

Base-Calling of Automated Sequencer Traces Using *Phred*

Genome Research

8, 186-194

DOI: 10.1101/gr.8.3.186

Citation Report

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1991	The complete mitochondrial genome of the large yellow croaker, <i>Larimichthys crocea</i> (Perciformes,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 58 Gene, 2009, 432, 33-43.	2.2	103
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1993	The complete mitochondrial genome of <i>Watersipora subtorquata</i> (Bryozoa, Gymnolaemata,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 58	2.2	15
1994	Complete mitochondrial genome of the sea cucumber <i>Apostichopus japonicus</i> (Echinodermata:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58 ground pattern. Gene, 2009, 439, 79-86.	2.2	35
1995	Harnessing genomics for evolutionary insights. Trends in Ecology and Evolution, 2009, 24, 192-200.	8.7	124

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1996	Channel catfish, <i>Ictalurus punctatus</i> Rafinesque 1818, tetraspanin membrane protein family: Characterization and expression analysis of CD81 cDNA. <i>Veterinary Immunology and Immunopathology</i> , 2009, 128, 431-436.	1.2	7
1997	Genetic characterization of the complete coding regions of genotype 3 hepatitis E virus isolated from Spanish swine herds. <i>Virus Research</i> , 2009, 139, 111-116.	2.2	25
1998	Genome-wide analysis reveals increased levels of transcripts related with infectivity in peanut lectin non-agglutinated promastigotes of <i>Leishmania infantum</i> . <i>Genomics</i> , 2009, 93, 551-564.	2.9	50
1999	Comparative sequence analysis of the SALT OVERLY SENSITIVE1 orthologous region in <i>Thellungiella halophila</i> and <i>Arabidopsis thaliana</i> . <i>Genomics</i> , 2009, 94, 196-203.	2.9	17
2000	Functional expression of five <i>Arabidopsis</i> fatty acyl-CoA reductase genes in <i>Escherichia coli</i> . <i>Journal of Plant Physiology</i> , 2009, 166, 787-796.	3.5	110
2001	Overexpression of Nrp/b (nuclear restrict protein in brain) suppresses the malignant phenotype in the C6/ST1 glioma cell line. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2009, 117, 107-116.	2.5	5
2002	Sequence and function of lysosomal and digestive cathepsin D-like proteinases of <i>Musca domestica</i> midgut. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 782-791.	2.7	54
2003	Purification, characterization and sequencing of the major β -1,3-glucanase from the midgut of <i>Tenebrio molitor</i> larvae. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 861-874.	2.7	53
2004	Male-enriched transcription of genes encoding ASPs and Kunitz-type protease inhibitors in <i>Ancylostoma</i> species. <i>Molecular and Cellular Probes</i> , 2009, 23, 298-303.	2.1	9
2005	Genomic sequence encoding diversity segments of the pig TCR β chain gene demonstrates productivity of highly diversified repertoire. <i>Molecular Immunology</i> , 2009, 46, 1212-1221.	2.2	25
2006	DNA sequence analysis of the conserved region around the SOD1 gene locus in recessively inherited ALS. <i>Neuroscience Letters</i> , 2009, 463, 64-69.	2.1	6
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2008	Analysis of the genome sequences of three <i>Drosophila melanogaster</i> spontaneous mutation accumulation lines. <i>Genome Research</i> , 2009, 19, 1195-1201.	5.5	343
2009	Next-Generation Sequencing Methods: Impact of Sequencing Accuracy on SNP Discovery. <i>Methods in Molecular Biology</i> , 2009, 578, 95-111.	0.9	41
2010	The complete mitochondrial genome sequence of the cutlassfish <i>Trichiurus japonicus</i> (Perciformes:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i> 133-142.	1.1	47
2011	Multiple linked β and α globin genes in Atlantic cod: A PCR based strategy of genomic exploration. <i>Marine Genomics</i> , 2009, 2, 169-181.	1.1	6
2012	Genomic organization of Atlantic salmon (<i>Salmo salar</i>) fatty acid binding protein (fabp2) genes reveals independent loss of duplicate loci in teleosts. <i>Marine Genomics</i> , 2009, 2, 193-200.	1.1	13
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2015	Large-Scale Sequencing and Analytical Processing of ESTs. <i>Methods in Molecular Biology</i> , 2009, 533, 153-187.	0.9	11
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2017	Genome analysis and genetic enhancement of tomato. <i>Critical Reviews in Biotechnology</i> , 2009, 29, 152-181.	9.0	16
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2019	Phylogeny and taxonomy of a diverse collection of <i>Bradyrhizobium</i> strains based on multilocus sequence analysis of the 16S rRNA gene, ITS region and <i>glnII</i> , <i>recA</i> , <i>atpD</i> and <i>dnaK</i> genes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2934-2950.	1.7	154
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2030	Population structure analyses and demographic history of the malaria vector <i>Anopheles albimanus</i> from the Caribbean and the Pacific regions of Colombia. <i>Malaria Journal</i> , 2009, 8, 259.	2.3	37
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2035	Genome-wide comparative analysis of the <i>Brassica rapa</i> gene space reveals genome shrinkage and differential loss of duplicated genes after whole genome triplication. <i>Genome Biology</i> , 2009, 10, R111.	9.6	183
2036	Improved base calling for the Illumina Genome Analyzer using machine learning strategies. <i>Genome Biology</i> , 2009, 10, R83.	9.6	212
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2044	An overview of recent developments in genomics and associated statistical methods. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2009, 367, 4313-4337.	3.4	27
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2047	Cloning and Characterization of Full-length Triticin cDNA and Genes from Wheat Varieties K-68 and Chinese Spring. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2009, 18, 21-28.	1.7	0
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2049	Identification of candidate genome regions controlling disease resistance in <i>Arachis</i> . <i>BMC Plant Biology</i> , 2009, 9, 112.	3.6	118
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2078	The JCVI standard operating procedure for annotating prokaryotic metagenomic shotgun sequencing data. <i>Standards in Genomic Sciences</i> , 2010, 2, 229-237.	1.5	55
2079	SeqTrim07: a pipeline for preprocessing sequence reads. <i>International Journal of Computational Intelligence in Bioinformatics and Systems Biology</i> , 2010, 1, 370.	0.1	0
2080	A quality management system application to investigate and troubleshoot process failures. <i>Clinical Governance</i> , 2010, 15, 102-112.	0.3	0
2081	Impact of asymptomatic nodavirus carrier state and intraperitoneal viral mimic injection on brain transcript expression in Atlantic cod (<i>Gadus morhua</i>). <i>Physiological Genomics</i> , 2010, 42, 266-280.	2.3	53
2083	A Polymerase Chain Reaction Assay for the Detection of <i>Xanthomonas campestris</i> pv. <i>musacearum</i> in Banana. <i>Plant Disease</i> , 2010, 94, 109-114.	1.4	26
2084	Phylogeography and historical demography of the neotropical stingless bee <i>Melipona quadrifasciata</i> (Hymenoptera, Apidae): incongruence between morphology and mitochondrial DNA. <i>Apidologie</i> , 2010, 41, 534-547.	2.0	78
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2092	The Mitochondrial Genomes of Two Scallops, <i>Argopecten irradians</i> and <i>Chlamys farreri</i> (Mollusca:). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Evolution, 2010, 70, 57-68.	1.8	38
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2110	PCR screening and sequence analysis of iol clusters in <i>Lactobacillus casei</i> strains isolated from koumiss. <i>Folia Microbiologica</i> , 2010, 55, 603-606.	2.3	3
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2112	Assessment of soil fungal communities using pyrosequencing. <i>Journal of Microbiology</i> , 2010, 48, 284-289.	2.8	116
2113	Expressed sequence tag analysis generated from a normalized full-length cDNA library of the root-knot nematode (<i>Meloidogyne incognita</i>). <i>Genes and Genomics</i> , 2010, 32, 553-562.	1.4	7
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2120	Genic markers for wild abortive (WA) cytoplasm based male sterility and its fertility restoration in rice. <i>Molecular Breeding</i> , 2010, 26, 275-292.	2.1	52
2121	Characterization and tissue expression of channel catfish (<i>Ictalurus punctatus</i> Rafinesque, 1818) ubiquitin carboxyl-terminal hydrolase L5 (UCHL5) cDNA. <i>Molecular Biology Reports</i> , 2010, 37, 1229-1234.	2.3	3
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2127	Identification of novel members in sweet orange carotenoid biosynthesis gene families. <i>Tree Genetics and Genomes</i> , 2010, 6, 905-914.	1.6	27
2128	Development and mapping of peach candidate genes involved in fruit quality and their transferability and potential use in other Rosaceae species. <i>Tree Genetics and Genomes</i> , 2010, 6, 995-1012.	1.6	23
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2130	â€Candidatus <i>Phlomobacter fragariae</i> â€™ and the proteobacterium associated with the low sugar content syndrome of sugar beet are related to bacteria of the arsenophonus clade detected in hemipteran insects. <i>European Journal of Plant Pathology</i> , 2010, 126, 123-127.	1.7	12
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2709	Complete genome sequence of <i>Terriglobus saanensis</i> type strain SP1PR4T, an Acidobacteria from tundra soil. <i>Standards in Genomic Sciences</i> , 2012, 7, 59-69.	1.5	20

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4004	Genetic and morphological variation in the circumpolar distribution range of <i>Sphagnum warnstorffii</i> : indications of vicariant divergence in a common peatmoss. <i>Botanical Journal of the Linnean Society</i> , 2019, 189, 408-423.	1.6	8
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4044	In-depth comparative analysis of Illumina [®] MiSeq run metrics: Development of a wet-lab quality assessment tool. <i>Molecular Ecology Resources</i> , 2019, 19, 377-387.	4.8	7
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4122	Phylogeny and biogeography of <i>Astraea</i> with new insights into the evolutionary history of <i>Crotoneae</i> (Euphorbiaceae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106738.	2.7	9

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4127	De novo genome assembly of <i>Candida glabrata</i> reveals cell wall protein complement and structure of dispersed tandem repeat arrays. <i>Molecular Microbiology</i> , 2020, 113, 1209-1224.	2.5	25
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4130	Live-cell PCR and one-step purification streamline DNA engineering. <i>FASEB Journal</i> , 2020, 34, 3448-3460.	0.5	3
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4145	First molecular detection of piroplasmids in non-hematophagous bats from Brazil, with evidence of putative novel species. <i>Parasitology Research</i> , 2021, 120, 301-310.	1.6	14
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