Mark Woon

Software Developer, Research, Biomedical Data Science

Bio

LINKS

- NIH Biosketch: https://www.ncbi.nlm.nih.gov/myncbi/1JIGcdoL-WvQf/cv/581201/
- ClinPGx: https://www.clinpgx.org
- PharmCAT: https://pharmcat.org

Publications

PUBLICATIONS

- **CLINPGX: A COMPREHENSIVE PHARMACOGENOMICS RE-SOURCE WITH TOOLS FOR ACCESSING CLINICAL GUIDANCE BY GENOTYPE**
  Whirl-Carrillo, M., Sangkuhl, K., Gong, L., Whaley, R., Woon, M., Thorn, C., Keseler, I., Klein, C., Tsermpini, E., Caudle, K., Ritchie, M., Klein, T.
  WILEY.2025
- **From sample to star alleles: a long-read pharmacogenomics pipeline powered by Twist target enrichment and PacBio HiFi sequencing**
  Holt, S., Harting, J., Han, T., Arbiza, L., Kingan, S., Souppe, A., Zhang, S., Baybayan, P., Lambert, C., Ferrao, H., Li, B., Sangkuhl, K., Woon, et al
  SPRINGERNATURE.2024: 701-702
- **Highly Scalable Pharmacogenomic Panel Testing with Hybrid Capture and Long-Read Sequencing**
  Gonzaludo, N., Kingan, S., Harting, J., Baybayan, P., Han, T., Arbiza, L., Li, B., Sangkuhl, K., Woon, M., Whaley, R., Whirl-Carrillo, M., Yang, Y., Klein, et al
  LIPPINCOTT WILLIAMS & WILKINS.2023: 183
- **Frequencies of pharmacogenomic alleles across biogeographic groups in a large-scale biobank.** *American journal of human genetics*
  Li, B., Sangkuhl, K., Whaley, R., Woon, M., Keat, K., Whirl-Carrillo, M., Ritchie, M. D., Klein, T. E.
  2023
- **How to Run the Pharmacogenomics Clinical Annotation Tool (PharmCAT).** *Clinical pharmacology and therapeutics*
  Li, B., Sangkuhl, K., Keat, K., Whaley, R. M., Woon, M., Verma, S., Dudek, S., Tuteja, S., Verma, A., Whirl-Carrillo, M., Ritchie, M. D., Klein, T. E.
  2022
- **PGxMine: Text mining for curation of PharmGKB.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  Lever, J. n., Barbarino, J. M., Gong, L. n., Huddart, R. n., Sangkuhl, K. n., Whaley, R. n., Whirl-Carrillo, M. n., Woon, M. n., Klein, T. E., Altman, R. B.
  2020; 25: 611–22
- **PGxMine: Text mining for curation of PharmGKB**
  Lever, J., Barbarino, J. M., Gong, L., Huddart, R., Sangkuhl, K., Whaley, R., Whirl-Carrillo, M., Woon, M., Klein, T. E., Altman, R. B.
  edited by Altman, R. B., Dunker, A. K., Hunter, L., Ritchie, M. D., Murray, T., Klein, T. E.
  WORLD SCIENTIFIC PUBL CO PTE LTD.2020: 611-622
- **Pharmacogenomics Clinical Annotation Tool (PharmCAT).** *Clinical pharmacology and therapeutics*
  Sangkuhl, K., Whirl-Carrillo, M., Whaley, R. M., Woon, M., Lavertu, A., Altman, R. B., Carter, L., Verma, A., Ritchie, M. D., Klein, T. E.
  2019
- **Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence** *PLOS GENETICS*
  Dewey, F. E., Chen, R., Cordero, S. P., Ormond, K. E., Caleshu, C., Karczewski, K. J., Whirl-Carrillo, M., Wheeler, M. T., Dudley, J. T., Byrnes, J. K., Cornejo, O. E., Knowles, J. W., Woon, et al

2011; 7 (9)

- **Clinical assessment incorporating a personal genome** *LANCET*

  Ashley, E. A., Butte, A. J., Wheeler, M. T., Chen, R., Klein, T. E., Dewey, F. E., Dudley, J. T., Ormond, K. E., Pavlovic, A., Morgan, A. A., Pushkarev, D., Neff, N. F., Hudgins, et al

  2010; 375 (9725): 1525-1535

- **The Phenotype and Genotype Experiment Object Model (PaGE-OM): A Robust Data Structure for Information Related to DNA Variation** *HUMAN MUTATION*

  Brookes, A. J., Lehvaslaiho, H., Muilu, J., Shigemoto, Y., Oroguchi, T., Tomiki, T., Mukaiyama, A., Konagaya, A., Kojima, T., Inoue, I., Kuroda, M., Mizushima, H., Thorisson, et al

  2009; 30 (6): 968-977

- **An XML-based interchange format for genotype-phenotype data** *HUMAN MUTATION*

  Whirl-Carrillo, M., Woon, M., Thorn, C. E., Klein, T. E., Altman, R. B.

  2008; 29 (2): 212-219

- **The pharmacogenetics and pharmacogenomics knowledge base: accentuating the knowledge** *NUCLEIC ACIDS RESEARCH*

  Hernandez-Boussard, T., Whirl-Carrillo, M., Hebert, J. M., Gong, L., Owen, R., Gong, M., Gor, W., Liu, F., Truong, C., Whaley, R., Woon, M., Zhou, T., Altman, et al

  2008; 36: D913-D918

- **Integrating large-scale genotype and phenotype data** *OMICS-A JOURNAL OF INTEGRATIVE BIOLOGY*

  Hernandez-Boussard, T., Woon, M., Klein, T. E., Altman, R. B.

  2006; 10 (4): 545-554

- **A resource to acquire and summarize pharmacogenetics knowledge in the literature** *11th World Congress on Medical Informatics*

  Rubin, D. L., Carrillo, M., Woon, M., Conroy, J., Klein, T. E., Altman, R. B.

  I O S PRESS.2004: 793–797

- **A personalized and automated dbSNP surveillance system** *2nd International Computational Systems Bioinformatics Conference*

  Liu, S., Lin, S., Woon, M., Klein, T. E., Altman, R. B.

  IEEE COMPUTER SOC.2003: 132–136