

## Main Scientific Publications

(See footnotes at end of the publication section)

### -- 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 Manakongtreeeep, 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.

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.

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 Uszczyńska-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 Laukitis, 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 Flück (2018). "Repeat associated mechanisms of genome evolution and function revealed by the *Mus caroli*" *Genome Res* 28: 448-459.

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MJ Gandal, JR Haney, NN Parkshak, 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.

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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 Ammour, 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.

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- 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.
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- 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.
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## -- 2015 --

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

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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.

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## Notes on Scientific Publications

(As of 1 Jan. 2019)

a) In total, 562 scientific publication.

Not including in press or submitted articles or popular pieces such as 12 published Op-Eds.

b) H-index for M Gerstein is 157

(according to Google Scholar, scholar.google.com/citations?user=YvjuUugAAAAJ)

c) Highly Cited Researchers (HCR) list inclusion.

On Thomson Reuters list, in 2014 to 2016. On succeeding Clarivate list, in 2017 & 2018.

d) Senior Author Status.

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

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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

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