CITATION REPORT List of articles citing



DOI: 10.1093/bioinformatics/btm404 Bioinformatics, 2007, 23, 2947-8.

Source: https://exaly.com/paper-pdf/42303745/citation-report.pdf

Version: 2024-04-09

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Рареі	IF	Citations
2207	Quantitative Proteomic Profiling of Peanut Allergens in Food Ingredients Used for Oral Food Challenges.		
2206	HosA, a MarR Family Transcriptional Regulator, Represses Nonoxidative Hydroxyarylic Acid Decarboxylase Operon and Is Modulated by 4Hydroxybenzoic Acid.		
2205			
2204	Insights into Thiotemplated Pyrrole Biosynthesis Gained from the Crystal Structure of Flavin-Dependent Oxidase in Complex with Carrier Protein.		
2203	Functional and Structural Analyses of the Split-Dehydratase Domain in the Biosynthesis of Macrolactam Polyketide Cremimycin.		
2202	1,4-Dioxane Biodegradation by Mycobacterium dioxanotrophicus PH-06 Is Associated with a Group6 Soluble Di-Iron Monooxygenase.		
2201	Highly Efficient Synthesis of Fructooligosaccharides by Extracellular Fructooligosaccharide-Producing Enzymes and Immobilized Cells of Aspergillus aculeatus M105 and Purification and Biochemical Characterization of a Fructosyltransferase from the Fungus.		
2200	Toward Automatic Rhodopsin Modeling as a Tool for High-Throughput Computational Photobiology.		
2199	Genomic Mushroom Hunting Decrypts Coprinoferrin, A Siderophore Secondary Metabolite Vital to Fungal Cell Development.		
2198	Structure-Based Screening of Uncharted Chemical Space for Atypical Adenosine Receptor Agonists.		
2197			
2196	Biosynthesis of t-Butyl in Apratoxin A: Functional Analysis and Architecture of a PKS Loading Module.		
2195			
2194	Differentiating Physicochemical Properties between Addictive and Nonaddictive ADHD Drugs Revealed by Molecular Dynamics Simulation Studies.		
2193	What Contributes to SerotoninNorepinephrine Reuptake Inhibitors Dual-Targeting Mechanism? The Key Role of Transmembrane Domain 6 in Human Serotonin and Norepinephrine Transporters Revealed by Molecular Dynamics Simulation.		
2192	Discovery and Characterization of 1Aminocyclopropane-1-carboxylic Acid Synthase of Bacterial Origin.		
2191	Discovery, Xray Crystallography and Antiviral Activity of Allosteric Inhibitors of Flavivirus NS2B-NS3 Protease.		

2190	Data-Driven Construction of Antitumor Agents with Controlled Polypharmacology.
2189	High-Resolution Structure and Inhibition of the Schizophrenia-Linked Pseudokinase ULK4.
2188	Molecular Mechanisms of the Bindings between Non-Amyloid Component Oligomers and Amylin Oligomers.
2187	A Phenylpyruvic Acid Reductase Is Required for Biosynthesis of Tropane Alkaloids.
2186	Two Trifunctional Leloir Glycosyltransferases as Biocatalysts for Natural Products Glycodiversification.
2185	pH-Dependent DNA Distortion and Repression of Gene Expression by Pectobacterium atrosepticum PecS.
2184	A Mononuclear Iron-Dependent Methyltransferase Catalyzes Initial Steps in Assembly of the Apratoxin A Polyketide Starter Unit.
2183	Structural Basis of Polyketide Synthase OMethylation.
2182	The Catalytic Mechanism of a Natural DielsAlderase Revealed in Molecular Detail.
2181	Nanomechanical and Thermophoretic Analyses of the Nucleotide-Dependent Interactions between the AAA+ Subunits of Magnesium Chelatase.
2180	Single-Amino Acid Modifications Reveal Additional Controls on the Proton Pathway of [FeFe]-Hydrogenase.
2179	Lipases That Activate at High Solvent Polarities.
2178	•
2177	
2176	Flap Endonuclease 1 Mutations A159V and E160D Cause Genomic Instability by Slowing Reaction on Double-Flap Substrates.
2175	Product Diversity Linked to Substrate Usage in Chain Elongation by Mixed-Culture Fermentation.
2174	Exploring Protein Stability by Comparative Molecular Dynamics Simulations of Homologous Hyperthermophilic, Mesophilic and Psychrophilic Proteins.
2173	Discovery of Selective Inhibitors Targeting Acetylcholinesterase 1 from Disease-Transmitting Mosquitoes.

Thienopyrimidinone Derivatives That Inhibit Bacterial tRNA (Guanine37N1)Methyltransferase (TrmD) by Restructuring the Active Site with a Tyrosine-Flipping Mechanism.

2171	Culturable diversity of Arctic phytoplankton during pack ice melting. 2020 , 8,	
	Molecular epidemiology and phylogenetic analysis of Dengue virus type-1 and 2 isolated in Malaysia. 2015 , 31, 615-20	4
	The maintenance of gestation and the initiation of lactation in the mouse in the absence of pituitary prolactin. 1971 , 27, 121-4	13
2168	River boundaries and species range size in Amazonian primates. 1992 , 140, 531-7	345
2167	Metal Specificity of Metallosensors. 2004 , 1-16	1
	Phylogeny and biogeography of a cosmopolitan frog radiation: Late cretaceous diversification resulted in continent-scale endemism in the family ranidae. 2006 , 55, 579-94	161
2165	The Pfam protein families database. 2008 , 36, D281-8	1806
	Cytotoxic and antiplasmodial substances from marine-derived fungi, Nodulisporium sp. and CRI247-01. 2008 , 69, 2621-6	48
	Survey of repetitive sequences in Silene latifolia with respect to their distribution on sex chromosomes. 2008 , 16, 961-76	79
	Comparison of the backbone dynamics of a natural and a consensus designed 3-TPR domain. 2008 , 41, 169-78	7
2161	New DNA markers for high molecular weight glutenin subunits in wheat. 2008 , 118, 177-83	108
2160	Genome-Wide Analysis of Repetitive Elements in Papaya. 2008 , 1, 191-201	22
	Crystal structures of Lymnaea stagnalis AChBP in complex with neonicotinoid insecticides imidacloprid and clothianidin. 2008 , 8, 71-81	110
2158	Glycogen branching enzyme: a novel deltamethrin resistance-associated gene from Culex pipiens pallens. 2008 , 103, 449-58	10
	Isolation, analysis and marker utility of novel miniature inverted repeat transposable elements from the barley genome. 2008 , 280, 275-85	23
	The artiodactyl APOBEC3 innate immune repertoire shows evidence for a multi-functional domain organization that existed in the ancestor of placental mammals. 2008 , 9, 104	146
2155	The crystal structure of the catalytic domain of a eukaryotic guanylate cyclase. 2008, 8, 42	74

(2008-2008)

2154	The small GTPase RhoH is an atypical regulator of haematopoietic cells. 2008 , 6, 6	26
2153	Stage debut for the elusive Drosophila insulin-like growth factor binding protein. 2008 , 7, 18	6
2152	Structure of the thioredoxin-like domain of yeast glutaredoxin 3. 2008 , 64, 927-32	15
2151	Structure of Deinococcus radiodurans tunicamycin-resistance protein (TmrD), a phosphotransferase. 2008 , 64, 479-86	5
2150	Purification, crystallization and initial crystallographic characterization of the Ginkgo biloba 11S seed globulin ginnacin. 2008 , 64, 641-4	3
2149	Crystallization and preliminary X-ray diffraction analysis of L-threonine dehydrogenase (TDH) from the hyperthermophilic archaeon Thermococcus kodakaraensis. 2008 , 64, 828-30	2
2148	Purification, crystallization and preliminary X-ray diffraction analysis of the CBS-domain pair from the Methanococcus jannaschii protein MJ0100. 2008 , 64, 936-41	4
2147	X-ray crystal structure of a CRISPR-associated protein, Cse2, from Thermus thermophilus HB8. 2008 , 73, 1063-7	22
2146	Crystal structure of an alkaline serine protease from Nesterenkonia sp. defines a novel family of secreted bacterial proteases. 2008 , 73, 1072-5	3
2145	Differential inhibitory activities and stabilisation of DNA aptamers against the SARS coronavirus helicase. 2008 , 9, 3037-45	86
2144	Sex-specific expression of SOX9 during gonadogenesis in the amphibian Xenopus tropicalis. 2008 , 237, 2996-3005	34
2143	Essential role for fibrillin-2 in zebrafish notochord and vascular morphogenesis. 2008 , 237, 2844-61	30
2142	MAP3Ks as central regulators of cell fate during development. 2008 , 237, 3102-14	91
2141	Requirement for a core 1 galactosyltransferase in the Drosophila nervous system. 2008 , 237, 3703-14	31
2140	Essential role for the alpha 1 chain of type VIII collagen in zebrafish notochord formation. 2008 , 237, 3715-26	38
2139	Analysis of binding residues between scorpion neurotoxins and D2 dopamine receptor: a computational docking study. 2008 , 38, 1056-67	6
2138	Classification of proteins based on similarity of two-dimensional protein maps. 2008 , 138, 11-22	4
2137	Substrate promiscuity of pyruvate kinase on various deoxynucleoside diphosphates for synthesis of deoxynucleoside triphosphates. 2008 , 43, 455-459	7

2136	Iron homeostasis strategies in acidophilic iron oxidizers: Studies in Acidithiobacillus and Leptospirillum. 2008 , 94, 175-179	11
2135	Comparative genome analysis of a Saccharomyces cerevisiae wine strain. 2008 , 8, 1185-95	124
2134	Human haptoglobin structure and functiona molecular modelling study. 2008 , 275, 5648-56	67
2133	Functional analysis of the aglycone-binding site of the maize beta-glucosidase Zm-p60.1. 2008 , 275, 6123-35	14
2132	Expression levels of FAS are regulated through an evolutionary conserved element in intron 2, which modulates cystic fibrosis disease severity. 2008 , 9, 689-96	19
2131	A discontinuous hammerhead ribozyme embedded in a mammalian messenger RNA. 2008 , 454, 899-902	142
2130	Identification of Holliday junction resolvases from humans and yeast. 2008 , 456, 357-61	307
2129	PhosphoPepa database of protein phosphorylation sites in model organisms. 2008, 26, 1339-40	178
2128	The detection of possible sensor histidine kinases regulating citrate/malate metabolism from the bovine rumen microbial ecosystem. 2008 , 47, 462-6	4
2127	Predominance of Gram-positive bacteria in house dust in the low-allergy risk Russian Karelia. 2008 , 10, 3317-25	98
2126	The tryptophan aminotransferase Tam1 catalyses the single biosynthetic step for tryptophan-dependent pigment synthesis in Ustilago maydis. 2008 , 68, 152-72	45
2125	Neutralizing activity of antibodies to the V3 loop region of HIV-1 gp120 relative to their epitope fine specificity. 2008 , 381, 251-60	50
2124	SciDBMaker: new software for computer-aided design of specialized biological databases. 2008 , 9, 121	14
2123	Improved accuracy of multiple ncRNA alignment by incorporating structural information into a MAFFT-based framework. 2008 , 9, 212	434
2122	In silico analysis of methyltransferase domains involved in biosynthesis of secondary metabolites. 2008 , 9, 454	65
2121	RIPCAL: a tool for alignment-based analysis of repeat-induced point mutations in fungal genomic sequences. 2008 , 9, 478	120
2120	Genomic organization of zebrafish microRNAs. 2008 , 9, 253	53
2119	Promoter-sharing by different genes in human genomeCPNE1 and RBM12 gene pair as an example. 2008 , 9, 456	18

2118	Phylogenetic distribution and membrane topology of the LytR-CpsA-Psr protein family. 2008, 9, 617	56
2117	PrimerSNP: a web tool for whole-genome selection of allele-specific and common primers of phylogenetically-related bacterial genomic sequences. 2008 , 8, 185	1
2116	Microbial iron management mechanisms in extremely acidic environments: comparative genomics evidence for diversity and versatility. 2008 , 8, 203	43
2115	Genomic analysis of bacteriophage epsilon 34 of Salmonella enterica serovar Anatum (15+). 2008 , 8, 227	31
2114	Assessment of genetic and functional diversity of phosphate solubilizing fluorescent pseudomonads isolated from rhizospheric soil. 2008 , 8, 230	120
2113	IgTree: creating Immunoglobulin variable region gene lineage trees. 2008, 338, 67-74	80
2112	Core structure of the yeast spt4-spt5 complex: a conserved module for regulation of transcription elongation. 2008 , 16, 1649-58	51
2111	Evolutionary analysis of the transferrin gene in Antarctic Notothenioidei: A history of adaptive evolution and functional divergence. 2008 , 1, 95-101	4
2110	Acidophilic haloarchaeal strains are isolated from various solar salts. 2008 , 4, 16	25
2109	Absence of Wolbachia endobacteria in the non-filariid nematodes Angiostrongylus cantonensis and A. costaricensis. 2008 , 1, 31	15
2108	The haem-copper oxygen reductase of Desulfovibrio vulgaris contains a dihaem cytochrome c in subunit II. 2008 , 1777, 1528-34	16
2107	Evolutionary and structural analyses of alpha-papillomavirus capsid proteins yields novel insights into L2 structure and interaction with L1. 2008 , 5, 150	22
2106	Bioinformatic analysis suggests that the Orbivirus VP6 cistron encodes an overlapping gene. 2008 , 5, 48	40
2105	The Groucho/TLE/Grg family of transcriptional co-repressors. 2008 , 9, 205	116
2104	The C-terminal half of the HrpN virulence protein of the fire blight pathogen Erwinia amylovora is essential for its secretion and for its virulence and avirulence activities. 2008 , 21, 1387-97	14
2103	Computational studies reveal phosphorylation-dependent changes in the unstructured R domain of CFTR. 2008 , 378, 1052-63	48
2102	Structural and functional studies of the Rap1 C-terminus reveal novel separation-of-function mutants. 2008 , 380, 520-31	30
2101	Solution structure of the C-terminal nucleoprotein-RNA binding domain of the vesicular stomatitis virus phosphoprotein. 2008 , 382, 525-38	57

2100	Crystal structure of the NanB sialidase from Streptococcus pneumoniae. 2008, 384, 436-49	66
2099	The structure of monoamine oxidase from Aspergillus niger provides a molecular context for improvements in activity obtained by directed evolution. 2008 , 384, 1218-31	70
2098	Structural and functional diversity of ferredoxin-NADP(+) reductases. 2008, 474, 283-91	113
2097	A novel serine protease from the snake venom of Agkistrodon blomhoffii ussurensis. 2008 , 52, 760-8	17
2096	Isolation, characterization and cloning of a cDNA encoding a new antifungal defensin from Phaseolus vulgaris L. seeds. 2008 , 29, 2090-100	55
2095	Molecular cloning, sequencing and characterization of channel catfish (Ictalurus punctatus, Rafinesque 1818) cathepsin S gene. 2008 , 126, 382-7	22
2094	Molecular epidemiology of rabies in Indonesia. 2008 , 135, 144-9	31
2093	Evolutionary conservation of human drug targets in organisms used for environmental risk assessments. 2008 , 42, 5807-13	412
2092	PHL1 of Cercospora zeae-maydis encodes a member of the photolyase/cryptochrome family involved in UV protection and fungal development. 2008 , 45, 1364-72	44
2091	Motif analysis of amphioxus, lamprey and invertebrate estrogen receptors: toward a better understanding of estrogen receptor evolution. 2008 , 371, 724-8	11
2090	A fatty acid elongase ELO with novel activity from Dictyostelium discoideum. 2008 , 374, 226-30	7
2089	Identification and characterization of mouse plexin B3 promoter. 2008 , 375, 11-5	1
2088	Trichoplax, the simplest known animal, contains an estrogen-related receptor but no estrogen receptor: Implications for estrogen receptor evolution. 2008 , 375, 623-7	33
2087	Mitochondrial 12S rRNA susceptibility mutations in aminoglycoside-associated and idiopathic bilateral vestibulopathy. 2008 , 377, 379-383	19
2086	Expression study of an alpha-l-fucosidase gene in the Drosophilidae family. 2008 , 420, 23-33	11
2085	Molecular cloning and sequencing of metallothionein in squamates: new insights into the evolution of the metallothionein genes in vertebrates. 2008 , 423, 48-56	18
2084	Comparative analysis of Xenopus tropicalis hepcidin I and hepcidin II genes. 2008, 426, 91-7	11
2083	Phospholipases A(2) in the genome of the sea anemone Nematostella vectensis. 2008 , 3, 226-33	10

(2008-2008)

2082	pallens. 2008 , 151, 230-5	15
2081	Structure, mechanism and regulation of pyruvate carboxylase. 2008 , 413, 369-87	299
2080	The N-clasp of human DNA polymerase kappa promotes blockage or error-free bypass of adenine-or guanine-benzo[a]pyrenyl lesions. 2008 , 36, 6571-84	39
2079	Protein-DNA interactions: structural, thermodynamic and clustering patterns of conserved residues in DNA-binding proteins. 2008 , 36, 5922-32	67
2078	Multiplex mass spectrometric genotyping of single nucleotide polymorphisms employing pyrrolidinyl peptide nucleic acid in combination with ion-exchange capture. 2008 , 80, 8178-86	32
2077	Aryl acid adenylating enzymes involved in siderophore biosynthesis: fluorescence polarization assay, ligand specificity, and discovery of non-nucleoside inhibitors via high-throughput screening. 2008 , 47, 11735-49	37
2076	Molecular engineering of conotoxins: the importance of loop size to alpha-conotoxin structure and function. 2008 , 51, 5575-84	28
2075	Molecular cloning and characterization of a candidate human growth-related and time-keeping constitutive cell surface hydroquinone (NADH) oxidase. 2008 , 47, 14028-38	37
2074	A PAS domain with an oxygen labile [4Fe-4S](2+) cluster in the oxygen sensor kinase NreB of Staphylococcus carnosus. 2008 , 47, 13921-32	42
2073	NMR studies of a heterotypic Sam-Sam domain association: the interaction between the lipid phosphatase Ship2 and the EphA2 receptor. 2008 , 47, 12721-8	52
2072	Characterization of the microbial community and polyketide biosynthetic potential in the palmerolide-producing tunicate Synoicum adareanum. 2008 , 71, 1812-8	45
2071	Caenorhabditis elegans gelsolin-like protein 1 is a novel actin filament-severing protein with four gelsolin-like repeats. 2008 , 283, 26071-80	22
2070	Residues in the HIV-1 capsid assembly inhibitor binding site are essential for maintaining the assembly-competent quaternary structure of the capsid protein. 2008 , 283, 32024-33	64
2069	Temperature sensitivity and cell division defects in an Escherichia coli strain with mutations in yghB and yqjA, encoding related and conserved inner membrane proteins. 2008 , 190, 4489-500	40
2068	PilF is an outer membrane lipoprotein required for multimerization and localization of the Pseudomonas aeruginosa Type IV pilus secretin. 2008 , 190, 6961-9	81
2067	Comparative Genomics. 2008,	2
2066	The Cryptococcus neoformans Rho-GDP dissociation inhibitor mediates intracellular survival and virulence. 2008 , 76, 5729-37	38
2065	BCR-ABL alternative splicing as a common mechanism for imatinib resistance: evidence from molecular dynamics simulations. 2008 , 7, 3834-41	52

2064	Construction of a rice glycosyltransferase phylogenomic database and identification of rice-diverged glycosyltransferases. 2008 , 1, 858-77	77
2063	Functional characterization of the plastidic phosphate translocator gene family from the thermo-acidophilic red alga Galdieria sulphuraria reveals specific adaptations of primary carbon partitioning in green plants and red algae. 2008 , 148, 1487-96	34
2062	The natural history of the myelin-derived nerve growth inhibitor Nogo-A. 2008 , 4, 83-9	12
2061	Nested Patch PCR enables highly multiplexed mutation discovery in candidate genes. 2008, 18, 1844-50	49
2060	The Plant Cytoskeleton: a Key Tool for Agro-Biotechnology. 2008,	15
2059	Evolution of CCR5 use before and during coreceptor switching. 2008, 82, 11758-66	34
2058	Crystal structure of the Thermus thermophilus 16 S rRNA methyltransferase RsmC in complex with cofactor and substrate guanosine. 2008 , 283, 26548-56	19
2057	A conserved arginine-containing motif crucial for the assembly and enzymatic activity of the mixed lineage leukemia protein-1 core complex. 2008 , 283, 32162-75	131
2056	A novel, evolutionarily conserved enhancer of cone photoreceptor-specific expression. 2008 , 283, 10881-91	11
2055	RcoM: a new single-component transcriptional regulator of CO metabolism in bacteria. 2008 , 190, 3336-43	49
2054	Molecular cloning and expression of the CRISP family of proteins in the boar. 2008 , 79, 1129-34	16
2053	Specific alignment of structured RNA: stochastic grammars and sequence annealing. <i>Bioinformatics</i> , 2008 , 24, 2677-83	31
2052	The major amino acid transporter superfamily has a similar core structure as Na+-galactose and Na+-leucine transporters. 2008 , 25, 567-70	35
2051	Classification, expression pattern, and E3 ligase activity assay of rice U-box-containing proteins. 2008 , 1, 800-15	93
2050	Incompatibilities involving yeast mismatch repair genes: a role for genetic modifiers and implications for disease penetrance and variation in genomic mutation rates. 2008 , 4, e1000103	30
2049	Identification of ancient remains through genomic sequencing. 2008, 18, 1347-53	46
2048	Implications of the binding of tamoxifen to the coactivator recognition site of the estrogen receptor. 2008 , 15, 851-70	46
2047	Comprehensive analysis of archaeal tRNA genes reveals rapid increase of tRNA introns in the order thermoproteales. 2008 , 25, 2709-16	55

(2008-2008)

2046	2008, 46, 2435-7	15
2045	Recent developments in the MAFFT multiple sequence alignment program. 2008 , 9, 286-98	2702
2044	Arabidopsis ARC6 coordinates the division machineries of the inner and outer chloroplast membranes through interaction with PDV2 in the intermembrane space. 2008 , 20, 2460-70	101
2043	The Helicobacter pylori HpyAXII restriction-modification system limits exogenous DNA uptake by targeting GTAC sites but shows asymmetric conservation of the DNA methyltransferase and restriction endonuclease components. 2008 , 36, 6893-906	39
2042	High and low temperatures differently affect infection density and vertical transmission of male-killing Spiroplasma symbionts in Drosophila hosts. 2008 , 74, 6053-9	53
2041	Standard and generalized McDonald-Kreitman test: a website to detect selection by comparing different classes of DNA sites. 2008 , 36, W157-62	101
2040	Novel astroviruses in insectivorous bats. 2008 , 82, 9107-14	205
2039	Maternal control of male-gamete delivery in Arabidopsis involves a putative GPI-anchored protein encoded by the LORELEI gene. 2008 , 20, 3038-49	137
2038	A core paired-type and POU homeodomain-containing transcription factor program drives retinal bipolar cell gene expression. 2008 , 28, 7748-64	88
2037	Independent losses of function in a polyphenol oxidase in rice: differentiation in grain discoloration between subspecies and the role of positive selection under domestication. 2008 , 20, 2946-59	58
2036	Dolichyl-phosphate-glucose is used to make O-glycans on glycoproteins of Trichomonas vaginalis. 2008 , 7, 1344-51	11
2035	Dlx genes pattern mammalian jaw primordium by regulating both lower jaw-specific and upper jaw-specific genetic programs. 2008 , 135, 2905-16	102
2034	Etiologic study of upper respiratory infections of household dogs. 2008 , 70, 563-9	52
2033	Global sequencing: a review of current molecular data and new methods available to assess microbial diversity. 2008 , 23, 253-68	58
2032	The Metal-Dependent Regulators FurA and FurB from Mycobacterium Tuberculosis. 2008 , 9, 1548-60	23
2031	The bacterial symbiont Wolbachia induces resistance to RNA viral infections in Drosophila melanogaster. 2008 , 6, e2	807
2030	Species specificity in major urinary proteins by parallel evolution. 2008 , 3, e3280	114
2029	Differentially evolved genes of Salmonella pathogenicity islands: insights into the mechanism of host specificity in Salmonella. 2008 , 3, e3829	40

2028	A nitrile hydratase in the eukaryote Monosiga brevicollis. 2008 , 3, e3976	21
2027	Phylogenetic analyses: A toolbox expanding towards Bayesian methods. 2008 , 2008, 683509	5
2026	Trichoplax, the simplest known animal, contains an estrogen-related receptor: Implications for the evolution of vertebrate and invertebrate estrogen receptors. 2008 ,	
2025	Trichoplax, the simplest known animal, contains an estrogen-related receptor but no estrogen receptor: Implications for estrogen receptor evolution. 2008 ,	
2024	Prediction of Functional Sites in SCOP Domains using Dynamics Perturbation Analysis. 2008,	1
2023	Grania (Annelida: Clitellata: Enchytraeidae) of the Great Barrier Reef, Australia, including four new species and a re-description of Grania trichaeta Jamieson, 1977. 2009 , 2165, 16-38	7
2022	Morphological disparity despite genetic similarity; new species of Lobosorchis Miller & amp; Cribb, 2005 (Digenea: Cryptogonimidae) from the Great Barrier Reef and the Maldives. 2009 , 1992, 37-52	21
2021	The intracellular domain of the low affinity p75 nerve growth factor receptor is a death effector domain. 2009 , 2, 539-41	5
2020	Anoctamin and transmembrane channel-like proteins are evolutionarily related. 2009, 24, 51-5	30
2019	A male-specific odorant receptor conserved through the evolution of sex pheromones in Ostrinia moth species. 2009 , 5, 319-30	57
2018	Characteristics of a Microcystin-Degrading Bacterium under Alkaline Environmental Conditions. 2009 , 2009, 954291	43
2017	Genomic signatures of influenza A pandemic (H1N1) 2009 virus. 2009 , 15, 1897-1903	55
2016	Unusual armadillo fold in the human general vesicular transport factor p115. 2009 , 4, e4656	20
2015	A novel puf-A gene predicted from evolutionary analysis is involved in the development of eyes and primordial germ-cells. 2009 , 4, e4980	28
2014	Panorama phylogenetic diversity and distribution of Type A influenza virus. 2009 , 4, e5022	74
2013	Dll1 haploinsufficiency in adult mice leads to a complex phenotype affecting metabolic and immunological processes. 2009 , 4, e6054	12
2012	Immunogenic Burkholderia pseudomallei outer membrane proteins as potential candidate vaccine targets. 2009 , 4, e6496	65
2011	A family of diverse Kunitz inhibitors from Echinococcus granulosus potentially involved in host-parasite cross-talk. 2009 , 4, e7009	30

2010	Comparative sequence and structural analyses of G-protein-coupled receptor crystal structures and implications for molecular models. 2009 , 4, e7011	63
2009	Analysis of blood stem cell activity and cystatin gene expression in a mouse model presenting a chromosomal deletion encompassing Csta and Stfa2l1. 2009 , 4, e7500	12
2008	Evolutionary trends of A(H1N1) influenza virus hemagglutinin since 1918. 2009 , 4, e7789	60
2007	Haplotype distribution and evolutionary pattern of miR-17 and miR-124 families based on population analysis. 2009 , 4, e7944	24
2006	Dissecting the role of critical residues and substrate preference of a Fatty Acyl-CoA Synthetase (FadD13) of Mycobacterium tuberculosis. 2009 , 4, e8387	21
2005	Evolutionary descent of prion genes from a ZIP metal ion transport ancestor. 2009,	0
2004	Exserohilum Leaf Spot on Tiger Grass. 2009 , 10, 1	10
2003	Broadly reactive pan-paramyxovirus reverse transcription polymerase chain reaction and sequence analysis for the detection of Canine distemper virus in a case of canine meningoencephalitis of unknown etiology. 2009 , 21, 844-9	14
2002	Reverse transcription loop-mediated isothermal amplification for the detection of Porcine reproductive and respiratory syndrome virus. 2009 , 21, 350-4	18
2001	Pup, a prokaryotic ubiquitin-like protein, is an intrinsically disordered protein. 2009 , 422, 207-15	83
2000	Genome-wide identification, structure and expression studies, and mutant collection of 22 early nodulin-like protein genes in Arabidopsis. 2009 , 73, 2452-9	44
1999	Component Vector method and Its Application in Detecting Similarities between Sequences. 2009,	
1998	The three-dimensional structure of carnocyclin A reveals that many circular bacteriocins share a common structural motif. 2009 , 284, 28674-81	69
1997	Ethylene regulates phosphorus remobilization and expression of a phosphate transporter (PhPT1) during petunia corolla senescence. 2009 , 60, 2179-90	54
1996	[FeFe] hydrogenase genetic diversity provides insight into molecular adaptation in a saline microbial mat community. 2009 , 75, 4620-3	45
1995	Ana3 is a conserved protein required for the structural integrity of centrioles and basal bodies. 2009 , 187, 355-63	37
1994	Mapping of disulfide bonds within the amino-terminal extracellular domain of the inhibitory glycine receptor. 2009 , 284, 36128-36136	12
1993	Amino acid changes in elongation factor Tu of Mycoplasma pneumoniae and Mycoplasma genitalium influence fibronectin binding. 2009 , 77, 3533-41	33

1992	Arabidopsis GRI is involved in the regulation of cell death induced by extracellular ROS. 2009, 106, 5412-7	54
1991	Structural and functional studies of the Thermus thermophilus 16S rRNA methyltransferase RsmG. 2009 , 15, 1693-704	13
1990	Phage T4 mobE promotes trans homing of the defunct homing endonuclease I-TevIII. 2009, 37, 7110-23	13
1989	Solution structure of eggcase silk protein and its implications for silk fiber formation. 2009 , 106, 8906-11	75
1988	Toward effective HIV vaccination: induction of binary epitope reactive antibodies with broad HIV neutralizing activity. 2009 , 284, 30627-42	13
1987	AID can restrict L1 retrotransposition suggesting a dual role in innate and adaptive immunity. 2009 , 37, 1854-67	55
1986	Structure, expression, and biological function of INSM1 transcription factor in neuroendocrine differentiation. 2009 , 23, 2024-33	100
1985	The CELLULOSE-SYNTHASE LIKE C (CSLC) family of barley includes members that are integral membrane proteins targeted to the plasma membrane. 2009 , 2, 1025-39	32
1984	PLecDom: a program for identification and analysis of plant lectin domains. 2009 , 37, W452-8	7
1983	Sulfolobus tokodaii ST0053 produces a novel thermostable, NAD-dependent medium-chain alcohol dehydrogenase. 2009 , 75, 1758-63	11
1982	Allelic diversities in rice starch biosynthesis lead to a diverse array of rice eating and cooking qualities. 2009 , 106, 21760-5	354
1981	Molecular basis for Bcl-2 homology 3 domain recognition in the Bcl-2 protein family: identification of conserved hot spot interactions. 2009 , 284, 17499-511	20
1980	Characterization of arrangement and expression of the T cell receptor gamma locus in the sandbar shark. 2009 , 106, 8591-6	48
1979	Testing taxonomic boundaries and the limit of DNA barcoding in the Siberian sturgeon, Acipenser baerii. 2009 , 20, 110-8	13
1978	Penicillin-binding protein 7/8 contributes to the survival of Acinetobacter baumannii in vitro and in vivo. 2009 , 199, 513-21	68
1977	Delftia lacustris sp. nov., a peptidoglycan-degrading bacterium from fresh water, and emended description of Delftia tsuruhatensis as a peptidoglycan-degrading bacterium. 2009 , 59, 2195-9	62
1976	Arabidopsis L-type lectin receptor kinases: phylogeny, classification, and expression profiles. 2009 , 60, 4383-96	132
1975	The p.Arg258Gly mutation in intracellular loop 2 of CFTR is associated with CFTR-related disorders. 2009 , 13, 765-8	3

1974	First records of mermithid nematodes (Nematoda: Mermithidae) parasitising stick insects (Insecta: Phasmatodea). 2009 , 36, 35-39	9
1973	A highly conserved retinoic acid responsive element controls wt1a expression in the zebrafish pronephros. 2009 , 136, 2883-92	72
1972	Functional analysis of alpha-DOX2, an active alpha-dioxygenase critical for normal development in tomato plants. 2009 , 151, 1421-32	30
1971	The laminin-binding protein Lbp from Streptococcus pyogenes is a zinc receptor. 2009 , 191, 5814-23	49
1970	ACC (1-aminocyclopropane-1-carboxylate) deaminase activity, a widespread trait in Burkholderia species, and its growth-promoting effect on tomato plants. 2009 , 75, 6581-90	160
1969	Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic Vibrio cholerae. 2009 , 106, 15442-7	297
1968	Neisseria meningitidis antigen NMB0088: sequence variability, protein topology and vaccine potential. 2009 , 58, 196-208	16
1967	Three-dimensional structure of CaV3.1: comparison with the cardiac L-type voltage-gated calcium channel monomer architecture. 2009 , 284, 22310-22321	39
1966	CO(2) uptake and fixation by a thermoacidophilic microbial community attached to precipitated sulfur in a geothermal spring. 2009 , 75, 4289-96	50
1965	Characterization of sulfoxygenation and structural implications of human flavin-containing monooxygenase isoform 2 (FMO2.1) variants S195L and N413K. 2009 , 37, 1785-91	9
1964	Repeat-associated plasticity in the Helicobacter pylori RD gene family. 2009, 191, 6900-10	8
1963	Gem-1 encodes an SLC16 monocarboxylate transporter-related protein that functions in parallel to the gon-2 TRPM channel during gonad development in Caenorhabditis elegans. 2009 , 181, 581-91	11
1962	Influence of heterologous MreB proteins on cell morphology of Bacillus subtilis. 2009, 155, 3611-3621	19
1961	Two variants of staphylococcal cassette chromosome mec type IVA in community-associated meticillin-resistant Staphylococcus aureus strains in South Korea. 2009 , 58, 1314-1321	5
1960	Identification of the determinant conferring permissive substrate usage in the telomere resolvase, ResT. 2009 , 284, 23293-301	12
1959	MAp44, a human protein associated with pattern recognition molecules of the complement system and regulating the lectin pathway of complement activation. 2009 , 183, 7371-8	146
1958	Characterization of Nda2, a plastoquinone-reducing type II NAD(P)H dehydrogenase in chlamydomonas chloroplasts. 2009 , 284, 4148-57	116
1957	Molecular basis of coiled coil coactivator recruitment by the aryl hydrocarbon receptor nuclear translocator (ARNT). 2009 , 284, 15184-92	26
	· · · · · · · · · · · · · · · · · · ·	

1956	The divalent metal transporter homologues SMF-1/2 mediate dopamine neuron sensitivity in caenorhabditis elegans models of manganism and parkinson disease. 2009 , 284, 35758-68	80
1955	Identification of sequences in the polysialyltransferases ST8Sia II and ST8Sia IV that are required for the protein-specific polysialylation of the neural cell adhesion molecule, NCAM. 2009 , 284, 15505-16	40
1954	Two lysine residues in the bacterial luciferase mobile loop stabilize reaction intermediates. 2009 , 284, 32827-34	17
1953	Structure of PhnP, a phosphodiesterase of the carbon-phosphorus lyase pathway for phosphonate degradation. 2009 , 284, 17216-17226	31
1952	Crystal structure of Epiphyas postvittana takeout 1 with bound ubiquinone supports a role as ligand carriers for takeout proteins in insects. 2009 , 284, 3496-503	38
1951	Lipoic acid synthesis and attachment in yeast mitochondria. 2009 , 284, 23234-42	84
1950	The gad2 promoter is a transcriptional target of estrogen receptor (ER)alpha and ER beta: a unifying hypothesis to explain diverse effects of estradiol. 2009 , 29, 8790-7	40
1949	A 25-amino acid sequence of the Arabidopsis TGD2 protein is sufficient for specific binding of phosphatidic acid. 2009 , 284, 17420-7	55
1948	Structural and mechanistic studies of a stabilized subunit dimer variant of Escherichia coli bacterioferritin identify residues required for core formation. 2009 , 284, 18873-81	19
1947	Expression of PIN genes in rice (Oryza sativa L.): tissue specificity and regulation by hormones. 2009 , 2, 823-831	140
1946	Novel mitochondrial complex II isolated from Trypanosoma cruzi is composed of 12 peptides including a heterodimeric Ip subunit. 2009 , 284, 7255-63	42
1945	In vivo mutational analysis of YtvA from Bacillus subtilis: mechanism of light activation of the general stress response. 2009 , 284, 24958-64	62
1944	Anaerobic respiration of elemental sulfur and thiosulfate by Shewanella oneidensis MR-1 requires psrA, a homolog of the phsA gene of Salmonella enterica serovar typhimurium LT2. 2009 , 75, 5209-17	93
1943	A chloroplastic UDP-glucose pyrophosphorylase from Arabidopsis is the committed enzyme for the first step of sulfolipid biosynthesis. 2009 , 21, 892-909	174
1942	Detection of 140 clinically relevant antibiotic-resistance genes in the plasmid metagenome of wastewater treatment plant bacteria showing reduced susceptibility to selected antibiotics. 2009 , 155, 2306-2319	330
1941	A sulfilimine bond identified in collagen IV. 2009 , 325, 1230-4	161
1940	Total ERK1/2 activity regulates cell proliferation. 2009 , 8, 705-11	73
1939	Nephrin mutations cause childhood- and adult-onset focal segmental glomerulosclerosis. 2009 , 76, 1268-76	92

1938	Myosin XI is required for actin-associated movement of plastid stromules. 2009 , 2, 1262-72	57
1937	Role of Acinetobacter baylyi Crc in catabolite repression of enzymes for aromatic compound catabolism. 2009 , 191, 2834-42	26
1936	Analysis of ColE1 MbeC unveils an extended ribbon-helix-helix family of nicking accessory proteins. 2009 , 191, 1446-55	30
1935	Binding Mode Analysis of Bacillus subtilis Obg with Ribosomal Protein L13 through Computational Docking Study. 2009 , 1, 9-14	1
1934	Morphology, molecular characterisation and systematic position of Hemiplectus muscorum Zell, 1991 (Nematoda: Plectida). 2009 , 11, 719-737	2
1933	Role of gluconic acid production in the regulation of biocontrol traits of Pseudomonas fluorescens CHA0. 2009 , 75, 4162-74	140
1932	Production of the phytohormone indole-3-acetic acid by estuarine species of the genus Vibrio. 2009 , 75, 2253-8	56
1931	Function, regulation, and transcriptional organization of the hemin utilization locus of Bartonella quintana. 2009 , 77, 307-16	30
1930	Interplay between two RND systems mediating antimicrobial resistance in Brucella suis. 2009 , 191, 2530-40	21
1929	Upstream regulatory region alterations found in human papillomavirus type 16 (HPV-16) isolates from cervical carcinomas increase transcription, ori function, and HPV immortalization capacity in culture. 2009 , 83, 7457-66	37
1928	Plant virus cell-to-cell movement is not dependent on the transmembrane disposition of its movement protein. 2009 , 83, 5535-43	34
1927	Streptomyces thinghirensis sp. nov., isolated from rhizosphere soil of Vitis vinifera. 2009 , 59, 3063-7	7
1926	Phylogenetic Analysis of Four Vibrio Strains of Pathogenic Bacteria Based on Hemolysin Genes and 16S rRNA Genes. 2009 ,	O
1925	Protinfo PPC: a web server for atomic level prediction of protein complexes. 2009 , 37, W519-25	20
1924	Common introns within orthologous genes: software and application to plants. 2009 , 10, 631-44	26
1923	Crystal structure of the conserved N-terminal domain of the peroxisomal matrix protein import receptor, Pex14p. 2009 , 106, 417-21	29
1922	Conserved waters mediate structural and functional activation of family A (rhodopsin-like) G protein-coupled receptors. 2009 , 106, 8555-60	201
1921	Cold adaptation of zinc metalloproteases in the thermolysin family from deep sea and arctic sea ice bacteria revealed by catalytic and structural properties and molecular dynamics: new insights into relationship between conformational flexibility and hydrogen bonding. 2009 , 284, 9257-69	57

1920	In silico prediction of horizontal gene transfer events in Lactobacillus bulgaricus and Streptococcus thermophilus reveals protocooperation in yogurt manufacturing. 2009 , 75, 4120-9	56
1919	The final step of hygromycin A biosynthesis, oxidation of C-5"-dihydrohygromycin A, is linked to a putative proton gradient-dependent efflux. 2009 , 53, 5163-72	6
1918	Surface colonization by marine roseobacters: integrating genotype and phenotype. 2009 , 75, 6027-37	102
1917	Identification of Amazonian trees with DNA barcodes. 2009 , 4, e7483	152
1916	Hepatitis C virus NS2 protein contributes to virus particle assembly via opposing epistatic interactions with the E1-E2 glycoprotein and NS3-NS4A enzyme complexes. 2009 , 83, 8379-95	109
1915	Egyptian glycogen storage disease type III - identification of six novel AGL mutations, including a large 1.5 kb deletion and a missense mutation p.L620P with subtype IIId. 2009 , 47, 1233-8	8
1914	Intra-tumor heterogeneity of MLH1 promoter methylation revealed by deep single molecule bisulfite sequencing. 2009 , 37, 4603-12	59
1913	The ESCRT-related CHMP1A and B proteins mediate multivesicular body sorting of auxin carriers in Arabidopsis and are required for plant development. 2009 , 21, 749-66	165
1912	NAD biosynthesis evolution in bacteria: lateral gene transfer of kynurenine pathway in Xanthomonadales and Flavobacteriales. 2009 , 26, 399-406	36
1911	Inactivation of PadR, the repressor of the phenolic acid stress response, by molecular interaction with Usp1, a universal stress protein from Lactobacillus plantarum, in Escherichia coli. 2009 , 75, 5273-83	34
1910	Patterns of variation in the evolution of carotenoid biosynthetic pathway enzymes of higher plants. 2009 , 100, 754-61	38
1909	Butyricimonas synergistica gen. nov., sp. nov. and Butyricimonas virosa sp. nov., butyric acid-producing bacteria in the family 'Porphyromonadaceae' isolated from rat faeces. 2009 , 59, 1748-53	92
1908	A novel role for Gtb1p in glucose trimming of N-linked glycans. 2009 , 19, 1408-16	15
1907	A comprehensive classification and evolutionary analysis of plant homeobox genes. 2009 , 26, 2775-94	248
1906	The modular architecture of meningococcal factor H-binding protein. 2009 , 155, 2873-2883	59
1905	Actinomyces hyovaginalis-associated lymphadenitis in a Nubian goat. 2009 , 21, 380-4	7
1904	A preliminary phylogeny of the 'didymocarpoid Gesneriaceae' based on three molecular data sets: Incongruence with available tribal classifications. 2009 , 96, 989-1010	57
1903	Origin, evolution and taxonomy of American Roccella (Roccellaceae, Ascomycetes). 2009 , 7, 307-317	18

1902	Properties of cytochrome bd plastoquinol oxidase from the cyanobacterium Synechocystis sp. PCC 6803. 2009 , 145, 395-401	17
1901	An Mrr-family nuclease motif in the single polypeptide restriction-modification enzyme LlaGI. 2009 , 37, 7231-8	10
1900	The barley magnesium chelatase 150-kd subunit is not an abscisic acid receptor. 2009 , 150, 157-66	80
1899	Proteomic identification and characterization of a novel peroxisomal adenine nucleotide transporter supplying ATP for fatty acid beta-oxidation in soybean and Arabidopsis. 2008 , 20, 3227-40	71
1898	Structural basis for the inhibition of human 5,10-methenyltetrahydrofolate synthetase by N10-substituted folate analogues. 2009 , 69, 7294-301	9
1897	Distinct Kinesin-14 mitotic mechanisms in spindle bipolarity. 2009 , 8, 3571-83	13
1896	The Yfr2 ncRNA family, a group of abundant RNA molecules widely conserved in cyanobacteria. 2009 , 6, 222-7	23
1895	Hormone-activated estrogen receptors in annelid invertebrates: implications for evolution and endocrine disruption. 2009 , 150, 1731-8	92
1894	Interrogating and predicting tolerated sequence diversity in protein folds: application to E. elaterium trypsin inhibitor-II cystine-knot miniprotein. 2009 , 5, e1000499	23
1893	Genotype distribution and sequence variation of hepatitis E virus, Hong Kong. 2009 , 15, 792-4	12
1892	Pseudomonas brassicacearum subsp. neoaurantiaca subsp. nov., orange-pigmented bacteria isolated from soil and the rhizosphere of agricultural plants. 2009 , 59, 2476-81	13
1891	Computational resources for protein modelling and drug discovery applications. 2009 , 9, 557-62	3
1890	KlAft, the Kluyveromyces lactis ortholog of Aft1 and Aft2, mediates activation of iron-responsive transcription through the PuCACCC Aft-type sequence. 2009 , 183, 93-106	19
1889	Molecular mimicry: an important virulence strategy employed by Legionella pneumophila to subvert host functions. 2009 , 4, 691-701	40
1888	The difficulty of avoiding false positives in genome scans for natural selection. 2009 , 19, 922-33	60
1887	Auxin-responsive genes AIR12 code for a new family of plasma membrane b-type cytochromes specific to flowering plants. 2009 , 150, 606-20	29
1886	Molecular evolution of the junctophilin gene family. 2009 , 37, 175-86	60
1885	HistoneHits: a database for histone mutations and their phenotypes. 2009 , 19, 674-81	42

1884	A new protein motif extraction framework based on constrained co-clustering. 2009,	3
1883	Factor VIII-von Willebrand factor complex inhibits osteoclastogenesis and controls cell survival. 2009 , 284, 31704-13	45
1882	Multiple antibiotic resistance in Arabidopsis is conferred by mutations in a chloroplast-localized transport protein. 2009 , 151, 559-73	57
1881	The transcriptional regulator Rv0485 modulates the expression of a pe and ppe gene pair and is required for Mycobacterium tuberculosis virulence. 2009 , 77, 4654-67	31
1880	Disease-causing 7.4 kb cis-regulatory deletion disrupting conserved non-coding sequences and their interaction with the FOXL2 promotor: implications for mutation screening. 2009 , 5, e1000522	76
1879	Genomic survey of the non-cultivatable opportunistic human pathogen, Enterocytozoon bieneusi. 2009 , 5, e1000261	105
1878	Sequence-based prediction of type III secreted proteins. 2009 , 5, e1000376	194
1877	Molecular decay of the tooth gene Enamelin (ENAM) mirrors the loss of enamel in the fossil record of placental mammals. 2009 , 5, e1000634	107
1876	HHP1 is involved in osmotic stress sensitivity in Arabidopsis. 2009 , 60, 1589-604	15
1875	Accurate prediction of peptide binding sites on protein surfaces. 2009 , 5, e1000335	116
,,	Accurate prediction of peptide binding sites on protein surfaces. 2009 , 5, e1000335 Fast statistical alignment. 2009 , 5, e1000392	116 252
1874	Fast statistical alignment. 2009 , 5, e1000392	
1874	Fast statistical alignment. 2009 , 5, e1000392 Selective inhibition of type III secretion activated signaling by the Salmonella effector AvrA. 2009 ,	252
1874	Fast statistical alignment. 2009 , 5, e1000392 Selective inhibition of type III secretion activated signaling by the Salmonella effector AvrA. 2009 , 5, e1000595	252 86
1874 1873 1872	Fast statistical alignment. 2009 , 5, e1000392 Selective inhibition of type III secretion activated signaling by the Salmonella effector AvrA. 2009 , 5, e1000595 Avian encephalomyelitis virus in reared pheasants: a case study. 2009 , 38, 251-6	252 86 18
1874 1873 1872	Fast statistical alignment. 2009, 5, e1000392 Selective inhibition of type III secretion activated signaling by the Salmonella effector AvrA. 2009, 5, e1000595 Avian encephalomyelitis virus in reared pheasants: a case study. 2009, 38, 251-6 Rapid evolution of sex pheromone-producing enzyme expression in Drosophila. 2009, 7, e1000168 NHE8 is an intracellular cation/H+ exchanger in renal tubules of the yellow fever mosquito Aedes aegypti. 2009, 296, F730-50	252 86 18
1874 1873 1872 1871 1870	Fast statistical alignment. 2009, 5, e1000392 Selective inhibition of type III secretion activated signaling by the Salmonella effector AvrA. 2009, 5, e1000595 Avian encephalomyelitis virus in reared pheasants: a case study. 2009, 38, 251-6 Rapid evolution of sex pheromone-producing enzyme expression in Drosophila. 2009, 7, e1000168 NHE8 is an intracellular cation/H+ exchanger in renal tubules of the yellow fever mosquito Aedes aegypti. 2009, 296, F730-50	252 86 18 171 43

1866	Oryza species. 2009 , 26, 2877-85	46
1865	Degenerate tetraploidy was established before bdelloid rotifer families diverged. 2009 , 26, 375-83	44
1864	Temporal trails of natural selection in human mitogenomes. 2009 , 26, 715-7	23
1863	From the gating charge response to pore domain movement: initial motions of Kv1.2 dynamics under physiological voltage changes. 2009 , 26, 397-421	12
1862	Redox-dependent regulation of the stress-induced zinc-finger protein SAP12 in Arabidopsis thaliana. 2009 , 2, 357-67	59
1861	Comparative ICE genomics: insights into the evolution of the SXT/R391 family of ICEs. 2009 , 5, e1000786	188
1860	Blastodinium galatheanum sp. nov. (Dinophyceae) a parasite of the planktonic copepod Acartia negligens (Crustacea, Calanoida) in the central Atlantic Ocean. 2009 , 44, 425-438	9
1859	Characterization of a multimeric, eukaryotic prolyl aminopeptidase: an inducible and highly specific intracellular peptidase from the non-pathogenic fungus Talaromyces emersonii. 2009 , 155, 3673-3682	26
1858	Feedback inhibition in the PhoQ/PhoP signaling system by a membrane peptide. 2009 , 5, e1000788	144
1857	Sepiapterin reductase regulation of endothelial tetrahydrobiopterin and nitric oxide bioavailability. 2009 , 297, H331-9	27
1856	Experimental determination of the evolvability of a transcription factor. 2009 , 106, 18650-5	59
1855	Dichotomous haplotypic lineages of the immunoproteasome subunit genes, PSMB8 and PSMB10, in the MHC class I region of a Teleost Medaka, Oryzias latipes. 2009 , 26, 769-81	14
1854	Mutagenesis and functional characterization of the RNA and protein components of the toxIN abortive infection and toxin-antitoxin locus of Erwinia. 2009 , 191, 6029-39	63
1853	Coupling phosphate homeostasis to cell cycle-specific transcription: mitotic activation of Saccharomyces cerevisiae PHO5 by Mcm1 and Forkhead proteins. 2009 , 29, 4891-905	15
1852	Structure of human Rad51 protein filament from molecular modeling and site-specific linear dichroism spectroscopy. 2009 , 106, 13248-53	47
1851	Comparative analysis between homoeologous genome segments of Brassica napus and its progenitor species reveals extensive sequence-level divergence. 2009 , 21, 1912-28	146
1850	Rapid evolution of mouse Y centromere repeat DNA belies recent sequence stability. 2009 , 19, 2202-13	40
1849	PolV(PolIVb) function in RNA-directed DNA methylation requires the conserved active site and an additional plant-specific subunit. 2009 , 106, 941-6	64

1848	Kalign2: high-performance multiple alignment of protein and nucleotide sequences allowing external features. 2009 , 37, 858-65	214
1847	Identification and classification of ncRNA molecules using graph properties. 2009, 37, e66	29
1846	Enhanced secretion of biologically active murine interleukin-12 by Lactococcus lactis. 2009 , 75, 869-71	14
1845	Aspergillus nidulans protein O-mannosyltransferases play roles in cell wall integrity and developmental patterning. 2009 , 8, 1475-85	36
1844	Probing the relationship between Gram-negative and Gram-positive S1 proteins by sequence analysis. 2009 , 37, 5578-88	72
1843	Efficient estimation of pairwise distances between genomes. <i>Bioinformatics</i> , 2009 , 25, 3221-7 7.2	36
1842	The intrinsically disordered N-terminal domain of thymidylate synthase targets the enzyme to the ubiquitin-independent proteasomal degradation pathway. 2009 , 284, 31597-607	27
1841	Functional analysis of the Streptomyces coelicolor NrdR ATP-cone domain: role in nucleotide binding, oligomerization, and DNA interactions. 2009 , 191, 1169-79	16
1840	A recurrent magnesium-binding motif provides a framework for the ribosomal peptidyl transferase center. 2009 , 37, 3134-42	50
1839	Web services at the European Bioinformatics Institute-2009. 2009 , 37, W6-10	60
1838	KazrinE is a desmosome-associated liprin that colocalises with acetylated microtubules. 2009 , 122, 4035-41	26
1837	Molecular detection of Canine distemper virus and the immunohistochemical characterization of the neurologic lesions in naturally occurring old dog encephalitis. 2009 , 21, 588-97	34
1836	Multiplex real-time PCR for rapid Staphylococcal cassette chromosome mec typing. 2009 , 47, 3692-706	80
1835	Why would phylogeneticists ignore computerized sequence alignment?. 2009 , 58, 150-8	62
1834	Crystal structure of a mammalian CTP: phosphocholine cytidylyltransferase catalytic domain reveals novel active site residues within a highly conserved nucleotidyltransferase fold. 2009 , 284, 33535-48	47
1833	Probing the haem d-binding site in cytochrome bd quinol oxidase by site-directed mutagenesis. 2009 , 145, 763-70	11
1832	Toxoplasma gondii cathepsin L is the primary target of the invasion-inhibitory compound morpholinurea-leucyl-homophenyl-vinyl sulfone phenyl. 2009 , 284, 26839-50	48
1831	Arabidopsis FAB1/PIKfyve proteins are essential for development of viable pollen. 2009 , 151, 1812-22	64

1830	The polychromatic Helitron landscape of the maize genome. 2009 , 106, 19916-21	85
1829	An eIF4E-binding protein regulates katanin protein levels in C. elegans embryos. 2009 , 187, 33-42	34
1828	MGEScan-non-LTR: computational identification and classification of autonomous non-LTR retrotransposons in eukaryotic genomes. 2009 , 37, e143	52
1827	Complete genome of the broad-host-range Erwinia amylovora phage phiEa21-4 and its relationship to Salmonella phage felix O1. 2009 , 75, 2139-47	54
1826	Characterization of DNA polymerase X from Thermus thermophilus HB8 reveals the POLXc and PHP domains are both required for 3'-5' exonuclease activity. 2009 , 37, 2037-52	22
1825	Comprehensive census of bacteria in clean rooms by using DNA microarray and cloning methods. 2009 , 75, 6559-67	74
1824	Nuclear magnetic resonance structure shows that the severe acute respiratory syndrome coronavirus-unique domain contains a macrodomain fold. 2009 , 83, 1823-36	44
1823	Downregulation of the T-cell receptor by human immunodeficiency virus type 2 Nef does not protect against disease progression. 2009 , 83, 12968-72	14
1822	Reducing the risk of adeno-associated virus (AAV) vector mobilization with AAV type 5 vectors. 2009 , 83, 3919-29	22
1821	A myocardium tropic adeno-associated virus (AAV) evolved by DNA shuffling and in vivo selection. 2009 , 106, 3946-51	157
1820	Characterization of mycobacteria from a major Brazilian outbreak suggests that revision of the taxonomic status of members of the Mycobacterium chelonae-M. abscessus group is needed. 2009 , 47, 2691-8	105
1819	Reproductive compensation favours male-killing Wolbachia in a live-bearing host. 2009 , 276, 4021-8	16
1818	Extreme convergence in stick insect evolution: phylogenetic placement of the Lord Howe Island tree lobster. 2009 , 276, 1055-62	91
1817	Deletion and overexpression of the Aspergillus nidulans GATA factor AreB reveals unexpected pleiotropy. 2009 , 155, 3868-3880	35
1816	In vivo display of a multisubunit enzyme complex on biogenic magnetic nanoparticles. 2009, 75, 7734-8	25
1815	High rate of N2 fixation by East Siberian cryophilic soil bacteria as determined by measuring acetylene reduction in nitrogen-poor medium solidified with gellan gum. 2009 , 75, 2811-9	27
1814	Matriptase-2 mutations in iron-refractory iron deficiency anemia patients provide new insights into protease activation mechanisms. 2009 , 18, 3673-83	54
1813	Crystallographic and mutational analyses of substrate recognition of endo-alpha-N-acetylgalactosaminidase from Bifidobacterium longum. 2009 , 146, 389-98	40

1812	The paralogous genes RADICAL-INDUCED CELL DEATH1 and SIMILAR TO RCD ONE1 have partially redundant functions during Arabidopsis development. 2009 , 151, 180-98	58
1811	AAC(6')-laf, a novel aminoglycoside 6'-N-acetyltransferase from multidrug-resistant Pseudomonas aeruginosa clinical isolates. 2009 , 53, 2327-34	18
1810	Identification of a novel sodium-dependent fructose transport activity in the hepatopancreas of the Atlantic lobster Homarus americanus. 2009 , 212, 1912-20	12
1809	Structural basis of Ist1 function and Ist1-Did2 interaction in the multivesicular body pathway and cytokinesis. 2009 , 20, 3514-24	73
1808	Informatics approaches to understanding TGFbeta pathway regulation. 2009 , 136, 3729-40	24
1807	Distinct functional specificities are associated with protein isoforms encoded by the Drosophila dorsal-ventral patterning gene pipe. 2009 , 136, 2779-89	9
1806	Prevotella falsenii sp. nov., a Prevotella intermedia-like organism isolated from monkey dental plaque. 2009 , 59, 319-22	10
1805	Parabacteroides gordonii sp. nov., isolated from human blood cultures. 2009 , 59, 2843-7	21
1804	Tensin1 requires protein phosphatase-1alpha in addition to RhoGAP DLC-1 to control cell polarization, migration, and invasion. 2009 , 284, 34713-22	37
1803	The Arabidopsis B-box zinc finger family. 2009 , 21, 3416-20	216
1802	Of bars and rings: Hof1-dependent cytokinesis in multiseptated hyphae of Ashbya gossypii. 2009 , 29, 771-83	31
1801	Eukaryote-to-eukaryote gene transfer events revealed by the genome sequence of the wine yeast Saccharomyces cerevisiae EC1118. 2009 , 106, 16333-8	307
1800	Pro-interleukin (IL)-1beta shares a core region of stability as compared with mature IL-1beta while maintaining a distinctly different configurational landscape: a comparative hydrogen/deuterium exchange mass spectrometry study. 2009 , 284, 26137-48	21
1799	Diversity of serine hydrolase activities of unchallenged and botrytis-infected Arabidopsis thaliana. 2009 , 8, 1082-93	76
1798	Distinct roles for CARMIL isoforms in cell migration. 2009 , 20, 5290-305	57
1797	Deep sequencing analysis of the Methanosarcina mazei Gil transcriptome in response to nitrogen availability. 2009 , 106, 21878-82	165
1796	Analysis of synthetic lethality reveals genetic interactions between the GTPase Snu114p and snRNAs in the catalytic core of the Saccharomyces cerevisiae spliceosome. 2009 , 183, 497-515-1SI-4SI	11
1795	Gibberellin modulates anther development in rice via the transcriptional regulation of GAMYB. 2009 , 21, 1453-72	264

1794	Three-dimensional EM structure of an intact activator-dependent transcription initiation complex. 2009 , 106, 19830-5	61
1793	Crystal structure of porcine reproductive and respiratory syndrome virus leader protease Nsp1alpha. 2009 , 83, 10931-40	54
1792	Iron translocation into and out of Listeria innocua Dps and size distribution of the protein-enclosed nanomineral are modulated by the electrostatic gradient at the 3-fold "ferritin-like" pores. 2009 , 284, 19101-9	50
1791	Type I cystatin (stefin) is a major component of Fasciola gigantica excretion/secretion product. 2009 , 167, 60-71	36
1790	A novel oxygenase from Pleurotus sapidus transforms valencene to nootkatone. 2009 , 61, 202-207	54
1789	Differences in biocatalytic behavior between two variants of StcI esterase from Aspergillus nidulans and its potential use in biocatalysis. 2009 , 61, 225-234	4
1788	High concentration of basidiolichens in a single family of agaricoid mushrooms (Basidiomycota: Agaricales: Hygrophoraceae). 2009 , 113, 1154-71	65
1787	Characterization of a small erythromycin resistance plasmid pLFE1 from the food-isolate Lactobacillus plantarum M345. 2009 , 61, 159-70	34
1786	Characterization of pACK4, a mobilizable plasmid from Staphylococcus simulans biovar staphylolyticus. 2009 , 62, 201-5	3
1785	Vertical adaptive radiation in ocean Prochlorococcus: Evolutionary implications of the Chl b/a ratio from molecular evidence. 2009 , 19, 1561-1568	1
1784	Structure and interdomain interactions of a hybrid domain: a disulphide-rich module of the fibrillin/LTBP superfamily of matrix proteins. 2009 , 17, 759-68	40
1783	The Kindlin protein family: new members to the club of focal adhesion proteins. 2009 , 19, 504-13	136
1782	Development of a novel real-time reverse-transcriptase PCR method for the detection of H275Y positive influenza A H1N1 isolates. 2009 , 158, 190-4	35
1781	Differentiation of C-strain "Riems" or CP7_E2alf vaccinated animals from animals infected by classical swine fever virus field strains using real-time RT-PCR. 2009 , 158, 114-22	38
1780	Concurrent quantitation of the A and D genotypes of hepatitis B virus. 2009 , 161, 265-70	3
1779	Molecular detection of native and invasive marine invertebrate larvae present in ballast and open water environmental samples collected in Puget Sound. 2009 , 369, 93-99	27
1778	Male engorgement factor: Role in stimulating engorgement to repletion in the ixodid tick, Dermacentor variabilis. 2009 , 55, 909-18	15
1777	XMPP for cloud computing in bioinformatics supporting discovery and invocation of asynchronous web services. 2009 , 10, 279	33

1776	Optimizing substitution matrix choice and gap parameters for sequence alignment. 2009 , 10, 396	27
1775	Exploratory visual analysis of conserved domains on multiple sequence alignments. 2009 , 10 Suppl 11, S7	4
1774	Insights into the evolution of sialic acid catabolism among bacteria. 2009 , 9, 118	127
1773	Independent inactivation of arginine decarboxylase genes by nonsense and missense mutations led to pseudogene formation in Chlamydia trachomatis serovar L2 and D strains. 2009 , 9, 166	13
1772	Zebrafish RNase T2 genes and the evolution of secretory ribonucleases in animals. 2009 , 9, 170	25
1771	Comprehensive computational analysis of Hmd enzymes and paralogs in methanogenic Archaea. 2009 , 9, 199	12
1770	Does evolutionary innovation in pharyngeal jaws lead to rapid lineage diversification in labrid fishes?. 2009 , 9, 255	84
1769	Estimating the phylogeny and divergence times of primates using a supermatrix approach. 2009 , 9, 259	212
1768	Phylogenomic analysis of the cystatin superfamily in eukaryotes and prokaryotes. 2009 , 9, 266	75
1767	Diversification of the cullin family. 2009 , 9, 267	38
1767 1766	Diversification of the cullin family. 2009 , 9, 267 Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate acid reductase gene family in plants. 2009 , 9, 90	38 71
, , ,	Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate	
1766	Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate acid reductase gene family in plants. 2009 , 9, 90 Analysis of tarantula skeletal muscle protein sequences and identification of transcriptional	71
1766 1765	Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate acid reductase gene family in plants. 2009 , 9, 90 Analysis of tarantula skeletal muscle protein sequences and identification of transcriptional isoforms. 2009 , 10, 117 Genomic organization and classification of the bovine WC1 genes and expression by peripheral	71
1766 1765 1764	Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate acid reductase gene family in plants. 2009, 9, 90 Analysis of tarantula skeletal muscle protein sequences and identification of transcriptional isoforms. 2009, 10, 117 Genomic organization and classification of the bovine WC1 genes and expression by peripheral blood gamma delta T cells. 2009, 10, 191 Complete sequence determination of a novel reptile iridovirus isolated from soft-shelled turtle and	71 20 44
1766 1765 1764 1763	Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate acid reductase gene family in plants. 2009, 9, 90 Analysis of tarantula skeletal muscle protein sequences and identification of transcriptional isoforms. 2009, 10, 117 Genomic organization and classification of the bovine WC1 genes and expression by peripheral blood gamma delta T cells. 2009, 10, 191 Complete sequence determination of a novel reptile iridovirus isolated from soft-shelled turtle and evolutionary analysis of Iridoviridae. 2009, 10, 224 Comparative genomics and evolution of conserved noncoding elements (CNE) in rainbow trout.	71 20 44 92
1766 1765 1764 1763 1762	Phylogenetic analysis, structural evolution and functional divergence of the 12-oxo-phytodienoate acid reductase gene family in plants. 2009, 9, 90 Analysis of tarantula skeletal muscle protein sequences and identification of transcriptional isoforms. 2009, 10, 117 Genomic organization and classification of the bovine WC1 genes and expression by peripheral blood gamma delta T cells. 2009, 10, 191 Complete sequence determination of a novel reptile iridovirus isolated from soft-shelled turtle and evolutionary analysis of Iridoviridae. 2009, 10, 224 Comparative genomics and evolution of conserved noncoding elements (CNE) in rainbow trout. 2009, 10, 278 Comparative analysis of plant genomes allows the definition of the "Phytolongins": a novel	71 20 44 92 10

1758	YY1's DNA-binding motifs in mammalian olfactory receptor genes. 2009 , 10, 576	7
1757	Evolutionary diversification of an ancient gene family (rhs) through C-terminal displacement. 2009 , 10, 584	69
1756	Comparative analysis of two Neisseria gonorrhoeae genome sequences reveals evidence of mobilization of Correia Repeat Enclosed Elements and their role in regulation. 2009 , 10, 70	24
1755	Genomic and systems evolution in Vibrionaceae species. 2009 , 10 Suppl 1, S11	13
1754	Word-based characterization of promoters involved in human DNA repair pathways. 2009 , 10 Suppl 1, S18	6
1753	Understanding diversity of human innate immunity receptors: analysis of surface features of leucine-rich repeat domains in NLRs and TLRs. 2009 , 10, 48	33
1752	Expression and subcellular localization of kinetoplast-associated proteins in the different developmental stages of Trypanosoma cruzi. 2009 , 9, 120	15
1751	High-level chromate resistance in Arthrobacter sp. strain FB24 requires previously uncharacterized accessory genes. 2009 , 9, 199	54
1750	Identification of a bacteriocin and its cognate immunity factor expressed by Moraxella catarrhalis. 2009 , 9, 207	7
1749	Evolutionary relationships among salivarius streptococci as inferred from multilocus phylogenies based on 16S rRNA-encoding, recA, secA, and secY gene sequences. 2009 , 9, 232	8
1748	RotaC: a web-based tool for the complete genome classification of group A rotaviruses. 2009 , 9, 238	322
1747	Systemic acquired resistance in soybean is regulated by two proteins, Orthologous to Arabidopsis NPR1. 2009 , 9, 105	62
1746	Seed storage protein gene promoters contain conserved DNA motifs in Brassicaceae, Fabaceae and Poaceae. 2009 , 9, 126	40
1745	'Who's who' in two different flower types of Calluna vulgaris (Ericaceae): morphological and molecular analyses of flower organ identity. 2009 , 9, 148	13
1744	Expression by Lawsonia intracellularis of type III secretion system components during infection. 2009 , 139, 298-303	16
1743	The capsid protein of infectious bursal disease virus contains a functional alpha 4 beta 1 integrin ligand motif. 2009 , 386, 360-72	44
1742	Molecular variability and genetic structure of the population of soybean mosaic virus based on the analysis of complete genome sequences. 2009 , 393, 91-103	103
1741	Biofilm formation and proteolytic activities of Pseudoalteromonas bacteria that were isolated from fish farm sediments. 2009 , 2, 361-9	22

1740	Phylogenetic and phenotypic relationships among Triatoma carcavalloi (Hemiptera: Reduviidae: Triatominae) and related species collected in domiciles in Rio Grande do Sul State, Brazil. 2009 , 34, 164-73	13
1739	The carboxyl terminus of Brca2 links the disassembly of Rad51 complexes to mitotic entry. 2009 , 19, 1075-85	68
1738	HSPB7 is a SC35 speckle resident small heat shock protein. 2009 , 1793, 1343-53	58
1737	Characterization of species-related differences in the pharmacology of tachykinin NK receptors 1, 2 and 3. 2009 , 77, 1522-30	34
1736	Best linear unbiased prediction of host-range of the facultative parasite Colletotrichum gloeosporioides f. sp. salsolae, a potential biological control agent of Russian thistle. 2009 , 51, 158-168	31
1735	Approaches to the study of the systematics of anaerobic, gram-negative, non-sporeforming rods: current status and perspectives. 2009 , 15, 179-94	50
1734	Interaction of the Thermoplasma acidophilum A1A0-ATP synthase peripheral stalk with the catalytic domain. 2009 , 583, 3121-6	5
1733	Comparative analysis of CRISPR loci in lactic acid bacteria genomes. 2009 , 131, 62-70	222
1732	Two homologous fungal carbonyl reductases with different substrate specificities. 2009 , 178, 295-302	5
1731	Molecular determinants of non-competitive antagonist binding to the mouse GPRC6A receptor. 2009 , 46, 323-32	44
1730	Insights into sequence-activity relationships amongst Baeyer-Villiger monooxygenases as revealed by the intragenomic complement of enzymes from Rhodococcus jostii RHA1. 2009 , 10, 1208-17	56
1729	A gene conversion hotspot in the human growth hormone (GH1) gene promoter. 2009 , 30, 239-47	12
1728	Structural insights on pathogenic effects of novel mutations causing pyruvate carboxylase deficiency. 2009 , 30, 734-40	27
1727	Pathogenic or not? And if so, then how? Studying the effects of missense mutations using bioinformatics methods. 2009 , 30, 703-14	184
1726	COLdb, a database linking genetic data to molecular function in fibrillar collagens. 2009 , 30, 946-51	23
1725	Copy number gain and oncogenic activity of YWHAZ/14-3-3zeta in head and neck squamous cell carcinoma. 2009 , 125, 603-11	53
1724	Phosphatidylserine decarboxylases, key enzymes of lipid metabolism. 2009 , 61, 151-62	64
1723	Docking studies of structurally diverse antimalarial drugs targeting PfATP6: no correlation between in silico binding affinity and in vitro antimalarial activity. 2009 , 4, 1469-79	31

1722	Cloning and spatiotemporal expression of zebrafish neuronal nicotinic acetylcholine receptor alpha 6 and alpha 4 subunit RNAs. 2009 , 238, 980-92	28
1721	Emx3 is required for the differentiation of dorsal telencephalic neurons. 2009 , 238, 1984-98	31
1720	In vivo post-transcriptional regulation of CD154 in mouse CD4+ T cells. 2009 , 39, 2224-32	14
1719	Transcriptional regulation of human eosinophil RNase2 by the liver-enriched hepatocyte nuclear factor 4. 2009 , 106, 317-26	2
1718	Beta-keratins of the crocodilian epidermis: composition, structure, and phylogenetic relationships. 2009 , 312, 42-57	47
1717	Generation and evaluation of a homology model of PfGSK-3. 2009 , 342, 327-32	7
1716	MeCP2 post-translational regulation through PEST domains: two novel hypotheses: potential relevance and implications for Rett syndrome. 2009 , 31, 561-9	19
1715	An unstructured protein with destructive potential: TPPP/p25 in neurodegeneration. 2009, 31, 676-86	37
1714	Molecular evolution of SPARC: absence of the acidic module and expression in the endoderm of the starlet sea anemone, Nematostella vectensis. 2009 , 219, 509-21	22
1713	Partial sequence of the beta-tubulin of Histomonas meleagridis and the activity of benzimidazoles against H. meleagridis in vitro. 2009 , 104, 1183-9	15
1712	The putative cyclooctadepsipeptide receptor depsiphilin of the canine hookworm Ancylostoma caninum. 2009 , 105 Suppl 1, S91-100	8
1711	Expression diversity and evolutionary dynamics of rice duplicate genes. 2009 , 281, 483-93	35
1710	Regions associated with repression of the barley (Hordeum vulgare) VERNALIZATION1 gene are not required for cold induction. 2009 , 282, 107-17	93
1709	Plant lectins: the ties that bind in root symbiosis and plant defense. 2009 , 282, 1-15	148
1708	Evolution of Tom, 297, 17.6 and rover retrotransposons in Drosophilidae species. 2009 , 282, 351-62	15
1707	A candidate for Lr19, an exotic gene conditioning leaf rust resistance in wheat. 2009 , 9, 325-34	28
1706	Molecular dynamics simulations of mouse ferrochelatase variants: what distorts and orientates the porphyrin?. 2009 , 14, 1119-28	4
1705	Fatty acids, unusual glycophospholipids and DNA analyses of thermophilic bacteria isolated from hot springs. 2009 , 13, 101-9	11

1704	Acanthamoeba T4 and T15 genotypes associated with keratitis infections in Italy. 2009 , 28, 607-12	46
1703	The complete nucleotide sequence and genome structure of potato latent virus. 2009, 154, 361-4	2
1702	The complete nucleotide sequence of potato virus T. 2009 , 154, 321-5	5
1701	The complete nucleotide sequence and genome organization of red clover vein mosaic virus (genus Carlavirus). 2009 , 154, 891-4	6
1700	Molecular characterization and detection of recombinant isolates of potato virus Y from China. 2009 , 154, 1303-12	32
1699	Identification and molecular characterization of a marafivirus in Rubus spp. 2009 , 154, 1729-35	17
1698	Complete genome sequence of turnip ringspot virus. 2009 , 154, 1851-3	4
1697	LAP3, a novel plant protein required for pollen development, is essential for proper exine formation. 2009 , 22, 167-77	49
1696	Mitochondrial genome sequence of Unionicola foili (Acari: Unionicolidae): a unique gene order with implications for phylogenetic inference. 2009 , 49, 305-16	24
1695	Prediction of epitopes in closely related proteins using a new algorithm. 2009 , 148, 869-73	7
1694	Long-term evolution of 5S ribosomal DNA seems to be driven by birth-and-death processes and selection in Ensis razor shells (Mollusca: Bivalvia). 2009 , 47, 635-44	30
1693	Glycogen synthase kinase-3 inhibition by 3-anilino-4-phenylmaleimides: insights from 3D-QSAR and docking. 2009 , 23, 113-27	17
1692	Species-specific differences in the Pro-Ala rich region of cardiac myosin binding protein-C. 2009 , 30, 303-6	31
1691	cDNA cloning and gene expression pattern following bacterial challenge of peroxinectin in Chinese shrimp Fenneropenaeus chinensis. 2009 , 36, 2333-9	18
1690	Structural model of the CopA copper ATPase of Enterococcus hirae based on chemical cross-linking. 2009 , 22, 363-75	20
1689	MicroRNA-17-3p is a prostate tumor suppressor in vitro and in vivo, and is decreased in high grade prostate tumors analyzed by laser capture microdissection. 2009 , 26, 965-79	40
1688	The tomato brassinosteroid receptor BRI1 increases binding of systemin to tobacco plasma membranes, but is not involved in systemin signaling. 2009 , 70, 603-16	44
1687	An abundant and heavily truncated non-LTR retrotransposon (LINE) family in Beta vulgaris. 2009 , 71, 585-97	18

1686	Molecular Evidence for Recombination in Prunus Necrotic Ringspot Virus. 2009 , 27, 189-198	4
1685	A novel species-specific satellite DNA family in the invasive root-knot nematode Meloidogyne mayaguensis and its potential use for diagnostics. 2009 , 125, 485-495	11
1684	Description of a new trans-generic Skb-RNase allele in apple. 2009 , 166, 83-94	10
1683	Patterns of DNA sequence variation at candidate gene loci in black poplar (Populus nigra L.) as revealed by single nucleotide polymorphisms. 2009 , 137, 141-50	30
1682	Sialylation in protostomes: a perspective from Drosophila genetics and biochemistry. 2009 , 26, 313-24	35
1681	Evolution of the pili nut genus (Canarium L., Burseraceae) and its cultivated species. 2009 , 56, 765-781	15
1680	Adlardia novaecaledoniae n. g., n. sp. (Digenea: Cryptogonimidae) from the fork-tailed threadfin bream Nemipterus furcosus (Val.) (Perciformes: Nemipteridae) off New Caledonia. 2009 , 73, 151-60	16
1679	Gynichthys diakidnus n. g., n. sp. (Digenea: Cryptogonimidae) from the grunt Plectorhinchus gibbosus (Lacβde, 1802) (Perciformes: Haemulidae) off the Great Barrier Reef, Australia. 2009 , 74, 103-12	11
1678	Recombination structure and genetic relatedness among members of the family Bromoviridae based on their RNAs 1 and 2 sequence analyses. 2009 , 38, 435-44	13
1677	Sequence signatures in envelope protein may determine whether flaviviruses produce hemorrhagic or encephalitic syndromes. 2009 , 39, 1-9	12
1676	Fine-scale vertical distribution of bacteria in the East Pacific deep-sea sediments determined via 16S rRNA gene T-RFLP and clone library analyses. 2009 , 25, 179-188	19
1675	Purification and characterization of an antimicrobial peptide produced by Pseudomonas sp. strain 4B. 2009 , 25, 205-213	9
1674	Modeling the 3-D structure of a recombinant laccase from Trametes trogii active at a pH close to neutrality. 2009 , 28, 375-83	8
1673	Computational analysis of the human HSPH/HSPA/DNAJ family and cloning of a human HSPH/HSPA/DNAJ expression library. 2009 , 14, 1-21	116
1672	Diversity of the enzymatic activity in the lipoxygenase gene family of Arabidopsis thaliana. 2009 , 44, 85-95	152
1671	Towards bioremediation of toxic unresolved complex mixtures of hydrocarbons: identification of bacteria capable of rapid degradation of alkyltetralins. 2009 , 9, 129-136	13
1670	Two fungi associated with necrotic leaflets of areca palms (Areca catechu). 2009, 8, 115-121	3
1669	Cloning, expression, and characterization of a novel anti-HIV lectin from the cultured cyanobacterium, Oscillatoria agardhii. 2009 , 75, 743-753	34

1668	Origin of the diclidophorid monogenean Neoheterobothrium hirame Ogawa, 1999, the causative agent of anemia in olive flounder Paralichthys olivaceus. 2009 , 75, 1167-1176	15
1667	Hybridization and polymorphic microsatellite markers for two lagomorph species (Genus Sylvilagus): implications for conservation. 2009 , 1, 419-424	8
1666	Development of primers for amplification and further research on the D-loop control region for the Common Spadefoot toad, Pelobates fuscus (Amphibia). 2009 , 1, 495-499	2
1665	A genetic analysis of in vivo selenate reduction by Salmonella enterica serovar Typhimurium LT2 and Escherichia coli K12. 2009 , 191, 519-28	50
1664	hShroom1 links a membrane bound protein to the actin cytoskeleton. 2009 , 66, 681-96	9
1663	To investigate protein evolution by detecting suppressed epitope structures. 2009 , 68, 448-60	35
1662	Phylogenetic analysis and molecular evolution of guanine deaminases: from guanine to dendrites. 2009 , 68, 227-35	18
1661	Evolution of phage-type RNA polymerases in higher plants: characterization of the single phage-type RNA polymerase gene from Selaginella moellendorffii. 2009 , 68, 528-38	15
1660	Birth and death of genes and functions in the beta-esterase cluster of Drosophila. 2009 , 69, 10-21	18
1659	A comparative approach shows differences in patterns of numt insertion during hominoid evolution. 2009 , 68, 688-99	29
1658	RBR ubiquitin ligases: Diversification and streamlining in animal lineages. 2009 , 69, 54-64	28
1657	Phylogenetic analysis of the NEEP21/calcyon/P19 family of endocytic proteins: evidence for functional evolution in the vertebrate CNS. 2009 , 69, 319-32	14
1656	Diversity and distribution of sediment nirS-encoding bacterial assemblages in response to environmental gradients in the eutrophied Jiaozhou Bay, China. 2009 , 58, 161-9	66
1655	Ancient photosynthetic eukaryote biofilms in an Atacama Desert coastal cave. 2009 , 58, 485-96	30
1654	Importance of malate synthase in the glyoxylate cycle of Ashbya gossypii for the efficient production of riboflavin. 2009 , 83, 529-39	18
1653	Molecular characterization of aromatic peroxygenase from Agrocybe aegerita. 2009 , 84, 885-97	92
1652	Molecular characterization of StcI esterase from Aspergillus nidulans. 2009 , 84, 917-26	
1651	X-ray crystal structure of a CRISPR-associated RAMP module [corrected] Cmr5 protein [corrected] from Thermus thermophilus HB8. 2009 , 75, 528-32	24

1650	The 2.1 A crystal structure of an acyl-CoA synthetase from Methanosarcina acetivorans reveals an alternate acyl-binding pocket for small branched acyl substrates. 2009 , 77, 685-98	15
1649	Crystal structure of ginkbilobin-2 with homology to the extracellular domain of plant cysteine-rich receptor-like kinases. 2009 , 77, 247-51	29
1648	Yeast Ste23p shares functional similarities with mammalian insulin-degrading enzymes. 2009 , 26, 595-610	12
1647	Electrospray ionization mass spectrometry as a critical tool for revealing new properties of snake venom phospholipase A2. 2009 , 23, 1158-66	6
1646	Structural model of rho1 GABAC receptor based on evolutionary analysis: Testing of predicted protein-protein interactions involved in receptor assembly and function. 2009 , 18, 2371-83	16
1645	The crystal structure of a TIR domain from Arabidopsis thaliana reveals a conserved helical region unique to plants. 2010 , 19, 155-61	47
1644	Structural plasticity of the phage P22 tail needle gp26 probed with xenon gas. 2009 , 18, 537-48	20
1643	Structures of alternatively spliced isoforms of human ketohexokinase. 2009 , 65, 201-11	26
1642	Application of molecular replacement to protein powder data from image plates. 2009, 65, 348-55	5
1641	Structure of a fatty-acid-binding protein from Bacillus subtilis determined by sulfur-SAD phasing using in-house chromium radiation. 2009 , 65, 440-8	12
1640	The three-dimensional structure of MAP kinase p38beta: different features of the ATP-binding site in p38beta compared with p38alpha. 2009 , 65, 777-85	26
1639	Structure of the C-terminal domain of nsp4 from feline coronavirus. 2009 , 65, 839-46	18
1638	Overproduction, purification and structure determination of human dual-specificity phosphatase 14. 2009 , 65, 1013-20	17
1637	Structures of the apo and holo forms of formate dehydrogenase from the bacterium Moraxella sp. C-1: towards understanding the mechanism of the closure of the interdomain cleft. 2009 , 65, 1315-25	26
1636	Crystallization and preliminary X-ray diffraction of chlorite dismutase from Dechloromonas aromatica RCB. 2009 , 65, 818-21	6
1635	Structure of the first PDZ domain of human PSD-93. 2009 , 65, 1254-7	9
1634	Muscle differentiation in a colonial ascidian: organisation, gene expression and evolutionary considerations. 2009 , 9, 48	14
1633	Hypermethylation of the DLC1 CpG island does not alter gene expression in canine lymphoma. 2009 , 10, 73	20

1632	Bioinformatic characterizations and prediction of K+ and Na+ ion channels effector toxins. 2009, 9, 4	10
1631	Gene composer: database software for protein construct design, codon engineering, and gene synthesis. 2009 , 9, 36	50
1630	Structural effects of clinically observed mutations in JAK2 exons 13-15: comparison with V617F and exon 12 mutations. 2009 , 9, 58	25
1629	Partially-supervised protein subclass discovery with simultaneous annotation of functional residues. 2009 , 9, 68	6
1628	Disruption of chromosome 11 in canine fibrosarcomas highlights an unusual variability of CDKN2B in dogs. 2009 , 5, 27	16
1627	Characterization of genes in the ASYMMETRIC LEAVES2/LATERAL ORGAN BOUNDARIES (AS2/LOB) family in Arabidopsis thaliana, and functional and molecular comparisons between AS2 and other family members. 2009 , 58, 525-37	99
1626	A microarray-based genotyping and genetic mapping approach for highly heterozygous outcrossing species enables localization of a large fraction of the unassembled Populus trichocarpa genome sequence. 2009 , 58, 1054-67	29
1625	The Populus homeobox gene ARBORKNOX2 regulates cell differentiation during secondary growth. 2009 , 60, 1000-14	100
1624	Acetylcholinesterase genes in the basal Hexapod Orchesella villosa. 2009 , 18, 45-54	5
1623	Diversity and spatial distribution of amoA-encoding archaea in the deep-sea sediments of the tropical West Pacific Continental Margin. 2009 , 106, 1482-93	50
1622	Structural and bioinformatic analysis of the Roman snail Cd-Metallothionein gene uncovers molecular adaptation towards plasticity in coping with multifarious environmental stress. 2009 , 18, 2426-43	28
1621	The archaeal RNA polymerase subunit P and the eukaryotic polymerase subunit Rpb12 are interchangeable in vivo and in vitro. 2009 , 71, 989-1002	15
1620	CsiA is a bacterial cell wall synthesis inhibitor contributing to DNA translocation through the cell envelope. 2009 , 72, 779-94	8
1619	Crystal structure of the Vibrio cholerae ferric uptake regulator (Fur) reveals insights into metal co-ordination. 2009 , 72, 1208-20	106
1618	The transcriptionally active regions in the genome of Bacillus subtilis. 2009 , 73, 1043-57	139
1617	The third pillar of bacterial signal transduction: classification of the extracytoplasmic function (ECF) sigma factor protein family. 2009 , 74, 557-81	303
1616	FATTY ACID DESATURASE4 of Arabidopsis encodes a protein distinct from characterized fatty acid desaturases. 2009 , 60, 832-9	75
1615	The evolution and diversity of TNF block haplotypes in European, Asian and Australian Aboriginal populations. 2009 , 10, 607-15	20

1614	Structure of a tetrameric MscL in an expanded intermediate state. 2009 , 461, 120-4	94
1613	Transport mechanism of a bacterial homologue of glutamate transporters. 2009 , 462, 880-5	348
1612	Bone morphogenetic protein heterodimers assemble heteromeric type I receptor complexes to pattern the dorsoventral axis. 2009 , 11, 637-43	174
1611	The evolutionary history of the SSX family of human C/T-antigens. 2009 , 43, 954-960	2
1610	MYC-induced myeloid leukemogenesis is accelerated by all six members of the antiapoptotic BCL family. 2009 , 28, 1274-9	90
1609	Characterization of genotypes of Enterocytozoon bieneusi in immunosuppressed and immunocompetent patient groups. 2009 , 56, 388-93	52
1608	Structurally delineating stromal interaction molecules as the endoplasmic reticulum calcium sensors and regulators of calcium release-activated calcium entry. 2009 , 231, 113-31	21
1607	5-MCA-NAT does not act through NQO2 to reduce intraocular pressure in New-Zealand white rabbit. 2009 , 47, 201-209	25
1606	TRAPP II complex assembly requires Trs33 or Trs65. 2009 , 10, 1831-44	30
1605	Mutation in sco affects cytochrome c assembly and alters oxidative stress resistance in Agrobacterium tumefaciens. 2009 , 293, 122-9	14
1604	Inactivation of thioredoxin-like gene alters oxidative stress resistance and reduces cytochrome c oxidase activity in Agrobacterium tumefaciens. 2009 , 295, 110-6	8
1603	A novel inorganic pyrophosphatase in Thermococcus onnurineus NA1. 2009 , 300, 68-74	17
1602	A reason for overlap peaks in direct sequencing of rRNA gene ITS in Pleurotus nebrodensis. 2009 , 305, 14-17	О
1601	Glutathione transferases in bacteria. 2009 , 276, 58-75	216
1600	Crystal structure of the parasite inhibitor chagasin in complex with papain allows identification of structural requirements for broad reactivity and specificity determinants for target proteases. 2009 , 276, 793-806	29
1599	Stability and fibril formation properties of human and fish transthyretin, and of the Escherichia coli transthyretin-related protein. 2009 , 276, 1999-2011	10
1598	Role of calcium phosphate nanoclusters in the control of calcification. 2009 , 276, 2308-23	63
1597	Characterization of a membrane-bound angiotensin-converting enzyme isoform in crayfish testis and evidence for its release into the seminal fluid. 2009 , 276, 4727-38	3

1596	Inactivating pentapeptide insertions in the fission yeast replication factor C subunit Rfc2 cluster near the ATP-binding site and arginine finger motif. 2009 , 276, 4803-13	3
1595	Structure analysis of the flavoredoxin from Desulfovibrio vulgaris Miyazaki F reveals key residues that discriminate the functions and properties of the flavin reductase family. 2009 , 276, 4840-53	1
1594	Identification of an atypical insect olfactory receptor subtype highly conserved within noctuids. 2009 , 276, 6537-47	17
1593	Cholesterol oxidase: biochemistry and structural features. 2009 , 276, 6826-43	71
1592	Cholesterol oxidase: physiological functions. 2009 , 276, 6844-56	61
1591	The N-terminus of mature human frataxin is intrinsically unfolded. 2009 , 276, 6669-76	20
1590	Functional and small-angle X-ray scattering studies of a new stationary phase survival protein E (SurE) from Xylella fastidiosaevidence of allosteric behaviour. 2009 , 276, 6751-62	6
1589	Functional significance of five noncanonical Ca2+-binding sites of human transglutaminase 2 characterized by site-directed mutagenesis. 2009 , 276, 7083-96	61
1588	Identifying coevolutionary patterns in human leukocyte antigen (HLA) molecules. 2010 , 64, 1429-45	3
1587	Identification of phosphatidylserine decarboxylases 1 and 2 from Pichia pastoris. 2009 , 9, 911-22	9
1586	Cloning and blood-meal dependent induction pattern of apolipophorin-III from Anopheles sinensis. 2009 , 39, 388-393	
1585	A land snail's view of a fragmented landscape. 2009 , 98, 839-850	9
1584	Resources and transgenesis techniques for functional genomics in Xenopus. 2009 , 51, 387-401	22
1583	An HLA-DR11/DQ3 haplotype with a DRB1*0301 sequence motif in the third hypervariable region of the HLA-DR beta-1 chain: molecular and serological analysis of its generation in a European Caucasian family. 2009 , 74, 330-5	2
1582	Translocons on the inner and outer envelopes of chloroplasts share similar evolutionary origin in Arabidopsis thaliana. 2009 , 22, 1418-28	11
1581	Detecting positive selection in the budding yeast genome. 2009 , 22, 2430-7	17
1580	Bacterial, archaeal and eukaryal community structures throughout soil horizons of harvested and naturally disturbed forest stands. 2009 , 11, 3045-62	143
1579	Diverse and dynamic populations of cyanobacterial podoviruses in the Chesapeake Bay unveiled through DNA polymerase gene sequences. 2009 , 11, 2884-92	55

1578	EspT triggers formation of lamellipodia and membrane ruffles through activation of Rac-1 and Cdc42. 2009 , 11, 217-29	57
1577	A developmentally regulated Myb domain protein regulates expression of a subset of stage-specific genes in Entamoeba histolytica. 2009 , 11, 898-910	41
1576	Tethyan relicts on continental coastlines of the northwestern Pacific Ocean and Australasia: molecular phylogeny and fossil record of batillariid gastropods (Caenogastropoda, Cerithioidea). 2009 , 38, 503-525	35
1575	DREAM2 challenge. 2009 , 1158, 196-204	
1574	Genetic variation of FUT3 in Ghanaians, Caucasians, and Mongolians. 2009 , 49, 959-66	19
1573	Patterns and consequences of vertebrate Emx gene duplications. 2009 , 11, 343-53	25
1572	TAXONOMIC STUDY OF TWO NEW GENERA OF FUSIFORM GREEN FLAGELLATES, TABRIS GEN. NOV. AND HAMAKKO GEN. NOV. (VOLVOCALES, CHLOROPHYCEAE)(1). 2009 , 45, 482-92	28
1571	TorsinA and dystonia: from nuclear envelope to synapse. 2009 , 109, 1596-609	45
1570	Functional dissection of the alpha-synuclein promoter: transcriptional regulation by ZSCAN21 and ZNF219. 2009 , 110, 1479-90	40
1569	Genetic differentiation within the inbred C57BL/6J mouse strain. 2009 , 278, 42-47	9
1568	Island populations have high conservation value for northern Australia's top marsupial predator ahead of a threatening process. 2009 , 278, 206-217	32
1567	Sterol metabolism in the oomycete Aphanomyces euteiches, a legume root pathogen. 2009 , 183, 291-300	32
1566	Nitrogen metabolism in the developing ear of maize (Zea mays): analysis of two lines contrasting in their mode of nitrogen management. 2009 , 184, 340-352	47
1565	Tyrosine sulfation: an increasingly recognised post-translational modification of secreted proteins. 2009 , 25, 299-317	120
1564	Bioinformatic analysis and in vitro site-directed mutagenesis of conserved amino acids in BphKLB400, a specific bacterial glutathione transferase. 2009 , 63, 928-932	2
1563	Bionectriol A, a polyketide glycoside from the fungus Bionectria sp. associated with the fungus-growing ant, Apterostigma dentigerum. 2009 , 50, 6834-6837	22
1562	Escape from the Ponto-Caspian: evolution and biogeography of an endemic goby species flock (Benthophilinae: Gobiidae: Teleostei). 2009 , 52, 84-102	80
1561	Phylogeny, taxonomy, and evolution of the endothelin receptor gene family. 2009 , 52, 677-87	13

1560	Slippery when wet: phylogeny and character evolution in the gelatinous cyanobacterial lichens (Peltigerales, Ascomycetes). 2009 , 53, 862-71	58
1559	Apicortin, a unique protein, with a putative cytoskeletal role, shared only by apicomplexan parasites and the placozoan Trichoplax adhaerens. 2009 , 9, 1275-86	19
1558	Toward the three-dimensional structure and lysophosphatidic acid binding characteristics of the LPA(4)/p2y(9)/GPR23 receptor: a homology modeling study. 2009 , 28, 70-9	7
1557	Thioredoxin reductase: A target for gold compounds acting as potential anticancer drugs. 2009 , 253, 1692-1707	445
1556	The dual function of the Mycobacterium tuberculosis FadD32 required for mycolic acid biosynthesis. 2009 , 16, 510-9	59
1555	Chemical inhibition of a subset of Arabidopsis thaliana GSK3-like kinases activates brassinosteroid signaling. 2009 , 16, 594-604	189
1554	Computational analyses of mammalian lactate dehydrogenases: human, mouse, opossum and platypus LDHs. 2009 , 33, 379-85	31
1553	Estimating sufficient statistics in co-evolutionary analysis by mutual information. 2009 , 33, 440-4	25
1552	SPlitSSI-SVM: an algorithm to reduce the misleading and increase the strength of domain signal. 2009 , 39, 1013-9	3
1551	Interactions of the M. tuberculosis UsfX with the cognate sigma factor SigF and the anti-anti sigma factor RsfA. 2009 , 1794, 541-53	10
1550	Structural characterization of the protein cce_0567 from Cyanothece 51142, a metalloprotein associated with nitrogen fixation in the DUF683 family. 2009 , 1794, 627-33	2
1549	Structural overview on the allosteric activation of cyclic AMP receptor protein. 2009 , 1794, 1299-308	44
1548	Proteolysis of the proofreading subunit controls the assembly of Escherichia coli DNA polymerase III catalytic core. 2009 , 1794, 1606-15	8
1547	The molecular basis for perforin oligomerization and transmembrane pore assembly. 2009 , 30, 684-95	102
1546	Behaviour of a peptide sequence from the GB virus C/hepatitis G virus E2 protein in Langmuir monolayers: its interaction with phospholipid membrane models. 2009 , 141, 153-61	13
1545	Enzymatic characterization and inhibition of the nuclear variant of human O-GlcNAcase. 2009 , 344, 1079-84	28
1544	Applicability of multigene family-specific antibodies toward studies of the subtilases in Arabidopsis thaliana. 2009 , 384, 114-22	2
1543	Molecular determinants of substrate and inhibitor specificities of the Penicillium griseofulvum family 11 xylanases. 2009 , 1794, 438-45	26

1542	The PLASTID DIVISION1 and 2 components of the chloroplast division machinery determine the rate of chloroplast division in land plant cell differentiation. 2009 , 21, 1769-80	106
1541	Molecular dynamics simulation of the heterodimeric mGluR2/5HT(2A) complex. An atomistic resolution study of a potential new target in psychiatric conditions. 2009 , 49, 1602-16	51
1540	PrimerHunter: a primer design tool for PCR-based virus subtype identification. 2009 , 37, 2483-92	30
1539	UniPrime2: a web service providing easier Universal Primer design. 2009 , 37, W209-13	18
1538	Directed evolution of a Bacillus chitinase. 2009 , 4, 501-9	21
1537	Symbiont flexibility in Thamnolia vermicularis (Pertusariales: Icmadophilaceae). 2009 , 112, 404-417	47
1536	Biochemical characterization of the catalytic domains of three different Clostridial collagenases. 2009 , 390, 11-8	24
1535	An unusual ERAD-like complex is targeted to the apicoplast of Plasmodium falciparum. 2009 , 8, 1134-45	125
1534	A missense mutation in CASK causes FG syndrome in an Italian family. 2009 , 84, 162-77	63
1533	Mutations in LOXHD1, an evolutionarily conserved stereociliary protein, disrupt hair cell function in mice and cause progressive hearing loss in humans. 2009 , 85, 328-37	108
1532	Bioinformatic search of plant protein kinases involved in the phosphorylation of microtubular proteins and the regulation of the cell cycle. 2009 , 43, 201-215	1
1531	Bioinformatics search for plant homologues of Ste20-like serine/threonine protein kinases. 2009 , 43, 419-428	2
1530	Arginine methylation analysis of the splicing-associated SR protein SFRS9/SRP30C. 2009, 14, 657-69	14
1529	Phylogeny of the a genomes of wild and cultivated wheat species. 2009 , 45, 1360-1367	15
1528	Specificity of Campylobacter jejuni adhesin PEB3 for phosphates and structural differences among its ligand complexes. 2009 , 48, 3057-67	26
1527	Nonadditivity in the recognition of single-stranded DNA by the schizosaccharomyces pombe protection of telomeres 1 DNA-binding domain, Pot1-DBD. 2009 , 48, 6864-75	15
1526	CLPH, a novel casein kinase 2-phosphorylated disordered protein, is specifically associated with postmeiotic germ cells in rat spermatogenesis. 2009 , 8, 2953-65	14
1525	The Mcm complex: unwinding the mechanism of a replicative helicase. 2009 , 73, 652-83	215

1524	Topological switching between an alpha-beta parallel protein and a remarkably helical molten globule. 2009 , 131, 8290-5	14
1523	Catalytic mechanism of SHCHC synthase in the menaquinone biosynthesis of Escherichia coli: identification and mutational analysis of the active site residues. 2009 , 48, 6921-31	29
1522	Ubiquitin C-terminal electrophiles are activity-based probes for identification and mechanistic study of ubiquitin conjugating machinery. 2009 , 4, 275-87	63
1521	Binding of Pseudomonas aeruginosa apobacterioferritin-associated ferredoxin to bacterioferritin B promotes heme mediation of electron delivery and mobilization of core mineral iron. 2009 , 48, 7420-31	56
1520	Global diversity in the human salivary microbiome. 2009 , 19, 636-43	320
1519	Characterization of a new plasmid-like prophage in a pandemic Vibrio parahaemolyticus O3:K6 strain. 2009 , 75, 2659-67	52
1518	The SH2 domains of inositol polyphosphate 5-phosphatases SHIP1 and SHIP2 have similar ligand specificity but different binding kinetics. 2009 , 48, 11075-83	17
1517	Functional role for the conformationally mobile phenylalanine 223 in the reaction of methylenetetrahydrofolate reductase from Escherichia coli. 2009 , 48, 7673-85	10
1516	Molecular evolution and functional divergence of sulfate transporter gene family in plants. 2009,	
1515	Form, function and phylogenetics of NITRs in bony fish. 2009 , 33, 135-44	40
1514	Isolation and expression profile of a gene encoding for the Signal Transducer and Activator of Transcription STAT2 in Atlantic salmon (Salmo salar). 2009 , 33, 821-9	20
1513	Evidence for the evolution of tenascin and fibronectin early in the chordate lineage. 2009, 41, 424-34	57
1512	The SGNH-hydrolase of Streptomyces coelicolor has (aryl)esterase and a true lipase activity. 2009 , 91, 390-400	34
1511	The first alpha-1,3-glucosidase from bacterial origin belonging to glycoside hydrolase family 31. 2009 , 91, 1434-42	15
1510	Mixed model analysis combining disease ratings and DNA sequences to determine host range of Uromyces salsolae for biological control of Russian thistle. 2009 , 49, 68-76	10
1510		10
	Uromyces salsolae for biological control of Russian thistle. 2009 , 49, 68-76 A small G protein Rhb1 and a GTPase-activating protein Tsc2 involved in nitrogen	

1506	Bovine Carboxylesterases: Evidence for Two CES1 and Five Families of CES Genes on Chromosome 18. 2009 , 4, 11-20	4
1505	Horse carboxylesterases: evidence for six CES1 and four families of CES genes on chromosome 3. 2009 , 4, 54-65	4
1504	A new class of mammalian carboxylesterase CES6. 2009 , 4, 209-17	13
1503	Characterization of dehydrodolichyl diphosphate synthase gene in rainbow trout (Oncorhynchus mykiss). 2009 , 152, 260-5	16
1502	Insights into the effect of detergents on the full-length rhomboid protease from Pseudomonas aeruginosa and its cytosolic domain. 2009 , 1788, 2444-53	18
1501	Clustering of disease-causing mutations on the domain-domain interfaces of ABCC6. 2009 , 379, 706-9	34
1500	Crystal structure of a methyltransferase from a no-known-vector Flavivirus. 2009, 382, 200-4	9
1499	Wnt5b stimulates adipogenesis by activating PPARgamma, and inhibiting the beta-catenin dependent Wnt signaling pathway together with Wnt5a. 2009 , 387, 207-11	77
1498	Structure of the Enterococcus faecalis EIIA(gnt) PTS component. 2009 , 388, 626-9	4
1497	Mutation-induced reinforcement of prestin-expressing cells. 2009 , 389, 569-74	5
1496	Channel catfish, Ictalurus punctatus, cysteine proteinases: cloning, characterisation and expression of cathepsin H and L. 2009 , 26, 332-8	33
1495	Characterization of the interferon genes in homozygous rainbow trout reveals two novel genes, alternate splicing and differential regulation of duplicated genes. 2009 , 26, 293-304	72
1494	Characterization, molecular modelling and developmental expression of zebrafish manganese superoxide dismutase. 2009 , 27, 318-24	30
1493	Evaluation of the effect of CpG hypermutability on human codon substitution. 2009, 431, 18-22	12
1492	The rapid evolution of signal peptides is mainly caused by relaxed selection on non-synonymous and synonymous sites. 2009 , 436, 8-11	30
1491	Splice variants of the human ZC3H14 gene generate multiple isoforms of a zinc finger polyadenosine RNA binding protein. 2009 , 439, 71-8	33
1490	The complete mitochondrial genome of Watersipora subtorquata (Bryozoa, Gymnolaemata, Ctenostomata) with phylogenetic consideration of Bryozoa. 2009 , 439, 17-24	13
1489	Aspartic proteases gene family in rice: Gene structure and expression, predicted protein features and phylogenetic relation. 2009 , 442, 108-18	49

1488	Differentially conserved staphylococcal SH3b_5 cell wall binding domains confer increased staphylolytic and streptolytic activity to a streptococcal prophage endolysin domain. 2009 , 443, 32-41	91
1487	Fast, adaptive evolution at a bacterial host-resistance locus: the PFam54 gene array in Borrelia burgdorferi. 2009 , 445, 26-37	37
1486	Evolution of the Schlafen genes, a gene family associated with embryonic lethality, meiotic drive, immune processes and orthopoxvirus virulence. 2009 , 447, 1-11	68
1485	Simple and fast classification of non-LTR retrotransposons based on phylogeny of their RT domain protein sequences. 2009 , 448, 207-13	72
1484	Automatic classification within families of transposable elements: application to the mariner Family. 2009 , 448, 227-32	25
1483	PII in higher plants: a modern role for an ancient protein. 2009 , 14, 505-11	62
1482	Cu(II) bis(thiosemicarbazone) radiopharmaceutical binding to serum albumin: further definition of species dependence and associated substituent effects. 2009 , 36, 495-504	28
1481	Genotypification of bovine group A rotavirus in M\(\text{\textit{Zico.}}\) 2009, 27, 6411-4	7
1480	Assessment of vaccine potential of the Neisseria-specific protein NMB0938. 2009 , 27, 6910-7	13
1479	Synthetic peptides from conserved regions of the Plasmodium falciparum early transcribed membrane and ring exported proteins bind specifically to red blood cell proteins. 2009 , 27, 6877-86	6
1478	Channel catfish, Ictalurus punctatus Rafinesque 1818, tetraspanin membrane protein family: characterization and expression analysis of CD81 cDNA. 2009 , 128, 431-6	6
1477	Channel catfish (Ictalurus punctatus Rafinesque, 1818) CD156a (ADAM metallopeptidase domain 8): cDNA clone, characterization and expression in tissues. 2009 , 132, 307-13	2
1476	The A312L 5'-UTR of Chlorella virus PBCV-1 is a translational enhancer in Arabidopsis thaliana. 2009 , 140, 138-46	8
1475	Molecular and phylogenetic analysis and vaccine strain match of human influenza A(H3N2) viruses isolated in Northern Greece between 2004 and 2008. 2009 , 145, 220-6	8
1474	The role of Xenopus Rx-L in photoreceptor cell determination. 2009 , 327, 352-65	17
1473	Grandparental stem cells in leech segmentation: differences in CDC42 expression are correlated with an alternating pattern of blast cell fates. 2009 , 336, 112-21	4
1472	Experimental and bioinformatic characterisation of the promoter region of the Marfan syndrome gene, FBN1. 2009 , 94, 233-40	18
1471	Consensus-degenerate hybrid oligonucleotide primers (CODEHOPs) for the detection of novel viruses in non-human primates. 2009 , 49, 32-41	17

	21
Characterization and distribution of NKD, a receptor for Drosophila tachykinin-related peptide 6. 2009 , 30, 545-56	64
Hylin a1, the first cytolytic peptide isolated from the arboreal South American frog Hypsiboas albopunctatus ("spotted treefrog"). 2009 , 30, 291-6	50
Molecular cloning and functional identification of a new K(+) channel blocker, LmKTx10, from the scorpion Lychas mucronatus. 2009 , 30, 675-80	16
Structural characterization of five post-translationally modified isomorphs of a novel putative delta-conotoxin from the vermivorous snail Conus delessertii from the Mexican Caribbean Sea. 2009 , 30, 458-66	10
Expression, purification and characterization of a group of lectin-like peptides from the spider Ornithoctonus huwena. 2009 , 30, 669-74	7
FGLamide Allatostatin genes in Arthropoda: introns early or late?. 2009 , 30, 1241-8	3
Identification, by RT-PCR, of four novel T-1-superfamily conotoxins from the vermivorous snail Conus spurius from the Gulf of Mexico. 2009 , 30, 1396-404	8
A novel antifungal peptide designed from the primary structure of a natural antimicrobial peptide purified from Argopecten purpuratus hemocytes. 2009 , 30, 1405-11	18
BAC library development for allotetraploid Leymus (Triticeae) wildryes enable comparative genetic analysis of lax-barrenstalk1 orthogene sequences and growth habit QTLs. 2009 , 177, 427-438	8
The AAA(+) motor complex of subunits CobS and CobT of cobaltochelatase visualized by single particle electron microscopy. 2009 , 167, 227-34	31
Crystal structure of MqnD (TTHA1568), a menaquinone biosynthetic enzyme from Thermus thermophilus HB8. 2009 , 168, 575-81	13
Differential regulation of transferrin 1 and 2 in Aedes aegypti. 2009 , 39, 234-44	28
The insect SNMP gene family. 2009 , 39, 448-56	191
The Anopheles gambiae salivary protein gSG6: an anopheline-specific protein with a blood-feeding role. 2009 , 39, 457-66	43
A novel growth hormone 1 gene-derived probe for Oncorhynchus masou formosanus distinguished from the Oncorhynchus subspecies. 2009 , 23, 103-6	6
Phylogenetic analysis of rubella viruses isolated in 2008 outbreak in Argentina. 2009 , 46, 286-9	5
HDMCP uncouples yeast mitochondrial respiration and alleviates steatosis in L02 and hepG2 cells by decreasing ATP and H2O2 levels: a novel mechanism for NAFLD. 2009 , 50, 1019-28	34
	peptides. 2009, 30, 467-76 Characterization and distribution of NKD, a receptor for Drosophila tachykinin-related peptide 6. 2009, 30, 545-56 Hylin a1, the first cytolytic peptide isolated from the arboreal South American frog Hypsiboas albopunctatus ("spotted treefrog"). 2009, 30, 291-6 Molecular cloning and functional identification of a new K(+) channel blocker, LmKTx10, from the scorpion Lychas mucronatus. 2009, 30, 675-80 Structural characterization of five post-translationally modified isomorphs of a novel putative delta-conotoxin from the vermivorous snail Conus delessertii from the Mexican Caribbean Sea. 2009, 30, 486-66 Expression, purification and characterization of a group of lectin-like peptides from the spider Ornithoctonus huwena. 2009, 30, 669-74 FGLamide Allatostatin genes in Arthropoda: introns early or late?. 2009, 30, 1241-8 Identification, by RT-PCR, of four novel T-1-superfamily conotoxins from the vermivorous snail Conus spurius from the Gulf of Mexico. 2009, 30, 1396-404 A novel antifungal peptide designed from the primary structure of a natural antimicrobial peptide purified from Argopecten purpuratus hemocytes. 2009, 30, 1405-11 BAC library development for allotetraploid Leymus (Triticeae) wildryes enable comparative genetic analysis of lax-barrenstalk1 orthogene sequences and growth habit QTLs. 2009, 177, 427-438 The AAA(+) motor complex of subunits CobS and CobT of cobaltochelatase visualized by single particle electron microscopy. 2009, 167, 227-34 Crystal structure of MqnD (TTHA1568), a menaquinone biosynthetic enzyme from Thermus thermophilus HBB. 2009, 168, 575-81 Differential regulation of transferrin 1 and 2 in Aedes aegypti. 2009, 39, 234-44 The insect SNMP gene family. 2009, 39, 448-56 The Anopheles gambiae salivary protein gSG6: an anopheline-specific protein with a blood-feeding role. 2009, 39, 457-66 Phylogenetic analysis of rubella viruses isolated in 2008 outbreak in Argentina. 2009, 46, 286-9

1452	Structure of human endothelin-converting enzyme I complexed with phosphoramidon. 2009 , 385, 178-87	40
1451	Properties of an ezrin mutant defective in F-actin binding. 2009 , 385, 1015-31	27
1450	Crystal structure of chlorite dismutase, a detoxifying enzyme producing molecular oxygen. 2009 , 387, 192-206	66
1449	Insights into how RNase R degrades structured RNA: analysis of the nuclease domain. 2009 , 387, 570-83	52
1448	The mouse thymosin beta15 gene family displays unique complexity and encodes a functional thymosin repeat. 2009 , 387, 809-25	12
1447	Contributions of the transmembrane domain and a key acidic motif to assembly and function of the TatA complex. 2009 , 388, 122-32	16
1446	Structural rearrangements in the active site of the Thermus thermophilus 16S rRNA methyltransferase KsgA in a binary complex with 5'-methylthioadenosine. 2009 , 388, 271-82	17
1445	Active-site gating regulates substrate selectivity in a chymotrypsin-like serine protease the structure of haemophilus influenzae immunoglobulin A1 protease. 2009 , 389, 559-74	58
1444	Structure and calcium-binding activity of LipL32, the major surface antigen of pathogenic Leptospira sp. 2009 , 390, 722-36	35
1443	Nonmyristoylated matrix protein from the Mason-Pfizer monkey virus forms oligomers. 2009 , 390, 967-80	9
1442	An evolutionarily conserved family of virion tail needles related to bacteriophage P22 gp26: correlation between structural stability and length of the alpha-helical trimeric coiled coil. 2009 , 391, 227-45	13
1441	Conformational adaptability of Redbeta during DNA annealing and implications for its structural relationship with Rad52. 2009 , 391, 586-98	50
1440	Histone deacetylases regulate multicellular development in the social amoeba Dictyostelium discoideum. 2009 , 391, 833-48	12
1439	Characterization of two novel aldo-keto reductases from Arabidopsis: expression patterns, broad substrate specificity, and an open active-site structure suggest a role in toxicant metabolism following stress. 2009 , 392, 465-80	101
1438	Archaeal aIF2B interacts with eukaryotic translation initiation factors eIF2alpha and eIF2Balpha: Implications for aIF2B function and eIF2B regulation. 2009 , 392, 701-22	28
1437	Insights into the biosynthesis of the Vibrio cholerae major autoinducer CAI-1 from the crystal structure of the PLP-dependent enzyme CqsA. 2009 , 392, 763-73	32
1436	Crystal structure of the three tandem FF domains of the transcription elongation regulator CA150.	
14,50	2009 , 393, 397-408	10

1434	A new cloning system using a mutant esterase containing MCS as an indicator for gene cloning. 2009 , 77, 302-7	6
1433	Use of molecular beacons and multi-allelic real-time PCR for detection of and discrimination between virulent Bacillus anthracis and other Bacillus isolates. 2009 , 78, 45-53	23
1432	Comparison of multiplex PCR, enzyme immunoassay and cell culture methods for the detection of enterotoxinogenic Bacillus cereus. 2009 , 78, 265-70	73
1431	Identification of mitochondrial Complex II subunits SDH3 and SDH4 and ATP synthase subunits a and b in Plasmodium spp. 2009 , 9, 443-53	28
1430	The rainbow trout TLR9 gene and its role in the immune responses elicited by a plasmid encoding the glycoprotein G of the viral haemorrhagic septicaemia rhabdovirus (VHSV). 2009 , 46, 1710-7	36
1429	A function for AAMP in Nod2-mediated NF-kappaB activation. 2009 , 46, 2647-54	25
1428	Molecular cloning and analysis of SSc5D, a new member of the scavenger receptor cysteine-rich superfamily. 2009 , 46, 2585-96	14
1427	Antigenic basis of diversity in the gammadelta T cell co-receptor WC1 family. 2009 , 46, 2565-75	28
1426	Predicted structural basis for CD1c presentation of mycobacterial branched polyketides and long lipopeptide antigens. 2009 , 47, 253-60	11
1425	Kinetic characterization and quaternary structure of glutamate racemase from the periodontal anaerobe Fusobacterium nucleatum. 2009 , 491, 16-24	11
1424	Polycyclic aromatic hydrocarbon-degrading species isolated from Hawaiian soils: Mycobacterium crocinum sp. nov., Mycobacterium pallens sp. nov., Mycobacterium rutilum sp. nov., Mycobacterium rufum sp. nov. and Mycobacterium aromaticivorans sp. nov. 2009 , 59, 378-87	72
1423	Do lichens domesticate photobionts like farmers domesticate crops? Evidence from a previously unrecognized lineage of filamentous cyanobacteria. 2009 , 96, 1409-18	91
1422	Transmembrane helical domain of the cannabinoid CB1 receptor. 2009 , 96, 3251-62	30
1421	Interactions of H562 in the S5 helix with T618 and S621 in the pore helix are important determinants of hERG1 potassium channel structure and function. 2009 , 96, 3600-10	35
1420	Spore-forming halophilic bacteria isolated from Arctic terrains: Implications for long-range transportation of microorganisms. 2009 , 3, 163-169	17
1419	Bruno negatively regulates germ cell-less expression in a BRE-independent manner. 2009 , 126, 503-16	9
1418	Teaching synthetic biology, bioinformatics and engineering to undergraduates: the interdisciplinary Build-a-Genome course. 2009 , 181, 13-21	48
1417	The human asparaginase-like protein 1 hASRGL1 is an Ntn hydrolase with beta-aspartyl peptidase activity. 2009 , 48, 11026-31	63

1416 The basic concepts of molecular modeling. 2009 , 467, 307-334	13
Intragenomic variation in the rDNA internal transcribed spacer Cumberlandia monodonta (Say, 1828). 2009 , 75, 419-421	(ITS1) in the freshwater mussel 8
Cloning, expression in Pichia pastoris, and characterization of a endo-1,4-beta-mannosidase from Aspergillus niger BK01. 2009	
Lack of functional and expression homology between human a enzymes: implications for modelling human cancers. 2009 , 8, 1	30
1412 Multiple-infection and recombination in HIV-1 within a longitu	dinal cohort of women. 2009 , 6, 54
Panorama phylogenetic diversity and distribution of type A inf internal gene sequences. 2009 , 6, 137	luenza viruses based on their six
Bioinformatic evidence for a stem-loop structure 5'-adjacent to gene in the bee paralysis dicistroviruses. 2009 , 6, 193	o the IGR-IRES and for an overlapping
Molecular characterization and the effect of salinity on cyanob Eastern Uttar Pradesh, India. 2009 , 5, 4	pacterial diversity in the rice fields of 33
1408 In silico analysis of the cyclophilin repertoire of apicomplexan	parasites. 2009 , 2, 27 23
Beyond Simple Homology Searches: Multiple Sequence Alignm 1, 11.3.1	ients and Phylogenetic Trees. 2009 , 4
1406 Submitting a Sequence to GenBank. 2009 , 1, 11.2.1	
1405 Subtyping of the influenza virus by high resolution mass spect	rometry. 2009 , 81, 3500-6 48
1404 The role of CLCA proteins in inflammatory airway disease. 200	9 , 71, 425-49 8 ₃
1403 Detection and quantitative assessment of horizontal gene trai	nsfer. 2009 , 532, 195-213 19
1402 Identification of a maize neocentromere in an oat-maize addit	on line. 2009 , 124, 228-38 64
Pivotal roles of the outer membrane polysaccharide export an protein families in export of extracellular polysaccharides in g	
Molecular features of 23 patients with glycogen storage disea p.R1147G associated with isolated glucosidase deficiency, alor	
Chapter 1: Variation in form and function the helix-turn-helix r 2009 , 69, 1-22	egulators of the GntR superfamily.

1398	Integrating Decision Tree and Hidden Markov Model (HMM) for Subtype Prediction of Human Influenza A Virus. 2009 , 52-58	4
1397	Phylogenetic and phenotypic relationships among Triatoma carcavalloi (Hemiptera: Reduviidae: Triatominae) and related species collected in domiciles in Rio Grande do Sul State, Brazil. 2009 , 34, 164-173	1
1396	Nomenclature Abstract for Porphyromonadaceae Krieg 2012 emend. Ormerod et al. 2016 2009,	
1395	Localization of the ATP-binding cassette (ABC) transport proteins PfMRP1, PfMRP2, and PfMDR5 at the Plasmodium falciparum plasma membrane. 2009 , 8, 205	40
1394	Tandem repeats modify the structure of human genes hosted in segmental duplications. 2009, 10, R137	15
1393	Development and application of versatile high density microarrays for genome-wide analysis of Streptomyces coelicolor: characterization of the HspR regulon. 2009 , 10, R5	32
1392	Structural modeling identified the tRNA-binding domain of Utp8p, an essential nucleolar component of the nuclear tRNA export machinery of Saccharomyces cerevisiae. 2009 , 87, 431-43	6
1391	Recent Advances in Transthyretin Evolution, Structure and Biological Functions. 2009,	10
1390	Genome Sequence Databases: Types of Data and Bioinformatic Tools. 2009 , 211-236	1
1389	Algorithms in Bioinformatics. 2009,	1
1389 1388	Algorithms in Bioinformatics. 2009, Maximum unbiased validation (MUV) data sets for virtual screening based on PubChem bioactivity data. 2009, 49, 169-84	208
3 ,	Maximum unbiased validation (MUV) data sets for virtual screening based on PubChem bioactivity	
1388	Maximum unbiased validation (MUV) data sets for virtual screening based on PubChem bioactivity data. 2009 , 49, 169-84	208
1388	Maximum unbiased validation (MUV) data sets for virtual screening based on PubChem bioactivity data. 2009 , 49, 169-84 CooC1 from Carboxydothermus hydrogenoformans is a nickel-binding ATPase. 2009 , 48, 11505-13	208
1388 1387 1386	Maximum unbiased validation (MUV) data sets for virtual screening based on PubChem bioactivity data. 2009, 49, 169-84 CooC1 from Carboxydothermus hydrogenoformans is a nickel-binding ATPase. 2009, 48, 11505-13 A Database of Selected Marine Genomics for Retrieving Distantly Related Proteins. 2009, Identification and characterization of gshA, a gene encoding the glutamate-cysteine ligase in the	208
1388 1387 1386	Maximum unbiased validation (MUV) data sets for virtual screening based on PubChem bioactivity data. 2009, 49, 169-84 CooC1 from Carboxydothermus hydrogenoformans is a nickel-binding ATPase. 2009, 48, 11505-13 A Database of Selected Marine Genomics for Retrieving Distantly Related Proteins. 2009, Identification and characterization of gshA, a gene encoding the glutamate-cysteine ligase in the halophilic archaeon Haloferax volcanii. 2009, 191, 5196-204 Identification of a cytoplasmic manganese superoxide dismutase (cMnSOD) in the red swamp	208 44 0
1388 1387 1386 1385	Maximum unbiased validation (MUV) data sets for virtual screening based on PubChem bioactivity data. 2009, 49, 169-84 CooC1 from Carboxydothermus hydrogenoformans is a nickel-binding ATPase. 2009, 48, 11505-13 A Database of Selected Marine Genomics for Retrieving Distantly Related Proteins. 2009, Identification and characterization of gshA, a gene encoding the glutamate-cysteine ligase in the halophilic archaeon Haloferax volcanii. 2009, 191, 5196-204 Identification of a cytoplasmic manganese superoxide dismutase (cMnSOD) in the red swamp crawfish, Procambarus clarkii: cDNA cloning and tissue expression. 2009, 26, 284-8	208 44 0 20 8

1380	Role of conjugative elements in the evolution of the multidrug-resistant pandemic clone Streptococcus pneumoniaeSpain23F ST81. 2009 , 191, 1480-9	129
1379	Evolutionary analysis of the Sub1 gene cluster that confers submergence tolerance to domesticated rice. 2009 , 103, 143-50	59
1378	Mitochondrial and chloroplastic targeting signals of NADP+-dependent isocitrate dehydrogenase. 2009 , 87, 963-74	7
1377	Signature peptides of influenza nucleoprotein for the typing and subtyping of the virus by high resolution mass spectrometry. 2009 , 134, 2253-61	26
1376	Dissection of USP catalytic domains reveals five common insertion points. 2009 , 5, 1797-808	110
1375	Identification of 3-hydroxy-2-(3-hydroxyphenyl)-4H-1-benzopyran-4-ones as isoform-selective PKC-zeta inhibitors and potential therapeutics for psychostimulant abuse. 2009 , 5, 927-30	10
1374	Photosensitivity in sponge due to cytochrome c oxidase?. 2009 , 8, 755-7	6
1373	Biological Feature Incorporated Alignment for Cross Species Analysis on Carbohydrate Binding Modules. 2009 ,	1
1372	Insect mitochondrial genomics 3: the complete mitochondrial genome sequences of representatives from two neuropteroid orders: a dobsonfly (order Megaloptera) and a giant lacewing and an owlfly (order Neuroptera). 2009 , 52, 31-8	38
1371	Rice Pi5-mediated resistance to Magnaporthe oryzae requires the presence of two coiled-coil-nucleotide-binding-leucine-rich repeat genes. 2009 , 181, 1627-38	201
1370	FastWrap: An efficient wrapper for tabular data extraction from the web. 2009,	7
1369	Estimating mutation distances from unaligned genomes. 2009 , 16, 1487-500	67
1368	Comparative genomics of the fungal pathogens Candida dubliniensis and Candida albicans. 2009 , 19, 2231-44	165
1367	Tiger species identification based on molecular approach. 2009 , 2, 310-312	6
1366	Human coronaviruses 229E and NL63: close yet still so far. 2009 , 108, 270-9	38
1365	Phylogeny of the "forgotten" cellular slime mold, Fonticula alba, reveals a key evolutionary branch within Opisthokonta. 2009 , 26, 2699-709	115
1364	Phylogenetic Relationships, Evolution, and Systematic Revision of the Septate Gregarines (Apicomplexa: Eugregarinorida: Septatorina). 2009 , 76, 167-190	50
1363	The complete mitochondrial genome of Diadegma semiclausum (hymenoptera: ichneumonidae) indicates extensive independent evolutionary events. 2009 , 52, 308-19	83

1362	Protein-repairing methionine sulfoxide reductases in photosynthetic organisms: gene organization, reduction mechanisms, and physiological roles. 2009 , 2, 202-17	92
1361	Zea mays annexins modulate cytosolic free Ca2+ and generate a Ca2+-permeable conductance. 2009 , 21, 479-93	118
1360	Characterization of 3-ketosteroid 9{alpha}-hydroxylase, a Rieske oxygenase in the cholesterol degradation pathway of Mycobacterium tuberculosis. 2009 , 284, 9937-46	114
1359	Two distinct groups of fungal catalase/peroxidases. 2009 , 37, 772-7	30
1358	Proteomic analyses of pancreatic cyst fluids. 2009 , 38, e33-42	66
1357	The HIV hide and seek game: an immunogenomic analysis of the HIV epitope repertoire. 2009 , 23, 1311-8	25
1356	Crystallization and preliminary X-ray diffraction analysis of ARO9, an aromatic aminotransferase from Saccharomyces cerevisiae. 2009 , 16, 450-3	3
1355	Are coral-dwelling crabs monophyletic? A phylogeny of the Trapezioidea (Crustacea : Decapoda : Brachyura). 2009 , 23, 402	17
1354	POPULATION STRUCTURE OF PHYTOPHTHORA INFESTANS IN THE VENEZUELAN ANDES (2004-2007). 2009 , 129-140	2
1353	Schistosoma kisumuensis n. sp. (Digenea: Schistosomatidae) from murid rodents in the Lake Victoria Basin, Kenya and its phylogenetic position within the S. haematobium species group. 2009 , 136, 987-1001	14
1352	A novel motif at the C-terminus of palmitoyltransferases is essential for Swf1 and Pfa3 function in vivo. 2009 , 419, 301-8	34
1351	Identification and characterization of the lipid-binding property of GrlR, a locus of enterocyte effacement regulator. 2009 , 420, 191-9	18
1350	Structure of human porphobilinogen deaminase at 2.8 A: the molecular basis of acute intermittent porphyria. 2009 , 420, 17-25	53
1349	Functional characterization of the early steps of tetrapyrrole biosynthesis and modification in Desulfovibrio vulgaris Hildenborough. 2009 , 420, 317-25	33
1348	Functional conservation of tRNase ZL among Saccharomyces cerevisiae, Schizosaccharomyces pombe and humans. 2009 , 422, 483-92	26
1347	Convergent evolution of coenzyme M biosynthesis in the Methanosarcinales: cysteate synthase evolved from an ancestral threonine synthase. 2009 , 424, 467-78	32
1346	Active site substitutions delineate distinct classes of eubacterial flap endonuclease. 2009 , 418, 285-92	15
1345	The haloarchaeal chromosome replication machinery. 2009 , 37, 108-13	17

1344	Occurrence of Erysiphe necator chasmothecia and their natural parasitism by Ampelomyces quisqualis. 2009 , 99, 704-10	16
1343	Characterization of a New Streptomyces Strain, DS3024, That Causes Potato Common Scab. 2009 , 93, 1329-1334	23
1342	A New 'Candidatus Liberibacter' Species Associated with Diseases of Solanaceous Crops. 2009 , 93, 208-214	188
1341	Identification and Properties of a Carlavirus Causing Chlorotic Mottle of Florists' Hydrangea (H. macrophylla) in the United States. 2009 , 93, 891-895	3
1340	Pathotypes and genetic relationship of worldwide collections of Elsinolspp. causing scab diseases of citrus. 2009 , 99, 721-8	33
1339	Evolutionary characterization of a highly repetitive sequence identified from the false killer whale (Pseudorca crassidens). 2009 , 84, 185-9	
1338	Cloning and tissue-specific expression of a delta-COP homologue in a freshwater and a brackish water-adapted strain of rainbow trout (Oncorhynchus mykiss). 2009 , 84, 239-43	3
1337	Morphological Identification and Phylogenetic Evaluation of the Cyanobacterium Anabaena Isolated from Urushizawa Dam and other Lakes and Reservoirs. 2009 , 32, 501-504	
1336	Using the Multiple Analysis Approach to Reconstruct Phylogenetic Relationships among Planktonic Foraminifera from Highly Divergent and Length-polymorphic SSU rDNA Sequences. 2009 , 3, 155-77	25
1335	Intracellular catalase/peroxidase from the phytopathogenic rice blast fungus Magnaporthe grisea: expression analysis and biochemical characterization of the recombinant protein. 2009 , 418, 443-51	21
1334	Protein domains as information processing units. 2009 , 10, 133-45	3
1333	A new role for Zn(II) aminopeptidases: antigenic peptide generation and destruction. 2009, 15, 3656-70	39
1332	Isolation and Molecular Identification of Klebsiella Pneumoniae Strains, Producing Diols from Glycerol. 2009 , 23, 814-817	3
1331	A diagnostic challenge: mild hemophilia B with normal activated partial thromboplastin time. 2010 , 21, 368-71	11
1330	Paleogenomic analysis of the short arm of chromosome 3 reveals the history of the African and Asian progenitors of cultivated rices. 2010 , 2, 132-9	3
1329	Quantitative gene expression profiles in real time from expressed sequence tag databases. 2010 , 14, 321-36	4
1328	Neobulgaria alba sp. nov. and its Phialophora-like anamorph in native forests and kiwifruit orchards in New Zealand. 2010 , 113, 385-396	8
1327	Recent patents and challenges on DNA microarray probe design technologies. 2010 , 4, 210-7	2

1326	Glomus candidum, a new species of arbuscular mycorrhizal fungi from North American grassland. 2010 , 113, 101-109	5
1325	Stereotyped patterns of B-cell receptor in splenic marginal zone lymphoma. 2010 , 95, 1792-6	74
1324	Comparative analysis of two fatty acid binding proteins from Fasciola gigantica. 2010 , 137, 1805-17	16
1323	A Parallel Non-Alignment Based Approach to Efficient Sequence Comparison using Longest Common Subsequences. 2010 , 256, 012012	
1322	Virus-induced gene silencing of plastidial soluble inorganic pyrophosphatase impairs essential leaf anabolic pathways and reduces drought stress tolerance in Nicotiana benthamiana. 2010 , 154, 55-66	53
1321	T1653 mutation in the enhancer II region of the hepatitis B virus genome in southern African Blacks with hepatocellular carcinoma. 2010 , 22, 541-5	6
1320	An algorithm for the reconstruction of consensus sequences of ancient segmental duplications and transposon copies in eukaryotic genomes. 2010 , 6, 147-62	3
1319	Proteome-wide identification of mycobacterial pupylation targets. 2010 , 6, 386	86
1318	Phylogenetics and revised taxonomy of the Australian freshwater cod genus, Maccullochella (Percichthyidae). 2010 , 61, 980	13
1317	Secondary structural analyses of ITS1 in Paramecium. 2010 , 25, 313-6	8
1316	Initial studies of the cytoplasmic FABP superfamily. 2010 , 86, 220-8	9
1315	New family of allomorphic jellyfishes, Drymonematidae (Scyphozoa, Discomedusae), emphasizes evolution in the functional morphology and trophic ecology of gelatinous zooplankton. 2010 , 219, 249-67	33
1314	Evolution of nickel hyperaccumulation by Stackhousia tryonii (Celastraceae), a serpentinite-endemic plant from Queensland, Australia. 2010 , 23, 415	11
1313	Investigation of the Transcriptome of Prairie Cord Grass, a New Cellulosic Biomass Crop. 2010 , 3,	17
1312	Complete mitochondrial genome of Cabot's tragopan, Tragopan caboti (Galliformes: Phasianidae). 2010 , 9, 1204-16	31
1311	Characterization of the complete mitochondrial genome of the Rock pigeon, Columba livia (Columbiformes: Columbidae). 2010 , 9, 1234-49	49
1310	Evolution of the Clustal Family of Multiple Sequence Alignment Programs. 2010 , 277-298	
1309	Identification, sequencing and characterization of a stress induced homologue of fructose bisphosphate aldolase from cotton. 2010 , 90, 41-48	7

1308	Update of human and mouse forkhead box (FOX) gene families. 2010 , 4, 345-52	143
1307	Pleistophora hyphessobryconis (Microsporidia) infecting zebrafish Danio rerio in research facilities. 2010 , 91, 47-56	49
1306	Rapid typing and subtyping of vaccine strains of the influenza virus with high resolution mass spectrometry. 2010 , 16, 321-9	14
1305	Crystal structure of the human transcription elongation factor DSIF hSpt4 subunit in complex with the hSpt5 dimerization interface. 2009 , 425, 373-80	23
1304	S-Glutathionyl-(chloro)hydroquinone reductases: a novel class of glutathione transferases. 2010 , 428, 419-27	34
1303	Functional Analysis of Genes. 2010 , 2, 1-16	2
1302	Flavitrack analysis of the structure and function of West Nile non-structural proteins. 2010 , 6, 134-46	15
1301	Structural assessment of the effects of amino acid substitutions on protein stability and protein protein interaction. 2010 , 3, 334-49	27
1300	Methyl esterase 1 (StMES1) is required for systemic acquired resistance in potato. 2010 , 23, 1151-63	78
1299	An In Planta Method for Assessing the Role of Basidiospores in Rhizoctonia Foliar Disease of Tomato. 2010 , 94, 515-520	24
1298	Isolation, characterization, and sensitivity to 2,4-diacetylphloroglucinol of isolates of Phialophora spp. from Washington wheat fields. 2010 , 100, 404-14	8
1297	DNA types of aspermic Fasciola species in Japan. 2010 , 72, 1371-4	25
1296	Identity of Tetragonia pentandraand taxonomy and distribution of Patellifolia (Chenopodiaceae). 2010 , 40, 5-11	9
1295	Comparative molecular evolution of trichoderma chitinases in response to mycoparasitic interactions. 2010 , 6, 1-26	46
1294	Rapid Screening for Gram-Negative and Gram-Positive Beer-Spoilage Firmicutes Using a Real-Time Multiplex PCR. 2010 , 68, 89-95	5
1293	Bioinformatic search for plant homologs of the protein kinase Bub1 key component of the mitotic spindle assembly checkpoint. 2010 , 44, 376-388	4
1292	Type I restriction-modification loci reveal high allelic diversity in clinical Helicobacter pylori isolates. 2010 , 15, 114-25	8
1291	Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation site motifs. 2010 , 3, ra12	262

1290	Occurrence of the Vibrio cholerae seventh pandemic VSP-I island and a new variant. 2010, 14, 1-7	30
1289	Homozygosity mapping reveals mutations of GRXCR1 as a cause of autosomal-recessive nonsyndromic hearing impairment. 2010 , 86, 138-47	52
1288	Evolutionary dynamics of the wnt gene family: a lophotrochozoan perspective. 2010 , 27, 1645-58	93
1287	Sensing by the membrane-bound sensor kinase DcuS: exogenous versus endogenous sensing of C(4)-dicarboxylates in bacteria. 2010 , 5, 1383-402	24
1286	ALTER: program-oriented conversion of DNA and protein alignments. 2010 , 38, W14-8	265
1285	Amaranth (Amaranthus hypochondriacus) vicilin subunit structure. 2010 , 58, 12957-63	19
1284	Immunoinformatics and systems biology methods for personalized medicine. 2010 , 662, 203-20	25
1283	Further refinement of the phylogeny of the Halobacteriaceae based on the full-length RNA polymerase subunit B' (rpoB') gene. 2010 , 60, 2398-2408	160
1282	Evolutionary relationships among scyphozoan jellyfish families based on complete taxon sampling and phylogenetic analyses of 18S and 28S ribosomal DNA. 2010 , 50, 436-55	56
1281	Computational approaches to 3D modeling of RNA. 2010 , 22, 283101	83
1280	Detection of fiber-digesting bacteria in the ceca of ostrich using specific primer sets. 2010 , 60, 112-6	13
1279	Novel integron gene cassette arrays identified in a global collection of multi-drug resistant non-typhoidal Salmonella enterica. 2010 , 60, 217-23	25
1278	RNA editing in six mitochondrial ribosomal protein genes of Didymium iridis. 2010 , 56, 203-13	11
1277	The alpha-kinase family: an exceptional branch on the protein kinase tree. 2010 , 67, 875-90	72
1276	Characterisations of odorant-binding proteins in the tsetse fly Glossina morsitans morsitans. 2010 , 67, 919-29	38
1275	Structure and function of interleukin-22 and other members of the interleukin-10 family. 2010 , 67, 2909-35	35
1274	Myoinhibiting peptides are the ancestral ligands of the promiscuous Drosophila sex peptide receptor. 2010 , 67, 3511-22	73
1273	Molecular evidence for species separation in the water mite Hygrobates nigromaculatus Lebert, 1879 (Acari, Hydrachnidia): evolutionary consequences of the loss of larval parasitism. 2010 , 72, 347-360	49

1272	Probing the structure of human glucose transporter 2 and analysis of protein ligand interactions. 2010 , 19, 836-853	7
1271	Molecular diagnosis of a previously unreported predator-prey association in coffee: Karnyothrips flavipes Jones (Thysanoptera: Phlaeothripidae) predation on the coffee berry borer. 2010 , 97, 291-8	25
1270	A new SNP haplotype associated with blue disease resistance gene in cotton (Gossypium hirsutum L.). 2010 , 120, 943-53	63
1269	The putative Bacillus subtilis L,D-transpeptidase YciB is a lipoprotein that localizes to the cell poles in a divisome-dependent manner. 2010 , 192, 57-68	3
1268	Molecular diversity of katG genes in the soil bacteria Comamonas. 2010 , 192, 175-84	4
1267	CspC and CspD are essential for Caulobacter crescentus stationary phase survival. 2010 , 192, 747-58	14
1266	Kosmotoga arenicorallina sp. nov. a thermophilic and obligately anaerobic heterotroph isolated from a shallow hydrothermal system occurring within a coral reef, southern part of the Yaeyama Archipelago, Japan, reclassification of Thermococcoides shengliensis as Kosmotoga shengliensis	32
1265	comb. nov., and emended description of the genus Kosmotoga. 2010 , 192, 811-9 The metabolic demands of swimming behavior influence the evolution of skeletal muscle fiber design in the brachyuran crab family Portunidae. 2010 , 157, 221-236	21
1264	The phylogenetic distribution of non-CTCF insulator proteins is limited to insects and reveals that BEAF-32 is Drosophila lineage specific. 2010 , 70, 74-84	30
1263	Evolution, homology conservation, and identification of unique sequence signatures in GH19 family chitinases. 2010 , 70, 466-78	50
1262	Evolution of the RpoS regulon: origin of RpoS and the conservation of RpoS-dependent regulation in bacteria. 2010 , 70, 557-71	36
1261	Evaluation of models of the mechanisms underlying intron loss and gain in Aspergillus fungi. 2010 , 71, 364-73	34
1260	Evolution of dopamine-related systems: biosynthesis, degradation and receptors. 2010 , 71, 374-84	10
1259	Nitrogen transformations and diversity of ammonia-oxidizing bacteria in a desert ephemeral stream receiving untreated wastewater. 2010 , 59, 46-58	14
1258	Comparison of 61 sequenced Escherichia coli genomes. 2010 , 60, 708-20	360
1257	Soil microbial abundance and diversity along a low precipitation gradient. 2010 , 60, 453-61	126
1256	Conformational studies of peptides representing a segment of TM7 from H+-VO-ATPase in SDS micelles. 2010 , 39, 639-46	6
1255	Camptosemin, a tetrameric lectin of Camptosema ellipticum: structural and functional analysis. 2010 , 39, 1193-205	4

1254	Lineage pattern, trans-species polymorphism, and selection pressure among the major lineages of feline MHC-DRB peptide-binding region. 2010 , 62, 307-17	16
1253	Haplotype variation, recombination, and gene conversion within the turkey MHC-B locus. 2010 , 62, 465-77	26
1252	Identification and characterization of a bacterial cytochrome P450 for the metabolism of diclofenac. 2010 , 85, 625-33	29
1251	Characterization of a recombinant amylolytic enzyme of hyperthermophilic archaeon Thermofilum pendens with extremely thermostable maltogenic amylase activity. 2010 , 85, 1821-30	20
1250	Discovery of a new tyrosinase-like enzyme family lacking a C-terminally processed domain: production and characterization of an Aspergillus oryzae catechol oxidase. 2010 , 86, 213-26	35
1249	Characterization of corrosive bacterial consortia isolated from petroleum-product-transporting pipelines. 2010 , 85, 1175-88	124
1248	A robust and extracellular heme-containing peroxidase from Thermobifida fusca as prototype of a bacterial peroxidase superfamily. 2010 , 86, 1419-30	150
1247	Functional expression of a thermophilic glucuronyl esterase from Sporotrichum thermophile: identification of the nucleophilic serine. 2010 , 87, 1765-72	44
1246	Functional analysis of glycoside hydrolase family 8 xylanases shows narrow but distinct substrate specificities and biotechnological potential. 2010 , 87, 2125-35	24
1245	Engineering of a fungal beta-galactosidase to remove product inhibition by galactose. 2010 , 87, 1773-82	38
1244	Regioselective hydroxylation of norisoprenoids by CYP109D1 from Sorangium cellulosum So ce56. 2010 , 88, 485-95	52
1243	A WD40-repeat gene from Malus x domestica is a functional homologue of Arabidopsis thaliana TRANSPARENT TESTA GLABRA1. 2010 , 29, 285-94	63
1242	GA3 stimulates the formation and germination of somatic embryos and the expression of a KNOTTED-like homeobox gene of Cocos nucifera (L.). 2010 , 29, 1049-59	31
1241	Ulva and Enteromorpha (Ulvaceae, Chlorophyta) from two sides of the Yellow Sea: analysis of nuclear rDNA ITS and plastid rbcL sequence data. 2010 , 28, 762-768	10
124 0	Alkylresorcylic acid synthesis by type III polyketide synthases from rice Oryza sativa. 2010, 71, 1059-67	27
1239	Gibberellin 3-oxidases in developing embryos of the southern wild cucumber, Marah macrocarpus. 2010 , 71, 2010-8	22
1238	Ecological leads for natural product discovery: Novel sesquiterpene hydroquinones from the red macroalga Peyssonnelia sp. 2010 , 66, 455-461	39
1237	In silico analysis of antibody triggering biofilm associated protein in Acinetobacter baumannii. 2010 , 266, 275-90	35

1236	Identification of forensically important blowfly species (Diptera: Calliphoridae) by high-resolution melting PCR analysis. 2010 , 124, 277-85	28
1235	Mitochondrial DNA diversity in a population from Santa Catarina (Brazil): predominance of the European input. 2010 , 124, 331-6	23
1234	Role of a novel disulfide bridge within the all-beta fold of soluble Rieske proteins. 2010 , 15, 271-81	6
1233	Changes in non-core regions stabilise plastocyanin from the thermophilic cyanobacterium Phormidium laminosum. 2010 , 15, 329-38	4
1232	Cloning, purification and characterisation of a recombinant purine nucleoside phosphorylase from Bacillus halodurans Alk36. 2010 , 14, 185-92	15
1231	Homology modeling and molecular dynamics simulations of HgiDII methyltransferase in complex with DNA and S-adenosyl-methionine: catalytic mechanism and interactions with DNA. 2010 , 16, 1213-22	1
1230	"Fuzzy oil drop" model applied to individual small proteins built of 70 amino acids. 2010 , 16, 1269-82	4
1229	Contribution of charged and polar residues for the formation of the E1-E2 heterodimer from Hepatitis C Virus. 2010 , 16, 1625-37	9
1228	A novel sequence-based method of predicting protein DNA-binding residues, using a machine learning approach. 2010 , 30, 99-105	7
1227	Differential expression of CHS7 and CHS8 genes in soybean. 2010 , 231, 741-53	47
1226	Cloning and characterization of a novel gene that encodes (S)-beta-bisabolene synthase from ginger, Zingiber officinale. 2010 , 232, 121-30	36
1226 1225		36 15
	ginger, Zingiber officinale. 2010 , 232, 121-30 Molecular and experimental evidence refuse the life cycle of Proctoeces lintoni (Fellodistomidae) in	
1225	ginger, Zingiber officinale. 2010 , 232, 121-30 Molecular and experimental evidence refuse the life cycle of Proctoeces lintoni (Fellodistomidae) in Chile. 2010 , 106, 737-40	15
1225	ginger, Zingiber officinale. 2010, 232, 121-30 Molecular and experimental evidence refuse the life cycle of Proctoeces lintoni (Fellodistomidae) in Chile. 2010, 106, 737-40 Large intron 14 rearrangement in APC results in splice defect and attenuated FAP. 2010, 127, 359-69 Conserved synteny at the protein family level reveals genes underlying Shewanella species' cold	15 15
1225 1224 1223	ginger, Zingiber officinale. 2010, 232, 121-30 Molecular and experimental evidence refuse the life cycle of Proctoeces lintoni (Fellodistomidae) in Chile. 2010, 106, 737-40 Large intron 14 rearrangement in APC results in splice defect and attenuated FAP. 2010, 127, 359-69 Conserved synteny at the protein family level reveals genes underlying Shewanella species' cold tolerance and predicts their novel phenotypes. 2010, 10, 97-110 Recharacterization of Chlamydomonas reinhardtii and its relatives with new isolates from Japan.	15 15 10
1225 1224 1223	ginger, Zingiber officinale. 2010, 232, 121-30 Molecular and experimental evidence refuse the life cycle of Proctoeces lintoni (Fellodistomidae) in Chile. 2010, 106, 737-40 Large intron 14 rearrangement in APC results in splice defect and attenuated FAP. 2010, 127, 359-69 Conserved synteny at the protein family level reveals genes underlying Shewanella species' cold tolerance and predicts their novel phenotypes. 2010, 10, 97-110 Recharacterization of Chlamydomonas reinhardtii and its relatives with new isolates from Japan. 2010, 123, 67-78	15 15 10 40

1218	Savicalin, a lipocalin from hemocytes of the soft tick, Ornithodoros savignyi. 2010 , 52, 313-26	10
1217	Putative recombination events and evolutionary history of five economically important viruses of fruit trees based on coat protein-encoding gene sequence analysis. 2010 , 48, 357-75	14
1216	Isolation and identification of Rhizoctonia-like fungi from roots of three orchid genera, Paphiopedilum, Dendrobium, and Cymbidium, collected in Chiang Rai and Chiang Mai provinces of Thailand. 2010 , 20, 459-71	55
1215	Craterellus fallax, a Black Trumpet mushroom from eastern North America with a broad host range. 2010 , 20, 569-75	10
1214	The complete nucleotide sequence of a new bipartite begomovirus from Brazil infecting Abutilon. 2010 , 155, 813-6	16
1213	Isolation and sequence analysis of Culex flavivirus from Culex interrogator and Culex quinquefasciatus in the Yucatan Peninsula of Mexico. 2010 , 155, 983-6	22
1212	Nucleotide sequence and genome organization of Dweet mottle virus and its relationship to members of the family Betaflexiviridae. 2010 , 155, 1523-7	10
1211	A putative new ampelovirus associated with grapevine leafroll disease. 2010 , 155, 1871-6	23
1210	Complete nucleotide sequence of Velvet tobacco mottle virus isolate K1. 2010 , 155, 1893-6	11
1209	Two novel begomoviruses belonging to different lineages infecting Rhynchosia minima. 2010 , 155, 2053-8	16
	Two novel begomoviruses belonging to different lineages infecting Rhynchosia minima. 2010 , 155, 2053-8 Manifold construction based on local distance invariance. 2010 , 2, 149-160	165
1208	Manifold construction based on local distance invariance. 2010 , 2, 149-160 Structural basis for the action of xyloglucan endotransglycosylases/hydrolases: insights from	5
1208	Manifold construction based on local distance invariance. 2010 , 2, 149-160 Structural basis for the action of xyloglucan endotransglycosylases/hydrolases: insights from homology modeling. 2010 , 2, 133-9 Cloning and nutritional regulation of polyunsaturated fatty acid desaturase and elongase of a	5
1208 1207 1206	Manifold construction based on local distance invariance. 2010 , 2, 149-160 Structural basis for the action of xyloglucan endotransglycosylases/hydrolases: insights from homology modeling. 2010 , 2, 133-9 Cloning and nutritional regulation of polyunsaturated fatty acid desaturase and elongase of a marine teleost, the nibe croaker Nibea mitsukurii. 2010 , 76, 463-472 Survey of mealybug (Hemiptera: Pseudococcidae) vectors of Ampelovirus and Vitivirus in vineyards	5 3 26
1208 1207 1206	Manifold construction based on local distance invariance. 2010, 2, 149-160 Structural basis for the action of xyloglucan endotransglycosylases/hydrolases: insights from homology modeling. 2010, 2, 133-9 Cloning and nutritional regulation of polyunsaturated fatty acid desaturase and elongase of a marine teleost, the nibe croaker Nibea mitsukurii. 2010, 76, 463-472 Survey of mealybug (Hemiptera: Pseudococcidae) vectors of Ampelovirus and Vitivirus in vineyards of northwestern Italy. 2010, 38, 401-409 Cloning and Characterization of the Gene Cluster Involved in the Production of the Circular	5 3 26 25
1208 1207 1206 1205	Manifold construction based on local distance invariance. 2010, 2, 149-160 Structural basis for the action of xyloglucan endotransglycosylases/hydrolases: insights from homology modeling. 2010, 2, 133-9 Cloning and nutritional regulation of polyunsaturated fatty acid desaturase and elongase of a marine teleost, the nibe croaker Nibea mitsukurii. 2010, 76, 463-472 Survey of mealybug (Hemiptera: Pseudococcidae) vectors of Ampelovirus and Vitivirus in vineyards of northwestern Italy. 2010, 38, 401-409 Cloning and Characterization of the Gene Cluster Involved in the Production of the Circular Bacteriocin Carnocyclin A. 2010, 2, 218-25	5 3 26 25

1200	Crystal structures of NAC domains of human nascent polypeptide-associated complex (NAC) and its NAC subunit. 2010 , 1, 406-416	19
1199	Crystal structure of the C-terminal domain of the e subunit of human translation initiation factor eIF2B. 2010 , 1, 595-603	11
1198	Cloning and expression pattern of a hemolin homologue from the diamondback moth, Plutella xylostella. 2010 , 32, 71-77	5
1197	Molecular cloning and functional analysis of the FSH receptor gene promoter from the volcano mouse (Neotomodon alstoni alstoni). 2010 , 37, 98-105	5
1196	The use of DNA identification in prosecuting wildlife-traffickers in Australia: do the penalties fit the crimes?. 2010 , 6, 211-6	12
1195	Physicochemical evolution and positive selection of the gymnosperm matK proteins. 2010 , 89, 81-9	4
1194	Biochemical and molecular characterization of thermo-alkali tolerant xylanase producing bacteria from thermal springs of Manikaran. 2010 , 50, 2-9	61
1193	First cellular approach of the effects of global warming on groundwater organisms: a study of the HSP70 gene expression. 2010 , 15, 259-70	27
1192	Sequence variations of PDHA1 gene in Triticeae species allow for identifying wheat-alien introgression lines. 2010 , 4, 137-144	4
1191	Sequence and expression analysis of the Arabidopsis IQM family. 2010 , 32, 191-198	6
1190	Cloning, overexpression, purification and preliminary characterization of human septin 8. 2010 , 29, 328-35	2
1189	Population genetic history of the dreissenid mussel invasions: expansion patterns across North America. 2010 , 12, 3687-3710	37
1188	A beta-barrel outer membrane protein facilitates cellular uptake of polychlorophenols in Cupriavidus necator. 2010 , 21, 431-9	17
1187	A molecular screening method for unisexual Ambystoma using mitochondrial DNA. 2010 , 11, 1177-1179	3
1186	Morphology and phylogeny of a non-toxic invasive Cylindrospermopsis raciborskii from a Mediterranean Lake. 2010 , 639, 115-128	51
1185	Genetic diversity in Australian ancient asexual Vestalenula (Ostracoda, Darwinulidae): little variability down under. 2010 , 641, 59-70	13
1184	Design, structure-based focusing and in silico screening of combinatorial library of peptidomimetic inhibitors of Dengue virus NS2B-NS3 protease. 2010 , 24, 195-212	28
1183	Molecular modeling of class I and II alleles of the major histocompatibility complex in Salmo salar. 2010 , 24, 1035-51	7

1182	A SNP haplotype associated with a gene resistant to Xanthomonas axonopodis pv. malvacearum in upland cotton (Gossypium hirsutum L.). 2010 , 25, 593-602	23
1181	High-resolution genetic map of the Rvi15 (Vr2) apple scab resistance locus. 2010 , 26, 561-572	21
1180	Recombination is suppressed in an alien introgression in peanut harboring Rma, a dominant root-knot nematode resistance gene. 2010 , 26, 357-370	93
1179	Characterization and tissue expression of channel catfish (Ictalurus punctatus Rafinesque, 1818) ubiquitin carboxyl-terminal hydrolase L5 (UCHL5) cDNA. 2010 , 37, 1229-34	2
1178	The complete mitochondrial genome of Evania appendigaster (Hymenoptera: Evaniidae) has low A+T content and a long intergenic spacer between atp8 and atp6. 2010 , 37, 1931-42	74
1177	Peptidylarginine deiminase gene is differentially expressed in freshwater and brackish water rainbow trout. 2010 , 37, 2333-9	28
1176	Genome-wide analysis of primary auxin-responsive Aux/IAA gene family in maize (Zea mays. L.). 2010 , 37, 3991-4001	86
1175	Variability of United States isolates of Macrophomina phaseolina based on simple sequence repeats and cross genus transferability to related genera within botryosphaeriaceae. 2010 , 170, 169-80	29
1174	Cryptic species of Euryakaina n. g. (Digenea: Cryptogonimidae) from sympatric lutjanids in the Indo-West Pacific. 2010 , 77, 185-204	24
1173	Characterisation of a cyclin-dependent kinase (CDKA) gene expressed during somatic embryogenesis of coconut palm. 2010 , 102, 251-258	36
1172	The pleiotropic protein kinase CK2 phosphorylates HTLV-1 Tax protein in vitro, targeting its PDZ-binding motif. 2010 , 41, 149-57	16
1171	Microbial community structure and diversity in a native forest wood-decomposed hollow-stump ecosystem. 2010 , 26, 233-240	14
1170	Cloning of triose phosphate isomerase gene from an antarctic psychrophilic Pseudomonas sp. by degenerate and splinkerette PCR. 2010 , 26, 1251-9	3
1169	Identification of novel members in sweet orange carotenoid biosynthesis gene families. 2010 , 6, 905-914	24
1168	A gene family encoding RING finger proteins in rice: their expansion, expression diversity, and co-expressed genes. 2010 , 72, 369-80	62
1167	Intracellular pH sensing is altered by plasma membrane PIP aquaporin co-expression. 2010 , 74, 105-18	58
1166	Deletion of the eIFiso4G subunit of the Arabidopsis eIFiso4F translation initiation complex impairs health and viability. 2010 , 74, 249-63	58
1165	Molecular diversity and metal accumulation of different Thlaspi praecox populations from Slovenia. 2010 , 330, 195-205	17

1164	Serpentine soil has little influence on the root-associated microbial community composition of the serpentine tolerant grass species Avenula sulcata. 2010 , 330, 393-405	15
1163	Comparative genomics of green sulfur bacteria. 2010 , 104, 137-52	11
1162	Molecular characterization of PRR13 and its tissue-specific expression in rainbow trout (Oncorhynchus mykiss). 2010 , 36, 1271-6	6
1161	Genomic screening in dioecious "yerba mate" tree (Ilex paraguariensis A. St. Hill., Aquifoliaceae) through representational difference analysis. 2010 , 138, 567-78	10
1160	TLRR (lrrc67) interacts with PP1 and is associated with a cytoskeletal complex in the testis. 2010 , 102, 173-89	22
1159	Cloning and functional expression of Rh50-like glycoprotein, a putative ammonia channel, in Aedes albopictus mosquitoes. 2010 , 56, 1599-610	16
1158	Assessment of 16S rRNA gene-based phylogenetic diversity and promising plant growth-promoting traits of Acinetobacter community from the rhizosphere of wheat. 2010 , 165, 627-38	45
1157	Arp1, an actin-related protein, in Plasmodium berghei. 2010 , 173, 88-96	8
1156	A novel thermostable cellulase from Fervidobacterium nodosum. 2010 , 66, 294-301	47
1155	Potent inhibition of the classical pathway of complement by a novel C1q-binding peptide derived from the human astrovirus coat protein. 2010 , 48, 305-13	41
1154	Characterization of the hemagglutinin gene of subtype H9 avian influenza viruses isolated in 2007-2009 in China. 2010 , 163, 186-9	24
1153	Typing of human and animal strains of influenza virus with conserved signature peptides of matrix M1 protein by high resolution mass spectrometry. 2010 , 165, 178-85	23
1152	The ABCs of multidrug resistance in malaria. 2010 , 26, 440-6	67
1151	Complex formation and light activation in membrane-embedded sensory rhodopsin II as seen by solid-state NMR spectroscopy. 2010 , 18, 293-300	46
1150	Crystal structures of Phd-Doc, HigA, and YeeU establish multiple evolutionary links between microbial growth-regulating toxin-antitoxin systems. 2010 , 18, 996-1010	59
1149	Evolutionary rates at codon sites may be used to align sequences and infer protein domain function. 2010 , 11, 151	5
1148	BISMAfast and accurate bisulfite sequencing data analysis of individual clones from unique and repetitive sequences. 2010 , 11, 230	188
1147	MTRAP: pairwise sequence alignment algorithm by a new measure based on transition probability between two consecutive pairs of residues. 2010 , 11, 235	8

1146	JCoDA: a tool for detecting evolutionary selection. 2010 , 11, 284	36
1145	Kinome-wide interaction modelling using alignment-based and alignment-independent approaches for kinase description and linear and non-linear data analysis techniques. 2010 , 11, 339	49
1144	CIG-DB: the database for human or mouse immunoglobulin and T cell receptor genes available for cancer studies. 2010 , 11, 398	9
1143	Clustering of protein families into functional subtypes using Relative Complexity Measure with reduced amino acid alphabets. 2010 , 11, 428	17
1142	Automatic detection of anchor points for multiple sequence alignment. 2010 , 11, 445	4
1141	Sigma-2: Multiple sequence alignment of non-coding DNA via an evolutionary model. 2010 , 11, 464	3
1140	ClustalXeed: a GUI-based grid computation version for high performance and terabyte size multiple sequence alignment. 2010 , 11, 467	11
1139	Non-coding RNA detection methods combined to improve usability, reproducibility and precision. 2010 , 11, 491	17
1138	Towards realistic benchmarks for multiple alignments of non-coding sequences. 2010 , 11, 54	19
1137	Gene processing control loops suggested by sequencing, splicing, and RNA folding. 2010 , 11, 602	4
1137	Gene processing control loops suggested by sequencing, splicing, and RNA folding. 2010 , 11, 602 Computational prediction of type III secreted proteins from gram-negative bacteria. 2010 , 11 Suppl 1, S47	4 59
	Computational prediction of type III secreted proteins from gram-negative bacteria. 2010 , 11 Suppl	
1136	Computational prediction of type III secreted proteins from gram-negative bacteria. 2010 , 11 Suppl 1, S47 Gene-centric association analysis for the correlation between the guanine-cytosine content levels	59
1136	Computational prediction of type III secreted proteins from gram-negative bacteria. 2010, 11 Suppl 1, S47 Gene-centric association analysis for the correlation between the guanine-cytosine content levels and temperature range conditions of prokaryotic species. 2010, 11 Suppl 11, S7 Large number of phosphotransferase genes in the Clostridium beijerinckii NCIMB 8052 genome	59 24
1136 1135 1134	Computational prediction of type III secreted proteins from gram-negative bacteria. 2010, 11 Suppl 1, S47 Gene-centric association analysis for the correlation between the guanine-cytosine content levels and temperature range conditions of prokaryotic species. 2010, 11 Suppl 11, S7 Large number of phosphotransferase genes in the Clostridium beijerinckii NCIMB 8052 genome and the study on their evolution. 2010, 11 Suppl 11, S9 Phylometrics: a pipeline for inferring phylogenetic trees from a sequence relationship network	59 24 20
1136 1135 1134 1133	Computational prediction of type III secreted proteins from gram-negative bacteria. 2010, 11 Suppl 1, S47 Gene-centric association analysis for the correlation between the guanine-cytosine content levels and temperature range conditions of prokaryotic species. 2010, 11 Suppl 11, S7 Large number of phosphotransferase genes in the Clostridium beijerinckii NCIMB 8052 genome and the study on their evolution. 2010, 11 Suppl 11, S9 Phylometrics: a pipeline for inferring phylogenetic trees from a sequence relationship network perspective. 2010, 11 Suppl 6, S18	59 24 20
1136 1135 1134 1133 1132	Computational prediction of type III secreted proteins from gram-negative bacteria. 2010, 11 Suppl 1, S47 Gene-centric association analysis for the correlation between the guanine-cytosine content levels and temperature range conditions of prokaryotic species. 2010, 11 Suppl 11, S7 Large number of phosphotransferase genes in the Clostridium beijerinckii NCIMB 8052 genome and the study on their evolution. 2010, 11 Suppl 11, S9 Phylometrics: a pipeline for inferring phylogenetic trees from a sequence relationship network perspective. 2010, 11 Suppl 6, S18 Divergence of imprinted genes during mammalian evolution. 2010, 10, 116	59 24 20 0 16

1128	Aquaporins in the wild: natural genetic diversity and selective pressure in the PIP gene family in five Neotropical tree species. 2010 , 10, 202	12
1127	Conservation and divergence of ADAM family proteins in the Xenopus genome. 2010 , 10, 211	17
1126	Diversifying selection and functional analysis of interleukin-4 suggests antagonism-driven evolution at receptor-binding interfaces. 2010 , 10, 223	16
1125	Phylogenetic analysis of ferlin genes reveals ancient eukaryotic origins. 2010 , 10, 231	39
1124	Distinct patterns of mitochondrial genome diversity in bonobos (Pan paniscus) and humans. 2010 , 10, 270	21
1123	Identification and analysis of candidate fungal tRNA 3'-end processing endonucleases tRNase Zs, homologs of the putative prostate cancer susceptibility protein ELAC2. 2010 , 10, 272	10
1122	Periostin shows increased evolutionary plasticity in its alternatively spliced region. 2010 , 10, 30	71
1121	Complete plastome sequences of Equisetum arvense and Isoetes flaccida: implications for phylogeny and plastid genome evolution of early land plant lineages. 2010 , 10, 321	100
112 0	Ancient origin of animal U-box ubiquitin ligases. 2010 , 10, 331	19
1119	Molecular phylogeny of pearl oysters and their relatives (Mollusca, Bivalvia, Pterioidea). 2010 , 10, 342	34
1118	Predicting genome-wide redundancy using machine learning. 2010 , 10, 357	8
1118	Predicting genome-wide redundancy using machine learning. 2010 , 10, 357 Difference in gene duplicability may explain the difference in overall structure of protein-protein interaction networks among eukaryotes. 2010 , 10, 358	8
	Difference in gene duplicability may explain the difference in overall structure of protein-protein	
1117	Difference in gene duplicability may explain the difference in overall structure of protein-protein interaction networks among eukaryotes. 2010 , 10, 358 Next generation sequencing and analysis of a conserved transcriptome of New Zealand's kiwi. 2010	8
1117	Difference in gene duplicability may explain the difference in overall structure of protein-protein interaction networks among eukaryotes. 2010, 10, 358 Next generation sequencing and analysis of a conserved transcriptome of New Zealand's kiwi. 2010, 10, 387 Mitochondrial phylogenomics of the Bivalvia (Mollusca): searching for the origin and mitogenomic	8
1117 1116 1115	Difference in gene duplicability may explain the difference in overall structure of protein-protein interaction networks among eukaryotes. 2010, 10, 358 Next generation sequencing and analysis of a conserved transcriptome of New Zealand's kiwi. 2010, 10, 387 Mitochondrial phylogenomics of the Bivalvia (Mollusca): searching for the origin and mitogenomic correlates of doubly uniparental inheritance of mtDNA. 2010, 10, 50 Functional evolution of the trace amine associated receptors in mammals and the loss of TAAR1 in	8 12 124
1117 1116 1115 1114	Difference in gene duplicability may explain the difference in overall structure of protein-protein interaction networks among eukaryotes. 2010, 10, 358 Next generation sequencing and analysis of a conserved transcriptome of New Zealand's kiwi. 2010, 10, 387 Mitochondrial phylogenomics of the Bivalvia (Mollusca): searching for the origin and mitogenomic correlates of doubly uniparental inheritance of mtDNA. 2010, 10, 50 Functional evolution of the trace amine associated receptors in mammals and the loss of TAAR1 in dogs. 2010, 10, 51	8 12 124 27

1110	target genes in bilaterian animals. 2010 , 11, 101	25
1109	Identification of candidates for cyclotide biosynthesis and cyclisation by expressed sequence tag analysis of Oldenlandia affinis. 2010 , 11, 111	26
1108	The Zur regulon of Corynebacterium glutamicum ATCC 13032. 2010 , 11, 12	50
1107	High-throughput genome sequencing of two Listeria monocytogenes clinical isolates during a large foodborne outbreak. 2010 , 11, 120	248
1106	The RST and PARP-like domain containing SRO protein family: analysis of protein structure, function and conservation in land plants. 2010 , 11, 170	73
1105	Genome-wide cloning and sequence analysis of leucine-rich repeat receptor-like protein kinase genes in Arabidopsis thaliana. 2010 , 11, 19	134
1104	Genome-wide comparative analysis of metacaspases in unicellular and filamentous cyanobacteria. 2010 , 11, 198	37
1103	Functional genomics of mountain pine beetle (Dendroctonus ponderosae) midguts and fat bodies. 2010 , 11, 215	54
1102	LEAPdb: a database for the late embryogenesis abundant proteins. 2010 , 11, 221	64
1101	Thioredoxin and glutathione systems differ in parasitic and free-living platyhelminths. 2010, 11, 237	32
1100	Genome-wide in silico screen for CCCH-type zinc finger proteins of Trypanosoma brucei, Trypanosoma cruzi and Leishmania major. 2010 , 11, 283	63
1099	Variable structure motifs for transcription factor binding sites. 2010 , 11, 30	15
1098	Bioinformatic analysis of Entamoeba histolytica SINE1 elements. 2010 , 11, 321	14
1097	Functional and evolutionary correlates of gene constellations in the Drosophila melanogaster genome that deviate from the stereotypical gene architecture. 2010 , 11, 322	1
1096	The proteolytic system of lactic acid bacteria revisited: a genomic comparison. 2010 , 11, 36	195
1096	A manual collection of Svt. Esvt. Rph3a. Rph3al. Doc2. and Dblc2 genes from 46 metazoan	195 41
	A manual collection of Syt, Esyt, Rph3a, Rph3al, Doc2, and Dblc2 genes from 46 metazoan genomesan open access resource for neuroscience and evolutionary biology. 2010 , 11, 37 Comparative mitogenomics of Braconidae (Insecta: Hymenoptera) and the phylogenetic utility of	

1092	Comparison of koala LPCoLN and human strains of Chlamydia pneumoniae highlights extended genetic diversity in the species. 2010 , 11, 442	27
1091	Chiropteran types I and II interferon genes inferred from genome sequencing traces by a statistical gene-family assembler. 2010 , 11, 444	36
1090	Mobile genetic element proliferation and gene inactivation impact over the genome structure and metabolic capabilities of Sodalis glossinidius, the secondary endosymbiont of tsetse flies. 2010 , 11, 449	58
1089	A three-way comparative genomic analysis of Mannheimia haemolytica isolates. 2010 , 11, 535	19
1088	The complete mitochondrial genome of the citrus red mite Panonychus citri (Acari: Tetranychidae): high genome rearrangement and extremely truncated tRNAs. 2010 , 11, 597	56
1087	Analyses of genome architecture and gene expression reveal novel candidate virulence factors in the secretome of Phytophthora infestans. 2010 , 11, 637	141
1086	Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. 2010 , 11, 702	132
1085	Specific patterns of gene space organisation revealed in wheat by using the combination of barley and wheat genomic resources. 2010 , 11, 714	21
1084	Genomic and transcriptomic analysis of the AP2/ERF superfamily in Vitis vinifera. 2010 , 11, 719	209
1083	The vertebrate makorin ubiquitin ligase gene family has been shaped by large-scale duplication and retroposition from an ancestral gonad-specific, maternal-effect gene. 2010 , 11, 721	33
1082	Trichomonas vaginalis vast BspA-like gene family: evidence for functional diversity from structural organisation and transcriptomics. 2010 , 11, 99	60
1081	Modeling neutral evolution of Alu elements using a branching process. 2010 , 11 Suppl 1, S11	8
1080	Bioinformatic search of plant microtubule-and cell cycle related serine-threonine protein kinases. 2010 , 11 Suppl 1, S14	20
1079	Diverse modes of reproduction in the marine free-living ciliate Glauconema trihymene. 2010 , 10, 108	7
1078	Species specificity, surface exposure, protein expression, immunogenicity, and participation in biofilm formation of Porphyromonas gingivalis HmuY. 2010 , 10, 134	52
1077	Comparative genomic analysis reveals evidence of two novel Vibrio species closely related to V. cholerae. 2010 , 10, 154	44
1076	Genes and pathways for CO2 fixation in the obligate, chemolithoautotrophic acidophile, Acidithiobacillus ferrooxidans, carbon fixation in A. ferrooxidans. 2010 , 10, 229	43
1075	PpiD is a player in the network of periplasmic chaperones in Escherichia coli. 2010 , 10, 251	43

1074	simulated infection conditions. 2010 , 10, 301	51
1073	Excision dynamics of Vibrio pathogenicity island-2 from Vibrio cholerae: role of a recombination directionality factor VefA. 2010 , 10, 306	21
1072	Carbon-dependent control of electron transfer and central carbon pathway genes for methane biosynthesis in the Archaean, Methanosarcina acetivorans strain C2A. 2010 , 10, 62	44
1071	The phylogenetic placement and biogeographical origins of the New Zealand stick insects (Phasmatodea). 2010 , 35, 207-225	51
1070	Direct optimization overly optimizes data. 2010 , 35, 199-206	22
1069	Analysis of promoter activity of members of the PECTATE LYASE-LIKE (PLL) gene family in cell separation in Arabidopsis. 2010 , 10, 152	54
1068	Molecular characterization of vernalization loci VRN1 in wild and cultivated wheats. 2010 , 10, 168	44
1067	The aconitate hydratase family from Citrus. 2010 , 10, 222	47
1066	Natural diversity of potato (Solanum tuberosum) invertases. 2010 , 10, 271	43
1065	Early activation of wheat polyamine biosynthesis during Fusarium head blight implicates putrescine as an inducer of trichothecene mycotoxin production. 2010 , 10, 289	83
1064	The YlmG protein has a conserved function related to the distribution of nucleoids in chloroplasts and cyanobacteria. 2010 , 10, 57	28
1063	Analysis of a c0t-1 library enables the targeted identification of minisatellite and satellite families in Beta vulgaris. 2010 , 10, 8	22
1062	Comparison of homoeolocus organisation in paired BAC clones from white clover (Trifolium repens L.) and microcolinearity with model legume species. 2010 , 10, 94	12
1061	Transcriptional regulation of the CRK/DUF26 group of receptor-like protein kinases by ozone and plant hormones in Arabidopsis. 2010 , 10, 95	175
1060	A novel spliced fusion of MLL with CT45A2 in a pediatric biphenotypic acute leukemia. 2010 , 10, 518	9
1059	Efficient recombinant expression and secretion of a thermostable GH26 mannan endo-1,4-beta-mannosidase from Bacillus licheniformis in Escherichia coli. 2010 , 9, 20	68
1058	The Plasmodium falciparum merozoite surface protein-1 19 KD antibody response in the Peruvian Amazon predominantly targets the non-allele specific, shared sites of this antigen. 2010 , 9, 3	13
1057	Local replication of simian immunodeficiency virus in the breast milk compartment of chronically-infected, lactating rhesus monkeys. 2010 , 7, 7	16

1056	The archaeo-eukaryotic GINS proteins and the archaeal primase catalytic subunit PriS share a common domain. 2010 , 5, 17	10
1055	The evolutionary rate variation among genes of HOG-signaling pathway in yeast genomes. 2010 , 5, 46	31
1054	Phylogenetic and regulatory region analysis of Wnt5 genes reveals conservation of a regulatory module with putative implication in pancreas development. 2010 , 5, 49	6
1053	Impact of antigenic and genetic drift on the serologic surveillance of H5N2 avian influenza viruses. 2010 , 6, 57	13
1052	Protein complex forming ability is favored over the features of interacting partners in determining the evolutionary rates of proteins in the yeast protein-protein interaction networks. 2010 , 4, 155	10
1051	Cloning of Nrul and Sbo13I restriction and modification sstems in E. coli and amino acid sequence comparison of M.Nrul and M.Sbo13I with other amino-methyltransferases. 2010 , 3, 139	1
1050	Comparative genomic sequence analysis of strawberry and other rosids reveals significant microsynteny. 2010 , 3, 168	9
1049	ANDES: Statistical tools for the ANalyses of DEep Sequencing. 2010 , 3, 199	18
1048	A molecular phylogeny of Hypnales (Bryophyta) inferred from ITS2 sequence-structure data. 2010 , 3, 320	17
1047	CUDASW++2.0: enhanced Smith-Waterman protein database search on CUDA-enabled GPUs based on SIMT and virtualized SIMD abstractions. 2010 , 3, 93	121
1046	Grellamoeba robusta gen. n., sp. n., a possible member of the family Acramoebidae Smirnov, Nassonova et Cavalier-Smith, 2008. 2010 , 46, 77-85	6
1045	Microbial diversity in ostrich ceca as revealed by 16S ribosomal RNA gene clone library and detection of novel Fibrobacter species. 2010 , 16, 83-93	47
1044	RECQL5 helicase: connections to DNA recombination and RNA polymerase II transcription. 2010 , 9, 345-53	23
1043	Unwinding the functions of the Pif1 family helicases. 2010 , 9, 237-49	156
1042	Current trends in antimicrobial agent research: chemo- and bioinformatics approaches. 2010 , 15, 540-6	58
1041	The electron transfer flavoprotein: ubiquinone oxidoreductases. 2010 , 1797, 1910-6	164
1040	Emerging structure-function relationships defining monoamine NSS transporter substrate and ligand affinity. 2010 , 79, 1083-91	25
1039	An angiotensin II type 1 receptor activation switch patch revealed through evolutionary trace analysis. 2010 , 80, 86-94	5

1038	BLUP, a new paradigm in host-range determination. 2010 , 53, 143-152	10
1037	AP-1 inhibitory peptides attenuate in vitro cortical neuronal cell death induced by kainic acid. 2010 , 1360, 8-16	16
1036	Molecular phylogeny of the Pycnonotus sinensis and Pycnonotus taivanus in Taiwan based on sequence variations of nuclear CHD and mitochondrial cytochrome b genes. 2010 , 38, 195-201	2
1035	Phylogenetic status of Vavilovia formosa (Fabaceae-Fabeae) based on nrDNA ITS and cpDNA sequences. 2010 , 38, 313-319	22
1034	Using a phylogenetic approach to selection of target plants in drug discovery of acetylcholinesterase inhibiting alkaloids in Amaryllidaceae tribe Galantheae. 2010 , 38, 1026-1034	25
1033	Selective pressure, putative recombination events and evolutionary relationships among members of the family Closteroviridae: A proposal for a new classification. 2010 , 38, 1185-1192	5
1032	Morin fosters apoptosis in experimental hepatocellular carcinogenesis model. 2010 , 183, 284-92	44
1031	Structure-function relationships of the alpha/beta-hydrolase fold domain of neuroligin: a comparison with acetylcholinesterase. 2010 , 187, 49-55	8
1030	Molecular and biochemical characterization of human galactokinase and its small molecule inhibitors. 2010 , 188, 376-85	37
1029	Rapid identification of lymnaeid snails and their infection with Fasciola gigantica in Thailand. 2010 , 126, 482-8	13
1028	A genomics method to identify pathogenicity-related proteins. Application to aminoacyl-tRNA synthetase-like proteins. 2010 , 584, 460-6	5
1027	Substrate specificity and evolutionary implications of a NifDK enzyme carrying NifB-co at its active site. 2010 , 584, 1487-92	30
1026	Structure of a polyisoprenoid binding domain from Saccharophagus degradans implicated in plant cell wall breakdown. 2010 , 584, 1577-84	17
1025	Evolution of 11beta-hydroxysteroid dehydrogenase-type 1 and 11beta-hydroxysteroid dehydrogenase-type 3. 2010 , 584, 2279-84	22
1024	Modulation of copper site properties by remote residues determines the stability of plastocyanins. 2010 , 584, 2346-50	5
1023	The amyloid fibrils of the constant domain of immunoglobulin light chain. 2010 , 584, 3348-53	16
1022	Ecdysone receptor homologs from mollusks, leeches and a polychaete worm. 2010 , 584, 4458-62	16
1021	Phylogenetic analysis and evolution of aromatic amino acid hydroxylase. 2010 , 584, 4775-82	25

1020	Growth hormone receptors in zebrafish (Danio rerio): adult and embryonic expression patterns. 2010 , 10, 214-25	35
1019	Expression of Ol-foxi3 and Na(+)/K(+)-ATPase in ionocytes during the development of euryhaline medaka (Oryzias latipes) embryos. 2010 , 10, 185-92	19
1018	Diversification of fasting regulated transcription in a cluster of duplicated nuclear hormone receptors in C. elegans. 2010 , 10, 227-36	3
1017	Probing for primary functions of prohibitin in Trypanosoma brucei. 2010 , 40, 73-83	19
1016	Identification and characterisation of an immunodiagnostic marker for cyathostomin developing stage larvae. 2010 , 40, 265-75	23
1015	LmxMPK4, an essential mitogen-activated protein kinase of Leishmania mexicana is phosphorylated and activated by the STE7-like protein kinase LmxMKK5. 2010 , 40, 969-78	20
1014	Developmental stages and molecular phylogeny of Hepatozoon tuatarae, a parasite infecting the New Zealand tuatara, Sphenodon punctatus and the tick, Amblyomma sphenodonti. 2010 , 40, 1311-5	13
1013	Genome-wide expression analysis of Saccharomyces pastorianus orthologous genes using oligonucleotide microarrays. 2010 , 110, 602-7	27
1012	Brachyspira intermedia strain diversity and relationships to the other indole-positive Brachyspira species. 2010 , 143, 246-54	27
1011	Genetic diversity of Porcine reproductive and respiratory syndrome virus (PRRSV) in selected herds in a pig-dense region of North-Western Germany. 2010 , 143, 213-23	14
1010	Avian metapneumovirus (AMPV) attachment protein involvement in probable virus evolution concurrent with mass live vaccine introduction. 2010 , 146, 24-34	44
1009	Molecular diversity assessed by VNTR and IS1296 typing of historical Mycoplasma mycoides subsp. mycoides SC strains. 2010 , 146, 295-302	1
1008	Classical swine fever virus in South-Eastern Europeretrospective analysis of the disease situation and molecular epidemiology. 2010 , 146, 276-84	19
1007	GAG-binding variants of tick-borne encephalitis virus. 2010 , 398, 262-72	41
1006	Evidence for ribosomal frameshifting and a novel overlapping gene in the genomes of insect-specific flaviviruses. 2010 , 399, 153-166	54
1005	Viral encephalitis of tilapia larvae: primary characterization of a novel herpes-like virus. 2010 , 399, 239-47	34
1004	Group-specific structural features of the 5'-proximal sequences of coronavirus genomic RNAs. 2010 , 401, 29-41	62
1003	Identification and complete genome analysis of three novel paramyxoviruses, Tuhoko virus 1, 2 and 3, in fruit bats from China. 2010 , 404, 106-16	52

1002	Characterization of the gene expression profile of human bocavirus. 2010 , 403, 145-54	106
1001	The complete genome and genetic characteristics of SRV-4 isolated from cynomolgus monkeys (Macaca fascicularis). 2010 , 405, 390-6	14
1000	Regulation of MYPT1 stability by the E3 ubiquitin ligase SIAH2. 2010 , 316, 68-77	19
999	Expression of leptin receptor gene in developing and adult zebrafish. 2010 , 166, 346-55	72
998	Neurohormones and neuropeptides encoded by the genome of Lottia gigantea, with reference to other mollusks and insects. 2010 , 167, 86-103	173
997	The brown shrimp (Crangon crangon L.) ecdysteroid receptor complex: cloning, structural modeling of the ligand-binding domain and functional expression in an EcR-deficient Drosophila cell line. 2010 , 168, 415-23	15
996	Characterization of the apical membrane antigen-1 in Italian strains of Babesia bigemina. 2010, 57, 52-6	15
995	Spatial and temporal expression patterns of Bmal delineate a circadian clock in the nervous system of Branchiostoma lanceolatum. 2010 , 518, 1837-46	5
994	Localized expression of urocortin genes in the developing zebrafish brain. 2010 , 518, 2978-95	28
993	A migratory role for EphrinB ligands in avian epicardial mesothelial cells. 2010 , 239, 598-609	10
992	Cabin1 expression suggests roles in neuronal development. 2010 , 239, 2443-51	15
991	Conservation, expression, and knockdown of zebrafish plxnb2a and plxnb2b. 2010 , 239, 2722-34	3
990	Zebrafish cx30.3: identification and characterization of a gap junction gene highly expressed in the skin. 2010 , 239, 2627-36	9
989	Developmental expression patterns of candidate cofactors for vertebrate six family transcription factors. 2010 , 239, 3446-66	18
988	Capillary electrophoresis for analysis of microheterogeneous glutelin subunits in rice (Oryza sativa L.). 2010 , 31, 3566-72	6
987	How many species of woolly monkeys inhabit Colombian forests?. 2010 , 72, 1131-40	12
986	Insights into multienzyme docking in hybrid PKS-NRPS megasynthetases revealed by heterologous expression and genetic engineering. 2010 , 11, 1069-75	12
985	Analysis of the sorangicin gene cluster reinforces the utility of a combined phylogenetic/retrobiosynthetic analysis for deciphering natural product assembly by trans-AT PKS. 2010 , 11, 1840-9	61

984	Probing enzyme promiscuity of SGNH hydrolases. 2010 , 11, 2158-67	60
983	Analysis of expressed sequence tags from a significant livestock pest, the stable fly (Stomoxys calcitrans), identifies transcripts with a putative role in chemosensation and sex determination. 2010 , 74, 179-204	17
982	Motif-based search for a novel fructosyl peptide oxidase from genome databases. 2010 , 106, 358-66	10
981	Functional characterization of propane-enhanced N-nitrosodimethylamine degradation by two actinomycetales. 2010 , 107, 924-32	34
980	Rhinovirus species and their clinical presentation among different risk groups of non-hospitalized patients. 2010 , 82, 2110-5	19
979	Cloning and characterization of poly(3-hydroxybutyrate) biosynthesis genes from Pseudomonas sp. USM 4-55. 2010 , 50, 179-89	6
978	Subcellular phosphoproteomics. 2010 , 29, 962-90	35
977	Characterization and phylogenetic analysis of vitellogenin coding sequences in the Antarctic fish Trematomus bernacchii. 2010 , 314, 645-52	6
976	Cloning, screening and characterization of ester hydrolases with enantioselectivity in typical bacteria. 2010 , 45, 475-480	6
975	Purification and characterization of a solvent stable aminopeptidase from Pseudomonas aeruginosa: Cloning and analysis of aminopeptidase gene conferring solvent stability. 2010 , 45, 757-764	17
974	Dimethyl isotope labeling assisted de novo peptide sequencing. 2010 , 21, 1957-65	22
973	Disruption of the H-bond network in the main access channel of catalase-peroxidase modulates enthalpy and entropy of Fe(III) reduction. 2010 , 104, 648-56	14
972	Evolutionary selection associated with the multi-function of overlapping genes in the hepatitis B virus. 2010 , 10, 84-8	23
971	A single Phe54Tyr substitution improves the catalytic activity and thermostability of Trigonopsis variabilis D-amino acid oxidase. 2010 , 27, 78-84	16
970	Classification studies based on a spectral representation of DNA. 2010 , 266, 667-74	10
969	gamma-Conglutin, the Lupinus albus XEGIP-like protein, whose expression is elicited by chitosan, lacks of the typical inhibitory activity against GH12 endo-glucanases. 2010 , 71, 142-8	28
968	Epigenetic chromatin modifiers in barley: III. Isolation and characterization of the barley GNAT-MYST family of histone acetyltransferases and responses to exogenous ABA. 2010 , 48, 98-107	31
967	Aquifex aeolicus membrane hydrogenase for hydrogen biooxidation: Role of lipids and physiological partners in enzyme stability and activity. 2010 , 35, 10778-10789	35

966	Detecting natural selection in RNA virus populations using sequence summary statistics. 2010 , 10, 421-30	21
965	Requirement of NMB0065 for connecting assembly and export of sialic acid capsular polysaccharides in Neisseria meningitidis. 2010 , 12, 476-87	15
964	Limited genetic diversity among Sarcocystis neurona strains infecting southern sea otters precludes distinction between marine and terrestrial isolates. 2010 , 169, 37-44	37
963	Molecular characterization of Sarcocystis neurona strains from opossums (Didelphis virginiana) and intermediate hosts from Central California. 2010 , 170, 20-9	23
962	Sarcocystis calchasi is distinct to Sarcocystis columbae sp. nov. from the wood pigeon (Columba palumbus) and Sarcocystis sp. from the sparrowhawk (Accipiter nisus). 2010 , 171, 7-14	35
961	Molecular analysis of clonal trichomonad isolates indicate the existence of heterogenic species present in different birds and within the same host. 2010 , 172, 53-64	59
960	Molecular and serologic evidence for Babesia bovis-like parasites in white-tailed deer (Odocoileus virginianus) in south Texas. 2010 , 172, 214-20	30
959	Analysis of a mitochondrial noncoding region for the identification of the most diffused Hypoderma species (Diptera, Oestridae). 2010 , 173, 317-23	4
958	A new species of Haemopis (Annelida: Hirudinea): evolution of North American terrestrial leeches. 2010 , 54, 226-34	11
957	Temporal speciation pattern in the western Mediterranean genus Tudorella P. Fischer, 1885 (Gastropoda, Pomatiidae) supports the Tyrrhenian vicariance hypothesis. 2010 , 54, 427-36	38
956	Evolutionary placement of Xanthomonadales based on conserved protein signature sequences. 2010 , 54, 524-34	24
955	Supermatrix and species tree methods resolve phylogenetic relationships within the big cats, Panthera (Carnivora: Felidae). 2010 , 56, 64-76	53
954	Phylogeography of endemic toads and post-Pliocene persistence of the Brazilian Atlantic Forest. 2010 , 55, 1018-31	172
953	Phylogeny of entelegyne spiders: affinities of the family Penestomidae (NEW RANK), generic phylogeny of Eresidae, and asymmetric rates of change in spinning organ evolution (Araneae, Araneoidea, Entelegynae). 2010 , 55, 786-804	82
952	Phylogeographic analysis and environmental niche modeling of the plain-bellied watersnake (Nerodia erythrogaster) reveals low levels of genetic and ecological differentiation. 2010 , 55, 985-95	23
951	The importance of taxon sampling in genomic studies: an example from the cyclooxygenases of teleost fishes. 2010 , 56, 451-5	9
950	Evolutionary affinity of billfishes (Xiphiidae and Istiophoridae) and flatfishes (Plueronectiformes): Independent and trans-subordinal origins of endothermy in teleost fishes. 2010 , 56, 897-904	29
949	Phylogeny and species boundaries of the endemic species complex, Eliurus antsingy and E. carletoni (Rodentia: Muroidea: Nesomyidae), in Madagascar using mitochondrial and nuclear DNA sequence data. 2010 , 57, 11-22	6

948	Phylogeny, historical biogeography and body size evolution in Pacific Island Crocodile skinks Tribolonotus (Squamata; Scincidae). 2010 , 57, 227-36	15
947	Domestication of olive fly through a multi-regional host shift to cultivated olives: comparative dating using complete mitochondrial genomes. 2010 , 57, 678-86	82
946	Expanded phylogeny of myxobacteria and evidence for cultivation of the 'unculturables'. 2010, 57, 878-87	62
945	Computational approaches for protein function prediction: a combined strategy from multiple sequence alignment to molecular docking-based virtual screening. 2010 , 1804, 1695-712	68
944	Global expression analysis of miRNA gene cluster and family based on isomiRs from deep sequencing data. 2010 , 34, 165-71	67
943	Expression and characterization of Bacillus licheniformis chitinase (ChiA), suitable for bioconversion of chitin waste. 2010 , 101, 4096-103	78
942	Selecting sequences that fold into a defined 3D structure: A new approach for protein design based on molecular dynamics and energetics. 2010 , 146, 76-84	14
941	A novel NADP+-dependent formate dehydrogenase from Burkholderia stabilis 15516: Screening, purification and characterization. 2010 , 46, 557-561	40
940	Structure of a family 3b' carbohydrate-binding module from the Cel9V glycoside hydrolase from Clostridium thermocellum: structural diversity and implications for carbohydrate binding. 2010 , 66, 33-43	16
939	The X-ray structure of Salmonella typhimurium uridine nucleoside phosphorylase complexed with 2,2'-anhydrouridine, phosphate and potassium ions at 1.86 A resolution. 2010 , 66, 51-60	18
938	Structure of nondiscriminating glutamyl-tRNA synthetase from Thermotoga maritima. 2010 , 66, 813-20	6
937	Structures of the nucleotide-binding domain of the human ABCB6 transporter and its complexes with nucleotides. 2010 , 66, 979-87	10
936	X-ray and molecular-dynamics studies on Mycobacterium leprae single-stranded DNA-binding protein and comparison with other eubacterial SSB structures. 2010 , 66, 1048-58	11
935	A new crystal form of human diamine oxidase. 2010 , 66, 137-42	9
934	Crystallization and preliminary X-ray diffraction analyses of the homodimeric glycine decarboxylase (P-protein) from the cyanobacterium Synechocystis sp. PCC 6803. 2010 , 66, 187-91	4
933	Structure of the newly found green turtle egg-white ribonuclease. 2010 , 66, 755-9	
932	Crystallization and preliminary X-ray studies of a galactose-specific lectin from the seeds of bitter gourd (Momordica charantia). 2010 , 66, 1037-40	8
931	Production, crystallization and preliminary X-ray analysis of CTP:inositol-1-phosphate cytidylyltransferase from Archaeoglobus fulgidus. 2010 , 66, 1463-5	2

930	Structure of dihydroorotase from Bacillus anthracis at 2.6 Iresolution. 2010 , 66, 1432-5	10
929	Structure of a tryptophanyl-tRNA synthetase containing an iron-sulfur cluster. 2010 , 66, 1326-34	16
928	Characterization of the first beta-class carbonic anhydrase from an arthropod (Drosophila melanogaster) and phylogenetic analysis of beta-class carbonic anhydrases in invertebrates. 2010 , 11, 28	57
927	Secreted fungal sulfhydryl oxidases: sequence analysis and characterisation of a representative flavin-dependent enzyme from Aspergillus oryzae. 2010 , 11, 31	11
926	Visceral regeneration in a sea cucumber involves extensive expression of survivin and mortalin homologs in the mesothelium. 2010 , 10, 117	45
925	Discriminant analysis of principal components: a new method for the analysis of genetically structured populations. 2010 , 11, 94	2650
924	Phylogeny and expression of carbonic anhydrase-related proteins. 2010 , 11, 25	58
923	Identification and expression analysis of splice variants of mouse enabled homologue during development and in adult tissues. 2010 , 11, 45	
922	Cytochrome P450 diversity and induction by gorgonian allelochemicals in the marine gastropod Cyphoma gibbosum. 2010 , 10, 24	21
921	Predicting the pathway involved in post-translational modification of elongation factor P in a subset of bacterial species. 2010 , 5, 3	53
920	Asymmetric and non-uniform evolution of recently duplicated human genes. 2010 , 5, 54	19
919	Sequence embedding for fast construction of guide trees for multiple sequence alignment. 2010 , 5, 21	74
918	Two-color STED microscopy reveals different degrees of colocalization between hexokinase-I and the three human VDAC isoforms. 2010 , 3, 4	90
917	A structural-based statistical approach suggests a cooperative activity of PUM1 and miR-410 in human 3'-untranslated regions. 2010 , 1, 17	18
916	Hybridisation as potential source of incongruence in the morphological and mitochondrial diversity of a Thai freshwater gastropod (Pachychilidae, Brotia H. Adams, 1866). 2010 , 86, 301-314	13
915	The importance of valine 114 in ligand binding in beta(2)-adrenergic receptor. 2010 , 19, 85-93	8
914	The short-chain oxidoreductase Q9HYA2 from Pseudomonas aeruginosa PAO1 contains an atypical catalytic center. 2010 , 19, 1097-103	1
913	Combining crystallography and molecular dynamics: the case of Schistosoma mansoni phospholipid glutathione peroxidase. 2010 , 78, 259-70	22

912	Cooperative nature of gating transitions in K(+) channels as seen from dynamic importance sampling calculations. 2010 , 78, 1105-19	13
911	Solution structure of the N-terminal domain of Bacillus subtilis delta subunit of RNA polymerase and its classification based on structural homologs. 2010 , 78, 1807-10	22
910	Self-association of TPR domains: Lessons learned from a designed, consensus-based TPR oligomer. 2010 , 78, 2131-43	41
909	The structure of Boo/Diva reveals a divergent Bcl-2 protein. 2010 , 78, 2181-6	22
908	Species specificity of the complement inhibitor compstatin investigated by all-atom molecular dynamics simulations. 2010 , 78, 2655-67	32
907	Generating stereochemically acceptable protein pathways. 2010 , 78, 2908-21	65
906	Docking by structural similarity at protein-protein interfaces. 2010 , 78, 3235-41	68
905	Structural refinement of the hERG1 pore and voltage-sensing domains with ROSETTA-membrane and molecular dynamics simulations. 2010 , 78, 2922-34	44
904	Structure of a putative BenF-like porin from Pseudomonas fluorescens Pf-5 at 2.6 A resolution. 2010 , 78, 3056-62	17
903	Structure-based prediction of protein-peptide specificity in Rosetta. 2010 , 78, 3437-49	34
902	CYP9A12 and CYP9A17 in the cotton bollworm, Helicoverpa armigera: sequence similarity, expression profile and xenobiotic response. 2010 , 66, 65-73	59
901	Characterization of conantokin Rl-A: molecular phylogeny as structure/function study. 2010 , 16, 375-82	9
900	Algorithmic and analytical methods in network biology. 2010 , 2, 277-292	23
899	Multifaceted activity of HIV Vpr/Vpx proteins: the current view of their virological functions. 2010 , 20, 68-76	25
898	GRAMINIFOLIA homolog expression in Streptocarpus rexii is associated with the basal meristems in phyllomorphs, a morphological novelty in Gesneriaceae. 2010 , 12, 61-73	13
897	Origin of animal epithelia: insights from the sponge genome. 2010 , 12, 601-17	79
896	INTRACELLULAR LOCALIZATION OF AN ENDOGENOUS CELLULOSE SYNTHASE OF MICRASTERIAS DENTICULATA (DESMIDIALES, CHLOROPHYTA) BY MEANS OF TRANSIENT GENETIC TRANSFORMATION1. 2010 , 46, 839-845	16
895	AN UNRECOGNIZED ANCIENT LINEAGE OF GREEN PLANTS PERSISTS IN DEEP MARINE WATERS1. 2010 , 46, 1288-1295	32

894	MOLECULAR PHYLOGENY OF GRACILARIA SPECIES INFERRED FROM MOLECULAR MARKERS BELONGING TO THREE DIFFERENT GENOMES1. 2010 , 46, 1322-1328	11
893	Gold nanoprobe assay for the identification of mycobacteria of the Mycobacterium tuberculosis complex. 2010 , 16, 1464-1469	46
892	Homoeologous nonreciprocal recombination in polyploid cotton. 2010 , 186, 123-34	105
891	Mobilization of retrotransposons in synthetic allotetraploid tobacco. 2010 , 186, 135-47	122
890	Genetic architecture of zinc hyperaccumulation in Arabidopsis halleri: the essential role of QTL x environment interactions. 2010 , 187, 355-367	72
889	Host-selective toxins, Ptr ToxA and Ptr ToxB, as necrotrophic effectors in the Pyrenophora tritici-repentis-wheat interaction. 2010 , 187, 911-9	158
888	Functional characterization of nonsynonymous single nucleotide polymorphisms in the human organic anion transporter 4 (hOAT4). 2010 , 159, 419-27	32
887	Alzheimer's beta-amyloid peptide blocks vascular endothelial growth factor mediated signaling via direct interaction with VEGFR-2. 2010 , 112, 66-76	65
886	Biogeochemical cycling and microbial diversity in the thrombolitic microbialites of Highborne Cay, Bahamas. 2010 , 8, 337-54	68
885	Cyclophilin D links programmed cell death and organismal aging in Podospora anserina. 2010 , 9, 761-75	44
884	Cloning and induction patterns of Cu/Zn superoxide dismutase in responses to immune elicitors and nucleopolyhedrovirus in the beet armyworm Spodoptera exigua. 2010 , 40, 336-342	1
883	Molecular identification of the Hyalesthes species (Hemiptera: Cixiidae) occurring in vineyard agroecosystems. 2010 , 157, 435-445	11
882	Two new species of trypanosomatid parasites isolated from Heteroptera in Costa Rica. 2010 , 57, 177-88	44
881	Lowering intercellular melatonin levels by transgenic analysis of indoleamine 2,3-dioxygenase from rice in tomato plants. 2010 , 49, 239-47	66
880	Novel PSI domains in plant and animal H+-inositol symporters. 2010 , 11, 767-81	14
879	The combined effects of rivers and refugia generate extreme cryptic fragmentation within the common ground skink (scincella lateralis). 2010 , 64, 409-28	43
878	Uncoordinated phylogeography of Borrelia burgdorferi and its tick vector, Ixodes scapularis. 2010 , 64, 2653-63	60
877	Biochemical characterization of an ecto-ATP diphosphohydrolase activity in Candida parapsilosis and its possible role in adenosine acquisition and pathogenesis. 2010 , 10, 735-46	15

876	Diversity, abundance and distribution of amoA-encoding archaea in deep-sea methane seep sediments of the Okhotsk Sea. 2010 , 72, 370-85	60
875	Geochemical constraints on the diversity and activity of H2 -oxidizing microorganisms in diffuse hydrothermal fluids from a basalt- and an ultramafic-hosted vent. 2010 , 74, 55-71	30
874	Temporal shifts of the Norway lobster (Nephrops norvegicus) gut bacterial communities. 2010, 74, 472-84	55
873	Identification and in vitro deoxynucleotidylation of the terminal protein of the linear plasmid pAL1 of Arthrobacter nitroguajacolicus R B 1a. 2010 , 304, 169-76	6
872	Diversity of Wolbachia in Odontotermes spp. (Termitidae) and Coptotermes heimi (Rhinotermitidae) using the multigene approach. 2010 , 307, 55-64	20
871	Discovery of novel Vibrio cholerae VSP-II genomic islands using comparative genomic analysis. 2010 , 308, 130-7	44
870	Diversity of Mycobacterium species from marine sponges and their sensitivity to antagonism by sponge-derived rifamycin-synthesizing actinobacterium in the genus Salinispora. 2010 , 313, 33-40	18
869	Characterization of a two-component signal transduction system that controls arsenite oxidation in the chemolithoautotroph NT-26. 2010 , 313, 20-8	37
868	Using regional comparative phylogeographic data from snake lineages to infer historical processes in Middle America. 2010 , 33, no-no	22
867	X-ray crystallographic and NMR studies of pantothenate synthetase provide insights into the mechanism of homotropic inhibition by pantoate. 2010 , 277, 697-712	3
866	Targeting mechanism of the retinoblastoma tumor suppressor by a prototypical viral oncoprotein. Structural modularity, intrinsic disorder and phosphorylation of human papillomavirus E7. 2010 , 277, 973-88	35
865	Physiological truncation and domain organization of a novel uracil-DNA-degrading factor. 2010 , 277, 1245-59	5
864	Crystal structure of a glycoside hydrolase family 6 enzyme, CcCel6C, a cellulase constitutively produced by Coprinopsis cinerea. 2010 , 277, 1532-42	24
863	A new phospholipase A2 isolated from the sea anemone Urticina crassicornis lits primary structure and phylogenetic classification. 2010 , 277, 2641-2653	22
862	Characterization of single-nucleotide polymorphism markers in the Mediterranean mussel, Mytilus galloprovincialis. 2010 , 41, e568-e575	14
861	Cl- homeostasis in includer and excluder citrus rootstocks: transport mechanisms and identification of candidate genes. 2010 , 33, 2012-27	46
860	Identification of protein factors and U3 snoRNAs from a Brassica oleracea RNP complex involved in the processing of pre-rRNA. 2010 , 61, 383-98	22
859	A single-repeat MYB transcription factor, GmMYB176, regulates CHS8 gene expression and affects isoflavonoid biosynthesis in soybean. 2010 , 62, 1019-34	86

858	The origin of the non-recombining region of sex chromosomes in Carica and Vasconcellea. 2010 , 63, 801-10	22
857	Evolutionary analysis of regulatory sequences (EARS) in plants. 2010 , 64, 165-76	21
856	Arabidopsis Qa-SNARE SYP2 proteins localized to different subcellular regions function redundantly in vacuolar protein sorting and plant development. 2010 , 64, 924-35	39
855	Data mining cDNAs reveals three new single stranded RNA viruses in Nasonia (Hymenoptera: Pteromalidae). 2010 , 19 Suppl 1, 99-107	30
854	Wing development genes of the pea aphid and differential gene expression between winged and unwinged morphs. 2010 , 19 Suppl 2, 63-73	67
853	Halloween genes and nuclear receptors in ecdysteroid biosynthesis and signalling in the pea aphid. 2010 , 19 Suppl 2, 187-200	61
852	Comparative analysis of detoxification enzymes in Acyrthosiphon pisum and Myzus persicae. 2010 , 19 Suppl 2, 155-64	165
851	Two Tor genes in the silkworm Bombyx mori. 2010 , 19, 727-35	24
850	Co-expression of leptin and oestrogen receptors in the preoptic-hypothalamic area. 2010 , 22, 996-1003	13
849	Characterization of a hotspot for mimicry: assembly of a butterfly wing transcriptome to genomic sequence at the HmYb/Sb locus. 2010 , 19 Suppl 1, 240-54	63
848	Rapid evolution and selection inferred from the transcriptomes of sympatric crater lake cichlid fishes. 2010 , 19 Suppl 1, 197-211	180
847	Ecological rather than geographical isolation dominates Quaternary formation of Mediterranean Cistus species. 2010 , 19, 1381-95	57
846	Evidence of selection at the ramosa1 locus during maize domestication. 2010 , 19, 1296-311	44
845	Fat frogs, mobile genes: unexpected phylogeographic patterns for the ornate chorus frog (Pseudacris ornata). 2010 , 19, 2501-15	9
844	Patterns of persistence and isolation indicate resilience to climate change in montane rainforest lizards. 2010 , 19, 2531-44	68
843	Evolution of host breadth in broad interactions: mycorrhizal specificity in East Asian and North American rattlesnake plantains (Goodyera spp.) and their fungal hosts. 2010 , 19, 3008-17	51
842	Rampant drift in artificially fragmented populations of the endangered tidewater goby (Eucyclogobius newberryi). 2010 , 19, 3315-27	20
841	Phylogeography of ninespine sticklebacks (Pungitius pungitius) in North America: glacial refugia and the origins of adaptive traits. 2010 , 19, 4061-76	45

840	Serpentine soils promote ectomycorrhizal fungal diversity. 2010 , 19, 5566-76	28
839	A localized multimeric anchor attaches the Caulobacter holdfast to the cell pole. 2010 , 76, 409-27	51
838	Structure determination and analysis of a haemolytic gingipain adhesin domain from Porphyromonas gingivalis. 2010 , 76, 861-73	25
837	Phase variation controls expression of Salmonella lipopolysaccharide modification genes by a DNA methylation-dependent mechanism. 2010 , 77, 337-53	90
836	Interaction specificity, toxicity and regulation of a paralogous set of ParE/RelE-family toxin-antitoxin systems. 2010 , 77, 236-51	77
835	Phylogenetic analyses of symbiotic genes and characterization of functional traits of Mesorhizobium spp. strains associated with the promiscuous species Acacia seyal Del. 2010 , 108, 818-830	20
834	A long-standing Pleistocene refugium in southern Africa and a mosaic of refugia in East Africa: insights from mtDNA and the common eland antelope. 2010 , 37, 571-581	38
833	A phylogeographical study of the toxic benthic dinoflagellate genusOstreopsisSchmidt. 2010 , 37, 830-841	114
832	Rhizobial hitchhikers from Down Under: invasional meltdown in a plant-bacteria mutualism?. 2010 ,	23
831	Amphitropic amphiantarctic disjunctions in Apiaceae subfamily Apioideae. 2010 , 37, no-no	10
830	Orthogonal use of a human tRNA synthetase active site to achieve multifunctionality. 2010 , 17, 57-61	63
829	An intramembrane aromatic network determines pentameric assembly of Cys-loop receptors. 2010 , 17, 90-8	75
828	Crystal structure of the conserved herpesvirus fusion regulator complex gH-gL. 2010 , 17, 882-8	192
827	Structural basis for cooperative RNA binding and export complex assembly by HIV Rev. 2010 , 17, 1337-42	124
826	The obligate endobacteria of arbuscular mycorrhizal fungi are ancient heritable components related to the Mollicutes. 2010 , 4, 862-71	106
825	Ubiquitous cyanobacterial podoviruses in the global oceans unveiled through viral DNA polymerase gene sequences. 2010 , 4, 1243-51	37
824	[FeFe]-hydrogenase in Yellowstone National Park: evidence for dispersal limitation and phylogenetic niche conservatism. 2010 , 4, 1485-95	56
	phytogenetic mene conservation. 2010 , 1, 1 105 25	

Fructose 1,6-bisphosphate aldolase/phosphatase may be an ancestral gluconeogenic enzyme. 2010 , 464, 1077-81	144
Stepwise [FeFe]-hydrogenase H-cluster assembly revealed in the structure of HydA(DeltaEFG). 2010 , 465, 248-51	248
The architecture of respiratory complex I. 2010 , 465, 441-5	513
Natural allelic variation underlying a major fitness trade-off in Arabidopsis thaliana. 2010 , 465, 632-6	273
The Ndc80 kinetochore complex forms oligomeric arrays along microtubules. 2010 , 467, 805-10	223
Origin of the human malaria parasite Plasmodium falciparum in gorillas. 2010 , 467, 420-5	381
Structural basis of semaphorin-plexin signalling. 2010 , 467, 1118-22	168
Characterization of a monomeric heat-labile classical alkaline phosphatase from Anabaena sp. PCC7120. 2010 , 75, 655-64	12
Microbial community of the chemocline of the meromictic Lake Shunet (Khakassia, Russia) during summer stratification. 2010 , 79, 253-261	23
An essential function for the centrosomal protein NEDD1 in zebrafish development. 2010 , 17, 1302-14	13
Viral security proteins: counteracting host defences. 2010 , 8, 867-78	45
Inclusion of nuclear intron sequence data helps to identify the Asian sister group of New World pitvipers. 2010 , 54, 172-8	28
Probing into the diversity of trypanosomatid flagellates parasitizing insect hosts in South-West China reveals both endemism and global dispersal. 2010 , 54, 243-53	54
An evolutionary conserved motif is responsible for immunoglobulin heavy chain packing in the B cell membrane. 2010 , 57, 1238-44	7
Uncovering an overlooked radiation: molecular phylogeny and biogeography of Madagascar's endemic river snails (Caenogastropoda: Pachychilidae: Madagasikara gen. nov.). 2010 , 99, 867-894	34
Genetic and morphological variation in a Mediterranean glacial refugium: evidence from Italian pygmy shrews, Sorex minutus (Mammalia: Soricomorpha). 2010 , 100, 774-787	33
Co-evolution of the premaxilla and jaw protrusion in cichlid fishes (Heroine: Cichlidae). 2010 , 100, 619-629	27
The phylogeny of the Pantropical genus Arrhipis Bonvouloir (Coleoptera, Eucnemidae). 2010 , 26, 14-22	1
	Stepwise [FeFe]-hydrogenase H-cluster assembly revealed in the structure of HydA(DeltaEFG). 2010, 465, 248-51 The architecture of respiratory complex I. 2010, 465, 441-5 Natural allelic variation underlying a major fitness trade-off in Arabidopsis thaliana. 2010, 465, 632-6 The Ndc80 kinetochore complex forms oligomeric arrays along microtubules. 2010, 467, 805-10 Origin of the human malaria parasite Plasmodium falciparum in gorillas. 2010, 467, 420-5 Structural basis of semaphorin-plexin signalling. 2010, 467, 1118-22 Characterization of a monomeric heat-labile classical alkaline phosphatase from Anabaena sp. PCC7120. 2010, 75, 655-64 Microbial community of the chemocline of the meromictic Lake Shunet (Khakassia, Russia) during summer stratification. 2010, 79, 253-261 An essential function for the centrosomal protein NEDD1 in zebrafish development. 2010, 17, 1302-14 Viral security proteins: counteracting host defences. 2010, 8, 867-78 Inclusion of nuclear intron sequence data helps to identify the Asian sister group of New World pitvipers. 2010, 54, 172-8 Probing into the diversity of trypanosomatid flagellates parasitizing insect hosts in South-West China reveals both endemism and global dispersal. 2010, 54, 243-53 An evolutionary conserved motif is responsible for immunoglobulin heavy chain packing in the B cell membrane. 2010, 57, 1238-44 Uncovering an overlooked radiation: molecular phylogeny and biogeography of Madagascar's endemic river snails (Caenogastropoda: Pachychilidae: Madagasikara gen. nov.). 2010, 99, 867-894 Cenetic and morphological variation in a Mediterranean glacial refugitum: evidence from Italian pygmy shrews, Sorex minutus (Mammalia: Soricomorpha). 2010, 100, 774-787 Co-evolution of the premaxilla and Jaw protrusion in cichlid fishes (Heroine: Cichlidae). 2010, 100, 619-629

804	Tracking the geographical spread of avian influenza (H5N1) with multiple phylogenetic trees. 2010 , 26, 1-13	107
803	Development and validation of a qPCR-based method for quantifying Shiga toxin-encoding and other lambdoid bacteriophages. 2010 , 12, 1194-204	29
802	Annotation and overview of the Pseudomonas savastanoi pv. savastanoi NCPPB 3335 draft genome reveals the virulence gene complement of a tumour-inducing pathogen of woody hosts. 2010 , 12, 1604-20	66
801	Natural transformation of Vibrio fischeri requires tfoX and tfoY. 2010 , 12, 2302-11	73
800	A thermophilic bacterial origin and subsequent constraints by redox, light and salinity on the evolution of the microbial mercuric reductase. 2010 , 12, 2904-17	82
799	Comparative analysis between protist communities from the deep-sea pelagic ecosystem and specific deep hydrothermal habitats. 2010 , 12, 2946-64	65
798	First description of giant Archaea (Thaumarchaeota) associated with putative bacterial ectosymbionts in a sulfidic marine habitat. 2010 , 12, 2371-83	58
797	Phylogenetic position of a rare loricated green alga, Cephalomonas granulata N. L. Higinb. (Volvocales, Chlorophyceae). 2010 , 58, 62-68	12
796	Chlorella variabilis and Micractinium reisseri sp. nov. (Chlorellaceae, Trebouxiophyceae): Redescription of the endosymbiotic green algae of Paramecium bursaria (Peniculia, Oligohymenophorea) in the 120th year. 2010 , 58, 188-201	63
795	Enhancing plant growth and fiber production by silencing GA 2-oxidase. 2010 , 8, 425-35	68
794	Structure and putative function of NFX1-like proteins in plants. 2010 , 12, 381-94	13
793	An update on the ABCC transporter family in plants: many genes, many proteins, but how many functions?. 2010 , 12 Suppl 1, 15-25	53
79 ²	Expression, localisation and phylogeny of a novel family of plant-specific membrane proteins. 2010 , 12 Suppl 1, 140-52	16
791	Flatfish at seamount hydrothermal vents show strong genetic divergence between volcanic arcs. 2010 , 31, 158-167	18
790	Secondary and tertiary structure modeling reveals effects of novel mutations in polycystic liver disease genes PRKCSH and SEC63. 2010 , 78, 47-56	38
7 ⁸ 9	Transmembrane nine proteins in yeast and Arabidopsis affect cellular metal contents without changing vacuolar morphology. 2010 , 140, 355-67	10
788	Wing pointedness associated with migratory distance in common-garden and comparative studies of stonechats (Saxicola torquata). 2010 , 23, 1050-63	67
787	Comparative rates of lower jaw diversification in cichlid adaptive radiations. 2010 , 23, 1456-67	36

786	Evolution of 11[beta]-Hydroxysteroid Dehydrogenase-Type 1 and 11[beta]-Hydroxysteroid Dehydrogenase-type 3. 2010 ,	
785	11[beta]-hydroxysteroid dehydrogenase-type 2 evolved from an ancestral 17[beta]-hydroxysteroid dehydrogenase-type 2. 2010 ,	
7 ⁸ 4	The interplay of descriptor-based computational analysis with pharmacophore modeling builds the basis for a novel classification scheme for feruloyl esterases. 2010 ,	
783	Epidemiological Baseline of Influenza Virus in Wild Aquatic Birds in Hong Kong during the Pre-H5N1 Endemic Era. 2010 ,	
782	A systematic review of the genus Chasmodes (Teleostei: Perciformes: Blenniidae). 2010 , 2558, 1	2
781	Two new Stephanostomum-like cercariae (Digenea: Acanthocolpidae) from Nassarius dorsatus and N. olivaceus (Gastropoda: Nassariidae) in Central Queensland, Australia. 2010 , 2445, 35	7
7 ⁸ 0	A new species of Pseudodiaptomus (Copepoda: Calanoida) from Japan, with notes on the closely related P. inopinus Burckhardt, 1913 from Kyushu Island. 2010 , 2623, 52	16
779	Joint Analysis of Near-Isogenic and Recombinant Inbred Line Populations Yields Precise Positional Estimates for Quantitative Trait Loci. 2010 , 3,	12
778	Finding the balance between the mathematical and biological optima in multiple sequence alignment. 2010 , 2, 7	23
777	Marine myxobacteria as a source of antibioticscomparison of physiology, polyketide-type genes and antibiotic production of three new isolates of Enhygromyxa salina. 2010 , 8, 2466-79	39
776	Circadian clock proteins in prokaryotes: hidden rhythms?. 2010 , 1, 130	28
775	Seasonal Expression of the Picocyanobacterial Phosphonate Transporter Gene phnD in the Sargasso Sea. 2010 , 1, 135	20
774	Kinase/phosphatase overexpression reveals pathways regulating hippocampal neuron morphology. 2010 , 6, 391	55
773	Of bits and bugson the use of bioinformatics and a bacterial crystal structure to solve a eukaryotic repeat-protein structure. 2010 , 5, e13402	19
772	Sequence and structural analysis of the chitinase insertion domain reveals two conserved motifs involved in chitin-binding. 2010 , 5, e8654	81
771	A humanized anti-VEGF rabbit monoclonal antibody inhibits angiogenesis and blocks tumor growth in xenograft models. 2010 , 5, e9072	44
770	Phylogenetic analysis of the MS4A and TMEM176 gene families. 2010 , 5, e9369	51
769	Phenotypic covariance of longevity, immunity and stress resistance in the caenorhabditis nematodes. 2010 , 5, e9978	33

768	A novel role for minimal introns: routing mRNAs to the cytosol. 2010 , 5, e10144	27
767	The enzyme and the cDNA sequence of a thermolabile and double-strand specific DNase from Northern shrimps (Pandalus borealis). 2010 , 5, e10295	21
766	Agrin binds BMP2, BMP4 and TGFbeta1. 2010 , 5, e10758	23
765	UBIAD1 mutation alters a mitochondrial prenyltransferase to cause Schnyder corneal dystrophy. 2010 , 5, e10760	47
764	GM-CSF increases mucosal and systemic immunogenicity of an H1N1 influenza DNA vaccine administered into the epidermis of non-human primates. 2010 , 5, e11021	53
763	Platelet-derived growth factor receptor beta is critical for zebrafish intersegmental vessel formation. 2010 , 5, e11324	35
762	The fate of miRNA* strand through evolutionary analysis: implication for degradation as merely carrier strand or potential regulatory molecule?. 2010 , 5, e11387	169
761	Identification of a novel Staphylococcus aureus two-component leukotoxin using cell surface proteomics. 2010 , 5, e11634	159
760	Structural disorder within Henipavirus nucleoprotein and phosphoprotein: from predictions to experimental assessment. 2010 , 5, e11684	63
759	Serpentine soils do not limit mycorrhizal fungal diversity. 2010 , 5, e11757	33
758	Extracellular and mixotrophic symbiosis in the whale-fall mussel Adipicola pacifica: a trend in evolution from extra- to intracellular symbiosis. 2010 , 5, e11808	34
757	Crystal structure of the RNA recognition motif of yeast translation initiation factor eIF3b reveals differences to human eIF3b. 2010 , 5, e12784	9
756	MicroRNA discovery and analysis of pinewood nematode Bursaphelenchus xylophilus by deep sequencing. 2010 , 5, e13271	30
755	Evolutionary history and population dynamics of hepatitis E virus. 2010 , 5, e14376	86
754	Robust computational analysis of rRNA hypervariable tag datasets. 2010 , 5, e15220	14
753	Apolipophorin-III mediates antiplasmodial epithelial responses in Anopheles gambiae (G3) mosquitoes. 2010 , 5, e15410	46
752	The Aquaporin gene family of the yellow fever mosquito, Aedes aegypti. 2010 , 5, e15578	75
751	Genome analysis of Treponema pallidum subsp. pallidum and subsp. pertenue strains: most of the genetic differences are localized in six regions. 2010 , 5, e15713	48

Computational internal sequence repeats analysis of accelerated evolution and the role of 750 extensins under abiotic and biotic stresses. 2010, 157 Phylogenetic relationships among Unionicola (Acari: Unionicolidae) mussel-mites of North America 6 749 based on mitochondrial cytochrome oxidase I sequences. 2010, 2537, 47 Simulated Atmospheric Nitrogen Deposition Alters Actinobacterial Community Composition in 748 55 Forest Soils. 2010, 74, 1157-1166 Structures of Heterotrimeric G Proteins and their Complexes. 2010, 119-128 747 Phylogenetic Diversity of the Cold Water Octocoral Paragorgia arborea (Linnaeus, 1758) off the 746 East Coast of Canada. 2010. 3. A new species of Lepidocephalichthys (Teleostei: Cobitidae) with distinctive sexual dimorphism and 745 comments on relationships in southern lineages of Cobitidae. 2010, 2557, 1 A Clustering Optimization Strategy for Molecular Taxonomy Applied to Planktonic Foraminifera 27 744 SSU rDNA. **2010**, 6, 97-112 Molecular phylogeny of edge hill virus supports its position in the yellow Fever virus group and 19 743 identifies a new genetic variant. 2010, 6, 91-6 Cocultivated bacteria can increase or decrease the culture lifetime of Chlorella vulgaris. 2010, 56, 413-8 742 10 Structural biology of DNA repair: spatial organisation of the multicomponent complexes of 741 23 nonhomologous end joining. 2010, 2010, MYB transcription factors orchestrating the developmental program of xylem vessels in 740 29 Arabidopsis roots. 2010, 27, 267-272 Staphylococcus aureus NrdH redoxin is a reductant of the class Ib ribonucleotide reductase. 2010, 739 24 192, 4963-72 Evolution of a distinct genomic domain in Drosophila: comparative analysis of the dot chromosome 738 25 in Drosophila melanogaster and Drosophila virilis. 2010, 185, 1519-34 Characterization of Streptococcus pyogenes beta-NAD+ glycohydrolase: re-evaluation of enzymatic 737 33 properties associated with pathogenesis. 2010, 285, 5683-94 Polymorphisms in the IGF1 gene and their effect on growth traits in Mexican beef cattle. 2010, 9, 875-83 736 33 Molecular characterization of ovine zygomycosis in central western Brazil. 2010, 22, 274-7 735 15 Isolation of Rickettsia parkeri and identification of a novel spotted fever group Rickettsia sp. from 734 91 Gulf Coast ticks (Amblyomma maculatum) in the United States. 2010, 76, 2689-96 Origin and evolution of the unique tetra-domain hemoglobin from the hydrothermal vent scale 733 24 worm Branchipolynoe. 2010, 27, 143-52

732	GIN transposons: genetic elements linking retrotransposons and genes. 2010 , 27, 1903-11	12
731	PTMScout, a Web resource for analysis of high throughput post-translational proteomics studies. 2010 , 9, 2558-70	37
730	BB0250 of Borrelia burgdorferi is a conserved and essential inner membrane protein required for cell division. 2010 , 192, 6105-15	28
729	Genomic analysis of codon, sequence and structural conservation with selective biochemical-structure mapping reveals highly conserved and dynamic structures in rotavirus RNAs with potential cis-acting functions. 2010 , 38, 7718-35	49
728	Vibrio casei sp. nov., isolated from the surfaces of two French red smear soft cheeses. 2010 , 60, 1745-1749	24
727	Implication of serine residues 271, 273, and 275 in the human immunodeficiency virus type 1 cofactor activity of lens epithelium-derived growth factor/p75. 2010 , 84, 740-52	18
726	Diagnosing cervical cancer and high-grade precursors by HPV16 transcription patterns. 2010 , 70, 249-56	56
725	DnaB proteolysis in vivo regulates oligomerization and its localization at oriC in Bacillus subtilis. 2010 , 38, 2851-64	14
724	Genetic and phenotypic characterization of GII-4 noroviruses that circulated during 1987 to 2008. 2010 , 84, 9595-607	57
723	Huntingtin facilitates polycomb repressive complex 2. 2010 , 19, 573-83	128
723 722	Huntingtin facilitates polycomb repressive complex 2. 2010 , 19, 573-83 Evidence for multiple independent origins of trans-splicing in Metazoa. 2010 , 27, 684-93	128 60
722	Evidence for multiple independent origins of trans-splicing in Metazoa. 2010 , 27, 684-93	60
722 721	Evidence for multiple independent origins of trans-splicing in Metazoa. 2010 , 27, 684-93 Arabidopsis thaliana XRN2 is required for primary cleavage in the pre-ribosomal RNA. 2010 , 38, 4487-502 An effector-targeted protease contributes to defense against Phytophthora infestans and is under	60
722 721 720	Evidence for multiple independent origins of trans-splicing in Metazoa. 2010 , 27, 684-93 Arabidopsis thaliana XRN2 is required for primary cleavage in the pre-ribosomal RNA. 2010 , 38, 4487-502 An effector-targeted protease contributes to defense against Phytophthora infestans and is under diversifying selection in natural hosts. 2010 , 154, 1794-804 Perturbed heme binding is responsible for the blistering phenotype associated with mutations in	60 81 121
722 721 720 719	Evidence for multiple independent origins of trans-splicing in Metazoa. 2010, 27, 684-93 Arabidopsis thaliana XRN2 is required for primary cleavage in the pre-ribosomal RNA. 2010, 38, 4487-502 An effector-targeted protease contributes to defense against Phytophthora infestans and is under diversifying selection in natural hosts. 2010, 154, 1794-804 Perturbed heme binding is responsible for the blistering phenotype associated with mutations in the Caenorhabditis elegans dual oxidase 1 (DUOX1) peroxidase domain. 2010, 285, 40991-1000	60 81 121
722 721 720 719 718	Evidence for multiple independent origins of trans-splicing in Metazoa. 2010, 27, 684-93 Arabidopsis thaliana XRN2 is required for primary cleavage in the pre-ribosomal RNA. 2010, 38, 4487-502 An effector-targeted protease contributes to defense against Phytophthora infestans and is under diversifying selection in natural hosts. 2010, 154, 1794-804 Perturbed heme binding is responsible for the blistering phenotype associated with mutations in the Caenorhabditis elegans dual oxidase 1 (DUOX1) peroxidase domain. 2010, 285, 40991-1000 Evidence for bacterial origin of heat shock RNA-1. 2010, 16, 274-9 The N-myc downstream regulated gene (NDRG) family: diverse functions, multiple applications.	60 81 121 19

714	Molecular basis for the resistance of an insect chymotrypsin to a potato type II proteinase inhibitor. 2010 , 107, 15016-21	49
713	Crystal structure of bovine CD1b3 with endogenously bound ligands. 2010 , 185, 376-86	15
712	Large-scale patterns in biodiversity of microbial eukaryotes from the abyssal sea floor. 2010 , 107, 115-20	86
711	Large-scale tRNA intron transposition in the archaeal order Thermoproteales represents a novel mechanism of intron gain. 2010 , 27, 2233-43	26
710	A BAFF-R mutation associated with non-Hodgkin lymphoma alters TRAF recruitment and reveals new insights into BAFF-R signaling. 2010 , 207, 2569-79	73
709	Unusual evolution of a catalytic core element in CCA-adding enzymes. 2010 , 38, 4436-47	17
708	Footprints of X-to-Y gene conversion in recent human evolution. 2010 , 27, 714-25	36
707	Vivaxin genes encode highly immunogenic, non-variant antigens on the Trypanosoma vivax cell-surface. 2022 , 16, e0010791	O
706	Phylogeographic structure of common sage (Salvia officinalis L.) reveals microrefugia throughout the Balkans and colonizations of the Apennines. 2022 , 12,	О
705	The Angolan bushveld lizards, genus Heliobolus Fitzinger, 1843 (Squamata: Lacertidae): Integrative taxonomy and the description of two new species. 72, 745-769	O
704	Compositional Dynamics of Gastrointestinal Tract Microbiomes Associated with Dietary Transition and Feeding Cessation in Lake Sturgeon Larvae. 2022 , 10, 1872	О
703	Paracoccus everestensis sp. nov., a novel bacterium with great antioxidant capacity isolated from the north slope of Mount Everest. 2022 , 72,	О
702	Taxonomic Delimitation of the Monostromatic Green Algal Genera Monostroma Thuret 1854 and Gayralia Vinogradova 1969 (Ulotrichales, Chlorophyta). 2022 , 14, 773	О
701	Bta06987, Encoding a Peptide of the AKH/RPCH Family: A Role of Energy Mobilization in Bemisia tabaci. 2022 , 13, 834	Ο
700	Genome-derived Microsatellite Markers in Lippia origanoides from Colombia. 1-18	О
699	KMer-Node2Vec: Learning Vector Representations of K-mers from the K-mer Graph.	Ο
698	Domestication-associated PHYTOCHROME C is a flowering time repressor and a key factor determining Setaria as a short-day plant.	Ο
697	Functional divergence of GLP genes between G. barbadense and G. hirsutum in response to Verticillium dahliae infection. 2022 , 114, 110470	1

696	Transcriptome characterization and profiling related to detoxification enzyme genes in Chilo sacchariphagus (Lepidoptera Crambidae). 2022 , 52, 404-427	О
695	Insights to the superoxide dismutase genes and its roles in Hevea brasiliensis under abiotic stress. 2022 , 12,	0
694	Machine learning reveals limited contribution of trans-only encoded variants to the HLA-DQ immunopeptidome by accurate and comprehensive HLA-DQ antigen presentation prediction.	0
693	Streptococcus ruminicola sp. nov., new species of the Streptococcus bovis/Streptococcus equinus complex (SBSEC) isolated from the rumen of Korean domestic ruminants. 2022 , 204,	Ο
692	Identification and structural modeling of the chlamydial RNA polymerase omega subunit.	Ο
691	Spatial Structure Formation by RsmE-Regulated Extracellular Secretions in Pseudomonas fluorescens Pf0-1.	Ο
690	The complete mitochondrial genome of Isochrysis galbana harbors a unique repeat structure and a specific trans-spliced cox1 gene. 13,	Ο
689	Grass Carp Prx 3 Elevates Host Antioxidant Activity and Induces Autophagy to Inhibit Grass Carp Reovirus (GCRV) Replication. 2022 , 11, 1952	1
688	Lysophosphatidic acid signaling via LPA 6 : a negative modulator of developmental oligodendrocyte maturation.	Ο
687	Comparative structural insight into the unidirectional catalysis of ornithine carbamoyltransferases from Psychrobacter sp. PAMC 21119. 2022 , 17, e0274019	Ο
686	Phylogeographic patterns of the yellow fever virus around the metropolitan region of SB Paulo, Brazil, 2016I019. 2022 , 16, e0010705	1
685	Complete genome sequence of a novel mitovirus isolated from the fungus Fusarium equiseti causing potato dry rot.	O
684	Microbial antagonism against phytopathogenic Botrytis cinerea in highbush blueberry (Vaccinium corymbosum L.) cultivars. Contribution of leaf-associated microorganisms from native Andean Ericaceae.	0
683	First Report on Molecular Identification of Moniezia expansa in Sheep from Mannavanur, Palani Hills, Tamil Nadu, India.	O
682	Import and Export of Mannosylerythritol Lipids by Ustilago maydis.	1
681	Genome-Wide Identification and Molecular Evolution of the Magnesium Transporter (MGT) Gene Family in Citrullus lanatus and Cucumis sativus. 2022 , 12, 2253	0
680	New Genetic Variants of Leptospira spp Characterized by MLST from Peruvian Isolates. 2022 , 2022, 1-13	0
679	Phylogenomic characterization and pangenomic insights into the surfactin-producing bacteria Bacillus subtilis strain RI4914.	O

678	Immune pathogenesis in pigeons during experimental Prohemistomum vivax infection. 9,	О
677	Comprehensive genomic characterization of cotton cationic amino acid transporter genes reveals that GhCAT10D regulates salt tolerance. 2022 , 22,	0
676	Antibiotic and metal resistance of Stenotrophomonas maltophilia isolates from Eboling permafrost of the Tibetan Plateau.	Ο
675	Characterization of a metagenome-derived thermostable xylanase from Tengchong hot spring.	O
674	High evidence targets of conserved plant microRNAs and the complexities of their ancient microRNA binding-sites.	0
673	Characterization of a novel thermophilic beta-glucosidase from Thermotoga sp. and its application in the transformation of notoginsenoside R1. 2022 , 12,	Ο
672	The Phosphofurin Acidic Cluster Sorting Protein 2 (PACS-2) E209K Mutation Responsible for PACS-2 Syndrome Increases Susceptibility to Apoptosis. 2022 , 7, 34378-34388	1
671	Exposure of dogs and cats to Borrelia miyamotoi infected Ixodes ricinus ticks in urban areas of the city of Pozna west-central Poland.	0
670	Desulfofustis limnaeus sp. nov., a freshwater sulfate-reducing bacterium isolated from marsh soil. 2022 , 204,	0
669	The genome of Areca catechu provides insights into sex determination of monoecious plants.	O
668	Production of Helvolic Acid in Metarhizium Contributes to Fungal Infection of Insects by Bacteriostatic Inhibition of the Host Cuticular Microbiomes.	0
((-		
667	Genetic Analysis and Fine Mapping of ZmGHT1 Conferring Glufosinate Herbicide Tolerance in Maize (Zea mays L.). 2022 , 23, 11481	0
666		0
	(Zea mays L.). 2022 , 23, 11481	
666	(Zea mays L.). 2022 , 23, 11481 Cytochrome P450 Genes Expressed in Phasmatodea Midguts. 2022 , 13, 873 Systematic analysis of the pectin methylesterase gene family in Nicotiana tabacum and reveal their	0
666	(Zea mays L.). 2022, 23, 11481 Cytochrome P450 Genes Expressed in Phasmatodea Midguts. 2022, 13, 873 Systematic analysis of the pectin methylesterase gene family in Nicotiana tabacum and reveal their multiple roles in plant development and abiotic stresses. 13,	0
666 665 664	Cytochrome P450 Genes Expressed in Phasmatodea Midguts. 2022, 13, 873 Systematic analysis of the pectin methylesterase gene family in Nicotiana tabacum and reveal their multiple roles in plant development and abiotic stresses. 13, BRCA2 BRC missense variants disrupt RAD51-dependent DNA repair. 11, Evolutionary relationship analysis of STARD gene family and VvSTARD5 improves tolerance of salt	0 0

660	Ribosomal MLST nucleotide identity (rMLST-NI), a rapid bacterial species identification method: application to Klebsiella and Raoultella genomic species validation. 2022 , 8,	0
659	A new species of Allobathynella (Crustacea, Bathynellacea, Parabathynellidae) from the hyporheic zone of the Hangang River, South Korea. 44, 85-101	O
658	Towards Understanding the Function of Aegerolysins. 2022 , 14, 629	0
657	Structural basis for strychnine activation of human bitter taste receptor TAS2R46. 2022 , 377, 1298-1304	1
656	Genome-Wide Identifiation and Expression Proling of the Wnt Gene Family in Three Rice Planthoppers: Sogatella furcifera, Laodelphax striatellus, and Nilaparvata lugens. 2022 , 22,	О
655	A revision of the Inocybe grammata group in North America including four new taxa.	Ο
654	Novel ECarotene and Astaxanthin-Producing Marine Planococcus sp.: Insights into Carotenogenesis Regulation and Genetic Aspects.	0
653	Genome-wide identification of the ZIP gene family in lettuce (Lactuca sativa L.) and expression analysis under different element stress. 2022 , 17, e0274319	O
652	Phylogeny and systematics of the genus Clonostachys.	О
651	Metabarcoding of mycetangia from the Dendroctonus frontalis species complex (Curculionidae: Scolytinae) reveals diverse and functionally redundant fungal assemblages. 13,	Ο
650	Genome-wide identification, evolution and function analysis of UGTs superfamily in cotton. 9,	0
649	Fungal Load of Groundwater Systems in Geographically Segregated Islands: A Step Forward in Fungal Control. 1-12	O
648	A review on bacterial and archaeal thermostable sulfur oxidoreductases (SORS)-an insight into the biochemical, molecular and in-silico structural comparative analysis of a neglected thermostable enzyme of industrial significance. 2022 , 204,	0
647	Genome-Wide Investigation and Characterization of SWEET Gene Family with Focus on Their Evolution and Expression during Hormone and Abiotic Stress Response in Maize. 2022 , 13, 1682	1
646	Influence of planting yellowhorn (Xanthoceras sorbifolium Bunge) on the bacterial and fungal diversity of fly ash. 10, e14015	0
645	Molecular characterization of two pedigrees with maternally inherited diabetes mellitus. 2022 , 7, 1724-1731	0
644	Suppression of the insect cuticular microbiomes by a fungal defensin to facilitate parasite infection.	0
643	Acrocarpospora catenulata sp. nov., a novel actinobacterium isolated from lake sediment. 2022 , 72,	О

642	New findings on the fungal species <i>Tricholoma matsutake</i> from Ukraine, and revision of its taxonomy and biogeography based on multilocus phylogenetic analyses. 2022 , 63, 197-214	1
641	Structure-Based Pathogenicity Relationship Identifier (SPRI): A Novel Structure-Guided Method to Evaluate Pathological Effect of Missense Mutations.	0
640	The Transcription Factor CsAtf1 Negatively Regulates the Cytochrome P450 Gene CsCyp51G1 to Increase Fludioxonil Sensitivity in Colletotrichum siamense. 2022 , 8, 1032	0
639	Organellar genome comparisons of Sargassum polycystum and S. plagiophyllum (Fucales, Phaeophyceae) with other Sargassum species. 2022 , 23,	O
638	An updated checklist of Collembola in Taiwan, with DNA barcoding of Papirioides jacobsoni Folsom, 1924 (Symphypleona, Dicyrtomidae). 1123, 123-146	0
637	Emergence and molecular characterization of the avian infectious bronchitis virus GI-23 in commercial broiler farms from South America.	О
636	Genome-wide identification of black pepper (Piper nigrum L.) Dof gene family and the differential gene screening in resistance to Phytophthora capsici.	0
635	Physiological insight into the conserved properties of Caenorhabditis elegans acid-sensing DEG/ENaCs.	О
634	Variation in the growth and toxin production of Gymnodinium catenatum under different laboratory conditions. 2022 , 169,	0
633	The linker domain of the initiator DnaA contributes to its ATP binding and membrane association in E. coli chromosomal replication. 2022 , 8,	О
632	Analysis of ancient and modern horse genomes reveals the critical impact of lncRNA-mediated epigenetic regulation on horse domestication. 13,	0
631	An activated form of NB-ARC protein RLS1 functions with cysteine-rich receptor-like protein RMC to trigger cell death in rice. 2022 , 100459	О
630	Isocitrate binds to the itaconic acid-responsive LysR-type transcriptional regulator RipR in Salmonella pathogenesis. 2022 , 102562	0
629	Genome-wide analysis and characterization of the LRR-RLK gene family provides insights into anthracnose resistance in common bean.	O
628	Description and genomic characterization of Jiella flava sp. nov., isolated from Acrostichum aureum. 2022 , 72,	0
627	Genome-wide identification of the auxin response factor (ARF) gene family in Magnolia sieboldii and functional analysis of MsARF5. 13,	О
626	Description of two new species Chattonella tenuiplastida sp. nov. and Chattonella malayana sp. nov. (Raphidophyceae) from South China Sea, with a report of wild fish mortality. 2022 , 118, 102322	0
625	Coleophora santonici Baldizzone & Taktīs (Lepidoptera, Coleophoridae), new species from Hungary bred from Artemisia santonicum. 2022 , 129,	О

624	The complex genome and adaptive evolution of polyploid Chinese pepper (Zanthoxylum armatum and Zanthoxylum bungeanum).	O
623	Structural insights into the substrate binding of phosphomevalonate kinase from the silkworm, Bombyx mori. 2022 , 150, 103849	O
622	Expression of coffee florigen CaFT1 reveals a sustained floral induction window associated with asynchronous flowering in tropical perennials. 2022 , 325, 111479	1
621	In silico prediction of B-cell and T-cell epitope of Ves g 5 and Vesp m 5 allergens. 2021 , 35, 72	O
620	Rapid detection of HPV16/18 based on CRISPR-Cas13a/Cas12a dual-channel system.	О
619	Morphological and Molecular Characterization of Tylenchorhynchus clarus Allen, 1955 and T. zeae Sethi & Sethi	O
618	Development and Validation of a Bioinformatic Workflow for the Rapid Detection of Viruses in Biosecurity. 2022 , 14, 2163	О
617	The Auxin/Indole-3-Acetic Acid (Aux/IAA) Gene Family Analysis of Four Rosaceae Genomes and Expression Patterns of PmIAAs in Prunus mume. 2022 , 8, 899	O
616	Bnakkale Boਬz∸ndan Yakalanan Kolyozūn (Scomber japonicus Houttuyn, 1782) Biyokimyasal ve Hematolojik Karakteristikleri ⊠erine Anisakis pegreffii (Nematoda: Anisakidae)ūin Etkisi.	О
615	How tectonic, volcanic and climatic processes in Andean Eky islands haped the diversification of endemic ground beetles. 2022 , 49, 2077-2090	O
614	Natural variation of Alfin-like family affects seed size and drought tolerance in rice.	1
613	Identification and evolutionary characterization of SFBB genes in Maliland its spontaneous self-compatible mutant [inzhui[[Pyrus bretschneideri]]. 2022 ,	O
612	A centenary tale: population genetic insights into the introduction history of the oriental fire-bellied toad (Bombina orientalis) in Beijing. 2022 , 22,	0
611	Population analysis of heavy metal and biocide resistance genes in Salmonella enterica from human clinical cases in New Hampshire, United States. 13,	O
610	One fold, many functions™23 family of peptidoglycan hydrolases. 13,	0
609	New Record of Echinoderms from Gili Ketapang Island by Combining DNA Barcoding and Morphology: A Baseline Report.	O
608	Polarly localized WPR proteins interact with PAN receptors and the actin cytoskeleton during maize stomatal development.	1
607	Revealing the contribution of GbPR10.5D1 to resistance against Verticillium dahliae and its regulation for structural defense and immune signaling.	O

606	Genome-wide identification and expression profiling of WUSCHEL-related homeobox (WOX) genes confer their roles in somatic embryogenesis, growth and abiotic stresses in banana. 2022 , 12,	0
605	Peptides that Mimic RS repeats modulate phase separation of SRSF1, revealing a reliance on combined stacking and electrostatic interactions.	Ο
604	Chemosensory-Related Genes in Marine Copepods. 2022 , 20, 681	Ο
603	Whole genome and transcriptome reveal flavone accumulation in Scutellaria baicalensis roots. 13,	O
602	Current genetic diversity of managed and commercially produced Apis mellifera colonies in Argentina inferred by wing geometric morphometrics and COI-COII mtDNA locus. 2022 , 53,	0
601	Genome-Wide Identification of Maize Protein Arginine Methyltransferase Genes and Functional Analysis of ZmPRMT1 Reveal Essential Roles in Arabidopsis Flowering Regulation and Abiotic Stress Tolerance. 2022 , 23, 12793	O
600	Genome-wide identification and comparative analysis of CLE family in rapeseed and its diploid progenitors. 13,	0
599	A second locus contributing to the differential expression of the blue sensitive opsin SWS2A in Lake Malawi cichlids.	Ο
598	tRNA methylation resolves codon usage bias at the limit of cell viability. 2022 , 41, 111539	Ο
597	Sequential action of a tRNA base editor in conversion of cytidine to pseudouridine. 2022, 13,	1
596	Cloning and characterization of thermophilic endoglucanase and its application in the transformation of ginsenosides. 2022 , 12,	1
595	Genome-Wide Analysis and Expression Profiling of Glutathione Reductase Gene Family in Oat (Avena sativa) Indicate Their Responses to Abiotic Stress during Seed Imbibition. 2022 , 23, 11650	O
594	Biochemical Characterization of GacI, a Bifunctional Glycosyltransferase P hosphatase Enzyme Involved in Acarbose Biosynthesis in Streptomyces glaucescens GLA.O.	0
593	A Novel ssDNA Aptamer Targeting Carcinoembryonic Antigen: Selection and Characterization. 2022 , 11, 1540	O
592	Host Plants Shape the Codon Usage Pattern of Turnip Mosaic Virus. 2022 , 14, 2267	0
591	Borna Disease Virus 1 Phosphoprotein Forms a Tetramer and Interacts with Host Factors Involved in DNA Double-Strand Break Repair and mRNA Processing. 2022 , 14, 2358	O
590	Genomic Insights into the Radiation-Resistant Capability of Sphingomonas qomolangmaensis S5-59T and Sphingomonas glaciei S8-45T, Two Novel Bacteria from the North Slope of Mount Everest. 2022 , 10, 2037	О
589	Aquimarina acroporae sp. nov., isolated from seawater surrounding scleractinian coral Acropora digitifera. 2022 , 72,	O

588	Complete chloroplast genome sequences of Phlomis fruticosa and Phlomoides strigosa and comparative analysis of the genus Phlomis sensu lato (Lamiaceae). 13,	O
587	Assessment of the Role of Free-Living and Farmed Fallow Deer (Dama dama) as A Potential Source of Human Infection with Multiple-Drug-Resistant Strains of Yersinia enterocolitica and Yersinia pseudotuberculosis. 2022 , 11, 1266	O
586	The complete mitochondrial genome of the woodwasp Euxiphydria potanini (Hymenoptera, Xiphydrioidea) and phylogenetic implications for symphytans. 2022 , 12,	0
585	Deep mutational scanning and machine learning reveal structural and molecular rules governing allosteric hotspots in homologous proteins. 11,	2
584	Tempo-spatial distribution of Ulva spp. micro-propagules in the Yellow Sea during and after green tide in 2019.	1
583	Discovery of a MUC3B gene reconstructs the membrane mucin gene cluster on human chromosome 7. 2022 , 17, e0275671	O
582	WRKY genes in black raspberry (Rubus occidentalis L.): duplicate and conquer.	0
581	The complex set of internal repeats in SpTransformer protein sequences result in multiple but limited alternative alignments. 13,	Ο
580	On the energetic differences of avian cryptochromes 4 from selected species. 2022 , 76,	1
579	Genetic architecture of behavioural resilience to ocean acidification.	O
578	HDOCK update for modeling protein- RNA / DNA complex structures. 2022, 31,	O
577	Molecular characterization and transcriptomic analysis of a novel polymycovirus in the fungus Talaromyces amestolkiae. 13,	O
576	HBcompare: Classifying Ligand Binding Preferences with Hydrogen Bond Topology. 2022 , 12, 1589	0
575	Genome-Wide Identification of the DOF Gene Family Involved in Fruitlet Abscission in Areca catechu L 2022 , 23, 11768	0
574	Horizontally transferred genes as RNA interference targets for aphid and whitefly control.	0
573	Phylogenetic reconstructions of Polynesian medicinal plant use reveal adaptive strategies to meet health needs.	O
572	Antibacterial Activity of Bacillus Strains against Acute Hepatopancreatic Necrosis Disease-Causing Vibrio campbellii in Pacific White Leg Shrimp. 2022 , 7, 287	0
571	Massive genome investigations reveal insights of prevalent introgression for environmental adaptation and triterpene biosynthesis in Ganoderma.	0

570	Ion transfer mechanisms in Mrp-type antiporters from high resolution cryoEM and molecular dynamics simulations. 2022 , 13,	1
569	Genome-Wide Analysis of the MYB-Related Transcription Factor Family in Pepper and Functional Studies of CaMYB37 Involvement in Capsaicin Biosynthesis. 2022 , 23, 11667	2
568	Genome-wide characterization of the UDP-glycosyltransferase gene family reveals their potential roles in leaf senescence in cotton. 2022 ,	1
567	Mitochondrial diversity and phylogenetic structure of Yellowcheek (Elopichthys bambusa) in the Yangtze River.	1
566	Cross-watershed distribution pattern challenging the elimination of Oncomelania hupensis, the intermediate host of Schistosoma japonica, in Sichuan province, China. 2022 , 15,	Ο
565	Complex statistical modelling for phylogenetic inference.	Ο
564	Accumulation of soxC-expressing cells facilitated by MMPreg is essential for blastema formation in annelids.	0
563	Exploring morphological evolution in relation to habitat moisture in the moss genus Fissidens using molecular data generated from herbarium specimens.	Ο
562	A Chlamydia psittaci Outbreak in Psittacine Birds in Sardinia, Italy. 2022 , 19, 14204	Ο
561	Stieleria sedimenti sp. nov., a Novel Member of the Family Pirellulaceae with Antimicrobial Activity Isolated in Portugal from Brackish Sediments. 2022 , 10, 2151	1
560	High level of somatic mutations detected in a diploid banana wild relative Musa basjoo.	О
559	Comparative analysis of the complete mitochondrial genomes of two species of Clupeiformes and the phylogenetic implications for Clupeiformes. 1-12	Ο
558	Genotyping of Coxiella burnetii from Cattle by Multispacer Sequence Typing and Multiple Locus Variable Number of Tandem Repeat Analysis in the Republic of Korea. 2022 , 13, 1927	Ο
557	Overexpression of EKetoacyl CoA Synthase 2B.1 from Chenopodium quinoa Promotes Suberin MonomersIProduction and Salt Tolerance in Arabidopsis thaliana. 2022 , 23, 13204	Ο
556	Genome-wide analysis of R2R3-MYB transcription factors in Japanese morning glory. 2022 , 17, e0271012	Ο
555	Characterization of WOX genes revealed drought tolerance, callus induction, and tissue regeneration in Gossypium hirsutum. 13,	Ο
554	Gracilaria gracilis and Nannochloropsis oceanica, singly or in combination, in diets alter the intestinal microbiota of European seabass (Dicentrarchus labrax). 9,	1
553	Geometric morphometric and molecular techniques for discriminating among three cryptic species of the Anopheles barbirostris complex (Diptera: Culicidae) in Thailand. 2022 , 8, e11261	1

552	Genome-wide characterization and expression analysis of the growth-regulating factor family in Saccharum. 2022 , 22,	0
551	Septins regulate virulence in Verticillium dahliae and differentially contribute to microsclerotial formation and stress responses. 2022 , 4,	O
550	Expanding spectrum, intrafamilial diversity, and therapeutic challenges from 15 patients with heterozygous CARD11-associated diseases: A single center experience. 13,	1
549	Phylogeny and Systematics of the Genus Tolypocladium (Ophiocordycipitaceae, Hypocreales). 2022 , 8, 1158	O
548	Genome-wide characterization of AINTEGUMENTA-LIKE family in Medicago truncatula reveals the significant roles of AINTEGUMENTAs in leaf growth. 13,	O
547	Genome-wide association study reveals a GLYCOGEN SYNTHASE KINASE 3 gene regulating plant height in Brassica napus. 13,	1
546	A homolog of low molecular weight protein tyrosine phosphatase isolated from Brucella melitensis displays an acidic dual specific phosphatase activity, nonessential for bacterial resistance to bactericidal factors and virulence. 2022 , 101904	O
545	Polar localization of CheO under hypoxia promotes Campylobacter jejuni chemotactic behavior within host. 2022 , 18, e1010953	O
544	Whole genome resequencing and comparative genome analysis of three Puccinia striiformis f. sp. tritici pathotypes prevalent in India. 2022 , 17, e0261697	O
543	Allosteric inhibition of the epidermal growth factor receptor through disruption of transmembrane interactions.	O
542	Genome-wide identification of RUB activating enzyme and conjugating enzyme gene families and their expression analysis under abiotic stresses in Capsicum annuum.	0
541	Leptospira spp. strains associated with Bovine Genital Leptospirosis (BGL). 2022, 173, 105841	O
540	The interferon-like proteins, Vagos, in Fenneropenaeus merguiensis elicit antimicrobial responses against WSSV and VPAHPND infection. 2022 , 131, 718-728	O
539	SAM1 domain of SASH1 harbors distinctive structural heterogeneity. 2022 , 214, 107914	O
538	Structural characterization and functional analysis of juvenile hormone acid methyltransferase JHAMT3 from the silkworm, Bombyx mori. 2022 , 151, 103863	O
537	Co-cultivation of microalgae-cyanobacterium under various nitrogen and phosphorus regimes to concurrently improve biomass, lipid accumulation and easy harvesting. 2022 , 188, 108706	O
536	Insight into the molecular structure and function of peptidoglycan recognition protein SC2 (PGRP-SC2) from Amphiprion clarkii: Investigating the role in innate immunity. 2022 , 131, 559-569	O
535	Purification and characterization of enolase as a novel allergen in Platanus acerifolia pollen. 2022 , 113, 109313	O

534	Recombination and incomplete concerted evolution of the ribosomal 18S (partial) -ITS1-5.8S-ITS2-28S (partial) rDNA in Cynoglossus trigrammus genome. 2022 , 105, 104513	0
533	A novel catfish cultured in South China is proved to be Silurus asotus based on morphological and molecular genomic identification. 2022 , 27, 101376	Ο
532	A new enantioselective dioxygenase for the (S)-enantiomer of the chiral herbicide dichlorprop in Sphingopyxis sp. DBS4. 2023 , 176, 105511	0
531	Genome Wide Characterization of CBL-CIPK Family Genes and Their Responsive Expression in Rosa chinensis. 2023 , 92, 349-368	0
530	In-vitro characterization of thrombolytic activity of staphylokinase produced by Staphylococcus aureus S1. 2022 ,	0
529	An opportunistic pathogenic Pseudomonas isolated from healthy brown alga Saccharina japonica. 2023 , 563, 738975	0
528	Plant-endophytic bacteria interactions associated with root and leaf microbiomes of Cattleya walkeriana and their effect on plant growth. 2023 , 309, 111656	1
527	Association of milk production traits with genetic variants in exon 5 and intron 3 of bovine growth hormone (bGH) gene in Sahiwal cattle. 2022 , 91,	O
526	Genomic Analysis of Halotolerant Bacterial Strains Martelella soudanensis NC18T and NC20. 2022,	О
525	CHARACTERIZATION of cox3 and rnl GENES ENCODED IN MITOCHONDRIA of Fusarium graminearum.	O
524	Teaching Computational Genomics and Bioinformatics on a High Performance Computing Cluster - A Primer.	О
523	Genome-wide identification and expression analysis of NAC family genes in Ginkgo biloba L	O
522	Identification and Expression Analysis of Odorant-Binding and Chemosensory Protein Genes in Virus Vector Nephotettix cincticeps. 2022 , 13, 1024	О
521	Genome-wide analysis of zinc finger-homeodomain (ZF-HD) transcription factors in diploid and tetraploid cotton.	Ο
520	Population genetic assessment of G igantocalamus malpenensis K.M. Wong (Poaceae: Bambusoideae: Bambuseae) and implications for bamboo silviculture.	0
519	SEPepQuant enables comprehensive protein isoform characterization in shotgun proteomics.	O
518	KINN: An alignment-free accurate phylogeny reconstruction method based on inner distance distributions of k-mer pairs in biological sequences. 2022 , 107662	O
517	Mitochondrial effects on fertility and longevity in Tigriopus californicus contradict predictions of the mother's curse hypothesis. 2022 , 289,	Ο

516	Molecular phylogeny of the spiny-surfaced species of the dinoflagellate Prorocentrum with the description of P. Thermophilum sp. nov. and P. criophilum sp. nov. (Prorocentrales, Dinophyceae).	O
515	Behavioral and genomic divergence between a generalist and a specialist fly. 2022, 41, 111654	O
514	Investigating the eukaryotic host-like SLiMs in microbial mimitopes and their potential as novel drug targets for treating autoimmune diseases. 13,	O
513	An ancient enzyme finds a new home: Prevalence and neofunctionalization of trypsin in marine phytoplankton.	O
512	Complete Mitochondrial Genome, Genetic Diversity and Phylogenetic Analysis of Pingpu Yellow Chicken (Gallus gallus). 2022 , 12, 3037	O
511	Functional Characterization and Structural Modeling of a Novel Glycine Oxidase from Variovorax paradoxus Iso1.	O
510	Bioinformatics analysis and function prediction of NBS-LRR gene family in Broussonetia papyrifera.	О
509	Preparation of chitooligosaccharides with a low degree of polymerization and anti-microbial properties using the novel chitosanase AqCsn1. 2022 , 106199	O
508	Evolution patterns of NBS genes in the genus Dendrobium and NBS-LRR gene expression in D. officinale by salicylic acid treatment. 2022 , 22,	O
507	Six novel Micromonospora species associated with the phyllosphere and roots of leguminous plants: Micromonospora alfalfae sp. nov., Micromonospora cabrerizensis sp. nov., Micromonospora foliorum sp. nov., Micromonospora hortensis sp. nov., Micromonospora salmantinae sp. nov., and	O
506	Mechanochemical tuning of a kinesin motor essential for malaria parasite transmission. 2022 , 13,	0
505	Identification and expression analysis of maize NF-YA subunit genes. 10, e14306	O
504	Molecular exposition of broad-spectrum antibacterial efficacy by p-coumaric acid from an edible mushroom Termitomyces heimii: in vitro and in silico approach.	O
503	An ancestral mycobacterial effector promotes dissemination of infection. 2022,	O
502	Genome-Wide Identification and In Silico Analysis of ZF-HD Transcription Factor Genes in Zea mays L 2022 , 13, 2112	1
501	Positive selection-driven fixation of a hominin-specific amino acid mutation related to dephosphorylation in IRF9. 2022 , 22,	O
500	Toxic Dinophysis acuminata in southern Chile: A comparative approach based on its first local in vitro culture and offshore-estuarine bloom dynamics. 2022 , 102918	1
499	Weed Hosts Represent an Important Reservoir of Turnip Yellows Virus and a Possible Source of Virus Introduction into Oilseed Rape Crop. 2022 , 14, 2511	1

498	Integrative approach clarifies the distinct taxonomic account of gryloblattids endemic to Hokkaido, Japan, with a description of two new species (Insecta, Grylloblattodea). 2022 ,	0
497	Environmental features drive lineage diversification in the Aricidea assimilis species complex (Annelida, Paraonidae) in the Mediterranean Sea. 2022 , 89, 1246-1258	Ο
496	Exploring clade differentiation of the Faecalibacterium prausnitzii complex. 2022, 105533	0
495	Jiella avicenniae sp. nov., a novel endophytic bacterium isolated from bark of Avicennia marina. 2022 , 204,	0
494	Antibacterial Properties and Potential Mechanism of Serum from Chinese Alligator. 2022, 10, 2210	0
493	Tobacco rattle virus-induced VcANS gene silencing in blueberry fruit. 2022 , 147054	0
492	Multi-Bioactivity of Protein Digests and Peptides from Oat (Avena sativa L.) Kernels in the Prevention of the Cardiometabolic Syndrome. 2022 , 27, 7907	1
491	Extreme harmful algal blooms, climate change, and potential risk of eutrophication in Patagonian fjords: insights from an exceptional Heterosigma akashiwo fish-killing event. 2022 , 102921	0
490	A glutathione-independent DJ-1/PfpI domain-containing tomato glyoxalaseIII2 , SlGLYIII2 , confers enhanced tolerance under salt and osmotic stresses.	0
489	Tegument protein UL21 of alpha-herpesvirus inhibits the innate immunity by triggering CGAS degradation through TOLLIP-mediated selective autophagy. 1-21	0
488	African Swine Fever Virus MGF110-7L Induces Host Cell Translation Suppression and Stress Granule Formation by Activating the PERK/PKR-eIF2Pathway.	3
487	Lack of mtDNA genetic diversity despite phenotypic variation and environmental heterogeneity in the exotic suckermouth armored catfish (Pterygoplichthys pardalis).	0
486	Is the Illegal Trade of Glass Eels (Anguilla anguilla) Increasing the Spread of Disease? A Case of EVEX. 2022 , 10, 2208	O
485	Screening, isolation and mechanism of a nematicidal extract from actinomycetes against the pine wood nematode Bursaphelenchus xylophilus. 2022 , e11713	0
484	Phosphorylation status of CPK28 affects its ubiquitination and protein stability.	O
483	Mutational patterns along different evolution paths of follicular lymphoma. 12,	O
482	Immunostimulatory activity of Lactococcus lactis LM1185 isolated from Hydrangea macrophylla.	О
481	A multifunctional LysM effector ofBotrytis cinereacontributes to plant infection.	0

480	Transcriptomic profiling analysis to identify genes associated with PA biosynthesis and insolubilization in the late stage of fruit development in C-PCNA persimmon. 2022 , 12,	2
479	Unsterile production of a polyhydroxyalkanoate copolymer by Halomonas cupida J9. 2022 , 223, 240-251	О
478	Ecological significance of G protein-coupled receptors in the Pacific oyster (Crassostrea gigas): Pervasive gene duplication and distinct transcriptional response to marine environmental stresses. 2022 , 185, 114269	О
477	Provenance of rhizobial symbionts is similar for invasive and non-invasive acacias introduced to California.	O
476	Genome-Wide Identification, Characterization, and Expression Analysis of CHS Gene Family Members in Chrysanthemum nankingense. 2022 , 13, 2145	0
475	The first complete genome of the simian malaria parasite Plasmodium brasilianum. 2022 , 12,	O
474	Identification of the GAPDH gene family in Citrullus lanatus and functional characteristics of ClGAPC2 in Arabidopsis thaliana.	O
473	Natural occurrence of entomopathogenic fungus, <i>Aschersonia aleyrodis</i> on citrus whitefly, <i>Dialeurodes citri</i> (Ashmead) in Kinnow mandarin in Punjab, India. 181-186	O
472	Genomes of Vibrio metoecus co-isolated with Vibrio cholerae extend our understanding of differences between these closely related species. 2022 , 14,	O
471	Evolution, Expansion and Characterization of Cannabinoid Synthase Gene Family in Cannabis Sativa.	О
470	Characterization of HcaA, a novel autotransporter protein inHelicobacter cinaedi, and its role in host cell adhesion.	0
469	Molecular detection of tick-borne rickettsial pathogens in ticks collected from domestic animals from Cauca, Colombia. 2022 , 106773	O
468	Genome-wide analysis of the SWEET genes in Taraxacum kok-saghyz Rodin: An insight into two latex-abundant isoforms. 2022 ,	1
467	Expression profile and molecular function of beclin-1 in Epinephelus akaara in response to immune stimuli and oxidative stress. 2023 , 132, 108490	O
466	Bird's-eye MApping of plasmids (BeMAp) for visualization and comparison of genomic structures of different plasmids by mapping antimicrobial resistance genes on spreadsheets. 2023 , 204, 106645	0
465	SKAP2 Modular Organization Differently Recognizes SRC Kinases Depending on Their Activation Status and Localization. 2023 , 22, 100451	O
464	Grape BES1 transcription factor gene VvBES1-3 confers salt tolerance in transgenic Arabidopsis. 2023 , 854, 147059	О
463	Genome-wide evolutionary analysis of AUX/IAA gene family in wheat identifies a novel gene TaIAA15-1A regulating flowering time by interacting with ARF. 2023 , 227, 285-296	O

462	Structural evolution of an amphibian-specific globin: A computational evolutionary biochemistry approach. 2023 , 45, 101055	О
461	Response of a temperate coral to temperature stress: A comparison of populations across sites. 2023 , 560, 151863	O
460	Inter and intra-specific relationship between goat fishes Upeneus vittatus (Forsskal, 1775) and Upeneus tragula based on their mtCOI gene from Palk Bay and Gulf of Mannar Coast (Mandapam, Tamil Nadu) of India. 2023 , 30, 101713	O
459	Prediction and verification of glycosyltransferase activity by bioinformatics analysis and protein engineering. 2023 , 4, 101905	O
458	Two dominant genes in barley (<i>Hordeum vulgare</i> L.) complementarily encode perfect resistance to <i>Japanese soil-borne wheat mosaic virus</i>. 2022 , 72, 372-382	0
457	Molecular characterisation of Giardia duodenalis from human and companion animal sources in the United Kingdom using an improved triosephosphate isomerase molecular marker. 2022 , 2, 100105	O
456	Association of lactation persistency with genetic variants of bovine growth hormone gene in Indian Sahiwal cows. 2022 , 90, 739-743	O
455	Colletotrichum spp. and other fungi associated with anthracnose on Coffea arabica L. in Mfida State, Venezuela. 2022 , 48, 99-111	O
454	Neisseria gonorrhoeae Ketol-Acid Reductoisomerase Is a Potential Therapeutic Target.	О
453	Potential Pathogenicity of Aeromonas spp. Recovered in River Water, Soil, and Vegetation from a Natural Recreational Area. 2022 , 11, 1382	O
452	Spike protein of SARS-CoV-2 Omicron variant: An in-silico study evaluating spike interactions and immune evasion. 10,	O
451	Structural differences in 3C-like protease (Mpro) from SARS-CoV and SARS-CoV-2: molecular insights revealed by Molecular Dynamics Simulations.	O
450	Development of a Taq-Man qPCR assay for trypanosomatid multi-species detection and quantification in insects.	0
449	Genetic diversity of rodent species sold in South African pet shops.	O
448	Genomic basis of the giga-chromosomes and giga-genome of tree peony Paeonia ostii. 2022, 13,	О
447	ConsensusPrimeA Bioinformatic Pipeline for Ideal Consensus Primer Design. 2022 , 2, 637-642	O
446	Dominant Elongase Activity of Elovl5a but Higher Expression of Elovl5b in Common Carp (Cyprinus carpio). 2022 , 23, 14666	1
445	Identification and Characterization of AP2/ERF Transcription Factors in Yellow Horn. 2022 , 23, 14991	1

444	Response regulator PorX coordinates oligonucleotide signalling and gene expression to control the secretion of virulence factors. 2022 , 50, 12558-12577	0
443	Global occurrence of the bacteria with capability for extracellular reduction of iodate. 13,	О
442	KNEMIDOKOPTES MITES AND THEIR EFFECTS ON THE GRIPPING POSITION OF THE FEET OF STELLER'S JAYS (CYANOCITTA STELLERI). 2022 , 58,	0
441	Genome-Scale Investigation of GARP Family Genes Reveals Their Pivotal Roles in Nutrient Stress Resistance in Allotetraploid Rapeseed. 2022 , 23, 14484	1
440	Multivalent Human Cytomegalovirus Glycoprotein B Nucleoside-Modified mRNA Vaccines Demonstrate a Greater Breadth in T cell but not Antibody Responses.	Ο
439	Dual-Mode Gold Nanoparticle-Based Method for Early Detection of Acanthamoeba. 2022 , 23, 14877	Ο
438	Sensing of a spore surface protein by a Drosophila chemosensory protein induces behavioral defense against fungal parasitic infections. 2022 ,	1
437	Immunoinformatics analysis of candidate proteins for controlling bovine paratuberculosis. 2022 , 17, e0277751	O
436	Characterization of feruloyl esterases from Pecoramyces sp. F1 and the synergistic effect in biomass degradation. 2023 , 39,	0
425		
435	Thermodynamic Architecture and Conformational Plasticity of GPCRs.	O
434	Thermodynamic Architecture and Conformational Plasticity of GPCRs. Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. 2022 , 185, 4587-46	
434	Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. 2022 , 185, 4587-46 MeGATAs, functional generalists in interactions between cassava growth and development, and	03.e 2 3
434	Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. 2022, 185, 4587-46 MeGATAs, functional generalists in interactions between cassava growth and development, and abiotic stresses.	03.e 2 3
434 433 432	Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. 2022, 185, 4587-46 MeGATAs, functional generalists in interactions between cassava growth and development, and abiotic stresses. Lacticaseibacillus kribbianus sp. nov., isolated from pig farm faeces dump. 2022, 72,	03.e23 0
434 433 432 431	Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. 2022, 185, 4587-46 MeGATAs, functional generalists in interactions between cassava growth and development, and abiotic stresses. Lacticaseibacillus kribbianus sp. nov., isolated from pig farm faeces dump. 2022, 72, Phylogeny and biogeography of the algal DMS-releasing enzyme. Geology, climate, and hydrochemistry shape the spatial patterns of multiple diversity facets and	03.e23 0
434 433 432 431 430	Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. 2022, 185, 4587-46 MeGATAs, functional generalists in interactions between cassava growth and development, and abiotic stresses. Lacticaseibacillus kribbianus sp. nov., isolated from pig farm faeces dump. 2022, 72, Phylogeny and biogeography of the algal DMS-releasing enzyme. Geology, climate, and hydrochemistry shape the spatial patterns of multiple diversity facets and functional traits of fishes. Genome-Wide Identification and Expression Analysis of the PME and PMEI Gene Families in	03.e23 0

426	Calcium-permeable channelrhodopsins for the photocontrol of calcium signalling. 2022, 13,	O
425	Three mitochondrial lineages and no Atlantic-Mediterranean barrier for the bogue Boops boops across its widespread distribution. 2022 , 12,	O
424	Quantification of Marine Picocyanobacteria on Water Column Particles and in Sediments Using Real-Time PCR Reveals Their Role in Carbon Export. 2022 , 7,	0
423	Emergence of Anaplasma Species Related to A. phagocytophilum and A. platys in Senegal. 2023 , 24, 35	O
422	Identification of the Xyloglucan Endotransglycosylase/Hydrolase (XTH) Gene Family Members Expressed in Boehmeria nivea in Response to Cadmium Stress. 2022 , 23, 16104	1
421	ERG11 Gene Variability and Azole Susceptibility in Malassezia pachydermatis.	O
420	Identification of Halophilic and Halotolerant Bacteria from the Root Soil of the Halophyte Sesuvium verrucosum Raf. 2022 , 11, 3355	1
419	Transcriptome analysis and identification of chemosensory genes in the larvae of Plagiodera versicolora. 2022 , 23,	O
418	Characterisation of key genotypic and phenotypic traits of clinical cystic fibrosisStaphylococcus aureusisolates.	0
417	Biosynthesis of Lyngbyastatins 1 and 3, Cytotoxic Depsipeptides from an Okeania sp. Marine Cyanobacterium.	O
416	Diversity dynamics of aerobic anoxygenic phototrophic bacteria in a freshwater lake.	O
415	Chloroplast genome assemblies and comparative analyses of commercially important Vaccinium berry crops. 2022 , 12,	1
414	Enhanced genome-wide association reveals the role of YABBY11-NGATHA-LIKE1 in leaf serration development of Populus.	0
413	Replitrons: a new group of eukaryotic transposons encoding HUH endonuclease.	O
412	Characterization and DNA Stable-Isotope Probing of Methanotrophic Bioaerosols. 2022, 10,	0
411	Genetic restoration of black rhinoceroses in South Africa: conservation implications.	O
410	Host-symbiont interactions in Angomonas deanei include the evolution of a host-derived dynamin ring around the endosymbiont division site. 2022 ,	0
409	De novo transcriptome analysis of the centrohelid Raphidocystis contractilis to identify genes involved in microtubule-based motility.	O

408	New globally distributed bacterial phyla within the FCB superphylum. 2022, 13,	0
407	Epidemiology of Type 3 Poliovirus AFP Cases in Israel between 1973 and 1988: Whole Genome Sequencing of RNA Extracted Directly from Archived Stocks to Avoid Re-Culturing Neurovirulent Wild Poliovirus. 2022 , 10, 2154	0
406	Modeling and analysis of the dynamics of communities of microbial DNA sequences in environments.	O
405	Characterisation of neonatalStaphylococcus capitisNRCS-A isolates compared with non NRCS-AStaphylococcus capitisfrom neonates and adults.	O
404	Genome-wide analysis of Hyperosmolality-gated calcium-permeable channel (OSCA) family members and their involvement in various osmotic stresses in Brassica napus. 2022 , 147137	О
403	Metabolic functional redundancy of the CYP9A subfamily members leads to P450 -mediated lambda -cyhalothrin resistance in Cydia pomonella.	1
402	18 S r DNA sequenceEtructure phylogeny of the Euglenophyceae (Euglenozoa, Euglenida).	0
401	Nucleic acid sensing by STING induces an interferon-like antiviral response in a marine invertebrate.	O
400	The Thylakoid Membrane Protein NTA1 Is An Assembly Factor of Cytochrome b6f Complex Essential for Chloroplast Development in Arabidopsis. 2022 , 100509	0
399	Comparative Transcriptome Analysis of CCCH Family in Roles of Flower Opening and Abiotic Stress in Osmanthus fragrans. 2022 , 23, 15363	O
398	Sourcing thermotolerant poly(ethylene terephthalate) hydrolase scaffolds from natural diversity. 2022 , 13,	3
397	Extensive reorganization of the chloroplast genome of Corydalis platycarpa: A comparative analysis of their organization and evolution with other Corydalis plastomes. 13,	0
396	Genome-Wide Characterization of Trehalose-6-Phosphate Synthase Gene Family of Brassica napus and Potential Links with Agronomic Traits. 2022 , 23, 15714	0
395	Structural basis of odorant recognition by a human odorant receptor.	1
394	Transposon-derived transcription factors across metazoans.	1
393	Transmission dynamics of human herpesvirus 6A, 6B and 7 from whole genome sequences of families. 2022 , 19,	O
392	Phylogeographic and morphological analysis ofBotrylloides nigerHerdman, 1886 from the northeastern Mediterranean Sea.	0
391	Identification and Expression Analysis of MPK and MKK Gene Families in Pecan (Carya illinoinensis). 2022 , 23, 15190	O

390	Phylogeography of hepatitis B virus: The role of Portugal in the early dissemination of HBV worldwide. 2022 , 17, e0276618	О
389	Auxin Biosynthesis Genes in Allotetraploid Oilseed Rape Are Essential for Plant Development and Response to Drought Stress. 2022 , 23, 15600	O
388	Identification of the riceRcgene as a main regulator of seed survival under dry storage conditions.	0
387	Capture-SELEX: Selection Strategy, Aptamer Identification, and Biosensing Application. 2022, 12, 1142	1
386	Impact of a biorepair treatment on the diversity of calcifying bacterial communities at the surface of cracked concrete walls. 2023 , 107, 187-200	O
385	Genome-wide identification, characterization, and evolutionary analysis of NBS genes and their association with disease resistance in Musa spp 2023 , 23,	O
384	Population structure of mud flounder Paralichthys orbignyanus from the south-western Atlantic Ocean.	0
383	Draft Genome of White-blotched River Stingray Provides Novel Clues for Niche Adaptation and Skeleton Formation. 2022 ,	Ο
382	Molecular Cloning and Characterization of a New Family VI Esterase from an Activated Sludge Metagenome. 2022 , 10, 2403	О
381	Length matters: functional flip of the short TatA transmembrane helix. 2022,	O
381	Length matters: functional flip of the short TatA transmembrane helix. 2022 , Characteristics of the ErmK Protein of Bacillus halodurans C-125.	0
380	Characteristics of the ErmK Protein of Bacillus halodurans C-125.	0
380 379	Characteristics of the ErmK Protein of Bacillus halodurans C-125. Pdif-mediated antibiotic resistance genes transfer in bacteria identified by pdifFinder. Comparative genomic analyses of four novel Ramlibacter species and the cellulose-degrading	0
380 379 378	Characteristics of the ErmK Protein of Bacillus halodurans C-125. Pdif-mediated antibiotic resistance genes transfer in bacteria identified by pdifFinder. Comparative genomic analyses of four novel Ramlibacter species and the cellulose-degrading properties of Ramlibacter cellulosilyticus sp. nov 2022, 12,	0 1 0
380 379 378 377	Characteristics of the ErmK Protein of Bacillus halodurans C-125. Pdif-mediated antibiotic resistance genes transfer in bacteria identified by pdifFinder. Comparative genomic analyses of four novel Ramlibacter species and the cellulose-degrading properties of Ramlibacter cellulosilyticus sp. nov 2022, 12, Identification and Characterization of Corynaridin, a Novel Linaridin from Corynebacterium lactis. Evolutionary reconstruction, nomenclature and functional meta-analysis of the Kiwellin protein	0 1 0
380 379 378 377	Characteristics of the ErmK Protein of Bacillus halodurans C-125. Pdif-mediated antibiotic resistance genes transfer in bacteria identified by pdifFinder. Comparative genomic analyses of four novel Ramlibacter species and the cellulose-degrading properties of Ramlibacter cellulosilyticus sp. nov 2022, 12, Identification and Characterization of Corynaridin, a Novel Linaridin from Corynebacterium lactis. Evolutionary reconstruction, nomenclature and functional meta-analysis of the Kiwellin protein family. 13, Morphology and genetics of grasshopper mice revisited in a paleontological framework:	0 1 0 0

372	Effects of Coleus amboinicus L. Essential Oil and Ethanolic Extracts on Planktonic Cells and Biofilm Formation of Microsporum canis Isolated from Feline Dermatophytosis. 2022 , 11, 1734	O
371	Differential critical residues on the overlapped region of the non-structural protein-1 recognized by flavivirus and dengue virus cross-reactive monoclonal antibodies. 2022 , 12,	O
370	Genome-wide identification of sucrose non-fermenting-1-related protein kinase genes in maize and their responses to abiotic stresses. 13,	0
369	Identification of an 任1 -♠)-Mannosyltransferase Contributing To Biosynthesis of the Fungal-Type Galactomannan ⊞ore-Mannan Structure in Aspergillus fumigatus. 2022 , 7,	1
368	The catalase-peroxidase PiCP1 plays a critical role in abiotic stress resistance, pathogenicity and asexual structure development in Phytophthora infestans.	0
367	Chromosome-scale genome assembly of Eustoma grandiflorum, the first complete genome sequence in the genus Eustoma.	O
366	The Delta variant wave in Tunisia: Genetic diversity, spatio-temporal distribution and evidence of the spread of a divergent AY.122 sub-lineage. 10,	O
365	Mitochondrial genome of Pseudopotamilla reniformis (Annelida: Sabellidae). 2023, 8, 149-151	O
364	Systematics and Phylogenetic Placement of Panicum L. Species within the Melinidinae Based on Morphological, Anatomical, and Molecular Data (Poaceae, Panicoideae, Paniceae). 2023 , 12, 399	O
363	Bioinformatic analysis of the coding region of the melatonin receptor 1b gene as a reliable DNA marker to resolve interspecific mammal phylogenetic relationships. 2023 , 20, 5430-5447	O
362	Genome-wide identification of acyl-CoA binding proteins and possible functional prediction in legumes. 13,	1
361	OsPRD2 is essential for double-strand break formation, but not spindle assembly during rice meiosis. 13,	O
360	Evaluation of Modern Techniques for Species Identification of Lutzia Mosquitoes (Diptera: Culicidae) in Thailand: Geometric Morphometrics and DNA Barcoding. 2023 , 14, 78	1
359	The identification of conserved sequence features of co-translationally decayed mRNAs and upstream open reading frames in angiosperm transcriptomes. 2023 , 7,	O
358	In-depth genetic characterization of the SARS-CoV-2 pandemic in a two-year frame in North Macedonia using second and third generation sequencing technologies. 2,	0
357	Identification and Characterization of CCD Gene Family in Rose (Rosa chinensis Jacq. Dld Blush) and Gene Co-Expression Network in Biosynthesis of Flower Scent. 2023 , 9, 115	1
356	Determinants of substrate specificity in a catalytically diverse family of acyl-ACP thioesterases from plants. 2023 , 23,	2
355	Genomically mined acoustic reporter genes for real-time in vivo monitoring of tumors and tumor-homing bacteria.	O

354	Fbxl4 Regulates the Photic Entrainment of Circadian Locomotor Rhythms in the Cricket Gryllus bimaculatus. 2023 , 40,	1
353	SARM suppresses TRIF, TRAF3, and IRF3/7 mediated antiviral signaling in large yellow croaker Larimichthys crocea. 13,	O
352	Saxitoxins-producing potential of the marine dinoflagellate Alexandrium affine and its environmental implications revealed by toxins and transcriptome profiling. 2023 , 105874	0
351	Overexpression of the Liriodendron chinense CONSTANS gene in Arabidopsis causes earlier flowering under long-day conditions.	O
350	LsSpt23p is a regulator of triacylglycerol synthesis in the oleaginous yeast Lipomyces starkeyi.	О
349	Genetic Divergence and Connectivity among Gene Pools of Polyprion americanus. 2023 , 13, 302	О
348	Expression and functional analysis of ace1 and ace2 reveal their differential roles in larval growth and insecticide sensitivity in Spodoptera frugiperda.	О
347	Review of the Mimeticus Subgroup of Culex (Culex) (Diptera: Culicidae), With an Assessment of the Specific Status of Three Nominal Species Described From India.	О
346	Virome analyses by next-generation sequencing (NGS) in chilli (Capsicum anuumL.) presented with diverse symptoms phenotype revealed the association of seven plant viruses.	О
345	Genome-Wide Identification and Expression Analysis of the Xyloglucan Endotransglucosylase/Hydrolase Gene Family in Sweet Potato [Ipomoea batatas (L.) Lam]. 2023 , 24, 775	О
344	Transcriptome-wide analysis of mRNA N 6 -methyladenosine modification in the embryonic development of Spodoptera frugiperda.	О
343	Genome-Wide Identification and Characterization of the Trehalose-6-Phosphate Synthetase Gene Family in Chinese Cabbage (Brassica rapa) and Plasmodiophora brassicae during Their Interaction. 2023 , 24, 929	О
342	Rapid prototyping enzyme homologs to improve titer of nicotinamide mononucleotide using a strategy combining cell-free protein synthesis with split GFP.	О
341	Genome-wide characterization of Ficus carica MADS-box transcription factors with a focus on their roles during fruit development.	О
340	Comprehensive Analysis and Functional Verification of the Pinus massoniana NBS-LRR Gene Family Involved in the Resistance to Bursaphelenchus xylophilus. 2023 , 24, 1812	0
339	Taxonomical and functional analysis of four arbuscular mycorrhizal fungi populations obtained from a Ricinus communis rhizospheric Cr(VI) polluted soil. 2023 , 100343	О
338	Development of a novel loop-mediated isothermal amplification assay for Elactamase gene identification using clinical isolates of Gram-negative bacteria. 12,	О
337	Is It in the Stars? Exploring the Relationships between Species Traits and Sea Star Wasting Disease. 000-000	О

336	A Clinical, Pathological, Epidemiological and Molecular Investigation of Recent Outbreaks of Peste des Petits Ruminants Virus in Domestic and Wild Small Ruminants in the Abu Dhabi Emirate, United Arab Emirates. 2023 , 10, 56	O
335	Golgi fucosyltransferase 1 reveals its important role in 日,4-fucose modification of N-glycan in CRISPR/Cas9 diatom Phaeodactylum tricornutum. 2023 , 22,	O
334	A cinnamyl alcohol dehydrogenase (CAD) like enzyme leads to a branch in the shikonin biosynthetic pathway inArnebia euchroma.	О
333	Biotransformations of nitriles mediated by in vivo nitrile hydratase of Rhodococcus erythropolis ATCC 4277 heterologously expressed in E. coli. 2023 , 5, 100760	O
332	Evolutionary Landscape of SOX Genes to Inform Genotype-to-Phenotype Relationships. 2023 , 14, 222	О
331	Identification of PLATZ genes in Malus and expression characteristics of MdPLATZs in response to drought and ABA stresses. 13,	O
330	Functional immune diversity in reindeer reveals a high Arctic population at risk. 10,	О
329	Modulation of the IKS channel by PIP2 requires two binding sites per monomer. 2023 , 3, 100073	O
328	Landscape structure is a key driver of soil protist diversity in meadows in the Swiss Alps.	О
327	Detection of Candidatus Phythoplasma prunorumlin Apricot Trees and its Associated Psyllid Samples. 2023 , 13, 199	O
326	Thermodynamic architecture and conformational plasticity of GPCRs. 2023, 14,	О
325	Role of the Nitrogen Metabolism Regulator TAM1 in Regulation of Cellulase Gene Expression in Trichoderma reesei.	Ο
324	Genome-wide identification of MAXs genes for strigolactones synthesis/signaling in solanaceous plants and analysis of their potential functions in tobacco. 11, e14669	0
323	Overexpression of Tomato ACL5 Gene in Tobacco Leads to Increased Plant Growth and Delayed the Onset of Leaf Senescence.	O
322	Discovery and Heterologous Expression of Unspecific Peroxygenases. 2023 , 13, 206	1
321	Assessment of potassium ion channel during electric signalling in biofilm formation of Acinetobacter baumannii for finding antibiofilm molecule. 2023 , 9, e12837	O
320	The role of functional and phylogenetic diversity in riparian tree vegetation on leaf litter breakdown in rivers.	0
319	Mitochondrial genome of the jack silverside, Atherinopsis californiensis (Atherinopsidae, Atheriniformes), a nearshore fish of the California Current Ecosystem. 2023 , 8, 13-17	O

318	A chromosome-level genome assembly enables the identification of the follicule stimulating hormone receptor as the master sex-determining gene in the flatfish Solea senegalensis.	0
317	Genome-wide analysis of wheat Di19 gene family and functional analysis of TaDi19-7 in transgenic Arabidopsis. 2023 , 206, 105192	O
316	Identification of probable inhibitors for the DNA polymerase of the Monkeypox virus through the virtual screening approach. 2023 , 229, 515-528	0
315	Genetic and functional characterization of multiple thermophilic organosulfur-removal systems reveals desulfurization potentials for waste residue oil cleaning. 2023 , 446, 130706	О
314	Gnawing pressure led to the expansion of JAZ genes in angiosperms. 2023 , 230, 123165	0
313	Estimation of heritabilities and quantitative trait loci for growth traits of bighead carp (Hypophthalmichthys nobilis). 2023 , 566, 739213	1
312	Description and genomic characterization of Nocardioides bruguierae sp. nov., isolated from Bruguiera gymnorhiza. 2023 , 46, 126391	O
311	Identification of genetic marker for CSN3 gene in Karan Fries (Holstein Friesian crossbred) population. 2018 , 88, 808-811	О
310	An AhRtaspase Axis Mediated Antiviral Apoptosis in an Arthropod. 2022, 209, 2022-2032	О
309	Description of Vishniacozyma terrae sp. nov. and Dioszegia terrae sp. nov., Two Novel Basidiomycetous Yeast Species Isolated from Soil in Korea. 2022 , 50, 439-447	O
308	Sparse and stereotyped encoding implicates a core glomerulus for ant alarm behavior.	О
307	A standalone incompatible insect technique enables mosquito suppression in the urban subtropics. 2022 , 5,	О
306	Horizontally transferred genes as RNA interference targets for aphid and whitefly control.	О
305	Cas9/gRNA-Mediated Mutations in PtrFLA40 and PtrFLA45 Reveal Redundant Roles in Modulating Wood Cell Size and SCW Synthesis in Poplar. 2023 , 24, 427	О
304	Discovery of entomopathogenic fungi across geographical regions in southern China on pine sawyer beetle Monochamus alternatus and implication for multi-pathogen vectoring potential of this beetle. 13,	O
303	Chromosome-level assembly of triploid genome of sichuan pepper (Zanthoxylum armatum). 2022,	O
302	Genome-Wide Identification and Analysis of the MAPK and MAPKK Gene Families in Potato (Solanum tuberosum L.). 2023 , 13, 93	0
301	Nuclear and Mitochondrial DNA Suggest That Nature Reserve Maintains Novel Haplotypes and Genetic Diversity of Honeybees (Apis cerana). 2022 , 58, 1513-1523	O

300	Structural and Functional Characterization of a New Bacterial Dipeptidyl Peptidase III Involved in Fruiting Body Formation in Myxobacteria. 2023 , 24, 631	1
299	Crystal Structure and Biochemical Analysis of a Cytochrome P450 Steroid Hydroxylase (BaCYP106A6) from Bacillus Species. 2022 ,	Ο
298	Flavobacterium potami sp. nov., a multi-metal resistance genes harbouring bacterium isolated from shallow river silt.	Ο
297	Colletotrichum species causing anthracnose disease on avocado fruit in Taiwan.	O
296	Characterizing Relevant MicroRNA Editing Sites in Parkinson Disease. 2023, 12, 75	О
295	Two new hypogean species of Triplophysa (Cypriniformes: Nemacheilidae) from the River Yangtze drainage in Guizhou, China. 2022 , 71,	O
294	Diversity of Mixotrophic Neutrophilic Thiosulfate- and Iron-Oxidizing Bacteria from Deep-Sea Hydrothermal Vents. 2023 , 11, 100	О
293	Compression-Complexity Measures for Analysis and Classification of Coronaviruses. 2023, 25, 81	O
292	Genome-Wide Identification and Analysis of the GRAS Transcription Factor Gene Family in Theobroma cacao. 2023 , 14, 57	О
291	Filogenia de los clidos actuales (Carnivora: Canidae) mediante anllsis de congruencia de caracteres bajo parsimonia. 2017 , 34, 85-102	O
290	Characterization of a lytic phage KFS-EC3 infecting multiple foodborne pathogens. 2022, 29, 1022-1034	O
289	Genome-scale metabolic reconstruction of 7,302 human microorganisms for personalized medicine.	1
288	Genome-Wide Identification of Kiwifruit SGR Family Members and Functional Characterization of SGR2 Protein for Chlorophyll Degradation. 2023 , 24, 1993	О
287	Species Identification of the Major Japanese Encephalitis Vectors within the Culex vishnui Subgroup (Diptera: Culicidae) in Thailand Using Geometric Morphometrics and DNA Barcoding. 2023 , 14, 131	O
286	Development of Molecular-Based Species Identification and Optimization of Reaction Conditions for Molecular Diagnosis of Three Major Asian Planthoppers (Hemiptera: Delphacidae). 2023 , 14, 124	О
285	Cryo-EM structure of adeno-associated virus 4 at 2.2 [resolution. 2023 , 79, 140-153	1
284	Anaeromicropila herbilytica gen. nov., sp. nov., a plant polysaccharide-decomposing anaerobic bacterium isolated from anoxic soil subjected to reductive soil disinfestation, and reclassification of Clostridium populeti as Anaeromicropila populeti comb. nov 2023 , 73,	Ο
283	The Impact of Multiple Sequence Alignment Error on Phylogenetic Estimation under Variable-Across-Phylogeny Substitution Models.	O

282	No loss of genetic divergence in Torymus sinensis following its release for Dryocosmus kuriphilus control in Europe.	O
281	Streptomyces guryensis sp. nov. exhibiting antimicrobial activity, isolated from riverside soil. 2023 , 73,	O
280	Food webs reveal coexistence mechanisms and community organization in carnivores. 2023,	O
279	Evolutionary fine-tuning of residual helix structure in disordered proteins manifests in complex structure and lifetime. 2023 , 6,	O
278	Identification and expression analyses of the olfactory-related genes in different tissues' transcriptome of a predacious soldier beetle, Podabrus annulatus (Coleoptera, Cantharidae).	О
277	A Data-Driven Approach to Construct a Molecular Map of Trypanosoma cruzi to Identify Drugs and Vaccine Targets. 2023 , 11, 267	O
276	Theoretical Studies on Selectivity of HPK1/JAK1 Inhibitors by Molecular Dynamics Simulations and Free Energy Calculations. 2023 , 24, 2649	О
275	Evolutionary diversification of methanotrophic ANME-1 archaea and their expansive virome. 2023 , 8, 231-245	O
274	Spatial and phylogenetic structure of Alpine stonefly assemblages across seven habitats using DNA-species.	O
273	A candidate transporter allowing symbiotic dinoflagellates to feed their coral hosts. 2023 , 3,	O
272	Telomerase-independent survival leads to a mosaic of complex subtelomere rearrangements inChlamydomonas reinhardtii.	O
271	A Computational Inter-Species Study on Safrole Phase I Metabolism-Dependent Bioactivation: A Mechanistic Insight into the Study of Possible Differences among Species. 2023 , 15, 94	O
270	Genetic, Antigenic, and Pathobiological Characterization of H9 and H6 Low Pathogenicity Avian Influenza Viruses Isolated in Vietnam from 2014 to 2018. 2023 , 11, 244	О
269	Importin alpha family NAAT/IBB domain: Functions of a pleiotropic long chameleon sequence. 2023	O
268	Identification of major quantitative trait loci and candidate genes for seed weight in soybean. 2023 , 136, 1-17	O
267	Reclassification of Clostridium cocleatum, Clostridium ramosum, Clostridium spiroforme and Clostridium saccharogumia as Thomasclavelia cocleata gen. nov., comb. nov., Thomasclavelia ramosa comb. nov., gen. nov., zen. nov., zen. nov., zen. nov., zen. nov., zen. nov. zen. zen. zen. zen. zen. zen. zen. zen	O
266	Iron-sulfur clusters are involved in post-translational arginylation. 2023 , 14,	О
265	Leaf blight of rice-paper plant, Tetrapanax papyrifer, caused by Neofusicoccum parvum: a potential source of stem rot diseases of mango and grape.	O

264	Phylogenetic Relationships in the Group Caespitosa of Paspalum L. (Poaceae, Panicoideae, Paspaleae). 2023 , 15, 134	O
263	Abscisic acid mediated strawberry receptacle ripening involves the interplay of multiple phytohormone signaling networks. 14,	0
262	Novel (E)-3-(1-substituted-1H-indazol-5-yl)-N-hydroxypropenamides as histone deacetylase inhibitors: design, synthesis and structurelictivity relationships.	0
261	Performance of Phenotypic Tests to Detect Lactamases in a Population of Lactamase Coproducing Enterobacteriaceae Isolates.	0
260	Identification and Structural Modeling of the RNA Polymerase Omega Subunits in Chlamydiae and Other Obligate Intracellular Bacteria.	0
259	Harnessing Novel Soil Bacteria for Beneficial Interactions with Soybean. 2023, 11, 300	0
258	Comparative Genomic Analysis Reveals Gene Content Diversity, Phylogenomic Contour, Putative Virulence Determinants, and Potential Diagnostic Markers within Pythium insidiosum Traits. 2023 , 9, 169	0
257	Genome-wide identification and characterisation of bHLH transcription factors in Artemisia annua. 2023 , 23,	O
256	Systematic identification of TPS genes in Gossypium and their characteristics in response to flooding stress. 14,	0
255	Ticks (Acari: Ixodidae, Argasidae) associated with wild birds in Argentina. 2023 , 14, 102135	O
254	Description of Defluviimonas salinarumsp. nov. with the potential of benzene-degradation isolated from saltern in the Yellow Seacoast. 2023 , 370,	0
253	Gene Structural Specificity and Expression of MADS-Box Gene Family in Camellia chekiangoleosa. 2023 , 24, 3434	O
252	Molecular characterization of a novel amalgavirus infecting Lilium spp. in China.	0
251	Genome-wide identification and expression analysis of the HD2 protein family and its response to drought and salt stress in Gossypium species. 14,	O
250	Cross-protection and cross-feeding between Klebsiella pneumoniae and Acinetobacter baumannii promotes their co-existence. 2023 , 14,	0
249	Development of a TaqMan qPCR assay for trypanosomatid multi-species detection and quantification in insects. 2023 , 16,	0
248	Design, synthesis, and evaluation of peptides derived from L1 protein against bovine papillomavirus-1/2 identified along Mexico cattle export route. 2023 , 67, 11-21	0
247	Evolutionary relevance of single nucleotide variants within the forebrain exclusive human accelerated enhancer regions. 2023 , 24,	O

246	Comprehensive genomic identification of cotton starch synthase genes reveals that GhSS9 regulates drought tolerance. 14,	O
245	Genome-wide identification and expression analysis of the anthocyanin-related genes during seed coat development in six Brassica species. 2023 , 24,	O
244	Molecular detection and characterization of Anaplasma spp. in cattle and sable antelope from Lusaka and North-Western provinces of Zambia. 2023 , 39, 100847	O
243	Analysis of the tick communities associated to domestic mammals in rural areas of the Yungas montane forest from Argentina. 2023 , 39, 100850	O
242	Cases of paternal inheritance and recombination of mictochondria in peas (Pisum L.).	O
241	The Keap1-Nrf2 signaling pathway regulates antioxidant defenses of Ctenopharyngodon idella induced by bacterial infection. 2023 , 108686	Ο
240	Sequence Characteristics and Expression Analysis of the Gene Encoding Sedoheptulose-1,7-Bisphosphatase, an Important Calvin Cycle Enzyme in Upland Cotton (Gossypium hirsutum L.). 2023 , 24, 6648	O
239	Environmental Factors Affect the Bacterial Community in Diaphorina citri, an Important Vector of [] Candidatus Liberibacter asiaticus[]2023, 11,	O
238	Genome-Wide Identification and Expression Analysis of the SHI-Related Sequence Family in Cassava. 2023 , 14, 870	O
237	New species of the genus Astyris (Gastropoda: Neogastropoda: Buccinoidea: Columbellidae) from the vicinity of hydrothermal vents of the Piip Volcano, southwestern Bering Sea. 2023 , 5263, 441-450	1
236	Isolation and characterization of a novel l-Methionine producer from Mahanadi river site in Sambalpur district of Odisha, India. 2023 , 49, 102659	O
235	Carbonic anhydrase activity identified in the powdered nacreous layer of Pinctada fucata. 2023 , 128, 22-29	O
234	BrSPA1 mutation resulted in earlier bolting of Chinese cabbage under short day conditions. 2023 , 315, 111962	O
233	Genome-wide identification and expression profiling of the bZIP gene family in Betula platyphylla and the functional characterization of BpChr04G00610 under low-temperature stress. 2023 , 198, 107676	O
232	Exceptional levels of species discovery ameliorate inferences of the biogeography and diversification of an Afrotropical catfish family. 2023 , 182, 107754	O
231	Soft rot disease of Belamcanda chinensis caused by Dickeya fangzhongdai in China. 2023 , 125, 101974	O
230	Structural analysis of factors related to FAM3C/ILEI dimerization and identification of inhibitor candidates targeting cancer treatment. 2023 , 104, 107869	O
229	Molecular characterization, expression analysis and function identification of TNF#n black rockfish (Sebastes schlegelii). 2023 , 236, 123912	O

228	The wheat TaF-box3, SCF ubiquitin ligase component, participates in the regulation of flowering time in transgenic Arabidopsis. 2023 , 331, 111668	O
227	Genome-wide identification and expression analysis of SUT gene family members in sugar beet (Beta vulgaris L.). 2023 , 870, 147422	O
226	Molecular and biochemical characterization of a recombinant glycosyl hydrolase family 3 Eglucosidase overexpressed in Escherichia. coli; bioprospecting metagenomes for cellulolytic processing function. 2023 , 542, 113118	0
225	Characterization of the Fasciclin-like arabinogalactan gene family in Brassica napus and the negative regulatory role of BnFLA39 in response to clubroot disease stress. 2023 , 196, 116400	О
224	Exploring particulate methane monooxygenase (pMMO) proteins using experimentation and computational molecular docking. 2023 , 35, 102634	0
223	Identification of Omega-class glutathione transferases in helminths of the Taeniidae family. 2023 , 254, 111559	O
222	Ortholinea nupchi n. sp. (Myxosporea: Ortholineidae) from the urinary bladder of the cultured olive flounder Paralichthys olivaceus, South Korea. 2023 , 94, 102734	O
221	New report of Halamphora subtropica (Bacillariophyta) from the Strait of Malacca and its growth and biochemical characterisation under nutrient deprivation. 2023 , 62, 102947	O
220	Effect of geographic isolation on genetic variation and population structure of Euphrasia nankotaizanensis, a threatened endemic alpine herb in Taiwan. 2023 , 9, e14228	0
219	Conserved Sequences in the 5? and 3? Untranslated Regions of Jingmenvirus Group Representatives. 2023 , 15, 971	O
218	Antarcticirhabdus aurantiaca gen. nov., sp. nov., isolated from Antarctic gravel soil. 2023, 73,	O
217	Expression and functional analysis of NAC transcription factors under five diverse growth stages reveal their regulatory roles during wood formation in Chinese cedar (Cryptomeria fortunei Hooibrenk). 2023 , 197, 116597	O
216	Dichotomous effects of oxidative metabolisms: A theoretical perspective on the dolomite problem. 2023 , 222, 104041	O
215	Rational design of a novel halotolerant ATP regeneration system for biocatalytic CTP production. 2023 , 98, 1025-1031	O
214	A Physcomitrella PIN protein acts in spermatogenesis and sporophyte retention. 2023 , 237, 2118-2135	O
213	Engineering of xylanases for the development of biotechnologically important characteristics. 2023 , 120, 1171-1188	O
212	Characterization of a Galactose Oxidase from Fusarium odoratissimum and Its Application in the Modification of Agarose. 2023 , 12, 603	0
211	Classification and Secondary Metabolite-Biosynthetic Gene Clusters of Marine Streptomyces Strains Including a Lobophorin- and Divergolide-Producer. 2023 , 2, 151-161	0

210	Cryobacterium zhongshanensis sp. nov., an actinobacterium isolated from Antarctic soil. 2023, 205,	Ο
209	Development of KLA-RGD integrated lipopeptide with the effect of penetrating membrane which target the $\mbox{\em B}$ receptor and the application of combined antitumor. 2023 , 223, 113186	O
208	Genomic identification of cotton SAC genes branded ovule and stress-related key genes in Gossypium hirsutum. 14,	0
207	Genetic Structure and Phylogeography of Commercial Mytilus unguiculatus in China Based on Mitochondrial COI and Cytb Sequences. 2023 , 8, 89	O
206	A comprehensive pharmacological analysis of fenoterol and its derivatives to unravel the role of \mathbb{Q} -adrenergic receptor in zebrafish. 2023 , 160, 114355	0
205	Next-Generation Sequencing of the Complete Huaibei Grey Donkey Mitogenome and Mitogenomic Phylogeny of the Equidae Family. 2023 , 13, 531	O
204	Isolation, Identification and Antimicrobial Activities of Four Bacteria Associated with Entomopathogenic Nematodes, Steinernema spp 2023 , 17, 309-319	Ο
203	New Insights into Plastid and Mitochondria Evolution in Wild Peas (Pisum L.). 2023, 15, 216	Ο
202	Teleost TRAF7, a protein functions in the host antiviral responses via NF- B and IRF3/7 mediated signaling. 10,	0
201	Diaporthe and Diplodia Species Associated with Walnut (Juglans regia L.) in Hungarian Orchards. 2023 , 9, 205	0
200	A Protein Co-Conservation Network Model Characterizes Mutation Effects on SARS-CoV-2 Spike Protein. 2023 , 24, 3255	0
199	PANAS: Pipeline and a Case Study to Obtain Synonymous and Nonsynonymous Substitution Rates in Genes of Platyhelminthes. 2023 , 90,	Ο
198	Interaction network among de novo purine nucleotide biosynthesis enzymes in Escherichia coli.	Ο
197	Olive Polyphenol Oxidase Gene Family. 2023 , 24, 3233	Ο
196	Characterization of Arnebia euchroma PGT homologs involved in the biosynthesis of shikonin. 2023 , 196, 587-595	0
195	An Update of the Cenchrinae (Poaceae, Panicoideae, Paniceae) and a New Genus for the Subtribe to Clarify the Dubious Position of a Species of Panicum L 2023 , 12, 749	O
194	Full sequencing and comparison of five venom metalloproteases of Trimeresurus gracilis: The PI-enzyme is most similar to okinalysin but the PIII-enzyme is most similar to Crotalus venom enzymes. 2023 , 225, 107053	0
193	452. Phylogenetic analysis of local cattle population in northern province of Sri Lanka. 2022 ,	Ο

192	Wound healing and regeneration in the reef building coral Acropora millepora. 10,	O
191	Integrated transcriptomic and metabolomic profiles reveal anthocyanin accumulation in Scutellaria baicalensis petal coloration. 2023 , 194, 116144	O
190	Overproduction of poly(3-hydroxybutyrate) by the extremely halophilic archaeon Haloarcula sp. CEJ40-10 using starchy substrate.	O
189	Evidence that genetic drift not adaptation drivesfast-Zandlarge-Zeffects inFicedulaflycatchers.	O
188	De-MISTED: Image-based classification of erroneous multiple sequence alignments using convolutional neural networks.	О
187	The Molecular Composition of Peptide Toxins in the Venom of Spider Lycosa coelestis as Revealed by cDNA Library and Transcriptomic Sequencing. 2023 , 15, 143	O
186	Mucormycosis-causing fungi in humans: a meta-analysis establishing the phylogenetic relationships using internal transcribed spacer (ITS) sequences. 2023 , 72,	O
185	A bacterial cold-active dye-decolorizing peroxidase from an Antarctic Pseudomonas strain. 2023 , 107, 1707-1724	O
184	Gaining Insight into Large Gene Families with the Aid of Bioinformatic Tools. 2023, 173-191	O
183	Genome-wide analysis of Panax MADS-box genes reveals role of PgMADS41 and PgMADS44 in modulation of root development and ginsenoside synthesis. 2023 , 233, 123648	O
182	Benzimidazole Derivatives Suppress Fusarium Wilt Disease via Interaction with ERG6 of Fusarium equiseti and Activation of the Antioxidant Defense System of Pepper Plants. 2023 , 9, 244	О
181	Transfection of Sponge Cells and Intracellular Localization of Cancer-Related MYC, RRAS2, and DRG1 Proteins. 2023 , 21, 119	0
180	Nonomuraea sediminis sp. nov., a novel actinobacterium with antimicrobial activity, isolated from sediment of Dianchi Lake. 2023 , 205,	O
179	Uncovering the involvement of DoDELLA1-interacting proteins in development by characterizing the DoDELLA gene family in Dendrobium officinale. 2023 , 23,	O
178	Characterization of Megabat-Favored, CA-Dependent Susceptibility to Retrovirus Infection. 2023 , 97,	O
177	Three Chitin Deacetylase Family Members of Beauveria bassiana Modulate Asexual Reproduction and Virulence of Fungi by Mediating Chitin Metabolism and Affect Fungal Parasitism and Saprophytic Life. 2023 , 11,	O
176	Laurasian legacies in the Gondwanan tree fern order Cyatheales.	0
175	Genome-wide analysis of R2R3-MYB genes in cultivated peanut (Arachis hypogaea L.): Gene duplications, functional conservation, and diversification. 14,	O

174	Prevalence of major parasitic nematodes associated with tomatoes (Solanum lycopersicum L.) in two districts of Jimma, Ethiopia. 2023 , 56, 158-174	0
173	Identification and characterization of two long-type peptidoglycan recognition proteins, PGRP-L1 and PGRP-L2, in the orange-spotted grouper, Epinephelus coioides. 2023 , 134, 108580	0
172	Diversity, Lifestyle, Genomics, and Their Functional Role of Cochliobolus, Bipolaris, and Curvularia Species in Environmental Remediation and Plant Growth Promotion under Biotic and Abiotic Stressors. 2023 , 9, 254	0
171	Engineered Glycosidase for Significantly Improved Production of Naturally Rare Vina-Ginsenoside R7. 2023 , 71, 3852-3861	O
170	Differentiation of the Flavescence dor phytoplasma genetic clusters by multiplex real-time PCR assay targeting the map gene.	0
169	Dysfunction of Prkcaa Links Social Behavior Defects with Disturbed Circadian Rhythm in Zebrafish. 2023 , 24, 3849	Ο
168	Sequence analysis of cytochrome b gene in Vietnamese isolates of Hemileia vastatrix, the causal agent of coffee leaf rust, in relation to potential QoI fungicide resistance.	0
167	Deep reinforcement learning-based pairwise DNA sequence alignment method compatible with embedded edge devices. 2023 , 13,	Ο
166	A novel phytopathogen Erwinia sorbitola sp. nov., isolated from the feces of ruddy shelducks. 13,	О
165	Genome-Wide Identification, Characterization, and Expression Analysis of SPIRAL1 Family Genes in Legume Species. 2023 , 24, 3958	Ο
164	Orthologs of Human-Disease-Associated Genes in Plants Are Involved in Regulating Leaf Senescence. 2023 , 13, 559	0
163	Cas9-orthologue-mediated cytosine and adenine base editors recognizing NNAAAA PAM sequences. 2200533	Ο
162	Characterization and expression profiles of the B-box gene family during plant growth and under low-nitrogen stress in Saccharum. 2023 , 24,	Ο
161	First report of Botrytis cinerea causing gray mold of pomegranate (Punica granatum L.) in Mexico.	0
160	Convergently selected NPF2.12 coordinates root growth and nitrogen use efficiency in wheat and barley.	0
159	Single nucleotide polymorphisms within exon four of the prolactin gene and their effect on milk traits in cattle populations of Ethiopia. 1-11	O
158	Genome-wide identification and analysis of the molecular evolution and expression of type-A response regulator genes in Populus deltoids. 2023 , 194, 116336	0
157	Sub-Genotyping of Acanthamoeba T4 Complex: Experience from North India. 2023 , 3, 69-78	O

156	Is a Modified Actin the Key to Toxin Resistance in the Nudibranch Chromodoris? A Biochemical and Molecular Approach. 2023 , 15, 304	0
155	Reciprocal regulatory balance within the CLEC16ARNF41 mitophagy complex depends on an intrinsically disordered protein region. 2023 , 299, 103057	Ο
154	Molecular identification and functional analysis of X-linked inhibitor of apoptosis -associated factor-1 (XAF1) in grass carp, Ctenopharyngodon idella. 2023 , 134, 108635	0
153	Identification and Functional Characterization of General Odorant Binding Proteins in Orthaga achatina. 2023 , 14, 216	O
152	Roseomonas acroporae sp. nov., isolated from coral Acropora digitifera. 2023 , 73,	0
151	Radiobacillus kanasensis sp. nov., a halotolerant bacterium isolated from woodland soil. 2023 , 73,	Ο
150	Comparative Analysis of Complete Mitochondrial Genome of Ariosoma meeki (Jordan and Snider, 1900), Revealing Gene Rearrangement and the Phylogenetic Relationships of Anguilliformes. 2023 , 12, 348	0
149	A magnesium transporter is involved in the cesium ion resistance of the high-concentration cesium ion-resistant bacterium Microbacterium sp. TS-1. 14,	Ο
148	Comprehensive study of rice YABBY gene family: evolution, expression and interacting proteins analysis. 11, e14783	0
147	Roadmap to the study of gene and protein phylogeny and evolution practical guide. 2023 , 18, e0279597	O
146	Three-dimensional models of antigens with serodiagnostic potential for leprosy: An in silico study. 13, 1-10	0
145	Deciphering the network of cholesterol biosynthesis in Paris polyphylla laid a base for efficient diosgenin production in plant chassis. 2023 , 76, 232-246	O
144	Temperature-induced modulation of stress-tolerant PGP genes bioprospected from Bacillus sp. IHBT-705 associated with saffron (Crocus sativus) rhizosphere: A natural -treasure trove of microbial biostimulants. 14,	0
143	Population structure and evolutionary history of the greater cane rat (Thryonomys swinderianus) from the Guinean Forests of West Africa. 14,	O
142	Characterization and functional analyses of wheat TaPR1 genes in response to stripe rust fungal infection. 2023 , 13,	0
141	Description of the Three Complete Mitochondrial Genomes of Sitta (S. himalayensis, S. nagaensis, and S. yunnanensis) and Phylogenetic Relationship (Aves: Sittidae). 2023 , 14, 589	O
140	The molecular phylogenetic position of Harpagocarpus (Polygonaceae) sheds new light on the infrageneric classification of Fagopyrum. 220, 109-126	0
139	Evaluating Compression-Based Phylogeny Estimation in the Presence of Incomplete Lineage Sorting. 2023 , 30, 250-260	O

138	A new and accurate qPCR protocol to detect plant pathogenic bacteria of the genus Candidatus Liberibacter In plants and insects. 2023 , 13,	O
137	New insights into the phylogenetic relationships of Japanese knotweed (Reynoutria japonica) and allied taxa in subtribe Reynoutriinae (Polygonaceae). 220, 83-108	O
136	Phylogenetic diversity of cacao (Theobroma cacao L.) genotypes in Colombia. 2022, 20, 203-214	0
135	Identification and Characterization of Phytocyanin Family Genes in Cotton Genomes. 2023, 14, 611	O
134	HPLC and DNA barcoding profiles for identification of the selected twelve Mucuna species and its application for detecting prohibited aphrodisiac Mucuna products. 2023 , 9, e14130	0
133	Subsurface aeration mitigates organic material mulching-induced anaerobic stress via regulating hormone signaling in Phyllostachys praecox roots. 14,	O
132	E-2 Glycoprotein Structural Variations Analysed within the CSFV 2.2. Genogroup in a C losed Grid Sampling Study from Meghalaya, India. 2023 , 14, 343-354	0
131	One-Pot Biosynthesis of 2-Keto-4-hydroxybutyrate from Cheap C1 Compounds Using Rationally Designed Pyruvate Aldolase and Methanol Dehydrogenase. 2023 , 71, 4328-4336	O
130	Disruption of T-box transcription factor eomesa results in abnormal development of median fins in Oujiang color common carp Cyprinus carpio. 2023 , 18, e0281297	0
129	Peptides that Mimic RS repeats modulate phase separation of SRSF1, revealing a reliance on combined stacking and electrostatic interactions. 12,	O
128	Transcriptome analysis of the endangered dung beetle Copris tripartitus (Coleoptera: Scarabaeidae) and characterization of genes associated to immunity, growth, and reproduction. 2023 , 24,	O
127	Phylogeny and systematics of the genus Clonostachys. 14,	O
126	Identification and characterization analysis of candidate genes controlling mushroom leaf development in Chinese kale by BSA-seq. 2023 , 43,	0
125	A new class A beta-lactamase gene blaCAE-1 coexists with blaAFM-1 in a novel untypable plasmid in Comamonas aquatica. 2023 , 13,	O
124	Complete Mitochondrial Genomes of Four Pelodiscus sinensis Strains and Comparison with Other Trionychidae Species. 2023 , 12, 406	0
123	Assessment of the Diversity, Distinctiveness and Conservation of Australia Central Queensland Coastal Rainforests Using DNA Barcoding. 2023 , 15, 378	O
122	Phylogeographic and Morphological Analysis of Botrylloides niger Herdman, 1886 from the Northeastern Mediterranean Sea. 2023 , 15, 367	0
121	Mutational signatures in wild typeEscherichia colistrains reveal dominance of DNA polymerase errors.	O

120	Transposon-derived transcription factors across metazoans. 11,	0
119	Transcript Isoform Diversity of Ampliconic Genes on the Y Chromosome of Great Apes.	O
118	Multigene phylogeny and morphology reveal two novel zombie-ant fungi in Ophiocordyceps (Ophiocordycipitaceae, Hypocreales). 2023 , 22,	0
117	Regulation of capsule spine formation in castor.	O
116	ZmG6PDH1 in glucose-6-phosphate dehydrogenase family enhances cold stress tolerance in maize. 14,	0
115	Identification of the rice Rc gene as a main regulator of seed survival under dry storage conditions.	O
114	Deladenus bonabensis n. sp. (Tylenchomorpha: Neotylenchidae) from East Azarbaijan province, northwestern Iran: A morphological and molecular phylogenetic study. 2023 , 55,	0
113	Investigation of a Listeria monocytogenes Chromosomal Immigration Control Region Reveals Diverse Restriction Modification Systems with Complete Sequence Type Conservation. 2023 , 11, 699	Ο
112	Human sirtuin 2 inhibitors, their mechanisms and binding modes. 2023 , 15, 291-311	0
111	Association of a variant upstream ofgrowth differentiation factor 11(GDF11) on carcass traits in crossbred beef cattle. 2023 , 7,	O
110	Genome-Wide Identification and Expression Analysis of NPF Genes in Cucumber (Cucumis sativus L.). 2023 , 12, 1252	0
109	Characterization of a bloom-associated alphaproteobacterial lineage, Clandidatus Phycosocius insights into freshwater algal-bacterial interactions. 2023 , 3,	O
108	HV1 mtDNA Reveals the High Genetic Diversity and the Ancient Origin of Vietnamese Dogs. 2023 , 13, 1036	O
107	Genome-Wide Analysis of MIKCC-Type MADS-Box Genes Reveals Their Involvement in Flower Development in Malus Lineage. 2023 , 9, 373	O
106	A molecular cell biology toolkit for the study of meiosis in the silkworm Bombyx mori.	0
105	Combinatorial interactions among natural structural variants of Brassica SOC1 promoters and SVP depict conservation of binding affinity despite molecular diversity.	O
104	TaBAS1 encoding a typical 2-Cys peroxiredoxin enhances salt tolerance in wheat. 14,	0
103	Relationship between Dubas Bug (Ommatissus lybicus) Infestation and the Development of Fungal-Induced Leaf Spots in Date Palms (Phoenix dactylifera). 2023 , 14, 283	O

102	Genome-wide identification of NHX (Na+/H+ antiporter) gene family in Cucurbita L. and functional analysis of CmoNHX1 under salt stress. 14,	0
101	Genome-wide characterization of trichome birefringence-like genes provides insights into fiber yield improvement. 14,	О
100	Role of nuclear receptors NlHR3 and NlFTZ-F1 in regulating molting and reproduction in Nilaparvata lugens (stl). 14,	O
99	Identification and Expression Analysis of the bHLH Gene Family Members in Diospyros kaki. 2023 , 9, 380	О
98	Asynchronous phylogeographic and demographic dynamics of rodent community in the low latitude Asia.	0
97	Identification and characterization of the Doublesex gene and its mRNA isoforms in the brine shrimp Artemia franciscana. 2023 , 480, 385-401	О
96	Phylogenetic Analysis of R2R3-MYB Family Genes in Tetrastigma hemsleyanum Diels et Gilg and Roles of ThMYB4 and ThMYB7 in Flavonoid Biosynthesis. 2023 , 13, 531	0
95	Genome-wide investigation of NLP gene family members in alfalfa (Medicago sativa L.): Evolution and expression profiles during development and stress.	О
94	Structural basis of odorant recognition by a human odorant receptor. 2023 , 615, 742-749	O
93	In situ structure of the red algal phycobilisome B SII B SI I IHC megacomplex. 2023 , 616, 199-206	О
92	Ensemble-based molecular docking and spectrofluorometric analysis of interaction between cytotoxin and tumor necrosis factor receptor 1. 1-15	0
91	Influence of High-Molecular-Weight Glutenin Subunit on Components and Multiscale Structure of Gluten and Dough Quality in Soft Wheat. 2023 , 71, 4943-4956	О
90	Whole genome characterization and diagnostics of prunus necrotic ringspot virus (PNRSV) infecting apricot in India. 2023 , 13,	0
89	Croceibacterium selenioxidans sp. nov., isolated from seleniferous soil. 2023 , 73,	О
88	Genome-wide identification and expression analysis of the U-box E3 ubiquitin ligase gene family related to salt tolerance in sorghum (Sorghum bicolor L.). 14,	0
87	Template-Based Modelling of the Structure of Fungal Effector Proteins.	О
86	Genome-Wide Identification of the Sweet Orange bZIP Gene Family and Analysis of Their Expression in Response to Infection by Penicillium digitatum. 2023 , 9, 393	O
85	Development and Clinical Application of a Multilocus Sequence Typing Scheme for Bacteroides fragilis Based on Whole-Genome Sequencing Data. 2023 , 11,	O

84	Insulambacter thermoxylanivorax sp. nov., a thermophilic xylanolytic bacterium isolated from compost. 2023 , 73,	0
83	The Identification and Expression Analysis of the Liriodendron chinense (Hemsl.) Sarg. SOD Gene Family. 2023 , 14, 628	O
82	Genome-wide identification and characterization of lipoxygenase genes related to the English grain aphid infestation response in wheat. 2023 , 257,	0
81	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.	O
80	Fungal Screening for Potential PET Depolymerization. 2023 , 15, 1581	O
79	Primate protein-ligand interfaces exhibit significant conservation and unveil human-specific evolutionary drivers. 2023 , 19, e1010966	O
78	Genome-Wide Identification and Analysis of the MADS-Box Transcription Factor Genes in Blueberry (Vaccinium spp.) and Their Expression Pattern during Fruit Ripening. 2023 , 12, 1424	0
77	Dual-Mechanism Glycolipidpeptide with High Antimicrobial Activity, Immunomodulatory Activity, and Potential Application for Combined Antibacterial Therapy. 2023 , 17, 6292-6316	O
76	Homology Modeling in the Twilight Zone: Improved Accuracy by Sequence Space Analysis. 2023 , 1-23	0
75	Encyclobrephus brevivitellus n. sp. (Digenea: Plagiorchioidea, Incertae sedis) Infecting the Mekong Snail-Eating Turtle, Malayemys subtrijuga , in the Mekong River, Vietnam, with Phylogenetic Analyses Based on rDNA. 2023 , 109,	O
74	An extended Tudor domain within Vreteno interconnects Gtsf1L and Ago3 for piRNA biogenesis inBombyx mori.	O
73	Two new siderophores produced by Pseudomonas sp. NCIMB 10586: The anti-oomycete non-ribosomal peptide synthetase-dependent mupirochelin and the NRPS-independent triabactin. 14,	O
72	Protein Kinase PoxMKK1 Regulates Plant-Polysaccharide-Degrading Enzyme Biosynthesis, Mycelial Growth and Conidiation in Penicillium oxalicum. 2023 , 9, 397	0
71	Coevolutionary analysis of the Philopteroides Mey, 2004 (Phthiraptera: Ischnocera) parasitizing bulbuls (Passeriformes: Pycnonotidae). 11,	O
7°	To all the gar I loved before: range-wide population genetic structure in Alligator gar.	О
69	Upregulation of ENKD1 disrupts cellular homeostasis to promote lymphoma development.	O
68	Investigation of cadmium and nickel biosorption by Pseudomonas sp. via response surface methodology. 2023 , 39,	0
67	Myosin light chain of shark fast skeletal muscle exhibits intrinsic urea-resistibility. 2023, 13,	O

66	Structure of the Newcastle Disease Virus L protein in complex with tetrameric phosphoprotein. 2023 , 14,	О
65	srdA mutations suppress the rseA/cpsA deletion mutant conidiation defect in Aspergillus nidulans. 2023 , 13,	Ο
64	Identification of Fungal and Bacterial Denitrification Inhibitors Targeting Copper Nitrite Reductase. 2023 , 71, 5172-5184	0
63	Contribution of Leaf-Associated Microorganisms from Native Andean Ericaceae against Botrytis cinerea in Vaccinium corymbosum Cultivars.	Ο
62	Comprehensive Analysis of the INDETERMINATE DOMAIN (IDD) Gene Family and Their Response to Abiotic Stress in Zea mays. 2023 , 24, 6185	0
61	Comparative Omics-Based Identification and Expression Analysis of a Two-Component System in Vigna radiata in Drought Stress. 2023 , 13, 989	Ο
60	Cancer Therapeutics: Structure-Based Drug Design of Inhibitors for a Novel Angiogenic Growth Factor. 2023 , 18, 72-88	0
59	THE TRUE REDWOOD SORREL: REINSTATEMENT OF OXALIS SMALLIANA (OXALIDACEAE) AS A SPECIES SEPARATE FROM OXALIS OREGANA. 2023 , 69,	Ο
58	Culturable Endophyte Fungi of the Well-Conserved Coastal Dune Vegetation Located on the East Coast of the Korean Peninsula. 2023 , 11, 734	О
57	A parasitological survey and the molecular detection of Entamoeba species in pigs of East Java, Indonesia. 2023 , 650-656	O
56	A Contribution to the Systematics of Sunda Shelf Angle-Headed Dragons (Agamidae: Gonocephalus) with the Description of New Taxa from Sumatra. 2023 , 37,	О
55	Identification and biodiversity patterns of Aspergillus species isolated from some soil invertebrates at high altitude using morphological characteristics and phylogenetic analyses. 11, e15035	Ο
54	Functional characterization of the GhNRT2.1e gene reveals its significant role in improving nitrogen use efficiency in Gossypium hirsutum. 11, e15152	0
53	Genome characterization of three potyviruses affecting maize in Argentina.	Ο
52	Chelativorans petroleitrophicus sp. nov., a paraffin oil-degrading bacterium isolated from a mixture of oil-based drill cuttings and paddy soil. 2023 , 73,	О
51	Genome-wide single nucleotide polymorphisms reveal recurrent waves of speciation in niche-pockets, in Europe's most venomous snake.	Ο
50	Lolliginicoccus levis gen. nov., sp. nov., a novel bacterium isolated from the brain of the Chiroteuthis picteti squid, and reclassification of two Hoyosella species as Lolliginicoccus suaedae comb. nov. and Lolliginicoccus lacisalsi comb. nov 2023 , 73,	О
49	Determinants of species-specific utilization of ACE2 by human and animal coronaviruses.	Ο

48	Delineating the functional role of thePPE50 (Rv3135) - PPE51 (Rv3136)gene cluster in the pathophysiology of Mycobacterium tuberculosis.	0
47	Characteristics, Comparative Analysis, and Phylogenetic Relationships of Chloroplast Genomes of Cultivars and Wild Relatives of Eggplant (Solanum melongena). 2023 , 45, 2832-2846	O
46	Diversity of GH51 \pm -arabinofuranosidase homolog sequences from subantarctic intertidal sediments.	0
45	Epigenetic mechanisms to propagate histone acetylation by p300/CBP.	O
44	New Insights into the Variation and Admixture of the Cave-Dwelling Spider Trogloneta yunnanensis in South China Karst. 2023 , 13, 1244	Ο
43	RAS gene mutations and histomorphometric measurements in oral squamous cell carcinoma. 1-9	Ο
42	Innate Immune Response of TmToll-3 Following Systemic Microbial Infection in Tenebrio molitor. 2023 , 24, 6751	0
41	Identification and validation of new MADS-box homologous genes in 3010 rice pan-genome.	Ο
40	Glycoside hydrolase family 5 gene Pp07886 in Pythium porphyrae: Identification, characterization, expression pattern, and activation of the host immunity. 2023 , 71, 103090	0
39	Paramecium: RNA sequenceEtructure phylogenetics. 2023 , 73,	O
38	Complete Genome of Rose Myrtle, Rhodomyrtus tomentosa, and Its Population Genetics in Thai Peninsula. 2023 , 12, 1582	0
37	Genome-Wide Identification and Expression Analysis of the TCP Genes in Jatropha curcas L. Reveals Its Roles in Involvement of Leaf Shape. 2023 , 14, 780	O
36	Aurantimonas marianensis sp. nov., isolated from deep-sea sediment of the Mariana Trench. 2023 , 73,	0
35	A novel narnavirus isolated from Colletotrichum curcumae strain 780-2T.	0
34	Antibacterial Activity of the Green Synthesized Plasmonic Silver Nanoparticles with Crystalline Structure against Gram-Positive and Gram-Negative Bacteria. 2023 , 13, 1327	0
33	PRELIMINARY EXAMINATION OF THE EXOSKELETAL MICROBIOTA OF ARMADILLIDIUM VULGARE (THE COMMON PILL BUG). 2023 , 67,	O
32	Anaplasma Species in Ticks Infesting Mammals of Sardinia, Italy. 2023 , 13, 1332	0
31	Overexpression of Global Regulator SCrp Leads to the Discovery of New Angucyclines in Streptomyces sp. XS-16. 2023 , 21, 240	O

30	Genetic Characterization of Raspberry Bushy Dwarf Virus Isolated from Red Raspberry in Kazakhstan. 2023 , 15, 975	Ο
29	Genomic Identification and Expression Analysis of Acid Invertase (AINV) Gene Family in Dendrobium officinale Kimura et Migo.	Ο
28	Genome-Wide Identification, Characterization, and Expression of TCP Genes Family in Orchardgrass. 2023 , 14, 925	Ο
27	Host phylogeny and environment shape the diversity of the salamander skin microbiome.	Ο
26	Chemosensory Protein 2 of Male Athetis lepigone Is Involved in the Perception of Sex Pheromones and Maize Volatiles.	0
25	Characterization of acetolactate synthase gene (ALS) in Echinochloa colona (L.) Link., a hexaploid weed species. 2023 , 41,	O
24	Single Copies of the 5S rRNA Inserted into 45S rDNA Intergenic Spacers in the Genomes of Nototheniidae (Perciformes, Actinopterygii). 2023 , 24, 7376	0
23	Heterologous Expression and Characterization of Tox A1 haplotype from India and its interaction with Tsn1 for Spot Blotch Susceptibility in spring wheat.	0
22	Copy number variation in tRNA isodecoder genes impairs mammalian development and balanced translation. 2023 , 14,	0
21	Distribution of the transcription factor islet-1 in the central nervous system of nonteleost actinopterygian fish: Relationship with cholinergic and catecholaminergic systems.	0
20	Genomic insight of sulfate reducing bacterial genus Desulfofaba reveals their metabolic versatility in biogeochemical cycling. 2023 , 24,	0
19	Enterocloster alcoholdehydrogenati sp. nov., a Novel Bacterial Species Isolated from the Feces of a Patient with Alcoholism. 2023 , 80,	0
18	A new sesquiterpene synthase catalyzing the formation of (R)-Ebisabolene from medicinal plant Colquhounia coccinea var. mollis and its anti-adipogenic and antibacterial activities. 2023 , 211, 113681	0
17	Integrative taxonomy reveals two new narrowly-endemic crayfish species (Decapoda: Cambaridae) from the Yadkin River Basin in western North Carolina, USA. 2023 , 5270, 207-230	O
16	Aeoliella straminimaris sp. nov., a novel member of the phylum Planctomycetota with an unusual filamentous structure. 2023 , 73,	0
15	Three Glycosyltransferase Mutants in a One-Pot Multi-enzyme System with Enhanced Efficiency for Biosynthesis of Quercetin-3,4?-O-diglucoside.	O
14	Detection of Viral Genes in Metarhizium anisopliae JEF-290-infected longhorned tick, Haemaphysalis longicornis using transcriptome analysis. 2023 , 107926	0
13	Machine learning reveals limited contribution of trans-only encoded variants to the HLA-DQ immunopeptidome. 2023 , 6,	0

12	Identification of Aspergillus niger Aquaporins Involved in Hydrogen Peroxide Signaling. 2023, 9, 499	O
11	Computational design and molecular dynamics simulations suggest the mode of substrate binding in ceramide synthases. 2023 , 14,	O
10	Phenotypic Characterization and Phylogeny of Godronia myrtilli (Anamorph: Topospora myrtilli) ausal Agent of Godronia Canker on Highbush Blueberry. 2023 , 12, 642	0
9	BK Polyomavirus Diversity After Hematopoietic Stem Cell Transplantation.	O
8	slr2103, a homolog of type-2 diacylglycerol acyltransferase genes, for plastoquinone-related neutral lipid synthesis and NaCl-stress acclimatization in a cyanobacterium, Synechocystis sp. PCC 6803. 14,	O
7	Sellimonas catena sp. nov., isolated from human faeces. 2023 , 73,	O
6	Identification, Characterization, and Growth-Promoting Effects of Bacterial Endophytes Isolated from Okra (Abelmoschus esculentus L.). 2023 , 13, 1226	0
5	Stability and functional evolution of a novel family of hyperstable apple snail egg proteins.	O
4	Genomic analyses provide insights into the polyploidization-driven herbicide adaptation in Leptochloa weeds.	0
3	A highly selective C-rhamnosyltransferase from Viola tricolor and insights into its mechanisms. 2023 ,	O
2	Oligosoma aureocola sp. nov. (Reptilia: Scincidae) from the northern Southland high country of Aotearoa/New Zealand. 2023 , 5285, 271-292	0
1	Molecular characterisation of the current high prevalence of the new CPV-2c variants in the Southern Vietnamese dogs signifies a widespread in the worldwide dog population.	O