

Bibliography

- Adams KL, Palmer JD. 2003. Evolution of mitochondrial gene content: gene loss and transfer to the nucleus. *Molecular phylogenetics and evolution* 29: 380-395.
- Ahn I, Jeong BJ, Bae SE, Jung J, Son HS. 2006. Genomic analysis of influenza A viruses, including avian flu (H5N1) strains. *European journal of epidemiology* 21: 511-519.
- Akashi H. 1994. Synonymous codon usage in *Drosophila melanogaster*: natural selection and translational accuracy. *Genetics* 136: 927-935.
- Akashi H. 1997. Codon bias evolution in *Drosophila*. Population genetics of mutation-selection drift. *Gene* 205: 269-278.
- Akashi H. 2001. Gene expression and molecular evolution. *Current opinion in genetics & development* 11: 660-666.
- Akashi H, Gojobori T. 2002. Metabolic efficiency and amino acid composition in the proteomes of *Escherichia coli* and *Bacillus subtilis*. *Proceedings of the National Academy of Sciences* 99: 3695-3700.
- Andersson S, Kurland C. 1990. Codon preferences in free-living microorganisms. *Microbiological Reviews* 54: 198-210.
- Anfinsen CB. 1977. Studies on the principles that govern the folding of protein chains. *Nobel Lectures in Molecular Biology* 401:1933-1975.
- Aota SI, Ikemura T. 1986. Diversity in G+ C content at the third position of codons in vertebrate genes and its cause. *Nucleic acids research* 14: 6345-6355.
- Arava Y, Boas FE, Brown PO, Herschlag D. 2005. Dissecting eukaryotic translation and its control by ribosome density mapping. *Nucleic acids research* 33: 2421-2432.
- Baba T, Ara T, Hasegawa M, Takai Y, Okumura Y, Baba M, Datsenko KA, Tomita M, Wanner BL, Mori H. 2006. Construction of *Escherichia coli* K-12 in-frame, single-gene knockout mutants: the Keio collection. *Molecular systems biology* 2: 2006.0008.
- Bahir I, Fromer M, Prat Y, Linial M. 2009. Viral adaptation to host: a proteome-based analysis of codon usage and amino acid preferences. *Molecular systems biology* 5: 2009.71.
- Baker D, Agard DA. 1994. Influenza hemagglutinin: kinetic control of protein function. *Structure* 2: 907-910.
- Barrai I, Volinia S, Scapoli C. 1995. The usage of oligopeptides in proteins correlates negatively with molecular weight. *International journal of peptide and protein research* 45: 326-331.
- Behura SK, Severson DW. 2012. Comparative analysis of codon usage bias and codon context patterns between dipteran and hymenopteran sequenced genomes. *PloS one* 7: e43111.

Bibliography

- Behura SK, Severson DW. 2013. Codon usage bias: causative factors, quantification methods and genome-wide patterns: with emphasis on insect genomes. *Biological Reviews* 88: 49-61.
- Berg OG. 1996. Selection intensity for codon bias and the effective population size of *Escherichia coli*. *Genetics* 142: 1379-1382.
- Bibb M, Findlay P, Johnson M. 1984. The relationship between base composition and codon usage in bacterial genes and its use for the simple and reliable identification of protein-coding sequences. *Gene* 30: 157-166.
- Biro JC. 2008. Studies on the Origin and Evolution of Codon Bias. arXiv preprint arXiv:0807.3901.
- Blier PU, Dufresne F, Burton RS. 2001. Natural selection and the evolution of mtDNA-encoded peptides: evidence for intergenic co-adaptation. *Trends in Genetics* 17: 400-406.
- Braun H-P, Emmermann M, Kruft V, Schmitz U. 1992. The general mitochondrial processing peptidase from potato is an integral part of cytochrome c reductase of the respiratory chain. *The EMBO Journal* 11: 3219.
- Brown GG, Gadaleta G, Pepe G, Saccone C, Sbisà E. 1986. Structural conservation and variation in the D-loop-containing region of vertebrate mitochondrial DNA. *Journal of molecular biology* 192: 503-511.
- Bulmer M. 1991. The selection-mutation-drift theory of synonymous codon usage. *Genetics* 129: 897-907.
- Burmann BM, Knauer SH, Sevostyanova A, Schweimer K, Mooney RA, Landick R, Artsimovitch I, Rösch P. 2012. An α helix to β barrel domain switch transforms the transcription factor RfaH into a translation factor. *cell* 150: 291-303.
- Butt AM, Nasrullah I, Tong Y. 2014. Genome-wide analysis of codon usage and influencing factors in chikungunya viruses. *PLoS One* 9: e90905.
- Campos JL, Zeng K, Parker DJ, Charlesworth B, Haddrill PR. 2013. Codon usage bias and effective population sizes on the X chromosome versus the autosomes in *Drosophila melanogaster*. *Molecular biology and evolution* 30: 811-823.
- Chamary J, Parmley JL, Hurst LD. 2006. Hearing silence: non-neutral evolution at synonymous sites in mammals. *Nature Reviews Genetics* 7: 98-108.
- Chaney JL, Clark PL, Gruner SM, Lattman EE, Hass MA, Mulder FA, Noda NN, Inagaki F, Taheri-Araghi S, Brown SD. 2015. Roles for Synonymous Codon Usage in Protein Biogenesis. *Annual review of biophysics* 44:143-66.
- Chen H, Sun S, Norenburg JL, Sundberg P. 2014. Mutation and Selection Cause Codon Usage and Bias in Mitochondrial Genomes of Ribbon Worms (*Nemertea*). *PloS one* 9(1): e85631.

Bibliography

- Chen JQ, Cammarata PR, Baines CP, Yager JD. 2009. Regulation of mitochondrial respiratory chain biogenesis by estrogens/estrogen receptors and physiological, pathological and pharmacological implications. *Biochimica et Biophysica Acta (BBA)-Molecular Cell Research* 1793: 1540-1570.
- Chen L, Yang D, Liu T, Nong X, Huang X, Xie Y, Fu Y, Zheng W, Zhang R, Wu X. 2013. Synonymous codon usage patterns in different parasitic platyhelminth mitochondrial genomes. *Genetics and molecular research: GMR* 12: 587.
- Chen Y. 2013. A comparison of synonymous codon usage bias patterns in DNA and RNA virus genomes: quantifying the relative importance of mutational pressure and natural selection. *BioMed research international* e406342.
- Choudhury MN, Chakraborty S. 2015. Codon usage pattern in human SPANX genes. *Bioinformation* 11: 454.
- Chung BK, Lee DY. 2012. Computational codon optimization of synthetic gene for protein expression. *BMC systems biology* 6: 134.
- Clark AG, Eisen MB, Smith DR, Bergman CM, Oliver B, Markow TA, Kaufman TC, Kellis M, Gelbart W, Iyer VN. 2007. Evolution of genes and genomes on the *Drosophila* phylogeny. *Nature* 450: 203-218.
- Clarke IV TF, Clark PL. 2008. Rare codons cluster. *PLoS One* 3: e3412.
- Clarke TF, Clark PL. 2010. Increased incidence of rare codon clusters at 5'and 3'gene termini: implications for function. *BMC genomics* 11: 1.
- Cutter AD, Wasmuth JD, Blaxter ML. 2006. The evolution of biased codon and amino acid usage in nematode genomes. *Molecular biology and evolution* 23: 2303-2315.
- Daidone V, Gallinaro L, Cattini MG, Pontara E, Bertomoro A, Pagnan A, Casonato A. 2011. An apparently silent nucleotide substitution (c. 7056C> T) in the von Willebrand factor gene is responsible for type 1 von Willebrand disease. *haematologica* 96: 881-887.
- Dilucca M, Cimini G, Semmoloni A, Deiana A, Giansanti A. 2015. Codon Bias Patterns of *E. coli*'s Interacting Proteins. *PLoS One* 10: e0142127.
- Ding YZ, You YN, Sun DJ, Chen H-t, Wang YI, Chang HY, Pan L, Fang YZ, Zhang Z-w, Zhou P. 2014. The Effects of the Context-Dependent Codon Usage Bias on the Structure of the nsp1 α of Porcine Reproductive and Respiratory Syndrome Virus. *BioMed research international* e 765320.
- Dohra H, Fujishima M, Suzuki H. 2015. Analysis of amino acid and codon usage in *Paramecium bursaria*. *FEBS letters* 589: 3113-3118.
- dos Reis M, Savva R, Wernisch L. 2004. Solving the riddle of codon usage preferences: a test for translational selection. *Nucleic acids research* 32: 5036-5044.
- Dowling DK, Friberg U, Lindell J. 2008. Evolutionary implications of non-neutral mitochondrial genetic variation. *Trends in Ecology & Evolution* 23: 546-554.

Bibliography

- Dreher TW. 2010. Viral tRNAs and tRNA-like structures. Wiley Interdisciplinary Reviews: RNA 1: 402-414.
- Drummond DA, Wilke CO. 2009. The evolutionary consequences of erroneous protein synthesis. Nature Reviews Genetics 10: 715-724.
- Du Y-Z, Dickerson C, Aylsworth AS, Schwartz CE. 1998. A silent mutation, C924T (G308G), in the L1CAM gene results in X linked hydrocephalus (HSAS). Journal of medical genetics 35: 456-462.
- Duan X, Yi S, Guo X, Wang W. 2015. A Comprehensive Analysis of Codon Usage Patterns in Blunt Snout Bream (*Megalobrama amblycephala*) Based on RNA-Seq Data. International journal of molecular sciences 16: 11996-12013.
- Duret L. 2002. Evolution of synonymous codon usage in metazoans. Current opinion in genetics & development 12: 640-649.
- Duret L, Mouchiroud D. 1999. Expression pattern and, surprisingly, gene length shape codon usage in *Caenorhabditis*, *Drosophila*, and *Arabidopsis*. Proceedings of the National Academy of Sciences 96: 4482-4487.
- Ellington WR. 2001. Evolution and physiological roles of phosphagen systems. Annual Review of Physiology 63: 289-325.
- Embley TM, Martin W. 2006. Eukaryotic evolution, changes and challenges. Nature 440: 623-630.
- Eyre-Walker A, Keightley PD. 1999. High genomic deleterious mutation rates in hominids. Nature 397: 344-347.
- Faa V, Coiana A, Incani F, Costantino L, Cao A, Rosatelli MC. 2010. A synonymous mutation in the CFTR gene causes aberrant splicing in an italian patient affected by a mild form of cystic fibrosis. The Journal of Molecular Diagnostics 12: 380-383.
- Fadiel A. 2010. Genome analysis of genbank known rabbit. World rabbit science 11:117-136.
- Fedyunin I, Lehnhardt L, Böhmer N, Kaufmann P, Zhang G, Ignatova Z. 2012. tRNA concentration fine tunes protein solubility. FEBS letters 586: 3336-3340.
- Fonseca RR, Johnson WE, O'Brien SJ, Ramos M, Antunes A. 2008. The adaptive evolution of the mammalian mitochondrial genome. BMC genomics 9: 1.
- Foster PG, Hickey DA. 1999. Compositional bias may affect both DNA-based and protein-based phylogenetic reconstructions. Journal of Molecular Evolution 48: 284-290.
- Francino MP, Ochman H. 2001. Deamination as the basis of strand-asymmetric evolution in transcribed *Escherichia coli* sequences. Molecular biology and evolution 18: 1147-1150.

Bibliography

- Freire-Picos MA, Gonzalez-Siso MI, Rodríguez-Belmonte E, Rodríguez-Torres AM, Ramil E, Cerdan ME. 1994. Codon usage in *Kluyveromyces lactis* and in yeast cytochrome c-encoding genes. *Gene* 139: 43-49.
- Fuglsang A. 2003. Codon optimizer: a freeware tool for codon optimization. *Protein expression and purification* 31: 247-249.
- Fung KL, Pan J, Ohnuma S, Lund PE, Pixley JN, Kimchi-Sarfaty C, Ambudkar SV, Gottesman MM. 2014. MDR1 synonymous polymorphisms alter transporter specificity and protein stability in a stable epithelial monolayer. *Cancer research* 74: 598-608.
- Garcia-Vallvé S, Guzmán E, Montero M, Romeu A. 2003. HGT-DB: a database of putative horizontally transferred genes in prokaryotic complete genomes. *Nucleic acids research* 31: 187-189.
- Gatherer D, McEwan NR. 1997. Small regions of preferential codon usage and their effect on overall codon bias-The case of the plp gene. *IUBMB Life* 43: 107-114.
- Gemmell NJ, Metcalf VJ, Allendorf FW. 2004. Mother's curse: the effect of mtDNA on individual fitness and population viability. *Trends in Ecology & Evolution* 19: 238-244.
- Gibson A, Gowri-Shankar V, Higgs PG, Rattray M. 2005. A comprehensive analysis of mammalian mitochondrial genome base composition and improved phylogenetic methods. *Molecular biology and evolution* 22: 251-264.
- Gingold H, Pilpel Y. 2011. Determinants of translation efficiency and accuracy. *Molecular systems biology* 7: 481.
- Goodarzi H, Torabi N, Najafabadi HS, Archetti M. 2008. Amino acid and codon usage profiles: adaptive changes in the frequency of amino acids and codons. *Gene* 407: 30-41.
- Grantham R, Gautier C, Gouy M. 1980. Codon frequencies in 119 individual genes confirm consistent choices of degenerate bases according to genome type. *Nucleic Acids Res* 8: 1893-1912.
- Green P, Ewing B, Miller W, Thomas PJ, Green ED. 2003. Transcription-associated mutational asymmetry in mammalian evolution. *Nature genetics* 33: 514-517.
- Grote A, Hiller K, Scheer M, Münch R, Nörtemann B, Hempel DC, Jahn D. 2005. JCat: a novel tool to adapt codon usage of a target gene to its potential expression host. *Nucleic acids research* 33: W526-W531.
- Gupta S, Bhattacharyya T, Ghosh TC. 2004. Synonymous codon usage in *Lactococcus lactis*: mutational bias versus translational selection. *Journal of Biomolecular Structure and Dynamics* 21: 527-535.
- Gustafsson C, Govindarajan S, Minshull J. 2004. Codon bias and heterologous protein expression. *Trends in biotechnology* 22: 346-353.
- Gyles C, Boerlin P. 2013. Horizontally transferred genetic elements and their role in pathogenesis of bacterial disease. *Veterinary Pathology Online*: 0300985813511131.

Bibliography

- Hartl DL, Moriyama EN, Sawyer SA. 1994. Selection intensity for codon bias. *Genetics* 138: 227-234.
- Hassan S, Mahalingam V, Kumar V. 2010. Synonymous codon usage analysis of thirty two mycobacteriophage genomes. *Advances in bioinformatics* e316936.
- Hay JM, Ruvinsky I, Hedges SB, Maxson LR. 1995. Phylogenetic relationships of amphibian families inferred from DNA sequences of mitochondrial 12S and 16S ribosomal RNA genes. *Molecular biology and evolution* 12: 928-937.
- Hebert PD, Cywinska A, Ball SL. 2003. Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London B: Biological Sciences* 270: 313-321.
- Hershberg R, Petrov DA. 2008. Selection on codon bias. *Annual review of genetics* 42: 287-299.
- Hey J, Kliman RM. 2002. Interactions between natural selection, recombination and gene density in the genes of *Drosophila*. *Genetics* 160: 595-608.
- Hoeijmakers JH. 2001. Genome maintenance mechanisms for preventing cancer. *Nature* 411: 366-374.
- Hussain T, Babar M, Musthafa M, Saif R, Hussain F, Aqeel M, Naveed N, Pervez M, Khan W, Ziaullah S. Mitochondrial ATP6 and ATP8 genes based molecular diversity and phylogenetic analysis in punjab urial (*Ovis vigneipunjabiensis*). *The journal of animal and plant sciences* 3(2):311-318.
- Ikemura T. 1981. Correlation between the abundance of *Escherichia coli* transfer RNAs and the occurrence of the respective codons in its protein genes. *Journal of molecular biology* 146: 1-21.
- Ikemura T. 1982. Correlation between the abundance of yeast transfer RNAs and the occurrence of the respective codons in protein genes: differences in synonymous codon choice patterns of yeast and *Escherichia coli* with reference to the abundance of isoaccepting transfer RNAs. *Journal of molecular biology* 158: 573-597.
- Ikemura T. 1985. Codon usage and tRNA content in unicellular and multicellular organisms. *Molecular biology and evolution* 2: 13-34.
- Jenkins GM, Holmes EC. 2003. The extent of codon usage bias in human RNA viruses and its evolutionary origin. *Virus research* 92: 1-7.
- Jha S, Komar AA. 2011. Birth, life and death of nascent polypeptide chains. *Biotechnology journal* 6: 623-640.
- Jia W, Higgs PG. 2008. Codon usage in mitochondrial genomes: distinguishing context-dependent mutation from translational selection. *Molecular biology and evolution* 25: 339-351.
- Jia X, Liu S, Zheng H, Li B, Qi Q, Wei L, Zhao T, He J, Sun J. 2015. Non-uniqueness of factors constraint on the codon usage in *Bombyx mori*. *BMC genomics* 16: 356.

Bibliography

- Kane JF. 1995. Effects of rare codon clusters on high-level expression of heterologous proteins in *Escherichia coli*. *Current Opinion in Biotechnology* 6: 494-500.
- Karakozova M, Kozak M, Wong CC, Bailey AO, Yates JR, Mogilner A, Zebroski H, Kashina A. 2006. Arginylation of β -actin regulates actin cytoskeleton and cell motility. *Science* 313: 192-196.
- Karlin S, Mrázek J. 1996. What drives codon choices in human genes? *Journal of molecular biology* 262: 459-472.
- Kaufmann WK, Paules RS. 1996. DNA damage and cell cycle checkpoints. *The FASEB Journal* 10: 238-247.
- Keightley PD, Lercher MJ, Eyre-Walker A. 2005. Evidence for widespread degradation of gene control regions in hominid genomes. *PLoS Biol* 3(2): e42.
- Kelkar YD, Phillips DS, Ochman H. 2015. Effects of Genic Base Composition on Growth Rate in G+ C-Rich Genomes. *G3: Genes| Genomes| Genetics*: G3. 115.016824.
- Kim CH, Oh Y, Lee TH. 1997. Codon optimization for high-level expression of human erythropoietin (EPO) in mammalian cells. *Gene* 199: 293-301.
- Kimchi-Sarfaty C, Oh JM, Kim I-W, Sauna ZE, Calcagno AM, Ambudkar SV, Gottesman MM. 2007. A "silent" polymorphism in the MDR1 gene changes substrate specificity. *Science* 315: 525-528.
- Kliman RM, Hey J. 2003. Hill–Robertson interference in *Drosophila melanogaster*: reply to Marais, Mouchiroud and Duret. *Genetical research* 81: 89-90.
- Knight RD, Freeland SJ, Landweber LF. 2001. Rewiring the keyboard: evolvability of the genetic code. *Nature Reviews Genetics* 2: 49-58.
- Kober KM, Pogson GH. 2013. Genome-wide patterns of codon bias are shaped by natural selection in the purple sea urchin, *Strongylocentrotus purpuratus*. *G3: Genes| Genomes| Genetics* 3: 1069-1083.
- Kramer EB, Farabaugh PJ. 2007. The frequency of translational misreading errors in *E. coli* is largely determined by tRNA competition. *Rna* 13: 87-96.
- Kramer G, Boehringer D, Ban N, Bukau B. 2009. The ribosome as a platform for cotranslational processing, folding and targeting of newly synthesized proteins. *Nature structural & molecular biology* 16: 589-597.
- Kunkel TA, Loeb LA. 1981. Fidelity of mammalian DNA polymerases. *Science* 213: 765-767.
- Lakshmanan LN, Gruber J, Halliwell B, Gunawan R. 2015. Are mutagenic non D-loop direct repeat motifs in mitochondrial DNA under a negative selection pressure? *Nucleic acids research*: gkv299.
- Li J, Zhou J, Wu Y, Yang S, Tian D. 2015. GC-content of synonymous codons profoundly influences amino acid usage. *G3: Genes| Genomes| Genetics* 5: 2027-2036.

Bibliography

- Lin K, Kuang Y, Joseph JS, Kolatkar PR. 2002. Conserved codon composition of ribosomal protein coding genes in *Escherichia coli*, *Mycobacterium tuberculosis* and *Saccharomyces cerevisiae*: lessons from supervised machine learning in functional genomics. Nucleic acids research 30: 2599-2607.
- Liu Q, Feng Y, Zhao Xa, Dong H, Xue Q. 2004. Synonymous codon usage bias in *Oryza sativa*. Plant Science 167: 101-105.
- Lobry J. 1996. Origin of replication of *Mycoplasma genitalium*. Science 272: 745-746.
- Luo X, Tang Z, Xia G, Wassmann K, Matsumoto T, Rizo J, Yu H. 2004. The Mad2 spindle checkpoint protein has two distinct natively folded states. Nature structural & molecular biology 11: 338-345.
- Macaya G, Thiery J-P, Bernardi G. 1976. An approach to the organization of eukaryotic genomes at a macromolecular level. Journal of molecular biology 108: 237-254.
- Malumbres M, Gil J, Martín JF. 1993. Codon preference in corynebacteria. Gene 134: 15-24.
- Matsukage A, Bohn E, Wilson S. 1975. DNA polymerase III of mouse myeloma. Partial purification and characterization. Biochemistry 14: 1006-1020.
- Mbaye F, Dem A, Fall M, Sembène M, Diop CA, Sénégal D. 2012. Implication of the Cytochrome B nucleotide and protein mutations in the occurrence of breast cancer in Senegal. Int Jour of Applied Biol and Phar Tech 3: 107-114.
- McEwan NR, Gatherer D. 1999. Codon indices as a predictor of gene functionality in a *Frankia* operon. Canadian Journal of Botany 77: 1287-1292.
- Mirsafian H, Mat Ripen A, Singh A, Teo PH, Merican AF, Mohamad SB. 2014. A Comparative Analysis of Synonymous Codon Usage Bias Pattern in Human Albumin Superfamily. The Scientific World Journal e639682.
- Modica-Napolitano JS, Singh KK. 2004. Mitochondrial dysfunction in cancer. Mitochondrion 4: 755-762.
- Moriyama EN, Powell JR. 1998. Gene length and codon usage bias in *Drosophila melanogaster*, *Saccharomyces cerevisiae* and *Escherichia coli*. Nucleic acids research 26: 3188-3193.
- Mueller S, Papamichail D, Coleman JR, Skiena S, Wimmer E. 2006. Reduction of the rate of poliovirus protein synthesis through large-scale codon deoptimization causes attenuation of viral virulence by lowering specific infectivity. Journal of virology 80: 9687-9696.
- Mukhopadhyay P, Basak S, Ghosh TC. 2007. Synonymous codon usage in different protein secondary structural classes of human genes: implication for increased non-randomness of GC3 rich genes towards protein stability. Journal of biosciences 32: 947-963.

Bibliography

- Nair RR, Nandhini MB, Sethuraman T, Doss G. 2013. Mutational pressure dictates synonymous codon usage in freshwater unicellular α -cyanobacterial descendant *Paulinella chromatophora* and β -cyanobacterium *Synechococcus elongatus* PCC6301. SpringerPlus 2: 492.
- Orešič M, Dehn MH, Korenblum DH, Shalloway DH. 2003. Tracing specific synonymous codon–secondary structure correlations through evolution. Journal of Molecular Evolution 56: 473-484.
- Pavlov IP, Anrep GVe. 2003. Conditioned reflexes: Courier Corporation. Courier Corporation.
- Peixoto L, Fernandez V, Musto H. 2004. The effect of expression levels on codon usage in *Plasmodium falciparum*. Parasitology 128: 245-251.
- Perez-Reyes E. 1998. Molecular characterization of a novel family of low voltage-activated, T-type, calcium channels. Journal of bioenergetics and biomembranes 30: 313-318.
- Perna NT, Kocher TD. 1995. Patterns of nucleotide composition at fourfold degenerate sites of animal mitochondrial genomes. Journal of Molecular Evolution 41: 353-358.
- Pesole G, Gissi C, De Chirico A, Saccone C. 1999. Nucleotide substitution rate of mammalian mitochondrial genomes. Journal of Molecular Evolution 48: 427-434.
- Plotkin JB, Kudla G. 2011. Synonymous but not the same: the causes and consequences of codon bias. Nature Reviews Genetics 12: 32-42.
- Plotkin JB, Robins H, Levine AJ. 2004. Tissue-specific codon usage and the expression of human genes. Proceedings of the National Academy of Sciences of the United States of America 101: 12588-12591.
- Plotkin JB, Dushoff J, Desai MM, Fraser HB. 2006. Codon usage and selection on proteins. Journal of Molecular Evolution 63: 635-653.
- Powell JR, Moriyama EN. 1997. Evolution of codon usage bias in *Drosophila*. Proceedings of the National Academy of Sciences 94: 7784-7790.
- Powell JR, Sezzi E, Moriyama EN, Gleason JM, Caccone A. 2003. Analysis of a shift in codon usage in *Drosophila*. Journal of Molecular Evolution 57: S214-S225.
- Prat Y, Fromer M, Linial N, Linial M. 2009. Codon usage is associated with the evolutionary age of genes in metazoan genomes. BMC evolutionary biology 9: 285.
- Ran W, Higgs PG. 2010. The influence of anticodon–codon interactions and modified bases on codon usage bias in bacteria. Molecular biology and evolution 27: 2129-2140.
- Rand DM, Kann LM. 1998. Mutation and selection at silent and replacement sites in the evolution of animal mitochondrial DNA. Mutation and Evolution. Genetica 102:393-407.
- Rand DM, Dorfsman M, Kann LM. 1994. Neutral and non-neutral evolution of *Drosophila* mitochondrial DNA. Genetics 138: 741-756.

Bibliography

- Rand DM, Haney RA, Fry AJ. 2004. Cytonuclear coevolution: the genomics of cooperation. *Trends in Ecology & Evolution* 19: 645-653.
- Rao Y, Wu G, Wang Z, Chai X, Nie Q, Zhang X. 2011. Mutation bias is the driving force of codon usage in the *Gallus gallus* genome. *DNA research* 18: 499-512.
- Rasmussen A-S, Arnason U. 1999. Phylogenetic studies of complete mitochondrial DNA molecules place cartilaginous fishes within the tree of bony fishes. *Journal of Molecular Evolution* 48: 118-123.
- Rocha EP. 2004. Codon usage bias from tRNA's point of view: redundancy, specialization, and efficient decoding for translation optimization. *Genome research* 14: 2279-2286.
- Romero H, Zavala A, Musto H. 2000. Codon usage in *Chlamydia trachomatis* is the result of strand-specific mutational biases and a complex pattern of selective forces. *Nucleic acids research* 28: 2084-2090.
- Romero H, Zavala A, Musto H, Bernardi G. 2003. The influence of translational selection on codon usage in fishes from the family Cyprinidae. *Gene* 317: 141-147.
- Sauna ZE, Kimchi-Sarfaty C. 2011. Understanding the contribution of synonymous mutations to human disease. *Nature Reviews Genetics* 12: 683-691.
- Scarpulla RC. 2008. Transcriptional paradigms in mammalian mitochondrial biogenesis and function. *Physiological reviews* 88: 611-638.
- Schwartz S, Meshorer E, Ast G. 2009. Chromatin organization marks exon-intron structure. *Nature structural & molecular biology* 16: 990-995.
- Shah P, Gilchrist MA. 2010. Effect of correlated tRNA abundances on translation errors and evolution of codon usage bias. *PLoS Genet* 6: e1001128.
- Sharma J, Chakraborty S, Uddin A. 2014. Codon Usage Bias in Two Hemipteran Insect Species: *Bemisia tabaci* and *Homalodisca coagulata*. *Advances in Biology* e145465.
- Sharp PM, Li W-H. 1986. An evolutionary perspective on synonymous codon usage in unicellular organisms. *Journal of Molecular Evolution* 24: 28-38.
- Sharp PM, Li W-H. 1987. The codon adaptation index-a measure of directional synonymous codon usage bias, and its potential applications. *Nucleic acids research* 15: 1281-1295.
- Sharp PM, Matassi G. 1994. Codon usage and genome evolution. *Current opinion in genetics & development* 4: 851-860.
- Sharp PM, Tuohy TM, Mosurski KR. 1986. Codon usage in yeast: cluster analysis clearly differentiates highly and lowly expressed genes. *Nucleic acids research* 14: 5125-5143.
- Sharp PM, Emery LR, Zeng K. 2010. Forces that influence the evolution of codon bias. *Philosophical Transactions of the Royal Society B: Biological Sciences* 365: 1203-1212.

Bibliography

- Sharp PM, Stenico M, Peden JF, Lloyd AT. 1993. Codon usage: mutational bias, translational selection, or both? Biochemical Society Transactions 21: 835.
- Sharp PM, Averof M, Lloyd AT, Matassi G, Peden JF. 1995. DNA sequence evolution: the sounds of silence. Philosophical Transactions of the Royal Society B: Biological Sciences 349: 241-247.
- Sharp PM, Cowe E, Higgins DG, Shields DC, Wolfe KH, Wright F. 1988. Codon usage patterns in *Escherichia coli*, *Bacillus subtilis*, *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Drosophila melanogaster* and *Homo sapiens*; a review of the considerable within-species diversity. Nucleic acids research 16: 8207-8211.
- Shay JW, Werbin H. 1992. New evidence for the insertion of mitochondrial DNA into the human genome: significance for cancer and aging. Mutation Research/DNAging 275: 227-235.
- Sheffield N, Song H, Cameron S, Whiting M. 2008. A comparative analysis of mitochondrial genomes in Coleoptera (Arthropoda: Insecta) and genome descriptions of six new beetles. Molecular biology and evolution 25: 2499-2509.
- Shen W, Wang D, Ye B, Shi M, Ma L, Zhang Y, Zhao Z. 2015. GC3 biased gene domains in mammalian genomes. Bioinformatics 31(19): 3081-3084.
- Shields DC, Sharp PM. 1987. Synonymous codon usage in *Bacillus subtilis* reflects both translational selection and mutational biases. Nucleic acids research 15: 8023-8040.
- Shields DC, Sharp PM, Higgins DG, Wright F. 1988. " Silent" sites in *Drosophila* genes are not neutral: evidence of selection among synonymous codons. Molecular biology and evolution 5: 704-716.
- Shoubridge EA. 2000. Mitochondrial DNA segregation in the developing embryo. Human Reproduction 15: 229-234.
- Sinclair JF, Ziegler MM, Baldwin TO. 1994. Kinetic partitioning during protein folding yields multiple native states. Nature structural & molecular biology 1: 320-326.
- Singer GA, Hickey DA. 2000. Nucleotide bias causes a genomewide bias in the amino acid composition of proteins. Molecular biology and evolution 17: 1581-1588.
- Singh KK, Sigala B, Sikder HA, Schwimmer C. 2001. Inactivation of *Saccharomyces cerevisiae* OGG1 DNA repair gene leads to an increased frequency of mitochondrial mutants. Nucleic acids research 29: 1381-1388.
- Stenico M, Lloyd AT, Sharp PM. 1994. Codon usage in *Caenorhabditis elegans*: delineation of translational selection and mutational biases. Nucleic Acids Research 22: 2437-2446.
- Stoletzki N, Eyre-Walker A. 2007. Synonymous codon usage in *Escherichia coli*: selection for translational accuracy. Molecular biology and evolution 24: 374-381.

Bibliography

- Subramanian A, Sarkar RR. 2015. Comparison of codon usage bias across *Leishmania* and Trypanosomatids to understand mRNA secondary structure, relative protein abundance and pathway functions. *Genomics* 106: 232-241.
- Sueoka N. 1988. Directional mutation pressure and neutral molecular evolution. *Proceedings of the National Academy of Sciences* 85: 2653-2657.
- Sun L, Petrounia IP, Yagasaki M, Bandara G, Arnold FH. 2001. Expression and stabilization of galactose oxidase in *Escherichia coli* by directed evolution. *Protein engineering* 14: 699-704.
- Supek F. 2015. The Code of Silence: Widespread Associations between Synonymous Codon Biases and Gene Function. *Journal of Molecular Evolution* 82(1):65-73.
- Supek F, Miñana B, Valcárcel J, Gabaldón T, Lehner B. 2014. Synonymous mutations frequently act as driver mutations in human cancers. *cell* 156: 1324-1335.
- Syvanen M. 2012. Evolutionary implications of horizontal gene transfer. *Annual review of genetics* 46: 341-358.
- Tanguy A, Bierne N, Saavedra C, Pina B, Bachère E, Kube M, Bazin E, Bonhomme F, Boudry P, Boulo V. 2008. Increasing genomic information in bivalves through new EST collections in four species: development of new genetic markers for environmental studies and genome evolution. *Gene* 408: 27-36.
- Tatarinova TV, Alexandrov NN, Bouck JB, Feldmann KA. 2010. GC3 biology in corn, rice, sorghum and other grasses. *BMC genomics* 11: 308.
- Taylor RW, Turnbull DM. 2005. Mitochondrial DNA mutations in human disease. *Nature Reviews Genetics* 6: 389-402.
- Tindle RW. 2002. Immune evasion in human papillomavirus-associated cervical cancer. *Nature Reviews Cancer* 2: 59-64.
- Torri AF, Englund PT. 1995. A DNA polymerase β in the mitochondrion of the trypanosomatid *Crithidia fasciculata*. *Journal of Biological Chemistry* 270: 3495-3497.
- Tuller T, Carmi A, Vestsigian K, Navon S, Dorfan Y, Zaborske J, Pan T, Dahan O, Furman I, Pilpel Y. 2010. An evolutionarily conserved mechanism for controlling the efficiency of protein translation. *cell* 141: 344-354.
- Uddin A, Chakraborty S. Mutation Pressure Dictates Codon Usage Pattern in Mitochondrial ATP8 in Some Mammalian Species. *International journal of science and research* 3(6):2206-2212.
- Uddin A, Chakraborty S. 2015. Synonymous codon usage pattern in mitochondrial CYB gene in pisces, aves, and mammals. *Mitochondrial DNA*: 1-10.
- Uddin A, Mazumder TH, Choudhury MN, Chakraborty S. Codon bias and gene expression of mitochondrial ND2 gene in chordates. *Bioinformation* 11(8):407-412.

Bibliography

- Urrutia AO, Hurst LD. 2001. Codon usage bias covaries with expression breadth and the rate of synonymous evolution in humans, but this is not evidence for selection. *Genetics* 159: 1191-1199.
- Vicario S, Moriyama EN, Powell JR. 2007. Codon usage in twelve species of *Drosophila*. *BMC evolutionary biology* 7: 226.
- Wallace DC. 2005. A mitochondrial paradigm of metabolic and degenerative diseases, aging, and cancer: a dawn for evolutionary medicine. *Annual review of genetics* 39: 359.
- Walter P, Blobel G. 1981. Translocation of proteins across the endoplasmic reticulum III. Signal recognition protein (SRP) causes signal sequence-dependent and site-specific arrest of chain elongation that is released by microsomal membranes. *The Journal of Cell Biology* 91: 557-561.
- Watanabe K, Yokobori SI. 2011. tRNA modification and genetic code variations in animal mitochondria. *Journal of nucleic acids* e623095.
- Wei L, He J, Jia X, Qi Q, Liang Z, Zheng H, Ping Y, Liu S, Sun J. 2014. Analysis of codon usage bias of mitochondrial genome in *Bombyx mori* and its relation to evolution. *BMC evolutionary biology* 14: 262.
- Wickner W, Schekman R. 2005. Protein translocation across biological membranes. *Science* 310: 1452-1456.
- Wiedmann M, Huth A, Rapoport TA. 1986. A signal sequence is required for the functions of the signal recognition particle. *Biochemical and biophysical research communications* 134: 790-796.
- Wilson RB, Roof DM. 1997. Respiratory deficiency due to loss of mitochondrial DNA in yeast lacking the frataxin homologue. *Nature genetics* 16: 352-357.
- Wise CA, Srámek M, Easteal S. 1998. Departure from neutrality at the mitochondrial NADH dehydrogenase subunit 2 gene in humans, but not in chimpanzees. *Genetics* 148: 409-421.
- Woolhead CA, McCormick PJ, Johnson AE. 2004. Nascent membrane and secretory proteins differ in FRET-detected folding far inside the ribosome and in their exposure to ribosomal proteins. *cell* 116: 725-736.
- Wright F. 1990. The ‘effective number of codons’ used in a gene. *Gene* 87: 23-29.
- Xia X. 1996. Maximizing transcription efficiency causes codon usage bias. *Genetics* 144: 1309-1320.
- Xu Y, Ma P, Shah P, Rokas A, Liu Y, Johnson CH. 2013. Non-optimal codon usage is a mechanism to achieve circadian clock conditionality. *Nature* 495: 116-120.
- Yang X, Luo X, Cai X. 2014. Analysis of codon usage pattern in *Taenia saginata* based on a transcriptome dataset. *Parasites & vectors* 7: 1-11.

Bibliography

- Zardoya R, Meyer A. 1997. The complete DNA sequence of the mitochondrial genome of a “living fossil,” the coelacanth (*Latimeria chalumnae*). *Genetics* 146: 995-1010.
- Zardoya R, Meyer A. 1998. Complete mitochondrial genome suggests diapsid affinities of turtles. *Proceedings of the National Academy of Sciences* 95: 14226-14231.
- Zhang F, Saha S, Shabalina SA, Kashina A. 2010. Differential arginylation of actin isoforms is regulated by coding sequence-dependent degradation. *Science* 329: 1534-1537.
- Zhang J-F, Nie L-W, Wang Y, Hu L-L. 2009. The complete mitochondrial genome of the large-headed frog, *Limnonectes bannaensis* (Amphibia: Anura), and a novel gene organization in the vertebrate mtDNA. *Gene* 442: 119-127.
- Zhang WJ, Zhou J, Li ZF, Wang L, Gu X, Zhong Y. 2007. Comparative Analysis of Codon Usage Patterns Among Mitochondrion, Chloroplast and Nuclear Genes in *Triticum aestivum* L. *Journal of Integrative Plant Biology* 49: 246-254.
- Zhang Z, Dai W, Wang Y, Lu C, Fan H. 2013. Analysis of synonymous codon usage patterns in torque teno sus virus 1 (TTSuV1). *Archives of virology* 158: 145-154.
- Zhao S, Zhang Q, Chen Z, Zhao Y, Zhong J. 2007. The factors shaping synonymous codon usage in the genome of *Burkholderia mallei*. *Journal of Genetics and Genomics* 34: 362-372.
- Zheng Y, Zhao WM, Wang H, Zhou Y-B, Luan Y, Qi M, Cheng YZ, Tang W, Liu J, Yu H. 2007. Codon usage bias in *Chlamydia trachomatis* and the effect of codon modification in the MOMP gene on immune responses to vaccination This paper is one of a selection of papers in this Special Issue, entitled International Symposium on Recent Advances in Molecular, Clinical, and Social Medicine, and has undergone the Journal's usual peer-review process. *Biochemistry and cell biology* 85: 218-226.
- Zhong J, Li Y, Zhao S, Liu S, Zhang Z. 2007. Mutation pressure shapes codon usage in the GC-Rich genome of foot-and-mouth disease virus. *Virus Genes* 35: 767-776.
- Zhou M, Guo J, Cha J, Chae M, Chen S, Barral JM, Sachs MS, Liu Y. 2013. Non-optimal codon usage affects expression, structure and function of clock protein FRQ. *Nature* 495: 111-115.
- Zuckerkandl E, Pauling L. 1965. Evolutionary divergence and convergence in proteins. *Evolving genes and proteins* 97: 97-166.