

Bibliography

- ALBERT R and BARABÁSI A. Statistical mechanics of complex networks. *Rev Mod Physics*, 74:47–97, 2002. 1.1.4
- ALOY P, CEULEMANS H, STARK A and RUSSELL RB. The relationship between sequence and interaction divergence in proteins. *J Mol Biol*, 332:989–998, 2003. 1.1.1.4, 2.3.4, 3.3.2.1, 3.4.1
- ALOY P and RUSSELL RB. The third dimension for protein interactions and complexes. *Trends Biochem Sci*, 27:633–638, 2002. 3.4.1
- ALOY P and RUSSELL RB. Ten thousand interactions for the molecular biologist. *Nat Biotechnol*, 22:1317–1321, 2004. 1.3.1, 2.1, 2.3.7, 2.3.7, 2.4.1, 2.4.2
- AURY JM, JAILLON O, DURET L, NOEL B, JUBIN C *et al.* Global trends of whole-genome duplications revealed by the ciliate *Paramecium tetraurelia*. *Nature*, 444:171–178, 2006. 4.1
- AXELSEN JB, LOTEM J, SACHS L and DOMANY E. Genes overexpressed in different human solid cancers exhibit different tissue-specific expression profiles. *Proc Natl Acad Sci USA*, 104:13122–13127, 2007. 4.2.4, 4.3.2
- BARABASI A and ALBERT R. Emergence of scaling in random networks. *Science*, 286:509–512, 1999. 1.1.4

- BARABASI AL and OLTVAI ZN. Network biology: understanding the cell's functional organization. *Nat Rev Genet*, 5:101–113, 2004. 1.1.4
- BARBUJANI G, MAGAGNI A, MINCH E and CAVALLI-SFORZA LL. An apportionment of human DNA diversity. *Proc Natl Acad Sci USA*, 94:4516–4519, 1997. 1.2.2
- BARTEL PL and FIELDS S. *The Yeast Two-Hybrid System (Advances in Molecular Biology)*. Oxford University Press, USA, 1st edition, 1997. 1.1.1.2
- BASU MK, CARMEL L, ROGOZIN IB and KOONIN EV. Evolution of protein domain promiscuity in eukaryotes. *Genome Res*, 18:449–461, 2008. 2.4.2
- BATZER MA and DEININGER PL. Alu repeats and human genomic diversity. *Nat Rev Genet*, 3:370–379, 2002. 1.2.1
- BERGGÅRD T, LINSE S and JAMES P. Methods for the detection and analysis of protein–protein interactions. *Proteomics*, 7:2833–2842, 2007. 1.1.1.1, 1.1.1.2
- BERMAN HM. The Protein Data Bank: a historical perspective. *Acta Crystallogr A*, 64:88–95, 2008. 1.5
- BIRCHLER J. The genetic basis of dosage compensation of alcohol dehydrogenase-1 in maize. *Genetics*, 97:625–637, 1981. 4.1
- BIRCHLER JA, BHADRA U, BHADRA MP and AUGER DL. Dosage-dependent gene regulation in multicellular eukaryotes: implications for dosage compensation, aneuploid syndromes, and quantitative traits. *Dev Biol*, 234:275–288, 2001. 4.1
- BIRCHLER JA, RIDDLE NC, AUGER DL and VEITIA RA. Dosage balance in gene regulation: biological implications. *Trends Genet*, 21:219–226, 2005. 4.1, 4.4.2
- BIRCHLER JA, YAO H and CHUDALAYANDI S. Biological consequences of dosage dependent gene regulatory systems. *Biochim Biophys Acta*, 1769:422–428, 2007. 4.1

- BLAKE WJ, KAERN M, CANTOR CR and COLLINS JJ. Noise in eukaryotic gene expression. *Nature*, 422:633–637, 2003. 4.4.2
- BLEKHMANN R, MAN O, HERRMANN L, BOYKO AR, INDAP A *et al.* Natural selection on genes that underlie human disease susceptibility. *Curr Biol*, 18:883–889, 2008. 1.2.3.1
- BOTSTEIN D and RISCH N. Discovering genotypes underlying human phenotypes: past successes for Mendelian disease, future approaches for complex disease. *Nature Genetics*, 33:228–237, 2003. 1.2.3.1
- BOYD W. Genetics and the human race: Definition of race on the basis of gene frequencies supplements definition from morphological characters. *Science*, 140:1057–1064, 1963. 1.2.3
- BRANDEN C and TOOZE J. *Introduction to Protein Structure*. Garland Publishing, 2nd edition, 1991. 1.1.1.4
- BRAVO J and ALOY P. Target selection for complex structural genomics. *Curr Opin Struct Biol*, 16:385–392, 2006. 2.4.1
- BREITKREUTZ BJ, STARK C, REGULY T, BOUCHER L, BREITKREUTZ A *et al.* The BioGRID interaction database: 2008 update. *Nucleic Acids Res*, 36:D637–640, 2008. 1.1.3, 2.2.1, 3.3.3
- BRUFORD EA, LUSH MJ, WRIGHT MW, SNEDDON TP, POVEY S and BIRNEY E. The HGNC database in 2008: a resource for the human genome. *Nucleic Acids Res*, 36:D445–448, 2008. 4.2.1
- BURATTI E, BARALLE M and BARALLE FE. Defective splicing, disease and therapy: searching for master checkpoints in exon definition. *Nucleic Acids Res*, 34:3494–3510, 2006. 3.1

- BURCKSTUMMER T, BENNETT KL, PRERADOVIC A, SCHUTZE G, HANTSCHHEL O, SUPERTI-FURGA G and BAUCH A. An efficient tandem affinity purification procedure for interaction proteomics in mammalian cells. *Nat Methods*, 3:1013–1019, 2006. 1.1.1.1
- BUSHELL KM, SOLLNER C, SCHUSTER-BÖCKLER B, BATEMAN A and WRIGHT GJ. Large-scale screening for novel low-affinity extracellular protein interactions. *Genome Res*, 18:622–630, 2008. 1.1.1.5, 1.4
- CAMON E, MAGRANE M, BARRELL D, LEE V, DIMMER E *et al.* The Gene Ontology Annotation (GOA) database: sharing knowledge in UniProt with Gene Ontology. *Nucleic Acids Res*, 32:D262–266, 2004. 4.2.9
- CHAKRABARTI P and JANIN J. Dissecting protein–protein recognition sites. *Proteins*, 47:334–343, 2002. 3.3.4.4, 3.9
- CHATR-ARYAMONTRI A, CEOL A, PALAZZI LM, NARDELLI G, SCHNEIDER MV, CASTAGNOLI L and CESARENI G. MINT: the Molecular INTeraction database. *Nucleic Acids Res*, 35:D572–574, 2007. 1.1.3, 2.2.1
- CHEUNG SW, SHAW CA, YU W, LI J, OU Z *et al.* Development and validation of a CGH microarray for clinical cytogenetic diagnosis. *Genet Med*, 7:422–432, 2005. 4.2.4
- CHITI F and DOBSON CM. Protein misfolding, functional amyloid, and human disease. *Annu Rev Biochem*, 75:333–366, 2006. 3.1
- CHOTHIA C. One thousand families for the molecular biologist. *Nature*, 357:543–544, 1992. 1.3
- CHOTHIA C and LESK AM. The relation between the divergence of sequence and structure in proteins. *EMBO J*, 5:823–826, 1986. 1.1.1.4, 3.3.2.1

BIBLIOGRAPHY

- COLLINS FS, GUYER MS and CHAKRAVARTI A. Variations on a theme: Cataloging human DNA sequence variation. *Science*, 278:1580–1581, 1997. 3.1
- CONRAD DF, ANDREWS TD, CARTER NP, HURLES ME and PRITCHARD JK. A high-resolution survey of deletion polymorphism in the human genome. *Nat Genet*, 38:75–81, 2006. 1.2.3
- CONRAD DF and HURLES ME. The population genetics of structural variation. *Nat Genet*, 39:S30–36, 2007. 4.1
- COOPER GM, NICKERSON DA and EICHLER EE. Mutational and selective effects on copy-number variants in the human genome. *Nat Genet*, 29:S22–29, 2007. 4.1, 4.3.3, 4.3.4, 4.4.3
- CUNNINGHAM BC and WELLS JA. High-resolution epitope mapping of hGH-receptor interactions by alanine-scanning mutagenesis. *Science*, 244:1081–1085, 1989. 1.1, 3.2.6
- CUSICK ME, KLITGORD N, VIDAL M and HILL DE. Interactome: gateway into systems biology. *Hum Mol Genet*, 14:R171–181, 2005. 2.1
- DANG V, KASSAHN K, MARCOS A and RAGAN M. Identification of human haploinsufficient genes and their genomic proximity to segmental duplications. *Eur J Hum Genet*, 2008. 4.4.4
- DARWIN C. *On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life*. John Murray, 1st edition, 1859. 1.2
- DEANE CM, SALWINSKI L, XENARIOS I and EISENBERG D. Protein interactions: two methods for assessment of the reliability of high throughput observations. *Mol Cell Proteomics*, 1:349–356, 2002. 1.1.2

- DEUTSCHBAUER AM, JARAMILLO DF, PROCTOR M, KUMM J, HILLENMEYER ME, DAVIS RW, NISLOW C and GIAEVER G. Mechanisms of haploinsufficiency revealed by genome-wide profiling in yeast. *Genetics*, 169:1915–1925, 2005. 4.1
- DEVLIN RH, HOLM DG and GRIGLIATTI TA. Autosomal dosage compensation in *Drosophila melanogaster* strains trisomic for the left arm of chromosome 2. *Proc Natl Acad Sci USA*, 79:1200–1204, 1982. 4.1, 4.4.2
- DISOTELL TR. Human genomic variation. *Genome Biol*, 1:5, 2000. 1.2.2
- VAN DONGEN S. *Graph clustering by flow simulation*. Ph.D. thesis, University of Utrecht, The Netherlands, 2000. 4.2.3
- DURBIN R, EDDY SR, KROGH A and MITCHISON G. *Biological Sequence Analysis*. Cambridge University Press, 1998. 1.3
- EDDY SR. *HMMER User's Guide: Biological sequence analysis using profile hidden Markov models, version 2.2*. Washington University School of Medicine, <http://hmmer.wustl.edu>, 2001. 3.2.4
- EDGAR RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res*, 32:1792–1797, 2004. 3
- EISENBERG E and LEVANON E. Preferential attachment in the protein network evolution. *Phys Rev Lett*, 91:138701, 2003. 1.1.4
- EL GHOZZI V, LEGEAI-MALLET L, ARESTA S, BENOIST C, MUNNICH A, DE GUNZBURG J and BONAVENTURE J. Saethre-Chotzen mutations cause TWIST protein degradation or impaired nuclear location. *Hum Mol Genet*, 9:813–819, 2000. 3.3.6.3
- ENRIGHT AJ, ILIOPOULOS I, KYRPIDES NC and OUZOUNIS CA. Protein interaction maps for complete genomes based on gene fusion events. *Nature*, 402:86–90, 1999. 1.3.1, 2.2.4

- EWING RM, CHU P, ELISMA F, LI H, TAYLOR P *et al.* Large-scale mapping of human protein–protein interactions by mass spectrometry. *Mol Syst Biol*, 3:89, 2007. 4.2.3
- FAWCETT T. An introduction to ROC analysis. *Pattern Recog Lett*, 27:861–874, 2006. 3.3.2.3
- FELDMAN MW, LEWONTIN RC and KING MC. Race: a genetic melting-pot. *Nature*, 424:374, 2003. 1.2.2
- FERRER-COSTA C, OROZCO M and DE LA CRUZ X. Characterization of disease-associated single amino acid polymorphisms in terms of sequence and structure properties. *J Mol Biol*, 315:771–786, 2002. 3.1, 3.4.2
- FIELDS S and SONG O. A novel genetic system to detect protein–protein interactions. *Nature*, 340:245–246, 1989. 1.1.1.2
- FINN RD, MARSHALL M and BATEMAN A. iPfam: visualization of protein–protein interactions in PDB at domain and amino acid resolutions. *Bioinformatics*, 21:410–412, 2005. 1.3.1, 2.1, 2.2.4, 3.2.2, 3.3.1
- FINN RD, MISTRY J, SCHUSTER-BÖCKLER B, GRIFFITHS-JONES S, HOLLICH V *et al.* Pfam: clans, web tools and services. *Nucleic Acids Res*, 34:D247–251, 2006. 1.4
- FINN RD, TATE J, MISTRY J, COGGILL PC, SAMMUT SJ *et al.* The Pfam protein families database. *Nucleic Acids Res*, 36:D281–288, 2008. 1, 1.3, 2.1
- FREEMAN JL, PERRY GH, FEUK L, REDON R, MCCARROLL SA *et al.* Copy number variation: new insights in genome diversity. *Genome Res*, 16:949–961, 2006. 1.2.3
- FU L. Alteration of protein–protein interactions of congenital cataract crystallin mutants. *Investig Ophthalmology & Vis Sci*, 44:1155–1159, 2003. 3.1

- GANDHI TKB, ZHONG J, MATHIVANAN S, KARTHICK L, CHANDRIKA KN *et al.* Analysis of the human protein interactome and comparison with yeast, worm and fly interaction datasets. *Nat Genet*, 38:285–293, 2006. 1, 2.4.3
- GAVIN AC, ALOY P, GRANDI P, KRAUSE R, BOESCHE M *et al.* Proteome survey reveals modularity of the yeast cell machinery. *Nature*, 440:631–636, 2006. 1.1.2, 2.3.5
- GERHART J and SCHACHMAN H. Distinct subunits for the regulation and catalytic activity of aspartate transcarbamylase. *Biochemistry*, 4:1054–1062, 1965. 1.1
- GERHART JC and PARDEE AB. The enzymology of control by feedback inhibition. *J Biol Chem*, 237:891–896, 1962. 1.1
- GIORGINI F and MUCHOWSKI PJ. Connecting the dots in Huntington’s disease with protein interaction networks. *Genome Biol*, 6:210–211, 2005. 3.1
- GLASER F, ROSENBERG Y, KESSEL A, PUPKO T and BEN-TAL N. The ConSurf-HSSP database: the mapping of evolutionary conservation among homologs onto PDB structures. *Proteins*, 58:610–617, 2005. 3.2.3
- GRACE CRR, PERRIN MH, GULYAS J, DIGRUCCIO MR, CANTLE JP, RIVIER JE, VALE WW and RIEK R. Structure of the N-terminal domain of a type B1 G protein-coupled receptor in complex with a peptide ligand. *Proc Natl Acad Sci USA*, 104:4858–4863, 2007. 3.2.6
- GRIGORIEV A. On the number of protein–protein interactions in the yeast proteome. *Nucleic Acids Res*, 31:4157–4161, 2003. 2.1
- GUINDON S and GASCUEL O. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Syst Biol*, 52:696–704, 2003. 4

- GULDENER U, MUNSTERKOTTER M, OESTERHELD M, PAGEL P, RUEPP A, MEWES H and STUMPFLEN V. MPact: the MIPS protein interaction resource on yeast. *Nucleic Acids Res*, 34:D436–441, 2006. 2.2.1, 3.3.3
- HAHN A, RAHNENFUHRER J, TALWAR P and LENGAUER T. Confirmation of human protein interaction data by human expression data. *BMC Bioinformatics*, 6:1, 2005. 4.3.2, 4.4.1
- HAMOSH A, SCOTT AF, AMBERGER JS, BOCCHINI CA and MCKUSICK VA. Online Mendelian Inheritance in Man (OMIM), a knowledgebase of human genes and genetic disorders. *Nucleic Acids Res*, 33:D514–517, 2005. 1.2.3.1, 3.1, 3.2.1
- HAN JDJ, DUPUY D, BERTIN N, CUSICK ME and VIDAL M. Effect of sampling on topology predictions of protein–protein interaction networks. *Nat Biotechnol*, 23:839–844, 2005. 1.1.4
- HART GT, RAMANI AK and MARCOTTE EM. How complete are current yeast and human protein-interaction networks? *Genome Biol*, 7:120, 2006. 1, 1.1.2
- HERMJAKOB H, MONTECCHI-PALAZZI L, BADER G, WOJCIK J, SALWINSKI L *et al.* The HUPO PSI’s molecular interaction format — a community standard for the representation of protein interaction data. *Nat Biotechnol*, 22:177–183, 2004. 2.2.1
- HONG B, SENISTERRA G, RABEH W, VEDADI M, LEONARDI R *et al.* Crystal structures of human pantothenate kinases: Insights into allosteric regulation and mutations linked to a neurodegeneration disorder. *J Biol Chem*, 282:27984–27993, 2007. 3.1
- HUBER LA. Is proteomics heading in the wrong direction? *Nat Rev Mol Cell Biol*, 4:74–80, 2003. 1.3

- HUGHES AL and NEI M. Pattern of nucleotide substitution at major histocompatibility complex class I loci reveals overdominant selection. *Nature*, 335:167–170, 1988. 1.2.1
- HUMPHREY W, DALKE A and SCHULTEN K. VMD – Visual Molecular Dynamics. *J Mol Graph*, 14:33–38, 1996. 3.2.9
- IAFRATE AJ, FEUK L, RIVERA MN, LISTEWNIK ML, DONAHOE PK, Qi Y, SCHERER SW and LEE C. Detection of large-scale variation in the human genome. *Nat Genet*, 36:949–951, 2004. 1.2.3, 4.2.7
- ISPOLATOV I, YURYEV A, MAZO I and MASLOV S. Binding properties and evolution of homodimers in protein–protein interaction networks. *Nucleic Acids Res*, 33:3629–3635, 2005. 3.3.3
- ITO T, CHIBA T, OZAWA R, YOSHIDA M, HATTORI M and SAKAKI Y. A comprehensive two-hybrid analysis to explore the yeast protein interactome. *Proc Natl Acad Sci USA*, 98:4569–4574, 2001. 1.1.2, 1.1.4
- ITZHAKI Z, AKIVA E, ALTUVIA Y and MARGALIT H. Evolutionary conservation of domain–domain interactions. *Genome Biol*, 7:R125, 2006. 2.1
- JAMES LC, KEEBLE AH, KHAN Z, RHODES DA and TROWSDALE J. Structural basis for PRYSPRY-mediated tripartite motif (TRIM) protein function. *Proc Natl Acad Sci USA*, 104:6200–6205, 2007. 3.2.6
- JANIN J, RODIER F, CHAKRABARTI P and BAHADUR RP. Macromolecular recognition in the Protein Data Bank. *Acta Crystallogr D Biol Crystallogr*, 63:1–8, 2007. 1.1
- JANSEN R, GREENBAUM D and GERSTEIN M. Relating whole-genome expression data with protein–protein interactions. *Genome Res*, 12:37–46, 2002. 4.1, 4.3.2
- JEONG H, MASON SP, BARABASI AL and OLTVAI ZN. Lethality and centrality in protein networks. *Nature*, 411:41–42, 2001. 1.1.4

- JHOTI H. High-throughput structural proteomics using x-rays. *Trends Biotechnol*, 19:S67–71, 2001. 1.1.1.4
- JIMENEZ-SANCHEZ G, CHILDS B and VALLE D. Human disease genes. *Nature*, 409:853–855, 2001. 3.3.4.3, 1
- JONES S and THORNTON JM. Principles of protein-protein interactions. *Proc Natl Acad Sci USA*, 93:13–20, 1996. 1.1
- JOTHI R, CHERUKURI PF, TASNEEM A and PRZYTYCKA TM. Co-evolutionary analysis of domains in interacting proteins reveals insights into domain–domain interactions mediating protein–protein interactions. *J Mol Biol*, 362:861–875, 2006. 2.1, 2.4.1, 2.4.3
- JUNTTILA MR, SAARINEN S, SCHMIDT T, KAST J and WESTERMARCK J. Single-step Strep-tag purification for the isolation and identification of protein complexes from mammalian cells. *Proteomics*, 5:1199–1203, 2005. 1.1.1.1
- KAFATOS FC, EFSTRATIADIS A, FORGET BG and WEISSMAN SM. Molecular evolution of human and rabbit beta-globin mRNAs. *Proc Natl Acad Sci USA*, 74:5618–5622, 1977. 1.2.1
- KAREV GP, WOLF YI, RZHETSKY AY, BEREZOVSKAYA FS and KOONIN EV. Birth and death of protein domains: a simple model of evolution explains power law behavior. *BMC Evol Biol*, 2:18, 2002. 1.1.4
- KELLIS M, BIRREN BW and LANDER ES. Proof and evolutionary analysis of ancient genome duplication in the yeast *Saccharomyces cerevisiae*. *Nature*, 428:617–624, 2004. 4.1
- KENDREW JC, BODO G, DINTZIS HM, PARRISH RG, WYCKOFF H and PHILLIPS DC.

- A three-dimensional model of the myoglobin molecule obtained by x-ray analysis. *Nature*, 181:662–666, 1958. 1.1.1.4
- KENT WJ, SUGNET CW, FUREY TS, ROSKIN KM, PRINGLE TH, ZAHLER AM and HAUSSLER D. The human genome browser at UCSC. *Genome Res*, 12:996–1006, 2002. 4.4
- KERRIEN S, ALAM-FARUQUE Y, ARANDA B, BANCARZ I, BRIDGE A *et al.* IntAct—open source resource for molecular interaction data. *Nucleic Acids Res*, 35:D561–565, 2007. 1.1.3, 2.2.1, 3.3.3, 4.2.3
- KERSEY P, BOWER L, MORRIS L, HORNE A, PETRYSZAK R *et al.* Integr8 and genome reviews: integrated views of complete genomes and proteomes. *Nucleic Acids Res*, 33:D297–302, 2005. 2.2.3
- KESTLER HA. ROC with confidence — a Perl program for receiver operator characteristic curves. *Comput Methods Programs Biomed*, 64:133–136, 2001. 3.7
- KHANIN R and WIT E. How scale-free are biological networks? *J Comput Biol*, 13:810–818, 2006. 1.1.4
- KIND J, VAQUERIZAS JM, GEBHARDT P, GENTZEL M, LUSCOMBE NM, BERTONE P and AKHTAR A. Genome-wide analysis reveals MOF as a key regulator of dosage compensation and gene expression in *Drosophila*. *Cell*, 133:813–828, 2008. 4.4.2
- KISSINGER CR, REJTO PA, PELLETIER LA, THOMSON JA, SHOWALTER RE *et al.* Crystal structure of human ABAD/HSD10 with a bound inhibitor: implications for design of Alzheimer’s disease therapeutics. *J Mol Biol*, 342:943–952, 2004. 3.3.6
- KLEIN C, PHILIPPE N, LE DEIST F, FRAITAG S, PROST C, DURANDY A, FISCHER A and GRISCELLI C. Partial albinism with immunodeficiency (Griscelli syndrome). *J Pediatr*, 125:886–895, 1994. 3.3.6.1

- KLEYWEGT GJ. Validation of protein crystal structures. *Acta Crystallogr D Biol Crystallogr*, 56:249–265, 2000. 1.1.1.4
- KLOTZ IM, LANGERMAN NR and DARNALL DW. Quaternary structure of proteins. *Annual Review of Biochemistry*, 39:25–62, 1970. 1.1
- KOEGEL M and UETZ P. Improving yeast two-hybrid screening systems. *Brief Funct Genomic Proteomic*, 6:302–312, 2007. 1.1.1.2
- KONDRASHOV FA and KOONIN EV. A common framework for understanding the origin of genetic dominance and evolutionary fates of gene duplications. *Trends Genet*, 20:287–290, 2004. 1.2.3.1, 4.1
- KONDRASHOV FA, ROGOZIN I, WOLF Y and KOONIN E. Selection in the evolution of gene duplications. *Genome Biol*, 3:2, 2002. 4.1
- KOURANOV A, XIE L, DE LA CRUZ J, CHEN L, WESTBROOK J, BOURNE PE and BERMAN HM. The RCSB PDB information portal for structural genomics. *Nucleic Acids Res*, 34:D302–305, 2006. 1.1.1.4, 2.1, 3.3.1
- KRISSINEL E and HENRICK K. Inference of macromolecular assemblies from crystalline state. *J Mol Biol*, 372:774–797, 2007. 1.1.1.4
- KROGAN NJ, CAGNEY G, YU H, ZHONG G, GUO X *et al.* Global landscape of protein complexes in the yeast *Saccharomyces cerevisiae*. *Nature*, 440:637–643, 2006. 4.2.3
- KROGH A, BROWN M, MIAN IS, SJOLANDER K and HAUSSLER D. Hidden Markov models in computational biology. applications to protein modeling. *J Mol Biol*, 235(5):1501–1531, 1994. 1.3
- KUHN K, BAKER SC, CHUDIN E, LIEU MH, OESER S *et al.* A novel, high-performance random array platform for quantitative gene expression profiling. *Genome Res*, 14:2347–2356, 2004. 4.2.5

- LAMOLET B, PULICHINO AM, LAMONERIE T, GAUTHIER Y, BRUE T, ENJALBERT A and DROUIN J. A pituitary cell-restricted T box factor, Tpit, activates POMC transcription in cooperation with Pitx homeoproteins. *Cell*, 104:849–859, 2001. 3.3.6.2
- LEANDRO J, NASCIMENTO C, DE ALMEIDA IT and LEANDRO P. Co-expression of different subunits of human phenylalanine hydroxylase: Evidence of negative interallelic complementation. *Biochim Biophys Acta*, 1762:544–550, 2006. 3.4.3
- LEE H, DENG M, SUN F and CHEN T. An integrated approach to the prediction of domain-domain interactions. *BMC Bioinformatics*, 7, 2006. 2.1, 2.4.1
- LEE JA and LUPSKI JR. Genomic rearrangements and gene copy-number alterations as a cause of nervous system disorders. *Neuron*, 52:103–121, 2006. 4.1
- LEHNER B, CROMBIE C, TISCHLER J, FORTUNATO A and FRASER AG. Systematic mapping of genetic interactions in *Caenorhabditis elegans* identifies common modifiers of diverse signaling pathways. *Nat Genet*, 38:896–903, 2006. 1.1.1.5
- LE MOS B, MEIKLEJOHN CD and HARTL DL. Regulatory evolution across the protein interaction network. *Nat Genet*, 36:1059–1060, 2004. 4.4.1
- LEWONTIN RC. The apportionment of human diversity. *Evolutionary Biology*, 6:391–398, 1972. 1.2.3
- LITTLER SJ and HUBBARD SJ. Conservation of orientation and sequence in protein domain–domain interactions. *J Mol Biol*, 345:1265–1279, 2005. 2.1
- LIVINGSTONE F. Anthropological implications of sickle cell gene distribution in west africa. *Am Anthropol*, 60:533–562, 1958. 1.2.3
- LOGSDON NJ, JONES BC, ALLMAN JC, IZOTOVA L, SCHWARTZ B, PESTKA S and WALTER MR. The IL-10R2 binding hot spot on IL-22 is located on the N-terminal

- helix and is dependent on N-linked glycosylation. *J Mol Biol*, 342:503–514, 2004. 3.2.6
- LU X, SHAW CA, PATEL A, LI J, COOPER ML *et al.* Clinical implementation of chromosomal microarray analysis: summary of 2513 postnatal cases. *PLoS ONE*, 2:e327, 2007. 3.1
- LUSCOMBE NM, QIAN J, ZHANG Z, JOHNSON T and GERSTEIN M. The dominance of the population by a selected few: power-law behaviour applies to a wide variety of genomic properties. *Genome Biol*, 3:R8, 2002. 1.1.4
- LYNCH M and CONERY JS. The evolutionary fate and consequences of duplicate genes. *Science*, 290:1151–1155, 2000. 4.1
- MACBEATH G and SCHREIBER SL. Printing proteins as microarrays for high-throughput function determination. *Science*, 289:1760–1763, 2000. 1.1.1.5
- MANI R, ST ONGE RP, HARTMAN JLT, GIAEVER G and ROTH FP. Defining genetic interaction. *Proc Natl Acad Sci USA*, 105:3461–3466, 2008. 1.1.1.5
- MARKHAM K, BAI Y and SCHMITT-ULMS G. Co-immunoprecipitations revisited: an update on experimental concepts and their implementation for sensitive interactome investigations of endogenous proteins. *Anal Bioanal Chem*, 389:461–473, 2007. 1.1.1.5
- MASLOV S and SNEPPEN K. Specificity and stability in topology of protein networks. *Science*, 296:910–913, 2002. 2.2.6
- MENASCHE G, PASTURAL E, FELDMANN J, CERTAIN S, ERSOY F *et al.* Mutations in RAB27A cause Griscelli syndrome associated with haemophagocytic syndrome. *Nat Genet*, 25:173–176, 2000. 3.3.6.1
- MENDEL J. Versuche über Pflanzenhybriden. *Verhandlungen des naturforschenden Vereines in Brünn*, 4:3–47, 1865. 1.2

- VON MERING C, KRAUSE R, SNEL B, CORNELL M, OLIVER SG, FIELDS S and BORK P. Comparative assessment of large-scale data sets of protein–protein interactions. *Nature*, 417:399–403, 2002. 1.1.2, 2.1
- MEWES HW, DIETMANN S, FRISHMAN D, GREGORY R, MANNHAUPT G *et al.* MIPS: analysis and annotation of genome information in 2007. *Nucleic Acids Res*, 36:D196–201, 2008. 1.1.1.3, 1.1.3
- MINTSERIS J and WENG Z. Structure, function, and evolution of transient and obligate protein–protein interactions. *Proc Natl Acad Sci USA*, 102:10930–10935, 2005. 4.3.4, 4.4.3
- MISHRA GR, SURESH M, KUMARAN K, KANNABIRAN N, SURESH S *et al.* Human protein reference database–2006 update. *Nucleic Acids Res*, 34:D411–414, 2006. 1.1.3, 2.2.1, 3.3.3
- MÜLLER CW and HERRMANN BG. Crystallographic structure of the T domain–DNA complex of the brachyury transcription factor. *Nature*, 389:884–888, 1997. 3.3.6.2
- NAIR SK and BURLEY SK. X-ray structures of Myc–Max and Mad–Max recognizing DNA: Molecular bases of regulation by proto-oncogenic transcription factors. *Cell*, 112:193–205, 2003. 3.3.6.3
- NEDUVA V and RUSSELL RB. Linear motifs: evolutionary interaction switches. *FEBS Lett*, 579:3342–3345, 2005. 2.3.5
- NG PC and HENIKOFF S. SIFT: Predicting amino acid changes that affect protein function. *Nucleic Acids Res*, 31:3812–3814, 2003. 3.3.2.2
- NG SK, ZHANG Z, TAN SH and LIN K. InterDom: a database of putative interacting protein domains for validating predicted protein interactions and complexes. *Nucleic Acids Res*, 31:251–4, 2003. 2.1

- NGUYEN DQ, WEBBER C and PONTING CP. Bias of selection on human copy-number variants. *PLoS Genet*, 2:e20, 2006. 4.1, 4.3.3, 4.3.4, 4.4.3
- NYE TMW, BERZUINI C, GILKS WR, BABU MM and TEICHMANN SA. Statistical analysis of domains in interacting protein pairs. *Bioinformatics*, 21:993–1001, 2005. 2.1
- OFMAN R, RUITER JPN, FEENSTRA M, DURAN M, POLL-THE BT *et al.* 2-Methyl-3-hydroxybutyryl-CoA dehydrogenase deficiency is caused by mutations in the HADH2 gene. *Am J Hum Genet*, 72:1300–1307, 2003. 3.3.6
- OFRAN Y and ROST B. Analysing six types of protein–protein interfaces. *J Mol Biol*, 325:377–387, 2003. 3.3.4.4
- OFRAN Y and ROST B. Protein–protein interaction hotspots carved into sequences. *PLoS Comput Biol*, 3:e119, 2007. 3.3.2.4
- ORR H. A test of Fisher’s theory of dominance. *Proc Natl Acad Sci USA*, 88:11413–11415, 1991. 4.1
- OSTERMEIER C and BRUNGER AT. Structural basis of Rab effector specificity: crystal structure of the small G protein Rab3A complexed with the effector domain of rabphilin-3a. *Cell*, 96:363–374, 1999. 3.3.6.1
- PAGEL P, WONG P and FRISHMAN D. A domain interaction map based on phylogenetic profiling. *J Mol Biol*, 344:1331–46, 2004. 2.1
- PAPP B, PAL C and HURST LD. Dosage sensitivity and the evolution of gene families in yeast. *Nature*, 424:194–197, 2003. 3.4.3, 4.1
- PARK J, LAPPE M and TEICHMANN SA. Mapping protein family interactions: intramolecular and intermolecular protein family interaction repertoires in the PDB and yeast. *J Mol Biol*, 307:929–38, 2001. 2.1

- PENG K, OBRADOVIC Z and VUCETIC S. Exploring bias in the protein data bank using contrast classifiers. *Pac Symp Biocomput*, 435–446, 2004. 2.1
- PERUTZ M, ROSSMANN M, CULLIS A, MUIRHEAD H, WILL G and NORTH A. Structure of haemoglobin: A three-dimensional fourier synthesis at 5.5Å resolution, obtained by X-ray analysis. *Nature*, 185:416–422, 1960. 1.1.1.4
- PLATZER P, UPENDER MB, WILSON K, WILLIS J, LUTTERBAUGH J *et al.* Silence of chromosomal amplifications in colon cancer. *Cancer Res*, 62:1134–1138, 2002. 4.4.2
- POWELL AJ, READ JA, BANFIELD MJ, GUNN-MOORE F, YAN SD *et al.* Recognition of structurally diverse substrates by type II 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding alcohol dehydrogenase (ABAD). *J Mol Biol*, 303:311–327, 2000. 3.3.6
- PRINCE VE and PICKETT FB. Splitting pairs: the diverging fates of duplicated genes. *Nat Rev Genet*, 3:827–837, 2002. 4.1
- PULICHINO AM, VALLETTE-KASIC S, COUTURE C, GAUTHIER Y, BRUE T *et al.* Human and mouse TPIT gene mutations cause early onset pituitary ACTH deficiency. *Genes Dev*, 17:711–716, 2003. 3.3.6.2
- R DEVELOPMENT CORE TEAM. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria, 2006. ISBN 3-900051-07-0. 3.2.8, 4.2.12
- RANDLES LG, LAPPALAINEN I, FOWLER SB, MOORE B, HAMILL SJ and CLARKE J. Using model proteins to quantify the effects of pathogenic mutations in Ig-like proteins. *J Biol Chem*, 281:24216–24226, 2006. 3.3.2.4
- REDON R, ISHIKAWA S, FITCH KR, FEUK L, PERRY GH *et al.* Global variation in

- copy number in the human genome. *Nature*, 444:444–454, 2006. 1.2.3, 3.1, 4.4, 4.3.1, 4.7, 4.3.3
- REGULY T, BREITKREUTZ A, BOUCHER L, BREITKREUTZ B, HON G *et al.* Comprehensive curation and analysis of global interaction networks in *Saccharomyces cerevisiae*. *J Biol*, 5:11, 2006. 1.1.1.3
- RIGAUT G, SHEVCHENKO A, RUTZ B, WILM M, MANN M and SERAPHIN B. A generic protein purification method for protein complex characterization and proteome exploration. *Nat Biotechnol*, 17:1030–1032, 1999. 1.1.1.1
- RILEY R, LEE C, SABATTI C and EISENBERG D. Inferring protein domain interactions from databases of interacting proteins. *Genome Biol*, 6:R89, 2005. 2.1, 2.4.1
- RISCH N and MERIKANGAS K. The future of genetic studies of complex human diseases. *Science*, 273:1516–1517, 1996. 1.2.3.1
- ROSS ED, MINTON A and WICKNER RB. Prion domains: sequences, structures and interactions. *Nat Cell Biol*, 7:1039–1044, 2005. 3.1
- RUAL JF, VENKATESAN K, HAO T, HIROZANE-KISHIKAWA T, DRICOT A *et al.* Towards a proteome-scale map of the human protein–protein interaction network. *Nature*, 437:1173–1178, 2005. 1.1.2, 4.2.3
- RUEPP A, BRAUNER B, DUNGER-KALTENBACH I, FRISHMAN G, MONTRONE C *et al.* CORUM: the comprehensive resource of mammalian protein complexes. *Nucleic Acids Res*, 36:D646–650, 2008. 4.2.2
- SALWINSKI L, MILLER CS, SMITH AJ, PETTIT FK, BOWIE JU and EISENBERG D. The Database of Interacting Proteins: 2004 update. *Nucleic Acids Res*, 32:D449–451, 2004. 1.1.3, 2.2.1, 3.3.3

- SAMMUT SJ, FINN RD and BATEMAN A. Pfam 10 years on: 10,000 families and still growing. *Brief Bioinform*, 9:210–219, 2008. 1.3
- SANCHEZ C, LACHAIZE C, JANODY F, BELLON B, RODER L, EUZENAT J, RECHENMANN F and JACQ B. Grasping at molecular interactions and genetic networks in *Drosophila melanogaster* using FlyNets, an internet database. *Nucleic Acids Res*, 27:89–94, 1999. 1.1.4
- SANKAR P and CHO MK. Genetics. toward a new vocabulary of human genetic variation. *Science*, 298:1337–1338, 2002. 1.2.2
- SAVAS S, TUZMEN S and OZCELIK H. Human SNPs resulting in premature stop codons and protein truncation. *Hum Genomics*, 2:274–286, 2006. 3.1
- SCHUSTER-BÖCKLER B and BATEMAN A. Visualizing profile–profile alignment: pairwise HMM logos. *Bioinformatics*, 21:2912–2913, 2005. 1.4
- SCHUSTER-BÖCKLER B and BATEMAN A. An introduction to hidden Markov models. *Curr Protoc Bioinformatics*, A3, 2007a. 1.3
- SCHUSTER-BÖCKLER B and BATEMAN A. Reuse of structural domain–domain interactions in protein networks. *BMC Bioinformatics*, 8:259, 2007b. 1.4
- SCHUSTER-BÖCKLER B and BATEMAN A. Protein interactions in human genetic diseases. *Genome Biol*, 9:9, 2008. 1.4
- SCHUSTER-BÖCKLER B, SCHULTZ J and RAHMANN S. HMM Logos for visualization of protein families. *BMC Bioinformatics*, 5, 2004. 3.2.5
- SEBAT J, LAKSHMI B, TROGE J, ALEXANDER J, YOUNG J *et al.* Large-scale copy number polymorphism in the human genome. *Science*, 305:525–528, 2004. 1.2.3
- SETO ML, LEE SJ, SZE RW and CUNNINGHAM ML. Another TWIST on Baller-Gerold syndrome. *Am J Med Genet*, 104:323–330, 2001. 3.3.6.3

- SHANY E, SAADA A, LANDAU D, SHAAG A, HERSHKOVITZ E and ELPELEG ON. Lipoamide dehydrogenase deficiency due to a novel mutation in the interface domain. *Biochem Biophys Res Commun*, 262:163–166, 1999. 3.3.4.2
- SHARAN R and IDEKER T. Modeling cellular machinery through biological network comparison. *Nat Biotech*, 24:427–433, 2006. 1
- SHE X, JIANG Z, CLARK RA, LIU G, CHENG Z *et al.* Shotgun sequence assembly and recent segmental duplications within the human genome. *Nature*, 431:927–930, 2004. 4.2.8
- SHINAWI M and CHEUNG SW. The array CGH and its clinical applications. *Drug Discov Today*, 13:760–770, 2008. 1.2.3
- SHY ME, JANI A, KRAJEWSKI K, GRANDIS M, LEWIS RA *et al.* Phenotypic clustering in MPZ mutations. *Brain*, 127:371–384, 2004. 3.1
- SIDHU SS, FAIRBROTHER WJ and DESHAYES K. Exploring protein-protein interactions with phage display. *Chembiochem*, 4:14–25, 2003. 1.1.1.5
- SING T, SANDER O, BEERENWINKEL N and LENGAUER T. ROCR: visualizing classifier performance in R. *Bioinformatics*, 21:3940–3941, 2005. 3.6
- SIVA N. 1000 Genomes project. *Nat Biotechnol*, 26:256, 2008. 1.2.2
- SMITH EA and CORN RM. Surface plasmon resonance imaging as a tool to monitor biomolecular interactions in an array based format. *Appl Spectrosc*, 57:320A–332A, 2003. 1.1.1.5
- SOPKO R, HUANG D, PRESTON N, CHUA G, PAPP B *et al.* Mapping pathways and phenotypes by systematic gene overexpression. *Mol Cell*, 21:319–330, 2006. 4.1
- SPRINZAK E, SATTATH S and MARGALIT H. How reliable are experimental protein–protein interaction data? *J Mol Biol*, 327:919–923, 2003. 1.1.2

BIBLIOGRAPHY

- STEINMETZ LM, SCHARFE C, DEUTSCHBAUER AM, MOKRANJAC D, HERMAN ZS *et al.* Systematic screen for human disease genes in yeast. *Nat Genet*, 31:400–404, 2002. 4.1
- STELZL U, WORM U, LALOWSKI M, HAENIG C, BREMBECK FH *et al.* A human protein–protein interaction network: a resource for annotating the proteome. *Cell*, 122:957–968, 2005. 4.2.3
- STRANGER BE, FORREST MS, DUNNING M, INGLE CE, BEAZLEY C *et al.* Relative impact of nucleotide and copy number variation on gene expression phenotypes. *Science*, 315:848–853, 2007. 4.2.5, 4.3.1
- STROM M, HUME AN, TARAFDER AK, BARKAGIANNI E and SEABRA MC. A family of Rab27-binding proteins. melanophilin links Rab27a and myosin Va function in melanosome transport. *J Biol Chem*, 277:25423–25430, 2002. 3.3.6.1
- STUMPF MPH, THORNE T, DE SILVA E, STEWART R, AN HJ, LAPPE M and WIUF C. Estimating the size of the human interactome. *Proc Natl Acad Sci USA*, 105:6959–6964, 2008. 1.1.2
- STUMPF MPH, WIUF C and MAY RM. Subnets of scale-free networks are not scale-free: sampling properties of networks. *Proc Natl Acad Sci USA*, 102:4221–4224, 2005. 1.1.4
- SU AI, WILTSHIRE T, BATALOV S, LAPP H, CHING KA *et al.* A gene atlas of the mouse and human protein-encoding transcriptomes. *Proc Natl Acad Sci USA*, 101:6062–6067, 2004. 4.2.5
- SVEDBERG T. Mass and size of protein molecules. *Nature*, 123:871, 1929. 1.1
- THE INTERNATIONAL HAPMAP CONSORTIUM. The international HapMap project. *Nature*, 426:789–796, 2003. 1.2.3

- THORN KS and BOGAN AA. ASEdb: a database of alanine mutations and their effects on the free energy of binding in protein interactions. *Bioinformatics*, 17:284–285, 2001. 1.1, 3.2.6, 3.3.2
- TONG AHY, LESAGE G, BADER GD, DING H, XU H *et al.* Global mapping of the yeast genetic interaction network. *Science*, 303:808–813, 2004. 1.1.1.5
- UETZ P, GIOT L, CAGNEY G, MANSFIELD T, JUDSON R *et al.* A comprehensive analysis of protein–protein interactions in *Saccharomyces cerevisiae*. *Nature*, 403:623–627, 2000. 1.1.2, 1.1.4
- VEITIA RA. Exploring the etiology of haploinsufficiency. *BioEssays*, 24:175–184, 2002. 3.4.3
- VEITIA RA. Gene dosage balance: deletions, duplications and dominance. *Trends Genet*, 21:33–35, 2005. 4.1
- VELANKAR S, MCNEIL P, MITTARD-RUNTE V, SUAREZ A, BARRELL D, APWEILER R and HENRICK K. E-MSD: an integrated data resource for bioinformatics. *Nucleic Acids Res*, 33:D262–265, 2005. 1.3.1
- VITKUP D, SANDER C and CHURCH GM. The amino-acid mutational spectrum of human genetic disease. *Genome Biol*, 4:R72, 2003. 3.3.4.4
- WALSH STR and KOSSIAKOFF AA. Crystal structure and site 1 binding energetics of human placental lactogen. *J Mol Biol*, 358:773–784, 2006. 3.2.6
- WANG Z and MOULT J. SNPs, protein structure, and disease. *Hum Mutat*, 17:263–270, 2001. 3.1
- WELLCOME TRUST CASE CONTROL CONSORTIUM. Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature*, 447:661–678, 2007. 1.2.3.1

- WILLIAMS AD, SHIVAPRASAD S and WETZEL R. Alanine scanning mutagenesis of A β (1–40) amyloid fibril stability. *J Mol Biol*, 357:1283–1294, 2006. 3.2.6
- WOLF YI, ROGOZIN IB and KOONIN EV. Coelomata and not ecdysozoa: evidence from genome-wide phylogenetic analysis. *Genome Res*, 14:29–36, 2004. 1.3
- WONG JMS, IONESCU D and INGLES CJ. Interaction between BRCA2 and replication protein A is compromised by a cancer-predisposing mutation in BRCA2. *Oncogene*, 22:28–33, 2003. 3.3.4.2
- WRIGHT S. Physiological and evolutionary theories of dominance. *Am Nat*, 68:24–53, 1934. 1.2.3.1, 4.1
- WU C, APWEILER R, BAIROCH A, NATALE D, BARKER W *et al.* The Universal Protein Resource (UniProt): an expanding universe of protein information. *Nucleic Acids Res*, 34:D187–191, 2006. 1.3, 3.1, 3.2.1
- YANG J, LUSK R and LI WH. Organismal complexity, protein complexity, and gene duplicability. *Proc Natl Acad Sci USA*, 100:15661–15665, 2003. 4.1, 4.4.3
- YANG Z. PAML: a program package for phylogenetic analysis by maximum likelihood. *Comput Appl Biosci*, 13:555–556, 1997. 4.2.11
- YUE P, LI Z and MOULT J. Loss of protein structure stability as a major causative factor in monogenic disease. *J Mol Biol*, 353:459–473, 2005. 3.1
- ZDOBNOV EM, LOPEZ R, APWEILER R and ETZOLD T. The EBI SRS server — Recent developments. *Bioinformatics*, 18:368–373, 2002. 3.2.1
- ZHU H, DOMINGUES FS, SOMMER I and LENGAUER T. NOXclass: prediction of protein-protein interaction types. *BMC Bioinformatics*, 7:27, 2006. 2.2.5, 3.2.3
- ZUCKERKANDL E and PAULING L. Molecular disease, evolution, and genetic heterogeneity. *Horiz Biochem*, 189–225, 1962. 1.2.1