Citation Report
List of articles citing

Initial sequencing and analysis of the human genome

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2248	Reflections on the origins of the human brain. 1-22		
2247	Strategies for Identifying RNA Splicing Regulatory Motifs and Predicting Alternative Splicing Events. **2008**, 4, e21		
2246	Birthday Honours. **1899**, 1, 1421-1422		
2245	Dancing Nucleotides. **1920**, 187-213		
2244	Quantitative chromatographic estimation of alpha-amino-acids. *Nature*, **1948**, 161, 763	50.4	48
2243	Prader-Willi and Angelman syndromes: update on genetic mechanisms and diagnostic complexities. **1999**, 12, 149-54		18
2242	Biological aspects of DNA/RNA quadruplexes. **2000**, 56, 209-27		157
2241	The Organism is dead. Long live the organism!. **2000**, 8, 286-315		18
2240	Overview of Electrophysiological Techniques. **2014**, 64, 11.1.1-17		10
2239	The human repertoire of odorant receptor genes and pseudogenes. **2001**, 2, 493-510		86
2238	The impact of microbial genomics on antimicrobial drug development. **2001**, 2, 259-69		20
2237	An overview of the genetic analysis of complex diseases, with reference to type 1 diabetes. **2001**, 15, 265-77		5
2236	The genetics of type 2 diabetes. **2001**, 15, 293-308		48
2235	Non-coding RNAs: the architects of eukaryotic complexity. **2001**, 2, 986-91		584
2234	Functionally gene-linked polymorphic regions and genetically controlled neurotransmitters metabolism. **2001**, 11, 431-9		18

2233	Variation of serotonergic gene expression: neurodevelopment and the complexity of response to psychopharmacologic drugs. **2001**, 11, 457-74	53
2232	Genetics and genomics in neuropsychopharmacology: the impact on drug discovery and development. **2001**, 11, 491-9	7
2231	Fully Automated Parallel Oligonucleotide Synthesizer. **2001**, 66, 1299-1314	19
2230	Evolutionary perspective on innate immune recognition. **2001**, 155, 705-10	66
2229	Delivery of neurotrophic factors to the central nervous system: pharmacokinetic considerations. **2001**, 40, 907-46	356
2228	The genetic architecture of quantitative traits. **2001**, 35, 303-39	820
2227	Comparative genomic sequencing reveals a strikingly similar architecture of a conserved syntenic region on human chromosome 11p15.3 (including gene ST5) and mouse chromosome 7. **2001**, 93, 284-90	16
2226	Use of cDNA microarrays to analyze dioxin-induced changes in human liver gene expression. **2001**, 122, 189-203	130
2225	Comprehensive analysis of a large genomic sequence at the putative B-cell chronic lymphocytic leukaemia (B-CLL) tumour suppresser gene locus. **2001**, 458, 55-70	18
2224	Hypothermia for traumatic brain injury--a good idea proved ineffective. **2001**, 344, 602-3	26
2223	Prediction of unidentified human genes on the basis of sequence similarity to novel cDNAs from cynomolgus monkey brain. **2002**, 3, RESEARCH0006	9
2222	What use is the human genome for understanding the mouse?. **2001**, 2, COMMENT2009	2
2221	What does a worm want with 20,000 genes?. **2001**, 2, COMMENT2008	28
2220	The olfactory receptor family album. **2001**, 2, REVIEWS1027	19
2219	Abundant protein domains occur in proportion to proteome size. **2001**, 2, RESEARCH0039	1
2218	The trappist's approach to pathfinding: elucidating brain wiring using secretory-trap mutagenesis. **2001**, 2, REVIEWS1026	2
2217	Nucleomorph genomes: much ado about practically nothing. **2001**, 2, REVIEWS1022	16
2216	A draft annotation and overview of the human genome. **2001**, 2, RESEARCH0025	34

2215	Genome cartography through domain annotation. **2001**, 2, Comment 2006	7
2214	Evolution of mammalian genome organization inferred from comparative gene mapping. **2001**, 2, REVIEWS0005	530
2213	Bases and spaces: resources on the web for accessing the draft human genome - II - after publication of the draft. **2001**, 2, REVIEWS2001	1
2212	The human olfactory receptor repertoire. **2001**, 2, RESEARCH0018	218
2211	Endogenous retroviruses in the human genome sequence. **2001**, 2, REVIEWS1017	169
2210	Towards a complete sequence of the human Y chromosome. **2001**, 2, REVIEWS1016	16
2209	Characterizing glycosylation pathways. **2001**, 2, REVIEWS0004	62
2208	Goodbye to 'one by one' genetics. **2001**, 2, COMMENT2004	4
2207	Twin peaks: the draft human genome sequence. **2001**, 2, COMMENT2003	
2206	Sequence interpretation. Making sense of the sequence. **2001**, 291, 1257-60	21
2205	Tech.Sight. Sequencing genomes and beyond. **2001**, 292, 515-7	15
2204	Gentica no mendeliana y crecimiento. El sndrome de Russel-Silver. **2001**, 54, 531-535	1
2203	The catalog of human hair keratins. II. Expression of the six type II members in the hair follicle and the combined catalog of human type I and II keratins. **2001**, 276, 35123-32	214
2202	Abundance, distribution, and transcriptional activity of repetitive elements in the maize genome. **2001**, 11, 1660-76	316
2201	Evolving genomic metaphors: a new look at the language of DNA. **2001**, 294, 86-7	72
2200	Human Genome Project: German Perspective. **2001**, 6995-6999	
2199	A new approach to decoding life: systems biology. **2001**, 2, 343-72	1187
2198	High-throughput proteomics: protein expression and purification in the postgenomic world. **2001**, 22, 159-64	142

2197	A train of thoughts on gene mapping. **2001**, 60, 149-53	12
2196	Implications of multilocus inheritance for gene-disease association studies. **2001**, 60, 215-20	39
2195	Estrogen receptors alpha and beta exhibit different estradiol and estrogen response element binding in the presence of nonspecific DNA. **2001**, 390, 253-64	12
2194	Androgens regulate the mammalian homologues of invertebrate sex determination genes tra-2 and fox-1. **2001**, 282, 499-506	25
2193	Sulfation of endothelial mucin by corneal keratan N-acetylglucosamine 6-O-sulfotransferase (GST-4beta). **2001**, 282, 928-33	14
2192	Evidence that caspase-13 is not a human but a bovine gene. **2001**, 285, 1150-4	39
2191	Characterization of tissue- and cell-type-specific expression of a novel human septin family gene, Bradeion. **2001**, 286, 547-53	19
2190	The genomic structure and promoter region of the human parkin gene. **2001**, 286, 863-8	36
2189	Analysis of the mammalian talin2 gene TLN2. **2001**, 286, 880-5	90
2188	Coparalogy: physical and functional clusterings in the human genome. **2001**, 288, 362-70	41
2187	New insights into the origin of the Gaucher disease-causing mutation N370S: extended haplotype analysis using the 5GC3.2, 5470 G/A, and ITG6.2 polymorphisms. **2001**, 27, 950-9	9
2186	PCR-CTPP: a new genotyping technique in the era of genetic epidemiology. **2001**, 1, 119-23	59
2185	Songbird genomics: analysis of 45 kb upstream of a polymorphic Mhc class II gene in red-winged blackbirds (Agelaius phoeniceus). **2001**, 75, 26-34	44
2184	Repetitive elements in the 5' untranslated region of a human zinc-finger gene modulate transcription and translation efficiency. **2001**, 76, 110-6	51
2183	Assessment of the total number of human transcription units. **2001**, 77, 71-8	49
2182	The human mitochondrial ribosomal protein genes: mapping of 54 genes to the chromosomes and implications for human disorders. **2001**, 77, 65-70	77
2181	The mouse genome sequence: status and prospects. **2001**, 77, 117-8	8
2180	From PREDs and open reading frames to cDNA isolation: revisiting the human chromosome 21 transcription map. **2001**, 78, 46-54	33

2179	Transduction of the human gene FAM8A1 by endogenous retrovirus during primate evolution. **2001**, 78, 38-45		31
2178	Complex high-resolution linkage disequilibrium and haplotype patterns of single-nucleotide polymorphisms in 2.5 Mb of sequence on human chromosome 21. **2001**, 78, 64-72		15
2177	Homology between a 173-kb region from mouse chromosome 10, telomeric to the Ifng locus, and human chromosome 12q15. **2001**, 78, 206-13		19
2176	Predicting the functional consequences of non-synonymous single nucleotide polymorphisms: structure-based assessment of amino acid variation. **2001**, 307, 683-706		321
2175	Large-scale analysis of the Alu Ya5 and Yb8 subfamilies and their contribution to human genomic diversity. **2001**, 311, 17-40		135
2174	Bacterial comparative genomic hybridization: a method for directly identifying lateral gene transfer. **2001**, 312, 1-5		24
2173	Rearrangement of side-chains in a Zif268 mutant highlights the complexities of zinc finger-DNA recognition. **2001**, 313, 309-15		60
2172	Cardiovascular genomics: estimating the total number of genes expressed in the human cardiovascular system. **2001**, 33, 1879-86		33
2171	Stability of membrane proteins: relevance for the selection of appropriate methods for high-resolution structure determinations. **2001**, 136, 144-57		73
2170	Regulation of alternative splicing of human tau exon 10 by phosphorylation of splicing factors. **2001**, 18, 80-90		93
2169	DNA methylation analysis by MethyLight technology. **2001**, 25, 456-62		103
2168	Heterozygosity: an expanding role in proteomics. **2001**, 74, 51-63		27
2167	Expression profiling of renal epithelial neoplasms: a method for tumor classification and discovery of diagnostic molecular markers. **2001**, 158, 1639-51		269
2166	Hemogen is a novel nuclear factor specifically expressed in mouse hematopoietic development and its human homologue EDAG maps to chromosome 9q22, a region containing breakpoints of hematological neoplasms. **2001**, 104, 105-11		48
2165	A physical map of the human genome. *Nature*, **2001**, 409, 934-41	50.4	732
2164	Mouse BAC ends quality assessment and sequence analyses. **2001**, 11, 1736-45		44
2163	Pharmacogenetics in Evidence-based practice--what to watch for. **2001**, 5, 109-10		
2162	Mitochondria and the quality of human gametes. **2001**, 68, 1535-7		9

2161	Mutations of the protocadherin gene PCDH15 cause Usher syndrome type 1F. **2001**, 69, 25-34	330
2160	High-resolution multipoint linkage-disequilibrium mapping in the context of a human genome sequence. **2001**, 69, 159-78	104
2159	Estimating the efficacy and efficiency of cascade genetic screening. **2001**, 69, 361-70	49
2158	Molecular characterization and gene content of breakpoint boundaries in patients with neurofibromatosis type 1 with 17q11.2 microdeletions. **2001**, 69, 516-27	112
2157	A genomewide scan for loci predisposing to type 2 diabetes in a U.K. population (the Diabetes UK Warren 2 Repository): analysis of 573 pedigrees provides independent replication of a susceptibility locus on chromosome 1q. **2001**, 69, 553-69	271
2156	Lower-than-expected linkage disequilibrium between tightly linked markers in humans suggests a role for gene conversion. **2001**, 69, 582-9	86
2155	An immune defect causing dominant chronic mucocutaneous candidiasis and thyroid disease maps to chromosome 2p in a single family. **2001**, 69, 791-803	34
2154	Mutations in CGI-58, the gene encoding a new protein of the esterase/lipase/thioesterase subfamily, in Chanarin-Dorfman syndrome. **2001**, 69, 1002-12	382
2153	On the evolution of protein folds: are similar motifs in different protein folds the result of convergence, insertion, or relics of an ancient peptide world?. **2001**, 134, 191-203	225
2152	Simulated refolding of stretched titin immunoglobulin domains. **2001**, 81, 2268-77	45
2151	The mammalian retinal degeneration B2 gene is not required for photoreceptor function and survival. **2001**, 107, 35-41	41
2150	Multiple alignment of complete sequences (MACS) in the post-genomic era. **2001**, 270, 17-30	54
2149	Generation of a P1 artificial chromosome library of the Southern pufferfish. **2001**, 272, 283-9	5
2148	Full-sized HERV-K (HML-2) human endogenous retroviral LTR sequences on human chromosome 21: map locations and evolutionary history. **2001**, 273, 51-61	16
2147	Identification of tumor suppressor candidate genes by physical and sequence mapping of the TSLC1 region of human chromosome 11q23. **2001**, 273, 181-9	14
2146	Identification and characterization of two novel calpain large subunit genes. **2001**, 274, 245-52	61
2145	Isochore chromosome maps of eukaryotic genomes. **2001**, 276, 47-56	79
2144	Misunderstandings about isochores. Part 1. **2001**, 276, 3-13	102

2143	Similar integration but different stability of Alus and LINEs in the human genome. **2001**, 276, 39-45	91
2142	Assignment of 118 novel cDNAs of cynomolgus monkey brain to human chromosomes. **2001**, 275, 31-7	19
2141	Compositional heterogeneity within and among isochores in mammalian genomes. II. Some general comments. **2001**, 276, 25-31	17
2140	Delineating relative homogeneous G+C domains in DNA sequences. **2001**, 276, 57-72	40
2139	Structural and functional features of eukaryotic mRNA untranslated regions. **2001**, 276, 73-81	320
2138	Human GABA(B)R genomic structure: evidence for splice variants in GABA(B)R1 but not GABA(B)R2. **2001**, 278, 63-79	43
2137	Human pigmentation genes: identification, structure and consequences of polymorphic variation. **2001**, 277, 49-62	282
2136	Co-transcriptional splicing of pre-messenger RNAs: considerations for the mechanism of alternative splicing. **2001**, 277, 31-47	143
2135	Cloning and genetic characterization of an evolutionarily conserved human olfactory receptor that is differentially expressed across species. **2001**, 278, 41-51	48
2134	A novel serine/threonine kinase gene, STK33, on human chromosome 11p15.3. **2001**, 280, 175-81	29
2133	The human melanocortin-1 receptor locus: analysis of transcription unit, locus polymorphism and haplotype evolution. **2001**, 281, 81-94	38
2132	Nucleocytoplasmic O-glycosylation: O-GlcNAc and functional proteomics. **2001**, 83, 575-81	72
2131	Alternative RNA splicing in the nervous system. **2001**, 65, 289-308	277
2130	The grand design. **2001**, 22, 166-7	3
2129	From genes to effective drugs for neurological and psychiatric diseases. **2001**, 22, 159-60	7
2128	Mining the genome for causes and cures of neurological disease. **2001**, 22, 161-2	5
2127	Useful G-protein-coupled receptor websites. **2001**, 22, 485-6	2
2126	Neuroscience in the post-genome era: an overview. **2001**, 24, 363-4	4

2125	Dual use of the transcriptional repressor (CtBP2)/ribbon synapse (RIBEYE) gene: how prevalent are multifunctional genes?. **2001**, 24, 555-7	15
2124	Homology evolving. **2001**, 16, 434-440	79
2123	The molecular natural history of the human genome. **2001**, 16, 420-422	4
2122	Charting the proteomes of organisms with unsequenced genomes by MALDI-quadrupole time-of-flight mass spectrometry and BLAST homology searching. **2001**, 73, 1917-26	530
2121	Gene expression profiling of cancer by use of DNA arrays: how far from the clinic?. **2001**, 2, 674-82	56
2120	Proteomics: an holistic analysis of nature's proteins. **2001**, 1, 513-20	15
2119	The human genome: an immuno-centric view of evolutionary strategies. **2001**, 22, 227-9	8
2118	Genome mining for human cancer genes: wherefore art thou?. **2001**, 7, 187-9	
2117	The impact of the Human Genome Project on medical genetics. **2001**, 7, 229-31	3
2116	Rethinking genetic strategies to study complex diseases. **2001**, 7, 512-6	17
2115	Genetics and genomics in infectious disease susceptibility. **2001**, 7, 521-6	30
2114	Genetics, genomics and beyond. **2001**, 7, 492-3	2
2113	Taking a functional genomics approach in molecular medicine. **2001**, 7, 494-501	19
2112	Using genetic variation to study human disease. **2001**, 7, 507-12	101
2111	Do plants have more genes than humans?. **2001**, 6, 195-6	9
2110	Do plants have more genes than humans? Yes, when it comes to ABC proteins. **2001**, 6, 347-8	21
2109	Organellar peptide deformylases: universality of the N-terminal methionine cleavage mechanism. **2001**, 6, 566-72	95
2108	Genetic Prediction: What are the Limits?. **2001**, 32, 619-633	8

2107	Computational analysis of human disease-associated genes and their protein products. **2001**, 11, 247-57	11
2106	Systematic approaches to mouse mutagenesis. **2001**, 11, 268-73	93
2105	Statistical inference of sequence-dependent mutation rates. **2001**, 11, 612-5	24
2104	Lateral and oblique gene transfer. **2001**, 11, 616-9	46
2103	Genome-wide variation in the human and fruitfly: a comparison. **2001**, 11, 627-34	82
2102	What controls the length of noncoding DNA?. **2001**, 11, 652-9	52
2101	Evolution of novel genes. **2001**, 11, 673-80	128
2100	Gene and genome duplication. **2001**, 11, 681-4	90
2099	Molecular mechanisms of prostate cancer. **2001**, 37 Suppl 7, S119-25	18
2098	Microbial genomics. **2001**, 9, 159	
2097	An abundance of bacterial ADP-ribosyltransferases--implications for the origin of exotoxins and their human homologues. **2001**, 9, 302-7; discussion 308	60
2096	Is KSHV lytic growth induced by a methylation-sensitive switch?. **2001**, 9, 464-6	4
2095	Exploiting genomics to discover new antibiotics. **2001**, 9, 611-7	82
2094	Comparative genomics of the human and mouse T cell receptor loci. **2001**, 15, 337-49	146
2093	Recognition of specific DNA sequences. **2001**, 8, 937-46	277
2092	Exon identity established through differential antagonism between exonic splicing silencer-bound hnRNP A1 and enhancer-bound SR proteins. **2001**, 8, 1351-61	298
2091	A genomic perspective on human proteases. **2001**, 498, 214-8	36
2090	Rapid functional analysis of protein-protein interactions by fluorescent C-terminal labeling and single-molecule imaging. **2001**, 502, 79-83	21

2089	Atomic structure of a glycerol channel and implications for substrate permeation in aqua(glycero)porins. **2001**, 504, 112-7	35
2088	Ht31: the first protein kinase A anchoring protein to integrate protein kinase A and Rho signaling. **2001**, 507, 264-8	52
2087	In silico screening for tumour-specific expressed sequences in human genome. **2001**, 508, 143-8	33
2086	Molecular profiling of cancer and drug-induced toxicity using new proteomic technologies. **2001**, 62, 803-819	5
2085	Toward gene therapy for disorders of globin synthesis. **2001**, 38, 382-92	24
2084	After the genome: DNA and human disease. **2001**, 104, 465-7	7
2083	Working in the post-genomic C. elegans world. **2001**, 105, 173-6	30
2082	Accounting for specificity in receptor tyrosine kinase signaling. **2001**, 106, 9-11	31
2081	Prions affect the appearance of other prions: the story of [PIN(+)]. **2001**, 106, 171-82	485
2080	A polymorphic genomic duplication on human chromosome 15 is a susceptibility factor for panic and phobic disorders. **2001**, 106, 367-79	184
2079	A comparison of the Celera and Ensembl predicted gene sets reveals little overlap in novel genes. **2001**, 106, 413-5	166
2078	Life, sex, and WT1 isoforms--three amino acids can make all the difference. **2001**, 106, 391-4	95
2077	A diverse family of GPCRs expressed in specific subsets of nociceptive sensory neurons. **2001**, 106, 619-32	491
2076	Of mice and genome sequence. **2001**, 107, 13-6	26
2075	Regulating axon branch stability: the role of p190 RhoGAP in repressing a retraction signaling pathway. **2001**, 107, 195-207	191
2074	Use of DNA arrays/microarrays in pancreatic research. **2001**, 1, 581-6	12
2073	Global methylation profiling of lung cancer identifies novel methylated genes. **2001**, 3, 314-23	60
2072	[Genetics and disease]. **2001**, 116, 736-7	0

2071	Microbial disease in humans: A genomic perspective. **2001**, 6, 243-52	5
2070	El largo camino hacia la secuenciaci□ del genoma humano: de los guisantes de Mendel a los escopetazos de Venter. Impacto en el conocimiento de las enfermedades cardiovasculares. **2001**, 13, 219-225	
2069	Genoma humano: gen□mica, gentica y aplicaciones en medicina. **2001**, 116, 672-675	0
2068	The growing impact of genetics on health care: do we have appropriate educational resources?. **2001**, 76, 769-71	6
2067	Innovative cancer drug targets: genomics, transcriptomics and clinomics. **2001**, 2, 911-5	7
2066	. **2001**, 16, 14-18	18
2065	Lithium-related genetics of bipolar disorder. **2001**, 33, 272-85	37
2064	Candidate gene studies of bipolar disorder. **2001**, 33, 248-56	37
2063	Patent status of the therapeutically important G-protein-coupled receptors. **2001**, 11, 1861-1887	26
2062	. **2001**, 15, 95-100	2
2061	Pharmacogenetic tactics and strategies: implications for paediatrics. **2001**, 3, 863-81	4
2060	Candidate genes for osteoporosis. Therapeutic implications. **2001**, 1, 11-9	7
2059	Proteomics. Making sense of genomic information for drug discovery. **2001**, 1, 29-35	5
2058	A simple analysis of gene expression and variability in gene arrays based on repeated observations. **2001**, 1, 145-52	12
2057	Finding genes influencing susceptibility to complex diseases in the post-genome era. **2001**, 1, 203-21	59
2056	Detecting rare mutations associated with cancer risk. **2001**, 1, 283-93	7
2055	High throughput genotyping technologies for pharmacogenomics. **2001**, 1, 295-302	16
2054	Information technology tools for efficient SNP studies. **2001**, 1, 303-14	3

2053	SSAHA: a fast search method for large DNA databases. **2001**, 11, 1725-9	720
2052	Predicting splice variant from DNA chip expression data. **2001**, 11, 1237-45	95
2051	Antidepressant drug discovery in the postgenomic era. **2001**, 2, 165-77	22
2050	Fighting infection using immunomodulatory agents. **2001**, 1, 641-53	40
2049	Src inhibitors: genomics to therapeutics. **2001**, 10, 1327-44	40
2048	Genomics. Genetic association by whole-genome analysis?. **2001**, 294, 1669-70	24
2047	Web Intelligence: Research and Development. **2001**,	10
2046	Computing in drug discovery: the design phase. **2001**, 3, 105-108	2
2045	Genetic signal analysis.	5
2044	Resistance to anti-peptide deformylase drugs. **2001**, 5, 415-418	12
2043	The birth and death of human single-nucleotide polymorphisms: new experimental evidence and implications for human history and medicine. **2001**, 10, 2195-8	31
2042	The Fall of the Null Hypothesis: Liabilities and Opportunities. **2001**, 65, 379	42
2041	Molecular reactions of protein phosphatases--insights from structure and chemistry. **2001**, 101, 2313-40	194
2040	Methyl-CpG-binding protein 2 represses LINE-1 expression and retrotransposition but not Alu transcription. **2001**, 29, 4493-501	141
2039	Recent developments in cationic lipid-mediated gene delivery and gene therapy. **2001**, 11, 1729-1752	28
2038	Analyses of p53 target genes in the human genome by bioinformatic and microarray approaches. **2001**, 276, 43604-10	125
2037	Estrogen receptor interaction with estrogen response elements. **2001**, 29, 2905-19	731
2036	What can psychiatric genetics offer suicidology?. **2001**, 22, 61-5	105

2035	Visualization challenges for a new cyber-pharmaceutical computing paradigm.	4
2034	The complete human olfactory subgenome. **2001**, 11, 685-702	489
2033	L□ra biologica post-genomica: dizionario per l□ndocrinologo clinico. **2001**, 2, 71-83	
2032	The new biology and drug research. **2001**, 8, 197-206	
2031	Automated construction of high-density comparative maps between rat, human, and mouse. **2001**, 11, 1935-43	38
2030	The contribution of exon-skipping events on chromosome 22 to protein coding diversity. **2001**, 11, 1848-53	39
2029	Comparing vertebrate whole-genome shotgun reads to the human genome. **2001**, 11, 1807-16	21
2028	The human genome revealed. **2001**, 11, 1803-4	3
2027	A streamlined process to phenotypically profile heterologous cDNAs in parallel using yeast cell-based assays. **2001**, 11, 1899-912	25
2026	Genome Organization. **2001**, 295-298	
2025	Thermodynamics of RNA Secondary Structure Formation. **2001**, 21-48	11
2024	Determinants of CpG islands: expression in early embryo and isochore structure. **2001**, 11, 1854-60	91
2023	Full-length cDNAs: more than just reaching the ends. **2001**, 6, 57-80	47
2022	Alternative splicing and diversity of renal transporters. **2001**, 281, F781-94	28
2021	Engineered antibodies take center stage. **2001**, 10, 127-142	61
2020	Bioinformatics: use in bacterial vaccine discovery. **2001**, 31, 636, 638, 640, passim	17
2019	Proteomics--structure and function. **2001**, 31, 156-8, 160	7
2018	Inherited Risks for Susceptibility to Dental Caries. **2001**, 65, 1038-1045	61

2017	Pharmacologic Advances in Orofacial Pain: From Molecules to Medicine. **2001**, 65, 1393-1403	7
2016	Open-system approaches to gene expression in the CNS. **2001**, 21, 8306-9	16
2015	Genetics of human complement component C4 and evolution the central MHC. **2001**, 6, D904-13	12
2014	What is Bioinformatics? A Proposed Definition and Overview of the Field. **2001**, 40, 346-358	218
2013	Sequence analysis of the human genome: implications for the understanding of nervous system function and disease. **2001**, 58, 1772-8	24
2012	Candidate genes and single nucleotide polymorphisms (SNPs) in the study of human disease. **2001**, 17, 89-98	84
2011	Genetic Determinants of Pediatric HIV-1 Infection: Vertical Transmission and Disease Progression Among Children. **2001**, 7, 583-589	18
2010	Alternative spliced transcripts as cancer markers. **2001**, 17, 67-75	53
2009	Preface. **2001**, 87, 3-3	
2008	Human endothelial cell response to gram-negative lipopolysaccharide assessed with cDNA microarrays. **2001**, 281, C1587-95	83
2007	Genetic determinants of coronary vasomotor tone in humans. **2001**, 281, H1465-8	10
2006	EEG1, a putative transporter expressed during epithelial organogenesis: comparison with embryonic transporter expression during nephrogenesis. **2001**, 281, F1148-56	14
2005	Deciphering therapeutic targets. **2001**, 30, 1086-8, 1090	1
2004	Opportunities for public health genetics trainees: results of an employer/workplace survey. **2001**, 4, 143-7	2
2003	Integrating genetic services into public health--guidance for state and territorial programs from the National Newborn Screening and Genetics Resource Center (NNSGRC). **2001**, 4, 175-96	12
2002	Cancer--emerging breakthrough drugs. **2001**, 30, 626-8, 630, 632	2
2001	The Arabidopsis SERRATE Gene Encodes a Zinc-Finger Protein Required for Normal Shoot Development. **2001**, 13, 1263-1280	144
2000	Fast and Specific Hybridization Using Flow-Through Microarrays on Porous Metal Oxide. **2001**, 47, 1931-1933	43

1999	Expanding the Boundaries: Enhancing Dentistry's Contribution to Overall Health and Well-Being of Children. **2001**, 65, 1323-1334	9
1998	The human gene map for performance and health-related fitness phenotypes. **2001**, 33, 855-67	62
1997	A Survey of Genetics Knowledge of Health Professionals: Implications for Physical Therapists. **2001**, 13, 156-163	3
1996	Rates of movement and distribution of transposable elements in Drosophila melanogaster: in situ hybridization vs Southern blotting data. **2001**, 78, 121-36	58
1995	Identification of disease-specific genes in chronic pancreatitis using DNA array technology. **2001**, 234, 769-78; discussion 778-9	49
1994	Implications of the Human Genome Project for obstetrics and gynecology. **2001**, 56, 437-43	4
1993	Commentary: A Historical Perspective on the US-Canada Connection in The Psychology of Aging*. **2001**, 20, 149-159	0
1992	Gene polymorphisms and musculoskeletal disease. **2001**, 12, 416-423	
1991	Regulation of the sodium transporters NHE3, NKCC2 and NCC in the kidney. **2001**, 10, 655-9	41
1990	Genomic approaches to the pathogenesis of hematologic malignancy. **2001**, 8, 252-61	19
1989	The impact of molecular biology on the practice of pediatric critical care medicine. **2001**, 2, 299-310	10
1988	The genetic basis of endometriosis. **2001**, 13, 309-14	91
1987	Human sulfotransferase SULT1C1 pharmacogenetics: gene resequencing and functional genomic studies. **2001**, 11, 747-56	47
1986	Identification of amyloid-beta binding sites using an antisense peptide approach. **2001**, 12, 2561-6	31
1985	Gene expression profiles for monitoring radiation exposure. **2001**, 97, 11-6	69
1984	The role of genetic testing and effect on patient care. **2001**, 137, 1515-9	2
1983	Human gene therapy: are we still expecting too much, too soon?. **2001**, 94, 337-9	
1982	.	1

1981	Integrating genotype and phenotype information: an overview of the PharmGKB project. Pharmacogenetics Research Network and Knowledge Base. **2001**, 1, 167-70	297
1980	Public health impact of genetic tests at the end of the 20th century. **2001**, 3, 405-10	42
1979	Single nucleotide polymorphism identification in candidate gene systems of obesity. **2001**, 1, 193-203	12
1978	Science, medicine, and the future: Postgenomic technologies: hunting the genes for common disorders. **2001**, 322, 1031-4	38
1977	Perspectives on the Molecular Basis of Developmental Defects in the Human Pituitary Region. **2001** , 4, 30-47	1
1976	Gene expression screening of human mast cells and eosinophils using high-density oligonucleotide probe arrays: abundant expression of major basic protein in mast cells. **2001**, 98, 1127-34	81
1975	Identification of disease genes by expression profiling. **2001**, 18, 882-9	10
1974	Genetics of COPD: present and future. **2001**, 18, 741-3	13
1973	New approaches to lymphoma diagnosis. **2001**, 2001, 194-220	60
1972	From Genomes to Drugs with Bioinformatics. **2001**, 1-25	
1971	Bioinformatics Support of Genome Sequencing Projects. **2001**, 25-48	1
1970	Genome Organization: Human. **2001**,	1
1969	p38 mitogen-activated protein kinase-independent induction of gadd45 expression in nerve growth factor-induced apoptosis in medulloblastomas. **2001**, 276, 41120-7	16
1968	Significance of the human genome sequence to drug discovery. **2001**, 1, 11-2	6
1967	Genomics Analysis of Genes Expressed in Maize Endosperm Identifies Novel Seed Proteins and Clarifies Patterns of Zein Gene Expression. **2001**, 13, 2297-2317	112
1966	Segmental duplications: organization and impact within the current human genome project assembly. **2001**, 11, 1005-17	488
1965	High-throughput variation detection and genotyping using microarrays. **2001**, 11, 1913-25	239
1964	Postgenomic prospects of success in drug development and pharmacotherapy. **2001**, 1, 6-9	1

1963	Chapter 21. The role of protein structure prediction in drug discovery. **2001**, 36, 211-225	
1962	Genome Organization. **2001**, 859-863	
1961	Human Genome Project. **2001**, 980-981	2
1960	Large-scale proteomics and its future impact on medicine. **2001**, 1, 15-9	9
1959	Mouse anxiety: the power of knockout. **2001**, 1, 187-92	15
1958	Clinical genetics: compassion, access, science, and advocacy. **2001**, 3, 426-9	10
1957	Functional genomics and systems engineering. **2001**, 34, 13-22	
1956	Environmental echoes. **2001**, 84, 105-24	18
1955	Identification and characterization of CaMKP-N, nuclear calmodulin-dependent protein kinase phosphatase. **2001**, 130, 833-40	26
1954	Drosophila P transposons in the human genome?. **2001**, 18, 1979-82	18
1953	The evolution of controlled multitasked gene networks: the role of introns and other noncoding RNAs in the development of complex organisms. **2001**, 18, 1611-30	335
1952	Scale-free behavior in protein domain networks. **2001**, 18, 1694-702	219
1951	Model Organisms as Models: Understanding the 'Lingua Franca' of the Human Genome Project. **2001**, 68, S251-S261	59
1950	Research needs for human nutrition in the post-genome-sequencing era. **2001**, 131, 3319-23	10
1949	Genetics update : impact of the human genome projects and identification of a stroke gene. **2001**, 32, 1239-41	77
1948	Current World Literature. **2001**, 10, 699-725	
1947	WD-repeat proteins: structure characteristics, biological function, and their involvement in human diseases. **2001**, 58, 2085-97	369
1946	Das ELSI-Programm des U.S.-amerikanischen Humangenomprojekts neue Perspektiven f die Medizinethik?. **2001**, 13, 243-252	

1945	Molecular diagnosis of gastric cancer: present and future. **2001**, 4, 113-21	80
1944	A statistical view of genome transcription?. **2001**, 53, 160-2	6
1943	CD150 is a member of a family of genes that encode glycoproteins on the surface of hematopoietic cells. **2001**, 53, 382-94	48
1942	CFFM4: a new member of the CD20/FcepsilonRIbeta family. **2001**, 53, 468-76	16
1941	CD2F-10: a new member of the CD2 subset of the immunoglobulin superfamily. **2001**, 53, 599-602	20
1940	Yeast--a panacea for the structure-function analysis of membrane proteins?. **2001**, 40, 157-71	43
1939	Computational analysis of full-length mouse cDNAs compared with human genome sequences. **2001**, 12, 673-7	11
1938	[Not Available]. **2001**, 44, 929-41	0
1937	Gene-diet interaction and plasma lipid response to dietary intervention. **2001**, 3, 200-8	32
1936	Use of gene markers to guide antihypertensive therapy. **2001**, 3, 410-5	5
1935	Impact of molecular medicine on neuropsychiatry: the clinician's perspective. **2001**, 3, 355-60	0
1934	A full-length and potentially active LINE element is integrated polymorphically within the IGL locus in a genomically unstable region of chromosome 22. **2001**, 109, 628-37	1
1933	A genome-wide survey of human thioredoxin and glutaredoxin family pseudogenes. **2001**, 109, 429-39	7
1932	A draft sequence of the rice (Oryza sativa ssp.indica) genome. **2001**, 46, 1937-1942	24
1931	Eureka? The draft of the human genome deciphered. **2001**, 43, 119-20	
1930	Review article: the genetics of inflammatory bowel disease. **2001**, 15, 731-48	115
1929	Neurofibromatosis type I as a model of autosomal dominant inheritance. **2001**, 18, 445-7	9
1928	The genetics of alopecia areata. **2001**, 14, 329-339	14

1927	The search for drug target molecules from genomics. **2001**, 88 Suppl 2, 11-7; discussion 49-50	12
1926	Beyond the Hox: how widespread is homeobox gene clustering?. **2001**, 199, 13-23	54
1925	Multiple personalities: synaptic target cells as introverts and extroverts. **2001**, 43, 503-8	4
1924	Towards understanding life itself. **2001**, 25, 313-5	1
1923	Regulation of new biomedical technologies: the next frontier. **2001**, 12, 297-298	
1922	Protein interaction databases. **2001**, 12, 334-9	76
1921	Mapping protein-protein interactions with combinatorial biology methods. **2001**, 12, 340-7	23
1920	General introduction to the importance of genomics in food biotechnology and nutrition. **2001**, 12, 483-7	10
1919	Genomics: food and nutrition. **2001**, 12, 516-22	38
1918	Functional genomics and target validation approaches using antisense oligonucleotide technology. **2001**, 12, 622-5	69
1917	In vivo drug target discovery: identifying the best targets from the genome. **2001**, 12, 626-31	45
1916	Custom DNA-binding proteins come of age: polydactyl zinc-finger proteins. **2001**, 12, 632-7	86
1915	From symptomatic treatments to causative therapy?. **2001**, 5, 352-9	3
1914	Protein tyrosine phosphatases: prospects for therapeutics. **2001**, 5, 416-23	324
1913	Chemogenomic approaches to drug discovery. **2001**, 5, 464-70	151
1912	Do plants have rhodopsin after all? A mystery of plant G protein-coupled signalling. **2001**, 39, 1027-1035	6
1911	Intramers as promising new tools in functional proteomics. **2001**, 8, 931-9	84
1910	Molecular linkage studies of bipolar disorders. **2001**, 3, 276-83	55

1909	Human synemin gene generates splice variants encoding two distinct intermediate filament proteins. **2001**, 268, 6435-49	62
1908	Siglecs in the immune system. **2001**, 103, 137-45	220
1907	Pharmacogenetics and pharmacogenomics. **2001**, 52, 345-7	92
1906	Scaffolding proteins organize multimolecular protein complexes for sensory signal transduction. **2001**, 14, 769-76	51
1905	The genetics of diabetes: a progress report. **2001**, 18, 246-250	2
1904	Current Awareness on Comparative and Functional Genomics. **2001**, 2, 345-352	78
1903	Definition of the gene content of the human genome: the need for deep experimental verification. **2001**, 2, 169-75	2
1902	Phage-display evolution of tyrosine kinases with altered nucleotide specificity. **2001**, 60, 220-8	19
1901	Preface to genomic pathology--a new frontier. **2001**, 195, 1-2	7
1900	Detection of novel gene expression in paraffin-embedded tissues by isotopic in situ hybridization in tissue microarrays. **2001**, 195, 87-96	26
1899	A substrate phage enzyme-linked immunosorbent assay to profile panels of proteases. **2001**, 294, 176-84	9
1898	Screening for soluble expression of recombinant proteins in a 96-well format. **2001**, 297, 79-85	101
1897	On cloning and clone libraries for finite and infinite length genomes. **2001**, 63, 933-50	
1896	The Complexity of Gene Placement. **2001**, 41, 225-243	3
1895	Letter to the editor: Chronicle for an orphan trait: comment on Hofer, Shair, Masmela, & Brunelli, "Developmental effects of selective breeding for an infantile trait: the rat pup ultrasonic isolation call". **2001**, 39, 251-6	5
1894	Automation in genotyping of single nucleotide polymorphisms. **2001**, 17, 475-92	186
1893	Using linked markers to infer the age of a mutation. **2001**, 18, 87-100	57
1892	Object-oriented approach to drug design enabled by NMR SOLVE: first real-time structural tool for characterizing protein-ligand interactions. **2001**, Suppl 37, 99-105	13

1891	Genomics approaches to drug discovery. **2001**, Suppl 37, 110-9	4
1890	Sp1 and krüppel-like factor family of transcription factors in cell growth regulation and cancer. **2001**, 188, 143-60	823
1889	Homeobox genes in normal and malignant cells. **2001**, 188, 161-9	181
1888	ERCC1: a comparative genomic perspective. **2001**, 38, 209-15	39
1887	Novel alternative PBX3 isoforms in leukemia cells with distinct interaction specificities. **2001**, 32, 275-80	27
1886	Virtual anthropology (VA): a call for glasnost in paleoanthropology. **2001**, 265, 193-201	52
1885	Methyl CpG-binding proteins and transcriptional repression. **2001**, 23, 1131-7	279
1884	Location analysis of DNA-bound proteins at the whole-genome level: untangling transcriptional regulatory networks. **2001**, 23, 473-6	20
1883	Empowering primary care health professionals in medical genetics: how soon? How fast? How far?. **2001**, 106, 223-32	122
1882	Loss of N-glycolylneuraminic acid in humans: Mechanisms, consequences, and implications for hominid evolution. **2001**, Suppl 33, 54-69	218
1881	NotI-MseII methylation-sensitive amplied fragment length polymorhism for DNA methylation analysis of human cancers. **2001**, 22, 1946-56	34
1880	Recent advances in DNA sequencing by capillary and microdevice electrophoresis. **2001**, 22, 4104-17	41
1879	Hepatocellular carcinoma: from bedside to proteomics. **2001**, 1, 1249-63	103
1878	Heart failure and apoptosis: electrophoretic methods support data from micro- and macro-arrays. A critical review of genomics and proteomics. **2001**, 1, 1481-8	25
1877	Medizinische Chemie: Herausforderungen und Chancen. **2001**, 113, 3443-3453	13
1876	Medicinal Chemistry: Challenges and Opportunities. **2001**, 40, 3341-3350	85
1875	Both normal and leukemic B lymphocytes express multiple isoforms of the human Aiolos gene. **2001**, 31, 3469-74	20
1874	The sequence of the human genome. **2001**, 291, 1304-51	10609

1873	Mass spectrometry for protein and peptide characterisation. **2001**, 58, 868-84	50
1872	Biology of mammalian L1 retrotransposons. **2001**, 35, 501-38	624
1871	Solitary human endogenous retroviruses-K LTRs retain transcriptional activity in vivo, the mode of which is different in different cell types. **2001**, 290, 83-90	25
1870	Effects of glia maturation factor overexpression in primary astrocytes on MAP kinase activation, transcription factor activation, and neurotrophin secretion. **2001**, 26, 1293-9	58
1869	From the laboratory to pharmaceutical care research--Part I. **2001**, 23, 205-9	5
1868	Introduction into Plant Genomics. **2001**, 35, 285-293	5
1867	Arrangements of macro- and microchromosomes in chicken cells. **2001**, 9, 569-84	155
1866	Non-random radial higher-order chromatin arrangements in nuclei of diploid human cells. **2001**, 9, 541-67	300
1865	Zinc biochemistry, physiology, and homeostasis recent insights and current trends. **2001**, 14, 187-190	111
1864	Localization of Human Ribosomal Gene DNA Probes on Barley Chromosomes. **2001**, 37, 1452-1454	3
1863	Gene mapping in fishes: a means to an end. **2001**, 111, 3-23	63
1862	Genetic mapping of Y-chromosomal DNA markers in Pacific salmon. **2001**, 111, 43-58	95
1861	Classical and molecular cytogenetics of the zebrafish, Danio rerio (Cyprinidae, Cypriniformes): an overview. **2001**, 111, 397-412	57
1860	Comparing function and structure between entire proteomes. **2001**, 10, 1970-9	223
1859	Genetic variations in human G protein-coupled receptors: implications for drug therapy. **2001**, 3, E22	40
1858	Predicted structures of two proteins involved in human diseases. **2001**, 35, 35-47	19
1857	Structural basis for control by phosphorylation. **2001**, 101, 2209-42	494
1856	Species-specific organization of CpG island promoters at mammalian homologous genes. **2001**, 2, 586-92	38

1855	Dynamic modules and heterogeneity of function: a lesson from tyrosine kinase receptors in endothelial cells. **2001**, 2, 763-7		24
1854	Mutation in Brca2 stimulates error-prone homology-directed repair of DNA double-strand breaks occurring between repeated sequences. **2001**, 20, 4704-16		325
1853	The exon-exon junction complex provides a binding platform for factors involved in mRNA export and nonsense-mediated mRNA decay. **2001**, 20, 4987-97		591
1852	Exon structure conservation despite low sequence similarity: a relic of dramatic events in evolution?. **2001**, 20, 5354-60		74
1851	High-throughput three-dimensional protein structure determination. **2001**, 12, 348-54		46
1850	Advances in proteome analysis by mass spectrometry. **2001**, 12, 607-12		80
1849	Tissue microarray profiling of cancer specimens and cell lines: opportunities and limitations. **2001**, 81, 1331-8		217
1848	Part three in the book of genes. *Nature*, **2001**, 414, 854-5	50.4	6
1847	The DNA sequence and comparative analysis of human chromosome 20. *Nature*, **2001**, 414, 865-71	50.4	177
1846	Putting the genes for type II diabetes on the map. **2001**, 7, 277-9		82
1845	Zeroing in on tolerance. **2001**, 7, 279-81		6
1844	Pharmacogenetic applications of the Human Genome project. **2001**, 7, 281-3		76
1843	Gazing into a crystal ball-cancer therapy in the post-genomic era. **2001**, 7, 283-5		23
1842	The heart of genomics. **2001**, 7, 287-8		3
1841	Piecing together the significance of splicing. **2001**, 19, 196		21
1840	The end of the beginning for genomic medicine. **2001**, 19, 207-9		24
1839	Mapping a role for SNPs in drug development. **2001**, 19, 209-11		12
1838	Harvesting the fruits of the human genome. **2001**, 27, 227-8		6

1837	The end of all human DNA maps?. **2001**, 27, 229-30	3
1836	Chipping away at the transcriptome. **2001**, 27, 232-4	18
1835	Variation is the spice of life. **2001**, 27, 234-6	730
1834	Comparative architecture of transposase and integrase complexes. **2001**, 8, 302-7	150
1833	Sequence diversity in CYP3A promoters and characterization of the genetic basis of polymorphic CYP3A5 expression. **2001**, 27, 383-91	1738
1832	Creation of genome-wide protein expression libraries using random activation of gene expression. **2001**, 19, 440-5	61
1831	Completeness in structural genomics. **2001**, 8, 559-66	282
1830	Mouse mutagenesis on target. **2001**, 28, 198-200	8
1829	Functional analysis of secreted and transmembrane proteins critical to mouse development. **2001**, 28, 241-9	354
1828	Stroke genomics: approaches to identify, validate, and understand ischemic stroke gene expression. **2001**, 21, 755-78	78
1827	The Nod2 gene in Crohn's disease: implications for future research into the genetics and immunology of Crohn's disease. **2001**, 7, 271-5	35
1826	An infectious transfer and expression system for genomic DNA loci in human and mouse cells. **2001** , 19, 1067-70	157
1825	The power of public access: the human genome project and the scientific process. **2001**, 29, 4-6	7
1824	Choreographing mRNA biogenesis. **2001**, 29, 6-7	16
1823	An evaluation of the draft human genome sequence. **2001**, 29, 88-91	26
1822	A radiation hybrid map of mouse genes. **2001**, 29, 201-5	61
1821	Genetic variation in the 5q31 cytokine gene cluster confers susceptibility to Crohn disease. **2001**, 29, 223-8	656
1820	High-resolution haplotype structure in the human genome. **2001**, 29, 229-32	1398

1819	The UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase gene is mutated in recessive hereditary inclusion body myopathy. **2001**, 29, 83-7		407
1818	The AZFc region of the Y chromosome features massive palindromes and uniform recurrent deletions in infertile men. **2001**, 29, 279-86		519
1817	A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2. **2001**, 29, 377-8		250
1816	Genome scanning with array CGH delineates regional alterations in mouse islet carcinomas. **2001**, 29, 459-64		246
1815	Evidence for genomic rearrangements mediated by human endogenous retroviruses during primate evolution. **2001**, 29, 487-9		165
1814	Conjugation between bacterial and mammalian cells. **2001**, 29, 375-6		135
1813	Computational identification of promoters and first exons in the human genome. **2001**, 29, 412-7		320
1812	Identification of Tapr (an airway hyperreactivity regulatory locus) and the linked Tim gene family. **2001**, 2, 1109-16		404
1811	Short tandem repeat (STR) haplotypes in HLA: an integrated 50-kb STR/linkage disequilibrium/gene map between the RING3 and HLA-B genes and identification of STR haplotype diversification in the class III region. **2001**, 9, 590-8		30
1810	Refinement of the PARK3 locus on chromosome 2p13 and the analysis of 14 candidate genes. **2001**, 9, 659-66		42
1809	Genomic organisation of the approximately 1.5 Mb Smith-Magenis syndrome critical interval: transcription map, genomic contig, and candidate gene analysis. **2001**, 9, 892-902		27
1808	Crk family adaptors-signalling complex formation and biological roles. **2001**, 20, 6348-71		405
1807	Transcript map and complete genomic sequence for the 310 kb region of minimal allele loss on chromosome segment 11p15.5 in non-small-cell lung cancer. **2001**, 20, 8154-64		24
1806	Human genome diversity: what about the other human genome project?. **2001**, 2, 222-7		25
1805	Guide to the draft human genome. *Nature*, **2001**, 409, 824-6	50.4	39
1804	Mining the draft human genome. *Nature*, **2001**, 409, 827-8	50.4	51
1803	Can sequencing shed light on cell cycling?. *Nature*, **2001**, 409, 844-6	50.4	84
1802	Evolutionary analyses of the human genome. *Nature*, **2001**, 409, 847-9	50.4	331

1801	Cancer and genomics. *Nature*, **2001**, 409, 850-2	50.4	108
1800	Human disease genes. *Nature*, **2001**, 409, 853-5	50.4	286
1799	Computational comparison of two draft sequences of the human genome. *Nature*, **2001**, 409, 856-9	50.4	50
1798	A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. *Nature*, **2001**, 409, 928-33	50.4	2398
1797	The physical maps for sequencing human chromosomes 1, 6, 9, 10, 13, 20 and X. *Nature*, **2001**, 409, 942-3	50.4	48
1796	Comparison of human genetic and sequence-based physical maps. *Nature*, **2001**, 409, 951-3	50.4	237
1795	Our genome unveiled. *Nature*, **2001**, 409, 814-6	50.4	212
1794	The draft sequences. Filling in the gaps. *Nature*, **2001**, 409, 818-20	50.4	47
1793	The draft sequences. Comparing species. *Nature*, **2001**, 409, 820-1	50.4	68
1792	To a future of genetic medicine. *Nature*, **2001**, 409, 822-3	50.4	132
1791	Chinese biology. A great leap forward. *Nature*, **2001**, 410, 10-2	50.4	18
1790	Emerging technologies in yeast genomics. **2001**, 2, 302-12		82
1789	Yesterday's polyploids and the mystery of diploidization. **2001**, 2, 333-41		564
1788	Protecting genetic privacy. **2001**, 2, 392-6		46
1787	Genome sequencing. A grin without a cat. *Nature*, **2001**, 410, 1040-1	50.4	6
1786	Linkage disequilibrium in the human genome. *Nature*, **2001**, 411, 199-204	50.4	1373
1785	Linking class-switch recombination with somatic hypermutation. **2001**, 2, 493-503		119
1784	Genome annotation: from sequence to biology. **2001**, 2, 493-503		249

1783	Functional genomics and the study of development, variation and evolution. **2001**, 2, 528-37		44
1782	The evolution of isochores. **2001**, 2, 549-55		308
1781	The ins and outs of signalling. *Nature*, **2001**, 411, 759-62	50.4	165
1780	Phylogenetic analyses do not support horizontal gene transfers from bacteria to vertebrates. *Nature*, **2001**, 411, 940-4	50.4	177
1779	Genes lost during evolution. *Nature*, **2001**, 411, 1013-4	50.4	61
1778	Strategies for the systematic sequencing of complex genomes. **2001**, 2, 573-83		112
1777	The role of selfish genetic elements in eukaryotic evolution. **2001**, 2, 597-606		303
1776	Faster, better, cheaper genotyping. *Nature*, **2001**, 412, 580-2	50.4	43
1775	Http://C. elegans: mining the functional genomic landscape. **2001**, 2, 681-9		20
1774	Segmental duplications: an 'expanding' role in genomic instability and disease. **2001**, 2, 791-800		220
1773	A tour of structural genomics. **2001**, 2, 801-9		131
1772	Mutations in a member of the ADAMTS gene family cause thrombotic thrombocytopenic purpura. *Nature*, **2001**, 413, 488-94	50.4	1394
1771	Positive selection of a gene family during the emergence of humans and African apes. *Nature*, **2001**, 413, 514-9	50.4	244
1770	Chromosomal microdeletions: dissecting del22q11 syndrome. **2001**, 2, 858-68		216
1769	Tn7: smarter than we thought. **2001**, 2, 806-14		163
1768	Sanger Centre welcomes gene funds with a new name. *Nature*, **2001**, 413, 660	50.4	
1767	Pharmacogenetics and cancer therapy. **2001**, 1, 99-108		200
1766	Non-coding RNA genes and the modern RNA world. **2001**, 2, 919-29		1012

1765	Accessing genetic variation: genotyping single nucleotide polymorphisms. **2001**, 2, 930-42	798
1764	BAC to the future: the use of bac transgenic mice for neuroscience research. **2001**, 2, 861-70	288
1763	To cycle or not to cycle: a critical decision in cancer. **2001**, 1, 222-31	1108
1762	The Surgeon General's Report and special-needs patients: a framework for action for children and their caregivers. **2001**, 21, 88-94	8
1761	Psychogeriatric Research: A Conceptual Introduction to Aging and Geriatric Neuroscience. **2001**, 1, 158-188	21
1760	Genome analysis with gene-indexing databases. **2001**, 91, 115-32	17
1759	FLEXGene repository: from sequenced genomes to gene repositories for high-throughput functional biology and proteomics. **2001**, 118, 155-65	44
1758	A status report on the sequencing and annotation of the P. falciparum genome. **2001**, 118, 133-8	9
1757	Study on construction of a cDNA library corresponding to an amino acid-specific tRNA and influence of the modified nucleotide upon nucleotide misincorporations in reverse transcription. **2001**, 1521, 81-8	7
1756	Nucleotide sequence and cell cycle-associated differential expression of ZF5128, a novel Kruppel type zinc finger protein gene. **2001**, 1522, 230-7	4
1755	Matching peptide mass spectra to EST and genomic DNA databases. **2001**, 19, 17-22	42
1754	Insights into protein function through large-scale computational analysis of sequence and structure. **2001**, 19, 61-66	16
1753	High-throughput structural proteomics using x-rays. **2001**, 19, 67-71	280
1752	Recent developments in computational proteomics. **2001**, 19, 266-72	43
1751	Gene expression microarrays and the integration of biological knowledge. **2001**, 19, 412-5	74
1750	High-throughput structural proteomics using x-rays. **2001**, 19, S67-71	26
1749	Insights into protein function through large-scale computational analysis of sequence and structure. **2001**, 19, S61-6	13
1748	Matching peptide mass spectra to EST and genomic DNA databases. **2001**, 19, S17-22	46

1747	Embryogenomics: developmental biology meets genomics. **2001**, 19, 511-8	58
1746	Plagiarized bacterial genes in the human book of life. **2001**, 17, 235-7	19
1745	In the name of the father: surnames and genetics. **2001**, 17, 353-7	121
1744	Footprints of primordial introns on the eukaryotic genome: still no clear traces. **2001**, 17, 499-501	18
1743	PDZ proteins and polarity: functions from the fly. **2001**, 17, 511-9	59
1742	Single nucleotide polymorphisms and recombination rate in humans. **2001**, 17, 481-5	234
1741	Retrotransposons rule in Carry-le-Rouet. **2001**, 17, 489-90	
1740	Unfolding the role of chaperones and chaperonins in human disease. **2001**, 17, 528-35	92
1739	How many nuclear hormone receptors are there in the human genome?. **2001**, 17, 554-6	179
1738	Common pitfalls in bioinformatics-based analyses: look before you leap. **2001**, 17, 541-5	16
1737	Recent duplication, domain accretion and the dynamic mutation of the human genome. **2001**, 17, 661-9	269
1736	A reassessment of the translation initiation codon in vertebrates. **2001**, 17, 685-7	96
1735	Genome of the apes. **2001**, 17, 637-45	64
1734	Harnessing the cellular immune system to the gene-prediction cart. **2001**, 17, 732-4	4
1733	Fungi and humans: closer than you think. **2001**, 17, 682-4	21
1732	The morning after. **2001**, 17, 688-9	
1731	Gene expression microarray analysis in cancer biology, pharmacology, and drug development: progress and potential. **2001**, 62, 1311-36	167
1730	Genomes, man, and machines. **2001**, 20, 18-9; 21	2

1729	Molecular mechanisms in neurologic disorders. **2001**, 8, 128-34	7
1728	Automated processing of raw DNA sequence data. **2001**, 20, 41-8	1
1727	Computational genomics. **2001**, 11, R155-8	15
1726	Genome evolution: sex and the transposable element. **2001**, 11, R296-9	82
1725	Mouse genomics: making sense of the sequence. **2001**, 11, R311-4	3
1724	Tapping into genome secrets. **2001**, 11, R416-7	
1723	Unfolding the genomes' structural secrets. **2001**, 11, R680-2	
1722	Insertional polymorphisms of full-length endogenous retroviruses in humans. **2001**, 11, 1531-5	263
1721	Kif1C, a kinesin-like motor protein, mediates mouse macrophage resistance to anthrax lethal factor. **2001**, 11, 1503-11	74
1720	Discovery of the human genome sequence in the public and private databases. **2001**, 11, R808-11	4
1719	Selection on Alu sequences?. **2001**, 11, R900-1	37
1718	Local protein synthesis in neurons. **2001**, 11, R901-3	11
1717	Imaging biochemistry inside cells. **2001**, 11, 203-11	403
1716	Alternative splicing of potassium channels: a dynamic switch of cellular excitability. **2001**, 11, 353-8	88
1715	A question of strategy. **2001**, 26, 207-8	4
1714	Microarrays go live--new prospects for proteomics. **2001**, 26, 639-41	18
1713	Beyond the "recognition code": structures of two Cys2His2 zinc finger/TATA box complexes. **2001**, 9, 717-23	102
1712	Expression profiling techniques for cardiac molecular phenotyping. **2001**, 11, 218-21	3

1711	Too many targets, not enough target validation. **2001**, 6, 397	8
1710	A genomic perspective on human proteases as drug targets. **2001**, 6, 681-688	83
1709	Transgenic knockouts as part of high-throughput, evidence-based target selection and validation strategies. **2001**, 6, 628-636	33
1708	Virogenomics: a novel approach to antiviral drug discovery. **2001**, 6, 621-627	27
1707	Too many targets, not enough target validation - Reply. **2001**, 6, 665-666	
1706	Animal models and human genome diversity: the pitfalls of inbred mice. **2001**, 6, 766-768	9
1705	News in brief. **2001**, 6, 820-822	
1704	Transgenic gene knockouts: a functional platform for the industry. **2001**, 6, 770-771	2
1703	Beyond the genome: turning data into knowledge. **2001**, 6, 881-883	6
1702	Recent developments in computational proteomics. **2001**, 6, 996-1004	19
1701	Genome acrobatics: understanding complex genomes. **2001**, 6, 1181-1182	2
1700	Structural genomics: lessons to be learnt. **2001**, 6, 1261-1262	3
1699	Pre-mRNA splicing in the new millennium. **2001**, 13, 302-9	399
1698	Immunoglobulin superfamily receptors: cis-interactions, intracellular adapters and alternative splicing regulate adhesion. **2001**, 13, 611-8	85
1697	Of weeds and men: what genomes teach us about plant cell biology. **2001**, 4, 478-87	23
1696	The human genome: what's in it for parasitologists?. **2001**, 17, 214	
1695	The Genomic Era and 21st Century Medicine: Its Potential Impact in Sepsis Research. **2001**, 4, 197-199	1
1694	FOUNTAIN: a JAVA open-source package to assist large sequencing projects. **2001**, 2, 6	6

1693	A comparative molecular analysis of developing mouse forelimbs and hindlimbs using serial analysis of gene expression (SAGE). **2001**, 11, 1686-98	56
1692	Genomic characterization of recent human LINE-1 insertions: evidence supporting random insertion. **2001**, 11, 2050-8	92
1691	Novel protein domains and repeats in Drosophila melanogaster: insights into structure, function, and evolution. **2001**, 11, 1996-2008	89
1690	Assembling puzzles from preassembled blocks. **2001**, 11, 1461-2	1
1689	Genomics analysis of genes expressed in maize endosperm identifies novel seed proteins and clarifies patterns of zein gene expression. **2001**, 13, 2297-317	189
1688	Chemosensitivity prediction by transcriptional profiling. **2001**, 98, 10787-92	534
1687	Cloning and characterization of a histone deacetylase, HDAC9. **2001**, 98, 10572-7	188
1686	The interplay of biology and technology. **2001**, 98, 10051-4	18
1685	Terminal-repeat retrotransposons in miniature (TRIM) are involved in restructuring plant genomes. **2001**, 98, 13778-83	173
1684	Association between divergence and interspersed repeats in mammalian noncoding genomic DNA. **2001**, 98, 14503-8	33
1683	Molecular characteristics of non-small cell lung cancer. **2001**, 98, 15203-8	111
1682	A protein kinase associated with apoptosis and tumor suppression: structure, activity, and discovery of peptide substrates. **2001**, 276, 38956-65	52
1681	The role of PTF1-P48 in pancreatic acinar gene expression. **2001**, 276, 44018-26	87
1680	Prediction of the coding sequences of unidentified human genes. XXII. The complete sequences of 50 new cDNA clones which code for large proteins. **2001**, 8, 319-27	29
1679	Molecular cloning of a third member of the potassium-dependent sodium-calcium exchanger gene family, NCKX3. **2001**, 276, 23161-72	87
1678	Anwendungen der DNA-Array-Technologie in der Laboratoriumsmedizin. Uses of DNA Microarray Technology in Laboratory Medicine. **2001**, 25, 469-476	
1677	Prediction of the coding sequences of unidentified human genes. XXI. The complete sequences of 60 new cDNA clones from brain which code for large proteins. **2001**, 8, 179-87	29
1676	Microarray probe selection strategies. **2001**, 2, 329-40	48

1675	Genomes, neuroscience, and neurology. **2001**, 58, 1755-7	2
1674	Understanding human disease mutations through the use of interspecific genetic variation. **2001**, 10, 2319-28	237
1673	The Human Genome Project and eye disease: clinical implications. **2001**, 119, 1710-1	2
1672	Human mast cell transcriptome project. **2001**, 125, 1-8	16
1671	The role of eosinophils in asthma: Sarastro or the Queen of the Night?. **2001**, 125, 290-6	13
1670	Neurogenetics in the postgenomic era. **2001**, 58, 1758-9	
1669	The human genome is sequenced: what does it mean and why is it important?. **2001**, 58, 1748-9	1
1668	Gene expression in the developing mouse retina by EST sequencing and microarray analysis. **2001**, 29, 4983-93	60
1667	Thoughts on the relationship of the human genome project to neurology. **2001**, 58, 1764-5	2
1666	Genetics moves into the medical mainstream. **2001**, 286, 2322-4	69
1665	Impact of the human genome sequence on neurology and neuroscience. **2001**, 58, 1750-1	0
1664	A computational scan for U12-dependent introns in the human genome sequence. **2001**, 29, 4006-13	110
1663	Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs. **2001**, 29, E108	18
1662	Computational inference of homologous gene structures in the human genome. **2001**, 11, 803-16	267
1661	Assembly of the working draft of the human genome with GigAssembler. **2001**, 11, 1541-8	92
1660	High-resolution BAC-based map of the central portion of mouse chromosome 5. **2001**, 11, 1746-57	1
1659	A Survey of Genetics Knowledge of Health Professionals: Implications for Physical Therapists. **2001**, 13, 156-163	3
1658	Evolutionary dynamics in a novel L2 clade of non-LTR retrotransposons in Deuterostomia. **2001**, 18, 2213-24	60

1657 A mammalian gene evolved from the integrase domain of an LTR retrotransposon. **2001**, 18, 1597-600 29

1656 Adaptive evolution in LINE-1 retrotransposons. **2001**, 18, 2186-94 82

1655 Local similarity in evolutionary rates extends over whole chromosomes in human-rodent and mouse-rat comparisons: implications for understanding the mechanistic basis of the male mutation bias. **2001**, 18, 2032-9 82

1654 Breakthrough of the year. The runners-up. **2001**, 294, 2443-7

1653 Shifting paradigms in gene-mapping methodology for complex traits. **2001**, 2, 195-202 23

1652 Structural genomics in endocrinology. **2001**, 2, 353-60

1651 Recent advances in computational genomics. **2001**, 2, 361-72 5

1650 New drug targets for genomic cancer therapy: successes, limitations, opportunities and future challenges. **2001**, 1, 33-47 42

1649 A high-resolution radiation hybrid map of the human genome draft sequence. **2001**, 291, 1298-302 111

1648 Vaccinia virus semaphorin A39R is a 50-55 kDa secreted glycoprotein that affects the outcome of infection in a murine intradermal model. **2001**, 82, 2083-2093 39

1647 Signal and noise in gene length distributions of decoded genomes.

1646 Genomics Analysis of Genes Expressed in Maize Endosperm Identifies Novel Seed Proteins and Clarifies Patterns of Zein Gene Expression. **2001**, 13, 2297 3

1645 Pharmacogenomics and the (ir)relevance of race. **2001**, 1, 104-8 20

1644 Site-specific molecular design and its relevance to pharmacogenomics and chemical biology. **2001**, 1, 38-47 4

1643 Signaling to the mammalian circadian clocks: in pursuit of the primary mammalian circadian photoreceptor. **2001**, 2001, re16 19

1642 DNA amplification on chromosome 7q in squamous cell carcinoma of the tongue. **2001**, 19, 851-5 1

1641 Where will the genome lead us? Dentistry in the 21st century. **2001**, 132, 801-7 10

1640 Molecular diagnostics in monogenic and multifactorial forms of type 2 diabetes. **2001**, 1, 403-12 35

1639	Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro. **2001**, 8, 85-95	115
1638	Supersensitivity to anandamide and enhanced endogenous cannabinoid signaling in mice lacking fatty acid amide hydrolase. **2001**, 98, 9371-6	1084
1637	Hundred-year search for the human genome. **2001**, 2, 1-8	3
1636	DNA microarrays in medical practice. **2001**, 323, 611-5	59
1635	Detection of cis-element clusters in higher eukaryotic DNA. **2001**, 17, 878-89	202
1634	Methylation-mediated proviral silencing is associated with MeCP2 recruitment and localized histone H3 deacetylation. **2001**, 21, 7913-22	92
1633	Gene expression profiling in human fetal liver and identification of tissue- and developmental-stage-specific genes through compiled expression profiles and efficient cloning of full-length cDNAs. **2001**, 11, 1392-403	43
1632	SERPINB12 is a novel member of the human ov-serpin family that is widely expressed and inhibits trypsin-like serine proteinases. **2001**, 276, 49320-30	34
1631	Segmental duplications: what's missing, misassigned, and misassembled--and should we care?. **2001** , 11, 653-6	80
1630	How will the human genome project change cardiovascular medicine?. **2001**, 86, 123-4	3
1629	Alu-mediated inactivation of the human CMP- N-acetylneuraminic acid hydroxylase gene. **2001**, 98, 11399-404	125
1628	Histone deacetylase 1 phosphorylation promotes enzymatic activity and complex formation. **2001**, 276, 47733-41	191
1627	Interdomain chaperoning between PSD-95, Dlg, and Zo-1 (PDZ) domains of glutamate receptor-interacting proteins. **2001**, 276, 43216-20	30
1626	A second uniquely human mutation affecting sialic acid biology. **2001**, 276, 40282-7	59
1625	Dynamic protein complexes: insights from mass spectrometry. **2001**, 276, 46685-8	52
1624	Differential cooperation between regulatory sequences required for human CD53 gene expression. **2001**, 276, 35405-13	14
1623	Networking proteins in yeast. **2001**, 98, 4277-8	78
1622	Genomic and phylogenetic perspectives on the evolution of prokaryotes. **2001**, 50, 497-512	30

1621	Krüppel-like factors: three fingers in many pies. **2001**, 276, 34355-8	487
1620	Unlimited access--limitless success. **2001**, 11, 637-8	5
1619	Genome-scale compositional comparisons in eukaryotes. **2001**, 11, 540-6	117
1618	Navigating the human transcriptome. **2001**, 98, 11837-8	13
1617	A computational analysis of sequence features involved in recognition of short introns. **2001**, 98, 11193-8	276
1616	Are we polyploids? A brief history of one hypothesis. **2001**, 11, 667-70	41
1615	Treasures in the attic: rolling circle transposons discovered in eukaryotic genomes. **2001**, 98, 8923-4	65
1614	Human Genome Project. **2001**,	1
1613	Identification and characterization of mammalian mitochondrial tRNA nucleotidyltransferases. **2001**, 276, 40041-9	84
1612	The complete gene sequence of titin, expression of an unusual approximately 700-kDa titin isoform, and its interaction with obscurin identify a novel Z-line to I-band linking system. **2001**, 89, 1065-72	493
1611	Bypass of heterology during strand transfer by Saccharomyces cerevisiae Rad51 protein. **2001**, 29, 5052-7	22
1610	The 1.4-Mb CMT1A duplication/HNPP deletion genomic region reveals unique genome architectural features and provides insights into the recent evolution of new genes. **2001**, 11, 1018-33	109
1609	The intronless and TATA-less human TAF(II)55 gene contains a functional initiator and a downstream promoter element. **2001**, 276, 25503-11	43
1608	Molecular indexing of human genomic DNA. **2001**, 29, E95	1
1607	A sequence-based integrated map of chromosome 22. **2001**, 11, 1290-5	14
1606	An isoform-specific inhibitory domain regulates the LHX3 LIM homeodomain factor holoprotein and the production of a functional alternate translation form. **2001**, 276, 36311-9	52
1605	Highlights of alternative splicing regulation session: yes, no, maybe--a history of paradigm shifts. **2001**, 2001, pe35	1
1604	Chapter 20. Bioinformatics in the drug discovery process. **2001**, 36, 201-210	1

1603	Genome-wide views of cancer. **2001**, 344, 601-2	68
1602	Sequence variation and disease in the wake of the draft human genome. **2001**, 10, 2209-14	24
1601	Pattern and timing of gene duplication in animal genomes. **2001**, 11, 1842-7	158
1600	Characterization and functional implications of the RNA binding properties of nuclear factor TDP-43, a novel splicing regulator of CFTR exon 9. **2001**, 276, 36337-43	462
1599	Agent interaction for bioinformatics data management. **2001**, 15, 917-947	13
1598	Molecular diagnostics in China. **2001**, 39, 1190-4	1
1597	Hypermutability at a poly(A/T) tract in the human germline. **2001**, 29, 4405-13	19
1596	Matrix-induced fragmentation of P3'-N5' phosphoramidate-containing DNA: high-throughput MALDI-TOF analysis of genomic sequence polymorphisms. **2001**, 29, 3864-72	40
1595	Birth of scale-free molecular networks and the number of distinct DNA and protein domains per genome. **2001**, 17, 988-96	123
1594	GST-PRIME: a genome-wide primer design software for the generation of gene sequence tags. **2001**, 29, 4373-7	16
1593	GeneLynx: a gene-centric portal to the human genome. **2001**, 11, 2151-7	44
1592	Molecular evolution of the homeodomain family of transcription factors. **2001**, 29, 3258-69	111
1591	Identification of genes potentially involved in rupture of human atherosclerotic plaques. **2001**, 89, 547-54	118
1590	Most of the human genome is transcribed. **2001**, 11, 1975-7	45
1589	Obscurin, a giant sarcomeric Rho guanine nucleotide exchange factor protein involved in sarcomere assembly. **2001**, 154, 123-36	225
1588	Comparative analysis for expressed genes by polymerase chain reaction using module-shuffling primers. **2001**, 91-2	
1587	DNA sequences from multiple amplifications reveal artifacts induced by cytosine deamination in ancient DNA. **2001**, 29, 4793-9	482
1586	Spidey: a tool for mRNA-to-genomic alignments. **2001**, 11, 1952-7	265

1585	The human genome sequence expedition: views from the "base camp". **2001**, 11, 645-51	14
1584	REPuter: the manifold applications of repeat analysis on a genomic scale. **2001**, 29, 4633-42	991
1583	Regulated transposition of a fish transposon in the mouse germ line. **2001**, 98, 6759-64	205
1582	Divergent origins and concerted expansion of two segmental duplications on chromosome 16. **2001**, 92, 462-8	22
1581	Genetically increased angiotensin I-converting enzyme level and renal complications in the diabetic mouse. **2001**, 98, 13330-4	119
1580	Principles of Data Mining and Knowledge Discovery. **2001**,	6
1579	Adaptins: the final recount. **2001**, 12, 2907-20	375
1578	Discovery of functional genes in the post-genome era by novel RNA-protein hybrid ribozymes. **2001**, 133-4	2
1577	Applications of yeast in drug discovery. **2001**, 57, 117-62	16
1576	Genomics and the transformation of neurology. **2001**, 286, 2869-70	
1575	The unending string. **2001**, 155, 1193-4	
1574	Genomic neurology: a new beginning. **2001**, 58, 1739-41	5
1573	Implications of the human genome for understanding human biology and medicine. **2001**, 286, 2296-307	93
1572	Identification of alternate polyadenylation sites and analysis of their tissue distribution using EST data. **2001**, 11, 1520-6	139
1571	Alternative splicing of CRH-R1 receptors in human and mouse skin: identification of new variants and their differential expression. **2001**, 15, 2754-6	145
1570	Milestone or genomania? The relevance of the Human Genome Project to biological aging and the age-related diseases. **2001**, 56, M529-37	4
1569	Molecular characterization of two natural hotspots in the Drosophila buzzatii genome induced by transposon insertions. **2001**, 11, 1353-64	59
1568	A clone-array pooled shotgun strategy for sequencing large genomes. **2001**, 11, 1619-23	41

1567	The AIDS research model: implications for other infectious diseases of global health importance. **2001**, 286, 458-61		8
1566	HERV-K(OLD): ancestor sequences of the human endogenous retrovirus family HERV-K(HML-2). **2001**, 75, 8917-26		45
1565	A novel mechanism for regulating transforming growth factor beta (TGF-beta) signaling. Functional modulation of type III TGF-beta receptor expression through interaction with the PDZ domain protein, GIPC. **2001**, 276, 39608-17		158
1564	Twin priming: a proposed mechanism for the creation of inversions in L1 retrotransposition. **2001**, 11, 2059-65		171
1563	Is the Individual Anything Other Than Culture?. **2001**, 7, 495-506		
1562	A human nuclease specific for G4 DNA. **2001**, 98, 12444-9		90
1561	Protein-protein interaction panel using mouse full-length cDNAs. **2001**, 11, 1758-65		89
1560	The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome. **2001**, 98, 12103-8		103
1559	LDB2000: sequence-based integrated maps of the human genome. **2001**, 17, 581-6		11
1558	A novel nuclear human poly(A) polymerase (PAP), PAP gamma. **2001**, 276, 33504-11		48
1557	Cloning and characterization of a novel mouse Siglec, mSiglec-F: differential evolution of the mouse and human (CD33) Siglec-3-related gene clusters. **2001**, 276, 45128-36		69
1556	CNS myelination and PLP gene dosage. **2001**, 2, 263-72		15
1555	Evolution of knowledge encapsulated in scientific definitions. **2001**, 44, 556-64		5
1554	Integration of cytogenetic landmarks into the draft sequence of the human genome. *Nature*, **2001**, 409, 953-8	50.4	262
1553	Genetic strategies for the personalization of antipsychotic treatment. **2001**, 1, 275-80		5
1552	Pharmacogenetics: the Rx perspective. **2001**, 1, 255-63		14
1551	Towards high-throughput genotyping of SNPs by dynamic allele-specific hybridization. **2001**, 1, 352-8		8
1550	The Human Genome Project, genetics and health. **2001**, 4, 77-80		13

1549 Racial profiling in medical research. **2001**, 344, 1392-3 323

1548 Fungal histidine kinases. **2001**, 2001, re1 71

1547 Modification of alternative splicing by antisense oligonucleotides as a potential chemotherapy for cancer and other diseases. **2001**, 1, 211-30 38

1546 Multiplex polymerase chain reaction (PCR) with color-tagged module-shuffling primers for comparing gene expression levels in various cells. **2001**, 29, E84 5

1545 Infectious diseases: considerations for the 21st century. **2001**, 32, 675-85 240

1544 Cambridge Healthtech Institute's 5th Annual Conference: impact of genomics on medicine. **2001**, 2, 297-301

1543 Applied neurogenomics. **2001**, 2, 143-52 8

1542 Microarrays: spotlight on gene function and pharmacogenomics. **2001**, 1, 155-75 16

1541 MALDI TOF mass spectrometry: an emerging platform for genomics and diagnostics. **2001**, 1, 11-8 20

1540 Identification and prevention of a GC content bias in SAGE libraries. **2001**, 29, E60-0 49

1539 Homology modelling and molecular dynamics studies of human placental tissue protein 13 (galectin-13). **2001**, 14, 875-80 69

1538 An Eulerian path approach to DNA fragment assembly. **2001**, 98, 9748-53 857

1537 Genomics, complexity and drug discovery: insights from Boolean network models of cellular regulation. **2001**, 2, 203-22 70

1536 Closing the gaps in genetics legislation and policy: a report by the new york state task force on life and the law. **2001**, 5, 275-80 4

1535 Model system for evaluation of alternative splicing: exon skipping. **2001**, 20, 807-13 14

1534 Nuclear Pre-mRNA Splicing in Plants. **2001**, 20, 523-571 48

1533 . **2001**, 12

1532 Molecular diversity of the HLA-B27 gene and its association with disease. **2001**, 11, 275-85 5

1531	Cytokines and Colony Stimulating Factors. **2002**,	
1530	Sampling rare events: statistics of local sequence alignments. **2002**, 65, 056102	61
1529	A comparative genomic analysis of two distant diptera, the fruit fly, Drosophila melanogaster, and the malaria mosquito, Anopheles gambiae. **2002**, 12, 57-66	50
1528	Transcriptional regulation: a genomic overview. **2002**, 1, e0085	33
1527	BLAT--the BLAST-like alignment tool. **2002**, 12, 656-64	5063
1526	A comparison of whole-genome shotgun-derived mouse chromosome 16 and the human genome. **2002**, 296, 1661-71	305
1525	The human ribosomal protein genes: sequencing and comparative analysis of 73 genes. **2002**, 12, 379-90	123
1524	Comparative genome and proteome analysis of Anopheles gambiae and Drosophila melanogaster. **2002**, 298, 149-59	455
1523	Bootstrapping and normalization for enhanced evaluations of pairwise sequence comparison. **2002**, 90, 1834-1847	33
1522	Discovery of five conserved beta -defensin gene clusters using a computational search strategy. **2002**, 99, 2129-33	423
1521	Functional genomics in reproductive medicine. **2002**, 5, 3-5	3
1520	Protein-based analysis of alternative splicing in the human genome.	3
1519	Engaging science and technology for drug development. **2002**, 1, 1	3
1518	Statistics of selectively neutral genetic variation. **2002**, 65, 040901	2
1517	Novel ENU-induced eye mutations in the mouse: models for human eye disease. **2002**, 11, 755-67	101
1516	An electrochemical detection scheme for identification of single nucleotide polymorphisms using hairpin-forming probes. **2002**, 30, e55	57
1515	Genomics and integrative analyses of division of labor in honeybee colonies. **2002**, 160 Suppl 6, S160-72	114
1514	Evidence for lateral transfer of genes encoding ferredoxins, nitroreductases, NADH oxidase, and alcohol dehydrogenase 3 from anaerobic prokaryotes to Giardia lamblia and Entamoeba histolytica. **2002**, 1, 181-90	112

1513	DNA probes on beads arrayed in a capillary, 'Bead-array', exhibited high hybridization performance. **2002**, 30, e87	33
1512	Current methods of gene prediction, their strengths and weaknesses. **2002**, 30, 4103-17	274
1511	Using bio-panning of FLITRX peptide libraries displayed on E. coli cell surface to study protein-protein interactions. **2003**, 205, 267-80	12
1510	Genomic medicine--a primer. **2002**, 347, 1512-20	468
1509	Biophysical characterization of proteins in the post-genomic era of proteomics. **2002**, 1, 415-20	11
1508	Structure and evolution of the Smith-Magenis syndrome repeat gene clusters, SMS-REPs. **2002**, 12, 729-38	72
1507	euGenes: a eukaryote genome information system. **2002**, 30, 145-8	34
1506	Evidence for a fast, intrachromosomal conversion mechanism from mapping of nucleotide variants within a homogeneous alpha-satellite DNA array. **2002**, 12, 1815-26	50
1505	Generalized gap model for bacterial artificial chromosome clone fingerprint mapping and shotgun sequencing. **2002**, 12, 1943-9	23
1504	A computational/functional genomics approach for the enrichment of the retinal transcriptome and the identification of positional candidate retinopathy genes. **2002**, 99, 14326-31	27
1503	In silico chromosome staining: reconstruction of Giemsa bands from the whole human genome sequence. **2002**, 99, 797-802	33
1502	Single nucleotide polymorphism mapping using genome-wide unique sequences. **2002**, 12, 1106-11	10
1501	Systematic identification of novel protein domain families associated with nuclear functions. **2002**, 12, 47-56	437
1500	The clinical impact of the Human Genome Project: inherited variants in cancer care. **2002**, 13 Suppl 4, 105-7	2
1499	Multiplex SNP genotyping in pooled DNA samples by a four-colour microarray system. **2002**, 30, e70	82
1498	Remarkable compartmentalization of transposable elements and pseudogenes in the heterochromatin of the Tetraodon nigroviridis genome. **2002**, 99, 13636-41	60
1497	Novel endogenous retrovirus in rabbits previously reported as human retrovirus 5. **2002**, 76, 7094-102	28
1496	Structural characterization of the human proteome. **2002**, 12, 1625-41	57

1495	Distinct sets of adjacent heterogeneous nuclear ribonucleoprotein (hnRNP) A1/A2 binding sites control 5' splice site selection in the hnRNP A1 mRNA precursor. **2002**, 277, 29745-52	60
1494	Genome-wide analysis of clustered Dorsal binding sites identifies putative target genes in the Drosophila embryo. **2002**, 99, 763-8	305
1493	Differential gene expression in premalignant human epidermis revealed by cluster analysis of serial analysis of gene expression (SAGE) libraries. **2002**, 16, 246-8	23
1492	tRNomics: analysis of tRNA genes from 50 genomes of Eukarya, Archaea, and Bacteria reveals anticodon-sparing strategies and domain-specific features. **2002**, 8, 1189-232	290
1491	Application of in silico positional cloning and bioinformatic mutation analysis to the study of eye diseases. **2002**, 3, 59-72	3
1490	Genetics and social class. **2002**, 56, 529-35	19
1489	A unique glutamic acid-lysine (EK) domain acts as a splicing inhibitor. **2002**, 277, 39485-92	12
1488	Interphase chromosomes in Arabidopsis are organized as well defined chromocenters from which euchromatin loops emanate. **2002**, 99, 14584-9	354
1487	The BNIP-2 and Cdc42GAP homology/Sec14p-like domain of BNIP-Salpha is a novel apoptosis-inducing sequence. **2002**, 277, 7483-92	35
1486	Intergenic mRNA molecules resulting from trans-splicing. **2002**, 277, 5882-90	109
1485	Tandem repeats in protein coding regions of primate genes. **2002**, 12, 909-15	62
1484	MODEL FOR THE GROWTH OF BACTERIAL GENOMES. **2002**, 16, 821-827	2
1483	GENOMIC ORGANIZATION AND HOPFIELD'S MODEL OF ASSOCIATIVE MEMORY. **2002**, 05, 361-369	
1482	Complementary profiling of gene expression at the transcriptome and proteome levels in Saccharomyces cerevisiae. **2002**, 1, 323-33	525
1481	Genetic and physiological data implicating the new human gene G72 and the gene for D-amino acid oxidase in schizophrenia. **2002**, 99, 13675-80	709
1480	Defects in pre-mRNA processing as causes of and predisposition to diseases. **2002**, 21, 803-18	71
1479	When pharmacogenomics goes public. **2002**, 21, 29-37	11
1478	Spline methods for the comparison of physical and genetic maps. **2002**, 9, 465-75	6

1477	Targeting HIV RNA with Small Molecules. 18-40	
1476	Oligo(dT) primer generates a high frequency of truncated cDNAs through internal poly(A) priming during reverse transcription. **2002**, 99, 6152-6	125
1475	Unique de novo mutation of BRCA2 in a woman with early onset breast cancer. **2002**, 39, 126-8	16
1474	RePS: a sequence assembler that masks exact repeats identified from the shotgun data. **2002**, 12, 824-31	48
1473	A bioinformatic strategy to rapidly characterize cDNA libraries. **2002**, 18, 949-52	14
1472	Selective stimulation of translational expression by Alu RNA. **2002**, 30, 3253-61	59
1471	INCONSISTENCIES BETWEEN MAPS OF HUMAN CHROMOSOME 22 CORRELATE WITH INCREASED FREQUENCY OF DISEASE-RELATED LOCI. **2002**, 10, 303-317	2
1470	Gene expression studies using microarrays: principles, problems, and prospects. **2002**, 26, 256-70	114
1469	On the sequencing of the human genome. **2002**, 99, 3712-6	112
1468	Selective inhibition of P-glycoprotein expression in multidrug-resistant tumor cells by a designed transcriptional regulator. **2002**, 302, 963-71	47
1467	Genome-wide identification of tissue-specific enhancers in the Ciona tadpole. **2002**, 99, 6802-5	85
1466	Linkage disequilibrium between the beta frequency of the human EEG and a GABAA receptor gene locus. **2002**, 99, 3729-33	246
1465	Paradigm shifts in late-Holocene climatology?. **2002**, 12, 239-249	6
1464	Critical residues within the BTB domain of PLZF and Bcl-6 modulate interaction with corepressors. **2002**, 22, 1804-18	177
1463	Genes in a refined Smith-Magenis syndrome critical deletion interval on chromosome 17p11.2 and the syntenic region of the mouse. **2002**, 12, 713-28	88
1462	Alu-containing exons are alternatively spliced. **2002**, 12, 1060-7	368
1461	Conformational changes that occur during M3 muscarinic acetylcholine receptor activation probed by the use of an in situ disulfide cross-linking strategy. **2002**, 277, 2247-57	63
1460	Enzyme activity profiles of the secreted and membrane proteome that depict cancer cell invasiveness. **2002**, 99, 10335-40	284

1459	Cross-referencing eukaryotic genomes: TIGR Orthologous Gene Alignments (TOGA). **2002**, 12, 493-502	115
1458	Evolutionary conservation of chromosome territory arrangements in cell nuclei from higher primates. **2002**, 99, 4424-9	311
1457	Methylation-mediated silencing of TMS1/ASC is accompanied by histone hypoacetylation and CpG island-localized changes in chromatin architecture. **2002**, 277, 4951-8	42
1456	The novel human protein arginine N-methyltransferase PRMT6 is a nuclear enzyme displaying unique substrate specificity. **2002**, 277, 3537-43	257
1455	Microarray analysis reveals a major direct role of DNA copy number alteration in the transcriptional program of human breast tumors. **2002**, 99, 12963-8	980
1454	Genome complexity reduction for SNP genotyping analysis. **2002**, 99, 2942-7	37
1453	CFTR is a pattern recognition molecule that extracts Pseudomonas aeruginosa LPS from the outer membrane into epithelial cells and activates NF-kappa B translocation. **2002**, 99, 6907-12	118
1452	Signals and their transduction pathways regulating alternative splicing: a new dimension of the human genome. **2002**, 11, 2409-16	153
1451	Cutting edge: CATERPILLER: a large family of mammalian genes containing CARD, pyrin, nucleotide-binding, and leucine-rich repeat domains. **2002**, 169, 4088-93	236
1450	Computer assisted cloning of human neutral alpha-glucosidase C (GANC): a new paralog in the glycosyl hydrolase gene family 31. **2002**, 99, 13642-6	8
1449	Alternative splice variants of doublecortin-like kinase are differentially expressed and have different kinase activities. **2002**, 277, 17696-705	50
1448	Probing the molecular basis for potent and selective protein-tyrosine phosphatase 1B inhibition. **2002**, 277, 41014-22	61
1447	Genes, pseudogenes, and Alu sequence organization across human chromosomes 21 and 22. **2002**, 99, 2930-5	55
1446	The first linkage disequilibrium (LD) maps: delineation of hot and cold blocks by diplotype analysis. **2002**, 99, 2228-33	155
1445	Evolution of the RNA polymerase II C-terminal domain. **2002**, 99, 6091-6	59
1444	Microarray Data Processing and Analysis. **2002**, 43-63	14
1443	E. coliGene Expression Protocols. **2002**,	1
1442	An International Campaign for Agricultural and Livestock Genomics (CALG). **2002**, 06, 958-965	

1441 Databases and tools for browsing genomes. **2002**, 3, 293-310 17

1440 Identifying novel transcripts and novel genes in the human genome by using novel SAGE tags. **2002**, 99, 12257-62 130

1439 Genomes to Life "Center for Molecular and Cellular Systems": a research program for identification and characterization of protein complexes. **2002**, 6, 287-303 6

1438 Developmental genomic approaches in model organisms. **2002**, 3, 153-78 28

1437 The human genome project and its impact on psychiatry. **2002**, 25, 1-50 67

1436 A conceptual scale for correlating cytogenetic and physical maps. **2002**, 97, 136-9

1435 Cytogenetic and molecular genetic aspects of essential thrombocythemia. **2002**, 108, 55-65 47

1434 Generation and characterization of a 12,000-rad radiation hybrid panel for fine mapping in pig. **2002**, 97, 219-28 56

1433 Identification and characterization of human taste receptor genes belonging to the TAS2R family. **2002**, 98, 45-53 81

1432 Human chromosome 3: integration of 60 NotI clones into a physical and gene map. **2002**, 98, 177-83 10

1431 Synthesis and polymerase incorporation of 5'-amino-2',5'-dideoxy-5'-N-triphosphate nucleotides. **2002**, 30, 3739-47 18

1430 Parallel construction of orthologous sequence-ready clone contig maps in multiple species. **2002**, 12, 1277-85 56

1429 Statistical significance of clusters of motifs represented by position specific scoring matrices in nucleotide sequences. **2002**, 30, 3214-24 90

1428 A genome wide scan for familial high myopia suggests a novel locus on chromosome 7q36. **2002**, 39, 118-24 92

1427 Gene Expression Profiling of Human Diseases by Serial Analysis of Gene Expression. **2002**, 9, 384-394 19

1426 Genome-wide comparison of differences in the integration sites of interspersed repeats between closely related genomes. **2002**, 30, e71 25

1425 Identification and analysis of over 2000 ribosomal protein pseudogenes in the human genome. **2002**, 12, 1466-82 151

1424 Epigenetic contributors to the discordance of monozygotic twins. **2002**, 62, 97-103 94

1423	The SCAN domain of ZNF174 is a dimer. **2002**, 277, 5448-52	30
1422	Theoretical analysis of alternative splice forms using computational methods. **2002**, 18 Suppl 2, S65-73	14
1421	Genetic testing for breast and ovarian cancer predisposition: cancer burden and responsibility. **2002**, 7, 469-84	153
1420	The rice genome. The cereal of the world's poor takes center stage. **2002**, 296, 53	64
1419	What is finished, and why does it matter. **2002**, 12, 669-71	50
1418	Functional cloning, sorting, and expression profiling of nucleic acid-binding proteins. **2002**, 12, 1175-84	6
1417	The role of lineage-specific gene family expansion in the evolution of eukaryotes. **2002**, 12, 1048-59	332
1416	Pattern of organization of human mitochondrial pseudogenes in the nuclear genome. **2002**, 12, 885-93	125
1415	Protein-protein interactions between large proteins: two-hybrid screening using a functionally classified library composed of long cDNAs. **2002**, 12, 1773-84	80
1414	Large-scale protein annotation through gene ontology. **2002**, 12, 785-94	73
1413	The EMBL Nucleotide Sequence Database. **2002**, 30, 21-6	117
1412	Recent improvements to the SMART domain-based sequence annotation resource. **2002**, 30, 242-4	535
1411	DNA Data Bank of Japan (DDBJ) for genome scale research in life science. **2002**, 30, 27-30	88
1410	Ethical issues in human genome epidemiology: a case study based on the Japanese American Family Study in Seattle, Washington. **2002**, 155, 585-92	16
1409	The impact of chip technology on cancer medicine. **2002**, 13 Suppl 4, 109-13	4
1408	Characterization of POMT2, a novel member of the PMT protein O-mannosyltransferase family specifically localized to the acrosome of mammalian spermatids. **2002**, 12, 771-83	94
1407	Can long-range microsatellite data be used to predict short-range linkage disequilibrium?. **2002**, 11, 1363-72	20
1406	Microsatellite evolution inferred from human-chimpanzee genomic sequence alignments. **2002**, 99, 8748-53	107

1405	Mutations in the DNAH11 (axonemal heavy chain dynein type 11) gene cause one form of situs inversus totalis and most likely primary ciliary dyskinesia. **2002**, 99, 10282-6	268
1404	A nonsense mutation in the gene encoding 2'-5'-oligoadenylate synthetase/L1 isoform is associated with West Nile virus susceptibility in laboratory mice. **2002**, 99, 11311-6	240
1403	Inactivation of CMP-N-acetylneuraminic acid hydroxylase occurred prior to brain expansion during human evolution. **2002**, 99, 11736-41	239
1402	Activation of clg, a novel dbl family guanine nucleotide exchange factor gene, by proviral insertion at evi24, a common integration site in B cell and myeloid leukemias. **2002**, 277, 13463-72	16
1401	Molecular identification of a novel carnitine transporter specific to human testis. Insights into the mechanism of carnitine recognition. **2002**, 277, 36262-71	142
1400	Molecular cloning of a fourth member of the potassium-dependent sodium-calcium exchanger gene family, NCKX4. **2002**, 277, 48410-7	79
1399	Sacred lotus, the long-living fruits of China Antique. **2002**, 12, 131-143	92
1398	A review of DNA sequencing techniques. **2002**, 35, 169-200	151
1397	ARROGANT: an application to manipulate large gene collections. **2002**, 18, 1410-7	9
1396	Olfactory Receptor Database: a metadata-driven automated population from sources of gene and protein sequences. **2002**, 30, 354-60	61
1395	Cross-species studies for target validation. **2002**, 1, 53-65	4
1394	Automated de novo identification of repeat sequence families in sequenced genomes. **2002**, 12, 1269-76	499
1393	HapScope: a software system for automated and visual analysis of functionally annotated haplotypes. **2002**, 30, 5213-21	29
1392	PATIKA: an integrated visual environment for collaborative construction and analysis of cellular pathways. **2002**, 18, 996-1003	114
1391	Highly efficient modification of bacterial artificial chromosomes (BACs) using novel shuttle vectors containing the R6Kgamma origin of replication. **2002**, 12, 1992-8	198
1390	Authorship for research groups. **2002**, 288, 3166-8	35
1389	Molecular mechanisms of TRS instability. **2002**, 516, 1-25	27
1388	Combined functional genomic maps of the C. elegans DNA damage response. **2002**, 295, 127-31	253

1387	Sustained expression of the novel EBV-induced zinc finger gene, ZNFEB, is critical for the transition of B lymphocyte activation to oncogenic growth transformation. **2002**, 168, 680-8	8
1386	Serial analysis of gene expression: technical considerations and applications to cardiovascular biology. **2002**, 91, 565-9	42
1385	Molecular fossils in the human genome: identification and analysis of the pseudogenes in chromosomes 21 and 22. **2002**, 12, 272-80	144
1384	Prediction of the coding sequences of mouse homologues of KIAA gene: I. The complete nucleotide sequences of 100 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries. **2002**, 9, 179-88	18
1383	Identification of candidate genes regulating HDL cholesterol using a chromosomal region expression array. **2002**, 12, 1693-702	19
1382	Identification of new herpesvirus gene homologs in the human genome. **2002**, 12, 1739-48	74
1381	A functional gene discovery in the Fas-mediated pathway to apoptosis by analysis of transiently expressed randomized hybrid-ribozyme libraries. **2002**, 30, 3609-14	31
1380	Evolutionary time and human memory. **2002**, 288, 3045-7	1
1379	Time and memory. **2002**, 59, 1699-700	1
1378	DBTSS: DataBase of human Transcriptional Start Sites and full-length cDNAs. **2002**, 30, 328-31	164
1377	Systematic sequencing of cDNA clones using the transposon Tn5. **2002**, 30, 2469-77	50
1376	Triple Repeat Diseases of the Nervous Systems. **2002**,	
1375	The structural basis of g-protein-coupled receptor function and dysfunction in human diseases. **2002**, 144-227	6
1374	Search for the second Peutz-Jeghers syndrome locus: exclusion of the STK13, PRKCG, KLK10, and PSCD2 genes on chromosome 19 and the STK11IP gene on chromosome 2. **2002**, 97, 171-8	43
1373	A novel interferon regulatory factor (IRF), IRF-10, has a unique role in immune defense and is induced by the v-Rel oncoprotein. **2002**, 22, 3942-57	80
1372	High-resolution organization of mouse telomeric and pericentromeric DNA. **2002**, 96, 125-9	29
1371	Copy and paste: the impact of a new non-L1 retroposon on the gonosomal heterochromatin of Microtus agrestis. **2002**, 96, 179-85	13
1370	Identification of a haplosufficient 3.6-Mb region in human chromosome 11q14.3-->q21. **2002**, 97, 158-62	24

1369	The KOX zinc finger genes: genome wide mapping of 368 ZNF PAC clones with zinc finger gene clusters predominantly in 23 chromosomal loci are confirmed by human sequences annotated in EnsEMBL. **2002**, 98, 147-53	21
1368	High-throughput selection of retrovirus producer cell lines leads to markedly improved efficiency of germ line-transmissible insertions in zebra fish. **2002**, 76, 2192-8	66
1367	Supportive evidence for the DYX3 dyslexia susceptibility gene in Canadian families. **2002**, 39, 125-6	59
1366	Partial trisomy 9p12p21.3 with a normal phenotype. **2002**, 39, 141-4	13
1365	Deletion of the OPA1 gene in a dominant optic atrophy family: evidence that haploinsufficiency is the cause of disease. **2002**, 39, e47	54
1364	Candidate gene studies in respiratory disease: avoiding the pitfalls. **2002**, 57, 377-8	5
1363	ANALYSIS OF THE EVOLVING PROTEOMES: PREDICTIONS OF THE NUMBER OF PROTEIN DOMAINS IN NATURE AND THE NUMBER OF GENES IN EUKARYOTIC ORGANISMS. **2002**, 10, 381-407	8
1362	The 'spectraplakins': cytoskeletal giants with characteristics of both spectrin and plakin families. **2002**, 115, 4215-25	138
1361	Progress in bioinformatics and the importance of being earnest. **2002**, 8, 1-54	8
1360	Paradigm shift in gene-finding method: From bench-top approach to desk-top approach (Review). **2002**, 10, 677	
1359	Genome-wide detection of tissue-specific alternative splicing in the human transcriptome. **2002**, 30, 3754-66	298
1358	Loss of heterozygosity at microsatellite markers from region p11-21 of chromosome 8 in microdissected breast tumor but not in peritumoral cells. **2002**, 21, 989	3
1357	Role of synaptotagmin in Ca2+-triggered exocytosis. **2002**, 366, 1-13	109
1356	Exclusion of the neuronal nicotinic acetylcholine receptor alpha7 subunit gene as a candidate for catatonic schizophrenia in a large family supporting the chromosome 15q13-22 locus. **2002**, 7, 220-3	23
1355	Map of candidate genes and STSs on 18p11.2, a bipolar disorder and schizophrenia susceptibility region. **2002**, 7, 337-9	11
1354	Efficient discovery of single-nucleotide polymorphisms in coding regions of human genes. **2002**, 2, 236-42	16
1353	Respective roles of calcitonin receptor-like receptor (CRLR) and receptor activity-modifying proteins (RAMP) in cell surface expression of CRLR/RAMP heterodimeric receptors. **2002**, 277, 14731-7	41
1352	Heterogeneous nuclear ribonucleoprotein (hnRNP) K is a component of an intronic splicing enhancer complex that activates the splicing of the alternative exon 6A from chicken beta-tropomyosin pre-mRNA. **2002**, 277, 16614-23	66

1351	Molecular enzymology of the catalytic domains of the Dnmt3a and Dnmt3b DNA methyltransferases. **2002**, 277, 20409-14	150
1350	Segmental polymorphisms in the proterminal regions of a subset of human chromosomes. **2002**, 12, 1673-8	31
1349	Selecting for functional alternative splices in ESTs. **2002**, 12, 1837-45	143
1348	Dasheng and RIRE2. A nonautonomous long terminal repeat element and its putative autonomous partner in the rice genome. **2002**, 130, 1697-705	52
1347	Functional genomics approaches to understanding brain disorders. **2002**, 3, 31-45	17
1346	Analyzing array data using supervised methods. **2002**, 3, 403-15	59
1345	Single cell expression analysis--pharmacogenomic potential. **2002**, 3, 809-22	6
1344	Optimized regulation of gene expression using artificial transcription factors. **2002**, 5, 685-94	29
1343	HUGE: a database for human large proteins identified in the Kazusa cDNA sequencing project. **2002** , 30, 166-8	71
1342	Combining multiple data sets in a likelihood analysis: which models are the best?. **2002**, 19, 2294-307	96
1341	Integrating genomics, bioinformatics, and classical genetics to study the effects of recombination on genome evolution. **2002**, 19, 1181-97	201
1340	Proliferation and deterioration of Rickettsia palindromic elements. **2002**, 19, 1234-43	14
1339	Molecular and genetic aspects of cardiac fatty acid homeostasis in health and disease. **2002**, 23, 774-87	5
1338	The presence of old Alus in GC-rich regions of the human genome - a genetic algorithm perspective.	
1337	The changing face of epidemiology in the genomics era. **2002**, 13, 472-80	33
1336	Human genome sequences: enigmatic variations. **2002**, 17, 457-61	1
1335	The Opitz syndrome gene Mid1 is transcribed from a human endogenous retroviral promoter. **2002**, 19, 1934-42	89
1334	Computational SNP discovery in DNA sequence data. **2003**, 212, 85-110	4

1333	A Kohonen self-organizing map for the functional classification of proteins based on one-dimensional sequence information.	0
1332	Patterns of insertion and deletion in contrasting chromatin domains. **2002**, 19, 2211-25	69
1331	Searching for evidence of positive selection in the human genome using patterns of microsatellite variability. **2002**, 19, 1143-53	83
1330	Applications of codon and rate variation models in molecular phylogeny. **2002**, 19, 1550-62	7
1329	Characterization of novel Alu- and tRNA-related SINEs from the tree shrew and evolutionary implications of their origins. **2002**, 19, 1964-72	70
1328	Deducing the origin of soluble adenylyl cyclase, a gene lost in multiple lineages. **2002**, 19, 2239-46	40
1327	Abundant raw material for cis-regulatory evolution in humans. **2002**, 19, 1991-2004	299
1326	Ancient lineages of non-LTR retrotransposons in the primitive eukaryote, Giardia lamblia. **2002**, 19, 619-30	55
1325	Analysis of lamprey and hagfish genes reveals a complex history of gene duplications during early vertebrate evolution. **2002**, 19, 1440-50	150
1324	A population-based study of Ashkenazi Jewish women's attitudes toward genetic discrimination and BRCA1/2 testing. **2002**, 4, 346-52	39
1323	Genetic approaches to the molecular understanding of type 2 diabetes. **2002**, 283, E217-25	73
1322	Pseudomonas-epithelial cell interactions dissected with DNA microarrays. **2002**, 121, 36S-39S	13
1321	Real and complex genomic signals.	1
1320	Transcriptional Regulation as a Pharmacologic Intervention. **2002**, 2, 1-9	1
1319	SNPs on human chromosomes 21 and 22 -- analysis in terms of protein features and pseudogenes. **2002**, 3, 393-402	14
1318	Information management systems for pharmacogenomics. **2002**, 3, 651-67	6
1317	A theory of sulcal-gap signalization. **2002**, 95, 375-406	
1316	How many SNPs does a genome-wide haplotype map require?. **2002**, 3, 379-91	86

1315	NetAffx. **2002**,	3
1314	The restriction scaffold problem. **2002**,	
1313	Tests for gene clustering. **2002**,	4
1312	The greedy path-merging algorithm for contig scaffolding. **2002**, 49, 603-615	61
1311	Parameter optimized surfaces (POPS): analysis of key interactions and conformational changes in the ribosome. **2002**, 30, 2950-60	80
1310	Functional characterisation of MeCP2 mutations found in male patients with X linked mental retardation. **2002**, 39, 132-6	14
1309	Identification of a locus for a form of spondyloepiphyseal dysplasia on chromosome 15q26.1: exclusion of aggrecan as a candidate gene. **2002**, 39, 634-8	8
1308	Getting ready for gene-based medicine. **2002**, 347, 1526-7	66
1307	Gene polymorphisms and the risk of myocardial infarction--an emerging relation. **2002**, 347, 1963-5	23
1306	Identification and characterization of the murine and human gene encoding the tuberoinfundibular peptide of 39 residues. **2002**, 143, 1047-57	36
1305	Pharmacogenomics in endocrinology. **2002**, 87, 2495-9	3
1304	Genomic studies of the spleen protein tyrosine kinase locus reveal a complex promoter structure and several genetic variants. **2002**, 43, 1627-35	2
1303	The use of chromosome-based vectors for animal transgenesis. **2002**, 9, 708-12	20
1302	Implications of pharmacogenomics in oral health. **2002**, 2, 148-51	3
1301	Genetic factors in atherosclerosis: status and perspectives. **2002**, 4, B14-B16	
1300	Some Historical and Future Aspects of Engineering Mechanics. **2002**, 128, 1242-1253	1
1299	[Biological Markers in Epidemiology: Concepts, applications, Perspectives (Part II)]. **2002**, 64, 145-52	0
1298	Chemical strategies for functional proteomics. **2002**, 1, 781-90	145

1297	Paroxysmal kinesigenic dyskinesia and generalized seizures: clinical and genetic analysis in a Spanish pedigree. **2002**, 33, 288-93	23
1296	The challenges of delivering pharmacogenomics into clinical pediatrics. **2002**, 2, 141-3	18
1295	Hormonal genomics. **2002**, 23, 369-81	18
1294	The missense mutation in the WKL1 gene not found in patients with bipolar affective disorder. **2002**, 7, 340-1	4
1293	Human chromosome 15q11-q14 regions of rearrangements contain clusters of LCR15 duplicons. **2002**, 10, 26-35	79
1292	Genetics of osteoporosis. **2002**, 23, 303-26	304
1291	A novel conditional Akt 'survival switch' reversibly protects cells from apoptosis. **2002**, 9, 233-44	47
1290	Identification of tandemly-repeated C/D snoRNA genes at the imprinted human 14q32 domain reminiscent of those at the Prader-Willi/Angelman syndrome region. **2002**, 11, 1527-38	172
1289	HERVd: database of human endogenous retroviruses. **2002**, 30, 205-6	61
1288	References. **2002**, 179-195	1
1287	Promoter proximal splice sites enhance transcription. **2002**, 16, 2792-9	196
1286	A duplication growth model of gene expression networks. **2002**, 18, 1486-93	144
1285	Functional substitution for TAF(II)250 by a retroposed homolog that is expressed in human spermatogenesis. **2002**, 11, 2341-6	70
1284	GFScan: a gene family search tool at genomic DNA level. **2002**, 12, 1142-9	7
1283	In sickness and in health: the importance of translational regulation. **2002**, 86, 322-4	12
1282	Medicinal chemistry in the new millennium. A glance into the future. **2002**, 74, 703-785	48
1281	Processed pseudogenes of human endogenous retroviruses generated by LINEs: their integration, stability, and distribution. **2002**, 12, 391-9	76
1280	Designer microarrays: from soup to nuts. **2002**, 57, B400-5	9

1279	Maternal transmission of P element transposase activity in Drosophila melanogaster depends on the last P intron. **2002**, 99, 9306-9	14
1278	Beyond the central dogma. **2002**, 18, 223-5	12
1277	A long terminal repeat retrotransposon of fission yeast has strong preferences for specific sites of insertion. **2002**, 1, 44-55	62
1276	Craniofacial anomalies, cataracts, congenital heart disease, sacral neural tube defects, and growth and developmental retardation in two sisters: a new autosomal recessive MCA/MR syndrome?. **2002**, 39, 145-8	3
1275	The impact of genomic and proteomic technologies on the development of new cancer drugs. **2002** , 13 Suppl 4, 115-24	15
1274	Genetic signal representation and analysis. **2002**,	10
1273	Neuroscience, genetics, and the future of psychiatric diagnosis. **2002**, 35, 139-44	37
1272	POTE, a highly homologous gene family located on numerous chromosomes and expressed in prostate, ovary, testis, placenta, and prostate cancer. **2002**, 99, 16975-80	67
1271	Deciphering protein complexes and protein interaction networks by tandem affinity purification and mass spectrometry: analytical perspective. **2002**, 1, 204-12	54
1270	Computational comparison of human genomic sequence assemblies for a region of chromosome 4. **2002**, 12, 424-9	9
1269	Signatures of domain shuffling in the human genome. **2002**, 12, 1642-50	71
1268	Common exon duplication in animals and its role in alternative splicing. **2002**, 11, 1561-7	120
1267	Evidence of positive selection acting at the human dopamine receptor D4 gene locus. **2002**, 99, 309-14	463
1266	Computer programs for eukaryotic gene prediction. **2002**, 3, 195-9	17
1265	Generation and comparative analysis of approximately 3.3 Mb of mouse genomic sequence orthologous to the region of human chromosome 7q11.23 implicated in Williams syndrome. **2002**, 12, 3-15	54
1264	Comparative genome analysis and pathway reconstruction. **2002**, 3, 245-56	13
1263	SNP genotyping on a genome-wide amplified DOP-PCR template. **2002**, 30, e125	32
1262	Cloning and characterization of human Siglec-11. A recently evolved signaling molecule that can interact with SHP-1 and SHP-2 and is expressed by tissue macrophages, including brain microglia. **2002**, 277, 24466-74	138

1261	Chemical Degradation of Polymers and Pyrolysis. **2002**, 65, 847-917	2
1260	Identifying transcription factor binding sites through Markov chain optimization. **2002**, 18 Suppl 2, S100-9	60
1259	Conserved helix 7 tyrosine acts as a multistate conformational switch in the 5HT2C receptor. Identification of a novel "locked-on" phenotype and double revertant mutations. **2002**, 277, 36577-84	99
1258	V-SINEs: a new superfamily of vertebrate SINEs that are widespread in vertebrate genomes and retain a strongly conserved segment within each repetitive unit. **2002**, 12, 316-24	85
1257	High throughput DNA sequencing with a microfabricated 96-lane capillary array electrophoresis bioprocessor. **2002**, 99, 574-9	224
1256	An efficient algorithm for large-scale detection of protein families. **2002**, 30, 1575-84	2433
1255	Translation initiation start prediction in human cDNAs with high accuracy. **2002**, 18, 343-50	62
1254	EZ-Retrieve: a web-server for batch retrieval of coordinate-specified human DNA sequences and underscoring putative transcription factor-binding sites. **2002**, 30, e121	24
1253	Comparison of whole genome assemblies of the human genome. **2002**, 30, 5004-14	4
1252	A microbead-based system for identifying and characterizing RNA-protein interactions by flow cytometry. **2002**, 1, 922-9	13
1251	The Molecular Biology Database Collection: 2002 update. **2002**, 30, 1-12	134
1250	Genomic analysis of the olfactory receptor region of the mouse and human T-cell receptor alpha/delta loci. **2002**, 12, 81-7	22
1249	Annotating the human proteome: the Human Proteome Survey Database (HumanPSD) and an in-depth target database for G protein-coupled receptors (GPCR-PD) from Incyte Genomics. **2002**, 30, 137-41	57
1248	The use of transgenic systems in pharmaceutical research. **2002**, 1, 119-30	10
1247	Short interspersed transposable elements (SINEs) are excluded from imprinted regions in the human genome. **2002**, 99, 327-32	133
1246	Current status of human chromosome 14. **2002**, 39, 81-90	19
1245	SKIP is an indispensable factor for Caenorhabditis elegans development. **2002**, 99, 9254-9	25
1244	Human paralogs of KIAA0187 were created through independent pericentromeric-directed and chromosome-specific duplication mechanisms. **2002**, 12, 67-80	21

1243	The mRNA of DEAD box protein p72 is alternatively translated into an 82-kDa RNA helicase. **2002**, 277, 1066-75	45
1242	Comparative genomics and evolution of proteins involved in RNA metabolism. **2002**, 30, 1427-64	383
1241	A new approach to genome mapping and sequencing: slalom libraries. **2002**, 30, E6	8
1240	Nutritional genomics. **2002**, 324, 1438-42	94
1239	NotI flanking sequences: a tool for gene discovery and verification of the human genome. **2002**, 30, 3163-70	17
1238	Linker-mediated recombinational subcloning of large DNA fragments using yeast. **2002**, 12, 190-7	58
1237	The ubiquitous nature of RNA chaperone proteins. **2002**, 72, 223-68	142
1236	A variant of osteogenesis imperfecta type IV with resolving kyphomelia is caused by a novel COL1A2 mutation. **2002**, 39, 128-32	5
1235	Classification of human B-ZIP proteins based on dimerization properties. **2002**, 22, 6321-35	347
1234	C2A activates a cryptic Ca(2+)-triggered membrane penetration activity within the C2B domain of synaptotagmin I. **2002**, 99, 1665-70	112
1233	Comparative genomic sequence analysis of the human chromosome 21 Down syndrome critical region. **2002**, 12, 1323-32	36
1232	SCREENING USING ANIMAL SYSTEMS. **2002**, 285-299	6
1231	On the importance of being co-transcriptional. **2002**, 115, 3865-71	241
1230	Intraproteomic networks: new forays into predicting interaction partners. **2002**, 12, 1156-8	
1229	Dissection of a complex enhancer element: maintenance of keratinocyte specificity but loss of differentiation specificity. **2002**, 22, 4293-308	35
1228	Soluble and transmembrane isoforms of novel interleukin-17 receptor-like protein by RNA splicing and expression in prostate cancer. **2002**, 277, 4309-16	101
1227	NASty effects on fibrillin pre-mRNA splicing: another case of ESE does it, but proposals for translation-dependent splice site choice live on. **2002**, 16, 1743-53	48
1226	Complexities of cancer research: mouse genetic models. **2002**, 43, 80-8	12

1225	Comparative mycobacterial genomics as a tool for drug target and antigen discovery. **2002**, 36, 78s-86s	54
1224	Prevalence of somatic alterations in the colorectal cancer cell genome. **2002**, 99, 3076-80	163
1223	SYSTERS, GeneNest, SpliceNest: exploring sequence space from genome to protein. **2002**, 30, 299-300	44
1222	Were vertebrates octoploid?. **2002**, 357, 531-44	169
1221	Utilizing the genome sequence of parasitic protozoa. Papers of a discussion meeting at The Royal Society. March 21-22, 2001. **2002**, 357, 3-116	3
1220	Technologies for the study of gene and protein expression in Plasmodium. **2002**, 357, 13-6	2
1219	Genomics and plant cells: application of genomics strategies to Arabidopsis cell biology. **2002**, 357, 731-6	8
1218	Functional genomics: lessons from yeast. **2002**, 357, 17-23	74
1217	ARACHNE: a whole-genome shotgun assembler. **2002**, 12, 177-89	378
1216	Progress and problems in defining susceptibility genes for rheumatic diseases. **2002**, 41, 361-4	5
1215	A scalable high-throughput chemical synthesizer. **2002**, 12, 1950-60	4
1214	High-throughput expression profiling techniques. **2002**, 27, 289-91	4
1213	Tracing the LINEs of human evolution. **2002**, 99, 10522-7	57
1212	On the sequencing and assembly of the human genome. **2002**, 99, 4145-6	37
1211	Functional second genes generated by retrotransposition of the X-linked ribosomal protein genes. **2002**, 30, 5369-75	38
1210	Dysmorphism, variable overgrowth, normal bone age, and severe developmental delay: a "Sotos-like" syndrome?. **2002**, 39, 148-52	6
1209	A deletion-generator compound element allows deletion saturation analysis for genomewide phenotypic annotation. **2002**, 99, 9948-53	48
1208	Single nucleotide polymorphism seeking long term association with complex disease. **2002**, 30, 3295-311	135

1207	The Gene Resource Locator: gene locus maps for transcriptome analysis. **2002**, 30, 221-5	10
1206	Validation of DNA sequences using mass spectrometry coupled with nucleoside mass tagging. **2002**, 12, 1135-41	9
1205	Large-scale analysis of the human and mouse transcriptomes. **2002**, 99, 4465-70	1248
1204	The genetics of tobacco use: methods, findings and policy implications. **2002**, 11, 119-24	76
1203	Predicting protein cellular localization using a domain projection method. **2002**, 12, 1168-74	81
1202	Very large G protein-coupled receptor-1, the largest known cell surface protein, is highly expressed in the developing central nervous system. **2002**, 277, 785-92	93
1201	Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones. **2002**, 9, 99-106	20
1200	Commentary: meta-analysis of individual participants' data in genetic epidemiology. **2002**, 156, 204-10	77
1199	Factor B and the mitochondrial ATP synthase complex. **2002**, 277, 6097-103	30
1198	Positional candidate cloning of a QTL in dairy cattle: identification of a missense mutation in the bovine DGAT1 gene with major effect on milk yield and composition. **2002**, 12, 222-31	642
1197	A question of size: the eukaryotic proteome and the problems in defining it. **2002**, 30, 1083-90	141
1196	Novel fluorescence labeling and high-throughput assay technologies for in vitro analysis of protein interactions. **2002**, 12, 487-92	38
1195	A common mechanism for mitotic inactivation of C2H2 zinc finger DNA-binding domains. **2002**, 16, 2985-90	108
1194	Acrofacial dysostosis in a patient with the TSC2-PKD1 contiguous gene syndrome. **2002**, 39, 136-41	13
1193	Active Alu element "A-tails": size does matter. **2002**, 12, 1333-44	105
1192	A low genomic number of recessive lethals in natural populations of bluefin killifish and zebrafish. **2002**, 296, 2398-401	44
1191	DNA microarrays: implications for cardiovascular medicine. **2002**, 91, 559-64	55
1190	The transcription cycle of RNA polymerase II in living cells. **2002**, 159, 777-82	215

1189	Mammalian selenoprotein in which selenocysteine (Sec) incorporation is supported by a new form of Sec insertion sequence element. **2002**, 22, 1402-11	127
1188	An ensemble method for identifying regulatory circuits with special reference to the qa gene cluster of Neurospora crassa. **2002**, 99, 16904-9	91
1187	Genes on human chromosome 19 show extreme divergence from the mouse orthologs and a high GC content. **2002**, 30, 1751-6	39
1186	The chAB4 and NF1-related long-range multisequence DNA families are contiguous in the centromeric heterochromatin of several human chromosomes. **2002**, 30, 2899-905	6
1185	Horizontal Gene Transfer and its Role in the Evolution of Prokaryotes. **2002**, 277-IX	4
1184	SRp30c is a repressor of 3' splice site utilization. **2002**, 22, 4001-10	51
1183	Whole-genome disassembly. **2002**, 99, 4143-4	32
1182	Consensus promoter identification in the human genome utilizing expressed gene markers and gene modeling. **2002**, 12, 462-9	43
1181	Psychiatric genetics in silico: databases and tools for psychiatric geneticists. **2002**, 12, 67-73	1
1180	Distribution of the second virial coefficients of globular proteins. **2002**, 60, 938-944	7
1179	More on vascular malformations. **2002**, 109, 2591-4; author reply 2594-5	10
1178	Repeat expansion detection (RED) and the RED cloning strategy. **2003**, 217, 51-60	
1177	Identifying protein production in wound healing: current techniques. **2002**, 11, 63-6	5
1176	[Pharmacogenomics: the frontiers of genome medicine]. **2002**, 120, 141-8	
1175	Developmental abnormalities in mouse embryos tetrasomic for chromosome 11: apparent similarity to embryos functionally disomic for the x chromosome. **2002**, 77, 269-76	6
1174	Chapter 10. The prospects for microbial genomics providing novel, exploitable, antibacterial targets. **2002**, 37, 95-104	1
1173	Military research needs in biomedical informatics. **2002**, 9, 509-19	8
1172	Retroposed new genes out of the X in Drosophila. **2002**, 12, 1854-9	327

1171	mRNA Splicing: Regulated and Differential. **2002**,	
1170	Haemophilia A and haemophilia B: molecular insights. **2002**, 55, 127-44	85
1169	Azole antifungals are potent inhibitors of cytochrome P450 mono-oxygenases and bacterial growth in mycobacteria and streptomycetes. **2002**, 148, 2937-2949	147
1168	Association between SAH, an acyl-CoA synthetase gene, and hypertriglyceridemia, obesity, and hypertension. **2002**, 105, 41-7	62
1167	TAPP1 and TAPP2 are targets of phosphatidylinositol 3-kinase signaling in B cells: sustained plasma membrane recruitment triggered by the B-cell antigen receptor. **2002**, 22, 5479-91	92
1166	Biochemie und Molekulargenetik 2001. **2002**, 50, 312-326	
1165	Dictionary-driven protein annotation. **2002**, 30, 3901-16	18
1164	Preface. **2002**, 13, 485	
1163	The era of genomics: impact on sepsis clinical trial design. **2002**, 30, S341-8	34
1162	Developments in laboratory techniques for prenatal diagnosis. **2002**, 14, 161-8	9
1161	Genetic Predisposition to Severe Sepsis. **2002**, 9, 229-237	1
1160	Human 3'-phosphoadenosine 5'-phosphosulfate synthetase 2 (PAPSS2) pharmacogenetics: gene resequencing, genetic polymorphisms and functional characterization of variant allozymes. **2002**, 12, 11-21	27
1159	Identification and ethnic distribution of major haplotypes in the gene GNB3 encoding the G-protein beta3 subunit. **2002**, 12, 209-20	80
1158	cDNA microarray analysis of global gene expression in sarcomas. **2002**, 14, 406-11	14
1157	Mammalian chemosensory receptors. **2002**, 13, A9-17	13
1156	Challenges in dyslipidemia. **2002**, 4, 141-6	
1155	Applications of advances in molecular biology and genomics to clinical cancer care. **2002**, 25, 110-22; quiz 123-4	5
1154	Genetics competency: new directions for nursing. **2002**, 13, 486-91	8

1153	Genetic analysis of Carney complex: current understanding and future questions. **2002**, 9, 244-249	3
1152	Gene-expression profiles in hereditary breast cancer. **2002**, 9, 1-6	4
1151	Status and potential of gene therapy in clinical medicine. Assessment of an emerging health technology through systematic survey of clinical gene therapy protocols and published results. **2002**, 18, 645-74	12
1150	Autosomal Dominant Inheritance Pattern for Trigger Thumb. **2002**, 109, 242	
1149	Application of high-throughput computing in bioinformatics. **2002**, 360, 1179-89	8
1148	Genomics and cancer. **2002**, 14, 79-85	19
1147	Recombinant expression of mammalian selenocysteine-containing thioredoxin reductase and other selenoproteins in Escherichia coli. **2002**, 347, 226-35	39
1146	Environmental factors affecting transcription of the human L1 retrotransposon. I. Steroid hormone-like agents. **2002**, 17, 193-200	24
1145	Histone gene complement, variant expression, and mRNA processing in a urochordate Oikopleura dioica that undergoes extensive polyploidization. **2002**, 19, 2247-60	13
1144	On the abundance and distribution of transposable elements in the genome of Drosophila melanogaster. **2002**, 19, 926-37	194
1143	Altered mRNA expression of Pax5 and Blimp-1 in B cells in multiple myeloma. **2002**, 100, 4629-39	37
1142	Genetic testing and psychology: New roles, new responsibilities.. **2002**, 57, 271-282	40
1141	Interactions between two fission yeast serine/arginine-rich proteins and their modulation by phosphorylation. **2002**, 368, 527-34	17
1140	Methods for Analysing mRNA Expression. 163-407	
1139	Marked increase in CC chemokine gene expression in both human and mouse mast cell transcriptomes following Fcepsilon receptor I cross-linking: an interspecies comparison. **2002**, 100, 3861-8	97
1138	Narrowing and genomic annotation of the commonly deleted region of the 5q- syndrome. **2002**, 99, 4638-41	213
1137	Role of Src in Signal Transduction Pathways. **2002**, 30, 11-17	67
1136	Evidence that the number of hematopoietic stem cells per animal is conserved in mammals. **2002**, 100, 2665-7	174

1135	Genomics, proteomics, and the new paradigm in biomedical research. **2002**, 4, 2S-9S	8
1134	A novel mutation vf causing abnormal vacuoles in the central nervous system maps on rat chromosome 8. **2002**, 51, 149-55	3
1133	High-Throughput and Industrial Methods for mRNA Expression Analysis. 409-622	1
1132	Familial isolated growth hormone deficiency: genetics and pathophysiology. **2002**, 49, 265-72	1
1131	Protein profiling and proteomic databases. **2002**, 299-312	
1130	Applications for microarrays in renal biology and medicine. **2002**, 10, 93-101	10
1129	Coffin-Lowry phenotype in a patient with a complex chromosome rearrangement. **2002**, 39, e41	3
1128	Setting the pace. **2002**, 55, 18-18	
1127	Expression of human smooth muscle calponin in transgenic mice revealed with a bacterial artificial chromosome. **2002**, 282, H1793-803	11
1126	Translational genomics in medical genetics. **2002**, 4, 468-71	5
1125	Protein modules and protein-protein interaction. Introduction. **2002**, 61, 1-8	27
1124	Sequence analysis of multidomain proteins: past perspectives and future directions. **2002**, 61, 75-98	10
1123	Chapter 19. Expanding and exploring cellular pathways for novel drug targets. **2002**, 37, 187-196	2
1122	The crucial role of the public health sciences in the postgenomic era. **2002**, 4, 21S-26S	8
1121	Quantitative analysis of in situ hybridization histochemistry. **2002**, 47, 135-70	4
1120	Microbial genomics for antibiotic target discovery. **2002**, 271-288	
1119	The role of biotechnology. **2002**, 21, 205-213	1
1118	References. **2002**, 305-345	

1117 Deciphering the Human Genome Project. 1-32

1116 Genomic Technology. 33-54

1115 Haemophilia A and haemophilia B: molecular insights. **2002**, 55, 1-18 51

1114 Finding genes for bipolar disorder in the functional genomics era: from convergent functional genomics to phenomics and back. **2002**, 7, 215-6, 223-6 18

1113 Gene density and human nucleotide polymorphism. **2002**, 19, 336-40 55

1112 Characterization of the intragenomic spread of the human endogenous retrovirus family HERV-W. **2002**, 19, 526-33 70

1111 Evolution of genome size in Drosophila. is the invader's genome being invaded by transposable elements?. **2002**, 19, 1154-61 67

1110 Risk Assessment at the Crossroads of the 21st Century: Opportunities and Challenges for Research. **2002**, 8, 1195-1202 2

1109 Signal processing and statistical methods in analysis of text and DNA. **2002**, 1

1108 Beyond the genome: Reconstituting the new genetics. **2002**, 21, 267-277 17

1107 Application of the human genome to obstetrics and gynecology. **2002**, 45, 711-29; discussion 730-2 7

1106 The Tower of Babel? An assessment of the development and state of genetic and SNP technologies. **2002**, 12, 59-61 1

1105 Gene expression profiling by DNA microarray technology. **2002**, 13, 35-50 30

1104 Multiple ribonuclease H-encoding genes in the Caenorhabditis elegans genome contrasts with the two typical ribonuclease H-encoding genes in the human genome. **2002**, 19, 1910-9 6

1103 Genome-wide analysis of the Emigrant family of MITEs of Arabidopsis thaliana. **2002**, 19, 2285-93 70

1102 Comparative genetics and evolution of annexin A13 as the founder gene of vertebrate annexins. **2002**, 19, 608-18 37

1101 Evolution of the phosphoglycerate mutase processed gene in human and chimpanzee revealing the origin of a new primate gene. **2002**, 19, 654-63 61

1100 Science, medicine, and the future: Bioinformatics. **2002**, 324, 1018-22 71

1099	Non-coding ribonucleic acids--a class of their own?. **2002**, 218, 143-219	7
1098	Molecular techniques for studying gene expression in carcinogenesis. **2002**, 20, 77-116	31
1097	Identification of a contact region between the tridecapeptide alpha-factor mating pheromone of Saccharomyces cerevisiae and its G protein-coupled receptor by photoaffinity labeling. **2002**, 41, 6128-39	37
1096	A novel family of calmodulin-binding transcription activators in multicellular organisms. **2002**, 277, 21851-61	199
1095	Genome-wide profiling of gene expression in 29 normal human tissues with a cDNA microarray. **2002**, 9, 35-45	77
1094	[beta]-defensins in lung host defense. **2002**, 64, 709-48	215
1093	Protein Microarrays on ITO Surfaces by a Direct Covalent Attachment Scheme. **2002**, 18, 6324-6329	36
1092	Basic Concepts of Gene Expression. 1-95	
1091	Array-based structure and gene expression relationship study of antitumor sulfonamides including N-[2-[(4-hydroxyphenyl)amino]-3-pyridinyl]-4-methoxybenzenesulfonamide and N-(3-chloro-7-indolyl)-1,4-benzenedisulfonamide. **2002**, 45, 4913-22	65
1090	Genomewide motif identification using a dictionary model. **2002**, 90, 1803-1810	16
1089	Purine and pyrimidine (P2) receptors as drug targets. **2002**, 45, 4057-93	283
1088	Tandem mass spectrometry of ribonuclease A and B: N-linked glycosylation site analysis of whole protein ions. **2002**, 74, 577-83	72
1087	Bench-to-bedside review: fulfilling promises of the Human Genome Project. **2002**, 6, 212-5	11
1086	A personal view of molecular technology and how it has changed biology. **2002**, 1, 399-409	43
1085	Tyr266 in the sixth transmembrane domain of the yeast alpha-factor receptor plays key roles in receptor activation and ligand specificity. **2002**, 41, 13681-9	26
1084	Proteomics approaches in drug discovery. **2002**, 74, 412A-419A	27
1083	Calcium signaling through protein kinases. The Arabidopsis calcium-dependent protein kinase gene family. **2002**, 129, 469-85	630
1082	An integrated physical and genetic map of the rice genome. **2002**, 14, 537-45	374

1081	Simultaneous sequencing of multiple polymerase chain reaction products and combined polymerase chain reaction with cycle sequencing in single reactions. **2002**, 161, 27-33	9
1080	A new method for large scale isolation of kidney glomeruli from mice. **2002**, 161, 799-805	418
1079	Gene expression studies on soft tissue tumors. **2002**, 161, 1531-4	14
1078	mRNA expression profiling of laser microbeam microdissected cells from slender embryonic structures. **2002**, 160, 801-13	85
1077	Retroelement distributions in the human genome: variations associated with age and proximity to genes. **2002**, 12, 1483-95	253
1076	The human genome browser at UCSC. **2002**, 12, 996-1006	5840
1075	Coordinate regulation of transcription and splicing by steroid receptor coregulators. **2002**, 298, 416-9	303
1074	The maternally transcribed gene p57(KIP2) (CDNK1C) is abnormally expressed in both androgenetic and biparental complete hydatidiform moles. **2002**, 11, 3267-72	98
1073	Ex vivo and in vitro studies of transgene expression in rat astrocytes transduced with lentiviral vectors. **2002**, 173, 22-30	33
1072	Physical and transcript map of the hereditary prostate cancer region at xq27. **2002**, 79, 41-50	23
1071	Wdr12, a mouse gene encoding a novel WD-Repeat Protein with a notchless-like amino-terminal domain. **2002**, 79, 77-86	17
1070	Candidate genes required for embryonic development: a comparative analysis of distal mouse chromosome 14 and human chromosome 13q22. **2002**, 79, 154-61	17
1069	Evolution of the regulators of G-protein signaling multigene family in mouse and human. **2002**, 79, 177-85	82
1068	A 3-Mb map of a large Segmental duplication overlapping the alpha7-nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14. **2002**, 79, 197-209	90
1067	Identification and characterization of a dense cluster of placenta-specific cysteine peptidase genes and related genes on mouse chromosome 13. **2002**, 79, 225-40	56
1066	Physical and transcript map of a 2-Mb region in Xp22.1 containing candidate genes for X-linked mental retardation and short stature. **2002**, 79, 274-7	2
1065	A technique for genome-wide identification of differences in the interspersed repeats integrations between closely related genomes and its application to detection of human-specific integrations of HERV-K LTRs. **2002**, 79, 413-22	35
1064	Novel paralogy relations among human chromosomes support a link between the phylogeny of doublesex-related genes and the evolution of sex determination. **2002**, 79, 333-43	85

1063	cDNA cloning, genomic structure, chromosomal mapping, and functional expression of a novel human alanine aminotransferase. **2002**, 79, 445-50	86
1062	Analysis of the human neurexin genes: alternative splicing and the generation of protein diversity. **2002**, 79, 587-97	145
1061	Guidelines for human gene nomenclature. **2002**, 79, 464-70	297
1060	Genomic organization of the interleukin-1 locus. **2002**, 79, 726-33	116
1059	Many human genes are transcribed from the antisense promoter of L1 retrotransposon. **2002**, 79, 628-34	186
1058	Ancient duplications of the human proglucagon gene. **2002**, 79, 741-6	33
1057	The misidentification of bacterial genes as human cDNAs: was the human D-1 tumor antigen gene acquired from bacteria?. **2002**, 79, 625-7	5
1056	An evaluation of the assembly of an approximately 15-Mb region on human chromosome 13q32-q33 linked to bipolar disorder and schizophrenia. **2002**, 79, 635-56	18
1055	A genetic, deletion, physical, and human homology map of the long fin region on zebrafish linkage group 2. **2002**, 79, 756-9	15
1054	Structure and evolution of neurexin genes: insight into the mechanism of alternative splicing. **2002**, 79, 849-59	221
1053	Nineteen additional unpredicted transcripts from human chromosome 21. **2002**, 79, 824-32	43
1052	Novel vertebrate genes and putative regulatory elements identified at kidney disease and NR2E1/fierce loci. **2002**, 80, 45-53	22
1051	Structure and chromosomal distribution of human mitochondrial pseudogenes. **2002**, 80, 71-7	113
1050	Transcription regulation of human chemokine receptor CCR3: evidence for a rare TATA-less promoter structure conserved between drosophila and humans. **2002**, 80, 86-95	12
1049	Functional and comparative genomic analysis of the piebald deletion region of mouse chromosome 14. **2002**, 80, 172-84	16
1048	A quantitative and validated SAGE transcriptome reference for adult mouse heart. **2002**, 80, 213-22	32
1047	Comparative analysis of human genome assemblies reveals genome-level differences. **2002**, 80, 138-9	9
1046	Sequencing, transcript identification, and quantitative gene expression profiling in the breast cancer loss of heterozygosity region 16q24.3 reveal three potential tumor-suppressor genes. **2002**, 80, 303-10	39

1045	DEFOG: a practical scheme for deciphering families of genes. **2002**, 80, 295-302	17
1044	A new gene family (FAM9) of low-copy repeats in Xp22.3 expressed exclusively in testis: implications for recombinations in this region. **2002**, 80, 259-67	45
1043	The human endogenous retrovirus family HERV-K(HML-3). **2002**, 80, 331-43	28
1042	Computational analysis of alternative splicing using EST tissue information. **2002**, 80, 326-30	35
1041	A new family of chimeric retrotranscripts formed by a full copy of U6 small nuclear RNA fused to the 3' terminus of l1. **2002**, 80, 402-6	92
1040	A Novel Endogenous Retrovirus-Related Element in the Human Genome Resembles a DNA Transposon: Evidence for an Evolutionary Link?. **2002**, 80, 453-455	14
1039	The Gene CSTF2T, Encoding the Human Variant CstF-64 Polyadenylation Protein CstF-64, Lacks Introns and May Be Associated with Male Sterility. **2002**, 80, 509-514	22
1038	Sequence analysis of the ly49 cluster in C57BL/6 mice: a rapidly evolving multigene family in the immune system. **2002**, 80, 646-61	66
1037	Characterization of disease-associated single amino acid polymorphisms in terms of sequence and structure properties. **2002**, 315, 771-86	171
1036	Towards proteome-wide production of monoclonal antibody by phage display. **2002**, 315, 1063-73	96
1035	Suppression of 15-lipoxygenase synthesis by hnRNP E1 is dependent on repetitive nature of LOX mRNA 3'-UTR control element DICE. **2002**, 315, 965-74	54
1034	Protein structure prediction constrained by solution X-ray scattering data and structural homology identification. **2002**, 316, 173-87	41
1033	Non-traditional Alu evolution and primate genomic diversity. **2002**, 316, 1033-40	69
1032	Global and gene-specific methylation patterns in cancer: aspects of tumor biology and clinical potential. **2002**, 75, 1-16	48
1031	Efficient isolation of regulatory sequences from human genome and BAC DNA. **2002**, 290, 1079-83	4
1030	Analysis of the human TrkB gene genomic organization reveals novel TrkB isoforms, unusual gene length, and splicing mechanism. **2002**, 290, 1054-65	129
1029	A rapid method to capture and screen for transcription factors by SELDI mass spectrometry. **2002**, 290, 1328-35	46
1028	A germline-specific splicing generates an extended ovo protein isoform required for Drosophila oogenesis. **2002**, 246, 366-76	12

1027	The Hox Paradox: More complex(es) than imagined. **2002**, 249, 1-15	91
1026	Gene transfer in bacteria: speciation without species?. **2002**, 61, 449-60	173
1025	Chromosomal distributions of breakpoints in cancer, infertility, and evolution. **2002**, 61, 497-501	22
1024	Active Alu elements are passed primarily through paternal germlines. **2002**, 61, 519-30	55
1023	Strategic use of affinity-based mass spectrometry techniques in the drug discovery process. **2002**, 74, 1-9	45
1022	Homogeneous glycopeptides and glycoproteins for biological investigation. **2002**, 71, 593-634	144
1021	Genomic and proteomic perspectives in cell culture engineering. **2002**, 94, 73-92	40
1020	The enemy at the gates? DNA adducts as biomarkers of exposure to exogenous and endogenous genotoxic agents. **2002**, 134, 51-6	16
1019	Friday, May 17. **2002**, 51, S92-S145	
1018	Future of genetics of mood disorders research. **2002**, 52, 457-77	108
1017	Emerging role of genomics in endometriosis research. **2002**, 78, 694-8	63
1016	Structure-based thermodynamic analysis of a coupled metal binding-protein folding reaction involving a zinc finger peptide. **2002**, 41, 15068-73	61
1015	Genomics Applications That Facilitate the Understanding of Drug Action and Toxicity. 83-125	2
1014	Pharmacogenomics and Drug Design. 143-157	
1013	Pharmacogenomics: Ensuring Equity Regarding Drugs Based on Genetic Difference. 515-524	
1012	Translation of Vascular Proteomics into Individualized Therapeutics. 525-530	
1011	The natural history of protein domains. **2002**, 31, 45-71	221
1010	Protein structure prediction and biomolecular recognition: from protein sequence to peptidomimetic design with the human beta3 integrin. **2002**, 13, 473-86	2

1009	Genetic contributions to addiction. **2002**, 53, 435-62	202
1008	Molecular mechanism of class switch recombination: linkage with somatic hypermutation. **2002**, 20, 165-96	479
1007	Clinical potential of proteomics in the diagnosis of ovarian cancer. **2002**, 2, 312-20	97
1006	Design, functional evaluation and biomedical applications of carbohydrate dendrimers (glycodendrimers). **2002**, 90, 269-90	77
1005	Mutational analysis of the connexin 36 gene (CX36) and exclusion of the coding sequence as a candidate region for catatonic schizophrenia in a large pedigree. **2002**, 58, 87-91	13
1004	Functional genomics and depression research. Beyond the monoamine hypothesis. **2002**, 12, 235-44	26
1003	Novel genes and functional relationships in the adult mouse gastrointestinal tract identified by microarray analysis. **2002**, 122, 1467-82	76
1002	Advances in in vivo bioluminescence imaging of gene expression. **2002**, 4, 235-60	768
1001	Overall DNA methylation and chromatin structure of normal and abnormal X chromosomes. **2002**, 99, 85-91	8
1000	Genetic markers in psychiatric genetics. **2003**, 77, 63-98	2
999	Sequence determination from overlapping fragments: a simple model of whole-genome shotgun sequencing. **2002**, 88, 068106	2
998	Primer on medical genomics part II: Background principles and methods in molecular genetics. **2002** , 77, 785-808	25
997	Serine-threonine protein phosphatase inhibitors: development of potential therapeutic strategies. **2002**, 45, 1151-75	204
996	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. **2002**, 99, 16899-903	1457
995	Plants compared to animals: the broadest comparative study of development. **2002**, 295, 1482-5	227
994	Exploiting natural product diversity. **2002**, 131-201	
993	FISH Techniques, FISH Probes and Their Applications in Medicine and Biology An Overview. **2002**, 3-50	3
992	Molecular mechanisms for genomic disorders. **2002**, 3, 199-242	237

991	Mycoplasmas and the Minimal Genome Concept. **2002**, 221-253	10
990	Practical Algorithms and Fixed-Parameter Tractability for the Single Individual SNP Haplotyping Problem. **2002**, 29-43	38
989	The Enhanced Suffix Array and Its Applications to Genome Analysis. **2002**, 449-463	43
988	Identification of an intronic TG repeat polymorphism in the human proteasome core particle PROS-27K gene. **2002**, 13, 139-43	3
987	The Human Y Chromosome Haplogroup Tree: Nomenclature and Phylogeography of Its Major Divisions. **2002**, 31, 303-321	63
986	DNA methylation patterns and epigenetic memory. **2002**, 16, 6-21	4960
985	The draft genome of Ciona intestinalis: insights into chordate and vertebrate origins. **2002**, 298, 2157-67	1354
984	Origin and evolution of avian microchromosomes. **2002**, 96, 97-112	172
983	Chemical diversity in the sialic acids and related alpha-keto acids: an evolutionary perspective. **2002** , 102, 439-69	992
982	Capillary electrophoresis for the analysis of biopolymers. **2002**, 74, 2833-50	94
981	Algorithms in Bioinformatics. **2002**,	3
980	Finding the needle in the haystack: why high-throughput screening is good for your health. **2002**, 4, 148-54	27
979	Microarray analysis of orthologous genes: conservation of the translational machinery across species at the sequence and expression level. **2003**, 4, R4	19
978	Computational comparison of two mouse draft genomes and the human golden path. **2003**, 4, R1	24
977	The repertoire of protein kinases encoded in the draft version of the human genome: atypical variations and uncommon domain combinations. **2002**, 3, RESEARCH0066	36
976	Whole-genome analysis of animal A- and B-type cyclins. **2002**, 3, RESEARCH0070	37
975	Assessing the impact of comparative genomic sequence data on the functional annotation of the Drosophila genome. **2002**, 3, RESEARCH0086	107
974	Isochores Merit the Prefix 'Iso'. **2002**, 3, preprint0009.1	

973 Finding signals that regulate alternative splicing in the post-genomic era. **2002**, 3, reviews0008 151

972 Variations in abundance: genome-wide responses to genetic variation and vice versa. **2002**, 3, reviews1029 12

971 Molecular archeology of L1 insertions in the human genome. **2002**, 3, research0052 146

970 On the importance of being finished. **2002**, 3, COMMENT2010 7

969 Sushi gets serious: the draft genome sequence of the pufferfish Fugu rubripes. **2002**, 3, reviews1025

968 The DNA-binding region of RAG 1 is not a homeodomain. **2002**, 3, INTERACTIONS1004 5

967 Transcriptome analysis of the retina. **2002**, 3, REVIEWS1022 23

966 The SWIRM domain: a conserved module found in chromosomal proteins points to novel chromatin-modifying activities. **2002**, 3, RESEARCH0039 74

965 ORMDL proteins are a conserved new family of endoplasmic reticulum membrane proteins. **2002**, 3, RESEARCH0027 130

964 Full-length messenger RNA sequences greatly improve genome annotation. **2002**, 3, RESEARCH0029 127

963 Phylogenetic analysis of the human basic helix-loop-helix proteins. **2002**, 3, RESEARCH0030 150

962 Estimation of genetic distances from human and mouse introns. **2002**, 3, RESEARCH0028 21

961 Evolution of gene fusions: horizontal transfer versus independent events. **2002**, 3, research0024 65

960 Is 'big biology' a commercial enterprise?. **2002**, 3, COMMENT2004

959 Untranslated regions of mRNAs. **2002**, 3, REVIEWS0004 637

958 Selection in the evolution of gene duplications. **2002**, 3, RESEARCH0008 491

957 Single Nucleotide Polymorphisms. **2002**, 5

956 Molecular Biology and Pathogenicity of Mycoplasmas. **2002**, 29

955	Main Sessions. **2002**, 81, S67-S74	
954	Rho GTPases in transformation and metastasis. **2002**, 84, 57-80	217
953	Primer on medical genomics part I: History of genetics and sequencing of the human genome. **2002**, 77, 773-82	20
952	Beneficial impact of genome projects on tuberculosis control. **2002**, 16, 145-61	
951	ARDS. The future. **2002**, 18, 177-96	7
950	Efecto del polimorfismo de la apolipoprotena E en el perfil lipoproteico y riesgo cardiovascular en una poblacin mediterrnea. **2002**, 118, 569-574	2
949	The future of reproductive cellular engineering in male infertility. **2002**, 29, 809-15	1
948	The Feline Genome Project. **2002**, 36, 657-86	55
947	Transposable elements in medaka fish. **2002**, 19, 1-6	18
946	Patterning and cell differentiation inHydra: novel genes and the limits to conservation. **2002**, 80, 1670-1677	30
945	Genetics in Society/Society in Genetics. **2002**, 11, 421-428	6
944	Screening regulatory sequences from bacterial artificial chromosome DNA of alpha- and beta-globin gene clusters. **2002**, 80, 415-20	2
943	The K(A)/K(S) ratio test for assessing the protein-coding potential of genomic regions: an empirical and simulation study. **2002**, 12, 198-202	175
942	Target validation and drug discovery using genomic and protein-protein interaction technologies. **2002**, 6, 517-31	10
941	Mammalian retroelements. **2002**, 12, 1455-65	289
940	Distribution and characterization of regulatory elements in the human genome. **2002**, 12, 1827-36	228
939	Deterministic mutation rate variation in the human genome. **2002**, 12, 1350-6	85
938	.	

937	Complex genomic signals.	0
936	Molecular characterization of a 2.7-kb, 12q13-specific, retroviral-related sequence isolated by RDA from monozygotic twin pairs discordant for schizophrenia. **2002**, 45, 381-90	19
935	Measuring conservation of contiguous sets of autosomal markers on bovine and porcine genomes in relation to the map of the human genome. **2002**, 45, 769-76	9
934	Target-assisted iterative screening reveals novel interactors for PSD95, Nedd4, Src, Abl and Crk proteins. **2002**, 19, 1015-29	14
933	The Pfam protein families database. **2002**, 30, 276-80	1839
932	Bioinformatics and rational drug design: tools for discovery and better understanding of biological targets and mode of action of drugs. **2002**, 95-9	16
931	Deductions about the number, organization, and evolution of genes in the tomato genome based on analysis of a large expressed sequence tag collection and selective genomic sequencing. **2002**, 14, 1441-56	259
930	Mathematics-assisted mapping in analysis of medical disease. **2002**, 34, 291-8	2
929	Pharmacogenomics for the treatment of dementia. **2002**, 34, 357-79	39
928	Genetic polymorphisms of matrix metalloproteinases: functional importance in the development of chronic obstructive pulmonary disease?. **2002**, 2, 167-75	23
927	Deductive genomics: a functional approach to identify innovative drug targets in the post-genome era. **2002**, 2, 263-71	17
926	Emerging ethical issues in pharmacogenomics: from research to clinical practice. **2002**, 2, 273-81	14
925	A new single nucleotide polymorphisms typing method and device by bioluminometric assay coupled with a photodiode array. **2002**, 13, 1779-1785	12
924	Recent discovery and development of protein tyrosine phosphatase inhibitors. **2002**, 12, 871-905	58
923	Molecular biologist's guide to proteomics. **2002**, 66, 39-63; table of contents	383
922	Simulation of microimages emitted by virtual array of testing oligonucleotides.	
921	Cancer genome targets: RAF-ing up tumor cells to overcome oncogene addiction. **2002**, 2, 611-4	15
920	Genetic approaches to the identification of interactions between membrane proteins in yeast. **2002**, 22, 471-81	12

919	Evolutionary dynamics of intron size, genome size, and physiological correlates in archosaurs. **2002**, 160, 539-52	83
918	Comparative mapping of Homo sapiens chromosome 4 (HSA4) and Sus scrofa chromosome 8 (SSC8) using orthologous genes representing different cytogenetic bands as landmarks. **2002**, 45, 147-56	19
917	The application of genetics to the discovery of better medicines. **2002**, 3, 257-63	15
916	Jak3 expression and genomic sequence in pediatric acute lymphoblastic leukemia. **2002**, 43, 2355-62	2
915	The Ensembl genome database project. **2002**, 30, 38-41	1084
914	Neurogenetics. **2002**,	
913	Identification of a syndecan 4 pseudogene. **2002**, 13, 353-7	
912	Histidine protein kinases: key signal transducers outside the animal kingdom. **2002**, 3, REVIEWS3013	256
911	Whole chromosome features of genomic signals.	1
910	Specific ablation of Stat3beta distorts the pattern of Stat3-responsive gene expression and impairs recovery from endotoxic shock. **2002**, 108, 331-44	114
909	Coordinated transcription of key pathways in the mouse by the circadian clock. **2002**, 109, 307-20	1831
908	Estimating the human gene count. **2002**, 109, 283-4	17
907	Bidirectional gene organization: a common architectural feature of the human genome. **2002**, 109, 807-9	276
906	Genomic deletions created upon LINE-1 retrotransposition. **2002**, 110, 315-25	368
905	Human l1 retrotransposition is associated with genetic instability in vivo. **2002**, 110, 327-38	375
904	HIV-1 integration in the human genome favors active genes and local hotspots. **2002**, 110, 521-9	1376
903	LINEs mobilize SINEs in the eel through a shared 3' sequence. **2002**, 111, 433-44	262
902	Thermodynamics of drug-DNA interactions. **2002**, 403, 1-15	313

901	Human caspase 12 has acquired deleterious mutations. **2002**, 293, 722-6	300
900	In silico sequence analysis of arylamine N-acetyltransferases: evidence for an absence of lateral gene transfer from bacteria to vertebrates and first description of paralogs in bacteria. **2002**, 293, 783-92	25
899	Overexpression of glia maturation factor in astrocytes leads to immune activation of microglia through secretion of granulocyte-macrophage-colony stimulating factor. **2002**, 294, 238-44	42
898	Genetic and physical maps of jerker (Espn(je)) on mouse chromosome 4. **2002**, 296, 1143-7	3
897	Identification of the novel splicing variants for the hPXR in human livers. **2002**, 298, 433-8	57
896	Pleckstrin homology domains and the cytoskeleton. **2002**, 513, 71-6	196
895	Protein domain analysis in the era of complete genomes. **2002**, 513, 129-34	46
894	Identification of ten exon deleted ERbeta mRNAs in human ovary, breast, uterus and bone tissues: alternate splicing pattern of estrogen receptor beta mRNA is distinct from that of estrogen receptor alpha. **2002**, 516, 133-8	64
893	Only the soluble form of the scavenger receptor CD163 acts inhibitory on phorbol ester-activated T-lymphocytes, whereas membrane-bound protein has no effect. **2002**, 526, 93-6	74
892	Human RhoGAP domain-containing proteins: structure, function and evolutionary relationships. **2002**, 528, 27-34	128
891	Tandem genomic arrangement of a G protein (Gna15) and G protein-coupled receptor (s1p(4)/lp(C1)/Edg6) gene. **2002**, 531, 99-102	11
890	Arrays in biological and chemical analysis. **2002**, 56, 289-99	12
889	Sub-proteome differential display: single gel comparison by 2D electrophoresis and mass spectrometry. **2002**, 318, 21-31	19
888	Transfer RNA gene-targeted retrotransposition of Dictyostelium TRE5-A into a chromosomal UMP synthase gene trap. **2002**, 318, 273-85	20
887	Studying genomes through the aeons: protein families, pseudogenes and proteome evolution. **2002**, 318, 1155-74	146
886	Structure-function analysis of the inverted terminal repeats of the sleeping beauty transposon. **2002**, 318, 1221-35	189
885	The Human Genome Project: a player's perspective. **2002**, 319, 931-42	22
884	Prediction of human protein function from post-translational modifications and localization features. **2002**, 319, 1257-65	274

883	Hetero-oligomerization among the TIF family of RBCC/TRIM domain-containing nuclear cofactors: a potential mechanism for regulating the switch between coactivation and corepression. **2002**, 320, 629-44		73
882	On the role of periodism in the origin of proteins. **2002**, 320, 833-40		29
881	A new method to detect related function among proteins independent of sequence and fold homology. **2002**, 323, 387-406		360
880	Common physical properties of DNA affecting target site selection of sleeping beauty and other Tc1/mariner transposable elements. **2002**, 323, 441-52		221
879	Digging deep for ancient relics: a survey of protein motifs in the intergenic sequences of four eukaryotic genomes. **2002**, 323, 811-22		17
878	Expression profiles of 109 apoptosis pathway-related genes in 82 mouse tissues and experimental conditions. **2002**, 297, 537-44		7
877	Steered molecular dynamics studies of titin I1 domain unfolding. **2002**, 83, 3435-45		104
876	Anti-malarial mosquitoes?. *Nature*, **2002**, 417, 387-8	50.4	34
875	Question 6 How would one retrieve the sequence of a gene, along with all annotated exons and introns, as well as a certain number of flanking bases for use in primer design?. **2002**, 32, 40-43		
874	Rapid development of nucleic acid diagnostics. **2002**, 90, 1708-1721		22
873	High risk/high priority: familial hypercholesterolemia--a paradigm for molecular medicine. **2002**, 2, 27-30; discussion 30-2		9
872	Gene expression profiles in Ciona intestinalis cleavage-stage embryos. **2002**, 112, 115-27		64
871	Molecular cloning, gene structure, expression profile and functional characterization of the mouse glutamate transporter (EAAT3) interacting protein GTRAP3-18. **2002**, 292, 81-90		45
870	Pharmacogenetics, pharmacogenomics and airway disease. **2002**, 3, 10		14
869	Detection of pleiotropic effects of quantitative trait loci in outbred populations using regression analysis. **2002**, 85, 3503-13		7
868	Genetic dissection of immunity to mycobacteria: the human model. **2002**, 20, 581-620		771
867	Genetics of asthma and related phenotypes. **2002**, 3, 47-51		14
866	DNA microarrays in otolaryngology-head and neck surgery. **2002**, 127, 196-204		6

865	Why mutation analysis does not always predict clinical consequences: explanations in the era of genomics. **2002**, 140, 502-6	37
864	Pediatric practice and education in the genomic/postgenomic era. **2002**, 141, 453-8	8
863	The map problem: a comparison of genetic and sequence-based physical maps. **2002**, 70, 101-7	24
862	Human-specific duplication and mosaic transcripts: the recent paralogous structure of chromosome 22. **2002**, 70, 83-100	150
861	Score tests for association between traits and haplotypes when linkage phase is ambiguous. **2002**, 70, 425-34	1581
860	Evidence for linkage of stature to chromosome 3p26 in a large U.K. Family data set ascertained for type 2 diabetes. **2002**, 70, 543-6	44
859	2001 ASHG Presidential Address. On black boxes and storytellers: lessons learned in human genetics. **2002**, 70, 285-96	2
858	A 117-kb microdeletion removing HOXD9-HOXD13 and EVX2 causes synpolydactyly. **2002**, 70, 547-55	86
857	Limb-girdle muscular dystrophy type 2H associated with mutation in TRIM32, a putative E3-ubiquitin-ligase gene. **2002**, 70, 663-72	197
856	Localization of a susceptibility gene for common forms of stroke to 5q12. **2002**, 70, 593-603	173
855	Fine-scale mapping of disease loci via shattered coalescent modeling of genealogies. **2002**, 70, 686-707	106
854	Revised 14.7-cM locus for the hyperparathyroidism-jaw tumor syndrome gene, HRPT2. **2002**, 70, 1376-7	14
853	Common deletion of SMAD4 in juvenile polyposis is a mutational hotspot. **2002**, 70, 1357-62	40
852	Systematic evaluation of map quality: human chromosome 22. **2002**, 70, 1398-410	15
851	A major predisposition locus for severe obesity, at 4p15-p14. **2002**, 70, 1459-68	113
850	Intron-size constraint as a mutational mechanism in Rothmund-Thomson syndrome. **2002**, 71, 165-7	60
849	A comprehensive analysis of recently integrated human Ta L1 elements. **2002**, 71, 312-26	129
848	Evidence consistent with human L1 retrotransposition in maternal meiosis I. **2002**, 71, 327-36	103

847	Human diallelic insertion/deletion polymorphisms. **2002**, 71, 854-62	255
846	Genetic linkage of attention-deficit/hyperactivity disorder on chromosome 16p13, in a region implicated in autism. **2002**, 71, 959-63	176
845	Combinatorial fluorescence energy transfer tags: new molecular tools for genomics applications. **2002**, 38, 110-121	5
844	The use of zinc finger peptides to study the role of specific factor binding sites in the chromatin environment. **2002**, 26, 76-83	39
843	Large nuclear RNP particles--the nuclear pre-mRNA processing machine. **2002**, 140, 123-30	22
842	Status and opportunities for genomics research with rainbow trout. **2002**, 133, 609-46	153
841	Dynamic antagonism between ETR-3 and PTB regulates cell type-specific alternative splicing. **2002**, 9, 649-58	161
840	Diabetes mutations delineate an atypical POU domain in HNF-1alpha. **2002**, 10, 1129-37	75
839	Constructing the vertebrate genome: evidence from eels that LINEs mobilize SINEs. **2002**, 10, 961-2	2
838	Synaptotagmin I functions as a calcium sensor to synchronize neurotransmitter release. **2002**, 36, 897-908	219
837	Repetitive DNA, genome system architecture and genome reorganization. **2002**, 153, 447-53	18
836	Impact of the Human Genome Project on the clinical management of sporadic cancers. **2002**, 3, 349-56	11
835	Protein sequence analysis in silico: application of structure-based bioinformatics to genomic initiatives. **2002**, 2, 574-80	11
834	CD200 and membrane protein interactions in the control of myeloid cells. **2002**, 23, 285-90	334
833	Is the number of genes we possess limited by the presence of an adaptive immune system?. **2002**, 23, 351-5	10
832	Translating basic cancer research into new cancer therapeutics. **2002**, 8, S1-9	59
831	Twenty pairs of sox: extent, homology, and nomenclature of the mouse and human sox transcription factor gene families. **2002**, 3, 167-70	408
830	MitoAnalyzer, a computer program and interactive web site to determine the effects of single nucleotide polymorphisms and mutations in human mitochondrial DNA. **2002**, 1, 321-6	12

829	Reconciling the many faces of lateral gene transfer. **2002**, 10, 1-4	179
828	Senescence and epigenetic dysregulation in cancer. **2002**, 34, 1475-90	47
827	Influence of the APOC3 -2854T>G polymorphism on plasma lipid levels: effect of age and gender. **2002**, 1583, 311-4	9
826	Familial dysautonomia. **2002**, 12, 307-11	274
825	Molecular-evolutionary mechanisms for genomic disorders. **2002**, 12, 312-9	126
824	Gene duplication and divergence in the early evolution of vertebrates. **2002**, 12, 393-6	40
823	The evolution of developmental regulatory pathways. **2002**, 12, 695-700	11
822	Variation in recombination rate across the genome: evidence and implications. **2002**, 12, 657-63	170
821	The evolution of spliceosomal introns. **2002**, 12, 701-10	124
820	Cancer genetics and their application to individualised medicine. **2002**, 38, 872-9	28
819	Challenges of PK/PD measurements in modern drug development. **2002**, 38, 2189-93	59
818	Modulation of the membrane-binding projection domain of tau protein: splicing regulation of exon 3. **2002**, 101, 109-21	22
817	The human zoo: endogenous retroviruses in the human genome. **2002**, 17, 91-97	33
816	Linking molecular insight and ecological research. **2002**, 17, 409-414	73
815	Role of heparan sulfate-2-O-sulfotransferase in the mouse. **2002**, 1573, 319-27	33
814	Pharmacological inhibitors of MAPK pathways. **2002**, 23, 40-5	377
813	Seven-transmembrane receptors: crystals clarify. **2002**, 23, 140-6	149
812	From genetics and genomics to drug discovery: yeast rises to the challenge. **2002**, 23, 544-7	24

811	Inhibition of mu and delta opioid receptor ligand binding by the peptide aldehyde protease inhibitor, leupeptin. **2002**, 105, 9-14	4
810	Cell line-specific translation of two laminin 5 beta3 chain isoforms. **2002**, 283, 237-44	10
809	Identification of six novel genes by experimental validation of GeneMachine predicted genes. **2002**, 284, 203-13	7
808	Structure of the human carboxypeptidase M gene. Identification of a proximal GC-rich promoter and a unique distal promoter that consists of repetitive elements. **2002**, 284, 189-202	18
807	Genomic organization and differential expression of Kalirin isoforms. **2002**, 284, 41-51	57
806	Genomic organization of the siglec gene locus on chromosome 19q13.4 and cloning of two new siglec pseudogenes. **2002**, 286, 259-70	25
805	Genomic organization, transcript variants and comparative analysis of the human nucleoporin 155 (NUP155) gene. **2002**, 288, 9-18	8
804	Characterization and in silico mapping of a novel murine zinc finger transcription factor. **2002**, 289, 49-59	2
803	Cysteine and tyrosine-rich 1 (CYYR1), a novel unpredicted gene on human chromosome 21 (21q21.2), encodes a cysteine and tyrosine-rich protein and defines a new family of highly conserved vertebrate-specific genes. **2002**, 290, 141-51	14
802	Generation of multiple farnesoid-X-receptor isoforms through the use of alternative promoters. **2002**, 290, 35-43	155
801	Human mitochondrial transcription factor A (mtTFA): gene structure and characterization of related pseudogenes. **2002**, 291, 223-32	29
800	The identification of a novel human homologue of the SH3 binding glutamic acid-rich (SH3BGR) gene establishes a new family of highly conserved small proteins related to Thioredoxin Superfamily. **2002**, 291, 233-9	47
799	Genomic organization and chromosomal localization of the mouse protein kinase C alpha gene. **2002**, 291, 11-6	2
798	Characterization of the SCAN box encoding RAZ1 gene: analysis of cDNA transcripts, expression, and cellular localization. **2002**, 296, 53-64	9
797	Fugu and human sequence comparison identifies novel human genes and conserved non-coding sequences. **2002**, 294, 35-44	55
796	Are isochore sequences homogeneous?. **2002**, 300, 129-39	33
795	Structure, function and DNA composition of Saccharomyces cerevisiae chromatin loops. **2002**, 300, 63-8	20
794	Natural selection at linked sites in humans. **2002**, 300, 31-42	28

793	Periodicity in prokaryotic and eukaryotic genomes identified by power spectrum analysis. **2002**, 300, 203-11	50
792	LINEs and SINE-like elements of the protist Entamoeba histolytica. **2002**, 297, 229-39	43
791	Angiomotin belongs to a novel protein family with conserved coiled-coil and PDZ binding domains. **2002**, 298, 69-77	110
790	Isochore chromosome maps of the human genome. **2002**, 300, 117-27	48
789	Study of statistical correlations in DNA sequences. **2002**, 300, 105-15	64
788	Localization of the gene-richest and the gene-poorest isochores in the interphase nuclei of mammals and birds. **2002**, 300, 169-78	102
787	Can mutation or fixation biases explain the allele frequency distribution of human single nucleotide polymorphisms (SNPs)?. **2002**, 300, 53-8	13
786	A simple and species-independent coding measure. **2002**, 300, 97-104	16
785	Isochores, GC3 and mutation biases in the human genome. **2002**, 300, 161-8	19
784	Wide intra-genomic G+C heterogeneity in human and chicken is mainly due to strand-symmetric directional mutation pressures: dGTP-oxidation and symmetric cytosine-deamination hypotheses. **2002**, 300, 141-54	24
783	Length distribution of long interspersed nucleotide elements (LINEs) and processed pseudogenes of human endogenous retroviruses: implications for retrotransposition and pseudogene detection. **2002**, 300, 189-94	44
782	Entire sequence of a mouse chromosomal segment containing the gene Rhced and a comparative analysis of the homologous human sequence. **2002**, 299, 165-72	9
781	An L1 element disrupts human bone sialoprotein promoter: lack of tissue-specific regulation by distalless5 (Dlx5) and runt homeodomain protein2 (Runx2)/core binding factor a1 (Cbfa1) elements. **2002**, 299, 205-17	32
780	Exploiting genomics in evolutionary developmental biology. **2002**, 1246, 217-229	
779	Chimpanzee genome project for understanding ourselves. **2002**, 1246, 183-187	
778	Oligo-capped cDNAs for promoter identification and annotation. **2002**, 1246, 233-239	1
777	A genome scientific view of ascidian development. **2002**, 1246, 117-124	
776	Organisation of the human genome and our tools for identifying disease genes. **2002**, 61, 11-31	7

775	Gene finding strategies. **2002**, 61, 53-71	33
774	Matrix remodeling in the ovary: regulation and functional role of the plasminogen activator and matrix metalloproteinase systems. **2002**, 187, 29-38	107
773	Reexamining the polyadenylation signal: were we wrong about AAUAAA?. **2002**, 190, 1-8	68
772	Using expressed sequence tag databases to identify ovarian genes of interest. **2002**, 191, 11-4	11
771	Regulation of the activity of Sp1-related transcription factors. **2002**, 195, 27-38	390
770	Current approaches for deciphering the molecular basis of combined anterior pituitary hormone deficiency in humans. **2002**, 197, 47-56	9
769	Exploring genetic regulatory networks in metazoan development: methods and models. **2002**, 10, 131-43	24
768	Discovery of novel targets of quinoline drugs in the human purine binding proteome. **2002**, 62, 1364-72	209
767	Successful virtual screening for novel inhibitors of human carbonic anhydrase: strategy and experimental confirmation. **2002**, 45, 3588-602	159
766	High-throughput screening for expression of heterologous proteins in the yeast Pichia pastoris. **2002**, 99, 51-62	106
765	A sequence-based map of the nine genes of the human interleukin-1 cluster. **2002**, 79, 718-25	166
764	Gene co-option in physiological and morphological evolution. **2002**, 18, 53-80	323
763	Functional complexity of intermediate filament cytoskeletons: from structure to assembly to gene ablation. **2003**, 223, 83-175	143
762	Functional genomics of immune responses. **2002**, 22, 891-910	2
761	Bridging genetics and genomics in neurology. **2002**, 20, 867-77, viii	
760	[Praise of complexity]. **2002**, 118, 782-3	
759	Current and future genetic screening for male infertility. **2002**, 29, 767-92	14
758	Primer on medical genomics. Part IV: Expression proteomics. **2002**, 77, 1185-96	21

757 [Unavoidable death and quest for immortality]. **2002**, 119, 99-102

756 RNase 8, a novel RNase A superfamily ribonuclease expressed uniquely in placenta. **2002**, 30, 1169-75 61

755 Identification of a novel human organic anion transporting polypeptide as a high affinity thyroxine transporter. **2002**, 16, 2283-96 261

754 Ischemia induces a translocation of the splicing factor tra2-beta 1 and changes alternative splicing patterns in the brain. **2002**, 22, 5889-99 81

753 Identification of genes that are downregulated in the absence of the POU domain transcription factor pou3f1 (Oct-6, Tst-1, SCIP) in sciatic nerve. **2002**, 22, 10217-31 38

752 New Generation Pharmacogenomic Tools: A SNP Linkage Disequilibrium Map, Validated SNP Assay Resource, and High-Throughput Instrumentation System for Large-Scale Genetic Studies. **2002**, 32, S48-S54 37

751 Making Sense of the Epithelial Barrier: What Molecular Biology and Genetics Tell Us About the Functions of Oral Mucosal and Epidermal Tissues. **2002**, 66, 564-574 91

750 Table_11.XLSX. **2018**,

749 Table_12.XLSX. **2018**,

748 Table_2.XLSX. **2018**,

747 Table_3.XLSX. **2018**,

746 Table_4.XLSX. **2018**,

745 Table_5.XLSX. **2018**,

744 Table_6.XLSX. **2018**,

743 Table_7.XLSX. **2018**,

742 Table_8.XLSX. **2018**,

741 Table_9.XLSX. **2018**,

740 Data_Sheet_1.docx. **2020**,

739 DataSheet_1.docx. **2020**,

738 DataSheet_2.docx. **2020**,

737 Table_1.docx. **2020**,

736 Table_2.docx. **2020**,

735 DataSheet_1.pdf. **2020**,

734 DataSheet_2.pdf. **2020**,

733 Image_1.pdf. **2020**,

732 Table_1.doc. **2020**,

731 Table_2.xls. **2020**,

730 Table_3.xlsx. **2020**,

729 Table_1.DOCX. **2020**,

728 Table_2.DOCX. **2020**,

727 Table_1.DOCX. **2020**,

726 DataSheet_1.pdf. **2019**,

725 DataSheet_2.csv. **2019**,

724 Table_2.xlsx. **2020**,

723 DataSheet_3.csv. **2019**,

722 DataSheet_4.csv. **2019**,

721 Table_3.DOCX. **2020**,

720 DataSheet_5.csv. **2019**,

719 DataSheet_6.csv. **2019**,

718 Data_Sheet_1.pdf. **2020**,

717 Image_1.JPEG. **2020**,

716 Image_2.jpg. **2020**,

715 Image_3.JPEG. **2020**,

714 Data_Sheet_1.pdf. **2018**,

713 Data_Sheet_1.zip. **2018**,

712 Data_Sheet_2.ZIP. **2018**,

711 Data_Sheet_1.PDF. **2020**,

710 Table_1.pdf. **2020**,

709 Table_2.pdf. **2020**,

708 Data_Sheet_1.PDF. **2019**,

707 Data_Sheet_2.zip. **2019**,

706 Data_Sheet_1.pdf. **2020**,

705 Image_1.TIF. **2018**,

704 Image_2.TIF. **2018**,

703 Table_1.xlsx. **2018**,

702 DataSheet_1.xlsx. **2019**,

701 Table_1.docx. **2020**,

700 Data_Sheet_1.pdf. **2019**,

699 Table_1.DOCX. **2018**,

698 Data_Sheet_1.docx. **2020**,

697 Table_1.DOCX. **2018**,

696 Table_2.DOCX. **2018**,

695 Table_3.DOCX. **2018**,

694 Presentation_1.PDF. **2018**,

693 Data_Sheet_1.DOCX. **2018**,

692 Data_Sheet_1.docx. **2018**,

691 Table_1.docx. **2018**,

690 Image_1.TIF. **2020**,

689 Table_1.pdf. **2020**,

688 Image_1.pdf. **2020**,

687 Table_1.docx. **2020**,

686 Table_2.xlsx. **2020**,

685 Table_3.docx. **2020**,

684 Table_4.docx. **2020**,

683 Data_Sheet_1.DOCX. **2020**,

682 Data_Sheet_2.DOCX. **2020**,

681 Table_1.xlsx. **2020**,

680 Table_2.xlsx. **2020**,

679 Table_3.xlsx. **2020**,

678 From Genotype to Phenotype: Polygenic Prediction of Complex Human Traits.. **2022**, 2467, 421-446

677 Genomic Prediction Methods Accounting for Nonadditive Genetic Effects.. **2022**, 2467, 219-243 0

676 [Web-based gene expression analysis-paving the way to decode healthy and diseased ocular tissue].. **2022**, 1 0

675 How to keep up with the analysis of classic and emerging neurotoxins: Age-resolved fitness tests in the animal model - a step-by-step protocol.. **2022**, 21, 344-353 0

674 DNA methylation is associated with muscle loss in community-dwelling older men -the Yakumo study- : a preliminary experimental study.. **2022**, 84, 60-68

673 Highly sensitive diagnostic method for colorectal cancer using the ratio of free DNA fragments in serum.. **2019**, 5, 14-20

672 Fundamentals of Genetics. **2022**, 2815-2846

671 DNA methylation: a historical perspective.. **2022**, 7

670 Functional dissection of human mitotic genes using CRISPR-Cas9 tiling screens.. **2022**,

669 Nuclear organization by satellite DNA, SAF-A/hnRNPU and matrix attachment regions.. **2022**, 2

668 A classical revival: Human satellite DNAs enter the genomics era.. **2022**, 1

667	Meet the Honorary Senior Advisor. **2022**, 2, 86-86	
666	Application of transposon systems in the transgenesis of bovine somatic and germ cells.. **2022**, 18, 156	0
665	Nutrigenomics and Green Technologies. **2022**, 509-528	
664	DeepRepeat: direct quantification of short tandem repeats on signal data from nanopore sequencing.. **2022**, 23, 108	2
663	Comprehensive human amniotic fluid metagenomics supports the sterile womb hypothesis.. **2022**, 12, 6875	2
662	Diagnosis of rare bleeding disorders.. **2022**, 28 Suppl 4, 119-124	2
661	The History and Future of Basic and Translational Cell-Free DNA Research at a Glance. **2022**, 12, 1192	
660	Precise Metabolomics Reveals a Diversity of Aging-Associated Metabolic Features.. **2022**, e2200130	0
659	Autoantibody Landscape Revealed by Wet Protein Array: Sum of Autoantibody Levels Reflects Disease Status. **2022**, 13,	1
658	The Brazilian Rare Genomes Project: Validation of Whole Genome Sequencing for Rare Diseases Diagnosis.. **2022**, 9, 821582	2
657	Metal Ion-Directed Specific DNA Structures and Their Functions. **2022**, 12, 686	0
656	Computational Approaches for Understanding Sequence Variation Effects on the 3D Genome Architecture.. **2022**,	
655	Reconstruction of full-length LINE-1 progenitors from ancestral genomes.. **2022**,	0
654	Nde1 is Required for Heterochromatin Compaction and Stability in Neocortical Neurons. **2022**, 104354	0
653	Disrupting Mechanisms that Regulate Genomic Repeat Elements to Combat Cancer and Drug Resistance. **2022**, 10,	1
652	Non-canonical nematode endogenous retroviruses resulting from RNA virus glycoprotein gene capture by a metavirus.. **2022**, 103,	
651	NF-B-Activated lncRNACASC9 Promotes Bladder Cancer Progression by Regulating the TK1 Expression.. **2022**, 2022, 9905776	
650	Radiogenomics: A Valuable Tool for the Clinical Assessment and Research of Ovarian Cancer.. **2022**, 46, 371-378	

649 Cancer-associated chromatin variants uncover the oncogenic role of transposable elements.. **2022**, 74, 101911 1

648 Epigenetics and Its Implications for Tissue Regeneration and Regenerative Medicine with a Focus on DNA-Methylation. **2021**, 1-52

647 Molecular imaging: Techniques and current clinical applications. 10-21 3

646 Introduction to Target Validation. **2022**, 61-82

645 Accuracy of multiple sequence alignment methods in the reconstruction of transposable element families.. **2022**, 4, lqac040 1

644 Advances in the diagnosis of heritable platelet disorders. **2022**, 100972

643 SVA retrotransposons and a low copy repeat in humans and great apes: a mobile connection.. **2022**, 0

642 Human endogenous retroviruses and hematological malignant tumors. **17**, Publish Ahead of Print,

641 A deep dive into genome assemblies of non-vertebrate animals. 2,

640 Reflections on antifreeze proteins and their evolution.. **2022**,

639 Free fatty acid receptor 4 deletion attenuates colitis by modulating Treg Cells via ZBED6-IL33 pathway.. **2022**, 80, 104060 1

638 A retrotransposon storm marks clinical phenoconversion to late-onset Alzheimer's disease.. **2022**, 1

637 Characterizing Fractal Genetic Variation in the Human Genome from the Hapmap Project.. **2022**, 2250028 0

636 Using Multiple Chromosomal Marker Analysis Tools, for DNA Profiling in Human Identification: New, Evolving and Productive Approach. **2022**, 1-23

635 Data Deduplication with Random Substitutions. **2022**, 1-1

634 Bioinformatics: The Interactome of Multidisciplinary Approaches. **2022**, 107-113

633 Omics Technologies for High-Throughput-Screening of Cell-Biomaterial Interactions. 1

632 Genome Project. **2022**, 2918-2922

631	A Versatile Hemolin With Pattern Recognitional Contributions to the Humoral Immune Responses of the Chinese Oak Silkworm Antheraea pernyi. **2022**, 13,		
630	Extrachromosomal DNA in Cancer. **2022**, 23,		0
629	Extensive mosaicism by somatic L1 retrotransposition in normal human cells.		
628	Genetics of bipolar disorder: insights into its complex architecture and biology from common and rare variants.		0
627	A High Throughput Cell-Based Screen Assay for LINE-1 ORF1p Expression Inhibitors Using the In-Cell Western Technique. **2022**, 13,		
626	TFIIIC-based chromatin insulators through eukaryotic evolution. **2022**, 146533		
625	State of the Art of Chemosensors in a Biomedical Context. **2022**, 10, 199		1
624	The first complete human genome. *Nature*,	50.4	1
623	Developmental Neuropathology and Neurodegeneration of Down Syndrome: Current Knowledge in Humans. **2022**, 10,		1
622	The past, present and future of genomics and bioinformatics: A survey of Brazilian scientists. **2022**, 45,		
621	Locus-Specific DNA Methylation Profiling of Human LINE-1 Retrotransposons. **2022**, 197-227		
620	Detecting Tandem Repeat Expansions Using Short-Read Sequencing for Clinical Use. **2022**, 15-42		0
619	Polymorphisms in common antihypertensive targets: Pharmacogenomic implications for the treatment of cardiovascular disease. **2022**, 141-182		
618	Meta-Analysis Suggests That Intron Retention Can Affect Quantification of Transposable Elements from RNA-Seq Data. **2022**, 11, 826		0
617	SARS-CoV-2 impacts the transcriptome and epigenome at the maternal-fetal interface in pregnancy.		
616	Superconserved receptors expressed in the brain: Expression, function, motifs and evolution of an orphan receptor family. **2022**, 108217		
615	Bridging the Gap Between Environmental Adversity and Neuropsychiatric Disorders: The Role of Transposable Elements. 13,		1
614	Short tandem repeats bind transcription factors to tune eukaryotic gene expression.		0

613	Disruption of Ecatenin-mediated negative feedback reinforces cAMP-induced neuronal differentiation in glioma stem cells. **2022**, 13,	0
612	The Role of Transposable Elements of the Human Genome in Neuronal Function and Pathology. **2022**, 23, 5847	1
611	Characterising genome architectures using genome decomposition analysis. **2022**, 23,	0
610	The Happy Hopping of Transposons: The Origins of V(D)J Recombination in Adaptive Immunity. 10,	
609	Antidiabetic Effect of Rehmanniae Radix Based on Regulation of TRPV1 and SCD1. 13,	
608	Satellite DNAs and human sex chromosome variation. **2022**,	0
607	Comprehensive In Silico Analysis of Retrotransposon Insertions within the Survival Motor Neuron Genes Involved in Spinal Muscular Atrophy. **2022**, 11, 824	
606	Splashed E-box and AP-1 motifs cooperatively drive regeneration-response and shape regeneration abilities.	
605	De Novo Assembly of Plasmodium knowlesi Genomes From Clinical Samples Explains the Counterintuitive Intrachromosomal Organization of Variant SICAvar and kir Multiple Gene Family Members. 13,	0
604	Splicing mutations in the CFTR gene as therapeutic targets.	1
603	A phenome-wide association study identifies effects of copy-number variation of VNTRs and multicopy genes on multiple human traits. **2022**, 109, 1065-1076	0
602	The Utility of Repetitive Cell-Free DNA in Cancer Liquid Biopsies. **2022**, 12, 1363	0
601	Epigenomic analysis reveals prevalent contribution of transposable elements to cis-regulatory elements, tissue-specific expression, and alternative promoters in zebrafish. gr.276052.121	1
600	Revisiting the miR-200 Family: A Clan of Five Siblings with Essential Roles in Development and Disease. **2022**, 12, 781	0
599	Genome-Wide Identification of Long Noncoding RNA and Their Potential Interactors in ISWI Mutants. **2022**, 23, 6247	
598	Small but Powerful: The Human Vault RNAs as Multifaceted Modulators of Pro-Survival Characteristics and Tumorigenesis. **2022**, 14, 2787	2
597	The effect of hemolysis on quality control metrics for noninvasive prenatal testing. **2022**, 15,	0
596	Position Effect Variegation: Role of the Local Chromatin Context in Gene Expression Regulation. **2022**, 56, 307-338	

595	A meditation on accelerating the development of small molecule medicines targeting RNA. 1-3	
594	Genomic instability and the link to infertility: A focus on microsatellites and genomic instability syndromes. **2022**, 274, 229-237	
593	Functional indications for transposase domestications Characterization of the human piggyBac transposase derived (PGBD) activities. **2022**, 834, 146609	1
592	Genetic etiologies of autism: Unpacking pathogenic mechanisms and characteristics. **2022**, 197-213	
591	Modifying Bacterial Artificial Chromosomes for Extended Genome Modification. **2022**, 67-90	
590	Transposable elements are associated with the variable response to influenza infection.	0
589	Old genes in new places: A taxon-rich analysis of interdomain lateral gene transfer events. **2022**, 18, e1010239	0
588	The Level of LINE-1 mRNA Is Increased in Extracellular Circulating Plasma RNA in Patients with Colorectal Cancer.	0
587	The Genomics of Auditory Function and Disease. **2022**, 23,	1
586	Slaying (Yet Again) the Brain-Eating Zombie Called the Isochore Theory A Segmentation Algorithm Used to Confirm the Existence of Isochores Creates Isochores Where None Exist. **2022**, 23, 6558	1
585	Genomic analysis in Entamoeba reveals intron gain and unbiased intron loss, transformed splicing signals, and a coevolved snRNA.	0
584	Blood-derived lncRNAs as biomarkers for cancer diagnosis: the Good, the Bad and the Beauty. **2022**, 6,	1
583	Revisiting the Tigger Transposon Evolution Revealing Extensive Involvement in the Shaping of Mammal Genomes. **2022**, 11, 921	0
582	Translational Significance of the LINE-1 Jumping Gene in Skeletal Muscle. Publish Ahead of Print,	
581	Did circular DNA shape the evolution of mammalian genomes?.	
580	Physlr: Next-Generation Physical Maps. **2022**, 2, 116-130	0
579	Timing and causes of the evolution of the germline mutation spectrum in humans.	0
578	Somatic retrotransposition in the developing rhesus macaque brain. gr.276451.121	

577	Transposable element-mediated rearrangements are prevalent in human genomes.	0
576	Satellite repeat RNA expression in epithelial ovarian cancer associates with a tumor immunosuppressive phenotype.	1
575	Moderne Sequenzierungsmethoden: Neue M□glichkeiten f□ die Geff□hedizin □auch bei kleiner Probenzahl?.	
574	Analysis of codon usage bias of WRKY transcription factors in Helianthus annuus. **2022**, 23,	2
573	Structure and Evolution of Neuronal Wiring Receptors and Ligands.	1
572	Onasemnogene abeparvovec for presymptomatic infants with three copies of SMN2 at risk for spinal muscular atrophy: the Phase III SPR1NT trial.	4
571	Application of Artificial intelligence in Drug Discovery. **2022**, 28,	0
570	PRMT1 is required for the generation of MHC-associated microglia and remyelination in the central nervous system. **2022**, 5, e202201467	0
569	Patterns and distribution of de novo mutations in multiplex Middle Eastern families.	
568	Influence of publication on university ranking: Citation, collaboration, and level of interdisciplinary research. 096100062211061	0
567	Structural insights into AT-rich DNA recognition by SALL family proteins.	
566	A complete, telomere-to-telomere human genome sequence presents new opportunities for evolutionary genomics. **2022**, 19, 635-638	0
565	paPAML: An Improved Computational Tool to Explore Selection Pressure on Protein-Coding Sequences. **2022**, 13, 1090	
564	A Modern Approach towards an Industry 4.0 Model: From Driving Technologies to Management. **2022**, 2022, 1-18	8
563	The Compleat Human Genome. **2022**, 1, 234-236	
562	The highly expressed ERV1 forms virus-like particles for regulating early embryonic development.	
561	Cancer: A pathologist journey from morphology to molecular. **2022**,	0
560	Structural Insights into At-Rich DNA Recognition by Sall Family Proteins.	

559	What Have Failed, Interrupted, and Withdrawn Antibody Therapies in Multiple Sclerosis Taught Us?. **2022**, 19, 785-807	0
558	S̈quence du gĥome : la fin du commencement. **2022**, 38, 609-611	0
557	Molecular Modelling Hurdle in the Next-Generation Sequencing Era. **2022**, 23, 7176	
556	Quantum technology a tool for sequencing of the ratio DSS/DNA modifications for the development of new DNA-binding proteins. **2022**, 9, 308-323	
555	The Location of Missense Variants in the Human GIP Gene Is Indicative for Natural Selection. 13,	
554	Estimating the rates of crossover and gene conversion from individual genomes.	
553	The HERV-K(HML-2) Transcriptome in Non-Diseased Tissue.	
552	Frequency and mechanisms of LINE-1 retrotransposon insertions at CRISPR/Cas9 sites. **2022**, 13,	1
551	L1 Retrotransposons: A Potential Endogenous Regulator for Schizophrenia. 13,	
550	3D spatial genome organization in the nervous system: From development and plasticity to disease. **2022**,	2
549	Comprehensive identification and characterization of the ́HERV-K (HML-9) group in the human genome. **2022**, 19,	3
548	Thousands of human mutation clusters are explained by short-range template switching. gr.276478.121	
547	A common genomic architecture for interacting with the external world.	
546	RE: Lower Exome Sequencing Coverage of Ancestrally African Patients in the Cancer Genome Atlas.	0
545	The Significance of MicroRNAs in the Molecular Pathology of Brain Metastases. **2022**, 14, 3386	
544	High-throughput method for the hybridisation-based targeted enrichment of long genomic fragments for PacBio third-generation sequencing. **2022**, 4,	0
543	Increased mutation rate and interlocus gene conversion within human segmental duplications.	0
542	Invertebrate neurones, genomes, phenotypic and target-based screening: Their contributions to the search for new chemical leads and new molecular targets for the control of pests, parasites and disease vectors. **2022**, 105175	

541	Effects of end-stage osteoarthritis on markers of skeletal muscle Long INterspersed Element-1 activity. **2022**, 15,	0
540	Role of Transposable Elements in Genome Stability: Implications for Health and Disease. **2022**, 23, 7802	0
539	The effects of sequencing depth on the assembly of coding and noncoding transcripts in the human genome. **2022**, 23,	0
538	Covalent Chemical Tools for Profiling Post-Translational Modifications. 10,	0
537	DNA damage and repair in age-related inflammation.	3
536	How Reproducibility Will Accelerate Discovery Through Collaboration in Physio-Logging. 13,	
535	Decoding the zebrafish genome. **2022**, 54, 917-919	1
534	Myocardial Injury Caused by Chronic Alcohol Exposure: A Pilot Study Based on Proteomics. **2022**, 27, 4284	0
533	Genomic map of candidate human imprint control regions: the imprintome. 1-24	2
532	Complex genomic rearrangements: an underestimated cause of rare diseases. **2022**,	1
531	Quantification of mutant allele expression at isoform level in cancer from RNA-seq data. **2022**, 4,	
530	LINE-1 promotes tumorigenicity and exacerbates tumor progression via stimulating metabolism reprogramming in non-small cell lung cancer. **2022**, 21,	0
529	Murine gammaherpesvirus 68 ORF45 stimulates B2 retrotransposon and pre-tRNA activation in a manner dependent on mitogen-activated protein kinase (MAPK) signaling.	0
528	ExoPLOT: Representation of alternative splicing in human tissues and developmental stages with transposed element (TE) involvement. **2022**, 110434	
527	Dynamic reprogramming of H3K9me3 at hominoid-specific retrotransposons during human preimplantation development. **2022**, 29, 1031-1050.e12	1
526	Transcriptional and reverse transcriptional regulation of host genes by human endogenous retroviruses in cancers. 13,	0
525	A Draft Human Pangenome Reference.	1
524	Uncovering the statistical physics of 3D chromosomal organization using data-driven modeling. **2022**, 75, 102418	0

523	Allelic frequencies distribution and forensic parameters of 23 autosomal short tandem repeats in the population of the State of Pernambuco, Brazil. **2022**, 59, 102112	
522	Sequestration of LINE -1 in cytosolic aggregates by MOV10 restricts retrotransposition.	0
521	Mutant KRAS regulates transposable element RNA and innate immunity via KRAB zinc-finger genes. **2022**, 40, 111104	0
520	Biallelic and gene-wide genomic substitution for endogenous intron and retroelement mutagenesis in human cells. **2022**, 13,	0
519	Baseline QOL, QOL-relevant HLA-restricted HERV gene-derived peptides, and survival outcomes in gastric cancer. **2022**, 30, 55-66	1
518	A quantification method of somatic mutations in normal tissues and their accumulation in pediatric patients with chemotherapy. **2022**, 119,	0
517	Artificial Intelligence, Healthcare, Clinical Genomics, and Pharmacogenomics Approaches in Precision Medicine. 13,	0
516	New Drug Development and Clinical Trial Design by Applying Genomic Information Management. **2022**, 14, 1539	0
515	The L1-ORF1p coiled coil enables formation of a tightly compacted nucleic acid-bound complex that is associated with retrotransposition.	
514	Neuronal nuclear tau and neurodegeneration. **2022**,	0
513	Retroviral glycoprotein-mediated immune suppression via the potassium channel KCa3.1 □A new strategy for amelioration of inflammatory bowel diseases. **2022**, 109081	
512	Chromatin structure in cancer. **2022**, 23,	2
511	Clinical Validation of Genome Reference Consortium Human Build 38 in a Laboratory Utilizing Next-Generation Sequencing Technologies.	0
510	Mutational analysis of 16 STR markers in Slovak population. 1-11	
509	Duplex sequencing identifies genomic features that determine susceptibility to benzo(a)pyrene-induced in vivo mutations. **2022**, 23,	0
508	Copyright Page. **2007**, iv-iv	
507	Preface. **2007**, xi-xvi	
506	Dedication. **2007**, v-vi	

505 Foreword. **2007**, vii-x

504 Foreword. **2009**, v-vi

503 Copyright Page. **2009**, iv-iv

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501 Introduction. **2009**, xiii-xvi

500 Copyright Page. **2011**, iv-iv

499 Foreword. **2011**, vii-viii

498 Dedication. **2011**, v-vi

497 List of abbreviations. **2011**, xix-xx

496 Epigraph. **2011**, xi-xii

495 Author's Preface. **2011**, ix-x

494 From molecules to genomic variations: Accelerating genome analysis via intelligent algorithms and architectures. **2022**, 20, 4579-4599 1

493 Ongoing endeavors to detect mobilization of transposable elements. **2022**, 55, 305-315

492 Long noncoding RNA profile of the intracranial artery in patients with moyamoya disease. **2022**, 1-8

491 Clinical application of microRNAs in glomerular diseases.

490 Next-Generation Pathology Using Multiplexed Immunohistochemistry: Mapping Tissue Architecture at Single-Cell Level. 12, 0

489 Evaluating Illumina-, Nanopore-, and PacBio-based genome assembly strategies with the bald notothen, Trematomus borchgrevinki. 1

488 Diversifying the genomic data science research community. **2022**, 32, 1231-1241

487	Long non-coding RNAs: a valuable biomarker for metabolic syndrome. **2022**, 297, 1169-1183	1
486	PML and PML-like exonucleases restrict retrotransposons in jawed vertebrates.	
485	Fixing reference errors efficiently improves sequencing results.	0
484	Mammalian genome innovation through transposon domestication.	1
483	SCIFER: approach for analysis of LINE-1 mRNA expression in single cells at a single locus resolution. **2022**, 13,	
482	Analysis of archaic human haplotypes suggests that 5hmC acts as an epigenetic guide for NCO recombination. **2022**, 20,	
481	Genome-wide single cell annotation of the human protein-coding genes.	
480	LncRNAs divide and rule: The master regulators of phase separation. 13,	1
479	Progress and opportunities through use of genomics in animal production. **2022**,	0
478	The Research Data Repository Facility. **2022**, 1-29	
477	Origination of LTR retroelement-derived NYNRIN coincides with therian placental emergence.	0
476	Starships are active eukaryotic transposable elements mobilized by a new family of tyrosine recombinases.	1
475	Mutational signatures and increased retrotransposon insertions in Xeroderma Pigmentosum variant skin tumors.	
474	Pan-African genome demonstrates how population-specific genome graphs improve high-throughput sequencing data analysis. **2022**, 13,	0
473	Long-term voluntary wheel running effects on markers of Long Interspersed Nuclear Element-1 in skeletal muscle, liver, and brain tissue of female rats.	1
472	All Quiet on the TE Front? The Role of Chromatin in Transposable Element Silencing. **2022**, 11, 2501	
471	Mouse L1s fade with age: a methylation-enforced mechanism for attenuation of L1 retrotransposition potential.	0
470	Multiscale Analysis of Pangenome Enables Improved Representation of Genomic Diversity For Repetitive And Clinically Relevant Genes.	0

469 Delineating mechanisms and design principles of Caenorhabditis elegans embryogenesis using in toto high-resolution imaging data and computational modeling. **2022**,

468 Reduced synaptic activity and dysregulated extracellular matrix pathways in midbrain neurons from Parkinson disease patients. **2022**, 8, 1

467 Quantitative assaying of SpCas9-NG with fluorescent reporters.

466 Comprehensive analysis of F8 large deletions: Characterization of full breakpoint junctions and description of a possible DNA breakage hotspot in intron 6. 0

465 Basics and Terminology. **2022**, 1-20

464 Therapeutic siRNA: State-of-the-Art and Future Perspectives. 1

463 The Neurodevelopmental Gene MSANTD2 Belongs to a Gene Family Formed by Recurrent Molecular Domestication of Harbinger Transposons at the Base of Vertebrates. **2022**, 39,

462 Hierarchical Interleaved Bloom Filter: Enabling ultrafast, approximate sequence queries.

461 A Tale of Native American Whole-Genome Sequencing and Other Technologies. **2022**, 14, 647

460 Breaking satellite silence: human satellite II RNA expression in ovarian cancer. **2022**, 132, 0

459 3rd-ChimeraMiner: A pipeline for integrated analysis of whole genome amplification generated chimeric sequences using long-read sequencing.

458 HSDatabase a database of highly similar duplicate genes from plants, animals, and algae.

457 Endogenous Retroviral Sequences Behave as Putative Enhancers Controlling Gene Expression through HP1-Regulated Long-Range Chromatin Interactions. **2022**, 11, 2392

456 Protein Design: From the Aspect of Water Solubility and Stability. 7

455 Placental DNA Methylation in pregnancies complicated by maternal diabetes and/or obesity: State of the Art and research gaps. 0

454 Tool and techniques study to plant microbiome current understanding and future needs: an overview. **2022**, 15, 209-225 1

453 Profiling human pathogenic repeat expansion regions by synergistic and multi-level impacts on molecular connections.

452 Recombination between heterologous human acrocentric chromosomes. 0

451	De Novo Somatic Mosaicism of CYBB Caused by Intronic LINE-1 Element Insertion Resulting in Chronic Granulomatous Disease.	1
450	The interplay of long noncoding RNAs and hepatitis B virus.	0
449	The retroelement Lx9 puts a brake on the immune response to virus infection. **2022**, 608, 757-765	0
448	Perspectives in plant evolutionary genetics: A field guide in 15 easy steps to modern tools in evolutionary genetics and genomics. 100,	1
447	Distinct composition and amplification dynamics of transposable elements in sacred lotus (Nelumbo nucifera Gaertn.).	
446	PerSVade: personalized structural variant detection in any species of interest. **2022**, 23,	0
445	The Era of Genomic Research for Lymphoma: Looking Back and Forward. **2022**, 3, 485-507	
444	Marsupial satellite DNA as faithful reflections of long terminal repeat (LTR) retroelement structure.	0
443	The first gapless, reference-quality, fully annotated genome from a Southern Han Chinese individual.	
442	Characterisation of retrotransposon insertion polymorphisms in whole genome sequencing data from individuals with amyotrophic lateral sclerosis. **2022**, 843, 146799	
441	The genetic and molecular features of the intronic pentanucleotide repeat expansion in spinocerebellar ataxia type 10. 13,	0
440	Transposable Elements Shaping the Epigenome. **2023**, 323-355	0
439	Genetics, mechanism, and pathophysiology of 22q11.2 deletion syndrome. **2022**, 34-52	0
438	Living in Peace with Coronaviruses. **2022**, 93-109	0
437	Transcriptomics. **2022**,	0
436	Chapter 1. Chemical Approaches for Beta-cell Biology. **2022**, 1-52	0
435	DNA damage, epigenetics, and aging. **2022**, 139-156	0
434	Higher-order Chromatin Organization in Diseases, from Chromosomal Position Effect to Phenotype Variegation. **2023**, 89-110	0

433	Circular RNAs: New Players in Cardiomyopathy. **2022**, 13, 1537	0
432	Decoding psychosis: from national genome project to national brain project. **2022**, 35, e100889	0
431	Introductory Chapter: Epigenetics and Optogenetics - The Science behind the Cover Blanket of Our Genome.	0
430	Early macrophage response to obesity encompasses Interferon Regulatory Factor 5 regulated mitochondrial architecture remodelling. **2022**, 13,	0
429	Using ncRNAs as Tools in Cancer Diagnosis and Treatment The Way towards Personalized Medicine to Improve Patients Health. **2022**, 23, 9353	1
428	The formation mechanism and homeostasis of extrachromosomal DNA.	0
427	Transposable elements derived microRNA expression patterns in TCGA dataset and evolutionary analysis for 10 species.	0
426	Web-based gene expression analysis paving the way to decode healthy and diseased ocular tissue.	0
425	BRAF and NRAS Mutation Status and Response to Checkpoint Inhibition in Advanced Melanoma. **2022**,	0
424	Functional precision cancer medicine: drug sensitivity screening enabled by cell culture models. **2022**,	0
423	Condensin I and condensin II proteins form a LINE-1 dependent super condensin complex and cooperate to repress LINE-1.	0
422	Transcriptional Regulation of Endogenous Retroviruses and Their Misregulation in Human Diseases. **2022**, 23, 10112	0
421	Multi-pathway DNA-repair reporters reveal competition between end-joining, single-strand annealing and homologous recombination at Cas9-induced DNA double-strand breaks. **2022**, 13,	1
420	Retrotransposon insertion as a novel mutational cause of spinal muscular atrophy.	0
419	The emerging roles and potential applications of circular RNAs in ovarian cancer: a comprehensive review.	0
418	Genomics and epigenetics guided identification of tissue-specific genomic safe harbors. **2022**, 23,	0
417	A primary hierarchically organized patient-derived model enables in depth interrogation of stemness driven by the coding and non-coding genome.	0
416	Multinomial Convolutions for Joint Modeling of Regulatory Motifs and Sequence Activity Readouts. **2022**, 13, 1614	0

415	Immune Isoform Atlas: Landscape of alternative splicing in human immune cells.	0
414	Scalable Functional Assays for the Interpretation of Human Genetic Variation. **2022**, 56,	0
413	Intragenic L1 Insertion: One Possibility of Brain Disorder. **2022**, 12, 1425	0
412	Biomarkers for immune checkpoint inhibitors in solid tumors.	0
411	In situ tools for chromatin structural epigenomics.	0
410	Mapping Retrotransposon LINE-1 Sequences into Two Cebidae Species and Homo sapiens Genomes and a Short Review on Primates. **2022**, 13, 1742	0
409	Chromosomes: Noncoding DNA (Including Satellite DNA). 1-18	0
408	Sources of Cancer Neoantigens beyond Single-Nucleotide Variants. **2022**, 23, 10131	1
407	Integration of TE Induces Cancer Specific Alternative Splicing Events. **2022**, 23, 10918	0
406	Climate change, human health, and the exposome: Utilizing OMIC technologies to navigate an era of uncertainty. 10,	0
405	The druggable genome: Twenty years later. 2,	0
404	Evolution of stickleback spines through independent cis-regulatory changes at HOXDB. **2022**, 6, 1537-1552	0
403	IRescue: single cell uncertainty-aware quantification of transposable elements expression.	0
402	Isoform-specific and ubiquitination dependent recruitment of Tet1 to replicating heterochromatin modulates methylcytosine oxidation. **2022**, 13,	0
401	ChimeraTE: A pipeline to detect chimeric transcripts derived from genes and transposable elements.	0
400	IEAtlas: an atlas of HLA-presented immune epitopes derived from non-coding regions.	1
399	Rapid genome sequencing for pediatrics.	0
398	Biocircuits in plants and eukaryotic algae. 13,	0

397	Data-Driven Dental, Oral, and Craniofacial Analytics: Here to Stay. **2022**, 101, 1255-1257	1
396	Emerging role of oncogenic long noncoding RNA as cancer biomarkers.	0
395	L1 retrotransposition is regulated post-transcriptionally In High-Grade Serous Ovarian Cancer.	0
394	A Comprehensive Review of Performance of Next-Generation Sequencing Platforms. **2022**, 2022, 1-12	9
393	Los retos de las ciencias a la concepci cristiana de lo humano. **2022**, 97, 395-421	0
392	QuickDeconvolution: fast and scalable deconvolution of linked-read sequencing data.	0
391	Statistical learning quantifies transposable element-mediated cis-regulation.	0
390	The 3D-Evo Space: Evolution of Gene Expression and Alternative Splicing Regulation. **2022**, 56,	0
389	Exploring Bacterial Attributes That Underpin Symbiont Life in the Monogastric Gut. **2022**, 88,	1
388	Mechanisms of mRNA processing defects in inherited THOC6 intellectual disability syndrome.	0
387	Analyzing RNA posttranscriptional modifications to decipher the epitranscriptomic code.	0
386	High-Resolution and Multidimensional Phenotypes Can Complement Genomics Data to Diagnose Diseases in the Neonatal Population.	0
385	Histone Modification Analysis of Low-Mappability Regions. **2023**, 163-185	0
384	Epigenetic centromere identity is precisely maintained through DNA replication but is uniquely specified among human cells.	0
383	Nef Suppresses LINE-1 Retrotransposition through Two Distinct Mechanisms.	0
382	Comparative Genomic Characterization of Relaxin Peptide Family in Cattle and Buffalo. **2022**, 2022, 1-11	0
381	Accurate prediction of functional states of cis-regulatory modules reveals common epigenetic rules in humans and mice. **2022**, 20,	0
380	Robot Telepresence as a Practical Tool for Responsible and Open Research in Trustworthy Autonomous Systems. **2022**, 100050	0

379	lncRNAs: Role in Regulation of Gene Expression.	1
378	Multiple Genome Analytics Framework: The Case of All SARS-CoV-2 Complete Variants. **2022**,	0
377	hAssembler: A hybrid de novo genome assembly approach for large genomes. **2020**, 90, 2000-2005	0
376	Epigenomic reprogramming in iAs-mediated carcinogenesis. **2022**,	0
375	Clinical genomics and precision medicine. **2022**, 45,	0
374	HSDatabase: a database of highly similar duplicate genes from plants, animals, and algae. **2022**, 2022,	0
373	Human Genomics, History. **2022**,	0
372	Pharmacogenetic Biomarkers and Personalized Medicine: Upcoming Concept in Pharmacotherapy. **2022**, 4289-4292	0
371	Cross-species transmission of an ancient endogenous retrovirus and convergent co-option of its envelope gene in two mammalian orders. **2022**, 18, e1010458	0
370	Human Endogenous Retroviruses and Toll-Like Receptors.	1
369	Multidistrict Host–Pathogen Interaction during COVID-19 and the Development Post-Infection Chronic Inflammation. **2022**, 11, 1198	0
368	Beyond Basic Diversity Estimates: Analytical Tools for Mechanistic Interpretations of Amplicon Sequencing Data. **2022**, 10, 1961	0
367	3L, three-Lactobacilli on recovering of microbiome and immune-damage by cyclophosphamide chemotherapy.	0
366	Sequencing and chromosome-scale assembly of the giantPleurodeles waltlgenome.	1
365	Navigating Transcriptomic Connectivity Mapping Workflows to Link Chemicals with Bioactivities.	0
364	Human Retrotransposons and Effective Computational Detection Methods for Next-Generation Sequencing Data. **2022**, 12, 1583	0
363	Alternative and aberrant splicing of human endogenous retroviruses in cancer. What about head and neck? A mini review. 12,	0
362	The Chemical Probes Portal: an expert review-based public resource to empower chemical probe assessment, selection and use.	3

361	Cancer Genomics and Evolution. 1-30	0
360	3D genome organization links non-coding disease-associated variants to genes. 10,	0
359	Bacterial DNA involvement in carcinogenesis. 12,	0
358	The function and clinical implication of circular RNAs in lung cancer. 12,	0
357	Investigating on the influence mechanism of sausage of sea bass on calcium absorption and transport based on Caco-2 cell monolayer model. 9,	0
356	Population designations in biomedical research: limitations and perspectives.	0
355	Counting Genes: A Human Genome Conundrum. **2022**, 1, 428-429	0
354	Structural studies of SALL family protein zinc finger cluster domains in complex with DNA reveal preferential binding to an AATA tetranucleotide motif. **2022**, 102607	1
353	Discovery of a MUC3B gene reconstructs the membrane mucin gene cluster on human chromosome 7. **2022**, 17, e0275671	0
352	Widespread expression of the ancient HERV-K (HML-2) provirus group in normal human tissues. **2022**, 20, e3001826	4
351	EUGENe: A Python toolkit for predictive analyses of regulatory sequences.	0
350	Quantum computing algorithms: getting closer to critical problems in computational biology.	0
349	The discovery of multiple active mys-related LTR-retroelements within the Neotominae subfamily of cricetid rodents.	0
348	Endogenous retroelements as alarms for disruptions to cellular homeostasis. **2022**,	0
347	Genetics of Thalassemia.	0
346	Transposable Elements as a Source of Novel Repetitive DNA in the Eukaryote Genome. **2022**, 11, 3373	1
345	SERPINE1 DNA Methylation Levels Quantified in Blood Cells at Five Years of Age Are Associated with Adiposity and Plasma PAI-1 Levels at Five Years of Age. **2022**, 23, 11833	0
344	PERSONALIZED MEDICINE: AN INNOVATION IN HEALTH-CARE SYSTEM. 4-9	0

343	Long non-coding RNAs and microRNAs as regulators of stress in cancer (Review). **2022**, 26,	1
342	SiRNA Molecules as Potential RNAi Therapeutics to Silence RdRP Region and N-Gene of SARS-CoV-2: An In Silico Approach.	0
341	A novel inflammation-related lncRNAs prognostic signature identifies LINC00346 in promoting proliferation, migration, and immune infiltration of glioma. 13,	0
340	Semi-automated assembly of high-quality diploid human reference genomes.	3
339	Bioeconomy in a changing world. **2022**, 100041	0
338	Liquid Biopsy in Cancer: Focus on Lymphoproliferative Disorders. **2022**, 14, 5378	0
337	G-PROTEIN COUPLED RECEPTOR 19 (GPR19) KNOCKOUT MICE DISPLAY SEX-DEPENDENT METABOLIC DYSFUNCTION.	0
336	Regularized sequence-context mutational trees capture variation in mutation rates across the human genome.	0
335	Hematogenous metastasis and tumor dormancy as concepts or dogma? The continuum of vessel co-option and angiotropic extravascular migratory metastasis as an alternative. 12,	0
334	Seropositivity-Dependent Association between LINE-1 Methylation and Response to Methotrexate Therapy in Early Rheumatoid Arthritis Patients. **2022**, 13, 2012	1
333	Novel Privacy Considerations for Large Scale Proteomics.	0
332	Evolution of bioinformatics and its impact on modern bio-science in the twenty-first century: Special attention to pharmacology, plant science and drug discovery. **2022**, 24, 100248	1
331	The landscape of hervRNAs transcribed from human endogenous retroviruses across human body sites. **2022**, 23,	0
330	GenomicKB: a knowledge graph for the human genome.	0
329	A Truncated Form of the p27 Cyclin-Dependent Kinase Inhibitor Translated from Pre-mRNA Causes G 2 -Phase Arrest.	0
328	Single-cell RNA sequencing highlights the functional role of human endogenous retroviruses in gallbladder cancer. **2022**, 85, 104319	0
327	A Systems Biology Approach on the Regulatory Footprint of Human Endogenous Retroviruses (HERVs). **2022**, 10, 98	1
326	Comprehensive analysis of the PRPF31 Gene in Retinitis Pigmentosa Patients: Four novel Alu -mediated Copy Number Variations at the PRPF31 locus.	0

325	The Impact of Leukemia on the Detection of Short Tandem Repeat (STR) Markers. **2022**,	0
324	Transgenic mice harboring direct repeat substrates reveal key underlying causes of homologous recombination in vivo. **2022**, 120, 103419	0
323	Cellular regulation and stability of DNA replication forks in eukaryotic cells. **2022**, 120, 103418	0
322	Spatial transcriptomics. **2023**, 175-197	0
321	Susceptibility and resilience to maternal immune activation are associated with differential expression of endogenous retroviral elements. **2023**, 107, 201-214	0
320	Interplay between activation of endogenous retroviruses and inflammation as common pathogenic mechanism in neurological and psychiatric disorders. **2023**, 107, 242-252	0
319	Proteomic studies of human and other vertebrate muscle proteins. **2004**, 69, 1283-1298	0
318	CENP-A: A Histone H3 Variant with Key Roles in Centromere Architecture in Healthy and Diseased States. **2022**, 221-261	0
317	Regulation of Biological Agents and Biotechnology. **2023**, 376-386	0
316	RNA interference is the basis of human antiviral defense. **2022**, 24, 1065-1074	0
315	Identification of non-coding silencer elements and their regulation of gene expression.	1
314	Small Non-Coding RNAs in Human Cancer. **2022**, 13, 2072	1
313	How to start a LINE: 5′switching rejuvenates LINE retrotransposons in tobacco and relatedNicotianaspecies.	0
312	Fast and accurate mapping of long reads to complete genome assemblies with VerityMap. gr.276871.122	0
311	Improved NGS-based detection of microsatellite instability using tumor-only data. 12,	0
310	A condensate forming tether for lariat debranching enzyme is defective in non-photosensitive trichothiodystrophy.	0
309	Retrotransposon insertions associated with risk of neurologic and psychiatric diseases.	0
308	VarSCAT: A computational tool for sequence context annotations of genomic variants.	0

307	Profiling human pathogenic repeat expansion regions by synergistic and multi-level impacts on molecular connections.	0
306	The single-cell expression profile of transposable elements and transcription factors in human early biparental and uniparental embryonic development. 10,	0
305	Modifier Factors of Cystic Fibrosis Phenotypes: A Focus on Modifier Genes. **2022**, 23, 14205	0
304	Making Sense of Ecology from a Genetic Perspective: Caenorhabditis elegans, Microbes and Behavior. **2022**, 12, 1084	0
303	A Primer on Chimerism Analysis: A Straightforward, Thorough Review.	0
302	A comprehensive review of the role of lncRNAs in gastric cancer (GC) pathogenesis, immune regulation, and their clinical applications. **2022**, 154221	0
301	Expression of retrotransposons contributes to aging in Drosophila.	0
300	Subcellular Fractionation for DIGE-Based Proteomics. **2023**, 351-362	2
299	Owl Monkey Alu Insertion Polymorphisms and Aotus Phylogenetics. **2022**, 13, 2069	1
298	The discovery of multiple active mys-related LTR-retroelements within the Neotominae subfamily of cricetid rodents.	0
297	Latch Verified Bulk-RNA Seq toolkit: a cloud-based suite of workflows for bulk RNA-seq quality control, analysis, and functional enrichment.	0
296	From the reference human genome to human pangenome: Premise, promise and challenge. 13,	0
295	Phased Genome Assemblies. **2023**, 273-286	0
294	Tissue Proteogenomic Landscape Reveals the Role of Uncharacterized SEL1L3 in Progression and Immunotherapy Response in Lung Adenocarcinoma.	0
293	Blood Group Genotyping. **2022**, 42, 645-668	0
292	Genetic variation and susceptibility to schizophrenia: Work in progress. **2022**, 318, 114949	0
291	Are studies of human gut microbiome the new fad following the SNP mainstream?. **2022**, 66, 929-930	0
290	Transposable element-mediated rearrangements are prevalent in human genomes. **2022**, 13,	0

289	Evolutionary insights from profiling LINE-1 activity at allelic resolution in a single human genome.	0
288	Deep mutational scanning to probe specificity determinants in proteins. **2023**, 31-71	0
287	Differentially expressed AC077690.1, AL049874.3 and AP001037.1 lncRNAs in prostate cancer. **2022**, 74, 359-366	0
286	The landscape of the repeated sequences in the human genome. **2023**, 157-170	0
285	Use of ubiquitous chromatin opening elements (UCOE) as tools to maintain transgene expression in biotechnology. **2023**, 21, 275-283	0
284	Are transposable elements enemies within?. **2023**, 185-200	0
283	Legal Trends in Bioethics. **2001**, 12, 176-185	0
282	Connecting Evolutionary Genomics to Cell Biology. **2016**, 356-362	0
281	Genome-wide association studies for thyroid physiology and diseases. **2022**,	0
280	The Human Genome. **2022**,	0
279	Boolean modelling in plant biology. **2022**, 3,	0
278	Genetic resources for general practitioners. **2022**, 3, 115-117	0
277	Broadening participation of biology students in computing: a mixed methods study among bioinformatics students. **2022**,	0
276	The coevolution between APOBEC3 and retrotransposons in primates. **2022**, 13,	0
275	Rad52 DNA annealing activity drives template switching associated with restarted DNA replication. **2022**, 13,	0
274	Epigenetic Mechanisms Underlying Melanoma Resistance to Immune and Targeted Therapies. **2022**, 14, 5858	0
273	Computer simulation of molecular recognition in biomolecular system: from in silico screening to generalized ensembles.	1
272	Recurrent co-domestication of PIF/Harbinger transposable element proteins in insects. **2022**, 13,	0

271	T3E: a tool for characterising the epigenetic profile of transposable elements using ChIP-seq data. **2022**, 13,	0
270	Discovery of the hidden coding information in cancers: Mechanisms and biological functions.	0
269	The coming decade in precision oncology: six riddles. **2023**, 23, 43-54	1
268	Modulation of human endogenous retroviruses and cytokines expression in peripheral blood mononuclear cells from autistic children and their parents. **2022**, 19,	1
267	Protection of the human gene research literature from contract cheating organizations known as research paper mills. **2022**, 50, 12058-12070	0
266	Cancer Stem Cells The Insight into Non-Coding RNAs. **2022**, 11, 3699	0
265	Effects of Different Methods and Genomic Relationship Matrices on Reliabilities of Genomic Selection in Dairy Cattle.	0
264	An Epigenetic LINE-1-Based Mechanism in Cancer. **2022**, 23, 14610	0
263	Epigenetics in Pancreatic Ductal Adenocarcinoma: Impact on Biology and Utilization in Diagnostics and Treatment. **2022**, 14, 5926	0
262	Single-cell multiomics reveals the complexity of TGF signalling to chromatin in iPSC-derived kidney organoids. **2022**, 5,	0
261	NPFFR2 Contributes to the Malignancy of Hepatocellular Carcinoma Development by Activating RhoA/YAP Signaling. **2022**, 14, 5850	0
260	[illegible] 200- [illegible] **2022**, 29-38	0
259	Next-Generation-Sequencing in der Augenheilkunde. **2022**, 119, 1317-1328	0
258	Generalized nuclear localization of retroelement transcripts. **2022**, 13,	0
257	Epigenetic Regulation of Fungal Genes Involved in Plant Colonization. **2023**, 255-281	0
256	Retrotransposon instability dominates the acquired mutation landscape of mouse induced pluripotent stem cells. **2022**, 13,	0
255	Proteogenomic characterization of MiT family translocation renal cell carcinoma. **2022**, 13,	0
254	Transposons Acting as Competitive Endogenous RNAs: In-Silico Evidence from Datasets Characterised by L1 Overexpression. **2022**, 10, 3279	0

253	LINE-1 Retrotransposition Assays in Embryonic Stem Cells. **2023**, 257-309	0
252	Nanopore Sequencing to Identify Transposable Element Insertions and Their Epigenetic Modifications. **2023**, 151-171	0
251	Time-resolved microfluidics unravels individual cellular fates during double-strand break repair. **2022**, 20,	0
250	Long non-coding RNA H19: a potential biomarker and therapeutic target in human malignant tumors.	0
249	Thirteen dubious ways to detect conserved structural RNAs.	0
248	Exon Elongation Added Intrinsically Disordered Regions to the Encoded Proteins and Facilitated the Emergence of the Last Eukaryotic Common Ancestor.	0
247	Engineering exosomes for bone defect repair. 10,	0
246	Oncoproteomics: insight into current proteomic technologies in cancer biomarker discovery and treatment.	0
245	The mutational dynamics of short tandem repeats in large, multigenerational families. **2022**, 23,	0
244	Event-based high throughput computing: A series of case studies on a massively parallel softcore machine.	0
243	Optimized CRISPR guide RNA library cloning reduces skew and enables more compact genetic screens.	0
242	A chromosome level genome assembly of longnose gar,Lepisosteus osseus.	0
241	Transposon-derived transcription factors across metazoans.	1
240	PDX1 is the cornerstone of pancreatic □cell functions and identity. 9,	0
239	Nano-Based Robotic Technologies for Plant Disease Diagnosis. **2023**, 327-359	0
238	Freddie: annotation-independent detection and discovery of transcriptomic alternative splicing isoforms using long-read sequencing.	0
237	Targets of histone H3 lysine 9 methyltransferases. 10,	0
236	Cancer Genomics. **2022**, 53, 723-731	1

235	Viral proteases as therapeutic targets. **2022**, 88, 101159	1
234	Chromatin-associated YTHDC1 coordinates heat-induced reprogramming of gene expression. **2022**, 41, 111784	0
233	Correction of transposase sequence bias in ATAC-seq data with rule ensemble modeling.	0
232	Integrating extrusion complex-associated pattern to predict cell type-specific long-range chromatin loops. **2022**, 25, 105687	0
231	Whole-genome identification of transposable elements reveals the equine repetitive element insertion polymorphism in Chinese horses.	0
230	Seeing the complete picture: proteins in top-down mass spectrometry.	1
229	Dysregulated thrombospondin 1 and miRNA-29a-3p in severe COVID-19. **2022**, 12,	0
228	A comprehensive investigation of human endogenous retroviral syncytin proteins and their receptors in men with normozoospermia and impaired semen quality.	0
227	Y chromosome sequence and epigenomic reconstruction across human populations.	0
226	Remnants of SIRE1 retrotransposons in human genome?. **2023**, 102,	0
225	The Role of Lead and Cadmium in Gynecological Malignancies. **2022**, 11, 2468	0
224	Whole genome analysis of clouded leopard species reveals an ancient divergence and distinct demographic histories. **2022**, 25, 105647	0
223	Exogenous chromosomes reveal how sequence composition drives chromatin assembly, activity, folding and compartmentalization.	0
222	Targeting riboswitches with beta-axial substituted cobalamins.	0
221	Perspectives on the future of dysmorphology.	0
220	An update on post-transcriptional regulation of retrotransposons.	0
219	0multifunctional Nanoparticles For Organelle-Specific Targeted Drug Delivery In Cancer Therapy. **2022**, 13,	0
218	Evolutionary analysis of endogenous intronic retroviruses in primates reveals an enrichment in transcription binding sites associated with key regulatory processes. 10, e14431	0

217	Is it the time to integrate novel sequencing technologies into clinical practice?. Publish Ahead of Print,	0
216	Genome-wide association studies of cardiovascular disease.	0
215	The genetic diversity and nutritional quality of proso millet (Panicum miliaceum) and its Philippine ecotype, the ancient grain Kabog millet□A review. **2023**, 100499	0
214	Epigenetics in Cancer Biology. **2022**,	0
213	Origin Matters: Using a Local Reference Genome Improves Measures in Population Genomics.	0
212	Bioinformatic method for determining single nucleotide polymorphisms on the example of gene <i>WIN</i> in <i>Glycine max</i>. **2023**, 12, 599-604	0
211	From □Omics to Multi-omics Technologies: the Discovery of Novel Causal Mediators.	2
210	The interferon stimulated gene-encoded protein HELZ2 inhibits human LINE-1 retrotransposition and LINE-1 RNA-mediated type I interferon induction. **2023**, 14,	0
209	The Field-Dependent Nature of PageRank Values in Citation Networks.	0
208	Association between night shift work and methylation of a subset of immune-related genes. 10,	0
207	NanoSTR: A method for detection of target short tandem repeats based on nanopore sequencing data. 10,	0
206	Endogenous Reverse Transcriptase Inhibition Attenuates TLR5-Mediated Inflammation.	0
205	Current advances in primate genomics: novel approaches for understanding evolution and disease.	0
204	The first gapless, reference-quality, fully annotated genome from a Southern Han Chinese individual.	0
203	Splashed E-box and AP-1 motifs cooperatively drive regeneration response and shape regeneration abilities.	0
202	Mathematical model of nuclear speckle morphology.	0
201	Examining the shared etiology of psychopathology with genome-wide association studies.	0
200	3L, three-Lactobacilli on recovering of microbiome and immune-damage by cyclophosphamide chemotherapy □A pilot experiment in rats□	0

199	Advances and Challenges of the Decade: The Ever-Changing Clinical and Genetic Landscape of Immunodeficiency. **2023**, 11, 107-115	0
198	Long-read metagenomics paves the way toward a complete microbial tree of life. **2023**, 20, 30-31	0
197	Using Single-Cell RNA Sequencing and MicroRNA Targeting Data to Improve Colorectal Cancer Survival Prediction. **2023**, 12, 228	1
196	Transcriptional Response in Human Jurkat T Lymphocytes to a near Physiological Hypergravity Environment and to One Common in Routine Cell Culture Protocols. **2023**, 24, 1351	0
195	Alternatively Spliced Isoforms of MUC4 and ADAM12 as Biomarkers for Colorectal Cancer Metastasis. **2023**, 13, 135	0
194	Comprehensive variant discovery in the era of complete human reference genomes. **2023**, 20, 17-19	0
193	Epigenetic centromere identity is precisely maintained through DNA replication but is uniquely specified among human cells. **2023**, 6, e202201807	0
192	Transferability of the PRS estimates for height and BMI obtained from the European ethnic groups to the Western Russian populations. 14,	0
191	3L, three-Lactobacilli on recovering of microbiome and immune-damage by cyclophosphamide chemotherapy A pilot experiment	0
190	Prediction of protein-coding small ORFs in multi-species using integrated sequence-derived features and the random forest model. **2023**, 210, 10-19	0
189	HSDecipher: A pipeline for comparative genomic analysis of highly similar duplicate genes in eukaryotic genomes. **2023**, 4, 102014	0
188	pfeRNAs- A Novel Class of Small Non-Coding RNAs With Real Translational Potential. **2023**, 284, 237-244	0
187	Endogenous Retrovirus Elements Are Co-Expressed with IFN Stimulation Genes in the JAKSTAT Pathway. **2023**, 15, 60	0
186	Chromatin modifier developmental pluripotency associated factor 4 (DPPA4) is a candidate gene for alcohol-induced developmental disorders. **2022**, 20,	0
185	[illegible] **2022**, 3-18	0
184	Drug Repurposing against KRAS Mutant G12C: A Machine Learning, Molecular Docking, and Molecular Dynamics Study. **2023**, 24, 669	0
183	Different structural variant prediction tools yield considerably different results in Caenorhabditis elegans. **2022**, 17, e0278424	0
182	An Update on Circular RNA in Pediatric Cancers. **2023**, 11, 36	0

181	CLIP-Seq Analysis Enables the Design of Ribosomal RNA Bait Oligonucleotides That Protect AgainstC9ORF72ALS/FTD-Associated Poly-GR Pathophysiology.	0
180	Identification and characterization of small molecule inhibitors of the LINE-1 retrotransposon endonuclease.	0
179	Expression of LINE-1 retrotransposon in early human spontaneous abortion tissues. **2022**, 101, e31964	0
178	Introduction to Genomic Diagnostics. **2019**, 38-75	0
177	Fundamentals of Genetics. **2021**, 1-32	0
176	Integrated ACMG approved genes and ICD codes for the translational research and precision medicine.	0
175	LINE-1 ORF1p as a candidate biomarker in high grade serous ovarian carcinoma. **2023**, 13,	0
174	Endogenous Retroviruses as Modulators of Innate Immunity. **2023**, 12, 162	0
173	Immunogenetics of Cancer. **2023**, 1-27	0
172	tRNA derived fragments:A novel player in gene regulation and applications in cancer. 13,	0
171	Transposable Elements Co-Option in Genome Evolution and Gene Regulation. **2023**, 24, 2610	0
170	The genome editing revolution. **2023**,	0
169	Microevolutionary dynamics of eccDNA in Chinese hamster ovary cells grown in fed-batch cultures under control and lactate-stressed conditions. **2023**, 13,	0
168	Industrial applications of thermophilic/hyperthermophilic enzymes. **2023**, 105-284	0
167	ChromDL: A Next-Generation Regulatory DNA Classifier.	0
166	Trends in modern drug discovery and development: A glance in the present millennium. **2023**, 27-38	0
165	Genome Evolution and the Future of Phylogenomics of Non-Avian Reptiles. **2023**, 13, 471	0
164	Noncoding RNAs and their role in bacterial infections. **2023**, 617-622	0

163	HiCLift: A fast and efficient tool for converting chromatin interaction data between genome assemblies.	0
162	Interchromosomal translocation in neural progenitor cells exposed to L1 retrotransposition. **2023**, 46,	0
161	FIMICS: A panel of long noncoding RNAs for cardiovascular conditions. **2023**, 9, e13087	0
160	Epigenetic Regulation of Macrophage Polarization in Cardiovascular Diseases. **2023**, 16, 141	0
159	Role of epigenetic factors in cancer progression induced by inactivation of tumor suppressors genes. **2023**, 33-44	0
158	Alternative splicing of PSMD13 mediated by genetic variants is significantly associated with endometrial cancer risk. 34,	0
157	Protein State-Dependent Chemical Biology.	0
156	Inference of Ancient Polyploidy Using Transcriptome Data. **2023**, 47-76	0
155	Genetics and Genomics Education for Physician Assistant Students: A Review of the Literature. **2023**, Publish Ahead of Print,	0
154	Rock, scissors, paper: How RNA structure informs function.	0
153	The role of structural variations in Alzheimer disease and other neurodegenerative diseases. 14,	0
152	Emerging Scientific Advances: How Do They Enter Dental Curricula and the Profession?. **2005**, 33, 805-809	0
151	Key challenges for toxicologists in the 21st century. **2023**, 703-718	0
150	Genomics in Treatment Development. **2023**, 363-385	0
149	Drug discovery: Standing on the shoulders of giants. **2023**, 207-338	0
148	Macromolecular chemistry: An introduction. **2023**, 71-128	0
147	Pitfalls of using sequence databases for heterologous expression studies a technical review.	0
146	Biomarkers (mRNAs and non-coding RNAs) for the diagnosis and prognosis of rheumatoid arthritis. 14,	0

145	A mentorship and incubation program using project-based learning to build a professional bioinformatics pipeline in Kenya. **2023**, 19, e1010904	0
144	Long-read sequencing in ecology and evolution: Understanding how complex genetic and epigenetic variants shape biodiversity. **2023**, 32, 1229-1235	0
143	Structurally divergent and recurrently mutated regions of primate genomes.	0
142	Climate-Related Human Biological Variation. **2023**, 140-166	0
141	The sound of silence: mechanisms and implications of HUSH complex function. **2023**, 39, 251-267	0
140	Characterization of genome-wide STR variation in 6487 human genomes. **2023**, 14,	0
139	The Three-Generation Pedigree. **2023**, 5, 77-91	0
138	Goat MyoD1: mRNA expression, InDel and CNV detection and their associations with growth traits. **2023**, 866, 147348	0
137	Nutrigenomics in the context of evolution. **2023**, 62, 102656	0
136	The Technology Behind Genomic Database. **2022**,	0
135	Epigenetic Mechanisms of Aging and Aging-Associated Diseases. **2023**, 12, 1163	0
134	Circular RNA circPlce1 regulates innate immune response in miiuy croaker, Miichthys miiuy. **2023**, 133, 108561	0
133	Detection for endogenous retroviral loci in Jungle fowl using whole-genome sequencing.	0
132	Potential health risks of mRNA-based vaccine therapy: A hypothesis. **2023**, 171, 111015	0
131	Exome/Genome Sequencing in Undiagnosed Syndromes. **2023**, 74, 489-502	1
130	Genes and Genomes. **2021**, 45-86	0
129	Assessing the functional impact of protein binding site definition.	0
128	Overview of single-cell RNA sequencing analysis and its application to spermatogenesis research. **2023**, 22,	0

127	Transcriptional activation of CSTB gene expression by transcription factor Sp3. **2023**, 649, 71-78	0
126	Interactions of an Artificial Zinc Finger Protein with Cd(II) and Hg(II): Competition and Metal and DNA Binding. **2023**, 11, 64	0
125	Exploring AlphaFold2?s Performance on Predicting Amino Acid Side-Chain Conformations and Its Utility in Crystal Structure Determination of B318L Protein. **2023**, 24, 2740	0
124	Recognition of transcription terminators during retrotransposition: How to keep a group II intron quiet. **2023**, 83, 332-334	0
123	Increased levels of endogenous retroviruses trigger fibroinflammation and play a role in kidney disease development. **2023**, 14,	0
122	Contribution of the TGF□ signaling pathway to pigmentation in sea cucumber (Apostichopus japonicus). 10,	0
121	Where are all the egg genes?. 11,	0
120	Modern Japanese ancestry-derived variants reveal the formation process of the current Japanese regional gradations. **2023**, 26, 106130	0
119	Genetics of Congenital Heart Disease. **2023**, 25-34	0
118	Human-specific genetics: new tools to explore the molecular and cellular basis of human evolution.	0
117	Insights into brain evolution through the genotype-phenotype connection. **2023**, 73-92	0
116	A chemoproteomic platform for reactive fragment profiling against the deubiquitinases.	0
115	Healthcare practitioners□ knowledge, attitudes and practices of genetics and genetic testing in low- or middle-income countries - A scoping review.	0
114	Cancer relevance of circulating antibodies against LINE-1 antigens in humans.	0
113	WGS Data Collections: How Do Genomic Databases Transform Medicine?. **2023**, 24, 3031	0
112	Widespread contribution of transposable elements to the rewiring of mammalian 3D genomes. **2023**, 14,	0
111	DNA-nanostructure-templated assembly of planar and curved lipid-bilayer membranes. 10,	0
110	The Genotype-Phenotype Correlation in Human 5□ Reductase Type 2 Deficiency: Classified and Analyzed from a SRD5A2 Structural Perspective. **2023**, 24, 3297	0

109	Murine Gammaherpesvirus 68 ORF45 Stimulates B2 Retrotransposon and Pre-tRNA Activation in a Manner Dependent on Mitogen-Activated Protein Kinase (MAPK) Signaling. **2023**, 11,	0
108	AI and ML for Development of Cell and Gene Therapy for Personalized Treatment. **2023**, 371-400	0
107	The Pol III transcriptome: Basic features, recurrent patterns, and emerging roles in cancer.	0
106	Deep learning for detecting and elucidating human T-cell leukemia virus type 1 integration in the human genome. **2023**, 4, 100674	0
105	DNA methylation trajectories during innate and adaptive immune responses of human B lymphocytes.	0
104	Gene–Environment Interactions in Repeat Expansion Diseases: Mechanisms of Environmentally Induced Repeat Instability. **2023**, 11, 515	0
103	An overview of bioinformatics courses delivered at the academic level in Italy: Reflections and recommendations from BITS. **2023**, 19, e1010846	0
102	Limited role of generation time changes in driving the evolution of the mutation spectrum in humans. 12,	0
101	Investigating the effects of Ceylon cinnamon water extract on HepG2 cells for Type 2 diabetes therapy. **2023**, 41, 254-267	0
100	Whole genome sequencing of Malaysian colorectal cancer patients reveals specific druggable somatic mutations. 9,	0
99	Computational prediction of protein folding rate using structural parameters and network centrality measures. **2023**, 155, 106436	0
98	Genomic structural variation: A complex but important driver of human evolution.	0
97	Molecular biology tools used to study hominin evolution. **2023**, 219-279	0
96	Lipid-based colloidal nanoparticles for applications in targeted vaccine delivery. **2023**, 5, 1853-1869	0
95	Epigenetic regulation in hematopoiesis and its implications in the targeted therapy of hematologic malignancies. **2023**, 8,	0
94	Alternative splicing of its 5′ untranslated region controls CD20 mRNA translation and enables resistance to CD20-directed immunotherapies.	0
93	Non-random Codon Usage of Synonymous and Non-synonymous Mutations in the Human HLA-A Gene. **2023**, 91, 169-191	0
92	FixItFelix: improving genomic analysis by fixing reference errors. **2023**, 24,	0

91	The Association between the Differential Expression of lncRNA and Type 2 Diabetes Mellitus in People with Hypertriglyceridemia. **2023**, 24, 4279	0
90	Zinc binding of a Cys2His2-type zinc finger protein is enhanced by the interaction with DNA. **2023**, 28, 301-315	1
89	Human Endogenous Retroviruses in Autism Spectrum Disorders: Recent Advances and New Perspectives at the Gene-Environment Interface.	0
88	Gene and schizophrenia in the pregenome and postgenome-wide association studies era: a bibliometric analysis and network visualization. **2023**, 33, 37-49	0
87	LINE-associated cryptic splicing induces dsRNA-mediated interferon response and tumor immunity.	0
86	Sex-based differences in placental DNA methylation profiles related to gestational age: an NIH ECHO meta-analysis. **2023**, 18,	0
85	RNA -mediated heterochromatin formation at repetitive elements in mammals. **2023**, 42,	0
84	Revealing the History and Mystery of RNA-Seq. **2023**, 45, 1860-1874	0
83	Influence of the Mediterranean Diet on Healthy Aging. **2023**, 24, 4491	0
82	Proteomics approaches in the identification of cancer biomarkers and drug discovery. **2023**, 77-120	0
81	Functional genomics of Chlamydomonas reinhardtii. **2023**, 65-84	0
80	cfSNV: a software tool for the sensitive detection of somatic mutations from cell-free DNA.	0
79	Requirements for establishment and epigenetic stability of mammalian heterochromatin.	0
78	Repeat DNA Sequences in Flax Genomes. **2023**, 19-36	0
77	Reference Genome Sequence of Flax. **2023**, 1-17	1
76	Genomes: Molecular Maps of Living Organisms. **2023**, 35-45	0
75	Genetics of psychotic disorders with focus on early-onset psychosis. **2023**, 51-80	0
74	Alternative biological screening methods. **2023**, 95-137	0

73	Computational genomics for understanding of DNA-DNA and protein-protein similarity. **2023**, 217-263	0
72	The discovery of multiple active mys-related LTR-retroelements within the Neotominae subfamily of cricetid rodents.	0
71	A new codon adaptation metric predicts vertebrate body size and tendency to protein disorder.	0
70	Psychotic disorders as a framework for precision psychiatry.	0
69	Prevalent use and evolution of exonic regulatory sequences in the human genome. **2023**, 3,	0
68	Human Lantern Ribozymes: Smallest Known Self-cleaving Ribozymes.	0
67	Whole-Exome Sequencing in Family Trios Reveals De Novo Mutations Associated with Type 1 Diabetes Mellitus. **2023**, 12, 413	0
66	The use of data independent acquisition based proteomic analysis and machine learning to reveal potential biomarkers for autism spectrum disorder. **2023**, 278, 104872	0
65	A Case Report of a Feto-Placental Mosaicism Involving a Segmental Aneuploidy: A Challenge for Genome Wide Screening by Non-Invasive Prenatal Testing of Cell-Free DNA in Maternal Plasma. **2023**, 14, 668	0
64	Human Population Genomics. **2023**, 87-102	0
63	L1 retrotransposons drive human neuronal transcriptome complexity and functional diversification.	0
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60	Strand asymmetries across genomic processes. **2023**, 21, 2036-2047	0
59	Variability in genome-engineering source materials: consider your starting point. **2023**, 8,	0
58	A deep population reference panel of tandem repeat variation.	0
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55	A single base pair duplication inSLC33A1gene causes fetal losses and neonatal lethality in Manech Tête Rousse dairy sheep.	0
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50	A systematic survey of LU domain-containing proteins reveals a novel human gene, LY6A, which encodes the candidate ortholog of mouse Ly-6A/Sca-1 and is aberrantly expressed in pituitary tumors.	0
49	Oncogenic zinc finger protein ZNF687 accelerates lung adenocarcinoma cell proliferation and tumor progression by activating the PI3K / AKT signaling pathway.	0
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46	How to start a LINE : 5? switching rejuvenates LINE retrotransposons in tobacco and related Nicotiana species.	0
45	Thermogenomic Analysis of Left-Handed Z-DNA Propensities in Genomes. **2023**, 195-215	0
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43	Methods to Study Z-DNA-Induced Genetic Instability. **2023**, 227-240	0
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37	Viruses, Microorganisms and Molecular Genetics. **2023**, 9-58	0
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35	Retroelement decay by the exonuclease XRN1 is a viral mimicry dependency in cancer.	0
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30	A Database of Restriction Maps to Expand the Utility of Bacterial Artificial Chromosomes.	0
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28	An Endogenous Retrovirus Vaccine Encoding an Envelope with a Mutated Immunosuppressive Domain in Combination with Anti-PD1 Treatment Eradicates Established Tumours in Mice. **2023**, 15, 926	0
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26	Molecular Diagnosis of Genetic Diseases of the Kidney: Primer for Pediatric Nephrologists. **2023**, 119-169	0
25	Place des outils mol□culaires dans les leuc□mies aigu□ my□o□des en 2023. **2023**, 2023, 52-63	0
24	The Allen Ancient DNA Resource (AADR): A curated compendium of ancient human genomes.	0
23	Transposable elements are associated with the variable response to influenza infection. **2023**, 100292	0
22	Structural RNA components supervise the sequential DNA cleavage in R2 retrotransposon.	0
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9	Evolution of piggyBac Transposons in Apoidea. **2023**, 14, 402	0
8	Detection of long terminal repeat loci derived from endogenous retrovirus in junglefowl using whole-genome sequencing. **2023**, 13,	0
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5	Genetic testing for diffuse lung diseases in children.	0
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1	Introns: the dark matter of the eukaryotic genome. 14,	0