

BIOGRAPHICAL SKETCH

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NAME Winston A. Hide		POSITION TITLE Associate Professor of Genomics and Bioinformatics, Department of Biostatistics, Harvard School of Public Health	
eRA COMMONS USER NAME (credential, e.g., agency login) WHIDE1			
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
University of Wales, Cardiff	B.Sc (Hons)	1981	Zoology
Temple University, Philadelphia	M.A.	1985	Molecular Genetics
Temple University, Philadelphia	Ph.D	1991	Molecular Genetics

A. Positions and Honors.**PROFESSIONAL EXPERIENCE:**

1991 **Postdoctoral Fellow**, Molecular Evolution, Baylor College of Medicine, Houston, TX
1991 **Postdoctoral Fellow**, Molecular Evolution, University of Texas
1992 **Postdoctoral Fellow**, Molecular Evolution, Smithsonian Natural History Museum, DC
1993 **Postdoctoral Fellow**, Algorithm Development, University of Houston, TX
1993 **Postdoctoral Fellow**, Genomics, Baylor College of Medicine, Houston, TX
1994 - 1995 **Director**; MasPar Computer Corporation, Genome Science Market Development
1995 **Consultant**, RW Johnson PRI (Johnson and Johnson Pharmaceuticals)
1996 - 2008 **Director and Professor of Genomics and Bioinformatics**, South African National Bioinformatics Institute, University of Western Cape
2003 **Kerr International Fellow**, Ludwig Institute for Cancer Research
2003 - Present **Director of Bioinformatics and Executive Board member**, South African AIDS Vaccine Initiative
2003 - Present **Executive Director of Bioinformatics**, Centre for the AIDS Programme of Research in South Africa
2007 - 2009 **Visiting Professor of Bioinformatics**, Department of Biostatistics Harvard School of Public Health
2007 - Present **Scientific Advisory Board**, Global Initiative on Sharing Avian Influenza Data (GISAID)
2009 **Associate Professor of Bioinformatics**, Department of Biostatistics Harvard School of Public Health

OTHER EXPERIENCE AND PROFESSIONAL MEMBERSHIP:

2001 - 2004 Member of board of directors and Education committee Chair, International Society for Computational Biology
2002 Advisor on bioinformatics and applied genomics, World Health Organization/Tropical Disease Research
2003 - present Executive committee member for Glossina genome sequencing project, World Health Organization / Tropical Disease Research

HONORS and AWARDS:

1991 Discover Magazine: Top fifty scientific discoveries of 1991
1998 National President's Award, Foundation for Research Development, South Africa
1999 Member of University of Western Cape Senate
2001 Appointed Professor of Genomics and Bioinformatics, University Western Cape
2007 Elected member of the Academy of Science of South Africa

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

1. VanBuren V, Piao Y, Dudekula DB, Qian Y, Carter MG, Martin PR, Stagg CA, Bassey UC, Aiba K, Hamatani T, Kargul GJ, Luo AG, Kelso J, **Hide W**, Ko MS. Assembly, verification, and initial annotation of the NIA mouse 7.4K cDNA clone set. *Genome Res*, 2002; 12(12): 1999-2003.
2. McCarthy MI, Smedley D, **Hide W**. New methods for finding disease-susceptibility genes: impact and potential. *Genome Biol*, 2003; 4(10): 119.
3. **Hide W**, Smedley D, McCarthy M, Kelso J. Application of eVOC: controlled vocabularies for unifying gene expression data. *C R Biol*, 2003; 326(10-11): 1089-96.
4. Kelso J, Visagie J, Theiler G, Christoffels A, Bardien S, Smedley D, Otgaar D, Greyling G, Jongeneel CV, McCarthy MI, Hide T, **Hide W**. eVOC: a controlled vocabulary for unifying gene expression data. *Genome Res*, 2003; 13(6A): 1222-30.
5. Lim YP, Hoog JO, Gardner P, Ranganathan S, Andersson S, Subbiah S, Tan TW, **Hide W**, Weiss AS. The S-Star trial bioinformatics course - An on-line learning success. *Biochemistry and Molecular Biology Education*, 2003; 31(1): 20-23.
6. Sharov AA et al., **Hide W**, Ko MS. Transcriptome analysis of mouse stem cells and early embryos. *PLoS Biol*, 2003; 1(3): E74.
7. Brentani H, et al. The generation and utilization of a cancer-oriented representation of the human transcriptome by using expressed sequence tags. *Proc Natl Acad Sci U S A*, 2003; 100(23): 13418-23.
8. Isokpehi RD, **Hide WA**. Integrative analysis of intraerythrocytic differentially expressed transcripts yields novel insights into the biology of *Plasmodium falciparum*. *Malar J*, 2003; 2(1): 38.
9. **Hide WA**, Isokpehi RD. Positive selection scanning of parasite DNA sequences. *Methods Mol Biol*, 2004; 270: 127-50.
10. Davila AMR, Majiwa PAO, Grisard EC, Aksoy S, **Hide W**. Response to Hertz-Fowler and Berriman: Continuing tsetse and Trypanosoma genome sequencing projects. *Trends in Parasitology*, 2004; 20(7): 309-310.
11. Swart EC, **Hide WA**, Seoighe C. FRAGS: estimation of coding sequence substitution rates from fragmentary data. *BMC Bioinformatics*, 2004; 5: 8.
12. Imanishi T, Itoh T, et al. Integrative annotation of 21,037 human genes validated by full-length cDNA clones. *PLoS Biol*, 2004; 2(6): e162.
13. Tiffin N, Kelso JF, Powell AR, Pan H, Bajic VB, **Hide WA**. Integration of text- and data-mining using ontologies successfully selects disease gene candidates. *Nucleic Acids Res*, 2005; 33(5): 1544-52. (Cited since 1996: 41).
14. Tanino M et al., **Hide W**, Okubo K. The Human Anatomic Gene Expression Library (H-ANGEL), the H-Inv integrative display of human gene expression across disparate technologies and platforms. *Nucleic Acids Res*, 2005; 33(Database issue): D567-72.
15. Aksoy S, Berriman M, Hall N, Hattori M, **Hide W**, Lehane MJ. A case for a *Glossina* genome project. *Trends Parasitol*, 2005; 21(3): 107-11.
16. Carninci P, Kasukawa T, et al. The transcriptional landscape of the mammalian genome. *Science*, 2005; 309(5740): 1559-63.
17. Ptitsyn A, **Hide W**. CLU: a new algorithm for EST clustering. *BMC Bioinformatics*, 2005; 6 Suppl 2: S3.
18. Tiffin N, Adie E, Turner F, Brunner HG, van Driel MA, Oti M, Lopez-Bigas N, Ouzounis C, Perez-Iratxeta C, Andrade-Navarro MA, Adeyemo A, Patti ME, Semple CA, **Hide W**. Computational disease gene identification: a concert of methods prioritizes type 2 diabetes and obesity candidate genes. *Nucleic Acids Res*, 2006; 34(10): 3067-81.
19. Bajic VB, Tan SL, Christoffels A, Schonbach C, Lipovich L, Yang L, Hofmann O, Kruger A, **Hide W**, Kai C, Kawai J, Hume DA, Carninci P, Hayashizaki Y. Mice and men: Their promoter properties. *Plos Genetics*, 2006; 2(4): 614-626.
20. Mehrle A, Rosenfelder H, Schupp I, del Val C, Arlt D, Hahne F, Bechtel S, Simpson J, Hofmann O, **Hide W**, Glatting KH, Huber W, Pepperkok R, Poustka A, Wiemann S. The LIFEdb database in 2006. *Nucleic Acids Res*, 2006; 34(Database issue): D415-8.
21. Lombard Z, Tiffin N, Hofmann O, Bajic VB, **Hide W**, Ramsay M. Computational selection and prioritization of candidate genes for fetal alcohol syndrome. *BMC Genomics*, 2007; 8: 389.

22. Schwegmann A, Guler R, Cutler AJ, Arendse B, Horsnell WG, Flemming A, Kottmann AH, Ryan G, **Hide W**, Leitges M, Seoighe C, Brombacher F. Protein kinase C delta is essential for optimal macrophage-mediated phagosomal containment of *Listeria monocytogenes*. *Proc Natl Acad Sci U S A*, 2007; 104(41): 16251-6.
23. Stevenson BJ, Iseli C, Panji S, Zahn-Zabal M, **Hide W**, Old LJ, Simpson AJ, Jongeneel CV. Rapid evolution of cancer/testis genes on the X chromosome. *BMC Genomics*, 2007; 8: 129.
24. Seoighe C, Ketwaroo F, Pillay V, Scheffler K, Wood N, Duffet R, Zvelebil M, Martinson N, McIntyre J, Morris L, **Hide W**. A model of directional selection applied to the evolution of drug resistance in HIV-1. *Mol Biol Evol*, 2007; 24(4): 1025-31.
25. Kruger A, Hofmann O, Carninci P, Hayashizaki Y, **Hide W**. Simplified ontologies allowing comparison of developmental mammalian gene expression. *Genome Biol*, 2007; 8(10): R229.
26. Kaur M, Schmeier S, MacPherson CR, Hofmann O, **Hide WA**, Taylor S, Willcox N, Bajic VB. Prioritizing genes of potential relevance to diseases affected by sex hormones: an example of myasthenia gravis. *BMC Genomics*. 2008 Oct 13;9:481. PMID: PMC2592250.
27. Hofmann O, Caballero OL, Stevenson BJ, Chen YT, Cohen T, Chua R, Maher CA, Panji S, Schaefer U, Kruger A, Lehvaslaiho M, Carninci P, Hayashizaki Y, Jongeneel CV, Simpson AJ, Old LJ, **Hide W**. Genome-wide analysis of cancer/testis gene expression. *Proc Natl Acad Sci U S A*. 2008 Dec 23;105(51):20422-7. PMID: PMC2603434.
28. Mathivanan S, Ahmed M et al. Human Proteinpedia enables sharing of human protein data. *Nat Biotechnol*, 2008; 26(2): 164-7.
29. Yamasaki C, Murakami K et al. The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. *Nucleic Acids Res*, 2008; 36(Database issue): D793-9.
30. Hazelhurst S, **Hide W**, Liptak Z, Nogueira R, Starfield R. An overview of the wcd EST clustering tool. *Bioinformatics*, 2008; 24(13):1542-1546.
31. Chopera DR, Woodman Z, Mlisana K, Mlotshwa M, Martin DP, Seoighe C, Treurnicht F, de Rosa DA, **Hide W**, Karim SA, Gray CM, Williamson C. Transmission of HIV-1 CTL escape variants provides HLA-mismatched recipients with a survival advantage. *PLoS Pathog*, 2008; 4(3): e1000033.
32. Howe D, Costanzo M, Fey P, Gojobori T, Hannick L, **Hide W**, Hill DP, Kania R, Schaeffer M, St Pierre S, Twigger S, White O, Yon Rhee S. Big data: The future of biocuration. *Nature*, 2008; 455(7209): 47-50.
33. Koscielny G et al. ASTD: The Alternative Splicing and Transcript Diversity database. *Genomics*. 2009 Mar;93(3):213-20.
34. Abrahams MR et al. Quantitating the multiplicity of infection with human immunodeficiency virus type 1 subtype C reveals a non-poisson distribution of transmitted variants. *J Virol*, 2009. 83(8): 3556-3567.
35. **CORE AUTHORSHIP†**, Suzuki H‡, et al. A complex transcriptional network controls growth arrest and differentiation in a human myeloid leukemia cell line. *Nature Genetics* 41(5): 553-62

PUBLISHED DATABASES AND SOFTWARE

- 1997 – STACKdb Sequence Tag Alignment and Consensus Knowledgebase www.sanbi.ac.za/Dbases.html
2000 – stackPACK transcript reconstruction and analysis system www.sanbi.ac.za/CODES
2002 – eVOC standardised gene expression term vocabulary. www.evocontology.org

C. Research Support.

ACTIVE

PS00108 (Jackson)
CDC

03/01/08 – 03/06/11

HIV Surveillance

Molecular surveillance by accurate detection of HIV-1 drug resistance mutations in patients on antiviral treatment in Southern Africa: An informatics approach. Role: PI on sub-award

R24 RR02186300-1A1 (Bumgardner)
NIH/NHGRI

08/01/07 – 08/01/10

A cDNA Sequence Resource for Baboon

Program Director/Principal Investigator (Hide, Winston, A):

To provide analysis of 150,000 Baboon ESTs and to distribute information on these via the international databases. Role: Co-Investigator

LSHG-CT-2007-037231 (Kel) 09/01/07 – 8/31/10

European Commission through the FP6 program

SYSCO

Consortium grant for the analysis of the transcriptome of Leishmania infected macrophage. Role: Consortium Co-PI.

COMPLETED

336707 (Hide) 04/30/02 – 12/31/08

South African National Bioinformatics Network

South African National Bioinformatics Network Node

Development and delivery of standards for the description of gene expression as ontologies. Role: PI

TW-03-008 (Altman) 06/01/04 – 05/29/08

NIH/Fogarty

STANFORD-SOUTH AFRICA Informatics Training for Global Health Grant

Develop and train biomedical informatics researchers and teachers in South Africa by extending the graduate curriculum at University Western Cape (UWC) with jointly developed and taught short courses from Stanford University and supporting visiting postgraduate students at Stanford University. Role: Co-PI

U19 AI51794 (Abdul) 07/01/02 – 06/30/07

NIH

CIPRA USA-South Africa Grant HIV

Development of database and delivery of analytical systems and analysis of HIV genetic diversity of South Africa as part of the CAPRISA programme. Highly integrated with other laboratories throughout South Africa. Strong training component. Role: Co-PI

A60312 (Hide) 09/2006 – 08/2007

World Health Organisation

Mobilising tsetse information to address disease

Development of web-based resource for tsetse community to use for analysis and access to tsetse transcript information. Role: PI

HQ/03/129082 and HQ/03/129095 (Hide) 01/2002 – 12/2007

World Health Organisation

African Regional Centre for training in bioinformatics

Development and provision of an annual standardized training course in pathogen genome bioinformatics of regional centers worldwide. Role: PI

A50331 (Hide) 08/2005 – 07/2006

World Health Organisation

Consolidation and functional annotation of reconstructed transcripts for Glossina

Consolidate and analyze transcript data for Glossina as part of worldwide consortium Role: PI

2038486 (Hide) 01/2006 – 12/2007

SA Foundation for Research Development

Institutional Development Program South Africa

Fund the development of research and postgraduate teaching. Role: PI