References

[1] C.F. Allex, J.W. Shavlik, and F.R. Blattner. Neural network input representations that produce accurate consensus sequences from dna fragment assemblies. *Bioinformatics*, 15(9):723–728, 1999.

[2] M.A. Andrade, N.P. Brown, C. Leroy, S. Hoersch, A. de Daruvar, C. Reich, A. Franchini, J. Tamames, A. Valencia, C. Ouzounis, and C. Sander. Automated genome sequence analysis and annotation. *Bioinformatics*, 15(5):391–412, 1999.

[3] V.N. Babenko, P.S. Kosarev, O.V. Vishnevsky, V.G. Levitsky, VV. Basin, and A.S. Frolov. Investigating extended regulatory regions of genomic dna sequences. *Bioinformatics*, 15(7):644–653, 1999.

[4] R. Backofen, S. Will, and E. Bornberg-Bauer. Application of constraint programming techniques for structure prediction of lattice proteins with extended alphabets. *Bioinformatics*, 15(3):234–242, 1999.

[5] P.G. Baker, C.A. Goble, S. Bechhofer, N.W. Paton, R. Stevens, and A. Brass. An ontology for bioinformatics applications. *Bioinformatics*, 15(6):510–520, 1999.

[6] Pierre Baldi, Søren Brunak, Yves Chauvin, and Anders Gorm Pedersen. Structural basis for triplet repeat disorders: A computational analysis. *Bioinformatics*, 15(11):918–929, 1999.

[7] Pierre Baldi, Søren Brunak, Paolo Frasconi, Giovanni Soda, and Gianluca Pollastri. Exploiting the past and the future in protein secondary structure prediction. *Bioinformatics*, 15(11):937–946, 1999.

[8] Arvind K. Bansal. An automated comparative analysis of 17 complete microbial genomes. *Bioinformatics*, 15(11):900–908, 1999.

[9] E. Barillot, U. Leser, P. Lijnzaad, C. Cussat-Blanc, K. Jungfer, F. Guyon, G. Vaysseix, C. Helgesen, and P. Rodriguez-Tome. A proposal for a standard corba interface for genome maps. *Bioinformatics*, 15(2):157–169, 1999.

[10] M.I. Bellgard, H.L. Hiew, A. Hunter, and M. Wiebrands. Orbit: An integrated environment for user-customized bioinformatics tools. *Bioinformatics*, 15(10):847–851, 1999.

[11] J. Bentz, A. Baucom, M. Hansen, and L. Gregoret. Dinamo: Interactive protein alignment and model building. *Bioinformatics*, 15(4):309–316, 1999.

[12] V.B. Berikov and I.B. Rogozin. Regression trees for analysis of mutational spectra in nucleotide sequences. *Bioinformatics*, 15(7):553–562, 1999.

[13] R.D. Blake, J.W. Bizzaro, J.D. Blake, G.R. Day, S.G. Delcourt, J. Knowles, K.A. Marx, SantaLucia, and Jr. J. Statistical mechanical simulation of polymeric dna melting with meltsim. *Bioinformatics*, 15(5):370–375, 1999.

[14] A. Bohne, E. Lang, and C.W. von der Lieth. Sweet — www-based rapid 3d construction of oligo- and polysaccharides. *Bioinformatics*, 15(9):767–768, 1999.

[15] D. Bouthinon and H. Soldano. A new method to predict the consensus secondary structure of a set of unaligned rna sequences. *Bioinformatics*, 15(10):785–798, 1999.

[16] L. Brun-Samarcq, S. Gallina, A. Philippi, F. Demenais, G. Vaysseix, and E. Barillot. Cope: A collaborative pedigree drawing environment. *Bioinformatics*, 15(4):345–346, 1999.

[17] K. Bucka-Lassen, O. Caprani, and J. Hein. Combining many multiple alignments in one improved alignment. *Bioinformatics*, 15(2):122–130, 1999.

[18] S. Bushnell, J. Budde, T. Catino, J. Cole, A. Derti, R. Kelso, M.L. Collins, G. Molino, P. Sheridan, J. Monahan, and M. Urdea. Probedesigner: For the design of probesets for branched dna (bdna) signal amplification assays. *Bioinformatics*, 15(5):348–355, 1999.

[19] M. Cariaso, P. Folta, M. Wagner, T. Kuczmarski, and G. Lennon. Imagene i: Clustering and ranking of i.m.a.g.e. cdna clones corresponding to known genes. *Bioinformatics*, 15(12):965–973, 1999.

[20] K.M. Chao. Calign: Aligning sequences with restricted affine gap penalties. *Bioinformatics*, 15(4):298–304, 1999.

[21] C.C. Chen, J.P. Singh, and R.B. Altman. Using imperfect secondary structure predictions to improve molecular structure computations. *Bioinformatics*, 15(1):53–65, 1999.

[22] A. Chou and J. Burke. Crawview: For viewing splicing variation, gene families, and polymorphism in clusters of ests and full-length sequences. *Bioinformatics*, 15(5):376–381, 1999.

[23] J.M. Comeron. K-estimator: Calculation of the number of nucleotide substitutions per site and the confidence intervals. *Bioinformatics*, 15(9):763–764, 1999.

[24] J. Conery and M. Lynch. Genetic simulation library. *Bioinformatics*, 15(1):85–86, 1999.

[25] G.G. Consalez, A. Cabibbo, A. Corradi, C. Alli, M. Sardella, R. Sitia, and R. Fesce. A computer-driven approach to pcr-based differential screening, alternative to differential display. *Bioinformatics*, 15(2):93–105, 1999.

[26] Florence Corpet, Jérôme Gouzy, and Daniel Kahn. Browsing protein families via the "rich family description" format. *Bioinformatics*, 15(12):1020–1027, 1999.

[27] T. Coupaye. Wrapping sts with corba: From textual data to distributed objects. *Bioinformatics*, 15(4):333–338, 1999.

[28] Eivind Coward. Shufflet: Shuffling sequences while conserving the k-let counts. *Bioinformatics*, 15(12):1058–1059, 1999.

[29] O.H. Crawford. A fast, stochastic threading algorithm for proteins. *Bioinformatics*, 15(1):66–71, 1999.

[30] V. Di Francesco, P.J. Munson, and J. Garnier. Foresst: Fold recognition from secondary structure predictions of proteins. *Bioinformatics*, 15(2):131–140, 1999.

[31] F. Drablos. Clustering of non-polar contacts in proteins. *Bioinformatics*, 15(6):501–509, 1999.

[32] F. Eisenhaber and P. Bork. Evaluation of human-readable annotation in biomolecular sequence databases with biological rule libraries. *Bioinformatics*, 15(7):528–535, 1999.

[33] L.B. Ellis and D. Kalumbi. Financing a future for public biological data. *Bioinformatics*, 15(9):717–722, 1999.

[34] A. Elofsson and E.L. Sonnhammer. A comparison of sequence and structure protein domain families as a basis for structural genomics. *Bioinformatics*, 15(6):480–500, 1999.

[35] D. Evers and R. Giegerich. Rna movies: Visualizing rna secondary structure spaces. *Bioinformatics*, 15(1):32–37, 1999.

[36] D. Fenyo. The biopolymer markup language. *Bioinformatics*, 15(4):339–340, 1999.

[37] E.S. Ferlanti, J.F. Ryan, I. Makalowska, and A.D. Baxevanis. Webblastt 2.0: An integrated solution for organizing and analyzing sequence data. *Bioinformatics*, 15(5):422–423, 1999.

[38] D. Fischer and D. Eisenberg. Erratum to "finding families for genomic orfans". *Bioinformatics*, 15(10):864–864, 1999. Originally in: Bioinformatics, Vol. 15, 1999, No. 9, 759-762.

[39] D. Fischer and D. Eisenberg. Finding families for genomic orfans. *Bioinformatics*, 15(9):759–762, 1999. see Erratum in Bioinformatics, Vol. 15, 1999, No. 10, 864-864.

[40] S. Fischer, J. Crabtree, B. Brunk, M. Gibson, and G.C. Overton. biowidgets: Data interaction components for genomics. *Bioinformatics*, 15(10):837–846, 1999.

[41] W. Fleischmann, S. Moller, A. Gateau, and R. Apweiler. A novel method for automatic functional annotation of proteins. *Bioinformatics*, 15(3):228–233, 1999.

[42] M. Forster, A. Heath, and M. Afzal. Application of distance geometry to 3d visualization of sequence relationships. *Bioinformatics*, 15(1):89–90, 1999.

[43] D. Gilbert, D. Westhead, N. Nagano, and J. Thornton. Motif-based searching in tops protein topology databases. *Bioinformatics*, 15(4):317–326, 1999.

[44] Véronique Giudicelli and Marie-Paule Lefranc. Ontology for immunogenetics: The imgt-ontology. *Bioinformatics*, 15(12):1047–1054, 1999.

[45] I. Goncalves, M. Robinson, G. Perriere, and D. Mouchiroud. Jadis: Computing distances between nucleic acid sequences. *Bioinformatics*, 15(5):424–425, 1999.

[46] J. Gorodkin, H.H. Staerfeldt, O. Lund, and S. Brunak. Matrixplot: Visualizing sequence constraints. *Bioinformatics*, 15(9):769–770, 1999.

[47] I. Goryanin, T.C. Hodgman, and E. Selkov. Mathematical simulation and analysis of cellular metabolism and regulation. *Bioinformatics*, 15(9):749–758, 1999.

[48] P. Gouet, E. Courcelle, D.I. Stuart, and F. Metoz. Espript: Analysis of multiple sequence alignments in postscript. *Bioinformatics*, 15(4):305–308, 1999.

[49] W.N. Grundy and T.L. Bailey. Family pairwise search with embedded motif models. *Bioinformatics*, 15(6):463–470, 1999.

[50] Y. Guermeur, C. Geourjon, P. Gallinari, and G. Deleage. Improved performance in protein secondary structure prediction by inhomogeneous score combination. *Bioinformatics*, 15(5):413–421, 1999.

[51] Vladimir G. Gusev, Lubov A. Nemytikova, and Nadia A. Chuzhanova. On the complexity measures of genetic sequences. *Bioinformatics*, 15(12):994–999, 1999.

[52] Eran Halperin, Simchon Faigler, and Raveh Gill-More. Frameplus: Aligning dna to protein sequences. *Bioinformatics*, 15(11):867–873, 1999.

[53] K. Han, D. Kim, and H.J. Kim. A vector-based method for drawing rna secondary structure. *Bioinformatics*, 15(4):286–297, 1999.

[54] J. Hanke, G. Lehmann, P. Bork, and J.G. Reich. Associative database of protein sequences. *Bioinformatics*, 15(9):741–748, 1999.

[55] E. Harley, A. Bonner, and N. Goodman. Revealing hidden interval graph structure in sts-content data. *Bioinformatics*, 15(4):278–285, 1999.

[56] S. Henikoff, J.G. Henikoff, and S. Pietrokovski. Blocks+: A non-redundant database of protein alignment blocks derived from multiple compilations. *Bioinformatics*, 15(6):471–479, 1999.

[57] H. Hermjakob, W. Fleischmann, and R. Apweiler. Swissknife — "lazy parsing" of swiss-prot entries. *Bioinformatics*, 15(9):771–772, 1999.

[58] G.Z. Hertz and G.D. Stormo. Identifying dna and protein patterns with statistically significant alignments of multiple sequences. *Bioinformatics*, 15(7):563–577, 1999.

[59] H. Herzel, O. Weiss, and E.N. Trifonov. 10-11 bp periodicities in complete genomes reflect protein structure and dna folding. *Bioinformatics*, 15(3):187–193, 1999.

[60] H. Hirakawa, S. Muta, and S. Kuhara. The hydrophobic cores of proteins predicted by wavelet analysis. *Bioinformatics*, 15(2):141–148, 1999.

[61] Thomas Huber, Anthony J. Russell, Daniel Ayers, and Andrew E. Torda. Sausage: Protein threading with flexible force fields. *Bioinformatics*, 15(12):1064–1065, 1999.

[62] V.L. Junker, R. Apweiler, and A. Bairoch. Representation of functional information in the swiss-prot data bank. *Bioinformatics*, 15(12):1066–1067, 1999.

[63] Y. Kallberg and B. Persson. Kind-a non-redundant protein database. *Bioinformatics*, 15(3):260–261, 1999.

[64] W. Kasprzak and B. Shapiro. Stem trace: An interactive visual tool for comparative rna structure analysis. *Bioinformatics*, 15(1):16–31, 1999.

[65] A. Klingenhoff, K. Frech, K. Quandt, and T. Werner. Functional promoter modules can be detected by formal models independent of overall nucleotide sequence similarity. *Bioinformatics*, 15(3):180–186, 1999.

[66] B. Knudsen and J. Hein. Rna secondary structure prediction using stochastic context-free grammars and evolutionary history. *Bioinformatics*, 15(6):446–454, 1999.

[67] S. Knudsen. Promoter2.0: For the recognition of polii promoter sequences. *Bioinformatics*, 15(5):356–361, 1999.

[68] A.V. Kochetov, M.P. Ponomarenko, A.S. Frolov, L.L. Kisselev, and N.A. Kolchanov. Prediction of eukaryotic mrna translational properties. *Bioinformatics*, 15(7):704–712, 1999.

[69] N.A. Kolchanov, M.P. Ponomarenko, A.S. Frolov, E.A. Ananko, F.A. Kolpakov, E.V. Ignatieva, O.A. Podkolodnaya, T.N. Goryachkovskaya, I.L. Stepanenko, T.I. Merkulova, V.V. Babenko, Y.V. Ponomarenko, A.V. Kochetov, N.L. Podkolodny, D.V. Vorobiev, S.V. Lavryushev, D.A. Grigorovich, Y.V. Kondrakhin, L. Milanesi, E. Wingender, V. Solovyev, and G.C. Overton. Integrated databases and computer systems for studying eukaryotic gene expression. *Bioinformatics*, 15(7):669–686, 1999.

[70] F.A. Kolpakov and E.A. Ananko. Interactive data input into the genenet database. *Bioinformatics*, 15(7):713–714, 1999.

[71] A. Krause, P. Nicodeme, E. Bornberg-Bauer, M. Rehmsmeier, and M. Vingron. Www access to the systers protein sequence cluster set. *Bioinformatics*, 15(3):262–263, 1999.

[72] S. Kurtz and C. Schleiermacher. Reputer: Fast computation of maximal repeats in complete genomes. *Bioinformatics*, 15(5):426–427, 1999.

[73] N.C. Kyrpides. Genomes online database (gold 1.0): A monitor of complete and ongoing genome projects world-wide. *Bioinformatics*, 15(9):773–774, 1999.

[74] Istvan Ladunga. Physean: Physical sequence analysis for the identification of protein domains on the basis of physical and chemical properties of amino acids. *Bioinformatics*, 15(12):1028–1038, 1999.

[75] R.F. Lascaris, W.H. Mager, and R.J. Planta. Dna-binding requirements of the yeast protein rap1p as selected in silico from ribosomal protein gene promoter sequences. *Bioinformatics*, 15(4):267–277, 1999.

[76] G. Lavorgna, A. Guffanti, G. Borsani, A. Ballabio, and E. Boncinelli. Targetfinder: Searching annotated sequence databases for target genes of transcription factors. *Bioinformatics*, 15(2):172–173, 1999.

[77] H.P. Lenhof, B. Morgenstern, and K. Reinert. An exact solution for the segment-to-segment multiple sequence alignment problem. *Bioinformatics*, 15(3):203–210, 1999.

[78] V.G. Levitsky, M.P. Ponomarenko, J.V. Ponomarenko, A.S. Frolov, and N.A. Kolchanov. Nucleosomal dna property database. *Bioinformatics*, 15(7):582–592, 1999.

[79] Allison Lim and Louxin Zhang. Webphylip: A web interface to phylip. *Bioinformatics*, 15(12):1068–1069, 1999.

[80] J.S. Liu and C.E. Lawrence. Bayesian inference on biopolymer models. *Bioinformatics*, 15(1):38–52, 1999.

[81] Alexander V. Lukashin and Joseph J. Rosa. Local multiple sequence alignment using dead-end elimination. *Bioinformatics*, 15(11):947–953, 1999.

[82] R.B. Lyngso, M. Zuker, and C.N. Pedersen. Fast evaluation of internal loops in rna secondary structure prediction. *Bioinformatics*, 15(6):440–445, 1999.

[83] R.R. Mallios. Class ii mhc quantitative binding motifs derived from a large molecular database with a versatile iterative stepwise discriminant analysis meta-algorithm. *Bioinformatics*, 15(6):432–439, 1999.

[84] M.E. Mangan and K.S. Frazer. An extensive list of genes that produce alternative transcripts in the mouse. *Bioinformatics*, 15(2):170–171, 1999.

[85] C. Medigue, F. Rechenmann, A. Danchin, and A. Viari. Imagene: An integrated computer environment for sequence annotation and analysis. *Bioinformatics*, 15(1):2–15, 1999.

[86] L. Mendoza, D. Thieffry, and E.R. Alvarez-Buylla. Genetic control of flower morphogenesis in arabidopsis thaliana: A logical analysis. *Bioinformatics*, 15(7):593–606, 1999.

[87] L. Milanesi, D. D'Angelo, and I.B. Rogozin. Genebuilder: Interactive in silico prediction of gene structure. *Bioinformatics*, 15(7):612–621, 1999.

[88] C. Miller, J. Gurd, and A. Brass. A rapid algorithm for sequence database comparisons: Application to the identification of vector contamination in the embl databases. *Bioinformatics*, 15(2):111–121, 1999.

[89] S. Moller, U. Leser, W. Fleischmann, and R. Apweiler. Edittotrembl: A distributed approach to high-quality automated protein sequence annotation. *Bioinformatics*, 15(3):219–227, 1999.

[90] B. Morgenstern. Dialign 2: Improvement of the segment-to-segment approach to multiple sequence alignment. *Bioinformatics*, 15(3):211–218, 1999.

[91] R. Mott. Local sequence alignments with monotonic gap penalties. *Bioinformatics*, 15(6):455–462, 1999.

[92] M.H. Mucchielli-Giorgi, S. Hazout, and P. Tuffery. Predacc: Prediction of solvent accessibility. *Bioinformatics*, 15(2):176–177, 1999.

[93] J. Murvai, K. Vlahovicek, E. Barta, S. Parthasarathy, H. Hegyi, F. Pfeiffer, and S. Pongor. The domain-server: Direct prediction of protein domain-homologies from blast search. *Bioinformatics*, 15(4):343–344, 1999.

[94] K. Nakata, T. Takai, and T. Kaminuma. Development of the receptor database (rdb): Application to the endocrine disruptor problem. *Bioinformatics*, 15(7):544–552, 1999.

[95] C. O'Donovan, M.J. Martin, E. Glemet, J.J. Codani, and R. Apweiler. Removing redundancy in swiss-prot and trembl. *Bioinformatics*, 15(3):258–259, 1999.

[96] U. Ohler, S. Harbeck, H. Niemann, E. Noth, and M.G. Reese. Interpolated markov chains for eukaryotic promoter recognition. *Bioinformatics*, 15(5):362–369, 1999.

[97] José L. Oliver, Ramón Román-Roldán, Javier Pérez, and Pedro Bernaola-Galván. Segment: Identifying compositional domains in dna sequences. *Bioinformatics*, 15(12):974–979, 1999.

[98] Y. Osada, R. Saito, and M. Tomita. Analysis of base-pairing potentials between 16s rrna and 5' utr for translation initiation in various prokaryotes. *Bioinformatics*, 15(7):578–581, 1999.

[99] Nathalie Pavy, Stephane Rombauts, Patrice Déhais, Catherine Mathé, Davuluri V.V. Ramana, Philippe Leroy, and Pierre Rouzé. Evaluation of gene prediction software using a genomic data set: Application to arabidopsis thaliana sequences. *Bioinformatics*, 15(11):887–899, 1999.

[100] Florencio Pazos, Burkhard Rost, and Alfonso Valencia. A platform for integrating threading results with protein family analyses. *Bioinformatics*, 15(12):1062–1063, 1999.

[101] S.C. Pegg and P.C. Babbitt. Shotgun: Getting more from sequence similarity searches. *Bioinformatics*, 15(9):729–740, 1999.

[102] Leonid Peshkin and Mikhail S. Gelfand. Segmentation of yeast dna using hidden markov models. *Bioinformatics*, 15(12):980–986, 1999.

[103] T. Pfeiffer, I. Sanchez-Valdenebro, J.C. Nuno, F. Montero, and S. Schuster. Metatool: For studying metabolic networks. *Bioinformatics*, 15(3):251–257, 1999.

[104] J.V. Ponomarenko, M.P. Ponomarenko, A.S. Frolov, D.G. Vorobyev, G.C. Overton, and N.A. Kolchanov. Conformational and physicochemical dna features specific for transcription factor binding sites. *Bioinformatics*, 15(7):654–668, 1999.

[105] M.P. Ponomarenko, J.V. Ponomarenko, A.S. Frolov, O.A. Podkolodnaya, D.G. Vorobyev, N.A. Kolchanov, and G.C. Overton. Oligonucleotide frequency matrices addressed to recognizing functional dna sites. *Bioinformatics*, 15(7):631–643, 1999.

[106] M.P. Ponomarenko, J.V. Ponomarenko, A.S. Frolov, N.L. Podkolodny, L.K. Savinkova, N.A. Kolchanov, and G.C. Overton. Identification of sequence-dependent dna features correlating to activity of dna sites interacting with proteins. *Bioinformatics*, 15(7):687–703, 1999.

[107] A.L. Ponomarev and R.K. Sachs. Polymer chromosome models and monte carlo simulations of radiation breaking dna. *Bioinformatics*, 15(12):957–964, 1999.

[108] R. Preissner, A. Goede, and C. Frommel. Homonyms and synonyms in the dictionary of interfaces in proteins (dip). *Bioinformatics*, 15(10):832–836, 1999.

[109] M. Rarey, B. Kramer, and T. Lengauer. Docking of hydrophobic ligands with interaction-based matching algorithms. *Bioinformatics*, 15(3):243–250, 1999.

[110] V.S. Reddy and A.S.N. Reddy. A plant calmodulin-binding motor is part kinesin and part myosin. *Bioinformatics*, 15(12):1055–1057, 1999.

[111] P. Riikonen and M. Vihinen. Mutbase: Maintenance and analysis of distributed mutation databases. *Bioinformatics*, 15(10):852–859, 1999.

[112] J. Rozas and R. Rozas. Dnasp version 3: An integrated program for molecular population genetics and molecular evolution analysis. *Bioinformatics*, 15(2):174–175, 1999.

[113] Roberto Sánchez. Modbase: A database of comparative protein structure models. *Bioinformatics*, 15(12):1060–1061, 1999.

[114] David Sankoff. Genome rearrangement with gene families. *Bioinformatics*, 15(11):909–917, 1999.

[115] M.A. Saqi, D.L. Wild, and M.J. Hartshorn. Protein analyst — a distributed object environment for protein sequence and structure analysis. *Bioinformatics*, 15(6):521–522, 1999.

[116] Alejandro A. Schäffer, Yuri I. Wolf, Chris P. Ponting, Eugene V. Koonin, L. Aravind, and Stephen F. Altschul. Impala: Matching a protein sequence against a collection of psi-blast-constructed position-specific score matrices. *Bioinformatics*, 15(12):1000–1011, 1999.

[117] P. Scordis, D.R. Flower, and T.K. Attwood. Fingerprintscan: Intelligent searching of the prints motif database. *Bioinformatics*, 15(10):799–806, 1999.

[118] Joachim Selbig, Theo Mevissen, and Thomas Lengauer. Decision tree-based formation of consensus protein secondary structure prediction. *Bioinformatics*, 15(12):1039–1046, 1999.

[119] G.A. Seluja, A. Farmer, M. McLeod, C. Harger, and P.A. Schad. Establishing a method of vector contamination identification in database sequences. *Bioinformatics*, 15(2):106–110, 1999.

[120] O. Shats, I.I. Vaisman, A. Shats, and S. Sherman. Secost: Sequence-conformation-structure database for amino acid residues in proteins. *Bioinformatics*, 15(6):525–526, 1999.

[121] Anton M. Shmatkov, Arik A. Melikyan, Felix L. Chernousko, and Mark Borodovsky. Finding prokaryotic genes by the "frame-by-frame" algorithm: Targeting gene starts and overlapping genes. *Bioinformatics*, 15(11):874–886, 1999.

[122] V. Sobolev, A. Sorokine, J. Prilusky, E.E. Abola, and M. Edelman. Automated analysis of interatomic contacts in proteins. *Bioinformatics*, 15(4):327–332, 1999.

[123] G.Y. Srinivasarao, L.S. Yeh, C.R. Marzec, B.C. Orcutt, and W.C. Barker. Pir-aln: A database of protein sequence alignments. *Bioinformatics*, 15(5):382–390, 1999.

[124] T.A. Tatusova, I. Karsch-Mizrachi, and J.A. Ostell. Complete genomes in www entrez: Data representation and analysis. *Bioinformatics*, 15(7):536–543, 1999.

[125] P. Thebault, P. Monestie, A. McGrath, and D.G. Higgins. Miah: Automatic alignment of eukaryotic ssu rrnas. *Bioinformatics*, 15(4):341–342, 1999.

[126] G.H. Thomas. Completing the e. coli proteome: A database of gene products characterised since the completion of the genome sequence. *Bioinformatics*, 15(10):860–861, 1999.

[127] J.D. Thompson, F. Plewniak, and O. Poch. Balibase: A benchmark alignment database for the evaluation of multiple alignment programs. *Bioinformatics*, 15(1):87–88, 1999.

[128] M. Tomita, K. Hashimoto, K. Takahashi, T.S. Shimizu, Y. Matsuzaki, F. Miyoshi, K. Saito, S. Tanida, K. Yugi, J.C. Venter, Hutchison III, and C.A. E-cell: Software environment for whole-cell simulation. *Bioinformatics*, 15(1):72–84, 1999.

[129] T. Tsunoda and T. Takagi. Estimating transcription factor bindability on dna. *Bioinformatics*, 15(7):622–630, 1999.

[130] S. Uliel, A. Fliess, A. Amir, and R. Unger. A simple algorithm for detecting circular permutations in proteins. *Bioinformatics*, 15(11):930–936, 1999.

[131] J.S. Varre, J.P. Delahaye, and E. Rivals. Transformation distances: A family of dissimilarity measures based on movements of segments. *Bioinformatics*, 15(3):194–202, 1999.

[132] A. Wagner. Genes regulated cooperatively by one or more transcription factors and their identification in whole eukaryotic genomes. *Bioinformatics*, 15(10):776–784, 1999.

[133] T. Wei and M. O'Connell. Targetdb: A database of peptides targeting proteins to subcellular locations. *Bioinformatics*, 15(9):765–766, 1999.

[134] H. Weissig and P.E. Bourne. An analysis of the protein data bank in search of temporal and global trends. *Bioinformatics*, 15(10):807–831, 1999.

[135] W. Wright, P. Scordis, and T.K. Attwood. Blast prints — alternative perspectives on sequence similarity. *Bioinformatics*, 15(6):523–524, 1999.

[136] Tetsushi Yada, Mitsuteru Nakao, Yasushi Totoki, and Kenta Nakai. Modeling and predicting transcriptional units of escherichia coli genes using hidden markov models. *Bioinformatics*, 15(12):987–993, 1999.

[137] J. Yuan, A. Amend, J. Borkowski, R. DelMarco, W. Bailey, Y. Liu, G. Xie, and R. Blevins. Multiclustal: A systematic method for surveying clustal w alignment parameters. *Bioinformatics*, 15(10):862–863, 1999.

[138] Zheng Zhang, Piotr Berman, Thomas Wiehe, and Webb Miller. Post-processing long pairwise alignments. *Bioinformatics*, 15(12):1012–1019, 1999.

[139] Y. Zhong, Y. Luo, S. Pramanik, and J.H. Beaman. Hiclas: A taxonomic database system for displaying and comparing biological classification and phylogenetic trees. *Bioinformatics*, 15(2):149–156, 1999.

[140] J. Zhu and M.Q. Zhang. Scpd: A promoter database of the yeast saccharomyces cerevisiae. *Bioinformatics*, 15(7):607–611, 1999.