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

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L Lochovsky, J Zhang, M Gerstein (2017). "MOAT: Efficient Detection of Highly Mutated Regions with the Mutations Overburdening Annotations Tool." *Bioinformatics*.

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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.

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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*.

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.

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Notes on Scientific Publications

a) 511 scientific publications in total.
   Not including in press or submitted articles or popular pieces such as Op-Eds.

b) H-index for M Gerstein is 138
   (according to Google Scholar, scholar.google.com/citations?user=YvjuUugAAAAJ)

c) On Thomson Reuters Highly Cited Researchers (HCR) List in '14, 2015 & 2016

d) 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:

Sudmant… 1000 Genomes Project, Mills*, **Gerstein***, Bashir*, Stegle*, Devine*, Lee*, Eichler*, Korbel* (2015). *Nature* 492: 438-42

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