

References

1. D. Bartel, MicroRNAs: target recognition and regulatory functions, *Cell* **136**, 215 (2009).
2. K. Chen and N. Rajewsky, Deep conservation of microRNA-target relationships and 3'UTR motifs in vertebrates, flies, and nematodes, *Cold Spring Harb. Symp. Quant. Biol.* **71**, 149 (2006).
3. J. Li, Y. Liu, X. Xin, T. S. Kim, E. A. Cabeza, J. Ren, R. Nielsen, J. L. Wrana and Z. Zhang, Evidence for positive selection on a number of microRNA regulatory interactions during recent human evolution, *PLoS Genetics* **8**, p. e1002578 (2012).
4. P. Paul, A. Chakraborty, D. Sarkar, M. Langthasa, M. Rahman, M. Bari, R. S. Singha, A. K. Malakar and S. Chakraborty, Interplay between miRNAs and human diseases, *Journal of Cellular Physiology* **233**, 2007 (2018).
5. G. Calin, C. Dumitru, M. Shimizu, R. Bichi, S. Zupo, E. Noch, H. Aldler, S. Rattan, M. Keating, K. Rai, L. Rassenti, T. Kipps, M. Negrini, F. Bullrich and C. Croce, Frequent deletions and down-regulation of microRNA genes miR15 and miR16 at 13q14 in chronic lymphocytic leukemia, *Proc Natl Acad Sci U S A* **99**, 15524 (2002).
6. L. B. Alexandrov and M. R. Stratton, Mutational signatures: the patterns of somatic mutations hidden in cancer genomes, *Current Opinion in Genetics & Development* **24**, 52 (2014).
7. L. B. Alexandrov, S. Nik-Zainal, D. C. Wedge, S. A. Aparicio, S. Behjati, A. V. Biankin, G. R. Bignell, N. Bolli, A. Borg, A.-L. Børresen-Dale *et al.*, Signatures of mutational processes in human cancer, *Nature* **500**, 415 (2013).
8. A. Kozomara, M. Birgaoanu and S. Griffiths-Jones, miRBase: from microRNA sequences to function, *Nucleic Acids Res.* **47**, D155 (2019).
9. V. Agarwal, G. Bell, J. Nam and D. Bartel, Predicting effective microRNA target sites in mammalian mRNAs, *eLife* **4**, p. e05005 (2015).
10. L. B. Alexandrov, J. Kim, N. J. Haradhvala, M. N. Huang, A. W. T. Ng, A. Boot, K. R. Covington, D. A. Gordenin, E. Bergstrom, N. Lopez-Bigas *et al.*, The repertoire of mutational signatures in human cancer, *bioRxiv* (2018).
11. J. Zhang, J. Baran, A. Cros, J. M. Guberman, S. Haider, J. Hsu, Y. Liang, E. Rivkin, J. Wang, B. Whitty *et al.*, International Cancer Genome Consortium Data Portal—a one-stop shop for cancer genomics data, *Database (Oxford)* **2011**, p. bar026 (2011).
12. A. Frankish, M. Diekhans, A.-M. Ferreira, R. Johnson, I. Jungreis, J. Loveland, J. M. 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, I. T. Fiddes, C. García Girón, J. M. Gonzalez, T. Grego, M. Hardy, T. Hourlier, T. Hunt, O. G. Izuogu, J. Lagarde, F. J. Martin, L. Martínez, S. Mohanan, P. Muir, F. C. P. Navarro, A. Parker, B. Pei, F. Pozo, M. Ruffier, B. M. Schmitt, E. Stapleton, M.-M. Suner, I. Sycheva, B. Uszczynska-Ratajczak, J. Xu, A. Yates, D. Zerbino, Y. Zhang, B. Aken, J. S. Choudhary, M. Gerstein, R. Guigó, T. J. P. Hubbard, M. Kellis, B. Paten, A. Reymond, M. L. Tress and P. Flicek, GENCODE reference annotation for the human and mouse genomes, *Nucleic Acids Research* **47**, D766 (2018).
13. Z. Huang, J. Shi, Y. Gao, C. Cui, S. Zhang, J. Li, Y. Zhou and C. Q, HMDD v3.0: a database for experimentally supported human microRNA-disease associations, *Nucleic Acids Res.* **47**, 1013 (2019).
14. D. C. Ellwanger, F. A. Büttner, H.-W. Mewes and V. Stümpflen, The sufficient minimal set of miRNA seed types, *Bioinformatics* **27**, 1346 (2011).
15. S. Werfel, S. Leierseder, B. Ruprecht, B. Kuster and S. Engelhardt, Preferential microRNA targeting revealed by in vivo competitive binding and differential Argonaute immunoprecipitation, *Nucleic Acids Research* **45**, 10218 (2017).
16. S. Krüger and R. M. Piro, decompTumor2Sig: identification of mutational signatures active in individual tumors, *BMC Bioinformatics* **20**, p. 152 (2019).