

***Education and Training***

University of Amsterdam	Philosophy	B.S.	1984
University of Amsterdam	Psychology	M.S.	1986
University of Amsterdam	Medicine	Ph.D.	1995
University of Amsterdam	Virology	Postdoc	1996

***Professional Experience:***

- 2002-present Staff member; PI, HCV Database Group at the Los Alamos National Laboratory; PI, HFV database project. Activities:
- manage a team to create and maintain the databases and website
  - design and supervise the construction of new web tools
  - oversee the content of the sequence database (including annotation)
  - do research and publish on viral evolution and molecular epidemiology
  - develop new methods and techniques for the field of sequence analysis
- 1999-2003 Staff member and co-PI, HIV Database and Analysis Group at the Los Alamos National Laboratory; editor, "AIDS Research and Human Retroviruses"; editor, "Human Retroviruses and AIDS". Activities:
- manage the HIV sequence database and website
  - co-manage the entire HIV database project (~20 employees) with the project PI
  - manage the production of the publication of "Human Retroviruses and AIDS", the project's annual HIV sequence variation compendium
  - supervise the research of postdocs and students
  - editor of the "Sequence Notes" section of the journal "AIDS Research and Human Retroviruses"
- 1995-1998 Post-doctoral positions at the HIV Database and Analysis Group at the Los Alamos National Laboratory (2 years), and at the Human Retrovirus Department of the University of Amsterdam (1.5 years). Editor of the Sequence Note section of AIDS Research and Human Retroviruses (1998-2000).

***Relevant Publications***

- 1: Eriksen MB, Jørgensen LB, Krarup H, Laursen AL, Christensen PB, Møller A, Schlichting P, Kuiken C, Bukh J, Weis N; DANHEP Group. Molecular and epidemiological profiles of hepatitis C virus genotype 4 in Denmark. *J Med Virol.* 2010 Nov;82(11):1869-77.
- 2: Kuiken C. Designing a low-cost drug resistance database for viral hepatitis. *Antivir Ther.* 2010;15(3 Pt B):517-20. Review.
- 3: Yusim K, Fischer W, Yoon H, Thurmond J, Fenimore PW, Lauer G, Korber B, Kuiken C. Genotype 1 and global hepatitis C T-cell vaccines designed to optimize coverage of genetic diversity. *J Gen Virol.* 2010 May;91(Pt 5):1194-206.
- 4: Kuiken C, Simmonds P. Nomenclature and numbering of the hepatitis C virus. *Methods Mol Biol.* 2009;510:33-53.
- 5: Hraber P, Kuiken C, Waugh M, Geer S, Bruno WJ, Leitner T. Classification of hepatitis C virus and human immunodeficiency virus-1 sequences with the branching index. *J Gen Virol.* 2008 Sep;89(Pt 9):2098-107.
- 6: Kuntzen T, Berical A, Ndjomou J, Bennett P, Schneidewind A, Lennon N, Birren BW, Kuiken C, Henn MR, Simmonds P, Allen TM. A set of reference sequences for the hepatitis C genotypes 4d, 4f, and 4k covering the full open reading frame. *J Med Virol.* 2008 Aug;80(8):1370-8.
- 7: Kemal KS, Beattie T, Dong T, Weiser B, Kaul R, Kuiken C, Sutton J, Lang D, Yang H, Peng YC, Collman R, Philpott S, Rowland-Jones S, Burger H. Transition from long-term nonprogression to HIV-1

- disease associated with escape from cellular immune control. *J Acquir Immune Defic Syndr.* 2008 Jun 1;48(2):119-26.
- 8: Thurmond J, Yoon H, Kuiken C, Yusim K, Perkins S, Theiler J, Bhattacharya T, Korber B, Fischer W. Web-based design and evaluation of T-cell vaccine candidates. *Bioinformatics.* 2008 Jul 15;24(14):1639-40.
- 9: Kuiken C, Hraber P, Thurmond J, Yusim K. The hepatitis C sequence database in Los Alamos. *Nucleic Acids Res.* 2008 Jan;36(Database issue):D512-6.
- 10: Hraber P, Kuiken C, Yusim K. Evidence for human leukocyte antigen heterozygote advantage against hepatitis C virus infection. *Hepatology.* 2007 Dec;46(6):1713-21.
- 11: Hraber PT, Leach RW, Reilly LP, Thurmond J, Yusim K, Kuiken C; Los Alamos HIV database team. Los Alamos hepatitis C virus sequence and human immunology databases: an expanding resource for antiviral research. *Antivir Chem Chemother.* 2007;18(3):113-23.
- 12: Lok AS, Zoulim F, Locarnini S, Bartholomeusz A, Ghany MG, Pawlotsky JM, Liaw YF, Mizokami M, Kuiken C; Hepatitis B Virus Drug Resistance Working Group. Antiviral drug-resistant HBV: standardization of nomenclature and assays and recommendations for management. *Hepatology.* 2007 Jul;46(1):254-65. Review.
- 13: Reinis M, Weiser B, Kuiken C, Dong T, Lang D, Nachman S, Zhang Y, Rowland-Jones S, Burger H. Genomic analysis of HIV type 1 strains derived from a mother and child pair of long-term nonprogressors. *AIDS Res Hum Retroviruses.* 2007 Feb;23(2):309-15.
- 14: Fischer W, Perkins S, Theiler J, Bhattacharya T, Yusim K, Funkhouser R, Kuiken C, Haynes B, Letvin NL, Walker BD, Hahn BH, Korber BT. Polyvalent vaccines for optimal coverage of potential T-cell epitopes in global HIV-1 variants. *Nat Med.* 2007 Jan;13(1):100-6.
- 15: Hraber PT, Fischer W, Bruno WJ, Leitner T, Kuiken C. Comparative analysis of hepatitis C virus phylogenies from coding and non-coding regions: the 5' untranslated region (UTR) fails to classify subtypes. *Virology.* 2006 Dec 14;3:103.
- 16: Kuiken C, Combet C, Bukh J, Shin-I T, Deleage G, Mizokami M, Richardson R, Sablon E, Yusim K, Pawlotsky JM, Simmonds P; Los Alamos HIV Database Group. A comprehensive system for consistent numbering of HCV sequences, proteins and epitopes. *Hepatology.* 2006 Nov;44(5):1355-61.
- 17: Bernardin F, Herring B, Page-Shafer K, Kuiken C, Delwart E. Absence of HCV viral recombination following superinfection. *J Viral Hepat.* 2006 Aug;13(8):532-7.
- 18: Zhang M, Schultz AK, Calef C, Kuiken C, Leitner T, Korber B, Morgenstern B, Stanke M. jpHMM at GOBICS: a web server to detect genomic recombinations in HIV-1. *Nucleic Acids Res.* 2006 Jul 1;34(Web Server issue):W463-5.
- 19: Schultz AK, Zhang M, Leitner T, Kuiken C, Korber B, Morgenstern B, Stanke M. A jumping profile Hidden Markov Model and applications to recombination sites in HIV and HCV genomes. *BMC Bioinformatics.* 2006 May 22;7:265.
- 20: Kuiken C, Mizokami M, Deleage G, Yusim K, Penin F, Shin-I T, Charavay C, Tao N, Crisan D, Grando D, Dalwani A, Geourjon C, Agrawal A, Combet C. Hepatitis C databases, principles and utility to researchers. *Hepatology.* 2006 May;43(5):1157-65.
- 21: Lu L, Nakano T, Li C, Fu Y, Miller S, Kuiken C, Robertson BH, Hagedorn CH. Hepatitis C virus complete genome sequences identified from China representing subtypes 6k and 6n and a novel, as yet unassigned subtype within genotype 6. *J Gen Virol.* 2006 Mar;87(Pt 3):629-34.
- 22: Yusim K, Richardson R, Tao N, Dalwani A, Agrawal A, Szinger J, Funkhouser R, Korber B, Kuiken C. Los alamos hepatitis C immunology database. *Appl Bioinformatics.* 2005;4(4):217-25.
- 23: Simmonds P, Bukh J, Combet C, Deléage G, Enomoto N, Feinstone S, Halfon P, Inchauspé G, Kuiken C, Maertens G, Mizokami M, Murphy DG, Okamoto H, Pawlotsky JM, Penin F, Sablon E, Shin-I T, Stuyver LJ, Thiel HJ, Viazov S, Weiner AJ, Widell A. Consensus proposals for a unified system of nomenclature of hepatitis C virus genotypes. *Hepatology.* 2005 Oct;42(4):962-73. Review.
- 24: Layden-Almer JE, Kuiken C, Ribeiro RM, Kunstman KJ, Perelson AS, Layden TJ, Wolinsky SM. Hepatitis C virus genotype 1a NS5A pretreatment sequence variation and viral kinetics in African American and white patients. *J Infect Dis.* 2005 Sep 15;192(6):1078-87.
- 25: Switzer WM, Salemi M, Shanmugam V, Gao F, Cong ME, Kuiken C, Bhullar V, Beer BE, Vallet D, Gautier-Hion A, Tooze Z, Villinger F, Holmes EC, Heneine W. Ancient co-speciation of simian foamy viruses and primates. *Nature.* 2005 Mar 17;434(7031):376-80.