

## References

- Araujo, P. R., Yoon, K., Ko, D., Smith, A. D., Qiao, M., Suresh, U., Burns, S. C., & Penalva, L. O. F. (2012). Before It Gets Started: Regulating Translation at the 5' UTR. *Comparative and Functional Genomics*, 2012, 1–8. <https://doi.org/10.1155/2012/475731>
- Barreau, C., Paillard, L., & Osborne, H. B. (2005). AU-rich elements and associated factors: are there unifying principles? *Nucleic Acids Research*, 33(22), 7138–7150. <https://doi.org/10.1093/nar/gki1012>
- Beaupere, C., Chen, R. B., Pelosi, W., & Labunskyy, V. M. (2017). Genome-wide Quantification of Translation in Budding Yeast by Ribosome Profiling. *Journal of Visualized Experiments*, 130. <https://doi.org/10.3791/56820>
- Bertoni, S., Cusan, M., Segatto, I., Citron, F., D'Andrea, S., Benevol, S., Avanzo, M., Dall'Acqua, A., Schiappacassi, M., Bristow, R. G., Belletti, B., & Baldassarre, G. (2017). Loss of p27kip1 increases genomic instability and induces radio-resistance in luminal breast cancer cells. *Scientific Reports*, 7, 595. <https://doi.org/10.1038/s41598-017-00734-3>
- Bhat, K. P., & Greer, S. F. (2011). Proteolytic and non-proteolytic roles of ubiquitin and the ubiquitin proteasome system in transcriptional regulation. *Biochimica et Biophysica Acta (BBA) - Gene Regulatory Mechanisms*, 1809(2), 150–155. <https://doi.org/10.1016/j.bbagr.2010.11.006>
- Boeke, D., Trautmann, S., Meurer, M., Wachsmuth, M., Godlee, C., Knop, M., & Kaksonen, M. (2014). Quantification of cytosolic interactions identifies E de1 oligomers as key organizers of endocytosis. *Molecular Systems Biology*, 10(11), 756. <https://doi.org/10.15252/msb.20145422>
- Brown, W., & Clancy, S. (2008). Translation: DNA to mRNA to Protein. *Undefined*. <https://www.semanticscholar.org/paper/Translation%3A-DNA-to-mRNA-to-Protein-Brown-Clancy/47c2de42fb5c28ba9ff9c0ef49f5e40605e4ac85>
- Budenholzer, L., Cheng, C. L., Li, Y., & Hochstrasser, M. (2017). Proteasome Structure and Assembly. *Journal of Molecular Biology*, 429(22), 3500–3524. <https://doi.org/10.1016/j.jmb.2017.05.027>

- Clausen, L., Abildgaard, A. B., Gersing, S. K., Stein, A., Lindorff-Larsen, K., & Hartmann-Petersen, R. (2019). Protein stability and degradation in health and disease. *Molecular Chaperones in Human Disorders*, 61–83. <https://doi.org/10.1016/bs.apcsb.2018.09.002>
- Cooper, G. M. (2015). *Translation of mRNA*. Nih.gov; Sinauer Associates. <https://www.ncbi.nlm.nih.gov/books/NBK9849/>
- Dawson, S., Apcher, S., Mee, M., Higashitsuji, H., Baker, R., Uhle, S., Dubiel, W., Fujita, J., & Mayer, R. J. (2002). Gankyrin is an ankyrin-repeat oncoprotein that interacts with CDK4 kinase and the S6 ATPase of the 26 S proteasome. *The Journal of Biological Chemistry*, 277(13), 10893–10902. <https://doi.org/10.1074/jbc.M107313200>
- Dominguez, R., & Holmes, K. C. (2011). Actin Structure and Function. *Annual Review of Biophysics*, 40(1), 169–186. <https://doi.org/10.1146/annurev-biophys-042910-155359>
- Ecroyd, H., & Carver, J. A. (2008). Unraveling the mysteries of protein folding and misfolding. *IUBMB Life*, 60(12), 769–774. <https://doi.org/10.1002/iub.117>
- Finley, D. (2009). Recognition and Processing of Ubiquitin-Protein Conjugates by the Proteasome. *Annual Review of Biochemistry*, 78(1), 477–513. <https://doi.org/10.1146/annurev.biochem.78.081507.101607>
- Ford, L. K., & Fioriti, L. (2020). Coiled-Coil Motifs of RNA-Binding Proteins: Dynamicity in RNA Regulation. *Frontiers in Cell and Developmental Biology*, 8. <https://doi.org/10.3389/fcell.2020.607947>
- Galmozzi, C. V., Merker, D., Friedrich, U. A., Döring, K., & Kramer, G. (2019). Selective ribosome profiling to study interactions of translating ribosomes in yeast. *Nature Protocols*, 14(8), 2279–2317. <https://doi.org/10.1038/s41596-019-0185-z>
- Gandin, V., Laia Masvidal, Hulea, L., Gravel, S., Cargnello, M., McLaughlan, S., Cai, Y., Preetika Balanathan, Morita, M., Arjuna Rajakumar, Luc Furic, Pollak, M., Porco, J. A., St-Pierre, J., Pelletier, J., Larsson, O., & Topisirovic, I. (2016). nanoCAGE reveals 5' UTR features that define

specific modes of translation of functionally related MTOR-sensitive mRNAs. *Genome Research*, 26(5), 636–648. <https://doi.org/10.1101/gr.197566.115>

Gross, S. R., & Kinzy, T. G. (2007). Improper Organization of the Actin Cytoskeleton Affects Protein Synthesis at Initiation. *Molecular and Cellular Biology*, 27(5), 1974–1989. <https://doi.org/10.1128/mcb.00832-06>

Hanssum, A., Zhong, Z., Rousseau, A., Krzyzosiak, A., Sigurdardottir, A., & Bertolotti, A. (2014). An Inducible Chaperone Adapts Proteasome Assembly to Stress. *Molecular Cell*, 55(4), 566–577. <https://doi.org/10.1016/j.molcel.2014.06.017>

Hershey, J. W. B., Sonenberg, N., & Mathews, M. B. (2012). Principles of Translational Control: An Overview. *Cold Spring Harbor Perspectives in Biology*, 4(12), a011528–a011528. <https://doi.org/10.1101/cshperspect.a011528>

Hinnebusch, A. G., Ivanov, I. P., & Sonenberg, N. (2016). Translational control by 5'-untranslated regions of eukaryotic mRNAs. *Science (New York, N.Y.)*, 352(6292), 1413–1416. <https://doi.org/10.1126/science.aad9868>

Isono, E., Nishihara, K., Saeki, Y., Yashiroda, H., Kamata, N., Ge, L., Ueda, T., Kikuchi, Y., Tanaka, K., Nakano, A., & Toh-e, A. (2007). The Assembly Pathway of the 19S Regulatory Particle of the Yeast 26S Proteasome. *Molecular Biology of the Cell*, 18(2), 569–580. <https://doi.org/10.1091/mbc.e06-07-0635>

Ito, S. (2020). Proteasome Inhibitors for the Treatment of Multiple Myeloma. *Cancers*, 12(2), 265. <https://doi.org/10.3390/cancers12020265>

Jackson, R. J., Hellen, C. U. T., & Pestova, T. V. (2010). The mechanism of eukaryotic translation initiation and principles of its regulation. *Nature Reviews Molecular Cell Biology*, 11(2), 113–127. <https://doi.org/10.1038/nrm2838>

Jan, M., Sperling, A. S., & Ebert, B. L. (2021). Cancer therapies based on targeted protein degradation — lessons learned with lenalidomide. *Nature Reviews Clinical Oncology*, 18(7), 401–417. <https://doi.org/10.1038/s41571-021-00479-z>

- Jia, L., Mao, Y., Ji, Q., Dersh, D., Yewdell, J. W., & Qian, S.-B. (2020). *Decoding mRNA translatability and stability from 5'UTR*. <https://doi.org/10.1101/2020.03.13.990887>
- K Geetha, R. (2021). Protein folding, misfolding, and coping mechanism of cells—A short discussion. *Open Journal of Cell and Protein Science*, 001–004. <https://doi.org/10.17352/ojcps.000003>
- Karathia, H., Vilaprinyo, E., Sorribas, A., & Alves, R. (2011). *Saccharomyces cerevisiae* as a Model Organism: A Comparative Study. *PLoS ONE*, 6(2), e16015. <https://doi.org/10.1371/journal.pone.0016015>
- Kastano, K., Mier, P., & Andrade-Navarro, M. A. (2021). The Role of Low Complexity Regions in Protein Interaction Modes: An Illustration in Huntington. *International Journal of Molecular Sciences*, 22(4), 1727. <https://doi.org/10.3390/ijms22041727>
- Keene, J. D. (2007). RNA regulons: coordination of post-transcriptional events. *Nature Reviews Genetics*, 8(7), 533–543. <https://doi.org/10.1038/nrg2111>
- Kock, M., Nunes, M. M., Hemann, M., Kube, S., Dohmen, R. J., Herzog, F., Ramos, P. C., & Wendler, P. (2015). Proteasome assembly from 15S precursors involves major conformational changes and recycling of the Pba1-Pba2 chaperone. *Nature Communications*, 6, 6123. <https://doi.org/10.1038/ncomms7123>
- Koellner, C. M., Mensink, K. A., & Highsmith, W. E. (2018). Basic Concepts in Human Molecular Genetics. *Molecular Pathology*, 99–120. <https://doi.org/10.1016/b978-0-12-802761-5.00005-5>
- Koh, W. S., Porter, J. R., & Batchelor, E. (2019). Tuning of mRNA stability through altering 3'-UTR sequences generates distinct output expression in a synthetic circuit driven by p53 oscillations. *Scientific Reports*, 9(1). <https://doi.org/10.1038/s41598-019-42509-y>
- Kozak, M., & Marko Kaksonen. (2022). Condensation of Ede1 promotes the initiation of endocytosis. *ELife*, 11. <https://doi.org/10.7554/elife.72865>

Laughery, M. F., Hunter, T., Brown, A., Hoopes, J., Ostbye, T., Shumaker, T., & Wyrick, J. J. (2015). New vectors for simple and streamlined CRISPR-Cas9 genome editing in *Saccharomyces cerevisiae*. *Yeast*, 32(12), 711–720. <https://doi.org/10.1002/yea.3098>

Laurent, J. M., Garge, R. K., Teufel, A. I., Wilke, C. O., Kachroo, A. H., & Marcotte, E. M. (2020). Humanization of yeast genes with multiple human orthologs reveals functional divergence between paralogs. *PLOS Biology*, 18(5), e3000627. <https://doi.org/10.1371/journal.pbio.3000627>

Lecker, S. H., Goldberg, A. L., & Mitch, W. E. (2006). Protein Degradation by the Ubiquitin-Proteasome Pathway in Normal and Disease States. *Journal of the American Society of Nephrology*, 17(7), 1807–1819. <https://doi.org/10.1681/asn.2006010083>

Leppek, K., Das, R., & Barna, M. (2017). Functional 5' UTR mRNA structures in eukaryotic translation regulation and how to find them. *Nature Reviews Molecular Cell Biology*, 19(3), 158–174. <https://doi.org/10.1038/nrm.2017.103>

Li, J., & Guo, Y. (2010). Gankyrin Oncoprotein: Structure, Function, and Involvement in Cancer. *Current Chemical Biology*, 4(1), 13–19. <https://doi.org/10.2174/2212796811004010013>

Li, Y., Li, S., & Wu, H. (2022). Ubiquitination-Proteasome System (UPS) and Autophagy Two Main Protein Degradation Machineries in Response to Cell Stress. *Cells*, 11(5), 851. <https://doi.org/10.3390/cells11050851>

Lino, C. A., Harper, J. C., Carney, J. P., & Timlin, J. A. (2018). Delivering CRISPR: a review of the challenges and approaches. *Drug Delivery*, 25(1), 1234–1257. <https://doi.org/10.1080/10717544.2018.1474964>

Liu, G.-H., Barkho, B. Z., Ruiz, S., Diep, D., Qu, J., Yang, S.-L., Panopoulos, A. D., Suzuki, K., Kurian, L., Walsh, C., Thompson, J., Boue, S., Fung, H. L., Sancho-Martinez, I., Zhang, K., III, J. Y., & Belmonte, J. C. I. (2011). Recapitulation of premature ageing with iPSCs from Hutchinson-Gilford progeria syndrome. *Nature*, 472(7342), 221–225. <https://doi.org/10.1038/nature09879>

Lu, R., & Drubin, D. G. (2017). Selection and stabilization of endocytic sites by Ede1, a yeast functional homologue of human Eps15. *Mol Biol Cell*, 28(5), 567–575. <https://doi.org/10.1091/mbc.e16-06-0391>

Magnuson, B., Ekim, B., & Fingar, Diane C. (2011). Regulation and function of ribosomal protein S6 kinase (S6K) within mTOR signalling networks. *Biochemical Journal*, 441(1), 1–21. <https://doi.org/10.1042/bj20110892>

Mayr, C. (2016). Evolution and Biological Roles of Alternative 3'UTRs. *Trends in Cell Biology*, 26(3), 227–237. <https://doi.org/10.1016/j.tcb.2015.10.012>

Mayr, C. (2017). Regulation by 3'-Untranslated Regions. *Annual Review of Genetics*, 51(1), 171–194. <https://doi.org/10.1146/annurev-genet-120116-024704>

Mayr, C. (2019). What Are 3' UTRs Doing? *Cold Spring Harbor Perspectives in Biology*, 11(10). <https://doi.org/10.1101/cshperspect.a034728>

Mishra, M., Huang, J., & Balasubramanian, M. K. (2014). The yeast actin cytoskeleton. *FEMS Microbiology Reviews*, 38(2), 213–227. <https://doi.org/10.1111/1574-6976.12064>

Mofers, A., Pellegrini, P., Linder, S., & D'Arcy, P. (2017). Proteasome-associated deubiquitinases and cancer. *Cancer and Metastasis Reviews*, 36(4), 635–653. <https://doi.org/10.1007/s10555-017-9697-6>

Murata, S., Yashiroda, H., & Tanaka, K. (2009). Molecular mechanisms of proteasome assembly. *Nature Reviews Molecular Cell Biology*, 10(2), 104–115. <https://doi.org/10.1038/nrm2630>

Nakamura, Y., Umehara, T., Tanaka, A., Horikoshi, M., Padmanabhan, B., & Yokoyama, S. (2007). Structural basis for the recognition between the regulatory particles Nas6 and Rpt3 of the yeast 26S proteasome. *Biochemical and Biophysical Research Communications*, 359(3), 503–509. <https://doi.org/10.1016/j.bbrc.2007.05.138>

Nandagopal, N., & Roux, P. P. (2015). Regulation of global and specific mRNA translation by the mTOR signaling pathway. *Translation*, 3(1), e983402. <https://doi.org/10.4161/21690731.2014.983402>

- Nijhawan, D., Zack, T. I., Ren, Y., Strickland, M. R., Lamothe, R., Schumacher, S. E., Tsherniak, A., Besche, H. C., Rosenbluh, J., Shehata, S., Cowley, G. S., Weir, B. A., Goldberg, A. L., Mesirov, J. P., Root, D. E., Bhatia, S. N., Beroukhim, R., & Hahn, W. C. (2012). Cancer Vulnerabilities Unveiled by Genomic Loss. *Cell*, 150(4), 842–854. <https://doi.org/10.1016/j.cell.2012.07.023>
- Oikonomou, P., Goodarzi, H., & Tavazoie, S. (2014). Systematic Identification of Regulatory Elements in Conserved 3' UTRs of Human Transcripts. *Cell Reports*, 7(1), 281–292. <https://doi.org/10.1016/j.celrep.2014.03.001>
- Petrocca, F., Altschuler, G., Tan, S., Mendillo, Marc L., Yan, H., Jerry, D. Joseph, Kung, Andrew L., Hide, W., Ince, Tan A., & Lieberman, J. (2013). A Genome-wide siRNA Screen Identifies Proteasome Addiction as a Vulnerability of Basal-like Triple-Negative Breast Cancer Cells. *Cancer Cell*, 24(2), 182–196. <https://doi.org/10.1016/j.ccr.2013.07.008>
- Pollard, T. D., & Cooper, J. A. (2009). Actin, a Central Player in Cell Shape and Movement. *Science*, 326(5957), 1208–1212. <https://doi.org/10.1126/science.1175862>
- Prosser, D. C., Drivas, T. G., Maldonado-Báez, L., & Wendland, B. (2011). Existence of a novel clathrin-independent endocytic pathway in yeast that depends on Rho1 and formin. *The Journal of Cell Biology*, 195(4), 657–671. <https://doi.org/10.1083/jcb.201104045>
- Rosenzweig, R., Osmulski, P. A., Gaczynska, M., & Glickman, M. H. (2008). The central unit within the 19S regulatory particle of the proteasome. *Nature Structural & Molecular Biology*, 15(6), 573–580. <https://doi.org/10.1038/nsmb.1427>
- Rousseau, A., & Bertolotti, A. (2016). An evolutionarily conserved pathway controls proteasome homeostasis. *Nature*, 536(7615), 184–189. <https://doi.org/10.1038/nature18943>
- Rousseau, A., & Bertolotti, A. (2018). Regulation of proteasome assembly and activity in health and disease. *Nature Reviews Molecular Cell Biology*, 19(11), 697–712. <https://doi.org/10.1038/s41580-018-0040-z>

Saeki, Y., Toh-e, A., Kudo, T., Kawamura, H., & Tanaka, K. (2009). Multiple Proteasome-Interacting Proteins Assist the Assembly of the Yeast 19S Regulatory Particle. *Cell*, 137(5), 900–913.  
<https://doi.org/10.1016/j.cell.2009.05.005>

Sagot, I., Pinson, B., Salin, B., & Daignan-Fornier, B. (2006). Actin Bodies in Yeast Quiescent Cells: An Immediately Available Actin Reserve? *Molecular Biology of the Cell*, 17(11), 4645–4655.  
<https://doi.org/10.1091/mbc.E06-04-0282>

Savinov, A., Brandsen, B. M., Angell, B. E., Cuperus, J. T., & Fields, S. (2021). Effects of sequence motifs in the yeast 3' untranslated region determined from massively parallel assays of random sequences. *Genome Biology*, 22(1). <https://doi.org/10.1186/s13059-021-02509-6>

Svitkina, T. (2018). The Actin Cytoskeleton and Actin-Based Motility. *Cold Spring Harbor Perspectives in Biology*, 10(1), a018267. <https://doi.org/10.1101/cshperspect.a018267>

Thines, L., Deschamps, A., Stribny, J., & Morsomme, P. (2019). Yeast as a Tool for Deeper Understanding of Human Manganese-Related Diseases. *Genes*, 10(7), 545.  
<https://doi.org/10.3390/genes10070545>

Thoreen, C. C., Chantranupong, L., Keys, H. R., Wang, T., Gray, N. S., & Sabatini, D. M. (2012). A unifying model for mTORC1-mediated regulation of mRNA translation. *Nature*, 485(7396), 109–113.  
<https://doi.org/10.1038/nature11083>

Tomko, R. J., & Hochstrasser, M. (2013). Molecular Architecture and Assembly of the Eukaryotic Proteasome. *Annual Review of Biochemistry*, 82(1), 415–445.  
<https://doi.org/10.1146/annurev-biochem-060410-150257>

Utomo, J. C., Hodgins, C. L., & Ro, D.-K. (2021). Multiplex Genome Editing in Yeast by CRISPR/Cas9 – A Potent and Agile Tool to Reconstruct Complex Metabolic Pathways. *Frontiers in Plant Science*, 12. <https://doi.org/10.3389/fpls.2021.719148>

Walerych, D., Lisek, K., Sommaggio, R., Piazza, S., Ciani, Y., Dalla, E., Rajkowska, K., Gaweda-Walerych, K., Ingallina, E., Tonelli, C., Morelli, M. J., Amato, A., Eterno, V., Zambelli, A., Rosato, A., Amati, B., Wiśniewski, J. R., & Del Sal, G. (2016). Proteasome machinery is instrumental in a common

gain-of-function program of the p53 missense mutants in cancer. *Nature Cell Biology*, 18(8), 897–909. <https://doi.org/10.1038/ncb3380>

Wang, Y., Zhang, L., He, Z., Deng, J., Zhang, Z., Liu, L., Ye, W., & Liu, S. (2020). Tunicamycin induces ER stress and inhibits tumorigenesis of head and neck cancer cells by inhibiting N-glycosylation. *American Journal of Translational Research*, 12(2), 541–550. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7061826/>

Wang, Z., & Kiledjian, M. (2000). The Poly(A)-Binding Protein and an mRNA Stability Protein Jointly Regulate an Endoribonuclease Activity. *Molecular and Cellular Biology*, 20(17), 6334–6341. <https://doi.org/10.1128/mcb.20.17.6334-6341.2000>

Webster, J. M., Darling, A. L., Uversky, V. N., & Blair, L. J. (2019). Small Heat Shock Proteins, Big Impact on Protein Aggregation in Neurodegenerative Disease. *Frontiers in Pharmacology*, 10. <https://doi.org/10.3389/fphar.2019.01047>

Wei, M., Fan, X., Ding, M., Li, R., Shao, S., Hou, Y., Meng, S., Tang, F., Li, C., & Sun, Y. (2020). Nuclear actin regulates inducible transcription by enhancing RNA polymerase II clustering. *Science Advances*, 6(16), eaay6515. <https://doi.org/10.1126/sciadv.aay6515>

Wiklund, L., Sokolowski, M., Carlsson, A., Rush, M., & Schwartz, S. (2002). Inhibition of Translation by UAUUUUAU and UAUUUUUUAU Motifs of the AU-rich RNA Instability Element in the HPV-1 Late 3' Untranslated Region. *Journal of Biological Chemistry*, 277(43), 40462–40471. <https://doi.org/10.1074/jbc.m205929200>

Williams, T. D., Cacioppo, R., Agrotis, A., Black, A., Zhou, H., & Rousseau, A. (2022). Actin remodelling controls proteasome homeostasis upon stress. *Nature Cell Biology*, 24(7), 1077–1087. <https://doi.org/10.1038/s41556-022-00938-4>

Xiang, K., & Bartel, D. P. (2021). The molecular basis of coupling between poly(A)-tail length and translational efficiency. *eLife*, 10, e66493. <https://doi.org/10.7554/eLife.66493>

Xie, Y., & Varshavsky, A. (2001). RPN4 is a ligand, substrate, and transcriptional regulator of the 26S proteasome: A negative feedback circuit. *Proceedings of the National Academy of Sciences*, 98(6), 3056–3061. <https://doi.org/10.1073/pnas.071022298>

Yang, M., Lu, Y., Piao, W., & Jin, H. (2022). The Translational Regulation in mTOR Pathway. *Biomolecules*, 12(6), 802. <https://doi.org/10.3390/biom12060802>

Young, M. E., Cooper, J. A., & Bridgman, P. C. (2004). Yeast actin patches are networks of branched actin filaments. *The Journal of Cell Biology*, 166(5), 629–635. <https://doi.org/10.1083/jcb.200404159>