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2197	Tests for comparing related amino-acid sequences. Cytochrome c and cytochrome c 551. <i>Journal of Molecular Biology</i> , 1971 , 61, 409-24	6.5	428
2196	Evolution of clupeine Z, a probable crossover product. 1971 , 229, 245-7		12
2195	Crossassociation: a method of comparing protein sequences. 1971 , 5, 287-313		24
2194	21 Vertebrate Lysozymes. 1972 , 7, 665-868		246
2193	Matching sequences under deletion-insertion constraints. 1972 , 69, 4-6		217
2192	Phylogenetic relationships of proteroglyphae toxins. 1972 , 10, 39-45		19
2191	A generalized homology correlation for various hormones and proteins. 1972 , 28, 1517-22		35
2190	Theoretical foundations for a quantitative approach to paleogenetics: Part II: Proteins. 1972 , 1, 134-49		25
2189	An application of information theory to genetic mutations and the matching of polypeptide sequences. 1973 , 42, 245-61		33
2188	Shortcuts, diversions, and maximal chainsin partially ordered sets. 1973 , 4, 287-293		16
2187	A test for nucleotide sequence homology. <i>Journal of Molecular Biology</i> , 1973 , 77, 169-64	6.5	34
2186	5S rRNA and t RNA: evidence for a common evolutionary origin. 1973 , 242, 80-2		8

2185 No Evidence for a Common Evolutionary Origin of 5S rRNA and tRNA (Reply). **1973**, 245, 127-128

Inferences from protein and nucleic acid sequences: Early molecular evolution, divergence of kingdoms and rates of change. 1974 , 5, 311-330	19
2183 A generalized method for matching informational macromolecular code sequences. 1974 , 4, 43-57	17
2182 Origins and implications of the D stagger in collagen. 1974 , 60, 858-64	35
Epidermal growth factor: internal duplication and probable relationship to pancreatic secretory trypsin inhibitor. 1974 , 60, 1020-8	81
2180 On the Theory and Computation of Evolutionary Distances. 1974 , 26, 787-793	326
Detecting Evolutionary Incompatibilities from Protein Sequences. 1975 , 24, 311	41
$_{2178}$ Phylogenies from amino acid sequences aligned with gaps: the problem of gap weighting. 1975 , 5, 1-24	27
2177 Evolution of 5sRNA. 1975 , 7, 75-86	64
2176 Evolution of sequences within protein superfamilies. 1975 , 62, 154-161	52
Detecting Evolutionary Incompatibilities From Protein Sequences. 1975 , 24, 311-332	2
A SIMPLE TEST FOR THE POSSIBLE SIMULTANEOUS EVOLUTIONARY DIVERGENCE OF TWO AMINO ACID POSITIONS. 1975 , 24, 609-613	47
2173 Matching code sequences utilizing context free quality measures. 1975 , 24, 25-30	10
2172 2 Evolutionary and Structural Relationships among Dehydrogenases. 1975 , 61-102	339
2171 Minimal Mutation Trees of Sequences. 1975 , 28, 35-42	379
[Cathepsin D from horse spleen. I. Purification and study of certain physicochemical properties]. 1976 , 58, 771-82	6
2169 Evidence for gene duplication in collagen. <i>Journal of Molecular Biology</i> , 1976 , 107, 159-74 6.5	; 32
The evolutionary origin of proinsulin. Amino acid sequence homology with the trypsin-related serine proteases detected and evaluated by new statistical methods. <i>Journal of Molecular Biology</i> , 6.5 1976 , 106, 639-61	39

2167	Sequence similarity between cholera toxin and glycoprotein hormones: implications for structure activity relationship and mechanism of action. 1976 , 69, 852-9	83
2166	Homology relationships among the small blue proteins. 1976 , 261, 344-6	90
2165	A Method for the Correction of Garbled Words Based on the Levenshtein Metric. 1976 , C-25, 172-178	131
2164	On certain homologies between proteins. 1976 , 7, 215-44	5
2163	Frequency of insertion-deletion, transversion, and transition in the evolution of 5S ribosomal RNA. 1976 , 7, 133-49	106
2162	Some biological sequence metrics. 1976 , 20, 367-387	267
2161	Bounds on the Complexity of the Longest Common Subsequence Problem. 1976 , 23, 1-12	145
2160	Primary structure of cholera toxin beta-chain: a glycoprotein hormone analog?. 1977 , 195, 299-301	100
2159	Algorithms for the Longest Common Subsequence Problem. 1977 , 24, 664-675	414
2158	Evolution of lipoproteins deduced from protein sequence data. 1977 , 57, 309-15	52
2157	Analysis of periodic patterns in amino acid sequences: collagen. 1977 , 16, 1271-97	56
2156	An encoding technique to facilitate the detection of homologies in biopolymer sequences. 1977 , 69, 767-9	
2155	Alignment statistic for identifying related protein sequences. 1977 , 9, 121-30	33
2154	The detection of amino acid sequence homology: a new scoring method based on the genetic code with allowance for redundancy. 1978 , 72, 1-8	1
2153	Application of the 'profiles of relationship' method to distantly related proteins. 1978, 12, 1-10	4
2152	A method for detecting distant evolutionary relationships between protein or nucleic acid sequences in the presence of deletions or insertions. 1978 , 11, 143-61	7
2151	The Complexity of Some Problems on Subsequences and Supersequences. 1978 , 25, 322-336	373
2150	Origins of prokaryotes, eukaryotes, mitochondria, and chloroplasts. 1978 , 199, 395-403	494

2149	RNA secondary structure: a complete mathematical analysis. 1978 , 42, 257-266		186
2148	Some Concepts for the Estimation of Evolutionary Relationships in Systematic Botany. 1978 , 3, 146		41
2147	ON THE ROLE OF INFORMATION AND HIERARCHY IN THE MODELING OF BIOMOLECULAR SYSTEMS. 1978 , 8, 223-236		1
2146	The heavy chain of human histocompatibility antigen HLA-B7 contains an immunoglobulin-like region. 1979 , 282, 266-70		118
2145	Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene. 1979 , 18, 559-68		235
2144	Regulation of gene expression: possible role of repetitive sequences. 1979 , 204, 1052-9		529
2143	Complete amino acid sequence of a papain-solubilized human histocompatibility antigen, HLA-B7. 2. Sequence determination and search for homologies. 1979 , 18, 5711-20		121
2142	On the evolution of blue proteins. 1979 , 61, 781-90		32
2141	Gene duplications in the structural evolution of chymotrypsin. <i>Journal of Molecular Biology</i> , 1979 , 128, 49-79	6.5	486
2140	Covalent structure of human haptoglobin: a serine protease homolog. 1980 , 77, 3388-92		218
2139	Complete amino acid sequence of pooled papain-solubilized HLA-A, -B, and -C antigens: relatedness to immunoglobulins and internal homologies. 1980 , 77, 1129-33		36
			36
	to immunoglobulins and internal homologies. 1980 , 77, 1129-33		
2138	to immunoglobulins and internal homologies. 1980 , 77, 1129-33 Origins of immunoglobulin heavy chain domains. 1980 , 15, 113-27 Sequence homologies among E. coli ribosomal proteins: evidence for evolutionarily related		15
2138	to immunoglobulins and internal homologies. 1980 , 77, 1129-33 Origins of immunoglobulin heavy chain domains. 1980 , 15, 113-27 Sequence homologies among E. coli ribosomal proteins: evidence for evolutionarily related groupings and internal duplications. 1980 , 15, 129-48 An evaluation of the significance of amino acid sequence homologies in human histocompatibility antigens (HLA-A and HLA-B) with immunoglobulins and other proteins, using relatively short		15 67
2138 2137 2136	Origins of immunoglobulin heavy chain domains. 1980, 15, 113-27 Sequence homologies among E. coli ribosomal proteins: evidence for evolutionarily related groupings and internal duplications. 1980, 15, 129-48 An evaluation of the significance of amino acid sequence homologies in human histocompatibility antigens (HLA-A and HLA-B) with immunoglobulins and other proteins, using relatively short sequences. 1980, 11, 573-92 Complete nucleotide sequence of mouse immunoglobulin mu gene and comparison with other	6.5	15 67 38
2138 2137 2136 2135	Origins of immunoglobulin heavy chain domains. 1980, 77, 1129-33 Sequence homologies among E. coli ribosomal proteins: evidence for evolutionarily related groupings and internal duplications. 1980, 15, 129-48 An evaluation of the significance of amino acid sequence homologies in human histocompatibility antigens (HLA-A and HLA-B) with immunoglobulins and other proteins, using relatively short sequences. 1980, 11, 573-92 Complete nucleotide sequence of mouse immunoglobulin mu gene and comparison with other immunoglobulin heavy chain genes. 1980, 8, 3933-45 Comparative analysis of the sequences of the three collagen chains alpha 1(I), alpha 2 and alpha	6.5	15 67 38 102

2131	Characterization of bacteriophage T4 and D RNA, a low-molecular-weight RNA of unknown function. 1981 , 210, 298-306		2
2130	Identification of common molecular subsequences. <i>Journal of Molecular Biology</i> , 1981 , 147, 195-7	6.5	6681
2129	An examination of the expected degree of sequence similarity that might arise in proteins that have converged to similar conformational states. The impact of such expectations on the search for homology between the structurally similar domains of rhodanese. <i>Journal of Molecular Biology</i> ,	6.5	46
2128	1981, 151, 179-97 Repetitive sequences of the sea urchin genome. III. Nucleotide sequences of cloned repeat elements. <i>Journal of Molecular Biology</i> , 1981, 149, 41-67	6.5	49
2127	ampC cephalosporinase of Escherichia coli K-12 has a different evolutionary origin from that of beta-lactamases of the penicillinase type. 1981 , 78, 4897-901		360
2126	Homology in protein sequences expressed by correlation coefficients. 1981 , 91, 347-61		62
2125	Comparative biosequence metrics. 1981 , 18, 38-46		209
2124	The uniqueness of protein sequences: A Monte Carlo analysis. 1981 , 43, 619-639		1
2123	Nucleotide sequence and formation of the transforming gene of a mouse sarcoma virus. 1981 , 289, 258	3-62	194
2122	Comparison of biosequences. 1981 , 2, 482-489		585
2121	The uniqueness of protein sequences: a Monte Carlo analysis. 1981 , 43, 619-39		3
2120	Similar amino acid sequences: chance or common ancestry?. 1981 , 214, 149-59		791
2119	Los Alamos sequence analysis package for nucleic acids and proteins. 1982 , 10, 183-96		229
2118	Pattern recognition in nucleic acid sequences. I. A general method for finding local homologies and symmetries. 1982 , 10, 247-63		324
2117	Hierarchical analysis of influenza A hemagglutinin gene sequences. 1982 , 10, 5375-89		2
2116	An efficient method for matching nucleic acid sequences. 1982 , 10, 133-9		37
2115	Structural similarities among gastrointestinal hormones and related active peptides. 1982 , 363, 475-83		9
2114	Automation of the computer handling of gel reading data produced by the shotgun method of DNA sequencing. 1982 , 10, 4731-51		735

2113	An interactive graphics program for comparing and aligning nucleic acid and amino acid sequences. 1982 , 10, 2951-61	817
2112	Amino acid sequence of a basic blue protein from cucumber seedlings. 1982 , 79, 6434-7	50
2111	SPELLING ERROR DETECTION AND CORRECTION BY COMPUTER: SOME NOTES AND A BIBLIOGRAPHY. 1982 , 38, 282-291	16
2110	Complete amino acid sequence of an HLA-DR antigen-like beta chain as predicted from the nucleotide sequence: similarities with immunoglobulins and HLA-A, -B, and -C antigens. 1982 , 79, 3687-91	286
2109	Model of the active site in the blue oxidases based on the ceruloplasmin-plastocyanin homology. 1982 , 79, 6767-71	41
2108	Classification of mouse VK groups based on the partial amino acid sequence to the first invariant tryptophan: impact of 14 new sequences from IgG myeloma proteins. 1982 , 19, 1619-30	153
2107	An improved algorithm for matching biological sequences. <i>Journal of Molecular Biology</i> , 1982 , 162, 705- & .5	1155
2106	Amino acid sequence homologies between Escherichia coli penicillin-binding protein 5 and class A beta-lactamases. 1982 , 139, 159-63	11
2105	Sequence of the malK gene in E.coli K12. 1982 , 10, 7449-58	145
2104	Ribosomal protein S1 is the product of a series of contiguous duplications. 1982 , 2, 405-12	12
2103	Homology among DNA-binding proteins suggests use of a conserved super-secondary structure. 1982 , 298, 447-51	424
2102	An unusual transposon with long terminal inverted repeats in the sea urchin Strongylocentrotus purpuratus. 1983 , 306, 342-7	55
2101	Efficient algorithms for searching for exact repetition of nucleotide sequences. 1983 , 19, 283-5	5
2100	CHARMM: A program for macromolecular energy, minimization, and dynamics calculations. 1983 , 4, 187-217	13044
2099	An efficient code searching for sequence homology and DNA duplication. 1983 , 100, 319-28	10
2098	Analysis of gene duplication repeats in the myosin rod. <i>Journal of Molecular Biology</i> , 1983 , 169, 15-30 6.5	67
2097	Primary structure of the imml immunity region of bacteriophage P22. <i>Journal of Molecular Biology</i> , 1983 , 168, 699-713	70
2096	An Overview of Sequence Comparison: Time Warps, String Edits, and Macromolecules. 1983 , 25, 201-237	194

2095	The effects of mutations, deletions and insertions of single amino acids on the three-dimensional structure of globins. 1983 , 161, 65-70	4
2094	Protein identification system: methods of searching for similar sequences.	2
2093	Establishing homologies in protein sequences. 1983 , 91, 524-45	953
2092	Angiotensinogen is related to the antitrypsin-antithrombin-ovalbumin family. 1983, 222, 417-9	195
2091	A common basis for similarity measures involving two strings 1983, 13, 17-40	15
2090	Molecular structure of ilvIH and its evolutionary relationship to ilvG in Escherichia coli K12. 1983 , 11, 5299-313	106
2089	The complete nucleotide sequence of the I-E alpha d immune response gene. 1983, 11, 5055-71	94
2088	Regulatory pattern identification in nucleic acid sequences. 1983 , 11, 2221-31	28
2087	Optimal sequence alignments. 1983 , 80, 1382-6	165
2086	Rapid similarity searches of nucleic acid and protein data banks. 1983 , 80, 726-30	1343
2085	Concerted evolution of the immunoglobulin VH gene family. 1984 , 1, 195-212	32
2084	Comparison of the entire genomes of bovine leukemia virus and human T-cell leukemia virus and characterization of their unidentified open reading frames 1984 , 3, 3231-3237	51
2083	Note added in proof. 1984 , 3, 3237-3237	
2082	Structure of the murine Ia-associated invariant (Ii) chain as deduced from a cDNA clone 1984 , 3, 873-877	31
2081	Comparative analysis of human and bovine papillomaviruses. 1984 , 1, 357-70	8
2080	The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefaciens plasmid pTiAch5 1984 , 3, 835-846	105
2079	A convenient method for locating sets of related short sequences in DNA sequences of any length. 1984 , 12, 257-62	1
2078	Fast optimal alignment. 1984 , 12, 175-9	73

2077	A convenient and adaptable package of computer programs for DNA and protein sequence management, analysis and homology determination. 1984 , 12, 643-55	276
2076	GENAS: a database system for nucleic acid sequence analysis. 1984 , 12, 89-99	59
2075	A new rule for analyzing homologous coding sequences in DNA. 1984 , 12, 159-73	1
2074	A fast homology program for aligning biological sequences. 1984 , 12, 447-55	57
2073	Use of statistical criteria for screening potential homologies in nucleic acid sequences. 1984 , 12, 203-13	95
2072	The diagonal-traverse homology search algorithm for locating similarities between two sequences. 1984 , 12, 751-66	26
2071	SEQAID: a DNA sequence assembling program based on a mathematical model. 1984, 12, 307-21	80
2070	A comprehensive set of sequence analysis programs for the VAX. 1984 , 12, 387-95	13899
2069	Modeling RNA Structure. 1984 , 2, 791-795	2
2068	Sequence comparison by exponentially-damped alignment. 1984 , 12, 457-64	32
2067	On the statistical assessment of similarities in DNA sequences. 1984 , 12, 5529-43	25
2066	Applications of parallel processing algorithms for DNA sequence analysis. 1984 , 12, 181-92	20
2065	Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of oncogene. 1984 , 224, 1456-9	109
2064	New algorithms for the LCS problem. 1984 , 29, 133-152	33
2063	General methods of sequence comparison. 1984 , 46, 473-500	143
2062	Pattern recognition in genetic sequences by mismatch density. 1984 , 46, 501-514	56
2061	Searching the protein sequence database. 1984 , 46, 545-52	9
2060	Algorithms for computing evolutionary similarity measures with length independent gap penalties. 1984, 46, 553-566	31

2059 A non-metric sequence alignment program. 1984 , 46, 579-90	2
2058 RNA secondary structures and their prediction. 1984 , 46, 591-621	279
2057 Properties of levenshtein metrics on sequences. 1984 , 46, 327-332	4
A note on the evaluation of similarity (homology) of short sequences with long sequences. 1984 , 46, 951-61	
2055 Computer-based characterization of epidermal growth factor precursor. 1984 , 307, 558-60	200
2054 A common function for polyoma virus large-T and papillomavirus E1 proteins?. 1984 , 311, 276-9	138
A developmental gene product of Bacillus subtilis homologous to the sigma factor of Escherichia coli. 1984 , 312, 376-8	89
2052 Cloning, sequence and expression of human interleukin-2 receptor. 1984 , 312, 768-71	269
Conformational changes in the globin family during evolution. 1. Analysis of the evolutionary role of insertions and deletions. 1984 , 21, 42-53	9
Evolution of the human sarcomeric-actin genes: evidence for units of selection within the 3' untranslated regions of the mRNAs. 1984 , 20, 202-14	103
Quantitation of base substitutions in eukaryotic 5S rRNA: selection for the maintenance of RNA secondary structure. 1984 , 20, 351-61	16
The alignment of sets of sequences and the construction of phyletic trees: an integrated method. 1984 , 20, 175-86	197
2047 The Context Dependent Comparison of Biological Sequences. 1984 , 44, 557-567	58
The amino acid sequence of two small ribosomal proteins from Bacillus stearothermophilus. 1984 , $^{204^6}$ 166, 343-6	15
Nucleotide sequence of the heat shock regulatory gene of E. coli suggests its protein product may be a transcription factor. 1984 , 38, 175-82	199
2044 The cellulolytic enzymes of Trichoderma reesei as a system of homologous proteins. 1984 , 167, 301-308	3 26
2043 A fast method of comparing protein structures. 1984 , 168, 97-102	21
Identification of a potential protease-coding gene in the genomes of bovine leukemia and human T-cell leukemia viruses. 1984 , 178, 79-82	18

2041	Nucleotide sequence of the brome mosaic virus genome and its implications for viral replication. Journal of Molecular Biology, 1984 , 172, 369-83	6.5	168
2040	Coding nucleotide sequence of 3-methylcholanthrene-inducible cytochrome P-450d cDNA from rat liver. 1984 , 81, 1649-53		129
2039	Expression of specific mRNAs during adipose differentiation: identification of an mRNA encoding a homologue of myelin P2 protein. 1984 , 81, 5468-72		301
2038	Molecular cloning and nucleotide sequence of cDNA for mRNA of mitochondrial cytochrome P-450(SCC) of bovine adrenal cortex. 1984 , 81, 4647-51		208
2037	Coagulation factors V and VIII and ceruloplasmin constitute a family of structurally related proteins. 1984 , 81, 6934-7		156
2036	Sequence of the bacteriophage SP01 gene coding for transcription factor 1, a viral homologue of the bacterial type II DNA-binding proteins. 1984 , 81, 7031-5		44
2035	Amino acid sequence homology among the major outer membrane proteins of Escherichia coli. 1984 , 81, 1048-52		55
2034	Bovine leukemia virus: unique structural features of its long terminal repeats and its evolutionary relationship to human T-cell leukemia virus. 1984 , 81, 4741-5		54
2033	Codon usage in the vertebrate hemoglobins and its implications. 1985 , 2, 390-8		12
2032	Significance of similarities in patterns: an application to beta interferon-related DNA on human chromosome 2. 1985 , 82, 4090-4		8
2031	Genomic structure of the cottontail rabbit (Shope) papillomavirus. 1985 , 82, 1580-4		99
2030	Conservation of nif- and species-specific domains within repeated promoter sequences from fast-growing Rhizobium species. 1985 , 13, 3407-18		12
2029	Complete nucleotide sequence of the genome of bovine leukemia virus: its evolutionary relationship to other retroviruses. 1985 , 82, 677-81		366
2028	Coding nucleotide sequence of rat NADPH-cytochrome P-450 oxidoreductase cDNA and identification of flavin-binding domains. 1985 , 82, 973-7		164
2027	Complete nucleotide sequence of the Drosophila transposable element copia: homology between copia and retroviral proteins. 1985 , 5, 1630-8		309
2026	Simultaneous comparison of three protein sequences. 1985 , 82, 3073-7		117
2025	Locating a nucleotide-binding site in the thymidine kinase of vaccinia virus and of herpes simplex virus by scoring triply aligned protein sequences. 1985 , 82, 6815-9		19
2024	Stanislaw M. Ulam's contributions to theoretical theory. 1985 , 10, 231-242		11

2023 The prediction of a protein and nucleic acid structure: Problems and prospects. 1985 , 4, 115-137	2
Cloning, sequence and expression of two distinct human interleukin-1 complementary DNAs. 1985 , 315, 641-7	1439
Gamma-interferon transcriptionally regulates an early-response gene containing homology to platelet proteins. 1985 , 315, 672-6	837
2020 The prokaryote-eukaryote interface. 1985 , 18, 223-40	15
2019 Computer modeling studies of the structure of a repressor. 1985 , 18, 3-14	5
2018 More homologies among the vertebrate plasma proteins. 1985 , 5, 877-84	3
2017 Multisequence comparisons in protein coding genes. Search for functional constraints. 1985 , 7, 239-50	5
2016 Similarities in the genomic sequence and coat protein structure of plant virsuses. 1985 , 8, 815-821	
2015 Sequence similarity ('homology') searching for molecular biologists. 1985 , 47, 437-74	8
Alignment of nucleotide or amino acid sequences on microcomputers, using a modification of 2014 Sellers' (1974) algorithm which avoids the need for calculation of the complete distance matrix. 1985 , 21, 3-10	4
2013 Aligning amino acid sequences: comparison of commonly used methods. 1984 , 21, 112-25	355
Comparison of the nucleotide sequence of soybean 18S rRNA with the sequences of other small-subunit rRNAs. 1984 , 21, 259-69	152
2011 U1 snRNA: the evolution of its primary and secondary structure. 1984 , 21, 323-33	10
2010 Algorithms for approximate string matching. 1985 , 64, 100-118	352
2009 Table of contents. 1985,	
2008 Optimal alignments of biological sequences on a microcomputer. 1985 , 1, 83-7	
2007 Sequence determination of the Sendai virus fusion protein gene. 1985 , 66 (Pt 2), 317-31	144
Nucleotide sequence and mutational analysis of an immunity repressor gene from Bacillus subtilis temperate phage phi 105. 1985 , 13, 5441-55	25

2005	Amino acid sequence analysis of human interleukin 1 (IL-1). Evidence for biochemically distinct forms of IL-1. 1985 , 162, 790-801		84
2004	Type II restriction endonucleases cleave single-stranded DNAs in general. 1985 , 13, 5747-60		39
2003	Nucleic acid and protein sequence databases. 1985 , 1, 11-7		1
2002	The SEQANAL and SEQTALK programs: a new method of access to high-resolution nucleotide sequence comparison and analysis programs from a remote laboratory mini- or microcomputer. 1985, 1, 241-7		
2001	Rapid and sensitive protein similarity searches. 1985 , 227, 1435-41		3665
2000	The primary structure of the imported mitochondrial protein, ornithine transcarbamylase from rat liver: mRNA levels during ontogeny. 1985 , 4, 147-56		28
1999	The statistical distribution of nucleic acid similarities. 1985 , 13, 645-56		168
1998	Structural relationship of human interferon alpha genes and pseudogenes. <i>Journal of Molecular Biology</i> , 1985 , 185, 227-60	6.5	177
1997	Sequence determination of the Sendai virus HN gene and its comparison to the influenza virus glycoproteins. 1985 , 41, 269-78		119
1996	Nucleotide sequence from the neurogenic locus notch implies a gene product that shares homology with proteins containing EGF-like repeats. 1985 , 43, 567-81		969
1995	A novel ras-related gene family. 1985 , 41, 31-40		408
1994	Simultaneous Solution of the RNA Folding, Alignment and Protosequence Problems. 1985 , 45, 810-825		407
1993	Complete complementary DNA of rat tyrosine aminotransferase messenger RNA. Deduction of the primary structure of the enzyme. <i>Journal of Molecular Biology</i> , 1985 , 184, 347-50	6.5	50
1992	Homologies between the protein encoded by a Drosophila segmentation gene and the papovavirus large T antigens. 1985 , 136, 205-212		
1991	The internally located telomeric sequences in the germ-line chromosomes of Tetrahymena are at the ends of transposon-like elements. 1985 , 43, 747-58		99
1990	Improving sequence-matching algorithms by working from both ends. <i>Journal of Molecular Biology</i> , 1985 , 181, 137-8	6.5	2
1989	Confidence limits for homology in protein or gene sequences. The c-myc oncogene and adenovirus E1a protein. <i>Journal of Molecular Biology</i> , 1985 , 185, 39-49	6.5	24
1988	The structure of the voltage-sensitive sodium channel. Inferences derived from computer-aided analysis of the Electrophorus electricus channel primary structure. 1985 , 193, 125-34		167

1987	Two functional domains conserved in major and alternate bacterial sigma factors. 1985 , 187, 11-5		78
1986	A dynamic programming algorithm to find all solutions in a neighborhood of the optimum. 1985 , 77, 179-188		54
1985	Sequence homologies and structural similarities between the polypeptides of yeast and beef heart cytochrome c oxidase. 1986 , 207, 11-7		38
1984	cDNA sequence of human beta-preprotachykinin, the common precursor to substance P and neurokinin A. 1986 , 208, 67-72		82
1983	The primary structure of the ribosomal A-protein (L12) from the moderate halophile NRCC 41227. 1986 , 64, 675-80		16
1982	Inhibition of iodine-125-labeled human follitropin binding to testicular receptor by epidermal growth factor and synthetic peptides. 1986 , 25, 2644-9		33
1981	Structure, evolution, and tissue-specific synthesis of human apolipoprotein AIV. 1986 , 25, 3962-70		92
1980	Structure of a Bacillus subtilis endo-beta-1,4-glucanase gene. 1986 , 14, 9159-70		77
1979	NADPH-cytochrome P-450 oxidoreductase: flavin mononucleotide and flavin adenine dinucleotide domains evolved from different flavoproteins. 1986 , 25, 1682-7		241
1978	Nucleotide sequence of the genes encoded in early region 2b of human adenovirus type 12. 1986 , 46, 187-95		35
1977	Cloning and sequencing of mRNAs coding for two adult alpha globin chains of the salamander Pleurodeles waltlii. 1986 , 42, 159-68		4
1976	Structural and regulatory divergence among site-specific recombination genes of lambdoid phage. Journal of Molecular Biology, 1986 , 189, 603-16	6.5	70
1975	Phosphocholine binding immunoglobulin Fab McPC603. An X-ray diffraction study at 2.7 A. <i>Journal of Molecular Biology</i> , 1986 , 190, 593-604	6.5	579
1974	Multiple sequence alignment. <i>Journal of Molecular Biology</i> , 1986 , 191, 153-61	6.5	106
1973	Nucleotide sequence of the phoR gene, a regulatory gene for the phosphate regulon of Escherichia coli. <i>Journal of Molecular Biology</i> , 1986 , 192, 549-56	6.5	117
1972	Maximum likelihood alignment of DNA sequences. <i>Journal of Molecular Biology</i> , 1986 , 190, 159-65	6.5	87
1971	Identification of protein sequence homology by consensus template alignment. <i>Journal of Molecular Biology</i> , 1986 , 188, 233-58	6.5	270
1970	The E35 stopper mutant of Neurospora crassa: precise localization of deletion endpoints in mitochondrial DNA and evidence that the deleted DNA codes for a subunit of NADH dehydrogenase. 1986, 5, 779-785		61

1969 Comparison of the malA regions of Escherichia coli and Klebsiella pneumoniae. 1986 , 168, 1220-7	30
1968 Using known substructures in protein model building and crystallography 1986 , 5, 819-822	595
Sequence and interspecies transfer of an aminoglycoside phosphotransferase gene (APH) of Bacillus circulans. Self-defence mechanism in antibiotic-producing organisms. 1986 , 233, 383-93	22
Computer analysis of retroviral pol genes: assignment of enzymatic functions to specific sequences and homologies with nonviral enzymes. 1986 , 83, 7648-52	463
1965 A measure of the similarity of sets of sequences not requiring sequence alignment. 1986 , 83, 5155-9	254
Gene products specifying adhesion of uropathogenic Escherichia coli are minor components of pili. 1964 1986, 83, 1891-5	112
1963 Common evolutionary origin of hepatitis B virus and retroviruses. 1986 , 83, 2531-5	173
Polymorphism of HLA-DR beta chains in DR4, -7, and -9 haplotypes: implications for the mechanisms of allelic variation. 1986 , 83, 9149-53	70
Repetitive segmental structure of the transducin beta subunit: homology with the CDC4 gene and identification of related mRNAs. 1986 , 83, 2162-6	379
1960 Comparison of sequences as a method for evaluation of the molecular similarity. 1986 , 7, 176-188	15
1959 Products of the "X" gene in hepatitis B and related viruses. 1986 , 6, 191-8	47
1958 Comprehensive molecular modelling system. 1986 , 4, 134-142	9
1957 A simple way to look at DNA. 1986 , 119, 319-28	150
Nucleotide sequence of the lig gene and primary structure of DNA ligase of Escherichia coli. 1986 , 204, 1-7	51
1955 Molecular structure and evolution of adrenergic and cholinergic receptors. 1986 , 1, 287-301	21
1954 Primary structure of the reaction center from Rhodopseudomonas sphaeroides. 1986 , 1, 312-25	140
Sequence conservation and region shuffling in an endoglucanase and an exoglucanase from Cellulomonas fimi. 1986 , 1, 335-41	58
Homologies in both primary and secondary structure between nuclear envelope and intermediate filament proteins. 1986 , 319, 463-8	760

1951	The amino-acid sequence of the nonspecific lipid transfer protein from germinated castor bean endosperms. 1986 , 870, 248-255	49
1950	Optimal sequence alignment using affine gap costs. 1986 , 48, 603-16	131
1949	A nonlinear measure of subalignment similarity and its significance levels. 1986 , 48, 617-32	43
1948	Locally optimal subalignments using nonlinear similarity functions. 1986 , 48, 633-60	32
1947	Constrained string editing. 1986 , 40, 267-284	25
1946	A method for the simultaneous alignment of three or more amino acid sequences. 1986 , 23, 267-78	60
1945	A comprehensive package for DNA sequence analysis in FORTRAN IV for the PDP-11. 1986 , 14, 239-54	13
1944	Improving the efficiency of dot-matrix similarity searches through use of an oligomer table. 1986 , 14, 597-610	14
1943	DNA sequence analysis: a procedure to find homologies among many sequences. 1986 , 14, 543-50	14
1942	The protein identification resource (PIR). 1986 , 14, 11-5	295
1942 1941	The protein identification resource (PIR). 1986, 14, 11-5 Computer program for the IBM personal computer which searches for approximate matches to short oligonucleotide sequences in long target DNA sequences. 1986, 14, 501-8	² 95
· ·	Computer program for the IBM personal computer which searches for approximate matches to	
1941	Computer program for the IBM personal computer which searches for approximate matches to short oligonucleotide sequences in long target DNA sequences. 1986 , 14, 501-8 An efficient string matching algorithm with k differences for nucleotide and amino acid sequences.	7
1941	Computer program for the IBM personal computer which searches for approximate matches to short oligonucleotide sequences in long target DNA sequences. 1986 , 14, 501-8 An efficient string matching algorithm with k differences for nucleotide and amino acid sequences. 1986 , 14, 31-46	7 26
1941 1940 1939	Computer program for the IBM personal computer which searches for approximate matches to short oligonucleotide sequences in long target DNA sequences. 1986, 14, 501-8 An efficient string matching algorithm with k differences for nucleotide and amino acid sequences. 1986, 14, 31-46 Algorithms for the search of amino acid patterns in nucleic acid sequences. 1986, 14, 99-107 Fast analysis of DNA and protein sequence on Apple IIe: restriction sites search, alignment of short	7 26 20
1941 1940 1939 1938	Computer program for the IBM personal computer which searches for approximate matches to short oligonucleotide sequences in long target DNA sequences. 1986, 14, 501-8 An efficient string matching algorithm with k differences for nucleotide and amino acid sequences. 1986, 14, 31-46 Algorithms for the search of amino acid patterns in nucleic acid sequences. 1986, 14, 99-107 Fast analysis of DNA and protein sequence on Apple IIe: restriction sites search, alignment of short sequence and dot matrix analysis. 1986, 14, 583-90 Molecular cloning of the closed circular provirus of human T cell leukaemia virus type I: a new open	7 26 20 16
1941 1940 1939 1938	Computer program for the IBM personal computer which searches for approximate matches to short oligonucleotide sequences in long target DNA sequences. 1986, 14, 501-8 An efficient string matching algorithm with k differences for nucleotide and amino acid sequences. 1986, 14, 31-46 Algorithms for the search of amino acid patterns in nucleic acid sequences. 1986, 14, 99-107 Fast analysis of DNA and protein sequence on Apple IIe: restriction sites search, alignment of short sequence and dot matrix analysis. 1986, 14, 583-90 Molecular cloning of the closed circular provirus of human T cell leukaemia virus type I: a new open reading frame in the gag-pol region. 1987, 68 (Pt 1), 213-8	7 26 20 16 28

1933	A hypervariable RFLP on chromosome 17p13 is defined by an arbitrary single copy probe p144-D6 [HGM9 No. D17S34]. 1987 , 15, 10605	43
1932	Pattern matching of biological sequences with limited storage. 1987 , 3, 17-20	4
1931	A quantitative approach to sequence comparisons of nitrogenase MoFe protein alpha- and beta-subunits including the newly sequenced nifK gene from Klebsiella pneumoniae. 1987 , 247, 277-85	20
1930	Structure and expression of human dihydropteridine reductase. 1987 , 84, 3329-33	54
1929	Three-dimensional structure of the bifunctional enzyme N-(5'-phosphoribosyl)anthranilate isomerase-indole-3-glycerol-phosphate synthase from Escherichia coli. 1987 , 84, 5690-4	95
1928	Origin of structural domains of the serum-albumin gene family and a predicted structure of the gene for vitamin D-binding protein. 1987 , 4, 364-79	26
1927	Distinct primary structures, ligand-binding properties and tissue-specific expression of four human muscarinic acetylcholine receptors 1987 , 6, 3923-3929	601
1926	Isolation and sequencing of cDNA clones encoding alpha and beta subunits of Drosophila melanogaster casein kinase II. 1987 , 7, 3409-17	165
1925	Isolation of cDNA clones encoding protein kinase C: evidence for a protein kinase C-related gene family. 1987 , 84, 1065-9	140
1924	Profile analysis: detection of distantly related proteins. 1987 , 84, 4355-8	1065
1923	The rudimentary gene of Drosophila melanogaster encodes four enzymic functions. <i>Journal of Molecular Biology</i> , 1987 , 193, 1-13	105
1922	Nucleotide sequence of the kanamycin resistance determinant of plasmid RP4: homology to other aminoglycoside 3'-phosphotransferases. 1987 , 18, 193-204	30
1921	Three-dimensional similarity mapping reveals nucleotide sequence relationships among human immunodeficiency virus (HIV) isolates. 1987 , 57, 247-53	1
1920	Complete nucleotide sequence of the M RNA segment of Uukuniemi virus encoding the membrane glycoproteins G1 and G2. 1987 , 160, 191-202	58
1919	Structure of the M2 protein gene of sonchus yellow net virus. 1987 , 161, 234-41	21
1918	Cloning and sequence analysis of the human brain beta-adrenergic receptor. Evolutionary relationship to rodent and avian beta-receptors and porcine muscarinic receptors. 1987 , 211, 200-6	93
1917	Sequence identity between a lysine-containing peptide from Leuconostoc mesenteroides glucose-6-phosphate dehydrogenase and an active site peptide from human erythrocyte glucose-6-phosphate dehydrogenase. 1987 , 211, 243-6	14
1916	Purification and amino acid sequencing of NAF, a novel neutrophil-activating factor produced by monocytes. 1987 , 149, 755-61	432
1918	relationship to rodent and avian beta-receptors and porcine muscarinic receptors. 1987 , 211, 200-6	

1915	Fowlpox virus thymidine kinase: nucleotide sequence and relationships to other thymidine kinases. 1987 , 156, 355-65	78
1914	Cloning and nucleotide sequence of Newcastle disease virus hemagglutinin-neuraminidase mRNA: identification of a putative sialic acid binding site. 1987 , 156, 12-24	94
1913	Sequence analysis of proteins. 1987 , 4, 27-40	
1912	A strategy for the rapid multiple alignment of protein sequences. Confidence levels from tertiary structure comparisons. <i>Journal of Molecular Biology</i> , 1987 , 198, 327-37	412
1911	A new algorithm for best subsequence alignments with application to tRNA-rRNA comparisons. Journal of Molecular Biology, 1987, 197, 723-8 6.5	205
1910	Determinants of a protein fold. Unique features of the globin amino acid sequences. <i>Journal of Molecular Biology</i> , 1987 , 196, 199-216	455
1909	Prediction of protein secondary structure and active sites using the alignment of homologous sequences. <i>Journal of Molecular Biology</i> , 1987 , 195, 957-61	375
1908	The primary structure of the ribosomal A-protein (L12) from the halophilic eubacterium Haloanaerobium praevalens. 1987 , 69, 1013-20	12
1907	Detecting homology of distantly related proteins with consensus sequences. <i>Journal of Molecular Biology</i> , 1987 , 198, 567-77	141
1906	Complete nucleotide sequence of bovine alpha-lactalbumin gene: comparison with its rat counterpart. 1987 , 69, 609-20	55
1905	The complete amino acid sequence of human serum retinol-binding protein. 1987 , 92, 115-46	13
1904	Cloning and Expression of the Fungal Expandase/hydroxylase Gene Involved in Cephalosporin Biosynthesis. 1987 , 5, 1207-1214	74
1903	Common evolutionary origin of the ilvGMEDA attenuation locus and tRNA(1Leu) in Escherichia coli. 1987 , 169, 2893-5	4
1902	Evolution of cytochrome P-450 proteins. 1987 , 4, 572-93	145
1901	The halo-opsin gene. II. Sequence, primary structure of halorhodopsin and comparison with bacteriorhodopsin. 1987 , 6, 265-273	146
1900	Evolution of the primary and secondary structures of the E1a mRNAs of the adenovirus. 1987 , 4, 300-14	15
1899	Bibliography. 1987 , 433-496	1
1898	Progressive sequence alignment as a prerequisite to correct phylogenetic trees. 1987 , 25, 351-60	1580

	enetic relationships between the kringle domains of human plasminogen, prothrombin, tissue inogen activator, urokinase, and coagulation factor XII. 1987 , 26, 358-69	48
	otide sequence of the delta-beta-globin intergenic segment in the macaque: structure and cionary rates in higher primates. 1987 , 24, 297-308	24
	ylS gene positive regulator of TOL plasmid pWWO: identification, sequence analysis and roduction leading to constitutive expression of meta cleavage operon. 1987 , 207, 349-54	58
	otide sequences and unusual electrophoretic behavior of the W chromosome-specific ting DNA units of the domestic fowl, Gallus gallus domesticus. 1987 , 96, 18-25	101
	icient string matching algorithm with K substitutions for nucleotide and amino acid nces. 1987 , 126, 483-90	4
	ction of secondary structure by evolutionary comparison: application to the alpha subunit of ophan synthase. 1987 , 2, 118-29	120
1891 PRON	UC: a software package for the analysis of protein and nucleic acid sequences. 1987 , 24, 27-36	2
1890 The u	se of folding patterns in the prediction of protein topologies. 1987 , 916, 54-65	3
1889 Theor	etical molecular biology: prospectives and perspectives. 1987 , 125, 219-35	30
1888 ls scra	pie Prp 27-30 related to AIDS virus?. 1987 , 325, 113-4	4
	pie Prp 27-30 related to AIDS virus?. 1987 , 325, 113-4 virus and scrapie protein genes. 1987 , 325, 581	4 7
1887 AIDS		
1887 AIDS	virus and scrapie protein genes. 1987 , 325, 581	7
1887 AIDS	virus and scrapie protein genes. 1987 , 325, 581 ledge-based prediction of protein structures and the design of novel molecules. 1987 , 326, 347-52 complete nucleotide sequence and structure of the gene encoding bovine phenylethanolamine	7 640
1887 AIDS	virus and scrapie protein genes. 1987, 325, 581 ledge-based prediction of protein structures and the design of novel molecules. 1987, 326, 347-52 complete nucleotide sequence and structure of the gene encoding bovine phenylethanolamine chyltransferase. 1988, 19, 367-76 on and nucleotide sequence of a cDNA clone encoding bovine adrenal tyrosine hydroxylase:	7 640 38
1887 AIDS 1886 Know 1885 The converse N-me 1884 comp 1883 Synor overse	virus and scrapie protein genes. 1987, 325, 581 ledge-based prediction of protein structures and the design of novel molecules. 1987, 326, 347-52 complete nucleotide sequence and structure of the gene encoding bovine phenylethanolamine chyltransferase. 1988, 19, 367-76 on and nucleotide sequence of a cDNA clone encoding bovine adrenal tyrosine hydroxylase: arative analysis of tyrosine hydroxylase gene products. 1988, 19, 440-9 ymous nucleotide substitution rates of beta-tubulin and histone genes conform to high	7 640 38 52
1887 AIDS 1886 Know 1885 The converse Norme 1884 comp 1883 Synor overse 1882 An events Evolution	virus and scrapie protein genes. 1987, 325, 581 ledge-based prediction of protein structures and the design of novel molecules. 1987, 326, 347-52 complete nucleotide sequence and structure of the gene encoding bovine phenylethanolamine chyltransferase. 1988, 19, 367-76 on and nucleotide sequence of a cDNA clone encoding bovine adrenal tyrosine hydroxylase: arative analysis of tyrosine hydroxylase gene products. 1988, 19, 440-9 ymous nucleotide substitution rates of beta-tubulin and histone genes conform to high ll genomic rates in rodents but not in sea urchins. 1988, 27, 56-64	7 640 38 52

1879	Parallel processing of biological sequence comparison algorithms. 1988 , 17, 259-275	44
1878	LOPAL and SCAMP: techniques for the comparison and display of protein structures. 1988 , 6, 190-196	17
1877	Abundant embryonic mRNA in field bean (Vicia faba L.) codes for a new class of seed proteins: cDNA cloning and characterization of the primary translation product. 1988 , 11, 321-34	35
1876	Cloning and sequencing of the genes encoding the large and the small subunits of the H2 uptake hydrogenase (hup) of Rhodobacter capsulatus. 1988 , 214, 97-107	100
1875	Computer-assisted primary and secondary structure analyses of DNA polymerases of herpes simplex, Epstein-Barr and varicella zoster viruses reveal conserved domains with some homology to DNA-binding domain in E. coli DNA pol I. 1988 , 1, 351-67	6
1874	Structural alignment and analysis of two distantly related proteins: Aplysia limacina myoglobin and sea lamprey globin. 1988 , 4, 240-50	9
1873	Epitope mapping with solid-phase peptides: identification of type-, subspecies-, species- and genus-reactive antibody binding domains on the major outer membrane protein of Chlamydia trachomatis. 1988 , 2, 673-9	69
1872	Identification of protein kinases by computer. 1988 , 333, 308	9
1871	A copia-like transposable element family in Arabidopsis thaliana. 1988, 336, 242-4	191
1870	The matching of protein sequences using color intrasequence homology displays. 1988 , 6, 135-140	17
1869	An efficient algorithm for comparing two protein sequences: Implementation for microcomputers. 1988 , 12, 21-25	3
1868	Sequence comparison with concave weighting functions. 1988 , 50, 97-120	79
1867	Similarity analysis of cognitive scripts. 1988 , 16, 36-42	7
1866	MPSA short communications. 1988 , 7, 187-188	7
1865	Generation of sequence diversity in the kinetoplast DNA minicircles of Leishmania mexicana amazonensis. 1988 , 30, 1-8	26
1864	Improvements in a secondary structure prediction method based on a search for local sequence homologies and its use as a model building tool. 1988 , 955, 283-95	90
· ·		90

1861	Cloning and molecular characterization of an oral papillomavirus of domestic rabbits. 1988, 162, 221-31	8
1860	slit: an EGF-homologous locus of D. melanogaster involved in the development of the embryonic central nervous system. 1988 , 55, 1047-59	234
1859	Amino acid substitutions in structurally related proteins. A pattern recognition approach. Determination of a new and efficient scoring matrix. <i>Journal of Molecular Biology</i> , 1988 , 204, 1019-29	282
1858	Isolation and characterization of a cDNA for mitochondrial manganese superoxide dismutase (SOD-3) of maize and its relation to other manganese superoxide dismutases. 1988 , 951, 61-70	57
1857	CLUSTAL: a package for performing multiple sequence alignment on a microcomputer. 1988 , 73, 237-44	3045
1856	Characterization of the gene encoding ovine beta-lactoglobulin. Similarity to the genes for retinol binding protein and other secretory proteins. <i>Journal of Molecular Biology</i> , 1988 , 199, 415-26	113
1855	A rapidly evolving region in the immunoglobulin heavy chain loci of rat and mouse: postulated role of (dC-dA)n.(dG-dT)n sequences. 1988 , 68, 93-100	25
1854	Sequence and expression of NUC1, the gene encoding the mitochondrial nuclease in Saccharomyces cerevisiae. 1988 , 16, 3297-312	87
1853	Human glucosamine-6-sulfatase cDNA reveals homology with steroid sulfatase. 1988 , 157, 218-24	44
1852	Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from Dictyostelium discoideum as deduced from the cDNA sequence. 1988 , 153, 359-64	33
1851	The Multiple Sequence Alignment Problem in Biology. 1988 , 48, 1073-1082	306
1850	Nucleotide sequence and gene organization of sea urchin mitochondrial DNA. <i>Journal of Molecular Biology</i> , 1988 , 202, 185-217	313
1849	A deduced gene product from the Drosophila neurogenic locus, enhancer of split, shows homology to mammalian G-protein beta subunit. 1988 , 55, 785-95	195
1848	Nucleotide sequence of the beta-D-phosphogalactoside galactohydrolase gene of Lactobacillus casei: comparison to analogous pbg genes of other gram-positive organisms. 1988 , 62, 263-76	72
1847	Multiple sequence alignment with hierarchical clustering. 1988 , 16, 10881-90	4155
1846	A second antigenic heat shock protein of Plasmodium falciparum. 1988 , 7, 71-8	40
1845	Purification and characterization of gibberellic Acid-induced cysteine endoproteases in barley aleurone layers. 1988 , 87, 95-103	107
1844	SCH9, a gene of Saccharomyces cerevisiae that encodes a protein distinct from, but functionally and structurally related to, cAMP-dependent protein kinase catalytic subunits. 1988 , 2, 517-27	165

1843	Automated sequence reading and analysis. 1988 , 16, 1847-56	10
1842	A program for template matching of protein sequences. 1988 , 4, 345-50	1
1841	IS150: distribution, nucleotide sequence and phylogenetic relationships of a new E. coli insertion element. 1988 , 16, 6789-802	63
1840	Molecular cloning, complementary deoxyribonucleic acid structure and predicted full-length amino acid sequence of the hormone-inducible regulatory subunit of 3'-5'-cyclic adenosine monophosphate-dependent protein kinase from human testis. 1988 , 2, 1364-73	101
1839	cDNA cloning and expression of a human platelet-derived growth factor (PDGF) receptor specific for B-chain-containing PDGF molecules. 1988 , 8, 3476-86	315
1838	Algorithms for identifying local molecular sequence features. 1988 , 4, 41-51	4
1837	Statistical analysis of DNA sequences. 1988 , 80, 395-406	13
1836	An algorithm for simultaneous comparison of several sequences. 1988 , 4, 89-92	2
1835	Statistical method for rapid homology search. 1988 , 16, 5169-73	12
1834	Nucleotide sequence of the pilin gene of Bacteroides nodosus 340 (serogroup D) and implications for the relatedness of serogroups. 1988 , 134, 575-84	2
1833	Alignment of multiple DNA and protein sequence data. 1988, 4, 213-4	
1832	Prediction of the recognition sites on 16S and 23S rRNAs from E. coli for the formation of 16S-23S rRNA complex. 1988 , 6, 587-92	3
1831	Multiple DNA and protein sequence alignment on a workstation and a supercomputer. 1988, 4, 467-71	0
1830	A flexible multiple sequence alignment program. 1988 , 16, 1683-91	64
1829	Two DNA-binding factors recognize specific sequences at silencers, upstream activating sequences, autonomously replicating sequences, and telomeres in Saccharomyces cerevisiae. 1988 , 8, 210-25	529
1828	6;7 chromosomal translocation in spontaneously arising rat immunocytomas: evidence for c-myc breakpoint clustering and correlation between isotypic expression and the c-myc target. 1988 , 8, 441-51	35
1827	Nucleotide sequence of the genetic loci encoding subunits of Bradyrhizobium japonicum uptake hydrogenase. 1988 , 85, 8395-9	104
1826	Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mo1: chromosomal localization and homology to the alpha subunits of integrins. 1988 , 85, 2776-80	29

1825	Improved tools for biological sequence comparison. 1988 , 85, 2444-8	9694
1824	A gene encoding the major beta tubulin of the mitotic spindle in Physarum polycephalum plasmodia. 1988 , 8, 1275-81	32
1823	Guanine nucleotide-binding proteins that enhance choleragen ADP-ribosyltransferase activity: nucleotide and deduced amino acid sequence of an ADP-ribosylation factor cDNA. 1988 , 85, 5488-91	96
1822	Efficient algorithms for molecular sequence analysis. 1988 , 85, 841-5	33
1821	Computer analysis of nucleic acid sequences. 1988 , 164, 765-93	24
1820	The active-site-serine penicillin-recognizing enzymes as members of the Streptomyces R61 DD-peptidase family. 1988 , 250, 313-24	325
1819	Hydrophobic-cluster analysis of plant protein sequences. A domain homology between storage and lipid-transfer proteins. 1988 , 255, 901-5	32
1818	Sequence and transcriptional start site of the Pseudomonas aeruginosa outer membrane porin protein F gene. 1988 , 170, 155-62	110
1817	Complete primary structure of human and rabbit lactase-phlorizin hydrolase: implications for biosynthesis, membrane anchoring and evolution of the enzyme 1988 , 7, 2705-2713	189
1816	Sequences of the bovine and yeast ADP-ribosylation factor and comparison to other GTP-binding proteins. 1988 , 85, 4620-4	193
1815	Viral cysteine proteases are homologous to the trypsin-like family of serine proteases: structural and functional implications. 1988 , 85, 7872-6	354
1814	A Xenopus ribosomal protein S6 kinase has two apparent kinase domains that are each similar to distinct protein kinases. 1988 , 85, 3377-81	242
1813	DNA sequence, structure, and tyrosine kinase activity of the Drosophila melanogaster Abelson proto-oncogene homolog. 1988 , 8, 843-53	74
1812	Structural and mutational analysis of E2 trans-activating proteins of papillomaviruses reveals three distinct functional domains 1988 , 7, 2823-2829	141
1811	Import of proteins into yeast mitochondria: the nuclear MAS2 gene encodes a component of the processing protease that is homologous to the MAS1-encoded subunit 1988 , 7, 3863-3871	109
1810	Pseudomonas aeruginosa diaminopimelate decarboxylase: evolutionary relationship with other amino acid decarboxylases. 1988 , 5, 549-59	17
1809	Homology of mycoplasma plasmid pADB201 and staphylococcal plasmid pE194. 1989 , 171, 593-5	42
1808	Phosphorylation of hepatic phenobarbital-inducible cytochrome P-450 1989 , 8, 3003-3010	43

1807	Identification of four conserved motifs among the RNA-dependent polymerase encoding elements 1989 , 8, 3867-3874	842
1806	Primary structure of sensory rhodopsin I, a prokaryotic photoreceptor 1989 , 8, 3963-3971	72
1805	Characterization of Acinetobacter calcoaceticus catM, a repressor gene homologous in sequence to transcriptional activator genes. 1989 , 171, 5410-21	71
1804	A possible homology between immunodeficiency virus p24 core protein and picornaviral VP2 coat protein: prediction of HIV p24 antigenic sites 1989 , 8, 779-785	48
1803	Cloning, nucleotide sequence, and characterization of genes encoding the secretion function of the Pasteurella haemolytica leukotoxin determinant. 1989 , 171, 916-28	223
1802	Fast and sensitive multiple sequence alignments on a microcomputer. 1989 , 5, 151-3	504
1801	Characterization of the glycinin gene family in soybean. 1989 , 1, 313-28	333
1800	Comparison of exon 5 sequences from 35 class I genes of the BALB/c mouse. 1989 , 170, 1837-58	36
1799	Coat protein of melon necrotic spot carmovirus is more similar to those of tombusviruses than those of carmoviruses. 1989 , 70 (Pt 11), 3033-42	31
1798	Identification and characterization of the potato leafroll virus putative coat protein gene. 1989 , 70 (Pt 3), 783-8	15
1797	Analysis of the complete nucleotide sequence of Chp1, a phage which infects avian Chlamydia psittaci. 1989 , 70 (Pt 12), 3381-90	47
1796	A fast and sensitive multiple sequence alignment algorithm. 1989 , 5, 115-21	35
1795	A Dictyostelium discoideum cDNA coding for a protein with homology to the rat ribosomal protein L7. 1989 , 17, 5393	12
1794	Transcription factor ATF cDNA clones: an extensive family of leucine zipper proteins able to selectively form DNA-binding heterodimers. 1989 , 3, 2083-90	877
1793	Similarity between the picornavirus VP3 capsid polypeptide and the Saccharomyces cerevisiae virus capsid polypeptide. 1989 , 17, 7487-93	4
1792	A G protein gamma subunit shares homology with ras proteins. 1989 , 244, 971-4	151
1791	A multiple sequence alignment algorithm for homologous proteins using secondary structure information and optionally keying alignments to functionally important sites. 1989 , 5, 141-50	2
1790	Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding. 1989 , 17, 2233-44	93

1789	MULTAN (2), a multiple string alignment program for nucleic acids and proteins. 1989 , 5, 51-2	1
1788	Cloning, characterization and heterologous expression of the Smal restriction-modification system. 1989 , 17, 9783-96	51
1787	The alignment of protein structures in three dimensions. 1989 , 51, 55-78	52
1786	A lambda gt11 cDNA recombinant that encodes Dirofilaria immitis paramyosin. 1989 , 35, 31-41	25
1785	Complete nucleotide sequence of the cucumber necrosis virus genome. 1989 , 169, 251-9	73
1784	Distinct lineages of influenza virus H4 hemagglutinin genes in different regions of the world. 1989 , 169, 408-17	82
1783	Similarities among plant virus (+) and (-) RNA termini imply a common ancestry with promoters of eukaryotic tRNAs. 1989 , 172, 415-27	35
1782	Nucleotide sequence of the Lassa virus (Josiah strain) S genome RNA and amino acid sequence comparison of the N and GPC proteins to other arenaviruses. 1989 , 168, 421-5	58
1781	Intra- and interspecies analyses of the carcinoembryonic antigen (CEA) gene family reveal independent evolution in primates and rodents. 1989 , 29, 126-34	37
1780	Scrambled duplications in the feline leukemia virus gag gene: a putative pattern for molecular evolution. 1989 , 29, 135-48	7
1779	Primate evolution of a human chromosome 1 hypervariable repetitive element. 1989 , 28, 212-9	8
1778	Deletions in processed pseudogenes accumulate faster in rodents than in humans. 1989 , 28, 279-85	123
1777	Amphibian albumins as members of the albumin, alpha-fetoprotein, vitamin D-binding protein multigene family. 1989 , 29, 344-54	52
1776	Effectiveness of measures requiring and not requiring prior sequence alignment for estimating the dissimilarity of natural sequences. 1989 , 29, 526-37	46
1775	Average values of a dissimilarity measure not requiring sequence alignment are twice the averages of conventional mismatch counts requiring sequence alignment for a computer-generated model system. 1989 , 29, 538-47	27
1774	A 28s ribosomal RNA phylogeny of certain cyclorrhaphous Diptera based upon a hypervariable region. 1989 , 14, 417-431	43
1773	Arginase of Agrobacterium Ti plasmid C58. DNA sequence, properties, and comparison with eucaryotic enzymes. 1989 , 184, 635-41	28
1772	Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the secretion of its gene product in transformants of different yeast genera. 1989 , 184, 699-706	37

1771	Evolutionary relationships among aminotransferases. Tyrosine aminotransferase, histidinol-phosphate aminotransferase, and aspartate aminotransferase are homologous proteins. 1989 , 186, 249-53		124
1770	Pattern recognition in the prediction of protein structure. I. Tripeptide conformational probabilities calculated from the amino acid sequence. 1989 , 10, 770-797		53
1769	Isolation and structural characterization of the bovine tyrosine hydroxylase gene. 1989 , 23, 31-40		37
1768	Supercomputers and biological sequence comparison algorithms. 1989 , 22, 497-515		4
1767	[Localization of the essential structure for binding of antiviral agents to thymidine kinase by studying sequence homologies]. 1989 , 322, 409-13		6
1766	Supercomputing and biomedical science. 1989 , 5, 197-205		1
1765	Evaluation of the molecular similarity and property prediction for QSAR purposes. 1989 , 6, 49-63		4
1764	The active site of cytochrome P-450 nifedipine oxidase: a model-building study. 1989 , 7, 206-11		25
1763	Molecular properties of the fungal plasma-membrane [H+]-ATPase. 1989, 21, 621-32		42
1762	Gap costs for multiple sequence alignment. 1989 , 138, 297-309		97
1761	cDNA cloning of artichoke mottled crinkle virus RNA and localization and sequencing of the coat protein gene. 1989 , 13, 685-92		16
1760	Analysis of the genes of the OEE1 and OEE3 proteins of the photosystem II complex from Chlamydomonas reinhardtii. 1989 , 12, 683-93		63
1759	Study of protein sequence comparison metrics on the connection machine CM-2. 1989 , 3, 255-269		12
1758	The class 1 outer membrane protein of Neisseria meningitidis: gene sequence and structural and immunological similarities to gonococcal porins. 1989 , 3, 131-9		97
1757	Isolation, molecular characterization and expression of the ushB gene of Salmonella typhimurium which encodes a membrane-bound UDP-sugar hydrolase. 1989 , 3, 177-86		9
1756	Sequence of an unusually large protein implicated in regulation of myosin activity in C. elegans. 1989 , 342, 45-50		355
1755	Protein structure alignment. <i>Journal of Molecular Biology</i> , 1989 , 208, 1-22	6.5	563
1754	Plasmid-partition functions of the P7 prophage. <i>Journal of Molecular Biology</i> , 1989 , 209, 393-406	6.5	56

1753	DNA sequence, organization and regulation of the qa gene cluster of Neurospora crassa. <i>Journal of Molecular Biology</i> , 1989 , 207, 15-34	6.5	148
1752	Weights for data related by a tree. Journal of Molecular Biology, 1989, 207, 647-53	6.5	122
1751	Human SSAV-related endogenous retroviral element: LTR-like sequence and chromosomal localization to 18q21. 1989 , 4, 68-75		32
1750	The protein encoded by a murine male germ cell-specific transcript is a putative ATP-dependent RNA helicase. 1989 , 57, 549-59		160
1749	Drosophila neuroglian: a member of the immunoglobulin superfamily with extensive homology to the vertebrate neural adhesion molecule L1. 1989 , 59, 447-60		369
1748	Cloning and nucleotide sequence analysis of genes coding for the major chlorophyll-binding protein of the moss Physcomitrella patens and the halotolerant alga Dunaliella salina. 1989 , 76, 299-312	2	49
1747	Structure and expression of the human gene encoding plasminogen activator inhibitor, PAI-1. 1989 , 84, 447-53		19
1746	Structure and expression in Escherichia coli K-12 of the L-asparaginase I-encoding ansA gene and its flanking regions. 1989 , 78, 37-46		39
1745	Computer Aided Protein Design: Methods and Applications. 1989 , 127-137		
1744	The Development of the Prediction of Protein Structure. 1989 , 193-316		56
1743	. 1989 , 77, 1056-1060		13
1743 1742	. 1989, 77, 1056-1060 Pattern analysis of RNA secondary structure similarity and consensus of minimal-energy folding. Journal of Molecular Biology, 1989, 207, 597-614	6.5	13 46
7 13	Pattern analysis of RNA secondary structure similarity and consensus of minimal-energy folding.	6.5	
1742	Pattern analysis of RNA secondary structure similarity and consensus of minimal-energy folding. Journal of Molecular Biology, 1989, 207, 597-614 Cloning and sequencing of cDNA clones encoding chicken lamins A and B1 and comparison of the		46
1742	Pattern analysis of RNA secondary structure similarity and consensus of minimal-energy folding. Journal of Molecular Biology, 1989, 207, 597-614 Cloning and sequencing of cDNA clones encoding chicken lamins A and B1 and comparison of the primary structures of vertebrate A- and B-type lamins. Journal of Molecular Biology, 1989, 208, 393-404	6.5	46 101
1742 1741 1740	Pattern analysis of RNA secondary structure similarity and consensus of minimal-energy folding. Journal of Molecular Biology, 1989, 207, 597-614 Cloning and sequencing of cDNA clones encoding chicken lamins A and B1 and comparison of the primary structures of vertebrate A- and B-type lamins. Journal of Molecular Biology, 1989, 208, 393-404 Are coiled-coil proteins evolutionarily related?. Journal of Molecular Biology, 1989, 206, 689-92	6.5	46 101 1
1742 1741 1740 1739	Pattern analysis of RNA secondary structure similarity and consensus of minimal-energy folding. <i>Journal of Molecular Biology</i> , 1989 , 207, 597-614 Cloning and sequencing of cDNA clones encoding chicken lamins A and B1 and comparison of the primary structures of vertebrate A- and B-type lamins. <i>Journal of Molecular Biology</i> , 1989 , 208, 393-404 Are coiled-coil proteins evolutionarily related?. <i>Journal of Molecular Biology</i> , 1989 , 206, 689-92 A method for multiple sequence alignment with gaps. <i>Journal of Molecular Biology</i> , 1989 , 209, 539-48	6.5	46 101 1 66

1735	Human testis cDNA for the regulatory subunit RII alpha of cAMP-dependent protein kinase encodes an alternate amino-terminal region. 1989 , 246, 57-64	72
1734	Sequence similarity between protein B and human apolipoprotein A-IV. 1989 , 249, 151-4	1
1733	Cloning, sequence analysis and chromosome localization of a Drosophila muscarinic acetylcholine receptor. 1989 , 255, 219-25	67
1732	Rat pineal S-antigen: sequence analysis reveals presence of alpha-transducin homologous sequence. 1989 , 247, 307-11	31
1731	The H+ ATPase regulatory subunit of Methanococcus thermolithotrophicus: amplification of an 800 bp fragment by polymerase chain reaction. 1989 , 251, 132-6	14
1730	A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly similar to the extracellular portion of mouse interleukin 1 receptor. 1989 , 258, 301-4	2 80
1729	Heterogeneity within the alkane-inducible cytochrome P450 gene family of the yeast Candida tropicalis. 1989 , 256, 128-34	24
1728	Schistosoma haematobium: analysis of eggshell protein genes and their expression. 1989 , 68, 17-30	17
1727	Trees, Stars, and Multiple Biological Sequence Alignment. 1989 , 49, 197-209	106
1726	Speeding up Dynamic Programming Algorithms for Finding Optimal Lattice Paths. 1989 , 49, 1552-1566	15
1725	Leaf Pairs and Tree Dissections. 1989, 2, 293-299	4
1724	A highly charged sequence of chick hsp90: a good candidate for interaction with steroid receptors. 1989 , 34, 369-74	14
1723	A template based method of pattern matching in protein sequences. 1989 , 54, 159-252	19
1722	Neural cadherin: role in selective cell-cell adhesion. 1989 , 245, 631-5	233
1721	Protein conformational prediction. 1989 , 14, 295-9	60
1720	Primary structure and functional expression of a mammalian skeletal muscle sodium channel. 1989 , 3, 33-49	521
1719		12
1718	Identification of members of the P-glycoprotein multigene family. 1989 , 9, 1224-32	179

1717	SSC1, an essential member of the yeast HSP70 multigene family, encodes a mitochondrial protein. 1989 , 9, 3000-8	245
1716	Cloning and structural characterization of the genes coding for adenosylcobalamin-dependent methylmalonyl-CoA mutase from Propionibacterium shermanii. 1989 , 260, 345-52	72
1715	Identification and characterization of PF4varl, a human gene variant of platelet factor 4. 1989 , 9, 1445-51	49
1714	A tool for multiple sequence alignment. 1989 , 86, 4412-5	376
1713	A ubiquitin carrier protein from wheat germ is structurally and functionally similar to the yeast DNA repair enzyme encoded by RAD6. 1989 , 86, 9861-5	46
1712	Identification of an epitope shared by the DNA-binding domain of glucocorticoid receptor and the B chain of insulin. 1989 , 86, 2138-42	2
1711	Molecular characterization of the plasmid-encoded lactose-PTS ofLactobacillus casei. 1989 , 63, 157-165	2
1710	Characterization of the Glycinin Gene Family in Soybean. 1989 , 1, 313	54
1709	Structure and expression of STK, a src-related gene in the simple metazoan Hydra attenuata. 1989 , 9, 4141-51	53
1708	Organization of the human lipoprotein lipase gene and evolution of the lipase gene family. 1989 , 86, 9647-51	202
1707	Complete nucleotide sequence of primitive vertebrate immunoglobulin light chain genes. 1989 , 86, 4684-8	56
1706	Isolation and characterization of cDNA encoding the alpha subunit of Cap $Z(36/32)$, an actin-capping protein from the Z line of skeletal muscle. 1989 , 86, 5800-4	43
1705	A Drosophila gene encoding a protein resembling the human beta-amyloid protein precursor. 1989 , 86, 2478-82	187
1704	Structural homology of complement protein C6 with other channel-forming proteins of complement. 1989 , 86, 2799-803	23
1703	Conservation of structural and functional domains in complement component C3 of Xenopus and mammals. 1989 , 86, 1323-7	39
1702	Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis ribosomal S6 kinase. 1989 , 9, 3850-9	163
1701	Expression and nucleotide sequence of the Lactobacillus bulgaricus beta-galactosidase gene cloned in Escherichia coli. 1989 , 171, 625-35	94
1700	Evolutionary relationship between the TonB-dependent outer membrane transport proteins: nucleotide and amino acid sequences of the Escherichia coli colicin I receptor gene. 1989 , 171, 1041-7	86

1699	Methodological aspects and potential of computer-aided protein engineering. 1990 , 4, 329-336	3
1698	Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes. 1990 , 87, 2264-8	1173
1697	Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is homologous to platelet-derived growth factor. 1990 , 87, 2628-32	318
1696	Hepatitis C virus shares amino acid sequence similarity with pestiviruses and flaviviruses as well as members of two plant virus supergroups. 1990 , 87, 2057-61	522
1695	Identification and characterization of a Dictyostelium discoideum ribosomal protein gene. 1990 , 18, 4695-701	12
1694	Structural analysis of sulphated glycoprotein 2 from amino acid sequence. Relationship to clusterin and serum protein 40,40. 1990 , 268, 571-8	70
1693	Three-way NeedlemanWunsch algorithm. 1990 , 183, 365-75	3
1692	Protein multiple sequence alignment and flexible pattern matching. 1990 , 183, 403-28	142
1691	Computer analysis of protein structure. 1990 , 182, 751-76	9
1690	Use of homology domains in sequence similarity detection. 1990 , 183, 133-46	1
1689	Sensitivity comparison of protein amino acid sequences. 1990 , 183, 352-65	14
1688	Multiple sequence comparison. 1990 , 183, 438-47	2
1687	Simultaneous comparison of several sequences. 1990 , 183, 447-56	10
1686	Functional similarities between retroviruses and the IS3 family of bacterial insertion sequences?. 1990 , 4, 1771-7	195
1685	Sequence and relatedness in other bacteria of the Pseudomonas aeruginosa oprP gene coding for the phosphate-specific porin P. 1990 , 4, 831-8	29
1684	Structural analysis of the pehA gene and characterization of its protein product, endopolygalacturonase, of Erwinia carotovora subspecies carotovora. 1990 , 4, 1037-44	65
1683	Disruption of the actin cytoskeleton in yeast capping protein mutants. 1990 , 344, 352-4	154
1682	Isolation and characterization of the gene for a yeast mitochondrial import receptor. 1990 , 347, 488-91	75

(1990-1990)

1681	limited proteolysis experiments. 1990 , 189, 221-7	29
1680	Characterization of matteuccin, the 2.2S storage protein of the ostrich fern. Evolutionary relationship to angiosperm seed storage proteins. 1990 , 192, 101-7	15
1679	Distribution of the number of matches between nucleotide sequences. 1990 , 52, 349-58	1
1678	Optimal sequence alignment allowing for long gaps. 1990 , 52, 359-73	46
1677	Consistency of optimal sequence alignments. 1990 , 52, 509-25	38
1676	Symposium 1: Structure and engineering of proteins: New developments. 1990 , 337, 1-3	
1675	Bloodstream and metacyclic variant surface glycoprotein gene expression sites of Trypanosoma brucei gambiense. 1990 , 41, 101-14	16
1674	Conservation of functional residues between yeast and E. coli inorganic pyrophosphatases. 1990 , 1038, 338-45	37
1673	Sequence similarity between alpha 2-macroglobulin from the horseshoe crab, Limulus polyphemus, and proteins of the alpha 2-macroglobulin family from mammals. 1990 , 96, 621-5	17
1672	Identification of conserved domains in the cell attachment proteins of the three serotypes of reovirus. 1990 , 174, 399-409	74
1671	Nucleotide sequence and genome organization of biologically active proviruses of the bovine immunodeficiency-like virus. 1990 , 175, 391-409	173
1670	Genome organization and taxonomic position of human papillomavirus type 47 inferred from its DNA sequence. 1990 , 177, 401-5	23
1669	An O(NP) sequence comparison algorithm. 1990 , 35, 317-323	61
1668	Differential regulation of genes for resveratrol synthase in cell cultures ofArachis hypogaea L. 1990 , 181, 169-75	65
1667	Phylogenetic relationships among Tetrahymena species determined using the polymerase chain reaction. 1990 , 30, 290-7	43
1666	Molecular anatomy: phyletic relationships derived from three-dimensional structures of proteins. 1990 , 30, 43-59	91
1665	Evolution of proteins of the cystatin superfamily. 1990 , 30, 60-71	251
1664	Identification of protein folds: matching hydrophobicity patterns of sequence sets with solvent accessibility patterns of known structures. 1990 , 7, 257-64	92

1663	Structural homology among the peroxidase enzyme family revealed by hydrophobic cluster analysis. 1990 , 8, 251-7	46
1662	Complexity of common subsequence and supersequence problems and related problems. 1990 , 25, 565-580	50
1661	Major histocompatibility complex class I genes of Peromyscus leucopus. 1990 , 32, 371-9	18
1660	Sequence conservation among the glucose transporter from the cyanobacterium Synechocystis sp. PCC 6803 and mammalian glucose transporters. 1990 , 14, 697-706	37
1659	CGEMA and VGAP: a Colour Graphics Editor for Multiple Alignment using a variable GAP penalty. Application to the muscarinic acetylcholine receptor. 1990 , 4, 131-45	18
1658	Class I major histocompatibility complex cDNA clones from sheep thymus: alternative splicing could make a long cytoplasmic tail. 1990 , 32, 77-87	28
1657	Unexpected close relationship between the large nonvirion proteins of filamentous potexviruses and spherical tymoviruses. 1990 , 3, 373-9	15
1656	Stochastic traits of molecular evolutionacceptance of point mutations in native actin genes. 1990 , 143, 287-306	11
1655	A rapid method of protein structure alignment. 1990 , 147, 517-51	115
1654	Parallel computation of multiple biological sequence comparisons. 1990 , 23, 310-31	2
1653	A program to find regions of similarity between homologous protein sequences using dot-matrix analysis. 1990 , 8, 11-5, 25	3
1652	Genetic sequences of hormone response elements share similarity with predicted alpha helices within DNA binding domains of steroid receptor proteins: A basis for site-specific recognition. 1990 , 20, 25-48	20
1651	Short interspersed repeats in rabbit DNA can provide functional polyadenylation signals. 1990 , 7, 1-8	18
1650	Structural characterization of the Salmonella typhimurium LT2 umu operon. 1990 , 172, 4979-87	47
1649	Transposition in Shigella dysenteriae: isolation and analysis of IS911, a new member of the IS3 group of insertion sequences. 1990 , 172, 4090-9	116
1648	Multiple nicotinic acetylcholine receptor genes are expressed in goldfish retina and tectum. 1990 , 10, 670-83	30
1647	Sequence analysis and mapping of the Salmonella typhimurium LT2 umuDC operon. 1990 , 172, 4964-78	57

1645	Cloning of the esterase-5 locus from Drosophila pseudoobscura and comparison with its homologue in D. melanogaster. 1990 , 7, 525-46	38
1644	Algorithms for Finding Patterns in Strings. 1990 , 255-300	86
1643	OP-1 cDNA encodes an osteogenic protein in the TGF-beta family 1990 , 9, 2085-2093	425
1642	Structural and functional characterization of tnpl, a recombinase locus in Tn21 and related beta-lactamase transposons. 1990 , 172, 3745-57	41
1641	Molecular studies on the mechanism of tetracycline resistance mediated by Tet(O). 1990, 34, 71-7	59
1640	Characterization of the promoter region of Tetrahymena genes. 1990 , 18, 323-9	54
1639	Variation among the dispersed (GATA)n sequences in Drosophila melanogaster. 1990, 33, 750-4	6
1638	A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor. 1990 , 87, 8331-5	250
1637	Nucleotide sequence and phylogeny of SHV-2 beta-lactamase. 1990 , 34, 1725-32	47
1636	Cloning of three human tyrosine phosphatases reveals a multigene family of receptor-linked protein-tyrosine-phosphatases expressed in brain. 1990 , 87, 7000-4	166
1635	Linguistic measure of taxonomic and functional relatedness of nucleotide sequences. 1990 , 7, 1251-68	40
1634	Cloning and characterization of cDNAs for murine macrophage inflammatory protein 2 and its human homologues. 1990 , 172, 911-9	263
1633	Biophysical studies on the morphology of baculovirus-expressed bluetongue virus tubules. 1990 , 71 (Pt 8), 1839-44	10
1632	Cloning and expression of the cDNA for a Drosophila insulin-degrading enzyme. 1990 , 4, 1580-91	61
1631	An ancient, highly conserved family of cysteine-rich protein domains revealed by cloning type I and type II murine macrophage scavenger receptors. 1990 , 87, 8810-4	270
1630	Nucleotide sequence and genomic organization of melon necrotic spot virus. 1990 , 71 (Pt 9), 1887-96	81
1629	Herpesviral deoxythymidine kinases contain a site analogous to the phosphoryl-binding arginine-rich region of porcine adenylate kinase; comparison of secondary structure predictions and conservation. 1990 , 71 (Pt 12), 2979-87	82
1628	cDNA clone encoding Drosophila transcription factor TFIID. 1990 , 87, 9148-52	69

Nucleotide sequence of segment S9 of the genome of rice gall dwarf virus. 1990 , 71 (Pt 8), 1861-3	25
1626 HIV-1 reverse transcriptase: structure predictions for the polymerase domain. 1990 , 6, 1061-72	6 7
Expression of the K-fgf proto-oncogene is controlled by 3' regulatory elements which are specific for embryonal carcinoma cells. 1990 , 10, 2475-84	83
Molecular Phylogeny of Selected Decapod Crustaceans Based on 18s rRNA Nucleotide Sequences. 1624 1990 , 10, 1	40
Phylogeny and evolution of antlered deer determined from mitochondrial DNA sequences. 1990 , 87, 6127-31	109
Sequence and structural similarities between the leucine-specific binding protein and leucyl-tRNA synthetase of Escherichia coli. 1990 , 87, 4561-5	9
1621 Protein database searches for multiple alignments. 1990 , 87, 5509-13	397
1620 Progressive alignment and phylogenetic tree construction of protein sequences. 1990 , 183, 375-87	276
1619 Similarities between putative transport proteins of plant viruses. 1990 , 71 (Pt 5), 1009-18	88
A family of positive regulators related to the Pseudomonas putida TOL plasmid XylS and the Escherichia coli AraC activators. 1990 , 18, 2149-52	86
1617 Hemolin: an insect-immune protein belonging to the immunoglobulin superfamily. 1990 , 250, 1729-3	32 224
1616 Phylogenetic relationships from three-dimensional protein structures. 1990 , 183, 670-90	55
Efficient recognition of immunoglobulin domains from amino acid sequences using a neural network. 1990 , 6, 319-24	5
1614 Consensus methods for DNA and protein sequence alignment. 1990 , 183, 221-37	31
1613 Hierarchical method to align large numbers of biological sequences. 1990 , 183, 456-74	27
1612 Digital signal processing methods for biosequence comparison. 1990 , 18, 3001-6	16
1611 Isolation of a Schizosaccharomyces pombe homologue to the rat ribosomal protein, L7. 1990 , 18, 45	90 15
1610 Mutation data matrix and its uses. 1990 , 183, 333-51	69

1609	Determination of reliable regions in protein sequence alignments. 1990 , 3, 565-9		67
1608	Cloning, sequencing, expression, and site-directed mutagenesis of the gene from Clostridium perfringens encoding pyruvoyl-dependent histidine decarboxylase. 1990 , 29, 132-9		32
1607	Mutational analysis of the phage T4 morphogenetic 31 gene, whose product interacts with the Escherichia coli GroEL protein. 1990 , 86, 19-25		30
1606	Prediction of protein structure from sequence. 1990 , 26, 1163-6		8
1605	Cloning and nucleotide sequence of the N-acetylmuramidase M1-encoding gene from Streptomyces globisporus. 1990 , 88, 81-6		34
1604	From comparisons of protein sequences and structures to protein modelling and design. 1990 , 15, 235-4	10	134
1603	Cloning, expression and sequence analysis of an endolysin-encoding gene of Lactobacillus bulgaricus bacteriophage mv1. 1990 , 94, 61-7		50
1602	Cloning and characterization of the Bacillus sphaericus genes controlling the bioconversion of pimelate into dethiobiotin. 1990 , 87, 63-70		90
1601	Receptor tyrosine kinases mediate cell-cell interactions during Drosophila development. 1990 , 2, 15-27		5
1600	Calculation of conformational ensembles from potentials of mean force. An approach to the knowledge-based prediction of local structures in globular proteins. <i>Journal of Molecular Biology</i> , 1990 , 213, 859-83	6.5	956
1599	Basic local alignment search tool. <i>Journal of Molecular Biology</i> , 1990 , 215, 403-10	6.5	65807
1598	Finding protein similarities with nucleotide sequence databases. 1990 , 183, 111-32		159
1597	Flexible protein sequence patterns. A sensitive method to detect weak structural similarities. Journal of Molecular Biology, 1990 , 212, 389-402	6.5	112
1596	Definition of general topological equivalence in protein structures. A procedure involving comparison of properties and relationships through simulated annealing and dynamic programming. <i>Journal of Molecular Biology</i> , 1990 , 212, 403-28	6.5	477
1595	Signal-regulator interactions. Genetic analysis of the effector binding site of xylS, the benzoate-activated positive regulator of Pseudomonas TOL plasmid meta-cleavage pathway operon. <i>Journal of Molecular Biology</i> , 1990 , 211, 373-82	6.5	83
1594	Cloning and analysis of the 5' region of the rat bone/liver/kidney/placenta alkaline phosphatase gene. A dual-function promoter. 1990 , 10, 38-47		17
1593	Rapid and sensitive sequence comparison with FASTP and FASTA. 1990 , 183, 63-98		1422
1592	Hydrophobic cluster analysis: procedures to derive structural and functional information from 2-D-representation of protein sequences. 1990 , 72, 555-74		298

1591	SequenceEditingAligner: a multiple sequence editor and aligner. 1990 , 7, 39-45	5
1590	Identification of a conserved protein motif in a group of growth factor receptors. 1990 , 272, 7-11	50
1589	An element of symmetry in yeast TATA-box binding protein transcription factor IID. Consequence of an ancestral duplication?. 1990 , 261, 223-5	14
1588	The amino acid sequence of a myotoxic phospholipase from the venom of Bothrops asper. 1990 , 278, 319-25	121
1587	Mode of assembly of amphipathic helical segments in model high-density lipoproteins. 1990 , 1043, 245-52	96
1586	Genomic DNA 5' to the mouse and human angiotensin-converting enzyme genes contains two distinct regions of conserved sequence. 1990 , 167, 1128-33	35
1585	Conserved residues of liquefying alpha-amylases are concentrated in the vicinity of active site. 1990 , 166, 61-5	11
1584	Efficient Parallel Algorithms for String Editing and Related Problems. 1990 , 19, 968-988	103
1583	Nucleotide sequence of the tick-borne, orthomyxo-like Dhori/Indian/1313/61 virus envelope gene. 1990 , 175, 10-8	14
1582	Identification and molecular characterization of insulin-like growth factor binding proteins (IGFBP-1, -2, -3, -4, -5 and -6). 1991 , 3, 243-66	490
1581	Enzymes depending on the pterin molybdenum cofactor: sequence families, spectroscopic properties of molybdenum and possible cofactor-binding domains. 1991 , 1057, 157-85	130
1580	. 1991 , 13, 1245-1255	12
1579	Recognition site mapping and receptor modelling: Application to 5-HT receptors. 1991 , 19, 397-406	9
1578	Murine gamma E-crystallin is distinct from murine gamma 2-crystallin. 1991 , 104, 265-70	20
1577	Nucleotide and deduced amino acid sequences of the gene encoding virion protein 16 of herpes simplex virus type 2. 1991 , 103, 235-8	22
1576	Identifying distantly related protein sequences. 1991 , 1, 321-326	11
1575	Molecular cloning and expression of a novel adhesion molecule, SC1. 1991 , 7, 535-45	178
1574	Characterization of a second alkane-inducible cytochrome P450-encoding gene, CYP52A2, from Candida tropicalis. 1991 , 106, 51-60	48

1573	A novel randomized iterative strategy for aligning multiple protein sequences. 1991 , 7, 479-84		38
1572	Yeast 6-phosphofructo-2-kinase: sequence and mutant. 1991 , 30, 10663-72		44
1571	Complement components C1r/C1s, bone morphogenic protein 1 and Xenopus laevis developmentally regulated protein UVS.2 share common repeats. 1991 , 282, 9-12		34
1570	Sequence similarity between opioid peptide precursors and DNA-binding proteins. 1991 , 282, 175-7		15
1569	Cellular mono(ADP-ribosyl) transferase inhibits protein synthesis. 1991, 283, 235-8		12
1568	Suboptimal sequence alignment in molecular biology. Alignment with error analysis. <i>Journal of Molecular Biology</i> , 1991 , 221, 403-20	6.5	79
1567	A new family of powerful multivariate statistical sequence analysis techniques. <i>Journal of Molecular Biology</i> , 1991 , 220, 877-87	6.5	56
1566	An efficient algorithm for identifying matches with errors in multiple long molecular sequences. Journal of Molecular Biology, 1991 , 221, 1367-78	6.5	37
1565	Schistosoma japonicum: analysis of eggshell protein genes, their expression, and comparison with similar genes from other schistosomes. 1991 , 72, 381-90		18
1564	The sequence of the Arbacia punctulata bindin cDNA and implications for the structural basis of species-specific sperm adhesion and fertilization. 1991 , 143, 282-8		33
1563	Comparative analysis of ribosomal protein L5 sequences from bacteria of the genus Thermus. 1991 , 73, 669-78		10
1562	The structure of the gene for ribosomal protein L5 in the archaebacterium Sulfolobus acidocaldarius. 1991 , 73, 679-82		7
1561	Searching protein sequence libraries: comparison of the sensitivity and selectivity of the Smith-Waterman and FASTA algorithms. 1991 , 11, 635-50		444
1560	Amino acid substitution matrices from an information theoretic perspective. <i>Journal of Molecular Biology</i> , 1991 , 219, 555-65	6.5	477
1559	A new method for building protein conformations from sequence alignments with homologues of known structure. <i>Journal of Molecular Biology</i> , 1991 , 217, 1-7	6.5	125
1558	A simple method to generate non-trivial alternate alignments of protein sequences. <i>Journal of Molecular Biology</i> , 1991 , 219, 727-32	6.5	40
1557	Motif recognition and alignment for many sequences by comparison of dot-matrices. <i>Journal of Molecular Biology</i> , 1991 , 218, 33-43	6.5	95
1556	Database algorithm for generating protein backbone and side-chain co-ordinates from a C alpha trace application to model building and detection of co-ordinate errors. <i>Journal of Molecular Biology</i> , 1991 , 218, 183-94	6.5	301

1555	Comparison of protein structures. 1991 , 1, 334-344	14
1554	Characterization and primary structure of proteins L28, L33 and L34 from Bacillus stearothermophilus ribosomes. 1991 , 73, 855-60	15
1553	VOSTORG: a package of microcomputer programs for sequence analysis and construction of phylogenetic trees. 1991 , 101, 251-4	53
1552	A method to identify protein sequences that fold into a known three-dimensional structure. 1991 , 253, 164-70	2411
1551	Galactose utilization in Lactobacillus helveticus: isolation and characterization of the galactokinase (galK) and galactose-1-phosphate uridyl transferase (galT) genes. 1991 , 173, 4464-73	41
1550	Constrained optimization and protein structure determination. 1991 , 261, C376-86	3
1549	Nucleotide and derived amino acid sequences of the major porin of Comamonas acidovorans and comparison of porin primary structures. 1991 , 173, 2196-205	34
1548	Similarity and Congruence as Criteria for Molecular Homology. 1991 ,	
1547	Subfamily relationships and clustering of rabbit C repeats. 1991 , 8, 1-30	26
1546	Cloning, nucleotide sequence, and characterization of mtr, the structural gene for a tryptophan-specific permease of Escherichia coli K-12. 1991 , 173, 108-15	55
1545	Three trans-acting regulatory functions control hydrogenase synthesis in Alcaligenes eutrophus. 1991 , 173, 1845-54	60
1544	Expression and nucleotide sequence of the Clostridium acetobutylicum beta-galactosidase gene cloned in Escherichia coli. 1991 , 173, 3084-95	51
1543	Nucleotide sequence of the Rhodobacter capsulatus fruK gene, which encodes fructose-1-phosphate kinase: evidence for a kinase superfamily including both phosphofructokinases of Escherichia coli. 1991 , 173, 3117-27	78
1542	Identification and sequence analysis of the hupR1 gene, which encodes a response regulator of the NtrC family required for hydrogenase expression in Rhodobacter capsulatus. 1991 , 173, 5928-32	56
1541	Metronidazole activation and isolation of Clostridium acetobutylicum electron transport genes. 1991 , 173, 1088-95	30
1540	Cloning and expression of a rat brain alpha 2B-adrenergic receptor. 1991 , 88, 1019-23	48
1539	Selection, expression, and nucleotide sequencing of the glutamate dehydrogenase gene of Peptostreptococcus asaccharolyticus. 1991 , 173, 6162-7	24
1538	Multiple trans-splicing events are required to produce a mature nad1 transcript in a plant mitochondrion. 1991 , 5, 1407-15	45

1537	Nucleotide sequences of the Acinetobacter calcoaceticus benABC genes for benzoate 1,2-dioxygenase reveal evolutionary relationships among multicomponent oxygenases. 1991 , 173, 5385-95	192
1536	Use of homologous sequences to improve protein secondary structure prediction. 1991 , 202, 45-59	8
1535	Modeling of mammalian P450s on basis of P450cam X-ray structure. 1991 , 206, 11-30	53
1534	Evolution of the major histocompatibility complex: molecular cloning of major histocompatibility complex class I from the amphibian Xenopus. 1991 , 88, 537-41	89
1533	cDNA cloning and sequencing of human fibrillarin, a conserved nucleolar protein recognized by autoimmune antisera. 1991 , 88, 931-5	166
1532	Evolution of retroposons by acquisition or deletion of retrovirus-like genes. 1991 , 8, 835-56	104
1531	Primary structure of xylene monooxygenase: similarities to and differences from the alkane hydroxylation system. 1991 , 173, 1690-5	148
1530	Different forms of Go alpha mRNA arise by alternative splicing of transcripts from a single gene on human chromosome 16. 1991 , 11, 1146-55	22
1529	A prion-like protein from chicken brain copurifies with an acetylcholine receptor-inducing activity. 1991 , 88, 7664-8	101
1528	Molecular dynamics of dopamine at the D2 receptor. 1991 , 88, 8111-5	95
1527	Rolling-circle replication of the plasmid pKYM isolated from a gram-negative bacterium. 1991 , 88, 10282-6	56
1526	A mutation in a Rhodobacter capsulatus gene encoding an integration host factor-like protein impairs in vivo hydrogenase expression. 1991 , 88, 10749-53	40
1525	Eliminated chromatin of Ascaris contains a gene that encodes a putative ribosomal protein. 1991 , 88, 1593-6	39
1524	The Neurospora crassa cyt-20 gene encodes cytosolic and mitochondrial valyl-tRNA synthetases and may have a second function in addition to protein synthesis. 1991 , 11, 4022-35	22
1523	Conservation of the gene for outer membrane protein OprF in the family Pseudomonadaceae: sequence of the Pseudomonas syringae oprF gene. 1991 , 173, 768-75	31
1522	A classification of glycosyl hydrolases based on amino acid sequence similarities. 1991 , 280 (Pt 2), 309-16	2550
1521	Gene organization and nucleotide sequence of the primase region of IncP plasmids RP4 and R751. 1991 , 2, 145-62	30
1520	Molecular cloning and expression of a new putative inositol 1,4,5-trisphosphate 3-kinase isoenzyme. 1991 , 278 (Pt 3), 883-6	73

1519	Human salivary cystatin S. Cloning, sequence analysis, hybridization in situ and immunocytochemistry. 1991 , 278 (Pt 3), 627-35	44
1518	Motifs of Immunoglobulin-Like Domains: Neurotrophic Factor Receptors trk and trkB are Members of the Immunoglobulin Family 1991 , 67, 188-192	1
1517	Nucleotide sequence analysis of the bovine respiratory syncytial virus fusion protein mRNA and expression from a recombinant vaccinia virus. 1991 , 181, 118-31	36
1516	Genome organization and nucleotide sequence of human papillomavirus type 39. 1991 , 181, 419-23	29
1515	Primary structure of a Plasmodium falciparum rhoptry antigen. 1991 , 49, 99-110	66
1514	Evolutionary relatedness of the predicted gene product of RNA segment 2 of the tick-borne Dhori virus and the PB1 polymerase gene of influenza viruses. 1991 , 182, 1-7	26
1513	The incorporation of reovirus cell attachment protein sigma 1 into virions requires the N-terminal hydrophobic tail and the adjacent heptad repeat region. 1991 , 182, 346-50	36
1512	Molecular cloning and characterization of a novel human gene homologous to the murine ecotropic retroviral receptor. 1991 , 185, 10-7	71
1511	Human papillomavirus type 58 DNA sequence. 1991 , 185, 424-7	33
1510	Sequence analysis of infectious pancreatic necrosis virus genome segment B and its encoded VP1 protein: a putative RNA-dependent RNA polymerase lacking the Gly-Asp-Asp motif. 1991 , 181, 541-52	106
1509	Early events in Epstein-Barr virus infection of human B lymphocytes. 1991 , 181, 595-608	246
1508	Isolation and molecular characterization of the swinepox virus thymidine kinase gene. 1991 , 183, 578-85	12
1507	Close tetrapod relationships of the coelacanth Latimeria indicated by haemoglobin sequences. 1991 , 351, 394-7	66
1506	Spinning in hyperspace. 1991 , 353, 388-389	6
1505	Origin of tetracycline efflux proteins: conclusions from nucleotide sequence analysis. 1991 , 5, 895-900	29
1504	Molecular characterization of the gor gene encoding glutathione reductase from Pseudomonas aeruginosa: determinants of substrate specificity among pyridine nucleotide-disulphide oxidoreductases. 1991 , 5, 163-171	29
1503	Peptide transport and chemotaxis in Escherichia coli and Salmonella typhimurium: characterization of the dipeptide permease (Dpp) and the dipeptide-binding protein. 1991 , 5, 1035-47	130
1502	Cloning and sequencing of the structural gene for the porin protein of Bordetella pertussis. 1991 , 5, 1649-56	29

1501 F	Primary structure of toad sperm protamines and nucleotide sequence of their cDNAs. 1991 , 196, 401-6	29
1500 €	nduced plant responses to pathogen attack. Analysis and heterologous expression of the key enzyme in the biosynthesis of phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63). 1991 , 196, 423-30	97
1499 <i>F</i>	Amino acid sequence analysis of the annexin super-gene family of proteins. 1991, 198, 749-60	126
1498 t	Primary structure and processing of the Candida tsukubaensis alpha-glucosidase. Homology with the rabbit intestinal sucrase-isomaltase complex and human lysosomal alpha-glucosidase. 1991 , 202, 657-64	20
1497 <i>F</i>	A review of algorithms for molecular sequence comparison. 1991 , 24, 72-96	16
	A parallel computing approach to genetic sequence comparison: the master-worker paradigm with nterworker communication. 1991 , 24, 152-69	10
1495	Sequence comparison on the connection machine. 1991 , 3, 89-107	
1494 [Dictyostelium discoideum gene family contains a long internal amino acid repeat. 1991 , 12, 133-8	5
1493 [Detection of flaviviruses by reverse-transcriptase polymerase chain reaction. 1991 , 33, 260-7	64
1492 F	Folding and function of the myelin proteins from primary sequence data. 1991 , 28, 1-17	64
	A fast unbiased comparison of protein structures by means of the Needleman-Wunsch algorithm. 1 991 , 32, 340-54	22
1490 (Average values of a dissimilarity measure not requiring sequence alignment are twice the averages of conventional mismatch counts requiring sequence alignment for a variety of computer-generated model systems. 1991 , 32, 521-8	8
1489 1	The evolution of rhodopsins and neurotransmitter receptors. 1991 , 33, 367-78	131
1488 <i>F</i>	An evolutionary model for maximum likelihood alignment of DNA sequences. 1991 , 33, 114-24	291
1487 <i>F</i>	A workbench for multiple alignment construction and analysis. 1991 , 9, 180-90	897
1,86	A workbench for multiple alignment construction and analysis. 1991 , 9, 180-90 Subunit structure of deglycosylated human and swine trachea and Cowper's gland mucin glycoproteins. 1991 , 102, 71-93	897
1486 S	Subunit structure of deglycosylated human and swine trachea and Cowper's gland mucin	

1483	Determination of steady-state mRNA levels of individual chlorophyll a/b binding protein genes of the tomato cab gene family. 1991 , 230, 413-22	31
1482	Computer-aided active-site-directed modeling of the herpes simplex virus 1 and human thymidine kinase. 1991 , 5, 385-404	23
1481	Topological maps of protein sequences. 1991 , 65, 451-8	32
1480	Nucleotide sequence, polymorphism, and evolution of ovine MHC class II DQA genes. 1991 , 34, 69-79	29
1479	B2-like repetitive sequence from the X chromosome of the American mink (Mustela vison). 1991 , 1, 165-70	8
1478	PROMOT: a FORTRAN program to scan protein sequences against a library of known motifs. 1991 , 7, 257-60	7
1477	'Size leap' algorithm: an efficient extraction of the longest common motifs from a molecular sequence set. Application to the DNA sequence reconstruction. 1991 , 7, 509-13	
1476	MASH: an interactive program for multiple alignment and consensus sequence construction for biological sequences. 1991 , 7, 195-202	2
1475	The complete nucleotide sequence of cucumber green mottle mosaic virus (SH strain) genomic RNA. 1991 , 72 (Pt 7), 1487-95	88
1474	Nucleotide sequence of tomato ringspot virus RNA-2. 1991 , 72 (Pt 7), 1505-14	47
1473	Parallel computation and FASTA: confronting the problem of parallel database search for a fast sequence comparison algorithm. 1991 , 7, 71-8	7
1472	Cloning and sequencing of PYBP, a pyrimidine-rich specific single strand DNA-binding protein. 1991 , 19, 5237-45	66
1471	Comparison of the sequences of class A beta-lactamases and of the secondary structure elements of penicillin-recognizing proteins. 1991 , 35, 2294-301	155
1470	Human autoantibody to RNA polymerase I transcription factor hUBF. Molecular identity of nucleolus organizer region autoantigen NOR-90 and ribosomal RNA transcription upstream binding factor. 1991 , 174, 1239-44	147
1469	Molecular cloning and sequencing of a pectinesterase gene from Pseudomonas solanacearum. 1991 , 137, 131-40	36
1468	Fast optimal alignment. 1991 , 7, 1-7	1
1467	Scanning protein sequence databanks using a distributed processing workstation network. 1991 , 7, 85-8	3
1466	Kinetics of angular and spectral characteristics of excimer laser radiation. 1991 , 21, 622-626	

1465	Nucleotide sequence and organization of genes flanking the transfer origin of promiscuous plasmid RP4. 1991 , 1, 303-27	79
1464	Cytochrome P450 family 4 in a cockroach: molecular cloning and regulation by regulation by hypertrehalosemic hormone. 1991 , 88, 4558-62	103
1463	Human catechol-O-methyltransferase: cloning and expression of the membrane-associated form. 1991 , 88, 1416-20	167
1462	Molecular cloning of a second form of rac protein kinase. 1991 , 2, 1001-9	146
1461	A rat brain mRNA encoding a transcriptional activator homologous to the DNA binding domain of retroviral integrases. 1991 , 19, 5269-74	89
1460	SQUIRREL: Sequence QUery, Information Retrieval and REporting Library. A program package for analyzing signals in nucleic acid sequences for the VAX. 1991 , 19, 6033-40	3
1459	Sodium and potassium ATPase of the teleost fish Catostomus commersoni. Sequence, protein structure and evolutionary conservation of the alpha-subunit. 1991 , 372, 279-86	22
1458	Identification of the porcine paramyxovirus LPMV matrix protein gene: comparative sequence analysis with other paramyxoviruses. 1991 , 72 (Pt 5), 1045-50	34
1457	The predicted protein sequence of a fish testis-specific alpha-tubulin cDNA shows conservation of isotype-specific amino acid substitutions. 1991 , 2, 47-51	5
1456	Molecular cloning of an invertebrate glutamate receptor subunit expressed in Drosophila muscle. 1991 , 254, 112-4	170
1455	Counting and discounting the universe of exons. 1991 , 253, 677-80	22
1454	Computer speed and sequence comparison. 1992 , 257, 1609-10	4
1453	. 1992,	1
1452	The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170 gene in an antigenic variant. 1992 , 12, 1194-201	43
1451	On the use of the transmembrane domain of bacteriorhodopsin as a template for modeling the three-dimensional structure of guanine nucleotide-binding regulatory protein-coupled receptors. 1992 , 89, 4009-12	87
1450	Unusual amino acid sequence of the second Ig-like domain of the feline CD4 protein. 1992 , 8, 1581-91	7
1449	Sparse dynamic programming I. 1992 , 39, 519-545	91

1447	Characterization of Chlorella virus PBCV-1 CviAII restriction and modification system. 1992, 20, 5351-6	35
1446	A variable gap penalty function and feature weights for protein 3-D structure comparisons. 1992 , 5, 43-51	72
1445	Identification of a second insulin-like growth factor in a fish species. 1992 , 89, 8913-7	103
1444	Functional assembly of a randomly cleaved protein. 1992 , 89, 1880-4	111
1443	Identification and expression of a cDNA clone encoding aspartate aminotransferase in carrot. 1992 , 100, 374-81	36
1442	Computer methods for locating kinetoplastid cryptogenes. 1992 , 20, 2717-24	13
1441	An efficient automated computer vision based technique for detection of three dimensional structural motifs in proteins. 1992 , 9, 769-89	69
1440	Cyclin-B homologs in Saccharomyces cerevisiae function in S phase and in G2. 1992 , 6, 2021-34	233
1439	Preferential expression of one beta-tubulin gene during flagellate development in Physarum. 1992 , 138, 229-38	15
1438	Sequence analysis of the Marburg virus nucleoprotein gene: comparison to Ebola virus and other non-segmented negative-strand RNA viruses. 1992 , 73 (Pt 2), 347-57	74
1437	Exhaustive matching of the entire protein sequence database. 1992 , 256, 1443-5	662
1436	hnRNP I, the polypyrimidine tract-binding protein: distinct nuclear localization and association with hnRNAs. 1992 , 20, 3671-8	281
1435	Identification and characterization of additional members of the cytochrome P450 multigene family CYP52 of Candida tropicalis. 1992 , 11, 767-80	62
1434		
1433	Proposed acquisition of an animal protein domain by bacteria. 1992 , 89, 8990-4	213
1432	Induction by fungal elicitor of S-adenosyl-L-methionine synthetase and S-adenosyl-L-homocysteine hydrolase mRNAs in cultured cells and leaves of Petroselinum crispum. 1992 , 89, 4713-7	146
1431	RNA polymerase-associated transcription specificity factor encoded by vaccinia virus. 1992 , 89, 3536-40	82
1430	Determining DNA sequence similarity using maximum independent set algorithms for interval graphs. 1992 , 326-337	21

1429	Human aspartylglucosaminidase. A biochemical and immunocytochemical characterization of the enzyme in normal and aspartylglucosaminuria fibroblasts. 1992 , 286 (Pt 2), 613-8	18
1428	Cloning, sequence analysis, and expression in Escherichia coli of a streptococcal plasmin receptor. 1992 , 174, 5204-10	178
1427	Temperature sensing in Yersinia pestis: regulation of yopE transcription by lcrF. 1992 , 174, 4275-86	56
1426	Nucleotide sequence, function, activation, and evolution of the cryptic asc operon of Escherichia coli K12. 1992 , 9, 688-706	68
1425	Sequencing and computer time. 1992 , 258, 1421	1
1424	Branched-chain amino acid biosynthesis genes in Lactococcus lactis subsp. lactis. 1992 , 174, 6580-9	110
1423	Characterization of a periplasmic thiol:disulfide interchange protein required for the functional maturation of secreted virulence factors of Vibrio cholerae. 1992 , 89, 6210-4	210
1422	At least five related, but distinct, hepatitis C viral genotypes exist. 1992 , 89, 7144-8	206
1421	Molecular mimicry of hepatitis B surface antigen by an anti-idiotype-derived synthetic peptide. 1992 , 89, 11900-4	56
1420	Parametric sequence comparisons. 1992 , 89, 6090-3	78
1419	Glutamate receptors of Drosophila melanogaster: cloning of a kainate-selective subunit expressed in the central nervous system. 1992 , 89, 10484-8	61
1418	A Bacteroides tetracycline resistance gene represents a new class of ribosome protection tetracycline resistance. 1992 , 36, 1005-12	95
1417	Nucleotide Sequence of the Gene for a Glutathione S-Transferase from Cell Suspension Cultures of Silene cucubalus. 1992 , 99, 1729-31	10
1416	Cloning and characterization of a Candida albicans maltase gene involved in sucrose utilization. 1992 , 174, 6992-6	67
1415	Regulation of secondary metabolism in Streptomyces spp. and overproduction of daunorubicin in Streptomyces peucetius. 1992 , 174, 144-54	157
1414	Phylogeny of five fungus-like protoctistan Phytophthora species, inferred from the internal transcribed spacers of ribosomal DNA. 1992 , 9, 636-53	155
1413	Differences in the E3 regions of the canine adenovirus type 1 and type 2. 1992 , 23, 119-33	21
1412	Dynamic programming algorithms for biological sequence comparison. 1992 , 210, 575-601	53

1411	•	1
1410	Phylogeny of LCR-1 and OXA-5 with class A and class D beta-lactamases. 1992 , 6, 1693-705	129
1409	Computer modeling of two inorganic pyrophosphatases. 1992 , 186, 122-8	5
1408	Exons I and VII of the gene (Ker10) encoding human keratin 10 undergo structural rearrangements within repeats. 1992 , 116, 245-51	1
1407	Sequences from a family of bovine Y-chromosomal repeats. 1992 , 13, 1267-73	29
1406	Comparative anatomy of the primate major histocompatibility complex DR subregion: evidence for combinations of DRB genes conserved across species. 1992 , 14, 340-9	43
1405	Mutations in the UL53 gene of HSV-1 abolish virus neurovirulence to mice by the intracerebral route of infection. 1992 , 26, 99-112	21
1404	Characterization of the allelic differences in the mouse cardiac alpha-myosin heavy chain coding sequence. 1992 , 13, 176-88	29
1403	Cloning, sequencing and expression of the gene encoding the extracellular neutral protease, vibriolysin, of Vibrio proteolyticus. 1992 , 112, 107-12	64
1402	A contig assembly program based on sensitive detection of fragment overlaps. 1992 , 14, 18-25	238
1401	Primary structure and alternative splice variants of gephyrin, a putative glycine receptor-tubulin linker protein. 1992 , 8, 1161-70	280
1400	The beta globin gene cluster of the prosimian primate Galago crassicaudatus: nucleotide sequence determination of the 41-kb cluster and comparative sequence analyses. 1992 , 13, 741-60	27
1399	Predicting de novo the folded structure of proteins. 1992 , 2, 402-412	45
1398	Sequence comparison of the Caenorhabditis elegans dpy-13 and col-34 genes, and their deduced collagen products. 1992 , 120, 261-6	9
1397	A novel zinc finger coiled-coil domain in a family of nuclear proteins. 1992 , 17, 344-5	221
1396	Expression cloning of a diphtheria toxin receptor: identity with a heparin-binding EGF-like growth factor precursor. 1992 , 69, 1051-61	500
1395	Antibody modeling using the conformational search program CONGEN. 1992 , 1, 96-106	23
1394	The yeast FBP26 gene codes for a fructose-2,6-bisphosphatase. 1992 , 31, 7126-33	28

1393	Identification and characterization of a nucleotide binding site on recombinant murine granulocyte/macrophage-colony stimulating factor. 1992 , 3, 484-92		4
1392	Evolutionary relationship of NAD(+)-dependent D-lactate dehydrogenase: comparison of primary structure of 2-hydroxy acid dehydrogenases. 1992 , 184, 60-6		52
1391	Conservation of sequences of subunits of mitochondrial complex I and their relationships with other proteins. 1992 , 1140, 105-34		264
1390	Three-dimensional structure of catalase from Micrococcus lysodeikticus at 1.5 A resolution. 1992 , 312, 127-31		75
1389	Sequence alignment approach to pick up conformationally similar protein fragments. <i>Journal of Molecular Biology</i> , 1992 , 223, 1053-61	5	27
1388	Evaluation of the sequence template method for protein structure prediction. Discrimination of the (beta/alpha)8-barrel fold. <i>Journal of Molecular Biology</i> , 1992 , 228, 170-87	5	32
1387	Genetic and functional analysis of the basic replicon of pPS10, a plasmid specific for Pseudomonas isolated from Pseudomonas syringae patovar savastanoi. <i>Journal of Molecular Biology</i> , 1992 , 223, 415-26.	5	64
1386	Topology fingerprint approach to the inverse protein folding problem. <i>Journal of Molecular Biology</i> , 1992 , 227, 227-38	5	317
1385	Is the bacteriophage lambda lysozyme an evolutionary link or a hybrid between the C and V-type lysozymes? Homology analysis and detection of the catalytic amino acid residues. <i>Journal of Molecular Biology</i> , 1992 , 228, 529-38	5	20
1384	Recognition of distantly related protein sequences using conserved motifs and neural networks. Journal of Molecular Biology, 1992 , 228, 951-62	5	27
1383	Dynamic expression of a cell surface protein during rearrangement of epithelial cells in the Manduca wing monolayer. 1992 , 152, 161-71		12
1382	Approximate matching of network expressions with spacers. 1992 , 372-386		
1381	A macrolide 3-O-acyltransferase gene from the midecamycin-producing species Streptomyces mycarofaciens. 1992 , 174, 5141-4		60
1380	Proline biosynthesis in Saccharomyces cerevisiae: molecular analysis of the PRO1 gene, which encodes gamma-glutamyl kinase. 1992 , 174, 4148-56		23
1379	Nucleotide sequence and transcriptional analysis of activator-regulator proteins for beta-lactamase in Streptomyces cacaoi. 1992 , 174, 2834-42		19
1378	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
1377	What limits affinity maturation of antibodies in Xenopusthe rate of somatic mutation or the ability to select mutants?. 1992 , 11, 4337-4347		136
1376	Dtrk, a Drosophila gene related to the trk family of neurotrophin receptors, encodes a novel class of neural cell adhesion molecule 1992 , 11, 391-404		114

1375	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
1374	A zinc finger protein from Candida albicans is involved in sucrose utilization. 1992 , 174, 222-32	37
1373	Cloning and nucleotide sequence of the leucyl-tRNA synthetase gene of Bacillus subtilis. 1992 , 174, 3928-35	36
1372	References Cited. 1992 , 1205-1286	
1371	Cloning and sequencing of the gene coding for alcohol dehydrogenase of Bacillus stearothermophilus and rational shift of the optimum pH. 1992 , 174, 1397-402	36
1370	Sequences of C mu and the VH1 family in LG7, a clonable strain of Xenopus, homozygous for the immunoglobulin loci. 1992 , 3, 13-24	10
1369	Nucleotide sequence of cDNA clones encoding the beta subunit of mitochondrial ATP synthase from the green alga Chlamydomonas reinhardtii: the precursor protein encoded by the cDNA contains both an N-terminal presequence and a C-terminal extension. 1992 , 19, 771-80	37
1368	Molecular analysis of a cruciferin storage protein gene family of Brassica napus. 1992 , 19, 1049-55	20
1367	An alfalfa (Medicago sativa L.) cDNA encoding an acidic leghemoglobin (MsLb3). 1992 , 20, 733-6	7
1366	Finite-state models in the alignment of macromolecules. 1992 , 35, 77-89	41
1365	The complete mitochondrial DNA sequence of the harbor seal, Phoca vitulina. 1992 , 34, 493-505	181
1364	An evolutionary model for the duplication and divergence of esterase genes in Drosophila. 1992 , 34, 506-21	23
1363	Progressive sequence alignment and molecular evolution of the Zn-containing alcohol dehydrogenase family. 1992 , 34, 522-35	135
1362	The influence of nearest neighbors on the rate and pattern of spontaneous point mutations. 1992 , 34, 189-200	103
1361	Chaos game representation of coding regions of human globin genes and alcohol dehydrogenase genes of phylogenetically divergent species. 1992 , 35, 261-9	17
1360	Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus (family Cricetidae). 1992 , 35, 351-3	3
1359	The refined 1.9-A X-ray crystal structure of D-Phe-Pro-Arg chloromethylketone-inhibited human alpha-thrombin: structure analysis, overall structure, electrostatic properties, detailed active-site geometry, and structure-function relationships. 1992 , 1, 426-71	530
1358	Protein classification artificial neural system. 1992 , 1, 667-77	93

1357	Intron locations and functional deletions in relation to the design and evolution of a subgroup of class I tRNA synthetases. 1992 , 1, 1387-91	20
1356	Fast structure alignment for protein databank searching. 1992 , 14, 139-67	126
1355	Selection of a representative set of structures from Brookhaven Protein Data Bank. 1992 , 14, 265-76	47
1354	Multiple protein sequence alignment from tertiary structure comparison: assignment of global and residue confidence levels. 1992 , 14, 309-23	542
1353	Evolution of structure and function of V-ATPases. 1992 , 24, 415-24	74
1352	Herpesvirus saimiri encodes homologues of G protein-coupled receptors and cyclins. 1992 , 355, 362-5	177
1351	Analysis of two gene regions involved in the expression of the imipenem-specific, outer membrane porin protein OprD ofPseudomonas aeruginosa. 1992 , 97, 267-273	25
1350	Short sequence in L1 region of human papillomaviruses correlates with clinical pictures and grouping by cross-hybridization. 1992 , 83, 315-9	9
1349	Coexistence of multiple codes in messenger RNA molecules. 1992 , 16, 153-163	6
1348	Efficient parallel implementation of sequence analysis algorithms using a global address space model. 1992 , 16, 51-77	
1347	Sequence analysis of eukaryotic retroid proteins. 1992 , 16, 121-136	21
1346	A neural network dynamics that resembles protein evolution. 1992 , 185, 395-401	10
1345	Molecular cloning of the cDNA encoding a receptor tyrosine kinase-related molecule with a catalytic region homologous to c-met. 1992 , 10, 309-14	17
1344	Maximum-likelihood estimation of the statistical distribution of Smith-Waterman local sequence similarity scores. 1992 , 54, 59-75	70
1343	A local algorithm for DNA sequence alignment with inversions. 1992 , 54, 521-36	42
1342	A survey of multiple sequence comparison methods. 1992 , 54, 563-98	75
1341	Poisson, compound Poisson and process approximations for testing statistical significance in sequence comparisons. 1992 , 54, 785-812	27
1340	Stage-specific expression of aldolase isoenzymes in the rodent malaria parasite Plasmodium berghei. 1992 , 52, 15-27	29

1339	Repeat structures in a Plasmodium falciparum protein (MESA) that binds human erythrocyte protein 4.1. 1992 , 50, 335-47	44
1338	Molecular modeling of the 3-D structure of cytochrome P-450scc. 1992 , 1160, 281-6	43
1337	The inference of evolutionary trees from molecular data. 1992 , 102, 643-59	4
1336	Mapping and molecular characterization of a functional thymidine kinase from Amsacta moorei entomopoxvirus. 1992 , 186, 507-16	26
1335	The glycoprotein of Thogoto virus (a tick-borne orthomyxo-like virus) is related to the baculovirus glycoprotein GP64. 1992 , 186, 640-6	77
1334	The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35. 1992 , 186, 770-6	18
1333	Human papillomavirus type 42: new sequences, conserved genome organization. 1992 , 186, 331-4	11
1332	Complete nucleotide sequence of the cloned infectious genome of Junonia coenia densovirus reveals an organization unique among parvoviruses. 1992 , 191, 202-22	53
1331	Amino acid sequence analysis of bovine rotavirus B223 reveals a unique outer capsid protein VP4 and confirms a third bovine VP4 type. 1992 , 191, 291-300	31
1330	Cloned DNA copies of cowpea severe mosaic virus genomic RNAs: infectious transcripts and complete nucleotide sequence of RNA 1. 1992 , 191, 607-18	31
1329	Molecular cloning and nucleotide sequence of a pestivirus genome, noncytopathic bovine viral diarrhea virus strain SD-1. 1992 , 191, 867-9	191
1328	Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence relationships with the flaviviruses and other viruses. 1992 , 187, 573-90	63
1327	Analysis of nucleotide sequence of the rightmost 43 kbp of herpesvirus saimiri (HVS) L-DNA: general conservation of genetic organization between HVS and Epstein-Barr virus. 1992 , 188, 296-310	26
1326	In vivo Paramecium mutants show that calmodulin orchestrates membrane responses to stimuli. 1992 , 13, 413-25	58
1325	Dynamic programming with convexity, concavity and sparsity. 1992 , 92, 49-76	41
1324	Identification and nucleotide sequence of a gene in feline herpesvirus type 1 homologous to the herpes simplex virus gene encoding the glycoprotein B. 1992 , 127, 387-97	23
1323	Determination of cross-linked amino acids in the protein pairs L3🛮 19 and L23ឋ 29 of Bacillus stearothermophilus ribosomes after treatment with diepoxybutane. 1992 , 11, 421-422	1
1322	Amino acid sequence comparison as an aid to determining evolutionary origins. 1992 , 11, 422-422	

1321 Probing the surface of the ribosome with antipeptide-antibodies. **1992**, 11, 422-423

Computer predictions of functional, topogenic, and antigenic domains in human immunodeficiency virus-2 envelope glycoprotein. 1992 , 6, 79-93	4
Phytochrome evolution: a phylogenetic tree with the first complete sequence of phytochrome from a cryptogamic plant (Selaginella martensii spring). 1992 , 56, 751-8	32
Detection and partial sequence of phytochrome genes in the ferns Anemia phyllitidis (L.)Sw (Schizaeaceae) and Dryopteris filix-mas L. (Polypodiaceae) by using polymerase-chain reaction technology. 1992 , 56, 759-63	15
Modeling rhodopsin, a member of G-protein coupled receptors, by computer graphics. Interpretation of chemical shifts of fluorinated rhodopsins. 1992 , 56, 883-93	12
Structural features and sites of expression of a new murine 65 kD and 48 kD hair-related keratin pair, associated with a special type of parakeratotic epithelial differentiation. 1992 , 50, 163-78	26
Phosphatidylinositol-glycan-specific phospholipase D is an amphiphilic glycoprotein that in serum is associated with high-density lipoproteins. 1992 , 206, 747-57	75
1314 Primary structures of ribosomal proteins L3 and L4 from Bacillus stearothermophilus. 1992 , 207, 877-8	5 18
1313 Inhibition of chloroplast ATPase by the K+ channel blocker alpha-dendrotoxin. 1992 , 210, 257-67	2
Cloning and expression of a heat-inducible hsp70 gene in two species of Hydra which differ in their stress response. 1992 , 210, 683-91	45
1311 Amino acid sequences and DP matching: A new method for alignment. 1992 , 63, 139-151	5
Molecular cloning and exon-intron mapping of the gene encoding human transmembrane secretory component (the poly-lg receptor). 1992 , 22, 2309-15	54
1309 Identifying periodic occurences of a template with applications to protein structure. 1993 , 45, 11-18	41
1308 No pain and gain! Experiences with Mentat on a biological application. 1993 , 5, 309-328	9
1307 Tertiary structure of calcineurin B by homology modeling. 1993 , 11, 47-52, 45	8
1306 Computation of biopolymers: a general approach to different problems. 1993 , 30, 1-19	37
1305 A novel method of multiple alignment of biopolymer sequences. 1993 , 30, 65-79	24
1304 Information enhancement methods for large scale sequence analysis. 1993 , 17, 191-201	87

1303	BLAZEEAn implementation of the Smith-Waterman sequence comparison algorithm on a massively parallel computer. 1993 , 17, 203-207	18
1302	General formulation and evaluation of agglomerative clustering methods with metric and non-metric distances. 1993 , 26, 1395-1406	20
1301	A protein alignment scoring system sensitive at all evolutionary distances. 1993 , 36, 290-300	120
1300	The nucleotide sequence of the mitochondrial DNA molecule of the grey seal, Halichoerus grypus, and a comparison with mitochondrial sequences of other true seals. 1993 , 37, 323-30	64
1299	The human complement component C8B gene: structure and phylogenetic relationship. 1993 , 92, 69-75	14
1298	Isolation and sequence analysis of cDNA for the dog T-cell receptor Tcr alpha and Tcr beta chains. 1993 , 38, 60-3	11
1297	Isolation of the DLD gene of Saccharomyces cerevisiae encoding the mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase. 1993 , 238, 315-24	62
1296	Isolation and characterization of a soybean cDNA clone encoding the plastid form of aspartate aminotransferase. 1993 , 21, 993-1009	27
1295	Structure of a cyanobacterial gene encoding the 50S ribosomal protein L9. 1993 , 21, 913-8	5
1294	BARE-1, a copia-like retroelement in barley (Hordeum vulgare L.). 1993 , 22, 829-46	174
1294 1293	BARE-1, a copia-like retroelement in barley (Hordeum vulgare L.). 1993, 22, 829-46 Molecular cloning and functional expression of a Talaromyces emersonii derived alpha-amylase encoding genetic determinant in a human cell line. 1993, 15, 1095-1100	174 O
<i>)</i>	Molecular cloning and functional expression of a Talaromyces emersonii derived alpha-amylase	
1293	Molecular cloning and functional expression of a Talaromyces emersonii derived alpha-amylase encoding genetic determinant in a human cell line. 1993 , 15, 1095-1100 Nucleotide sequence analysis of the 5.8S rDNA and adjacent ITS2 region of Candida albicans and related species. 1993 , 9, 1199-206	0
1293 1292	Molecular cloning and functional expression of a Talaromyces emersonii derived alpha-amylase encoding genetic determinant in a human cell line. 1993 , 15, 1095-1100 Nucleotide sequence analysis of the 5.8S rDNA and adjacent ITS2 region of Candida albicans and related species. 1993 , 9, 1199-206	93
1293 1292 1291 1290	Molecular cloning and functional expression of a Talaromyces emersonii derived alpha-amylase encoding genetic determinant in a human cell line. 1993, 15, 1095-1100 Nucleotide sequence analysis of the 5.8S rDNA and adjacent ITS2 region of Candida albicans and related species. 1993, 9, 1199-206 A homology model of human interferon alpha-2. 1993, 17, 62-74 Structural relationships of homologous proteins as a fundamental principle in homology modeling.	o 93 22
1293 1292 1291 1290	Molecular cloning and functional expression of a Talaromyces emersonii derived alpha-amylase encoding genetic determinant in a human cell line. 1993, 15, 1095-1100 Nucleotide sequence analysis of the 5.8S rDNA and adjacent ITS2 region of Candida albicans and related species. 1993, 9, 1199-206 A homology model of human interferon alpha-2. 1993, 17, 62-74 Structural relationships of homologous proteins as a fundamental principle in homology modeling. 1993, 17, 138-51	o 93 22 81
1293 1292 1291 1290 1289	Molecular cloning and functional expression of a Talaromyces emersonii derived alpha-amylase encoding genetic determinant in a human cell line. 1993, 15, 1095-1100 Nucleotide sequence analysis of the 5.8S rDNA and adjacent ITS2 region of Candida albicans and related species. 1993, 9, 1199-206 A homology model of human interferon alpha-2. 1993, 17, 62-74 Structural relationships of homologous proteins as a fundamental principle in homology modeling. 1993, 17, 138-51 A method to recognize distant repeats in protein sequences. 1993, 17, 391-41	93228159

1205	Nerve growth factor antibodies recognize neurotrophin-3. 1993 , 18, 705-9	12
1284	Sequence and structural homology among membrane-associated domains of CFTR and certain transporter proteins. 1993 , 12, 279-90	19
1283	A novel dimer configuration revealed by the crystal structure at 2.4 A resolution of human interleukin-5. 1993 , 363, 172-6	241
1282	Organization of the genes necessary for hydrogenase expression in Rhodobacter capsulatus. Sequence analysis and identification of two hyp regulatory mutants. 1993 , 8, 15-29	82
1281	Iron-hydroxamate uptake systems in Bacillus subtilis: identification of a lipoprotein as part of a binding protein-dependent transport system. 1993 , 8, 111-21	124
1280	A structural motif in the variant surface glycoproteins of Trypanosoma brucei. 1993 , 362, 603-9	193
1279	Characterization of the diphtheria toxin receptor-binding domain. 1993 , 7, 585-91	5
1278	Bacterial ureases: structure, regulation of expression and role in pathogenesis. 1993 , 9, 907-13	165
1277	Differential processing of the ferritin heavy chain mRNA in human liver and adult human brain. 1993 , 61, 2140-6	10
1276	Microbial hydrogenases: primary structure, classification, signatures and phylogeny. 1993 , 10, 243-69	140
1276 1275	Microbial hydrogenases: primary structure, classification, signatures and phylogeny. 1993 , 10, 243-69 Application of polymerase chain reaction with specific and arbitrary primers to identification and differentiation of Leishmania parasites. 1993 , 114, 99-104	140
,	Application of polymerase chain reaction with specific and arbitrary primers to identification and	
1275	Application of polymerase chain reaction with specific and arbitrary primers to identification and differentiation of Leishmania parasites. 1993 , 114, 99-104 A step towards understanding the folding mechanism of horseradish peroxidase. Tryptophan	23
1275 1274	Application of polymerase chain reaction with specific and arbitrary primers to identification and differentiation of Leishmania parasites. 1993 , 114, 99-104 A step towards understanding the folding mechanism of horseradish peroxidase. Tryptophan fluorescence and circular dichroism equilibrium studies. 1993 , 212, 227-35 Human 4-hydroxyphenylpyruvate dioxygenase. Primary structure and chromosomal localization of	23 73
1275 1274 1273	Application of polymerase chain reaction with specific and arbitrary primers to identification and differentiation of Leishmania parasites. 1993, 114, 99-104 A step towards understanding the folding mechanism of horseradish peroxidase. Tryptophan fluorescence and circular dichroism equilibrium studies. 1993, 212, 227-35 Human 4-hydroxyphenylpyruvate dioxygenase. Primary structure and chromosomal localization of the gene. 1993, 213, 1081-9 Aminotransferases: demonstration of homology and division into evolutionary subgroups. 1993,	237329
1275 1274 1273	Application of polymerase chain reaction with specific and arbitrary primers to identification and differentiation of Leishmania parasites. 1993, 114, 99-104 A step towards understanding the folding mechanism of horseradish peroxidase. Tryptophan fluorescence and circular dichroism equilibrium studies. 1993, 212, 227-35 Human 4-hydroxyphenylpyruvate dioxygenase. Primary structure and chromosomal localization of the gene. 1993, 213, 1081-9 Aminotransferases: demonstration of homology and division into evolutionary subgroups. 1993, 214, 549-61	23 73 29 331
1275 1274 1273 1272	Application of polymerase chain reaction with specific and arbitrary primers to identification and differentiation of Leishmania parasites. 1993, 114, 99-104 A step towards understanding the folding mechanism of horseradish peroxidase. Tryptophan fluorescence and circular dichroism equilibrium studies. 1993, 212, 227-35 Human 4-hydroxyphenylpyruvate dioxygenase. Primary structure and chromosomal localization of the gene. 1993, 213, 1081-9 Aminotransferases: demonstration of homology and division into evolutionary subgroups. 1993, 214, 549-61 Probing the membrane topology of Candida tropicalis cytochrome P450. 1993, 216, 477-85 Cloning, site-specific mutagenesis, expression and characterization of full-length chloroplast	23732933117

1267	A molecular model of the serine protease domain of activated protein C: application to the study of missense mutations causing protein C deficiency. 1993 , 84, 290-300	21
1266	Cloning, nucleotide sequence, and efficient expression of the gene coding for thermostable aldehyde dehydrogenase from Bacillus stearothermophilus, and characterization of the enzyme. 1993, 76, 161-167	11
1265	Cloning and nucleotide sequence of the gene coding for a subunit of the respiratory NADH dehydrogenase from Bacillus stearothermophilus. 1993 , 75, 454-456	2
1264	Recurring structural motifs in proteins with different functions. 1993 , 3, 131-9	43
1263	Structural similarity of DNA-binding domains of bacteriophage repressors and the globin core. 1993 , 3, 141-8	160
1262	Alpha plus beta folds revisited: some favoured motifs. 1993 , 1, 105-20	142
1261	Molecular characterization of a dense granule antigen (Gra 2) associated with the network of the parasitophorous vacuole in Toxoplasma gondii. 1993 , 58, 71-82	71
1260	Cloning and characterization of a bovine alpha interferon receptor. 1993 , 1173, 314-9	18
1259	Comparisons between the 12S rRNA, 16S rRNA, NADH1 and COI genes of sperm and fin whale mitochondrial DNA. 1993 , 21, 115-122	13
1258	A multiple sequence comparison method. 1993 , 55, 465-86	8
1257	Comparative sequence analysis of the coat proteins of biologically distinct citrus tristeza closterovirus isolates. 1993 , 7, 255-64	41
1256	PCR detection of the sheep-associated agent of malignant catarrhal fever. 1993 , 132, 145-59	187
1255	Identification and nucleotide sequence of a gene in feline herpesvirus type 1 homologous to the herpes simplex virus gene encoding the glycoprotein H. 1993 , 132, 183-91	11
1254	De novo and inverse folding predictions of protein structure and dynamics. 1993 , 7, 397-438	69
1253	Protein fold recognition. 1993 , 7, 439-56	63
1252	Boltzmann's principle, knowledge-based mean fields and protein folding. An approach to the computational determination of protein structures. 1993 , 7, 473-501	316
1251	Divergent evolution may link human immunodeficiency virus GP41 to human CD4. 1993 , 36, 448-57	5
1250	Evolution of protein complexity: the blue copper-containing oxidases and related proteins. 1993 , 36, 41-66	140

1249	Phyletic relationships of protein structures based on spatial preference of residues. 1993, 36, 67-78	8
1248	Amino acid sequence similarities between low molecular weight endo-1,4-beta-xylanases and family H cellulases revealed by clustering analysis. 1993 , 321, 135-9	51
1247	cDNA cloning of rat proteasome subunit RC7-I, a homologue of yeast PRE1 essential for chymotrypsin-like activity. 1993 , 332, 52-6	11
1246	Glutamate receptors of Drosophila melanogaster. Primary structure of a putative NMDA receptor protein expressed in the head of the adult fly. 1993 , 324, 171-7	75
1245	Homology of the NifS family of proteins to a new class of pyridoxal phosphate-dependent enzymes. 1993 , 322, 159-64	38
1244	The MAP kinase-activated protein kinase 2 contains a proline-rich SH3-binding domain. 1993 , 336, 143-7	34
1243	T cell receptor delta gene repertoire and diversity of intestinal intraepithelial lymphocytes in athymic mice. 1993 , 30, 813-9	7
1242	Analysis of the nucleotide and derived amino acid sequences of the SsoII restriction endonuclease and methyltransferase. 1993 , 124, 13-9	29
1241	Genetic analysis of a Pseudomonas locus encoding a pathway for biphenyl/polychlorinated biphenyl degradation. 1993 , 130, 47-55	166
1240	FPGA implementation of systolic sequence alignment. 1993 , 183-191	14
1240	FPGA implementation of systolic sequence alignment. 1993 , 183-191 Topology, structure and evolution of two families of proteins involved in antibiotic and antiseptic resistance in eukaryotes and prokaryotesan analysis. 1993 , 124, 1-11	14
	Topology, structure and evolution of two families of proteins involved in antibiotic and antiseptic	
1239	Topology, structure and evolution of two families of proteins involved in antibiotic and antiseptic resistance in eukaryotes and prokaryotesan analysis. 1993 , 124, 1-11 mei-3, a recombination and repair gene of Neurospora crassa, encodes a RecA-like protein. 1993 ,	111
1239	Topology, structure and evolution of two families of proteins involved in antibiotic and antiseptic resistance in eukaryotes and prokaryotesan analysis. 1993 , 124, 1-11 mei-3, a recombination and repair gene of Neurospora crassa, encodes a RecA-like protein. 1993 , 294, 223-34	32
1239 1238 1237	Topology, structure and evolution of two families of proteins involved in antibiotic and antiseptic resistance in eukaryotes and prokaryotesan analysis. 1993, 124, 1-11 mei-3, a recombination and repair gene of Neurospora crassa, encodes a RecA-like protein. 1993, 294, 223-34 Analysing molecular sequences using consensus. 1993, 31, 211-218 Purification, cloning, and cofactor independence of glutamate racemase from Lactobacillus. 1993,	111 32 4
1239 1238 1237 1236	Topology, structure and evolution of two families of proteins involved in antibiotic and antiseptic resistance in eukaryotes and prokaryotesan analysis. 1993, 124, 1-11 mei-3, a recombination and repair gene of Neurospora crassa, encodes a RecA-like protein. 1993, 294, 223-34 Analysing molecular sequences using consensus. 1993, 31, 211-218 Purification, cloning, and cofactor independence of glutamate racemase from Lactobacillus. 1993, 32, 3981-90	111 32 4 101
1239 1238 1237 1236	Topology, structure and evolution of two families of proteins involved in antibiotic and antiseptic resistance in eukaryotes and prokaryotesan analysis. 1993, 124, 1-11 mei-3, a recombination and repair gene of Neurospora crassa, encodes a RecA-like protein. 1993, 294, 223-34 Analysing molecular sequences using consensus. 1993, 31, 211-218 Purification, cloning, and cofactor independence of glutamate racemase from Lactobacillus. 1993, 32, 3981-90 The expected number of matches in optimal global sequence alignments. 1993, 31, 219-230	111 32 4 101 6

1231	Sequence of a gene encoding beta-lactamase from Streptomyces cellulosae. 1993 , 124, 111-4	8
1230	The regional distribution of extracellularly regulated kinase-1 and -2 messenger RNA in the adult rat central nervous system. 1993 , 56, 741-57	49
1229	Two related localized mRNAs from Xenopus laevis encode ubiquitin-like fusion proteins. 1993 , 128, 181-8	78
1228	Molecular evolution of bacterial cell-surface proteins. 1993 , 18, 136-40	54
1227	Chitin synthase-encoding gene(s) of the Zygomycete fungus Phycomyces blakesleeanus. 1993 , 134, 129-34	14
1226	The dacA gene of Bacillus stearothermophilus coding for D-alanine carboxypeptidase: cloning, structure and expression in Escherichia coli and Pichia pastoris. 1993 , 131, 35-41	33
1225	Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes. 1993 , 132, 227-36	49
1224	Not much to malign multalin 4.0. 1993 , 18, 106-107	3
1223	Avian herpesvirus as a live viral vector for the expression of heterologous antigens. 1993 , 11, 349-58	41
1222	Learning and alignment methods applied to protein structure prediction. 1993 , 75, 353-61	4
1221	Phylogeny of immune recognition: fine specificity of fish immune repertoires to cytochrome C. 1993 , 17, 229-40	7
1220	The RING finger. A novel protein sequence motif related to the zinc finger. 1993 , 684, 174-92	382
1219	Cloning of higher plant omega-3 fatty acid desaturases. 1993 , 103, 467-76	252
1218	Molecular characterization of two human autoantigens: unique cDNAs encoding 95- and 160-kD proteins of a putative family in the Golgi complex. 1993 , 178, 49-62	133
1217	Molecular characterization of a kinesin-related antigen of Leishmania chagasi that detects specific antibody in African and American visceral leishmaniasis. 1993 , 90, 775-9	308
1216	MASCOT: multiple alignment system for protein sequences based on three-way dynamic programming. 1993 , 9, 161-7	82
1215	Sequence and distribution of Xenopus laevis E-cadherin transcripts. 1993 , 1, 265-77	9
1214	A Comparison of Spelling-Correction Methods for the Identification of Word Forms in Historical Text Databases. 1993 , 8, 143-152	8

12	213	Identification of coding regions in genomic DNA sequences: an application of dynamic programming and neural networks. 1993 , 21, 607-13	138
12	212	An efficient algorithm to locate all locally optimal alignments between two sequences allowing for gaps. 1993 , 9, 729-34	7
12	211	Algorithms and software tools for ordering clone libraries: application to the mapping of the genome of Schizosaccharomyces pombe. 1993 , 21, 1965-74	66
12	210	An algorithm for the identification of similar oligopeptides between amino acid sequences. 1993 , 9, 93-100	
12	209	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
12	208	Multiple sequence alignment by parallel simulated annealing. 1993 , 9, 267-73	11
12	207	An approach to systematic detection of protein structural motifs. 1993 , 9, 153-9	3
12	206		1
12	205	•	
12	204	Characterization of a new oriental-mustard (Brassica juncea) allergen, Bra j IE: detection of an allergenic epitope. 1993 , 293 (Pt 3), 625-32	91
12	203	•	8
12	202	Defining topological equivalences in protein structures by means of a dynamic programming algorithm. 1993 , 6, 373-6	12
12	201	Molecular biology and evolution of filoviruses. 1993 , 7, 81-100	112
12	200	Changing endonuclease EcoRII Tyr308 to Phe abolishes cleavage but not recognition: possible homology with the Int-family of recombinases. 1993 , 21, 2599-603	32
11	199	Functional homology of protein kinases required for sexual differentiation in Schizosaccharomyces pombe and Saccharomyces cerevisiae suggests a conserved signal transduction module in eukaryotic organisms. 1993 , 4, 107-20	151
11	198	Analysis of DNA sequence data: phylogenetic inference. 1993 , 224, 456-87	80
11	197	The 3' conserved segment of integrons contains a gene associated with multidrug resistance to antiseptics and disinfectants. 1993 , 37, 761-8	241
11	196	Analysis of DNA sequences. 1993 , 2, 225-39	1

1195	Bacterial ice nucleation. 1993 , 34, 203-37	71
1194	Optimal alignment between groups of sequences and its application to multiple sequence alignment. 1993 , 9, 361-70	47
1193	Profile sequence analysis and database searches on a transputer machine connected to a Macintosh computer. 1993 , 9, 25-8	
1192	Multiple alignment of sequences on parallel computers. 1993 , 9, 397-402	1
1191	Transferrin in a cockroach: molecular cloning, characterization, and suppression by juvenile hormone. 1993 , 90, 1320-4	91
1190	Structure-function correlations of calcium binding and calcium channel activities based on 3-dimensional models of human annexins I, II, III, V and VII. 1993 , 10, 1067-89	25
1189	SF-assemblin, the structural protein of the 2-nm filaments from striated microtubule associated fibers of algal flagellar roots, forms a segmented coiled coil. 1993 , 121, 837-45	44
1188	The XylS/AraC family of regulators. 1993 , 21, 807-10	152
1187	Application of Systematic Conformational Search to Protein Modeling. 1993 , 10, 151-174	40
1186	3-Ketoacyl-acyl carrier protein synthase III from spinach (Spinacia oleracea) is not similar to other condensing enzymes of fatty acid synthase. 1993 , 103, 1361-7	54
1185	Multiple antibiotic resistance in Pseudomonas aeruginosa: evidence for involvement of an efflux operon. 1993 , 175, 7363-72	565
1184	Cloning and expression of a member of a new cytochrome P-450 family: cytochrome P-450lin (CYP111) from Pseudomonas incognita. 1993 , 175, 6028-37	26
1183	The sigma 54 bacterial enhancer-binding protein family: mechanism of action and phylogenetic relationship of their functional domains. 1993 , 175, 6067-74	362
1182	Osteoblast-specific factor 2: cloning of a putative bone adhesion protein with homology with the insect protein fasciclin I. 1993 , 294 (Pt 1), 271-8	505
1181	Evolution of the Adh locus in the Drosophila willistoni group: the loss of an intron, and shift in codon usage. 1993 , 10, 605-18	27
1180	Sequence analysis of the beta-N-acetylhexosaminidase gene of Vibrio vulnificus: evidence for a common evolutionary origin of hexosaminidases. 1993 , 90, 6751-5	33
1179	Evidence that facilitative glucose transporters may fold as beta-barrels. 1993 , 90, 11658-62	37
1178	Mycobacterium tuberculosis expresses two chaperonin-60 homologs. 1993 , 90, 2608-12	126

1177	Alteration of a yeast SH3 protein leads to conditional viability with defects in cytoskeletal and budding patterns. 1993 , 13, 5070-84	161
1176	PROTEIN CLASSIFICATION ARTIFICIAL NEURAL SYSTEM: A FILTER PROGRAM FOR DATABASE SEARCH. 1993 ,	
1175	Sequence analysis of teleost retina-specific lactate dehydrogenase C: evolutionary implications for the vertebrate lactate dehydrogenase gene family. 1993 , 90, 242-6	37
1174	A genotype of hepatitis D virus that occurs in northern South America. 1993 , 90, 9016-20	216
1173	Maize mitochondrial manganese superoxide dismutases are encoded by a differentially expressed multigene family. 1993 , 90, 9310-4	71
1172	Differentiation of major genotypes of Giardia intestinalis by polymerase chain reaction analysis of a gene encoding a trophozoite surface antigen. 1993 , 106 (Pt 4), 347-56	38
1171	A small diffusible signal molecule is responsible for the global control of virulence and exoenzyme production in the plant pathogen Erwinia carotovora 1993 , 12, 2467-2476	337
1170	Mutational and functional analysis of dominant SPT2 (SIN1) suppressor alleles in Saccharomyces cerevisiae. 1993 , 13, 5393-407	18
1169	Identification of the transcriptional activator pobR and characterization of its role in the expression of pobA, the structural gene for p-hydroxybenzoate hydroxylase in Acinetobacter calcoaceticus. 1993 , 175, 4499-506	76
1168	Structural genes for thiamine biosynthetic enzymes (thiCEFGH) in Escherichia coli K-12. 1993 , 175, 982-92	97
1167	The plasmid-encoded urease gene cluster of the family Enterobacteriaceae is positively regulated by UreR, a member of the AraC family of transcriptional activators. 1993 , 175, 3459-67	46
1166	Sequence analysis and interposon mutagenesis of the hupT gene, which encodes a sensor protein involved in repression of hydrogenase synthesis in Rhodobacter capsulatus. 1993 , 175, 7404-12	47
1165	L1 A-monomer tandem arrays have expanded during the course of mouse L1 evolution. 1993 , 10, 552-70	22
1164	Molecular evolution of a multigene family in group A streptococci. 1994 , 11, 208-19	50
1163	Cloning and characterization of an autonomous replication sequence from Coxiella burnetii. 1994 , 176, 5233-43	43
1162	Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells with 17 immunoglobulin-like domains 1994 , 13, 4490-4503	197
1161	Phylogenetic and molecular characterization of a 23S rRNA gene positions the genus Campylobacter in the epsilon subdivision of the Proteobacteria and shows that the presence of transcribed spacers is common in Campylobacter spp. 1994 , 176, 4597-609	60
1160	Reading the molecular clock from the decay of internal symmetry of a gene. 1994 , 91, 3413-7	5

1159	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
1158	Cloning and characterization of a c-myc intron binding protein (MIBP1). 1994 , 22, 5679-85	27
1157	Hidden Markov models of biological primary sequence information. 1994 , 91, 1059-63	301
1156	Multiple sequence alignment using simulated annealing. 1994 , 10, 419-26	45
1155	Further improvement in methods of group-to-group sequence alignment with generalized profile operations. 1994 , 10, 379-87	15
1154	A structure-based model for the halophilic adaptation of dihydrofolate reductase from Halobacterium volcanii. 1994 , 7, 213-20	30
1153	Pentapeptide identified as a monoclonal antibody binding site in the serine-protease domain of t-PA. 1994 , 375, 471-80	3
1152	A method for fast database search for all k-nucleotide repeats. 1994 , 22, 4828-36	47
1151	CD and DNA binding studies of a proline repeat-containing segment of the replication arrest protein Tus. 1994 , 22, 5024-30	10
1150	Structure, expression and chromosomal localization of human p80-coilin gene. 1994 , 22, 4462-9	47
1149	Sequence analysis of PER-1 extended-spectrum beta-lactamase from Pseudomonas aeruginosa and comparison with class A beta-lactamases. 1994 , 38, 104-14	129
1148	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
1147	Molecular characterization and tissue distribution of ZO-2, a tight junction protein homologous to ZO-1 and the Drosophila discs-large tumor suppressor protein. 1994 , 124, 949-61	384
1146	Cloning and sequence analysis of the gene for a carbapenem-hydrolyzing class A beta-lactamase, Sme-1, from Serratia marcescens S6. 1994 , 38, 1262-70	155
1145	Characterization and cloning of a receptor for BMP-2 and BMP-4 from NIH 3T3 cells. 1994 , 14, 5961-74	310
1144	A global approach for contig construction. 1994 , 10, 401-8	4
1143	SEQSEE: a comprehensive program suite for protein sequence analysis. 1994 , 10, 121-32	26
1142	Constrained multiple sequence alignment using XALIGN. 1994 , 10, 687-8	10

ADVANCE and ADAM: two algorithms for the analysis of global similarity between homologous informational sequences. **1994**, 10, 3-5

1140	Knowledge-based protein modeling. 1994 , 29, 1-68	174
1139	. 1994,	2
1138		1
1137	Characterization of the gene encoding the A-type inclusion body protein of mousepox virus. 1994 , 8, 125-35	23
1136	A statistical analysis of side-chain conformations in proteins: comparison with ECEPP predictions. 1994 , 13, 283-96	12
1135	Analysis of the introns in genes encoding small G proteins. 1994 , 26, 497-505	20
1134	Molecular evolution of the HSP70 multigene family. 1994 , 38, 1-17	388
1133	Genomic alignment. 1994 , 38, 310-6	14
1132	H-2T24 and PemaT24: orthologous expressed MHC class Ib genes from mouse and Peromyscus maniculatus. 1994 , 39, 412-7	3
1131	Nucleotide composition as a driving force in the evolution of retroviruses. 1994 , 38, 506-32	70
1130	Immunoglobulin light chain class multiplicity and alternative organizational forms in early vertebrate phylogeny. 1994 , 40, 83-99	85
1129	Molecular identification of the ten subunits of cytochrome-c reductase from potato mitochondria. 1994 , 193, 99-106	26
1128	Determinants of the factor IX mutational spectrum in haemophilia B: an analysis of missense mutations using a multi-domain molecular model of the activated protein. 1994 , 94, 594-608	13
1127	A gene from the fungal plant pathogen Nectria haematococca that encodes the phytoalexin-detoxifying enzyme pisatin demethylase defines a new cytochrome P450 family. 1994 , 243, 506-14	68
1126	A dehydrin cognate protein from pea (Pisum sativum L.) with an atypical pattern of expression. 1994 , 26, 805-16	56
1125	Evolutionary relationships among proteins in the phytohemagglutinin-arcelin-alpha-amylase inhibitor family of the common bean and its relatives. 1994 , 26, 1103-13	96
1124	Structure-based identification and clustering of protein families and superfamilies. 1994 , 8, 5-27	41

1123	Protein sequence comparisons: searching databases and aligning sequences. 1994 , 5, 24-8	7
1122	Self-organized neural maps of human protein sequences. 1994 , 3, 507-21	42
1121	The three-dimensional profile method using residue preference as a continuous function of residue environment. 1994 , 3, 687-95	35
1120	Discovering structural correlations in alpha-helices. 1994 , 3, 1847-57	56
1119	Multiple protein structure alignment. 1994 , 3, 1858-70	105
1118	Different protein sequences can give rise to highly similar folds through different stabilizing interactions. 1994 , 3, 1938-44	31
1117	A structural model for the prostate disease marker, human prostate-specific antigen. 1994 , 3, 2033-44	65
1116	Protein structural similarities predicted by a sequence-structure compatibility method. 1994 , 3, 2055-63	54
1115	Residue-residue contact substitution probabilities derived from aligned three-dimensional structures and the identification of common folds. 1994 , 3, 2366-77	16
1114	Structural modeling and electrostatic properties of aspartate transcarbamylase from Saccharomyces cerevisiae. 1994 , 19, 230-43	12
1113	Poly(ADP-ribose) polymerase: structural conservation among different classes of animals and its implications. 1994 , 138, 25-32	23
1112	LYC1 is the structural gene for lysine N-6-acetyl transferase in yeast. 1994 , 25, 24-9	11
1111	The human OX40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen. 1994 , 24, 677-83	115
1110	Molecular cloning of a Drosophila melanogaster gene coding for an homologue of human carboxypeptidase E. 1994 , 27, 169-78	4
1109	On the use of mild hydrophobic interaction chromatography for "method scouting" protein purification strategies in aqueous two-phase systems: a study using model proteins. 1994 , 44, 626-35	14
1108	Sensitive methods for determining the relatedness of proteins with limited sequence homology. 1994 , 5, 361-71	5
1107	The evolution and recognition of protein sequence repeats. 1994 , 18, 233-43	16
1106	Structural model of antagonist and agonist binding to the angiotensin II, AT1 subtype, G protein coupled receptor. 1994 , 1, 211-21	53

1105	. 1994,	1
1104	Approximate string matching using withinword parallelism. 1994 , 24, 337-362	17
1103	The large subunit of the pig heart mitochondrial membrane-bound beta-oxidation complex is a long-chain enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase bifunctional enzyme. 1994 , 109, 557-66	4
1102	Purification, characterization and partial sequencing of the heart fatty acid-binding protein from Bufo arenarum. 1994 , 107, 567-72	4
1101	Analysis of a single-domain P-glycoprotein-like gene in the early-diverging protist Trichomonas vaginalis. 1994 , 66, 127-37	32
1100	Identification and characterization of the developmentally regulated pattern of expression in the testis of a mouse gene exhibiting similarity to the family of phosphodiesterases. 1994 , 1217, 203-6	4
1099	Assessment of homology with the helical mimicry algorithm. 1994 , 1204, 181-8	
1098	Amino-acid sequence of a trypsin/chymotrypsin inhibitor from giant taro (Alocasia macrorrhiza). 1994 , 1204, 189-94	7
1097	Amino-acid sequences of the alpha- and beta-subunits of hemerythrin from Lingula reevii. 1994 , 1208, 277-85	16
1096	CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. 1994 , 22, 4673-80	52822
1095	Studies on molecular evolution and structural features of double-headed inhibitors of hmylase and trypsin in plants. 1994 , 73, 43-54	4
1094	Analysis of sequences of two different classes of kinetoplast DNA minicircles of aLeishmania spp 1994 , 19, 171-182	5
1093	Parametric and ensemble sequence alignment algorithms. 1994 , 56, 743-67	16
1092	Membrane-bound Bacillus cytochromes c and their phylogenetic position among bacterial class I cytochromes c. 1994 , 122, 203-10	23
1091	The large type II 70-kDa keratin of mouse epidermis is the ortholog of human keratin K2e. 1994 , 102, 165-70	16
1090	Issues in searching molecular sequence databases. 1994 , 6, 119-29	691
1089	Protein superfamilies and domain superfolds. 1994 , 372, 631-4	706
1088	The Lactococcus lactis sex-factor aggregation gene cluA. 1994 , 12, 655-63	41

1087	A novel, small endoglucanase gene, egl5, from Trichoderma reesei isolated by expression in yeast. 1994 , 13, 219-28	122
1086	The fimbrial gene cluster of Haemophilus influenzae type b. 1994 , 13, 673-84	68
1085	The functional units of a peptostreptococcal protein L. 1994 , 12, 911-20	22
1084	Non-motile mutants of Helicobacter pylori and Helicobacter mustelae defective in flagellar hook production. 1994 , 14, 691-703	85
1083	The dipeptide permease of Escherichia coli closely resembles other bacterial transport systems and shows growth-phase-dependent expression. 1994 , 14, 1077-92	55
1082	Comparison of two crystal structures of TGF-beta2: the accuracy of refined protein structures. 1994 , 50, 85-92	20
1081	Conservation analysis and structure prediction of the protein serine/threonine phosphatases. Sequence similarity with diadenosine tetraphosphatase from Escherichia coli suggests homology to the protein phosphatases. 1994 , 220, 225-37	143
1080	Characterization and primary structure of amphioxus troponin C. 1994 , 221, 537-46	9
1079	Approximate string matching and local similarity. 1994 , 259-273	35
1078	Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor. 1994 , 76, 793-802	248
1078		248
	gamma receptor. 1994 , 76, 793-802	
1077	gamma receptor. 1994 , 76, 793-802 Comparing nucleotide and protein sequences by linguistic methods. 1994 , 35, 257-72 Isolation, sequence and expression of a cDNA encoding a Class I heat shock protein (HSP17.2) in	5
1077 1076 1075	gamma receptor. 1994, 76, 793-802 Comparing nucleotide and protein sequences by linguistic methods. 1994, 35, 257-72 Isolation, sequence and expression of a cDNA encoding a Class I heat shock protein (HSP17.2) in maize. 1994, 97, 169-175 A basis for new approaches to the chemotherapy of AIDS: novel genes in HIV-1 potentially encode	5
1077 1076 1075	Comparing nucleotide and protein sequences by linguistic methods. 1994, 35, 257-72 Isolation, sequence and expression of a cDNA encoding a Class I heat shock protein (HSP17.2) in maize. 1994, 97, 169-175 A basis for new approaches to the chemotherapy of AIDS: novel genes in HIV-1 potentially encode selenoproteins expressed by ribosomal frameshifting and termination suppression. 1994, 37, 2637-54	5 8 55
1077 1076 1075	Comparing nucleotide and protein sequences by linguistic methods. 1994, 35, 257-72 Isolation, sequence and expression of a cDNA encoding a Class I heat shock protein (HSP17.2) in maize. 1994, 97, 169-175 A basis for new approaches to the chemotherapy of AIDS: novel genes in HIV-1 potentially encode selenoproteins expressed by ribosomal frameshifting and termination suppression. 1994, 37, 2637-54 A New Type of Cytochrome c from Synechocystis PCC6803. 1994, 144, 259-264 Analysis of the yeast NSR1 gene and protein domain comparison between Nsr1 and human hnRNP	5 8 55 27
1077 1076 1075 1074	Comparing nucleotide and protein sequences by linguistic methods. 1994, 35, 257-72 Isolation, sequence and expression of a cDNA encoding a Class I heat shock protein (HSP17.2) in maize. 1994, 97, 169-175 A basis for new approaches to the chemotherapy of AIDS: novel genes in HIV-1 potentially encode selenoproteins expressed by ribosomal frameshifting and termination suppression. 1994, 37, 2637-54 A New Type of Cytochrome c from Synechocystis PCC6803. 1994, 144, 259-264 Analysis of the yeast NSR1 gene and protein domain comparison between Nsr1 and human hnRNP type A1. 1994, 148, 59-66 The p53-associated protein MDM2 contains a newly characterized zinc-binding domain called the	5 8 55 27 3

1069	Schizosaccharomyces malidevorans and Sz. octosporus homologues of Sz. pombe rad9, a gene that mediates radioresistance and cell-cycle progression. 1994 , 150, 281-6	9
1068	The IHF proteins of Rhodobacter capsulatus and Pseudomonas aeruginosa. 1994 , 76, 951-7	10
1067	. 1994,	36
1066	Immunochemical and molecular analysis of antigen binding to lipid anchored and soluble forms of an MHC independent human alpha/beta T cell receptor. 1994 , 31, 857-72	1
1065	Resonance Raman evidence for an Fe-O-Fe center in stearoyl-ACP desaturase. Primary sequence identity with other diiron-oxo proteins. 1994 , 33, 12776-86	186
1064	Sequence alignment and penalty choice. Review of concepts, case studies and implications. <i>Journal of Molecular Biology</i> , 1994 , 235, 1-12	178
1063	Sequencing and expression of the aroA gene from Dichelobacter nodosus. 1994 , 145, 97-101	2
1062	A mouse cDNA encoding a protein with zinc-fingers and a KRAB domain shows similarity to human profilaggrin. 1994 , 149, 299-304	6
1061	RNA sequence analysis using covariance models. 1994 , 22, 2079-88	586
1060	The gene encoding the kappa-carrageenase of Alteromonas carrageenovora is related to beta-1,3-1,4-glucanases. 1994 , 139, 105-9	56
1059	. 1994,	1
1058	Recent developments in linear-space alignment methods: a survey. 1994 , 1, 271-91	37
1057	Motif-biased protein sequence alignment. 1994 , 1, 297-310	11
1056	Prediction and site-specific mutagenesis of residues in transmembrane alpha-helices of proton-pumping nicotinamide nucleotide transhydrogenases from Escherichia coli and bovine heart mitochondria. 1994 , 33, 7691-700	48
1055	Eight histidine residues are catalytically essential in a membrane-associated iron enzyme, stearoyl-CoA desaturase, and are conserved in alkane hydroxylase and xylene monooxygenase. 1994 , 33, 12787-94	649
1054	Pattern recognition metric for comparison of protein structures based on amino acid sequences. 1994 , 240, 667-723	
1053	Cloning and expression in Escherichia coli of a dog thyroid cDNA encoding a novel inositol 1,4,5-trisphosphate 5-phosphatase. 1994 , 300 (Pt 1), 85-90	46
1052	Molecular cloning of the rat analogue of human CD59: structural comparison with human CD59 and identification of a putative active site. 1994 , 304 (Pt 2), 595-601	66

1051 Structural Correlations in Families of Homologous Proteins. **1994**, 669-683

Identification of the pcaRKF gene cluster from Pseudomonas putida: involvement i biodegradation, and transport of 4-hydroxybenzoate. 1994 , 176, 6479-88	n chemotaxis,
1049 Comparative analysis of multiple protein-sequence alignment methods. 1994 , 11, 5	
Organization of the hao gene cluster of Nitrosomonas europaea: genes for two tet cytochromes. 1994 , 176, 3148-53	raheme c 66
$_{ m 1047}$ Computational chemistry and molecular modeling of electron-transfer proteins. 19	994 , 243, 559-607 3
A mutation in the indole-3-acetic acid biosynthesis pathway of Pseudomonas syring affects growth in Phaseolus vulgaris and syringomycin production. 1994 , 176, 1374	gae pv. syringae -82
Human cytoplasmic isoleucyl-tRNA synthetase: selective divergence of the anticod domain and acquisition of a new structural unit. 1994 , 91, 7435-9	on-binding 51
1044 MALIGN: A Multiple Sequence Alignment Program. 1994 , 85, 417-418	127
Src kinase associates with a member of a distinct subfamily of protein-tyrosine photocontaining an ezrin-like domain. 1994 , 91, 7477-81	esphatases 77
Identification and analysis of a Saccharomyces cerevisiae copper homeostasis gene homeodomain protein. 1994 , 14, 7792-804	encoding a
Molecular cloning of bullfrog saxiphilin: a unique relative of the transferrin family to saxitoxin. 1994 , 91, 2478-82	chat binds 68
Neighboring base composition and transversion/transition bias in a comparison of chloroplast noncoding regions. 1995 , 92, 9717-21	rice and maize 88
Safety Assessment of Potatoes Resistant to Colorado Potato Beetle. 1995 , 148-158	3 11
Characterization of honeybee (Apis mellifera L.) chromosomes using repetitive DN. fluorescence in situ hybridization. 1995 , 86, 145-50	A probes and 22
Cloning and functional expression of a Shaker-related voltage-gated potassium characteristics Schistosoma mansoni (Trematoda: Digenea). 1995 , 110 (Pt 2), 171-80	annel gene from 23
Cloning, expression and chromosomal localization of the rat pancreatitis-associate gene. 1995 , 307 (Pt 1), 9-16	d protein III 27
The structure of the quinoprotein alcohol dehydrogenase of Acetobacter aceti more methanol dehydrogenase from Methylobacterium extorquens. 1995 , 308 (Pt 2), 37	
Structure of the quinoprotein glucose dehydrogenase of Escherichia coli modelled methanol dehydrogenase from Methylobacterium extorquens. 1995 , 312 (Pt 3), 67	

[24] Estimation of genetic heterogeneity in primate T-cell lymphoma/leukemia viruses by PCR. **1995**, 358-380

1032 Drug design based on receptor modeling using a system B IOCES [E][1 1995 , 23, 49-81	
The proline-rich P65 protein of Mycoplasma pneumoniae is a component of the Triton X-100-insoluble fraction and exhibits size polymorphism in the strains M129 and FH. 1995 , 177, 3370-8	64
1030 Molecular phylogeny of the red panda (Ailurus fulgens). 1995 , 86, 413-22	38
Predicting coiled coils by use of pairwise residue correlations. 1995 , 92, 8259-63	593
1028 . 1995 , 28, 57-67	26
Phylogenetic Analysis of Seven New Isolates of Ammonia-Oxidizing Bacteria Based on 16S rRNA Gene Sequences. 1995 , 18, 549-559	74
Mutational effects on the spectroscopic properties and biological activities of oxidized bovine adrenodoxin, and their structural implications. 1995 , 231, 226-35	33
Cartography of ribosomal proteins of the 30S subunit from the halophilic Haloarcula marismortui and complete sequence analysis of protein HS26. 1995 , 234, 24-31	3
cDNA Cloning and Characterization of Rat Salivary Glycoproteins. Novel Members of the Proline-Rich-Protein Multigene Families. 1995 , 228, 343-350	
Molecular cloning and sequence of two novel P-type adenosinetriphosphatases from Plasmodium falciparum. 1995 , 227, 214-25	29
1022 A rapid and sensitive method of identification of HTLV-II subtypes. 1995 , 45, 1-9	15
GapIII, a new brain-enriched member of the GTPase-activating protein family. 1995 , 41, 846-58	48
1020 12-Lipoxygenase isoenzymes in mouse skin tumor development. 1995 , 14, 118-29	63
Cloning and expression of a rat placental cDNA encoding a novel cathepsin L-related protein. 1995 , 40, 146-56	18
1018 Cloning of a novel rat placental prolactin-like protein C-related cDNA. 1995 , 41, 167-76	5
String alignment with substitution, insertion, deletion, squashing, and expansion operations. 1995 , 83, 89-107	6
Amino acid sequence of the ribosomal protein HS23 from the halophilic Haloarcula marismortui and homology studies to other ribosomal proteins. 1995 , 14, 189-95	3

1015 Approximate regular expression pattern matching with concave gap penalties. 1995 , 14, 85-121	7
Mitochondrial citrate synthase from potato: predominant expression in mature leaves and young flower buds. 1995 , 196, 756-764	46
1013 Linear-space algorithms that build local alignments from fragments. 1995 , 13, 106-134	19
1012 Super-pattern matching. 1995 , 13, 211-243	15
Existence of two ferredoxin-glutamate synthases in the cyanobacterium Synechocystis sp. PCC 6803. Isolation and insertional inactivation of gltB and gltS genes. 1995 , 27, 753-67	34
1010 Investigating hypothetical products from noncoding frames (HyPNoFs). 1995 , 40, 570-7	2
Different evolutionary histories of kringle and protease domains in serine proteases: a typical example of domain evolution. 1995 , 40, 331-6	26
The size distribution of insertions and deletions in human and rodent pseudogenes suggests the logarithmic gap penalty for sequence alignment. 1995 , 40, 464-73	123
1007 Phylogenetic position of Dictyostelium inferred from multiple protein data sets. 1995 , 41, 238-46	20
Structure-based sequence alignment of elongation factors Tu and G with related GTPases involved in translation. 1995 , 41, 1096	32
Evolution of immunoglobulin heavy chain variable region genes: a VH family can last for 150-200 million years or longer. 1995 , 41, 18-28	33
Mitochondrial citrate synthase from potato: predominant expression in mature leaves and young flower buds. 1995 , 196, 756	
Structural superposition of proteins with unknown alignment and detection of topological similarity using a six-dimensional search algorithm. 1995 , 23, 187-95	55
1002 Evaluation of comparative protein modeling by MODELLER. 1995 , 23, 318-26	930
Assessment of a protein fold recognition method that takes into account four physicochemical properties: side-chain packing, solvation, hydrogen-bonding, and local conformation. 1995 , 23, 370-	5 11
1000 Progress in fold recognition. 1995 , 23, 376-86	86
999 Homology modeling by the ICM method. 1995 , 23, 403-14	139
998 Modeling substrate binding in Thermus thermophilus isopropylmalate dehydrogenase. 1995 , 4, 84-	92 18

997	A three-dimensional model of aromatase cytochrome P450. 1995 , 4, 1065-80	162
996	Gibbs motif sampling: detection of bacterial outer membrane protein repeats. 1995 , 4, 1618-32	333
995	Pseudotorsional OCCO backbone angle as a single descriptor of protein secondary structure. 1995 , 4, 1633-43	9
994	Evidence from sequence information that the interleukin-1 receptor is a transmembrane GTPase. 1995 , 4, 1851-9	15
993	The use of side-chain packing methods in modeling bacteriophage repressor and cro proteins. 1995 , 4, 2300-9	22
992	Paired natural cysteine mutation mapping: aid to constraining models of protein tertiary structure. 1995 , 4, 2405-10	15
991	Evolution of the chaperonin families (Hsp60, Hsp10 and Tcp-1) of proteins and the origin of eukaryotic cells. 1995 , 15, 1-11	247
990	Membrane topology and site-specific mutagenesis of Pseudomonas aeruginosa porin OprD. 1995 , 16, 931-41	54
989	Analysis of the sequence of a new cryptic plasmid, pRJF2, from a rumen bacterium of the genus Butyrivibrio: comparison with other Butyrivibrio plasmids and application in the development of cloning vector. 1995 , 130, 137-43	27
988	Purification and partial characterization of a novel thermophilic carboxylesterase with high mesophilic specific activity. 1995 , 17, 816-25	34
987	Generation of type VIII collagen-specific antibodies. 1995 , 188, 51-62	2
986	Towards understanding the role of the first extracellular loop for the binding of peptide hormones to G-protein coupled receptors. 1995 , 70, 255-62	14
985	Extensive diversity in repeat unit sequences of the cDNA encoding the polyprotein antigen/allergen from the bovine lungworm Dictyocaulus viviparus. 1995 , 72, 77-88	40
984	Molecular cloning of two types of cDNA encoding subunit RC6-I of rat proteasomes. 1995 , 1264, 45-52	15
983	Coupling hundreds of workstations for parallel molecular sequence analysis. 1995 , 25, 291-304	11
982	. 1995,	1
981	A lipopolysaccharide-binding domain of the Campylobacter fetus S-layer protein resides within the conserved N terminus of a family of silent and divergent homologs. 1995 , 177, 1734-41	63
980	Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of lamprey fructose bisphosphate aldolases and the evolution of aldolase genes. 1995 , 117, 545-53	16

979	Nin1p, a regulatory subunit of the 26S proteasome, is necessary for activation of Cdc28p kinase of Saccharomyces cerevisiae 1995 , 14, 3105-3115	75
978	A spontaneous hemadsorption-negative mutant of Mycoplasma pneumoniae exhibits a truncated adhesin-related 30-kilodalton protein and lacks the cytadherence-accessory protein HMW1. 1995 , 177, 843-6	45
977	Characterization of Actinobacillus pleuropneumoniae riboflavin biosynthesis genes. 1995, 177, 7265-70	25
976	Sequence variability within the tobacco retrotransposon Tnt1 population 1995 , 14, 2670-2678	50
975	Expression and kinetic characterization of recombinant human stomach alcohol dehydrogenase. Active-site amino acid sequence explains substrate specificity compared with liver isozymes. 1995 , 270, 3625-30	67
974	Identification and characterization of three members of the human SR family of pre-mRNA splicing factors 1995 , 14, 4336-4349	202
973	Visualization of biological sequence similarity search results.	5
972	Characterization of an LysR family protein, SmeR from Serratia marcescens S6, its effect on expression of the carbapenem-hydrolyzing beta-lactamase Sme-1, and comparison of this regulator with other beta-lactamase regulators. 1995 , 39, 629-37	41
971	A variant of the alpha 2 subunit of soluble guanylyl cyclase contains an insert homologous to a region within adenylyl cyclases and functions as a dominant negative protein. 1995 , 270, 21109-13	60
970	The use of graph theoretical methods for the comparison of the structures of biological macromolecules. 1995 , 73-103	6
969	Site-Specific Inactivation of Bacterial Genes Involved in Plant Rotting. 1995 , 9, 14-28	
968	Computational Techniques in Macromolecular Structural Analysis. 1995 , 433-490	1
967	Systolic Implementation of Smith and Waterman Algorithm on a SIMD Coprocessor. 1995 , 155-166	1
966	Deregulation of translational control of the 65-kDa regulatory subunit (PR65 alpha) of protein phosphatase 2A leads to multinucleated cells. 1995 , 270, 21374-81	39
965	Sequence analysis of sarcosine oxidase and nearby genes reveals homologies with key enzymes of folate one-carbon metabolism. 1995 , 270, 18252-9	66
964	The molecular basis of ornithine transcarbamylase deficiency: modelling the human enzyme and the effects of mutations. 1995 , 32, 680-8	37
963	A heuristic approach to RNA secondary structure prediction. 1995 ,	
962	Structural basis for the extreme thermostability of D-glyceraldehyde-3-phosphate dehydrogenase from Thermotoga maritima: analysis based on homology modelling. 1995 , 8, 779-89	25

961	Murine transcription factor alpha A-crystallin binding protein I. Complete sequence, gene structure, expression, and functional inhibition via antisense RNA. 1995 , 270, 1221-9	36
960	The Sry-related HMG box-containing gene Sox6 is expressed in the adult testis and developing nervous system of the mouse. 1995 , 23, 3365-72	132
959	Delineation of the minimal hepatitis B surface antigen-specific B- and T-cell epitope contained within an anti-idiotype-derived pentadecapeptide. 1995 , 92, 1575-9	12
958	A reliable sequence alignment method based on probabilities of residue correspondences. 1995 , 8, 999-1009	68
957	C2, and unusual filamentous bacterial virus: protein sequence and conformation, DNA size and conformation, and nucleotide/subunit ratio. 1995 , 34, 4077-87	5
956	Altering the regiospecificity of androstenedione hydroxylase activity in P450s 2a-4/5 by a mutation of the residue at position 481. 1995 , 34, 5054-9	21
955	Human alanyl-tRNA synthetase: conservation in evolution of catalytic core and microhelix recognition. 1995 , 34, 10340-9	33
954	Three-dimensional structure of butyryl-CoA dehydrogenase from Megasphaera elsdenii. 1995 , 34, 2163-71	97
953	Statistics of sequence-structure threading. 1995 , 5, 236-44	127
952	Primary sequence determination and molecular modelling of the variable region of an antiMUC1 mucin monoclonal antibody. 1995 , 31A, 214-21	2
951	Cloning, sequencing and expression of serine/threonine kinase-encoding genes from Streptomyces coelicolor A3(2). 1995 , 153, 99-104	50
950	Identification of a fliG homologue in Treponema denticola. 1995 , 161, 69-73	10
949	The upstream region of the SP-B gene: intrinsic promoter activity and glucocorticoid responsiveness related to a new DNA-binding protein. 1995 , 165, 285-90	2
948	Tyrosine phosphorylation of the tetragonal paracrystalline array of Aeromonas hydrophila: molecular cloning and high-level expression of the S-layer protein gene. <i>Journal of Molecular</i> 6.5 <i>Biology</i> , 1995 , 245, 568-81	45
947	Identification and analysis of multigene families by comparison of exon fingerprints. <i>Journal of Molecular Biology</i> , 1995 , 249, 342-59	26
946	An assessment of amino acid exchange matrices in aligning protein sequences: the twilight zone revisited. <i>Journal of Molecular Biology</i> , 1995 , 249, 816-31	154
945	Prediction of protein three-dimensional structures in insertion and deletion regions: a procedure for searching data bases of representative protein fragments using geometric scoring criteria. 6.5 Journal of Molecular Biology, 1995, 253, 114-31	107
944	Detection of alpha/beta-hydrolase fold in the cell surface esterases of Acinetobacter species using an analysis of 3D profiles. 1995 , 371, 231-5	6

943	Cloning and sequencing of a human thioredoxin reductase. 1995 , 373, 5-9	163
942	Protein sequence randomness and sequence/structure correlations. 1995 , 68, 1531-9	11
941	Searching for Representations to Improve Protein Sequence Fold-Class Prediction. 1995 , 21, 151-175	
940	Computer manipulation of DNA and protein sequences. 2001 , Chapter 7, Unit7.7	1
939	Genome analysis: Pattern search in biological macromolecules. 1995 , 261-285	5
938	Computational methods for protein sequence analysis. 2001 , Chapter 2, Unit2.1	
937		
936		
935	EEA1, an early endosome-associated protein. EEA1 is a conserved alpha-helical peripheral membrane protein flanked by cysteine "fingers" and contains a calmodulin-binding IQ motif. 1995 , 270, 13503-11	582
934	Searching for representations to improve protein sequence fold-class prediction. 1995 , 21, 151-175	1
933	Cornering and catching the common protein fold. 1995 , 1, 188-94	4
932	Detection of related positive-strand RNA virus genomes by reverse transcription/polymerase chain reaction using degenerate primers for common replicase sequences. 1995 , 39, 365-75	9
931	Differential glycosylation of the ectodomain of the primary envelope glycoprotein of two strains of lactate dehydrogenase-elevating virus that differ in neuropathogenicity. 1995 , 39, 331-40	13
930	Molecular dynamics simulation of fungal cellulose-binding domains: differences in molecular rigidity but a preserved cellulose binding surface. 1995 , 8, 443-50	41
929	Using CLUSTAL for multiple sequence alignments. 1996 , 266, 383-402	1239
928	Novel approaches to vaccine development against HBV. 1996 , 44, 67-73	11
927	A faster algorithm for approximate string matching. 1996 , 1-23	20
926	Homology modeling of metabotropic glutamate receptors. (mGluRs) structural motifs affecting binding modes and pharmacological profile of mGluR1 agonists and competitive antagonists. 1996 , 39, 3998-4006	55

925	A segment-based dynamic programming algorithm for predicting gene structure. 1996 , 3, 375-94		9
924	A mouse kidney- and liver-expressed cDNA having homology with a prokaryotic parathion hydrolase (phosphotriesterase)-encoding gene: abnormal expression in injured and polycystic kidneys. 1996 , 168, 157-63		18
923	Cloning and characterization of the Saccharomyces cerevisiae C-22 sterol desaturase gene, encoding a second cytochrome P-450 involved in ergosterol biosynthesis. 1996 , 169, 105-9		95
922	A general method for fast multiple sequence alignment. 1996 , 172, GC33-41		19
921	The restriction-modification system of Pasteurella haemolytica is a member of a new family of type I enzymes. 1996 , 178, 89-96		24
920	Long pentraxins: an emerging group of proteins with diverse functions. 1996 , 7, 191-202		123
919	Cloning, sequencing and immunological characterization of Dac g 3, a major allergen from Dactylis glomerata pollen. 1996 , 33, 797-806		18
918	A variable region of Anticarsia gemmatalis nuclear polyhedrosis virus contains tandemly repeated DNA sequences. 1996 , 41, 123-32		47
917	Searching for a family of orphan sequences with SAMBA, a parallel hardware dedicated to biological applications. 1996 , 78, 311-4		3
916	Automated biostratigraphic correlation of palynological records on the basis of shapes of pollen curves and evaluation of next-best solutions. 1996 , 124, 17-37		4
915	Sequence, genomic organization, and chromosomal localization of the human LPAP (PTPRCAP) and mouse CD45-AP/LSM-1 genes. 1996 , 38, 79-83		6
914	Residue-residue potentials with a favorable contact pair term and an unfavorable high packing density term, for simulation and threading. <i>Journal of Molecular Biology</i> , 1996 , 256, 623-44	6.5	988
913	Energy functions that discriminate X-ray and near native folds from well-constructed decoys. <i>Journal of Molecular Biology</i> , 1996 , 258, 367-92	6.5	348
912	A surface of minimum area metric for the structural comparison of proteins. <i>Journal of Molecular Biology</i> , 1996 , 258, 871-92	6.5	53
911	Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium falciparum. <i>Journal of Molecular Biology</i> , 1996 , 261, 155-72	6.5	473
910	Significant improvement in accuracy of multiple protein sequence alignments by iterative refinement as assessed by reference to structural alignments. <i>Journal of Molecular Biology</i> , 1996 , 264, 823-38	6.5	257
909	Molecular cloning and expression of mouse procalcitonin. 1996 , 226, 420-5		13
908	Acasp, a gene encoding a cathepsin D-like aspartic protease from the hookworm Ancylostoma caninum. 1996 , 227, 294-302		45

907	Cloning and sequence analysis of the dimethylsulfoxide reductase structural gene from Rhodobacter capsulatus. 1996 , 1276, 176-80	24
906	A structure-based model for cytochrome P450cam-putidaredoxin interactions. 1996 , 78, 723-33	105
905	Cloning and nucleotide sequence analysis of the Streptococcus mutans membrane-bound, proton-translocating ATPase operon. 1996 , 183, 87-96	46
904	Near-optimal sequence alignment. 1996 , 6, 346-52	38
903	Uracil metabolismUMP synthesis from orotic acid or uridine and conversion of uracil to beta-alanine: enzymes and cDNAs. 1996 , 53, 1-78	62
902	Local alignment statistics. 1996 , 266, 460-80	473
901	Enlarged similarity of nucleic acid sequences. 1996 , 3, 157-64	6
900	Determining divergence times of the major kingdoms of living organisms with a protein clock. 1996 , 271, 470-7	495
899	A subfamily of P-type ATPases with aminophospholipid transporting activity. 1996 , 272, 1495-7	434
898	The hexose transporter family of Saccharomyces cerevisiae. 1996 , 166, 283-92	223
897	Genomic organization of a mouse MHC class II region including the H2-M and Lmp2 loci. 1996 , 43, 204-14	15
896	. 1996 , 7, 425-438	6
895	Kestrel: a programmable array for sequence analysis.	3
894	Nucleotide Structure and Characterization of the Murine Blood Coagulation Factor VII Gene. 1996 , 76, 0957-0964	6
893	Identification of a third secondary carrier (DcuC) for anaerobic C4-dicarboxylate transport in Escherichia coli: roles of the three Dcu carriers in uptake and exchange. 1996 , 178, 7241-7	65
892	Autoregulation of the plasmid addiction operon of bacteriophage P1. 1996 , 271, 18705-10	65
891	Multiple DNA and protein sequence alignment based on segment-to-segment comparison. 1996 , 93, 12098-103	239
890	The expressed protein in glyphosate-tolerant soybean, 5-enolpyruvylshikimate-3-phosphate synthase from Agrobacterium sp. strain CP4, is rapidly digested in vitro and is not toxic to acutely gavaged mice. 1996 , 126, 728-40	124

889	Approaches to detection of distantly related proteins by database searches. 1996 , 21, 1118-22, 1124-5	3
888	Neuroserpin, an axonally secreted serine protease inhibitor 1996 , 15, 2944-2953	141
887	A Wzz (Cld) protein determines the chain length of K lipopolysaccharide in Escherichia coli O8 and O9 strains. 1996 , 178, 1903-7	40
886	Integration of multiple repeats of geminiviral DNA into the nuclear genome of tobacco during evolution. 1996 , 93, 759-64	144
885	The catalytic domain of acanthamoeba myosin I heavy chain kinase. II. Expression of active catalytic domain and sequence homology to p21-activated kinase (PAK). 1996 , 271, 27056-62	50
884	Identification of Agrobacterium tumefaciens genes that direct the complete catabolism of octopine. 1996 , 178, 1872-80	35
883	Ti plasmid-encoded genes responsible for catabolism of the crown gall opine mannopine by Agrobacterium tumefaciens are homologs of the T-region genes responsible for synthesis of this opine by the plant tumor. 1996 , 178, 3275-84	44
882	The intracellular domain of the second chain of the interferon-gamma receptor is interchangeable between species. 1996 , 16, 1039-45	9
881	Large-scale search for genes on which positive selection may operate. 1996 , 13, 685-90	320
880	DNA Sequence Alignment and Critical Phenomena. 1996 , 463, 75	
880 879	DNA Sequence Alignment and Critical Phenomena. 1996, 463, 75 BRO1, a novel gene that interacts with components of the Pkc1p-mitogen-activated protein kinase pathway in Saccharomyces cerevisiae. 1996, 16, 2585-93	67
	BRO1, a novel gene that interacts with components of the Pkc1p-mitogen-activated protein kinase	67 202
879	BRO1, a novel gene that interacts with components of the Pkc1p-mitogen-activated protein kinase pathway in Saccharomyces cerevisiae. 1996 , 16, 2585-93	,
879 878	BRO1, a novel gene that interacts with components of the Pkc1p-mitogen-activated protein kinase pathway in Saccharomyces cerevisiae. 1996 , 16, 2585-93 Molecular cloning and characterization of the human anaphylatoxin C3a receptor. 1996 , 271, 20231-4 A Bacteroides thetaiotaomicron outer membrane protein that is essential for utilization of	202
879 878 877	BRO1, a novel gene that interacts with components of the Pkc1p-mitogen-activated protein kinase pathway in Saccharomyces cerevisiae. 1996, 16, 2585-93 Molecular cloning and characterization of the human anaphylatoxin C3a receptor. 1996, 271, 20231-4 A Bacteroides thetaiotaomicron outer membrane protein that is essential for utilization of maltooligosaccharides and starch. 1996, 178, 823-30 Two glycosyltransferase genes, lgtF and rfaK, constitute the lipooligosaccharide ice (inner core	202
879 878 877 876	BRO1, a novel gene that interacts with components of the Pkc1p-mitogen-activated protein kinase pathway in Saccharomyces cerevisiae. 1996, 16, 2585-93 Molecular cloning and characterization of the human anaphylatoxin C3a receptor. 1996, 271, 20231-4 A Bacteroides thetaiotaomicron outer membrane protein that is essential for utilization of maltooligosaccharides and starch. 1996, 178, 823-30 Two glycosyltransferase genes, lgtF and rfaK, constitute the lipooligosaccharide ice (inner core extension) biosynthesis operon of Neisseria meningitidis. 1996, 178, 6677-84 p-Cumate catabolic pathway in Pseudomonas putida Fl: cloning and characterization of DNA	202 120 57
879 878 877 876	BRO1, a novel gene that interacts with components of the Pkc1p-mitogen-activated protein kinase pathway in Saccharomyces cerevisiae. 1996, 16, 2585-93 Molecular cloning and characterization of the human anaphylatoxin C3a receptor. 1996, 271, 20231-4 A Bacteroides thetaiotaomicron outer membrane protein that is essential for utilization of maltooligosaccharides and starch. 1996, 178, 823-30 Two glycosyltransferase genes, lgtF and rfaK, constitute the lipooligosaccharide ice (inner core extension) biosynthesis operon of Neisseria meningitidis. 1996, 178, 6677-84 p-Cumate catabolic pathway in Pseudomonas putida Fl: cloning and characterization of DNA carrying the cmt operon. 1996, 178, 1351-62 Effect of regulatory protein levels on utilization of starch by Bacteroides thetaiotaomicron. 1996,	202 120 57 103

871	Combined DNA and protein alignment. 1996 , 266, 402-18	21
870	Discrimination of common protein folds: application of protein structure to sequence/structure comparisons. 1996 , 266, 575-98	43
869	Three-dimensional profiles for measuring compatibility of amino acid sequence with three-dimensional structure. 1996 , 266, 598-616	11
868	Chloroplastic aspartate aminotransferase from Arabidopsis thaliana: an examination of the relationship between the structure of the gene and the spatial structure of the protein. 1996 , 319 (Pt 3), 969-76	17
867	Molecular cloning and expression in COS-1 cells of pig kidney aminopeptidase P. 1996 , 319 (Pt 1), 197-201	21
866	A Ti plasmid-encoded enzyme required for degradation of mannopine is functionally homologous to the T-region-encoded enzyme required for synthesis of this opine in crown gall tumors. 1996 , 178, 3285-92	28
865	ORK1, a potassium-selective leak channel with two pore domains cloned from Drosophila melanogaster by expression in Saccharomyces cerevisiae. 1996 , 93, 13256-61	159
864	Amino acid sequence of catechol 1,2-dioxygenase (pyrocatechase) isozyme alpha alpha from Pseudomonas arvilla C-1. 1996 , 39, 781-8	
863	A non-local gap-penalty for profile alignment. 1996 , 58, 1-18	4
862	Carboxy-terminal sequence divergence and processing of the polyprotein antigen from Dirofilaria immitis. 1996 , 82, 51-65	23
861	Cloning and sequence analysis of a hypothalamic cDNA encoding a D1c dopamine receptor in tilapia. 1996 , 1308, 17-22	9
860	Use of the intestinal and hepatic bile acid transporters for drug delivery. 1996 , 20, 59-82	22
859	Cloning, nucleotide sequence, and characterization of the genes encoding enzymes involved in the degradation of cumene to 2-hydroxy-6-oxo-7-methylocta-2,4-dienoic acid in Pseudomonas fluorescens IP01. 1996 , 81, 187-196	46
858	Conservation of neutralizing determinants between the sporozoite surface antigens of Theileria annulata and Theileria parva. 1996 , 82, 229-41	24
857	Characterization of two new preproGnRH mRNAs in the tree shrew: first direct evidence for mesencephalic GnRH gene expression in a placental mammal. 1996 , 104, 7-19	101
856	Computer-Aided Receptor Modelling of Human Opioid Receptors: (Mu, Kappa & Delta). 1996 , 2, 362-369	7
855	A non-local gap-penalty for profile alignment. 1996 , 58, 1-18	
854	Prediction of the three-dimensional structure of the rap-1A protein from its homology to the ras-gene-encoded p21 protein. 1996 , 15, 11-5	5

853	Computational sequence analysis of matrix metalloproteinases. 1996 , 15, 137-60	95
852	Identification and analysis of the simian varicella virus thymidine kinase gene. 1996 , 141, 43-55	11
851	Genomic organization of a mouse MHC class II region including the H2-M and Lmp2 loci. 1996 , 43, 204-214	15
850	Organization and chromosomal localization of a B1-like containing repeat of Microtus subarvalis. 1996 , 7, 593-7	21
849	Analysis of the amino acid sequences of plant Bowman-Birk inhibitors. 1996 , 42, 560-9	88
848	Characterization of the human small-ribosomal-subunit proteins by N-terminal and internal sequencing, and mass spectrometry. 1996 , 239, 144-9	52
847	cDNA cloning and functional analysis of the p97 subunit of the 26S proteasome, a polypeptide identical to the type-1 tumor-necrosis-factor-receptor-associated protein-2/55.11. 1996 , 239, 912-21	47
846	Crystallization and crystal packing of recombinant 3 (or 17) beta-hydroxysteroid dehydrogenase from Comamonas testosteroni ATTC 11996. 1996 , 236, 144-8	13
845	OPTIMIZATION ALIGNMENT: THE END OF MULTIPLE SEQUENCE ALIGNMENT IN PHYLOGENETICS?. 1996 , 12, 1-9	541
844	A prespore-specific gene of Dictyostelium discoideum encodes the small subunit of ribonucleotide reductase. 1996 , 1309, 100-8	10
843	Optimum superimposition of protein structures: ambiguities and implications. 1996 , 1, 123-32	112
842	From secondary structure to three-dimensional structure: Improved dihedral angle probability distribution function for use with energy searches for native structures of polypeptides and proteins. 1996 , 17, 1453-1480	2
841	Accessing the Kabat antibody sequence database by computer. 1996 , 25, 130-3	77
840	A protein structure comparison methodology. 1996 , 20, 359-380	37
839	Structural basis of p21H-ras molecular switch inhibition by a neutralizing antibody. 1996 , 14, 42-50, 28-9	1
838	Nonoverlapping local alignments (weighted independent sets of axis-parallel rectangles). 1996 , 71, 41-53	45
837	Structure and function of the Bacillus SpoIIE protein and its localization to sites of sporulation septum assembly. 1996 , 19, 1047-60	94
836	Definition of a consensus DNA-binding site for the Escherichia coli pleiotropic regulatory protein, FruR. 1996 , 21, 257-66	33

835	A flexible motif search technique based on generalized profiles. 1996 , 20, 3-23	228
834	Evolutionary algorithms in computer-aided molecular design. 1996 , 10, 337-58	102
833	Extremely thermostable L(+)-lactate dehydrogenase from Thermotoga maritima: cloning, characterization, and crystallization of the recombinant enzyme in its tetrameric and octameric state. 1996 , 5, 862-73	17
832	Protein fold recognition using sequence-derived predictions. 1996 , 5, 947-55	279
831	Self-consistently optimized statistical mechanical energy functions for sequence structure alignment. 1996 , 5, 1043-59	63
830	The 1.8-A X-ray structure of the Escherichia coli PotD protein complexed with spermidine and the mechanism of polyamine binding. 1996 , 5, 1984-90	50
829	A partial sequence for nitric oxide synthase from a goldfish (Carassius auratus) macrophage cell line. 1996 , 74, 374-9	47
828	ABGEN: a knowledge-based automated approach for antibody structure modeling. 1996 , 14, 323-8	45
827	Statistical Analysis of Protein Sequences. 1996 , 121-160	2
826	cDNA cloning and characterization of a novel nucleolar protein. 1996 , 7, 1015-24	60
826 825	cDNA cloning and characterization of a novel nucleolar protein. 1996 , 7, 1015-24 Controlling substrate preference and transglycosylation activity of neopullulanase by manipulating steric constraint and hydrophobicity in active center. 1996 , 271, 17321-9	60
	Controlling substrate preference and transglycosylation activity of neopullulanase by manipulating	
825	Controlling substrate preference and transglycosylation activity of neopullulanase by manipulating steric constraint and hydrophobicity in active center. 1996 , 271, 17321-9 Human placental leucine aminopeptidase/oxytocinase. A new member of type II	63
825 824	Controlling substrate preference and transglycosylation activity of neopullulanase by manipulating steric constraint and hydrophobicity in active center. 1996, 271, 17321-9 Human placental leucine aminopeptidase/oxytocinase. A new member of type II membrane-spanning zinc metallopeptidase family. 1996, 271, 56-61 Receptor recognition and specificity of interleukin-8 is determined by residues that cluster near a	63
825 824 823	Controlling substrate preference and transglycosylation activity of neopullulanase by manipulating steric constraint and hydrophobicity in active center. 1996, 271, 17321-9 Human placental leucine aminopeptidase/oxytocinase. A new member of type II membrane-spanning zinc metallopeptidase family. 1996, 271, 56-61 Receptor recognition and specificity of interleukin-8 is determined by residues that cluster near a surface-accessible hydrophobic pocket. 1996, 271, 8228-35 Relationship between thermal stability and 3-D structure in a homology model of	63 156 58
825 824 823	Controlling substrate preference and transglycosylation activity of neopullulanase by manipulating steric constraint and hydrophobicity in active center. 1996, 271, 17321-9 Human placental leucine aminopeptidase/oxytocinase. A new member of type II membrane-spanning zinc metallopeptidase family. 1996, 271, 56-61 Receptor recognition and specificity of interleukin-8 is determined by residues that cluster near a surface-accessible hydrophobic pocket. 1996, 271, 8228-35 Relationship between thermal stability and 3-D structure in a homology model of 3-isopropylmalate dehydrogenase from Escherichia coli. 1996, 9, 663-70 Hypothesis for a serine proteinase-like domain at the COOH terminus of Slowpoke	63 156 58
825 824 823 822	Controlling substrate preference and transglycosylation activity of neopullulanase by manipulating steric constraint and hydrophobicity in active center. 1996, 271, 17321-9 Human placental leucine aminopeptidase/oxytocinase. A new member of type II membrane-spanning zinc metallopeptidase family. 1996, 271, 56-61 Receptor recognition and specificity of interleukin-8 is determined by residues that cluster near a surface-accessible hydrophobic pocket. 1996, 271, 8228-35 Relationship between thermal stability and 3-D structure in a homology model of 3-isopropylmalate dehydrogenase from Escherichia coli. 1996, 9, 663-70 Hypothesis for a serine proteinase-like domain at the COOH terminus of Slowpoke calcium-activated potassium channels. 1996, 108, 473-84	63 156 58 11

[1996-1996]

817	analysis of its yeast homologue, sen3p. 1996 , 7, 853-70	49
816	Extreme sequence heteroplasmy in bat mitochondrial DNA. 1996 , 377, 661-7	17
815	Platypus insulin: indications from the amino acid sequence of significant differences in structure from porcine insulin. 1996 , 377, 147-53	2
814	Purification, characterization, and partial amino acid sequencing of an amphibian liver fatty acid binding protein. 1996 , 74, 109-15	25
813	Progressive multiple alignment with constraints. 1996 , 3, 563-72	22
812	An algorithm for finding maximal common subtopologies in a set of protein structures. 1996 , 3, 289-306	87
811	Similarity detection and localization. 1996 , 76, 2591-2594	57
810	Progressive alignment of amino acid sequences and construction of phylogenetic trees from them. 1996 , 266, 368-82	87
809	High-speed automated DNA sequencing in ultrathin slab gels. 1996 , 271, 219-37	4
808	Approximate matching of network expressions with spacers. 1996 , 3, 33-51	19
807	A graph theoretic approach to the analysis of DNA sequencing data. 1996 , 6, 80-91	30
806	Structural alignments of P450s and extrapolations to the unknown. 1996 , 272, 315-26	64
805	Fast and sound two-step algorithms for multiple alignment of nucleic sequences.	1
804	Cell adhesion molecules NgCAM and axonin-1 form heterodimers in the neuronal membrane and cooperate in neurite outgrowth promotion. 1996 , 135, 1593-607	114
803	The tight junction protein ZO-2 contains three PDZ (PSD-95/Discs-Large/ZO-1) domains and an alternatively spliced region. 1996 , 271, 25723-6	86
802	Glutathione-independent prostaglandin D synthase as a lead molecule for designing new functional proteins. 1996 , 9, 1067-82	40
801	Evolutionary Relationships of Chaperonins. 1996 , 27-64	14
800	Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes. 1996 , 24, 628-39	42

799 Genomanalyse und WWW: Vom Klon zum Klick. 1996, 38, 8-15

798	Detection of non-topological motifs in protein structures. 1996 , 9, 1103-19	28
797	Modeling Drug R eceptor Interactions. 1996 , 235-336	10
796	Converting sequence block alignments into structural insights. 1996 , 266, 662-80	3
795	The Molecular Structure of P450S: The Conserved and the Variable Elements. 1996 , 14, 57-79	2
794	Characterization of the cholecystokinin and gastrin genes from the bullfrog, Rana catesbeiana: evolutionary conservation of primary and secondary sites of gene expression. 1997 , 138, 1719-27	35
793	Cloning of the functional promoter for human insulin-like growth factor binding protein-4 gene: endogenous regulation. 1997 , 138, 332-43	23
792	Kestrel: design of an 8-bit SIMD parallel processor.	7
791	Sequence comparison using a relational database approach.	
790	Extracting protein alignment models from the sequence database. 1997 , 25, 1665-77	178
789	Human lysyl-tRNA synthetase accepts nucleotide 73 variants and rescues Escherichia coli double-defective mutant. 1997 , 272, 22809-16	65
788	Comparative analysis of the genomes of the bacteria Mycoplasma pneumoniae and Mycoplasma genitalium. 1997 , 25, 701-12	225
787	Protein distance constraints predicted by neural networks and probability density functions. 1997 , 10, 1241-8	104
786	Activated levels of rRNA synthesis in fission yeast are driven by an intergenic rDNA region positioned over 2500 nucleotides upstream of the initiation site. 1997 , 25, 659-67	15
785	Sequence and RFLP analysis of the elongation factor Tu gene used in differentiation and classification of phytoplasmas. 1997 , 143 (Pt 10), 3381-3389	153
7 ⁸ 4	A bank of protein family patterns for rapid identification of possible functions of amino acid sequences. 1997 , 13, 115-22	
783	The deferred path heuristic for the generalized tree alignment problem. 1997 , 4, 415-31	13
782	RAGA: RNA sequence alignment by genetic algorithm. 1997 , 25, 4570-80	86

781	Genetic Engineering and Design Problems. 1997 , 47-68	17
780	Reduced space sequence alignment. 1997 , 13, 45-53	20
779	A comparative study of duplications in bacteria and eukaryotes: the importance of telomeres. 1997 , 14, 1062-74	52
778	SEQMAN. 1997 , 75-89	49
777	Expression cloning and characterization of ROAT1. The basolateral organic anion transporter in rat kidney. 1997 , 272, 30088-95	337
776	Use of site-directed chemical modification to study an essential lysine in Escherichia coli leader peptidase. 1997 , 272, 9994-10003	66
775	Multiple Sequence Alignment. 1997 , 165-183	3
774	Sequence alignment with tandem duplication. 1997 , 4, 351-67	45
773	Nucleotide sequence analysis of the Streptococcus gordonii glucosyltransferase gene, gtfG. 1997 , 7, 83-95	38
772	Elasmobranchs express separate cholecystokinin and gastrin genes. 1997 , 94, 10221-6	34
771	Fast algorithms for aligning sequences with restricted affine gap penalties. 1997 , 264-273	
770	Cloning and characterization of four genes of Rhizobium leguminosarum bv. trifolii involved in exopolysaccharide production and nodulation. 1997 , 10, 290-301	52
769	p-Cymene catabolic pathway in Pseudomonas putida F1: cloning and characterization of DNA encoding conversion of p-cymene to p-cumate. 1997 , 179, 3171-80	116
768	Bibliography. 1997 , 505-523	1
767	Characterization of four outer membrane proteins that play a role in utilization of starch by Bacteroides thetaiotaomicron. 1997 , 179, 643-9	155
766	Sequence Navigator. 1997 , 145-154	2
765	Antibody-mediated inhibition of the growth of larvae from an insect causing cutaneous myiasis in a mammalian host. 1997 , 94, 8939-44	74
764	Proteolytic fragmentation reveals the oligomeric and domain structure of porcine aminopeptidase A. 1997 , 36, 3000-7	26

 $\,763\,$ $\,$ RMESH algorithms for parallel string matching.

762	Bona Fide Predictions of Protein Secondary Structure Using Transparent Analyses of Multiple Sequence Alignments. 1997 , 97, 2725-2844		41
761	Guinea pig and bovine zeta-crystallins have distinct functional characteristics highlighting replacements in otherwise similar structures. 1997 , 36, 5353-62		31
760	Neurotrypsin, a novel multidomain serine protease expressed in the nervous system. 1997 , 9, 207-19		96
759	Cloning of Candida albicans genes conferring resistance to azole antifungal agents: characterization of CDR2, a new multidrug ABC transporter gene. 1997 , 143 (Pt 2), 405-416		499
758	Molecular approaches to structure-function analysis of interleukin-8. 1997 , 287, 45-58		8
757	Expression of the sex determining cascade genes Sex-lethal and doublesex in the phorid fly Megaselia scalaris. 1997 , 40, 211-4		62
756	Caenorhabditis elegans has two isozymic forms, CE-1 and CE-2, of fructose-1,6-bisphosphate aldolase which are encoded by different genes. 1997 , 339, 226-34		13
755	Identification and mutational analysis of the immunodominant IgE binding epitopes of the major peanut allergen Ara h 2. 1997 , 342, 244-53		315
754	Human neuroserpin (PI12): cDNA cloning and chromosomal localization to 3q26. 1997 , 40, 55-62		61
753	Molecular characterization of human neogenin, a DCC-related protein, and the mapping of its gene (NEO1) to chromosomal position 15q22.3-q23. 1997 , 41, 414-21		32
752	Factors affecting the ability of energy functions to discriminate correct from incorrect folds. Journal of Molecular Biology, 1997 , 266, 831-46	6.5	147
75 ¹	A 3D-1D substitution matrix for protein fold recognition that includes predicted secondary structure of the sequence. <i>Journal of Molecular Biology</i> , 1997 , 267, 1026-38	6.5	144
75°	Solution structure of recombinant human interleukin-6. <i>Journal of Molecular Biology</i> , 1997 , 268, 468-81	6.5	65
749	Contact area difference (CAD): a robust measure to evaluate accuracy of protein models. <i>Journal of Molecular Biology</i> , 1997 , 268, 678-85	6.5	81
748	Protein evolution viewed through Escherichia coli protein sequences: introducing the notion of a structural segment of homology, the module. <i>Journal of Molecular Biology</i> , 1997 , 268, 857-68	6.5	92
747	Protein thermal stability, hydrogen bonds, and ion pairs. <i>Journal of Molecular Biology</i> , 1997 , 269, 631-43	8 6.5	580
746	The foldon universe: a survey of structural similarity and self-recognition of independently folding units. <i>Journal of Molecular Biology</i> , 1997 , 272, 95-105	6.5	66

745	Do aligned sequences share the same fold?. <i>Journal of Molecular Biology</i> , 1997 , 273, 355-68	6.5	203
744	The RAD52 epistasis group in mammalian double strand break repair. 1997 , 9, 181-8		79
743	Protein structure: what is it possible to predict now?. 1997 , 7, 60-71		65
742	unc-8, a DEG/ENaC family member, encodes a subunit of a candidate mechanically gated channel that modulates C. elegans locomotion. 1997 , 18, 107-19		171
741	Characterization of bacterially expressed rat estrogen receptor beta ligand binding domain by mass spectrometry: structural comparison with estrogen receptor alpha. 1997 , 62, 621-31		36
740	Comparative mutational analysis of peptidyl prolyl cis/trans isomerases: active sites of Escherichia coli trigger factor and human FKBP12. 1997 , 407, 184-90		57
739	Intermittent divergence of the protein tyrosine kinase family during animal evolution. 1997 , 412, 540-6		26
738	String taxonomy using learning automata. 1997 , 27, 354-65		18
737	The MHC class II-restricted T cell response of C57BL/6 mice to human C-reactive protein: homology to self and the selection of T cell epitopes and T cell receptors. 1997 , 34, 115-24		8
736	Isolation of the cDNA and characterization of mRNA expression of ribosomal protein S19 from the soft-shell clam, Mya arenaria. 1997 , 197, 295-304		12
735	Expression of Escherichia coli TehA gives resistance to antiseptics and disinfectants similar to that conferred by multidrug resistance efflux pumps. 1997 , 41, 440-4		53
734	Aspartate transcarbamylase from the deep-sea hyperthermophilic archaeon Pyrococcus abyssi: genetic organization, structure, and expression in Escherichia coli. 1997 , 179, 4143-57		32
733	Phylogeny and Evolution of 12S rDNA in Gruiformes (Aves). 1997 , 121-158		34
732	Transposon mutagenesis reinforces the correlation between Mycoplasma pneumoniae cytoskeletal protein HMW2 and cytadherence. 1997 , 179, 2668-77		71
731	The flgE gene of Campylobacter coli is under the control of the alternative sigma factor sigma54. 1997 , 179, 4647-53		27
730	Phylogenetic relationships of Bacillus thuringiensis delta-endotoxin family proteins and their functional domains. 1997 , 179, 2793-801		116
729	An evaluation of the environmental impact and of the safety of compact and modular equipment using SF6 up to 36 kV. 1997 ,		
728	Polymerase chain reaction (PCR) detection of porcine Chlamydia trachomatis and ruminant Chlamydia psittaci serovar 1 DNA in formalin-fixed intestinal specimens from swine. 1997 , 44, 185-91		14

727	2. Sequence Comparison Viaalignment and Gibbs Sampling: A Formal Analysis of the Emergence of the Modern Sociological Article. 1997 , 27, 47-87	34
726	Representative noise-free complete-link classification with application to protein structures. 1997 , 30, 467-482	1
725	The mouse mammary tumor associated gene INT3 is a unique member of the NOTCH gene family (NOTCH4). 1997 , 14, 1883-90	171
724	Effect of glucose transport inhibitors on vincristine efflux in multidrug-resistant murine erythroleukaemia cells overexpressing the multidrug resistance-associated protein (MRP) and two glucose transport proteins, GLUT1 and GLUT3. 1997 , 75, 161-8	20
723	CATHa hierarchic classification of protein domain structures. 1997 , 5, 1093-108	2063
722	Sequence conservation in the attachment glycoprotein and antigenic diversity among bovine respiratory syncytial virus isolates. 1997 , 54, 201-21	18
721	Mixed infections with porcine Chlamydia trachomatis/pecorum and infections with ruminant Chlamydia psittaci serovar 1 associated with abortions in swine. 1997 , 58, 251-60	42
720	Protein thermal stability: hydrogen bonds or internal packing?. 1997 , 2, S40-6	192
719	Cloning and characterization of the Oxytricha granulifera chaperonin containing tailless complex polypeptide 1 gamma gene. 1997 , 247, 877-83	10
718	Polarised expression of human intestinal N-benzoyl-L-tyrosyl-p-aminobenzoic acid hydrolase (human meprin) alpha and beta subunits in Madin-Darby canine kidney cells. 1997 , 247, 920-32	41
717	Anti-insect toxin 5 (AaIT5) from Androctonus australis. 1997 , 246, 496-501	23
716	Detection of lactate dehydrogenase-elevating virus in transplantable mouse tumors by biological assay and RT-PCR assays and its removal from the tumor cell. 1997 , 65, 227-36	19
715	Molecular analysis and characterization of a protein involved in the replication of intracellular Toxoplasma gondii. 1997 , 90, 403-13	5
714	Cloning, sequencing, expression and characterization of three anti-estradiol-17beta Fab fragments. 1997 , 1351, 192-202	8
713	Evolutionary motif and its biological and structural significance. 1997 , 44 Suppl 1, S38-43	8
712	Phylogenetic reconstruction of the Felidae using 16S rRNA and NADH-5 mitochondrial genes. 1997 , 44 Suppl 1, S98-116	143
711	Comparison of protein structures using 3D profile alignment. 1997 , 44 Suppl 1, S163-73	24
710	Analysis and organization of protein sequence data: a retrospective spanning four decades. 1997 , 16, 459-62	

709	Computational sequence analysis of the tissue inhibitor of metalloproteinase family. 1997 , 16, 237-55	87
708	Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. 1997 , 25, 3389-402	53786
707	The tax gene sequences form two divergent monophyletic lineages corresponding to types I and II of simian and human T-cell leukemia/lymphotropic viruses. 1997 , 231, 96-104	17
706	Oat blue dwarf marafivirus resembles the tymoviruses in sequence, genome organization, and expression strategy. 1997 , 232, 217-29	51
705	Comparison of the rotavirus gene 6 from different species by sequence analysis and localization of subgroup-specific epitopes using site-directed mutagenesis. 1997 , 237, 89-96	88
704	Molecular cloning and expression of two cDNAs encoding asparagine synthetase in soybean. 1997 , 33, 301-11	43
703	Comparison of sequences of RNAs 3 and 4 of rice stripe virus from China with those of Japanese isolates. 1997 , 15, 99-103	27
702	Needleman Wunsch Algorithm Using Multi-threading Approach. 2020 , 289-300	Ο
701	Harnessing Static Analysis to Help Learn Pseudo-Inverses of String Manipulating Procedures for Automatic Test Generation. 2020 , 180-201	
700	Full leave DDE 2020, 4, 105, 200	
700	Full Issue PDF. 2020 , 4, 195-289	
699	A Similarity-Calculation Method of Geometric Problems for Adaptive e-Learning. 2020 , 311-318	
		1
699	A Similarity-Calculation Method of Geometric Problems for Adaptive e-Learning. 2020 , 311-318	1
699 698	A Similarity-Calculation Method of Geometric Problems for Adaptive e-Learning. 2020, 311-318 Multiple Sequence Alignment Optimization Using Meta-Heuristic Techniques. 2020, 565-579 Constructing a Bioinformatics Platform with Web and Mobile Services Based on NVIDIA Jetson TK1.	1
699 698 697	A Similarity-Calculation Method of Geometric Problems for Adaptive e-Learning. 2020, 311-318 Multiple Sequence Alignment Optimization Using Meta-Heuristic Techniques. 2020, 565-579 Constructing a Bioinformatics Platform with Web and Mobile Services Based on NVIDIA Jetson TK1. 2020, 629-644 Grouping Users Through Pair Wise Sequence Alignment and Graph Traversal Based on Web Page	1
699 698 697 696	A Similarity-Calculation Method of Geometric Problems for Adaptive e-Learning. 2020, 311-318 Multiple Sequence Alignment Optimization Using Meta-Heuristic Techniques. 2020, 565-579 Constructing a Bioinformatics Platform with Web and Mobile Services Based on NVIDIA Jetson TK1. 2020, 629-644 Grouping Users Through Pair Wise Sequence Alignment and Graph Traversal Based on Web Page Navigation Behaviour. 2020, 1770-1791	1
699 698 697 696	A Similarity-Calculation Method of Geometric Problems for Adaptive e-Learning. 2020, 311-318 Multiple Sequence Alignment Optimization Using Meta-Heuristic Techniques. 2020, 565-579 Constructing a Bioinformatics Platform with Web and Mobile Services Based on NVIDIA Jetson TK1. 2020, 629-644 Grouping Users Through Pair Wise Sequence Alignment and Graph Traversal Based on Web Page Navigation Behaviour. 2020, 1770-1791 An Overview of Search and Match Algorithms Complexity and Performance. 2020, 457-471 Different Approaches to Solving the Problem of Reconstructing the Distance Matrix Between DNA	1

691 A Brief History of Bioinformatics Told by Data Visualization. 2020, 235-246

690	Some New Approaches to Comparative Evaluation of Algorithms for Calculating Distances Between Genomic Sequences. 2020 , 633-642	
689	Machine Boss: Rapid Prototyping of Bioinformatic Automata.	O
688	Dynamic homology and circularity in cladistic analysis. 2020 , 35, 1	5
687	DisCovER: distance- and orientation-based covariational threading for weakly homologous proteins.	2
686	SOLD2: Self-supervised Occlusion-aware Line Description and Detection. 2021 ,	9
685	Predicting Human Scanpaths in Visual Question Answering. 2021,	1
684	Assessment of Mutation Susceptibility in DNA Sequences with Word Vectors. 2020, 3, 1-6	1
683	On the interactions of the receptor-binding domain of SARS-CoV-1 and SARS-CoV-2 spike proteins with monoclonal antibodies and the receptor ACE2.	2
682	Characterizing Loop Acceleration in Heterogeneous Computing. 2021,	
681	Block aligner: fast and flexible pairwise sequence alignment with SIMD-accelerated adaptive blocks.	О
680	RNALigands: a database and web server for RNA - ligand interactions. 2021 ,	O
679	Citrullination was introduced into animals by horizontal gene transfer from cyanobacteria. 2021,	2
678	Discovering the Ultimate Limits of Protein Secondary Structure Prediction. 2021, 11,	O
677	VirusLab: A Tool for Customized SARS-CoV-2 Data Analysis. 2021 , 10, 27	2
676	Ancestral sequences of a large promiscuous enzyme family correspond to bridges in sequence space in a network representation. 2021 , 18, 20210389	
675	Evaluation of Saccadic Scanpath Prediction: Subjective Assessment Database and Recurrent Neural Network Based Metric. 2021 , 43, 4378-4395	3
674	GADP-align: A genetic algorithm and dynamic programming-based method for structural alignment of proteins. 2021 , 11, 271-279	

673	Communication vs Synchronisation in Parallel String Comparison. 2020,	0
672	Using Phoneme Representations to Build Predictive Models Robust to ASR Errors. 2020 ,	2
671	Humic acids enrich the plant microbiota with bacterial candidates for the suppression of pathogens.	
670	CRAFT: Compact genome Representation towards large-scale Alignment-Free daTabase.	
669	The ITS region provides a reliable DNA barcode for identifying reishi/lingzhi (Ganoderma) from herbal supplements.	
668	A Review of Kernel Methods Based Approaches to Classification and Clustering of Sequential Patterns. 72-92	
667	FPGA-Based Accelerators for Bioinformatics Applications. 605-635	
666	Genomics Perspectives of Bioethanol Producing Zymomonas Mobilis. 1354-1377	
665	Improving PSI-BLASTE Fold Recognition Performance through Combining Consensus Sequences and Support Vector Machine. 1667-1675	
664	Improving PSI-BLASTE Fold Recognition Performance through Combining Consensus Sequences and Support Vector Machine. 51-59	
663	Cooperation Between Expert Knowledge and Data Mining Discovered Knowledge. 198-221	
662	Merging Multi-Version Texts: a Generic Solution to the Overlap Problem.	1
661	Complexity of Common Subsequence Problems. 1977, 393-398	
660	Molecular modeling of the three-dimensional structure of the human interleukin-11. 2002 , 51-54	
659	Bioinformatics. 2006 , 657-695	
658	4.8.2 Sequences and homologies. 196-202	
657	4.8.8 References for 4.8. 241-243	
656	Data Mining in Protein Binding Cavities. 2005 , 354-361	

655	Neurocomputing for Certain Bioinformatics Tasks. 2005, 439-454
654	Improving Biological Sequence Property Distances by Using a Genetic Algorithm. 2001 , 539-546
653	Sequence Analysis. 2003 , 281-297
652	Protein Structure Comparison and Classification. 2007 , 147-180
651	Local Structure Prediction of Proteins. 2007 , 207-254
650	Deciphering the Structures of Genomic DNA Sequences Using Recurrence Time Statistics. 2007 , 321-337
649	Biological Sequence Search and Analysis. 2009 , 47-62
648	Bioinformatics: A New Approach for the Challenges of Molecular Biology. 2007 , 295-309
647	Semi-Automatic Semantic Analysis of Rituals. Chances and Challenges.
646	Applying SIMD Approach to Whole Genome Comparison on Commodity Hardware. 2008 , 1220-1229
645	Bioinformatik. 2008 , 332-345
644	Analyse von Biochips: Von der Sequenz zum System. 2008 , 63-100
643	Preliminary Analysis of the Cell BE Processor Limitations for Sequence Alignment Applications. 2008, 53-64
642	An Algorithm for Multiple and Global Alignments. 2008 , 479-488
641	Gene Machine' [A Hardware/Software Platform for Analyzing Genome Data. 2008 , 517-527
640	Alignment Methods. 2007 , 81-115
639	A Multi-Stack Based Phylogenetic Tree Building Method. 2007 , 49-60
638	Improved Prediction of Protein Secondary Structures Using Adaptively Weighted Profiles. 2007 , 83-94

637	Exhaustive Peptide Searching Using Relations. 2007 , 13-24	2
636	Manifestation and Exploitation of Invariants in Bioinformatics. 2007 , 365-377	
635	Alignments with Non-overlapping Moves, Inversions and Tandem Duplications in O(n 4) Time. 2007, 151-164	
634	Biological Sequence Comparison Application in Heterogeneous Environments with Dynamic Programming Algorithms. 2007 , 46-56	
633	An Optimized Distance Function for Comparison of Protein Binding Sites. 2007 , 93-100	
632	Local Context Selection for Aligning Sentences in Parallel Corpora. 2007, 82-93	1
631	A Parallel BSP Algorithm for Irregular Dynamic Programming. 2007 , 151-160	5
630	Improved Alignment of Protein Sequences Based on Common Parts. 2008, 87-99	
629	SimSearch: A New Variant of Dynamic Programming Based on Distance Series for Optimal and Near-Optimal Similarity Discovery in Biological Sequences. 2009 , 206-216	
628	The Relation between Indel Length and Functional Divergence: A Formal Study. 2008, 330-341	1
627	Explore Residue Significance in Peptide Classification. 2008 , 706-713	
626	Matching Techniques in Genomic Sequences for Motif Searching. 2009 , 319-330	
625	A performance evaluation of a local DNA sequence alignment algorithm on a cluster of workstations.	2
624	Generating Representative Test Sequences from Real Workload for Minimizing DRAM Verification Overhead. 2020 , 25, 1-23	
623	Evaluating the Performance of Sensor-based Bout Detection Algorithms: The Transition Pairing Method. 2020 , 3, 219-227	3
622	Sequence Alignment By Modified Teaching Learning Based Optimization Algorithm (M-TLBO). 2021 , 1441-1454	1
621	A 3D Structural Interactome to Explore the Impact of Evolutionary Divergence, Population Variation, and Small-molecule Drugs on SARS-CoV-2-Human Protein-Protein Interactions.	
620	Analysis of a Randomized Controlled Trial of Student Performance in Parallel Programming using a New Measurement Technique. 2020 , 20, 1-28	0

619	YACOS. 2020 ,	O
618	CIAlign - A highly customisable command line tool to clean, interpret and visualise multiple sequence alignments.	3
617	Refining pairwise sequence alignments of membrane proteins by the incorporation of anchors.	
616	Evaluation of distributed DNA representations on the classification of conserved non-coding elements. 2020 ,	O
615	Short-range template switching in great ape genomes explored using a pair hidden Markov model.	
614	Quantitative metaproteomics of patient fecal microbiota identifies host and microbial proteins associated with ulcerative colitis.	
613	CRISPAltRations: a validated cloud-based approach for interrogation of double-strand break repair mediated by CRISPR genome editing.	
612	Seed-and-vote based in-memory accelerator for DNA read mapping. 2020 ,	5
611	TraceSim: a method for calculating stack trace similarity. 2020 ,	0
610	KELSA: A Knowledge-Enriched Local Sequence Alignment Algorithm for Comparing Patient Medical Records. 2021 , 227-240	
609	Detection in the Genomes of Higher Organisms of Highly Fuzzy Megasatellite Repeats.	
608	Classifying Protein Structures by Using Protein Ray Based Descriptor, KNN and FuzzyKNN Classification Methods. 2020 ,	O
607	Weighted automata computation of edit distances with consolidations and fragmentations. 2020 , 282, 104652	
606	Complete nucleotide sequence of the Drosophila transposable element copia: homology between copia and retroviral proteins. 1985 , 5, 1630-1638	156
605	DNA sequence, structure, and tyrosine kinase activity of the Drosophila melanogaster Abelson proto-oncogene homolog. 1988 , 8, 843-853	23
604	A gene encoding the major beta tubulin of the mitotic spindle in Physarum polycephalum plasmodia. 1988 , 8, 1275-1281	11
603	Identification of members of the P-glycoprotein multigene family. 1989 , 9, 1224-1232	43
602	Identification and characterization of PF4varl, a human gene variant of platelet factor 4. 1989 , 9, 1445-1451	13

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583	Repetitive zinc-binding domains in the protein transcription factor IIIA from Xenopus oocytes. 1985 , 4, 1609-14	779
582	Dtrk, a Drosophila gene related to the trk family of neurotrophin receptors, encodes a novel class of neural cell adhesion molecule. 1992 , 11, 391-404	32
581	What limits affinity maturation of antibodies in Xenopusthe rate of somatic mutation or the ability to select mutants?. 1992 , 11, 4337-47	31
580	The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefaciens plasmid pTiAch5. 1984 , 3, 835-46	73
579	Structure of the murine Ia-associated invariant (Ii) chain as deduced from a cDNA clone. 1984, 3, 873-7	22
578	Comparison of the entire genomes of bovine leukemia virus and human T-cell leukemia virus and characterization of their unidentified open reading frames. 1984 , 3, 3231-7	27
577	The E35 stopper mutant of Neurospora crassa: precise localization of deletion endpoints in mitochondrial DNA and evidence that the deleted DNA codes for a subunit of NADH dehydrogenase. 1986 , 5, 779-85	25
576	Using known substructures in protein model building and crystallography. 1986 , 5, 819-22	174
575	Variable domain-linked oligosaccharides of a human monoclonal IgG: structure and influence on antigen binding. 1999 , 338 (Pt 2), 529-38	16
574	Molecular cloning and expression of adenosine kinase from Leishmania donovani: identification of unconventional P-loop motif. 1999 , 339 (Pt 3), 667-73	6
573	Fish macrophages express a cyclo-oxygenase-2 homologue after activation. 1999 , 340 (Pt 1), 153-9	10
572	Isolation, sequence and expression of a cDNA encoding the alpha-chain of the feline CD8. 1994 , 81, 127-31	7
571	A Web-based GIS for health care decision-support. 2005 , 365-9	2
570	Cloning and sequencing of a processed pseudogene derived from a human class III alcohol dehydrogenase gene. 1990 , 46, 85-91	26
569	Expression of very low density lipoprotein receptor in the vascular wall. Analysis of human tissues by in situ hybridization and immunohistochemistry. 1996 , 148, 1985-97	55
568	Sequence alignment by cross-correlation. 2005 , 16, 453-8	8
567	Crystallin gene mutations in Indian families with inherited pediatric cataract. 2008, 14, 1157-70	128
566	Mutations in NYX of individuals with high myopia, but without night blindness. 2007 , 13, 330-6	32

565	NEMO: Extraction and normalization of organization names from PubMed affiliations. 2010, 5, 50-75	16
564	Local alignment tool for clinical history: temporal semantic search of clinical databases. 2010 , 2010, 437-41	3
563	Alignment and clustering of breast cancer patients by longitudinal treatment history. 2011 , 2011, 760-7	4
562	Genetic and phenotypic characteristics of three Mainland Chinese families with choroideremia. 2012 , 18, 309-16	10
561	Molecular and Morphological Characterization and Biological Control Capabilities of a Pasteuria ssp. Parasitizing Rotylenchulus reniformis, the Reniform Nematode. 2010 , 42, 207-17	5
560	An enhanced algorithm for multiple sequence alignment of protein sequences using genetic algorithm. 2015 , 14, 1232-55	3
559	Combining Kernel and Model Based Learning for HIV Therapy Selection. 2017 , 2017, 239-248	12
558	Foundations for Studying Clinical Workflow: Development of a Composite Inter-Observer Reliability Assessment for Workflow Time Studies. 2019 , 2019, 617-626	1
557	An Interprofessional Approach to Clinical Workflow Evaluation Focused on the Electronic Health Record Using Time motion Study Methods. 2019 , 2019, 1187-1196	2
556	is conserved between and psychrophilic, polar-collected fungi. 2021 , 2021,	
555	A Genetic Linkage Map for Zebrafish: Comparative Analysis and Localization of Genes and Expressed Sequences. 1999 , 9, 334-347	97
554	Modeling Lengthy Behavioral Log Data for Customer Churn Management: A Representation Learning Approach.	
553	Protocol Reverse-Engineering Methods and Tools: A Survey. 2022 , 182, 238-254	1
552	Biological sequence analysis. 2022 , 33-47	
551	Introduction to basics of bioinformatics. 2022 , 1-15	О
550	Unsupervised Binary Protocol Clustering Based on Maximum Sequential Patterns. 2022 , 130, 483-498	O
549	. 2021,	О
548	HLS Portability from Intel to Xilinx: A Case Study. 2021 ,	

547	Pangenome evolution in environmentally transmitted symbionts of deep-sea mussels is governed by vertical inheritance.	
546	Shine: To explore specific, sensitive and conserved biomarkers from massive microbial genomic data within intrapopulations.	
545	Missense variants reveal functional insights into the human ARID family of gene regulators.	
544	Spatial ecology of Bay of Quinte walleye (Sander vitreus): Annual timing, extent, and patterns of migrations in eastern Lake Ontario. 2021 , 48, 159-159	O
543	Visual Sequential Search Test Analysis: An Algorithmic Approach. 2021 , 9, 2952	1
542	OAIPM: Optimal Algorithm to Identify Point Mutation Between DNA Sequences. 2022 , 393-401	
541	A 3D structural SARS-CoV-2-human interactome to explore genetic and drug perturbations. 2021 , 18, 1477-1488	3
540	A generic approach to detect design patterns in model transformations using a string-matching algorithm. 1	
539	Sampling the conformational landscapes of transporters and receptors with AlphaFold2.	1
538	Concepts and Coefficients Based on John L. Holland Theory of Vocational Choice Examining the R Package holland. 2021 , 3, 728-750	2
537	Efficient computation of Hash Hirschberg protein alignment utilizing hyper threading multi-core sharing technology.	4
536	Response : Computer Speed and Sequence Comparison. 1992 , 257, 1609-1610	5
535	Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. 2001 , 11, 281-289	4
534	DiagAF: A More Accurate and Efficient Pre-Alignment Filter for Sequence Alignment. 2021 , PP,	O
533	Genomic variants reducing expression of two endocytic receptors in 46,XY differences of sex development 2022 ,	
532	Does clustering of DNA barcodes agree with botanical classification directly at high taxonomic levels? Trees in French Guiana as a case study 2022 ,	1
531	ScRpb4, Encoding an RNA Polymerase Subunit from Sugarcane, Is Ubiquitously Expressed and Resilient to Changes in Response to Stress Conditions. 2022 , 12, 81	
530	Wide-angle, monocular head tracking using passive markers 2021 , 368, 109453	O

529	Real-time pattern matching and ranking for early prediction of industrial alarm floods. 2022, 120, 105004	2
528	An Attack Signatures Generation Sequence Alignment Algorithm Based on Production Rules. 2018,	
527	Symbiotic Bacterial Flora Changes in Response to Low Temperature in Reticulitermes speratus KMT001. 2018 , 46, 713-725	1
526	Lyrics Recognition and Syllable Assignment of Medieval Music Manuscripts. 2020 ,	
525	A Platoon Matching Approach for the Estimation of Arterial Travel Time Distributions. 2020,	
524	Classification of Protein Structures by Making Fuzzy-Rough Feature Selection. 2020,	
523	Dynamic Programming Applications: A Suvrvey. 2020 ,	O
522	SeedEx: A Genome Sequencing Accelerator for Optimal Alignments in Subminimal Space. 2020,	2
521	Comparison of the Smith-Waterman and Needleman-Wunsch algorithms for online similarity analysis of industrial alarm floods. 2020 ,	2
520	The SARS-CoV-2 and its Similarity to Other Bat-Derived SARS-like Coronaviruses: A Data-Driven Study.	
519	Parallelization of Global Sequence Alignment on Graphics Processing Unit. 2020,	O
518	FPGA Implementation of DNA Sequence Alignment with Traceback. 2020,	
517	Smart Grid System Security Protection by Deep Neural Network. 2021,	
516	Alignment Free Sequence Similarity Estimation using Local Binary Pattern on DNA Trajectory Images. 2021 ,	
515	State-Only Imitation Learning for Dexterous Manipulation. 2021,	6
514	Egocentric Biochemical Video-and-Language Dataset. 2021 ,	2
513	SLDP and LIPA mediate lipid droplet-plasma membrane tethering in Arabidopsis thaliana.	
512	Learning process patterns via multiple sequence alignment. 2022 , 159, 107676	О

511	Improved Genomic Identification, Clustering, and Serotyping of Shiga Toxin-Producing Using Cluster/Serotype-Specific Gene Markers 2021 , 11, 772574	0
510	The Metaxin Mitochondrial Import Proteins: Multiple Metaxin-like Proteins in Fungi.	O
509	Mitochondrial Processing Peptidases-Structure, Function and the Role in Human Diseases 2022 , 23,	2
508	A Simple Yet Robust Algorithm for Automatic Extraction of Parallel Sentences: A Case Study on Arabic-English Wikipedia Articles. 2022 , 10, 401-420	O
507	Using Sequence Analysis to Identify Conversational Motifs in Supportive Interactions. 026540752110666	0
506	Semantic Metadata Annotation Services in the Biomedical Domain Literature Review. 2022, 12, 796	1
505	The effect of dimerization and ligand binding on the dynamics of Kaposi's sarcoma-associated herpesvirus protease 2022 ,	1
504	Sub-Messages Extraction for Industrial Control Protocol Reverse Engineering.	
503	Differences between Omicron SARS-CoV-2 RBD and other variants in their ability to interact with cell receptors and monoclonal antibodies.	0
502	Redefining the coenzyme A transferase superfamily with a large set of manually-annotated proteins 2022 ,	2
501	The bacterial density of clinical rectal swabs is highly variable, correlates with sequencing contamination, and predicts patient risk of extraintestinal infection 2022 , 10, 2	1
500	LaRA 2: parallel and vectorized program for sequence-structure alignment of RNA sequences 2022 , 23, 18	O
499	Removing the Bottleneck: Introducing cMatch - A Lightweight Tool for Construct-Matching in Synthetic Biology 2021 , 9, 785131	0
498	Screening and identification of phytochemical drug molecules against mutant BRCA1 receptor of breast cancer using computational approaches 2022 ,	1
497	Evolutionary analyses of the gasdermin family suggest conserved roles in infection response despite loss of pore-forming functionality 2022 , 20, 9	4
496	SignalP 6.0 predicts all five types of signal peptides using protein language models 2022,	56
495	Improving the time and space complexity of the WFA algorithm and generalizing its scoring.	0
494	Sequence graph transform (SGT): a feature embedding function for sequence data mining. 1	1

493 Matching Regular Expressions on uncertain data. **2022**, 84, 532

Quantitative metaproteomics and activity-based protein profiling of patient fecal microbiome interfies host and microbial serine-type endopeptidase activity associated with ulcerative colitis 4 2022, 100197 491 MeShClust v3.0: High-quality clustering of DNA sequences using the mean shift algorithm and alignment-free identity scores. 490 MeShClust v3.0: High-quality clustering of DNA sequences using the mean shift algorithm and alignment-free identity scores. 480 Evolutionary rewiring of regulatory networks contributes to phenotypic differences between human and mouse orthologous genes. 2022. 480 The involvement of type IV pili and the phytochrome CphA in gliding motility, lateral motility and photophobotaxis of the cyanobacterium Phormidium lacuna. 2022, 17, e0249509 OPERATOR OF Perception System Efficient Characterization Method for Big Automotive Datasets Used for Perception System Development and Verification. 2022, 10, 12629-12643 A glimpse on metazoan ZNFX1 helicases, ancient players of antiviral innate immunity 2022, 121, 456-456 OPERATOR OF Perception System Extracting Formats of Service Messages with Varying Payloads. 2022, 22, 1-31 481 Digital Technology und Artificial Intelligence Facing COVID-19. 2022, 1229-1240 482 Dataflow Acceleration for Short Read Alignment on NGS data. 2022, 1-1 483 A survey on the algorithm and development of multiple sequence alignment 2022, OPERATOR OF STATES OF STATE			
491 alignment-free identity scores. 490 Evolutionary rewiring of regulatory networks contributes to phenotypic differences between human and mouse orthologous genes 2022. 489 The involvement of type IV pill and the phytochrome CphA in gliding motility, lateral motility and photophobotaxis of the cyanobacterium Phormidium lacuna 2022, 17, e0249509 488 Efficient Characterization Method for Big Automotive Datasets Used for Perception System Development and Verification. 2022, 10, 12629-12643 487 A glimpse on metazoan ZNFX1 helicases, ancient players of antiviral innate immunity 2022, 121, 456-456 o 488 Extracting Formats of Service Messages with Varying Payloads. 2022, 22, 1-31 489 Digital Technology und Artificial Intelligence Facing COVID-19. 2022, 1229-1240 484 Dataflow Acceleration for Short Read Alignment on NGS data. 2022, 1-1 485 A survey on the algorithm and development of multiple sequence alignment 2022, 486 Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast 2022, 11, 487 Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 488 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 489 Molecular identification and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, 480 Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	492	identifies host and microbial serine-type endopeptidase activity associated with ulcerative colitis	4
human and mouse orthologous genes 2022, The involvement of type IV pili and the phytochrome CphA in gliding motility, lateral motility and photophobotaxis of the cyanobacterium Phormidium lacuna 2022, 17, e0249509 Efficient Characterization Method for Big Automotive Datasets Used for Perception System Development and Verification. 2022, 10, 12629-12643 487 A glimpse on metazoan ZNFX1 helicases, ancient players of antiviral innate immunity 2022, 121, 456-456 o 488 Extracting Formats of Service Messages with Varying Payloads. 2022, 22, 1-31 489 Digital Technology und Artificial Intelligence Facing COVID-19. 2022, 1229-1240 484 Dataflow Acceleration for Short Read Alignment on NGS data. 2022, 1-1 485 A survey on the algorithm and development of multiple sequence alignment 2022, 482 Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast 2022, 11, 480 Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	491		1
photophobotaxis of the cyanobacterium Phormidium lacuna. 2022, 17, e0249509 Efficient Characterization Method for Big Automotive Datasets Used for Perception System Development and Verification. 2022, 10, 12629-12643 A glimpse on metazoan ZNFX1 helicases, ancient players of antiviral innate immunity 2022, 121, 456-456 Extracting Formats of Service Messages with Varying Payloads. 2022, 22, 1-31 Digital Technology und Artificial Intelligence Facing COVID-19. 2022, 1229-1240 Dataflow Acceleration for Short Read Alignment on NGS data. 2022, 1-1 A survey on the algorithm and development of multiple sequence alignment 2022, Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast 2022, 11, Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	490		O
Development and Verification. 2022, 10, 12629-12643 487 A glimpse on metazoan ZNFX1 helicases, ancient players of antiviral innate immunity 2022, 121, 456-456 488 Extracting Formats of Service Messages with Varying Payloads. 2022, 22, 1-31 489 Digital Technology und Artificial Intelligence Facing COVID-19. 2022, 1229-1240 484 Dataflow Acceleration for Short Read Alignment on NGS data. 2022, 1-1 483 A survey on the algorithm and development of multiple sequence alignment 2022, 482 Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast 2022, 11, 481 Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 480 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	489		O
286 Extracting Formats of Service Messages with Varying Payloads. 2022, 22, 1-31 485 Digital Technology und Artificial Intelligence Facing COVID-19. 2022, 1229-1240 484 Dataflow Acceleration for Short Read Alignment on NGS data. 2022, 1-1 485 A survey on the algorithm and development of multiple sequence alignment 2022, 486 Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast 2022, 11, 481 Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 480 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 479 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, 480 Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	488		1
Digital Technology und Artificial Intelligence Facing COVID-19. 2022, 1229-1240 484 Dataflow Acceleration for Short Read Alignment on NGS data. 2022, 1-1 483 A survey on the algorithm and development of multiple sequence alignment 2022, 60 482 Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast 2022, 11, 481 Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 480 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 479 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	487	A glimpse on metazoan ZNFX1 helicases, ancient players of antiviral innate immunity 2022 , 121, 456-456	О
Dataflow Acceleration for Short Read Alignment on NGS data. 2022, 1-1 A survey on the algorithm and development of multiple sequence alignment 2022, Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast 2022, 11, Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	486	Extracting Formats of Service Messages with Varying Payloads. 2022 , 22, 1-31	
A survey on the algorithm and development of multiple sequence alignment 2022, Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast 2022, 11, Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	485	Digital Technology und Artificial Intelligence Facing COVID-19. 2022 , 1229-1240	
Barcoded Bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast 2022, 11, Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	484	Dataflow Acceleration for Short Read Alignment on NGS data. 2022 , 1-1	
yeast 2022, 11, Molecular signature characters complement taxonomic diagnoses: a bioinformatic approach exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	483	A survey on the algorithm and development of multiple sequence alignment 2022,	O
exemplified by ciliated protists (Ciliophora, Oligotrichea) 2022, 107433 Molecular and Epidemiological Characterization of Emerging Immune-Escape Variants of SARS-CoV-2 2022, 9, 811004 Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	482		3
Tools and Techniques for Collection and Analysis of Internet-of-Things malware: A systematic state-of-art review. 2022, Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	481		О
state-of-art review. 2022 , Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of	480		1
	479		3
" Pacific flagrish, Eptatretus stoutii 2022 ,	478	Molecular identification and post-prandial regulation of glucose carrier proteins in the hindgut of Pacific hagfish, Eptatretus stoutii 2022 ,	
Chemistry-informed Macromolecule Graph Representation for Similarity Computation, 477 Unsupervised and Supervised Learning. 4	477		4
Sequence alignment of folk song melodies reveals cross-cultural regularities of musical evolution 476 2022,	476		4

475	AutoDSE: Enabling Software Programmers to Design Efficient FPGA Accelerators. 2022, 27, 1-27	3
474	Seventh International Conference on Methods in Protein Sequence Analysis. July 3-8, 1988, West Berlin, F.R.G. Short communications. 1988 , 7, 187-324	
473	Inferences from protein and nucleic acid sequences: early molecular evolution, divergence of kingdoms and rates of change. 1974 , 5, 311-30	8
472	Mitochondrial citrate synthase from potato: predominant expression in mature leaves and young flower buds. 1995 , 196, 756-64	11
471	Structure-based sequence alignment of elongation factors Tu and G with related GTPases involved in translation. 1995 , 41, 1096-104	15
470	Evolution of genes and taxa: a primer. 2000 , 42, 1-23	22
469	The long and winding road of molecular data in phylogenetic analysis. 2014 , 47, 443-78	2
468	FPGA Acceleration of Pre-Alignment Filters for Short Read Mapping With HLS. 2022 , 10, 22079-22100	1
467	How Do MSA Programs Work?. 2022 , 17-34	
466	Informative RNA base embedding for RNA structural alignment and clustering by deep representation learning 2022 , 4, lqac012	O
465	A flexible kinetic assay efficiently sorts prospective biocatalysts for PET plastic subunit hydrolysis 2022 , 12, 8119-8130	О
464	HyText 🖟 Scene-Text Extraction Method for Video Retrieval. 2022 , 182-193	О
463	Chant editing and analysis program: a tool for analyzing liturgical chant. 2022, 14, 82-95	
462	Extracting Land Use Change Patterns of Rural Town Settlements with Sequence Alignment Method. 2022 , 11, 313	4
461	A new paradigm of multiheme cytochrome evolution by grafting and pruning protein modules.	
460	Employment Pathways during Economic Recession and Recovery and Adult Health 2022, 63, 105-124	О
459	nPoRe: n-Polymer Realigner for improved pileup variant calling.	
458	Molecular and structural insights for the regulation of terpenoids in Ocimum basilicum and Ocimum tenuiflorum. 1	2

457	GenStore: a high-performance in-storage processing system for genome sequence analysis. 2022,	1
456	Computer Aided Written Character Feature Extraction in Progressive Supranuclear Palsy and Parkinson's Disease 2022 , 22,	1
455	Plastics degradation by hydrolytic enzymes: the Plastics-Active Enzymes Database - PAZy 2022,	4
454	Low-Cost Algorithms for Metabolic Pathway Pairwise Comparison 2022 , 7,	Ο
453	SEED LIPID DROPLET PROTEIN1, SEED LIPID DROPLET PROTEIN2 and LIPID DROPLET PLASMA MEMBRANE ADAPTOR mediate lipid droplet-plasma membrane tethering 2022 ,	0
452	Accelerating Minimap2 for accurate long read alignment on GPUs.	Ο
451	A spatial genome aligner for multiplexed DNA-FISH.	0
450	Lane Detection and Pixel-Level Tracking for Autonomous Vehicles.	
449	Aegilops sharonensis genome-assisted identification of stem rust resistance gene Sr62 2022 , 13, 1607	2
448	Evolution of transposable element-derived enhancer activity.	
447	TraceSim: An Alignment Method for Computing Stack Trace Similarity. 2022, 27, 1	Ο
446	NATURAL SEMANTIC INFORMATION-BASED EYE TRACKING USING IMPROVED NEEDLEMANIWUNSCH AND SUBSMATCH METHODS.	
445	Sampling alternative conformational states of transporters and receptors with AlphaFold2 2022 , 11,	8
444	PASIV: A Pooled Approach-Based Workflow to Overcome Toxicity-Induced Design of Experiments Failures and Inefficiencies 2022 ,	Ο
443	Developing new genetic algorithm based on integer programming for multiple sequence alignment. 2022 , 26, 3863-3870	
442	SHOOT: phylogenetic gene search and ortholog inference 2022 , 23, 85	3
441	Alkaloid Biosynthetic Enzyme Generates Diastereomeric Pair Two Distinct Mechanisms 2022,	3
440	PLO3S : Protein LOcal Surficial Similarity Screening.	

439	Protein Language Model Performs Efficient Homology Detection.		1
438	Application of the MAHDS Method for Multiple Alignment of Highly Diverged Amino Acid Sequences 2022 , 23,		
437	Fast protein structure comparison through effective representation learning with contrastive graph neural networks 2022 , 18, e1009986		1
436	CIAlign: A highly customisable command line tool to clean, interpret and visualise multiple sequence alignments 2022 , 10, e12983		3
435	Zika virus NS4A hijacks host ANKLE2 to promote viral replication.		
434	Diverse Protein Architectures and \(\textit{H}\)Methylation Patterns Define Split Borosin RiPP Biosynthetic Gene Clusters 2022 ,		1
433	Phylogeography and species delimitation of the Neotropical frog complex (Hylidae: Scinax granulatus).		
432	Tracking of Diversity and Evolution in the Brown Rot Fungi , , and 2022 , 13, 854852		1
431	bpRNA-align: Improved RNA Secondary Structure Global Alignment for Comparing and Clustering RNA Structures.		
430	A tool for feature extraction from biological sequences 2022,		1
429	Differences between inexperienced and experienced safety supervisors in identifying construction hazards: Seeking insights for training the inexperienced. 2022 , 52, 101602		1
428	Parameter-Free Ordered Partial Match Alignment with Hidden State Time Warping. 2022 , 12, 3783		1
427	Developments in Algorithms for Sequence Alignment: A Review 2022, 12,		1
426	Missense variants reveal functional insights into the human ARID family of gene regulators <i>Journal of Molecular Biology</i> , 2022 , 167529	6.5	1
426 425		6.5	0
	Journal of Molecular Biology, 2022, 167529 Toward a Period-specific Optimized Neural Network for OCR Error Correction of Historical Hebrew	6.5	
425	Journal of Molecular Biology, 2022, 167529 Toward a Period-specific Optimized Neural Network for OCR Error Correction of Historical Hebrew Texts. 2022, 15, 1-20	6.5	

The Alignment Module. 2022, 271-295 421 The SeqAn Library (Versions 1 and 2). 2022, 7-32 420 Heterogeneous Network Propagation with Optimal Similarity Measure for Drug-Target 419 Associations. 2021, RExACtor: Automatic Regular Expression Signature Generation for Stateless Packet Inspection. 418 A Corpus for Measuring Retrieval Performance of Process Matching Methods. 2021, 417 Net-Shape-Based Automated Detection of Integrated-Circuit Layout Plagiarism. 2021, 10, 3181 416 House fly larval grazing alters dairy cattle manure microbial communities.. 2021, 21, 346 415 O Hydrogen bonds meet self-attention: all you need for protein structure embedding. 2021, \circ 414 Investigating intra-individual variability of face scanning in autistic children.. 2021, 13623613211064373 413 Assessment of Sex Bias in Housekeeping Gene Expression in Adipose Tissue Through the Massive 412 Analysis of Transcriptomics Data. COMPARATIVE ANALYSIS OF HUMAN AND LIVESTOCK #RECEPTORS FOR SARS-COV-2. 62, 120-129 411 modulates the gut microbiota and produces anti-cancer metabolites to protect against colorectal 410 13 tumourigenesis.. 2021, Diverse Protein Architectures and EN-Methylation Patterns Define Split Borosin RiPP Biosynthetic 409 Gene Clusters. Synchronization of acquisition devices in neuroimaging: An application using co-registration of eye 408 movements and electroencephalography.. 2021, GCAEMDA: Predicting miRNA-disease associations via graph convolutional autoencoder. 2021, 17, e1009655 407 406 Coronavirus Genome Sequence Similarity and Protein Sequence Classification. 2021, 3, 3-18 Graph Attention Mechanism-based Deep Tensor Factorization for Predicting disease-associated 405 1 miRNA-miRNA pairs. 2021, In-Silico Screening of Prime PCOS Biomarkers for the Identification of a Potential Model Organism. 404 **2021**, 448-454

403	EdClust: A heuristic sequence clustering method with higher sensitivity 2021, 2150036	0
402	Protein Sequence Similarities between the Homo Sapiens and Mammal Specie. 2021 ,	
401	Detecting damage in rudder stocks under load using electro-mechanical susceptance: Frequency-warping and semi-supervised approaches. 1045389X2110643	3
400	High-performance computing for SARS-CoV-2 RNAs clustering: a data science-based genomics approach 2021 , 19, e49	
399	Plant Natriuretic Peptide Active Domain Forms Amyloid-like Fibrils in a pH-Dependent Manner 2021 , 11,	
398	Could Small Neurotoxins-Peptides be Expressed during SARS-CoV-2 Infection?. 2021 , 22, 557-563	0
397	GENPPI: standalone software for creating protein interaction networks from genomes 2021 , 22, 596	0
396	Exploring Unsupervised Learning Methods for Automated Protocol Analysis. 2021,	
395	Reprogramming Mycobacterium tuberculosis CRISPR System for Gene Editing and Genome-wide RNA Interference Screening 2021 ,	1
394	Prokaryotic communities in the historic silver mine Reiche Zeche. 2021 , 26, 2	1
393	Probing Allosteric Hsp70 Inhibitors by Molecular Modelling Studies to Expedite the Development of Novel Combined F508del CFTR Modulators 2021 , 14,	1
392	Plasmodium vivax malaria serological exposure markers: assessing the degree and implications of cross-reactivity with P. knowlesi.	
391	ASSD: Arabic Semantic Similarity Dataset. 2021 ,	
390	Dynamic order Markov model for categorical sequence clustering 2021 , 8, 154	O
389	Evolutionary dynamics of piRNA clusters in Drosophila. 2021,	2
388	Multi-relation graph embedding for predicting miRNA-target gene interactions by integrating gene sequence information 2022 , PP,	
387	XAI and Strategy Extraction via Reward Redistribution. 2022 , 177-205	
386	Empirical Study of Protein Feature Representation on Deep Belief Networks Trained with Small Data for Secondary Structure Prediction 2022 , PP,	

(2020-2022)

385	BiRDS - Binding Residue Detection from Protein Sequences Using Deep ResNets 2022,	0
384	Strain wars 3: Differences in infectivity and pathogenicity between Delta and Omicron strains of SARS-CoV-2 can be explained by thermodynamic and kinetic parameters of binding and growth 2022 , 100217	3
383	PPVED: A machine learning tool for predicting the effect of single amino acid substitution on protein function in plants 2022 ,	O
382	Optimal gap-affine alignment in O(s) space.	O
381	Shedding light on silica biomineralization by comparative analysis of the silica-associated proteomes from three diatom species 2022 ,	0
380	Great Minds Think Alike? Spatial Search Processes Can Be More Idiosyncratic When Guided by More Accurate Information 2022 , 46, e13132	
379	Neutralizing Dromedary-Derived Nanobodies Against Botl-Like Toxin From the Most Hazardous Scorpion Venom in the Middle East and North Africa Region 2022 , 13, 863012	0
378	US-align: Universal Structure Alignments of Proteins, Nucleic Acids, and Macromolecular Complexes.	О
377	Overview of structural variation calling: Simulation, identification, and visualization 2022, 145, 105534	Ο
376	A multi-layer multi-kernel neural network for determining associations between non-coding RNAs and diseases. 2022 , 493, 91-105	1
375	Chapter 11. Application of Molecular Modelling to Speed-up the Lead Discovery Process. 281-316	
374	Global Pairwise Protein Sequence Alignment via Mixed-Integer Linear Optimization. 2008, 1427-1434	
373	Mixed 0-1 Linear Programming Approach for DNA Transcription Element Identification. 2008, 2199-2210	
372	DataSheet_1.docx. 2019 ,	
371	Presentation_1.zip. 2020 ,	
370	Image_1.TIF. 2020 ,	
369	Image_2.TIF. 2020 ,	
368	Table_1.xlsx. 2020 ,	



(2018-2019)



331	Table_5.XLSX. 2018 ,	
330	Table_6.XLS. 2018 ,	
329	Table_7.XLS. 2018 ,	
328	Table_8.XLS. 2018 ,	
327	Table_9.XLS. 2018 ,	
326	Data_Sheet_1.pdf. 2019 ,	
325	Prediction of binding miRNAs involved with immune genes to the SARS-CoV-2 by using sequence features extraction and One-class SVM 2022 , 30, 100958	
324	Le changement linguistique au XVIIe s. : nouvelles approches scriptom[] triques. 2022 , 138, 02006	O
323	Hidden Markov Method. 2022 , 71-76	
322	OUP accepted manuscript.	Ο
321	Benchmarking a New Paradigm: Experimental Analysis and Characterization of a Real Processing-in-Memory System. 2022 , 1-1	2
320	Visual Attention Analysis Of Pathologists Examining Whole Slide Images Of Prostate Cancer. 2022 ,	1
319	A Contrastive Learning Pre-Training Method for Motif Occupancy Identification 2022 , 23,	
318	Computational Saturation Mutagenesis to Investigate the Effects of Neurexin-1 Mutations on AlphaFold Structure. 2022 , 13, 789	O
317	Faster SARS-CoV-2 sequence validation and annotation for GenBank using VADR 2022,	
316	PROVAL: A framework for comparison of protein sequence embeddings. 2022 , 100044	1
315	Sattahipmycin, a Hexacyclic Xanthone Produced by a Marine-Derived 2022 ,	O
314	In silico Comparisons of the Ethylene Response Factor 1 (ERF1) Gene Between Malaysian Wild Banana (Musa acuminata ssp. malaccensis) and Pisang Klutuk Wulung (Musa balbisiana). 2022 , 45, 519-545	

Retraction ATPase Motors from Three Orthologous Type IVa Pilus Systems Support Promiscuous 313 Retraction of the Vibrio cholerae Competence Pilus.. 2022, e0012622 DMSP Production by Coral-Associated Bacteria. 2022, 9, 312 iLncDA-LTR: Identification of lncRNA-disease associations by learning to rank. 2022, 105605 311 \circ Accuracy of multiple sequence alignment methods in the reconstruction of transposable element 310 families.. 2022, 4, lgac040 Bi-alignments with affine gaps costs.. 2022, 17, 10 309 Alarm management techniques to improve process safety. 2022, 308 Bibliography. 2022, 213-236 307 306 Sequence analysis. **2022**, 83-96 CrisprVi: a software for visualizing and analyzing CRISPR sequences of prokaryotes. 2022, 23, 305 Antibody repertoire sequencing analysis. 2022, 304 Effects of exercise and sleep deprivation on reaction severity during oral peanut challenge: a 303 0 randomised controlled trial. 2022, Revealing druggable cryptic pockets in the Nsp-1 of SARS-CoV-2 and other ⊯coronaviruses by 302 \circ simulations and crystallography. A survey of mapping algorithms in the long-reads era. 301 1 Effects of habitat and sampling time on bacterial community composition and diversity in the gut 300 of the female house fly, Musca domestica Linnaeus (Diptera: Muscidae). Scanpath Comparison using ScanGraph for Education and Learning Purposes. 2022, 299 1 298 Predicting Decision-Making during an Intelligence Test via Semantic Scanpath Comparisons. 2022, Study on reference-based FASTQ genome sequences compression. 2022, 297 Molecular dynamics and intrinsic disorder analysis of the SARS-CoV-2 Nsp1 structural changes 296 caused by substitution and deletion mutations. 1-10

295	A super robust and efficient DNA storage architecture based on modulation encoding and decoding.	O
294	Genomic and Biological Profile of a Novel Bacteriophage, Vibrio phage Virtus, Which Improves Survival of Sparus aurata Larvae Challenged with Vibrio harveyi. 2022 , 11, 630	2
293	SoftVN. 2022 ,	O
292	Nature Inspired Algorithms for Solving Multiple Sequence Alignment Problem: A Review.	
291	SeMiner: Side-Information-Based Semantics Miner for Proprietary Industrial Control Protocols. 2022 , 1-1	
290	Robust Pose Estimation via Hybrid Point and Twin Line Reprojection for RGB-D Vision Navigation. 2022 , 71, 1-19	1
289	An Improved Chemical Reaction Optimization Approach for Solving Multiple Sequence Alignment Problem. 2022 ,	
288	Clustering of Usage Traces for Regression Test Cases Selection. 2022,	
287	Principal Component Analysis Provides Insights on the Evolutionary Divergence of Conotoxins. 2022 ,	O
286	Environmental DNA (eDNA) metabarcoding surveys show evidence of non-indigenous freshwater species invasion to new parts of Eastern Europe. 6,	
285	Plasmodium vivax malaria serological exposure markers: Assessing the degree and implications of cross-reactivity with P. knowlesi. 2022 , 3, 100662	O
284	4D-Dynamic Representation of DNA/RNA Sequences: Studies on Genetic Diversity of Echinococcus multilocularis in Red Foxes in Poland. 2022 , 12, 877	
283	Terpenoid analogues as putative therapeutic agents towards glutathione peroxidase (GPX4) in neurodegenerative disorders: a dynamic computational approach. 1-11	О
282	Batch alignment via retention orders for preprocessing large-scale multi-batch LC-MS experiments.	
281	New streaming algorithms for high dimensional EMD and MST. 2022,	1
280	A new paradigm of multiheme cytochrome evolution by grafting and pruning protein modules.	2
279	Iso-FRET: an isothermal competition assay to analyze quadruplex formation in vitro.	O
278	A Prospective Study on Resilience Among Children with Different Migrant and Left-behind Trajectories.	

277	Insights into the structural peculiarities of the N-terminal and receptor binding domains of the spike protein from the SARS-CoV-2 Omicron variant. 2022 , 105735	2
276	Temporal Alignment of Longitudinal Microbiome Data. 13,	
275	Analyzing Student SQL Solutions via Hierarchical Clustering and Sequence Alignment Scores. 2022,	1
274	Pangenome evolution in environmentally transmitted symbionts of deep-sea mussels is governed by vertical inheritance.	O
273	Sequential Properties Representation Scheme for Recurrent Neural Network-Based Prediction of Therapeutic Peptides.	1
272	Sequence-sensitive elastic network captures dynamical features necessary for miR-125a maturation.	O
271	AnySeq/GPU. 2022 ,	
270	Computer-assisted pronunciation training Speech synthesis is almost all you need. 2022,	2
269	Computational Reconstruction and Analysis of Structural Models of Avian Cryptochrome 4.	2
268	MeShClust v3.0: high-quality clustering of DNA sequences using the mean shift algorithm and alignment-free identity scores. 2022 , 23,	1
267	Computational method for the systematic alignment of analogue series with structure-activity relationship transfer potential across different targets. 2022 , 239, 114558	0
266	Spike Train Distance. 2022 , 3232-3245	
265	POInT: A Tool for Modeling Ancient Polyploidies Using Multiple Polyploid Genomes. 2022 , 81-91	
264	Protein-Protein Interaction Design with Transformers.	
263	SALoBa: Maximizing Data Locality and Workload Balance for Fast Sequence Alignment on GPUs. 2022 ,	
262	Classification of Protein Structures Using Deep Learning Models. 2022,	
261	VarCLR. 2022 ,	0
260	Proposal of Smith-Waterman algorithm on FPGA to accelerate the forward and backtracking steps. 2022 , 17, e0254736	

259	Cas-CLOVER is a novel high-fidelity nuclease for safe and robust generation of TSCM-enriched allogeneic CAR-T cells. 2022 ,	O
258	A Physcomitrella PIN protein acts in spermatogenesis and sporophyte abortion.	
257	Early DSE and Automatic Generation of Coarse Grained Merged Accelerators.	
256	Progress in and Opportunities for Applying Information Theory to Computational Biology and Bioinformatics. 2022 , 24, 925	
255	Fast trimer statistics facilitate accurate decoding of large random DNA barcode sets even at large sequencing error rates	
254	Differences between Omicron SARS-CoV-2 RBD and other variants in their ability to interact with cell receptors and monoclonal antibodies. 1-21	O
253	Protein structure prediction improves the quality of amino-acid sequence alignment.	0
252	RNAloops: a database of RNA multiloops.	1
251	Response of soil bacterial community to biochar application in a boreal pine forest.	O
250	PhenoTrack3D: an automatic high-throughput phenotyping pipeline to track maize organs over time.	
249	Tandem repeats ubiquitously flank and contribute to translation initiation sites. 2022, 23,	O
248	Tangled gene-for-gene interactions mediate co-evolution of the rice NLR immune receptor Pik and blast fungus effector proteins.	O
247	Sub-messages extraction for industrial control protocol reverse engineering. 2022, 194, 1-14	
246	Appendices. 2006 , 311-318	
245	Preface. 2006 , vii-x	
244	Dedication. 2006 , v-vi	
243	Copyright Page. 2006 , iv-iv	
242	Preface. 2014 , vii-viii	

241 Copyright Page. **2014**, iv-iv

240	Foreword. 2014, v-vi	
239	Gelato: Feedback-driven and Guided Security Analysis of Client-side Web Applications. 2022,	
238	Efficient GPU Implementation of AFP-Based Algorithms to Accelerate Comparative Bioinformatic Analysis of Protein Structures in 3D-Space. 2022 , 43, 904-915	
237	Harnessing machine translation methods for sequence alignment.	
236	Explaining human mobility predictions through a pattern matching algorithm. 2022, 11,	
235	Convolutional Neural Network Applied to SARS-CoV-2 Sequence Classification. 2022 , 22, 5730	
234	An easy way to improve scoring of memory span tasks: The edit distance, beyond florrect recall in the correct serial position[]	О
233	CRISPR comparison toolkit (CCTK): Rapid identification, visualization, and analysis of CRISPR array diversity.	0
232	Regularized DTW in Offline Music Score-Following for Sight-Singing Based on Sol-fa Name Recognition. 2022 ,	
231	Fragment Libraries Designed to Be Functionally Diverse Recover Protein Binding Information More Efficiently Than Standard Structurally Diverse Libraries. 2022 , 65, 11404-11413	1
230	CBMDB: A Database for Accessing, Analyzing, and Mining CBM Information. 2022 , 12, 7842	
229	Cryptosporulation in Kurthia spp. forces a rethinking of asporogenesis in Firmicutes.	
228	WITCH-NG: Efficient and Accurate Alignment of Datasets with Sequence Length Heterogeneity.	
227	mintRULS: Prediction of miRNAThRNA Target Site Interactions Using Regularized Least Square Method. 2022 , 13, 1528	0
226	Supervised Machine Learning Algorithms for Ground Motion Time Series Classification from InSAR Data. 2022 , 14, 3821	O

A key regulator with a MIF-like domain orchestrates cellular differentiation and virulence in the fungal pathogen Magnaporthe oryzae.

Glycoinformatics in the Artificial Intelligence Era.

225

О

223	A general optimization framework for dynamic time warping.	O
222	Cross-Border Transmissions of the Delta Substrain AY.29 During Tokyo Olympic and Paralympic Games. 13,	O
221	TnSmu1 is a functional integrative and conjugative element in Streptococcus mutans that when expressed causes growth arrest of host bacteria.	1
220	Poxviral ANKR/F-box Proteins: Substrate Adapters for Ubiquitylation and More. 2022 , 11, 875	1
219	A key F27I substitution within HCDR1 facilitates the rapid maturation of P2C-1F11-like neutralizing antibodies in a SARS-CoV-2-infected donor. 2022 , 111335	
218	Sequence analysis: Its past, present, and future. 2022 , 102772	1
217	classLog: Logistic regression for the classification of genetic sequences.	
216	Team building without boundaries. 2022,	
215	Intersection two-vehicle crash scenario specification for automated vehicle safety evaluation using sequence analysis and Bayesian networks. 2022 , 176, 106814	0
214	Sequence Alignment. 2022 , 87-111	O
214	Strain wars 4 - Darwinian evolution through Gibbs glasses: Gibbs energies of binding and growth explain evolution of SARS-CoV-2 from Hu-1 to BA.2. 2022 , 575, 36-42	0
· ·	Strain wars 4 - Darwinian evolution through Gibbs[glasses: Gibbs energies of binding and growth	
213	Strain wars 4 - Darwinian evolution through Gibbs Glasses: Gibbs energies of binding and growth explain evolution of SARS-CoV-2 from Hu-1 to BA.2. 2022 , 575, 36-42	1
213	Strain wars 4 - Darwinian evolution through Gibbs Glasses: Gibbs energies of binding and growth explain evolution of SARS-CoV-2 from Hu-1 to BA.2. 2022, 575, 36-42 Modular structure of complex II: An evolutionary perspective. 2023, 1864, 148916 Design and experimental validation of an optimized microalgae-bacteria consortium for the	1 O
213	Strain wars 4 - Darwinian evolution through Gibbs[glasses: Gibbs energies of binding and growth explain evolution of SARS-CoV-2 from Hu-1 to BA.2. 2022, 575, 36-42 Modular structure of complex II: An evolutionary perspective. 2023, 1864, 148916 Design and experimental validation of an optimized microalgae-bacteria consortium for the bioremediation of glyphosate in continuous photobioreactors. 2023, 441, 129921 Self-Supervised Pre-Trained Speech Representation Based End-to-End Mispronunciation Detection	1 O
213 212 211 210	Strain wars 4 - Darwinian evolution through Gibbs lasses: Gibbs energies of binding and growth explain evolution of SARS-CoV-2 from Hu-1 to BA.2. 2022, 575, 36-42 Modular structure of complex II: An evolutionary perspective. 2023, 1864, 148916 Design and experimental validation of an optimized microalgae-bacteria consortium for the bioremediation of glyphosate in continuous photobioreactors. 2023, 441, 129921 Self-Supervised Pre-Trained Speech Representation Based End-to-End Mispronunciation Detection and Diagnosis of Mandarin. 2022, 1-1	1 O 2
213 212 211 210 209	Strain wars 4 - Darwinian evolution through Gibbs[glasses: Gibbs energies of binding and growth explain evolution of SARS-CoV-2 from Hu-1 to BA.2. 2022, 575, 36-42 Modular structure of complex II: An evolutionary perspective. 2023, 1864, 148916 Design and experimental validation of an optimized microalgae-bacteria consortium for the bioremediation of glyphosate in continuous photobioreactors. 2023, 441, 129921 Self-Supervised Pre-Trained Speech Representation Based End-to-End Mispronunciation Detection and Diagnosis of Mandarin. 2022, 1-1 Learning to Match Product Codes. 2022, 29-41	1 O 2 O

205	d-StructMAn: Containerized structural annotation on the scale from genetic variants to whole proteomes. 2022 , 11,	0
204	Semi-Weakly-Supervised Learning of Complex Actions from Instructional Task Videos. 2022,	O
203	PubTables-1M: Towards comprehensive table extraction from unstructured documents. 2022,	2
202	Automatic Field Extraction of Extended TLV for Binary Protocol Reverse Engineering. 2022,	О
201	Interpreting alignment-free sequence comparison: what makes a score a good score?. 2022, 4,	O
200	Multiple genome alignment in the telomere-to-telomere assembly era. 2022 , 23,	O
199	US-align: universal structure alignments of proteins, nucleic acids, and macromolecular complexes. 2022 , 19, 1109-1115	2
198	The impact of biochar on wood-inhabiting bacterial community and its function in a boreal pine forest. 2022 , 17,	O
197	Intron size minimisation in teleosts. 2022 , 23,	2
196	CANTATABrediction of missing links in Boolean networks using genetic programming.	O
196 195	CANTATABrediction of missing links in Boolean networks using genetic programming. Molecular insights into the interaction of apo-lactoferrin with the receptor binding domain of the SARS-CoV-2 spike protein: a molecular dynamics simulation study. 1-14	0
	Molecular insights into the interaction of apo-lactoferrin with the receptor binding domain of the	
195	Molecular insights into the interaction of apo-lactoferrin with the receptor binding domain of the SARS-CoV-2 spike protein: a molecular dynamics simulation study. 1-14 A comparison of techniques for deriving clustering and switching scores from verbal fluency word	0
195 194	Molecular insights into the interaction of apo-lactoferrin with the receptor binding domain of the SARS-CoV-2 spike protein: a molecular dynamics simulation study. 1-14 A comparison of techniques for deriving clustering and switching scores from verbal fluency word lists. 13,	0
195 194 193	Molecular insights into the interaction of apo-lactoferrin with the receptor binding domain of the SARS-CoV-2 spike protein: a molecular dynamics simulation study. 1-14 A comparison of techniques for deriving clustering and switching scores from verbal fluency word lists. 13, Predicting miRNA-disease associations based on multi-view information fusion. 13, Identification of three novel genes in <i>Phenuiviridae</i> detected from	0 0
195 194 193	Molecular insights into the interaction of apo-lactoferrin with the receptor binding domain of the SARS-CoV-2 spike protein: a molecular dynamics simulation study. 1-14 A comparison of techniques for deriving clustering and switching scores from verbal fluency word lists. 13, Predicting miRNA-disease associations based on multi-view information fusion. 13, Identification of three novel genes in <i>Phenuiviridae</i> detected from <i>Aedes</i> mosquitoes in Hokkaido, Japan. 2022, Flap structure within receptor binding domain of SARS-CoV-2 spike periodically obstructs hACE2	0 0
195 194 193 192	Molecular insights into the interaction of apo-lactoferrin with the receptor binding domain of the SARS-CoV-2 spike protein: a molecular dynamics simulation study. 1-14 A comparison of techniques for deriving clustering and switching scores from verbal fluency word lists. 13, Predicting miRNA-disease associations based on multi-view information fusion. 13, Identification of three novel genes in <i>Phenuiviridae</i> detected from <i>Aedes</i> mosquitoes in Hokkaido, Japan. 2022, Flap structure within receptor binding domain of SARS-CoV-2 spike periodically obstructs hACE2 Binding subdomain bearing similarities to HIV-1 protease flap. 2022, 12,	00000

187	Toward Efficient Similarity Search under Edit Distance on Hybrid Architectures. 2022 , 13, 452	O
186	A unified approach to sequential and non-sequential structure alignment of proteins, RNAs and DNAs. 2022 , 105218	O
185	Evolutionary conservation of sequence motifs at sites of protein modification.	0
184	Inferring and perturbing cell fate regulomes in human brain organoids.	O
183	Network Communication Protocol Reverse Engineering Based on Auto-Encoder. 2022, 2022, 1-14	0
182	Chapter 11 Experimentation for Business-to-Business Mission-Critical Systems: A Case Study. 2020 , 351-371	O
181	Chapter 10 Requirements Engineering Challenges and Practices in Large-Scale Agile System Development. 2020 , 293-350	0
180	Chapter 13 Engineering Al Systems. 2021 , 407-425	O
179	Chapter 3 Efficient and Effective Exploratory Testing of Large-Scale Software Systems. 2021 , 51-81	1
178	Introduction to the Continuous Architecture Theme. 2022 , 85-86	O
177	Introduction to the Continuous Delivery Theme. 2022 , 3-5	O
176	Introduction to the Customer Data and Ecosystem-Driven Development Theme. 2022 , 287-291	O
175	Target-Absent Human Attention. 2022 , 52-68	0
174	Introduction to the Al Engineering Theme. 2022 , 399-405	O
173	Introduction to the Metrics Theme. 2022 , 155-161	0
172	FaST. 2022 ,	O
171	Robust RGB-D Visual Odometry Using Point and Line Features. 2022 ,	0
170	An 85-amino-acid polypeptide from Myrmeleon bore larvae (antlions) homologous to heat shock factor binding protein 1 with antiproliferative activity against MG-63 osteosarcoma cells in vitro. 2022 , 16, 201-211	O

169	SoftMatch: Comparing Scanpaths Using Combinatorial Spatio-Temporal Sequences with Fractal Curves. 2022 , 22, 7438	0
168	Vector-clustering Multiple Sequence Alignment: Aligning into the twilight zone of protein sequence similarity with protein language models.	Ο
167	Tn Smu1 is a functional integrative and conjugative element in Streptococcus mutans that when expressed causes growth arrest of host bacteria.	О
166	Write Me and III Tell You Secrets IWrite-After-Write Effects On Intel CPUs. 2022 ,	O
165	Hybridization order is not the driving factor behind biases in duplicate gene losses among the hexaploid Solanaceae. 2022 , 289,	1
164	Seed-chain-extend alignment is accurate and runs in close toO(mlogn) time for similar sequences: a rigorous average-case analysis.	О
163	Changing Employment and Work Schedule Patterns over the 30 Working Years A Sequential Cluster Analysis. 2022 , 19, 13677	0
162	Heterogeneous network propagation with forward similarity integration to enhance drugEarget association prediction. 8, e1124	O
161	In silico functional annotation of hypothetical proteins from the Bacillus paralicheniformis strain Bac84 reveals proteins with biotechnological potentials and adaptational functions to extreme environments. 2022 , 17, e0276085	0
160	RecGraph: adding recombinations to sequence-to-graph alignments.	
		Ο
159	GenSLMs: Genome-scale language models reveal SARS-CoV-2 evolutionary dynamics.	0
159 158		
0,9	GenSLMs: Genome-scale language models reveal SARS-CoV-2 evolutionary dynamics.	0
158	GenSLMs: Genome-scale language models reveal SARS-CoV-2 evolutionary dynamics. RabbitTClust: enabling fast clustering analysis of millions bacteria genomes with MinHash sketches.	0
158	GenSLMs: Genome-scale language models reveal SARS-CoV-2 evolutionary dynamics. RabbitTClust: enabling fast clustering analysis of millions bacteria genomes with MinHash sketches. Alignment-free Comparison of Metagenomics Sequences via Approximate String Matching. Contrastive study of minimum edit distance and cosine similarity measures in the context of word	0 0
158 157 156	GenSLMs: Genome-scale language models reveal SARS-CoV-2 evolutionary dynamics. RabbitTClust: enabling fast clustering analysis of millions bacteria genomes with MinHash sketches. Alignment-free Comparison of Metagenomics Sequences via Approximate String Matching. Contrastive study of minimum edit distance and cosine similarity measures in the context of word suggestions for misspelled Marathi words.	0 0
158 157 156	GenSLMs: Genome-scale language models reveal SARS-CoV-2 evolutionary dynamics. RabbitTClust: enabling fast clustering analysis of millions bacteria genomes with MinHash sketches. Alignment-free Comparison of Metagenomics Sequences via Approximate String Matching. Contrastive study of minimum edit distance and cosine similarity measures in the context of word suggestions for misspelled Marathi words. Heuristic Pairwise Alignment in Database Environments. 2022, 13, 2005 Bioinformatic Analysis of B- and T-cell Epitopes from SARS-CoV-2 Structural Proteins and their	0 0 0

151	Leptospiral lipopolysaccharide mediated Hog1 phosphorylation in Saccharomyces cerevisiae directs activation of autophagy. 2022 , 173, 105840	0
150	Multiple Sequence Alignment based on deep Q network with negative feedback policy. 2022 , 101, 107780	0
149	Chapter 1 Climbing the Stairway to Heaven. 2012 , 7-22	4
148	Chapter 2 Modeling Continuous Integration Practice Differences in Industry Software Development. 2013 , 23-49	O
147	Chapter 5 Expectations and Challenges from Scaling Agile in Mechatronics-Driven Companies DA Comparative Case Study. 2015 , 119-130	0
146	Chapter 7 MESRAM IA Method for Assessing Robustness of Measurement Programs in Large Software Development Organizations and Its Industrial Evaluation. 2015 , 163-209	1
145	Chapter 12 The Evolution of Continuous Experimentation in Software Product Development: From Data to a Data-Driven Organization at Scale. 2017 , 373-395	0
144	Chapter 4 Technical Debt Tracking: Current State of Practice: A Survey and Multiple Case Study in 15 Large Organizations. 2018 , 87-118	0
143	Chapter 9 SimSAX: A Measure of Project Similarity Based on Symbolic Approximation Method and Software Defect Inflow. 2019 , 253-283	0
142	Chapter 6 Lightweight Consistency Checking for Agile Model-Based Development in Practice. 2019 , 131-151	0
141	Chapter 8 Recognizing Lines of Code Violating Company-Specific Coding Guidelines Using Machine Learning. 2019 , 211-251	0
140	Almost Rerere: Learning to resolve conflicts in distributed projects. 2022 , 1-18	0
139	Flow Graph to Video Grounding for Weakly-Supervised Multi-step Localization. 2022 , 319-335	0
138	Surfing the Wavefront of Genome Alignment. 2022 ,	O
137	A Hardware Accelerator for Long Sequence Alignment with the Bit-Vector Scoring Scheme and Divide-and-Conquer Traceback. 2022 ,	0
136	Using trace alignments for measuring the similarity between a physical and its digital twin. 2022,	0
135	ProsegDL: Binary Protocol Format Extraction by Deep Learning-based Field Boundary Identification. 2022 ,	0
134	In silico characterization, molecular docking, and dynamic simulation of a novel fungal cell-death suppressing effector, MoRlpA as potential cathepsin B-like cysteine protease inhibitor during rice blast infection. 1-18	O

133	Fast trimer statistics facilitate accurate decoding of large random DNA barcode sets even at large sequencing error rates	О
132	Vetinformatics from functional genomics to drug discovery: Insights into decoding complex molecular mechanisms of livestock systems in veterinary science. 9,	O
131	Distantly Related Homologue of UhpT in Pseudomonas aeruginosa. 2022 , 1, 266-278	0
130	Deep learning in drug discovery: an integrative review and future challenges.	1
129	In silico and in vitro arboviral MHC class I-restricted-epitope signatures reveal immunodominance and poor overlapping patterns. 13,	1
128	Human Nucleolar Protein 7 (NOL7) is required for pre-rRNA transcription and pre-18S rRNA processing.	Ο
127	Omicron BA.2.75 Sublineage (Centaurus) Follows the Expectations of the Evolution Theory: Less Negative Gibbs Energy of Biosynthesis Indicates Decreased Pathogenicity. 2022 , 13, 937-952	1
126	VarSCAT: A computational tool for sequence context annotations of genomic variants.	Ο
125	End-to-end learning of multiple sequence alignments with differentiable Smith-Waterman.	О
124	Comparison of phylogenetic placements to pairwise alignments for taxonomic assignment of ciliate OTUs.	Ο
123	SeqCP: A sequence-based algorithm for searching circularly permuted proteins. 2022,	О
122	Construction of gene co-expression networks in cultured silkworm cells and identification of previously uncharacterized lepidopteran-specific genes required for chromosome dynamics. 2022 , 103875	О
121	Improving the IR spectra alignment algorithm with spectra deconvolution and combination with Raman or VCD spectroscopy.	О
120	A High-Logic-Density, Low-Power Control Character Detection and Identification Circuit for the JESD204B Data Link Layer. 2022 , 1-1	Ο
119	A novel pattern-based edit distance for automatic log parsing. 2022,	О
118	Revealing druggable cryptic pockets in the Nsp1 of SARS-CoV-2 and other 毗oronaviruses by simulations and crystallography. 11,	O
117	Biology and medicine in the landscape of quantum advantages. 2022 , 19,	О
116	Recent advances in machine learning methods for predicting LncRNA and disease associations. 12,	Ο

115	Evaluation of genome and base editing tools in maize protoplasts. 13,	0
114	Traceback Memory Reduction for Three-Sequence Alignment Algorithm with Affine Gap Models. 2022 ,	О
113	Systematic analysis of paralogous regions in 41,755 exomes uncovers clinically relevant variation.	0
112	PhenoTrack3D: an automatic high-throughput phenotyping pipeline to track maize organs over time. 2022 , 18,	1
111	Opposite roles of MAPKKK17 and MAPKKK21 against Tetranychus urticae in Arabidopsis. 13,	0
110	Exhaustive Mutational Analysis of scv ORF3a: an Essential Component in the Pathogen's Infectivity Cycle.	O
109	Mirage28 high-quality spliced protein-to-genome mappings produce accurate multiple-sequence alignments of isoforms.	0
108	Investigating graph neural network for RNA structural embedding.	О
107	LncRNA-disease association identification using graph auto-encoder and learning to rank.	0
106	Design of MMP-1 inhibitors via SAR transfer and experimental validation. 2022 , 12,	O
105	A rapid phylogeny-based method for accurate community profiling of large-scale metabarcoding datasets.	0
104	The development of an automatic speech recognition model using interview data from long-term care for older adults.	o
103	Sequence-sensitive elastic network captures dynamical features necessary for miR-125a maturation. 2022 , 18, e1010777	0
102	mapquik: Efficient low-divergence mapping of long reads in minimizer space.	O
101	Deciphering clinical abbreviations with a privacy protecting machine learning system. 2022, 13,	0
100	Human gait-labeling uncertainty and a hybrid model for gait segmentation. 16,	1
99	Comparison of two approaches in multichannel sequence analysis using the Swiss Household Panel. 2022 , 1-32	0
98	On the choice of negative examples for prediction of host-pathogen protein interactions. 2,	О

97	Extending the Bag Distance for String Similarity Search. 2023, 4,	О
96	Detection of positive selection acting on protein surfaces at the whole-genome scale in the human malaria parasite Plasmodium falciparum. 2022 , 105397	O
95	Principal Component and Structural Element Analysis Provide Insights into the Evolutionary Divergence of Conotoxins. 2023 , 12, 20	0
94	Oligoclonal Development of B Cells Bearing Discrete Ig Chains in Chicken Single Germinal Centers. 1998 , 160, 4232-4241	10
93	Fast Longest Common Subsequence with General Integer Scoring Support on GPUs. 2014,	0
92	Efficient Parallel Implementations of Multiple Sequence Alignment using BSP/CGM Model. 2014,	O
91	Sensitive inference of alignment-safe intervals from biodiverse protein sequence clusters using EMERALD.	O
90	FAXC Proteins of Vertebrates and Invertebrates: Relationship to Metaxin Proteins.	O
89	An improved dynamic time warping method combing distance density clustering for eye movement analysis.	0
88	A spatial genome aligner for resolving chromatin architectures from multiplexed DNA FISH.	O
87	ProFeatX: A parallelized protein feature extraction suite for machine learning. 2023, 21, 796-801	0
86	Bioinformatic analysis of the effect of SNPs in the pig TERT gene on the structural and functional characteristics of the enzyme to develop new genetic markers of productivity traits.	О
85	Hardness and approximation of multiple sequence alignment with column score. 2023, 946, 113683	О
84	Levenshtein graphs: Resolvability, automorphisms & amp; determining sets. 2023, 346, 113310	O
83	DLCSS: Dynamic Longest Common Subsequences. 2022,	0
82	KANALYZER: a method to identify variations of discriminative k-mers in genomic sequences. 2022,	O
81	A Guide to In Silico Drug Design. 2023 , 15, 49	0
80	Imaging of Gव् Proteins in Mouse and Human Organs and Tissues. 2023 , 15, 57	O

79	CorrectSpeech: A Fully Automated System for Speech Correction and Accent Reduction. 2022,	O
78	Mitigating the effects of temporal distortion in a copy-detection based playback attack detector. 2022 ,	O
77	TLR4 and MD2 variation among horses with differential TNFD aseline concentrations and response to intravenous lipopolysaccharide infusion. 2023 , 13,	O
76	Tailoring the Host Range of Ackermannviridae Bacteriophages through Chimeric Tailspike Proteins. 2023 , 15, 286	O
75	Strain Tracking with Uncertainty Quantification.	O
74	MetaDamage tool: Examining post-mortem damage in sedaDNA on a metagenomic scale. 10,	O
73	Synchro-Sub, an adaptive multi-algorithm framework for real-time subtitling synchronisation of multi-type TV programmes.	O
72	Identification of novel amyloidosis in dogs: Es1-casein acquires amyloidogenicity in mammary tumor by overexpression and N-terminal truncation. 030098582211485	1
71	Disentangling the complex gene interaction networks between rice and the blast fungus identifies a new pathogen effector. 2023 , 21, e3001945	O
70	The arithmetic topology of genetic alignments. 2023 , 86,	O
70 69	The arithmetic topology of genetic alignments. 2023 , 86, Biochemical and Genetic Evidence Supports Fyv6 as a Second-Step Splicing Factor inSaccharomyces cerevisiae.	0
	Biochemical and Genetic Evidence Supports Fyv6 as a Second-Step Splicing Factor inSaccharomyces	
69	Biochemical and Genetic Evidence Supports Fyv6 as a Second-Step Splicing Factor inSaccharomyces cerevisiae.	О
69 68	Biochemical and Genetic Evidence Supports Fyv6 as a Second-Step Splicing Factor inSaccharomyces cerevisiae. Faster SARS-CoV-2 sequence validation and annotation for GenBank using VADR. 2023, 5, A Linear Memory CTC-Based Algorithm for Text-to-Voice Alignment of Very Long Audio	0
69 68 67	Biochemical and Genetic Evidence Supports Fyv6 as a Second-Step Splicing Factor inSaccharomyces cerevisiae. Faster SARS-CoV-2 sequence validation and annotation for GenBank using VADR. 2023, 5, A Linear Memory CTC-Based Algorithm for Text-to-Voice Alignment of Very Long Audio Recordings. 2023, 13, 1854	0 0
69 68 67 66	Biochemical and Genetic Evidence Supports Fyv6 as a Second-Step Splicing Factor inSaccharomyces cerevisiae. Faster SARS-CoV-2 sequence validation and annotation for GenBank using VADR. 2023, 5, A Linear Memory CTC-Based Algorithm for Text-to-Voice Alignment of Very Long Audio Recordings. 2023, 13, 1854 nPoRe: n-polymer realigner for improved pileup-based variant calling. 2023, 24,	0 0
69 68 67 66	Biochemical and Genetic Evidence Supports Fyv6 as a Second-Step Splicing Factor inSaccharomyces cerevisiae. Faster SARS-CoV-2 sequence validation and annotation for GenBank using VADR. 2023, 5, A Linear Memory CTC-Based Algorithm for Text-to-Voice Alignment of Very Long Audio Recordings. 2023, 13, 1854 nPoRe: n-polymer realigner for improved pileup-based variant calling. 2023, 24, Evolutionary conservation of sequence motifs at sites of protein modification. 2023, 299, 104617 Towards the accurate alignment of over a million protein sequences: Current state of the art. 2023,	O O O

61	New Short RNA Motifs Potentially Relevant in the SARS-CoV-2 Genome. 2022 , 23, 424-440	Ο
60	A Physcomitrella PIN protein acts in spermatogenesis and sporophyte retention. 2023 , 237, 2118-2135	O
59	Crafting negative training datasets for a high-performance classification of bacterial proteins secreted via non-classical pathways.	0
58	Employing string similarity metrics of partners to estimate audit team continuity: determinant and its effects on audit outcomes and pricing. 2023 , 45, 314-339	Ο
57	A comprehensive rRNA variation atlas in health and disease.	1
56	Quantitative comparison of protein-protein interaction interface using physicochemical feature-based descriptors of surface patches. 10,	O
55	Sequence and structure alignments in post-AlphaFold era. 2023 , 79, 102539	О
54	MOOCs Learning Pathways Recommendation Based on Sequence Alignment. 2022,	Ο
53	Optimal gap-affine alignment inO(s) space. 2023 , 39,	Ο
52	Pairwise Sequence Alignment. 2022 , 57-83	Ο
52 51	Pairwise Sequence Alignment. 2022, 57-83 bpRNA-align: improved RNA secondary structure global alignment for comparing and clustering RNA structures. 2023, 29, 584-595	0
	bpRNA-align: improved RNA secondary structure global alignment for comparing and clustering	
51	bpRNA-align: improved RNA secondary structure global alignment for comparing and clustering RNA structures. 2023 , 29, 584-595	0
51	bpRNA-align: improved RNA secondary structure global alignment for comparing and clustering RNA structures. 2023, 29, 584-595 SCARECROW-like GRAS protein PES positively regulates petunia floral scent production. HMM-based profiling identifies the binding to divalent cations and nucleotides as common	0
51 50 49	bpRNA-align: improved RNA secondary structure global alignment for comparing and clustering RNA structures. 2023, 29, 584-595 SCARECROW-like GRAS protein PES positively regulates petunia floral scent production. HMM-based profiling identifies the binding to divalent cations and nucleotides as common denominators of suramin targets. 3, MSGCL: inferring miRNA@isease associations based on multi-view self-supervised graph structure	0 0
51 50 49 48	bpRNA-align: improved RNA secondary structure global alignment for comparing and clustering RNA structures. 2023, 29, 584-595 SCARECROW-like GRAS protein PES positively regulates petunia floral scent production. HMM-based profiling identifies the binding to divalent cations and nucleotides as common denominators of suramin targets. 3, MSGCL: inferring miRNAdisease associations based on multi-view self-supervised graph structure contrastive learning. 2023, 24,	o o o
51 50 49 48 47	bpRNA-align: improved RNA secondary structure global alignment for comparing and clustering RNA structures. 2023, 29, 584-595 SCARECROW-like GRAS protein PES positively regulates petunia floral scent production. HMM-based profiling identifies the binding to divalent cations and nucleotides as common denominators of suramin targets. 3, MSGCL: inferring miRNABisease associations based on multi-view self-supervised graph structure contrastive learning. 2023, 24, An Experimental Comparison of Clone Detection Techniques using Java Bytecode. 2022, Deep reinforcement learning-based pairwise DNA sequence alignment method compatible with	0 0 0

43	Analyzing Passing Sequences for the Prediction of Goal-Scoring Opportunities. 2023, 27-40	О
42	Krein support vector machine classification of antimicrobial peptides. 2023 , 2, 502-511	O
41	Reconstructing B cell lineage trees with minimum spanning tree and genotype abundances. 2023 , 24,	О
40	Exploring microbial functional biodiversity at the protein family levelErom metagenomic sequence reads to annotated protein clusters. 3,	O
39	Processing genome-wide association studies within a repository of heterogeneous genomic datasets. 2023 , 24,	0
38	Computational genomics for understanding of DNA-DNA and protein-protein similarity. 2023 , 217-263	O
37	Sequence Analysis. 2022 , 415-437	О
36	Dynamic kernel matching for non-conforming data: A case study of T cell receptor datasets. 2023 , 18, e0265313	O
35	Closely relatedBacteroidesof the murine intestinal microbiota affect each other growth positively or negatively.	O
34	High degree of individual repeatability found in the annual migrations of walleye (Sander vitreus) in eastern Lake Ontario. 2023 ,	O
33	WITCH-NG: efficient and accurate alignment of datasets with sequence length heterogeneity. 2023 , 3,	0
32	Challenges and perspectives in recurrence analyses of event time series. 9,	О
31	Query Similarity of Various Linguistic Levels for Hybridized Conversational Agents. 2023,	O
30	AMHMDA: attention aware multi-view similarity networks and hypergraph learning for miRNAdisease associations identification. 2023 , 24,	O
29	Impact and characterization of serial structural variations across humans and great apes.	О
28	Insight into biosorption of hexavalent chromium using isolated species Aspergillus Proliferans LA: A systemic and In silico studies. 2023 , 7, 83	O
27	Identification of potential selective autophagy receptors from protein-content profiling of autophagosomes.	О
26	Lower respiratory tract microbiome composition and community interactions in smokers. 2023 , 5,	О

25	Toward IoT Device Fingerprinting from Proprietary Protocol Traffic via Key-Blocks Aware Approach. 2023 , 103145	О
24	Purification and Biological Properties of Raniseptins-3 and -6, Two Antimicrobial Peptides from Boana raniceps (Cope, 1862) Skin Secretion. 2023 , 13, 576	O
23	Study of the error correction capability of multiple sequence alignment algorithm (MAFFT) in DNA storage. 2023 , 24,	О
22	Rhetoric Mining: A New Text-Analytics Approach for Quantifying Persuasion.	O
21	Reference-free phylogeny from sequencing data. 2023 , 16,	O
20	Design and Pharmacological Characterization of 41 Integrin Cyclopeptide Agonists: Computational Investigation of Ligand Determinants for Agonism versus Antagonism. 2023, 66, 5021-5040	O
19	Transposon-sequencing across multipleMycobacterium abscessusisolates reveals significant functional genomic diversity among strains.	О
18	Genome Alignments. 2023,	O
17	Shine: A novel strategy to extract specific, sensitive and well-conserved biomarkers from massive microbial genomic datasets. 2023 , 24,	O
16	Place and immigrant labour market integration: A sequence analysis approach. 096977642311663	O
15	Application of Needleman-Wunsch Algorithm in Image Comparison. 2022,	О
14	New insights into the genome and transmission of the microsporidian pathogen Nosema muscidifuracis. 14,	O
13	Chromatin context-dependent regulation and epigenetic manipulation of prime editing.	O
12	Complex Networks Analyses of Antibiofilm Peptides: An Emerging Tool for Next-Generation AntimicrobialsDiscovery. 2023 , 12, 747	O
11	Integration of mRNA and miRNA Analysis Reveals the Post-Transcriptional Regulation of Salt Stress Response in Hemerocallis fulva. 2023 , 24, 7290	О
10	Gibberellin 2-Oxidases in Potato (Solanum tuberosum L.): Cloning, Characterization, In Silico Analysis and Molecular Docking.	O
9	GraphPart: Homology partitioning for biological sequence analysis.	О
8	PaxDB 5.0: curated protein quantification data suggests adaptive proteome changes.	O

7	Deciphering the sex bias in housekeeping gene expression in adipose tissue: a comprehensive meta-analysis of transcriptomic studies. 2023 , 14,	0
6	Histone divergence inTrypanosoma bruceiresults in unique alterations to nucleosome structure.	O
5	An image cryptography method by highly error-prone DNA storage channel. 11,	O
4	Protein Structure Prediction in Structural Genomics without Alignment Using Support Vector Machine with Fuzzy Logic. 2023 ,	O
3	Playing the System: Can Puzzle Players Teach us How to Solve Hard Problems?. 2023,	0
2	RNA-NRD: a non-redundant RNA structural dataset for benchmarking and functional analysis. 2023 , 5,	O
1	Weighted Edit Distance Computation: Strings, Trees, and Dyck. 2023 ,	О