# Gary D Stormo

List of Publications by Year
in descending order

| | | | |
|---|---|---|---|
| 173 papers | 17,449 citations | 16451<br>64 h-index | 15266<br>126 g-index |
| 178 all docs | 178 docs citations | 178 times ranked | 16050 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Directed Evolution of an Enhanced POU Reprogramming Factor for Cell Fate Engineering. Molecular Biology and Evolution, 2021, 38, 2854-2868. | 8.9 | 11 |
| 2 | Redefining fundamental concepts of transcription initiation in bacteria. Nature Reviews Genetics, 2020, 21, 699-714. | 16.3 | 100 |
| 3 | Alternative Splicing During the *Chlamydomonas* *reinhardtii* Cell Cycle. G3: Genes, Genomes, Genetics, 2020, 10, 3797-3810. | 1.8 | 15 |
| 4 | Autoregulation of yeast ribosomal proteins discovered by efficient search for feedback regulation. Communications Biology, 2020, 3, 761. | 4.4 | 11 |
| 5 | Comparison of discriminative motif optimization using matrix and DNA shape-based models. BMC Bioinformatics, 2018, 19, 86. | 2.6 | 10 |
| 6 | Is Autogenous Posttranscriptional Gene Regulation Common?. RNA Technologies, 2018, , 217-227. | 0.3 | 0 |
| 7 | Quantitative profiling of BATF family proteins/JUNB/IRF hetero-trimers using Spec-seq. BMC Molecular Biology, 2018, 19, 5. | 3.0 | 8 |
| 8 | Review of the algal biology program within the National Alliance for Advanced Biofuels and Bioproducts. Algal Research, 2017, 22, 187-215. | 4.6 | 69 |
| 9 | Quantitative specificity of STAT1 and several variants. Nucleic Acids Research, 2017, 45, 8199-8207. | 14.5 | 11 |
| 10 | BEESEM: estimation of binding energy models using HT-SELEX data. Bioinformatics, 2017, 33, 2288-2295. | 4.1 | 34 |
| 11 | SMARCAD1 Contributes to the Regulation of Naive Pluripotency by Interacting with Histone Citrullination. Cell Reports, 2017, 18, 3117-3128. | 6.4 | 40 |
| 12 | Coop-Seq Analysis Demonstrates that Sox2 Evokes Latent Specificities in the DNA Recognition by Pax6. Journal of Molecular Biology, 2017, 429, 3626-3634. | 4.2 | 4 |
| 13 | Measuring quantitative effects of methylation on transcription factor–DNA binding affinity. Science Advances, 2017, 3, eaao1799. | 10.3 | 62 |
| 14 | Quantitative profiling of selective Sox/POU pairing on hundreds of sequences in parallel by Coop-seq. Nucleic Acids Research, 2017, 45, 832-845. | 14.5 | 30 |
| 15 | Inherent limitations of probabilistic models for protein-DNA binding specificity. PLoS Computational Biology, 2017, 13, e1005638. | 3.2 | 19 |
| 16 | Combinatorial *Cis*-regulation in *Saccharomyces* Species. G3: Genes, Genomes, Genetics, 2016, 6, 653-667. | 1.8 | 10 |
| 17 | DNA Structure Helps Predict Protein Binding. Cell Systems, 2016, 3, 216-218. | 6.2 | 4 |
| 18 | A quantitative understanding of lac repressor's binding specificity and flexibility. Quantitative Biology, 2015, 3, 69-80. | 0.5 | 13 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 19 | Determination of specificity influencing residues for key transcription factor families. Quantitative Biology, 2015, 3, 115-123. | 0.5 | 2 |
| 20 | DNA Motif Databases and Their Uses. Current Protocols in Bioinformatics, 2015, 51, 2.15.1-2.15.6. | 25.8 | 16 |
| 21 | Response Element Composition Governs Correlations between Binding Site Affinity and Transcription in Glucocorticoid Receptor Feed-forward Loops. Journal of Biological Chemistry, 2015, 290, 19756-19769. | 3.4 | 32 |
| 22 | Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363. | 12.8 | 91 |
| 23 | Spec-seq: determining protein-DNA-binding specificity by sequencing. Briefings in Functional Genomics, 2015, 14, 30-38. | 2.7 | 35 |
| 24 | High-Resolution Specificity from DNA Sequencing Highlights Alternative Modes of Lac Repressor Binding. Genetics, 2014, 198, 1329-1343. | 2.9 | 46 |
| 25 | An improved predictive recognition model for Cys2-His2 zinc finger proteins. Nucleic Acids Research, 2014, 42, 4800-4812. | 14.5 | 66 |
| 26 | Discriminative motif optimization based on perceptron training. Bioinformatics, 2014, 30, 941-948. | 4.1 | 19 |
| 27 | Innate Host Defense Requires TFEB-Mediated Transcription of Cytoprotective and Antimicrobial Genes. Immunity, 2014, 40, 896-909. | 14.3 | 284 |
| 28 | Modeling the specificity of protein–DNA interactions. Quantitative Biology, 2013, 1, 115-130. | 0.5 | 173 |
| 29 | Using defined finger–finger interfaces as units of assembly for constructing zinc-finger nucleases. Nucleic Acids Research, 2013, 41, 2455-2465. | 14.5 | 27 |
| 30 | Identification of Cilia Genes That Affect Cell-Cycle Progression Using Whole-Genome Transcriptome Analysis in <i>Chlamydomonas reinhardtti</i>. G3: Genes, Genomes, Genetics, 2013, 3, 979-991. | 1.8 | 64 |
| 31 | Global analysis of Drosophila Cys2-His2 zinc finger proteins reveals a multitude of novel recognition motifs and binding determinants. Genome Research, 2013, 23, 928-940. | 5.5 | 70 |
| 32 | An Overview of RNA Sequence Analyses: Structure Prediction, ncRNA Gene Identification, and RNAi Design. Current Protocols in Bioinformatics, 2013, 43, 12.1.1-12.1.3. | 25.8 | 26 |
| 33 | Novel Modeling of Combinatorial miRNA Targeting Identifies SNP with Potential Role in Bone Density. PLoS Computational Biology, 2012, 8, e1002830. | 3.2 | 38 |
| 34 | Conserved Motifs and Prediction of Regulatory Modules in Caenorhabditis elegans. G3: Genes, Genomes, Genetics, 2012, 2, 469-481. | 1.8 | 17 |
| 35 | Improved Models for Transcription Factor Binding Site Identification Using Nonindependent Interactions. Genetics, 2012, 191, 781-790. | 2.9 | 123 |
| 36 | ScerTF: a comprehensive database of benchmarked position weight matrices for Saccharomyces species. Nucleic Acids Research, 2012, 40, D162-D168. | 14.5 | 73 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 37 | Fast, Sensitive Discovery of Conserved Genome-Wide Motifs. Journal of Computational Biology, 2012, 19, 139-147. | 1.6 | 5 |
| 38 | Recognition models to predict DNA-binding specificities of homeodomain proteins. Bioinformatics, 2012, 28, i84-i89. | 4.1 | 36 |
| 39 | Exploring the DNA-recognition potential of homeodomains. Genome Research, 2012, 22, 1889-1898. | 5.5 | 26 |
| 40 | An optimized two-finger archive for ZFN-mediated gene targeting. Nature Methods, 2012, 9, 588-590. | 19.0 | 114 |
| 41 | An Introduction to Recognizing Functional Domains. Current Protocols in Bioinformatics, 2011, 34, Unit 2.1. | 25.8 | 3 |
| 42 | Quantitative analysis demonstrates most transcription factors require only simple models of specificity. Nature Biotechnology, 2011, 29, 480-483. | 17.5 | 161 |
| 43 | Assessing the Effects of Symmetry on Motif Discovery and Modeling. PLoS ONE, 2011, 6, e24908. | 2.5 | 3 |
| 44 | A nutrientâ€sensitive interaction between Sirt1 and HNFâ€1Î± regulates <i>Crp</i> expression. Aging Cell, 2011, 10, 305-317. | 6.7 | 21 |
| 45 | Maximally Efficient Modeling of DNA Sequence Motifs at All Levels of Complexity. Genetics, 2011, 187, 1219-1224. | 2.9 | 30 |
| 46 | A modified bacterial one-hybrid system yields improved quantitative models of transcription factor specificity. Nucleic Acids Research, 2011, 39, e83-e83. | 14.5 | 25 |
| 47 | Novel sequence-based method for identifying transcription factor binding sites in prokaryotic genomes. Bioinformatics, 2010, 26, 2672-2677. | 4.1 | 21 |
| 48 | Determining the specificity of proteinâ€"DNA interactions. Nature Reviews Genetics, 2010, 11, 751-760. | 16.3 | 264 |
| 49 | Detecting Coevolution of Functionally Related Proteins for Automated Protein Annotation. , 2010, , 99-105. | | 2 |
| 50 | Motif Discovery Using Expectation Maximization and Gibbsâ€™ Sampling. Methods in Molecular Biology, 2010, 674, 85-95. | 0.9 | 11 |
| 51 | Modeling the Quantitative Specificity of DNA-Binding Proteins from Example Binding Sites. PLoS ONE, 2009, 4, e6736. | 2.5 | 8 |
| 52 | An Introduction to Sequence Similarity (â€œHomologyâ€) Searching. Current Protocols in Bioinformatics, 2009, 27, Unit 3.1 3.1.1-7. | 25.8 | 21 |
| 53 | Discovering structural <i>cis</i> â€regulatory elements by modeling the behaviors of mRNAs. Molecular Systems Biology, 2009, 5, 268. | 7.2 | 32 |
| 54 | Discovering cis-Regulatory RNAs in Shewanella Genomes by Support Vector Machines. PLoS Computational Biology, 2009, 5, e1000338. | 3.2 | 20 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 55 | Inferring Binding Energies from Selected Binding Sites. PLoS Computational Biology, 2009, 5, e1000590. | 3.2 | 188 |
| 56 | Improving Gene-finding in Chlamydomonas reinhardtii:GreenGenie2. BMC Genomics, 2009, 10, 210. | 2.8 | 18 |
| 57 | The AP-1 transcription factor Batf controls TH17 differentiation. Nature, 2009, 460, 405-409. | 27.8 | 524 |
| 58 | The *cis*-regulatory map of *Shewanella* genomes. Nucleic Acids Research, 2008, 36, 5376-5390. | 14.5 | 17 |
| 59 | Computational identification of the normal and perturbed genetic networks involved in myeloid differentiation and acute promyelocytic leukemia. Genome Biology, 2008, 9, R38. | 9.6 | 26 |
| 60 | Analysis of Homeodomain Specificities Allows the Family-wide Prediction of Preferred Recognition Sites. Cell, 2008, 133, 1277-1289. | 28.9 | 401 |
| 61 | Genome wide screens in yeast to identify potential binding sites and target genes of DNA-binding proteins. Nucleic Acids Research, 2008, 36, e8-e8. | 14.5 | 24 |
| 62 | Context-dependent DNA recognition code for C2H2 zinc-finger transcription factors. Bioinformatics, 2008, 24, 1850-1857. | 4.1 | 47 |
| 63 | TRANSCRIPTIONAL PROFILES OF HUMAN EPITHELIAL CELLS IN RESPONSE TO HEAT. Shock, 2008, 29, 623-630. | 2.1 | 19 |
| 64 | RNA Sampler: a new sampling based algorithm for common RNA secondary structure prediction and structural alignment. Bioinformatics, 2007, 23, 1883-1891. | 4.1 | 61 |
| 65 | A global approach to identify differentially expressed genes in cDNA (two-color) microarray experiments. Bioinformatics, 2007, 23, 2073-2079. | 4.1 | 22 |
| 66 | Identification of muscle-specific regulatory modules in Caenorhabditis elegans. Genome Research, 2007, 17, 348-357. | 5.5 | 38 |
| 67 | PAP: a comprehensive workbench for mammalian transcriptional regulatory sequence analysis. Nucleic Acids Research, 2007, 35, W238-W244. | 14.5 | 23 |
| 68 | Computational identification and functional validation of regulatory motifs in cartilage-expressed genes. Genome Research, 2007, 17, 1438-1447. | 5.5 | 30 |
| 69 | Putting numbers on the network connections. BioEssays, 2007, 29, 717-721. | 2.5 | 11 |
| 70 | Evidence for Active Maintenance of Inverted Repeat Structures Identified by a Comparative Genomic Approach. PLoS ONE, 2007, 2, e262. | 2.5 | 14 |
| 71 | An Introduction to Recognizing Functional Domains. Current Protocols in Bioinformatics, 2006, 15, Unit 2.1. | 25.8 | 3 |
| 72 | Training of the next generation of biostatisticians: a call to action in the U.S.. Statistics in Medicine, 2006, 25, 3415-3429. | 1.6 | 37 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 73 | An Overview of RNA Structure Prediction and Applications to RNA Gene Prediction and RNA i Design. Current Protocols in Bioinformatics, 2006, 13, Unit 12.1. | 25.8 | 7 |
| 74 | Molecular Diagnostics in Sepsis: From Bedside to Bench. Journal of the American College of Surgeons, 2006, 203, 585-598.e1. | 0.5 | 38 |
| 75 | An improved map of conserved regulatory sites for Saccharomyces cerevisiae. BMC Bioinformatics, 2006, 7, 113. | 2.6 | 617 |
| 76 | Direct, Androgen Receptor-Mediated Regulation of the FKBP5 Gene via a Distal Enhancer Element. Endocrinology, 2006, 147, 590-598. | 2.8 | 151 |
| 77 | Using mRNAs lengths to accurately predict the alternatively spliced gene products in Caenorhabditis elegans. Bioinformatics, 2006, 22, 1239-1244. | 4.1 | 3 |
| 78 | Target Selectivity of Vertebrate Notch Proteins. Journal of Biological Chemistry, 2006, 281, 5106-5119. | 3.4 | 197 |
| 79 | A systematic model to predict transcriptional regulatory mechanisms based on overrepresentation of transcription factor binding profiles. Genome Research, 2006, 16, 405-413. | 5.5 | 65 |
| 80 | PLASTICITY OF THE HUMAN INNATE IMMUNE RESPONSE TO ACUTE INFECTION DURING CRITICAL ILLNESS: DEVELOPMENT OF THE RIBOLEUKOGRAM.. Critical Care Medicine, 2006, 34, A47. | 0.9 | 0 |
| 81 | Quantitative analysis of EGR proteins binding to DNA: assessing additivity in both the binding site and the protein. BMC Bioinformatics, 2005, 6, 176. | 2.6 | 22 |
| 82 | PolyMAPr: Programs for polymorphism database mining, annotation, and functional analysis. Human Mutation, 2005, 25, 110-117. | 2.5 | 37 |
| 83 | Procom: a web-based tool to compare multiple eukaryotic proteomes. Bioinformatics, 2005, 21, 1693-1694. | 4.1 | 7 |
| 84 | Editing efficiency of a Drosophila gene correlates with a distant splice site selection. Rna, 2005, 11, 563-566. | 3.5 | 15 |
| 85 | Identifying the conserved network of cis-regulatory sites of a eukaryotic genome. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17400-17405. | 7.1 | 68 |
| 86 | Combining SELEX with quantitative assays to rapidly obtain accurate models of protein-DNA interactions. Nucleic Acids Research, 2005, 33, e141-e141. | 14.5 | 75 |
| 87 | Application of genome-wide expression analysis to human health and disease. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4801-4806. | 7.1 | 238 |
| 88 | Making connections between novel transcription factors and their DNA motifs. Genome Research, 2005, 15, 312-320. | 5.5 | 49 |
| 89 | Pairwise local structural alignment of RNA sequences with sequence similarity less than 40%. Bioinformatics, 2005, 21, 1815-1824. | 4.1 | 138 |
| 90 | enoLOGOS: a versatile web tool for energy normalized sequence logos. Nucleic Acids Research, 2005, 33, W389-W392. | 14.5 | 199 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 91 | Computational technique for improvement of the position-weight matrices for the DNA/protein binding sites. Nucleic Acids Research, 2005, 33, 2290-2301. | 14.5 | 73 |
| 92 | An Iterated loop matching approach to the prediction of RNA secondary structures with pseudoknots. Bioinformatics, 2004, 20, 58-66. | 4.1 | 213 |
| 93 | The Neuropeptide Pigment-Dispersing Factor Coordinates Pacemaker Interactions in the Drosophila Circadian System. Journal of Neuroscience, 2004, 24, 7951-7957. | 3.6 | 296 |
| 94 | A graph theoretical approach for predicting common RNA secondary structure motifs including pseudoknots in unaligned sequences. Bioinformatics, 2004, 20, 1591-1602. | 4.1 | 92 |
| 95 | Novel transcription regulatory elements in Caenorhabditis elegans muscle genes. Genome Research, 2004, 14, 2457-2468. | 5.5 | 27 |
| 96 | ILM: a web server for predicting RNA secondary structures with pseudoknots. Nucleic Acids Research, 2004, 32, W146-W149. | 14.5 | 32 |
| 97 | RNA interference of achaete-scute homolog 1 in mouse prostate neuroendocrine cells reveals its gene targets and DNA binding sites. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5559-5564. | 7.1 | 46 |
| 98 | Quantitative modeling of DNA-protein interactions: effects of amino acid substitutions on binding specificity of the Mnt repressor. Nucleic Acids Research, 2004, 32, 4026-4032. | 14.5 | 16 |
| 99 | Expression profiling using random genomic DNA microarrays identifies differentially expressed genes associated with three major developmental stages of the protozoan parasite Leishmania major. Molecular and Biochemical Parasitology, 2004, 136, 71-86. | 1.1 | 109 |
| 100 | Training the Next Generation of Informaticians: The Impact of "BISTI" and Bioinformatics--A Report from the American College of Medical Informatics. Journal of the American Medical Informatics Association: JAMIA, 2004, 11, 167-172. | 4.4 | 52 |
| 101 | PromoLign: A database for upstream region analysis and SNPs. Human Mutation, 2004, 23, 534-539. | 2.5 | 33 |
| 102 | Comparative Genomics Identifies a Flagellar and Basal Body Proteome that Includes the BBS5 Human Disease Gene. Cell, 2004, 117, 541-552. | 28.9 | 721 |
| 103 | Analysis of Chlamydomonas reinhardtii Genome Structure Using Large-Scale Sequencing of Regions on Linkage Groups I and III. Journal of Eukaryotic Microbiology, 2003, 50, 145-155. | 1.7 | 24 |
| 104 | An Introduction to Recognizing Functional Domains. Current Protocols in Bioinformatics, 2003, 00, 2.1.1. | 25.8 | 1 |
| 105 | New Tricks for an Old Dogma. Molecular Cell, 2003, 11, 1419-1420. | 9.7 | 10 |
| 106 | Computational identification of the Spo0A-phosphate regulon that is essential for the cellular differentiation and development in Gram-positive spore-forming bacteria. Nucleic Acids Research, 2003, 31, 6891-6903. | 14.5 | 27 |
| 107 | Combining phylogenetic data with co-regulated genes to identify regulatory motifs. Bioinformatics, 2003, 19, 2369-2380. | 4.1 | 227 |
| 108 | EVOLUTION: Heirlooms in the Attic. Science, 2003, 302, 997-999. | 12.6 | 13 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 109 | An Overview of RNA Structure Prediction. Current Protocols in Bioinformatics, 2003, 4, 12.1.1. | 25.8 | 0 |
| 110 | Identification of a Novel cis-Regulatory Element Involved in the Heat Shock Response in Caenorhabditis elegans Using Microarray Gene Expression and Computational Methods. Genome Research, 2002, 12, 701-712. | 5.5 | 262 |
| 111 | Influence of the period-dependent circadian clock on diurnal, circadian, and aperiodic gene expression in Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9562-9567. | 7.1 | 167 |
| 112 | Specificity of Mnt 'master residue' obtained from in vivo and in vitro selections. Nucleic Acids Research, 2002, 30, 5539-5548. | 14.5 | 6 |
| 113 | Putting the Leishmania genome to work: functional genomics by transposon trapping and expression profiling. Philosophical Transactions of the Royal Society B: Biological Sciences, 2002, 357, 47-53. | 4.0 | 27 |
| 114 | Sepsis gene expression profiling: Murine splenic compared with hepatic responses determined by using complementary DNA microarrays. Critical Care Medicine, 2002, 30, 2711-2721. | 0.9 | 51 |
| 115 | Probabilistic Code for DNA Recognition by Proteins of the EGR Family. Journal of Molecular Biology, 2002, 323, 701-727. | 4.2 | 109 |
| 116 | Mining genome databases to identify and understand new gene regulatory systems. Current Opinion in Microbiology, 2002, 5, 149-153. | 5.1 | 34 |
| 117 | Additivity in protein-DNA interactions: how good an approximation is it?. Nucleic Acids Research, 2002, 30, 4442-4451. | 14.5 | 284 |
| 118 | Is there a code for protein-DNA recognition? Probab(ilistical)ly?. BioEssays, 2002, 24, 466-475. | 2.5 | 94 |
| 119 | Role of gene expression microarray analysis in finding complex disease genes. Genetic Epidemiology, 2002, 23, 37-56. | 1.3 | 31 |
| 120 | INJURY IN THE ERA OF GENOMICS. Shock, 2001, 15, 165-170. | 2.1 | 43 |
| 121 | Discovering common stem-loop motifs in unaligned RNA sequences. Nucleic Acids Research, 2001, 29, 2135-2144. | 14.5 | 122 |
| 122 | Do mRNAs act as direct sensors of small molecules to control their expression?. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9465-9467. | 7.1 | 85 |
| 123 | Selection of optimal DNA oligos for gene expression arrays. Bioinformatics, 2001, 17, 1067-1076. | 4.1 | 213 |
| 124 | Non-independence of Mnt repressor-operator interaction determined by a new quantitative multiple fluorescence relative affinity (QuMFRA) assay. Nucleic Acids Research, 2001, 29, 2471-2478. | 14.5 | 169 |
| 125 | A Comparative Genomics Approach to Prediction of New Members of Regulons. Genome Research, 2001, 11, 566-584. | 5.5 | 113 |
| 126 | Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. Richard Durbin , Sean R. Eddy , Anders Krogh , Graeme Mitchison. Quarterly Review of Biology, 2000, 75, 313-314. | 0.1 | 6 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 127 | Improved statistical methods reveal direct interactions between 16S and 23S rRNA. Nucleic Acids Research, 2000, 28, 4938-4943. | 14.5 | 6 |
| 128 | <title>Probing protein: DNA interactions using a uniform monolayer of DNA and surface plasmon resonance</title>. , 2000, , . | | 5 |
| 129 | Gene-Finding Approaches for Eukaryotes. Genome Research, 2000, 10, 394-397. | 5.5 | 95 |
| 130 | Specificity, free energy and information content in protein–DNA interactions. Trends in Biochemical Sciences, 1998, 23, 109-113. | 7.5 | 312 |
| 131 | Information Content and Free Energy in DNA–Protein Interactions. Journal of Theoretical Biology, 1998, 195, 135-137. | 1.7 | 41 |
| 132 | PromFD 1.0: a computer program that predicts eukaryotic pol II promoters using strings and IMD matrices. Bioinformatics, 1997, 13, 29-35. | 4.1 | 12 |
| 133 | Finding the most significant common sequence and structure motifs in a set of RNA sequences. Nucleic Acids Research, 1997, 25, 3724-3732. | 14.5 | 188 |
| 134 | Quantitative specificity of the Mnt repressor. Journal of Molecular Biology, 1997, 271, 178-194. | 4.2 | 81 |
| 135 | DNA sequence classification using DAWGs. Lecture Notes in Computer Science, 1997, , 339-352. | 1.3 | 10 |
| 136 | Recognizing Functional Domains in Biological Sequences. , 1997, , 105-116. | | 0 |
| 137 | [2] Escherichia coli promoter sequences: Analysis and prediction. Methods in Enzymology, 1996, 273, 30-42. | 1.0 | 69 |
| 138 | Multi-alphabet consensus algorithm for identification of low specificity protein-DNA interactions. Nucleic Acids Research, 1995, 23, 1434-1440. | 14.5 | 21 |
| 139 | A consensus sequence for binding of Lrp to DNA. Journal of Bacteriology, 1995, 177, 4872-4880. | 2.2 | 130 |
| 140 | Identification of Protein Coding Regions In Genomic DNA. Journal of Molecular Biology, 1995, 248, 1-18. | 4.2 | 195 |
| 141 | Detection of deletions in the mitochondrial genome ofCaenorhabditis elegans. Nucleic Acids Research, 1994, 22, 1075-1078. | 14.5 | 73 |
| 142 | Quantitative DNA Sequencing to Determine the Relative Protein-DNA Binding Constants to Multiple DNA Sequences. Analytical Biochemistry, 1994, 219, 230-239. | 2.4 | 7 |
| 143 | Quantitative analysis of ribosome binding sites in E.coli. Nucleic Acids Research, 1994, 22, 1287-1295. | 14.5 | 147 |
| 144 | Specificity of the Mnt Protein. Journal of Molecular Biology, 1993, 229, 821-826. | 4.2 | 16 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 145 | Identification of coding regions in genomic DNA sequences: an application of dynamic programming and neural networks. Nucleic Acids Research, 1993, 21, 607-613. | 14.5 | 180 |
| 146 | Analysis of five presumptive protein-coding sequences clustered between the primosome genes, 41 and 61, of bacteriophages T4, T2, and T6. Journal of Virology, 1993, 67, 2305-2316. | 3.4 | 17 |
| 147 | Identifying constraints on the higher-order structure of RNA: continued development and application of comparative sequence analysis methods. Nucleic Acids Research, 1992, 20, 5785-5795. | 14.5 | 285 |
| 148 | Splicing signals inDrosophila: intron size, information content, and consensus sequences. Nucleic Acids Research, 1992, 20, 4255-4262. | 14.5 | 419 |
| 149 | Expectation maximization algorithm for identifying protein-binding sites with variable lengths from unaligned DNA fragments. Journal of Molecular Biology, 1992, 223, 159-170. | 4.2 | 132 |
| 150 | Translation initiation in Escherichia coli: sequences within the ribosome-binding site. Molecular Microbiology, 1992, 6, 1219-1229. | 2.5 | 329 |
| 151 | [22] Probing information content of DNA-binding sites. Methods in Enzymology, 1991, 208, 458-468. | 1.0 | 11 |
| 152 | Specificity of the Mnt protein determined by binding to randomized operators.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 5699-5703. | 7.1 | 30 |
| 153 | [7] High-level translation initiation. Methods in Enzymology, 1990, 185, 89-93. | 1.0 | 270 |
| 154 | [13] Consensus patterns in DNA. Methods in Enzymology, 1990, 183, 211-221. | 1.0 | 165 |
| 155 | Identification of consensus patterns in unaligned DNA sequences known to be functionally related. Bioinformatics, 1990, 6, 81-92. | 4.1 | 222 |
| 156 | Sequence requirements of the hammerhead RNA self-cleavage reaction. Biochemistry, 1990, 29, 10695-10702. | 2.5 | 489 |
| 157 | Excess information at bacteriophage T7 genomic promoters detected by a random cloning technique. Nucleic Acids Research, 1989, 17, 659-674. | 14.5 | 69 |
| 158 | Identifying protein-binding sites from unaligned DNA fragments.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 1183-1187. | 7.1 | 400 |
| 159 | Computer Methods for Analyzing Sequence Recognition of Nucleic Acids. Annual Review of Biophysics and Biophysical Chemistry, 1988, 17, 241-263. | 12.2 | 95 |
| 160 | Autogenous regulatory site on the bacteriophage T4 gene 32 messenger RNA. Journal of Molecular Biology, 1988, 201, 517-535. | 4.2 | 146 |
| 161 | Translational Regulation in Bacteriophages. , 1987, , 27-49. | | 10 |
| 162 | Information content of binding sites on nucleotide sequences. Journal of Molecular Biology, 1986, 188, 415-431. | 4.2 | 872 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 163 | Quantitative analysis of the relationship between nucleotide sequence and functional activity. Nucleic Acids Research, 1986, 14, 6661-6679. | 14.5 | 156 |
| 164 | Sequence landscapes. Nucleic Acids Research, 1986, 14, 141-158. | 14.5 | 47 |
| 165 | Translationsl regulation of expression of the bacteriophage T4 lysozyme gene. Nucleic Acids Research, 1986, 14, 5813-5826. | 14.5 | 139 |
| 166 | Translation Initiation. , 1986, , 195-224. | | 96 |
| 167 | Delila system tools. Nucleic Acids Research, 1984, 12, 129-140. | 14.5 | 45 |
| 168 | lacZ translation initiation mutations. Journal of Molecular Biology, 1984, 177, 663-683. | 4.2 | 115 |
| 169 | The bacteriophage T4regAgene: primary sequence of a translational repressor. Nucleic Acids Research, 1984, 12, 5979-5993. | 14.5 | 34 |
| 170 | A design for computer nucleic-acid-sequence storage, retrieval, and manipulation. Nucleic Acids Research, 1982, 10, 3013-3024. | 14.5 | 60 |
| 171 | Characterization of translational initiation sites inE. coli. Nucleic Acids Research, 1982, 10, 2971-2996. | 14.5 | 729 |
| 172 | Autoregulation of gene expression. Journal of Molecular Biology, 1982, 162, 795-818. | 4.2 | 111 |
| 173 | Use of the 'Perceptron' algorithm to distinguish translational initiation sites inE. coli. Nucleic Acids Research, 1982, 10, 2997-3011. | 14.5 | 649 |