Basic local alignment search tool

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2174	.		
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2141	.	
2140	.	
2139	.	
2138	.	
2137	.	
2136	Solid tumor cancer markers and applications to steroid hormone research. **2001**, 176, 329-40	
2135	Sequence databases and the Internet. **2001**, 167, 215-23	1
2134	Influence of surgical procedures on the curse of multiple sclerosis. **1961**, 11, 81-2	5
2133	Vitamin B12 unsaturated binding capacity of sera from various animals. **1962**, 109, 179-81	6
2132	Effects of androstenes, 5alpha-androstanes, 5beta-androstanes, oestrenes and oestratrienes on serum gonadotrophin levels and ventral prostate weights in gonadectomized, adult male rats. **1976**, 83, 201-10	10
2131	A hypervariable RFLP on chromosome 17p13 is defined by an arbitrary single copy probe p144-D6 [HGM9 No. D17S34]. **1987**, 15, 10605	43
2130	The NF1 locus encodes a protein functionally related to mammalian GAP and yeast IRA proteins. **1990**, 63, 851-9	727
2129	Identification of FAP locus genes from chromosome 5q21. **1991**, 253, 661-5	2047
2128	Identifying distantly related protein sequences. **1991**, 1, 321-326	11
2127	Nucleotide sequence of the RAD57 gene of Saccharomyces cerevisiae. **1991**, 105, 139-40	101
2126	DM-GRASP, a novel immunoglobulin superfamily axonal surface protein that supports neurite extension. **1991**, 7, 209-20	180

2125	The first lipocalin with enzymatic activity. **1991**, 16, 363		50
2124	Improved sensitivity of nucleic acid database searches using application-specific scoring matrices. **1991**, 3, 66-70		99
2123	New developments of a transcription factors database. **1991**, 16, 445-7		48
2122	cDNA cloning of the type 1 neurofibromatosis gene: complete sequence of the NF1 gene product. **1991**, 11, 931-40		350
2121	Templates, consensus patterns and motifs. **1991**, 1, 327-333		13
2120	Complementary DNA sequencing: expressed sequence tags and human genome project. **1991**, 252, 1651-6		1893
2119	Expression cloning and characterization of the TGF-beta type III receptor. **1991**, 67, 797-805		576
2118	Nanos is the localized posterior determinant in Drosophila. **1991**, 66, 637-47		416
2117	The TEA domain: a novel, highly conserved DNA-binding motif. **1991**, 66, 11-2		139
2116	Oskar organizes the germ plasm and directs localization of the posterior determinant nanos. **1991**, 66, 37-50		689
2115	The candidate gene for the X-linked Kallmann syndrome encodes a protein related to adhesion molecules. **1991**, 67, 423-35		600
2114	The fat tumor suppressor gene in Drosophila encodes a novel member of the cadherin gene superfamily. **1991**, 67, 853-68		392
2113	Searching protein sequence libraries: comparison of the sensitivity and selectivity of the Smith-Waterman and FASTA algorithms. **1991**, 11, 635-50		444
2112	Amino acid substitution matrices from an information theoretic perspective. *Journal of Molecular Biology*, **1991**, 219, 555-65	6.5	477
2111	Lysyl oxidase and rrg messenger RNA. **1991**, 253, 802		176
2110	Mutations in the two flagellin genes of Rhizobium meliloti. **1991**, 173, 3716-23		20
2109	A putative zinc finger protein, Saccharomyces cerevisiae Vps18p, affects late Golgi functions required for vacuolar protein sorting and efficient alpha-factor prohormone maturation. **1991**, 11, 5813-24		83
2108	Two putative subunits of a peptide pump encoded in the human major histocompatibility complex class II region. **1991**, 88, 10094-8		150

2107	Cloning and characterization of a receptor-class phosphotyrosine phosphatase gene expressed on central nervous system axons in Drosophila melanogaster. **1991**, 88, 11266-70	33
2106	Characterization of a murine gene expressed from the inactive X chromosome. **1991**, 351, 325-9	471
2105	Identification of self peptides bound to purified HLA-B27. **1991**, 353, 326-9	802
2104	Spinning in hyperspace. **1991**, 353, 388-389	6
2103	A gene deleted in Kallmann's syndrome shares homology with neural cell adhesion and axonal path-finding molecules. **1991**, 353, 529-36	764
2102	A strong propensity toward loop formation characterizes the expressed reading frames of the D segments at the Ig H and T cell receptor loci. **1991**, 21, 3021-5	23
2101	Cloning of a Saccharomyces cerevisiae gene encoding a protein homologous to allantoicase of Neurospora crassa. **1991**, 7, 993-5	10
2100	A platform for biological sequence comparison on parallel computers. **1991**, 7, 237-47	7
2099	Characterization and molecular cloning of polypyrimidine tract-binding protein: a component of a complex necessary for pre-mRNA splicing. **1991**, 5, 1237-51	294
2098	Kinetics of angular and spectral characteristics of excimer laser radiation. **1991**, 21, 622-626	
2097	Characterization of cDNAs encoding the polypyrimidine tract-binding protein. **1991**, 5, 1224-36	222
2096	sar1, a gene from Schizosaccharomyces pombe encoding a protein that regulates ras1. **1991**, 2, 453-65	76
2095	Software tools for analyzing pairwise alignments of long sequences. **1991**, 19, 4663-7	30
2094	Similarities in amino acid sequences of Drosophila eag and cyclic nucleotide-gated channels. **1991**, 254, 730	112
2093	Visualization and Characterization of Tobacco Mosaic Virus Movement Protein Binding to Single-Stranded Nucleic Acids. **1992**, 4, 397	2
2092	Bovine sequences in rodent DNA. **1992**, 20, 2892	6
2091	Accessing the Literature and Data Bases of Molecular Biology. **1992**, 41, 268-269	
2090	Sequence pattern matching on a massively parallel computer. **1992**, 8, 377-83	

2089	Corruption of genomic databases with anomalous sequence. **1992**, 20, 2741-7	28
2088	Chance and statistical significance in protein and DNA sequence analysis. **1992**, 257, 39-49	167
2087	Aligning two sequences within a specified diagonal band. **1992**, 8, 481-7	63
2086	Genomic DNA sequences of mitochondrial tRNA genes in fungi Penicillium chrysogenum KCTC1262: tRNA(arg), tRNA(asn) and tRNA(tyr) genes. **1992**, 20, 5842	1
2085	The Caenorhabditis elegans unc-93 gene encodes a putative transmembrane protein that regulates muscle contraction. **1992**, 117, 143-55	43
2084	Pumilio is essential for function but not for distribution of the Drosophila abdominal determinant Nanos. **1992**, 6, 2312-26	164
2083	Association of a 59-kilodalton immunophilin with the glucocorticoid receptor complex. **1992**, 256, 1315-8	296
2082	Identification of a streptomycin resistance gene and a partial Tn3 transposon coding for a beta-lactamase in a periodontal strain of Eikenella corrodens. **1992**, 36, 740-3	15
2081	Protein Sequence and Structure Comparison On Massively Parallel Computers. **1992**, 6, 138-146	4
2080	Cloning and mapping of the alpha-adducin gene close to D4S95 and assessment of its relationship to Huntington disease. **1992**, 1, 669-75	22
2079	Expression of antisense or sense RNA of an ankyrin repeat-containing gene blocks chloroplast differentiation in arabidopsis. **1992**, 4, 1575-88	71
2078	tra-2 encodes a membrane protein and may mediate cell communication in the Caenorhabditis elegans sex determination pathway. **1992**, 3, 461-73	111
2077	A simple method for global sequence comparison. **1992**, 20, 131-6	8
2076	Geminivirus replication proteins are related to prokaryotic plasmid rolling circle DNA replication initiator proteins. **1992**, 73 (Pt 10), 2763-6	126
2075	Nucleotide sequence analysis of a unique near-terminal region of the tumorigenic poxvirus, Shope fibroma virus. **1992**, 73 (Pt 11), 2903-11	10
2074	Effects of null mutations and overexpression of capping protein on morphogenesis, actin distribution and polarized secretion in yeast. **1992**, 119, 1151-62	115
2073	PATMAT: a searching and extraction program for sequence, pattern and block queries and databases. **1992**, 8, 249-54	27
2072	Isolation of a Saccharomyces cerevisiae long chain fatty acyl:CoA synthetase gene (FAA1) and assessment of its role in protein N-myristoylation. **1992**, 117, 515-29	76

2071	A new approach to understanding T cell development: the isolation and characterization of immature CD4-, CD8-, CD3- T cell cDNAs by subtraction cloning. **1992**, 3, 761-73	10
2070	A novel DNA-binding protein with regulatory and protective roles in starved Escherichia coli. **1992**, 6, 2646-54	589
2069	Visualization and characterization of tobacco mosaic virus movement protein binding to single-stranded nucleic acids. **1992**, 4, 397-411	254
2068	{BLR 1313} - Patents - Venter - NIH - cDNA - ESTs. **1992**, 11, 241-317	
2067	Molecular cloning of a candidate chicken prion protein. **1992**, 89, 9097-101	104
2066	Transmission-blocking antibodies recognize microfilarial chitinase in brugian lymphatic filariasis. **1992**, 89, 1548-52	98
2065	Glycosylation in Saccharomyces cerevisiae: cloning and characterization of an alpha-1,2-mannosyltransferase structural gene. **1992**, 2, 77-84	74
2064	Determining DNA sequence similarity using maximum independent set algorithms for interval graphs. **1992**, 326-337	21
2063	Nucleotide sequence and expression of a cDNA encoding rabbit liver cytosolic serine hydroxymethyltransferase. **1992**, 286 (Pt 1), 117-23	23
2062	Characterization of the DNA-binding activity of GCR1: in vivo evidence for two GCR1-binding sites in the upstream activating sequence of TPI of Saccharomyces cerevisiae. **1992**, 12, 2690-700	95
2061	Nucleotide sequence and transcriptional regulation of the yeast recombinational repair gene RAD51. **1992**, 12, 3235-46	242
2060	Isolation of a gene encoding a chaperonin-like protein by complementation of yeast amino acid transport mutants with human cDNA. **1992**, 89, 6060-4	18
2059	The yeast nuclear gene suv3 affecting mitochondrial post-transcriptional processes encodes a putative ATP-dependent RNA helicase. **1992**, 89, 6813-7	86
2058	Cloning, expression, and localization of a rat brain high-affinity glycine transporter. **1992**, 89, 7189-93	224
2057	A developmentally regulated chlamydial gene with apparent homology to eukaryotic histone H1. **1992**, 89, 2125-9	75
2056	Tsp: a tail-specific protease that selectively degrades proteins with nonpolar C termini. **1992**, 89, 295-9	172
2055	Cloning and expression of an NADP(+)-dependent alcohol dehydrogenase gene of Entamoeba histolytica. **1992**, 89, 10188-92	57
2054	Amino acid substitution matrices from protein blocks. **1992**, 89, 10915-9	4190

2053	Expression cloning of a human dual-specificity phosphatase. **1992**, 89, 12170-4	177
2052	Identification of a human src homology 2-containing protein-tyrosine-phosphatase: a putative homolog of Drosophila corkscrew. **1992**, 89, 11239-43	323
2051	Isolation and characterization of human cDNA clones encoding a high mobility group box protein that recognizes structural distortions to DNA caused by binding of the anticancer agent cisplatin. **1992**, 89, 2307-11	226
2050	Isolation of rsp-1, a novel cDNA capable of suppressing v-Ras transformation. **1992**, 12, 3750-6	74
2049	DPH5, a methyltransferase gene required for diphthamide biosynthesis in Saccharomyces cerevisiae. **1992**, 12, 4026-37	68
2048	Cloning and sequencing of Escherichia coli murZ and purification of its product, a UDP-N-acetylglucosamine enolpyruvyl transferase. **1992**, 174, 5748-52	109
2047	Sequence of the human factor VIII-associated gene is conserved in mouse. **1992**, 13, 862-5	24
2046	The nucleotide sequence of recG, the distal spo operon gene in Escherichia coli K-12. **1992**, 110, 95-9	30
2045	Organization, structure, and function of 95 kb of DNA spanning the murine T-cell receptor C alpha/C delta region. **1992**, 13, 1209-30	124
2044	The human Y chromosome: a 43-interval map based on naturally occurring deletions. **1992**, 258, 52-9	420
2043	Dynamic programming algorithms for biological sequence comparison. **1992**, 210, 575-601	53
2042	Archaebacterial virus SSV1 encodes a putative DnaA-like protein. **1992**, 20, 1143	25
2041	DnaC protein contains a modified ATP-binding motif and belongs to a novel family of ATPases including also DnaA. **1992**, 20, 1997	46
2040	A family of DNA virus genes that consists of fused portions of unrelated cellular genes. **1992**, 17, 213-4	45
2039	Conserved sequence motifs in the initiator proteins for rolling circle DNA replication encoded by diverse replicons from eubacteria, eucaryotes and archaebacteria. **1992**, 20, 3279-85	502
2038	A new group of putative RNA helicases. **1992**, 17, 495-7	71
2037	CLIP-170 links endocytic vesicles to microtubules. **1992**, 70, 887-900	335
2036	A targeting sequence directs DNA methyltransferase to sites of DNA replication in mammalian nuclei. **1992**, 71, 865-73	859

2035	ERCC6, a member of a subfamily of putative helicases, is involved in Cockayne's syndrome and preferential repair of active genes. **1992**, 71, 939-53	628
2034	Conservation of a 23-kDa human transplantation antigen in mammalian species. **1992**, 14, 959-64	8
2033	Fasciclin IV: sequence, expression, and function during growth cone guidance in the grasshopper embryo. **1992**, 9, 831-45	289
2032	Expression of murine cyclin B1 mRNAs and genetic mapping of related genomic sequences. **1992**, 13, 1018-30	34
2031	A transposon-like element in the deletion-prone region of the dystrophin gene. **1992**, 13, 594-600	37
2030	cDNA surveying of specific tissue expression of human chromosome 19 sequences. **1992**, 14, 263-9	5
2029	Conservation of gene organization and trans-splicing in the glyceraldehyde-3-phosphate dehydrogenase-encoding genes of Caenorhabditis briggsae. **1992**, 121, 227-35	29
2028	Sequences of the bovine herpesvirus 1 homologue of herpes simplex virus type-1 alpha-trans-inducing factor (UL48). **1992**, 119, 259-63	20
2027	Similarities in amino acid sequences of Aplysia ADP-ribosyl cyclase and human lymphocyte antigen CD38. **1992**, 17, 495	222
2026	A contig assembly program based on sensitive detection of fragment overlaps. **1992**, 14, 18-25	238
2025	Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences. **1992**, 12, 838-41	30
2024	Sequence-tagged sites (STSs) for a set of mapped markers on chromosome 21. **1992**, 14, 498-502	12
2023	A putative Ras GTPase activating protein acts as a negative regulator of signaling by the Sevenless receptor tyrosine kinase. **1992**, 68, 1007-19	284
2022	corkscrew encodes a putative protein tyrosine phosphatase that functions to transduce the terminal signal from the receptor tyrosine kinase torso. **1992**, 70, 225-36	378
2021	Genetic isolation of ADA2: a potential transcriptional adaptor required for function of certain acidic activation domains. **1992**, 70, 251-65	408
2020	A major palmitoylated membrane protein of human erythrocytes shows homology to yeast guanylate kinase and to the product of a Drosophila tumor suppressor gene. **1992**, 68, 621-2	41
2019	Expression cloning of the TGF-beta type II receptor, a functional transmembrane serine/threonine kinase. **1992**, 68, 775-85	971
2018	Molecular basis of myotonic dystrophy: expansion of a trinucleotide (CTG) repeat at the 3' end of a transcript encoding a protein kinase family member. **1992**, 68, 799-808	2045

(1992-1992)

2017	A suppressor of TBP mutations encodes an RNA polymerase III transcription factor with homology to TFIIB. **1992**, 71, 221-30		156
2016	Molecular cloning of cDNAs encoding the GAP-associated protein p190: implications for a signaling pathway from ras to the nucleus. **1992**, 69, 539-49		323
2015	SHR3: a novel component of the secretory pathway specifically required for localization of amino acid permeases in yeast. **1992**, 71, 463-78		188
2014	The argos gene encodes a diffusible factor that regulates cell fate decisions in the Drosophila eye. **1992**, 69, 963-75		222
2013	Transcriptionally active chimeric gene derived from the fusion of the AML1 gene and a novel gene on chromosome 8 in t(8;21) leukemic cells. **1992**, 63, 81-8		134
2012	Finding errors in DNA sequences. **1992**, 89, 4698-702		34
2011	Limit distributions of maximal segmental score among Markov-dependent partial sums. **1992**, 24, 113-140		84
2010	Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts. **1992**, 184, 922-9		58
2009	The second cholera toxin, Zot, and its plasmid-encoded and phage-encoded homologues constitute a group of putative ATPases with an altered purine NTP-binding motif. **1992**, 312, 3-6		41
2008	A subgroup of class alpha glutathione S-transferases. Cloning of cDNA for mouse lung glutathione S-transferase GST 5.7. **1992**, 313, 173-6		50
2007	Prediction of gene structure. *Journal of Molecular Biology*, **1992**, 226, 141-57	6.5	258
2006	Isolation of DNA damage-inducible promoters in Escherichia coli: regulation of polB (dinA), dinG, and dinH by LexA repressor. **1992**, 174, 3377-85		71
2005	Mutational analysis reveals functional similarity between NARX, a nitrate sensor in Escherichia coli K-12, and the methyl-accepting chemotaxis proteins. **1992**, 174, 3667-75		50
2004	Interaction of LexA repressor with the asymmetric dinG operator and complete nucleotide sequence of the gene. **1992**, 174, 5110-6		24
2003	Physical mapping of repetitive extragenic palindromic sequences in Escherichia coli and phylogenetic distribution among Escherichia coli strains and other enteric bacteria. **1992**, 174, 4583-93		61
2002	Nucleotide sequences of the genes regulating O-polysaccharide antigen chain length (rol) from Escherichia coli and Salmonella typhimurium: protein homology and functional complementation. **1992**, 174, 5228-36		95
2001	Frequent transpositions of Drosophila melanogaster HeT-A transposable elements to receding chromosome ends.. **1992**, 11, 4459-4469		113
2000	Limit distributions of maximal segmental score among Markov-dependent partial sums. **1992**, 24, 113-140		29

1999	Cloning, characterization, and expression of a human calcitonin receptor from an ovarian carcinoma cell line. **1992**, 90, 1726-35	146
1998	Chloroplast RNA polymerase genes of Chlamydomonas reinhardtii exhibit an unusual structure and arrangement. **1992**, 21, 485-97	33
1997	The murine MHC encodes a mammalian homolog of bacterial ribosomal protein S13. **1992**, 2, 87-95	11
1996	Protein classification artificial neural system. **1992**, 1, 667-77	93
1995	Comprehensive sequence analysis of the 182 predicted open reading frames of yeast chromosome III. **1992**, 1, 1677-90	98
1994	Comparative analysis of the beta transducin family with identification of several new members including PWP1, a nonessential gene of Saccharomyces cerevisiae that is divergently transcribed from NMT1. **1992**, 13, 41-56	87
1993	A systematic search for protein signature sequences. **1992**, 14, 16-28	25
1992	Mapping the putative RNA helicase genes by sequence overlapping. **1992**, 8, 973-5	
1991	Prune function?. **1992**, 355, 504-5	3
1990	Sequence identification of 2,375 human brain genes. **1992**, 355, 632-4	723
1989	DNA sequencing. The worm turns and delivers. **1992**, 356, 14-5	13
1988	The C. elegans genome sequencing project: a beginning. **1992**, 356, 37-41	465
1987	Gene patents. **1992**, 356, 738	2
1986	Proto-vav and gene expression. **1992**, 358, 113	34
1985	The Lowe's oculocerebrorenal syndrome gene encodes a protein highly homologous to inositol polyphosphate-5-phosphatase. **1992**, 358, 239-42	408
1984	The gene lin-3 encodes an inductive signal for vulval development in C. elegans. **1992**, 358, 470-6	327
1983	Automated DNA sequencing and analysis of 106 kilobases from human chromosome 19q13.3. **1992**, 1, 34-9	82
1982	Human CCAAT displacement protein is homologous to the Drosophila homeoprotein, cut. **1992**, 1, 50-5	188

1981	A survey of expressed genes in Caenorhabditis elegans. **1992**, 1, 114-23	342
1980	Caenorhabditis elegans expressed sequence tags identify gene families and potential disease gene homologues. **1992**, 1, 124-31	170
1979	Expressed genes, Alu repeats and polymorphisms in cosmids sequenced from chromosome 4p16.3. **1992**, 1, 348-53	45
1978	A trithorax-like gene is interrupted by chromosome 11q23 translocations in acute leukaemias. **1992** , 2, 113-8	408
1977	Single pass sequencing and physical and genetic mapping of human brain cDNAs. **1992**, 2, 180-5	164
1976	Cloning of the alpha-adducin gene from the Huntington’s disease candidate region of chromosome 4 by exon amplification. **1992**, 2, 223-7	43
1975	dlg-R proteins: modified guanylate kinases. **1992**, 2, 256-7	19
1974	Sequence signals:Artifact or reality?. **1992**, 16, 89-91	4
1973	Structure prediction and modelling. **1992**, 3, 338-47	
1972	Evolution of Glutathione S-Transferases Associated with Insecticide Resistance in Drosophila. **1992**, 53-70	6
1971	AAtDB, anArabidopsis thaliana database. **1992**, 10, 308-309	17
1970	Poisson, compound Poisson and process approximations for testing statistical significance in sequence comparisons. **1992**, 54, 785-812	27
1969	Molecular sequence accuracy: analysing imperfect data. **1992**, 8, 52-5	14
1968	Cloning and sequencing of a human cDNA from cytolytic NK/T cells with homology to yeast SEC7. **1992**, 1132, 75-8	59
1967	Data exchange and inter-database communication in genome projects. **1992**, 10, 58-61	4
1966	Herpesvirus saimiri has a gene specifying a homologue of the cellular membrane glycoprotein CD59. **1992**, 190, 527-30	97
1965	A signature for the HMG-1 box DNA-binding proteins. **1993**, 15, 539-46	248
1964	Cloning and characterization of a Lambert-Eaton myasthenic syndrome antigen. **1993**, 33, 113-20	61

1963	Selective expression of the chicken platelet-derived growth factor alpha (PDGF alpha) receptor during limb bud development. **1993**, 198, 14-21	10
1962	Infidelity in the structure of ectopic transcripts: a novel exon in lymphocyte dystrophin transcripts. **1993**, 2, 293-9	31
1961	Sequence analysis of translationally controlled maternal mRNAs from Urechis caupo. **1993**, 14, 485-91	14
1960	Separation of acidic barley endosperm proteins by two-dimensional electrophoresis. **1993**, 14, 1060-6	25
1959	SWISS-2DPAGE: a database of two-dimensional gel electrophoresis images. **1993**, 14, 1232-8	118
1958	No pain and gain!Experiences with Mentat on a biological application. **1993**, 5, 309-328	9
1957	Computer-assisted dissection of rolling circle DNA replication. **1993**, 30, 241-68	149
1956	Statistics of local complexity in amino acid sequences and sequence databases. **1993**, 17, 149-163	466
1955	Information enhancement methods for large scale sequence analysis. **1993**, 17, 191-201	87
1954	BLAZEAn implementation of the Smith-Waterman sequence comparison algorithm on a massively parallel computer. **1993**, 17, 203-207	18
1953	Classification neural networks for rapid sequence annotation and automated database organization. **1993**, 17, 219-227	14
1952	A protein alignment scoring system sensitive at all evolutionary distances. **1993**, 36, 290-300	120
1951	Genomic structure of the human CD53 gene. **1993**, 38, 272-9	12
1950	Characterization of beta 2-microglobulin transcripts from two teleost species. **1993**, 38, 27-34	60
1949	A novel coding sequence belonging to a new multicopy gene family mapping within the human MHC class I region. **1993**, 38, 47-53	72
1948	Molecular and genetic characterization of SPT4, a gene important for transcription initiation in Saccharomyces cerevisiae. **1993**, 237, 449-59	51
1947	Cloning and analysis of the mating type genes from Cochliobolus heterostrophus. **1993**, 238, 270-84	146
1946	The myrosinase (thioglucoside glucohydrolase) gene family in Brassicaceae. **1993**, 23, 511-24	54

1945	A histidine decarboxylase-like mRNA is involved in tomato fruit ripening. **1993**, 23, 627-31	26
1944	Arabidopsis thaliana cor15b, an apparent homologue of cor15a, is strongly responsive to cold and ABA, but not drought. **1993**, 23, 1073-7	100
1943	Transposition pattern of a modified Ds element in tomato. **1993**, 21, 1109-19	14
1942	BARE-1, a copia-like retroelement in barley (Hordeum vulgare L.). **1993**, 22, 829-46	174
1941	Opa-like repeats in the genome of the Medfly Ceratitis capitata. **1993**, 92, 43-53	3
1940	The isolation and nucleotide sequence of the pyruvate decarboxylase gene from Kluyveromyces marxianus. **1993**, 24, 274-7	17
1939	Sequence of the open reading frame of the FLO1 gene from Saccharomyces cerevisiae. **1993**, 9, 423-7	106
1938	The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae encodes a putative serine/threonine protein kinase. **1993**, 9, 543-9	4
1937	DNA sequence analysis of the YCN2 region of chromosome XI in Saccharomyces cerevisiae. **1993**, 9, 661-7	16
1936	CLG1, a new cyclin-like gene of Saccharomyces cerevisiae. **1993**, 9, 929-31	9
1935	Synonymous codon usage in Kluyveromyces lactis. **1993**, 9, 1219-28	28
1934	Performance evaluation of amino acid substitution matrices. **1993**, 17, 49-61	333
1933	P-glycoprotein structure and evolutionary homologies. **1993**, 12, 1-32	30
1932	Synthesis of the foetal protein fetuin by early developing neurons in the immature neocortex. **1993** , 22, 266-72	30
1931	Complementation of the DNA repair defect in xeroderma pigmentosum group G cells by a human cDNA related to yeast RAD2. **1993**, 363, 182-5	197
1930	Alteration in a new gene encoding a putative membrane-organizing protein causes neuro-fibromatosis type 2. **1993**, 363, 515-21	1205
1929	No HMG-1 box signature. **1993**, 363, 590	7
1928	Database of ancient sequences. **1993**, 364, 19-20	17

1927	Group II self-splicing introns in bacteria. **1993**, 364, 358-61	213
1926	Neurotransmission and secretion. **1993**, 364, 582	12
1925	Isolation of a Miller-Dieker lissencephaly gene containing G protein beta-subunit-like repeats. **1993**, 364, 717-21	906
1924	Characterization of the pufferfish (Fugu) genome as a compact model vertebrate genome. **1993**, 366, 265-8	533
1923	The yeast DOA4 gene encodes a deubiquitinating enzyme related to a product of the human tre-2 oncogene. **1993**, 366, 313-9	360
1922	Isolation of a candidate gene for Menkes disease that encodes a potential heavy metal binding protein. **1993**, 3, 14-9	645
1921	Identification of protein coding regions by database similarity search. **1993**, 3, 266-72	1390
1920	3,400 new expressed sequence tags identify diversity of transcripts in human brain. **1993**, 4, 256-67	283
1919	Genomic scanning for expressed sequences in Xp21 identifies the glycerol kinase gene. **1993**, 4, 367-72	38
1918	Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library. **1993**, 4, 373-80	322
1917	Fusion of a fork head domain gene to PAX3 in the solid tumour alveolar rhabdomyosarcoma. **1993**, 5, 230-5	774
1916	The Wilson disease gene is a copper transporting ATPase with homology to the Menkes disease gene. **1993**, 5, 344-50	1153
1915	Characterization of comE, a late competence operon of Bacillus subtilis required for the binding and uptake of transforming DNA. **1993**, 10, 99-111	65
1914	Sequence and properties of mecA, a negative regulator of genetic competence in Bacillus subtilis. **1993**, 9, 365-73	53
1913	Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325° to 333deg. **1993**, 10, 371-384	143
1912	Characterisation of a highly repeated DNA sequence from Mycobacterium bovis. **1993**, 111, 147-52	27
1911	Primary structure analysis of a duplicated region in the amplifiable AUD6 locus of Streptomyces ambofaciens DSM40697. **1993**, 113, 49-56	11
1910	The salivary glands of the vector mosquito, Aedes aegypti, express a novel member of the amylase gene family. **1993**, 1, 223-32	52

1909	Molecular cloning and characterization of an Echinococcus granulosus cDNA encoding malate dehydrogenase. **1993**, 60, 157-60	16
1908	Molecular cloning of a rho family gene of Entamoeba histolytica. **1993**, 58, 177-80	38
1907	Molecular cloning of a rac family protein kinase and identification of a serine/threonine protein kinase gene family of Entamoeba histolytica. **1993**, 60, 161-70	18
1906	Cloning and functional analysis of an extrachromosomally amplified multidrug resistance-like gene in Leishmania enriettii. **1993**, 60, 195-208	80
1905	The cDNA sequence of an abundant Entamoeba histolytica 20-kilodalton protein containing four repetitive domains. **1993**, 60, 323-6	4
1904	The dihydroorotate dehydrogenase gene homologue of Plasmodium falciparum. **1993**, 60, 349-51	14
1903	Restriction polymorphisms and fingerprint patterns from an interspersed repetitive element of Plasmodium falciparum DNA. **1993**, 61, 137-42	36
1902	A Babesia equi gene encodes a surface protein with homology to Theileria species. **1993**, 62, 121-4	49
1901	Molecular cloning of the gene for a novel ABC superfamily transporter of Entamoeba histolytica. **1993**, 62, 131-4	7
1900	Molecular cloning and localization of an abundant novel protein of Plasmodium berghei. **1993**, 59, 223-34	11
1899	A cDNA from Schistosoma mansoni eggs sharing sequence features of mammalian cystatin. **1993**, 57, 175-6	5
1898	cDNA sequence for mouse caltractin. **1993**, 1216, 126-8	27
1897	Cloning of a unique human homologue of the Escherichia coli DNAJ heat shock protein. **1993**, 1174, 111-3	55
1896	Identification of a ras gene in the slime mold Physarum polycephalum. **1993**, 1173, 357-9	6
1895	Nucleotide and predicted amino acid sequence of a new member of the ras gene family from the slime mold Physarum polycephalum. **1993**, 1174, 299-302	5
1894	Constrained sequence alignment. **1993**, 55, 503-24	9
1893	The closteroviruses, capilloviruses and other similar viruses: a short review. **1993**, 74 (Pt 8), 1475-83	29
1892	Fowlpox virus encodes a protein related to human deoxycytidine kinase: further evidence for independent acquisition of genes for enzymes of nucleotide metabolism by different viruses. **1993**, 7, 289-95	7

1891	Identification and partial sequence of the BchA gene of Rhodospirillum rubrum. **1993**, 27, 85-90	3
1890	An approach for building an integrated environment for molecular biology databases. **1993**, 1, 303-327	1
1889	Cell-to-cell movement of plant viruses. Insights from amino acid sequence comparisons of movement proteins and from analogies with cellular transport systems. **1993**, 133, 239-57	124
1888	Book reviews. **1993**, 10, 125-156	
1887	Compositional properties of coding sequences and mammalian phylogeny. **1993**, 37, 109-16	33
1886	Isolation of the cyclosporin-sensitive T cell transcription factor NFATp. **1993**, 262, 750-4	370
1885	Cloning of the human taurine transporter and characterization of taurine uptake in thyroid cells. **1993**, 318, 139-44	104
1884	Nucleotide sequence of cDNA encoding the fire ant venom protein Sol i II. **1993**, 319, 138-40	18
1883	Primary structure of the 5 S subunit of transcarboxylase as deduced from the genomic DNA sequence. **1993**, 330, 191-6	14
1882	A hybrid protein kinase-RNase in an interferon-induced pathway?. **1993**, 334, 149-52	43
1881	The 3' terminal region of a gene encoding a cysteine-rich surface protein in Giardia duodenalis. **1993**, 23, 785-92	3
1880	Molecular cloning of the branched-chain alpha-keto acid dehydrogenase kinase and the CoA-dependent methylmalonate semialdehyde dehydrogenase. **1993**, 33, 255-65	3
1879	Primary structure of Xenopus laevis S10, a ribosomal protein that cross-reacts with antibodies to immunoglobulin light chains. **1993**, 30, 387-94	
1878	Arabidopsis ethylene-response gene ETR1: similarity of product to two-component regulators. **1993**, 262, 539-44	1328
1877	Identification and regional localization of a human IMP dehydrogenase-like locus (IMPDHL1) at 16p13.13. **1993**, 18, 687-9	1
1876	A transducin-like gene maps to the autosomal dominant polycystic kidney disease gene region. **1993**, 18, 709-11	14
1875	RNase T shares conserved sequence motifs with DNA proofreading exonucleases. **1993**, 21, 2521-2	31
1874	Helicases: amino acid sequence comparisons and structure-function relationships. **1993**, 3, 419-429	962

1873	A common set of conserved motifs in a vast variety of putative nucleic acid-dependent ATPases including MCM proteins involved in the initiation of eukaryotic DNA replication. **1993**, 21, 2541-7	354
1872	A highly conserved sequence motif defining the family of MutT-related proteins from eubacteria, eukaryotes and viruses. **1993**, 21, 4847	93
1871	A human DNA segment encompassing leucine and methionine tRNA pseudogenes localized on chromosome 6. **1993**, 136, 157-66	2
1870	Efficient similarity search in sequence databases. **1993**, 69-84	759
1869	Specificity and promiscuity among naturally processed peptides bound to HLA-DR alleles. **1993**, 178, 27-47	821
1868	The orphan receptors NGFI-B and steroidogenic factor 1 establish monomer binding as a third paradigm of nuclear receptor-DNA interaction. **1993**, 13, 5794-804	361
1867	ZO-1, DlgA and PSD-95/SAP90: homologous proteins in tight, septate and synaptic cell junctions. **1993**, 44, 85-9	193
1866	A human putative lymphocyte G0/G1 switch gene homologous to a rodent gene encoding a zinc-binding potential transcription factor. **1993**, 12, 73-88	58
1865	The use of deficiencies to determine essential gene content in the let-56-unc-22 region of Caenorhabditis elegans. **1993**, 36, 1148-56	4
1864	An intron within the 16S ribosomal RNA gene of the archaeon Pyrobaculum aerophilum. **1993**, 90, 2547-50	68
1863	Identification of receptor tyrosine kinases in the embryonic chicken lens. **1993**, 12, 759-63	16
1862	cDNA sequence, gene structure, and cholinesterase-like domains of an esterase from Caenorhabditis elegans mapped to chromosome V. **1993**, 3, 347-56	4
1861	Site-directed mutagenesis of putative active-site amino acid residues of 3,2-trans-enoyl-CoA isomerase, conserved within the low-homology isomerase/hydratase enzyme family. **1993**, 32, 11405-12	42
1860	Novel zinc finger motif in the basal transcriptional machinery: three-dimensional NMR studies of the nucleic acid binding domain of transcriptional elongation factor TFIIS. **1993**, 32, 9944-59	115
1859	Isoabzymes: structurally and mechanistically similar catalytic antibodies from the same immunization. **1993**, 32, 12128-35	34
1858	Molecular cloning and expression of the catalytic subunit of bovine pyruvate dehydrogenase phosphatase and sequence similarity with protein phosphatase 2C. **1993**, 32, 8987-93	100
1857	Sequence similarity of phospholipase A2 activating protein and the G protein beta-subunits: a new concept of effector protein activation in signal transduction?. **1993**, 18, 292-3	32
1856	Cloning and characterization of a cDNA encoding chicken liver alpha-N-acetylgalactosaminidase. **1993**, 137, 309-14	14

1855	Sequence similarities between cell regulation factors, heat shock proteins and RNA helicases. **1993**, 18, 125-127	17
1854	Alternatively spliced isoforms of the NMDAR1 glutamate receptor subunit: differential expression in the basal ganglia of the rat. **1993**, 152, 161-4	54
1853	The Gene for a 74 kDa DNA Polymerase from the Archaeon Sulfolobus solfataricus. **1993**, 16, 665-671	8
1852	Epimorphin is related to a new class of neuronal and yeast vesicle targeting proteins. **1993**, 18, 124-5	26
1851	Nucleotide sequence of XhoI O fragment of ectromelia virus DNA reveals significant differences from vaccinia virus. **1993**, 30, 73-88	33
1850	Cloning of the Eh cdc2 gene from Entamoeba histolytica encoding a protein kinase p34cdc2 homologue. **1993**, 127, 203-7	58
1849	A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox is likely to encode the NADH ubiquinone oxidoreductase subunit B15. **1993**, 133, 233-5	1
1848	The rat trkC locus encodes multiple neurogenic receptors that exhibit differential response to neurotrophin-3 in PC12 cells. **1993**, 10, 975-90	276
1847	Neuromusculin, a Drosophila gene expressed in peripheral neuronal precursors and muscles, encodes a cell adhesion molecule. **1993**, 11, 673-87	40
1846	Collapsin: a protein in brain that induces the collapse and paralysis of neuronal growth cones. **1993**, 75, 217-27	993
1845	bottleneck acts as a regulator of the microfilament network governing cellularization of the Drosophila embryo. **1993**, 75, 373-85	76
1844	Independent domains of the Sdc-3 protein control sex determination and dosage compensation in C. elegans. **1993**, 72, 349-64	61
1843	The eyes absent gene: genetic control of cell survival and differentiation in the developing Drosophila eye. **1993**, 72, 379-95	512
1842	Identification of essential components of the S. cerevisiae kinetochore. **1993**, 73, 761-74	193
1841	Passover: a gene required for synaptic connectivity in the giant fiber system of Drosophila. **1993**, 73, 967-77	78
1840	Pseudomonas syringae pv. syringae harpinPss: a protein that is secreted via the Hrp pathway and elicits the hypersensitive response in plants. **1993**, 73, 1255-66	445
1839	A multisubunit complex associated with the RNA polymerase II CTD and TATA-binding protein in yeast. **1993**, 73, 1361-75	414
1838	Drosophila TAFII40 interacts with both a VP16 activation domain and the basal transcription factor TFIIB. **1993**, 75, 519-30	399

1837	Identification of human activin and TGF beta type I receptors that form heteromeric kinase complexes with type II receptors. **1993**, 75, 671-80	613
1836	Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates programmed cell death. **1993**, 74, 609-19	5361
1835	The human mutator gene homolog MSH2 and its association with hereditary nonpolyposis colon cancer. **1993**, 75, 1027-38	2386
1834	A Y chromosome gene family with RNA-binding protein homology: candidates for the azoospermia factor AZF controlling human spermatogenesis. **1993**, 75, 1287-95	446
1833	Dual roles of a multiprotein complex from S. cerevisiae in transcription and DNA repair. **1993**, 75, 1379-87	302
1832	The semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules. **1993**, 75, 1389-99	767
1831	Sonic hedgehog mediates the polarizing activity of the ZPA. **1993**, 75, 1401-16	1972
1830	Complementation cloning of an MHC class II transactivator mutated in hereditary MHC class II deficiency (or bare lymphocyte syndrome). **1993**, 75, 135-146	673
1829	Evolution and taxonomy of positive-strand RNA viruses: implications of comparative analysis of amino acid sequences. **1993**, 28, 375-430	801
1828	Cloning and characterization of alpha PS1, a novel Drosophila melanogaster integrin. **1993**, 43, 21-36	47
1827	Isolation and characterization of cDNA clones encoding the Drosophila homolog of the HMG-box SSRP family that recognizes specific DNA structures. **1993**, 21, 1643-6	40
1826	Identification and characterization of MPG1, a gene involved in pathogenicity from the rice blast fungus Magnaporthe grisea. **1993**, 5, 1575-90	701
1825	Map-based cloning of a protein kinase gene conferring disease resistance in tomato. **1993**, 262, 1432-6	1242
1824	H-2Dd exploits a four residue peptide binding motif. **1993**, 178, 1877-92	80
1823	SpoIIAB is an anti-sigma factor that binds to and inhibits transcription by regulatory protein sigma F from Bacillus subtilis. **1993**, 90, 2325-9	187
1822	The gene for C10, a member of the beta-chemokine family, is located on mouse chromosome 11 and contains a novel second exon not found in other chemokines. **1993**, 12, 839-47	21
1821	NAB2: a yeast nuclear polyadenylated RNA-binding protein essential for cell viability. **1993**, 13, 2730-41	164
1820	The third human homolog of a murine gene encoding an inhibitor of stem cell proliferation is truncated and linked to a CpG island-containing upstream sequence. **1993**, 12, 157-75	2

1819	Efficient loading of identical viral peptide onto class II molecules by antigenized immunoglobulin and influenza virus. **1993**, 178, 1795-9	45
1818	The developmentally-regulated Drosophila gene rox8 encodes an RRM-type RNA binding protein structurally related to human TIA-1-type nucleolysins. **1993**, 21, 3699-704	25
1817	The position end-set tree: a small automaton for word recognition in biological sequences. **1993**, 9, 343-8	1
1816	hnRNP G: sequence and characterization of a glycosylated RNA-binding protein. **1993**, 21, 4210-7	135
1815	Functional requirement of a site-specific ribose methylation in ribosomal RNA. **1993**, 262, 1886-9	119
1814	The signal recognition particle database (SRPDB). **1993**, 21, 3019-20	20
1813	Escherichia coli dinG gene encodes a putative DNA helicase related to a group of eukaryotic helicases including Rad3 protein. **1993**, 21, 1497	30
1812	The fission yeast prp4+ gene involved in pre-mRNA splicing codes for a predicted serine/threonine kinase and is essential for growth. **1993**, 21, 4079-83	48
1811	A human retinoic acid receptor gamma isoform is homologous to the murine retinoic acid receptor gamma 7. **1993**, 21, 2520	3
1810	Phosphatidylinositol 4-kinase: gene structure and requirement for yeast cell viability. **1993**, 262, 1444-8	192
1809	Genomic sequence of mitochondrial genes coding for ATPase subunit 6 and small subunit ribosomal RNA from Penicillium chrysogenum: a key for molecular systematics on fungi. **1993**, 21, 4393	2
1808	ADA3: a gene, identified by resistance to GAL4-VP16, with properties similar to and different from those of ADA2. **1993**, 13, 5981-9	113
1807	Isolation of a putative transcriptional regulator from the region of 22q11 deleted in DiGeorge syndrome, Shprintzen syndrome and familial congenital heart disease. **1993**, 2, 2099-107	129
1806	DNA-mediated transformation of bloodstream-form Trypanosoma brucei. **1993**, 21, 2537-8	61
1805	Stimulation of gene expression by introns: conversion of an inhibitory intron to a stimulatory intron by alteration of the splice donor sequence. **1993**, 21, 5901-8	32
1804	Bovine filensin possesses primary and secondary structure similarity to intermediate filament proteins. **1993**, 121, 847-53	83
1803	A special-purpose processor for gene sequence analysis. **1993**, 9, 221-6	6
1802	The development of sequence-tagged sites for human chromosome 4. **1993**, 2, 1271-88	49

1801	SpoU protein of Escherichia coli belongs to a new family of putative rRNA methylases. **1993**, 21, 5519	30
1800	Purification and cDNA cloning of HeLa cell p54nrb, a nuclear protein with two RNA recognition motifs and extensive homology to human splicing factor PSF and Drosophila NONA/BJ6. **1993**, 21, 4085-92	139
1799	The M.AluI DNA-(cytosine C5)-methyltransferase has an unusually large, partially dispensable, variable region. **1993**, 21, 905-11	19
1798	.	1
1797	Contamination of cDNA sequences in databases. **1993**, 259, 1677-8	19
1796	Identification and Characterization of MPG1, a Gene Involved in Pathogenicity from the Rice Blast Fungus Magnaporthe grisea. **1993**, 5, 1575	98
1795	.	8
1794	Strong conservation of non-coding sequences during vertebrates evolution: potential involvement in post-transcriptional regulation of gene expression. **1993**, 21, 2315-22	146
1793	Brief report: a single neoplastic clone in sequential biopsy specimens from a patient with primary gastric-mucosa-associated lymphoid-tissue lymphoma and Sj�gren’s syndrome. **1993**, 329, 172-5	67
1792	An expanding family of helicases within the ’DEAD/H’ superfamily. **1993**, 21, 751-2	120
1791	Classification of protein sequences by their dipeptide composition. **1993**, 9, 205-9	21
1790	A variant Tc4 transposable element in the nematode C. elegans could encode a novel protein. **1993**, 21, 59-67	20
1789	Approximate string-matching over suffix trees. **1993**, 228-242	60
1788	A quality control algorithm for DNA sequencing projects. **1993**, 21, 3829-38	29
1787	FASTPAT: a fast and efficient algorithm for string searching in DNA sequences. **1993**, 9, 541-5	
1786	A closely related group of RNA-dependent RNA polymerases from double-stranded RNA viruses. **1993**, 21, 5667-9	173
1785	Analysis of the RNA-recognition motif and RS and RGG domains: conservation in metazoan pre-mRNA splicing factors. **1993**, 21, 5803-16	610
1784	GenBank. **1993**, 21, 2963-5	236

1783	Designer algorithms for cryptogene searches. **1993**, 31, 269-273	
1782	Developmental regulation of a murine T-cell-specific tyrosine kinase gene, Tsk. **1993**, 90, 669-73	120
1781	The alpha and beta subunits of nematode actin capping protein function in yeast. **1993**, 4, 907-17	26
1780	Molecular cloning of a zinc finger protein which binds to the heptamer of the signal sequence for V(D)J recombination. **1993**, 21, 5067-73	43
1779	Identification and molecular characterization of E-MAP-115, a novel microtubule-associated protein predominantly expressed in epithelial cells. **1993**, 123, 357-71	96
1778	Cloning and functional characterization of early B-cell factor, a regulator of lymphocyte-specific gene expression. **1993**, 7, 760-73	216
1777	An Alu element retroposition in two families with Huntington disease defines a new active Alu subfamily. **1993**, 21, 3379-83	44
1776	Identification of human chromosome 9 specific genes using exon amplification. **1993**, 2, 1915-20	27
1775	The exon trapping assay partly discriminates against alternatively spliced exons. **1993**, 21, 2217-21	23
1774	The human hnRNP M proteins: identification of a methionine/arginine-rich repeat motif in ribonucleoproteins. **1993**, 21, 439-46	80
1773	Identification of a major soluble protein in mitochondria from nonphotosynthetic tissues as NAD-dependent formate dehydrogenase. **1993**, 102, 1171-7	109
1772	The three rows gene of Drosophila melanogaster encodes a novel protein that is required for chromosome disjunction during mitosis. **1993**, 4, 1161-74	34
1771	Isolation of the Rb-related p130 through its interaction with CDK2 and cyclins. **1993**, 7, 2378-91	389
1770	Dominant missense mutations in a novel yeast protein related to mammalian phosphatidylinositol 3-kinase and VPS34 abrogate rapamycin cytotoxicity. **1993**, 13, 6012-23	242
1769	Sequence-specific endonucleolytic cleavage and protection of mRNA in Xenopus and Drosophila. **1993**, 7, 1620-31	88
1768	Flightin, a novel myofibrillar protein of Drosophila stretch-activated muscles. **1993**, 121, 587-98	93
1767	Cloning and characterization of PSF, a novel pre-mRNA splicing factor. **1993**, 7, 393-406	292
1766	DNA sequence of the putA gene from Salmonella typhimurium: a bifunctional membrane-associated dehydrogenase that binds DNA. **1993**, 21, 1676	18

1765	Ancient conserved regions in new gene sequences and the protein databases. **1993**, 259, 1711-6	170
1764	Differential 3' polyadenylation of the Huntington disease gene results in two mRNA species with variable tissue expression. **1993**, 2, 1541-5	89
1763	Molecular analysis of the INCENPs (inner centromere proteins): separate domains are required for association with microtubules during interphase and with the central spindle during anaphase. **1993**, 123, 373-85	89
1762	Evolutionary relationships among group II intron-encoded proteins and identification of a conserved domain that may be related to maturase function. **1993**, 21, 4991-7	185
1761	Identification of a Candida utilis gene encoding ribosomal protein L7: evidence for two divergent subclasses of the eukaryotic ribosomal protein L7 family. **1993**, 21, 3577	2
1760	Streptomyces aureofaciens whiB gene encoding putative transcription factor essential for differentiation. **1993**, 21, 2512	12
1759	Profile sequence analysis and database searches on a transputer machine connected to a Macintosh computer. **1993**, 9, 25-8	
1758	SMC1: an essential yeast gene encoding a putative head-rod-tail protein is required for nuclear division and defines a new ubiquitous protein family. **1993**, 123, 1635-48	253
1757	Computer-assisted identification of a putative methyltransferase domain in NS5 protein of flaviviruses and lambda 2 protein of reovirus. **1993**, 74 (Pt 4), 733-40	193
1756	EMBLSearch: a CDROM based database query system. **1993**, 9, 71-77	
1755	A 127 kDa component of a UV-damaged DNA-binding complex, which is defective in some xeroderma pigmentosum group E patients, is homologous to a slime mold protein. **1993**, 21, 4111-8	97
1754	Structure and expression of the human trithorax-like gene 1 involved in acute leukemias. **1993**, 90, 4738-42	33
1753	MEF2C, a MADS/MEF2-family transcription factor expressed in a laminar distribution in cerebral cortex. **1993**, 90, 1546-50	185
1752	Genetic and biochemical analysis of an endonuclease encoded by the IncN plasmid pKM101. **1993**, 21, 4867-72	49
1751	Identification and characterization of a sphere organelle protein. **1993**, 122, 767-73	94
1750	Multiple antibiotic resistance in Pseudomonas aeruginosa: evidence for involvement of an efflux operon. **1993**, 175, 7363-72	565
1749	Cloning and characterization of subunit genes of ribonucleotide reductase, a cell-cycle-regulated enzyme, from Plasmodium falciparum. **1993**, 90, 12020-4	43
1748	A chromosomally encoded two-component sensory transduction system is required for virulence of Agrobacterium tumefaciens. **1993**, 175, 6614-25	156

1747	The cell-bound fructosyltransferase of Streptococcus salivarius: the carboxyl terminus specifies attachment in a Streptococcus gordonii model system. **1993**, 175, 4520-7	38
1746	A new cold-induced alfalfa gene is associated with enhanced hardening at subzero temperature. **1993**, 102, 873-9	167
1745	Characterization of the cobalamin (vitamin B12) biosynthetic genes of Salmonella typhimurium. **1993**, 175, 3303-16	231
1744	Cloning, sequence analysis, and hyperexpression of the genes encoding phosphotransacetylase and acetate kinase from Methanosarcina thermophila. **1993**, 175, 6822-9	74
1743	Cloning and DNA sequence of the gene coding for Clostridium thermocellum cellulase Ss (CelS), a major cellulosome component. **1993**, 175, 1293-302	97
1742	Nucleotide sequence of the adi gene, which encodes the biodegradative acid-induced arginine decarboxylase of Escherichia coli. **1993**, 175, 1221-34	76
1741	A cytotoxic early gene of Bacillus subtilis bacteriophage SPO1. **1993**, 175, 7887-900	23
1740	Characterization of the katG gene encoding a catalase-peroxidase required for the isoniazid susceptibility of Mycobacterium tuberculosis. **1993**, 175, 4255-9	184
1739	The opsX locus of Xanthomonas campestris affects host range and biosynthesis of lipopolysaccharide and extracellular polysaccharide. **1993**, 175, 5839-50	77
1738	A novel membrane-associated c-type cytochrome, cyt cy, can mediate the photosynthetic growth of Rhodobacter capsulatus and Rhodobacter sphaeroides.. **1993**, 12, 1283-1292	109
1737	An overview of computer software developed to search biological sequence databases. **1993**, 3, 243-52	
1736	PUB1 is a major nuclear and cytoplasmic polyadenylated RNA-binding protein in Saccharomyces cerevisiae. **1993**, 13, 6102-13	76
1735	Evidence that the SKI antiviral system of Saccharomyces cerevisiae acts by blocking expression of viral mRNA. **1993**, 13, 4331-41	101
1734	Gene in the region of the Friedreich ataxia locus encodes a putative transmembrane protein expressed in the nervous system. **1993**, 90, 109-13	72
1733	Applications and statistics for multiple high-scoring segments in molecular sequences. **1993**, 90, 5873-7	305
1732	Opsins from the lateral eyes and ocelli of the horseshoe crab, Limulus polyphemus. **1993**, 90, 6150-4	52
1731	The Arabidopsis endoplasmic reticulum retention receptor functions in yeast. **1993**, 90, 11433-7	102
1730	Gene sequence tags from Plasmodium falciparum genomic DNA fragments prepared by the "genease" activity of mung bean nuclease. **1993**, 90, 9867-71	38

1729	Phosducin-like protein: an ethanol-responsive potential modulator of guanine nucleotide-binding protein function. **1993**, 90, 10831-5	85
1728	Isolation of cDNAs for perilipins A and B: sequence and expression of lipid droplet-associated proteins of adipocytes. **1993**, 90, 12035-9	207
1727	Nuclear dot antigens may specify transcriptional domains in the nucleus. **1993**, 13, 6170-9	85
1726	AFR1 acts in conjunction with the alpha-factor receptor to promote morphogenesis and adaptation. **1993**, 13, 6876-88	38
1725	A U5 small nuclear ribonucleoprotein particle protein involved only in the second step of pre-mRNA splicing in Saccharomyces cerevisiae. **1993**, 13, 2959-70	65
1724	On the directional specificity of ribosome frameshifting at a "hungry" codon. **1993**, 90, 5469-73	53
1723	Analysis of a replication initiation sequence from the adenosine deaminase region of the mouse genome. **1993**, 13, 5931-42	44
1722	Hyperactive recombination in the mitochondrial DNA of the natural death nuclear mutant of Neurospora crassa. **1993**, 13, 6778-88	27
1721	Relatedness of an RNA-binding motif in human immunodeficiency virus type 1 TAR RNA-binding protein TRBP to human P1/dsI kinase and Drosophila staufen. **1993**, 13, 2193-202	128
1720	Cloning of the STE5 gene of Saccharomyces cerevisiae as a suppressor of the mating defect of cdc25 temperature-sensitive mutants. **1993**, 90, 5474-8	25
1719	Cloning, heterologous expression, and chromosomal localization of human inositol polyphosphate 1-phosphatase. **1993**, 90, 5833-7	17
1718	A Drosophila single-strand DNA/RNA-binding factor contains a high-mobility-group box and is enriched in the nucleolus. **1993**, 90, 6488-92	36
1717	Linking yeast genetics to mammalian genomes: identification and mapping of the human homolog of CDC27 via the expressed sequence tag (EST) data base. **1993**, 90, 10031-5	52
1716	IDENTIFICATION OF GENES IN GENOMIC AND EST SEQUENCES. **1993**,	
1715	Cloning of human erythroid dematin reveals another member of the villin family. **1993**, 90, 6651-5	63
1714	Identification of additional members of human G-protein-coupled receptor kinase multigene family. **1993**, 90, 9398-402	50
1713	RNA sequence of astrovirus: distinctive genomic organization and a putative retrovirus-like ribosomal frameshifting signal that directs the viral replicase synthesis. **1993**, 90, 10539-43	221
1712	The Escherichia coli hflA locus encodes a putative GTP-binding protein and two membrane proteins, one of which contains a protease-like domain. **1993**, 90, 10866-70	69

1711	Bradyrhizobium japonicum rhizobitoxine genes and putative enzyme functions: expression requires a translational frameshift. **1993**, 90, 2641-5	21
1710	Two novel transmembrane protein tyrosine kinases expressed during Caenorhabditis elegans hypodermal development. **1993**, 13, 7133-43	21
1709	Molecular cloning of a diverged homeobox gene that is rapidly down-regulated during the G0/G1 transition in vascular smooth muscle cells. **1993**, 13, 3722-33	122
1708	Genomic mapping with I-Ceu I, an intron-encoded endonuclease specific for genes for ribosomal RNA, in Salmonella spp., Escherichia coli, and other bacteria. **1993**, 90, 6874-8	319
1707	Cloning a plant amino acid transporter by functional complementation of a yeast amino acid transport mutant. **1993**, 90, 7441-5	120
1706	Downregulation of Ke 6, a novel gene encoded within the major histocompatibility complex, in murine polycystic kidney disease. **1993**, 13, 1847-53	37
1705	Cloning and characterization of subunits of the T-cell receptor and murine leukemia virus enhancer core-binding factor. **1993**, 13, 3324-39	416
1704	Isolation of STD1, a high-copy-number suppressor of a dominant negative mutation in the yeast TATA-binding protein. **1993**, 13, 3650-9	19
1703	Structures of genes nasA and nasB, encoding assimilatory nitrate and nitrite reductases in Klebsiella pneumoniae M5al. **1993**, 175, 2370-8	68
1702	Characterization of NGG1, a novel yeast gene required for glucose repression of GAL4p-regulated transcription.. **1993**, 12, 5255-5265	45
1701	Guanosine diphosphatase is required for protein and sphingolipid glycosylation in the Golgi lumen of Saccharomyces cerevisiae. **1993**, 122, 307-23	166
1700	A ubiquitin carrier protein cDNA from developing alfalfa embryos. **1993**, 102, 1049-50	2
1699	eps15, a novel tyrosine kinase substrate, exhibits transforming activity. **1993**, 13, 5814-28	250
1698	Developmental regulation of the gene for formate dehydrogenase in Neurospora crassa. **1993**, 175, 3703-9	30
1697	Anabaena sp. strain PCC 7120 bifA gene encoding a sequence-specific DNA-binding protein cloned by in vivo transcriptional interference selection. **1993**, 175, 4025-35	79
1696	Molecular cloning and expression of hctB encoding a strain-variant chlamydial histone-like protein with DNA-binding activity. **1993**, 175, 4274-81	65
1695	Purification and characterization of maleylacetate reductase from Alcaligenes eutrophus JMP134(pJP4). **1993**, 175, 6745-54	54
1694	Heat shock and development induce synthesis of a low-molecular-weight stress-responsive protein in the myxobacterium Stigmatella aurantiaca. **1993**, 175, 7479-82	32

1693	Location of IS200 on the genomic cleavage map of Salmonella typhimurium LT2. **1993**, 175, 7624-8	12
1692	Cloning, sequencing, expression, and complementation analysis of the Escherichia coli K1 kps region 1 gene, kpsE, and identification of an upstream open reading frame encoding a protein with homology to GutQ. **1993**, 175, 8018-23	19
1691	Characterization of intergenic spacers in two rrn operons of Enterococcus hirae ATCC 9790. **1993**, 175, 3213-9	32
1690	Characterization of a membrane-associated ATPase from Methanococcus voltae, a methanogenic member of the Archaea. **1993**, 175, 5677-82	23
1689	Identification of a purC gene from Streptococcus pneumoniae. **1993**, 175, 6364-7	7
1688	Autogenous transcriptional activation of a thiostrepton-induced gene in Streptomyces lividans.. **1993**, 12, 3183-3191	105
1687	The proposed plant connexin is a protein kinase-like protein. **1993**, 5, 998-9	23
1686	Component A2 of methylcoenzyme M reductase system from Methanobacterium thermoautotrophicum delta H: nucleotide sequence and functional expression by Escherichia coli. **1993**, 175, 3195-203	16
1685	Escherichia coli mutants lacking NADH dehydrogenase I have a competitive disadvantage in stationary phase. **1993**, 175, 5642-7	74
1684	The cbb operons of the facultative chemoautotroph Alcaligenes eutrophus encode phosphoglycolate phosphatase. **1993**, 175, 7329-40	54
1683	Transcriptional analysis of the Aeromonas salmonicida S-layer protein gene vapA. **1993**, 175, 7968-75	24
1682	The glnB region of the Escherichia coli chromosome. **1993**, 175, 7441-9	28
1681	The Rhizobium meliloti rhizopine mos locus is a mosaic structure facilitating its symbiotic regulation. **1993**, 175, 5193-204	48
1680	Yeast G1 cyclins CLN1 and CLN2 and a GAP-like protein have a role in bud formation.. **1993**, 12, 5277-5286	125
1679	Identification of genes encoding components of the swarmer cell flagellar motor and propeller and a sigma factor controlling differentiation of Vibrio parahaemolyticus. **1993**, 175, 3361-71	62
1678	Spontaneous pmrA mutants of Salmonella typhimurium LT2 define a new two-component regulatory system with a possible role in virulence. **1993**, 175, 4154-64	145
1677	SKN7, a yeast multicopy suppressor of a mutation affecting cell wall beta-glucan assembly, encodes a product with domains homologous to prokaryotic two-component regulators and to heat shock transcription factors. **1993**, 175, 6908-15	147
1676	Characterization of a guanine nucleotide dissociation stimulator for a ras-related GTPase.. **1993**, 12, 339-347	134

1675	A cDNA for Arabidopsis cytosol ribosomal protein S11. **1993**, 102, 695-6	8
1674	Rhs elements of Escherichia coli K-12: complex composites of shared and unique components that have different evolutionary histories. **1993**, 175, 2799-808	67
1673	A dominant negative mutant of 2-5A-dependent RNase suppresses antiproliferative and antiviral effects of interferon.. **1993**, 12, 3297-3304	212
1672	An Aeromonas salmonicida gene which influences a-protein expression in Escherichia coli encodes a protein containing an ATP-binding cassette and maps beside the surface array protein gene. **1993**, 175, 3105-14	24
1671	Characterization of genetic elements required for site-specific integration of the temperate lactococcal bacteriophage phi LC3 and construction of integration-negative phi LC3 mutants. **1993**, 175, 1745-55	76
1670	Functional conservation of vertebrate seven-up related genes in neurogenesis and eye development.. **1993**, 12, 1403-1414	57
1669	Complete nucleotide sequence of a circular plasmid from the Lyme disease spirochete, Borrelia burgdorferi. **1994**, 176, 2706-17	51
1668	Gene expression during phorbol ester-induced differentiation of cultured human megakaryoblastic cells. **1994**, 266, C1231-9	15
1667	Subunits of the Saccharomyces cerevisiae signal recognition particle required for its functional expression.. **1994**, 13, 4390-4400	76
1666	Identification of a high affinity NH4+ transporter from plants.. **1994**, 13, 3464-3471	288
1665	PIK1, an essential phosphatidylinositol 4-kinase associated with the yeast nucleus.. **1994**, 13, 2352-2361	91
1664	Mucoid-to-nonmucoid conversion in alginate-producing Pseudomonas aeruginosa often results from spontaneous mutations in algT, encoding a putative alternate sigma factor, and shows evidence for autoregulation. **1994**, 176, 6677-87	174
1663	PopA1, a protein which induces a hypersensitivity-like response on specific Petunia genotypes, is secreted via the Hrp pathway of Pseudomonas solanacearum.. **1994**, 13, 543-553	187
1662	Characterization of the rfc region of Shigella flexneri. **1994**, 176, 733-47	132
1661	Algal-CAMs: isoforms of a cell adhesion molecule in embryos of the alga Volvox with homology to Drosophila fasciclin I.. **1994**, 13, 4212-4222	104
1660	A family of proteins containing a conserved domain that mediates interaction with the yeast SNF1 protein kinase complex.. **1994**, 13, 5878-5886	99
1659	Sequencing, chromosomal inactivation, and functional expression in Escherichia coli of ppsR, a gene which represses carotenoid and bacteriochlorophyll synthesis in Rhodobacter sphaeroides. **1994**, 176, 2869-76	111
1658	The inhibitor of DNA replication encoded by the Drosophila gene plutonium is a small, ankyrin repeat protein.. **1994**, 13, 462-470	36

1657	Yeast chromosome III: new gene functions.. **1994**, 13, 493-503	74
1656	Stch encodes the ATPase core of a microsomal stress 70 protein.. **1994**, 13, 1216-1225	42
1655	MotY, a component of the sodium-type flagellar motor. **1994**, 176, 4219-25	90
1654	Molecular analysis of the rfb gene cluster of a group D2 Salmonella enterica strain: evidence for its origin from an insertion sequence-mediated recombination event between group E and D1 strains. **1994**, 176, 4357-65	87
1653	Membrane topology of Escherichia coli diacylglycerol kinase. **1994**, 176, 5459-65	60
1652	BglR protein, which belongs to the BglG family of transcriptional antiterminators, is involved in beta-glucoside utilization in Lactococcus lactis. **1994**, 176, 5681-5	61
1651	MotX, the channel component of the sodium-type flagellar motor. **1994**, 176, 5988-98	85
1650	Molecular cloning and characterization of outer membrane protein E of Moraxella (Branhamella) catarrhalis. **1994**, 176, 6636-43	30
1649	Excision of a P4-like cryptic prophage leads to Alp protease expression in Escherichia coli. **1994**, 176, 2068-81	100
1648	Analysis of duplicated gene sequences associated with tfdR and tfdS in Alcaligenes eutrophus JMP134. **1994**, 176, 2348-53	62
1647	A cryptic miniplasmid from the hyperthermophilic bacterium Thermotoga sp. strain RQ7. **1994**, 176, 2759-62	33
1646	A Sec62p-related component of the secretory protein translocon from Drosophila displays developmentally complex behavior.. **1994**, 13, 5253-5261	22
1645	RAD26, the functional S. cerevisiae homolog of the Cockayne syndrome B gene ERCC6.. **1994**, 13, 5361-5369	172
1644	Characterization and expression of transcripts induced by oxygen deprivation in maize (Zea mays L.). **1994**, 104, 387-94	40
1643	Tn5401, a new class II transposable element from Bacillus thuringiensis. **1994**, 176, 2835-45	56
1642	A peroxide/ascorbate-inducible catalase from Haemophilus influenzae is homologous to the Escherichia coli katE gene product. **1994**, 176, 2914-21	47
1641	Identification and structure of the nasR gene encoding a nitrate- and nitrite-responsive positive regulator of nasFEDCBA (nitrate assimilation) operon expression in Klebsiella pneumoniae M5al. **1994**, 176, 5077-85	35
1640	Identification of a novel gene, aut, involved in autotrophic growth of Alcaligenes eutrophus. **1994**, 176, 5401-8	8

1639	Functional similarity and physical association between GCN5 and ADA2: putative transcriptional adaptors.. **1994**, 13, 4807-4815	203
1638	Cloning and nucleotide sequence of the cyclic AMP receptor protein-regulated Salmonella typhimurium pepE gene and crystallization of its product, an alpha-aspartyl dipeptidase. **1994**, 176, 166-72	25
1637	Identification of flagellar synthesis regulatory and structural genes in a sigma D-dependent operon of Bacillus subtilis. **1994**, 176, 4492-500	57
1636	Conduction of pEC22, a plasmid coding for MR.EcoT22I, mediated by a resident Tn3-like transposon, Tn5396. **1994**, 176, 5059-67	16
1635	The mannitol repressor (MtlR) of Escherichia coli. **1994**, 176, 840-7	24
1634	Cloning, characterization, and nucleotide sequence analysis of the argH gene from Campylobacter jejuni TGH9011 encoding argininosuccinate lyase. **1994**, 176, 1865-71	9
1633	Functions involved in bacteriophage P2-induced host cell lysis and identification of a new tail gene. **1994**, 176, 4974-84	45
1632	FptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate siderophore receptor homologous to hydroxamate siderophore receptors. **1994**, 176, 307-19	116
1631	Complete DNA sequence of yeast chromosome II.. **1994**, 13, 5795-5809	172
1630	Cloning and expression of the MEP1 gene encoding an ammonium transporter in Saccharomyces cerevisiae.. **1994**, 13, 3456-3463	216
1629	Metabotropic glutamate receptor mRNA expression in the basal ganglia of the rat. **1994**, 14, 3005-18	473
1628	Analysis of a Het- mutation in Anabaena sp. strain PCC 7120 implicates a secondary metabolite in the regulation of heterocyst spacing. **1994**, 176, 2282-92	151
1627	NUP145 encodes a novel yeast glycine-leucine-phenylalanine-glycine (GLFG) nucleoporin required for nuclear envelope structure. **1994**, 125, 955-69	125
1626	Isolation and characterization of a gene, pmrD, from Salmonella typhimurium that confers resistance to polymyxin when expressed in multiple copies. **1994**, 176, 3589-97	41
1625	ACT3: a putative centractin homologue in S. cerevisiae is required for proper orientation of the mitotic spindle. **1994**, 127, 129-38	104
1624	Cloning, nucleotide sequence, mutagenesis, and mapping of the Bacillus subtilis pbpD gene, which codes for penicillin-binding protein 4. **1994**, 176, 7197-205	36
1623	Self-splicing group I intron in cyanobacterial initiator methionine tRNA: evidence for lateral transfer of introns in bacteria.. **1994**, 13, 4629-4635	50
1622	Subcellular relocalization of a long-chain fatty acid CoA ligase by a suppressor mutation alleviates a respiration deficiency in Saccharomyces cerevisiae.. **1994**, 13, 5531-5538	33

1621	The reductive acetyl coenzyme A pathway: sequence and heterologous expression of active methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase from Clostridium thermoaceticum. **1994**, 176, 6127-30	54
1620	The gene coding for polynucleotide phosphorylase in Photorhabdus sp. strain K122 is induced at low temperatures. **1994**, 176, 3775-84	31
1619	Heterologous expression of the bchM gene product from Rhodobacter capsulatus and demonstration that it encodes S-adenosyl-L-methionine:Mg-protoporphyrin IX methyltransferase. **1994**, 176, 5290-6	65
1618	Purification and cloning of a nucleotide excision repair complex involving the xeroderma pigmentosum group C protein and a human homologue of yeast RAD23.. **1994**, 13, 1831-1843	268
1617	The DNA polymerase gene from the methanogenic archaeon Methanococcus voltae. **1994**, 176, 6402-3	3
1616	A plasmid from the methylotrophic actinomycete Amycolatopsis methanolica capable of site-specific integration. **1994**, 176, 7087-90	36
1615	Physical characterization of the flagella and flagellins from Methanospirillum hungatei. **1994**, 176, 7491-8	18
1614	The virR gene, a member of a class of two-component response regulators, regulates the production of perfringolysin O, collagenase, and hemagglutinin in Clostridium perfringens. **1994**, 176, 1616-23	126
1613	Genetic characterization of polypeptide deformylase, a distinctive enzyme of eubacterial translation.. **1994**, 13, 914-923	194
1612	ESI3, a stress-induced gene from Lophopyrum elongatum. **1994**, 104, 799-800	36
1611	Domain structure of the Acetogenium kivui surface layer revealed by electron crystallography and sequence analysis. **1994**, 176, 1224-33	211
1610	In Situ Hybridization for Ribosomal RNA Sequences: A Rapid Sensitive Method for Diagnosis of Infectious Pathogens in Anatomic Pathology Substrates.. **1994**, 27, 601-606	23
1609	The Drosophila sex determination gene snf encodes a nuclear protein with sequence and functional similarity to the mammalian U1A snRNP protein. **1994**, 8, 914-25	81
1608	Arabidopsis TCH3 encodes a novel Ca2+ binding protein and shows environmentally induced and tissue-specific regulation. **1994**, 6, 1553-65	105
1607	The DNA polymerase genes of several HMU-bacteriophages have similar group I introns with highly divergent open reading frames. **1994**, 22, 3715-21	45
1606	NRSub: a non-redundant data base for the Bacillus subtilis genome. **1994**, 22, 5525-9	25
1605	A sequence compilation and comparison of exons that are alternatively spliced in neurons. **1994**, 22, 1515-26	91
1604	Disruptions in Golgi structure and membrane traffic in a conditional lethal mammalian cell mutant are corrected by epsilon-COP. **1994**, 125, 1213-24	139

1603	Neogenin, an avian cell surface protein expressed during terminal neuronal differentiation, is closely related to the human tumor suppressor molecule deleted in colorectal cancer. **1994**, 127, 2009-20	134
1602	The POZ domain: a conserved protein-protein interaction motif. **1994**, 8, 1664-77	614
1601	Insect iridescent virus type 6 encodes a polypeptide related to the largest subunit of eukaryotic RNA polymerase II. **1994**, 75 (Pt 7), 1557-67	24
1600	ScII: an abundant chromosome scaffold protein is a member of a family of putative ATPases with an unusual predicted tertiary structure. **1994**, 127, 303-18	235
1599	The Caenorhabditis elegans muscle-affecting gene unc-87 encodes a novel thin filament-associated protein. **1994**, 127, 79-93	56
1598	Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII. **1994**, 265, 2077-82	266
1597	LISTA, LISTA-HOP and LISTA-HON: a comprehensive compilation of protein encoding sequences and its associated homology databases from the yeast Saccharomyces. **1994**, 22, 3459-61	4
1596	Screening of the closterovirus genome by degenerate primer-mediated polymerase chain reaction. **1994**, 75 (Pt 6), 1415-22	33
1595	NAP57, a mammalian nucleolar protein with a putative homolog in yeast and bacteria. **1994**, 127, 1505-14	225
1594	SRD1, a S. cerevisiae gene affecting pre-rRNA processing contains a C2/C2 zinc finger motif. **1994**, 22, 1265-71	17
1593	Cloning of mid-G1 serum response genes and identification of a subset regulated by conditional myc expression. **1994**, 5, 375-88	51
1592	Computer Analysis of Sequence Data. **1994**,	0
1591	CRAC, a cytosolic protein containing a pleckstrin homology domain, is required for receptor and G protein-mediated activation of adenylyl cyclase in Dictyostelium. **1994**, 126, 1537-45	151
1590	Eukaryotic RNAse H shares a conserved domain with caulimovirus proteins that facilitate translation of polycistronic RNA. **1994**, 22, 4163-6	17
1589	Characterization of the yeast (1-->6)-beta-glucan biosynthetic components, Kre6p and Skn1p, and genetic interactions between the PKC1 pathway and extracellular matrix assembly. **1994**, 127, 567-79	132
1588	Can SINEs: a family of tRNA-derived retroposons specific to the superfamily Canoidea. **1994**, 22, 2726-30	51
1587	A putative regulatory gene downstream of recA is conserved in gram-negative and gram-positive bacteria. **1994**, 22, 1313-4	41
1586	A FUSCA gene of Arabidopsis encodes a novel protein essential for plant development. **1994**, 6, 25-41	188

1585	Bidirectional promoter of the mouse thymidylate synthase gene. **1994**, 22, 4044-9	28
1584	Expression of cone transducin, Gz alpha, and other G-protein alpha-subunit messenger ribonucleic acids in pancreatic islets. **1994**, 135, 31-7	39
1583	A FUSCA Gene of Arabidopsis Encodes a Novel Protein Essential for Plant Development. **1994**, 6, 25	8
1582	The gene encoding a major component of the lateral elements of synaptonemal complexes of the rat is related to X-linked lymphocyte-regulated genes. **1994**, 14, 1137-46	324
1581	En bloc incorporation of coatomer subunits during the assembly of COP-coated vesicles. **1994**, 124, 883-92	124
1580	Control of Arabidopsis Flower and Seed Development by the Homeotic Gene APETALA2. **1994**, 6, 1211	13
1579	Stowaway: A New Family of Inverted Repeat Elements Associated with the Genes of Both Monocotyledonous and Dicotyledonous Plants. **1994**, 6, 907	1
1578	Isoforms of apolipoprotein A-I in the serum of brown bullheads (Ameiurus nebulosus) with liver cancer. **1994**, 72, 1522-1527	6
1577	Control of Arabidopsis flower and seed development by the homeotic gene APETALA2. **1994**, 6, 1211-25	909
1576	Arabidopsis ABA response gene ABI1: features of a calcium-modulated protein phosphatase. **1994**, 264, 1448-52	725
1575	Characterization of a repetitive element detected by NheI in the genomes of Salmo species. **1994**, 37, 639-45	8
1574	Cloning and characterization of pig muscle cDNAs by an expressed sequence tag approach. **1994**, 5, 1-13	9
1573	The RNA of RNase MRP is required for normal processing of ribosomal RNA. **1994**, 91, 659-63	196
1572	The relative expression of human histone H2A genes is similar in different types of proliferating cells. **1994**, 13, 161-70	10
1571	Anabaena xisF gene encodes a developmentally regulated site-specific recombinase. **1994**, 8, 74-83	63
1570	The translation initiation factor eIF-4B contains an RNA-binding region that is distinct and independent from its ribonucleoprotein consensus sequence. **1994**, 14, 2307-16	108
1569	A novel FK506- and rapamycin-binding protein (FPR3 gene product) in the yeast Saccharomyces cerevisiae is a proline rotamase localized to the nucleolus. **1994**, 127, 623-39	74
1568	A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common "D35E" motif. **1994**, 91, 942-6	306

1567	Mobile inverted-repeat elements of the Tourist family are associated with the genes of many cereal grasses. **1994**, 91, 1411-5	199
1566	Cytoplasmic dynein and actin-related protein Arp1 are required for normal nuclear distribution in filamentous fungi. **1994**, 127, 139-149	270
1565	Cloning and characterization of a new human Xq13 gene, encoding a putative helicase. **1994**, 3, 1957-64	49
1564	Ponticulin is an atypical membrane protein. **1994**, 126, 1421-31	46
1563	STU1, a suppressor of a beta-tubulin mutation, encodes a novel and essential component of the yeast mitotic spindle. **1994**, 127, 1973-84	64
1562	Identification and characterization of Drosophila relatives of the yeast transcriptional activator SNF2/SWI2. **1994**, 14, 2225-34	166
1561	Vma21p is a yeast membrane protein retained in the endoplasmic reticulum by a di-lysine motif and is required for the assembly of the vacuolar H(+)-ATPase complex. **1994**, 5, 1039-50	108
1560	Localization of an alpha 1,2 galactosyltransferase activity to the Golgi apparatus of Schizosaccharomyces pombe. **1994**, 5, 519-28	57
1559	Stowaway: a new family of inverted repeat elements associated with the genes of both monocotyledonous and dicotyledonous plants. **1994**, 6, 907-16	307
1558	LDLC encodes a brefeldin A-sensitive, peripheral Golgi protein required for normal Golgi function. **1994**, 127, 679-91	60
1557	A new kinesin-like protein (Klp1) localized to a single microtubule of the Chlamydomonas flagellum. **1994**, 125, 1313-26	97
1556	Navigating the Brookhaven Protein Data Bank. **1994**, 10, 551-7	
1555	Gnome--an Internet-based sequence analysis tool. **1994**, 10, 547-50	1
1554	The signal recognition particle database (SRPDB). **1994**, 22, 3483-4	19
1553	Association of intestinal peptide transport with a protein related to the cadherin superfamily. **1994**, 264, 430-3	172
1552	Evidence for a group II intron in Escherichia coli inserted into a highly conserved reading frame associated with mobile DNA sequences. **1994**, 22, 1167-71	35
1551	Isolation and characterization of a Saccharomyces cerevisiae peptide transport gene. **1994**, 14, 104-15	125
1550	The hnRNP F protein: unique primary structure, nucleic acid-binding properties, and subcellular localization. **1994**, 22, 1059-67	125

1549	Identification of a novel family of human endogenous retroviruses and characterization of one family member, HERV-K(C4), located in the complement C4 gene cluster. **1994**, 22, 5211-7	52
1548	Characterization of the PNT1 pentamidine resistance gene of Saccharomyces cerevisiae. **1994**, 38, 2850-6	15
1547	Prediction of an rRNA methyltransferase domain in human tumor-specific nucleolar protein P120. **1994**, 22, 2476-8	33
1546	SWAP pre-mRNA splicing regulators are a novel, ancient protein family sharing a highly conserved sequence motif with the prp21 family of constitutive splicing proteins. **1994**, 22, 4510-9	24
1545	A simple tool to search for sequence motifs that are conserved in BLAST outputs. **1994**, 10, 457-9	9
1544	HOVERGEN: a database of homologous vertebrate genes. **1994**, 22, 2360-5	199
1543	Identification of a mariner-like repetitive sequence in C. elegans. **1994**, 22, 1719-23	38
1542	Tandemly repeated pentanucleotides in DNA sequences of eucaryotes. **1994**, 22, 3412-7	13
1541	Back-propagation and counter-propagation neural networks for phylogenetic classification of ribosomal RNA sequences. **1994**, 22, 4291-9	39
1540	DsaV methyltransferase and its isoschizomers contain a conserved segment that is similar to the segment in Hhai methyltransferase that is in contact with DNA bases. **1994**, 22, 4482-8	10
1539	CD and DNA binding studies of a proline repeat-containing segment of the replication arrest protein Tus. **1994**, 22, 5024-30	10
1538	Human natural resistance-associated macrophage protein: cDNA cloning, chromosomal mapping, genomic organization, and tissue-specific expression. **1994**, 180, 1741-52	219
1537	A distributed system for DNA/protein database similarity searches. **1994**, 10, 277-80	
1536	A novel transmembrane transporter encoded by the XPCT gene in Xq13.2. **1994**, 3, 1133-9	99
1535	Hierarchical Access System for Sequence Libraries in Europe (HASSLE): a tool to access sequence databases remotely. **1994**, 10, 31-4	1
1534	Fast subsequence matching in time-series databases. **1994**, 23, 419-429	426
1533	GRSF-1: a poly(A)+ mRNA binding protein which interacts with a conserved G-rich element. **1994**, 22, 2334-43	47
1532	Lymphotactin: a cytokine that represents a new class of chemokine. **1994**, 266, 1395-9	568

1531	The unusually long small subunit ribosomal RNA of Phreatamoeba balamuthi. **1994**, 22, 465-9	63
1530	Characterization of serine proteinase inhibitors in dry seeds of cultivated pasture grass species. **1994**, 4, 335-345	2
1529	LagC is required for cell-cell interactions that are essential for cell-type differentiation in Dictyostelium. **1994**, 8, 948-58	121
1528	The Arabidopsis GA1 locus encodes the cyclase ent-kaurene synthetase A of gibberellin biosynthesis. **1994**, 6, 1509-18	470
1527	Characterization of the KLP68D kinesin-like protein in Drosophila: possible roles in axonal transport. **1994**, 127, 1041-8	60
1526	Induction of pseudohyphal growth by overexpression of PHD1, a Saccharomyces cerevisiae gene related to transcriptional regulators of fungal development. **1994**, 14, 2100-12	249
1525	Discovery of group I introns in the nuclear small subunit ribosomal RNA genes of Acanthamoeba. **1994**, 22, 592-6	49
1524	Two classes of homeodomain proteins specify the multiple a mating types of the mushroom Coprinus cinereus. **1994**, 6, 1467-75	65
1523	Dorsal midline fate in Drosophila embryos requires twisted gastrulation, a gene encoding a secreted protein related to human connective tissue growth factor. **1994**, 8, 1489-501	117
1522	Saccharomyces cerevisiae contains four fatty acid activation (FAA) genes: an assessment of their role in regulating protein N-myristoylation and cellular lipid metabolism. **1994**, 127, 751-62	147
1521	Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones. **1994**, 106, 1241-55	606
1520	Differential localization and sequence analysis of capping protein beta-subunit isoforms of vertebrates. **1994**, 127, 453-65	126
1519	Human CENP-A contains a histone H3 related histone fold domain that is required for targeting to the centromere. **1994**, 127, 581-92	363
1518	Extreme evolutionary conservation of QM, a novel c-Jun associated transcription factor. **1994**, 3, 723-8	47
1517	SMS1, a high-copy suppressor of the yeast mas6 mutant, encodes an essential inner membrane protein required for mitochondrial protein import. **1994**, 5, 529-38	88
1516	Sequence similarity of putative transposases links the maize Mutator autonomous element and a group of bacterial insertion sequences. **1994**, 22, 2634-6	95
1515	Identification of the erythrocyte binding domains of Plasmodium vivax and Plasmodium knowlesi proteins involved in erythrocyte invasion. **1994**, 180, 497-506	327
1514	Nuclear mRNA accumulation causes nucleolar fragmentation in yeast mtr2 mutant. **1994**, 5, 1253-63	67

1513	Molecular cloning and characterization of a brassinosteroid-regulated gene from elongating soybean (Glycine max L.) epicotyls. **1994**, 104, 161-70	193
1512	Cloning and Characterization of Two Members of the Pto Gene Family: the Pto Bacterial Resistance Gene and the Fen Insecticide Sensitivity Gene.. **1994**, 273-282	
1511	The yeast homolog of H 58, a mouse gene essential for embryogenesis, performs a role in the delivery of proteins to the vacuole. **1994**, 8, 1379-87	23
1510	Identification of genes encoding zinc finger proteins, non-histone chromosomal HMG protein homologue, and a putative GTP phosphohydrolase in the genome of Chilo iridescent virus. **1994**, 22, 158-66	18
1509	Cloning by synteny: identifying C. briggsae homologues of C. elegans genes. **1994**, 22, 4414-8	58
1508	Cloning and molecular characterization of a novel chromosome specific centromere sequence of Chinese hamster. **1994**, 22, 3728-36	15
1507	Characterization of nuclear polyadenylated RNA-binding proteins in Saccharomyces cerevisiae. **1994**, 127, 1173-84	117
1506	Subtraction hybridisation and shot-gun sequencing: a new approach to identify symbiotic loci. **1994**, 22, 1335-41	42
1505	The lin-15 locus encodes two negative regulators of Caenorhabditis elegans vulval development. **1994**, 5, 395-411	201
1504	Control of leaf and chloroplast development by the Arabidopsis gene pale cress. **1994**, 6, 1253-64	101
1503	Construction of an equalized cDNA library from human brain by semi-solid self-hybridization system. **1994**, 1, 91-6	3
1502	Molecular cloning of the small (gamma) subunit of human TFIIA reveals functions critical for activated transcription. **1994**, 8, 2324-35	138
1501	The E subunit of vacuolar H(+)-ATPase localizes close to the centromere on human chromosome 22. **1994**, 3, 335-9	17
1500	The Drosophila segment polarity gene dishevelled encodes a novel protein required for response to the wingless signal. **1994**, 8, 118-30	327
1499	Dosage-dependent modulation of glucose repression by MSN3 (STD1) in Saccharomyces cerevisiae. **1994**, 14, 1972-8	45
1498	Using the FASTA program to search protein and DNA sequence databases. **1994**, 24, 307-31	115
1497	Combined use of sequence similarity and codon bias for coding region identification. **1994**, 1, 39-50	81
1496	Computer Analysis of Sequence Data. **1994**,	2

1495	Codon usage in Caenorhabditis elegans: delineation of translational selection and mutational biases. **1994**, 22, 2437-46	242
1494	An Arabidopsis Peptide Transporter Is a Member of a New Class of Membrane Transport Proteins. **1994**, 6, 1289	11
1493	Arabidopsis TCH3 Encodes a Novel Ca 2+ Binding Protein and Shows Environmentally Induced and Tissue-Specific Regulation. **1994**, 6, 1553	52
1492	Knowledge-based protein modeling. **1994**, 29, 1-68	174
1491	Molecular cloning of a chick cochlea cDNA encoding a subunit of DNA replication factor C/activator 1. **1994**, 13, 857-63	9
1490	Interaction of a protein phosphatase with an Arabidopsis serine-threonine receptor kinase. **1994**, 266, 793-5	265
1489	Proximity matching using fixed-queries trees. **1994**, 198-212	63
1488	Purification and initial characterization of a potential plant vacuolar targeting receptor. **1994**, 91, 3403-7	220
1487	A hidden Markov model that finds genes in E. coli DNA. **1994**, 22, 4768-78	219
1486	RFLP mapping of partially sequenced leaf cDNA clones in maize. **1994**, 88, 717-21	32
1485	Nucleotide sequence of the 3' terminal region of the RNA of two filamentous grapevine viruses. **1994**, 137, 249-61	44
1484	Analysis of the population structure of three phenotypically different PSTVd isolates. **1994**, 138, 233-45	34
1483	Chilo iridescent virus encodes a putative helicase belonging to a distinct family within the "DEAD/H" superfamily: implications for the evolution of large DNA viruses. **1994**, 8, 151-8	19
1482	The DNA rearrangement associated with facioscapulohumeral muscular dystrophy involves a heterochromatin-associated repetitive element: implications for a role of chromatin structure in the pathogenesis of the disease. **1994**, 2, 225-34	127
1481	Intracellular aminopeptidases in Streptomyces lividans 66. **1994**, 13, 24-9	14
1480	Antisense inhibition of low-affinity nerve growth factor receptor in kidney cultures: power and pitfalls. **1994**, 14, 439-57	15
1479	The application of antisense oligonucleotide technology to the brain: some pitfalls. **1994**, 14, 507-21	86
1478	Functional assignment of Erwinia herbicola Eho10 carotenoid genes expressed in Escherichia coli. **1994**, 245, 406-16	68

1477	Alternative splicing of the mouse amelogenin primary RNA transcript. **1994**, 55, 302-10	89
1476	An analysis of the sequence of part of the right arm of chromosome II of S. cerevisiae reveals new genes encoding an amino-acid permease and a carboxypeptidase. **1994**, 26, 1-7	8
1475	Similarity between putative ATP-binding sites in land plant plastid ORF2280 proteins and the FtsH/CDC48 family of ATPases. **1994**, 25, 379-83	29
1474	Analysis of cDNA sequences from mouse testis. **1994**, 5, 557-65	22
1473	Sequence analysis of a radiation-induced deletion breakpoint fusion in mouse. **1994**, 5, 518-9	2
1472	Evolution of the proteinase inhibitor I family and apparent lack of hypervariability in the proteinase contact loop. **1994**, 39, 644-54	20
1471	Similarity landscapes: a way to detect many structural and sequence motifs in both introns and exons. **1994**, 38, 188-203	4
1470	Molecular evolution of the HSP70 multigene family. **1994**, 38, 1-17	388
1469	Evolutionary relationships of bacterial and archaeal glutamine synthetase genes. **1994**, 38, 566-76	120
1468	On the evolution of arginases and related enzymes. **1994**, 39, 101-4	53
1467	Chromosomal localization of the human histone H2A.X gene to 11q23.2-q23.3 by fluorescence in situ hybridization. **1994**, 94, 303-6	18
1466	The identification of nuclear and mitochondrial genes by sequencing randomly chosen clones from a marsupial mammary gland cDNA library. **1994**, 32, 181-90	6
1465	A low-copy-number Sorghum DNA sequence that detects hypervariable EcoRV fragments. **1994**, 89, 64-9	1
1464	Molecular cloning of two Solanum chacoense S-alleles and a hypothesis concerning their evolution. **1994**, 7, 169	11
1463	Molecular and genetic characterization of the rhizopine catabolism (mocABRC) genes of Rhizobium meliloti L5-30. **1994**, 245, 11-24	59
1462	Molecular genetic analysis of the nagH gene encoding a hyaluronidase of Clostridium perfringens. **1994**, 243, 215-24	61
1461	The evolutionary origin of the 35 kb circular DNA of Plasmodium falciparum: new evidence supports a possible rhodophyte ancestry. **1994**, 243, 249-52	99
1460	The Caenorhabditis elegans unc-60 gene encodes proteins homologous to a family of actin-binding proteins. **1994**, 242, 346-57	102

1459	Molecular characterization of a novel tobacco pathogenesis-related (PR) protein: a new plant chitinase/lysozyme. **1994**, 245, 246-54	36
1458	Multicopy suppressors, mssA and mssB, of an smbA mutation of Escherichia coli. **1994**, 243, 9-16	30
1457	A superfamily of proteins involved in different secretion pathways in gram-negative bacteria: modular structure and specificity of the N-terminal domain. **1994**, 243, 112-8	152
1456	The smallest known eukaryotic genomes encode a protein gene: towards an understanding of nucleomorph functions. **1994**, 243, 600-4	19
1455	Identification of the XorII methyltransferase gene and a vsr homolog from Xanthomonas oryzae pv. oryzae. **1994**, 244, 383-90	23
1454	Inactivation of SSM4, a new Saccharomyces cerevisiae gene, suppresses mRNA instability due to rna14 mutations. **1994**, 245, 323-33	18
1453	Non-homologous recombination within the major histocompatibility complex creates a transcribed hybrid sequence. **1994**, 5, 771-6	13
1452	Structure and evolution of a member of a new subfamily of GTP-binding proteins mapping to the human MHC class I region. **1994**, 5, 100-5	43
1451	Functional complementation of a yeast vesicular transport mutation ypt1-1 by a Brassica napus cDNA clone encoding a small GTP-binding protein. **1994**, 26, 1725-35	30
1450	Analysis of the molecular basis of Pseudomonas syringae pv. tomato resistance in tomato. **1994**, 79, 187-193	3
1449	Expression and genomic organization of a dinoflagellate gene family. **1994**, 25, 23-31	35
1448	Genomic organization of the canrep repetitive DNA in Brassica juncea. **1994**, 26, 817-32	8
1447	Environmental stress-mediated differential 3' end formation of chloroplast RNA-binding protein transcripts. **1994**, 26, 833-49	18
1446	Domain conservation in several volvocalean cell wall proteins. **1994**, 26, 947-60	28
1445	Cloning and characterization of five cDNAs for genes differentially expressed during fruit development of kiwifruit (Actinidia deliciosa var. deliciosa). **1994**, 25, 877-86	121
1444	Synechocystis sp. PCC6803 fusB gene, located outside of the str operon, encodes a polypeptide related to protein synthesis factor EF-G. **1994**, 25, 735-8	1
1443	The major biotinyl protein from Pisum sativum seeds covalently binds biotin at a novel site. **1994**, 26, 265-73	28
1442	Partial sequencing and mapping of clones from two maize cDNA libraries. **1994**, 26, 1085-101	80

1441	The barley 60 kDa jasmonate-induced protein (JIP60) is a novel ribosome-inactivating protein. **1994** , 6, 815-24	117
1440	Protein sequence comparisons: searching databases and aligning sequences. **1994**, 5, 24-8	7
1439	The sequence of 29.7 kb from the right arm of chromosome II reveals 13 complete open reading frames, of which ten correspond to new genes. **1994**, 10 Suppl A, S1-11	5
1438	The sequence of an 8.8 kb segment on the left arm of chromosome II from Saccharomyces cerevisiae reveals four new open reading frames including homologs of animal DNA polymerase alpha-primases and bacterial GTP cyclohydrolase II. **1994**, 10 Suppl A, S13-24	7
1437	Sequence around the centromere of Saccharomyces cerevisiae chromosome II: similarity of CEN2 to CEN4. **1994**, 10 Suppl A, S41-6	25
1436	Sequencing of a 13.2 kb segment next to the left telomere of yeast chromosome XI revealed five open reading frames and recent recombination events with the right arms of chromosomes III and V. **1994**, 10 Suppl A, S81-91	20
1435	Molecular characterization of the SPT23 gene: a dosage-dependent suppressor of Ty-induced promoter mutations from Saccharomyces cerevisiae. **1994**, 10, 81-92	22
1434	Mapping and sequencing of two yeast genes belonging to the ATP-binding cassette superfamily. **1994**, 10, 377-83	62
1433	A Saccharomyces cerevisiae gene encoding a potential adenine phosphoribosyltransferase. **1994**, 10, 659-62	9
1432	LTE1 of Saccharomyces cerevisiae is a 1435 codon open reading frame that has sequence similarities to guanine nucleotide releasing factors. **1994**, 10, 953-8	13
1431	The nucleotide sequence of TTP1, a gene encoding a predicted type II membrane protein. **1994**, 10, 1111-5	5
1430	The sequence of 12.5 kb from the right arm of chromosome II predicts a new N-terminal sequence for the IRA1 protein and reveals two new genes, one of which is a DEAD-box helicase. **1994**, 10, 1227-34	9
1429	The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies 24 open reading frames including NUC1, PRP21 (SPP91), CDC6, CRY2, the gene for S24, a homologue to the aconitase gene ACO1 and two homologues to chromosome III genes. **1994**, 10, 1235-49	15
1428	Sequence of a segment of yeast chromosome II shows two novel genes, one almost entirely hydrophobic and the other extremely asparagine-serine rich. **1994**, 10, 1251-6	2
1427	The sequence of a 22.4 kb DNA fragment from the left arm of yeast chromosome II reveals homologues to bacterial proline synthetase and murine alpha-adaptin, as well as a new permease and a DNA-binding protein. **1994**, 10, 1489-96	13
1426	Cloning and sequence of REV7, a gene whose function is required for DNA damage-induced mutagenesis in Saccharomyces cerevisiae. **1994**, 10, 1503-9	30
1425	DNA sequence analysis of a 10.4 kbp region on the right arm of yeast chromosome XVI positions GPH1 and SGV1 adjacent to KRE6, and identifies two novel tRNA genes. **1994**, 10, 1527-30	2
1424	The nucleotide sequence and initial characterization of pyruvate decarboxylase from the yeast Hanseniaspora uvarum. **1994**, 10, 1581-9	13

1423	A 21.7 kb DNA segment on the left arm of yeast chromosome XIV carries WHI3, GCR2, SPX18, SPX19, an homologue to the heat shock gene SSB1 and 8 new open reading frames of unknown function. **1994**, 10, 1639-45	8
1422	Analysis of a 17.4 kb DNA segment of yeast chromosome II encompassing the ribosomal protein L19 as well as proteins with homologies to components of the hnRNP and snRNP complexes and to the human proliferation-associated p120 antigen. **1994**, 10, 1663-73	9
1421	Sequencing the yeast genome: an international achievement. **1994**, 10, 1689-706	21
1420	Sequence relationships between integral inner membrane proteins of binding protein-dependent transport systems: evolution by recurrent gene duplications. **1994**, 3, 325-44	54
1419	Conserved sequence pattern in a wide variety of phosphoesterases. **1994**, 3, 356-8	93
1418	Modular arrangement of proteins as inferred from analysis of homology. **1994**, 3, 482-92	174
1417	Self-organized neural maps of human protein sequences. **1994**, 3, 507-21	42
1416	Unexpected sequence similarity between nucleosidases and phosphoribosyltransferases of different specificity. **1994**, 3, 1081-8	31
1415	Self-splicing group I and group II introns encode homologous (putative) DNA endonucleases of a new family. **1994**, 3, 1117-20	110
1414	Recognition of related proteins by iterative template refinement (ITR). **1994**, 3, 1315-28	45
1413	The sequence of a subtilisin-type protease (aerolysin) from the hyperthermophilic archaeum Pyrobaculum aerophilum reveals sites important to thermostability. **1994**, 3, 1329-40	48
1412	A new family of carbon-nitrogen hydrolases. **1994**, 3, 1344-6	100
1411	A quantitative methodology for the de novo design of proteins. **1994**, 3, 1871-82	10
1410	Eukaryotic translation elongation factor 1 gamma contains a glutathione transferase domain--study of a diverse, ancient protein superfamily using motif search and structural modeling. **1994**, 3, 2045-54	127
1409	Analysis of hydrophobicity in the alpha and beta chemokine families and its relevance to dimerization. **1994**, 3, 2064-72	29
1408	High-sensitivity sequencing of large proteins: partial structure of the rapamycin-FKBP12 target. **1994**, 3, 2435-46	57
1407	A P-loop-like motif in a widespread ATP pyrophosphatase domain: implications for the evolution of sequence motifs and enzyme activity. **1994**, 20, 347-55	107
1406	Membrane topology of PLP in CNS myelin: evaluation of models. **1994**, 19, 975-81	12

1405	cDNA approaches to isolation of the mouse mutant weaver gene. **1994**, 19, 1359-62	1
1404	Sublinear approximate string matching and biological applications. **1994**, 12, 327-344	106
1403	A sublinear algorithm for approximate keyword searching. **1994**, 12, 345-374	104
1402	The TV-tree: An index structure for high-dimensional data. **1994**, 3, 517-542	286
1401	Software tools and databases for bacterial systematics and their dissemination via global networks. **1993**, 64, 205-29	6
1400	Typing of human papillomaviruses in cervical carcinoma biopsies from Cape Town. **1994**, 43, 231-7	29
1399	Isolation, characterization, and expression of cDNA clones that encode rat UDP-galactose: ceramide galactosyltransferase. **1994**, 38, 234-42	91
1398	Molecular cloning and characterization of rat brain 2',3'-cyclic nucleotide 3'-phosphodiesterase isoform 2. **1994**, 38, 243-7	42
1397	GRASP: a novel heparin-binding serum glycoprotein that mediates oligodendrocyte-substratum adhesion. **1994**, 39, 457-73	13
1396	A deductive database system for analyzing human nucleotide sequence data. **1994**, 36, 171-9	1
1395	AML1 fusion transcripts in t(3;21) positive leukemia: evidence of molecular heterogeneity and usage of splicing sites frequently involved in the generation of normal AML1 transcripts. **1994**, 11, 226-36	36
1394	Immunoselection of GRP94/endoplasmin from a KNRK cell-specific lambda gt11 library using antibodies directed against a putative heparanase amino-terminal peptide. **1994**, 56, 286-94	22
1393	Isolation of cDNA clones from an osteosarcoma-ROS17/2.8 library by differential hybridization. **1994**, 54, 273-80	2
1392	A rapid simple in situ hybridization method for herpes simplex virus employing a synthetic biotin-labeled oligonucleotide probe: a comparison with immunohistochemical methods for HSV detection. **1994**, 8, 105-15	25
1391	Organization of N-methyl-D-aspartate glutamate receptor gene expression in the basal ganglia of the rat. **1994**, 343, 1-16	349
1390	The human OX40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen. **1994**, 24, 677-83	115
1389	The human myocardial two-dimensional gel protein database: update 1994. **1994**, 15, 1459-65	66
1388	Molecular evolution: codes, clocks, genes and genomes. **1994**, 16, 699-703	6

1387	Purification of a 24 kD parasitism-specific hemolymph protein from pharate pupae of the Caribbean fruit fly, Anastrepha suspensa. **1994**, 27, 265-85	9
1386	Cloning and developmental expression of the chick type II and type III TGF beta receptors. **1994**, 199, 12-27	53
1385	Sensitive methods for determining the relatedness of proteins with limited sequence homology. **1994**, 5, 361-71	5
1384	Can informatics keep pace with molecular biology?. **1994**, 26, 69-77	
1383	Computer network resources and advanced level teaching of biochemical sciences. **1994**, 22, 40-44	3
1382	Some useful statistical properties of position-weight matrices. **1994**, 18, 287-94	34
1381	DNA sequence from Cretaceous period bone fragments. **1994**, 266, 1229-32	206
1380	Mutation of a mutL homolog in hereditary colon cancer. **1994**, 263, 1625-9	1661
1379	Polymerase chain reaction as a tool for developing stress protein probes. **1994**, 13, 1221-1229	13
1378	Fatty acid binding protein in locust and mammalian muscle. Comparison of structure, function and regulation. **1994**, 109, 199-208	19
1377	Alu sequences in the coding regions of mRNA: a source of protein variability. **1994**, 10, 188-93	242
1376	A functional superfamily of sodium/solute symporters. **1994**, 1197, 133-66	177
1375	Cloning of the glucose 6-phosphate dehydrogenase gene from Plasmodium falciparum. **1994**, 64, 313-26	37
1374	Sequence, expression and evolution of the globins of the parasitic nematode Nippostrongylus brasiliensis. **1994**, 68, 1-14	27
1373	Cloning and expression of the gene for an NADP(+)-dependent aldehyde dehydrogenase of Entamoeba histolytica. **1994**, 63, 157-61	11
1372	An amplified DNA element in Leishmania encodes potential integral membrane and nucleotide-binding proteins. **1994**, 66, 11-20	28
1371	Analysis of expressed sequence tags from Plasmodium falciparum. **1994**, 66, 97-104	84
1370	Primary structure of the Entamoeba histolytica gene (Ehvma1) encoding the catalytic peptide of a putative vacuolar membrane proton-transporting ATPase (V-ATPase). **1994**, 66, 165-9	12

1369	A gene coding for a high-molecular mass rhoptry protein of Plasmodium yoelii. **1994**, 65, 171-7	61
1368	Variation in the two internal transcribed spacers and 5.8S ribosomal RNA from five isolates of the marine parasite Perkinsus (Protista, Apicomplexa). **1994**, 65, 179-82	56
1367	Trypanosoma brucei mitochondrial CR4 gene encodes an extensively edited mRNA with completely edited sequence only in bloodstream forms. **1994**, 64, 65-74	44
1366	Molecular cloning of ras and rap genes from Entamoeba histolytica. **1994**, 64, 111-20	21
1365	Primary structure of an Entamoeba histolytica nicotinamide nucleotide transhydrogenase. **1994**, 68, 323-8	22
1364	Primary structure and expression of a human CTP:phosphocholine cytidylyltransferase. **1994**, 1219, 328-34	41
1363	Cloning, sequencing and expression of dinoflagellate luciferase DNA from a marine alga, Gonyaulax polyedra. **1994**, 1219, 449-56	26
1362	Yeast homologue of mammalian Ran binding protein 1. **1994**, 1219, 711-2	16
1361	Remotely related sequences and structures: analysis and predictive modelling. **1994**, 12, 154-8	4
1360	High-performance searching of biosequence databases. **1994**, 12, 76-80	5
1359	The WW domain: a signalling site in dystrophin?. **1994**, 19, 531-3	350
1358	New genes in old sequence: a strategy for finding genes in the bacterial genome. **1994**, 19, 309-13	65
1357	Amino acid sequence motif of group I intron endonucleases is conserved in open reading frames of group II introns. **1994**, 19, 402-4	133
1356	Direct sequencing of terminal regions of genomic P1 clones. A general strategy for the design of sequence-tagged site markers. **1994**, 11, 117-28	18
1355	Expression patterns of novel genes during mouse preimplantation embryogenesis. **1994**, 37, 121-9	136
1354	Molecular cloning and developmental expression of an mRNA encoding the 27 kDa outer dense fiber protein of rat spermatozoa. **1994**, 37, 229-40	73
1353	PDC2, a yeast gene essential for synthesis of pyruvate decarboxylase, encodes a novel transcription factor. **1994**, 73, 17-32	12
1352	Plasma proteins as early biomarkers of exposure to carcinogenic aromatic amines. **1994**, 93, 221-34	2

1351	Analysis of region-specific library constructed by sequence-independent amplification of microdissected fragments surrounding weaver (wv) gene on mouse chromosome 16. **1994**, 20, 401-8	6
1350	Bacterial genomics. **1994**, 14, 139-60	134
1349	Cloning and sequence analysis of a recA-like gene from Streptomyces venezuelae ISP5230. **1994**, 118, 51-6	14
1348	Nucleotide sequence and analysis of the gene in Borrelia burgdorferi encoding the immunogenic P39 antigen. **1994**, 119, 381-7	49
1347	Sequence and characterization of the Escherichia coli genome between the ndk and gcpE genes. **1994**, 121, 293-6	3
1346	Two mutant alleles of mukB, a gene essential for chromosome partition in Escherichia coli. **1994**, 123, 27-31	20
1345	Genetic evidence that hepA gene is involved in the normal deposition of the envelope of both heterocysts and akinetes in Anabaena variabilis ATCC 29413. **1994**, 123, 63-7	23
1344	Cloning and DNA sequence analysis of bmpC, a gene encoding a potential membrane lipoprotein of Borrelia burgdorferi. **1994**, 123, 75-82	17
1343	The use of PCR to monitor the population abundance of six human intestinal bacterial species in an in vitro semicontinuous culture system. **1994**, 124, 229-237	18
1342	Isolation of genes from complex sources of mammalian genomic DNA using exon amplification. **1994**, 6, 98-105	267
1341	Issues in searching molecular sequence databases. **1994**, 6, 119-29	691
1340	Genomic sequence sampling: a strategy for high resolution sequence-based physical mapping of complex genomes. **1994**, 7, 40-7	63
1339	Striking sequence similarity over almost 100 kilobases of human and mouse T-cell receptor DNA. **1994**, 7, 48-53	145
1338	A physical map and candidate genes in the BRCA1 region on chromosome 17q12-21. **1994**, 7, 472-9	78
1337	Identification and characterization of the gene causing type 1 spinocerebellar ataxia. **1994**, 7, 513-20	310
1336	Molecular cloning of Drosophila TFIID subunits. **1994**, 367, 484-7	104
1335	Evolutionary conservation of components of the protein translocation complex. **1994**, 367, 654-7	253
1334	2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. **1994**, 368, 32-8	1449

1333	Calcium channel beta-subunit binds to a conserved motif in the I-II cytoplasmic linker of the alpha 1-subunit. **1994**, 368, 67-70	582
1332	A model for high-throughput automated DNA sequencing and analysis core facilities. **1994**, 368, 474-5	34
1331	An RNA-binding protein associated with Src through its SH2 and SH3 domains in mitosis. **1994**, 368, 867-71	377
1330	A mammalian protein targeted by G1-arresting rapamycin-receptor complex. **1994**, 369, 756-8	1617
1329	The ancient regulatory-protein family of WD-repeat proteins. **1994**, 371, 297-300	1311
1328	Yeast TAFIIS in a multisubunit complex required for activated transcription. **1994**, 371, 523-7	149
1327	An unusual member of the nuclear hormone receptor superfamily responsible for X-linked adrenal hypoplasia congenita. **1994**, 372, 635-41	720
1326	A protein kinase involved in the regulation of inflammatory cytokine biosynthesis. **1994**, 372, 739-46	3044
1325	Characterization of the mutX gene of Streptococcus pneumoniae as a homologue of Escherichia coli mutT, and tentative definition of a catalytic domain of the dGTP pyrophosphohydrolases. **1994**, 11, 323-30	59
1324	Multiple signalling systems controlling expression of luminescence in Vibrio harveyi: sequence and function of genes encoding a second sensory pathway. **1994**, 13, 273-86	528
1323	Pathogenesis-related proteins in ozone-exposed Norway spruce [Picea abies (Karst) L.]. **1994**, 126, 81-89	25
1322	The citrulline biosynthetic operon, argC-F, and a ribose transport operon, rbs, from Bacillus subtilis are negatively regulated by Spo0A. **1994**, 11, 87-98	19
1321	Characterization of the dTDP-rhamnose biosynthetic genes encoded in the rfb locus of Shigella flexneri. **1994**, 11, 281-92	79
1320	The identification of rofA, a positive-acting regulatory component of prtF expression: use of an m gamma delta-based shuttle mutagenesis strategy in Streptococcus pyogenes. **1994**, 11, 671-84	98
1319	Cloning, sequencing, and characterization of multicopy suppressors of a mukB mutation in Escherichia coli. **1994**, 13, 301-12	75
1318	Anthrax toxin lethal factor contains a zinc metalloprotease consensus sequence which is required for lethal toxin activity. **1994**, 13, 1093-100	266
1317	Sequence and function of LuxO, a negative regulator of luminescence in Vibrio harveyi. **1994**, 12, 403-12	138
1316	MycDB: an integrated mycobacterial database. **1994**, 12, 517-34	41

1315	Two mutations that block heterocyst differentiation have different effects on akinete differentiation in Nostoc ellipsosporum. **1994**, 12, 679-84	54
1314	Identification and molecular analysis of a locus that regulates extracellular toxin production in Clostridium perfringens. **1994**, 12, 761-77	170
1313	Bacterial binding protein-dependent permeases: characterization of distinctive signatures for functionally related integral cytoplasmic membrane proteins. **1994**, 12, 993-1004	114
1312	A Haemophilus influenzae IgA protease-like protein promotes intimate interaction with human epithelial cells. **1994**, 14, 217-33	145
1311	Identification and characterization of an intervening sequence within the 23S ribosomal RNA genes of Campylobacter jejuni. **1994**, 14, 235-41	30
1310	Overexpression of flbA, an early regulator of Aspergillus asexual sporulation, leads to activation of brlA and premature initiation of development. **1994**, 14, 323-34	179
1309	Common ancestry between IncN conjugal transfer genes and macromolecular export systems of plant and animal pathogens. **1994**, 14, 655-68	116
1308	Crystal structure of a bacterial chitinase at 2.3 A resolution. **1994**, 2, 1169-80	378
1307	The sequence complexity of exons trapped from the mouse genome. **1994**, 4, 983-9	15
1306	Isolation and characterization of retinoic acid-inducible cDNA clones in F9 cells: one of the early inducible clones encodes a novel protein sharing several highly homologous regions with a Drosophila polyhomeotic protein. **1994**, 57, 39-50	99
1305	Cloning of metalloprotease genes in the carpet viper (Echis pyramidum leakeyi). Further members of the metalloprotease/disintegrin gene family. **1994**, 224, 483-8	45
1304	Purification of a novel 43-kDa protein (p43) intermediary in the activation of steroidogenesis from rat adrenal gland. **1994**, 224, 709-16	21
1303	Molecular cloning and tissue-specific RNA processing of a murine receptor-type protein tyrosine phosphatase. **1994**, 226, 773-82	11
1302	Unique primary structure of 2-nitropropane dioxygenase from Hansenula mrakii. **1994**, 226, 841-6	10
1301	A protein kinase isolated from porcine brain microvessels is similar to a class of heat-shock proteins. **1994**, 225, 805-9	11
1300	Induction of metallothionein and stomatin by interleukin-6 and glucocorticoids in a human amniotic cell line. **1994**, 223, 411-8	15
1299	Molecular analysis of ribosomal DNA from the aphid Amphorophora idaei and an associated fungal organism. **1994**, 3, 183-9	33
1298	Organization and sequence of the HpaII restriction-modification system and adjacent genes. **1994**, 142, 9-15	26

1297	Approximate string matching and local similarity. **1994**, 259-273	35
1296	Linkage of kdr-type resistance and the para-homologous sodium channel gene in German cockroaches (Blattella germanica). **1994**, 24, 647-54	70
1295	Isolation of exons from cloned DNA by exon trapping. **2001**, Chapter 6, Unit 6.1	
1294	Ethnic variation in frequency of an allelic polymorphism of human Fc gamma RIIA determined with allele specific oligonucleotide probes. **1994**, 173, 207-17	125
1293	Characterization of a rearrangement in the c-MYB promoter in the acute lymphoblastic leukemia cell line CCRF-CEM. **1994**, 75, 31-9	5
1292	The C. elegans gene odr-7 encodes an olfactory-specific member of the nuclear receptor superfamily. **1994**, 79, 971-80	148
1291	Mutation of a meiosis-specific MutS homolog decreases crossing over but not mismatch correction. **1994**, 79, 1069-80	322
1290	The polycystic kidney disease 1 gene encodes a 14 kb transcript and lies within a duplicated region on chromosome 16. The European Polycystic Kidney Disease Consortium. **1994**, 77, 881-94	665
1289	The diastrophic dysplasia gene encodes a novel sulfate transporter: positional cloning by fine-structure linkage disequilibrium mapping. **1994**, 78, 1073-87	650
1288	The product of the tobacco mosaic virus resistance gene N: similarity to toll and the interleukin-1 receptor. **1994**, 78, 1101-15	1078
1287	A complete Alu element within the coding sequence of a central gene. **1994**, 78, 173-4	14
1286	Characterization and relationship of Dpp receptors encoded by the saxophone and thick veins genes in Drosophila. **1994**, 78, 251-61	278
1285	Blimp-1, a novel zinc finger-containing protein that can drive the maturation of B lymphocytes into immunoglobulin-secreting cells. **1994**, 77, 297-306	626
1284	The FET3 gene of S. cerevisiae encodes a multicopper oxidase required for ferrous iron uptake. **1994**, 76, 403-10	608
1283	A repeating amino acid motif shared by proteins with diverse cellular roles. **1994**, 76, 789-91	578
1282	The Drosophila easily shocked gene: a mutation in a phospholipid synthetic pathway causes seizure, neuronal failure, and paralysis. **1994**, 79, 23-33	180
1281	The netrins define a family of axon outgrowth-promoting proteins homologous to C. elegans UNC-6. **1994**, 78, 409-24	1117
1280	EMB30 is essential for normal cell division, cell expansion, and cell adhesion in Arabidopsis and encodes a protein that has similarity to Sec7. **1994**, 77, 1051-62	300

1279	Pericentrin, a highly conserved centrosome protein involved in microtubule organization. **1994**, 76, 639-50	495
1278	A yeast actin-related protein homologous to that in vertebrate dynactin complex is important for spindle orientation and nuclear migration. **1994**, 78, 669-79	205
1277	CPEB is a specificity factor that mediates cytoplasmic polyadenylation during Xenopus oocyte maturation. **1994**, 79, 617-27	381
1276	RAFT1: a mammalian protein that binds to FKBP12 in a rapamycin-dependent fashion and is homologous to yeast TORs. **1994**, 78, 35-43	1186
1275	Sensitive detection of Ross River virus--a one-tube nested RT-PCR. **1994**, 49, 47-58	23
1274	Inhibition of the G1-S transition of the cell cycle by inhibitors of deoxyhypusine hydroxylation. **1994** , 1221, 115-24	112
1273	Molecular cloning of an Entamoeba histolytica gene encoding a putative mos family serine/threonine-kinase. **1994**, 1222, 122-4	9
1272	Comparing nucleotide and protein sequences by linguistic methods. **1994**, 35, 257-72	5
1271	The effect of aluminium treatment on wheat roots: expression of heat shock, histone and SHH genes. **1994**, 98, 37-45	7
1270	Regulation of plant nodule-specific genes expressed in alfalfa nodules arrested at an early stage of development. **1994**, 101, 65-73	7
1269	Novel cDNA clones obtained by antibody screening of a mouse cerebellar cDNA expression library. **1994**, 25, 183-91	6
1268	Heterogeneity of IgG antibody responses to cloned Onchocerca volvulus antigens in microfiladermia positive individuals from Esmeraldas Province, Ecuador. **1994**, 16, 201-9	9
1267	Correlation approach to identify coding regions in DNA sequences. **1994**, 67, 64-70	161
1266	Identification of genes encoding ribosomal protein L33 from Bacillus licheniformis, Thermus thermophilus and Thermotoga maritima. **1994**, 139, 135-6	9
1265	Using the FASTA program to search protein and DNA sequence databases. **1994**, 25, 365-89	49
1264	Conservation of K+ Channel Properties in Gene Subfamilies. **1994**, 5-16	4
1263	Genetic characterization of ompH mutants in the deep-sea bacterium Photobacterium sp. strain SS9. **1994**, 162, 323-8	24
1262	A New Type of Cytochrome c from Synechocystis PCC6803. **1994**, 144, 259-264	27

1261	Brain lipid-binding protein (BLBP): a novel signaling system in the developing mammalian CNS. **1994**, 12, 895-908	463
1260	The pectin lyase-encoding gene (pnl) family from Glomerella cingulata: characterization of pnlA and its expression in yeast. **1994**, 142, 141-6	42
1259	Conservation in human and mouse Pur alpha of a motif common to several proteins involved in initiation of DNA replication. **1994**, 149, 311-4	57
1258	Taxon Specific Hybridization Probes for Fiber-digesting Bacteria Suggest Novel Gut-associated Fibrobacter. **1994**, 17, 418-424	42
1257	Grandori and Carey reply. **1994**, 19, 235	1
1256	Identifying differences in mRNA expression by representational difference analysis of cDNA. **1994**, 22, 5640-8	788
1255	The Drosophila melanogaster ribosomal S6 kinase II-encoding sequence. **1994**, 144, 309-10	22
1254	PAD1 encodes phenylacrylic acid decarboxylase which confers resistance to cinnamic acid in Saccharomyces cerevisiae. **1994**, 142, 107-12	127
1253	An Anopheles gambiae cDNA predicts a protein similar to a yeast Suil translation factor. **1994**, 141, 299-300	3
1252	Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization of the BC cDNA reveals strong homology to surfactant protein-D. **1994**, 141, 277-81	18
1251	A specific amino acid repeat in squalene and oxidosqualene cyclases. **1994**, 19, 157-8	129
1250	Ancient conserved regions in gene sequences. **1994**, 4, 404-412	16
1249	Sequence of the region downstream of the Vitreoscilla hemoglobin gene: vgb is not part of a multigene operon. **1994**, 42, 304-8	17
1248	Cloning, characterization and insertional inactivation of the Lactobacillus helveticus D(-) lactate dehydrogenase gene. **1994**, 41, 432-9	33
1247	Comparison of the two major ARS elements of the ura4 replication origin region with other ARS elements in the fission yeast, Schizosaccharomyces pombe. **1994**, 103, 414-22	40
1246	Comparison of two active HeT-A retroposons of Drosophila melanogaster. **1994**, 103, 90-8	54
1245	A novel RNA-binding motif in omnipotent suppressors of translation termination, ribosomal proteins and a ribosome modification enzyme?. **1994**, 22, 2166-7	101
1244	The primary structure of a lipoxygenase from the shoots of etiolated lentil seedlings derived from its cDNA. **1994**, 1211, 239-42	16

1243	Glutamate receptor expression in rat striatum: effect of deafferentation. **1994**, 647, 209-19		66
1242	Identification of cDNA clones expressed selectively during the critical period for visual cortex development by subtractive hybridization. **1994**, 639, 73-84		30
1241	Characterization of the paramagnetic iron-containing redox centres of Thiosphaera pantotropha periplasmic nitrate reductase. **1994**, 345, 76-80		50
1240	Cloning of an Arabidopsis histidine transporting protein related to nitrate and peptide transporters. **1994**, 347, 185-9		91
1239	One of the retinoic acid-inducible cDNA clones in mouse embryonal carcinoma F9 cells encodes a novel isoenzyme of fructose 1,6-bisphosphatase. **1994**, 348, 201-5		11
1238	Autoimmunity in stiff-Man syndrome with breast cancer is targeted to the C-terminal region of human amphiphysin, a protein similar to the yeast proteins, Rvs167 and Rvs161. **1994**, 351, 73-9		128
1237	Predicted secondary structure of the 20 S proteasome and model structure of the putative peptide channel. **1994**, 354, 45-9		17
1236	Characterisation of a complementary DNA encoding a novel plant enzyme with sucrolytic activity. **1994**, 354, 123-7		7
1235	Primary structure of a multimeric protein, homologous to the PEP-utilizing enzyme family and isolated from a hyperthermophilic archaebacterium. **1994**, 356, 345-50		12
1234	The chaperone connection to the origins of the eukaryotic organelles. **1994**, 341, 146-51		87
1233	Drosophila kelch motif is derived from a common enzyme fold. *Journal of Molecular Biology*, **1994**, 236, 1277-82	6.5	164
1232	Paired box gene expression in Wilms' tumor. **1994**, 29, 134-41		30
1231	Identification and characterization of a cDNA encoding ribosomal protein S12 from Xenopus laevis. **1994**, 150, 331-3		1
1230	Sequence and expression of murine cDNAs encoding Xlr3a and Xlr3b, defining a new X-linked lymphocyte-regulated Xlr gene subfamily. **1994**, 150, 345-50		19
1229	The yeast FKS1 gene encodes a novel membrane protein, mutations in which confer FK506 and cyclosporin A hypersensitivity and calcineurin-dependent growth. **1994**, 151, 61-71		78
1228	Open reading frames flanking the peptidyl-tRNA hydrolase-encoding gene of Escherichia coli. **1994**, 151, 153-6		3
1227	Characterization of the macromolecular synthesis (MMS) operon from Listeria monocytogenes. **1994**, 151, 161-6		21
1226	Organization and sequence of the SalI restriction-modification system. **1994**, 151, 167-72		8

1225	The MID2 gene encodes a putative integral membrane protein with a Ca(2+)-binding domain and shows mating pheromone-stimulated expression in Saccharomyces cerevisiae. **1994**, 151, 203-8		47
1224	Escherichia coli contains a set of genes homologous to those involved in protein secretion, DNA uptake and the assembly of type-4 fimbriae in other bacteria. **1994**, 150, 9-15		28
1223	Cloning, analysis and expression of the HindIII R-M-encoding genes. **1994**, 150, 75-80		24
1222	Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent protein kinase I. **1994**, 1224, 156-60		20
1221	Histones, HMG, HU, IHF: Même combat. **1994**, 76, 901-8		89
1220	A genomic region encoding stonefish (Synanceja horrida) stonustoxin beta-subunit contains an intron. **1994**, 32, 1684-8		9
1219	Expression cloning and characterization of a novel adipocyte long chain fatty acid transport protein. **1994**, 79, 427-36		756
1218	Identification of a T cell-specific transcriptional enhancer 3’ of the human T cell receptor gamma locus. **1994**, 31, 315-22		9
1217	Characterization of a C alpha gene of swine. **1994**, 31, 633-42		34
1216	Variability in an MHCMosa class II beta chain-encoding gene in striped bass (Morone saxatilis). **1994**, 18, 325-42		41
1215	Sonic hedgehog and Fgf-4 act through a signaling cascade and feedback loop to integrate growth and patterning of the developing limb bud. **1994**, 79, 993-1003		722
1214	Sequence alignment and penalty choice. Review of concepts, case studies and implications. *Journal of Molecular Biology*, **1994**, 235, 1-12	6.5	178
1213	Sequence of a lipase-encoding gene isolated from Serratia proteamaculans 8805142. **1994**, 141, 137-8		1
1212	Cloning and expression of the hup encoding a histone-like protein of Campylobacter jejuni. **1994**, 146, 83-6		10
1211	The LEU1 gene of Ustilago maydis. **1994**, 140, 131-5		11
1210	Members of a family of Drosophila putative odorant-binding proteins are expressed in different subsets of olfactory hairs. **1994**, 12, 35-49		302
1209	The addition of 5’-coding information to a 3’-directed cDNA library improves analysis of gene expression. **1994**, 146, 199-207		1
1208	The penicillin amidase of Arthrobacter viscosus (ATCC 15294). **1994**, 143, 79-83		27

1207	Sequences of the rplJL operon containing the L10 and L7/L12 genes from Brucella abortus. **1994**, 140, 137-8	19
1206	The modular structure of NifU proteins. **1994**, 19, 199-200	27
1205	The SRCR superfamily: a family reminiscent of the Ig superfamily. **1994**, 19, 5-8	310
1204	Identification of the putative repressor-encoding gene cI of the temperate lactococcal bacteriophage Tuc2009. **1994**, 144, 93-5	36
1203	From genome sequences to protein function. **1994**, 4, 393-403	48
1202	FMN- or DNA-binding?. **1994**, 19, 234-5	4
1201	A mouse cDNA encoding a protein with zinc-fingers and a KRAB domain shows similarity to human profilaggrin. **1994**, 149, 299-304	6
1200	The aminopeptidase N-encoding pepN gene of Streptomyces lividans 66. **1994**, 141, 115-9	20
1199	A conserved domain in putative bacterial and bacteriophage transglycosylases. **1994**, 19, 106-7	46
1198	Cloning of the putative glycogen branching enzyme gene, glgB, from Streptomyces aureofaciens. **1994**, 1200, 334-6	9
1197	Barley beta-glucosidase: expression during seed germination and maturation and partial amino acid sequences. **1994**, 1199, 52-8	20
1196	Yeast protein controlling inter-organelle communication is related to bacterial phosphatases containing the Hsp 70-type ATP-binding domain. **1994**, 19, 156-7	36
1195	Two genes encoding ribosomal protein L3 of Schizosaccharomyces pombe and their proximal promoter regions. **1994**, 142, 119-22	7
1194	Isolation and sequence analysis of a Caenorhabditis elegans cDNA which encodes a 14-3-3 homologue. **1994**, 147, 215-8	11
1193	Identification of a ToxR-activated gene, tagE, that lies within the accessory colonization factor gene cluster of Vibrio cholerae O395. **1994**, 148, 91-5	15
1192	Differential expression of metabotropic glutamate receptors in the hippocampus and entorhinal cortex of the rat. **1994**, 21, 283-92	117
1191	Sequence of the RAD55 gene of Saccharomyces cerevisiae: similarity of RAD55 to prokaryotic RecA and other RecA-like proteins. **1994**, 142, 103-6	93
1190	Rhizobium meliloti homologs of Escherichia coli mur genes. **1994**, 148, 87-90	1

1189	An aroA homologue from Synechocystis sp. PCC 6803. **1994**, 144, 145-6	3
1188	Phylogenetic relationships among bacteriorhodopsins. **1994**, 145, 273-85	13
1187	A merR homologue at 74 minutes on the Escherichia coli genome. **1994**, 146, 131-2	7
1186	Ca2+ channel regulation by a conserved beta subunit domain. **1994**, 13, 495-503	237
1185	RNA sequence analysis using covariance models. **1994**, 22, 2079-88	586
1184	Isolation of human simple repeat loci by hybridization selection. **1994**, 3, 599-65	426
1183	Infusion into the brain of an antisense oligonucleotide to the immediate-early gene c-fos suppresses production of fos and produces a behavioral effect. **1994**, 63, 917-24	91
1182	Homology between Borrelia burgdorferi OspC and members of the family of Borrelia hermsii variable major proteins. **1994**, 143, 105-10	51
1181	Sequence of the rec-2 locus of Haemophilus influenzae: homologies to comE-ORF3 of Bacillus subtilis and msbA of Escherichia coli. **1994**, 146, 95-100	30
1180	Identification and purification of an agrin receptor from Torpedo postsynaptic membranes: a heteromeric complex related to the dystroglycans. **1994**, 12, 1173-80	283
1179	Characterization of the CNRE-1 family of repetitive DNA elements in Cryptococcus neoformans. **1994**, 144, 103-6	15
1178	Cloning, sequencing and expression of stress genes from the ethanol-producing bacterium Zymomonas mobilis: the groESL operon. **1994**, 148, 51-7	24
1177	Expression of the division-controlling gene ftsZ during growth and sporulation of the filamentous bacterium Streptomyces griseus. **1994**, 147, 21-8	25
1176	Identification and sequencing of the Thermotoga maritima lacZ gene, part of a divergently transcribed operon. **1994**, 147, 101-6	19
1175	A versatile tool for retrieving molecular sequences. **1994**, 19, 94-96	6
1174	The nature and expression of int-5, a novel MMTV integration locus gene in carcinogen-induced mammary tumors. **1994**, 87, 179-86	24
1173	Cloning of a gene encoding a human leukocyte protein characterised by extensive heptad repeats. **1994**, 144, 221-8	13
1172	Features of the cellodextrinase gene from Fibrobacter succinogenes S85. **1994**, 40, 592-6	18

1171	RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant disease resistance genes. **1994**, 265, 1856-60	822
1170	Sensing starvation: a homoserine lactone--dependent signaling pathway in Escherichia coli. **1994**, 265, 537-9	204
1169	The raspberry locus of Drosophila melanogaster includes an inosine monophosphate dehydrogenase like coding sequence. **1994**, 37, 333-44	6
1168	Cloning, molecular characterization, and expression of the genes encoding the lytic functions of lactococcal bacteriophage phi LC3: a dual lysis system of modular design. **1994**, 40, 658-65	105
1167	Isolation of the tomato Cf-9 gene for resistance to Cladosporium fulvum by transposon tagging. **1994**, 266, 789-93	804
1166	An invariant T cell receptor alpha chain is used by a unique subset of major histocompatibility complex class I-specific CD4+ and CD4-8- T cells in mice and humans. **1994**, 180, 1097-106	876
1165	.	2
1164	Identification of herpesvirus-like DNA sequences in AIDS-associated Kaposi's sarcoma. **1994**, 266, 1865-9	4854
1163	Recent developments in linear-space alignment methods: a survey. **1994**, 1, 271-91	37
1162	Motif-biased protein sequence alignment. **1994**, 1, 297-310	11
1161	A portable search engine and browser for the Entrez database. **1994**, 1, 293-5	7
1160	Biological evaluation of d2, an algorithm for high-performance sequence comparison. **1994**, 1, 199-215	51
1159	Sera from JRA patients contain antibodies against a defined epitope in chromosomal protein HMG-17. **1994**, 17, 23-30	7
1158	. **1994**,	
1157	Functional domains within FEN-1 and RAD2 define a family of structure-specific endonucleases: implications for nucleotide excision repair. **1994**, 8, 1344-55	231
1156	Membrane topology of liver microsomal cytochrome P450 2B4 determined via monoclonal antibodies directed to the halt-transfer signal. **1994**, 33, 6945-51	39
1155	Molecular evolution of SRP cycle components: functional implications. **1994**, 22, 1933-47	75
1154	The molecular diversity of the 5S rRNA gene in barley (Hordeum vulgare). **1994**, 37, 992-8	49

1153	The Hermes transposable element from the house fly, Musca domestica, is a short inverted repeat-type element of the hobo, Ac, and Tam3 (hAT) element family. **1994**, 64, 87-97	147
1152	DNA sequence of a gene in Escherichia coli encoding a putative tripartite transcription factor with receiver, ATPase and DNA binding domains. **1994**, 5, 17-24	7
1151	A library of yeast genomic MCM1 binding sites contains genes involved in cell cycle control, cell wall and membrane structure, and metabolism. **1994**, 14, 348-59	74
1150	ISWAC: proposed system for the integrated assembly of chromosomes. **1994**, 5, 67-76	
1149	A survey of genes expressed in undifferentiated mouse embryonal carcinoma F9 cells: characterization of low-abundance mRNAs. **1994**, 116, 128-39	21
1148	Bacillus subtilis lon protease prevents inappropriate transcription of genes under the control of the sporulation transcription factor sigma G. **1994**, 176, 6528-37	76
1147	cDNA cloning and amino acid sequence of human mitochondrial delta 3 delta 2-enoyl-CoA isomerase: comparison of the human enzyme with its rat counterpart, mitochondrial short-chain isomerase. **1994**, 300 (Pt 1), 1-5	9
1146	Dephosphorylation of cofilin in stimulated platelets: roles for a GTP-binding protein and Ca2+. **1994** , 301 (Pt 1), 41-7	74
1145	Structural comparisons lead to the definition of a new superfamily of NAD(P)(H)-accepting oxidoreductases: the single-domain reductases/epimerases/dehydrogenases (the 'RED' family). **1994**, 304 (Pt 1), 95-9	71
1144	Characterization of cDNA for murine tripeptidyl-peptidase II reveals alternative splicing. **1994**, 304 (Pt 2), 517-23	23
1143	Regulation of the DOPA Decarboxylase Gene During Drosophila Development. **1994**, 3, 55-86	7
1142	UTP: alpha-D-glucose-1-phosphate uridylyltransferase of Escherichia coli: isolation and DNA sequence of the galU gene and purification of the enzyme. **1994**, 176, 2611-8	86
1141	On the Correlation of Protein Structure with Local Sequence Patterns. **1994**, 685-703	
1140	Isolation and sequence analysis of polyketide synthase genes from the daunomycin-producing Streptomyces sp. strain C5. **1994**, 176, 6270-80	67
1139	Structure of the O antigen of Escherichia coli K-12 and the sequence of its rfb gene cluster. **1994**, 176, 4144-56	258
1138	The XbaI-BlnI-CeuI genomic cleavage map of Salmonella paratyphi B. **1994**, 176, 1014-24	42
1137	Plasmid location of Borrelia purine biosynthesis gene homologs. **1994**, 176, 6427-32	85
1136	Molecular cloning and expression of the Candida albicans beta-N-acetylglucosaminidase (HEX1) gene. **1994**, 176, 2640-7	73

1135	Evidence for effect of random genetic drift on G+C content after lateral transfer of fucose pathway genes to Escherichia coli K-12. **1994**, 11, 829-38	26
1134	Genetic control of bacterial suicide: regulation of the induction of PBSX in Bacillus subtilis. **1994**, 176, 5820-30	40
1133	Characterization of genes in the cellulose-synthesizing operon (acs operon) of Acetobacter xylinum: implications for cellulose crystallization. **1994**, 176, 5735-52	230
1132	The Alcaligenes eutrophus H16 hoxX gene participates in hydrogenase regulation. **1994**, 176, 4385-93	148
1131	Independent phylogenetic origins of methanotrophic and chemoautotrophic bacterial endosymbioses in marine bivalves. **1994**, 176, 1932-8	67
1130	A LuxR-LuxI type regulatory system activates Agrobacterium Ti plasmid conjugal transfer in the presence of a plant tumor metabolite. **1994**, 176, 2796-806	411
1129	Differential expression of a new dominant agouti allele (Aiapy) is correlated with methylation state and is influenced by parental lineage. **1994**, 8, 1463-72	220
1128	Combined nickel-cobalt-cadmium resistance encoded by the ncc locus of Alcaligenes xylosoxidans 31A. **1994**, 176, 7045-54	168
1127	Isolation and characterization of a second exe operon required for extracellular protein secretion in Aeromonas hydrophila. **1994**, 176, 6819-26	54
1126	A new gene required for cellulose production and a gene encoding cellulolytic activity in Acetobacter xylinum are colocalized with the bcs operon. **1994**, 176, 665-72	129
1125	Isolation, characterization, and nucleotide sequence of IS1202, an insertion sequence of Streptococcus pneumoniae. **1994**, 176, 4437-43	35
1124	A third genetic locus required for the formation of heterocysts in Anabaena sp. strain PCC 7120. **1994**, 176, 5277-83	46
1123	Plasmid-borne cadmium resistance genes in Listeria monocytogenes are similar to cadA and cadC of Staphylococcus aureus and are induced by cadmium. **1994**, 176, 3040-8	110
1122	Plasmid-borne cadmium resistance genes in Listeria monocytogenes are present on Tn5422, a novel transposon closely related to Tn917. **1994**, 176, 3049-61	69
1121	Purification and characterization of Clostridium perfringens 120-kilodalton collagenase and nucleotide sequence of the corresponding gene. **1994**, 176, 149-56	104
1120	Chloroperoxidase from Streptomyces lividans: isolation and characterization of the enzyme and the corresponding gene. **1994**, 176, 2339-47	53
1119	Bacillus subtilis F0F1 ATPase: DNA sequence of the atp operon and characterization of atp mutants. **1994**, 176, 6802-11	105
1118	A mutation in the indole-3-acetic acid biosynthesis pathway of Pseudomonas syringae pv. syringae affects growth in Phaseolus vulgaris and syringomycin production. **1994**, 176, 1374-82	69

1117	Extension of the mitochondrial transporter super-family: sequences of five members from the nematode worm, Caenorhabditis elegans. **1994**, 4, 281-91	21
1116	Intrinsic and extrinsic approaches for detecting genes in a bacterial genome. **1994**, 22, 4756-67	91
1115	Phylogenetic Utility of Partial Dna Sequences of G6pdh at Different Taxonomic Levels in Hexapoda with Emphasis on Diptera. **1994**, 87, 723-736	30
1114	Transcription factor IID in the Archaea: sequences in the Thermococcus celer genome would encode a product closely related to the TATA-binding protein of eukaryotes. **1994**, 91, 4180-4	85
1113	Codon reiteration and the evolution of proteins. **1994**, 91, 4298-302	73
1112	Identification of Drosophila cytoskeletal proteins by induction of abnormal cell shape in fission yeast. **1994**, 91, 4589-93	57
1111	The bat gene of Halobacterium halobium encodes a trans-acting oxygen inducibility factor. **1994**, 91, 5475-9	41
1110	MecB of Bacillus subtilis, a member of the ClpC ATPase family, is a pleiotropic regulator controlling competence gene expression and growth at high temperature. **1994**, 91, 5788-92	138
1109	Rch1, a protein that specifically interacts with the RAG-1 recombination-activating protein. **1994**, 91, 6156-60	154
1108	Evolution of the Glx-tRNA synthetase family: the glutaminyl enzyme as a case of horizontal gene transfer. **1994**, 91, 8670-4	129
1107	Discovery of myosin genes by physical mapping in Dictyostelium. **1994**, 91, 9446-50	42
1106	Individual chaperones required for Yop secretion by Yersinia. **1994**, 91, 10493-7	235
1105	Ubiquitous receptor: a receptor that modulates gene activation by retinoic acid and thyroid hormone receptors. **1994**, 91, 10809-13	209
1104	The human CAN protein, a putative oncogene product associated with myeloid leukemogenesis, is a nuclear pore complex protein that faces the cytoplasm. **1994**, 91, 1519-23	217
1103	The sequence, and its evolutionary implications, of a Thermococcus celer protein associated with transcription. **1994**, 91, 3854-6	39
1102	Commitment of yeast pre-mRNA to the splicing pathway requires a novel U1 small nuclear ribonucleoprotein polypeptide, Prp39p. **1994**, 14, 3623-33	57
1101	Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity. **1994**, 14, 6809-18	33
1100	MID1, a novel Saccharomyces cerevisiae gene encoding a plasma membrane protein, is required for Ca2+ influx and mating. **1994**, 14, 8259-71	199

1099	The Saccharomyces cerevisiae checkpoint gene BUB1 encodes a novel protein kinase. **1994**, 14, 8282-91	196
1098	The yeast UME5 gene regulates the stability of meiotic mRNAs in response to glucose. **1994**, 14, 3446-58	80
1097	Rapid and accurate estimates of statistical significance for sequence data base searches. **1994**, 91, 4625-8	128
1096	TraI, a LuxI homologue, is responsible for production of conjugation factor, the Ti plasmid N-acylhomoserine lactone autoinducer. **1994**, 91, 4639-43	185
1095	Molecular cloning, tissue distribution, and expression of a 14-kDa bile acid-binding protein from rat ileal cytosol. **1994**, 91, 4741-5	116
1094	Inactivation of the Podospora anserina vegetative incompatibility locus het-c, whose product resembles a glycolipid transfer protein, drastically impairs ascospore production. **1994**, 91, 5927-31	79
1093	Two cellular proteins that bind to wild-type but not mutant p53. **1994**, 91, 6098-102	347
1092	A catalogue of genes in the cardiovascular system as identified by expressed sequence tags. **1994**, 91, 10645-9	93
1091	An intron in the thymidylate synthase gene of Bacillus bacteriophage beta 22: evidence for independent evolution of a gene, its group I intron, and the intron open reading frame. **1994**, 91, 11669-73	39
1090	Sequence and structure comparison suggest that methionine aminopeptidase, prolidase, aminopeptidase P, and creatinase share a common fold. **1994**, 91, 2473-7	145
1089	Variant forms of a group I intron in nuclear small-subunit rRNA genes of the marine red alga Porphyra spiralis var. amplifolia. **1994**, 11, 195-207	31
1088	Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (rfb) of Escherichia coli K-12 W3110: identification of genes that confer group 6 specificity to Shigella flexneri serotypes Y and 4a. **1994**, 176, 4133-43	77
1087	Cloning and nucleotide sequence analysis of the colH gene from Clostridium histolyticum encoding a collagenase and a gelatinase. **1994**, 176, 6489-96	82
1086	RocR, a novel regulatory protein controlling arginine utilization in Bacillus subtilis, belongs to the NtrC/NifA family of transcriptional activators. **1994**, 176, 1234-41	101
1085	4-Hydroxybenzoate-coenzyme A ligase from Rhodopseudomonas palustris: purification, gene sequence, and role in anaerobic degradation. **1994**, 176, 634-41	71
1084	Cloning and expression of an Azotobacter vinelandii mannuronan C-5-epimerase gene. **1994**, 176, 2846-53	110
1083	Residues essential for the function of SecE, a membrane component of the Escherichia coli secretion apparatus, are located in a conserved cytoplasmic region. **1994**, 91, 2557-61	62
1082	Lipid synthesis in mycobacteria: characterization of the biotin carboxyl carrier protein genes from Mycobacterium leprae and M. tuberculosis. **1994**, 176, 2525-31	26

1081	Length of the coupling sequence of Tn916. **1994**, 176, 3386-8	26
1080	Organization and evolution of naphthalene catabolic pathways: sequence of the DNA encoding 2-hydroxychromene-2-carboxylate isomerase and trans-o-hydroxybenzylidenepyruvate hydratase-aldolase from the NAH7 plasmid. **1994**, 176, 7757-62	74
1079	Trehalose-6-phosphate hydrolase of Escherichia coli. **1994**, 176, 5654-64	100
1078	The nasFEDCBA operon for nitrate and nitrite assimilation in Klebsiella pneumoniae M5al. **1994**, 176, 2551-9	62
1077	Identification of a putative alternate sigma factor and characterization of a multicomponent regulatory cascade controlling the expression of Pseudomonas syringae pv. syringae Pss61 hrp and hrmA genes. **1994**, 176, 1025-36	231
1076	Cloning and expression of a cDNA encoding a brain-specific Na(+)-dependent inorganic phosphate cotransporter. **1994**, 91, 5607-11	270
1075	A carbonic anhydrase from the archaeon Methanosarcina thermophila. **1994**, 91, 6909-13	220
1074	Cloning of casbene synthase cDNA: evidence for conserved structural features among terpenoid cyclases in plants. **1994**, 91, 8497-501	122
1073	Cloning mammalian genes by expression selection of genetic suppressor elements: association of kinesin with drug resistance and cell immortalization. **1994**, 91, 3744-8	120
1072	Prokaryotic expression cloning of a novel human tyrosine kinase. **1994**, 14, 982-8	41
1071	Alpha 1(XVIII), a collagen chain with frequent interruptions in the collagenous sequence, a distinct tissue distribution, and homology with type XV collagen. **1994**, 91, 4234-8	143
1070	Cloning of human basic A1, a distinct 59-kDa dystrophin-associated protein encoded on chromosome 8q23-24. **1994**, 91, 4446-50	117
1069	Alternatively spliced isoforms of the putative renal Na-K-Cl cotransporter are differentially distributed within the rabbit kidney. **1994**, 91, 4544-8	246
1068	Analysis of the Streptomyces coelicolor sigE gene reveals the existence of a subfamily of eubacterial RNA polymerase sigma factors involved in the regulation of extracytoplasmic functions. **1994**, 91, 7573-7	441
1067	Direct isolation of genes encoded within a homogeneously staining region by chromosome microdissection. **1994**, 91, 9121-5	37
1066	Construction and characterization of a normalized cDNA library. **1994**, 91, 9228-32	355
1065	Retrotransposons in the flanking regions of normal plant genes: a role for copia-like elements in the evolution of gene structure and expression. **1994**, 91, 11792-6	233
1064	Detection of conserved segments in proteins: iterative scanning of sequence databases with alignment blocks. **1994**, 91, 12091-5	241

1063	Molecular cloning and functional expression of the bumetanide-sensitive Na-K-Cl cotransporter. **1994**, 91, 2201-5	362
1062	Repression of the genes for lysine biosynthesis in Saccharomyces cerevisiae is caused by limitation of Lys14-dependent transcriptional activation. **1994**, 14, 6411-8	64
1061	Isolation and characterization of a novel transcription factor that binds to and activates insulin control element-mediated expression. **1994**, 14, 6704-14	19
1060	Mutations in the Saccharomyces cerevisiae CDC1 gene affect double-strand-break-induced intrachromosomal recombination. **1994**, 14, 8037-50	19
1059	One exon of the human LSF gene includes conserved regions involved in novel DNA-binding and dimerization motifs. **1994**, 14, 5076-87	54
1058	A mutation in the second largest subunit of TFIIIC increases a rate-limiting step in transcription by RNA polymerase III. **1994**, 14, 822-30	53
1057	A novel synapse-associated noncoding RNA. **1994**, 14, 7095-104	50
1056	PEBP2 alpha B/mouse AML1 consists of multiple isoforms that possess differential transactivation potentials. **1994**, 14, 3242-52	198
1055	Effects on protein synthesis produced by pairing depolarization with serotonin, an analogue of associative learning in Aplysia. **1994**, 91, 4150-4	7
1054	Specific protein-protein interactions between the essential mammalian spliceosome-associated proteins SAP 61 and SAP 114. **1994**, 91, 6403-7	35
1053	Flavin reductase: sequence of cDNA from bovine liver and tissue distribution. **1994**, 91, 9322-6	24
1052	AtVPS34, a phosphatidylinositol 3-kinase of Arabidopsis thaliana, is an essential protein with homology to a calcium-dependent lipid binding domain. **1994**, 91, 11398-402	150
1051	Mobile Minos elements from Drosophila hydei encode a two-exon transposase with similarity to the paired DNA-binding domain. **1994**, 91, 4746-50	77
1050	The LCB2 gene of Saccharomyces and the related LCB1 gene encode subunits of serine palmitoyltransferase, the initial enzyme in sphingolipid synthesis. **1994**, 91, 7899-902	183
1049	Isolation of unknown genes from human bone marrow by differential screening and single-pass cDNA sequence determination. **1994**, 91, 11869-73	12
1048	MDS1, a dosage suppressor of an mck1 mutant, encodes a putative yeast homolog of glycogen synthase kinase 3. **1994**, 14, 831-9	74
1047	Isolation of a thyroid hormone-responsive gene by immunoprecipitation of thyroid hormone receptor-DNA complexes. **1994**, 14, 7621-32	28
1046	Regulation by protein-tyrosine phosphatase PTP2 is distinct from that by PTP1 during Dictyostelium growth and development. **1994**, 14, 5154-64	28

1045	The Arabidopsis GA1 Locus Encodes the Cyclase ent-Kaurene Synthetase A of Gibberellin Biosynthesis. **1994**, 6, 1509	63
1044	Mammalian DNA ligase III: molecular cloning, chromosomal localization, and expression in spermatocytes undergoing meiotic recombination. **1995**, 15, 5412-22	99
1043	The yeast carboxyl-terminal repeat domain kinase CTDK-I is a divergent cyclin-cyclin-dependent kinase complex. **1995**, 15, 5716-24	124
1042	FKBP51, a novel T-cell-specific immunophilin capable of calcineurin inhibition. **1995**, 15, 4395-402	137
1041	Identification of a gene involved in the biosynthesis of cyclopropanated mycolic acids in Mycobacterium tuberculosis. **1995**, 92, 6630-4	167
1040	Identification of cDNA clones encoding valosin-containing protein and other plant plasma membrane-associated proteins by a general immunoscreening strategy. **1995**, 92, 4457-61	49
1039	Identification of a nonneuronal isoform of synaptotagmin. **1995**, 92, 5895-9	74
1038	Ligand-induced endocytosis of epidermal growth factor receptors that are defective in binding adaptor proteins. **1995**, 92, 8719-23	79
1037	A common fold for peptide synthetases cleaving ATP to ADP: glutathione synthetase and D-alanine:d-alanine ligase of Escherichia coli. **1995**, 92, 1172-6	105
1036	The sak1+ gene of Schizosaccharomyces pombe encodes an RFX family DNA-binding protein that positively regulates cyclic AMP-dependent protein kinase-mediated exit from the mitotic cell cycle. **1995**, 15, 1479-88	60
1035	ELF-2, a new member of the Eph ligand family, is segmentally expressed in mouse embryos in the region of the hindbrain and newly forming somites. **1995**, 15, 4921-9	149
1034	The 94- to 97-kDa mouse macrophage membrane protein that recognizes oxidized low density lipoprotein and phosphatidylserine-rich liposomes is identical to macrosialin, the mouse homologue of human CD68. **1995**, 92, 9580-4	287
1033	Cloning and characterization of a cellular apoptosis susceptibility gene, the human homologue to the yeast chromosome segregation gene CSE1. **1995**, 92, 10427-31	159
1032	Intron phase correlations and the evolution of the intron/exon structure of genes. **1995**, 92, 12495-9	216
1031	A type 1 serine/threonine kinase receptor that can dorsalize mesoderm in Xenopus. **1995**, 92, 6474-8	11
1030	Construction of a 2.8-megabase yeast artificial chromosome contig and cloning of the human methylthioadenosine phosphorylase gene from the tumor suppressor region on 9p21. **1995**, 92, 6489-93	67
1029	The biosynthetic gene cluster for the polyketide immunosuppressant rapamycin. **1995**, 92, 7839-43	397
1028	Protein secretion by enteropathogenic Escherichia coli is essential for transducing signals to epithelial cells. **1995**, 92, 7991-5	218

1027	Complete sequence of the bithorax complex of Drosophila. **1995**, 92, 8398-402	147
1026	The urease locus of Mycobacterium tuberculosis and its utilization for the demonstration of allelic exchange in Mycobacterium bovis bacillus Calmette-Guf̂in. **1995**, 92, 8768-72	91
1025	Identification and characterization of putative transposable DNA elements in solanaceous plants and Caenorhabditis elegans. **1995**, 92, 8886-90	47
1024	Enhanced expression of an insulin growth factor-like binding protein (mac25) in senescent human mammary epithelial cells and induced expression with retinoic acid. **1995**, 92, 4472-6	175
1023	Isolation and characterization of a MAGE gene family in the Xp21.3 region. **1995**, 92, 4987-91	85
1022	Rapid mass spectrometric peptide sequencing and mass matching for characterization of human melanoma proteins isolated by two-dimensional PAGE. **1995**, 92, 5072-6	200
1021	Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulated by cellular O2 tension. **1995**, 92, 5510-4	4772
1020	Isolation of multiple sequences from the Plasmodium falciparum genome that encode conserved domains homologous to those in erythrocyte-binding proteins. **1995**, 92, 7100-4	100
1019	Dominance of one bacterial phylotype at a Mid-Atlantic Ridge hydrothermal vent site. **1995**, 92, 7232-6	172
1018	Functional complementation of the ste6 gene of Saccharomyces cerevisiae with the pfmdr1 gene of Plasmodium falciparum. **1995**, 92, 8921-5	76
1017	Murine eotaxin: an eosinophil chemoattractant inducible in endothelial cells and in interleukin 4-induced tumor suppression. **1995**, 92, 8960-4	308
1016	A protein-binding domain, EH, identified in the receptor tyrosine kinase substrate Eps15 and conserved in evolution. **1995**, 92, 9530-4	135
1015	The genome of Caenorhabditis elegans. **1995**, 92, 10836-40	120
1014	Growth and developmental functions of a human immunodeficiency virus Tat-binding protein/26S protease subunit homolog from Dictyostelium discoideum. **1995**, 15, 1725-36	8
1013	Definition of a metal-dependent/Li(+)-inhibited phosphomonoesterase protein family based upon a conserved three-dimensional core structure. **1995**, 92, 5149-53	144
1012	Identification of NAB1, a repressor of NGFI-A- and Krox20-mediated transcription. **1995**, 92, 6873-7	229
1011	Nodulating strains of Rhizobium loti arise through chromosomal symbiotic gene transfer in the environment. **1995**, 92, 8985-9	358
1010	Programmed DNA rearrangement of a cyanobacterial hupL gene in heterocysts. **1995**, 92, 791-5	132

1009	A Nodule-Specific Gene Encoding a Subtilisin-Like Protease Is Expressed in Early Stages of Actinorhizal Nodule Development. **1995**, 7, 785	1
1008	Functional expression of a myo-inositol/H+ symporter from Leishmania donovani. **1995**, 15, 5508-15	58
1007	Isolation of a gene encoding a functional zinc finger protein homologous to erythroid Krüppel-like factor: identification of a new multigene family. **1995**, 15, 5957-65	216
1006	Identification of a new family of tissue-specific basic helix-loop-helix proteins with a two-hybrid system. **1995**, 15, 3813-22	601
1005	Purification and characterization of nitric oxide synthase (NOSNoc) from a Nocardia species. **1995**, 177, 5122-8	103
1004	Identification of Rhizobium-specific intergenic mosaic elements within an essential two-component regulatory system of Rhizobium species. **1995**, 177, 5485-94	69
1003	The gene for the longest known Escherichia coli protein is a member of helicase superfamily II. **1995**, 177, 5393-400	32
1002	Identification of genes negatively regulated by Fis: Fis and RpoS comodulate growth-phase-dependent gene expression in Escherichia coli. **1995**, 177, 938-47	109
1001	Identification and characterization of two nitrogen-regulated genes of the cyanobacterium Synechococcus sp. strain PCC7942 required for maximum efficiency of nitrogen assimilation. **1995**, 177, 290-6	57
1000	Cloning and characterization of the Streptomyces peucetius dnrQS genes encoding a daunosamine biosynthesis enzyme and a glycosyl transferase involved in daunorubicin biosynthesis. **1995**, 177, 6688-92	89
999	Purification from Fusobacterium mortiferum ATCC 25557 of a 6-phosphoryl-O-alpha-D-glucopyranosyl:6-phosphoglucohydrolase that hydrolyzes maltose 6-phosphate and related phospho-alpha-D-glucosides. **1995**, 177, 2505-12	41
998	Characterization of the lactococcal abiD1 gene coding for phage abortive infection. **1995**, 177, 3818-23	79
997	Identification of two targets of the type III protein secretion system encoded by the inv and spa loci of Salmonella typhimurium that have homology to the Shigella IpaD and IpaA proteins. **1995**, 177, 7078-85	210
996	A new regulatory element modulates homoserine lactone-mediated autoinduction of Ti plasmid conjugal transfer. **1995**, 177, 449-58	126
995	Characterization of four superoxide dismutase genes from a filamentous cyanobacterium. **1995**, 177, 964-72	49
994	Identification and sequence analysis of lpfABCDE, a putative fimbrial operon of Salmonella typhimurium. **1995**, 177, 2087-97	146
993	Molecular and expression analysis of the Rhizobium meliloti phosphoenolpyruvate carboxykinase (pckA) gene. **1995**, 177, 1452-60	62
992	Aerobic and anaerobic regulation in Rhodobacter sphaeroides 2.4.1: the role of the fnrL gene. **1995** , 177, 6422-31	115

991	Organization and growth phase-dependent transcription of methane genes in two regions of the Methanobacterium thermoautotrophicum genome. **1995**, 177, 2460-8	46
990	Degradation of the thiocarbamate herbicide EPTC (S-ethyl dipropylcarbamothioate) and biosafening by Rhodococcus sp. strain NI86/21 involve an inducible cytochrome P-450 system and aldehyde dehydrogenase. **1995**, 177, 676-87	152
989	The octopine-type Ti plasmid pTiA6 of Agrobacterium tumefaciens contains a gene homologous to the chromosomal virulence gene acvB. **1995**, 177, 892-7	29
988	Genomic DNA sequencing methods. **1995**, 48, 551-69	21
987	Identification of cutC and cutF (nlpE) genes involved in copper tolerance in Escherichia coli. **1995**, 177, 4207-15	90
986	Genes required for cellulose synthesis in Agrobacterium tumefaciens. **1995**, 177, 1069-75	179
985	Analysis of the syrB and syrC genes of Pseudomonas syringae pv. syringae indicates that syringomycin is synthesized by a thiotemplate mechanism. **1995**, 177, 4009-20	82
984	Isolation of a novel paraquat-inducible (pqi) gene regulated by the soxRS locus in Escherichia coli. **1995**, 177, 2673-8	41
983	Identification of a second cellulose synthase gene (acsAII) in Acetobacter xylinum. **1995**, 177, 5276-83	75
982	Sequence, expression, and function of the gene for the nonphosphorylating, NADP-dependent glyceraldehyde-3-phosphate dehydrogenase of Streptococcus mutans. **1995**, 177, 2622-7	61
981	aldB, an RpoS-dependent gene in Escherichia coli encoding an aldehyde dehydrogenase that is repressed by Fis and activated by Crp. **1995**, 177, 3166-75	65
980	Glutathione is required for maximal transcription of the cobalamin biosynthetic and 1,2-propanediol utilization (cob/pdu) regulon and for the catabolism of ethanolamine, 1,2-propanediol, and propionate in Salmonella typhimurium LT2. **1995**, 177, 5434-9	52
979	Analysis of clustered genes encoding both early and late steps in daunomycin biosynthesis by Streptomyces sp. strain C5. **1995**, 177, 536-43	55
978	Parallelism in LASSAP, a large scale sequence comparisons package. **1995**, 787-792	
977	Cellular localization of dopamine D2 receptor messenger RNA in the rat trigeminal ganglion. **1995**, 81, 1181-5	7
976	Localization and Characterization of a Novel 20 kDa Polypeptide in the Chloroplast of the Green Alga Dunaliella salina. **1995**,	
975	Homology model building of the HMG-1 box structural domain. **1995**, 23, 1019-29	22
974	The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain. **1995**, 306 (Pt 2), 505-12	49

973	Isolation and characterization of cDNA clones encoding pig gastric mucin. **1995**, 308 (Pt 1), 89-96	24
972	Purification and characterization of the cell-wall-associated and extracellular alpha-glucosidases from Saccharomycopsis fibuligera. **1995**, 308 (Pt 3), 753-60	12
971	The embryonic RNA helicase gene (ERH): a new member of the DEAD box family of RNA helicases. **1995**, 308 (Pt 3), 839-46	23
970	Structure of the human aggrecan gene: exon-intron organization and association with the protein domains. **1995**, 309 (Pt 2), 535-42	58
969	The napEDABC gene cluster encoding the periplasmic nitrate reductase system of Thiosphaera pantotropha. **1995**, 309 (Pt 3), 983-92	133
968	Evolutionary conservation of the vertebrate Ah (dioxin) receptor: amplification and sequencing of the PAS domain of a teleost Ah receptor cDNA. **1995**, 310 (Pt 2), 383-7	55
967	The DAG family of glycosyl hydrolases combines two previously identified protein families. **1995**, 311 (Pt 1), 349-50	18
966	Purification and characterization of a uterine retinol-binding protein in the bitch. **1995**, 311 (Pt 2), 407-15	15
965	Factor IX Zutphen: a Cys18-->Arg mutation results in formation of a heterodimer with alpha 1-microglobulin and the inability to form a calcium-induced conformation. **1995**, 311 (Pt 3), 753-9	11
964	Cloning of the Schizosaccharomyces pombe gene encoding diadenosine 5’,5"’-P1,P4-tetraphosphate (Ap4A) asymmetrical hydrolase: sequence similarity with the histidine triad (HIT) protein family. **1995**, 312 (Pt 3), 925-32	78
963	Cloning of electron-transferring flavoprotein from Megasphaera elsdenii. **1995**, 23, 379S	3
962	Purification and characterization of three extracellular (1-->3)-beta-D-glucan glucohydrolases from the filamentous fungus Acremonium persicinum. **1995**, 308 (Pt 3), 733-41	34
961	Molecular cloning and expression of cDNA encoding the rat UDP-N-acetylglucosamine:alpha-6-D-mannoside beta-1,2-N-acetylglucosaminyltransferase II. **1995**, 270, 15211-21	47
960	Cloning and nucleotide sequence of the gene coding for the major 25-kilodalton outer membrane protein of Brucella abortus. **1995**, 177, 1911-4	35
959	The potential role of basic fibroblast growth factor in the transformation of cultured primary human fetal astrocytes and the proliferation of human glioma (U-87) cells. **1995**, 37, 723-30; discussion 730-2	16
958	Derived structure of the putative sialic acid transporter from Escherichia coli predicts a novel sugar permease domain. **1995**, 177, 6005-10	63
957	The novel flightless-I gene brings together two gene families, actin-binding proteins related to gelsolin and leucine-rich-repeat proteins involved in Ras signal transduction. **1995**, 12, 405-14	41
956	Homologs of the Shigella IpaB and IpaC invasins are required for Salmonella typhimurium entry into cultured epithelial cells. **1995**, 177, 3965-71	258

955	Novel DNA binding motifs in the DNA repair enzyme endonuclease III crystal structure.. **1995**, 14, 4108-4120	378
954	Molecular cloning and sequence analysis of expansins--a highly conserved, multigene family of proteins that mediate cell wall extension in plants. **1995**, 92, 9245-9	206
953	Genes encoded on a cyanobacterial plasmid are transcriptionally regulated by sulfur availability and CysR. **1995**, 177, 2143-50	48
952	Identification of Lrp-regulated genes by inverse PCR and sequencing: regulation of two mal operons of Escherichia coli by leucine-responsive regulatory protein. **1995**, 177, 2679-83	26
951	Genetic analysis of the modABCD (molybdate transport) operon of Escherichia coli. **1995**, 177, 4851-6	89
950	Cloning and characterization of MgtE, a putative new class of Mg2+ transporter from Bacillus firmus OF4. **1995**, 177, 1233-8	99
949	Retrovirus gene traps. **1995**, 254, 263-75	9
948	Serum induction of RhoG expression. **1995**, 256, 151-62	
947	Chapter 24 LargeScale Complementary DNA Sequencing Methods. **1995**, 571-582	8
946	MentatApplying the Object-Oriented Paradigm to Parallel Processing. **1995**, 223-242	
945	[7] Receptor cloning: High-throughput sequencing of cDNA tags for identification of novel genes. **1995**, 25, 126-141	
944	[20] Computational Analyses Aiding Identification and Characterization of Proteins, Genes, and Operons. **1995**, 375-386	1
943	In gel digestion of SDS PAGE-Separated proteins: Observations from internal sequencing of 25 proteins. **1995**, 6, 143-152	28
942	Comparative methods for identifying functional domains in protein sequences. **1995**, 1, 129-47	4
941	Identification and isolation of a gene required for nitrate assimilation and anaerobic growth of Bacillus subtilis. **1995**, 177, 1112-5	50
940	MOP2 (SLA2) affects the abundance of the plasma membrane H(+)-ATPase of Saccharomyces cerevisiae. **1995**, 270, 6815-23	49
939	Genetic analysis of the dTDP-rhamnose biosynthesis region of the Escherichia coli VW187 (O7:K1) rfb gene cluster: identification of functional homologs of rfbB and rfbA in the rff cluster and correct location of the rffE gene. **1995**, 177, 5539-46	89
938	Capsular polysaccharide biosynthesis and pathogenicity in Erwinia stewartii require induction by an N-acylhomoserine lactone autoinducer. **1995**, 177, 5000-8	232

937	Cloning and characterization of a polyketide synthase gene from Streptomyces fradiae Tü2717, which carries the genes for biosynthesis of the angucycline antibiotic urdamycin A and a gene probably involved in its oxygenation. **1995**, 177, 6126-36	81
936	Characterization of the polyketide synthase gene (pksL1) required for aflatoxin biosynthesis in Aspergillus parasiticus. **1995**, 177, 6246-54	96
935	Molecular analysis of a metalloprotease from Proteus mirabilis. **1995**, 177, 5790-8	60
934	Two highly similar multidrug transporters of Bacillus subtilis whose expression is differentially regulated. **1995**, 177, 3904-10	159
933	Phage inhibition, colicin resistance, and tellurite resistance are encoded by a single cluster of genes on the IncHI2 plasmid R478. **1995**, 177, 5016-27	80
932	AinS and a new family of autoinducer synthesis proteins. **1995**, 177, 6946-51	157
931	Characterization of the proton/glutamate symport protein of Bacillus subtilis and its functional expression in Escherichia coli. **1995**, 177, 2863-9	47
930	Genetic and molecular characterization of the polar flagellum of Vibrio parahaemolyticus. **1995**, 177, 1595-609	92
929	Characterization of MarR, the repressor of the multiple antibiotic resistance (mar) operon in Escherichia coli. **1995**, 177, 3414-9	169
928	The sequence of phosphatidylinositol-4-phosphate 5-kinase defines a novel family of lipid kinases. **1995**, 270, 2881-4	118
927	Lateral transfer of rfb genes: a mobilizable ColE1-type plasmid carries the rfbO:54 (O:54 antigen biosynthesis) gene cluster from Salmonella enterica serovar Borreze. **1995**, 177, 5247-53	35
926	The disease-resistance gene Pto and the fenthion-sensitivity gene fen encode closely related functional protein kinases. **1995**, 92, 4181-4	50
925	Cloning and sequencing of CATR1.3, a human gene associated with tumorigenic conversion. **1995**, 92, 6409-13	7
924	Identification of the Bacillus subtilis pur operon repressor. **1995**, 92, 7455-9	76
923	Identification and characterization of a TFIID-like multiprotein complex from Saccharomyces cerevisiae. **1995**, 92, 8224-8	118
922	Identification of a member of the interferon regulatory factor family that binds to the interferon-stimulated response element and activates expression of interferon-induced genes. **1995**, 92, 11657-61	329
921	Mutations altering the mitochondrial-cytoplasmic distribution of Mod5p implicate the actin cytoskeleton and mRNA 3’ ends and/or protein synthesis in mitochondrial delivery. **1995**, 15, 6884-94	71
920	Synthetic lethality of sep1 (xrn1) ski2 and sep1 (xrn1) ski3 mutants of Saccharomyces cerevisiae is independent of killer virus and suggests a general role for these genes in translation control. **1995**, 15, 2719-27	78

919	Identification genes that are differentially expressed during aging in Caenorhabditis elegans. **1995**, 50, B245-53	19
918	Cellular Localization of Dopamine D2 Receptor Messenger RNA in the Rat Trigeminal Ganglion. **1995**, 81, 1181-1185	18
917	Rapid method for detection of Aspergillus 5S ribosomal RNA using a genus-specific oligonucleotide probe. **1995**, 103, 48-51	47
916	Transposon tagging of tobacco mosaic virus resistance gene N: its possible role in the TMV-N-mediated signal transduction pathway. **1995**, 92, 4175-80	95
915	Extraordinary divergence and positive Darwinian selection in a fusagenic protein coating the acrosomal process of abalone spermatozoa. **1995**, 92, 4957-61	117
914	Molecular cloning and expression of the 32-kDa subunit of human TFIID reveals interactions with VP16 and TFIIB that mediate transcriptional activation. **1995**, 92, 5788-92	105
913	Molecular cloning of the transcription factor TFIIB homolog from Sulfolobus shibatae. **1995**, 92, 6077-81	49
912	Sequence analysis of a mannitol dehydrogenase cDNA from plants reveals a function for the pathogenesis-related protein ELI3. **1995**, 92, 7148-52	102
911	Sequence analysis of the cis-regulatory regions of the bithorax complex of Drosophila. **1995**, 92, 8403-7	32
910	Cloning, expression, and function of TFC5, the gene encoding the B" component of the Saccharomyces cerevisiae RNA polymerase III transcription factor TFIIIB. **1995**, 92, 9786-90	94
909	Sequence similarity analysis of Escherichia coli proteins: functional and evolutionary implications. **1995**, 92, 11921-5	96
908	The salivary gland-specific apyrase of the mosquito Aedes aegypti is a member of the 5'-nucleotidase family. **1995**, 92, 694-8	209
907	A small RNA acts as an antisilencer of the H-NS-silenced rcsA gene of Escherichia coli. **1995**, 92, 2003-7	195
906	Mutation avoidance and DNA repair proficiency in Ustilago maydis are differentially lost with progressive truncation of the REC1 gene product. **1995**, 15, 5329-38	23
905	Wiskott-Aldrich syndrome protein physically associates with Nck through Src homology 3 domains. **1995**, 15, 5725-31	298
904	Interaction cloning of Rabin3, a novel protein that associates with the Ras-like GTPase Rab3A. **1995**, 15, 1137-43	70
903	The Saccharomyces SHP1 gene, which encodes a regulator of phosphoprotein phosphatase 1 with differential effects on glycogen metabolism, meiotic differentiation, and mitotic cell cycle progression. **1995**, 15, 2037-50	65
902	Expression and functional analysis of a baculovirus gene encoding a truncated protein kinase homolog. **1995**, 206, 314-23	32

901	Analysis of 45 kb of DNA located at the left end of the chlorella virus PBCV-1 genome. **1995**, 206, 339-52	54
900	Alterations in gene expression associated with changes in the state of endothelial differentiation. **1995**, 58, 217-26	19
899	Two different subunits of importin cooperate to recognize nuclear localization signals and bind them to the nuclear envelope. **1995**, 5, 383-92	425
898	Conserved sequence motifs in bacterial and bacteriophage chaperonins. **1995**, 20, 14-5	32
897	Ready for a motif submission? A proposed checklist. **1995**, 20, 104	34
896	Common sequence and structural features in the heat-shock factor and Ets families of DNA-binding domains. **1995**, 20, 225-6	15
895	Dali: a network tool for protein structure comparison. **1995**, 20, 478-80	1275
894	The first prokaryotic lipocalins. **1995**, 20, 498-9	23
893	Molecular Tools for the Genetic Modification of Dairy Lactobacilli. **1995**, 18, 493-503	11
892	Evolutionary Analysis of the Spotted Fever and Thyphus Groups of Rickettsia Using 16S rRNA Gene Sequences. **1995**, 18, 52-61	86
891	Molecular Cloning and DNA Sequence Analysis of Pepl, a Leucyl Aminopeptidase Gene from Lactobacillus delbrueckii Subsp. Lactis DSM7290. **1995**, 228, 570-578	19
890	Characterization of a 45-kDa flavoprotein and evidence for a rubredoxin, two proteins that could participate in electron transport from H2 to CO2 in methanogenesis in Methanobacterium thermoautotrophicum. **1995**, 231, 628-38	29
889	The energy conserving N5-methyltetrahydromethanopterin:coenzyme M methyltransferase complex from Methanobacterium thermoautotrophicum is composed of eight different subunits. **1995**, 228, 640-8	60
888	Examination of fibronectin distribution and its sources in the regenerating newt limb by immunocytochemistry and in situ hybridization. **1995**, 202, 153-64	28
887	Molecular cloning of tyrosine kinases in the early Xenopus embryo: identification of Eck-related genes expressed in cranial neural crest cells of the second (hyoid) arch. **1995**, 203, 119-40	32
886	Thrombospondin-4 is expressed by early osteogenic tissues in the chick embryo. **1995**, 203, 477-90	50
885	Purification and characterization of fatty acid-binding protein from aerobic muscle of the Antarctic icefish Chaenocephalus aceratus. **1995**, 273, 190-203	24
884	Proteins of crustacean exoskeleton: IV. Partial amino acid sequences of exoskeletal proteins from the Bermuda land crab, Gecarcinus lateralis, and comparisons to certain insect proteins. **1995**, 273, 389-400	13

883	Zebrafish neurons express two L1-related molecules during early axonogenesis. **1995**, 42, 547-61	57
882	Tissue-specific variation in the length of the 5' untranslated region of the beta A-inhibin mRNA in sheep. **1995**, 40, 1-8	2
881	Cloning and partial characterization of the cDNA encoding the fox sperm protein FSA-Acr.1 with similarities to the SP-10 antigen. **1995**, 40, 242-52	22
880	Modulation of gene expression in the preimplantation mouse embryo by TGF-alpha and TGF-beta. **1995**, 41, 133-9	43
879	Allelic polymorphism in the hamster oviductin gene is due to a variable number of mucin-like tandem repeats. **1995**, 42, 388-96	16
878	The major dermatomyositis-specific Mi-2 autoantigen is a presumed helicase involved in transcriptional activation. **1995**, 38, 1389-99	117
877	A 200-amino acid ATPase module in search of a basic function. **1995**, 17, 639-50	326
876	In situ hybridization reveals transient laminin B-chain expression by individual glial and muscle cells in embryonic leech central nervous system. **1995**, 27, 1-14	9
875	Filarin, a novel invertebrate intermediate filament protein present in axons and perikarya of developing and mature leech neurons. **1995**, 27, 227-39	16
874	MDScope ▯a visual computing environment for structural biology. **1995**, 91, 111-133	39
873	Immunodominance with progenitor B cell diversity in the neutralizing antibody repertoire to influenza infection. **1995**, 25, 1803-9	12
872	Human CD6 possesses a large, alternatively spliced cytoplasmic domain. **1995**, 25, 2765-9	31
871	Separation of heat-stable proteins from Thermus thermophilus HB8 by two-dimensional electrophoresis. **1995**, 16, 1060-6	18
870	Sequence analysis of wheat grain allergens separated by two-dimensional electrophoresis with immobilized pH gradients. **1995**, 16, 1115-9	66
869	Demethylation of a repetitive DNA sequence in human cancers. **1995**, 16, 227-32	29
868	Characterization of a gene trap insertion into a novel gene, cordon-bleu, expressed in axial structures of the gastrulating mouse embryo. **1995**, 17, 141-54	60
867	Tyrosine protein kinase expression in long-term quiescent WI-38 cells following growth factor simulation. **1995**, 59, 42-52	1
866	Molecular cloning of a mouse epithelial protein-tyrosine phosphatase with similarities to submembranous proteins. **1995**, 59, 418-30	52

865	Genomic structure of a cytoplasmic dynein heavy chain gene from the nematode Caenorhabditis elegans. **1995**, 32, 26-36	21
864	In situ hybridization analysis of CHOT1, a creatine transporter, in the rat central nervous system. **1995**, 351, 94-103	40
863	Differential expression of mGluR5 metabotropic glutamate receptor mRNA by rat striatal neurons. **1995**, 354, 241-52	167
862	The Tri4 gene of Fusarium sporotrichioides encodes a cytochrome P450 monooxygenase involved in trichothecene biosynthesis. **1995**, 248, 95-102	95
861	A pAO1-encoded molybdopterin cofactor gene (moaA) of Arthrobacter nicotinovorans: characterization and site-directed mutagenesis of the encoded protein. **1995**, 164, 142-51	25
860	The Aspergillus parasiticus polyketide synthase gene pksA, a homolog of Aspergillus nidulans wA, is required for aflatoxin B1 biosynthesis. **1995**, 248, 270-7	107
859	Characterization of the let-653 gene in Caenorhabditis elegans. **1995**, 248, 719-26	32
858	Sequence and transcriptional analysis of a near-terminal region of the orf virus genome. **1995**, 11, 21-9	13
857	Predicted structure of the adenovirus DNA binding protein. **1995**, 9, 171-5	1
856	Sequence and transcriptional analysis of an orf virus gene encoding ankyrin-like repeat sequences. **1995**, 9, 277-82	19
855	Cloning and sequence homology of a rat UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase. **1995**, 12, 901-9	33
854	Guest Editor’s foreword. **1995**, 13, 1-6	
853	Linear-space algorithms that build local alignments from fragments. **1995**, 13, 106-134	19
852	Primary structure and eubacterial relationships of the pyruvate:Ferredoxin oxidoreductase of the amitochondriate eukaryoteTrichomonas vaginalis. **1995**, 41, 388-396	110
851	A homolog of the Rhizobium meliloti nitrogen fixation gene fixN is involved in the production of a microaerobically induced oxidase activity in the phytopathogenic bacterium Agrobacterium tumefaciens. **1995**, 247, 206-15	22
850	An unusual group 2 LEA gene family in citrus responsive to low temperature. **1995**, 29, 11-23	52
849	Molecular cloning and expression of a turgor-responsive gene in Brassica napus. **1995**, 27, 541-51	64
848	Molecular characterization of a glyoxysomal citrate synthase that is synthesized as a precursor of higher molecular mass in pumpkin. **1995**, 27, 377-90	56

847	Complete sequence of the binary vector Bin 19. **1995**, 27, 405-9	118
846	Atypical phytochrome gene structure in the green alga Mesotaenium caldariorum. **1995**, 29, 1127-42	79
845	The macrophage-specific membrane protein Nramp controlling natural resistance to infections in mice has homologues expressed in the root system of plants. **1995**, 29, 1181-96	41
844	The maize GapC4 promoter confers anaerobic reporter gene expression and shows homology to the maize anthocyanin regulatory locus C1. **1995**, 29, 1293-8	15
843	Structure and expression of LeMA-1, a tomato protein belonging to the SEC18-PAS1-CDC48-TBP-1 protein family of putative Mg(2+)-dependent ATPases. **1995**, 27, 1109-18	17
842	A role for glutamate decarboxylase during tomato ripening: the characterisation of a cDNA encoding a putative glutamate decarboxylase with a calmodulin-binding site. **1995**, 27, 1143-51	46
841	Characterization of the nuclear gene encoding mitochondrial aconitase in the marine red alga Gracilaria verrucosa. **1995**, 28, 635-46	17
840	Specificity in the immobilisation of cell wall proteins in response to different elicitor molecules in suspension-cultured cells of French bean (Phaseolus vulgaris L.). **1995**, 28, 1075-87	59
839	Identification and characterization of genes with unstable transcripts (GUTs) in tobacco. **1995**, 28, 27-38	29
838	Characterization of cDNA clones for differentially expressed genes in embryos of dormant and nondormant Avena fatua L. caryopses. **1995**, 28, 113-22	72
837	A salinity-induced gene from the halophyte M. crystallinum encodes a glycolytic enzyme, cofactor-independent phosphoglyceromutase. **1995**, 29, 213-26	46
836	Essential light chain of Drosophila nonmuscle myosin II. **1995**, 16, 491-8	16
835	Expression of the Ruminococcus flavefaciens cellodextrinase gene in Saccharomyces cerevisiae. **1995**, 17, 481-486	6
834	Pervasive migration of organellar DNA to the nucleus in plants. **1995**, 41, 397-406	83
833	A Drosophila hsp70 gene contains long, antiparallel, coupled open reading frames (LAC ORFs) conserved in homologous loci. **1995**, 41, 414-20	28
832	Statistical analysis of vertebrate sequences reveals that long genes are scarce in GC-rich isochores. **1995**, 40, 308-17	210
831	Gypsy/Ty3-class retrotransposons integrated in the DNA of herring, tunicate, and echinoderms. **1995**, 40, 13-24	41
830	Phylogenetic relationships among transposon-like elements in human and primate DNA. **1995**, 40, 127-35	5

829	The molecular cloning of a phospholipase A2 from Bothrops jararacussu snake venom: evolution of venom group II phospholipase A2's may imply gene duplications. **1995**, 41, 174-9	41
828	Major histocompatibility complex class II A gene polymorphism in the striped bass. **1995**, 41, 229-38	43
827	Three new immunoglobulin kappa variable (Igk-V) gene segments in the mouse. **1995**, 41, 334	1
826	A BC200-derived element and Z-DNA as structural markers in annexin I genes: relevance to Alu evolution and annexin tetrad formation. **1995**, 41, 979-85	10
825	The RecA protein as a model molecule for molecular systematic studies of bacteria: comparison of trees of RecAs and 16S rRNAs from the same species. **1995**, 41, 1105-23	176
824	Caenorhabditis elegans contains genes encoding two new members of the Zn-containing alcohol dehydrogenase family. **1995**, 41, 46-53	12
823	Primary structure and eubacterial relationships of the pyruvate:Ferredoxin oxidoreductase of the amitochondriate eukaryote Trichomonas vaginalis. **1995**, 41, 388	2
822	Hamster cDNA homologs to the mouse immunoglobulin IgG2 constant and Igh-VH10 genes. **1995**, 42, 225-6	5
821	Hamster cDNA homologs to the mouse immunoglobulin kappa constant and Igk-V 45.1 genes. **1995** , 42, 227-8	5
820	A genomic clone containing a telomere array maps near the centromere of mouse chromosome 6. **1995**, 6, 96-102	9
819	Characterization of murine mannose-binding protein genes Mbl1 and Mbl2 reveals features common to other collectin genes. **1995**, 6, 103-10	56
818	Characterization and mapping of three new mammalian ATP-binding transporter genes from an EST database. **1995**, 6, 114-7	25
817	Localization of three genes expressed in retina on mouse chromosome 11. **1995**, 6, 142-4	9
816	Molecular cloning of the meiosis-induced rec10 gene of Schizosaccharomyces pombe. **1995**, 27, 440-6	26
815	Cloning and analysis of the nuclear gene MRP-S9 encoding mitochondrial ribosomal protein S9 of Saccharomyces cerevisiae. **1995**, 28, 26-31	11
814	Intron-encoded open reading frame of the GIY-YIG subclass in a plastid gene. **1995**, 28, 97-9	7
813	A group-I intron in the mitochondrial small subunit ribosomal RNA gene of Sclerotinia sclerotiorum. **1995**, 27, 166-76	24
812	The novel nuclear gene DSS-1 of Saccharomyces cerevisiae is necessary for mitochondrial biogenesis. **1995**, 28, 108-12	57

811	A family of rapidly evolving genes from the sex reversal critical region in Xp21. **1995**, 6, 571-80	48
810	Identifying genes within microdissected genomic DNA: isolation of brain expressed genes from a translocation region associated with inherited mental illness. **1995**, 6, 257-62	5
809	The murine form of TXK, a novel TEC kinase expressed in thymus maps to chromosome 5. **1995**, 6, 476-80	9
808	New MADS box domains in Asparagus officinalis L.. **1995**, 8, 318	4
807	The CLS2 gene encodes a protein with multiple membrane-spanning domains that is important Ca2+ tolerance in yeast. **1995**, 246, 269-81	30
806	Abscisic acid-dependent and -independent regulation of gene expression by progressive drought in Arabidopsis thaliana. **1995**, 246, 10-8	164
805	Twintrons are not unique to the Euglena chloroplast genome: structure and evolution of a plastome cpn60 gene from a cryptomonad. **1995**, 246, 128-31	21
804	Recombination between heterologous linear and circular mitochondrial plasmids in the fungus Neurospora. **1995**, 249, 25-36	15
803	A chlorophyll synthetase gene from Arabidopsis thaliana. **1995**, 249, 58-64	58
802	The transformation booster sequence from Petunia hybrida is a retrotransposon derivative that binds to the nuclear scaffold. **1995**, 247, 614-22	30
801	Two enzymes together capable of cysteine biosynthesis are encoded on a cyanobacterial plasmid. **1995**, 247, 623-32	33
800	A novel zinc finger protein encoded by a couch potato homologue from Solanum tuberosum enables a sucrose transport-deficient yeast strain to grow on sucrose. **1995**, 247, 759-63	16
799	Overexpression of a novel member of the mitochondrial carrier family rescues defects in both DNA and RNA metabolism in yeast mitochondria. **1995**, 246, 426-36	38
798	Regulation of the expression of three housekeeping genes encoding subunits of the Neurospora crassa vacuolar ATPase. **1995**, 249, 317-27	9
797	Extension of the Rhizobium meliloti succinoglycan biosynthesis gene cluster: identification of the exsA gene encoding an ABC transporter protein, and the exsB gene which probably codes for a regulator of succinoglycan biosynthesis. **1995**, 249, 487-97	58
796	Monitoring the efficacy of hybrid selection during positional cloning: the search for BRCA1. **1995**, 6, 873-9	6
795	The mushroom-inducing gene Frt1 of Schizophyllum commune encodes a putative nucleotide-binding protein. **1995**, 247, 358-66	17
794	Molecular cloning and characterization of the dpy-20 gene of Caenorhabditis elegans. **1995**, 247, 367-78	31

793	A lipase of Aeromonas hydrophila showing nonhemolytic phospholipase C activity. **1995**, 31, 28-33	19
792	Analysis of the cbbF genes from Alcaligenes eutrophus that encode fructose-1,6-/sedoheptulose-1,7-bisphosphatase. **1995**, 31, 55-61	22
791	Identification, characterization, and localization to chromosome 17q21-22 of the human TBX2 homolog, member of a conserved developmental gene family. **1995**, 6, 793-7	41
790	The detection of the mRNAs of procollagen types I, II and III in human fetal fingers by in situ hybridization using digoxigenin-labelled oligonucleotide probes. **1995**, 27, 309-17	9
789	The cycHJKL genes of Rhizobium meliloti involved in cytochrome c biogenesis are required for "respiratory" nitrate reduction ex planta and for nitrogen fixation during symbiosis. **1995**, 247, 39-47	46
788	The cytidylyltransferase superfamily: identification of the nucleotide-binding site and fold prediction. **1995**, 22, 259-66	81
787	Fold recognition and ab initio structure predictions using hidden Markov models and beta-strand pair potentials. **1995**, 23, 398-402	62
786	Nucleotide sequence and analysis of the centromeric region of yeast chromosome IX. **1995**, 11, 61-78	19
785	The sequence of a 13.5 kb DNA segment from the left arm of yeast chromosome XIV reveals MER1; RAP1; a new putative member of the DNA replication complex and a new putative serine/threonine phosphatase gene. **1995**, 11, 85-91	9
784	The IFH1 gene product interacts with a fork head protein in Saccharomyces cerevisiae. **1995**, 11, 261-70	29
783	Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the RPD3, PAS8 and KRE1 loci, five new open reading frames. **1995**, 11, 567-72	15
782	Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading frames, including TPS2, PPH3, RAD55, SED1, PDC2, AFR1, SSS1, SLU7 and a tRNA for arginine. **1995**, 11, 673-9	3
781	Sequence, map position and genome organization of the RPL17B gene, encoding ribosomal protein L17b in Saccharomyces cerevisiae. **1995**, 11, 761-6	
780	The DNA sequence of a 7941 bp fragment of the left arm of chromosome VII of Saccharomyces cerevisiae contains four open reading frames including the multicopy suppressor gene of the pop2 mutation and a putative serine/threonine protein kinase gene. **1995**, 11, 767-74	12
779	SSU71, encoding the largest subunit of TFIIF, is located on the right arm of chromosome VII in Saccharomyces cerevisiae. **1995**, 11, 789-91	3
778	The Saccharomyces cerevisiae FLO1 flocculation gene encodes for a cell surface protein. **1995**, 11, 809-22	66
777	Sequence and functional analysis of a 7.2 kb DNA fragment containing four open reading frames located between RPB5 and CDC28 on the right arm of chromosome II. **1995**, 11, 865-71	10
776	A new essential gene located on Saccharomyces cerevisiae chromosome IX. **1995**, 11, 885-90	23

775	Molecular cloning of the GTP-cyclohydrolase structural gene RIB1 of Pichia guilliermondii involved in riboflavin biosynthesis. **1995**, 11, 945-52	17
774	The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV from Saccharomyces cerevisiae. **1995**, 11, 967-74	9
773	An 8.2 kb DNA segment from chromosome XIV carries the RPD3 and PAS8 genes as well as the Saccharomyces cerevisiae homologue of the thiamine-repressed nmt1 gene and a chromosome III-duplicated gene for a putative aryl-alcohol dehydrogenase. **1995**, 11, 987-91	6
772	Sequence analysis of a 9873 bp fragment of the left arm of yeast chromosome XV that contains the ARG8 and CDC33 genes, a putative riboflavin synthase beta chain gene, and four new open reading frames. **1995**, 11, 1061-7	5
771	Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the Tyl-H3 retrotransposon, the suf1(+) frameshift suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-1a and a delta element. **1995**, 11, 1069-75	10
770	Sequencing analysis of a 24.7 kb fragment of yeast chromosome XIV identifies six known genes, a new member of the hexose transporter family and ten new open reading frames. **1995**, 11, 1077-85	14
769	The sequence of 24.3 kb from chromosome X reveals five complete open reading frames, all of which correspond to new genes, and a tandem insertion of a Ty1 transposon. **1995**, 11, 1179-86	11
768	The sequence of an 11.1 kb fragment on the left arm of Saccharomyces cerevisiae chromosome VII reveals six open reading frames including NSP49, KEM1 and four putative new genes. **1995**, 11, 1187-94	4
767	DNA sequence analysis of a 13 kbp fragment of the left arm of yeast chromosome XV containing seven new open reading frames. **1995**, 11, 1281-8	13
766	Isolation of phosphoribosylpyrophosphate synthetase (PRS1) gene from Candida albicans. **1995**, 11, 1295-302	6
765	Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, and a novel putative serine/threonine protein kinase gene. **1995**, 11, 1303-10	7
764	The sequence of a 27 kb segment on the right arm of chromosome VII from Saccharomyces cerevisiae reveals MOL1, NAT2, RPL30B, RSR1, CYS4, PEM1/CHO2, NSR1 genes and ten new open reading frames. **1995**, 11, 1421-7	4
763	The mae1 gene of Schizosaccharomyces pombe encodes a permease for malate and other C4 dicarboxylic acids. **1995**, 11, 1485-91	76
762	Nucleotide sequence of the GDS1 gene of Saccharomyces cerevisiae. **1995**, 11, 1513-8	2
761	The sequence of an 11.1 kb DNA fragment between ADH4 and ADE5 on the left arm of chromosome VII reveals the presence of eight open reading frames. **1995**, 11, 1519-23	2
760	An overview of membrane transport proteins in Saccharomyces cerevisiae. **1995**, 11, 1575-611	222
759	Identification of a eukaryotic-like protein kinase gene in Archaebacteria. **1995**, 4, 126-9	27
758	Comparison of methods for searching protein sequence databases. **1995**, 4, 1145-60	214

757	A putative FAD-binding domain in a distinct group of oxidases including a protein involved in plant development. **1995**, 4, 1243-4	37
756	The SEA module: a new extracellular domain associated with O-glycosylation. **1995**, 4, 1421-5	109
755	Multidomain organization of eukaryotic guanine nucleotide exchange translation initiation factor eIF-2B subunits revealed by analysis of conserved sequence motifs. **1995**, 4, 1608-17	53
754	Gibbs motif sampling: detection of bacterial outer membrane protein repeats. **1995**, 4, 1618-32	333
753	Predicting the structure of the light-harvesting complex II of Rhodospirillum molischianum. **1995**, 4, 1670-82	38
752	New protein functions in yeast chromosome VIII. **1995**, 4, 2424-8	27
751	Ethanol utilization regulatory protein: profile alignments give no evidence of origin through aldehyde and alcohol dehydrogenase gene fusion. **1995**, 4, 2621-4	2
750	Molecular diagnosis of Marteilia sydneyi (Paramyxea) in Sydney rock oysters, Saccostrea commercialis (Angas). **1995**, 18, 507-510	15
749	A missense mutation in rpoD results in an A-signalling defect in Myxococcus xanthus. **1995**, 18, 943-52	39
748	A new RNA polymerase sigma factor, sigma F, is required for the late stages of morphological differentiation in Streptomyces spp. **1995**, 17, 37-48	102
747	SepA, the major extracellular protein of Shigella flexneri: autonomous secretion and involvement in tissue invasion. **1995**, 17, 123-35	168
746	Identification and characterization of a cell envelope protein of Haemophilus influenzae contributing to phase variation in colony opacity and nasopharyngeal colonization. **1995**, 17, 555-64	52
745	An rpoE-like locus controls outer membrane protein synthesis and growth at cold temperatures and high pressures in the deep-sea bacterium Photobacterium sp. strain SS9. **1995**, 17, 713-26	77
744	Functional conservation of the Salmonella and Shigella effectors of entry into epithelial cells. **1995**, 17, 781-9	118
743	Molecular characterization and transcriptional analysis of a multidrug resistance gene cloned from the pristinamycin-producing organism, Streptomyces pristinaespiralis. **1995**, 17, 989-99	48
742	The unrelated surface proteins ActA of Listeria monocytogenes and IcsA of Shigella flexneri are sufficient to confer actin-based motility on Listeria innocua and Escherichia coli respectively. **1995**, 18, 413-23	153
741	Expression of two csg operons is required for production of fibronectin- and Congo red-binding curli polymers in Escherichia coli K-12. **1995**, 18, 661-670	387
740	Plasmodium falciparum protein associated with the invasion junction contains a conserved oxidoreductase domain. **1995**, 15, 463-71	20

739	The genetic basis of colony opacity in Streptococcus pneumoniae: evidence for the effect of box elements on the frequency of phenotypic variation. **1995**, 16, 215-27	50
738	The fimA locus of Streptococcus parasanguis encodes an ATP-binding membrane transport system. **1995**, 15, 849-63	91
737	The tyrosine-6 hydroxyl of gamma delta resolvase is not required for the DNA cleavage and rejoining reactions. **1995**, 15, 865-70	25
736	Characterization and distribution of two insertion sequences, IS1191 and iso-IS981, in Streptococcus thermophilus: does intergeneric transfer of insertion sequences occur in lactic acid bacteria co-cultures?. **1995**, 16, 69-78	64
735	Cloning and expression of a murein hydrolase lipoprotein from Escherichia coli. **1995**, 16, 761-8	65
734	A novel locus of Yersinia enterocolitica serotype O:3 involved in lipopolysaccharide outer core biosynthesis. **1995**, 17, 575-94	123
733	Lipopolysaccharide with an altered O-antigen produced in Escherichia coli K-12 harbouring mutated, cloned Shigella flexneri rfb genes. **1995**, 18, 209-23	29
732	Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology. **1995**, 16, 955-67	71
731	The molecular characterization of a set of cDNAs differentially expressed during Douglas-fir germination and early seedling development. **1995**, 95, 456-464	15
730	Protein Modeling by E-mail. **1995**, 13, 658-660	519
729	Comparative sequence analysis of the human and pufferfish Huntington's disease genes. **1995**, 10, 67-76	135
728	Horizontal SINE transfer between vertebrate classes. **1995**, 10, 131-2	31
727	The polycystic kidney disease 1 (PKD1) gene encodes a novel protein with multiple cell recognition domains. **1995**, 10, 151-60	716
726	Cloning a balanced translocation associated with DiGeorge syndrome and identification of a disrupted candidate gene. **1995**, 10, 269-78	137
725	The mouse dystonia musculorum gene is a neural isoform of bullous pemphigoid antigen 1. **1995**, 10, 301-6	228
724	Recurrent rearrangements in the high mobility group protein gene, HMGI-C, in benign mesenchymal tumours. **1995**, 10, 436-44	484
723	Mutation of a new sodium channel gene, Scn8a, in the mouse mutant 'motor endplate disease'. **1995**, 10, 461-5	257
722	Epileptic seizures caused by inactivation of a novel gene, jerky, related to centromere binding protein-B in transgenic mice. **1995**, 11, 71-5	79

721	A gene (PEX) with homologies to endopeptidases is mutated in patients with X-linked hypophosphatemic rickets. The HYP Consortium. **1995**, 11, 130-6	912
720	Beta-sarcoglycan: characterization and role in limb-girdle muscular dystrophy linked to 4q12. **1995**, 11, 257-65	433
719	Beta-sarcoglycan (A3b) mutations cause autosomal recessive muscular dystrophy with loss of the sarcoglycan complex. **1995**, 11, 266-73	405
718	p53 activates expression of HIC-1, a new candidate tumour suppressor gene on 17p13.3. **1995**, 1, 570-7	376
717	Increased obese mRNA expression in omental fat cells from massively obese humans. **1995**, 1, 953-6	453
716	Adenoviral E1A-associated protein p300 as a functional homologue of the transcriptional co-activator CBP. **1995**, 374, 85-8	535
715	Cloning of a gene bearing missense mutations in early-onset familial Alzheimer's disease. **1995**, 375, 754-60	3425
714	A new family of outwardly rectifying potassium channel proteins with two pore domains in tandem. **1995**, 376, 690-5	359
713	Familial Alzheimer's disease in kindreds with missense mutations in a gene on chromosome 1 related to the Alzheimer's disease type 3 gene. **1995**, 376, 775-8	1749
712	Mechanosensory signalling in C. elegans mediated by the GLR-1 glutamate receptor. **1995**, 378, 78-81	281
711	Mariner transposons in humans. **1995**, 378, 672	71
710	Cloning and analysis of a Cryptosporidium parvum gene encoding a protein with homology to cytoplasmic form Hsp70. **1995**, 42, 416-22	65
709	Cloning and nucleotide sequence of a gene upstream of the eaeA gene of enterohemorrhagic Escherichia coli O157:H7. **1995**, 133, 35-9	9
708	Characterization of the smtA gene encoding an S-adenosylmethionine-dependent methyltransferase of Escherichia coli. **1995**, 133, 59-63	14
707	A potential anti-oxidant protein in a ferrous iron-oxidizing Sulfolobus species. **1995**, 134, 91-5	11
706	Amino acid transporters of lower eukaryotes: regulation, structure and topogenesis. **1995**, 16, 53-75	93
705	Purification and partial characterization of an outer membrane protein involved in the adhesion of Rahnella aquatilis to wheat roots. **1995**, 16, 19-24	10
704	Isolation of insertion elements from gram-positive Brevibacterium, Corynebacterium and Rhodococcus strains using the Bacillus subtilis sacB gene as a positive selection marker. **1995**, 126, 1-6	47

703	A highly conserved N-terminal sequence for teleost vitellogenin with potential value to the biochemistry, molecular biology and pathology of vitellogenesis. **1995**, 46, 255-263	37
702	A tonoplast intrinsic protein (TIP) is present in seeds, roots and somatic embryos of Norway spruce (Picea abies). **1995**, 95, 288-295	16
701	Modeling mutations and homologous proteins. **1995**, 6, 437-51	129
700	Characterization of cDNA clones containing CCA trinucleotide repeats derived from human brain. **1995**, 21, 279-84	11
699	Human cDNA clones that modify radiomimetic sensitivity of ataxia-telangiectasia (group A) cells. **1995**, 21, 99-111	16
698	Identification of the human neuronal nicotinic cholinergic alpha 2 receptor locus, (CHRNA2), within an 8p21 mapped locus, by sequence homology with rat DNA. **1995**, 21, 147-50	7
697	Molecular analysis and breakpoint definition of a set of human chromosome 21 somatic cell hybrids. **1995**, 21, 415-28	14
696	The first intron of the BCR gene contains two minor alternative exons. **1995**, 19, 963-70	4
695	X-HUSAR, an X-based graphical interface for the analysis of genomic sequences. **1995**, 46, 131-41	41
694	Purification and characterization of a protease-resistant cellulase from Aspergillus niger. **1995**, 79, 125-130	67
693	A ran-binding motif in nuclear pore proteins. **1995**, 5, 192-193	3
692	A secreted calreticulin protein in ixodid tick (Amblyomma americanum) saliva. **1995**, 41, 369-375	69
691	A group of NotI jumping and linking clones cover 2.5 Mb in the 3p21-p22 region suspected to contain a tumor suppressor gene. **1995**, 81, 144-50	26
690	dinP, a new gene in Escherichia coli, whose product shows similarities to UmuC and its homologues. **1995**, 347, 1-7	51
689	Characterisation of an immunodominant glycoprotein antigen of Onchocerca volvulus with homologues in other filarial nematodes and Caenorhabditis elegans. **1995**, 69, 185-95	46
688	Primary structure of a putative adenylate kinase gene of Giardia lamblia. **1995**, 71, 279-83	8
687	Cloning and sequencing of an excretory/secretory antigen from Ostertagia ostertagi fourth-stage larvae containing multiple tandem repeats. **1995**, 72, 239-41	13
686	Cloning and characterization of a putative calcium-transporting ATPase gene from Schistosoma mansoni. **1995**, 72, 129-39	25

685	cDNA expressed sequence tags of Trypanosoma brucei rhodesiense provide new insights into the biology of the parasite. **1995**, 73, 75-90	109
684	Cloning and characterization of a Plasmodium falciparum cyclophilin gene that is stage-specifically expressed. **1995**, 73, 111-21	38
683	Linkage and expression of the argininosuccinate lyase/delta-crystallin genes of the duck: insertion of a CR1 element in the intergenic spacer. **1995**, 1261, 25-34	7
682	Primary sequence of a putative pyrophosphate-linked phosphofructokinase gene of Giardia lamblia. **1995**, 1260, 218-22	16
681	Cloning and sequence analysis of a novel member of the single-stranded DNA binding protein family. **1995**, 1261, 143-6	2
680	Nucleotide sequence of a gene cluster encoding ribosomal proteins in the thermoacidophilic crenarchaeon Sulfolobus acidocaldarius. **1995**, 1261, 315-8	7
679	The putative Drosophila NMDARA1 gene is located on the second chromosome and is ubiquitously expressed in embryogenesis. **1995**, 1261, 301-3	15
678	Proteome-Wide Detection and Annotation of Receptor Tyrosine Kinases (RTKs): RTK-PRED and the TyReK Database. **2023**, 13, 270	0
677	Systematic In Silico Assessment of Antimicrobial Resistance Dissemination across the Global Plasmidome. **2023**, 12, 281	0
676	Molecular Identification of Asian Hornet Vespa velutina nigrithorax Prey from Larval Gut Contents: A Promising Method to Study the Diet of an Invasive Pest. **2023**, 13, 511	0
675	Biofouling and biocorrosion by microbiota from a marine oil pipeline: A metagenomic and proteomic approach. **2023**, 11, 109413	0
674	Elucidating the functional roles of prokaryotic proteins using big data and artificial intelligence. **2023**, 47,	0
673	AmiP from hyperthermophilic Thermus parvatiensis prophage is a thermoactive and ultrathermostable peptidoglycan lytic amidase. **2023**, 32,	0
672	Comparative Genome-Wide Analysis of Two Caryopteris x Clandonensis Cultivars: Insights on the Biosynthesis of Volatile Terpenoids. **2023**, 12, 632	0
671	Annotated sequence First report of Soybean chlorotic blotch virus infecting Okra (Abelmoschus esculentus) in Cameroon.	0
670	A Comparison of Different Matrices for the Laboratory Diagnosis of the Epizootic American Foulbrood of Honey Bees. **2023**, 10, 103	1
669	Genetic diversity among reptilian orthoreoviruses isolated from pet snakes and lizards. 10,	0
668	Reanalysis of ribosome profiling datasets reveals a function of rocaglamide A in perturbing the dynamics of translation elongation via eIF4A. **2023**, 14,	0

667	Contrasting Genetic Diversity of Listeria Pathogenicity Islands 3 and 4 Harbored by Nonpathogenic Listeria spp.. **2023**, 89,	0
666	KinFams: De-Novo Classification of Protein Kinases Using CATH Functional Units. **2023**, 13, 277	0
665	Alphaviruses Detected in Mosquitoes in the North-Eastern Regions of South Africa, 2014 to 2018. **2023**, 15, 414	0
664	A Novel Relapsing Fever Group Borrelia Isolated from Ornithodoros Ticks of the Brazilian Caatinga. **2023**, 11, 370	0
663	Nematode mitochondrial metagenomics: A new tool for biodiversity analysis.	0
662	Non-destructive insect metabarcoding as a surveillance tool for the Australian grains industry: a first trial for the iMapPESTS smart trap. 7,	0
661	Role of Alternative Elicitor Transporters in the Onset of Plant Host Colonization by Streptomyces scabiei 87-22. **2023**, 12, 234	0
660	Characterization of an atypical but widespread type IV secretion system for transfer of the integrative and conjugative element (ICEclc) inPseudomonas putida. **2023**, 51, 2345-2362	0
659	In vitro culture of the zoonotic nematode Anisakis pegreffii (Nematoda, Anisakidae). **2023**, 16,	0
658	Phylogeny analysis of whole protein-coding genes in metagenomic data detected an environmental gradient for the microbiota. **2023**, 18, e0281288	0
657	Whole-genome sequence of synthetically derived Brassica napus inbred cultivar Da-Ae. **2023**, 13,	0
656	Plant Growth Promotion, Phytohormone Production and Genomics of the Rhizosphere-Associated Microalga, Micractinium rhizosphaerae sp. nov.. **2023**, 12, 651	0
655	Pyridoxal 5′phosphate synthesis and salvage in Bacteria and Archaea: predicting pathway variant distributions and holes. **2023**, 9,	0
654	CD99 and the Chicken Alloantigen D Blood System. **2023**, 14, 402	0
653	Epigenetically controlled tumor antigens derived from splice junctions between exons and transposable elements. **2023**, 8,	0
652	Centromere repositioning and shifts in wheat evolution. **2023**, 100556	1
651	Molecular Analysis of MgO Nanoparticle-Induced Immunity against Fusarium Wilt in Tomato. **2023**, 24, 2941	0
650	De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. **2023**, 24, 2904	0

649	Identification of potential novel membrane drug targets of Acinetobacter baumannii ATCC 19606 using subtractive proteomics approach. **2022**, 38, 186-194	0
648	Genomics discovery of giant fungal viruses from subsurface oceanic crustal fluids. **2023**, 3,	0
647	Protein Therapeutic Target Candidates Against Acinetobacter baumannii, a Pathogen of Concern to Planetary Health: A Network-Based Integrative Omics Drug Discovery Approach. **2023**, 27, 62-74	0
646	CRISPR/Cas9 mediated gene editing in non-model nematode Panagrolaimus sp. PS1159. 5,	0
645	De novo transcriptome assembly from the nodal root growth zone of hydrated and water-deficit stressed maize inbred line FR697. **2023**, 13,	0
644	HPV and molecular mimicry in systemic lupus erythematosus and an impact of compiling B-cell epitopes and MHC-class II binding profiles with in silico evidence. 1-9	0
643	Development of Nuclear DNA Markers for Applications in Genetic Diversity Study of Oil Palm-Pollinating Weevil Populations. **2023**, 14, 157	0
642	A highly multiplexed assay to monitor pathogenicity, fungicide resistance and gene flow in the fungal wheat pathogen Zymoseptoria tritici. **2023**, 18, e0281181	0
641	CrAssphage May Be Viable Markers of Contamination in Pristine and Contaminated River Water. **2023**, 8,	0
640	The chickpea root rot complex in Saskatchewan, Canada- detection of emerging pathogens and their relative pathogenicity. 14,	0
639	Sequence and structure alignments in post-AlphaFold era. **2023**, 79, 102539	0
638	Tychonema sp. BBK16 Characterisation: Lifestyle, Phylogeny and Related Phages. **2023**, 15, 442	0
637	Diaporthe and Diplodia Species Associated with Walnut (Juglans regia L.) in Hungarian Orchards. **2023**, 9, 205	0
636	The Satellite DNAs Populating the Genome of Trigona hyalinata and the Sharing of a Highly Abundant satDNA in Trigona Genus. **2023**, 14, 418	1
635	Integrative description of Macrobiotus kosmali sp. nov. (hufelandi group) from the Island of Madeira (Portugal). **2023**, 90, 126-138	0
634	Deducing genotypes for loci of interest from SNP array data via haplotype sharing, demonstrated for apple and cherry. **2023**, 18, e0272888	0
633	A Novel Pathogenic Avipoxvirus Infecting Vulnerable Cook’s Petrel (Pterodroma cookii) in Australia Demonstrates a High Genomic and Evolutionary Proximity with South African Avipoxviruses. **2023**, 11,	0
632	Complete mitochondrial genome of a livebearing freshwater fish (Cyprinodontiformes: Poeciliidae): Poecilia parae. **2023**, 8, 215-219	0

631	Complete Genome Sequences of Two Thermophilic Indigenous Bacteria Isolated from Wheat Straw, Thermoclostridium stercorarium subsp. Strain RKWS1 and Thermoanaerobacter sp. Strain RKWS2. **2023**, 12,	0
630	Optimal gap-affine alignment inO(s) space. **2023**, 39,	0
629	The protein family of pyruvate:quinone oxidoreductases: Amino acid sequence conservation and taxonomic distribution. **2023**, 1864, 148958	0
628	The rubber tree kinome: Genome-wide characterization and insights into coexpression patterns associated with abiotic stress responses. 14,	0
627	Characterisation of the Upper Respiratory Tract Virome of Feedlot Cattle and Its Association with Bovine Respiratory Disease. **2023**, 15, 455	0
626	PanViTa: Pan Virulence and resisTance analysis. 3,	1
625	Pet Rats as the Likely Reservoir for Human Seoul Orthohantavirus Infection. **2023**, 15, 467	0
624	Inputs of seabird guano alter microbial growth, community composition and the phytoplankton□bacterial interactions in a coastal system.	0
623	Two new species of Astrothelium from Sud Yungas in Bolivia and the first discovery of vegetative propagules in the family Trypetheliaceae (lichen-forming Dothideomycetes, Ascomycota). 95, 83-100	0
622	The Ancestral Mitotic State: Closed Orthomitosis With Intranuclear Spindles in the Syncytial Last Eukaryotic Common Ancestor. **2023**, 15,	0
621	How Can Omics Inform Diabetic Foot Ulcer Clinical Management? A Whole Genome Comparison of Four Clinical Strains of Staphylococcus aureus. **2023**, 27, 51-61	0
620	Phytophthora Species Involved in Alnus glutinosa Decline in Portugal. **2023**, 12, 276	0
619	Novel microRNAs associated with the immune response to cucumber mosaic virus in hot pepper (Capsicum annuum L.). **2023**, 124, 101963	0
618	TET2 guards against unchecked BATF3-induced CAR T cell expansion. **2023**, 615, 315-322	1
617	Macroevolutionary diversity of traits and genomes in the model yeast genus Saccharomyces. **2023**, 14,	0
616	Insights into the convergent evolution of fructan biosynthesis in angiosperms from the highly characteristic chicory genome. **2023**, 238, 1245-1262	0
615	AlphaFold2-multimer guided high-accuracy prediction of typical and atypical ATG8-binding motifs. **2023**, 21, e3001962	0
614	Candida auris biofilm: a review on model to mechanism conservation. **2023**, 21, 295-308	0

613	Discovery of a coronavirus in the Eurasian badger (Meles meles) belonging to a putative new genus. **2023**, 109, 105406	0
612	Biodegradation of Microtoxic Phenylpropanoids (Phenylpropanoic Acid and Ibuprofen) by Bacteria and the Relevance for Their Removal from Wastewater Treatment Plants. **2023**, 14, 442	0
611	Syntenic Cell Wall QTLs as Versatile Breeding Tools: Intraspecific Allelic Variability and Predictability of Biomass Quality Loci in Target Plant Species. **2023**, 12, 779	0
610	Uncovering a Complex Virome Associated with the Cacao Pathogens Ceratocystis cacaofunesta and Ceratocystis fimbriata. **2023**, 12, 287	0
609	Nectary development in Cleome violacea. 13,	1
608	InParanoiDB 9: Ortholog Groups for Protein Domains and Full-Length Proteins. **2023**, 168001	0
607	Global epidemiology and clinical outcomes of carbapenem-resistant Pseudomonas aeruginosa and associated carbapenemases (POP): a prospective cohort study. **2023**, 4, e159-e170	0
606	A comparison of free-living and sponge-associated bacterial communities from a remote oceanic island with a focus on calcareous sponges. **2023**, 99,	0
605	Diverse Microbial Hot Spring Mat Communities at Black Canyon of the Colorado River.	0
604	Characterization of antibiotic resistomes by reprogrammed bacteriophage-enabled functional metagenomics in clinical strains. **2023**, 8, 410-423	0
603	The role of non-additive gene action on gene expression variation in plant domestication. **2023**, 14,	0
602	A Novel DNAzyme-Based Fluorescent Biosensor for Detection of RNA-Containing Nipah Henipavirus. **2023**, 13, 252	0
601	Expansion and loss of sperm nuclear basic protein genes in Drosophila correspond with genetic conflicts between sex chromosomes. 12,	0
600	Functional control and metabolic integration of stolen organelles in a photosynthetic ciliate. **2023**, 33, 973-980.e5	0
599	Simulated heat waves promote the growth but suppress the N2 fixation rates of Dolichospermum spp. and cyanobacterial communities in temperate lakes. **2023**, 147, 109983	0
598	Aggregation-resistant proteins are adjusted during drought in sugarcane plants. **2023**, 45,	0
597	Response of the obligate halophile fungus Aspergillus loretoensis to stress salinity. **2023**, 11, 26-33	0
596	A Mitosome With Distinct Metabolism in the Uncultured Protist ParasiteParamikrocytos canceri(Rhizaria, Ascetosporea). **2023**, 15,	0

595	Diverse DNA virus genomes identified in fecal samples of Mexican free-tailed bats (Tadarida brasiliensis) captured in Chiricahua Mountains of southeast Arizona (USA). **2023**, 580, 98-111	0
594	A high-quality reference genome of the kelp surfperch,Brachyistius frenatus(Embiotocidae), a wide-ranging Eastern Pacific reef fish with no pelagic larval stage.	0
593	Identification of potentially zoonotic parasites in captive orangutans and semi-captive mandrills: Phylogeny and morphological comparison. **2023**, 85,	0
592	Complete Genome Sequence of the Lysogenic Pseudomonas Bacteriophage Fyn8. **2023**, 12,	0
591	Capsular Polysaccharide Is Essential for the Virulence of the Antimicrobial-Resistant Pathogen Enterobacter hormaechei.	0
590	Periodontal disease is associated with increased gut colonization of pathogenic Haemophilus parainfluenzae in patients with Crohn's disease. **2023**, 42, 112120	0
589	Pseudomonas Phage ZCPS1 Endolysin as a Potential Therapeutic Agent. **2023**, 15, 520	2
588	Draft Genome Sequence of Exophiala Strain HKRS030, a Fungus Capable of Reducing Iron but Not Nitrate. **2023**, 12,	0
587	Dark Fermentation of Arundo donax: Characterization of the Anaerobic Microbial Consortium. **2023** , 16, 1813	0
586	Maternal Donor and Genetic Variation of Lagerstroemia indica Cultivars. **2023**, 24, 3606	0
585	Amniotes co-opt intrinsic genetic instability to protect germ-line genome integrity. **2023**, 14,	0
584	Differential Loss of OAS Genes Indicates Diversification of Antiviral Immunity in Mammals. **2023**, 11, 419	0
583	Variation of butyrate production in the gut microbiome in type 2 diabetes patients.	1
582	IMperm: a fast and comprehensive IMmune Paired-End Reads Merger for sequencing data. **2023**, 24,	0
581	HexSDF Is Required for Synthesis of a Novel Glycolipid That Mediates Daptomycin and Bacitracin Resistance in C. difficile.	0
580	Unsupervised cross-domain translation via deep learning and adversarial attention neural networks and application to music-inspired protein designs. **2023**, 4, 100692	0
579	Molecular evidence of Ehrlichia canis, associated risk factors and hematobiochemical analysis in client owned and shelter cats of Pakistan. **2023**, 94, 101959	0
578	Biotechnologically potential genes in a polysaccharide-degrading epibiont of the Indonesian brown algae Hydroclathrus sp.. **2023**, 21,	0

577	Identification of bacterial and fungal pathogens directly from clinical blood cultures using whole genome sequencing. **2023**, 115, 110580	0
576	Prevalence of major parasitic nematodes associated with tomatoes (Solanum lycopersicum L.) in two districts of Jimma, Ethiopia. **2023**, 56, 158-174	0
575	Physcomitrium patens PpRIC, an ancestral CRIB-domain ROP effector, inhibits auxin-induced differentiation of apical initial cells. **2023**, 42, 112130	0
574	RAREFAN: A webservice to identify REPINs and RAYTs in bacterial genomes. 3,	0
573	Recent transposable element bursts are associated with the proximity to genes in a fungal plant pathogen. **2023**, 19, e1011130	0
572	Structural analysis of human G-protein-coupled receptor 17 ligand binding sites. **2023**, 124, 533-544	0
571	Tree-Level Growth Patterns and Genetic Associations Depict Drought Legacies in the Relict Forests of Abies marocana. **2023**, 12, 873	0
570	A computational investigation on Rho-related GTP-binding protein RhoB through molecular modeling and molecular dynamics simulation study.	0
569	Phosphorylation status of a conserved residue in the adenylate cyclase of Botrytis cinerea is involved in regulating photomorphogenesis, circadian rhythm, and pathogenicity. 14,	0
568	Population Structure, Demographic History, and Adaptation of Giant Honeybees in China Revealed by Population Genomic Data. **2023**, 15,	0
567	Initiation of fatty acid biosynthesis in Pseudomonas putida KT2440. **2023**, 76, 193-203	0
566	On the origin and evolution of RNA editing in metazoans. **2023**, 42, 112112	0
565	Fructilactobacillus cliffordii sp. nov., Fructilactobacillus hinvesii sp. nov., Fructilactobacillus myrtifloralis sp. nov., Fructilactobacillus carniphilus sp. nov. and Fructobacillus americanaquae sp. nov., five novel lactic acid bacteria isolated from insects or flowers of Kangaroo Island, South Australia. **2023**, 73,	0
564	Differentially Expressed Genes and Molecular Susceptibility to Human Age-Related Diseases. **2023**, 24, 3996	0
563	Taxonomically Restricted Genes inBacillusmay Form Clusters of Homologs and Can be Traced to a Large Reservoir of Noncoding Sequences. **2023**, 15,	0
562	Sizing Up the Onychophoran Genome: Repeats, Introns, and Gene Family Expansion Contribute to Genome Gigantism inEpiperipatus broadwayi. **2023**, 15,	0
561	Genome-wide identification and characterization of major RNAi genes highlighting their regulatory factors in Cowpea (Vigna unguiculata(L.) Walp.).	0
560	Insights into the ecological generalist lifestyle of Clonostachys fungi through analysis of their predicted secretomes. 14,	0

559	Genetic analysis of the frozen microbiome at 7900 m a.s.l., on the South Col of Sagarmatha (Mount Everest). **2023**, 55,	0
558	S-Locus Genotyping in Japanese Plum by High Throughput Sequencing Using a Synthetic S-Loci Reference Sequence. **2023**, 24, 3932	0
557	Haemosporidian infection prevalence varies temporally and spatially and Leucocytozoon infections are male biased in Song Sparrows.	0
556	EvolClustDB: Exploring Eukaryotic Gene Clusters with Evolutionarily Conserved Genomic Neighbourhoods. **2023**, 168013	0
555	Transcriptomics-Driven Characterization of LUZ100, a T7-like Pseudomonas Phage with Temperate Features.	0
554	Next-Generation DNA Barcoding for Fish Identification Using High-Throughput Sequencing in Tai Lake, China. **2023**, 15, 774	0
553	Unusual prophages in Mycobacterium abscessus genomes and strain variations in phage susceptibilities. **2023**, 18, e0281769	0
552	Using the Culex pipiens sperm proteome to identify elements essential for mosquito reproduction. **2023**, 18, e0280013	0
551	Bioinformatics Analysis of Mutations Sheds Light on the Evolution of Dengue NS1 Protein With Implications in the Identification of Potential Functional and Druggable Sites. **2023**, 40,	0
550	Early antitermination in the atypical coliphage mEp021 mediated by the Gp17 protein. **2023**, 168,	0
549	Machine learning-enabled retrobiosynthesis of molecules. **2023**, 6, 137-151	1
548	OrthoPhy: A Program to Construct Ortholog Data Sets Using Taxonomic Information. **2023**, 15,	0
547	Molecular survey of hemotropic mycoplasmas in crab-eating raccoons (Procyon cancrivorus) in southern Brazil. **2023**, 32,	0
546	Insights into the prey of Vespa mandarinia (Hymenoptera: Vespidae) in Washington state, obtained from metabarcoding of larval feces. 3,	0
545	A Bacillaceae consortium positively impacts arbuscular mycorrhizal fungus colonisation, plant phosphate nutrition, and tuber yield in Solanum tuberosum cv. Jazzy. **2023**, 89, 235-250	0
544	Characterization of the arbuscular mycorrhizal fungal community associated with rosewood (Pterocarpus tinctorius Welw.) in Miombo forests, Democratic Republic of Congo.	0
543	Virulence and pathogenicity determinants in whole genome sequence of Fusarium udum causing wilt of pigeon pea. 14,	0
542	Variation of length and sequence of the nuclear ribosomal DNA internal transcribed spacer 1 supports □ermit-to-king□crab hypothesis. **2023**, 52, 31-48	0

541	Bioactivity Profiling and Untargeted Metabolomics of Microbiota Associated with Mesopelagic Jellyfish Periphylla Periphylla. **2023**, 21, 129	0
540	Sequence Analysis of the Arcelin-Phytohaemagglutinin-□Amylase Inhibitor (APA) Locus in Three Phylogenetically Arrayed Phaseolus vulgaris Clones. **2022**, 22,	0
539	Fusarium sacchari associated with stem rot in sweet corn in Brazil. 53,	0
538	Precipitation is the main axis of tropical plant phylogenetic turnover across space and time. **2023**, 9,	0
537	Effects of field inoculation of potato tubers with the arbuscular mycorrhizal fungus Rhizophagus irregularis DAOM 197198 are cultivar dependent. **2023**, 89, 213-226	0
536	DNA sequencing in the classroom: complete genome sequence of two earwig (Dermaptera; Insecta) species. **2023**, 56,	0
535	Identification and Genetic Characterization of MERS-Related Coronavirus Isolated from Nathusius□ Pipistrelle (Pipistrellus nathusii) near Zvenigorod (Moscow Region, Russia). **2023**, 20, 3702	2
534	CvkR is a MerR-type transcriptional repressor of class 2 type V-K CRISPR-associated transposase systems. **2023**, 14,	0
533	A multi-method approach for assessing the distribution of a rare, burrowing North American crayfish species. 11, e14748	0
532	Diversification of the shell shape and size in Baikal Candonidae ostracods inferred from molecular phylogeny. **2023**, 13,	0
531	Genomic Islands Identified in Highly Resistant Serratia sp. HRI: A Pathway to Discover New Disinfectant Resistance Elements. **2023**, 11, 515	0
530	VPAgs-Dataset4ML: A Dataset to Predict Viral Protective Antigens for Machine Learning-Based Reverse Vaccinology. **2023**, 8, 41	0
529	The opportunities and challenges posed by the new generation of deep learning-based protein structure predictors. **2023**, 79, 102543	0
528	Chromosome-level genome assembly and population genomics of Mongolian racerunner (Eremias argus) provide insights into high-altitude adaptation in lizards. **2023**, 21,	0
527	Bat pluripotent stem cells reveal unusual entanglement between host and viruses. **2023**, 186, 957-974.e28	0
526	MetaGenePipe: An Automated, Portable Pipeline for Contig-based Functional and Taxonomic Analysis. **2023**, 8, 4851	0
525	Fungal Integrated Histomolecular Diagnosis Using Targeted Next-Generation Sequencing on Formalin-Fixed Paraffin-Embedded Tissues. **2023**, 61,	0
524	The associated risk of Blastocystis infection in cancer: A case control study. 13,	0

523	Sunsetting Binding MOAD with its last data update and the addition of 3D-ligand polypharmacology tools. **2023**, 13,	0
522	Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. **2023**, 227-246	0
521	A MALDI-TOF MS library for rapid identification of human commensal gut bacteria from the class Clostridia. 14,	0
520	Phylogeography of Ramalina ́farinacea (Lichenized Fungi, Ascomycota) in the Mediterranean Basin, Europe, and Macaronesia. **2023**, 15, 310	0
519	Bacterial community structure in the alcyoniid Lobophytum pauciflorum.	0
518	Population genomics and phylogeography of four Australasian waterfowl. 1-13	0
517	Exploring Class I polyhydroxyalkanoate synthases with broad substrate specificity for polymerization of structurally diverse monomer units. 11,	0
516	Genome Sequence of Pseudomonas sp. Strain So3.2b, Isolated from a Soil Sample from Robert Island (Antarctic Specially Protected Area 112), Antarctic. **2023**, 12,	0
515	Trichoderma harzianum as a potential biological agent in control of the charcoal root rot of sugar beet.	0
514	Synthesis of 12-aminododecenoic acid by coupling transaminase to oxylipin pathway enzymes. **2023**, 107, 2209-2221	0
513	Community-wide collaboration is a must to reinstall trust in bioinformatics solutions and biomedical interpretation. **2023**, 20,	0
512	Complete Genome Sequence of Rhodopseudomonas sp. Strain P2A-2r, Isolated from Arctic Soil. **2023**, 12,	0
511	Identification of B and T Cell Epitopes to Design an Epitope-Based Peptide Vaccine against the Cell Surface Binding Protein of Monkeypox Virus: An Immunoinformatics Study. **2023**, 2023, 1-14	0
510	Effects of dielectric barrier discharge plasma and plasma-activated water on the surface microbial diversity of fresh goji berries during storage. **2023**, 313, 111920	0
509	Comparative Genomic Analysis and Physiological Properties of Limosilactobacillus fermentum SMFM2017-NK2 with Ability to Inflammatory Bowel Disease. **2023**, 11, 547	0
508	Field plus lab experiments help identify freezing tolerance and associated genes in subtropical evergreen broadleaf trees: A case study of Camellia oleifera. 14,	0
507	Meta-omics elucidates key degraders in a bacterial tris(2-butoxyethyl) phosphate (TBOEP)-degrading enrichment culture. **2023**, 233, 119774	0
506	Quantifying and visualizing Nitrospirillum amazonense strain CBAmC in sugarcane after using different inoculation methods.	0

505	Global Molecular Response of Paracoccidioides brasiliensis to Zinc Deprivation: Analyses at Transcript, Protein and MicroRNA Levels. **2023**, 9, 281	o
504	Importance of mobile genetic element immunity in numerically abundant Trichodesmium clades. **2023**, 3,	o
503	The Arabidopsis INNER NO OUTER (INO) gene acts exclusively and quantitatively in regulation of ovule outer integument development. **2023**, 7,	o
502	Alteration of a Shiga toxin-encoding phage associated with a change in toxin production level and disease severity in Escherichia coli. **2023**, 9,	o
501	Highly accurate genome assembly of an improved high-yielding silkworm strain, Nichi01. **2023**, 13,	o
500	Moniliella zaluziensis sp. nov., a black yeast related to fruit trees of the Rosaceae family. **2023**, 73,	o
499	A bivalent remipede toxin promotes calcium release via ryanodine receptor activation. **2023**, 14,	o
498	A chromosome-level genome assembly of an early matured aromatic Japonica rice variety Qigeng10 to accelerate rice breeding for high grain quality in Northeast China. 14,	o
497	Large-Scale Immunopeptidome Analysis Reveals Recurrent Posttranslational Splicing of Cancer- and Immune-Associated Genes. **2023**, 22, 100519	o
496	Hannaella floricola sp. nov., a novel basidiomycetous yeast species isolated from a flower of Lantana camara in Portugal. **2023**, 73,	o
495	Mitochondrial DNA variants in a cohort from Argentina with suspected Leber▯ hereditary optic neuropathy (LHON). **2023**, 18, e0275703	o
494	Genome-wide analysis of long non-coding RNAs (lncRNAs) in tea plants (Camellia sinensis) lateral roots in response to nitrogen application. 14,	o
493	Loss of function of ADNP by an intragenic inversion.	o
492	Composition and Patterns of Taxa Assemblages in the Western Channel Assessed by 18S Sequencing, Microscopy and Flow Cytometry. **2023**, 11, 480	o
491	Development of a specific real-time PCR assay for simultaneous detection and differentiation ofCoxiella burnetiistrains from environmental soil samples. **2023**, 76,	o
490	The genetic and evolutionary basis of gene expression variation in East Africans. **2023**, 24,	o
489	Identification of conserved genomic signatures specific to Bifidobacterium species colonising the human gut. **2023**, 13,	o
488	A Compendium for Novel Marker-Based Breeding Strategies in Eggplant. **2023**, 12, 1016	o

487	Intracellular Helix-Loop-Helix Domain Modulates Inactivation Kinetics of Mammalian TRPV5 and TRPV6 Channels. **2023**, 24, 4470	0
486	Draft genomes of three closely related low light-adapted Prochlorococcus. **2023**, 24,	0
485	Recommendations for Developing Molecular Assays for Microbial Pathogen Detection Using Modern In Silico Approaches. **2023**,	0
484	Three-dimensional models of antigens with serodiagnostic potential for leprosy: An in silico study. 13, 1-10	0
483	A comparative study across the parasitic plants of Cuscuta subgenus Grammica (Convolvulaceae) reveals a possible loss of the plastid genome in its section Subulatae. **2023**, 257,	0
482	A snapshot of climate drivers and temporal variation of Ixodes ovatus abundance from a giant panda living in the wild. **2023**, 20, 162-169	0
481	Different diagnostic approaches for the characterization of the fungal community and Fusarium species complex composition of Italian durum wheat grain and correlation with secondary metabolite accumulation.	0
480	Systematic identification and characterization of viral small RNAs from small RNA-Seq data. **2023**, 95,	0
479	A Novel Circular Rep-Encoding Single-Stranded DNA from Holstein Calves. **2023**, 12,	0
478	Krein support vector machine classification of antimicrobial peptides. **2023**, 2, 502-511	0
477	Benchmarking and Validation of a Bioinformatics Workflow for Meat Species Identification Using 16S rDNA Metabarcoding. **2023**, 12, 968	0
476	A Blind-Identification Test on Criconema annuliferum (de Man, 1921) Micoletzky, 1925 Species Complex Corroborate the Hyper-Cryptic Species Diversity Using Integrative Taxonomy. **2023**, 12, 1044	0
475	ProteInfer, deep neural networks for protein functional inference. 12,	1
474	In silico approaches for the quest of the novel enzymes. **2023**, 65-78	0
473	Protein sequence analysis. **2023**, 217-223	0
472	Computational strategies and tools for protein tertiary structure prediction. **2023**, 225-242	0
471	Whole-genome re-sequencing provides key genomic insights in farmed Arctic charr (Salvelinus alpinus) populations of anadromous and landlocked origin from Scandinavia.	0
470	Genome-Wide Identification, Characterization and Experimental Expression Analysis of CNGC Gene Family in Gossypium. **2023**, 24, 4617	0

469	Functional genomics of Chlamydomonas reinhardtii. **2023**, 65-84	0
468	Fungal Pathogens Associated with Aerial Symptoms of Avocado (Persea americana Mill.) in Tenerife (Canary Islands, Spain) Focused on Species of the Family Botryosphaeriaceae. **2023**, 11, 585	1
467	Bartonella spp. Infections Identified by Molecular Methods, United States. **2023**, 29, 467-476	0
466	Vibrio natriegens genome-scale modeling reveals insights into halophilic adaptations and resource allocation. **2023**, 19,	0
465	Structurally Different Yet Functionally Similar: Aptamers Specific for the Ebola Virus Soluble Glycoprotein and GP1,2 and Their Application in Electrochemical Sensing. **2023**, 24, 4627	0
464	Genome-wide association mapping for pre-harvest sprouting in European winter wheat detects novel resistance QTL, pleiotropic effects, and structural variation in multiple genomes.	0
463	Molecular exploration of fossil eggshell uncovers hidden lineage of giant extinct bird. **2023**, 14,	0
462	Competitive interactions between culturable bacteria are highly non-additive. 12,	0
461	Clonal Expansion of Multidrug-Resistant Streptococcus dysgalactiae Subspecies equisimilis Causing Bacteremia, Japan, 2005�021. **2023**, 29, 528-539	0
460	Predicting locations of cryptic pockets from single protein structures using the PocketMiner graph neural network. **2023**, 14,	1
459	Design and Optimization of a Monkeypox virus Specific Serological Assay. **2023**, 12, 396	0
458	Chromene-dihydropyrimidinone and xanthene-dihydropyrimidinone hybrids: design, synthesis, and antibacterial and antibiofilm activities.	0
457	A population of stem cells with strong regenerative potential discovered in deer antlers. **2023**, 379, 840-847	1
456	Complete genome sequences of newly discovered Dioscorea bacilliform AL virus and Dioscorea bacilliform SN virus isolates from Dioscorea bulbifera L. in northeastern Brazil.	0
455	Divergent TLR2 and TLR4 Activation by Fungal Spores and Species Diversity in Dust from Waste Sorting Plants. **2023**, 89,	0
454	Individual Genomic Loci and mRNA Levels of Immune Biomarkers Associated with Pneumonia Susceptibility in Baladi Goats. **2023**, 10, 185	0
453	Characterization of eyes, photoreceptors, and opsins in developmental stages of the arrow worm Spadella cephaloptera (Chaetognatha).	0
452	A cytosine-patch sequence motif identified in the conserved region of lincRNA-p21 interacts with the KH3 domain of hnRNPK. **2023**, 5, 100099	0

451	A tetramerization domain in prokaryotic and eukaryotic transcription regulators homologous to p53. **2023**, 79, 259-267	0
450	Genome Sequences of Five Microbacterium foliorum Phages, GaeCeo, NeumannU, Eightball, Chivey, and Hiddenleaf. **2023**, 12,	0
449	Isolation, molecular characterization of indigenous Metarhizium anisopliae (Metchnikoff) isolate, using ITS-5.8s rDNA region, and its efficacy against the Helicoverpa armigera (Hubner) (Lepidoptera: Noctuidae). **2023**, 33,	0
448	Adaptive laboratory evolution to hypersaline conditions´of lactic acid bacteria isolated from seaweed. **2023**, 75, 21-30	0
447	Culturable Diversity of Lichen-Associated Yeasts through Enrichment Strategies. **2023**, 4, 152-170	0
446	Effects of representative point mutations on dynamic behavior of the DISC1Ndel1 complex: a molecular dynamics study. 1-7	0
445	Dual domestications and origin of traits in grapevine evolution. **2023**, 379, 892-901	1
444	Molecular mapping of genomic regions and identification of possible candidate genes associated with gynoecious sex expression in bitter gourd. 14,	0
443	Transcription of MERVL retrotransposons is required for preimplantation embryo development. **2023**, 55, 484-495	0
442	Brace yourselves, winter is coming: the winter activity, natural diet, and prey preference of winter-active spiders on pear trees.	0
441	Identification and expression analysis of C2H2-zinc finger protein genes reveals their role in stress tolerance in Brassica napus.	0
440	Life Continuously Acquires New Information in Dialogue with the Environment. **2023**, 159-170	0
439	Sequence Analysis: Deciphering the Language of Life. **2023**, 3-22	0
438	Shrimp Glucose-6-phosphatase 2 (G6Pase 2): a second isoform of G6Pase in the Pacific white shrimp and regulation of G6Pase 1 and 2 isoforms via HIF-1 during hypoxia and reoxygenation in juveniles.	0
437	Mechanical weeding enhances ecosystem multifunctionality and profit in industrial oil palm.	0
436	Polybacterial shift in benthic river biofilms attributed to organic pollution a prospect of a new biosentinel?. **2023**, 54, 348-359	0
435	A bacterial genome assembly and annotation laboratory using a virtual machine.	0
434	Identification and characterization analysis of candidate genes controlling mushroom leaf development in´Chinese kale by BSA-seq. **2023**, 43,	0

433	Exploring microbial functional biodiversity at the protein family level□From metagenomic sequence reads to annotated protein clusters. 3,	0
432	Call repertoire of Ptychadena uzungwensis (Anura: Ptychadenidae) to complement molecular and morphological identification of the species from the Soutpansberg, South Africa.. 1-14	0
431	Transcriptomics and Proteomics of Haemonchus contortus in Response to Ivermectin Treatment. **2023**, 13, 919	0
430	Bacterial Endosymbionts Identified From Leafhopper (Hemiptera: Cicadellidae) Vectors of Phytoplasmas. **2023**, 52, 243-253	0
429	Sequence Analysis. **2022**, 415-437	0
428	Corynebacterium guaraldiae sp. nov.: a new species of Corynebacterium from human infections.	0
427	Eremophilanolide sulfoxides and eremophilanolides from the mangrove fungus TBRC-BCC 64093. **2023**, 136, 133354	0
426	Chaetomium globosum KPC3: An Antagonistic Fungus Against the Potato Cyst Nematode, Globodera rostochiensis. **2023**, 80,	0
425	Isolation and characterization of a novel Tenacibaculum species and a corresponding bacteriophage from a Mediterranean fish hatchery: Description of Tenacibaculum larymnensis sp. nov. and Tenacibaculum phage Larrie. 14,	0
424	Etiological Structure, Clinical and Epidemiological Characteristics of Infections Transmitted by Ixodic Ticks in the Sverdlovsk Region at the Present Stage. **2023**, 22, 38-58	0
423	Characterization of Ly108-H1 Signaling Reveals Ly108-3 Expression and Additional Strain-Specific Differences in Lupus Prone Mice. **2023**, 24, 5024	0
422	Structural and Functional Classification of G-Quadruplex Families within the Human Genome. **2023**, 14, 645	0
421	Characterization of the complete mitochondrial genome of the brazilian cownose ray Rhinoptera brasiliensis (Myliobatiformes, Rhinopteridae) in the western Atlantic and its phylogenetic implications.	0
420	Membrane lipid adaptation of soil Bacteroidetes isolates to temperature and pH. 14,	0
419	Study on mosaic disease of sponge gourd (Luffa cylindrica L.) caused by tomato leaf curl New Delhi virus.	0
418	Recent Applications and Strategies to Enhance Performance of Electrochemical Reduction of CO2 Gas into Value-Added Chemicals Catalyzed by Whole-Cell Biocatalysts. **2023**, 11, 766	0
417	Genome Sequence of Gordonia terrae Phage APunk. **2023**, 12,	0
416	Zinc/iron-regulated transporter-like protein gene family in Theobroma cacao L: Characteristics, evolution, function and 3D structure analysis. 14,	0

415	Analysis of Bacterial Diversity in Fermented Grains of Baijiu Based on Culturomics and Amplicon Sequencing. **2023**, 9, 260	0
414	Discovery and comparative genomic analysis of a novel equine anellovirus, representing the first complete Mutorquevirus genome. **2023**, 13,	0
413	Song features correlate with male reproductive success and avian malaria infection in a promiscuous songbird with female-only parental care.	0
412	Time trees and clock genes: a systematic review and comparative analysis of contemporary avian migration genetics.	0
411	Modulation of the rumen microbiome of dairy cows by inclusion of a live yeast supplement in a total mixed ration.	0
410	Phylogenetic History and Phylogeographic Patterns of the European Wildcat (Felis´silvestris) Populations. **2023**, 13, 953	0
409	The terrestrial isopod symbiont □Candidatus Hepatincola porcellionum□is a potential nutrient scavenger related to Holosporales symbionts of protists. **2023**, 3,	0
408	Hic Sunt Dracones: Molecular Docking in Uncharted Territories with Structures from AlphaFold2 and RoseTTAfold. **2023**, 63, 2218-2225	0
407	Monitoring the birds and the bees: Environmental DNA metabarcoding of flowers detects plant□animal interactions.	0
406	Evolution of mitogenomic gene order in Orthoptera.	0
405	Ecological distribution and genetic diversity of Azolla in Uganda. **2023**, 23,	0
404	Isolation of an Ecotropic Porcine Endogenous Retrovirus PERV-C from a Yucatan SLA D/D Inbred Miniature Swine. **2023**, 97,	0
403	Complete genome sequence of a novel member of the genus Polerovirus from Cnidium officinale in South Korea. **2023**, 168,	0
402	Immunoinformatics - Role in the Identification of New Classes of Antimicrobials. **2023**, 339-358	0
401	Novel crAssphage isolates exhibit conserved gene order and purifying selection of the host specificity protein.	0
400	A hydrogenotrophic Sulfurimonas is globally abundant in deep-sea oxygen-saturated hydrothermal plumes. **2023**, 8, 651-665	0
399	Investigation of a Listeria monocytogenes Chromosomal Immigration Control Region Reveals Diverse Restriction Modification Systems with Complete Sequence Type Conservation. **2023**, 11, 699	0
398	Association of soil fungal community composition with incidence of Fusarium wilt of banana in Malaysia. **2023**, 115, 178-186	0

397	Developing Growth Promotion Strategies for Cressa truxillensis to Improve Success of Restoration Activities. **2023**, 122,	0
396	Extensive sequence duplication in Arabidopsis revealed by pseudo-heterozygosity. **2023**, 24,	0
395	An improved assembly of the pearl millet reference genome using Oxford Nanopore long reads and optical mapping.	0
394	Investigation of the ultrastructures and retinal arrangements of larval stomatopod eyes. **2023**, 73, 101251	0
393	Isolation and selection of sauerkraut lactic acid bacteria producing exopolysaccharides. **2023**, 58, 02001	0
392	Athalassotoga. 1-6	0
391	Hybrid vigor in Eucalyptus increases resistance against Phytophthora root rot. **2023**, 22,	0
390	Epidermal threads reveal the origin of hagfish slime. 12,	0
389	Mesoaciditoga. 1-6	0
388	Impact Assessment of vB_KpnP_K1-ULIP33 Bacteriophage on the Human Gut Microbiota Using a Dynamic In Vitro Model. **2023**, 15, 719	0
387	Molecular surveillance detects the zoonotic nematode parasite Toxocara in soils from public spaces in a Minnesota community. **2023**, 93,	0
386	How Rare Are Argonautoidea Octopuses in the Mediterranean? New Data from Stranding Events, Stomach Contents and Genetics. **2023**, 12, 420	0
385	Bizarre Morphology Obscures Real Affiliation: An Integrative Study of Enigmatic Cephalaspid Philine denticulata from Arctic Waters Reveals Its Unique Phylogenetic Position. **2023**, 15, 395	0
384	Phylogeny of Serpulidae (Annelida, Polychaeta) Inferred from Morphology and DNA Sequences, with a New Classification. **2023**, 15, 398	0
383	SSP: An In Silico Tool for Salmonella Species Serotyping Using the Sequences of O-Antigen Biosynthesis Proteins and H-Antigen Filament Proteins. **2023**, 168046	0
382	Computational insight into structural basis of human ELOVL1 inhibition. **2023**, 157, 106786	0
381	Raveneliopsis, a new genus of ravenelioid rust fungi on Cenostigma (Caesalpinioideae) from the Brazilian Cerrado and Caatinga. **2023**, 115, 263-276	0
380	Efficient short time pretreatment on lignocellulosic waste using an isolated fungus Trametes sp. W-4 for the enhancement of biogas production. **2023**, 9, e14573	0

379	Evaluation of DNA metabarcoding for identifying fish eggs: a case study on the West Florida Shelf. 11, e15016	0
378	Bacillus thuringiensis Cyt Proteins as Enablers of Activity of Cry and Tpp Toxins against Aedes albopictus. **2023**, 15, 211	0
377	From tetraploid to diploid, a pangenomic approach to identify genes lost during synthetic diploidization of Eragrostis curvula. 14,	0
376	Pineapple mealybug wilt-associated viruses 1, 2, and 3 are associated with mealybug wilt disease of pineapple in Peru.	0
375	Target-driven machine learning-enabled virtual screening (TAME-VS) platform for early-stage hit identification. 10,	0
374	African army ants at the forefront of virome surveillance in a remote tropical forest. 3,	0
373	Fine mapping and candidate gene analysis of qFL-A12-5: a fiber length-related QTL introgressed from Gossypium barbadense into Gossypium hirsutum. **2023**, 136,	0
372	Seasonality of biogeochemically relevant microbial genes in a coastal ocean microbiome.	0
371	Spatial Study of Enzymatic Activities from Bacterial Isolates in a Mediterranean Urban Park. **2023**, 12, 655	0
370	Performance of Eversa Transform 2.0 Lipase in Ester Production Using Babassu Oil (Orbignya sp.) and Tucuman Oil (Astrocaryum vulgar): A Comparative Study between Liquid and Immobilized Forms in Fe3O4 Nanoparticles. **2023**, 13, 571	1
369	The tropical cookbook: Termite diet and phylogenetics□over geographical origin□drive the microbiome and functional genetic structure of nests. 14,	0
368	Identification, Biocontrol Activity, and Field Application Effect of Bacillus´velezensis Yb-1. **2023**, 9, 376	0
367	The inoculation with Ensifer meliloti sv. rigiduloides improves considerably the growth of Robinia pseudoacacia under lead-stress.	0
366	Identification of Neotropical Culex Mosquitoes by MALDI-TOF MS Profiling. **2023**, 8, 168	0
365	Peptide derived from progranulin of the carcinogenic liver fluke, Opisthorchis viverrini stimulates cell hyperproliferation and proinflammatory cytokine production..	0
364	Bioinformatics Approaches Applied to the Discovery of Antifungal Peptides. **2023**, 12, 566	0
363	Insight into biosorption of hexavalent chromium using isolated species Aspergillus Proliferans LA: A systemic and In silico studies. **2023**, 7, 83	0
362	Draft Genome Sequence of a Delftia sp., a Member of an Electroactive Community Enriched from Wastewater from the Indian Institute of Technology Delhi, India. **2023**, 12,	0

361	Pleomorphic Variants of Borreliella (syn. Borrelia) burgdorferi Express Evolutionary Distinct Transcriptomes. **2023**, 24, 5594	0
360	Using AlphaFold to predict the impact of single mutations on protein stability and function. **2023**, 18, e0282689	1
359	Molecular Basis of RNA-Driven ATP Hydrolysis in DExH-Box Helicases. **2023**, 145, 6691-6701	0
358	Population structure and adaptive differentiation in the sea cucumber Apostichopus californicus and implications for spatial resource management. **2023**, 18, e0280500	0
357	Genome-wide identification and characterization of tissue-specific non-coding RNAs in black pepper (Piper nigrum L.). 14,	0
356	Evolutionary-scale prediction of atomic-level protein structure with a language model. **2023**, 379, 1123-1130	2
355	Spathaspora brunopereirae sp. nov. and Spathaspora domphillipsii sp. nov., two d-xylose-fermenting ascosporogenous yeasts from Amazonian Forest biomes. **2023**, 73,	0
354	Palidis: fast discovery of novel insertion sequences. **2023**, 9,	0
353	Isolation of bacteriophages infecting Xanthomonas oryzae pv. oryzae and genomic characterization of novel phage vB_XooS_NR08 for biocontrol of bacterial leaf blight of rice. 14,	0
352	Bioinformatic and Statistical Analysis of Microbiome Data. **2023**, 183-229	0
351	Fungal diversity and surfactant-producing fungi in oil contaminated environments. **2023**, 134,	0
350	Identification of the Coding-Complete Genome Sequence of a Novel Cytorhabdovirus in Tilia cordata Showing Extensive Leaf Chloroses. **2023**, 12,	0
349	Comparative genomics reveals the diversification of triterpenoid biosynthesis and origin of ocotillol-type triterpenes in Panax. **2023**, 100591	0
348	Cervicovaginal Human Papillomavirus Genomes, Microbiota Composition and Cytokine Concentrations in South African Adolescents. **2023**, 15, 758	0
347	Genome-Wide Identification and Characterization of Bovine Fibroblast Growth Factor (FGF) Gene and Its Expression during Adipocyte Differentiation. **2023**, 24, 5663	0
346	Helicobacter kumamotonensis sp. nov., isolated from human clinical specimens. **2023**, 73,	0
345	A genetic linkage map and improved genome assembly of the termite symbiont Termitomyces cryptogamus. **2023**, 24,	0
344	Multiple factors driving the acquisition efficiency of apple proliferation phytoplasma in Cacopsylla melanoneura.	0

343	Insights into the genomic evolution and the alkali tolerance mechanisms of Agaricus sinodeliciosus by comparative genomic and transcriptomic analyses. **2023**, 9,	0
342	Whole-genome sequencing reveals putative underlying mechanisms of biocontrol capability of IBFCBF-5. **2023**, 45,	0
341	Antiviral immune response reveals host-specific virus infections in natural ant populations. 14,	0
340	Characterization and Comparative Genomic Analysis of Three Virulent E. coli Bacteriophages with the Potential to Reduce Antibiotic-Resistant Bacteria in the Environment. **2023**, 24, 5696	0
339	Machine Learning-Based Prediction of Orphan Genes and Analysis of Different Hybrid Features of Monocot and Eudicot Plants. **2023**, 12, 1433	0
338	Integrative multi-omics analysis of three early diverged rosid species reveals an ancient hierarchical cold-responsive regulatory network. **2023**, 175,	0
337	In the light of evolution: keratins as exceptional tumor biomarkers. 11, e15099	0
336	Analyzing CRISPR screens in non-conventional microbes. **2023**, 50,	0
335	Systematic analysis of prophage elements in actinobacterial genomes reveals a remarkable phylogenetic diversity. **2023**, 13,	0
334	The complete mitochondrial genome of Anthrenus museorum (Coleoptera: Bostrichiformia: Dermestidae) from China. **2023**, 8, 405-409	0
333	Bacteriolytic Potential of Enterococcus Phage iF6 Isolated from Sextaphag Therapeutic Phage Cocktail and Properties of Its Endolysins, Gp82 and Gp84. **2023**, 15, 767	0
332	Classification of Family Domain of Amino Acid Sequences Using CNN-LSTM. **2023**, 645-653	0
331	Increased zinc levels facilitate phenotypic detection of ceftazidime-avibactam resistance in metallo-β-lactamase-producing Gram-negative bacteria. 13,	0
330	Functional and Proteomic Insights into Aculeata Venoms. **2023**, 15, 224	0
329	Adaptation Strategies to High Hydrostatic Pressures in Pseudothermotoga species Revealed by Transcriptional Analyses. **2023**, 11, 773	0
328	Genetics of destemming in pepper: A step towards mechanical harvesting. 14,	0
327	Using Next-Generation Sequencing to Disentangle the Diet and Incidence of Intestinal Parasites of Falkland Flightless Steamer Duck Tachyeres brachypterus and Patagonian Crested Duck Lophonetta specularioides Sharing a South Atlantic Island. **2023**, 14, 731	0
326	Endorhizosphere of indigenous succulent halophytes: a valuable resource of plant growth promoting bacteria. **2023**, 18,	0

325	An informatic workflow for the enhanced annotation of excretory/secretory proteins of Haemonchus contortus. **2023**,	0
324	Collection of triatomines from sylvatic habitats by a Trypanosoma cruzi-infected scent detection dog in Texas, USA. **2023**, 17, e0010813	0
323	Incidental invertebrate-derived DNA detection of invasive and threatened species in temperate dry Southeast Australian forest.	0
322	Single-Cell Genomics Reveals the Divergent Mitochondrial Genomes of Retaria (Foraminifera and Radiolaria).	0
321	High Andean Steppes of Southern Chile Contain Little-Explored Peltigera Lichen Symbionts. **2023**, 9, 372	0
320	Ectodermal Wnt signaling, cell fate determination, and polarity of the skate gill arch skeleton. 12,	0
319	Rickettsial DNA and a trans-splicing rRNA group I intron in the unorthodox mitogenome of the fern Haplopteris ensiformis. **2023**, 6,	0
318	Axenic in vitro cultivation and genome diploidization of the moss Vesicularia montagnei for horticulture utilization. 14,	0
317	Plastid Genome Assembly Using Long-read data.	0
316	LSTM-GRU Based Deep Learning Model with Word2Vec for Transcription Factors in Primates.	0
315	Comparative transcriptome profiling of high and low grain-iron containing Indian barnyard millet (Echinochloa frumentacea L.) genotypes during different stages of grain development.	0
314	Structural analysis and molecular dynamics simulation studies of HIV-1 antisense protein predict its potential role in HIV replication and pathogenesis. 14,	0
313	Comparative analysis of the MYB gene family in seven Ipomoea species. 14,	0
312	Immunoinformatics aided approach for predicting potent cytotoxic T cell epitopes of respiratory syncytial virus. 1-13	0
311	Biocatalytic potential of Pseudolycoriella CAZymes (Sciaroidea, Diptera) in degrading plant and fungal cell wall polysaccharides. **2023**, 26, 106449	0
310	Broad-Spectrum Antifungal, Biosurfactants and Bioemulsifier Activity of Bacillus subtilis subsp. spizizeniiA Potential Biocontrol and Bioremediation Agent in Agriculture. **2023**, 12, 1374	0
309	Nanopore Cas9-targeted sequencing enables accurate and simultaneous identification of transgene integration sites, their structure and epigenetic status in recombinant Chinese hamster ovary cells.	0
308	Structural Study of the Cobetia marina Bacteriophage 1 (Carin-1) by Cryo-EM.	0

307	Brevundimonas and Serratia as host systems for assessing associated environmental viromes and phage diversity by complementary approaches. 14,	0
306	Lower respiratory tract microbiome composition and community interactions in smokers. **2023**, 5,	0
305	Elucidating the molecular mechanisms of essential oils' insecticidal action using a novel cheminformatics protocol. **2023**, 13,	0
304	Genome Sequence of Mycobacteriophage Bassalto. **2023**, 12,	0
303	Phytolith Content Negatively Affects Forage Quality of Eragrostis curvula (Schrad.) Nees. **2023**, 13, 924	0
302	Evidence of Zelkova carpinifolia as a potential host of Tuber uncinatum in Hyrcanian temperate forests.	0
301	Evolutionary history of two evergreen Rhododendron species as revealed by chromosome-level genome assembly. 14,	0
300	Metabarcoding the zooplankton species of the Saudi Arabian Gulf: A study employing mock communities and two gene markers. **2023**,	0
299	Genetic studies of heat stress regulation in goat during hot climatic condition. **2023**, 113, 103528	0
298	Differences in gut bacterial community composition between modern and slower-growing broiler breeder lines: Implications of growth selection on microbiome composition. 14,	0
297	Genome-Wide Identification and Expression Analysis of the Cytochrome P450 Gene Family in Bemisia tabaci MED and Their Roles in the Insecticide Resistance. **2023**, 24, 5899	0
296	Erythrocyte miRNA-92a-3p interactions with PfEMP1 as determinants of clinical malaria. **2023**, 23,	0
295	Freshwater Lichens, Including New Species in the Genera Verrucaria, Placopyrenium and Circinaria, Associated with Lobothallia hydrocharis (Poelt & Nimis) Sohrabi & Nimis from Watercourses of Sardinia. **2023**, 9, 380	0
294	Toward novel treatment against filariasis: Insight into genome-wide co-evolutionary analysis of filarial nematodes and Wolbachia. 14,	0
293	Studies on Argentine Phylacia species (Hypoxylaceae) using a polythetic taxonomic approach. **2023**, 22,	0
292	Purification and Biological Properties of Raniseptins-3 and -6, Two Antimicrobial Peptides from Boana raniceps (Cope, 1862) Skin Secretion. **2023**, 13, 576	0
291	Gene clustering and co-expression analysis for the identification of putative transcription factors associated with the genes of secondary metabolic pathways in Plantago ovata Forsk. and its wild allies.	0
290	A short-chain carbonyl reductase mutant is an efficient catalyst in the production of (R)-1,3-butanediol.	0

289	The persistence and stabilization of auxiliary genes in the human skin virome. **2023**, 20,	0
288	Insulin, dibutyryl-cAMP, and glucose modulate expression of patatin-like domain containing protein 7 in cultured human myotubes. 14,	0
287	Spatiotemporal transitions in Pseudo-nitzschia species assemblages and domoic acid along the Alaska coast. **2023**, 18, e0282794	0
286	From primordial clocks to circadian oscillators. **2023**, 616, 183-189	0
285	Spherical Body Protein 4 from Babesia bigemina: A Novel Gene That Contains Conserved B-Cell Epitopes and Induces Cross-Reactive Neutralizing Antibodies in Babesia ovata. **2023**, 12, 495	0
284	Discovering the Repeatome of Five Species Belonging to the Asteraceae Family: A Computational Study. **2023**, 12, 1405	0
283	Persistence of a Wild-Type Virulent Aeromonas hydrophila Isolate in Pond Sediments from Commercial Catfish Ponds: A Laboratory Study. **2023**, 10, 236	0
282	An In Silico Deep Learning Approach to Multi-Epitope Vaccine Design: A Hepatitis E Virus Case Study. **2023**, 11, 710	0
281	Heavy Metal Pollution Impacts Soil Bacterial Community Structure and Antimicrobial Resistance at the Birmingham 35th Avenue Superfund Site. **2023**, 11,	0
280	Crosstalk between Gut Microbiota and Epigenetic Markers in Obesity Development: Relationship between Ruminococcus, BMI, and MACROD2/SEL1L2 Methylation. **2023**, 15, 1550	0
279	Coccoloba-associated xerocomoid boletes (Boletaceae) from the Caribbean and Mexico: Tropicoboletus ruborculus gen. et comb. nov., revision of Xerocomus coccolobae, phylogenetic assessment of Singerocomus guadelupae comb. nov., and type studies of Xerocomus caeruleonigrescens, X. cuneipes, and X. pseudoboletinus var. pini-caribaeae. **2023**, 22,	0
278	Unraveling the Aquaporin-3 Inhibitory Effect of Rottlerin by Experimental and Computational Approaches. **2023**, 24, 6004	0
277	Fine-mapping and candidate gene analysis of the Mcgy1 locus responsible for gynoecy in bitter gourd (Momordica spp.). **2023**, 136,	0
276	An updated catalogue of diverse type II polyketide synthase biosynthetic gene clusters captured from large-scale nucleotide databases. **2023**, 9,	0
275	Homology Modeling in the Twilight Zone: Improved Accuracy by Sequence Space Analysis. **2023**, 1-23	0
274	Computational Approaches for Peroxisomal Protein Localization. **2023**, 405-411	0
273	Exploring and targeting potential druggable antimicrobial resistance targets ArgS, SecY and MurA in Staphylococcus sciuri with TCM inhibitors through subtractive genomics strategy.	0
272	Longitudinal changes in subgingival biofilm composition following periodontal treatment.	0

271	Effects of Starvation on the Physiology and Liver Transcriptome of Yellowcheek (Elopichthys bambusa). **2023**, 8, 175	0
270	The challenges of defining the human nasopharyngeal resistome. **2023**,	0
269	Traditional Fermented Foods: Introducing the Fructan Link **2023**, 147-166	0
268	Pseudolepraria, a new leprose genus revealed in Ramalinaceae (Ascomycota, Lecanoromycetes, Lecanorales) to accommodate Lepraria stephaniana. 96, 97-112	0
267	Dispersal-Limited Symbionts Exhibit Unexpectedly Wide Variation in Host Specificity.	0
266	Metabiotics Signature through Genome Sequencing and In Vitro Inhibitory Assessment of a Novel Lactococcus lactis Strain UTNCys6-1 Isolated from Amazonian Camu-Camu Fruits. **2023**, 24, 6127	0
265	Amazon Biobank: a collaborative genetic database for bioeconomy development. **2023**, 23,	0
264	Quantification of heavy metals and mercury-resistant bacteria in artisanal and small-scale gold mining sites, Maniema region, Democratic Republic of the Congo. **2023**, 17,	0
263	Infant gut microbiome composition correlated with type 1 diabetes acquisition in the general population: the ABIS study.	0
262	Genomic analysis of Vibrio harveyi strain PH1009, a potential multi-drug resistant pathogen due to acquisition of toxin genes. **2023**, 9, e14926	0
261	How to start a LINE : 5? switching rejuvenates LINE retrotransposons in tobacco and related Nicotiana species.	0
260	An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype.	0
259	Genomic diversity of non-diarrheagenic fecal Escherichia coli from children in sub-Saharan Africa and south Asia and their relatedness to diarrheagenic E. coli. **2023**, 14,	0
258	Antimicrobial peptides act on the rumen microbiome and metabolome affecting the performance of castrated bulls. **2023**, 14,	0
257	POSMM: an efficient alignment-free metagenomic profiler that complements alignment-based profiling. **2023**, 18,	0
256	Phylogenetic analysis of Plenodomus lingam and Plenodomus biglobosus isolates in Hungary.	0
255	Whitish truffles found in Finland: soil characteristics, and identification based on morphological and molecular properties. **2023**, 205,	0
254	De novo transcriptome assemblies of five major European oilseed rape insect pests. **2023**, 24,	0

253	Genomic rearrangements and evolutionary changes in 3D chromatin topologies in the cotton tribe (Gossypieae). **2023**, 21,	0
252	A highly conserved and globally prevalent cryptic plasmid is among the most numerous mobile genetic elements in the human gut.	0
251	Species composition and insecticide resistance in malaria vectors in Ellibou, southern C▯e d▯voire and first finding of Anopheles arabiensis in C▯e d▯voire. **2023**, 22,	0
250	The Torreya grandis genome illuminates the origin and evolution of gymnosperm-specific sciadonic acid biosynthesis. **2023**, 14,	0
249	QTL mapping and transcriptome analysis identify novel QTLs and candidate genes in Brassica villosa for quantitative resistance against Sclerotinia sclerotiorum. **2023**, 136,	0
248	Evolution of tetraspanin antigens in the zoonotic Asian blood fluke Schistosoma japonicum. **2023**, 16,	0
247	Identification of Fungal and Bacterial Denitrification Inhibitors Targeting Copper Nitrite Reductase. **2023**, 71, 5172-5184	0
246	Genome and Genetic Engineering of the House Cricket (Acheta domesticus): A Resource for Sustainable Agriculture. **2023**, 13, 589	0
245	Cloning and structural basis of fluorescent protein color variants from identical species of sea anemone, Diadumene lineata.	0
244	High-throughput miRNA sequencing and identification of a novel ICE1-targeting miRNA in response to low temperature stress in Eucalyptus camaldulensis.	0
243	High-resolution single-molecule long-fragment rRNA gene amplicon sequencing of bacterial and eukaryotic microbial communities. **2023**, 3, 100437	0
242	Population Genetic Structure of a Rare Butterfly in a Fragmented South Florida Ecosystem. **2023**, 14, 321	0
241	Rhetoric Mining: A New Text-Analytics Approach for Quantifying Persuasion.	0
240	Patterns of within-host spread of Chlamydia trachomatis between vagina, endocervix and rectum revealed by comparative genomic analysis. 14,	0
239	Screening and Application of Novel Homofermentative Lactic Acid Bacteria Results in Low-FODMAP Whole-Wheat Bread. **2023**, 9, 336	0
238	Biological Methanation in an Anaerobic Biofilm Reactor▯race Element and Mineral Requirements for Stable Operation. **2023**, 11, 1013	0
237	SARS-CoV-2 variant identification using a genome tiling array and genotyping probes.	0
236	In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem. **2023**, 11,	0

235	Correlation of Redondovirus and Entamoeba gingivalis Detections in the Human Oral Cavity Suggests That This Amoeba Is Possibly the Redondovirus Host. **2023**, 24, 6303	0
234	LTR Retroelements and Bird Adaptation to Arid Environments. **2023**, 24, 6332	0
233	Marker-assisted breeding (MAB) on apple and pear and new approaches for QTLs and major gene genotyping involved in disease resistance. **2023**, 221-230	0
232	Microbiome and Physicochemical Features Associated with Differential Listeria monocytogenes Growth in Soft, Surface-Ripened Cheeses.	0
231	A phylogenomic approach to resolving interrelationships of polyclad flatworms, with implications for life-history evolution. **2023**, 10,	0
230	Biodiversity, biogeography, and connectivity of polychaetes in the world's largest marine minerals exploration frontier.	0
229	Identification of Novel Tau-Tubulin Kinase 2 Inhibitors Using Computational Approaches. **2023**, 8, 13026-13037	0
228	Three chigger species (Trombidiformes: Trombiculidae) co-parasitizing a domestic cat in Brazil, including pathogen monitoring. 1-8	0
227	MarR-Dependent Transcriptional Regulation of mmpSL5 Induces Ethionamide Resistance in Mycobacterium abscessus. **2023**, 67,	0
226	Comparative Study of Microbial Diversity in Different Coastal Aquifers: Determining Factors. **2023**, 15, 1337	0
225	Pioneer colonizers: Bacteria that alter the chicken intestinal morphology and development of the microbiota. 14,	0
224	Evidence of Zelkova carpinifolia as a potential host of Tuber uncinatum in Hyrcanian temperate forests.	0
223	A Novel RT-LAMP for the Detection of Different Genotypes of Crimean–Congo Haemorrhagic Fever Virus in Patients from Spain. **2023**, 24, 6411	0
222	Diversity of trematodes from the amphibian anomaly P hotspot: Role of planorbid snails. **2023**, 18, e0281740	0
221	Phylogenomics and morphological evolution of the mega-diverse genus Artemisia (Asteraceae: Anthemideae): implications for its circumscription and infrageneric taxonomy.	0
220	Genome-Wide Pathway Exploration of the Epidermidibacterium keratini EPI-7T. **2023**, 11, 870	0
219	The evolution of morphological development is congruent with the species phylogeny in the genus Streptomyces. 14,	0
218	Chromosome-level genome assembly of the critically endangered Baer's pochard (Aythya baeri). **2023**, 10,	0

217	HERV-K (HML-2) insertion polymorphisms in the 8q24.13 region and their potential etiological associations with acute myeloid leukemia. **2023**, 168,	0
216	Human seven-βstrand (METTL) methyltransferases - conquering the universe of protein lysine methylation. **2023**, 104661	0
215	The Gut Microbiota of Broilers Reared with and without Antibiotic Treatment. **2023**, 11, 876	0
214	Powassan Virus Infection Detected by Metagenomic Next-Generation Sequencing, Ohio, USA. **2023**, 29, 838-841	0
213	Protein Structure Prediction: Challenges, Advances, and the Shift of Research Paradigms. **2023**,	0
212	Fungal Diversity Associated with Thirty-Eight Lichen Species Revealed a New Genus of Endolichenic Fungi, Intumescentia gen. nov. (Teratosphaeriaceae). **2023**, 9, 423	0
211	Using metatranscriptomics to better understand the role of microbial nitrogen cycling in coastal sediment benthic flux denitrification efficiency.	0
210	A novel method for visualizing in-vivo rates of protein degradation provides insight into how TRIM28 regulates muscle size. **2023**, 26, 106526	0
209	Rehabilitation and release of confiscated songbirds into the wild: A pilot study. 10,	0
208	Genome structures resolve the early diversification of teleost fishes. **2023**, 379, 572-575	0
207	Polydomus karssenii gen. nov. sp. nov. is a dark septate endophyte with a bifunctional lifestyle parasitising eggs of plant parasitic cyst nematodes (Heterodera spp.). **2023**, 14,	0
206	Different Response Mechanisms of Rhizosphere Microbial Communities in Two Species of Amorphophallus to Pectobacterium carotovorum subsp. carotovorum Infection. **2023**, 39, 207-219	0
205	Entropic analysis of antigen-specific CDR3 domains identifies essential binding motifs shared by CDR3s with different antigen specificities. **2023**, 14, 273-284.e5	0
204	RNA-seq analysis revealed considerable genetic diversity and enabled the development of specific KASP markers for Psathyrostachys huashanica. 14,	0
203	Sulfurospirillum tamanensis sp. nov., a Facultatively Anaerobic Alkaliphilic Bacterium from a Terrestrial Mud Volcano. **2023**, 92, 21-29	0
202	Rapid genomic surveillance of SARS-CoV-2 in a dense urban community of Kathmandu Valley using sewage samples. **2023**, 18, e0283664	0
201	Discrete patterns of microbiome variability across timescales in a wild rodent population. **2023**, 23,	0
200	An OmpW-dependent T4-like phage infects Serratia sp. ATCC 39006. **2023**, 9,	0

199	Saccharopolyspora sp. NFXS83 in Marine Biotechnological Applications: From Microalgae Growth Promotion to the Production of Secondary Metabolites. **2023**, 11, 902	0
198	In silico annotation of a hypothetical protein from Listeria monocytogenes EGD-e unfolds a toxin protein of the type II secretion system. **2023**, 21, e7	0
197	Enzyme function prediction using contrastive learning. **2023**, 379, 1358-1363	0
196	Five new Graphium species from hardwood trees in Poland. 1-18	0
195	Lolliginicoccus levis gen. nov., sp. nov., a novel bacterium isolated from the brain of the Chiroteuthis picteti squid, and reclassification of two Hoyosella species as Lolliginicoccus suaedae comb. nov. and Lolliginicoccus lacisalsi comb. nov.. **2023**, 73,	0
194	Organelle genome-based markers in deciphering mitonuclear conflict displaying floral malformations and distinguishing cytoplasm types in snowball cauliflower. **2023**, 507-512	0
193	A First Insight into the Microbial and Viral Communities of Comau Fjord A Unique Human-Impacted Ecosystem in Patagonia (42? S). **2023**, 11, 904	0
192	Gene loss during a transition to multicellularity. **2023**, 13,	0
191	Distinct cervical tissue-adherent and luminal microbiome communities correlate with mucosal host gene expression and protein levels in Kenyan sex workers. **2023**, 11,	0
190	T cell immune deficiency rather than chromosome instability predisposes patients with short telomere syndromes to squamous cancers. **2023**, 41, 807-817.e6	0
189	Genomic profiling and characteristics of a C1 degrading heterotrophic fresh-water bacterium Paracoccus sp. strain DMF.	0
188	When does the female bias arise? Insights from the sex determination cascade of a flea beetle with a strongly skewed sex ratio. **2023**, 23,	0
187	First report of wilt disease in cashew (Anacardium´occidentale L.) caused by Fusarium decemcellulare in Kerala, India. **2023**, 4,	0
186	Virus-Host Dynamics in Archaeal Groundwater Biofilms and the Associated Bacterial Community Composition. **2023**, 15, 910	0
185	Acarospora sultanii sp. nov. (Acarosporaceae, Lichen Forming Ascomycota) from Darel Valley, Gilgit Baltistan, Pakistan. **2022**, 49, S40-S44	0
184	Genome-Wide Analysis of the Odorant Receptor Gene Family in Solenopsis invicta, Ooceraea biroi, and Monomorium pharaonis (Hymenoptera: Formicidae). **2023**, 24, 6624	0
183	Studying pathogens degrades BLAST-based pathogen identification. **2023**, 13,	0
182	Major proliferation of transposable elements shaped the genome of the soybean rust pathogen Phakopsora pachyrhizi. **2023**, 14,	0

181	Morphological and genetic variability in cosmopolitan tardigrade species - Paramacrobiotus fairbanksi Schill, F�ster, Dandekar &amp; Wolf, 2010.	0
180	Aquitalea palustris sp. nov., isolated from a wild cranberry bog in the Cape Cod National Seashore. **2023**, 73,	0
179	Genome Alignments. **2023**,	0
178	Fortuitously compatible protein surfaces primed allosteric control in cyanobacterial photoprotection.	0
177	Concatenated 16S rRNA sequence analysis improves bacterial taxonomy. 11, 1530	0
176	Potential Effects of High Temperature and Heat Wave on Nanorana pleskei Based on Transcriptomic Analysis. **2023**, 45, 2937-2949	0
175	The complete plastid genome and nuclear ribosomal transcription unit sequences of <i>Spiraea prunifolia</i> f. <i>simpliciflora</i> (Rosaceae). **2023**, 53, 32-37	0
174	Evolutionary loss of the �-adrenergic receptor in salmonids. **2023**, 338, 114279	0
173	Resolving the phylogeny of Thladiantha (Cucurbitaceae) with three different targeted-capture pipelines.	0
172	Copper Efflux System Required in Murine Lung Infection by Haemophilus influenzae Composed of a Canonical ATPase Gene and Tandem Chaperone Gene Copies.	0
171	Metagenomic study for the identification of viruses infecting soybean in Pakistan.	0
170	transXpress: a Snakemake pipeline for streamlined de novo transcriptome assembly and annotation. **2023**, 24,	0
169	Shine: A novel strategy to extract specific, sensitive and well-conserved biomarkers from massive microbial genomic datasets. **2023**, 24,	0
168	Characterization and genetic diversity of MHC class II DRB genes in the Arabian camel (Camelus dromedarius).	0
167	Diexanthema hakuhomaruae sp. nov. (Copepoda: Siphonostomatoida: Nicothoidae) from the Hadal Zone in the Northwestern Pacific, with an 18S Molecular Phylogeny.	0
166	Comparative transcriptome analysis of juniper branches infected by Gymnosporangium spp. highlights their different infection strategies associated with cytokinins. **2023**, 24,	0
165	Lint percentage and boll weight QTLs in three excellent upland cotton (Gossypium hirsutum): ZR014121, CCRI60, and EZ60. **2023**, 23,	0
164	Environmental DNA survey indicates arrival of quagga mussel in Ticino River basin. 82,	0

163	Vibrio type III secretion system 2 is not restricted to the Vibrionaceae and encodes differentially distributed repertoires of effector proteins. **2023**, 9,	0
162	Etiology of oncogenic fusions in 5,190 childhood cancers and its clinical and therapeutic implication. **2023**, 14,	0
161	Morphological and molecular comparison as a useful tool for identification of the three centric marine diatoms (Bacillariophyceae: Chaetoceros). **2023**, 205,	0
160	Age estimation of Asian elephants (Elephas maximus) using methylation-sensitive high-resolution melting (MS-HRM).	0
159	Sampling strategies for sugarcane using either clonal replicates or diverse genotypes can bias the conclusions of RNA-Seq studies. **2023**, 46,	0
158	Spontaneously Produced Lysogenic Phages Are an Important Component of the Soybean Bradyrhizobium Mobilome.	0
157	Viruses interact with hosts that span distantly related microbial domains in dense hydrothermal mats.	0
156	Nisin S, a Novel Nisin Variant Produced by Ligilactobacillus salivarius P1CEA3. **2023**, 24, 6813	0
155	Exploring the microbiome of oral epithelial dysplasia as a predictor of malignant progression. **2023**, 23,	0
154	A methodology for the selection and characterization of riboflavin-overproducing Weissella cibaria strains after treatment with roseoflavin. 14,	0
153	Transcriptome-Assisted SNP Marker Discovery for Phytophthora infestans Resistance in Solanum lycopersicum L.. **2023**, 24, 6798	0
152	Chemical and genomic characterization of a potential probiotic treatment for stony coral tissue loss disease. **2023**, 6,	0
151	Three Aedes species infested by mermithids in France. **2023**, 30, 12	0
150	Purified cellulase-mediated simultaneous sugar utilization by Bacillus albus isolated from Similipal, Odisha, India.	0
149	Effect of bean common mosaic virus on seed germination and yield of cowpea (Vigna unguiculata [L.] Walp.) breeding lines and characterisation of virus strains.	0
148	Genome-based classification of Pedobacter polysacchareus sp. nov., isolated from Antarctic soil producing exopolysaccharide.	0
147	Genomic insights into the c-di-GMP signaling and biofilm development in the saprophytic spirochete Leptospira biflexa. **2023**, 205,	0
146	Maturases and Group II Introns in the Mitochondrial Genomes of the Deepest Jakobid Branch.	0

145	Tropical super flies: Integrating Cas9 into Drosophila ananassae and its phenotypic effects. **2023**, 147, 104516	o
144	Complete Genome Sequences of Chop, DelRio, and GrandSlam, Three Gordonia Phages Isolated from Soil in Central Arkansas.	o
143	An ancient metalloenzyme evolves through metal preference modulation.	o
142	The effect of petroleum levels on some soil biological properties under phytoremediation and bioaugmentation.	o
141	A Culturomics-Based Bacterial Synthetic Community for Improving Resilience towards Arsenic and Heavy Metals in the Nutraceutical Plant Mesembryanthemum crystallinum. **2023**, 24, 7003	o
140	Genome Sequence of Arthrobacter sp. Strain ATA002, a Seed Endophytic Bacterium from the Atacama Desert.	o
139	The First Swedish Outbreak with VIM-2-Producing Pseudomonas aeruginosa, Occurring between 2006 and 2007, Was Probably Due to Contaminated Hospital Sinks. **2023**, 11, 974	o
138	Comparative epidemic expansion of SARS-CoV-2 variants Delta and Omicron in the Brazilian State of Amazonas. **2023**, 14,	o
137	Allergenicity evaluation of five types of commercial food-derived oligopeptide products.	o
136	Genomic surveillance uncovers a pandemic clonal lineage of the wheat blast fungus. **2023**, 21, e3002052	o
135	Monkeypox virus: phylogenomics, host□pathogen interactome and mutational cascade. **2023**, 9,	o
134	A review of Ellescus (Coleoptera: Curculionidae) in North America: new species and synonyms revealed through integrative taxonomy. **2023**, 155,	o
133	In Silico Analysis of a GH3 □Glucosidase from Microcystis aeruginosa CACIAM 03. **2023**, 11, 998	o
132	First Study on profiling of gut microbiome in wild and captive Sumatran orangutans (Pongo abelii). **2023**, 717-727	o
131	Targeting the I7L Protease: A Rational Design for Anti-Monkeypox Drugs?. **2023**, 24, 7119	o
130	Staphylococcal diversity in atopic dermatitis from an individual to a global scale. **2023**, 31, 578-592.e6	o
129	Near-atomic architecture of Singapore grouper iridovirus and implications for giant virus assembly. **2023**, 14,	o
128	High-quality chromosome-level genome assembly of the plant bug Pachypeltis micranthus provides insights into the availability of Mikania micrantha control.	o

127	Dengue and chikungunya virus loads in the mosquito Aedes aegypti are determined by distinct genetic architectures. **2023**, 19, e1011307	0
126	A2TEA: Identifying trait-specific evolutionary adaptations. 11, 1137	0
125	Evaluation of the Deterioration of Untreated Commercial Polystyrene by Psychrotrophic Antarctic Bacterium. **2023**, 15, 1841	0
124	Chromosome-length genome assemblies and cytogenomic analyses of pangolins reveal remarkable chromosome counts and plasticity. **2023**, 31,	0
123	Sponge diversification in marine lakes: Implications for phylogeography and population genomic studies on sponges. **2023**, 13,	0
122	MicroalgaBacteria Community with High Level Carbon Dioxide Acclimation and Nitrogen-fixing Ability. **2023**, 125957	0
121	Condyloma acuminata: An evaluation of the immune response at cellular and molecular levels. **2023**, 18, e0284296	0
120	De novo transcriptome assembly of Iphiculus spongiosus Adams & White, 1849 (Decapoda; Brachyura; Leucosioidea) using full-length isoform sequencing. **2023**, 102960	0
119	Previously uncharacterized rectangular bacterial structures in the dolphin mouth. **2023**, 14,	0
118	Constellation of the endophytic mycobiome in spring and winter wheat cultivars grown under various conditions. **2023**, 13,	0
117	A multispecies corridor in a fragmented landscape: Evaluating effectiveness and identifying high-priority target areas. **2023**, 18, e0283258	0
116	Synthesis of SARS-CoV-2 Mpro inhibitors bearing a cinnamic ester warhead with in vitro activity against human coronaviruses.	0
115	Anaplasma Species in Ticks Infesting Mammals of Sardinia, Italy. **2023**, 13, 1332	0
114	Bloodmeal host identities among sympatric Glossina austeni and Glossina pallidipes tsetse flies in Shimba Hills National Reserve, Kwale, Kenya. 4,	0
113	Whole genome analysis of two sympatric human Mansonella: Mansonella perstans and Mansonella sp DEUX13,	0
112	A´new extremophile ostracod crustacean from the Movile Cave sulfidic chemoautotrophic ecosystem in Romania. **2023**, 13,	0
111	Volatiles of fungal cultivars act as cues for host-selection in the fungus-farming ambrosia beetle Xylosandrus germanus. 14,	0
110	Integration of mRNA and miRNA Analysis Reveals the Post-Transcriptional Regulation of Salt Stress Response in Hemerocallis fulva. **2023**, 24, 7290	0

109	Integrated Omics approach for Prediction of Operons like gene clusters in plants: Tools, Techniques, and Future aspects. **2023**, 947-954	0
108	Ruthenium biochanin-A complex ameliorates lung carcinoma through the downregulation of the TGF-/PPAR/PI3K/TNF-pathway in association with caspase-3-mediated apoptosis.	0
107	The structure and function of YTHDF epitranscriptomic m6A readers. **2023**,	0
106	Bioinformatic identification of ClpI, a distinct class of Clp unfoldases in Actinomycetota. 14,	0
105	Screening and Identification of the Strain Pediococcus acidilactici and Its Application in Fermentation of CornSoybean Meal Uncooked Materials. **2023**, 9, 383	0
104	Application of sequence semantic and integrated cellular geography approach to study alternative biogenesis of exonic circular RNA. **2023**, 24,	0
103	Haplotype-resolved genomes of two buckwheat crops provide insights into their contrasted rutin concentrations and reproductive systems. **2023**, 21,	0
102	Integrated transcriptome catalog of Tenualosa ilisha as a resource for gene discovery and expression profiling. **2023**, 10,	0
101	Uniparental Inheritance and Recombination as Strategies to Avoid Competition and Combat Mullers Ratchet among Mitochondria in Natural Populations of the Fungus Amanita phalloides. **2023**, 9, 476	0
100	Incidence of Begomovirus and Crinivirus in tomato and potato crops in ParanState, Brazil. **2023**, 53,	0
99	Transcriptomic alterations in the sweet orange vasculature correlate with growth repression induced by a variant of citrus tristeza virus. 14,	0
98	Draft Genome Sequences and Genome Characterization of Three Toxigenic and Two Nontoxigenic Clostridioides difficile Clinical Isolates from Florida, USA.	0
97	Surface ID: A Geometry-aware System for Protein Molecular Surface Comparison.	0
96	A Method Based on Temporal Embedding for the Pairwise Alignment of Dynamic Networks. **2023**, 25, 665	0
95	Complete Genome Sequence of Klebsiella pneumoniae Bacteriophage KpS110, Encoding Five Tail-Associated Proteins with Putative Polysaccharide Depolymerase Domains.	0
94	Independent Effects of HIV and Antiretroviral Therapy on the Oral Microbiome Identified by Multivariate Analyses.	0
93	Three marine species of the genus Fulvivirga, rich sources of carbohydrate-active enzymes degrading alginate, chitin, laminarin, starch, and xylan. **2023**, 13,	0
92	Definition of the transcriptional units of inherited retinal disease genes by meta-analysis of human retinal transcriptome data. **2023**, 24,	0

91	Genomics reveals broad hybridization in deeply divergent Palearctic grass and water snakes (Natrix spp.). **2023**, 107787	0
90	Probable Airborne Transmission of Burkholderia pseudomallei Causing an Urban Outbreak of Melioidosis during Typhoon Season in Hong Kong, China..	0
89	Long-reads-based transcriptome dataset from leaves of lime, Citrus aurantiifolia (Christm.) Swingle treated by ethephon and abscisic acid. **2023**, 109167	0
88	Inhibitory effect of natural compounds on Dihydropteroate synthase of Mycobacterium leprae: Molecular dynamic study. 1-16	0
87	Identification and susceptibility testing of oral candidiasis in advanced cancer patients. **2023**, 23,	0
86	C-phycoerythrin production from Anabaena sp. BTA 903: Optimization, production kinetics, thermodynamic, and stability analysis.	0
85	Transgressive and parental dominant gene expression and cytosine methylation during seed development in Brassica napus hybrids. **2023**, 136,	0
84	Distribution, diversity and diversification from a DNA barcoding perspective: the case ofGammarusradiation in Europe□ oldest inland waterbody - the ancient Lake Ohrid.	0
83	Endophytic Trichoderma species from rubber trees native to the Brazilian Amazon, including four new species. 14,	0
82	Population genomic analysis provides evidence of the past success and future potential of South China tiger captive conservation. **2023**, 21,	0
81	Identification of IPT9 in Brachiaria brizantha (syn. Urochloa brizantha) and expression analyses during ovule development in sexual and apomictic plants.	0
80	Genomic variations and mutational analysis of South Indian isolates of BmNPV.	0
79	Co-evolution of large inverted repeats and G-quadruplex DNA in fungal mitochondria may facilitate mitogenome stability: the case of Malassezia. **2023**, 13,	0
78	MRF: a tool to overcome the barrier of inconsistent genome annotations and perform comparative genomics studies for the largest animal DNA virus. **2023**, 20,	0
77	Expression of Microcystis Biosynthetic Gene Clusters in Natural Populations Suggests Temporally Dynamic Synthesis of Novel and Known Secondary Metabolites in Western Lake Erie.	0
76	Fungal feeding preferences and molecular gut content analysis of two abundant oribatid mite species (Acari: Oribatida) under the canopy of Prosopis laevigata (Fabaceae) in a semi-arid land.	0
75	High diversity and isolated distribution of aquatic heterotrophic protists in salars of the Atacama Desert at different salinities. **2023**, 125987	0
74	State-of-the-art of data analyses in environmental DNA approaches towards its applicability to sustainable fisheries management. 10,	0

73	Multi-factorial examination of amplicon sequencing workflows from sample preparation to bioinformatic analysis. **2023**, 23,	0
72	Genomic Analysis of Infectious Bursal Disease Virus in Nigeria: Identification of Unique Mutations of Yet Unknown Biological Functions in Both Segments A and B. **2023**, 11, 867	0
71	Detection of a Diverse Endophyte Assemblage within Fungal Communities Associated with the Arundo Leaf Miner, Lasioptera donacis (Diptera: Cecidomyiidae). **2023**, 15, 571	0
70	Oxidative Stability and Microbial Ecology of Fresh Beef with Extremely Long Shelf-Life. **2023**, 2023, 1-13	0
69	Phosphorus amendment alters soil arbuscular mycorrhizal fungal functional guild compositions in a subtropical forest.	0
68	Evolutionary relationship between DOF multigene transcription factors and the regulation of lipid biosynthesis in oilseeds.	0
67	Molecular Screening of Haemogregarine Hemoparasites (Apicomplexa: Adeleorina: Haemogregarinidae) in Populations of Native and Introduced Pond Turtles in Eastern Europe. **2023**, 11, 1063	0
66	A scuticociliate causes mass mortality of Diadema antillarum in the Caribbean Sea. **2023**, 9,	1
65	The embryology, metamorphosis, and muscle development of Schizocardium karankawa sp. nov. (Enteropneusta) from the Gulf of Mexico. **2023**, 14,	0
64	Sugiyamaella bielyi f. a., sp. nov. and Sugiyamaella amazoniana f. a., sp. nov., two yeast species isolated from passalid beetles and rotting wood in Amazonia. **2023**, 73,	0
63	Identification and expression analysis of SQUAMOSA´promoter-binding protein (SBP) genes in mungbean.	0
62	Atypical flavobacteria recovered from diseased fish in the Western United States. 13,	0
61	PAUSE: principled feature attribution for unsupervised gene expression analysis. **2023**, 24,	0
60	Presence and activity of nitrogen-fixing bacteria in Scots pine needles in a boreal forest: a nitrogen-addition experiment.	0
59	Towards resolving Nothophaeocryptopus and Rhizosphaera inhabitants of spruce needles.	0
58	E. coli ST11 (O157:H7) does not encode a functional AcrF efflux pump. **2023**, 169,	0
57	Detection of gut microflora and enzymes using metagenomics and metaproteomics in silkworm, Bombyx mori.	0
56	Genome-environment associations along elevation gradients in two snowbed species of the North-Eastern Calcareous Alps. **2023**, 23,	0

55	Canine piroplasmids: Molecular detection and laboratory characterization in dogs from Brasilia, Brazil, with the first molecular evidence of dog exposure to a novel opossum-associated Babesia sp.. **2023**, 14, 102181	0
54	Identification of combinatorial mutations associated with colistin resistance in Shewanella algae. **2023**, 105143	0
53	Mirusviruses link herpesviruses to giant viruses.	0
52	De novo transcriptome sequencing and gene co-expression reveal a genomic basis for drought sensitivity and evidence of a rapid local adaptation on Atlas cedar (Cedrus atlantica). 14,	0
51	Extensive genome analysis identifies novel plasmid families in Clostridium perfringens. **2023**, 9,	0
50	Exploring halophilic environments as a source of new antibiotics. 1-30	0
49	A Bacteriological Comparison of the Hemolymph from Healthy and Moribund Unionid Mussel Populations in the Upper Midwestern U.S.A. Prompts the Development of Diagnostic Assays to Detect Yokenella regensburgei. **2023**, 11, 1068	0
48	Insights into the Molecular Basis of Huanglongbing Tolerance in Persian Lime (Citrus latifolia Tan.) through a Transcriptomic Approach. **2023**, 24, 7497	0
47	The evolution of two transmissible cancers in Tasmanian devils. **2023**, 380, 283-293	0
46	The prevalence and molecular detection of bovine cysticercosis and its impact on slaughtered cattle in Egypt.	0
45	Identification and analysis of the secretome of plant pathogenic fungi reveals lifestyle adaptation. 14,	0
44	Generative design of de novo proteins based on secondary-structure constraints using an attention-based diffusion model. **2023**,	0
43	Molecular identification of Bartonella spp. and Rickettsia felis in fox fleas, Chile. **2023**, 101983	0
42	Evolution of immunogenetic components encoding ultralong CDR H3.	0
41	DivBrowse□interactive visualization and exploratory data analysis of variant call matrices. **2022**, 12,	0
40	Distribution and molecular evolution of the anti-CRISPR family AcrIF7. **2023**, 21, e3002072	0
39	Screening of marine Actinomycetia with bioactive metabolites from nearshore and deep sea marine sediments in southwestern Taiwan.	0
38	Putting hornets on the genomic map. **2023**, 13,	0

37	Molecular modeling approach for cancer drug therapy. **2023**, 11-18	0
36	Screening for Multifarious Plant Growth Promoting and Biocontrol Attributes in Bacillus Strains Isolated from Indo Gangetic Soil for Enhancing Growth of Rice Crops. **2023**, 11, 1085	0
35	Characterization and Genomic Analysis of the Naphthalene-Degrading Delftia tsuruhatensis ULwDis3 Isolated from Seawater. **2023**, 11, 1092	0
34	Metagenomic Detection of Divergent Insect- and Bat-Associated Viruses in Plasma from Two African Individuals Enrolled in Blood-Borne Surveillance. **2023**, 15, 1022	0
33	Diversity, distribution, and functional potentials of magroviruses from marine and brackish waters. 14,	0
32	Genetic differentiation of Gracilaria changii and Gracilaria firma (Gracilariaceae, Rhodophyta) based on chloroplast genome. **2023**,	0
31	Disentangling temporal associations in marine microbial networks. **2023**, 11,	0
30	Description of Sporanaerobium hydrogeniformans gen. nov., sp. nov., an obligately anaerobic, hydrogen producing bacterium of Lachnospiraceae family isolated from Aravali hot spring in India.	0
29	Human Milk Microbiota Profile Affected by Prematurity in Argentinian Lactating Women. **2023**, 11, 1090	0
28	Thalassemia, a New Hemoglobinopathy Category.	0
27	New Representative of the Species Prosthecodimorpha hirschii from a Methanotrophic Enrichment Culture: Phenotypic Traits and Genome Analysis. **2023**, 92, 129-136	0
26	Novel Catabolic Pathway for 4-Nitroaniline in a Rhodococcus sp. Strain JS360. **2023**, 131473	0
25	Photobacterium predominate the microbial communities of muscle of European plaice (Pleuronectes platessa) caught in the Norwegian sea independent of skin and gills microbiota, fishing season, and storage conditions. **2023**, 110222	0
24	How diverse a genus can be: An integrated multi-layered analysis into Desmonostoc (Nostocaceae, Cyanobacteriota). **2023**, 126422	0
23	A burst of genomic innovation at the origin of placental mammals mediated embryo implantation. **2023**, 6,	0
22	In silico structural and functional characterization of hypothetical proteins from Monkeypox virus. **2023**, 21,	0
21	A Cross-Inoculation Experiment Reveals that Ophidiomyces ophiodiicola and Nannizziopsis guarroi Can Each Infect Both Snakes and Lizards.	0
20	Some Physciaceae lichens from Pakistan. **2023**, 2023,	0

19	Ceftriaxone resistant Salmonella enterica serovar Paratyphi A identified in a case of enteric fever: first case report from Pakistan. **2023**, 23,	0
18	Complete Genome of ‘Candidatus Phytoplasma rubi’ RS, a Phytopathogenic Bacterium Associated with Rubus Stunt Disease. **2023**, 12,	0
17	Carbazole Degradation and Genetic Analyses of Sphingobium sp. Strain BS19 Isolated from Antarctic Soil. **2023**, 15, 7197	0
16	Draft Genome Sequences of 27 Rhizogenic Agrobacterium Biovar 1 Strains, the Causative Agent of Hairy Root Disease. **2023**, 12,	0
15	Molecular and phenotypic characterization of Hemicriconemoides rosae (Rathour et al., 2003) from mustard rhizosphere in India. **2023**, 84,	0
14	Draft Genome Sequences of Pseudomonas Isolates Derived from Glyphosate-Treated Sediments. **2023**, 12,	0
13	Investigating the cecal microbiota of broilers raised in extensive and intensive production systems.	0
12	Millipede gut-derived microbes as a potential source of cellulolytic enzymes. **2023**, 39,	0
11	Pseudomonas petrae sp. nov. isolated from regolith samples in Antarctica. **2023**, 46, 126424	0
10	High-throughput and high-accuracy single-cell RNA isoform analysis using PacBio circular consensus sequencing. **2023**, 14,	0
9	Detection of long terminal repeat loci derived from endogenous retrovirus in junglefowl using whole-genome sequencing. **2023**, 13,	0
8	Identification by High-Throughput Real-Time PCR of 30 Major Circulating Listeria monocytogenes Clonal Complexes in Europe.	0
7	A ParDE toxin–antitoxin system is responsible for the maintenance of the Yersinia virulence plasmid but not for type III secretion-associated growth inhibition. 13,	0
6	Genome-directed discovery of antiproliferative bafilomycins from a deepsea-derived Streptomyces samsunensis. **2023**, 106599	0
5	NON-TARGET-SITE RESISTANCE DUE TO RAPID PHYSIOLOGICAL RESPONSE IN 2, 4-D RESISTANT Conyza sumatrensis : REDUCED 2, 4-D TRANSLOCATION AND AUXIN-INDUCED GENE EXPRESSION.	0
4	Salinity stress mitigation on Zea mays L. seedling by halotolerant bacteria. **2023**, 1160, 012004	0
3	Using Genomics To Investigate an Outbreak of Vancomycin-Resistant Enterococcus faecium ST78 at a Large Tertiary Hospital in Queensland.	0
2	First report of whole genome sequence of septicemic Pasteurella multocida serovar B:2 “Soron” strain isolated from swine.	0

1	Genomics of Aminoglycoside Resistance in Pseudomonas aeruginosa Bloodstream Infections at a United States Academic Hospital.	0