B, Robertson D, Gao F, Hahn B. 1998. Updated proposal of reference sequences of HIV-1 genetic subtypes. Pp. III19-III24 *in* B. Korber *et al.* Human Retroviruses and AIDS 1997: a compilation and analysis of nucleic acid and amino acid sequences. Los Alamos National Laboratory, Los Alamos, NM.
- Leitner T**. 1997. Genetic subtypes of HIV-1. Pp. (III)28-(III)40 *in* G. Myers, B. Korber, B. Foley *et al.* Human retroviruses and AIDS 1996: a compilation and analysis

of nucleic acid and amino acid sequences. Los Alamos National Laboratory, Los Alamos, NM.

**Leitner T.** 1997. Genetiska subtyper av HIV-1. Pp. 327-331 (in Swedish) in L.

Moberg. Perspektiv på HIV. Stiftelsen Noaks Ark-Röda Korset, Stockholm.

**Leitner T, Albert J.** 1996. A new genetic subtype of HIV-1. Pp. (III)147-(III)150. in G.

Myers, B. Korber, B. H. Hahn et al. Human retroviruses and AIDS: a compilation and analysis of nucleic acid and amino acid sequences. Los Alamos National Laboratory, Los Alamos, NM.

**Leitner T.** 1996. Genetic variation of HIV-1. Thesis. Karolinska Institute, Stockholm, Sweden.

## Other publications

**Leitner T, Metzker ML, Zwickl D, Brown JM, Geretti AM, Vandamme A, Albert A, Hillis DM.** 2011. Guidelines for HIV in court cases. *Nature* 473:284.

Lemey P, Hillis D, Candelas FG, Milinkovitch M, **Leitner T.** 2006. Molecular evidence backs accused medics – Expert opinion. *Nature* 444: 658-659.

WHO-UNAIDS Network for HIV Isolation and Characterization. 2002. WHO-UNAIDS guidelines for standard HIV isolation and characterization procedures. WHO, Geneva, Switzerland.

Agosto M, Allan J, Benson C, Berger EA, Blumenthal R, Burton D, Clements J, Coffin J, Connor R, Cullen B, Desrosiers R, Dimitrov D, Doms R, Emerman M, Feinberg M, Fultz P, Gerard C, Gonsalves G, Haase A, Haigwood N, Hirsch V, Ho D, Hoxie JA, Hu SL, Hunter E, Johnson P, Kawata PA, Korber B, Kuiken C, Learn GH, **Leitner T**, Lewis G, Link D, Luban J, Luzuriaga K, Malim M, Marx P, McCune JM, Montefiori D, Moore J, Morrow C, Mosier D, Muesing M, Nixon D, Nunberg J, Overbaugh J, Parren P, Planelles V, Pope M, Posnett DN, Siliciano R, Steinman R, Stevenson M, Swanstrom R, Walker BD, Wolinsky S, Zingale D. 1998. AIDS vaccine development. *Science* 208:803-805.

UNAIDS Virus Network. Report of the Technical Working Group. 1998.

Characterisation of globally prevalent HIV strains in relation to HIV vaccine development. WHO, Geneva, Switzerland.