


Stanford



Purvesh Khatri

Associate Professor (Research) of Medicine (Biomedical Informatics - Research Institute for Immunity, Transplantation and Infection) and of Biomedical Data Science

 NIH Biosketch available Online

 Curriculum Vitae available Online

CONTACT INFORMATION

• Alternate Contact

Natasha Haulman - Administrative Assistant

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Bio

ACADEMIC APPOINTMENTS

- Associate Professor (Research), Medicine
- Associate Professor (Research), Biomedical Data Science
- Member, Bio-X
- Member, Child Health Research Institute
- Faculty Fellow, Stanford ChEM-H

ADMINISTRATIVE APPOINTMENTS

- Assistant Professor, Institute for Immunity, Transplantation and Infection, (2014- present)

Teaching

COURSES

2018-19

- Essential Methods in Computational and Systems Immunology: IMMUNOL 207 (Spr)
- Seminars in Computational and Systems Immunology: IMMUNOL 310 (Sum)

2017-18

- Essential Methods in Computational and Systems Immunology: IMMUNOL 207 (Spr)
- Seminars in Computational and Systems Immunology: IMMUNOL 310 (Sum)

2016-17

- Essential Methods in Computational and Systems Immunology: IMMUNOL 207 (Spr)
- Seminars in Computational and Systems Immunology: IMMUNOL 310 (Sum)

2015-16

- Advanced Computational and Systems Immunology: IMMUNOL 208 (Aut)
- Essential Methods in Computational and Systems Immunology: IMMUNOL 207 (Spr)

- Seminars in Computational and Systems Immunology: IMMUNOL 310 (Sum)

STANFORD ADVISEES

Med Scholar Project Advisor

Tej Azad

Doctoral Dissertation Reader (AC)

Lichy Han

Postdoctoral Faculty Sponsor

Guangbo Chen, Denis Dermadi Bebek, Michele Donato, Simone Thair, Francesco Vallania, Hayley Warsinske

Doctoral Dissertation Advisor (AC)

Erika Bongen, Ananthakrishnan Ganesan

Postdoctoral Research Mentor

Denis Dermadi Bebek, Simone Thair, Hayley Warsinske

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Immunology (Phd Program)

Publications

PUBLICATIONS

- **A multi-cohort study of the immune factors associated with M. tuberculosis infection outcomes.** *Nature*
Roy Chowdhury, R., Vallania, F., Yang, Q., Lopez Angel, C. J., Darboe, F., Penn-Nicholson, A., Rozot, V., Nemes, E., Malherbe, S. T., Ronacher, K., Walzl, G., Hanekom, W., Davis, et al
2018
- **KLRD1-expressing natural killer cells predict influenza susceptibility** *GENOME MEDICINE*
Bongen, E., Vallania, F., Utz, P. J., Khatri, P.
2018; 10: 45
- **Single-Cell Chromatin Modification Profiling Reveals Increased Epigenetic Variations with Aging.** *Cell*
Cheung, P., Vallania, F., Warsinske, H. C., Donato, M., Schaffert, S., Chang, S. E., Dvorak, M., Dekker, C. L., Davis, M. M., Utz, P. J., Khatri, P., Kuo, A. J.
2018
- **A community approach to mortality prediction in sepsis via gene expression analysis** *NATURE COMMUNICATIONS*
Sweeney, T. E., Perumal, T. M., Henao, R., Nichols, M., Howrylak, J. A., Choi, A. M., Bermejo-Martin, J. F., Almansa, R., Tamayo, E., Davenport, E. E., Burnham, K. L., Hinds, C. J., Knight, et al
2018; 9: 694
- **Antigen Identification for Orphan T Cell Receptors Expressed on Tumor-Infiltrating Lymphocytes** *CELL*
Gee, M. H., Han, A., Lofgren, S. M., Beausang, J. F., Mendoza, J. L., Birnbaum, M. E., Bethune, M. T., Fischer, S., Yang, X., Gomez-Eerland, R., Bingham, D. B., Sibener, L. V., Fernandes, et al
2018; 172 (3): 549+
- **Unsupervised Analysis of Transcriptomics in Bacterial Sepsis Across Multiple Datasets Reveals Three Robust Clusters.** *Critical care medicine*
Sweeney, T. E., Azad, T. D., Donato, M., Haynes, W. A., Perumal, T. M., Henao, R., Bermejo-Martin, J. F., Almansa, R., Tamayo, E., Howrylak, J. A., Choi, A., Parnell, G. P., Tang, et al
2018
- **Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses** *SCIENCE IMMUNOLOGY*

- Avey, S., Cheung, F., Fermin, D., Frelinger, J., Gaujoux, R., Gottardo, R., Khatri, P., Kleinstein, S. H., Kotliarov, Y., Meng, H., Sauteraud, R., Shen-Orr, S. S., Tsang, et al
2017; 2 (14)
- **Methods to increase reproducibility in differential gene expression via meta-analysis.** *Nucleic acids research*
Sweeney, T. E., Haynes, W. A., Vallania, F., Ioannidis, J. P., Khatri, P.
2017; 45 (1)
 - **Robust classification of bacterial and viral infections via integrated host gene expression diagnostics.** *Science translational medicine*
Sweeney, T. E., Wong, H. R., Khatri, P.
2016; 8 (346): 346ra91-?
 - **Genome-wide expression for diagnosis of pulmonary tuberculosis: a multicohort analysis.** *The Lancet. Respiratory medicine*
Sweeney, T. E., Braviak, L., Tato, C. M., Khatri, P.
2016; 4 (3): 213-224
 - **Integrated, Multi-cohort Analysis Identifies Conserved Transcriptional Signatures across Multiple Respiratory Viruses** *IMMUNITY*
Andres-Terre, M., McGuire, H. M., Pouliot, Y., Bongen, E., Sweeney, T. E., Tato, C. M., Khatri, P.
2015; 43 (6): 1199-1211
 - **A comprehensive time-course-based multicohort analysis of sepsis and sterile inflammation reveals a robust diagnostic gene set** *SCIENCE TRANSLATIONAL MEDICINE*
Sweeney, T. E., Shidham, A., Wong, H. R., Khatri, P.
2015; 7 (287)
 - **A Meta-analysis of Lung Cancer Gene Expression Identifies PTK7 as a Survival Gene in Lung Adenocarcinoma.** *Cancer research*
Chen, R., Khatri, P., Mazur, P. K., Polin, M., Zheng, Y., Vaka, D., Hoang, C. D., Shrager, J., Xu, Y., Vicent, S., Butte, A. J., Sweet-Cordero, E. A.
2014; 74 (10): 2892-2902
 - **A common rejection module (CRM) for acute rejection across multiple organs identifies novel therapeutics for organ transplantation.** *journal of experimental medicine*
Khatri, P., Roedder, S., Kimura, N., De Vusser, K., Morgan, A. A., Gong, Y., Fischbein, M. P., Robbins, R. C., Naesens, M., Butte, A. J., Sarwal, M. M.
2013; 210 (11): 2205-2221
 - **Ten Years of Pathway Analysis: Current Approaches and Outstanding Challenges** *PLOS COMPUTATIONAL BIOLOGY*
Khatri, P., Sirota, M., Butte, A. J.
2012; 8 (2)
 - **Cell type-specific gene expression differences in complex tissues** *NATURE METHODS*
Shen-Orr, S. S., Tibshirani, R., Khatri, P., Bodian, D. L., Staedtler, F., Perry, N. M., Hastie, T., Sarwal, M. M., Davis, M. M., Butte, A. J.
2010; 7 (4): 287-289
 - **A systems biology approach for pathway level analysis** *GENOME RESEARCH*
Draghici, S., Khatri, P., Tarca, A. L., Amin, K., Done, A., Voichita, C., Georgescu, C., Romero, R.
2007; 17 (10): 1537-1545
 - **Spermatozoal RNA profiles of normal fertile men** *LANCET*
Ostermeier, G. C., Dix, D. J., Miller, D., Khatri, P., Krawetz, S. A.
2002; 360 (9335): 772-777
 - **Fragile Histidine Triad (FHIT), a Novel Modifier Gene in Pulmonary Arterial Hypertension.** *American journal of respiratory and critical care medicine*
Dannewitz Prosseda, S., Tian, X., Kuramoto, K., Boehm, M., Sudheendra, D., Miyagawa, K., Zhang, F., Solow-Cordero, D., Saldivar, J. C., Austin, E. D., Loyd, J. E., Wheeler, L., Andruska, et al
2018
 - **Future Research Directions in Pneumonia NHLBI Working Group Report** *AMERICAN JOURNAL OF RESPIRATORY AND CRITICAL CARE MEDICINE*
Dela Cruz, C. S., Wunderink, R. G., Christiani, D. C., Cormier, S. A., Crothers, K., Doerschuk, C. M., Evans, S. E., Goldstein, D. R., Khatri, P., Kobzik, L., Kolls, J. K., Levy, B. D., Metersky, et al
2018; 198 (2): 256-63
 - **Single-cell epigenetics - Chromatin modification atlas unveiled by mass cytometry.** *Clinical immunology (Orlando, Fla.)*

Cheung, P., Vallania, F., Dvorak, M., Chang, S. E., Schaffert, S., Donato, M., Rao, A., Mao, R., Utz, P. J., Khatri, P., Kuo, A. J.
2018

- **Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations** *SCIENTIFIC REPORTS*
Tomczak, A., Mortensen, J. M., Winnenburg, R., Liu, C., Alessi, D. T., Swamy, V., Vallania, F., Lofgren, S., Haynes, W., Shah, N. H., Musen, M. A., Khatri, P.
2018; 8: 5115
- **Gene annotation bias impedes biomedical research** *SCIENTIFIC REPORTS*
Haynes, W. A., Tomczak, A., Khatri, P.
2018; 8: 1362
- **Inflammatory macrophage-associated 3-gene signature predicts subclinical allograft injury and graft survival.** *JCI insight*
Azad, T. D., Donato, M., Heylen, L., Liu, A. B., Shen-Orr, S. S., Sweeney, T. E., Maltzman, J. S., Naesens, M., Khatri, P.
2018; 3 (2)
- **A Human Genome-wide RNAi Screen Reveals Diverse Modulators that Mediate IRE1 β -XBP1 Activation.** *Molecular cancer research : MCR*
Yang, Z., Zhang, J., Jiang, D., Khatri, P., Solow-Cordero, D. E., Toesca, D. A., Koumenis, C., Denko, N. C., Giaccia, A. J., Le, Q. T., Koong, A. C.
2018
- **Multicohort Analysis of Whole-Blood Gene Expression Data Does Not Form a Robust Diagnostic for Acute Respiratory Distress Syndrome.** *Critical care medicine*
Sweeney, T. E., Thomas, N. J., Howrylak, J. A., Wong, H. R., Rogers, A. J., Khatri, P.
2018; 46 (2): 244–51
- **Pediatric Sepsis Endotypes Among Adults With Sepsis** *CRITICAL CARE MEDICINE*
Wong, H. R., Sweeney, T. E., Hart, K. W., Khatri, P., Lindsell, C. J.
2017; 45 (12): e1289–e1291
- **Higher Baseline Monocyte Count Is Associated with More Extensive Skin Involvement and Higher Mortality in Systemic Sclerosis**
Mohan, V., Khatri, P., Theodore, S., Charles, J., Hau Pham, Nair, D., Scott, M., Reveille, J. D., Mayes, M. D., Assassi, S.
WILEY.2017
- **Unique transcriptomic response to sepsis is observed among patients of different age groups** *PLOS ONE*
Raymond, S. L., Lopez, M., Baker, H. V., Larson, S. D., Efron, P. A., Sweeney, T. E., Khatri, P., Moldawer, L. L., Wynn, J. L.
2017; 12 (9): e0184159
- **A B-Cell Gene Signature Correlates With the Extent of Gluten-Induced Intestinal Injury in Celiac Disease.** *Cellular and molecular gastroenterology and hepatology*
Garber, M. E., Saldanha, A., Parker, J. S., Jones, W. D., Kaukinen, K., Laurila, K., Lähdeaho, M., Khatri, P., Khosla, C., Adelman, D. C., Mäki, M.
2017; 4 (1): 1-17
- **Validation of the Sepsis MetaScore for Diagnosis of Neonatal Sepsis.** *Journal of the Pediatric Infectious Diseases Society*
Sweeney, T. E., Wynn, J. L., Cernada, M., Serna, E., Wong, H. R., Baker, H. V., Vento, M., Khatri, P.
2017
- **Chemical Space Mimicry for Drug Discovery** *JOURNAL OF CHEMICAL INFORMATION AND MODELING*
Yuan, W., Jiang, D., Nambiar, D. K., Liew, L. P., Hay, M. P., Bloomstein, J., Lu, P., Turner, B., Le, Q., Tibshirani, R., Khatri, P., Moloney, M. G., Koong, et al
2017; 57 (4): 875-882
- **The authors reply.** *Critical care medicine*
Sweeney, T. E., Khatri, P.
2017; 45 (4): e457-e458
- **Gene Expression Analysis to Assess the Relevance of Rodent Models to Human Lung Injury.** *American journal of respiratory cell and molecular biology*
Sweeney, T. E., Lofgren, S., Khatri, P., Rogers, A. J.
2017
- **The authors reply.** *Critical care medicine*
Sweeney, T. E., Khatri, P.
2017; 45 (3)

- **Septic Cardiomyopathy: Getting to the Heart of the Matter.** *Critical care medicine*
Sweeney, T. E., Khatri, P.
2017; 45 (3): 556-557
- **An integrative approach unveils FOSL1 as an oncogene vulnerability in KRAS-driven lung and pancreatic cancer.** *Nature communications*
Vallejo, A., Perurena, N., Guruceaga, E., Mazur, P. K., Martinez-Canarias, S., Zandueta, C., Valencia, K., Arricibita, A., Gwinn, D., Sayles, L. C., Chuang, C., Guembe, L., Bailey, et al
2017; 8: 14294-?
- **Benchmarking Sepsis Gene Expression Diagnostics Using Public Data** *CRITICAL CARE MEDICINE*
Sweeney, T. E., Khatri, P.
2017; 45 (1): 1-10
- **Comprehensive Analysis of the Unfolded Protein Response in Breast Cancer Subtypes.** *JCO precision oncology*
Jiang, D., Turner, B., Song, J., Li, R., Diehn, M., Le, Q., Khatri, P., Koong, A. C.
2017; 2017
- **Integrated, multicohort analysis of systemic sclerosis identifies robust transcriptional signature of disease severity.** *JCI insight*
Lofgren, S., Hinchcliff, M., Carns, M., Wood, T., Aren, K., Arroyo, E., Cheung, P., Kuo, A., Valenzuela, A., Haemel, A., Wolters, P. J., Gordon, J., Spiera, et al
2016; 1 (21)
- **Complement pathway amplifies caspase-11-dependent cell death and endotoxin-induced sepsis severity.** *journal of experimental medicine*
Napier, B. A., Brubaker, S. W., Sweeney, T. E., Monette, P., Rothmeier, G. H., Gertszolf, N. A., Puschnik, A., Carette, J. E., Khatri, P., Monack, D. M.
2016; 213 (11): 2365-2382
- **Coordination of stress signals by the lysine methyltransferase SMYD2 promotes pancreatic cancer.** *Genes & development*
Reynoird, N., Mazur, P. K., Stellfeld, T., Flores, N. M., Lofgren, S. M., Carlson, S. M., Brambilla, E., Hainaut, P., Kaznowska, E. B., Arrowsmith, C. H., Khatri, P., Stresemann, C., Gozani, et al
2016; 30 (7): 772-785
- **META-ANALYSIS OF CONTINUOUS PHENOTYPES IDENTIFIES A GENE SIGNATURE THAT CORRELATES WITH COPD DISEASE STATUS.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Scott, M., Vallania, F., Khatri, P.
2016; 22: 266-275
- **EMPOWERING MULTI-COHORT GENE EXPRESSION ANALYSIS TO INCREASE REPRODUCIBILITY.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Haynes, W. A., Vallania, F., Liu, C., Bongen, E., Tomczak, A., Andres-Terrè, M., Lofgren, S., Tam, A., Deisseroth, C. A., Li, M. D., Sweeney, T. E., Khatri, P.
2016; 22: 144-153
- **Comprehensive Validation of the FAIM3:PLAC8 Ratio in Time-matched Public Gene Expression Data.** *American journal of respiratory and critical care medicine*
Sweeney, T. E., Khatri, P.
2015; 192 (10): 1260-1261
- **The center for expanded data annotation and retrieval.** *Journal of the American Medical Informatics Association*
Musen, M. A., Bean, C. A., Cheung, K., Dumontier, M., Durante, K. A., Gevaert, O., Gonzalez-Beltran, A., Khatri, P., Kleinstein, S. H., O'Connor, M. J., Pouliot, Y., Rocca-Serra, P., Sansone, et al
2015; 22 (6): 1148-1152
- **Combined inhibition of BET family proteins and histone deacetylases as a potential epigenetics-based therapy for pancreatic ductal adenocarcinoma.** *Nature medicine*
Mazur, P. K., Herner, A., Mello, S. S., Wirth, M., Hausmann, S., Sánchez-Rivera, F. J., Lofgren, S. M., Kuschma, T., Hahn, S. A., Vangala, D., Trajkovic-Arsic, M., Gupta, A., Heid, et al
2015; 21 (10): 1163-1171
- **A COMPREHENSIVE TIME-BASED META-ANALYSIS OF SIRS AND SEPSIS REVEALS A ROBUST DISCRIMINATORY GENE SET** *44th Critical Care Congress of the Society-of-Critical-Care-Medicine*
Sweeney, T., Shidham, A., Wong, H., Khatri, P.
LIPPINCOTT WILLIAMS & WILKINS.2014

- **SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer.** *Nature*
Mazur, P. K., Reynoird, N., Khatri, P., Jansen, P. W., Wilkinson, A. W., Liu, S., Barbash, O., Van Aller, G. S., Huddleston, M., Dhanak, D., Tummino, P. J., Kruger, R. G., Garcia, et al
2014; 510 (7504): 283-287
- **Multiplex meta-analysis of medulloblastoma expression studies with external controls.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Morgan, A. A., Achrol, A. S., Li, M. D., Khatri, P. J., Cheshier, S. H.
2014: 99-109
- **Integrated multi-cohort transcriptional meta-analysis of neurodegenerative diseases.** *Acta neuropathologica communications*
Li, M. D., Burns, T. C., Morgan, A. A., Khatri, P.
2014; 2: 93-?
- **A Drug Repositioning Approach Identifies Tricyclic Antidepressants as Inhibitors of Small Cell Lung Cancer and Other Neuroendocrine Tumors** *CANCER DISCOVERY*
Jahchan, N. S., Dudley, J. T., Mazur, P. K., Flores, N., Yang, D., Palmerton, A., Zmoos, A., Vaka, D., Tran, K. Q., Zhou, M., Krasinska, K., Riess, J. W., Neal, et al
2013; 3 (12): 1364-1377
- **Cross-Species Functional Analysis of Cancer-Associated Fibroblasts Identifies a Critical Role for CLCF1 and IL-6 in Non-Small Cell Lung Cancer In Vivo** *CANCER RESEARCH*
Vicent, S., Sayles, L. C., Vaka, D., Khatri, P., Gevaert, O., Chen, R., Zheng, Y., Gillespie, A. K., Clarke, N., Xu, Y., Shrager, J., Hoang, C. D., Plevritis, et al
2012; 72 (22): 5744-5756
- **A Peripheral Blood Diagnostic Test for Acute Rejection in Renal Transplantation** *AMERICAN JOURNAL OF TRANSPLANTATION*
Li, L., Khatri, P., Sigdel, T. K., Tran, T., Ying, L., Vitalone, M. J., Chen, A., Hsieh, S., Dai, H., Zhang, M., Naesens, M., Zarkhin, V., Sansanwal, et al
2012; 12 (10): 2710-2718
- **Non-HLA Antibodies to Immunogenic Epitopes Predict the Evolution of Chronic Renal Allograft Injury** *JOURNAL OF THE AMERICAN SOCIETY OF NEPHROLOGY*
Sigdel, T. K., Li, L., Tran, T. Q., Khatri, P., Naesens, M., Sansanwal, P., Dai, H., Hsieh, S., Sarwal, M. M.
2012; 23 (4): 750-763
- **Profiling of Autoantibodies in IgA Nephropathy, an Integrative Antibiotics Approach** *CLINICAL JOURNAL OF THE AMERICAN SOCIETY OF NEPHROLOGY*
Sigdel, T. K., Woo, S. H., Dai, H., Khatri, P., Li, L., Myers, B., Sarwal, M. M., Lafayette, R. A.
2011; 6 (12): 2775-2784
- **Progressive histological damage in renal allografts is associated with expression of innate and adaptive immunity genes** *KIDNEY INTERNATIONAL*
Naesens, M., Khatri, P., Li, L., Sigdel, T. K., Vitalone, M. J., Chen, R., Butte, A. J., Salvatierra, O., Sarwal, M. M.
2011; 80 (12): 1364-1376
- **Applications of Translational Bioinformatics in Transplantation** *CLINICAL PHARMACOLOGY & THERAPEUTICS*
Khatri, P., Sarwal, M. M., Butte, A. J.
2011; 90 (2): 323-327
- **Biomarkers in solid organ transplantation: establishing personalized transplantation medicine.** *Genome medicine*
Roedder, S., Vitalone, M., Khatri, P., Sarwal, M. M.
2011; 3 (6): 37-?
- **Comparison of multiplex meta analysis techniques for understanding the acute rejection of solid organ transplants** *AMIA Summit on Translational Bioinformatics*
Morgan, A. A., Khatri, P., Jones, R. H., Sarwal, M. M., Butte, A. J.
BIOMED CENTRAL LTD.2010
- **A microarray analysis of the effects of moderate hypothermia and rewarming on gene expression by human hepatocytes (HepG2)** *CELL STRESS & CHAPERONES*
Sonna, L. A., Kuhlmeier, M. M., Khatri, P., Chen, D., Lilly, C. M.
2010; 15 (5): 687-702

- **Meta-Analysis of Solid Organ Transplant Data Sets Identifies Differentially Expressed microRNAs Common in Heart, Kidney and Liver Allografts** *10th American Transplant Congress*
Khatri, P., Jones, R. H., Butte, A. J., Sarwal, M. M.
WILEY-BLACKWELL.2010: 61-61
- **NetPath: a public resource of curated signal transduction pathways** *GENOME BIOLOGY*
Kandasamy, K., Mohan, S. S., Raju, R., Keerthikumar, S., Kumar, G. S., Venugopal, A. K., Telikicherla, D., Navarro, J. D., Mathivanan, S., Pecquet, C., Gollapudi, S. K., Tattikota, S. G., Mohan, et al
2010; 11 (1)
- **Predicting Novel Human Gene Ontology Annotations Using Semantic Analysis** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*
Done, B., Khatri, P., Done, A., Draghici, S.
2010; 7 (1): 91-99
- **Using gene arrays in diagnosis of rejection** *CURRENT OPINION IN ORGAN TRANSPLANTATION*
Khatri, P., Sarwal, M. M.
2009; 14 (1): 34-39
- **A novel signaling pathway impact analysis** *BIOINFORMATICS*
Tarca, A. L., Draghici, S., Khatri, P., Hassan, S. S., Mittal, P., Kim, J., Kim, C. J., Kusanovic, J. P., Romero, R.
2009; 25 (1): 75-82
- **Identifying Uncertainty Regions in Support Vector Machines using Geometric Margin and Convex Hulls** *2008 IEEE INTERNATIONAL JOINT CONFERENCE ON NEURAL NETWORKS, VOLS 1-8*
Voichita, C., Khatri, P., Draghici, S.
2008: 3319-3324
- **Onto-Tools: new additions and improvements in 2006** *NUCLEIC ACIDS RESEARCH*
Khatri, P., Voichita, C., Kattan, K., Ansari, N., Khatri, A., Georgescu, C., Tarca, A. L., Draghici, S.
2007; 35: W206-W211
- **Semantic analysis of genome annotations using weighting schemes** *2007 IEEE SYMPOSIUM ON COMPUTATIONAL INTELLIGENCE IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY*
Done, B., Khatri, P., Done, A., Draghici, S.
2007: 212-218
- **A system biology approach for the steady-state analysis of gene signaling networks** *PROGRESS IN PATTERN RECOGNITION, IMAGE ANALYSIS AND APPLICATIONS, PROCEEDINGS*
Khatri, P., Draghici, S., Tarca, A. L., Hassan, S. S., Romero, R.
2007; 4756: 32-41
- **Babel's tower revisited: a universal resource for cross-referencing across annotation databases** *BIOINFORMATICS*
Draghici, S., Sellamuthu, S., Khatri, P.
2006; 22 (23): 2934-2939
- **New Onto-Tools: Promoter-Express, nsSNPCounter and Onto-Translate** *NUCLEIC ACIDS RESEARCH*
Khatri, P., Desai, V., Tarca, A. L., Sellamuthu, S., Wildman, D. E., Romero, R., Draghici, S.
2006; 34: W626-W631
- **Reliability and reproducibility issues in DNA microarray measurements** *TRENDS IN GENETICS*
Draghici, S., Khatri, P., Eklund, A. C., Szallasi, Z.
2006; 22 (2): 101-109
- **Ontological analysis of gene expression data: current tools, limitations, and open problems** *BIOINFORMATICS*
Khatri, P., Draghici, S.
2005; 21 (18): 3587-3595
- **A semantic analysis of the annotations of the human genome** *BIOINFORMATICS*
Khatri, P., Done, B., Rao, A., Done, A., Draghici, S.

2005; 21 (16): 3416-3421

- **Recent additions and improvements to the Onto-Tools** *NUCLEIC ACIDS RESEARCH*
Khatri, P., Sellamuthu, S., Malhotra, P., Amin, K., Done, A., Draghici, S.
2005; 33: W762-W765
- **Identification of genomic signatures for the design of assays for the detection and monitoring of anthrax threats** *PACIFIC SYMPOSIUM ON BIOCOMPUTING 2005*
Draghici, S., Khatri, P., Liu, Y. H., CHASE, K. J., Bode, E. A., Kulesh, D. A., Wasieloski, L. P., Norwood, D. A., Reifman, J.
2005: 248-259
- **A novel bioinformatics technique for predicting condition-specific transcription factor binding sites** *PROCEEDINGS OF THE 2005 IEEE SYMPOSIUM ON COMPUTATIONAL INTELLIGENCE IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY*
Desai, V., Khatri, P., Done, A., Fridman, A., Tainsky, M., Draghici, S.
2005: 202-207
- **Onto-Tools: an ensemble of web-accessible, ontology-based tools for the functional design and interpretation of high-throughput gene expression experiments** *NUCLEIC ACIDS RESEARCH*
Khatri, P., Bhavsar, P., Bawa, G., Draghici, S.
2004; 32: W449-W456
- **Onto-Tools, the toolkit of the modern biologist: Onto-Express, Onto-Compare, Onto-Design and Onto-Translate** *NUCLEIC ACIDS RESEARCH*
Draghici, S., Khatri, P., Bhavsar, P., Shah, A., Krawetz, S. A., Tainsky, M. A.
2003; 31 (13): 3775-3781
- **Assessing the functional bias of commercial microarrays using the onto-compare database** *BIOTECHNIQUES*
Draghici, S., Khatri, P., Shah, A., Tainsky, M. A.
2003: 55-61
- **Global functional profiling of gene expression** *GENOMICS*
Draghici, S., Khatri, P., Martins, R. P., Ostermeier, G. C., Krawetz, S. A.
2003; 81 (2): 98-104
- **Profiling gene expression using onto-express** *GENOMICS*
Khatri, P., Draghici, S., Ostermeier, G. C., Krawetz, S. A.
2002; 79 (2): 266-270