

Bibliography

- Aas JA, Paster BJ, Stokes LN, Olsen I and Dewhirst FE (2005). Defining the normal bacterial flora of the oral cavity. *J Clin Microbiol* **43**: 5721-32.
- Abrahamsson TR, Jakobsson T, Bottcher MF, Fredrikson M, *et al.* (2007). Probiotics in prevention of IgE-associated eczema: a double-blind, randomized, placebo-controlled trial. *J Allergy Clin Immunol* **119**: 1174-80.
- Abubucker S, Segata N, Goll J, Schubert AM, *et al.* (2012). Metabolic reconstruction for metagenomic data and its application to the human microbiome. *PLoS Comput Biol* **8**: e1002358.
- Adlerberth I and Wold AE (2009). Establishment of the gut microbiota in Western infants. *Acta Paediatr* **98**: 229-38.
- Akashi H and Gojobori T (2002). Metabolic efficiency and amino acid composition in the proteomes of *Escherichia coli* and *Bacillus subtilis*. *Proc Natl Acad Sci U S A* **99**: 3695-700.
- Alakomi HL, Skytta E, Saarela M, Mattila-Sandholm T, *et al.* (2000). Lactic acid permeabilizes gram-negative bacteria by disrupting the outer membrane. *Appl Environ Microbiol* **66**: 2001-5.
- Ali A, Naz A, Soares SC, Bakhtiar M, *et al.* (2015). Pan-genome analysis of human gastric pathogen *H. pylori*: comparative genomics and pathogenomics approaches to identify regions associated with pathogenicity and prediction of potential core therapeutic targets. *Biomed Res Int* **2015**: 139580.
- Allsop AE (1998). Bacterial genome sequencing and drug discovery. *Curr Opin Biotechnol* **9**: 637-42.
- Alm RA, Bina J, Andrews BM, Doig P, *et al.* (2000). Comparative genomics of *Helicobacter pylori*: analysis of the outer membrane protein families. *Infect Immun* **68**: 4155-68.
- Altermann E, Russell WM, Azcarate-Peril MA, Barrangou R, *et al.* (2005). Complete genome sequence of the probiotic lactic acid bacterium *Lactobacillus acidophilus* NCFM. *Proc Natl Acad Sci U S A* **102**: 3906-12.
- Altschul SF, Gish W, Miller W, Myers EW and Lipman DJ (1990). Basic local alignment search tool. *J Mol Biol* **215**: 403-10.
- Altschul SF, Gish W, Miller W, Myers EW and Lipman DJ (1990). Basic local alignment search tool. *J Mol Biol* **215**: 403-10.
- Amineni U, Pradhan D and Marisetty H (2010). In silico identification of common putative drug targets in *Leptospira interrogans*. *J Chem*

- Biol* **3**: 165-73.
- An D, Dong X and Dong Z (2005). Prokaryote diversity in the rumen of yak (*Bos grunniens*) and Jinnan cattle (*Bos taurus*) estimated by 16S rDNA homology analyses. *Anaerobe* **11**: 207-15.
- Anderson KL and Salyers AA (1989). Biochemical evidence that starch breakdown by *Bacteroides thetaiotaomicron* involves outer membrane starch-binding sites and periplasmic starch-degrading enzymes. *J Bacteriol* **171**: 3192-8.
- Andersson GE and Sharp PM (1996). Codon usage in the *Mycobacterium* tuberculosis complex. *Microbiology* **142** (Pt 4): 915-25.
- Ang MY, Heydari H, Jakubovics NS, Mahmud MI, et al. (2014). FusoBase: an online *Fusobacterium* comparative genomic analysis platform. *Database (Oxford)* **2014**:
- Angelotti MC, Bhuiyan SB, Chen G and Wan XF (2007). CodonO: codon usage bias analysis within and across genomes. *Nucleic Acids Res* **35**: W132-6.
- Anishetty S, Pulimi M and Pennathur G (2005). Potential drug targets in *Mycobacterium tuberculosis* through metabolic pathway analysis. *Comput Biol Chem* **29**: 368-78.
- Apajalahti JH, Sarkilahti LK, Maki BR, Heikkinen JP, et al. (1998). Effective recovery of
- Arpaia N, Campbell C, Fan X, Dikiy S, et al. (2013). Metabolites produced by commensal bacteria promote peripheral regulatory T-cell generation. *Nature* **504**: 451-5.
- Arthur JC, Perez-Chanona E,
- Muhlbauer M, Tomkovich S, et al. (2012). Intestinal inflammation targets cancer-inducing activity of the microbiota. *Science* **338**: 120-3.
- Arumugam M, Raes J, Pelletier E, Le Paslier D, et al. (2011). Enterotypes of the human gut microbiome. *Nature* **473**: 174-80.
- Aziz RK, Bartels D, Best AA, DeJongh M, et al. (2008). The RAST Server: rapid annotations using subsystems technology. *BMC Genomics* **9**: 75.
- Backert S, Ziska E, Brinkmann V, Zimny-Arndt U, et al. (2000). Translocation of the *Helicobacter pylori* CagA protein in gastric epithelial cells by a type IV secretion apparatus. *Cell Microbiol* **2**: 155-64.
- Backhed F, Ley RE, Sonnenburg JL, Peterson DA and Gordon JI (2005). Host-bacterial mutualism in the human intestine. *Science* **307**: 1915-20.
- Apajalahti JH, Särkilahti LK, Mäki BR, Heikkinen JP, Nurminen PH and Holben WE. Effective recovery of bacterial DNA and percent-guanine-plus-cytosine-based analysis of community structure in the gastrointestinal tract of broiler chickens. *Appl Environ Microbiol* **64**: 4084-8.
- Baddini Feitoza A, Fernandes Pereira A, Ferreira da Costa N and Goncalves Ribeiro B (2009). Conjugated linoleic acid (CLA): effect modulation of body composition and lipid profile. *Nutr Hosp* **24**: 422-8.
- Baker W, van den Broek A, Camon E, Hingamp P, et al. (2000). The EMBL nucleotide sequence database. *Nucleic Acids Res* **28**: 19-23.
- Barh D, Tiwari S, Jain N, Ali A, et al.

- (2011). In silico subtractive genomics for target identification in human bacterial pathogens. *Drug Develop Res* **72**: 162-177.
- Bashir A, Klammer AA, Robins WP, Chin CS, et al. (2012). A hybrid approach for the automated finishing of bacterial genomes. *Nat Biotechnol* **30**: 701-7.
- Ben David Y, Dassa B, Borovok I, Lamed R, et al. (2015). Ruminococcal cellulosome systems from rumen to human. *Environ Microbiol* **17**: 3407-26.
- Bendtsen JD, Nielsen H, von Heijne G and Brunak S (2004). Improved prediction of signal peptides: SignalP 3.0. *J Mol Biol* **340**: 783-95.
- Benson DA, Clark K, Karsch-Mizrachi I, Lipman DJ, et al. (2000). GenBank. *Nucleic Acids Res* **43**: D30-5.
- Berman H, Henrick K, Nakamura H and Markley JL (2007). The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. *Nucleic Acids Res* **35**: D301-3.
- Bernstein FC, Koetzle TF, Williams GJ, Meyer EF, Jr., et al. (1977). The Protein Data Bank. A computer-based archival file for macromolecular structures. *Eur J Biochem* **80**: 319-24.
- Bhattacharya T, Ghosh TS and Mande SS (2015). Global Profiling of Carbohydrate Active Enzymes in Human Gut Microbiome. *PLoS One* **10**: e0142038.
- Biely P (2012). Microbial carbohydrate esterases deacetylating plant polysaccharides. *Biotechnol Adv* **30**: 1575-88.
- Bik EM, Eckburg PB, Gill SR, Nelson KE, et al. (2006). Molecular analysis of the bacterial microbiota in the human stomach. *Proc Natl Acad Sci U S A* **103**: 732-7.
- Binnewies TT, Hallin PF, Staerfeldt HH and Ussery DW (2005). Genome Update: proteome comparisons. *Microbiology* **151**: 1-4.
- Birney E, Clamp M and Hubbard T (2002). Databases and tools for browsing genomes. *Annu Rev Genomics Hum Genet* **3**: 293-310.
- Blaser MJ and Atherton JC (2004). Helicobacter pylori persistence: biology and disease. *J Clin Invest* **113**: 321-33.
- Boekhorst J, Wels M, Kleerebezem M and Siezen RJ (2006). The predicted secretome of Lactobacillus plantarum WCFS1 sheds light on interactions with its environment. *Microbiology* **152**: 3175-83.
- Bolotin A, Wincker P, Mauger S, Jaillon O, et al. (2001). The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403. *Genome Res* **11**: 731-53.
- Boraston AB, Bolam DN, Gilbert HJ and Davies GJ (2004). Carbohydrate-binding modules: fine-tuning polysaccharide recognition. *Biochem J* **382**: 769-81.
- Borenstein E (2012). Computational systems biology and in silico modeling of the human microbiome. *Brief Bioinform* **13**: 769-80.
- Bottacini F, Medini D, Pavesi A, Turroni F, et al. (2010). Comparative genomics of the genus *Bifidobacterium*. *Microbiology* **156**: 3243-54.
- Bottacini F, Milani C, Turroni F, Sanchez B, et al. (2012). *Bifidobacterium asteroides* PRL2011 genome analysis reveals clues for colonization of

- the insect gut. *PLoS One* **7**: e44229.
- Bourriaud C, Robins RJ, Martin L, Kozlowski F, *et al.* (2005). Lactate is mainly fermented to butyrate by human intestinal microfloras but inter-individual variation is evident. *J Appl Microbiol* **99**: 201-12.
- Brulc JM, Yeoman CJ, Wilson MK, Berg Miller ME, *et al.* (2011). Cellulosomics, a gene-centric approach to investigating the intraspecific diversity and adaptation of *Ruminococcus flavefaciens* within the rumen. *PLoS One* **6**: e25329.
- Buchan JR, Aucott LS and Stansfield I (2006). tRNA properties help shape codon pair preferences in open reading frames. *Nucleic Acids Res* **34**: 1015-27.
- Canani RB, Cirillo P, Terrin G, Cesarano L, *et al.* (2007). Probiotics for treatment of acute diarrhoea in children: randomised clinical trial of five different preparations. *Bmj* **335**: 340.
- Cannarozzi G, Schraudolph NN, Faty M, von Rohr P, *et al.* (2010). A role for codon order in translation dynamics. *Cell* **141**: 355-67.
- Canny, G.O. and McCormick, B.A. (2008). Bacteria in the intestine, helpful residents or enemies from within? *Infect Immun* **76**: 3360-73.
- Cantarel BL, Coutinho PM, Rancurel C, Bernard T, *et al.* (2009). The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. *Nucleic Acids Res* **37**: D233-8.
- Cantarel BL, Lombard V and Henrissat B (2012). Complex carbohydrate utilization by the healthy human microbiome. *PLoS One* **7**: e28742.
- Cantarel, B.L., Coutinho, P.M., Rancurel, C., *et al.* (2009). The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. *Nucleic Acids Res* **37**: D233-8.
- Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, *et al.* (2011). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proc Natl Acad Sci U S A* **108 Suppl 1**: 4516-22.
- Cario E, Gerken G and Podolsky DK (2007). Toll-like receptor 2 controls mucosal inflammation by regulating epithelial barrier function. *Gastroenterology* **132**: 1359-74.
- Carr R, Shen-Orr SS and Borenstein E (2013). Reconstructing the genomic content of microbiome taxa through shotgun metagenomic deconvolution. *PLoS Comput Biol* **9**: e1003292.
- Carvalho FA, Aitken JD, Vijay-Kumar M and Gewirtz AT (2012). Toll-like receptor-gut microbiota interactions: perturb at your own risk! *Annu Rev Physiol* **74**: 177-98.
- Cash HL, Whitham CV, Behrendt CL and Hooper LV (2006). Symbiotic bacteria direct expression of an intestinal bactericidal lectin. *Science* **313**: 1126-30.
- Castellarin M, Warren RL, Freeman JD, Dreolini L, *et al.* (2012). *Fusobacterium nucleatum* infection is prevalent in human colorectal carcinoma. *Genome Res* **22**: 299-306.
- Chalker AF, Minehart HW, Hughes NJ, Koretke KK, *et al.* (2001). Systematic identification of selective essential genes in *Helicobacter pylori* by genome prioritization and

- allelic replacement mutagenesis. *J Bacteriol* **183**: 1259-68.
- Chassard C, Delmas E, Robert C and Bernalier-Donadille A (2010). The cellulose-degrading microbial community of the human gut varies according to the presence or absence of methanogens. *FEMS Microbiol Ecol* **74**: 205-13.
- Chassard C, Delmas E, Robert C, Lawson PA and Bernalier-Donadille A (2012). Ruminococcus champanellensis sp. nov., a cellulose-degrading bacterium from human gut microbiota. *Int J Syst Evol Microbiol* **62**: 138-43.
- Chawley P, Samal HB, Prava J, Suar M and Mahapatra RK (2014). Comparative genomics study for identification of drug and vaccine targets in *Vibrio cholerae*: MurA ligase as a case study. *Genomics* **103**: 83-93.
- Chen X and Zhang J (2013). Why are genes encoded on the lagging strand of the bacterial genome? *Genome Biol Evol* **5**: 2436-2439.
- Chiller K, Selkin BA and Murakawa GJ (2001). Skin microflora and bacterial infections of the skin. *J Investig Dermatol Symp Proc* **6**: 170-4.
- Christopherson MR, Dawson JA, Stevenson DM, Cunningham AC, et al. (2014). Unique aspects of fiber degradation by the ruminal ethanologen *Ruminococcus albus* 7 revealed by physiological and transcriptomic analysis. *BMC Genomics* **15**: 1066.
- Clarke J, Wu HC, Jayasinghe L, Patel A, et al. (2009). Continuous base identification for single-molecule nanopore DNA sequencing. *Nat Nanotechnol* **4**: 265-70.
- Clayton TA, Baker D, Lindon JC, Everett JR and Nicholson JK (2009). Pharmacometabolic identification of a significant host-microbiome metabolic interaction affecting human drug metabolism. *Proc Natl Acad Sci U S A* **106**: 14728-33.
- Cockburn DW, Orlovsky NI, Foley MH, Kwiatkowski KJ, et al. (2015). Molecular details of a starch utilization pathway in the human gut symbiont *Eubacterium rectale*. *Mol Microbiol* **95**: 209-30.
- Collins MD, Lawson PA, Willems A, Cordoba JJ, et al. (1994). The phylogeny of the genus *Clostridium*: proposal of five new genera and eleven new species combinations. *Int J Syst Bacteriol* **44**: 812-26.
- Comeron JM and Aguade M (1998). An evaluation of measures of synonymous codon usage bias. *J Mol Evol* **47**: 268-74.
- Corr SC, Li Y, Riedel CU, O'Toole PW, et al. (2007). Bacteriocin production as a mechanism for the antiinfective activity of *Lactobacillus salivarius* UCC118. *Proc Natl Acad Sci U S A* **104**: 7617-21.
- Crowther GJ, Shanmugam D, Carmona SJ, Doyle MA, et al. (2010). Identification of attractive drug targets in neglected-disease pathogens using an in silico approach. *PLoS Negl Trop Dis* **4**: e804.
- Cutter AD, Wasmuth JD and Blaxter ML (2006). The evolution of biased codon and amino acid usage in nematode genomes. *Mol Biol Evol* **23**: 2303-15.
- Damte D, Suh JW, Lee SJ, Yohannes SB, et al. (2013). Putative drug

- and vaccine target protein identification using comparative genomic analysis of KEGG annotated metabolic pathways of *Mycoplasma hyopneumoniae*. *Genomics* **102**: 47-56.
- D'Arcy PF (1985). Nitrofurantoin. *Annals of Pharmacotherapy* **19**: 540-547.
- Darfeuille-Michaud A, Boudeau J, Bulois P, Neut C, et al. (2004). High prevalence of adherent-invasive *Escherichia coli* associated with ileal mucosa in Crohn's disease. *Gastroenterology* **127**: 412-21.
- Das S, Paul S and Dutta C (2006). Evolutionary constraints on codon and amino acid usage in two strains of human pathogenic actinobacteria *Tropheryma whipplei*. *J Mol Evol* **62**: 645-58.
- Das S, Paul S, Chatterjee S and Dutta C (2005). Codon and amino acid usage in two major human pathogens of genus *Bartonella*--optimization between replicational-transcriptional selection, translational control and cost minimization. *DNA Res* **12**: 91-102.
- Dekker FJ and Haisma HJ (2009). Histone acetyl transferases as emerging drug targets. *Drug discovery today* **14**: 942-948.
- DeSantis TZ, Hugenholtz P, Larsen N, Rojas M, et al. (2006). Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Appl Environ Microbiol* **72**: 5069-72.
- Devillard E, McIntosh FM, Duncan SH and Wallace RJ (2007). Metabolism of linoleic acid by human gut bacteria: different routes for biosynthesis of conjugated linoleic acid. *J Bacteriol* **189**: 2566-70.
- Devillard E, McIntosh FM, Paillard D, Thomas NA, et al. (2009). Differences between human subjects in the composition of the faecal bacterial community and faecal metabolism of linoleic acid. *Microbiology* **155**: 513-20.
- Dicksved J, Halfvarson J, Rosenquist M, Jarnerot G, et al. (2008). Molecular analysis of the gut microbiota of identical twins with Crohn's disease. *Isme J* **2**: 716-27.
- Dicksved J (2008). Exploring the human intestinal microbiome in health and disease, University of Agricultural Sciences, Uppsala. PhD.
- dos Reis M, Savva R and Wernisch L (2004). Solving the riddle of codon usage preferences: a test for translational selection. *Nucleic Acids Res* **32**: 5036-44.
- dos Reis M, Wernisch L and Savva R (2003). Unexpected correlations between gene expression and codon usage bias from microarray data for the whole *Escherichia coli* K-12 genome. *Nucleic Acids Res* **31**: 6976-85.
- Duffield M, Cooper I, McAlister E, Bayliss M, et al. (2010). Predicting conserved essential genes in bacteria: in silico identification of putative drug targets. *Mol Biosyst* **6**: 2482-2489.
- Duret L (2000). tRNA gene number and codon usage in the *C. elegans* genome are co-adapted for optimal translation of highly expressed genes. *Trends Genet* **16**: 287-9.
- Duret L and Mouchiroud D (1999). Expression pattern and, surprisingly, gene length shape codon usage in *Caenorhabditis*,

- Drosophila, and Arabidopsis. *Proc Natl Acad Sci U S A* **96**: 4482-7.
- Durkin HG, Bazin H and Waksman BH (1981). Origin and fate of IgE-bearing lymphocytes. I. Peyer's patches as differentiation site of cells. Simultaneously bearing IgA and IgE. *J Exp Med* **154**: 640-8.
- Easom CA and Clarke DJ (2008). Motility is required for the competitive fitness of entomopathogenic *Photorhabdus luminescens* during insect infection. *BMC Microbiol* **8**: 168.
- Eckburg PB, Bik EM, Bernstein CN, Purdom E, et al. (2005). Diversity of the human intestinal microbial flora. *Science* **308**: 1635-8.
- Edlund A, Soule T, Sjoling S and Jansson JK (2006). Microbial community structure in polluted Baltic Sea sediments. *Environ Microbiol* **8**: 223-32.
- El Kaoutari A, Armougom F, Gordon JI, Raoult D and Henrissat B (2013). The abundance and variety of carbohydrate-active enzymes in the human gut microbiota. *Nat Rev Microbiol* **11**: 497-504.
- Elson CO (2002). Genes, microbes, and T cells--new therapeutic targets in Crohn's disease. *N Engl J Med* **346**: 614-6.
- Emerson JB, Thomas BC, Andrade K, Allen EE, et al. (2012). Dynamic viral populations in hypersaline systems as revealed by metagenomic assembly. *Appl Environ Microbiol* **78**: 6309-20.
- Eyre-Walker A (1996). Synonymous codon bias is related to gene length in *Escherichia coli*: selection for translational accuracy? *Mol Biol Evol* **13**: 864-72.
- Fedorov A, Saxonov S and Gilbert W (2002). Regularities of context-dependent codon bias in eukaryotic genes. *Nucleic Acids Res* **30**: 1192-7.
- Fenstermacher D (2005). Introduction to bioinformatics. *J American Society Information Science and Technol* **56**: 440-446.
- Fleischmann RD, Adams MD, White O, Clayton RA, et al. (1995). Whole-genome random sequencing and assembly of *Haemophilus influenzae*. *Rd. Science* **269**: 496-512.
- Flint HJ, Scott KP, Duncan SH, Louis P and Forano E (2012). Microbial degradation of complex carbohydrates in the gut. *Gut Microbes* **3**: 289-306.
- Fock KM, Graham DY and Malfertheiner P (2013). *Helicobacter pylori* research: historical insights and future directions. *Nat Rev Gastroenterol Hepatol* **10**: 495-500.
- Franceschini A, Szklarczyk D, Frankild S, Kuhn M, et al. (2013). STRING v9. 1: protein-protein interaction networks, with increased coverage and integration. *Nucleic Acids Res* **41**: D808-D815.
- Frank DN, St Amand AL, Feldman RA, Boedeker EC, et al. (2007). Molecular-phylogenetic characterization of microbial community imbalances in human inflammatory bowel diseases. *Proc Natl Acad Sci U S A* **104**: 13780-5.
- Fredrick K and Ibba M (2010). How the sequence of a gene can tune its translation. *Cell* **141**: 227-9.
- Freiberg C, Wieland B, Spaltmann F, Ehlert K, et al. (2001). Identification of novel essential *Escherichia coli*

- genes conserved among pathogenic bacteria. *J Mol Microbiol Biotechnol* **3**: 483-489.
- Fukiya S, Arata M, Kawashima H, Yoshida D, et al. (2009). Conversion of cholic acid and chenodeoxycholic acid into their 7-oxo derivatives by *Bacteroides intestinalis* AM-1 isolated from human feces. *FEMS Microbiol Lett* **293**: 263-70.
- Fuller R (1986). Probiotics. *Soc Appl Bacteriol Symp Ser* **15**: 1S-7S.
- Furusawa Y, Obata Y, Fukuda S, Endo TA, et al. (2013). Commensal microbe-derived butyrate induces the differentiation of colonic regulatory T cells. *Nature* **504**: 446-50.
- Gasteiger E, Gattiker A, Hoogland C, Ivanyi I, et al. (2003). ExPASy: the proteomics server for in-depth protein knowledge and analysis. *Nucleic Acids Res* **31**: 3784-3788.
- Gebbers JO and Laissue JA (1989). Immunologic structures and functions of the gut. *Schweiz Arch Tierheilkd* **131**: 221-38.
- Gerritsen J, Smidt H, Rijkers GT and de Vos WM (2011). Intestinal microbiota in human health and disease: the impact of probiotics. *Genes Nutr* **6**: 209-40.
- Ghosh S, Prava J, Samal HB, Suar M and Mahapatra RK (2014). Comparative genomics study for the identification of drug and vaccine targets in *Staphylococcus aureus*: MurA ligase enzyme as a proposed candidate. *J Microbiol Methods* **101**: 1-8.
- Goldberg SM, Johnson J, Busam D, Feldblyum T, et al. (2006). A Sanger/pyrosequencing hybrid approach for the generation of high-quality draft assemblies of marine microbial genomes. *Proc Natl Acad Sci U S A* **103**: 11240-5.
- Gordon JH and Dubos R (1970). The anaerobic bacterial flora of the mouse cecum. *J Exp Med* **132**: 251-60.
- Gosalbes MJ, Abellan JJ, Durban A, Perez-Cobas AE, et al. (2012). Metagenomics of human microbiome: beyond 16s rDNA. *Clin Microbiol Infect* **18 Suppl 4**: 47-9.
- Graham DY (2000). *Helicobacter pylori* infection is the primary cause of gastric cancer. *J Gastroenterol* **35 Suppl 12**: 90-7.
- Grantham R, Gautier C, Gouy M, Jacobzone M and Mercier R (1981). Codon catalog usage is a genome strategy modulated for gene expressivity. *Nucleic Acids Res* **9**: r43-74.
- Greenacre MJ (1984). Theory and applications of correspondence analysis. London, Academic Press.
- Gu W, Zhou T, Ma J, Sun X and Lu Z (2004). The relationship between synonymous codon usage and protein structure in *Escherichia coli* and *Homo sapiens*. *Biosystems* **73**: 89-97.
- Guinane CM and Cotter PD (2013). Role of the gut microbiota in health and chronic gastrointestinal disease: understanding a hidden metabolic organ. *Therap Adv Gastroenterol* **6**: 295-308.
- Guo FB and Yu XJ (2007). Separate base usages of genes located on the leading and lagging strands in *Chlamydia muridarum* revealed by the Z curve method. *BMC Genomics* **8**: 366.
- Guo FB and Yuan JB (2009). Codon

- usages of genes on chromosome, and surprisingly, genes in plasmid are primarily affected by strand-specific mutational biases in *Lawsonia intracellularis*. *DNA Res* **16**: 91-104.
- Guo FB, Ye YN, Zhao HL, Lin D and Wei W (2012). Universal pattern and diverse strengths of successive synonymous codon bias in three domains of life, particularly among prokaryotic genomes. *DNA Res* **19**: 477-85.
- Gupta SK and Ghosh TC (2001). Gene expressivity is the main factor in dictating the codon usage variation among the genes in *Pseudomonas aeruginosa*. *Gene* **273**: 63-70.
- Gutman GA and Hatfield GW (1989). Nonrandom utilization of codon pairs in *Escherichia coli*. *Proc Natl Acad Sci U S A* **86**: 3699-703.
- Gutman GA and Hatfield GW (1989). Nonrandom utilization of codon pairs in *Escherichia coli*. *Proc Natl Acad Sci U S A* **86**: 3699-703.
- Hajduk PJ, Huth JR and Tse C (2005). Predicting protein druggability. *Drug Discov Today* **10**: 1675-1682.
- Hamer HM, Jonkers D, Venema K, Vanhoutvin S, et al. (2008). Review article: the role of butyrate on colonic function. *Aliment Pharmacol Ther* **27**: 104-19.
- Handelsman J (2004). Metagenomics: application of genomics to uncultured microorganisms. *Microbiol Mol Biol Rev* **68**: 669-85.
- Harris MA, Reddy CA and Carter GR (1976). Anaerobic bacteria from the large intestine of mice. *Appl Environ Microbiol* **31**: 907-12.
- Hasan S, Daugelat S, Rao PS and Schreiber M (2006). Prioritizing genomic drug targets in pathogens: application to *Mycobacterium tuberculosis*. *PLoS Comput Biol* **2**: e61.
- He B, Xu W, Santini PA, Polydorides AD, et al. (2007). Intestinal bacteria trigger T cell-independent immunoglobulin A (2) class switching by inducing epithelial-cell secretion of the cytokine APRIL. *Immunity* **26**: 812-26.
- Heizer EM, Jr., Raiford DW, Raymer ML, Doom TE, et al. (2006). Amino acid cost and codon-usage biases in 6 prokaryotic genomes: a whole-genome analysis. *Mol Biol Evol* **23**: 1670-80.
- Henrissat B, Coutinho PM and Davies GJ (2001). A census of carbohydrate-active enzymes in the genome of *Arabidopsis thaliana*. *Plant Mol Biol* **47**: 55-72.
- Henry CS, DeJongh M, Best AA, Frybarger PM, et al. (2010). High-throughput generation, optimization and analysis of genome-scale metabolic models. *Nat Biotechnol* **28**: 977-82.
- Hesper B and Hogeweg P (1970). Bioinformatica: een werkconcept. *Kameleon* **1**: 28-29.
- Hess M, Sczyrba A, Egan R, Kim TW, et al. (2011). Metagenomic discovery of biomass-degrading genes and genomes from cow rumen. *Science* **331**: 463-7.
- Hooper LV (2009). Do symbiotic bacteria subvert host immunity? *Nat Rev Microbiol* **7**: 367-74.
- Hooper LV and Gordon JI (2001). Commensal host-bacterial relationships in the gut. *Science* **292**: 1115-8.

- Hooper LV, Stappenbeck TS, Hong CV and Gordon JI (2003). Angiogenins: a new class of microbicidal proteins involved in innate immunity. *Nat Immunol* **4**: 269-73.
- Hou ZC and Yang N (2002). [Analysis of factors shaping *S. pneumoniae* codon usage]. *Yi Chuan Xue Bao* **29**: 747-52.
- Hou ZC and Yang N (2003). Factors affecting codon usage in *Yersinia pestis*. *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao (Shanghai)* **35**: 580-6.
- Hsiao WW, Ung K, Aeschliman D, Bryan J, et al. (2005). Evidence of a large novel gene pool associated with prokaryotic genomic islands. *PLoS Genet* **1**: e62.
- Hucka M, Finney A, Sauro HM, Bolouri H, et al. (2003). The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. *Bioinformatics* **19**: 524-31.
- Hull MW and Chow AW (2007). Indigenous microflora and innate immunity of the head and neck. *Infect Dis Clin North Am* **21**: 265-82, v.
- Hurst LD (2002). The Ka/Ks ratio: diagnosing the form of sequence evolution. *Trends Genet* **18**: 486.
- Hurst LD and Pal C (2001). Evidence for purifying selection acting on silent sites in BRCA1. *Trends Genet* **17**: 62-5.
- Huson DH, Mitra S, Ruscheweyh HJ, Weber N and Schuster SC (2011). Integrative analysis of environmental sequences using MEGAN4. *Genome Res* **21**: 1552-60.
- Ikemura T (1981). Correlation between the abundance of *Escherichia coli* transfer RNAs and the occurrence of the respective codons in its protein genes. *J Mol Biol* **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. *J Mol Biol* **158**: 573-97.
- Ikemura T (1985). Codon usage and tRNA content in unicellular and multicellular organisms. *Mol Biol Evol* **2**: 13-34.
- Irwin B, Heck JD and Hatfield GW (1995). Codon pair utilization biases influence translational elongation step times. *J Biol Chem* **270**: 22801-6.
- Ishibashi N, Yaeshima T and Hayasawa H (1997). Bifidobacteria: their significance in human intestinal health. *Mal J Nutr* **3**: 149-159.
- Jandhyala SM, Talukdar R, Subramanyam C, Vuuyuru H, et al. (2015). Role of the normal gut microbiota. *World J Gastroenterol* **21**: 8787-803.
- Jensen LJ, Kuhn M, Stark M, Chaffron S, et al. (2009). STRING "a global view on proteins and their functional interactions in 630 organisms. *Nucleic Acids Res* **37**: D412-D416.
- Jernberg C, Lofmark S, Edlund C and Jansson JK (2007). Long-term ecological impacts of antibiotic administration on the human intestinal microbiota. *Isme J* **1**: 56-66.
- Jernberg C, Sullivan A, Edlund C and Jansson JK (2005). Monitoring of antibiotic-induced alterations in the human intestinal microflora and detection of

- probiotic strains by use of terminal restriction fragment length polymorphism. *Appl Environ Microbiol* **71**: 501-6.
- Jiao D, Ye Y and Tang H (2013). Probabilistic inference of biochemical reactions in microbial communities from metagenomic sequences. *PLoS Comput Biol* **9**: e1002981.
- Johansson ME, Phillipson M, Petersson J, Velcich A, et al. (2008). The inner of the two Muc2 mucin-dependent mucus layers in colon is devoid of bacteria. *Proc Natl Acad Sci U S A* **105**: 15064-9.
- Jordan IK, Rogozin IB, Wolf YI and Koonin EV (2002). Essential genes are more evolutionarily conserved than are nonessential genes in bacteria. *Genome Res* **12**: 962-968.
- Jordan KW, Nordenstam J, Lauwers GY, Rothenberger DA, et al. (2009). Metabolomic characterization of human rectal adenocarcinoma with intact tissue magnetic resonance spectroscopy. *Dis Colon Rectum* **52**: 520-5.
- Kahali B, Basak S and Ghosh TC (2007). Reinvestigating the codon and amino acid usage of *S. cerevisiae* genome: a new insight from protein secondary structure analysis. *Biochem Biophys Res Commun* **354**: 693-9.
- Kajander K, Myllyluoma E, Rajilic-Stojanovic M, Kyronpalo S, et al. (2008). Clinical trial: multispecies probiotic supplementation alleviates the symptoms of irritable bowel syndrome and stabilizes intestinal microbiota. *Aliment Pharmacol Ther* **27**: 48-57.
- Kanaya S, Yamada Y, Kudo Y and Ikemura T (1999). Studies of codon usage and tRNA genes of 18 unicellular organisms and quantification of *Bacillus subtilis* tRNAs: gene expression level and species-specific diversity of codon usage based on multivariate analysis. *Gene* **238**: 143-55.
- Kanehisa M and Goto S (2000). KEGG: kyoto encyclopedia of genes and genomes. *Nucleic Acids Res* **28**: 27-30.
- Kanehisa M, Araki M, Goto S, Hattori M, et al. (2008). KEGG for linking genomes to life and the environment. *Nucleic Acids Res* **36**: D480-D484.
- Kapatral V, Ivanova N, Anderson I, Reznik G, et al. (2003). Genome analysis of *F. nucleatum* sub spp *vincentii* and its comparison with the genome of *F. nucleatum* ATCC 25586. *Genome Res* **13**: 1180-9.
- Kaplan CW and Kitts CL (2003). Variation between observed and true Terminal Restriction Fragment length is dependent on true TRF length and purine content. *J Microbiol Methods* **54**: 121-5.
- Karlin S and Mrazek J (1996). What drives codon choices in human genes? *J Mol Biol* **262**: 459-72.
- Karlsson FH, Ussery DW, Nielsen J and Nookaew I (2011). A closer look at bacteroides: phylogenetic relationship and genomic implications of a life in the human gut. *Microb Ecol* **61**: 473-85.
- Karlsson FH (2014). Systems Biology of the Gut Microbiome in Metabolic Diseases, University of Technology, Sweden. **PhD**.
- Kelly DJ (1998). The physiology and metabolism of the human gastric pathogen *Helicobacter pylori*. *Adv Microb Physiol* **40**: 137-89.

- Kim JF, Jeong H, Yu DS, Choi SH, *et al.* (2009). Genome sequence of the probiotic bacterium *Bifidobacterium animalis* subsp. *lactis* AD011. *J Bacteriol* **191**: 678-9.
- Kim YS and Ho SB (2010). Intestinal goblet cells and mucins in health and disease: recent insights and progress. *Curr Gastroenterol Rep* **12**: 319-30.
- Kitts CL (2001). Terminal restriction fragment patterns: a tool for comparing microbial communities and assessing community dynamics. *Curr Issues Intest Microbiol* **2**: 17-25.
- Klaenhammer T, Altermann E, Arigoni F, Bolotin A, *et al.* (2002). Discovering lactic acid bacteria by genomics. *Antonie Van Leeuwenhoek* **82**: 29-58.
- Kleerebezem M, Boekhorst J, van Kranenburg R, Molenaar D, *et al.* (2003). Complete genome sequence of *Lactobacillus plantarum* WCFS1. *Proc Natl Acad Sci U S A* **100**: 1990-5.
- Knox C, Law V, Jewison T, Liu P, *et al.* (2011). DrugBank 3.0: a comprehensive resource for 'omics' research on drugs. *Nucleic Acids Res* **39**: D1035-D1041.
- Kostic AD, Gevers D, Pedamallu CS, Michaud M, *et al.* (2012). Genomic analysis identifies association of *Fusobacterium* with colorectal carcinoma. *Genome Res* **22**: 292-8.
- Krause DO, Dalrymple BP, Smith WJ, Mackie RI and McSweeney CS (1999a). 16S rDNA sequencing of *Ruminococcus albus* and *Ruminococcus flavefaciens*: design of a signature probe and its application in adult sheep. *Microbiology* **145** (Pt 7): 1797-807.
- Krause DO, McSweeney CS and Forster RJ. (1999b). Molecular ecological methods to study fibrolytic ruminal bacteria: phylogeny, competition and persistence. In *8th Int. Symp. Microb. Ecol. Canada Soc. Microb. Ecol., Halifax, Canada*, pp. 15-19.
- Kristiansson E, Hugenholtz P and Dalevi D (2009). ShotgunFunctionalizeR: an R-package for functional comparison of metagenomes. *Bioinformatics* **25**: 2737-8.
- Kruis W, FriÅ P, Pokrotnieks J, LukÅj M, *et al.* (2004). Maintaining remission of ulcerative colitis with the probiotic *Escherichia coli* Nissle 1917 is as effective as with standard mesalazine. *Gut* **53**: 1617-1623.
- Kuczynski J, Lauber CL, Walters WA, Parfrey LW, *et al.* (2011). Experimental and analytical tools for studying the human microbiome. *Nat Rev Genet* **13**: 47-58.
- Kumar N, Mariappan V, Baddam R, Lankapalli AK, *et al.* (2015). Comparative genomic analysis of *Helicobacter pylori* from Malaysia identifies three distinct lineages suggestive of differential evolution. *Nucleic Acids Res* **43**: 324-35.
- Kunz C, Kuntz S and Rudloff S (2009). Intestinal flora. *Adv Exp Med Biol* **639**: 67-79.
- Kurokawa K, Itoh T, Kuwahara T, Oshima K, *et al.* (2007). Comparative metagenomics revealed commonly enriched gene sets in human gut microbiomes. *DNA Res* **14**: 169-81.
- Kusters JG, van Vliet AH and Kuipers EJ (2006). Pathogenesis of

- Helicobacter pylori infection. *Clin Microbiol Rev* **19**: 449-90.
- Kutsukake K and Iino T (1994). Role of the FliA-FlgM regulatory system on the transcriptional control of the flagellar regulon and flagellar formation in *Salmonella typhimurium*. *J Bacteriol* **176**: 3598-605.
- Lafay B, Atherton JC and Sharp PM (2000). Absence of translationally selected synonymous codon usage bias in *Helicobacter pylori*. *Microbiology* **146 (Pt 4)**: 851-60.
- Lafay B, Lloyd AT, McLean MJ, Devine KM, *et al.* (1999). Proteome composition and codon usage in spirochaetes: species-specific and DNA strand-specific mutational biases. *Nucleic Acids Res* **27**: 1642-9.
- Lairson LL, Henrissat B, Davies GJ and Withers SG (2008). Glycosyltransferases: structures, functions, and mechanisms. *Biochemistry* **77**: 521.
- Langille MG, Zaneveld J, Caporaso JG, McDonald D, *et al.* (2013). Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. *Nat Biotechnol* **31**: 814-21.
- Langmead B, Trapnell C, Pop M and Salzberg SL (2009). Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol* **10**: R25.
- Larsen PE and Dai Y (2015). Metabolome of human gut microbiome is predictive of host dysbiosis. *Gigascience* **4**: 42.
- Lasken RS (2012). Genomic sequencing of uncultured microorganisms from single cells. *Nat Rev Microbiol* **10**: 631-40.
- Lau A-S-Y and Lioong M-T (2014). Lactic Acid Bacteria and Bifidobacteria-Inhibited *Staphylococcus epidermidis*. *Wounds* **26**: 121-131.
- Lawson PA and Finegold SM (2015). Reclassification of *Ruminococcus obeum* as *Blautia obeum* comb. nov. *Int J Syst Evol Microbiol* **65**: 789-93.
- Le Novere N, Bornstein B, Broicher A, Courtot M, *et al.* (2006). BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems. *Nucleic Acids Res* **34**: D689-91.
- LeBlanc JG, Milani C, de Giori GS, Sesma F, *et al.* (2013). Bacteria as vitamin suppliers to their host: a gut microbiota perspective. *Curr Opin Biotechnol* **24**: 160-8.
- Lehours P, Zheng Z, Skoglund A, Megraud F and Engstrand L (2009). Is there a link between the lipopolysaccharide of *Helicobacter pylori* gastric MALT lymphoma associated strains and lymphoma pathogenesis? *PLoS One* **4**: e7297.
- Leimena MM, Ramiro-Garcia J, Davids M, van den Bogert B, *et al.* (2013). A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. *BMC Genomics* **14**: 530.
- Lepage P, Hasler R, Spehlmann ME, Rehman A, *et al.* (2011). Twin study indicates loss of interaction between microbiota

- and mucosa of patients with ulcerative colitis. *Gastroenterology* **141**: 227-36.
- Levasseur A, Drula E, Lombard V, Coutinho PM and Henrissat B (2013). Expansion of the enzymatic repertoire of the CAZy database to integrate auxiliary redox enzymes. *Biotechnol Biofuels* **6**: 41.
- Leversen NA, de Souza GA, Malen H, Prasad S, et al. (2009). Evaluation of signal peptide prediction algorithms for identification of mycobacterial signal peptides using sequence data from proteomic methods. *Microbiology* **155**: 2375-83.
- Levy R and Borenstein E (2013). Metabolic modeling of species interaction in the human microbiome elucidates community-level assembly rules. *Proc Natl Acad Sci U S A* **110**: 12804-9.
- Ley RE (2010). Obesity and the human microbiome. *Curr Opin Gastroenterol* **26**: 5-11.
- Ley RE, Backhed F, Turnbaugh P, Lozupone CA, et al. (2005). Obesity alters gut microbial ecology. *Proc Natl Acad Sci U S A* **102**: 11070-5.
- Ley RE, Peterson DA and Gordon JI (2006a). Ecological and evolutionary forces shaping microbial diversity in the human intestine. *Cell* **124**: 837-48.
- Ley RE, Turnbaugh PJ, Klein S and Gordon JI (2006). Microbial ecology: human gut microbes associated with obesity. *Nature* **444**: 1022-3.
- Liu G, Wu J, Yang H and Bao Q (2010). Codon Usage Patterns in *Corynebacterium glutamicum*: Mutational Bias, Natural Selection and Amino Acid Conservation. *Comp Funct Genomics* **2010**: 343569.
- Liu WT, Marsh TL, Cheng H and Forney LJ (1997). Characterization of microbial diversity by determining terminal restriction fragment length polymorphisms of genes encoding 16S rRNA. *Appl Environ Microbiol* **63**: 4516-22.
- Ljungh A and Wadstrom T (2006). Lactic acid bacteria as probiotics. *Curr Issues Intest Microbiol* **7**: 73-89.
- Lobry JR and Gautier C (1994). Hydrophobicity, expressivity and aromaticity are the major trends of amino-acid usage in 999 *Escherichia coli* chromosome-encoded genes. *Nucleic Acids Res* **22**: 3174-80.
- Lochhead P and El-Omar EM (2007). *Helicobacter pylori* infection and gastric cancer. *Best Pract Res Clin Gastroenterol* **21**: 281-97.
- Loftus EV, Jr. (2004). Clinical epidemiology of inflammatory bowel disease: Incidence, prevalence, and environmental influences. *Gastroenterology* **126**: 1504-17.
- Lombard V, Bernard T, Rancurel C, Brumer H, et al. (2010). A hierarchical classification of polysaccharide lyases for glycogenomics. *Biochem J* **432**: 437-44.
- Lombard V, Golaconda Ramulu H, Drula E, Coutinho PM and Henrissat B (2014). The carbohydrate-active enzymes database (CAZy) in 2013. *Nucleic Acids Res* **42**: D490-5.
- Lopez P and Philippe H (2001). Composition strand asymmetries in prokaryotic genomes: mutational bias and biased gene orientation. *C R Acad Sci III* **324**: 201-8.
- Lowe TM and Eddy SR (1997).

- tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res* **25**: 955-64.
- Lukjancenko O, Ussery DW and Wassenaar TM (2012). Comparative genomics of *Bifidobacterium*, *Lactobacillus* and related probiotic genera. *Microb Ecol* **63**: 651-73.
- Lukjancenko O, Wassenaar TM and Ussery DW (2010). Comparison of 61 sequenced *Escherichia coli* genomes. *Microb Ecol* **60**: 708-20.
- Luo C, Tsementzi D, Kyripides N, Read T and Konstantinidis KT (2012). Direct comparisons of Illumina vs. Roche 454 sequencing technologies on the same microbial community DNA sample. *PLoS One* **7**: e30087.
- Luo H and Moran MA (2013). Assembly-free metagenomic analysis reveals new metabolic capabilities in surface ocean bacterioplankton. *Environ Microbiol Rep* **5**: 686-96.
- Luscombe NM, Greenbaum D and Gerstein M (2001). What is bioinformatics? An introduction and overview. *Yearbook of Medical Informatics* **1**: 83-99.
- Lutgendorff F, Akkermans LM and Soderholm JD (2008). The role of microbiota and probiotics in stress-induced gastro-intestinal damage. *Curr Mol Med* **8**: 282-98.
- Ma YP, Ke H, Liang ZL, Liu ZX, et al. (2016). Multiple Evolutionary Selections Involved in Synonymous Codon Usages in the *Streptococcus agalactiae* Genome. *Int J Mol Sci* **17**: 277.
- Macfarlane S and Macfarlane GT (2003). Regulation of short-chain fatty acid production. *Proc Nutr Soc* **62**: 67-72.
- Mackie RI, Sghir A and Gaskins HR (1999). Developmental microbial ecology of the neonatal gastrointestinal tract. *Am J Clin Nutr* **69**: 1035S-1045S.
- Magwira CA, Kullin B, Lewandowski S, Rodgers A, et al. (2012). Diversity of faecal oxalate-degrading bacteria in black and white South African study groups: insights into understanding the rarity of urolithiasis in the black group. *J Appl Microbiol* **113**: 418-28.
- Mahowald MA, Rey FE, Seedorf H, Turnbaugh PJ, et al. (2009). Characterizing a model human gut microbiota composed of members of its two dominant bacterial phyla. *Proc Natl Acad Sci USA* **106**: 5859-64.
- Mandar R and Mikelsaar M (1996). Transmission of mother's microflora to the newborn at birth. *Biol Neonate* **69**: 30-5.
- Marais G and Duret L (2001). Synonymous codon usage, accuracy of translation, and gene length in *Caenorhabditis elegans*. *J Mol Evol* **52**: 275-80.
- Marcabal A, Kashyap PC, Nelson TA, Aronov PA, et al. (2013). A metabolomic view of how the human gut microbiota impacts the host metabolome using humanized and gnotobiotic mice. *Isme J* **7**: 1933-43.
- Marin L, Miguelez EM, Villar CJ and Lombo F (2015). Bioavailability of dietary polyphenols and gut microbiota metabolism: antimicrobial properties. *Biomed Res Int* **2015**: 905215.
- Markowitz VM, Chen IM, Chu K, Szeto E, et al. (2014). IMG/M 4 version of the integrated metagenome comparative

- analysis system. *Nucleic Acids Res* **42**: D568-73.
- Markowitz VM, Ivanova N, Palaniappan K, Szeto E, et al. (2006). An experimental metagenome data management and analysis system. *Bioinformatics* **22**: e359-67.
- Martens EC, Koropatkin NM, Smith TJ and Gordon JI (2009). Complex glycan catabolism by the human gut microbiota: the Bacteroidetes Sus-like paradigm. *J Biol Chem* **284**: 24673-7.
- Martinez C, Antolin M, Santos J, Torrejon A, et al. (2008). Unstable composition of the fecal microbiota in ulcerative colitis during clinical remission. *Am J Gastroenterol* **103**: 643-8.
- Martinez-Medina M, Aldeguer X, Gonzalez-Huix F, Acero D and Garcia-Gil LJ (2006). Abnormal microbiota composition in the ileocolonic mucosa of Crohn's disease patients as revealed by polymerase chain reaction-denaturing gradient gel electrophoresis. *Inflamm Bowel Dis* **12**: 1136-45.
- Martin-Galiano AJ, Wells JM and de la Campa AG (2004). Relationship between codon biased genes, microarray expression values and physiological characteristics of *Streptococcus pneumoniae*. *Microbiology* **150**: 2313-25.
- Mastronunzio JE, Tisa LS, Normand P and Benson DR (2008). Comparative secretome analysis suggests low plant cell wall degrading capacity in *Frankia* symbionts. *BMC Genomics* **9**: 47.
- Mathiesen G, Sveen A, Brurberg MB, Fredriksen L, et al. (2009).
- Genome-wide analysis of signal peptide functionality in *Lactobacillus plantarum* WCFS1. *BMC Genomics* **10**: 425.
- Mathiesen G, Sveen A, Piard JC, Axelsson L and Eijsink VG (2008). Heterologous protein secretion by *Lactobacillus plantarum* using homologous signal peptides. *J Appl Microbiol* **105**: 215-26.
- McCoy AN, Araujo-Perez F, Azcarate-Peril A, Yeh JJ, et al. (2013). *Fusobacterium* is associated with colorectal adenomas. *PLoS One* **8**: e53653.
- McFadden JJ, Butcher PD, Chiodini R and Hermon-Taylor J (1987). Crohn's disease-isolated mycobacteria are identical to *Mycobacterium paratuberculosis*, as determined by DNA probes that distinguish between mycobacterial species. *J Clin Microbiol* **25**: 796-801.
- McInerney JO (1998). Replicational and transcriptional selection on codon usage in *Borrelia burgdorferi*. *Proc Natl Acad Sci U S A* **95**: 10698-703.
- McNulty NP, Yatsunenko T, Hsiao A, Faith JJ, et al. (2011). The impact of a consortium of fermented milk strains on the gut microbiome of gnotobiotic mice and monozygotic twins. *Sci Transl Med* **3**: 106ra106.
- Medini D, Donati C, Tettelin H, Massignani V and Rappuoli R (2005). The microbial pan-genome. *Curr Opin Genet Dev* **15**: 589-94.
- Meyer F, Paarmann D, D'Souza M, Olson R, et al. (2008). The metagenomics RAST server - a public resource for the automatic phylogenetic and functional analysis of metagenomes. *BMC*

- Bioinformatics* **9**: 386.
- Milani C, Lugli GA, Duranti S, Turroni F, et al. (2014). Genomic encyclopedia of type strains of the genus *Bifidobacterium*. *Appl Environ Microbiol* **80**: 6290-302.
- Mira A, Pushker R, Legault BA, Moreira D and Rodriguez-Valera F (2004). Evolutionary relationships of *Fusobacterium nucleatum* based on phylogenetic analysis and comparative genomics. *BMC Evol Biol* **4**: 50.
- Mirande C, Kadlecikova E, Matulova M, Capek P, et al. (2010). Dietary fibre degradation and fermentation by two xylanolytic bacteria *Bacteroides xyloisolvans* XB1A and *Roseburia intestinalis* XB6B4 from the human intestine. *J Appl Microbiol* **109**: 451-60.
- Mitsuoka T (1990). Bifidobacteria and their role in human health. *Journal of Industrial Microbiology* **6**: 263-267.
- Miyasaka H (2002). Translation initiation AUG context varies with codon usage bias and gene length in *Drosophila melanogaster*. *J Mol Evol* **55**: 52-64.
- Moller S, Croning MD and Apweiler R (2001). Evaluation of methods for the prediction of membrane spanning regions. *Bioinformatics* **17**: 646-53.
- Monstein HJ, Tiveljung A, Kraft CH, Borch K and Jonasson J (2000). Profiling of bacterial flora in gastric biopsies from patients with *Helicobacter pylori*-associated gastritis and histologically normal control individuals by temperature gradient gel electrophoresis and 16S rDNA sequence analysis. *J Med Microbiol* **49**: 817-22.
- Morgan XC, Tickle TL, Sokol H, Gevers D, et al. (2012). Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. *Genome Biol* **13**: R79.
- Moriyama EN and Powell JR (1997). Codon usage bias and tRNA abundance in *Drosophila*. *J Mol Evol* **45**: 514-23.
- Moriyama EN and Powell JR (1998). Gene length and codon usage bias in *Drosophila melanogaster*, *Saccharomyces cerevisiae* and *Escherichia coli*. *Nucleic Acids Res* **26**: 3188-93.
- Nakamura Y, Gojobori T and Ikemura T (2000). Codon usage tabulated from international DNA sequence databases: status for the year 2000. *Nucleic Acids Res* **28**: 292.
- Nakano Y, Takeshita T, Kamio N, Shiota S, et al. (2014). Supervised machine learning-based classification of oral malodor based on the microbiota in saliva samples. *Artif Intell Med* **60**: 97-101.
- Nammi, D., Srimath-Tirumala-Peddinti, R.C. and Neelapu, N.R. (2016) Identification of Drug Targets in *Helicobacter pylori* by in silico Analysis: Possible Therapeutic Implications for Gastric cancer. *Curr Cancer Drug Targets* **16**: 79-98.
- Narasingaraopu P, Podell S, Ugalde JA, Brochier-Armanet C, et al. (2012). De novo metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. *Isme J* **6**: 81-93.
- Navas-Molina JA, Peralta-Sanchez JM, Gonzalez A, McMurdie PJ, et al. (2013). Advancing our understanding of the human

- microbiome using QIIME. *Methods Enzymol* **531**: 371-444.
- Naya H, Romero H, Carels N, Zavala A and Musto H (2001). Translational selection shapes codon usage in the GC-rich genome of Chlamydomonas reinhardtii. *FEBS Lett* **501**: 127-30.
- Nayak KC (2009). Mutational bias and gene expression level shape codon usage in Thermobifida fusca YX. *In Silico Biol* **9**: 337-53.
- Nayak KC (2012). Comparative study on factors influencing the codon and amino acid usage in Lactobacillus sakei 23K and 13 other lactobacilli. *Mol Biol Rep* **39**: 535-45.
- Neelapu NR and Pavani T (2013). Identification of novel drug targets in HpB38, HpP12, HpG27, HpShi470, HpSJM180 strains of Helicobacter pylori : an in silico approach for therapeutic intervention. *Curr Drug Targets* **14**: 601-11.
- Neelapu NR, Mutha NV and Akula S (2015). Identification of potential drug targets in Helicobacter pylori strain HPG1 by in silico genome analysis. *Infect Disord Drug Targets* **15**: 106-17.
- Neish AS (2009). Microbes in gastrointestinal health and disease. *Gastroenterology* **136**: 65-80.
- Nicholson JK, Holmes E and Wilson ID (2005). Gut microorganisms, mammalian metabolism and personalized health care. *Nat Rev Microbiol* **3**: 431-8.
- Ning Z, Cox AJ and Mullikin JC (2001). SSAHA: a fast search method for large DNA databases. *Genome Res* **11**: 1725-9.
- Nogueira T, Touchon M and Rocha EP (2012). Rapid evolution of the sequences and gene repertoires of secreted proteins in bacteria. *PLoS One* **7**: e49403.
- Nwaka S and Hudson A (2006). Innovative lead discovery strategies for tropical diseases. *Nature Reviews Drug Discovery* **5**: 941-955.
- Oberhardt MA, Palsson BO and Papin JA (2009). Applications of genome-scale metabolic reconstructions. *Mol Syst Biol* **5**: 320.
- Ohama T, Muto A and Osawa S (1990). Role of GC-biased mutation pressure on synonymous codon choice in *Micrococcus luteus*, a bacterium with a high genomic GC-content. *Nucleic Acids Res* **18**: 1565-9.
- O'Hara AM and Shanahan F (2006). The gut flora as a forgotten organ. *EMBO Rep* **7**: 688-93.
- Ohkubo S, Muto A, Kawauchi Y, Yamao F and Osawa S (1987). The ribosomal protein gene cluster of *Mycoplasma capricolum*. *Mol Gen Genet* **210**: 314-22.
- Okayama T, Tamura T, Gojobori T, Tateno Y, et al. (1998). Formal design and implementation of an improved DDBJ DNA database with a new schema and object-oriented library. *Bioinformatics* **14**: 472-8.
- O'Sullivan O, O'Callaghan J, Sangrador-Vegas A, McAuliffe O, et al. (2009). Comparative genomics of lactic acid bacteria reveals a niche-specific gene set. *BMC Microbiol* **9**: 50.
- Overbeek R, Begley T, Butler RM, Choudhuri JV, et al. (2005). The subsystems approach to genome annotation and its use

- in the project to annotate 1000 genomes. *Nucleic Acids Res* **33**: 5691-702.
- Palmer KL, Godfrey P, Griggs A, Kos VN, et al. (2012). Comparative genomics of enterococci: variation in *Enterococcus faecalis*, clade structure in *E. faecium*, and defining characteristics of *E. gallinarum* and *E. casseliflavus*. *MBio* **3**: e00318-11.
- Papanikou E, Karamanou S and Economou A (2007). Bacterial protein secretion through the translocase nanomachine. *Nat Rev Microbiol* **5**: 839-51.
- Parvege MM, Rahman M and Hossain MS (2014). Genome-wide Analysis of *Mycoplasma hominis* for the Identification of Putative Therapeutic Targets. *Drug Target Insights* **8**: 51-62.
- Pearson WR and Lipman DJ (1988). Improved tools for biological sequence comparison. *Proc Natl Acad Sci U S A* **85**: 2444-8.
- Peden JF (1999). Analysis of codon usage, University of Nottingham, UK. **PhD**.
- Pei Z, Bini EJ, Yang L, Zhou M, et al. (2004). Bacterial biota in the human distal esophagus. *Proc Natl Acad Sci U S A* **101**: 4250-5.
- Peixoto L, Zavala A, Romero H and Musto H (2003). The strength of translational selection for codon usage varies in the three replicons of *Sinorhizobium meliloti*. *Gene* **320**: 109-16.
- Perez-Iratxeta C, Andrade-Navarro MA and Wren JD (2007). Evolving research trends in bioinformatics. *Brief Bioinform* **8**: 88-95.
- Petersen TN, Brunak S, von Heijne G and Nielsen H (2011). SignalP 4.0: discriminating signal peptides from transmembrane regions. *Nat Methods* **8**: 785-6.
- Petrof EO, Kojima K, Ropeleski MJ, Musch MW, et al. (2004). Probiotics inhibit nuclear factor -kappaB and induce heat shock proteins in colonic epithelial cells through proteasome inhibition. *Gastroenterology* **127**: 1474-87.
- Pintar J and Starmer WT (2003). The costs and benefits of killer toxin production by the yeast *Pichia kluyveri*. *Antonie Van Leeuwenhoek* **83**: 89-97.
- Plotkin JB and Kudla G (2011). Synonymous but not the same: the causes and consequences of codon bias. *Nat Rev Genet* **12**: 32-42.
- Plottel CS and Blaser MJ (2011). Microbiome and malignancy. *Cell Host Microbe* **10**: 324-35.
- Pothoulakis C (1996). Pathogenesis of *Clostridium difficile*-associated diarrhoea. *Eur J Gastroenterol Hepatol* **8**: 1041-7.
- Precup J and Parker J (1987). Missense misreading of asparagine codons as a function of codon identity and context. *J Biol Chem* **262**: 11351-5.
- Qin J, Li R, Raes J, Arumugam M, et al. (2010). A human gut microbial gene catalogue established by metagenomic sequencing. *Nature* **464**: 59-65.
- Qin J, Li Y, Cai Z, Li S, et al. (2012). A metagenome-wide association study of gut microbiota in type 2 diabetes. *Nature* **490**: 55-60.
- Rajilic-Stojanovic M and de Vos WM (2014). The first 1000 cultured species of the human gastrointestinal microbiota. *FEMS Microbiol Rev* **38**: 996-1047.
- Rajilic-Stojanovic M, Shanahan F,

- Guarner F and de Vos WM (2013). Phylogenetic analysis of dysbiosis in ulcerative colitis during remission. *Inflamm Bowel Dis* **19**: 481-8.
- Ranganathan S and Garg G (2009). Secretome: clues into pathogen infection and clinical applications. *Genome Med* **1**: 113.
- Rasko DA, Rosovitz MJ, Myers GS, Mongodin EF, et al. (2008). The pangenome structure of *Escherichia coli*: comparative genomic analysis of *E. coli* commensal and pathogenic isolates. *J Bacteriol* **190**: 6881-93.
- Ravcheev DA, Godzik A, Osterman AL and Rodionov DA (2013). Polysaccharides utilization in human gut bacterium *Bacteroides thetaiotaomicron*: comparative genomics reconstruction of metabolic and regulatory networks. *BMC Genomics* **14**: 873.
- Reumann S, Inoue K and Keegstra K (2005). Evolution of the general protein import pathway of plastids (review). *Mol Membr Biol* **22**: 73-86.
- Reuter G (2001). The *Lactobacillus* and *Bifidobacterium* microflora of the human intestine: composition and succession. *Curr Issues Intest Microbiol* **2**: 43-53.
- Robert C and Bernalier-Donadille A (2003). The cellulolytic microflora of the human colon: evidence of microcrystalline cellulose-degrading bacteria in methane-excreting subjects. *FEMS Microbiol Ecol* **46**: 81-9.
- Robinson M, Lilley R, Little S, Emtage JS, et al. (1984). Codon usage can affect efficiency of translation of genes in *Escherichia coli*. *Nucleic Acids Res* **12**: 6663-71.
- Rocha EP (2004). Codon usage bias from tRNA's point of view: redundancy, specialization, and efficient decoding for translation optimization. *Genome Res* **14**: 2279-86.
- Rocha EP and Danchin A (2003). Essentiality, not expressiveness, drives gene-strand bias in bacteria. *Nat Genet* **34**: 377-8.
- Romero H, Zavala A and 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 Res* **28**: 2084-90.
- Romero H, Zavala A and 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 Res* **28**: 2084-90.
- Romero H, Zavala A, Musto H and Bernardi G (2003). The influence of translational selection on codon usage in fishes from the family Cyprinidae. *Gene* **317**: 141-7.
- Ron EZ (2006). Host specificity of septicemic *Escherichia coli*: human and avian pathogens. *Curr Opin Microbiol* **9**: 28-32.
- Rosenstein JK, Wanunu M, Merchant CA, Drndic M and Shepard KL (2012). Integrated nanopore sensing platform with sub-microsecond temporal resolution. *Nat Methods* **9**: 487-92.
- Rouli L, Merhej V, Fournier PE and Raoult D (2015) The bacterial pangenome as a new tool for analysing pathogenic bacteria. *New Microbes New Infect* **7**: 72

- 85.
- Round JL, Lee SM, Li J, Tran G, *et al.* (2011). The Toll-like receptor 2 pathway establishes colonization by a commensal of the human microbiota. *Science* **332**: 974-7.
- Roy A, Bhattacharya S, Bothra AK and Sen A (2013). A database for Mycobacterium secretome analysis: 'MycoSec' to accelerate global health research. *OMICS* **17**: 502-9.
- Roy A, Mukhopadhyay S, Sarkar I and Sen A (2015). Comparative investigation of the various determinants that influence the codon and amino acid usage patterns in the genus *Bifidobacterium*. *World J Microbiol Biotechnol* **31**: 959-81.
- Saha JR, Butler VP, Jr., Neu HC and Lindenbaum J (1983). Digoxin-inactivating bacteria: identification in human gut flora. *Science* **220**: 325-7.
- Saier MH, Jr. (1994). Protein uptake into *E. coli* during *Bdellovibrio* infection. A process of reverse secretion? *FEBS Lett* **337**: 14-7.
- Saier MH, Jr. (2006). Protein secretion and membrane insertion systems in gram-negative bacteria. *J Membr Biol* **214**: 75-90.
- Salyers AA, West SE, Vercellotti JR and Wilkins TD (1977). Fermentation of mucins and plant polysaccharides by anaerobic bacteria from the human colon. *Appl Environ Microbiol* **34**: 529-33.
- Salzman NH, Underwood MA and Bevins CL (2007). Paneth cells, defensins, and the commensal microbiota: a hypothesis on intimate interplay at the intestinal mucosa. *Semin Immunol* **19**: 70-83.
- Samal HB, Prava J, Suar M and Mahapatra RK (2015). Comparative genomics study of *Salmonella Typhimurium* LT2 for the identification of putative therapeutic candidates. *J Theor Biol* **369**: 67-79.
- Sanchez B, Urdaci MC and Margolles A (2010). Extracellular proteins secreted by probiotic bacteria as mediators of effects that promote mucosa-bacteria interactions. *Microbiology* **156**: 3232-42.
- Sarkar M, Maganti L, Ghoshal N and Dutta C (2012). In silico quest for putative drug targets in *Helicobacter pylori* HPAG1: molecular modeling of candidate enzymes from lipopolysaccharide biosynthesis pathway. *J Mol Model* **18**: 1855-66.
- Sartor RB (2004). Therapeutic manipulation of the enteric microflora in inflammatory bowel diseases: antibiotics, probiotics, and prebiotics. *Gastroenterology* **126**: 1620-33.
- Sartor RB (2008). Microbial influences in inflammatory bowel diseases. *Gastroenterology* **134**: 577-94.
- Sau K and Deb A (2009). Temperature influences synonymous codon and amino acid usage biases in the phages infecting extremely thermophilic prokaryotes. *In Silico Biol* **9**: 1-9.
- Savage DC (1970). Associations of indigenous microorganisms with gastrointestinal mucosal epithelia. *Am J Clin Nutr* **23**: 1495-501.
- Savage DC (1977). Microbial ecology of the gastrointestinal tract. *Annu Rev Microbiol* **31**: 107-33.
- Scanlan PD, Shanahan F, O'Mahony C and Marchesi JR (2006). Culture-independent analyses of

- temporal variation of the dominant fecal microbiota and targeted bacterial subgroups in Crohn's disease. *J Clin Microbiol* **44**: 3980-8.
- Schadt EE, Turner S and Kasarskis A (2010). A window into third-generation sequencing. *Hum Mol Genet* **19**: R227-40.
- Schott T, Kondadi PK, Hanninen ML and Rossi M (2011). Comparative genomics of *Helicobacter pylori* and the human-derived *Helicobacter bizzozeronii* CIII-1 strain reveal the molecular basis of the zoonotic nature of non-pylori gastric *Helicobacter* infections in humans. *BMC Genomics* **12**: 534.
- Searls DB (2000). Bioinformatics tools for whole genomes. *Annu Rev Genomics Hum Genet* **1**: 251-79.
- Sekirov I, Russell SL, Antunes LC and Finlay BB (2010). Gut microbiota in health and disease. *Physiol Rev* **90**: 859-904.
- Seligmann H (2003). Cost-minimization of amino acid usage. *J Mol Evol* **56**: 151-61.
- Sen A, Sur S, Bothra AK, Benson DR, et al. (2008). The implication of life style on codon usage patterns and predicted highly expressed genes for three *Frankia* genomes. *Antonie Van Leeuwenhoek* **93**: 335-46.
- Sen G, Sur S, Bose D, Mondal U, et al. (2007). Analysis of codon usage patterns and predicted highly expressed genes for six phytopathogenic *Xanthomonas* genomes shows a high degree of conservation. *In Silico Biol* **7**: 547-58.
- Shapiro E, Biezuner T and Linnarsson S (2013). Single-cell sequencing-based technologies will revolutionize whole-organism science. *Nat Rev Genet* **14**: 618-30.
- Sharon I, Bercovici S, Pinter RY and Shlomi T (2011). Pathway-based functional analysis of metagenomes. *J Comput Biol* **18**: 495-505.
- Sharp PM and Li WH (1986). An evolutionary perspective on synonymous codon usage in unicellular organisms. *J Mol Evol* **24**: 28-38.
- Sharp PM and Li WH (1987). The codon Adaptation Index--a measure of directional synonymous codon usage bias, and its potential applications. *Nucleic Acids Res* **15**: 1281-95.
- Sharp PM, Cowe E, Higgins DG, Shields DC, et al. (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 Res* **16**: 8207-11.
- Sharp PM, Stenico M, Peden JF and Lloyd AT (1993). Codon usage: mutational bias, translational selection, or both? *Biochemical Society Transactions* **21**: 835.
- Shende K, Mishra A, Gothwal R and Iqbal M (2013). Comparative codon usage pattern analysis of *Eubacterium eligens*, *E. limosum* and *E. rectal*. *Recent Research in Science and Technology* **5**:
- Shi X, Huang J, Liang C, Liu S, et al. (2001). Is there a close relationship between synonymous codon bias and codon-anticodon binding strength in human genes? *Chinese Science Bulletin* **46**:

- 1015-1019.
- Sidhu H, Hoppe B, Hesse A, Tenbrock K, *et al.* (1998). Absence of *Oxalobacter formigenes* in cystic fibrosis patients: a risk factor for hyperoxaluria. *Lancet* **352**: 1026-9.
- Sievers F, Wilm A, Dineen D, Gibson TJ, *et al.* (2011). Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Mol Syst Biol* **7**: 539.
- Siezen RJ, Francke C, Renckens B, Boekhorst J, *et al.* (2012) Complete resequencing and reannotation of the *Lactobacillus plantarum* WCFS1 genome. *J Bacteriol* **194**: 195-6.
- Smith DR and Chapman MR (2010). Economical evolution: microbes reduce the synthetic cost of extracellular proteins. *MBio* **1**:
- Smith MG, Hold GL, Tahara E and El-Omar EM (2006). Cellular and molecular aspects of gastric cancer. *World J Gastroenterol* **12**: 2979-90.
- Smith PM, Howitt MR, Panikov N, Michaud M, *et al.* (2013). The microbial metabolites, short-chain fatty acids, regulate colonic Treg cell homeostasis. *Science* **341**: 569-73.
- Sokol H, Pigneur B, Watterlot L, Lakhdari O, *et al.* (2008). *Faecalibacterium prausnitzii* is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients. *Proc Natl Acad Sci U S A* **105**: 16731 -6.
- Sokol H, Seksik P, Furet JP, Firmesse O, *et al.* (2009). Low counts of *Faecalibacterium prausnitzii* in colitis microbiota. *Inflamm Bowel Dis* **15**: 1183-9.
- Sonnenburg JL, Xu J, Leip DD, Chen CH, *et al.* (2005). Glycan foraging in vivo by an intestine-adapted bacterial symbiont. *Science* **307**: 1955-9.
- Stappenbeck TS, Hooper LV and Gordon JI (2002). Developmental regulation of intestinal angiogenesis by indigenous microbes via Paneth cells. *Proc Natl Acad Sci U S A* **99**: 15451-5.
- Statnikov A, Henaff M, Narendra V, Konganti K, *et al.* (2013). A comprehensive evaluation of multiclassification methods for microbiomic data. *Microbiome* **1**: 11.
- Storf S, Pfeiffer F, Dilks K, Chen ZQ and Imam S (2010). Mutational and bioinformatic analysis of haloarchaeal lipobox-containing proteins. *Archaea* **16**: pii 410975
- Stumm G, Russ A and Nehls M (2002). Deductive genomics: a functional approach to identify innovative drug targets in the post-genome era. *Am J Pharmacogenomics* **2**: 263-71.
- Suen G, Stevenson DM, Bruce DC, Chertkov O, *et al.* (2011). Complete genome of the cellulolytic ruminal bacterium *Ruminococcus albus* 7. *J Bacteriol* **193**: 5574-5.
- Sun J and Chang EB (2014). Exploring gut microbes in human health and disease: Pushing the envelope. *Genes Dis* **1**: 132-139.
- Szklarczyk D, Franceschini A, Kuhn M, Simonovic M, *et al.* (2011). The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. *Nucleic Acids Res* **39**: D561-D568.
- Szklarczyk D, Franceschini A, Wyder S, Forslund K, *et al.* (2014).

- STRING v10: protein-protein interaction networks, integrated over the tree of life. *Nucleic Acids Res* **43**: D447-52.
- Tamura K, Stecher G, Peterson D, Filipski A and Kumar S (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Mol Biol Evol* **30**: 2725-9.
- Tasse L, Bercovici J, Pizzut-Serin S, Robe P, et al. (2010). Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. *Genome Res* **20**: 1605-12.
- Tatusov RL, Fedorova ND, Jackson JD, Jacobs AR, et al. (2003). The COG database: an updated version includes eukaryotes. *BMC Bioinformatics* **4**: 41.
- Thakur S, Normand P, Daubin V, Tisa LS and Sen A (2013). Contrasted evolutionary constraints on secreted and non-secreted proteomes of selected Actinobacteria. *BMC Genomics* **14**: 474.
- Thiele I and Palsson BO (2010). A protocol for generating a high-quality genome-scale metabolic reconstruction. *Nat Protoc* **5**: 93-121.
- Tilg H and Kaser A (2011). Gut microbiome, obesity, and metabolic dysfunction. *J Clin Invest* **121**: 2126-32.
- Tjalsma H, Antelmann H, Jongbloed JD, Braun PG, et al. (2004). Proteomics of protein secretion by *Bacillus subtilis*: separating the "secrets" of the secretome. *Microbiol Mol Biol Rev* **68**: 207-33.
- Tjalsma H, Antelmann H, Jongbloed JD, Braun PG, et al. (2004). Proteomics of protein secretion by *Bacillus subtilis*: separating the "secrets" of the secretome. *Microbiol Mol Biol Rev* **68**: 207-33.
- separating the "secrets" of the secretome. *Microbiol Mol Biol Rev* **68**: 207-33.
- Tomme P, Van Tilbeurgh H, Pettersson G, Van Damme J, et al. (1988). Studies of the cellulolytic system of *Trichoderma reesei* QM 9414. Analysis of domain function in two cellobiohydrolases by limited proteolysis. *Eur J Biochem* **170**: 575-81.
- Townsend DM and Tew KD (2003). The role of glutathione-S-transferase in anti-cancer drug resistance. *Oncogene* **22**: 7369-7375.
- Tremaroli V and Backhed F (2012). Functional interactions between the gut microbiota and host metabolism. *Nature* **489**: 242-9.
- Trott O and Olson AJ (2010). AutoDock Vina: improving the speed and accuracy of docking with a new scoring function, efficient optimization, and multithreading. *J Comput Chem* **31**: 455-61.
- Tuller T, Veksler-Lublinsky I, Gazit N, Kupiec M, et al. (2011). Composite effects of gene determinants on the translation speed and density of ribosomes. *Genome Biol* **12**: R110.
- Turnbaugh PJ, Hamady M, Yatsunenko T, Cantarel BL, et al. (2009a). A core gut microbiome in obese and lean twins. *Nature* **457**: 480-4.
- Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, et al. (2006). An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature* **444**: 1027-31.
- Turnbaugh PJ, Ridaura VK, Faith JJ, Rey FE, et al. (2009b). The effect of diet on the human gut

- microbiome: a metagenomic analysis in humanized gnotobiotic mice. *Sci Transl Med* **1**: 6ra14.
- Turroni F, Duranti S, Bottacini F, Guglielmetti S, et al. (2014). Bifidobacterium bifidum as an example of a specialized human gut commensal. *Front Microbiol* **5**: 437.
- van Baarlen P, Troost FJ, van Hemert S, van der Meer C, et al. (2009). Differential NF- κ B pathways induction by Lactobacillus plantarum in the duodenum of healthy humans correlating with immune tolerance. *Proc Natl Acad Sci U S A* **106**: 2371-6.
- Velagapudi VR, Hezaveh R, Reigstad CS, Gopalacharyulu P, et al. (2010). The gut microbiota modulates host energy and lipid metabolism in mice. *J Lipid Res* **51**: 1101-12.
- Ventura M, Canchaya C, Tauch A, Chandra G, et al. (2007). Genomics of Actinobacteria: tracing the evolutionary history of an ancient phylum. *Microbiol Mol Biol Rev* **71**: 495-548.
- Ventura M, Canchaya C, Tauch A, Chandra G, et al. (2007). Genomics of Actinobacteria: tracing the evolutionary history of an ancient phylum. *Microbiol Mol Biol Rev* **71**: 495-548.
- Verstraeten H (2008). Cutting edge: the vaginal microflora and bacterial vaginosis. *Verh K Acad Geneeskd Belg* **70**: 147-74.
- Vert JP. (2002). Support vector machine prediction of signal peptide cleavage site using a new class of kernels for strings. *Pac Symp Biocomput* **2002**: 649-660.
- Vesth T, Lagesen K, Acar O and Ussery D (2013). CMG-biotools, a free workbench for basic comparative microbial genomics. *PLoS One* **8**: e60120.
- Vesth T, Ozen A, Andersen SC, Kaas RS, et al. (2013). Veillonella, Firmicutes: Microbes disguised as Gram negatives. *Stand Genomic Sci* **9**: 431-48.
- von Heijne G (1984). How signal sequences maintain cleavage specificity. *J Mol Biol* **173**: 243-51.
- von Heijne G (1989). The structure of signal peptides from bacterial lipoproteins. *Protein Eng* **2**: 531-4.
- von Heijne G (1990). The signal peptide. *J Membr Biol* **115**: 195-201.
- Wallace BD, Wang H, Lane KT, Scott JE, et al. (2010). Alleviating cancer drug toxicity by inhibiting a bacterial enzyme. *Science* **330**: 831-5.
- Wan XF, Xu D, Kleinhofs A and Zhou J (2004). Quantitative relationship between synonymous codon usage bias and GC composition across unicellular genomes. *BMC Evol Biol* **4**: 19.
- Wang M, Ahrne S, Antonsson M and Molin G (2004). T-RFLP combined with principal component analysis and 16S rRNA gene sequencing: an effective strategy for comparison of fecal microbiota in infants of different ages. *J Microbiol Methods* **59**: 53-69.
- Wang M, Karlsson C, Olsson C, Adlerberth I, et al. (2008). Reduced diversity in the early fecal microbiota of infants with atopic eczema. *J Allergy Clin Immunol* **121**: 129-34.
- Wang S, Sim TB, Kim Y-S and Chang Y-T (2004). Tools for target

- identification and validation. *Curr Opin Chem Biol* **8**: 371-377.
- Wegmann U, Louis P, Goesmann A, Henrissat B, *et al.* (2014). Complete genome of a new Firmicutes species belonging to the dominant human colonic microbiota ('Ruminococcus bicirculans') reveals two chromosomes and a selective capacity to utilize plant glucans. *Environ Microbiol* **16**: 2879-90.
- Wei W and Guo FB (2010). Strong Strand Composition Bias in the Genome of *Ehrlichia canis* Revealed by Multiple Methods. *Open Microbiol J* **4**: 98-102.
- Wei YX, Zhang ZY, Liu C, Malakar PK and Guo XK (2012). Safety assessment of *Bifidobacterium longum* JDM301 based on complete genome sequences. *World J Gastroenterol* **18**: 479-88.
- Weinstock GM (2012). Genomic approaches to studying the human microbiota. *Nature* **489**: 250-6.
- Westermann AJ, Gorski SA and Vogel J (2012). Dual RNA-seq of pathogen and host. *Nat Rev Microbiol* **10**: 618-30.
- Wexler HM (2007). *Bacteroides*: the good, the bad, and the nitty-gritty. *Clin Microbiol Rev* **20**: 593-621.
- White BA, Lamed R, Bayer EA and Flint HJ (2014). Biomass utilization by gut microbiomes. *Annu Rev Microbiol* **68**: 279-96.
- Whitman WB, Coleman DC and Wiebe WJ (1998). Prokaryotes: the unseen majority. *Proc Natl Acad Sci U S A* **95**: 6578-83.
- Wilke A, Harrison T, Wilkening J, Field D, *et al.* (2012). The M5nr: a novel non-redundant database containing protein sequences and annotations from multiple sources and associated tools. *BMC Bioinformatics* **13**: 141.
- Williams GJ and Thorson JS (2009). Natural product glycosyltransferases: properties and applications. *Adv Enzymol Relat Areas Mol Biol* **76**: 55-119.
- Wilson AC, Carlson SS and White TJ (1977). Biochemical evolution. *Annual review of biochemistry* **46**: 573-639.
- Wong EH, Smith DK, Rabadian R, Peiris M and Poon LL (2010). Codon usage bias and the evolution of influenza A viruses. Codon Usage Biases of Influenza Virus. *BMC Evol Biol* **10**: 253.
- Wright F (1990). The 'effective number of codons' used in a gene. *Gene* **87**: 23-9.
- Wu G, Culley DE and Zhang W (2005). Predicted highly expressed genes in the genomes of *Streptomyces coelicolor* and *Streptomyces avermitilis* and the implications for their metabolism. *Microbiology* **151**: 2175-87.
- Xia X (2013). DAMBE5: a comprehensive software package for data analysis in molecular biology and evolution. *Mol Biol Evol* **30**: 1720-8.
- Xiong X, Frank DN, Robertson CE, Hung SS, *et al.* (2012). Generation and analysis of a mouse intestinal metatranscriptome through Illumina based RNA-sequencing. *PLoS One* **7**: e36009.
- Xu G, Strong MJ, Lacey MR, Baribault C, *et al.* (2014). RNA CoMPASS: a dual approach for

- pathogen and host transcriptome analysis of RNA-seq datasets. *PLoS One* **9**: e89445.
- Xu J, Bjursell MK, Himrod J, Deng S, et al. (2003). A genomic view of the human-Bacteroides thetaiotaomicron symbiosis. *Science* **299**: 2074-6.
- Yamazaki S, Tsuyuki S, Akashiba H, Kamimura H, et al. (1991). Immune response of *Bifidobacterium*-monoassociated mice. *Bifidobacteria and Microflora* **10**: 19-31.
- Yan F, Cao H, Cover TL, Washington MK, et al. (2011). Colon-specific delivery of a probiotic-derived soluble protein ameliorates intestinal inflammation in mice through an EGFR-dependent mechanism. *J Clin Invest* **121**: 2242-53.
- Yoon SH, Han MJ, Jeong H, Lee CH, et al. (2012). Comparative multi-omics systems analysis of *Escherichia coli* strains B and K -12. *Genome Biol* **13**: R37.
- Yoshimura HH, Graham DY, Estes MK and Merkal RS (1987). Investigation of association of mycobacteria with inflammatory bowel disease by nucleic acid hybridization. *J Clin Microbiol* **25**: 45-51.
- Yu CS, Chen YC, Lu CH and Hwang JK (2006). Prediction of protein subcellular localization. *Proteins: Struct, Funct, Bioinf* **64**: 643-651.
- Yu CS, Lin CJ and Hwang JK (2004). Predicting subcellular localization of proteins for Gram-negative bacteria by support vector machines based on n-peptide compositions. *Protein Sci* **13**: 1402-1406.
- Zakham F, Aouane O, Ussery D, Benjouad A and Ennaji MM (2012) Computational genomics -proteomics and Phylogeny analysis of twenty one mycobacterial genomes (Tuberculosis & non Tuberculosis strains). *Microb Inform Exp* **2**: 7.
- Zanotti G and Cendron L (2014). Structural and functional aspects of the *Helicobacter pylori* secretome. *World J Gastroenterol* **20**: 1402-23.
- Ze X, Ben David Y, Laverde-Gomez JA, Dassa B, et al. (2015). Unique Organization of Extracellular Amylases into Amylosomes in the Resistant Starch-Utilizing Human Colonic Firmicutes Bacterium *Ruminococcus bromii*. *MBio* **6**: e01058-15.
- Ze X, Duncan SH, Louis P and Flint HJ (2012). *Ruminococcus bromii* is a keystone species for the degradation of resistant starch in the human colon. *Isme J* **6**: 1535-43.
- Ze X, Le Mougen F, Duncan SH, Louis P and Flint HJ (2013). Some are more equal than others: the role of "keystone" species in the degradation of recalcitrant substrates. *Gut Microbes* **4**: 236-40.
- Zelante T, Iannitti RG, Cunha C, De Luca A, et al. (2013). Tryptophan catabolites from microbiota engage aryl hydrocarbon receptor and balance mucosal reactivity via interleukin-22. *Immunity* **39**: 372-85.
- Zhang H, DiBaise JK, Zuccolo A, Kudrna D, et al. (2009). Human gut microbiota in obesity and after gastric bypass. *Proc Natl Acad Sci U S A* **106**: 2365-70.
- Zhang R, Ou HY and Zhang CT (2004). DEG: a database of

- essential genes. *Nucleic Acids Res* **32**: D271-D272.
- Zhang YM, Shao ZQ, Yang LT, Sun XQ, *et al.* (2013). Non-random arrangement of synonymous codons in archaea coding sequences. *Genomics* **101**: 362-7.
- Zhao KN, Liu WJ and Frazer IH (2003). Codon usage bias and A+T content variation in human papillomavirus genomes. *Virus Res* **98**: 95-104.
- Zhong J, Li Y, Zhao S, Liu S and Zhang Z (2007). Mutation pressure shapes codon usage in the GC-Rich genome of foot-and-mouth disease virus. *Virus Genes* **35**: 767-76.
- Zhou JH, Gao ZL, Zhang J, Ding YZ, *et al.* (2013). The analysis of codon bias of foot-and-mouth disease virus and the adaptation of this virus to the hosts. *Infect Genet Evol* **14**: 105-10.
- Zhou M and Li X (2009). Analysis of synonymous codon usage patterns in different plant mitochondrial genomes. *Mol Biol Rep* **36**: 2039-46.
- Zhou M, Theunissen D, Wels M and Siezen RJ (2010). LAB-Secretome: a genome-scale comparative analysis of the predicted extracellular and surface-associated proteins of Lactic Acid Bacteria. *BMC Genomics* **11**: 651.
- Zijnge V, Welling GW, Degener JE, van Winkelhoff AJ, *et al.* (2006). Denaturing gradient gel electrophoresis as a diagnostic tool in periodontal microbiology. *J Clin Microbiol* **44**: 3628-33.
- Zoetendal EG, Akkermans AD and De Vos WM (1998). Temperature gradient gel electrophoresis analysis of 16S rRNA from human fecal samples reveals stable and host-specific communities of active bacteria. *Appl Environ Microbiol* **64**: 3854-9.
- Zoetendal EG, Collier CT, Koike S, Mackie RI and Gaskins HR (2004). Molecular ecological analysis of the gastrointestinal microbiota: a review. *J Nutr* **134**: 465-72.