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Ad, O., Hoffman, K. S., Cairns, A. G., Featherston, A. L., Miller, S. J., Söll, D., & Schepartz, A. (2019). Translation of Diverse Aramid- and 1,3-Dicarbonyl-peptides by Wild Type Ribosomes *in Vitro*. *ACS Central Science*. doi:10.1021/acscentsci.9b00460

Alexander, L. M., Goldman, D. H., Wee, L. M., & Bustamante, C. (2019). Non-equilibrium dynamics of a nascent polypeptide during translation suppress its misfolding. *Nature Communications*, 10(1), 2709. doi:10.1038/s41467-019-10647-6

Allen-Benton, M., Findlay, H. E., & Booth, P. J. (2019). Probing membrane protein properties using droplet interface bilayers. *Experimental Biology and Medicine*, 244(8), 709-720. doi:10.1177/1535370219847939

Almutairi, M. M., Svetlov, M. S., Hansen, D. A., Khabibullina, N. F., Klepacki, D., Kang, H. Y., Mankin, A. S. (2017). Co-produced natural ketolides methymycin and pikromycin inhibit bacterial growth by preventing synthesis of a limited number of proteins. *Nucleic Acids Res*, 45(16), 9573-9582. doi:10.1093/nar/gkx673

Alumasa, J. N., Manzanillo, P. S., Peterson, N. D., Lundrigan, T., Baughn, A. D., Cox, J. S., & Keiler, K. C. (2017). Ribosome Rescue Inhibitors Kill Actively Growing and Nonreplicating Persister *Mycobacterium tuberculosis* Cells. *ACS Infect Dis*, 3(9), 634-644. doi:10.1021/acsinfecdis.7b00028

Anne, D., Elise de, R., Pauline van, N., Mischa van der, H., Katy, W., Johannes, K., Christophe, D. (2019). Modelling cell-free RNA and protein synthesis with minimal systems. *Physical Biology*, 16(2), 025001.

Assad, N., Tillo, D., Ray, S., Dzienny, A., FitzGerald, P. C., & Vinson, C. (2019). GABPα and CREB1 Binding to Double Nucleotide Polymorphisms of Their Consensus Motifs and Cooperative Binding to the Composite ETS ⇔ CRE Motif (ACCGGAAGTGACGTCA). *ACS Omega*, 4(6), 9904-9910. doi:10.1021/acsomega.9b00540

Assah, E., Goh, W., Zheng, X. T., Lim, T. X., Li, J., Lane, D., Tan, Y. N. (2018). Rapid Colorimetric Detection of p53 Protein Function using DNA-Gold Nanoconjugates with Applications for Drug Discovery and Cancer Diagnostics. *Colloids and Surfaces B: Biointerfaces*. doi:<https://doi.org/10.1016/j.colsurfb.2018.05.007>

Au - Pardatscher, G., Au - Schwarz-Schilling, M., Au - Sagredo, S., & Au - Simmel, F. C. (2018). Functional Surface-immobilization of Genes Using Multistep Strand Displacement Lithography. *JoVE*(140), e58634. doi:doi:10.3791/58634

Aufinger, L., & Simmel, F. C. (2018). Artificial Gel-Based Organelles for Spatial Organization of Cell-Free Gene Expression Reactions. *Angew Chem Int Ed Engl*, 57(52), 17245-17248. doi:10.1002/anie.201809374

Bailey, J. K., Shen, W., Liang, X. H., & Crooke, S. T. (2017). Nucleic acid binding proteins affect the subcellular distribution of phosphorothioate antisense oligonucleotides. *Nucleic Acids Res*, 45(18), 10649-10671. doi:10.1093/nar/gkx709

Baumgardt, K., Gilet, L., Figaro, S., & Condon, C. (2018). The essential nature of YqfG, a YbeY homologue required for 3' maturation of *Bacillus subtilis* 16S ribosomal RNA is suppressed by deletion of RNase R. *Nucleic Acids Research*, gky488-gky488. doi:10.1093/nar/gky488

Beri, J., Nash, T., Martin, R. M., & Bereman, M. S. (2017). Exposure to BMAA mirrors molecular processes linked to neurodegenerative disease. *Proteomics*, 17(17-18), 1700161-n/a. doi:10.1002/pmic.201700161

Bhattacharya, A., Brea, R. J., Niederholtmeyer, H., & Devaraj, N. K. (2019). A minimal biochemical route towards de novo formation of synthetic phospholipid membranes. *Nature Communications*, 10(1), 300. doi:10.1038/s41467-018-08174-x

Blanken, D., van Nies, P., & Danelon, C. (2019). Quantitative imaging of gene-expressing liposomes reveals rare favorable phenotypes. *Physical Biology*, 16(4), 045002. doi:10.1088/1478-3975/ab0c62

Boles, K. S., Kannan, K., Gill, J., Felderman, M., Gouvis, H., Hubby, B., Gibson, D. G. (2017). Digital-to-biological converter for on-demand production of biologics. *Nat Biotechnol*, 35(7), 672-675. doi:10.1038/nbt.3859

Bray, M. S., Bowman, J. C., Petrov, A. S., Reddi, A. R., Williams, L. D., & Glass, J. B. (2018). Ferrous iron mediates translation. *bioRxiv*. doi:10.1101/256958

Bulutoglu, B., Dooley, K., Szilvay, G., Blenner, M., & Banta, S. (2017). Catch and Release: Engineered Allosterically Regulated beta-Roll Peptides Enable On/Off Biomolecular Recognition. *ACS Synth Biol*, 6(9), 1732-1741. doi:10.1021/acssynbio.7b00089

Bulutoglu, B., Haghpanah, J., Campbell, E., & Banta, S. A. (2017). Engineered Biomolecular Recognition of RDX Using a Thermostable Alcohol Dehydrogenase as a Protein Scaffold. *ChemBioChem*, n/a-n/a. doi:10.1002/cbic.201700539

Caveney, P. M., Norred, S. E., Chin, C. W., Boreyko, J. B., Razooky, B. S., Retterer, S. T., Simpson, M. L. (2017). Resource Sharing Controls Gene Expression Bursting. *ACS Synth Biol*, 6(2), 334-343. doi:10.1021/acssynbio.6b00189

Chang, J.-C., Swank, Z., Keiser, O., Maerkli, S. J., & Amstad, E. (2018). Microfluidic device for real-time formulation of reagents and their subsequent encapsulation into double emulsions. *Scientific Reports*, 8(1), 8143. doi:10.1038/s41598-018-26542-x

Charon, J., Manteca, A., & Innis, A. (2018). Using the bacterial ribosome as a discovery platform for peptide-based antibiotics. *Biochemistry*. doi:10.1021/acs.biochem.8b00927

Chauvier, A., Picard-Jean, F., Berger-Dancause, J.-C., Bastet, L., Naghdi, M. R., Dubé, A., Lafontaine, D. A. (2017). Transcriptional pausing at the translation start site operates as a critical checkpoint for riboswitch regulation. *Nature Communications*, 8, 13892. doi:10.1038/ncomms13892http://www.nature.com/articles/ncomms13892#supplementary-information

Chen, J., & Gottesman, S. (2017). Hfq links translation repression to stress-induced mutagenesis in *E. coli*. *Genes Dev.* doi:10.1101/gad.302547.117

Chuzel, L., Ganatra, M. B., Rapp, E., Henrissat, B., & Taron, C. H. (2018). Functional metagenomics identifies an exosialidase with an inverting catalytic mechanism that defines a new glycoside hydrolase family (GH156). *Journal of Biological Chemistry*. doi:10.1074/jbc.RA118.003302

Cintrón, M., Zeng, J.-M., Barth, V. C., Cruz, J. W., Husson, R. N., & Woychik, N. A. (2019). Accurate target identification for Mycobacterium tuberculosis endoribonuclease toxins requires expression in their native host. *Scientific Reports*, 9(1), 5949. doi:10.1038/s41598-019-41548-9

Cochrane, W. G., Hackler, A. L., Cavett, V. J., Price, A. K., & Paegel, B. M. (2017). Integrated, Continuous Emulsion Creamer. *Anal Chem*, 89(24), 13227-13234. doi:10.1021/acs.analchem.7b03070

Crowe-McAuliffe, C., Graf, M., Huter, P., Takada, H., Abdelshahid, M., Nováček, J., Wilson, D. N. (2018). Structural basis for antibiotic resistance mediated by the *Bacillus subtilis* ABCF ATPase VmlR. *Proceedings of the National Academy of Sciences*, 115(36), 8978-8983. doi:10.1073/pnas.1808535115

da Silva, E. S., Gomez-Vallejo, V., Lopez-Gallego, F., & Llop, J. (2017). Biocatalysis in Radiochemistry; Enzymatic Incorporation of PET radionuclides into molecules of biomedical interest. *J Labelled Comp Radiopharm*, n/a-n/a. doi:10.1002/jlcr.3592

Dabrowski-Tumanski, P., Piejko, M., Niewieczerzal, S., Stasiak, A., & Sulkowska, J. I. (2018). Protein Knotting by Active Threading of Nascent Polypeptide Chain Exiting From the Ribosome Exit Channel. *The Journal of Physical Chemistry B*. doi:10.1021/acs.jpcb.8b07634

Delarue, M., Brittingham, G. P., Pfeffer, S., Surovtsev, I. V., Pinglay, S., Kennedy, K. J., Holt, L. J. (2018). mTORC1 Controls Phase Separation and the Biophysical Properties of the Cytoplasm by Tuning Crowding. *Cell*. doi:<https://doi.org/10.1016/j.cell.2018.05.042>

Diefenbach, X. W., Farasat, I., Guetschow, E. D., Welch, C. J., Kennedy, R. T., Sun, S., & Moore, J. C. (2018). Enabling Biocatalysis by High-Throughput Protein Engineering Using Droplet Microfluidics Coupled to Mass Spectrometry. *ACS Omega*, 3(2), 1498-1508. doi:10.1021/acsomega.7b01973

Dillon, N. A., Peterson, N. D., Feaga, H. A., Keiler, K. C., & Baughn, A. D. (2017). Anti-tubercular Activity of Pyrazinamide is Independent of trans-Translation and RpsA. *Scientific Reports*, 7(1), 6135. doi:10.1038/s41598-017-06415-5

Dopp, B. J. L., Tamiev, D. D., & Reuel, N. F. (2018). Cell-free supplement mixtures: Elucidating the history and biochemical utility of additives used to support *in vitro* protein synthesis in *E. coli* extract. *Biotechnology Advances*. doi:<https://doi.org/10.1016/j.biotechadv.2018.12.006>

Dopp, J. L., & Reuel, N. F. (2018). Process optimization for scalable *E. coli* extract preparation for cell-free protein synthesis. *Biochemical Engineering Journal*. doi:<https://doi.org/10.1016/j.bej.2018.06.021>

Doshi, R., McGrath, A. P., Piñeros, M., Szewczyk, P., Garza, D. M., Kochian, L. V., & Chang, G. (2017). Functional characterization and discovery of modulators of SbMATE, the agronomically important aluminium tolerance transporter from Sorghum bicolor. *Scientific Reports*, 7(1), 17996. doi:[10.1038/s41598-017-18146-8](https://doi.org/10.1038/s41598-017-18146-8)

Durner, E., Ott, W., Nash, M. A., & Gaub, H. E. (2017). Post-Translational Sortase-Mediated Attachment of High-Strength Force Spectroscopy Handles. *ACS Omega*, 2(6), 3064-3069. doi:[10.1021/acsomega.7b00478](https://doi.org/10.1021/acsomega.7b00478)

Duyen, T. T., Matsuura, H., Ujiie, K., Muraoka, M., Harada, K., & Hirata, K. (2017). Paper-based colorimetric biosensor for antibiotics inhibiting bacterial protein synthesis. *J Biosci Bioeng*, 123(1), 96-100. doi:[10.1016/j.jbiosc.2016.07.015](https://doi.org/10.1016/j.jbiosc.2016.07.015)

Essuman, K., Summers, D. W., Sasaki, Y., Mao, X., DiAntonio, A., & Milbrandt, J. (2017). The SARM1 Toll/Interleukin-1 Receptor Domain Possesses Intrinsic NAD(+) Cleavage Activity that Promotes Pathological Axonal Degeneration. *Neuron*, 93(6), 1334-1343 e1335. doi:[10.1016/j.neuron.2017.02.022](https://doi.org/10.1016/j.neuron.2017.02.022)

Essuman, K., Summers, D. W., Sasaki, Y., Mao, X., Yim, A. K. Y., DiAntonio, A., & Milbrandt, J. (2018). TIR Domain Proteins Are an Ancient Family of NAD(+)-Consuming Enzymes. *Curr Biol*, 28(3), 421-430 e424. doi:[10.1016/j.cub.2017.12.024](https://doi.org/10.1016/j.cub.2017.12.024)

Farias-Rico, J. A., Goetz, S. K., Marino, J., & von Heijne, G. (2017). Mutational analysis of protein folding inside the ribosome exit tunnel. *FEBS Lett*, 591(1), 155-163. doi:[10.1002/1873-3468.12504](https://doi.org/10.1002/1873-3468.12504)

Fausther, M., E, G. L., & Dranoff, J. A. (2017). Liver myofibroblasts of murine origins express mesothelin: Identification of novel rat mesothelin splice variants. *PLoS ONE*, 12(9), e0184499. doi:[10.1371/journal.pone.0184499](https://doi.org/10.1371/journal.pone.0184499)

Fernández, C., & Giraldo, R. (2018). Modulation of the Aggregation of the Prion-like Protein RepA-WH1 by Chaperones in a Cell-Free Expression System and in Cytomimetic Lipid Vesicles. *ACS Synthetic Biology*. doi:[10.1021/acssynbio.8b00283](https://doi.org/10.1021/acssynbio.8b00283)

Fernández, C., Rivas, G., Giraldo, R., & Jiménez, M. (2017). Chapter Five - Reconstruction of Cytotoxic Bacterial Protein Assemblies in Lipid Vesicles. In M. R. Aleš Iglič & J. G.-S. Ana (Eds.), *Advances in Biomembranes and Lipid Self-Assembly* (Vol. Volume 26, pp. 173-193): Academic Press.

Fleming, S. R., Bartges, T. E., Vinogradov, A. A., Kirkpatrick, C. L., Goto, Y., Suga, H., Bowers, A. A. (2019). Flexizyme-Enabled Benchtop Biosynthesis of Thiopeptides. *Journal of the American Chemical Society*, 141(2), 758-762. doi:10.1021/jacs.8b11521

Florin, T., Maracci, C., Graf, M., Karki, P., Klepacki, D., Berninghausen, O., Mankin, A. S. (2017). An antimicrobial peptide that inhibits translation by trapping release factors on the ribosome. *Nature Structural & Molecular Biology*, 24, 752. doi:10.1038/nsmb.3439

Fomenkov, A., Sun, Z., Dila, D. K., Anton, B. P., Roberts, R. J., & Raleigh, E. A. (2017). EcoBLMcrX, a classical modification-dependent restriction enzyme in *Escherichia coli* B: Characterization *in vivo* and *in vitro* with a new approach to cleavage site determination. *PLoS ONE*, 12(6), e0179853. doi:10.1371/journal.pone.0179853

Fracasso, G., Korner, Y., Gonzales, D. T. T., & Dora Tang, T. Y. (2019). *In vitro* gene expression and detergent-free reconstitution of active proteorhodopsin in lipid vesicles. *Exp Biol Med (Maywood)*, 244(4), 314-322. doi:10.1177/1535370218820290

Gan, Q., & Fan, C. (2017). Increasing the fidelity of noncanonical amino acid incorporation in cell-free protein synthesis. *Biochim Biophys Acta*, 1861(11 Pt B), 3047-3052. doi:10.1016/j.bbagen.2016.12.002

Garenne, D., & Noireaux, V. (2019). Cell-free transcription–translation: engineering biology from the nanometer to the millimeter scale. *Current Opinion in Biotechnology*, 58, 19-27. doi:<https://doi.org/10.1016/j.copbio.2018.10.007>

Ghanem, A., Schweitzer, K., & Naumann, M. (2019). Catalytic domain of deubiquitinylase USP48 directs interaction with Rel homology domain of nuclear factor kappaB transcription factor RelA. *Molecular Biology Reports*. doi:10.1007/s11033-019-04587-z

Gregorio, N. E., Levine, M. Z., & Oza, J. P. (2019). A User's Guide to Cell-Free Protein Synthesis. *Methods and Protocols*, 2(1), 24.

Gupta, S., Sarkar, S., Katranidis, A., & Bhattacharya, J. (2019). Development of a Cell-Free Optical Biosensor for Detection of a Broad Range of Mercury Contaminants in Water: A Plasmid DNA-Based Approach. *ACS Omega*, 4(5), 9480-9487. doi:10.1021/acsomega.9b00205

Guzmán, G. I., Sandberg, T. E., LaCroix, R. A., Nyerges, Á., Papp, H., de Raad, M., Feist, A. M. (2019). Enzyme promiscuity shapes adaptation to novel growth substrates. *Molecular Systems Biology*, 15(4), e8462. doi:10.15252/msb.20188462

Hadzi, S., Garcia-Pino, A., Haesaerts, S., Jurenas, D., Gerdes, K., Lah, J., & Loris, R. (2017). Ribosome-dependent *Vibrio cholerae* mRNase HigB2 is regulated by a beta-strand sliding mechanism. *Nucleic Acids Res*, 45(8), 4972-4983. doi:10.1093/nar/gkx138

Hamadani, K. M., Howe, J., Jensen, M. K., Wu, P., Cate, J. H. D., & Marqsee, S. (2017). An *in vitro* tag-and-modify protein sample generation method for single-molecule fluorescence resonance energy transfer. *J Biol Chem*, 292(38), 15636-15648. doi:10.1074/jbc.M117.791723

Harris, N. J., Charalambous, K., Findlay, H. E., & Booth, P. J. (2018). Lipids modulate the insertion and folding of the nascent chains of alpha helical membrane proteins. *Biochemical Society Transactions*. doi:10.1042/bst20170424

Harris, N. J., Reading, E., Ataka, K., Grzegorzewski, L., Charalambous, K., Liu, X., Booth, P. J. (2017). Structure formation during translocon-unassisted co-translational membrane protein folding. *Scientific Reports*, 7(1), 8021. doi:10.1038/s41598-017-08522-9

Hoernes, T. P., & Erlacher, M. D. (2017). Methylated mRNA Nucleotides as Regulators for Ribosomal Translation. In A. Lusser (Ed.), *RNA Methylation: Methods and Protocols* (pp. 283-294). New York, NY: Springer New York.

Hong, J., Brandt, N., Abdul-Rahman, F., Yang, A., Hughes, T., & Gresham, D. (2018). An incoherent feedforward loop facilitates adaptive tuning of gene expression. *eLife*, 7, e32323. doi:10.7554/eLife.32323

Horiya, S., Bailey, J. K., & Krauss, I. J. (2017). Chapter Four - Directed Evolution of Glycopeptides Using mRNA Display. In B. Imperiali (Ed.), *Methods in Enzymology* (Vol. 597, pp. 83-141): Academic Press.

Hou, N., Yan, Z., Fan, K., LI, H., Zhao, R., Xia, Y., Xun, L. (2019). OxyR senses reactive sulfane sulfur and activates genes for its removal in *Escherichia coli*. *bioRxiv*, 561019. doi:10.1101/561019

Huang, A., Nguyen, P. Q., Stark, J. C., Takahashi, M. K., Donghia, N., Ferrante, T., Collins, J. J. (2018). BioBits™ Explorer: A modular synthetic biology education kit. *Science Advances*, 4(8). doi:10.1126/sciadv.aat5105

Huang, W.-P., Cho, C.-P., & Chang, K.-Y. (2018). mRNA-Mediated Duplexes Play Dual Roles in the Regulation of Bidirectional Ribosomal Frameshifting. *International Journal of Molecular Sciences*, 19(12), 3867.

Huter, P., Arenz, S., Bock, L. V., Graf, M., Frister, J. O., Heuer, A., Wilson, D. N. (2017). Structural Basis for Polyproline-Mediated Ribosome Stalling and Rescue by the Translation Elongation Factor EF-P. *Mol Cell*, 68(3), 515-527 e516. doi:10.1016/j.molcel.2017.10.014

Jacobs, M. L., Boyd, M. A., & Kamat, N. P. (2019). Diblock copolymers enhance folding of a mechanosensitive membrane protein during cell-free expression. *Proceedings of the National Academy of Sciences*, 116(10), 4031-4036. doi:10.1073/pnas.1814775116

Jain, M., Fleites, L. A., & Gabriel, D. W. (2017). A Small Wolbachia Protein Directly Represses Phage Lytic Cycle Genes in "Candidatus Liberibacter asiaticus" within Psyllids. *mSphere*, 2(3). doi:10.1128/mSphereDirect.00171-17

Jerlström Hultqvist, J., Warsi, O., Söderholm, A., Knopp, M., Eckhard, U., Vorontsov, E., Andersson, D. I. (2018). A bacteriophage enzyme induces bacterial metabolic perturbation that confers a novel promiscuous function. *Nature Ecology & Evolution*, 2(8), 1321-1330. doi:10.1038/s41559-018-0568-5

Jia, H., & Schwille, P. (2019). Bottom-up synthetic biology: reconstitution in space and time. *Current Opinion in Biotechnology*, 60, 179-187. doi:<https://doi.org/10.1016/j.copbio.2019.05.008>

Jiang, L., Zhao, J., Lian, J., & Xu, Z. (2018). Cell-free protein synthesis enabled rapid prototyping for metabolic engineering and synthetic biology. *Synthetic and Systems Biotechnology*. doi:<https://doi.org/10.1016/j.synbio.2018.02.003>

Jimeno, S., Camarillo, R., Mejías-Navarro, F., Fernández-Ávila, M. J., Soria-Bretones, I., Prados-Carvajal, R., & Huertas, P. (2018). The Helicase PIF1 Facilitates Resection over Sequences Prone to Forming G4 Structures. *Cell Reports*, 24(12), 3262-3273.e3264. doi:<https://doi.org/10.1016/j.celrep.2018.08.047>

Jin, L., Kamat, N. P., Jena, S., & Szostak, J. W. (2018). Fatty Acid/Phospholipid Blended Membranes: A Potential Intermediate State in Protocellular Evolution. *Small*, 14(15), e1704077. doi:[10.1002/smll.201704077](https://doi.org/10.1002/smll.201704077)

Josipovic, I., Pfluger, B., Fork, C., Vasconez, A. E., Oo, J. A., Hitzel, J., Leisegang, M. S. (2018). Long noncoding RNA LISPR1 is required for S1P signaling and endothelial cell function. *J Mol Cell Cardiol*, 116, 57-68. doi:[10.1016/j.yjmcc.2018.01.015](https://doi.org/10.1016/j.yjmcc.2018.01.015)

Jurenas, D., Chatterjee, S., Konijnenberg, A., Sobott, F., Droogmans, L., Garcia-Pino, A., & Van Melderen, L. (2017). AtaT blocks translation initiation by N-acetylation of the initiator tRNA(fMet). *Nat Chem Biol*, 13(6), 640-646. doi:[10.1038/nchembio.2346](https://doi.org/10.1038/nchembio.2346)

Jurénas, D., Van Melderen, L., & Garcia-Pino, A. (2019). Mechanism of regulation and neutralization of the AtaR–AtaT toxin–antitoxin system. *Nature Chemical Biology*. doi:[10.1038/s41589-018-0216-z](https://doi.org/10.1038/s41589-018-0216-z)

Kalkreuter, E., Keeler, A. M., Malico, A. A., Bingham, K. S., Gayen, A. K., & Williams, G. J. (2019). Development of a Genetically Encoded Biosensor for Detection of Polyketide Synthase Extender Units in *Escherichia coli*. *ACS Synthetic Biology*, 8(6), 1391-1400. doi:[10.1021/acssynbio.9b00078](https://doi.org/10.1021/acssynbio.9b00078)

Kaye, E. G., Booker, M., Kurland, J. V., Conicella, A. E., Fawzi, N. L., Bulyk, M. L., Larschan, E. (2018). Differential Occupancy of Two GA-Binding Proteins Promotes Targeting of the Drosophila Dosage Compensation Complex to the Male X Chromosome. *Cell Reports*, 22(12), 3227-3239. doi:<https://doi.org/10.1016/j.celrep.2018.02.098>

Kempf, N., Remes, C., Ledesch, R., Zuchner, T., Hofig, H., Ritter, I., Fitter, J. (2017). A Novel Method to Evaluate Ribosomal Performance in Cell-Free Protein Synthesis Systems. *Sci Rep*, 7, 46753. doi:[10.1038/srep46753](https://doi.org/10.1038/srep46753)

Kinoshita, E., Kinoshita-Kikuta, E., Karata, K., Kawano, T., Nishiyama, A., Yamato, M., & Koike, T. (2017). Specific glutamic acid residues in targeted proteins induce exaggerated retardations in Phos-tag SDS-PAGE migration. *Electrophoresis*, 38(8), 1139-1146. doi:[10.1002/elps.201600520](https://doi.org/10.1002/elps.201600520)

Knauf, G. A., Cunningham, A. L., Kazi, M. I., Riddington, I. M., Crofts, A. A., Cattoir, V., Davies, B. W. (2018). Exploring the Antimicrobial Action of Quaternary Amines against *Acinetobacter baumannii*. *mBio*, 9(1). doi:[10.1128/mBio.02394-17](https://doi.org/10.1128/mBio.02394-17)

Koren, I., Timms, R. T., Kula, T., Xu, Q., Li, M. Z., & Elledge, S. J. (2018). The Eukaryotic Proteome Is Shaped by E3 Ubiquitin Ligases Targeting C-Terminal Degrons. *Cell*. doi:<https://doi.org/10.1016/j.cell.2018.04.028>

Kreamer, N. N. K., Chopra, R., Caughlan, R. E., Fabbro, D., Fang, E., Gee, P., Uehara, T. (2018). Acylated-acyl carrier protein stabilizes the *Pseudomonas aeruginosa* WaaP lipopolysaccharide heptose kinase. *Scientific Reports*, 8(1), 14124. doi:10.1038/s41598-018-32379-1

Kudva, R., Pardo-Avila, F., Sandhu, H., Carroni, M., Bernstein, H. D., & Von Heijne, G. (2018). The Shape of the Ribosome Exit Tunnel Affects Cotranslational Protein Folding. *bioRxiv*. doi:10.1101/274191

Kummer, E., Leibundgut, M., Rackham, O., Lee, R. G., Boehringer, D., Filipovska, A., & Ban, N. (2018). Unique features of mammalian mitochondrial translation initiation revealed by cryo-EM. *Nature*, 560(7717), 263-267. doi:10.1038/s41586-018-0373-y

Kusmierenk, M., Hoßmann, J., Witte, R., Opitz, W., Vollmer, I., Volk, M., Dersch, P. (2019). A bacterial secreted translocator hijacks riboregulators to control type III secretion in response to host cell contact. *PLOS Pathogens*, 15(6), e1007813. doi:10.1371/journal.ppat.1007813

Lagoutte, P., Lugari, A., Elie, C., Potisopon, S., Donnat, S., Mignon, C., Stadthagen, G. (2019). Combination of ribosome display and next generation sequencing as a powerful method for identification of affibody binders against β -lactamase CTX-M15. *N Biotechnol*. doi:<https://doi.org/10.1016/j.nbt.2019.01.004>

Lavickova, B., & Maerkl, S. J. (2018). A simple, robust, and low-cost method to produce the PURE cell-free system. *bioRxiv*, 420570. doi:10.1101/420570

Lavickova, B., & Maerkl, S. J. (2019). A Simple, Robust, and Low-Cost Method To Produce the PURE Cell-Free System. *ACS Synthetic Biology*, 8(2), 455-462. doi:10.1021/acssynbio.8b00427

Layton, C. J., McMahon, P. L., & Greenleaf, W. J. (2018). Large-scale, quantitative protein assays on a high-throughput DNA sequencing chip. *bioRxiv*. doi:10.1101/342808

Lenz, M., Meissner, J., Quertinmont, L., Lutz, S., Kastner, J., & Nestl, B. M. (2017). Asymmetric Ketone Reduction by Imine Reductases. *ChemBioChem*, 18(3), 253-256. doi:10.1002/cbic.201600647

Leroy, M., Piton, J., Gilet, L., Pellegrini, O., Proux, C., Coppee, J. Y., Condon, C. (2017). Rae1/YacP, a new endoribonuclease involved in ribosome-dependent mRNA decay in *Bacillus subtilis*. *EMBO J*, 36(9), 1167-1181. doi:10.15252/embj.201796540

Li, C., Liu, S., Liu, P., Wang, Y., Xu, C., Tao, J., & He, C. (2018). The YebN Leader RNA Acts as a Mn²⁺ Sensor Required for the Interaction of *Xanthomonas oryzae* and Rice. *Molecular Plant-Microbe Interactions*. doi:10.1094/MPMI-02-18-0043-R

Li, J., Wassie, B., & Church, G. M. (2017). Physiological Assembly Of Functionally Active 30S Ribosomal Subunits From *In Vitro* Synthesized Parts. *bioRxiv*. doi:10.1101/137745

Li, J., Zhang, C., Huang, P., Kuru, E., Benson, E. T. C. F., Li, T., & Church, G. M. (2017). Dissecting limiting factors of the Protein synthesis Using Recombinant Elements (PURE) system. *bioRxiv*. doi:10.1101/099838

Li, J., Zhang, C., Huang, P., Kuru, E., Forster-Benson, E. T. C., Li, T., & Church, G. M. (2017). Dissecting limiting factors of the Protein synthesis Using Recombinant Elements (PURE) system. *Translation*, 5(1), e1327006. doi:10.1080/21690731.2017.1327006

Li, X., Jiang, Y., Chong, S., & Walt, D. R. (2018). Bottom-up single-molecule strategy for understanding subunit function of tetrameric β -galactosidase. *Proceedings of the National Academy of Sciences*. doi:10.1073/pnas.1805690115

Lim, M. C. C., Maubach, G., Sokolova, O., Feige, M. H., Diezko, R., Buchbinder, J., Naumann, M. (2017). Pathogen-induced ubiquitin-editing enzyme A20 bifunctionally shuts off NF-kappaB and caspase-8-dependent apoptotic cell death. *Cell Death Differ*, 24(9), 1621-1631. doi:10.1038/cdd.2017.89

Liu, K., Maciuba, K., & Kaiser, C. M. (2019). The Ribosome Cooperates with a Chaperone to Guide Multi-domain Protein Folding. *Molecular cell*. doi:<https://doi.org/10.1016/j.molcel.2019.01.043>

Liu, K., Rehfus, J. E., Mattson, E., & Kaiser, C. M. (2017). The ribosome destabilizes native and non-native structures in a nascent multidomain protein. *Protein Sci*, 26(7), 1439-1451. doi:10.1002/pro.3189

Liu, N., Hargreaves, V. V., Zhu, Q., Kurland, J. V., Hong, J., Kim, W., Orkin, S. H. (2018). Direct Promoter Repression by BCL11A Controls the Fetal to Adult Hemoglobin Switch. *Cell*. doi:<https://doi.org/10.1016/j.cell.2018.03.016>

Ma, D., Shen, L., Wu, K., Diehnelt, C. W., & Green, A. A. (2018). Low-Cost Detection of Norovirus Using Paper-Based Cell-Free Systems and Synbody-Based Viral Enrichment. *Synthetic Biology*, ysy018-ysy018. doi:10.1093/synbio/ysy018

Makki, A., Rada, P., Žářský, V., Kereičhe, S., Kováčik, L., Novotný, M., Tachezy, J. (2019). Triplet-pore structure of a highly divergent TOM complex of hydrogenosomes in *Trichomonas vaginalis*. *PLOS Biology*, 17(1), e3000098. doi:10.1371/journal.pbio.3000098

Mardirossian, M., Barrière, Q., Timchenko, T., Müller, C., Pacor, S., Mergaert, P., Wilson, D. N. (2018). Fragments of the Nonlytic Proline-Rich Antimicrobial Peptide Bac5 Kill *Escherichia coli* Cells by Inhibiting Protein Synthesis. *Antimicrobial Agents and Chemotherapy*, 62(8), e00534-00518. doi:10.1128/aac.00534-18

Mardirossian, M., Pérébaskine, N., Benincasa, M., Gambato, S., Hofmann, S., Huter, P., Wilson, D. N. (2018). The Dolphin Proline-Rich Antimicrobial Peptide Tur1A Inhibits Protein Synthesis by Targeting the Bacterial Ribosome. *Cell Chemical Biology*. doi:<https://doi.org/10.1016/j.chembiol.2018.02.004>

- Mariani, L., Weinand, K., Vedenko, A., Barrera, L. A., & Bulyk, M. L. (2017). Identification of Human Lineage-Specific Transcriptional Coregulators Enabled by a Glossary of Binding Modules and Tunable Genomic Backgrounds. *Cell Syst*, 5(3), 187-201 e187. doi:10.1016/j.cels.2017.06.015
- Meydan, S., Marks, J., Klepacki, D., Sharma, V., Baranov, P. V., Firth, A. E., Mankin, A. S. (2019). Retapamulin-assisted ribosome profiling reveals the alternative bacterial proteome. *bioRxiv*, 520783. doi:10.1101/520783
- Meydan, S., Marks, J., Klepacki, D., Sharma, V., Baranov, P. V., Firth, A. E., Mankin, A. S. (2019). Retapamulin-Assisted Ribosome Profiling Reveals the Alternative Bacterial Proteome. *Molecular cell*. doi:<https://doi.org/10.1016/j.molcel.2019.02.017>
- Migas, U. M., Quinn, M. K., & McManus, J. J. (2017). Protein self-assembly following *in situ* expression in artificial and mammalian cells. *Integr Biol (Camb)*, 9(5), 444-450. doi:10.1039/c6ib00240d
- Moore, S. J., MacDonald, J. T., & Freemont, P. S. (2017). Cell-free synthetic biology for *in vitro* prototype engineering. *Biochem Soc Trans*, 45(3), 785-791. doi:10.1042/BST20170011
- Moriizumi, Y., Tabata, K. V., Miyoshi, D., & Noji, H. (2019). Osmolyte-Enhanced Protein Synthesis Activity of a Reconstituted Translation System. *ACS Synthetic Biology*. doi:10.1021/acssynbio.8b00513
- Mückl, A., Schwarz-Schilling, M., Fischer, K., & Simmel, F. C. (2018). Filamentation and restoration of normal growth in *Escherichia coli* using a combined CRISPRi sgRNA/antisense RNA approach. *PLoS ONE*, 13(9), e0198058. doi:10.1371/journal.pone.0198058
- Müller, P., Gimpel, M., Wildenhain, T., & Brantl, S. (2019). A new role for CsrA: promotion of complex formation between an sRNA and its mRNA target in *Bacillus subtilis*. *RNA Biol*, 16(7), 972-987. doi:10.1080/15476286.2019.1605811
- Nguyen, D. T. T., Richter, D., Michel, G., Mitschka, S., Kolanus, W., Cuevas, E., & Wulczyn, F. G. (2017). The ubiquitin ligase LIN41/TRIM71 targets p53 to antagonize cell death and differentiation pathways during stem cell differentiation. *Cell Death Differ*, 24(6), 1063-1078. doi:10.1038/cdd.2017.54
- Notari, L., Martinez-Carranza, M., Stenmark, P., & Von Heijne, G. (2018). Cotranslational folding of a pentarepeat β -helix protein. *bioRxiv*. doi:10.1101/255810
- Nshogozabahizi, J. C., Aubrey, K. L., Ross, J. A., & Thakor, N. (2019). Applications and limitations of regulatory RNA elements in synthetic biology and biotechnology. *Journal of Applied Microbiology*, 0(ja). doi:10.1111/jam.14270
- Osterman, I. A., Khabibullina, N. F., Komarova, E. S., Kasatsky, P., Kartsev, V. G., Bogdanov, A. A., Polikanov, Y. S. (2017). Madumycin II inhibits peptide bond formation by forcing the peptidyl transferase center into an inactive state. *Nucleic Acids Res*, 45(12), 7507-7514. doi:10.1093/nar/gkx413

Pantel, L., Florin, T., Dobosz-Bartoszek, M., Racine, E., Sarciaux, M., Serri, M., Gualtieri, M. (2018). Odilorhabdins, Antibacterial Agents that Cause Miscoding by Binding at a New Ribosomal Site. *Molecular Cell*, 70(1), 83-94.e87. doi:<https://doi.org/10.1016/j.molcel.2018.03.001>

Pardatscher, G., Schwarz-Schilling, M., Daube, S. S., Bar-Ziv, R. H., & Simmel, F. C. (2018). Gene Expression on DNA Biochips Patterned with Strand-Displacement Lithography. *Angew Chem Int Ed Engl*, 57(17), 4783-4786. doi:[10.1002/anie.201800281](https://doi.org/10.1002/anie.201800281)

Pardee, K. (2018). Perspective: Solidifying the impact of cell-free synthetic biology through lyophilization. *Biochemical Engineering Journal*, 138, 91-97. doi:<https://doi.org/10.1016/j.bej.2018.07.008>

Park, H., McGibbon, L. C., Potts, A. H., Yakhnin, H., Romeo, T., & Babitzke, P. (2017). Translational Repression of the RpoS Antiadapter IraD by CsrA Is Mediated via Translational Coupling to a Short Upstream Open Reading Frame. *mBio*, 8(4). doi:[10.1128/mBio.01355-17](https://doi.org/10.1128/mBio.01355-17)

Penvose, A., Keenan, J. L., Bray, D., Ramlall, V., & Siggers, T. (2019). Comprehensive study of nuclear receptor DNA binding provides a revised framework for understanding receptor specificity. *Nature Communications*, 10(1), 2514. doi:[10.1038/s41467-019-10264-3](https://doi.org/10.1038/s41467-019-10264-3)

Petroll, K., Kopp, D., Care, A., Bergquist, P. L., & Sunna, A. (2018). Tools and strategies for constructing cell-free enzyme pathways. *Biotechnology Advances*. doi:<https://doi.org/10.1016/j.biotechadv.2018.11.007>

Praetorius, F., & Dietz, H. (2017). Self-assembly of genetically encoded DNA-protein hybrid nanoscale shapes. *Science*, 355(6331). doi:[10.1126/science.aam5488](https://doi.org/10.1126/science.aam5488)

Puckette, M., Clark, B. A., Smith, J. D., Turecek, T., Martel, E., Gabbert, L., Rasmussen, M. (2017). Foot-and-Mouth Disease (FMD) Virus 3C Protease Mutant L127P: Implications for FMD Vaccine Development. *J Virol*, 91(22). doi:[10.1128/JVI.00924-17](https://doi.org/10.1128/JVI.00924-17)

Pyrihová, E., Motyčková, A., Voleman, L., Wandyszewska, N., Fišer, R., Seydlová, G., Doležal, P. (2018). A Single Tim Translocase in the Mitosomes of Giardia intestinalis Illustrates Convergence of Protein Import Machines in Anaerobic Eukaryotes. *Genome Biology and Evolution*, 10(10), 2813-2822. doi:[10.1093/gbe/evy215](https://doi.org/10.1093/gbe/evy215)

Raad, M., Modavi, C., Sukovich, D. J., & Anderson, J. C. (2017). Observing Biosynthetic Activity Utilizing Next Generation Sequencing and the DNA Linked Enzyme Coupled Assay. *ACS Chem Biol*, 12(1), 191-199. doi:[10.1021/acschembio.6b00652](https://doi.org/10.1021/acschembio.6b00652)

Rajaratnam, G., Supeinthiran, A., Meier, R., & Su, K. F. Y. (2018). CRISPR/Cas9 deletions in a conserved exon of Distal-less generates gains and losses in a recently acquired morphological novelty in flies. *iScience*, 10, 222-233. doi:<https://doi.org/10.1016/j.isci.2018.11.036>

Ramakrishnan, R., Houben, B., Rousseau, F., & Schymkowitz, J. (2019). Differential proteostatic regulation of insoluble and abundant proteins. *Bioinformatics*. doi:[10.1093/bioinformatics/btz214](https://doi.org/10.1093/bioinformatics/btz214)

- Ranjan, N., & Leidel, S. A. (2019). The epitranscriptome in translation regulation: mRNA and tRNA modifications as the two sides of the same coin? *FEBS Letters*, 593(13), 1483-1493. doi:10.1002/1873-3468.13491
- Ray, S., Tillo, D., Assad, N., Ufot, A., Deppmann, C., Durell, S. R., Vinson, C. (2018). Replacing C189 in the bZIP domain of Zta with S, T, V, or A changes DNA binding specificity to four types of double-stranded DNA. *Biochem Biophys Res Commun*, 501(4), 905-912. doi:10.1016/j.bbrc.2018.05.080
- Ricci, V., Attah, V., Overton, T., Grainger, D. C., & Piddock, L. J. V. (2017). CsrA maximizes expression of the AcrAB multidrug resistance transporter. *Nucleic Acids Res*, 45(22), 12798-12807. doi:10.1093/nar/gkx929
- Rycroft, J. A., Gollan, B., Grabe, G. J., Hall, A., Cheverton, A. M., Larrouy-Maumus, G., Helaine, S. (2018). Activity of acetyltransferase toxins involved in *Salmonella* persister formation during macrophage infection. *Nature Communications*, 9(1), 1993. doi:10.1038/s41467-018-04472-6
- Sadler, F. W., Dodevski, I., & Sarkar, C. A. (2017). RNA Thermometers for the PURExpress System. *ACS Synth Biol*. doi:10.1021/acssynbio.7b00294
- Samelson, A. J., Bolin, E., Costello, S. M., Sharma, A. K., O'Brien, E. P., & Marqusee, S. (2018). Kinetic and structural comparison of a protein's cotranslational folding and refolding pathways. *Science Advances*, 4(5). doi:10.1126/sciadv.aas9098
- Schneider, B., Weigel, W., Sztukowska, M., & Demuth, D. R. (2018). Identification and functional characterization of type II toxin/antitoxin systems in *Aggregatibacter actinomycetemcomitans*. *Mol Oral Microbiol*, 33(3), 224-233. doi:10.1111/omi.12215
- Seip, B., Sacheau, G., Dupuy, D., & Innis, C. A. (2018). High-throughput inverse toeprinting reveals the complete sequence dependence of ribosome-targeting antibiotics. *bioRxiv*, 298794. doi:10.1101/298794
- Seip, B., Sacheau, G., Dupuy, D., & Innis, C. A. (2018). Ribosomal stalling landscapes revealed by high-throughput inverse toeprinting of mRNA libraries. *Life Science Alliance*, 1(5). doi:10.26508/lsa.201800148
- Senoussi, A., Lee Tin Wah, J., Shimizu, Y., Robert, J., Jaramillo, A., Findeiss, S., Estevez-Torres, A. (2018). Quantitative Characterization of Translational Riboregulators Using an *in Vitro* Transcription–Translation System. *ACS Synthetic Biology*, 7(5), 1269-1278. doi:10.1021/acssynbio.7b00387
- Sharma, K., Hongo, A., Nishigaki, K., Takamura, Y., & Biyani, M. (2018). ‘Head-to-Head’ mRNA display for the translation of multi-copied proteins with a free C-terminus. *Anal Biochem*, 557, 77-83. doi:<https://doi.org/10.1016/j.ab.2018.07.015>

- Shokri, L., Inukai, S., Hafner, A., Weinand, K., Hens, K., Vedenko, A., Bulyk, M. L. (2019). A Comprehensive Drosophila melanogaster Transcription Factor Interactome. *Cell Reports*, 27(3), 955-970.e957. doi:<https://doi.org/10.1016/j.celrep.2019.03.071>
- Srivastava, R., Zalisko, B. E., Keenan, R. J., & Howell, S. H. (2017). The GET System Inserts the Tail-Anchored Protein, SYP72, into Endoplasmic Reticulum Membranes. *Plant Physiol*, 173(2), 1137-1145. doi:10.1104/pp.16.00928
- Sterk, M., Romilly, C., & Wagner, E Gerhart H. (2018). Unstructured 5'-tails act through ribosome standby to override inhibitory structure at ribosome binding sites. *Nucleic Acids Research*, gky073-gky073. doi:10.1093/nar/gky073
- Steyer, D. J., & Kennedy, R. T. (2019). High-Throughput Nanoelectrospray Ionization-Mass Spectrometry Analysis of Microfluidic Droplet Samples. *Analytical Chemistry*, 91(10), 6645-6651. doi:10.1021/acs.analchem.9b00571
- Su, T., Cheng, J., Sohmen, D., Hedman, R., Berninghausen, O., von Heijne, G., Beckmann, R. (2017). The force-sensing peptide VemP employs extreme compaction and secondary structure formation to induce ribosomal stalling. *eLife*, 6, e25642. doi:10.7554/eLife.25642
- Takahashi, M. K., Tan, X., Dy, A. J., Braff, D., Akana, R. T., Furuta, Y., Collins, J. J. (2018). A low-cost paper-based synthetic biology platform for analyzing gut microbiota and host biomarkers. *Nature Communications*, 9(1), 3347. doi:10.1038/s41467-018-05864-4
- Tang, T. D., Cecchi, D., Fracasso, G., Accardi, D., Coutable-Pennarun, A., Mansy, S. S., Mann, S. (2017). Gene-Mediated Chemical Communication in Synthetic Protocell Communities. *ACS Synth Biol*. doi:10.1021/acssynbio.7b00306
- Tereshchenkov, A. G., Dobosz-Bartoszek, M., Osterman, I. A., Marks, J., Sergeeva, V. A., Kasatsky, P., Polikanov, Y. S. (2018). Binding and Action of Amino Acid Analogs of Chloramphenicol upon the Bacterial Ribosome. *J Mol Biol*. doi:10.1016/j.jmb.2018.01.016
- Tillo, D., Ray, S., Syed, K. S., Gaylor, M. R., He, X., Wang, J., Vinson, C. (2017). The Epstein-Barr Virus B-ZIP Protein Zta Recognizes Specific DNA Sequences Containing 5-Methylcytosine and 5-Hydroxymethylcytosine. *Biochemistry*, 56(47), 6200-6210. doi:10.1021/acs.biochem.7b00741
- Tran, S. T. P., Hipolito, C. J., Suzuki, H., Xie, R., Kim Tuyen, H. D., Dijke, P. t., Kato, M. (2019). Generation of non-standard macrocyclic peptides specifically binding TSC-22 homologous gene-1. *Biochemical and Biophysical Research Communications*, 516(2), 445-450. doi:<https://doi.org/10.1016/j.bbrc.2019.06.035>
- VanDuisse, C. M., Parks, A. R., & Escalante-Semerena, J. C. (2017). A Toxin Involved in *Salmonella* Persistence Regulates Its Activity by Acetylating Its Cognate Antitoxin, a Modification Reversed by CobB Sirtuin Deacetylase. *mBio*, 8(3). doi:10.1128/mBio.00708-17

Verdorfer, T., & Gaub, H. E. (2018). Ligand Binding Stabilizes Cellulosomal Cohesins as Revealed by AFM-based Single-Molecule Force Spectroscopy. *Scientific Reports*, 8(1), 9634. doi:10.1038/s41598-018-27085-x

Wang, S., Yang, C. I., & Shan, S. O. (2017). SecA mediates cotranslational targeting and translocation of an inner membrane protein. *J Cell Biol*, 216(11), 3639-3653. doi:10.1083/jcb.201704036

Wang, X., Arceci, A., Bird, K., Mills, C. A., Choudhury, R., Kernan, J. L., Emanuele, M. J. (2017). VprBP/DCAF1 Regulates the Degradation and Nonproteolytic Activation of the Cell Cycle Transcription Factor FoxM1. *Mol Cell Biol*, 37(13). doi:10.1128/MCB.00609-16

Wensel, D., Sun, Y., Li, Z., Zhang, S., Picarillo, C., McDonagh, T., Davis, J. (2017). Discovery and Characterization of a Novel CD4-Binding Adnectin with Potent Anti-HIV Activity. *Antimicrob Agents Chemother*, 61(8). doi:10.1128/AAC.00508-17

Wick, S., Walsh, D. I., Bobrow, J., Hamad-Schifferli, K., Kong, D. S., Thorsen, T., Carr, P. A. (2019). PERSIA for Direct Fluorescence Measurements of Transcription, Translation, and Enzyme Activity in Cell-Free Systems. *ACS Synthetic Biology*, 8(5), 1010-1025. doi:10.1021/acssynbio.8b00450

Widowati, E. W., Bamberg-Lemper, S., & Becker, W. (2018). Mutational analysis of two residues in the DYRK homology box of the protein kinase DYRK1A. *BMC Research Notes*, 11(1), 297. doi:10.1186/s13104-018-3416-4

Widowati, E. W., Ernst, S., Hausmann, R., Müller-Newen, G., & Becker, W. (2018). Functional characterization of DYRK1A missense variants associated with a syndromic form of intellectual deficiency and autism. *Biology Open*, 7(4). doi:10.1242/bio.032862

Wilcox, B., Osterman, I., Serebryakova, M., Lukyanov, D., Komarova, E., Gollan, B., Severinov, K. (2018). *Escherichia coli* ItaT is a type II toxin that inhibits translation by acetylating isoleucyl-tRNA^{Ille}. *Nucleic Acids Research*, gky560-gky560. doi:10.1093/nar/gky560

Wruck, F., Katranidis, A., Nierhaus, K. H., Buldt, G., & Hegner, M. (2017). Translation and folding of single proteins in real time. *Proc Natl Acad Sci USA*, 114(22), E4399-E4407. doi:10.1073/pnas.1617873114

Xu, C., Liu, K., Lei, M., Yang, A., Li, Y., Hughes, T. R., & Min, J. (2017). DNA Sequence Recognition of Human CXXC Domains and Their Structural Determinants. *Structure*. doi:10.1016/j.str.2017.11.022

Yakhnin, H., Aichele, R., Ades, S. E., Romeo, T., & Babitzke, P. (2017). Circuitry linking the global Csr and sigma(E)-dependent cell envelope stress response systems. *J Bacteriol*. doi:10.1128/JB.00484-17

Yamaguchi, A., Iraha, F., Ohtake, K., & Sakamoto, K. (2018). Pyrrollysyl-tRNA Synthetase with a Unique Architecture Enhances the Availability of Lysine Derivatives in Synthetic Genetic Codes. *Molecules*, 23(10), 2460.

Yeom, J., Pontes, M. H., Choi, J., & Groisman, E. A. (2018). A protein that controls the onset of a *Salmonella* virulence program. *The EMBO Journal*. doi:10.15252/embj.201796977

Yeom, J., Wayne, K. J., & Groisman, E. A. (2017). Sequestration from Protease Adaptor Confers Differential Stability to Protease Substrate. *Mol Cell*, 66(2), 234-246 e235. doi:10.1016/j.molcel.2017.03.009

Yin, Y., Morgunova, E., Jolma, A., Kaasinen, E., Sahu, B., Khund-Sayeed, S., Taipale, J. (2017). Impact of cytosine methylation on DNA binding specificities of human transcription factors. *Science*, 356(6337). doi:10.1126/science.aaj2239

Yoon, K. A., Park, Y. H., Koh, Y. H., & Lee, S. H. (2017). Bioactivity and molecular characterization of bombolitins from *Bombus ardens*, *B. consobrinus*, *B. terrestris* and *B. ussurensis*. *Journal of Asia-Pacific Entomology*, 20(4), 1190-1196. doi:10.1016/j.aspen.2017.08.020

You, C., Dai, X., & Wang, Y. (2017). Position-dependent effects of regioisomeric methylated adenine and guanine ribonucleosides on translation. *Nucleic Acids Res*, 45(15), 9059-9067. doi:10.1093/nar/gkx515

Yue, K., Zhu, Y., & Kai, L. (2019). Cell-Free Protein Synthesis: Chassis toward the Minimal Cell. *Cells*, 8(4), 315.

Zhang, S.-Q., Ma, K.-Y., Schonnesen, A. A., Zhang, M., He, C., Sun, E., Jiang, N. (2018). High-throughput determination of the antigen specificities of T cell receptors in single cells. *Nat Biotechnol*. doi:10.1038/nbt.4282

Zubaite, G., Simutis, K., Galinis, R., Milkus, V., Kiseliovav, V., & Mazutis, L. (2017). Droplet Microfluidics Approach for Single-DNA Molecule Amplification and Condensation into DNA-Magnesium-Pyrophosphate Particles. *Micromachines*, 8(2), 62.

Zuo, Z., Roy, B., Chang, Y. K., Granas, D., & Stormo, G. D. (2017). Measuring quantitative effects of methylation on transcription factor-DNA binding affinity. *Sci Adv*, 3(11), eaao1799. doi:10.1126/sciadv.aao1799



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