Main Scientific Publications
(See footnotes at end of the publication section)

-- 2019 --

JS Johnson, D Spakowicz, BY Hong, LM Petersen, P Demkowicz, L Chen, SR Leopold, BM Hanson, HO Agresta, M Gerstein, E Sodergren, GM Weinstock (2019). " Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis." *Nat Commun*. 10: 5029

J Warrell, MB Gerstein (2019). "Hierarchical PAC-Bayes Bounds via Deep Probabilistic Programming." Bayesian Deep Learning Workshop at NeurIPS.

M Koupenova, E Mick, HA Corkrey, A Singh, SE Tanriverdi, O Vitseva, D Levy, AM Keeler, M Ezzaty Mirhashemi, MK ElMallah, M Gerstein, J Rozowsky, K Tanriverdi, JE Freedman (2019). "Pollen-derived RNAs Are Found in the Human Circulation." *iScience* 19: 916-926.

S Lou, KA Cotter, T Li, J Liang, H Mohsen, J Liu, J Zhang, S Cohen, J Xu, H Yu, MA Rubin, M Gerstein (2019). "GRAM: A GeneRAlized Model to predict the molecular effect of a non-coding variant in a cell-type specific manner." *PLoS Genet* 15: e1007860.

S Kumar, D Clarke, MB Gerstein (2019). "Leveraging protein dynamics to identify cancer mutational hotspots using 3D structures." *Proc Natl Acad Sci U S A* 116: 18962-18970.

D Greenbaum, M Gerstein (2019). "Sharing data." *Science* 365:764.

FC Navarro, J Hoops, L Bellfy, E Cerveira, Q Zhu, C Zhang, C Lee, MB Gerstein (2019). "TeXP: Deconvolving the effects of pervasive and autonomous transcription of transposable elements." *PLoS Comput Biol* 15: e1007293.

D Polioudakis, L de la Torre-Ubieta, J Langerman, AG Elkins, X Shi, JL Stein, CK Vuong, S Nichterwitz, M Gevorgian, CK Opland, D Lu, W Connell, EK Ruzzo, JK Lowe, T Hadzic, FI Hinz, S Sabri, WE Lowry, MB Gerstein, K Plath, DH Geschwind (2019). "A Single-Cell Transcriptomic Atlas of Human Neocortical Development during Mid-gestation." *Neuron* 103: 785-801e8.

B Wang, C Yan, S Lou, P Emani, B Li, M Xu, X Kong, W Meyerson, YT Yang, D Lee, M Gerstein (2019). "Building a Hybrid Physical-Statistical Classifier for Predicting the Effect of Variants Related to Protein-Drug Interactions." *Structure* 27: 1469-1481e3.

FCP Navarro, H Mohsen, C Yan, S Li, M Gu, W Meyerson, M Gerstein (2019). "Genomics and data science: an application within an umbrella." *Genome Biol* 20: 109.

MJP Chaisson, AD Sanders, X Zhao, A Malhotra, D Porubsky, T Rausch, EJ Gardner, OL Rodriguez, L Guo, RL Collins, X Fan, J Wen, RE Handsaker, S Fairley, ZN Kronenberg, X Kong, F Hormozdiari, D Lee, AM Wenger, AR Hastie, D Antaki, T Anantharaman, PA Audano, H Brand, S Cantsilieris, H Cao, E Cerveira, C Chen, X Chen, CS Chin, Z Chong, NT Chuang, CC Lambert, DM Church, L Clarke, A Farrell, J Flores, T Galeev, DU Gorkin, M Gujral, V Guryev, WH Heaton, J Korlach, S Kumar, JY Kwon, ET Lam, JE Lee, J Lee, WP Lee, SP Lee, S Li, P Marks, K Viaud-Martinez, S Meiers, KM Munson, FCP Navarro, BJ Nelson, C Nodzak, A Noor, S Kyriazopoulou-Panagiotopoulou, AWC Pang, Y Qiu, G Rosanio, M Ryan, A Stutz, DCJ Spierings, A Ward, AE Welch, M Xiao, W Xu, C Zhang, Q Zhu, X Zheng-Bradley, E Lowy, S Yakneen, S McCarroll, G Jun, L Ding, CL Koh, B Ren, P Flicek, K Chen, MB Gerstein, PY Kwok, PM Lansdorp, GT Marth, J Sebat, X Shi, A Bashir, K Ye, SE Devine, ME Talkowski, RE Mills, T Marschall, JO Korbel, EE Eichler, C Lee (2019). "Multi-platform discovery of haplotype-resolved structural variation in human genomes." *Nat Commun* 10: 1784.

J Rozowsky, RR Kitchen, JJ Park, TR Galeev, J Diao, J Warrell, W Thistlethwaite, SL Subramanian, A Milosavljevic, M Gerstein (2019). "exceRpt: A Comprehensive Analytic Platform for Extracellular RNA Profiling." *Cell Syst* 8: 352-357e3.

OD Murillo, W Thistlethwaite, J Rozowsky, SL Subramanian, R Lucero, N Shah, AR Jackson, S Srinivasan, A Chung, CD Laurent, RR Kitchen, T Galeev, J Warrell, JA Diao, JA Welsh, K Hanspers, A Riutta, S Burgstaller-Muehlbacher, RV Shah, A Yeri, LM Jenkins, ME Ahsen, C Cordon-Cardo, N Dogra, SM Gifford, JT Smith, G Stolovitzky, AK Tewari, BH Wunsch, KK Yadav, KM Danielson, J Filant, C Moeller, P Nejad, A Paul, B Simonson, DK Wong, X Zhang, L Balaj, R Gandhi, AK Sood, RP Alexander, L Wang, C Wu, DTW Wong, DJ Galas, K Van Keuren-Jensen, T Patel, JC Jones, S Das, KH Cheung, AR Pico, AI Su, RL Raffai, LC Laurent, ME Roth, MB Gerstein, A Milosavljevic (2019). "exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids." *Cell* 177: 463-477e15.

S Das, Extracellular RNA Communication Consortium, KM Ansel, M Bitzer, XO Breakefield, A Charest, DJ Galas, MB Gerstein, M Gupta, A Milosavljevic, MT McManus, T Patel, RL Raffai, J Rozowsky, ME Roth, JA Saugstad, K Van Keuren-Jensen, AM Weaver, LC Laurent (2019). "The Extracellular RNA Communication Consortium: Establishing Foundational Knowledge and Technologies for Extracellular RNA Research." *Cell* 177: 231-242.

EY Ho, Q Cao, M Gu, RW Chan, Q Wu, M Gerstein, KY Yip (2019). "Shaping the nebulous enhancer in the era of high-throughput assays and genome editing." *Brief Bioinform*. bbz030

GG Yardmc, H Ozadam, MEG Sauria, O Ursu, KK Yan, T Yang, A Chakraborty, A Kaul, BR Lajoie, F Song, Y Zhan, F Ay, M Gerstein, A Kundaje, Q Li, J Taylor, F Yue, J Dekker, WS Noble (2019). "Measuring the reproducibility and quality of Hi-C data." *Genome Biol* 20: 57.

A Moro, TP Driscoll, LC Boraas, W Armero, DM Kasper, N Baeyens, C Jouy, V Mallikarjun, J Swift, SJ Ahn, D Lee, J Zhang, M Gu, M Gerstein, M Schwartz, S Nicoli (2019). "MicroRNA-dependent regulation of biomechanical genes establishes tissue stiffness homeostasis." *Nat Cell Biol* 21: 348-358.

JE Posey, AH O'Donnell-Luria, JX Chong, T Harel, SN Jhangiani, ZH Coban Akdemir, S Buyske, D Pehlivan, CMB Carvalho, S Baxter, N Sobreira, P Liu, N Wu, JA Rosenfeld, S Kumar, D Avramopoulos, JJ White, KF Doheny, PD Witmer, C Boehm, VR Sutton, DM Muzny, E Boerwinkle, M Gunel, DA Nickerson, S Mane, DG MacArthur, RA Gibbs, A Hamosh, RP Lifton, TC Matise, HL Rehm, M Gerstein, MJ Bamshad, D Valle, JR Lupski, Centers for Mendelian Genomics (2019). "Insights into genetics, human biology and disease gleaned from family based genomic studies." *Genet Med* 21: 798-812.

S Li, MB Gerstein (2019). "Next-Generation Sequencing to Diagnose Suspected Genetic Disorders." *N Engl J Med* 380: 200.

-- 2018 --

PsychENCODE Consortium (2018). "Revealing the brain's molecular architecture." *Science* 362: 1262-1263.

D Wang, S Liu, J Warrell, H Won, X Shi, FCP Navarro, D Clarke, M Gu, P Emani, YT Yang, M Xu, MJ Gandal, S Lou, J Zhang, JJ Park, C Yan, SK Rhie, K Manakongtreecheep, H Zhou, A Nathan, M Peters, E Mattei, D Fitzgerald, T Brunetti, J Moore, Y Jiang, K Girdhar, GE Hoffman, S Kalayci, ZH Gumus, GE Crawford, PsychENCODE Consortium, P Roussos, S Akbarian, AE Jaffe, KP White, Z Weng, N Sestan, DH Geschwind, JA Knowles, MB Gerstein (2018). "Comprehensive functional genomic resource and integrative model for the human brain." *Science* 362: eaat8464.

MJ Gandal, P Zhang, E Hadjimichael, RL Walker, C Chen, S Liu, H Won, H van Bakel, M Varghese, Y Wang, AW Shieh, J Haney, S Parhami, J Belmont, M Kim, P Moran Losada, Z Khan, J Mleczko, Y Xia, R Dai, D Wang, YT Yang, M Xu, K Fish, PR Hof, J Warrell, D Fitzgerald, K White, AE Jaffe, PsychENCODE Consortium, MA Peters, M Gerstein, C Liu, LM Iakoucheva, D Pinto, DH Geschwind (2018). "Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder." *Science* 362.

M Li, G Santpere, Y Imamura Kawasawa, OV Evgrafov, FO Gulden, S Pochareddy, SM Sunkin, Z Li, Y Shin, Y Zhu, AMM Sousa, DM Werling, RR Kitchen, HJ Kang, M Pletikos, J Choi, S Muchnik, X Xu, D Wang, B Lorente-Galdos, S Liu, P Giusti-Rodriguez, H Won, CA de Leeuw, AF Pardinas, BrainSpan Consortium, PsychENCODE Consortium, PsychENCODE Developmental Subgroup, M Hu, F Jin, Y Li, MJ Owen, MC O'Donovan, JTR Walters, D Posthuma, P Levitt, DR Weinberger, TM Hyde, JE Kleinman, DH Geschwind, MJ Hawrylycz, MW State, SJ Sanders, PF Sullivan, MB Gerstein, ES Lein, JA Knowles, N Sestan (2018). "Integrative functional genomic analysis of human brain development and neuropsychiatric risks." *Science* 362: 1264.

A Amiri, G Coppola, S Scuderi, F Wu, T Roychowdhury, F Liu, S Pochareddy, Y Shin, A Safi, L Song, Y Zhu, AMM Sousa, PsychENCODE Consortium, M Gerstein, GE Crawford, N Sestan, A Abyzov, FM Vaccarino (2018). "Transcriptome and epigenome landscape of human cortical development modeled in organoids." *Science* 362.

X Kong, M Gerstein (2018). "Text mining systems biology: Turning the microscope back on the observer" *Current Opinion in Systems Biology* 11:117-122.

W Shi, CKY Ng, RS Lim, T Jiang, S Kumar, X Li, VB Wali, S Piscuoglio, MB Gerstein, AB Chagpar, B Weigelt, L Pusztai, JS Reis-Filho, C Hatzis (2018). "Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity." *Cell Rep* 25: 1446-1457.

A Frankish, M Diekhans, AM Ferreira, R Johnson, I Jungreis, J Loveland, JM Mudge, C Sisu, J Wright, J Armstrong, I Barnes, A Berry, A Bignell, S Carbonell Sala, J Chrast, F Cunningham, T Di Domenico, S Donaldson, IT Fiddes, C Garcia Giron, JM Gonzalez, T Grego, M Hardy, T Hourlier, T Hunt, OG Izuogu, J Lagarde, FJ Martin, L Martinez, S Mohanan, P Muir, FCP Navarro, A Parker, B Pei, F Pozo, M Ruffier, BM Schmitt, E Stapleton, MM Suner, I Sycheva, B Uszczynska-Ratajczak, J Xu, A Yates, D Zerbino, Y Zhang, B Aken, JS Choudhary, M Gerstein, R Guigo, TJP Hubbard, M Kellis, B Paten, A Reymond, ML Tress, P Flicek (2018). "GENCODE reference annotation for the human and mouse genomes." *Nucleic Acids Res*.

J Lilue, AG Doran, IT Fiddes, M Abrudan, J Armstrong, R Bennett, W Chow, J Collins, S Collins, A Czechanski, P Danecek, M Diekhans, DD Dolle, M Dunn, R Durbin, D Earl, A Ferguson-Smith, P Flicek, J Flint, A Frankish, B Fu, M Gerstein, J Gilbert, L Goodstadt, J Harrow, K Howe, X Ibarra-Soria, M Kolmogorov, CJ Lelliott, DW Logan, J Loveland, CE Mathews, R Mott, P Muir, S Nachtweide, FCP Navarro, DT Odom, N Park, S Pelan, SK Pham, M Quail, L Reinholdt, L Romoth, L Shirley, C Sisu, M Sjoberg-Herrera, M Stanke, C Steward, M Thomas, G Threadgold, D Thybert, J Torrance, K Wong, J Wood, B Yalcin, F Yang, DJ Adams, B Paten, TM Keane (2018). "Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci." *Nat Genet* 50: 1574-1583.

D Greenbaum, M Gerstein (2018). "What's next for humanity?" *Science* 362 (6415):648.

D Greenbaum, M Gerstein (2018). "Human History, Human Genomes" *Cell* 174:1043-1044.

V Onuchic, E Lurie, I Carrero, P Pawliczek, RY Patel, J Rozowsky, T Galeev, Z Huang, RC Altshuler, Z Zhang, RA Harris, C Coarfa, L Ashmore, JW Bertol, WD Fakhouri, F Yu, M Kellis, M Gerstein, A Milosavljevic (2018). "Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci." *Science* 361.

BC Carlyle, RR Kitchen, J Zhang, RS Wilson, TT Lam, JS Rozowsky, KR Williams, N Sestan, MB Gerstein, AC Nairn (2018). "Isoform-Level Interpretation of High-Throughput Proteomics Data Enabled by Deep Integration with RNA-seq." *J Proteome Res* 17: 3431-3444.

AP Arkin, RW Cottingham, CS Henry, NL Harris, RL Stevens, S Maslov, P Dehal, D Ware, F Perez, S Canon, MW Sneddon, ML Henderson, WJ Riehl, D Murphy-Olson, SY Chan, RT Kamimura, S Kumari, MM Drake, TS Brettin, EM Glass, D Chivian, D Gunter, DJ Weston, BH Allen, J Baumohl, AA Best, B Bowen, SE Brenner, CC Bun, JM Chandonia, JM Chia, R Colasanti, N Conrad, JJ Davis, BH Davison, M DeJongh, S Devoid, E Dietrich, I Dubchak, JN Edirisinghe, G Fang, JP Faria, PM Frybarger, W Gerlach, M Gerstein, A Greiner, J Gurtowski, HL Haun, F He, R Jain, MP Joachimiak, KP Keegan, S Kondo, V Kumar, ML Land, F Meyer, M Mills, PS Novichkov, T Oh, GJ Olsen, R Olson, B Parrello, S Pasternak, E Pearson, SS Poon, GA Price, S Ramakrishnan, P Ranjan, PC Ronald, MC Schatz, SMD Seaver, M Shukla, RA Sutormin, MH Syed, J Thomason, NL Tintle, D Wang, F Xia, H Yoo, S Yoo, D Yu (2018). "KBase: The United States Department of Energy Systems Biology Knowledgebase." *Nat Biotechnol* 36: 566-569.

A Harmanci, M Gerstein (2018). "Analysis of sensitive information leakage in functional genomics signal profiles through genomic deletions" *Nat Commun* 9: 2453.

KW Barber, P Muir, RV Szeligowski, S Rogulina, M Gerstein, JR Sampson, FJ Isaacs, J Rinehart (2018). "Encoding human serine phosphopeptides in bacteria for proteome-wide identification of phosphorylation-dependent interactions." *Nat Biotechnol* 36: 638-644.

P McGillivray, D Clarke, W Meyerson, J Zhang, D Lee, M Gu, S Kumar, H Zhou, MB Gerstein (2018). "Network Analysis as a Grand Unifier in Biomedical Data Science" *Annual Review of Biomedical Data Science* Vol. 1.

D Thybert, M Roller, FCP Navarro, I Fiddes, I Streeter, C Feig, D Martin-Galvez, M Kolmogorov, V Janousek, W Akanni, B Aken, S Aldridge, V Chakrapani, W Chow, L Clarke, C Cummins, A Doran, M Dunn, L Goodstadt, K Howe, M Howell, AA Josselin, RC Karn, CM Laukaitis, L Jingtao, F Martin, M Muffato, S Nachtweide, MA Quail, C Sisu, M Stanke, K Stefflova, C Van Oosterhout, F Veyrunes, B Ward, F Yang, G Yazdanifar, A Zadissa, DJ Adams, A Brazma, M Gerstein, B Paten, S Pham, TM Keane, DT Odom, P Flicek (2018). "Repeat associated mechanisms of genome evolution and function revealed by the Mus caroli" *Genome Res* 28: 448-459.

P McGillivray, R Ault, M Pawashe, R Kitchen, S Balasubramanian, M Gerstein (2018). "A comprehensive catalog of predicted functional upstream open reading frames in humans." *Nucleic Acids Res* 46: 3326-3338.

T Becker, WP Lee, J Leone, Q Zhu, C Zhang, S Liu, J Sargent, K Shanker, A Mil-Homens, E Cerveira, M Ryan, J Cha, FCP Navarro, T Galeev, M Gerstein, RE Mills, DG Shin, C Lee, A Malhotra (2018). "FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods." *Genome Biol* 19: 38.

MJ Gandal, JR Haney, NN Parikshak, V Leppa, G Ramaswami, C Hartl, AJ Schork, V Appadurai, A Buil, TM Werge, C Liu, KP White, CommonMind Consortium, PsychENCODE Consortium, iPSYCH-BROAD Working Group, S Horvath, DH Geschwind (2018). "Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap." *Science* 359: 693-697.

MB Gerstein, FCP Navarro (2018). "Gene names can confound most-searched listings." *Nature* 553: 405.

BD Piening, W Zhou, K Contrepois, H Rost, GJ Gu Urban, T Mishra, BM Hanson, EJ Bautista, S Leopold, CY Yeh, D Spakowicz, I Banerjee, C Chen, K Kukurba, D Perelman, C Craig, E Colbert, D Salins, S Rego, S Lee, C Zhang, J Wheeler, MR Sailani, L Liang, C Abbott, M Gerstein, A Mardinoglu, U Smith, DL Rubin, S Pitteri, E Sodergren, TL McLaughlin, GM Weinstock, MP Snyder (2018). "Integrative Personal Omics Profiles during Periods of Weight Gain and Loss." *Cell Syst* 6: 157-170e8.

-- 2017 --

KE Kaczor-Urbanowicz, Y Kim, F Li, T Galeev, RR Kitchen, M Gerstein, K Koyano, SH Jeong, X Wang, D Elashoff, SY Kang, SM Kim, K Kim, S Kim, D Chia, X Xiao, J Rozowsky, DTW Wong (2017). "Novel approaches for bioinformatic analysis of salivary RNA sequencing data for development." *Bioinformatics* 34: 1-8.

MM Kudron, A Victorsen, L Gevirtzman, LW Hillier, WW Fisher, D Vafeados, M Kirkey, AS Hammonds, J Gersch, H Ammouri, ML Wall, J Moran, D Steffen, M Szynkarek, S Seabrook-Sturgis, N Jameel, M Kadaba, J Patton, R Terrell, M Corson, TJ Durham, S Park, S Samanta, M Han, J Xu, KK Yan, SE Celniker, KP White, L Ma, M Gerstein, V Reinke, RH Waterston (2017). "The ModERN Resource: Genome-Wide Binding Profiles for Hundreds of Drosophila and Caenorhabditis elegans Transcription Factors." *Genetics* 208: 937-949.

BC Carlyle, RR Kitchen, JE Kanyo, EZ Voss, M Pletikos, AMM Sousa, TT Lam, MB Gerstein, N Sestan, AC Nairn (2017). "A multiregional proteomic survey of the postnatal human brain." *Nat Neurosci* 20: 1787-1795.

AMM Sousa, Y Zhu, MA Raghanti, RR Kitchen, M Onorati, ATN Tebbenkamp, B Stutz, KA Meyer, M Li, YI Kawasawa, F Liu, RG Perez, M Mele, T Carvalho, M Skarica, FO Gulden, M Pletikos, A Shibata, AR Stephenson, MK Edler, JJ Ely, JD Elsworth, TL Horvath, PR Hof, TM Hyde, JE Kleinman, DR Weinberger, M Reimers, RP Lifton, SM Mane, JP Noonan, MW State, ES Lein, JA Knowles, T Marques-Bonet, CC Sherwood, MB Gerstein, N Sestan (2017). "Molecular and cellular reorganization of neural circuits in the human lineage." *Science* 358: 1027-1032.

L Lochovsky, J Zhang, M Gerstein (2017). "MOAT: efficient detection of highly mutated regions with the Mutations Overburdening Annotations Tool." *Bioinformatics* 34: 1031-1033.

Q Cao, C Anyansi, X Hu, L Xu, L Xiong, W Tang, MTS Mok, C Cheng, X Fan, M Gerstein, ASL Cheng, KY Yip (2017). "Reconstruction of enhancer-target networks in 935 samples of human primary cells, tissues and cell lines." *Nat Genet* 49: 1428-1436.

S Balasubramanian, Y Fu, M Pawashe, P McGillivray, M Jin, J Liu, KJ Karczewski, DG MacArthur, M Gerstein (2017). "Using ALoFT to determine the impact of putative loss-of-function variants in protein-coding genes." *Nat Commun* 8: 382.

KK Yan, S Lou, M Gerstein (2017). "MrTADFinder: A network modularity based approach to identify topologically associating domains in multiple resolutions." *PLoS Comput Biol* 13: e1005647.

SME Sahraeian, M Mohiyuddin, R Sebra, H Tilgner, PT Afshar, KF Au, N Bani Asadi, MB Gerstein, WH Wong, MP Snyder, E Schadt, HYK Lam (2017). "Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis." *Nat Commun* 8: 59.

Y Zhang, S Li, A Abyzov, MB Gerstein (2017). "Landscape and variation of novel retroduplications in 26 human populations." *PLoS Comput Biol* 13: e1005567.

S Kumar, M Gerstein (2017). "Cancer genomics: Less is more in the hunt for driver mutations." *Nature* 547: 40-41.

P Dhingra, Y Fu, M Gerstein, E Khurana (2017). "Using FunSeq2 for Coding and Non-Coding Variant Annotation and Prioritization." *Curr Protoc Bioinformatics* 57: 15111-151117.

P Alves, S Liu, D Wang, M Gerstein (2017). "Multiple-Swarm Ensembles: Improving the Predictive Power and Robustness of Predictive Models and Its Use in Computational Biology." *IEEE/ACM Trans Comput Biol Bioinform* 15: 926-933.

V Despic, M Dejung, M Gu, J Krishnan, J Zhang, L Herzel, K Straube, MB Gerstein, F Butter, KM Neugebauer (2017). "Dynamic RNA-protein interactions underlie the zebrafish maternal-to-zygotic transition." *Genome Res* 27: 1184-1194.

D Greenbaum, J Rozowsky, V Stodden, M Gerstein (2017). "Structuring supplemental materials in support of reproducibility." *Genome Biol* 18: 64.

KK Yan, GG Yardimci, C Yan, WS Noble, M Gerstein (2017). "HiC-spector: a matrix library for spectral and reproducibility analysis of Hi-C contact maps." *Bioinformatics* 33: 2199-2201.

S Li, BM Shuch, MB Gerstein (2017). "Whole-genome analysis of papillary kidney cancer finds significant noncoding alterations." *PLoS Genet* 13: e1006685.

DM Kasper, A Moro, E Ristori, A Narayanan, G Hill-Teran, E Fleming, M Moreno-Mateos, CE Vejnar, J Zhang, D Lee, M Gu, M Gerstein, A Giraldez, S Nicoli (2017). "MicroRNAs Establish Uniform Traits during the Architecture of Vertebrate Embryos." *Dev Cell* 40: 552-565e5.

E Mick, R Shah, K Tanriverdi, V Murthy, M Gerstein, J Rozowsky, R Kitchen, MG Larson, D Levy, JE Freedman (2017). "Stroke and Circulating Extracellular RNAs." *Stroke* 48: 828-834.

A Abyzov, L Tomasini, B Zhou, N Vasmatzis, G Coppola, M Amenduni, R Pattni, M Wilson, M Gerstein, S Weissman, AE Urban, FM Vaccarino (2017). "One thousand somatic SNVs per skin fibroblast cell set baseline of mosaic mutational load with patterns that suggest proliferative origin." *Genome Res* 27: 512-523.

-- 2016 --

J Chen, B Wang, L Regan, M Gerstein (2016). "Intensification: A Resource for Amplifying Population-Genetic Signals with Protein Repeats." *J Mol Biol* 429: 435-445.

S Kumar, D Clarke, M Gerstein (2016). "Localized structural frustration for evaluating the impact of sequence variants." *Nucleic Acids Res* 44: 10062-10073.

D Wang, F He, S Maslov, M Gerstein (2016). "DREISS: Using State-Space Models to Infer the Dynamics of Gene Expression Driven by External and Internal Regulatory Networks." *PLoS Comput Biol* 12: e1005146.

D Greenbaum, M Gerstein (2016). "Opinion: GMOs Are Not "Frankenfoods"" *The Scientist* (30 Aug

CC Yang, EH Andrews, MH Chen, WY Wang, JJ Chen, M Gerstein, CC Liu, C Cheng (2016). "iTAR: a web server for identifying target genes of transcription factors using ChIP-seq or ChIP-chip data." *BMC Genomics* 17: 632.

SW Choo, M Rayko, TK Tan, R Hari, A Komissarov, WY Wee, AA Yurchenko, S Kliver, G Tamazian, A Antunes, RK Wilson, WC Warren, KP Koepfli, P Minx, K Krasheninnikova, A Kotze, DL Dalton, E Vermaak, IC Paterson, P Dobrynin, FT Sitam, JJ Rovie-Ryan, WE Johnson, AM Yusoff, SJ Luo, KV Karuppannan, G Fang, D Zheng, MB Gerstein, L Lipovich, SJ O'Brien, GJ Wong (2016). "Pangolin genomes and the evolution of mammalian scales and immunity." *Genome Res* 26: 1312-1322.

R Shah, K Tanriverdi, D Levy, M Larson, M Gerstein, E Mick, J Rozowsky, R Kitchen, V Murthy, E Mikalev, JE Freedman (2016). "Discordant Expression of Circulating microRNA from Cellular and Extracellular Sources." *PLoS One* 11: e0153691.

JE Freedman, M Gerstein, E Mick, J Rozowsky, D Levy, R Kitchen, S Das, R Shah, K Danielson, L Beaulieu, FC Navarro, Y Wang, TR Galeev, A Holman, RY Kwong, V Murthy, SE Tanriverdi, M Koupenova-Zamor, E Mikhalev, K Tanriverdi (2016). "Diverse human extracellular RNAs are widely detected in human plasma." *Nat Commun* 7: 11106.

KH Cheung, S Keerthikumar, P Roncaglia, SL Subramanian, ME Roth, M Samuel, S Anand, L Gangoda, S Gould, R Alexander, D Galas, MB Gerstein, AF Hill, RR Kitchen, J Lotvall, T Patel, DC Procaccini, P Quesenberry, J Rozowsky, RL Raffai, A Shypitsyna, AI Su, C Thery, K Vickers, MH Wauben, S Mathivanan, A Milosavljevic, LC Laurent (2016). "Extending gene ontology in the context of extracellular RNA and vesicle communication." *J Biomed Semantics* 7: 19.

J Chen, J Rozowsky, TR Galeev, A Harmanci, R Kitchen, J Bedford, A Abyzov, Y Kong, L Regan, M Gerstein (2016). "A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals." *Nat Commun* 7: 11101.

D Clarke, A Sethi, S Li, S Kumar, RWF Chang, J Chen, M Gerstein (2016). "Identifying Allosteric Hotspots with Dynamics: Application to Inter- and Intra-species Conservation." *Structure* 24: 826-837.

KK Yan, D Wang, A Sethi, P Muir, R Kitchen, C Cheng, M Gerstein (2016). "Cross-Disciplinary Network Comparison: Matchmaking Between Hairballs." *Cell Syst* 2: 147-157.

D Greenbaum, M Gerstein (2016). "Who Owns Your DNA?" *Cell* 165:257-258.

F He, S Yoo, D Wang, S Kumari, M Gerstein, D Ware, S Maslov (2016). "Large-scale atlas of microarray data reveals the distinct expression landscape of different tissues in Arabidopsis." *Plant J* 86: 472-80.

P Muir, S Li, S Lou, D Wang, DJ Spakowicz, L Salichos, J Zhang, GM Weinstock, F Isaacs, J Rozowsky, M Gerstein (2016). "The real cost of sequencing: scaling computation to keep pace with data generation." *Genome Biol* 17: 53.

D Wang, KK Yan, J Rozowsky, E Pan, M Gerstein (2016). "Temporal Dynamics of Collaborative Networks in Large Scientific Consortia." *Trends Genet* 32: 251-253.

A Harmanci, M Gerstein (2016). "Quantification of private information leakage from phenotype-genotype data: linking attacks." *Nat Methods* 13: 251-6.

E Khurana, Y Fu, D Chakravarty, F Demichelis, MA Rubin, M Gerstein (2016). "Role of non-coding sequence variants in cancer." *Nat Rev Genet* 17: 93-108.

A Abyzov, S Li, MB Gerstein (2016). "Understanding genome structural variations." *Oncotarget* 7: 7370-1.

-- 2015 --

Cancer Genome Atlas Research Network. "The Molecular Taxonomy of Primary Prostate Cancer." *Cell* 163: 1011-25.

S Purushotham, MR Min, CJ Kuo, M Gerstein (2015). " Knowledge Based Factorized High Order Sparse Learning Models." NIPS Workshop on Machine Learning in Computational Biology.

A Abyzov, S Li, MB Gerstein (2015). "Understanding genome structural variations." *Oncotarget* .

A Sethi, D Clarke, J Chen, S Kumar, TR Galeev, L Regan, M Gerstein (2015). "Reads meet rotamers: structural biology in the age of deep sequencing." *Curr Opin Struct Biol* 35: 125-34.

S Akbarian, C Liu, JA Knowles, FM Vaccarino, PJ Farnham, GE Crawford, AE Jaffe, D Pinto, S Dracheva, DH Geschwind, J Mill, AC Nairn, A Abyzov, S Pochareddy, S Prabhakar, S Weissman, PF Sullivan, MW State, Z Weng, MA Peters, KP White, MB Gerstein, A Amiri, C Armoskus, AE Ashley-Koch, T Bae, A Beckel-Mitchener, BP Berman, GA Coetzee, G Coppola, N Francoeur, M Fromer, R Gao, K Grennan, J Herstein, DH Kavanagh, NA Ivanov, Y Jiang, RR Kitchen, A Kozlenkov, M Kundakovic, M Li, Z Li, S Liu, LM Mangravite, E Mattei, E Markenscoff-Papadimitriou, FC Navarro, N North, L Omberg, D Panchision, N Parikshak, J Poschmann, AJ Price, M Purcaro, TE Reddy, P Roussos, S Schreiner, S Scuderi, R Sebra, M Shibata, AW Shieh, M Skarica, W Sun, V Swarup, A Thomas, J Tsuji, H van Bakel, D Wang, Y Wang, K Wang, DM Werling, AJ Willsey, H Witt, H Won, CC Wong, GA Wray, EY Wu, X Xu, L Yao, G Senthil, T Lehner, P Sklar, N Sestan (2015). "The PsychENCODE project." *Nat Neurosci* 18: 1707-12.

D Greenbaum, M Gerstein (2015). ""Illuminating the Genome's Dark Matter," *Cell* 163:1047-1048.

Cancer Genome Atlas Research Network, WM Linehan, PT Spellman, CJ Ricketts, CJ Creighton, SS Fei, C Davis, DA Wheeler, BA Murray, L Schmidt, CD Vocke, M Peto, AA Al Mamun, E Shinbrot, A Sethi, S Brooks, WK Rathmell, AN Brooks, KA Hoadley, AG Robertson, D Brooks, R Bowlby, S Sadeghi, H Shen, DJ Weisenberger, M Bootwalla, SB Baylin, PW Laird, AD Cherniack, G Saksena, S Haake, J Li, H Liang, Y Lu, GB Mills, R Akbani, MD Leiserson, BJ Raphael, P Anur, D Bottaro, L Albiges, N Barnabas, TK Choueiri, B Czerniak, AK Godwin, AA Hakimi, TH Ho, J Hsieh, M Ittmann, WY Kim, B Krishnan, MJ Merino, KR Mills Shaw, VE Reuter, E Reznik, CS Shelley, B Shuch, S Signoretti, R Srinivasan, P Tamboli, G Thomas, S Tickoo, K Burnett, D Crain, J Gardner, K Lau, D Mallery, S Morris, JD Paulauskis, RJ Penny, C Shelton, WT Shelton, M Sherman, E Thompson, P Yena, MT Avedon, J Bowen, JM Gastier-Foster, M Gerken, KM Leraas, TM Lichtenberg, NC Ramirez, T Santos, L Wise, E Zmuda, JA Demchok, I Felau, CM Hutter, M Sheth, HJ Sofia, R Tarnuzzer, Z Wang, L Yang, JC Zenklusen, J Zhang, B Ayala, J Baboud, S Chudamani, J Liu, L Lolla, R Naresh, T Pihl, Q Sun, Y Wan, Y Wu, A Ally, M Balasundaram, S Balu, R Beroukhim, T Bodenheimer, C Buhay, YS Butterfield, R Carlsen, SL Carter, H Chao, E Chuah, A Clarke, KR Covington, M Dahdouli, N Dewal, N Dhalla, HV Doddapaneni, JA Drummond, SB Gabriel, RA Gibbs, R Guin, W Hale, A Hawes, DN Hayes, RA Holt, AP Hoyle, SR Jefferys, SJ Jones, CD Jones, D Kalra, C Kovar, L Lewis, J Li, Y Ma, MA Marra, M Mayo, S Meng, M Meyerson, PA Mieczkowski, RA Moore, D Morton, LE Mose, AJ Mungall, D Muzny, JS Parker, CM Perou, J Roach, JE Schein, SE Schumacher, Y Shi, JV Simons, P Sipahimalani, T Skelly, MG Soloway, C Sougnez, A Tam, D Tan, N Thiessen, U Veluvolu, M Wang, MD Wilkerson, T Wong, J Wu, L Xi, J Zhou, J Bedford, F Chen, Y Fu, M Gerstein, D Haussler, K Kasaian, P Lai, S Ling, A Radenbaugh, D Van Den Berg, JN Weinstein, J Zhu, M Albert, I Alexopoulou, JJ Andersen, JT Auman, J Bartlett, S Bastacky, J Bergsten, ML Blute, L Boice, RJ Bollag, J Boyd, E Castle, YB Chen, JC Cheville, E Curley, B Davies, A DeVolk, R Dhir, L Dike, J Eckman, J Engel, J Harr, R Hrebinko, M Huang, L Huelsenbeck-Dill, M Iacocca, B Jacobs, M Lobis, JK Maranchie, S McMeekin, J Myers, J Nelson, J Parfitt, A Parwani, N Petrelli, B Rabeno, S Roy, AL Salner, J Slaton, M Stanton, RH Thompson, L Thorne, K Tucker, PM Weinberger, C Winemiller, LA Zach, R Zuna (2015). "Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma." *N Engl J Med* 374: 135-45.

The 1000 Genomes Project Consortium (2015). "A global reference for human genetic variation." *Nature* 526: 68–74.

PH Sudmant, T Rausch, E Gardner, R Handsaker, A Abyzov, J Huddleston, Y Zhang, K Ye, G Jun, M Fritz, M Konkel, A Malhotra, A Stütz, X Shi, F Paolo Casale, J Chen, F Hormozdiari, G Dayama, K Chen, M Malig, M Chaisson, K Walter, S Meiers, S Kashin, E Garrison, A Auton, H Lam, XJ Mu, C Alkan, D Antaki, T Bae, E Cerveira, P Chines, Z Chong, L Clarke, E Dal, L Ding, S Emery, X Fan, M Gujral, F Kahveci, J Kidd, Y Kong, E Lameijer, S McCarthy, P Flicek, R Gibbs, G Marth, C Mason, A Menelaou, D Muzny, B Nelson, A Noor, N Parrish, M Pendleton, A Quitadamo, B Raeder, E Schadt, M Romanovitch, A Schlattl, R Sebra, A Shabalin, A Untergasser, J Walker, M Wang, F Yu, C Zhang, J Zhang, X Zheng-Bradley, W Zhou, T Zichner, J Sebat, M Batzer, S McCarroll, The 1000 Genomes Project Consortium, R Mills, M Gerstein, A Bashir, O Stegle, S Devine, C Lee, E Eichler, JO Korbel (2015). "An integrated map of structural variation in 2,504 human genomes." *Nature* 526: 75–81.

JC Mu, P Tootoonchi Afshar, M Mohiyuddin, X Chen, J Li, N Bani Asadi, MB Gerstein, WH Wong, HY Lam (2015). "Leveraging long read sequencing from a single individual to provide a comprehensive resource for benchmarking variant calling methods." *Sci Rep* 5: 14493.

LT Fang, PT Afshar, A Chhibber, M Mohiyuddin, Y Fan, JC Mu, G Gibeling, S Barr, NB Asadi, MB Gerstein, DC Koboldt, W Wang, WH Wong, HY Lam (2015). "An ensemble approach to accurately detect somatic mutations using SomaticSeq." *Genome Biol* 16: 197.

EE Duffy, M Rutenberg-Schoenberg, CD Stark, RR Kitchen, MB Gerstein, MD Simon (2015). "Tracking Distinct RNA Populations Using Efficient and Reversible Covalent Chemistry." *Mol Cell* 59: 858-66.

L Lochovsky, J Zhang, Y Fu, E Khurana, M Gerstein (2015). "LARVA: an integrative framework for large-scale analysis of recurrent variants in noncoding annotations." *Nucleic Acids Res* .

PP Kuksa, MR Min, R Dugar, M Gerstein (2015). "High-order neural networks and kernel methods for peptide-MHC binding prediction." *Bioinformatics* .

J Mariani, G Coppola, P Zhang, A Abyzov, L Provini, L Tomasini, M Amenduni, A Szekely, D Palejev, M Wilson, M Gerstein, EL Grigorenko, K Chawarska, KA Pelphrey, JR Howe, FM Vaccarino. (2015) "FOXG1-Dependent Dysregulation of GABA/Glutamate Neuron Differentiation in Autism Spectrum Disorders." *Cell* Jul 16;162(2):375-90.

A Abyzov, S Li, DR Kim, M Mohiyuddin, AM Stütz, NF Parrish, XJ Mu, W Clark, K Chen, M Hurles, JO Korbel, HY Lam, C Lee, MB Gerstein (2015). "Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms." *Nat Commun* 6: 7256.

D Greenbaum, M Gerstein (2015). "The computer connection." *Science* 347: 956.

M Mohiyuddin, JC Mu, J Li, N Bani Asadi, MB Gerstein, A Abyzov, WH Wong, HY Lam (2015). "MetaSV: an accurate and integrative structural-variant caller for next generation sequencing."*Bioinformatics* 31: 2741-4.

D Wang, KK Yan, C Sisu, C Cheng, J Rozowsky, W Meyerson, MB Gerstein (2015). "Loregic: a method to characterize the cooperative logic of regulatory factors." *PLoS Comput Biol* 11: e1004132.

C Cheng, E Andrews, KK Yan, M Ung, D Wang, M Gerstein (2015). "An approach for determining and measuring network hierarchy applied to comparing the phosphorylome and the regulome." *Genome Biol* 16: 63.

-- 2014 --

JC Mu, M Mohiyuddin, J Li, N Bani Asadi, MB Gerstein, A Abyzov, WH Wong, HY Lam (2014). "VarSim: a high-fidelity simulation and validation framework for high-throughput genome sequencing with cancer applications." *Bioinformatics* 31: 1469-71.

RR Kitchen, JS Rozowsky, MB Gerstein, AC Nairn (2014). "Decoding neuroproteomics: integrating the genome, translatome and functional anatomy." *Nat Neurosci* 17: 1491-9.

MR Min, X Ning, Y Qi, C Cheng, A Bonner, M Gerstein (2014). "Ensemble Learning Based Sparse High-Order Boltzmann Machine for Unsupervised Feature Interaction Identification." NIPS Workshop on Machine Learning in Computational Biology.

MR Min, X Ning, C Cheng, M Gerstein (2014). "Interpretable Sparse High-Order Boltzmann Machines." JMLR W&CP 33: 614-622 (AISTATS 2014).

A Harmanci, J Rozowsky, M Gerstein (2014). "MUSIC: identification of enriched regions in ChIP-Seq experiments using a mappability-corrected multiscale signal processing framework." *Genome Biol* 15: 474.

Y Fu, Z Liu, S Lou, J Bedford, XJ Mu, KY Yip, E Khurana, M Gerstein (2014). "FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer." *Genome Biol* 15: 480.

AP Boyle, CL Araya, C Brdlik, P Cayting, C Cheng, Y Cheng, K Gardner, LW Hillier, J Janette, L Jiang, D Kasper, T Kawli, P Kheradpour, A Kundaje, JJ Li, L Ma, W Niu, EJ Rehm, J Rozowsky, M Slattery, R Spokony, R Terrell, D Vafeados, D Wang, P Weisdepp, YC Wu, D Xie, KK Yan, EA Feingold, PJ Good, MJ Pazin, H Huang, PJ Bickel, SE Brenner, V Reinke, RH Waterston, M Gerstein, KP White, M Kellis, M Snyder (2014). "Comparative analysis of regulatory information and circuits across distant species." *Nature* 512: 453-6.

MB Gerstein, J Rozowsky, KK Yan, D Wang, C Cheng, JB Brown, CA Davis, L Hillier, C Sisu, JJ Li, B Pei, AO Harmanci, MO Duff, S Djebali, RP Alexander, BH Alver, R Auerbach, K Bell, PJ Bickel, ME Boeck, NP Boley, BW Booth, L Cherbas, P Cherbas, C Di, A Dobin, J Drenkow, B Ewing, G Fang, M Fastuca, EA Feingold, A Frankish, G Gao, PJ Good, R Guigó, A Hammonds, J Harrow, RA Hoskins, C Howald, L Hu, H Huang, TJ Hubbard, C Huynh, S Jha, D Kasper, M Kato, TC Kaufman, RR Kitchen, E Ladewig, J Lagarde, E Lai, J Leng, Z Lu, M MacCoss, G May, R McWhirter, G Merrihew, DM Miller, A Mortazavi, R Murad, B Oliver, S Olson, PJ Park, MJ Pazin, N Perrimon, D Pervouchine, V Reinke, A Reymond, G Robinson, A Samsonova, GI Saunders, F Schlesinger, A Sethi, FJ Slack, WC Spencer, MH Stoiber, P Strasbourger, A Tanzer, OA Thompson, KH Wan, G Wang, H Wang, KL Watkins, J Wen, K Wen, C Xue, L Yang, K Yip, C Zaleski, Y Zhang, H Zheng, SE Brenner, BR Graveley, SE Celniker, TR Gingeras, R Waterston (2014). "Comparative analysis of the transcriptome across distant species." *Nature* 512: 445-8.

C Sisu, B Pei, J Leng, A Frankish, Y Zhang, S Balasubramanian, R Harte, D Wang, M Rutenberg-Schoenberg, W Clark, M Diekhans, J Rozowsky, T Hubbard, J Harrow, MB Gerstein (2014). "Comparative analysis of pseudogenes across three phyla." *Proc Natl Acad Sci U S A* 111: 13361-6.

KK Yan, D Wang, J Rozowsky, H Zheng, C Cheng, M Gerstein (2014). "OrthoClust: an orthology-based network framework for clustering data across multiple species." *Genome Biol* 15: R100.

DG MacArthur, TA Manolio, DP Dimmock, HL Rehm, J Shendure, GR Abecasis, DR Adams, RB Altman, SE Antonarakis, EA Ashley, JC Barrett, LG Biesecker, DF Conrad, GM Cooper, NJ Cox, MJ Daly, MB Gerstein, DB Goldstein, JN Hirschhorn, SM Leal, LA Pennacchio, JA Stamatoyannopoulos, SR Sunyaev, D Valle, BF Voight, W Winckler, C Gunter (2014). "Guidelines for investigating causality of sequence variants in human disease." *Nature* 508: 469-76.

M Kellis, B Wold, MP Snyder, BE Bernstein, A Kundaje, GK Marinov, LD Ward, E Birney, GE Crawford, J Dekker, I Dunham, LL Elnitski, PJ Farnham, EA Feingold, M Gerstein, MC Giddings, DM Gilbert, TR Gingeras, ED Green, R Guigo, T Hubbard, J Kent, JD Lieb, RM Myers, MJ Pazin, B Ren, JA Stamatoyannopoulos, Z Weng, KP White, RC Hardison (2014). "Defining functional DNA elements in the human genome." *Proc Natl Acad Sci U S A* 111: 6131-8.

JA Miller, SL Ding, SM Sunkin, KA Smith, L Ng, A Szafer, A Ebbert, ZL Riley, JJ Royall, K Aiona, JM Arnold, C Bennet, D Bertagnolli, K Brouner, S Butler, S Caldejon, A Carey, C Cuhaciyan, RA Dalley, N Dee, TA Dolbeare, BA Facer, D Feng, TP Fliss, G Gee, J Goldy, L Gourley, BW Gregor, G Gu, RE Howard, JM Jochim, CL Kuan, C Lau, CK Lee, F Lee, TA Lemon, P Lesnar, B McMurray, N Mastan, N Mosqueda, T Naluai-Cecchini, NK Ngo, J Nyhus, A Oldre, E Olson, J Parente, PD Parker, SE Parry, A Stevens, M Pletikos, M Reding, K Roll, D Sandman, M Sarreal, S Shapouri, NV Shapovalova, EH Shen, N Sjoquist, CR Slaughterbeck, M Smith, AJ Sodt, D Williams, L Zöllei, B Fischl, MB Gerstein, DH Geschwind, IA Glass, MJ Hawrylycz, RF Hevner, H Huang, AR Jones, JA Knowles, P Levitt, JW Phillips, N Sestan, P Wohnoutka, C Dang, A Bernard, JG Hohmann, ES Lein (2014). "Transcriptional landscape of the prenatal human brain." *Nature* 508: 199-206.

-- 2013 --

KY Yip, C Cheng, M Gerstein (2013). "Machine learning and genome annotation: a match meant to be?" *Genome Biol* 14: 205.

E Khurana, Y Fu, J Chen, M Gerstein (2013). "Interpretation of genomic variants using a unified biological network approach." *PLoS Comput Biol* 9: e1002886.

MR Min, X Ning, C Cheng, M Gerstein (2013). " Interpretable Sparse High-Order Boltzmann Machines for Transcription Factor Interaction Identification." NIPS Workshop on Machine Learning in Computational Biology.

T Steijger, JF Abril, PG Engström, F Kokocinski, The RGASP Consortium, JF Abril, M Akerman, T Alioto, G Ambrosini, SE Antonarakis, J Behr, P Bertone, R Bohnert, P Bucher, N Cloonan, T Derrien, S Djebali, J Du, S Dudoit, PG Engström, M Gerstein, TR Gingeras, D Gonzalez, SM Grimmond, R Guigó, L Habegger, J Harrow, TJ Hubbard, C Iseli, G Jean, A Kahles, F Kokocinski, J Lagarde, J Leng, G Lefebvre, S Lewis, A Mortazavi, P Niermann, G Rätsch, A Reymond, P Ribeca, H Richard, J Rougemont, J Rozowsky, M Sammeth, A Sboner, MH Schulz, SM Searle, ND Solorzano, V Solovyev, M Stanke, T Steijger, BJ Stevenson, H Stockinger, A Valsesia, D Weese, S White, BJ Wold, J Wu, TD Wu, G Zeller, D Zerbino, MQ Zhang, TJ Hubbard, R Guigó, J Harrow, P Bertone (2013). "Assessment of transcript reconstruction methods for RNA-seq." *Nat Methods* 10:1177.

D Greenbaum, J Chen, M Gerstein (2013). "Deep Inside Champions, Just Genes?" *Science* 342: 560.

E Khurana, Y Fu, V Colonna, XJ Mu, HM Kang, T Lappalainen, A Sboner, L Lochovsky, J Chen, A Harmanci, J Das, A Abyzov, S Balasubramanian, K Beal, D Chakravarty, D Challis, Y Chen, D Clarke, L Clarke, F Cunningham, US Evani, P Flicek, R Fragoza, E Garrison, R Gibbs, ZH Gumus, J Herrero, N Kitabayashi, Y Kong, K Lage, V Liluashvili, SM Lipkin, DG MacArthur, G Marth, D Muzny, TH Pers, GR Ritchie, JA Rosenfeld, C Sisu, X Wei, M Wilson, Y Xue, F Yu, 1000 Genomes Project Consortium, ET Dermitzakis, H Yu, MA Rubin, C Tyler-Smith, M Gerstein (2013). "Integrative annotation of variants from 1092 humans: application to cancer genomics." *Science* 342: 1235587

A Abyzov, R Iskow, O Gokcumen, DW Radke, S Balasubramanian, B Pei, L Habegger, The 1000 Genomes Project Consortium, C Lee, M Gerstein (2013). "Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division." *Genome Res*. 12: 2042

C Cheng, Y Fu, L Shen, M Gerstein (2013). "Identification of yeast cell cycle regulated genes based on genomic features." *BMC Syst Biol* 7: 70.

Y Zhang, R Haraksingh, F Grubert, A Abyzov, M Gerstein, S Weissman, AE Urban (2013). "Child development and structural variation in the human genome." *Child Dev* 84: 34-48.

R Kittler, J Zhou, S Hua, L Ma, Y Liu, E Pendleton, C Cheng, M Gerstein, KP White (2013). "A comprehensive nuclear receptor network for breast cancer cells." *Cell Rep* 3: 538-51.

H Tilgner, D Raha, L Habegger, M Mohiuddin, M Gerstein, M Snyder (2013). "Accurate identification and analysis of human mRNA isoforms using deep long read sequencing." *G3* (Bethesda) 3: 387-97.

SB Montgomery, DL Goode, E Kvikstad, CA Albers, ZD Zhang, XJ Mu, G Ananda, B Howie, KJ Karczewski, KS Smith, V Anaya, R Richardson, J Davis, 1000 Genomes Project Consortium, DG MacArthur, A Sidow, L Duret, M Gerstein, KD Makova, J Marchini, G McVean, G Lunter (2013). "The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes." *Genome Res 23*: 749-61.

WF Doolittle, P Fraser, MB Gerstein, BR Graveley, S Henikoff, C Huttenhower, A Oshlack, CP Ponting, JL Rinn, MC Schatz, J Ule, D Weigel, GM Weinstock (2013). "Sixty years of genome biology." *Genome Biol* 14: 113.

E Khurana, Y Fu, J Chen, M Gerstein (2013). "Interpretation of genomic variants using a unified biological network approach." *PLoS Comput Biol* 9: e1002886.

-- 2012 --

PC Lin, YL Chiu, S Banerjee, K Park, JM Mosquera, E Giannopoulou, P Alves, AK Tewari, MB Gerstein, H Beltran, AM Melnick, O Elemento, F Demichelis, MA Rubin (2012). "Epigenetic repression of miR-31 disrupts androgen receptor homeostasis and contributes to prostate cancer progression." Cancer Res 73: 1232-44.

A Abyzov, J Mariani, D Palejev, Y Zhang, MS Haney, L Tomasini, AF Ferrandino, LA Rosenberg Belmaker, A Szekely, M Wilson, A Kocabas, NE Calixto, EL Grigorenko, A Huttner, K Chawarska, S Weissman, AE Urban*, M Gerstein*, FM Vaccarino* (2012). "Somatic copy number mosaicism in human skin revealed by induced pluripotent stem cells." *Nature* 492: 438-42

1000 Genomes Project Consortium (2012). "An integrated map of genetic variation from 1,092 human genomes." *Nature* 491: 56-65.

M Gerstein (2012). "Genomics: ENCODE leads the way on big data." *Nature* 489: 208.

ENCODE Project Consortium (2012). "An integrated encyclopedia of DNA elements in the human genome." *Nature* 489: 57-74.

MB Gerstein, A Kundaje, M Hariharan, SG Landt, KK Yan, C Cheng, XJ Mu, E Khurana, J Rozowsky, R Alexander, R Min, P Alves, A Abyzov, N Addleman, N Bhardwaj, AP Boyle, P Cayting, A Charos, DZ Chen, Y Cheng, D Clarke, C Eastman, G Euskirchen, S Frietze, Y Fu, J Gertz, F Grubert, A Harmanci, P Jain, M Kasowski, P Lacroute, J Leng, J Lian, H Monahan, H O'Geen, Z Ouyang, EC Partridge, D Patacsil, F Pauli, D Raha, L Ramirez, TE Reddy, B Reed, M Shi, T Slifer, J Wang, L Wu, X Yang, KY Yip, G Zilberman-Schapira, S Batzoglou, A Sidow, PJ Farnham, RM Myers, SM Weissman, M Snyder (2012). "Architecture of the human regulatory network derived from ENCODE data." *Nature* 489: 91-100.

S Djebali, CA Davis, A Merkel, A Dobin, T Lassmann, A Mortazavi, A Tanzer, J Lagarde, W Lin, F Schlesinger, C Xue, GK Marinov, J Khatun, BA Williams, C Zaleski, J Rozowsky, M Röder, F Kokocinski, RF Abdelhamid, T Alioto, I Antoshechkin, MT Baer, NS Bar, P Batut, K Bell, I Bell, S Chakrabortty, X Chen, J Chrast, J Curado, T Derrien, J Drenkow, E Dumais, J Dumais, R Duttagupta, E Falconnet, M Fastuca, K Fejes-Toth, P Ferreira, S Foissac, MJ Fullwood, H Gao, D Gonzalez, A Gordon, H Gunawardena, C Howald, S Jha, R Johnson, P Kapranov, B King, C Kingswood, OJ Luo, E Park, K Persaud, JB Preall, P Ribeca, B Risk, D Robyr, M Sammeth, L Schaffer, LH See, A Shahab, J Skancke, AM Suzuki, H Takahashi, H Tilgner, D Trout, N Walters, H Wang, J Wrobel, Y Yu, X Ruan, Y Hayashizaki, J Harrow, M Gerstein, T Hubbard, A Reymond, SE Antonarakis, G Hannon, MC Giddings, Y Ruan, B Wold, P Carninci, R Guigó, TR Gingeras (2012). "Landscape of transcription in human cells." *Nature* 489: 101-8.

J Harrow, A Frankish, JM Gonzalez, E Tapanari, M Diekhans, F Kokocinski, BL Aken, D Barrell, A Zadissa, S Searle, I Barnes, A Bignell, V Boychenko, T Hunt, M Kay, G Mukherjee, J Rajan, G

Despacio-Reyes, G Saunders, C Steward, R Harte, M Lin, C Howald, A Tanzer, T Derrien, J Chrast, N Walters, S Balasubramanian, B Pei, M Tress, JM Rodriguez, I Ezkurdia, J van Baren, M Brent, D Haussler, M Kellis, A Valencia, A Reymond, M Gerstein, R Guigó, TJ Hubbard (2012). "GENCODE: the reference human genome annotation for The ENCODE Project." *Genome Res* 22: 1760-74.

KY Yip, C Cheng, N Bhardwaj, JB Brown, J Leng, A Kundaje, J Rozowsky, E Birney, P Bickel, M Snyder, M Gerstein (2012). "Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors." *Genome Biol* 13: R48.

C Cheng, R Alexander, R Min, J Leng, KY Yip, J Rozowsky, KK Yan, X Dong, S Djebali, Y Ruan, CA Davis, P Carninci, T Lassman, TR Gingeras, R Guigó, E Birney, Z Weng, M Snyder, M Gerstein (2012). "Understanding transcriptional regulation by integrative analysis of transcription factor binding data." *Genome Res* 22: 1658-67.

SG Landt, GK Marinov, A Kundaje, P Kheradpour, F Pauli, S Batzoglou, BE Bernstein, P Bickel, JB Brown, P Cayting, Y Chen, G DeSalvo, C Epstein, KI Fisher-Aylor, G Euskirchen, M Gerstein, J Gertz, AJ Hartemink, MM Hoffman, VR Iyer, YL Jung, S Karmakar, M Kellis, PV Kharchenko, Q Li, T Liu, XS Liu, L Ma, A Milosavljevic, RM Myers, PJ Park, MJ Pazin, MD Perry, D Raha, TE Reddy, J Rozowsky, N Shoresh, A Sidow, M Slattery, JA Stamatoyannopoulos, MY Tolstorukov, KP White, S Xi, PJ Farnham, JD Lieb, BJ Wold, M Snyder (2012). "ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia." *Genome Res* 22: 1813-31.

B Pei, C Sisu, A Frankish, C Howald, L Habegger, XJ Mu, R Harte, S Balasubramanian, A Tanzer, M Diekhans, A Reymond, TJ Hubbard, J Harrow, MB Gerstein (2012). "The GENCODE pseudogene resource." *Genome Biol* 13: R51.

X Dong, MC Greven, A Kundaje, S Djebali, JB Brown, C Cheng, TR Gingeras, M Gerstein, R Guigó, E Birney, Z Weng (2012). "Modeling gene expression using chromatin features in various cellular contexts." *Genome Biol* 13: R53.

JQ Wu, M Seay, VP Schulz, M Hariharan, D Tuck, J Lian, J Du, M Shi, Z Ye, M Gerstein, MP Snyder, S Weissman (2012). "Tcf7 is an important regulator of the switch of self-renewal and differentiation in a multipotential hematopoietic cell line." *PLoS Genet* 8: e1002565.

HY Lam, C Pan, MJ Clark, P Lacroute, R Chen, R Haraksingh, M O'Huallachain, MB Gerstein, JM Kidd, CD Bustamante, M Snyder (2012). "Detecting and annotating genetic variations using the HugeSeq pipeline." *Nat Biotechnol* 30: 226-9.

J Cotney, J Leng, S Oh, LE DeMare, SK Reilly, MB Gerstein, JP Noonan (2012). "Chromatin state signatures associated with tissue-specific gene expression and enhancer activity in the embryonic limb." *Genome Res* 22: 1069-80.

M Vidal, DW Chan, M Gerstein, M Mann, GS Omenn, D Tagle, S Sechi, S Sechi, Workshop Participants (2012). "The human proteome - a scientific opportunity for transforming diagnostics, therapeutics, and healthcare." *Clin Proteomics* 9: 6.

MJ Bamshad, JA Shendure, D Valle, A Hamosh, JR Lupski, RA Gibbs, E Boerwinkle, RP Lifton, M Gerstein, M Gunel, S Mane, DA Nickerson, DA Nickerson, Centers for Mendelian Genomics (2012). "The Centers for Mendelian Genomics: a new large-scale initiative to identify the genes underlying rare Mendelian conditions." *Am J Med Genet A* 158A: 1523-5.

L Habegger, S Balasubramanian, DZ Chen, E Khurana, A Sboner, A Harmanci, J Rozowsky, D Clarke, M Snyder, M Gerstein (2012). "VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment." *Bioinformatics* 28: 2267-9.

G Zilberman-Schapira, J Chen, M Gerstein (2012). "On sports and genes." *Recent Pat DNA Gene Seq* 6: 180-8.

D Clarke, N Bhardwaj, MB Gerstein (2012). "Novel insights through the integration of structural and functional genomics data with protein networks." J Struct Biol 179: 320-6.

TA Gianoulis, MA Griffin, DJ Spakowicz, BF Dunican, CJ Alpha, A Sboner, AM Sismour, C Kodira, M Egholm, GM Church, MB Gerstein*, SA Strobel* (2012). "Genomic analysis of the hydrocarbon-producing, cellulolytic, endophytic fungus Ascocoryne sarcoides." *PLoS Genet* 8: e1002558.

R Chen, GI Mias, J Li-Pook-Than, L Jiang, HY Lam, R Chen, E Miriami, KJ Karczewski, M Hariharan, FE Dewey, Y Cheng, MJ Clark, H Im, L Habegger, S Balasubramanian, M O'Huallachain, JT Dudley, S Hillenmeyer, R Haraksingh, D Sharon, G Euskirchen, P Lacroute, K Bettinger, AP Boyle, M Kasowski, F Grubert, S Seki, M Garcia, M Whirl-Carrillo, M Gallardo, MA Blasco, PL Greenberg, P Snyder, TE Klein, RB Altman, AJ Butte, EA Ashley, M Gerstein, KC Nadeau, H Tang, M Snyder (2012). "Personal omics profiling reveals dynamic molecular and medical phenotypes." *Cell* 148: 1293-307.

DG MacArthur, S Balasubramanian, A Frankish, N Huang, J Morris, K Walter, L Jostins, L Habegger, JK Pickrell, SB Montgomery, CA Albers, ZD Zhang, DF Conrad, G Lunter, H Zheng, Q Ayub, MA DePristo, E Banks, M Hu, RE Handsaker, JA Rosenfeld, M Fromer, M Jin, XJ Mu, E Khurana, K Ye, M Kay, GI Saunders, MM Suner, T Hunt, IH Barnes, C Amid, DR Carvalho-Silva, AH Bignell, C Snow, B Yngvadottir, S Bumpstead, DN Cooper, Y Xue, IG Romero, IG Romero, 1000 Genomes Project Consortium, J Wang, Y Li, RA Gibbs, SA McCarroll, ET Dermitzakis, JK Pritchard, JC Barrett, J Harrow, ME Hurles, MB Gerstein*, C Tyler-Smith* (2012). "A systematic survey of loss-of-function variants in human protein-coding genes." *Science* 335: 823-8.

G Li, X Ruan, RK Auerbach, KS Sandhu, M Zheng, P Wang, HM Poh, Y Goh, J Lim, J Zhang, HS Sim, SQ Peh, FH Mulawadi, CT Ong, YL Orlov, S Hong, Z Zhang, S Landt, D Raha, G Euskirchen, CL Wei, W Ge, H Wang, C Davis, KI Fisher-Aylor, A Mortazavi, M Gerstein, T Gingeras, B Wold, Y Sun, MJ Fullwood, E Cheung, E Liu, WK Sung, M Snyder, Y Ruan (2012). "Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation." *Cell* 148: 84-98.

J Du, J Leng, L Habegger, A Sboner, D McDermott, M Gerstein (2012). "IQSeq: integrated isoform quantification analysis based on next-generation sequencing." *PLoS One* 7: e29175.

-- 2011 --

N Bhardwaj, D Clarke, M Gerstein (2011). "Systematic control of protein interactions for systems biology." *Proc Natl Acad Sci U S A* 108: 20279-80.

HY Lam, MJ Clark, R Chen, R Chen, G Natsoulis, M O'Huallachain, FE Dewey, L Habegger, EA Ashley, MB Gerstein, AJ Butte, HP Ji, M Snyder (2011). "Performance comparison of whole-genome sequencing platforms." *Nat Biotechnol* . 30: 78-82.

D Greenbaum, A Sboner, XJ Mu, M Gerstein (2011). "Genomics and privacy: implications of the new reality of closed data for the field." *PLoS Comput Biol* 7: e1002278.

RR Haraksingh, A Abyzov, M Gerstein, AE Urban, M Snyder (2011). "Genome-wide mapping of copy number variation in humans: comparative analysis of high resolution array platforms." *PLoS One* 6: e27859.

C Cheng, KK Yan, W Hwang, J Qian, N Bhardwaj, J Rozowsky, ZJ Lu, W Niu, P Alves, M Kato, M Snyder, M Gerstein (2011). "Construction and analysis of an integrated regulatory network derived from high-throughput sequencing data." *PLoS Comput Biol* 7: e1002190.

C Cheng, C Shou, KY Yip, MB Gerstein (2011). "Genome-wide analysis of chromatin features identifies histone modification sensitive and insensitive yeast transcription factors." *Genome Biol* 12: R111.

D Greenbaum, M Gerstein (2011). "The role of cloud computing in managing the deluge of potentially private genetic data." *Am J Bioeth* 11: 39-41.

C Cheng, R Min, M Gerstein (2011). "TIP: A probabilistic method for identifying transcription factor target genes from ChIP-seq binding profiles." *Bioinformatics* 27: 3221-7.

SC Flores, MB Gerstein (2011). "Predicting protein ligand binding motions with the conformation explorer." *BMC Bioinformatics* 12: 417.

KY Yip, L Utz, S Sitwell, X Hu, SS Sidhu, BE Turk, M Gerstein, PM Kim (2011). "Identification of specificity determining residues in peptide recognition domains using an information theoretic approach applied to large-scale binding maps." *BMC Biol* 9: 53.

C Cheng, M Gerstein (2011). "Modeling the relative relationship of transcription factor binding and histone modifications to gene expression levels in mouse embryonic stem cells." *Nucleic Acids Res* 40: 553-68.

MR Tanas, A Sboner, AM Oliveira, MR Erickson-Johnson, J Hespelt, PJ Hanwright, J Flanagan, Y Luo, K Fenwick, R Natrajan, C Mitsopoulos, M Zvelebil, BL Hoch, SW Weiss, M Debiec-Rychter, R Sciot, RB West, AJ Lazar, A Ashworth, JS Reis-Filho, CJ Lord, MB Gerstein, MA Rubin, BP Rubin (2011). "Identification of a disease-defining gene fusion in epithelioid hemangioendothelioma." *Sci Transl Med* 3: 98ra82.

N Bhardwaj, A Abyzov, D Clarke, C Shou, MB Gerstein (2011). "Integration of protein motions with molecular networks reveals different mechanisms for permanent and transient interactions." *Protein Sci* 20: 1745-54.

A Sboner, XJ Mu, D Greenbaum, RK Auerbach, MB Gerstein (2011). "The real cost of sequencing: higher than you think!" *Genome Biol* 12: 125.

J Rozowsky, A Abyzov, J Wang, P Alves, D Raha, A Harmanci, J Leng, R Bjornson, Y Kong, N Kitabayashi, N Bhardwaj, M Rubin, M Snyder, M Gerstein (2011). "AlleleSeq: analysis of allele-specific expression and binding in a network framework." *Mol Syst Biol* 7: 522.

ZD Zhang, J Du, H Lam, A Abyzov, AE Urban, M Snyder, M Gerstein (2011). "Identification of genomic indels and structural variations using split reads." *BMC Genomics* 12: 375.

MB Clark, PP Amaral, FJ Schlesinger, ME Dinger, RJ Taft, JL Rinn, CP Ponting, PF Stadler, KV Morris, A Morillon, JS Rozowsky, MB Gerstein, C Wahlestedt, Y Hayashizaki, P Carninci, TR Gingeras, JS Mattick (2011). "The reality of pervasive transcription." *PLoS Biol* 9: e1000625; discussion e1001102.

KK Yan, M Gerstein (2011). "The spread of scientific information: insights from the web usage statistics in PLoS article-level metrics." *PLoS One* 6: e19917.

XJ Mu, ZJ Lu, Y Kong, HY Lam, MB Gerstein (2011). "Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project." *Nucleic Acids Res* 39: 7058-76.

D Greenbaum, M Gerstein (2011). "Social considerations in research: consider them but don't use them." *Am J Bioeth* 11: 31-2.

ENCODE Project Consortium, RM Myers, J Stamatoyannopoulos, M Snyder, I Dunham, RC Hardison, BE Bernstein, TR Gingeras, WJ Kent, E Birney, B Wold, GE Crawford (2011). "A user's guide to the encyclopedia of DNA elements (ENCODE)." *PLoS Biol* 9: e1001046.

J Fasolo, A Sboner, MG Sun, H Yu, R Chen, D Sharon, PM Kim, M Gerstein, M Snyder (2011). "Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes." *Genes Dev* 25: 767-78.

TA Gianoulis, A Agarwal, M Snyder, MB Gerstein (2011). "The CRIT framework for identifying cross patterns in systems biology and application to chemogenomics." *Genome Biol* 12: R32.

N Nègre, CD Brown, L Ma, CA Bristow, SW Miller, U Wagner, P Kheradpour, ML Eaton, P Loriaux, R Sealfon, Z Li, H Ishii, RF Spokony, J Chen, L Hwang, C Cheng, RP Auburn, MB Davis, M Domanus, PK Shah, CA Morrison, J Zieba, S Suchy, L Senderowicz, A Victorsen, NA Bild, AJ Grundstad, D Hanley, DM MacAlpine, M Mannervik, K Venken, H Bellen, R White, M Gerstein, S Russell, RL Grossman, B Ren, JW Posakony, M Kellis, KP White (2011). "A cis-regulatory map of the Drosophila genome." *Nature* 471: 527-31.

GM Euskirchen, RK Auerbach, E Davidov, TA Gianoulis, G Zhong, J Rozowsky, N Bhardwaj, MB Gerstein, M Snyder (2011). "Diverse roles and interactions of the SWI/SNF chromatin remodeling complex revealed using global approaches." *PLoS Genet* 7: e1002008.

D Lipman, P Flicek, S Salzberg, M Gerstein, R Knight (2011). "Closure of the NCBI SRA and implications for the long-term future of genomics data storage." *Genome Biol*. 2011;12 :402.

J Jee, J Rozowsky, KY Yip, L Lochovsky, R Bjornson, G Zhong, Z Zhang, Y Fu, J Wang, Z Weng, M Gerstein (2011). "ACT: aggregation and correlation toolbox for analyses of genome tracks." *Bioinformatics* 27: 1152-4.

A Karpikov, J Rozowsky, M Gerstein (2011). "Tiling array data analysis: a multiscale approach using wavelets." *BMC Bioinformatics* 12: 57.

A Abyzov, AE Urban, M Snyder, M Gerstein (2011). "CNVnator: an approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing." *Genome Res* 21: 974-84.

C Cheng, KK Yan, KY Yip, J Rozowsky, R Alexander, C Shou, M Gerstein (2011). "A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets." *Genome Biol* 12: R15.

MF Berger, MS Lawrence, F Demichelis, Y Drier, K Cibulskis, AY Sivachenko, A Sboner, R Esgueva, D Pflueger, C Sougnez, R Onofrio, SL Carter, K Park, L Habegger, L Ambrogio, T Fennell, M Parkin, G Saksena, D Voet, AH Ramos, TJ Pugh, J Wilkinson, S Fisher, W Winckler, S Mahan, K Ardlie, J Baldwin, JW Simons, N Kitabayashi, TY MacDonald, PW Kantoff, L Chin, SB Gabriel, MB Gerstein, TR Golub, M Meyerson, A Tewari, ES Lander, G Getz, MA Rubin, LA Garraway (2011). "The genomic complexity of primary human prostate cancer." *Nature* 470: 214-20.

RE Mills, K Walter, C Stewart, RE Handsaker, K Chen, C Alkan, A Abyzov, SC Yoon, K Ye, RK Cheetham, A Chinwalla, DF Conrad, Y Fu, F Grubert, I Hajirasouliha, F Hormozdiari, LM Iakoucheva, Z Iqbal, S Kang, JM Kidd, MK Konkel, J Korn, E Khurana, D Kural, HY Lam, J Leng, R Li, Y Li, CY Lin, R Luo, XJ Mu, J Nemesh, HE Peckham, T Rausch, A Scally, X Shi, MP Stromberg, AM Stütz, AE Urban, JA Walker, J Wu, Y Zhang, ZD Zhang, MA Batzer, L Ding, GT Marth, G McVean, J Sebat, M Snyder, J Wang, K Ye, EE Eichler*, MB Gerstein*, ME Hurles*, C Lee*, SA McCarroll*, JO Korbel*, 1000 Genomes Project (2011). "Mapping copy number variation by population-scale genome sequencing." *Nature* 470: 59-65.

C Shou, N Bhardwaj, HY Lam, KK Yan, PM Kim, M Snyder, MB Gerstein (2011). "Measuring the evolutionary rewiring of biological networks." *PLoS Comput Biol* 7: e1001050.

A Abyzov, M Gerstein (2011). "AGE: defining breakpoints of genomic structural variants at single-nucleotide resolution, through optimal alignments with gap excision." *Bioinformatics* 27: 595-603.

S Balasubramanian, L Habegger, A Frankish, DG MacArthur, R Harte, C Tyler-Smith, J Harrow, M Gerstein (2011). "Gene inactivation and its implications for annotation in the era of personal genomics." *Genes Dev* 25: 1-10.

FM Vaccarino, AE Urban, HE Stevens, A Szekely, A Abyzov, EL Grigorenko, M Gerstein, S Weissman (2011). "Annual Research Review: The promise of stem cell research for neuropsychiatric disorders." *J Child Psychol Psychiatry* 52: 504-16.

ZJ Lu, KY Yip, G Wang, C Shou, LW Hillier, E Khurana, A Agarwal, R Auerbach, J Rozowsky, C Cheng, M Kato, DM Miller, F Slack, M Snyder, RH Waterston, V Reinke, MB Gerstein (2011). "Prediction and characterization of noncoding RNAs in C. elegans by integrating conservation, secondary structure, and high-throughput sequencing and array data." *Genome Res* 21: 276-85.

W Niu, ZJ Lu, M Zhong, M Sarov, JI Murray, CM Brdlik, J Janette, C Chen, P Alves, E Preston, C Slightham, L Jiang, AA Hyman, SK Kim, RH Waterston, M Gerstein, M Snyder, V Reinke (2011). "Diverse transcription factor binding features revealed by genome-wide ChIP-seq in C. elegans." *Genome Res* 21: 245-54.

L Habegger, A Sboner, TA Gianoulis, J Rozowsky, A Agarwal, M Snyder, M Gerstein (2011). "RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries." *Bioinformatics* 27: 281-3.

D Pflueger, S Terry, A Sboner, L Habegger, R Esgueva, PC Lin, MA Svensson, N Kitabayashi, BJ Moss, TY MacDonald, X Cao, T Barrette, AK Tewari, MS Chee, AM Chinnaiyan, DS Rickman, F Demichelis, MB Gerstein, MA Rubin (2011). "Discovery of non-ETS gene fusions in human prostate cancer using next-generation RNA sequencing." *Genome Res* 21: 56-67.

-- 2010 --

Reproducible Research: Addressing the need for data and code sharing in computational science. Yale Law School Roundtable on Data and Code Sharing (2010) Computing in Science & Engineering 12(5): 8-13 (Sept/Oct).

MB Gerstein, ZJ Lu, EL Van Nostrand, C Cheng, BI Arshinoff, T Liu, KY Yip, R Robilotto, A Rechtsteiner, K Ikegami, P Alves, A Chateigner, M Perry, M Morris, RK Auerbach, X Feng, J Leng, A Vielle, W Niu, K Rhrissorrakrai, A Agarwal, RP Alexander, G Barber, CM Brdlik, J Brennan, JJ Brouillet, A Carr, MS Cheung, H Clawson, S Contrino, LO Dannenberg, AF Dernburg, A Desai, L Dick, AC Dosé, J Du, T Egelhofer, S Ercan, G Euskirchen, B Ewing, EA Feingold, R Gassmann, PJ Good, P Green, F Gullier, M Gutwein, MS Guyer, L Habegger, T Han, JG Henikoff, SR Henz, A Hinrichs, H Holster, T Hyman, AL Iniguez, J Janette, M Jensen, M Kato, WJ Kent, E Kephart, V Khivansara, E Khurana, JK Kim, P Kolasinska-Zwierz, EC Lai, I Latorre, A Leahey, S Lewis, P Lloyd, L Lochovsky, RF Lowdon, Y Lubling, R Lyne, M MacCoss, SD Mackowiak, M Mangone, S McKay, D Mecenas, G Merrihew, DM Miller, A Muroyama, JI Murray, SL Ooi, H Pham, T Phippen, EA Preston, N Rajewsky, G Rätsch, H Rosenbaum, J Rozowsky, K Rutherford, P Ruzanov, M Sarov, R Sasidharan, A Sboner, P Scheid, E Segal, H Shin, C Shou, FJ Slack, C Slightam, R Smith, WC Spencer, EO Stinson, S Taing, T Takasaki, D Vafeados, K Voronina, G Wang, NL Washington, CM Whittle, B Wu, KK Yan, G Zeller, Z Zha, M Zhong, X Zhou, modENCODE Consortium, J Ahringer, S Strome, KC Gunsalus, G Micklem, XS Liu, V Reinke, SK Kim, LW Hillier, S Henikoff, F Piano, M Snyder, L Stein, JD Lieb, RH Waterston (2010). "Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project." *Science* 330: 1775-87.

N Bhardwaj, PM Kim, MB Gerstein (2010). "Rewiring of transcriptional regulatory networks: hierarchy, rather than connectivity, better reflects the importance of regulators." *Sci Signal* 3: ra79.

X Li, TA Gianoulis, KY Yip, M Gerstein, M Snyder (2010). "Extensive in vivo metabolite-protein interactions revealed by large-scale systematic analyses." *Cell* 143: 639-50.

ZD Zhang, MB Gerstein (2010). "Detection of copy number variation from array intensity and sequencing read depth using a stepwise Bayesian model." *BMC Bioinformatics* 11: 539.

1000 Genomes Project Consortium, RM Durbin, GR Abecasis, DL Altshuler, A Auton, LD Brooks, RM Durbin, RA Gibbs, ME Hurles, GA McVean (2010). "A map of human genome variation from population-scale sequencing." *Nature* 467: 1061-73.

A Sboner, L Habegger, D Pflueger, S Terry, DZ Chen, JS Rozowsky, AK Tewari, N Kitabayashi, BJ Moss, MS Chee, F Demichelis, MA Rubin, MB Gerstein (2010). "FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data." *Genome Biol* 11: R104.

KH Cheung, M Samwald, RK Auerbach, MB Gerstein (2010). "Structured digital tables on the Semantic Web: toward a structured digital literature." *Mol Syst Biol* 6: 403.

RP Alexander, G Fang, J Rozowsky, M Snyder, MB Gerstein (2010). "Annotating non-coding regions of the genome." *Nat Rev Genet* 11: 559-71.

E Khurana, HY Lam, C Cheng, N Carriero, P Cayting, MB Gerstein (2010). "Segmental duplications in the human genome reveal details of pseudogene formation." *Nucleic Acids Res* 38: 6997-7007.

A Agarwal, D Koppstein, J Rozowsky, A Sboner, L Habegger, LW Hillier, R Sasidharan, V Reinke, RH Waterston, M Gerstein (2010). "Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays." *BMC Genomics* 11: 383.

ME Holford, E Khurana, KH Cheung, M Gerstein (2010). "Using semantic web rules to reason on an ontology of pseudogenes." *Bioinformatics* 26: i71-8.

N Bhardwaj, MB Carson, A Abyzov, KK Yan, H Lu, MB Gerstein (2010). "Analysis of combinatorial regulation: scaling of partnerships between regulators with the number of governed targets." *PLoS Comput Biol* 6: e1000755.

NR Voss, M Gerstein (2010). "3V: cavity, channel and cleft volume calculator and extractor." *Nucleic Acids Res* 38: W555-62.

HY Lam, PM Kim, J Mok, R Tonikian, SS Sidhu, BE Turk, M Snyder, MB Gerstein (2010). "MOTIPS: automated motif analysis for predicting targets of modular protein domains." *BMC Bioinformatics* 11: 243.

KK Yan, G Fang, N Bhardwaj, RP Alexander, M Gerstein (2010). "Comparing genomes to computer operating systems in terms of the topology and evolution of their regulatory control networks." *Proc Natl Acad Sci U S A* 107: 9186-91.

PV Patel, TA Gianoulis, RD Bjornson, KY Yip, DM Engelman, MB Gerstein (2010). "Analysis of membrane proteins in metagenomics: networks of correlated environmental features and protein families." *Genome Res* 20: 960-71.

Y Lee, X Yang, Y Huang, H Fan, Q Zhang, Y Wu, J Li, R Hasina, C Cheng, MW Lingen, MB Gerstein, RR Weichselbaum, HR Xing, YA Lussier (2010). "Network modeling identifies molecular functions targeted by miR-204 to suppress head and neck tumor metastasis." *PLoS Comput Biol* 6: e1000730.

G Fang, N Bhardwaj, R Robilotto, MB Gerstein (2010). "Getting started in gene orthology and functional analysis." *PLoS Comput Biol* 6: e1000703.

N Bhardwaj, KK Yan, MB Gerstein (2010). "Analysis of diverse regulatory networks in a hierarchical context shows consistent tendencies for collaboration in the middle levels." *Proc Natl Acad Sci U S A* 107: 6841-6.

M Kasowski, F Grubert, C Heffelfinger, M Hariharan, A Asabere, SM Waszak, L Habegger, J Rozowsky, M Shi, AE Urban, MY Hong, KJ Karczewski, W Huber, SM Weissman, MB Gerstein, JO Korbel, M Snyder (2010). "Variation in transcription factor binding among humans." *Science* 328: 232-5.

A Sboner, F Demichelis, S Calza, Y Pawitan, SR Setlur, Y Hoshida, S Perner, HO Adami, K Fall, LA Mucci, PW Kantoff, M Stampfer, SO Andersson, E Varenhorst, JE Johansson, MB Gerstein, TR Golub, MA Rubin, O Andrén (2010). "Molecular sampling of prostate cancer: a dilemma for predicting disease progression." *BMC Med Genomics* 3: 8.

ZD Zhang, A Frankish, T Hunt, J Harrow, M Gerstein (2010). "Identification and analysis of unitary pseudogenes: historic and contemporary gene losses in humans and other primates." *Genome Biol* 11: R26.

N Bhardwaj, M Gerstein, H Lu (2010). "Genome-wide sequence-based prediction of peripheral proteins using a novel semi-supervised learning technique." *BMC Bioinformatics* 11 Suppl 1: S6.

JQ Wu, L Habegger, P Noisa, A Szekely, C Qiu, S Hutchison, D Raha, M Egholm, H Lin, S Weissman, W Cui, M Gerstein, M Snyder (2010). "Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing." *Proc Natl Acad Sci U S A* 107: 5254-9.

M Snyder, J Du, M Gerstein (2010). "Personal genome sequencing: current approaches and challenges." *Genes Dev* 24: 423-31.

M Zhong, W Niu, ZJ Lu, M Sarov, JI Murray, J Janette, D Raha, KL Sheaffer, HY Lam, E Preston, C Slightham, LW Hillier, T Brock, A Agarwal, R Auerbach, AA Hyman, M Gerstein, SE Mango, SK

Kim, RH Waterston, V Reinke, M Snyder (2010). "Genome-wide identification of binding sites defines distinct functions for Caenorhabditis elegans PHA-4/FOXA in development and environmental response." *PLoS Genet* 6: e1000848.

J Mok, PM Kim, HY Lam, S Piccirillo, X Zhou, GR Jeschke, DL Sheridan, SA Parker, V Desai, M Jwa, E Cameroni, H Niu, M Good, A Remenyi, JL Ma, YJ Sheu, HE Sassi, R Sopko, CS Chan, C De Virgilio, NM Hollingsworth, WA Lim, DF Stern, B Stillman, BJ Andrews, MB Gerstein, M Snyder, BE Turk (2010). "Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation site motifs." *Sci Signal* 3: ra12.

D Raha, Z Wang, Z Moqtaderi, L Wu, G Zhong, M Gerstein, K Struhl, M Snyder (2010). "Close association of RNA polymerase II and many transcription factors with Pol III genes." *Proc Natl Acad Sci U S A* 107: 3639-44.

KY Yip, RP Alexander, KK Yan, M Gerstein (2010). "Improved reconstruction of in silico gene regulatory networks by integrating knockout and perturbation data." *PLoS One* 5: e8121.

HY Lam, XJ Mu, AM Stütz, A Tanzer, PD Cayting, M Snyder, PM Kim, JO Korbel, MB Gerstein (2010). "Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library." *Nat Biotechnol* 28: 47-55.

A Abyzov, R Bjornson, M Felipe, M Gerstein (2010). "RigidFinder: a fast and sensitive method to detect rigid blocks in large macromolecular complexes." *Proteins* 78: 309-24.

-- 2009 --

Science and the Law: Grappling with the Gulf. D Greenbaum, MB Gerstein (2009) Science 323: 210.

A Canaan, I Haviv, AE Urban, VP Schulz, S Hartman, Z Zhang, D Palejev, AB Deisseroth, J Lacy, M Snyder, M Gerstein, SM Weissman (2009). "EBNA1 regulates cellular gene expression by binding cellular promoters." *Proc Natl Acad Sci U S A* 106: 22421-6.

D Greenbaum, M Gerstein (2009). "Social networking and personal genomics: suggestions for optimizing the interaction." *Am J Bioeth* 9: 15-9.

R Tonikian, X Xin, CP Toret, D Gfeller, C Landgraf, S Panni, S Paoluzi, L Castagnoli, B Currell, S Seshagiri, H Yu, B Winsor, M Vidal, MB Gerstein, GD Bader, R Volkmer, G Cesareni, DG Drubin, PM Kim, SS Sidhu, C Boone (2009). "Bayesian modeling of the yeast SH3 domain interactome predicts spatiotemporal dynamics of endocytosis proteins." *PLoS Biol* 7: e1000218.

YJ Liu, D Zheng, S Balasubramanian, N Carriero, E Khurana, R Robilotto, MB Gerstein (2009). "Comprehensive analysis of the pseudogenes of glycolytic enzymes in vertebrates: the anomalously high number of GAPDH pseudogenes highlights a recent burst of retrotrans-positional activity." *BMC Genomics* 10: 480.

A Sboner, A Karpikov, G Chen, M Smith, D Mattoon, M Dawn, L Freeman-Cook, B Schweitzer, MB Gerstein (2009). "Robust-linear-model normalization to reduce technical variability in functional protein microarrays." *J Proteome Res* 8: 5451-64.

C Cheng, N Bhardwaj, M Gerstein (2009). "The relationship between the evolution of microRNA targets and the length of their UTRs." *BMC Genomics* 10: 431.

Y Arinaminpathy, E Khurana, DM Engelman, MB Gerstein (2009). "Computational analysis of membrane proteins: the largest class of drug targets." *Drug Discov Today* 14: 1130-5.

C Cheng, X Fu, P Alves, M Gerstein (2009). "mRNA expression profiles show differential regulatory effects of microRNAs between estrogen receptor-positive and estrogen receptor-negative breast cancer." *Genome Biol* 10: R90.

RK Auerbach, G Euskirchen, J Rozowsky, N Lamarre-Vincent, Z Moqtaderi, P Lefrançois, K Struhl, M Gerstein, M Snyder (2009). "Mapping accessible chromatin regions using Sono-Seq." *Proc Natl Acad Sci U S A* 106: 14926-31.

KY Yip, PM Kim, D McDermott, M Gerstein (2009). "Multi-level learning: improving the prediction of protein, domain and residue interactions by allowing information flow between levels." *BMC Bioinformatics* 10: 241.

A Rzhetsky, M Seringhaus, MB Gerstein (2009). "Getting started in text mining: part two." *PLoS Comput Biol* 5: e1000411.

D Pflueger, DS Rickman, A Sboner, S Perner, CJ LaFargue, MA Svensson, BJ Moss, N Kitabayashi, Y Pan, A de la Taille, R Kuefer, AK Tewari, F Demichelis, MS Chee, MB Gerstein, MA Rubin (2009). "N-myc downstream regulated gene 1 (NDRG1) is fused to ERG in prostate cancer." *Neoplasia* 11: 804-11.

X Guo, Z Zhang, MB Gerstein, D Zheng (2009). "Small RNAs originated from pseudogenes: cis- or trans-acting?" *PLoS Comput Biol* 5: e1000449.

RP Alexander, PM Kim, T Emonet, MB Gerstein (2009). "Understanding modularity in molecular networks requires dynamics." *Sci Signal* 2: pe44.

R Sasidharan, A Agarwal, J Rozowsky, M Gerstein (2009). "An approach to comparing tiling array and high throughput sequencing technologies for genomic transcript mapping." *BMC Res Notes* 2: 150.

K Talbert-Slagle, S Marlatt, FN Barrera, E Khurana, J Oates, M Gerstein, DM Engelman, AM Dixon, D Dimaio (2009). "Artificial transmembrane oncoproteins smaller than the bovine papillomavirus E5 protein redefine sequence requirements for activation of the platelet-derived growth factor beta receptor." *J Virol* 83: 9773-85.

JO Korbel, T Tirosh-Wagner, AE Urban, XN Chen, M Kasowski, L Dai, F Grubert, C Erdman, MC Gao, K Lange, EM Sobel, GM Barlow, AS Aylsworth, NJ Carpenter, RD Clark, MY Cohen, E Doran, T Falik-Zaccai, SO Lewin, IT Lott, BC McGillivray, JB Moeschler, MJ Pettenati, SM Pueschel, KW Rao, LG Shaffer, M Shohat, AJ Van Riper, D Warburton, S Weissman, MB Gerstein, M Snyder, JR Korenberg (2009). "The genetic architecture of Down syndrome phenotypes revealed by high-resolution analysis of human segmental trisomies." *Proc Natl Acad Sci U S A* 106: 12031-6.

J Du, RD Bjornson, ZD Zhang, Y Kong, M Snyder, MB Gerstein (2009). "Integrating sequencing technologies in personal genomics: optimal low cost reconstruction of structural variants." *PLoS Comput Biol* 5: e1000432.

SE Celniker, LA Dillon, MB Gerstein, KC Gunsalus, S Henikoff, GH Karpen, M Kellis, EC Lai, JD Lieb, DM MacAlpine, G Micklem, F Piano, M Snyder, L Stein, KP White, RH Waterston, modENCODE Consortium (2009). "Unlocking the secrets of the genome." *Nature* 459: 927-30.

Y Xia, EA Franzosa, MB Gerstein (2009). "Integrated assessment of genomic correlates of protein evolutionary rate." *PLoS Comput Biol* 5: e1000413.

L Ni, C Bruce, C Hart, J Leigh-Bell, D Gelperin, L Umansky, MB Gerstein, M Snyder (2009). "Dynamic and complex transcription factor binding during an inducible response in yeast." *Genes Dev* 23: 1351-63.

N Bhardwaj, M Gerstein (2009). "Relating protein conformational changes to packing efficiency and disorder." *Protein Sci* 18: 1230-40.

M Snyder, S Weissman, M Gerstein (2009). "Personal phenotypes to go with personal genomes." *Mol Syst Biol* 5: 273.

C Cheng, LM Li, P Alves, M Gerstein (2009). "Systematic identification of transcription factors associated with patient survival in cancers." *BMC Genomics* 10: 225.

Y Mishima, C Abreu-Goodger, AA Staton, C Stahlhut, C Shou, C Cheng, M Gerstein, AJ Enright, AJ Giraldez (2009). "Zebrafish miR-1 and miR-133 shape muscle gene expression and regulate sarcomeric actin organization." *Genes Dev* 23: 619-32.

JO Korbel, A Abyzov, XJ Mu, N Carriero, P Cayting, Z Zhang, M Snyder, MB Gerstein (2009). "PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data." *Genome Biol* 10: R23.

KS Keating, SC Flores, MB Gerstein, LA Kuhn (2009). "StoneHinge: hinge prediction by network analysis of individual protein structures." *Protein Sci* 18: 359-71.

TA Gianoulis, J Raes, PV Patel, R Bjornson, JO Korbel, I Letunic, T Yamada, A Paccanaro, LJ Jensen, M Snyder, P Bork, MB Gerstein (2009). "Quantifying environmental adaptation of metabolic pathways in metagenomics." *Proc Natl Acad Sci U S A* 106: 1374-9.

P Lefrançois, GM Euskirchen, RK Auerbach, J Rozowsky, T Gibson, CM Yellman, M Gerstein, M Snyder (2009). "Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing." *BMC Genomics* 10: 37.

F Demichelis, SR Setlur, R Beroukhim, S Perner, JO Korbel, CJ Lafargue, D Pflueger, C Pina, MD Hofer, A Sboner, MA Svensson, DS Rickman, A Urban, M Snyder, M Meyerson, C Lee, MB Gerstein, R Kuefer, MA Rubin (2009). "Distinct genomic aberrations associated with ERG rearranged prostate cancer." *Genes Chromosomes Cancer* 48: 366-80.

X Zhang, Z Lian, C Padden, MB Gerstein, J Rozowsky, M Snyder, TR Gingeras, P Kapranov, SM Weissman, PE Newburger (2009). "A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster." *Blood* 113: 2526-34.

S Balasubramanian, D Zheng, YJ Liu, G Fang, A Frankish, N Carriero, R Robilotto, P Cayting, M Gerstein (2009). "Comparative analysis of processed ribosomal protein pseudogenes in four mammalian genomes." *Genome Biol* 10: R2.

J Rozowsky, G Euskirchen, RK Auerbach, ZD Zhang, T Gibson, R Bjornson, N Carriero, M Snyder, MB Gerstein (2009). "PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls." *Nat Biotechnol* 27: 66-75.

SC Popescu, GV Popescu, S Bachan, Z Zhang, M Gerstein, M Snyder, SP Dinesh-Kumar (2009). "MAPK target networks in Arabidopsis thaliana revealed using functional protein microarrays." *Genes Dev* 23: 80-92.

LY Wang, A Abyzov, JO Korbel, M Snyder, M Gerstein (2009). "MSB: a mean-shift-based approach for the analysis of structural variation in the genome." *Genome Res* 19: 106-17.

Z Wang, M Gerstein, M Snyder (2009). "RNA-Seq: a revolutionary tool for transcriptomics." *Nat Rev Genet* 10: 57-63.

KY Yip, M Gerstein (2009). "Training set expansion: an approach to improving the reconstruction of biological networks from limited and uneven reliable interactions." *Bioinformatics* 25: 243-50.

HY Lam, E Khurana, G Fang, P Cayting, N Carriero, KH Cheung, MB Gerstein (2009). "Pseudofam: the pseudogene families database." *Nucleic Acids Res* 37: D738-43.

-- 2008 --

Genomics Confounds Gene Classification. M Seringhaus, M Gerstein (2008) American Scientist 96:466-473 (Nov-Dec).

M Seringhaus, J Rozowsky, T Royce, U Nagalakshmi, J Jee, M Snyder, M Gerstein (2008). "Mismatch oligonucleotides in human and yeast: guidelines for probe design on tiling microarrays." *BMC Genomics* 9: 635.

AY Yam, Y Xia, HT Lin, A Burlingame, M Gerstein, J Frydman (2008). "Defining the TRiC/CCT interactome links chaperonin function to stabilization of newly made proteins with complex topologies." *Nat Struct Mol Biol* 15: 1255-62.

D Greenbaum, J Du, M Gerstein (2008). "Genomic anonymity: have we already lost it?" *Am J Bioeth* 8: 71-4.

Y Hasin, T Olender, M Khen, C Gonzaga-Jauregui, PM Kim, AE Urban, M Snyder, MB Gerstein, D Lancet, JO Korbel (2008). "High-resolution copy-number variation map reflects human olfactory receptor diversity and evolution." *PLoS Genet* 4: e1000249.

PM Kim, HY Lam, AE Urban, JO Korbel, J Affourtit, F Grubert, X Chen, S Weissman, M Snyder, MB Gerstein (2008). "Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history." *Genome Res* 18: 1865-74.

ZD Zhang, J Rozowsky, M Snyder, J Chang, M Gerstein (2008). "Modeling ChIP sequencing in silico with applications." *PLoS Comput Biol* 4: e1000158.

R Sasidharan, A Smith, M Gerstein (2008). "Transmembrane protein oxygen content and compartmentalization of cells." *PLoS One* 3: e2726.

A Rzhetsky, M Seringhaus, M Gerstein (2008). "Seeking a new biology through text mining." *Cell* 134: 9-13.

R Sasidharan, M Gerstein (2008). "Genomics: protein fossils live on as RNA." *Nature* 453: 729-31.

JO Korbel, PM Kim, X Chen, AE Urban, S Weissman, M Snyder, MB Gerstein (2008). "The current excitement about copy-number variation: how it relates to gene duplications and protein families." *Curr Opin Struct Biol* 18: 366-74.

YJ Huang, D Hang, LJ Lu, L Tong, MB Gerstein, GT Montelione (2008). "Targeting the human cancer pathway protein interaction network by structural genomics." *Mol Cell Proteomics* 7: 2048-60.

Z Lian, A Karpikov, J Lian, MC Mahajan, S Hartman, M Gerstein, M Snyder, SM Weissman (2008). "A genomic analysis of RNA polymerase II modification and chromatin architecture related to 3' end RNA polyadenylation." *Genome Res* 18: 1224-37.

KD Mertz, F Demichelis, A Sboner, MS Hirsch, P Dal Cin, K Struckmann, M Storz, S Scherrer, DM Schmid, RT Strebel, NM Probst-Hensch, M Gerstein, H Moch, MA Rubin (2008). "Association of cytokeratin 7 and 19 expression with genomic stability and favorable prognosis in clear cell renal cell cancer." *Int J Cancer* 123: 569-76.

U Nagalakshmi, Z Wang, K Waern, C Shou, D Raha, M Gerstein, M Snyder (2008). "The transcriptional landscape of the yeast genome defined by RNA sequencing." *Science* 320: 1344-9.

SC Flores, KS Keating, J Painter, F Morcos, K Nguyen, EA Merritt, LA Kuhn, MB Gerstein (2008). "HingeMaster: normal mode hinge prediction approach and integration of complementary predictors." *Proteins* 73: 299-319.

ZD Zhang, G Weinstock, M Gerstein (2008). "Rapid evolution by positive Darwinian selection in T-cell antigen CD4 in primates." *J Mol Evol* 66: 446-56.

PE Bourne, JL Fink, M Gerstein (2008). "Open access: taking full advantage of the content." *PLoS Comput Biol* 4: e1000037.

PM Kim, A Sboner, Y Xia, M Gerstein (2008). "The role of disorder in interaction networks: a structural analysis." *Mol Syst Biol* 4: 179.

M Seringhaus, M Gerstein (2008). "Manually structured digital abstracts: a scaffold for automatic text mining." *FEBS Lett* 582: 1170.

DS Johnson, W Li, DB Gordon, A Bhattacharjee, B Curry, J Ghosh, L Brizuela, JS Carroll, M Brown, P Flicek, CM Koch, I Dunham, M Bieda, X Xu, PJ Farnham, P Kapranov, DA Nix, TR Gingeras, X Zhang, H Holster, N Jiang, RD Green, JS Song, SA McCuine, E Anton, L Nguyen, ND Trinklein, Z Ye, K Ching, D Hawkins, B Ren, PC Scacheri, J Rozowsky, A Karpikov, G Euskirchen, S Weissman, M Gerstein, M Snyder, A Yang, Z Moqtaderi, H Hirsch, HP Shulha, Y Fu, Z Weng, K Struhl, RM Myers, JD Lieb, XS Liu (2008). "Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets." *Genome Res* 18: 393-403.

MR Seringhaus, PD Cayting, MB Gerstein (2008). "Uncovering trends in gene naming." *Genome Biol* 9: 401.

JQ Wu, J Du, J Rozowsky, Z Zhang, AE Urban, G Euskirchen, S Weissman, M Gerstein, M Snyder (2008). "Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome." *Genome Biol* 9: R3.

ZD Zhang, P Cayting, G Weinstock, M Gerstein (2008). "Analysis of nuclear receptor pseudogenes in vertebrates: how the silent tell their stories." *Mol Biol Evol* 25: 131-43.

KY Yip, P Patel, PM Kim, DM Engelman, D McDermott, M Gerstein (2008). "An integrated system for studying residue coevolution in proteins." *Bioinformatics* 24: 290-2.

-- 2007 --

Semantic Web Approach to Database Integration in the Life Sciences. KH Cheung, AK Smith, KYL Yip, CJO Baker, MB Gerstein (2007) in Semantic Web: Revolutionizing Knowledge Discovery in the Life Sciences (eds. C Baker and K Cheung, Springer, NY), pp. 11-30. Semantic Web Standards: Legal and Social Issues and Implications. D Greenbaum, M Gerstein (2007) in Semantic Web: Revolutionizing Knowledge Discovery in the Life Sciences (eds. C Baker and K Cheung, Springer, NY), pp. 413-433.

PM Kim, JO Korbel, MB Gerstein (2007). "Positive selection at the protein network periphery: evaluation in terms of structural constraints and cellular context." *Proc Natl Acad Sci U S A* 104: 20274-9.

SR Setlur, TE Royce, A Sboner, JM Mosquera, F Demichelis, MD Hofer, KD Mertz, M Gerstein, MA Rubin (2007). "Integrative microarray analysis of pathways dysregulated in metastatic prostate cancer." *Cancer Res* 67: 10296-303.

A Smith, K Cheung, M Krauthammer, M Schultz, M Gerstein (2007). "Leveraging the structure of the Semantic Web to enhance information retrieval for proteomics." *Bioinformatics* 23: 3073-9.

AJ McClellan, Y Xia, AM Deutschbauer, RW Davis, M Gerstein, J Frydman (2007). "Diverse cellular functions of the Hsp90 molecular chaperone uncovered using systems approaches." *Cell* 131: 121-35.

JO Korbel, AE Urban, JP Affourtit, B Godwin, F Grubert, JF Simons, PM Kim, D Palejev, NJ Carriero, L Du, BE Taillon, Z Chen, A Tanzer, AC Saunders, J Chi, F Yang, NP Carter, ME Hurles, SM Weissman, TT Harkins, MB Gerstein, M Egholm, M Snyder (2007). "Paired-end mapping reveals extensive structural variation in the human genome." *Science* 318: 420-6.

EZ Yu, AE Burba, M Gerstein (2007). "PARE: a tool for comparing protein abundance and mRNA expression data." *BMC Bioinformatics* 8: 309.

AR Borneman, TA Gianoulis, ZD Zhang, H Yu, J Rozowsky, MR Seringhaus, LY Wang, M Gerstein, M Snyder (2007). "Divergence of transcription factor binding sites across related yeast species." *Science* 317: 815-9.

S Orchard, L Salwinski, S Kerrien, L Montecchi-Palazzi, M Oesterheld, V Stümpflen, A Ceol, A Chatr-aryamontri, J Armstrong, P Woollard, JJ Salama, S Moore, J Wojcik, GD Bader, M Vidal, ME Cusick, M Gerstein, AC Gavin, G Superti-Furga, J Greenblatt, J Bader, P Uetz, M Tyers, P Legrain, S Fields, N Mulder, M Gilson, M Niepmann, L Burgoon, J De Las Rivas, C Prieto, VM Perreau, C Hogue, HW Mewes, R Apweiler, I Xenarios, D Eisenberg, G Cesareni, H Hermjakob (2007). "The minimum information required for reporting a molecular interaction experiment (MIMIx)." *Nat Biotechnol* 25: 894-8.

TE Royce, JS Rozowsky, MB Gerstein (2007). "Toward a universal microarray: prediction of gene expression through nearest-neighbor probe sequence identification." *Nucleic Acids Res* 35: e99.

AR Borneman, ZD Zhang, J Rozowsky, MR Seringhaus, M Gerstein, M Snyder (2007). "Transcription factor binding site identification in yeast: a comparison of high-density oligonucleotide and PCR-based microarray platforms." *Funct Integr Genomics* 7: 335-45.

SC Flores, MB Gerstein (2007). "FlexOracle: predicting flexible hinges by identification of stable domains." *BMC Bioinformatics* 8: 215.

LJ Lu, A Sboner, YJ Huang, HX Lu, TA Gianoulis, KY Yip, PM Kim, GT Montelione, MB Gerstein (2007). "Comparing classical pathways and modern networks: towards the development of an edge ontology." *Trends Biochem Sci* 32: 320-31.

ENCODE Project Consortium (2007). "Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project." *Nature* 447: 799-816.

GM Euskirchen, JS Rozowsky, CL Wei, WH Lee, ZD Zhang, S Hartman, O Emanuelsson, V Stolc, S Weissman, MB Gerstein, Y Ruan, M Snyder (2007). "Mapping of transcription factor binding regions in mammalian cells by ChIP: comparison of array- and sequencing-based technologies." *Genome Res* 17: 898-909.

S Washietl, JS Pedersen, JO Korbel, C Stocsits, AR Gruber, J Hackermüller, J Hertel, M Lindemeyer, K Reiche, A Tanzer, C Ucla, C Wyss, SE Antonarakis, F Denoeud, J Lagarde, J Drenkow, P Kapranov, TR Gingeras, R Guigó, M Snyder, MB Gerstein, A Reymond, IL Hofacker, PF Stadler (2007). "Structured RNAs in the ENCODE selected regions of the human genome." *Genome Res* 17: 852-64.

D Zheng, A Frankish, R Baertsch, P Kapranov, A Reymond, SW Choo, Y Lu, F Denoeud, SE Antonarakis, M Snyder, Y Ruan, CL Wei, TR Gingeras, R Guigó, J Harrow, MB Gerstein (2007). "Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution." *Genome Res* 17: 839-51.

ZD Zhang, A Paccanaro, Y Fu, S Weissman, Z Weng, J Chang, M Snyder, MB Gerstein (2007). "Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions." *Genome Res* 17: 787-97.

JS Rozowsky, D Newburger, F Sayward, J Wu, G Jordan, JO Korbel, U Nagalakshmi, J Yang, D Zheng, R Guigó, TR Gingeras, S Weissman, P Miller, M Snyder, MB Gerstein (2007). "The DART classification of unannotated transcription within the ENCODE regions: associating transcription with known and novel loci." *Genome Res* 17: 732-45.

ND Trinklein, U Karaöz, J Wu, A Halees, S Force Aldred, PJ Collins, D Zheng, ZD Zhang, MB Gerstein, M Snyder, RM Myers, Z Weng (2007). "Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome." *Genome Res* 17: 720-31.

MB Gerstein, C Bruce, JS Rozowsky, D Zheng, J Du, JO Korbel, O Emanuelsson, ZD Zhang, S Weissman, M Snyder (2007). "What is a gene, post-ENCODE? History and updated definition." *Genome Res* 17: 669-81.

TE Royce, NJ Carriero, MB Gerstein (2007). "An efficient pseudomedian filter for tiling microrrays." *BMC Bioinformatics* 8: 186.

JO Korbel, AE Urban, F Grubert, J Du, TE Royce, P Starr, G Zhong, BS Emanuel, SM Weissman, M Snyder, MB Gerstein (2007). "Systematic prediction and validation of breakpoints associated with copy-number variants in the human genome." *Proc Natl Acad Sci U S A* 104: 10110-5.

H Yu, R Jansen, G Stolovitzky, M Gerstein (2007). "Total ancestry measure: quantifying the similarity in tree-like classification, with genomic applications." *Bioinformatics* 23: 2163-73.

L Wu, SI Hwang, K Rezaul, LJ Lu, V Mayya, M Gerstein, JK Eng, DH Lundgren, DK Han (2007). "Global survey of human T leukemic cells by integrating proteomics and transcriptomics profiling." *Mol Cell Proteomics* 6: 1343-53.

SC Flores, LJ Lu, J Yang, N Carriero, MB Gerstein (2007). "Hinge Atlas: relating protein sequence to sites of structural flexibility." *BMC Bioinformatics* 8: 167.

ZD Zhang, J Rozowsky, HY Lam, J Du, M Snyder, M Gerstein (2007). "Tilescope: online analysis pipeline for high-density tiling microarray data." *Genome Biol* 8: R81.

M Gerstein, M Seringhaus, S Fields (2007). "Structured digital abstract makes text mining easy." *Nature* 447: 142.

AK Smith, KH Cheung, KY Yip, M Schultz, MK Gerstein (2007). "LinkHub: a Semantic Web system that facilitates cross-database queries and information retrieval in proteomics." *BMC Bioinformatics* 8 Suppl 3: S5.

X Zhu, M Gerstein, M Snyder (2007). "Getting connected: analysis and principles of biological networks." *Genes Dev* 21: 1010-24.

M Gerstein, SM Douglas (2007). "RNAi development." *PLoS Comput Biol* 3: e80.

H Yu, PM Kim, E Sprecher, V Trifonov, M Gerstein (2007). "The importance of bottlenecks in protein networks: correlation with gene essentiality and expression dynamics." *PLoS Comput Biol* 3: e59.

TE Royce, JS Rozowsky, MB Gerstein (2007). "Assessing the need for sequence-based normalization in tiling microarray experiments." *Bioinformatics* 23: 988-97.

D Zheng, MB Gerstein (2007). "The ambiguous boundary between genes and pseudogenes: the dead rise up, or do they?" *Trends Genet* 23: 219-24.

L Li, X Wang, R Sasidharan, V Stolc, W Deng, H He, J Korbel, X Chen, W Tongprasit, P Ronald, R Chen, M Gerstein, XW Deng (2007). "Global identification and characterization of transcriptionally active regions in the rice genome." *PLoS One* 2: e294.

SC Popescu, GV Popescu, S Bachan, Z Zhang, M Seay, M Gerstein, M Snyder, SP Dinesh-Kumar (2007). "Differential binding of calmodulin-related proteins to their targets revealed through high-density Arabidopsis protein microarrays." *Proc Natl Acad Sci U S A* 104: 4730-5.

MG Smith, TA Gianoulis, S Pukatzki, JJ Mekalanos, LN Ornston, M Gerstein, M Snyder (2007). "New insights into Acinetobacter baumannii pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis." *Genes Dev* 21: 601-14.

Z Zhang, AW Pang, M Gerstein (2007). "Comparative analysis of genome tiling array data reveals many novel primate-specific functional RNAs in human." *BMC Evol Biol* 7 Suppl 1: S14.

MR Seringhaus, MB Gerstein (2007). "Publishing perishing? Towards tomorrow's information architecture." *BMC Bioinformatics* 8: 17.

M Seringhaus, M Gerstein (2007). "Chemistry Nobel rich in structure." *Science* 315: 40-1.

H Yu, K Nguyen, T Royce, J Qian, K Nelson, M Snyder, M Gerstein (2007). "Positional artifacts in microarrays: experimental verification and construction of COP, an automated detection tool." *Nucleic Acids Res* 35: e8.

O Emanuelsson, U Nagalakshmi, D Zheng, JS Rozowsky, AE Urban, J Du, Z Lian, V Stolc, S Weissman, M Snyder, MB Gerstein (2007). "Assessing the performance of different high-density tiling microarray strategies for mapping transcribed regions of the human genome." *Genome Res* 17: 886-97.

JE Karro, Y Yan, D Zheng, Z Zhang, N Carriero, P Cayting, P Harrrison, M Gerstein (2007). "Pseudogene.org: a comprehensive database and comparison platform for pseudogene annotation." *Nucleic Acids Res* 35: D55-60.

M Gerstein, D Greenbaum, K Cheung, PL Miller (2007). "An interdepartmental Ph.D. program in computational biology and bioinformatics: the Yale perspective." *J Biomed Inform* 40: 73-9.

-- 2006 --

The Death of the Scientific Paper. Seringhaus M, Gerstein M (2006). The Scientist. 20(9): 25. Analytical Evolutionary Model for Protein Fold Occurrence in Genomes, Accounting for the Effects of Gene Duplication, Deletion, Acquisition and Selective Pressure. M Kamal, N Luscombe, J Qian, M Gerstein (2006) in Power Laws, Scale-Free Networks and Genome Biology (edited by EV Koonin, YI Wolf, GP Karev; Springer, New York), pages 165-193.

J Rozowsky, J Wu, Z Lian, U Nagalakshmi, JO Korbel, P Kapranov, D Zheng, S Dyke, P Newburger, P Miller, TR Gingeras, S Weissman, M Gerstein, M Snyder (2006). "Novel transcribed regions in the human genome." *Cold Spring Harb Symp Quant Biol* 71: 111-6.

PM Kim, LJ Lu, Y Xia, MB Gerstein (2006). "Relating three-dimensional structures to protein networks provides evolutionary insights." *Science* 314: 1938-41.

A Smith, M Gerstein (2006). "Data mining on the web." *Science* 314: 1682; author reply 1682.

Y Liu, J Li, L Sam, CS Goh, M Gerstein, YA Lussier (2006). "An integrative genomic approach to uncover molecular mechanisms of prokaryotic traits." *PLoS Comput Biol* 2: e159.

X Zhu, M Gerstein, M Snyder (2006). "ProCAT: a data analysis approach for protein microarrays." *Genome Biol* 7: R110.

LY Wang, M Snyder, M Gerstein (2006). "BoCaTFBS: a boosted cascade learner to refine the binding sites suggested by ChIP-chip experiments." *Genome Biol* 7: R102.

AE Burba, U Lehnert, EZ Yu, M Gerstein (2006). "Helix Interaction Tool (HIT): a web-based tool for analysis of helix-helix interactions in proteins." *Bioinformatics* 22: 2735-8.

J Du, JS Rozowsky, JO Korbel, ZD Zhang, TE Royce, MH Schultz, M Snyder, M Gerstein (2006). "A supervised hidden markov model framework for efficiently segmenting tiling array data in transcriptional and chIP-chip experiments: systematically incorporating validated biological knowledge." *Bioinformatics* 22: 3016-24.

CS Goh, TA Gianoulis, Y Liu, J Li, A Paccanaro, YA Lussier, M Gerstein (2006). "Integration of curated databases to identify genotype-phenotype associations." *BMC Genomics* 7: 257.

KY Yip, H Yu, PM Kim, M Schultz, M Gerstein (2006). "The tYNA platform for comparative interactomics: a web tool for managing, comparing and mining multiple networks." *Bioinformatics* 22: 2968-70.

H Yu, M Gerstein (2006). "Genomic analysis of the hierarchical structure of regulatory networks." *Proc Natl Acad Sci U S A* 103: 14724-31.

T Srikantha, AR Borneman, KJ Daniels, C Pujol, W Wu, MR Seringhaus, M Gerstein, S Yi, M Snyder, DR Soll (2006). "TOS9 regulates white-opaque switching in Candida albicans." *Eukaryot Cell* 5: 1674-87.

TE Royce, JS Rozowsky, NM Luscombe, O Emanuelsson, H Yu, X Zhu, M Snyder, MB Gerstein (2006). "Extrapolating traditional DNA microarray statistics to tiling and protein microarray technologies." *Methods Enzymol* 411: 282-311.

R Pinard, A de Winter, GJ Sarkis, MB Gerstein, KR Tartaro, RN Plant, M Egholm, JM Rothberg, JH Leamon (2006). "Assessment of whole genome amplification-induced bias through high-throughput, massively parallel whole genome sequencing." *BMC Genomics* 7: 216.

D Zheng, MB Gerstein (2006). "A computational approach for identifying pseudogenes in the ENCODE regions." *Genome Biol* 7 Suppl 1: S13.1-10.

M Seringhaus, A Paccanaro, A Borneman, M Snyder, M Gerstein (2006). "Predicting essential genes in fungal genomes." *Genome Res* 16: 1126-35.

M Gerstein, D Zheng (2006). "The real life of pseudogenes." *Sci Am* 295: 48-55.

H Yu, Y Xia, V Trifonov, M Gerstein (2006). "Design principles of molecular networks revealed by global comparisons and composite motifs." *Genome Biol* 7: R55.

NR Voss, M Gerstein, TA Steitz, PB Moore (2006). "The geometry of the ribosomal polypeptide exit tunnel." *J Mol Biol* 360: 893-906.

M Seringhaus, A Kumar, J Hartigan, M Snyder, M Gerstein (2006). "Genomic analysis of insertion behavior and target specificity of mini-Tn7 and Tn3 transposons in Saccharomyces cerevisiae." *Nucleic Acids Res* 34: e57.

M Gerstein (2006). "Tools needed to navigate landscape of the genome." *Nature* 440: 740.

Z Zhang, N Carriero, D Zheng, J Karro, PM Harrison, M Gerstein (2006). "PseudoPipe: an automated pseudogene identification pipeline." *Bioinformatics* 22: 1437-9.

NJ Krogan, G Cagney, H Yu, G Zhong, X Guo, A Ignatchenko, J Li, S Pu, N Datta, AP Tikuisis, T Punna, JM Peregrín-Alvarez, M Shales, X Zhang, M Davey, MD Robinson, A Paccanaro, JE Bray, A Sheung, B Beattie, DP Richards, V Canadien, A Lalev, F Mena, P Wong, A Starostine, MM Canete, J Vlasblom, S Wu, C Orsi, SR Collins, S Chandran, R Haw, JJ Rilstone, K Gandi, NJ Thompson, G Musso, P St Onge, S Ghanny, MH Lam, G Butland, AM Altaf-Ul, S Kanaya, A Shilatifard, E O'Shea, JS Weissman, CJ Ingles, TR Hughes, J Parkinson, M Gerstein, SJ Wodak, A Emili, JF Greenblatt (2006). "Global landscape of protein complexes in the yeast Saccharomyces cerevisiae." *Nature* 440: 637-43.

AE Urban, JO Korbel, R Selzer, T Richmond, A Hacker, GV Popescu, JF Cubells, R Green, BS Emanuel, MB Gerstein, SM Weissman, M Snyder (2006). "High-resolution mapping of DNA copy alterations in human chromosome 22 using high-density tiling oligonucleotide arrays." *Proc Natl Acad Sci U S A* 103: 4534-9.

H Yu, A Paccanaro, V Trifonov, M Gerstein (2006). "Predicting interactions in protein networks by completing defective cliques." *Bioinformatics* 22: 823-9.

AR Borneman, JA Leigh-Bell, H Yu, P Bertone, M Gerstein, M Snyder (2006). "Target hub proteins serve as master regulators of development in yeast." *Genes Dev* 20: 435-48.

Y Xia, LJ Lu, M Gerstein (2006). "Integrated prediction of the helical membrane protein interactome in yeast." *J Mol Biol* 357: 339-49.

S Flores, N Echols, D Milburn, B Hespenheide, K Keating, J Lu, S Wells, EZ Yu, M Thorpe, M Gerstein (2006). "The Database of Macromolecular Motions: new features added at the decade mark." *Nucleic Acids Res* 34: D296-301.

P Bertone, V Trifonov, JS Rozowsky, F Schubert, O Emanuelsson, J Karro, MY Kao, M Snyder, M Gerstein (2006). "Design optimization methods for genomic DNA tiling arrays." *Genome Res* 16: 271-81.

-- 2005 --

Inferring Protein-Protein Interactions Using Interaction Network Topologies. A Paccanaro, V Trifonov, H Yu, M Gerstein (2005). International Joint Conference on Neural Networks (IJCNN, Jul. 31-Aug. 4, Montreal, Canada), pages 161 - 166, vol. 1. Protein Interaction Prediction by Integrating Genomic Features and Protein Interaction Network Analysis. LJ Lu, Y Xia, H Yu, A Rives, H Lu, F Schubert, M Gerstein (2005). Data Analysis and Visualization in Genomics and Proteomics (Wiley, NY).

DM Gelperin, MA White, ML Wilkinson, Y Kon, LA Kung, KJ Wise, N Lopez-Hoyo, L Jiang, S Piccirillo, H Yu, M Gerstein, ME Dumont, EM Phizicky, M Snyder, EJ Grayhack (2005). "Biochemical and genetic analysis of the yeast proteome with a movable ORF collection." *Genes Dev* 19: 2816-26.

J Ptacek, G Devgan, G Michaud, H Zhu, X Zhu, J Fasolo, H Guo, G Jona, A Breitkreutz, R Sopko, RR McCartney, MC Schmidt, N Rachidi, SJ Lee, AS Mah, L Meng, MJ Stark, DF Stern, C De Virgilio, M Tyers, B Andrews, M Gerstein, B Schweitzer, PF Predki, M Snyder (2005). "Global analysis of protein phosphorylation in yeast." *Nature* 438: 679-84.

SE Hartman, P Bertone, AK Nath, TE Royce, M Gerstein, S Weissman, M Snyder (2005). "Global changes in STAT target selection and transcription regulation upon interferon treatments." *Genes Dev* 19: 2953-68.

V Stolc, L Li, X Wang, X Li, N Su, W Tongprasit, B Han, Y Xue, J Li, M Snyder, M Gerstein, J Wang, XW Deng (2005). "A pilot study of transcription unit analysis in rice using oligonucleotide tiling-path microarray." *Plant Mol Biol* 59: 137-49.

A Smith, D Greenbaum, SM Douglas, M Long, M Gerstein (2005). "Network security and data integrity in academia: an assessment and a proposal for large-scale archiving." *Genome Biol* 6: 119.

SM Douglas, GT Montelione, M Gerstein (2005). "PubNet: a flexible system for visualizing literature derived networks." *Genome Biol* 6: R80.

T Coric, D Zheng, M Gerstein, CM Canessa (2005). "Proton sensitivity of ASIC1 appeared with the rise of fishes by changes of residues in the region that follows TM1 in the ectodomain of the channel." *J Physiol* 568: 725-35.

LJ Lu, Y Xia, A Paccanaro, H Yu, M Gerstein (2005). "Assessing the limits of genomic data integration for predicting protein networks." *Genome Res* 15: 945-53.

TE Royce, JS Rozowsky, P Bertone, M Samanta, V Stolc, S Weissman, M Snyder, M Gerstein (2005). "Issues in the analysis of oligonucleotide tiling microarrays for transcript mapping." *Trends Genet* 21: 466-75.

KH Cheung, KY Yip, A Smith, R Deknikker, A Masiar, M Gerstein (2005). "YeastHub: a semantic web use case for integrating data in the life sciences domain." *Bioinformatics* 21 Suppl 1: i85-96.

D Zheng, Z Zhang, PM Harrison, J Karro, N Carriero, M Gerstein (2005). "Integrated pseudogene annotation for human chromosome 22: evidence for transcription." *J Mol Biol* 349: 27-45.

P Bertone, M Gerstein, M Snyder (2005). "Applications of DNA tiling arrays to experimental genome annotation and regulatory pathway discovery." *Chromosome Res* 13: 259-74.

Y Gilad, SA Rifkin, P Bertone, M Gerstein, KP White (2005). "Multi-species microarrays reveal the effect of sequence divergence on gene expression profiles." *Genome Res* 15: 674-80.

PM Harrison, D Zheng, Z Zhang, N Carriero, M Gerstein (2005). "Transcribed processed pseudogenes in the human genome: an intermediate form of expressed retrosequence lacking protein-coding ability." *Nucleic Acids Res* 33: 2374-83.

D Huber, D Boyd, Y Xia, MH Olma, M Gerstein, J Beckwith (2005). "Use of thioredoxin as a reporter to identify a subset of Escherichia coli signal sequences that promote signal recognition particle-dependent translocation." *J Bacteriol* 187: 2983-91.

TB Acton, KC Gunsalus, R Xiao, LC Ma, J Aramini, MC Baran, YW Chiang, T Climent, B Cooper, NG Denissova, SM Douglas, JK Everett, CK Ho, D Macapagal, PK Rajan, R Shastry, LY Shih, GV Swapna, M Wilson, M Wu, M Gerstein, M Inouye, JF Hunt, GT Montelione (2005). "Robotic cloning and Protein Production Platform of the Northeast Structural Genomics Consortium." *Methods Enzymol* 394: 210-43.

S Balasubramanian, Y Xia, E Freinkman, M Gerstein (2005). "Sequence variation in G-protein-coupled receptors: analysis of single nucleotide polymorphisms." *Nucleic Acids Res* 33: 1710-21.

H Grosshans, T Johnson, KL Reinert, M Gerstein, FJ Slack (2005). "The temporal patterning microRNA let-7 regulates several transcription factors at the larval to adult transition in C. elegans." *Dev Cell* 8: 321-30.

V Alexandrov, U Lehnert, N Echols, D Milburn, D Engelman, M Gerstein (2005). "Normal modes for predicting protein motions: a comprehensive database assessment and associated Web tool." *Protein Sci* 14: 633-43.

NR Voss, M Gerstein (2005). "Calculation of standard atomic volumes for RNA and comparison with proteins: RNA is packed more tightly." *J Mol Biol* 346: 477-92.

D Greenbaum, A Smith, M Gerstein (2005). "Impediments to database interoperation: legal issues and security concerns." *Nucleic Acids Res* 33: D3-4.

N Carriero, MV Osier, KH Cheung, PL Miller, M Gerstein, H Zhao, B Wu, S Rifkin, J Chang, H Zhang, K White, K Williams, M Schultz (2005). "A high productivity/low maintenance approach to high-performance computation for biomedicine: four case studies." *J Am Med Inform Assoc* 12: 90-8.

-- 2004 --

An XML-Based Approach to Integrating Heterogeneous Yeast Genome Data. KH Cheung, D Pan, A Smith, M Seringhaus, SM Douglas, M Gerstein. 2004 International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS); pp 236-242.

U Lehnert, Y Xia, TE Royce, CS Goh, Y Liu, A Senes, H Yu, ZL Zhang, DM Engelman, M Gerstein (2004). "Computational analysis of membrane proteins: genomic occurrence, structure prediction and helix interactions." *Q Rev Biophys* 37: 121-46.

EJ White, O Emanuelsson, D Scalzo, T Royce, S Kosak, EJ Oakeley, S Weissman, M Gerstein, M Groudine, M Snyder, D Schübeler (2004). "DNA replication-timing analysis of human chromosome 22 at high resolution and different developmental states." *Proc Natl Acad Sci U S A* 101: 17771-6.

P Berman, P Bertone, B Dasgupta, M Gerstein, MY Kao, M Snyder (2004). "Fast optimal genome tiling with applications to microarray design and homology search." *J Comput Biol* 11: 766-85.

P Bertone, V Stolc, TE Royce, JS Rozowsky, AE Urban, X Zhu, JL Rinn, W Tongprasit, M Samanta, S Weissman, M Gerstein*, M Snyder* (2004). "Global identification of human transcribed sequences with genome tiling arrays." *Science* 306: 2242-6.

ENCODE Project Consortium (2004). "The ENCODE (ENCyclopedia Of DNA Elements) Project." *Science* 306: 636-40.

N Lin, B Wu, R Jansen, M Gerstein, H Zhao (2004). "Information assessment on predicting protein-protein interactions." *BMC Bioinformatics* 5: 154.

DA Hall, H Zhu, X Zhu, T Royce, M Gerstein, M Snyder (2004). "Regulation of gene expression by a metabolic enzyme." *Science* 306: 482-4.

A Kumar, M Seringhaus, MC Biery, RJ Sarnovsky, L Umansky, S Piccirillo, M Heidtman, KH Cheung, CJ Dobry, MB Gerstein, NL Craig, M Snyder (2004). "Large-scale mutagenesis of the yeast genome using a Tn7-derived multipurpose transposon." *Genome Res* 14: 1975-86.

R Jansen, M Gerstein (2004). "Analyzing protein function on a genomic scale: the importance of gold-standard positives and negatives for network prediction." *Curr Opin Microbiol* 7: 535-45.

NM Luscombe, MM Babu, H Yu, M Snyder, SA Teichmann, M Gerstein (2004). "Genomic analysis of regulatory network dynamics reveals large topological changes." *Nature* 431: 308-12.

Y Liu, PM Harrison, V Kunin, M Gerstein (2004). "Comprehensive analysis of pseudogenes in prokaryotes: widespread gene decay and failure of putative horizontally transferred genes." *Genome Biol* 5: R64.

Z Zhang, M Gerstein (2004). "Large-scale analysis of pseudogenes in the human genome." *Curr Opin Genet Dev* 14: 328-35.

Z Wunderlich, TB Acton, J Liu, G Kornhaber, J Everett, P Carter, N Lan, N Echols, M Gerstein, B Rost, GT Montelione (2004). "The protein target list of the Northeast Structural Genomics Consortium." *Proteins* 56: 181-7.

MM Babu, NM Luscombe, L Aravind, M Gerstein, SA Teichmann (2004). "Structure and evolution of transcriptional regulatory networks." *Curr Opin Struct Biol* 14: 283-91.

Y Xia, H Yu, R Jansen, M Seringhaus, S Baxter, D Greenbaum, H Zhao, M Gerstein (2004). "Analyzing cellular biochemistry in terms of molecular networks." *Annu Rev Biochem* 73: 1051-87.

JL Rinn, JS Rozowsky, IJ Laurenzi, PH Petersen, K Zou, W Zhong, M Gerstein, M Snyder (2004). "Major molecular differences between mammalian sexes are involved in drug metabolism and renal function." *Dev Cell* 6: 791-800.

D Greenbaum, SM Douglas, A Smith, J Lim, M Fischer, M Schultz, M Gerstein (2004). "Computer security in academia-a potential roadblock to distributed annotation of the human genome." *Nat Biotechnol* 22: 771-2.

H Yu, NM Luscombe, HX Lu, X Zhu, Y Xia, JD Han, N Bertin, S Chung, M Vidal, M Gerstein (2004). "Annotation transfer between genomes: protein-protein interologs and protein-DNA regulogs." *Genome Res* 14: 1107-18.

H Yu, D Greenbaum, H Xin Lu, X Zhu, M Gerstein (2004). "Genomic analysis of essentiality within protein networks." *Trends Genet* 20: 227-31.

LL Freeman-Cook, AM Dixon, JB Frank, Y Xia, L Ely, M Gerstein, DM Engelman, D DiMaio (2004). "Selection and characterization of small random transmembrane proteins that bind and activate the platelet-derived growth factor beta receptor." *J Mol Biol* 338: 907-20.

CS Goh, D Milburn, M Gerstein (2004). "Conformational changes associated with protein-protein interactions." *Curr Opin Struct Biol* 14: 104-9.

G Euskirchen, TE Royce, P Bertone, R Martone, JL Rinn, FK Nelson, F Sayward, NM Luscombe, P Miller, M Gerstein, S Weissman, M Snyder (2004). "CREB binds to multiple loci on human chromosome 22." *Mol Cell Biol* 24: 3804-14.

R Das, M Gerstein (2004). "A method using active-site sequence conservation to find functional shifts in protein families: application to the enzymes of central metabolism, leading to the identification of an anomalous isocitrate dehydrogenase in pathogens." *Proteins* 55: 455-63.

M Gerstein, N Echols (2004). "Exploring the range of protein flexibility, from a structural proteomics perspective." *Curr Opin Chem Biol* 8: 14-9.

Y Liu, M Gerstein, DM Engelman (2004). "Transmembrane protein domains rarely use covalent domain recombination as an evolutionary mechanism." *Proc Natl Acad Sci U S A* 101: 3495-7.

Z Zhang, N Carriero, M Gerstein (2004). "Comparative analysis of processed pseudogenes in the mouse and human genomes." *Trends Genet* 20: 62-7.

CS Goh, N Lan, SM Douglas, B Wu, N Echols, A Smith, D Milburn, GT Montelione, H Zhao, M Gerstein (2004). "Mining the structural genomics pipeline: identification of protein properties that affect high-throughput experimental analysis." *J Mol Biol* 336: 115-30.

H Yu, X Zhu, D Greenbaum, J Karro, M Gerstein (2004). "TopNet: a tool for comparing biological sub-networks, correlating protein properties with topological statistics." *Nucleic Acids Res* 32: 328-37.

V Alexandrov, M Gerstein (2004). "Using 3D Hidden Markov Models that explicitly represent spatial coordinates to model and compare protein structures." *BMC Bioinformatics* 5: 2.

S Li, CM Armstrong, N Bertin, H Ge, S Milstein, M Boxem, PO Vidalain, JD Han, A Chesneau, T Hao, DS Goldberg, N Li, M Martinez, JF Rual, P Lamesch, L Xu, M Tewari, SL Wong, LV Zhang, GF Berriz, L Jacotot, P Vaglio, J Reboul, T Hirozane-Kishikawa, Q Li, HW Gabel, A Elewa, B Baumgartner, DJ Rose, H Yu, S Bosak, R Sequerra, A Fraser, SE Mango, WM Saxton, S Strome, S Van Den Heuvel, F Piano, J Vandenhaute, C Sardet, M Gerstein, L Doucette-Stamm, KC Gunsalus, JW Harper, ME Cusick, FP Roth, DE Hill, M Vidal (2004). "A map of the interactome network of the metazoan C. elegans." *Science* 303: 540-3.

-- 2003 --

WG Krebs, J Tsai, V Alexandrov, J Junker, R Jansen, M Gerstein (2003). "Tools and databases to analyze protein flexibility; approaches to mapping implied features onto sequences." *Methods Enzymol* 374: 544-84.

D Greenbaum, J Lim, M Gerstein (2003). "An analysis of the present system of scientific publishing: what's wrong and where to go from here" *Interdisc Sci Rev* 28: 293-302.

Z Lian, G Euskirchen, J Rinn, R Martone, P Bertone, S Hartman, T Royce, K Nelson, F Sayward, N Luscombe, J Yang, JL Li, P Miller, AE Urban, M Gerstein, S Weissman, M Snyder (2003).

"Identification of novel functional elements in the human genome." *Cold Spring Harb Symp Quant Biol* 68: 317-22.

Y Kluger, H Yu, J Qian, M Gerstein (2003). "Relationship between gene co-expression and probe localization on microarray slides." *BMC Genomics* 4: 49.

Z Zhang, PM Harrison, Y Liu, M Gerstein (2003). "Millions of years of evolution preserved: a comprehensive catalog of the processed pseudogenes in the human genome." *Genome Res* 13: 2541-58.

Y Jiao, H Yang, L Ma, N Sun, H Yu, T Liu, Y Gao, H Gu, Z Chen, M Wada, M Gerstein, H Zhao, LJ Qu, XW Deng (2003). "A genome-wide analysis of blue-light regulation of Arabidopsis transcription factor gene expression during seedling development." *Plant Physiol* 133: 1480-93.

Z Zhang, M Gerstein (2003). "Reconstructing genetic networks in yeast." *Nat Biotechnol* 21: 1295-7.

PM Harrison, N Carriero, Y Liu, M Gerstein (2003). "A "polyORFomic" analysis of prokaryote genomes using disabled-homology filtering reveals conserved but undiscovered short ORFs." *J Mol Biol* 333: 885-92.

R Jansen, H Yu, D Greenbaum, Y Kluger, NJ Krogan, S Chung, A Emili, M Snyder, JF Greenblatt, M Gerstein (2003). "A Bayesian networks approach for predicting protein-protein interactions from genomic data." *Science* 302: 449-53.

J Qian, J Lin, NM Luscombe, H Yu, M Gerstein (2003). "Prediction of regulatory networks: genome-wide identification of transcription factor targets from gene expression data." *Bioinformatics* 19: 1917-26.

R Martone, G Euskirchen, P Bertone, S Hartman, TE Royce, NM Luscombe, JL Rinn, FK Nelson, P Miller, M Gerstein, S Weissman, M Snyder (2003). "Distribution of NF-kappaB-binding sites across human chromosome 22." *Proc Natl Acad Sci U S A* 100: 12247-52.

Z Zhang, M Gerstein (2003). "Patterns of nucleotide substitution, insertion and deletion in the human genome inferred from pseudogenes." *Nucleic Acids Res* 31: 5338-48.

D Greenbaum, C Colangelo, K Williams, M Gerstein (2003). "Comparing protein abundance and mRNA expression levels on a genomic scale." *Genome Biol* 4: 117.

D Greenbaum, M Gerstein (2003). "A universal legal framework as a prerequisite for database interoperability." *Nat Biotechnol* 21: 979-82.

Z Zhang, M Gerstein (2003). "The human genome has 49 cytochrome c pseudogenes, including a relic of a primordial gene that still functions in mouse." *Gene* 312: 61-72.

H Yu, NM Luscombe, J Qian, M Gerstein (2003). "Genomic analysis of gene expression relationships in transcriptional regulatory networks." *Trends Genet* 19: 422-7.

J Qian, Y Kluger, H Yu, M Gerstein (2003). "Identification and correction of spurious spatial correlations in microarray data." *Biotechniques* 35: 42-4, 46, 48.

M Gerstein, JM Thornton (2003). "Sequences and topology." *Curr Opin Struct Biol* 13: 341-3.

NM Luscombe, TE Royce, P Bertone, N Echols, CE Horak, JT Chang, M Snyder, M Gerstein (2003). "ExpressYourself: A modular platform for processing and visualizing microarray data." *Nucleic Acids Res* 31: 3477-82.

Z Zhang, M Gerstein (2003). "Of mice and men: phylogenetic footprinting aids the discovery of regulatory elements." *J Biol* 2: 11.

PM Harrison, M Gerstein (2003). "A method to assess compositional bias in biological sequences and its application to prion-like glutamine/asparagine-rich domains in eukaryotic proteomes." *Genome Biol* 4: R40.

MS Kimber, F Vallee, S Houston, A Necakov, T Skarina, E Evdokimova, S Beasley, D Christendat, A Savchenko, CH Arrowsmith, M Vedadi, M Gerstein, AM Edwards (2003). "Data mining

crystallization databases: knowledge-based approaches to optimize protein crystal screens." *Proteins* 51: 562-8.

CS Goh, N Lan, N Echols, SM Douglas, D Milburn, P Bertone, R Xiao, LC Ma, D Zheng, Z Wunderlich, T Acton, GT Montelione, M Gerstein (2003). "SPINE 2: a system for collaborative structural proteomics within a federated database framework." *Nucleic Acids Res* 31: 2833-8.

Z Zhang, M Gerstein (2003). "Identification and characterization of over 100 mitochondrial ribosomal protein pseudogenes in the human genome." *Genomics* 81: 468-80.

M Snyder, M Gerstein (2003). "Genomics. Defining genes in the genomics era." *Science* 300: 258-60.

R Jansen, HJ Bussemaker, M Gerstein (2003). "Revisiting the codon adaptation index from a whole-genome perspective: analyzing the relationship between gene expression and codon occurrence in yeast using a variety of models." *Nucleic Acids Res* 31: 2242-51.

Y Kluger, R Basri, JT Chang, M Gerstein (2003). "Spectral biclustering of microarray data: coclustering genes and conditions." *Genome Res* 13: 703-16.

M Gerstein, A Edwards, CH Arrowsmith, GT Montelione (2003). "Structural genomics: current progress." *Science* 299: 1663.

JL Rinn, G Euskirchen, P Bertone, R Martone, NM Luscombe, S Hartman, PM Harrison, FK Nelson, P Miller, M Gerstein, S Weissman, M Snyder (2003). "The transcriptional activity of human Chromosome 22." *Genes Dev* 17: 529-40.

PM Harrison, D Milburn, Z Zhang, P Bertone, M Gerstein (2003). "Identification of pseudogenes in the Drosophila melanogaster genome." *Nucleic Acids Res* 31: 1033-7.

A Savchenko, A Yee, A Khachatryan, T Skarina, E Evdokimova, M Pavlova, A Semesi, J Northey, S Beasley, N Lan, R Das, M Gerstein, CH Arrowmith, AM Edwards (2003). "Strategies for structural proteomics of prokaryotes: Quantifying the advantages of studying orthologous proteins and of using both NMR and X-ray crystallography approaches." *Proteins* 50: 392-9.

N Lan, GT Montelione, M Gerstein (2003). "Ontologies for proteomics: towards a systematic definition of structure and function that scales to the genome level." *Curr Opin Chem Biol* 7: 44-54.

N Echols, D Milburn, M Gerstein (2003). "MolMovDB: analysis and visualization of conformational change and structural flexibility." *Nucleic Acids Res* 31: 478-82.

-- 2002 --

J Tsai, M Gerstein (2002). "Calculations of protein volumes: sensitivity analysis and parameter database." *Bioinformatics* 18: 985-95.

A Kumar, S Agarwal, JA Heyman, S Matson, M Heidtman, S Piccirillo, L Umansky, A Drawid, R Jansen, Y Liu, KH Cheung, P Miller, M Gerstein, GS Roeder, M Snyder (2002). "Subcellular localization of the yeast proteome." *Genes Dev* 16: 707-19.

D Greenbaum, R Jansen, M Gerstein (2002). "Analysis of mRNA expression and protein abundance data: an approach for the comparison of the enrichment of features in the cellular population of proteins and transcripts." *Bioinformatics* 18: 585-96.

H Hegyi, J Lin, D Greenbaum, M Gerstein (2002). "Structural genomics analysis: characteristics of atypical, common, and horizontally transferred folds." *Proteins* 47: 126-41.

P Harrison, A Kumar, N Lan, N Echols, M Snyder, M Gerstein (2002). "A small reservoir of disabled ORFs in the yeast genome and its implications for the dynamics of proteome evolution." *J Mol Biol* 316: 409-19.

PM Harrison, M Gerstein (2002). "Studying genomes through the aeons: protein families, pseudogenes and proteome evolution." *J Mol Biol* 318: 1155-74.

PM Harrison, A Kumar, N Lang, M Snyder, M Gerstein (2002). "A question of size: the eukaryotic proteome and the problems in defining it." *Nucleic Acids Res* 30: 1083-90.

PM Harrison, H Hegyi, S Balasubramanian, NM Luscombe, P Bertone, N Echols, T Johnson, M Gerstein (2002). "Molecular fossils in the human genome: identification and analysis of the pseudogenes in chromosomes 21 and 22." *Genome Res* 12: 272-80.

R Jansen, D Greenbaum, M Gerstein (2002). "Relating whole-genome expression data with protein-protein interactions." *Genome Res* 12: 37-46.

M Gerstein, N Lan, R Jansen (2002). "Proteomics. Integrating interactomes." *Science* 295: 284-7.

Towards a systematic definition of protein function that scales to the genome level: Defining function in terms of interactions. N Lan, R Jansen, M Gerstein (2002). Proceedings of the IEEE 90:1848-1858 .

M Gerstein, J Junker (2002). "Blurring the boundaries between scientific 'papers' and biological databases" *Nature Yearbook of Science and Technology* : 210-212 (ed. D Butler, Palgrave Macmillan Publishers).

Fast optimal genome tiling with applications to microarray design and homology search. P Berman, P Bertone, B DasGupta, M Gerstein, M-Y Kao, M Snyder. (2002) Proceedings of the 2nd International Workshop on Algorithms in Bioinformatics. Springer-Verlag LNCS 2452: 419-433 .

R Jansen, N Lan, J Qian, M Gerstein (2002). "Integration of genomic datasets to predict protein complexes in yeast." *J Struct Funct Genomics* 2: 71-81.

CE Horak, NM Luscombe, J Qian, P Bertone, S Piccirrillo, M Gerstein, M Snyder (2002). "Complex transcriptional circuitry at the G1/S transition in Saccharomyces cerevisiae." *Genes Dev* 16: 3017-33.

KH Cheung, K White, J Hager, M Gerstein, V Reinke, K Nelson, P Masiar, R Srivastava, Y Li, J Li, H Zhao, J Li, DB Allison, M Snyder, P Miller, K Williams (2002). "YMD: a microarray database for large-scale gene expression analysis." *Proc AMIA Symp* : 140-4.

D Schneider, Y Liu, M Gerstein, DM Engelman (2002). "Thermostability of membrane protein helix-helix interaction elucidated by statistical analysis." *FEBS Lett* 532: 231-6.

A Mateos, J Dopazo, R Jansen, Y Tu, M Gerstein, G Stolovitzky (2002). "Systematic learning of gene functional classes from DNA array expression data by using multilayer perceptrons." *Genome Res* 12: 1703-15.

ZL Zhang, PM Harrison, M Gerstein (2002). "Digging deep for ancient relics: a survey of protein motifs in the intergenic sequences of four eukaryotic genomes." *J Mol Biol* 323: 811-22.

J Lin, J Qian, D Greenbaum, P Bertone, R Das, N Echols, A Senes, B Stenger, M Gerstein (2002). "GeneCensus: genome comparisons in terms of metabolic pathway activity and protein family sharing." *Nucleic Acids Res* 30: 4574-82.

Z Lian, Y Kluger, DS Greenbaum, D Tuck, M Gerstein, N Berliner, SM Weissman, PE Newburger (2002). "Genomic and proteomic analysis of the myeloid differentiation program: global analysis of gene expression during induced differentiation in the MPRO cell line." *Blood* 100: 3209-20.

Y Liu, DM Engelman, M Gerstein (2002). "Genomic analysis of membrane protein families: abundance and conserved motifs." *Genome Biol* 3: research0054.

Z Zhang, P Harrison, M Gerstein (2002). "Identification and analysis of over 2000 ribosomal protein pseudogenes in the human genome." *Genome Res* 12: 1466-82.

AM Edwards, B Kus, R Jansen, D Greenbaum, J Greenblatt, M Gerstein (2002). "Bridging structural biology and genomics: assessing protein interaction data with known complexes." *Trends Genet* 18: 529-36.

WG Krebs, V Alexandrov, CA Wilson, N Echols, H Yu, M Gerstein (2002). "Normal mode analysis of macromolecular motions in a database framework: developing mode concentration as a useful classifying statistic." *Proteins* 48: 682-95.

NM Luscombe, J Qian, Z Zhang, T Johnson, M Gerstein (2002). "The dominance of the population by a selected few: power-law behaviour applies to a wide variety of genomic properties." *Genome Biol* 3: RESEARCH0040.

G Giaever, AM Chu, L Ni, C Connelly, L Riles, S Véronneau, S Dow, A Lucau-Danila, K Anderson, B André, AP Arkin, A Astromoff, M El-Bakkoury, R Bangham, R Benito, S Brachat, S Campanaro, M Curtiss, K Davis, A Deutschbauer, KD Entian, P Flaherty, F Foury, DJ Garfinkel, M Gerstein, D Gotte, U Güldener, JH Hegemann, S Hempel, Z Herman, DF Jaramillo, DE Kelly, SL Kelly, P Kötter, D LaBonte, DC Lamb, N Lan, H Liang, H Liao, L Liu, C Luo, M Lussier, R Mao, P Menard, SL Ooi, JL Revuelta, CJ Roberts, M Rose, P Ross-Macdonald, B Scherens, G Schimmack, B Shafer, DD Shoemaker, S Sookhai-Mahadeo, RK Storms, JN Strathern, G Valle, M Voet, G Volckaert, CY Wang, TR Ward, J Wilhelmy, EA Winzeler, Y Yang, G Yen, E Youngman, K Yu, H Bussey, JD Boeke, M Snyder, P Philippsen, RW Davis, M Johnston (2002). "Functional profiling of the Saccharomyces cerevisiae genome." *Nature* 418: 387-91.

S Balasubramanian, P Harrison, H Hegyi, P Bertone, N Luscombe, N Echols, P McGarvey, Z Zhang, M Gerstein (2002). "SNPs on human chromosomes 21 and 22 -- analysis in terms of protein features and pseudogenes." *Pharmacogenomics* 3: 393-402.

N Echols, P Harrison, S Balasubramanian, NM Luscombe, P Bertone, Z Zhang, M Gerstein (2002). "Comprehensive analysis of amino acid and nucleotide composition in eukaryotic genomes, comparing genes and pseudogenes." *Nucleic Acids Res* 30: 2515-23.

CE Horak, MC Mahajan, NM Luscombe, M Gerstein, SM Weissman, M Snyder (2002). "GATA-1 binding sites mapped in the beta-globin locus by using mammalian chIp-chip analysis." *Proc Natl Acad Sci U S A* 99: 2924-9.

Y Liu, NM Luscombe, V Alexandrov, P Bertone, P Harrison, Z Zhang, M Gerstein (2002). "Structural genomics: a new era for pharmaceutical research." *Genome Biol* 3: REPORTS4004.

A Kumar, PM Harrison, KH Cheung, N Lan, N Echols, P Bertone, P Miller, MB Gerstein, M Snyder (2002). "An integrated approach for finding overlooked genes in yeast." *Nat Biotechnol* 20: 58-63.

-- 2001 --

J Qian, NM Luscombe, M Gerstein (2001). "Protein family and fold occurrence in genomes: power-law behaviour and evolutionary model." *J Mol Biol* 313: 673-81.

J Qian, M Dolled-Filhart, J Lin, H Yu, M Gerstein (2001). "Beyond synexpression relationships: local clustering of time-shifted and inverted gene expression profiles identifies new, biologically relevant interactions." *J Mol Biol* 314: 1053-66.

H Hegyi, M Gerstein (2001). "Annotation transfer for genomics: measuring functional divergence in multi-domain proteins." *Genome Res* 11: 1632-40.

NM Luscombe, D Greenbaum, M Gerstein (2001). "What is bioinformatics? A proposed definition and overview of the field." *Methods Inf Med* 40: 346-58.

R Das, J Junker, D Greenbaum, MB Gerstein (2001). "Global perspectives on proteins: comparing genomes in terms of folds, pathways and beyond." *Pharmacogenomics J* 1: 115-25.

H Zhu, M Bilgin, R Bangham, D Hall, A Casamayor, P Bertone, N Lan, R Jansen, S Bidlingmaier, T Houfek, T Mitchell, P Miller, RA Dean, M Gerstein, M Snyder (2001). "Global analysis of protein activities using proteome chips." *Science* 293: 2101-5.

V Alexandrov, M Gerstein (2001). "Calculating populations of subcellular compartments using density matrix formalism" *International Journal of Quantum Chemistry* 85: 693-696.

WK Olson, M Bansal, SK Burley, RE Dickerson, M Gerstein, SC Harvey, U Heinemann, XJ Lu, S Neidle, Z Shakked, H Sklenar, M Suzuki, CS Tung, E Westhof, C Wolberger, HM Berman (2001). "A standard reference frame for the description of nucleic acid base-pair geometry." *J Mol Biol* 313: 229-37.

J Tsai, N Voss, M Gerstein (2001). "Determining the minimum number of types necessary to represent the sizes of protein atoms." *Bioinformatics* 17: 949-56.

D Greenbaum, NM Luscombe, R Jansen, J Qian, M Gerstein (2001). "Interrelating different types of genomic data, from proteome to secretome: 'oming in on function." *Genome Res* 11: 1463-8.

M Gerstein, F M Richards (2001). "Protein Geometry: Distances, Areas, and Volumes" *International Tables for Crystallography* : (Volume F, Chapter 22.1.1, pages 531-539; M Rossmann & E Arnold, editors; Dordrecht: Kluwer).

P Harrison, M Gerstein (2001). " A Bauhaus for Biologists: An Introduction to Protein Architecture by A. M. Lesk" *Trends Biochem Sci* 26: 204-205.

P Bertone, M Gerstein (2001). "Integrative data mining: the new direction in bioinformatics." *IEEE Eng Med Biol Mag* 20: 33-40.

Z Lian, L Wang, S Yamaga, W Bonds, Y Beazer-Barclay, Y Kluger, M Gerstein, PE Newburger, N Berliner, SM Weissman (2001). "Genomic and proteomic analysis of the myeloid differentiation program." *Blood* 98: 513-24.

YV Subrahmanyam, S Yamaga, Y Prashar, HH Lee, NP Hoe, Y Kluger, M Gerstein, JD Goguen, PE Newburger, SM Weissman (2001). "RNA expression patterns change dramatically in human neutrophils exposed to bacteria." *Blood* 97: 2457-68.

P Bertone, Y Kluger, N Lan, D Zheng, D Christendat, A Yee, AM Edwards, CH Arrowsmith, GT Montelione, M Gerstein (2001). "SPINE: an integrated tracking database and data mining approach for identifying feasible targets in high-throughput structural proteomics." *Nucleic Acids Res* 29: 2884-98.

M Gerstein, B Honig (2001). "Sequences and Topology" *Current Opinion in Structural Biology* 11: 327-329.

N Luscombe, D Greenbaum, M Gerstein (2001). "What is Bioinformatics? A Proposed Definition and Overview of the Field" *Intl. Medical Informatics Association* : (Yearbook, Pages 83-99).

PM Harrison, N Echols, MB Gerstein (2001). "Digging for dead genes: an analysis of the characteristics of the pseudogene population in the Caenorhabditis elegans genome." *Nucleic Acids Res* 29: 818-30.

J Qian, B Stenger, CA Wilson, J Lin, R Jansen, SA Teichmann, J Park, WG Krebs, H Yu, V Alexandrov, N Echols, M Gerstein (2001). "PartsList: a web-based system for dynamically ranking protein folds based on disparate attributes, including whole-genome expression and interaction information." *Nucleic Acids Res* 29: 1750-64.

An XML Application for Genomic Data Interoperation. Cheung KH, Liu Y, Kumar K, Snyder M, Gerstein M, Miller P. IEEE International Symposium on Bio-Informatics and Biomedical Engineering (BIBE) 2001, pp. 97-103 .

-- 2000 --

M Gerstein (2000). "Integrative database analysis in structural genomics." *Nat Struct Biol* 7 Suppl: 960-3.

R Das, H Hegyi, M Gerstein (2000). "Genome analyses of spirochetes: a study of the protein structures, functions and metabolic pathways in Treponema pallidum and Borrelia burgdorferi." *J Mol Microbiol Biotechnol* 2: 387-92.

D Christendat, A Yee, A Dharamsi, Y Kluger, M Gerstein, CH Arrowsmith, AM Edwards (2000). "Structural proteomics: prospects for high throughput sample preparation." *Prog Biophys Mol Biol* 73: 339-45.

H Zhu, JF Klemic, S Chang, P Bertone, A Casamayor, KG Klemic, D Smith, M Gerstein, MA Reed, M Snyder (2000). "Analysis of yeast protein kinases using protein chips." *Nat Genet* 26: 283-9.

A Drawid, R Jansen, M Gerstein (2000). "Genome-wide analysis relating expression level with protein subcellular localization." *Trends Genet* 16: 426-30.

M Gerstein, R Jansen (2000). "The current excitement in bioinformatics-analysis of whole-genome expression data: how does it relate to protein structure and function?" *Curr Opin Struct Biol* 10: 574-84.

R Das, M Gerstein (2000). "The stability of thermophilic proteins: a study based on comprehensive genome comparison." *Funct Integr Genomics* 1: 76-88.

GJ Naylor, M Gerstein (2000). "Measuring shifts in function and evolutionary opportunity using variability profiles: a case study of the globins." *J Mol Evol* 51: 223-33.

D Christendat, A Yee, A Dharamsi, Y Kluger, A Savchenko, JR Cort, V Booth, CD Mackereth, V Saridakis, I Ekiel, G Kozlov, KL Maxwell, N Wu, LP McIntosh, K Gehring, MA Kennedy, AR Davidson, EF Pai, M Gerstein, AM Edwards, CH Arrowsmith (2000). "Structural proteomics of an archaeon." *Nat Struct Biol* 7: 903-9.

A Drawid, M Gerstein (2000). "A Bayesian system integrating expression data with sequence patterns for localizing proteins: comprehensive application to the yeast genome." *J Mol Biol* 301: 1059-75.

S Balasubramanian, T Schneider, M Gerstein, L Regan (2000). "Proteomics of Mycoplasma genitalium: identification and characterization of unannotated and atypical proteins in a small model genome." *Nucleic Acids Res* 28: 3075-82.

M Gerstein, J Lin, H Hegyi (2000). "Protein folds in the worm genome." *Pac Symp Biocomput* : 30-41.

M Gerstein (2000). "Annotation of the human genome." *Science* 288: 1590.

J Lin, M Gerstein (2000). "Whole-genome trees based on the occurrence of folds and orthologs: implications for comparing genomes on different levels." *Genome Res* 10: 808-18.

WG Krebs, M Gerstein (2000). "The morph server: a standardized system for analyzing and visualizing macromolecular motions in a database framework." *Nucleic Acids Res* 28: 1665-75.

A Senes, M Gerstein, DM Engelman (2000). "Statistical analysis of amino acid patterns in transmembrane helices: the GxxxG motif occurs frequently and in association with beta-branched residues at neighboring positions." *J Mol Biol* 296: 921-36.

CA Wilson, J Kreychman, M Gerstein (2000). "Assessing annotation transfer for genomics: quantifying the relations between protein sequence, structure and function through traditional and probabilistic scores." *J Mol Biol* 297: 233-49.

R Jansen, M Gerstein (2000). "Analysis of the yeast transcriptome with structural and functional categories: characterizing highly expressed proteins." *Nucleic Acids Res* 28: 1481-8.

-- 1999 --

P Ross-Macdonald, PS Coelho, T Roemer, S Agarwal, A Kumar, R Jansen, KH Cheung, A Sheehan, D Symoniatis, L Umansky, M Heidtman, FK Nelson, H Iwasaki, K Hager, M Gerstein, P Miller, GS Roeder, M Snyder (1999). "Large-scale analysis of the yeast genome by transposon tagging and gene disruption." *Nature* 402: 413-8.

M Gerstein, C Chothia (1999). "Perspectives: signal transduction. Proteins in motion." *Science* 285: 1682-3.

M Gerstein, R Jansen, T Johnson, J Tsai, W Krebs (1999). " Motions in a Database Framework: from Structure to Sequence" *Rigidity Theory and Applications* : 401-442 (ed. M F Thorpe and P M Duxbury, Kluwer Academic/Plenum Publishers).

M Gerstein (1999). "E-publishing on the Web: promises, pitfalls, and payoffs for bioinformatics." *Bioinformatics* 15: 429-31.

ES Brodkin, M Gerstein (1999). ""E-biomed" and clinical research." *N Engl J Med* 341: 1080; author reply 1081.

J Tsai, R Taylor, C Chothia, M Gerstein (1999). "The packing density in proteins: standard radii and volumes." *J Mol Biol* 290: 253-66.

SA Teichmann, C Chothia, M Gerstein (1999). "Advances in structural genomics." *Curr Opin Struct Biol* 9: 390-9.

M Gerstein (1999). "Building the future of biocomputing." *Nature* 399: 101.

H Hegyi, M Gerstein (1999). "The relationship between protein structure and function: a comprehensive survey with application to the yeast genome." *J Mol Biol* 288: 147-64.

M Gerstein (1999). "Forging links in an electronic paper chain." *Nature* 398: 20.

-- 1998 --

M Gerstein, H Hegyi (1998). "Comparing genomes in terms of protein structure: surveys of a finite parts list." *FEMS Microbiol Rev* 22: 277-304.

M Gerstein (1998). "How representative are the known structures of the proteins in a complete genome? A comprehensive structural census." *Fold Des* 3: 497-512.

M Gerstein (1998). "Patterns of protein-fold usage in eight microbial genomes: a comprehensive structural census." *Proteins* 33: 518-34.

M Gerstein, M Levitt (1998). "Simulating water and the molecules of life." *Sci Am* 279: 100-5.

M Gerstein (1998). "Measurement of the effectiveness of transitive sequence comparison, through a third 'intermediate' sequence." *Bioinformatics* 14: 707-14.

M Gerstein, W Krebs (1998). "A database of macromolecular motions." *Nucleic Acids Res* 26: 4280-90.

J Fu, M Gerstein, PR David, AL Gnatt, DA Bushnell, AM Edwards, RD Kornberg (1998). "Repeated tertiary fold of RNA polymerase II and implications for DNA binding." *J Mol Biol* 280: 317-22.

M Levitt, M Gerstein (1998). "A unified statistical framework for sequence comparison and structure comparison." *Proc Natl Acad Sci U S A* 95: 5913-20.

M Gerstein, M Levitt (1998). "Comprehensive assessment of automatic structural alignment against a manual standard, the scop classification of proteins." *Protein Sci* 7: 445-56.

-- 1997 --

M Gerstein (1997). "A structural census of genomes: comparing bacterial, eukaryotic, and archaeal genomes in terms of protein structure." *J Mol Biol* 274: 562-76.

M Gerstein, M Levitt (1997). "A structural census of the current population of protein sequences." *Proc Natl Acad Sci U S A* 94: 11911-6.

C Chothia, M Gerstein (1997). "Protein evolution. How far can sequences diverge?" *Nature* 385: 579, 581.

M Levitt, M Gerstein, E Huang, S Subbiah, J Tsai (1997). "Protein folding: the endgame." *Annu Rev Biochem* 66: 549-79.

R Schmidt, M Gerstein, RB Altman (1997). "LPFC: an Internet library of protein family core structures." *Protein Sci* 6: 246-8.

-- 1996 --

R Becker, M Gerstein (1996). Practicing Cyberlaw in the Year 2000. *New Jersey Lawyer Magazine* 179: 12-27 (September).

J Tsai, M Gerstein, M Levitt (1996). Keeping the Shape but Changing the Charges: A Simulation Study of Urea and its Isosteric Analogues. *Journal of Chemical Physics* 104: 9417-9430.

M Gerstein, C Chothia (1996). "Packing at the protein-water interface." *Proc Natl Acad Sci U S A* 93: 10167-72.

M Gerstein, M Levitt (1996). "Using iterative dynamic programming to obtain accurate pairwise and multiple alignments of protein structures." *Proc Int Conf Intell Syst Mol Biol* 4: 59-67.

-- 1995 --

M Gerstein, RB Altman (1995). "Using a measure of structural variation to define a core for the globins." *Comput Appl Biosci* 11: 633-44.

M Suzuki, M Gerstein (1995). "Binding geometry of alpha-helices that recognize DNA." *Proteins* 23: 525-35.

M Gerstein, RB Altman (1995). "Average core structures and variability measures for protein families: application to the immunoglobulins." *J Mol Biol* 251: 161-75.

M Gerstein, J Tsai, M Levitt (1995). "The volume of atoms on the protein surface: calculated from simulation, using Voronoi polyhedra." *J Mol Biol* 249: 955-66.

RB Altman, C Hughes, MB Gerstein (1995). "Methods for displaying macromolecular structural uncertainty: application to the globins." *J Mol Graph* 13: 142-52, 109-2.

M Suzuki, N Yagi, M Gerstein (1995). "DNA recognition and superstructure formation by helix-turn-helix proteins." *Protein Eng* 8: 329-38.

M Suzuki, SE Brenner, M Gerstein, N Yagi (1995). "DNA recognition code of transcription factors." *Protein Eng* 8: 319-28.

-- 1994 --

Purcell's early work on NMR: Contingency versus Inevitability . M Gerstein (1994) American Journal of Physics 62: 596-601.

M Suzuki, M Gerstein, N Yagi (1994). "Stereochemical basis of DNA recognition by Zn fingers." *Nucleic Acids Res* 22: 3397-405.

Y Harpaz, M Gerstein, C Chothia (1994). "Volume changes on protein folding." *Structure* 2: 641-9.

M Gerstein, AM Lesk, C Chothia (1994). "Structural mechanisms for domain movements in proteins." *Biochemistry* 33: 6739-49.

M Suzuki, D Neuhaus, M Gerstein, S Aimoto (1994). "Solution structure of the DNA binding octapeptide repeat of the K10 gene product." *Protein Eng* 7: 461-70.

M Gerstein, EL Sonnhammer, C Chothia (1994). "Volume changes in protein evolution." *J Mol Biol* 236: 1067-78.

RB Altman, M Gerstein (1994). "Finding an average core structure: application to the globins." *Proc Int Conf Intell Syst Mol Biol* 2: 19-27.

-- 1993 --

Simulation of Water around a Model Protein Helix. 1. Two-dimensional Projections of Solvent Structure. M Gerstein, R Lynden-Bell (1993) Journal of Physical Chemistry 97: 2982-2991. Simulation of Water around a Model Protein Helix. 2. The Relative Contributions of Packing, Hydrophobicity, and Hydrogen Bonding. M Gerstein, R Lynden-Bell (1993) Journal of Physical Chemistry 97: 2991-2999..

M Gerstein, BF Anderson, GE Norris, EN Baker, AM Lesk, C Chothia (1993). "Domain closure in lactoferrin. Two hinges produce a see-saw motion between alternative close-packed interfaces." *J Mol Biol* 234: 357-72.

M Suzuki, M Gerstein, T Johnson (1993). "An NMR study on the DNA-binding SPKK motif and a model for its interaction with DNA." *Protein Eng* 6: 565-74.

M Gerstein, RM Lynden-Bell (1993). "What is the natural boundary of a protein in solution?" *J Mol Biol* 230: 641-50.

M Gerstein, G Schulz, C Chothia (1993). "Domain closure in adenylate kinase. Joints on either side of two helices close like neighboring fingers." *J Mol Biol* 229: 494-501.

S Subramaniam, M Gerstein, D Oesterhelt, R Henderson (1993). "Electron diffraction analysis of structural changes in the photocycle of bacteriorhodopsin." *EMBO J* 12: 1-8.

-- 1992 --

A Resolution-Sensitive Procedure for Comparing Protein Surfaces and its Application to the Comparison of Antigen-Combining Sites. M Gerstein (1992) Acta Crystallographica A48: 271-276.

I De Baere, L Liu, L Moens, J Van Beeumen, C Gielens, J Richelle, C Trotman, J Finch, M Gerstein, M Perutz (1992). "Polar zipper sequence in the high-affinity hemoglobin of Ascaris suum: amino acid sequence and structural interpretation." *Proc Natl Acad Sci U S A* 89: 4638-42.

-- 1991 --

M Gerstein, C Chothia (1991). "Analysis of protein loop closure. Two types of hinges produce one motion in lactate dehydrogenase." *J Mol Biol* 220: 133-49.

-- 1987 --

Inverse Problem for Synchrotron Radiation in the Presence of Noise. N Fisch, A Kritz, M Gerstein (1987) Proceedings of the Sixth Joint Workshop on Electron Cyclotron Emission and Electron Cyclotron Resonance Heating. (eds. A Riviere, A Costley), 23-30 (Oxford, 16-17 September).

Notes on Scientific Publications
(As of 31 Dec. 2019)

a) <u>In total</u>, 580 scientific publication.
Not including in press or submitted articles or popular pieces, such as 12 published newspaper Op-Eds. This list does include a few significant CS-oriented conference papers but other than that mostly excludes conference procedings and workshops.

b) <u>H-index</u> for M Gerstein is 166
(according to Google Scholar, scholar.google.com/citations?user=YvjuUugAAAAJ)

c) <u>Highly Cited Researchers (HCR)</u> list inclusion.
On Thomson Reuters list, in 2014 to 2016. On succeeding Clarivate list, in 2017 to 2019.

d) <u>Senior Author Status</u>.
In the publication list, if M Gerstein is not a last or first author, he is **not** considered to be a "corresponding" or "senior" author except as noted by the asterisks (*) in the list below:

Li… PsychENCODE Consortium… Sanders, Sullivan,
      Gerstein*, Lein*, Knowles*, Sestan* ('18). *Science* 362: 1264

Carlyle... Sestan, **Gerstein***, Nairn* ('18). *J Proteome Res* 17: 3431

Sudmant… 1000 Genomes Project, Mills*, **Gerstein***, Bashir*, Stegle*, Devine*, Lee*, Eichler*,
      Korbel* ('15). *Nature* 526: 75

Abyzov... Urban*, **Gerstein***, Vaccarino* ('12) *Nature* 492: 438

Gianoulis... **Gerstein***, Strobel* ('12). *PLoS Genet* 8: e1002558

MacArthur... 1000 Genomes Project... **Gerstein***, Tyler-Smith* ('12). *Science* 335: 823

Mills... Eichler*, **Gerstein***, Hurles*, Lee*, McCarroll*, Korbel*,
      1000 Genomes Project ('11). *Nature* 470: 59

Bertone... **Gerstein***, Snyder* ('04). *Science* 306: 2242