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**Velvet: algorithms for de novo short read assembly using de Bruijn graphs**

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2216	The diploid genome sequence of an Asian individual. <b>2008</b> , 456, 60-5		744
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1826	Comparative studies of de novo assembly tools for next-generation sequencing technologies. <b>2011</b> , 27, 2031-7	103
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1760	Genome sequence of strain IMCC2047, a novel marine member of the Gammaproteobacteria. <b>2011</b> , 193, 3688-9	6
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1750	Complete genome sequence of the nicotine-degrading <i>Pseudomonas putida</i> strain S16. <b>2011</b> , 193, 5541-2	53

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1641	Full genome sequence of bluetongue virus serotype 4 from China. <b>2012</b> , 86, 13122-3		8
1640	Purifying selection, sequence composition, and context-specific indel mutations shape intraspecific variation in a bacterial endosymbiont. <b>2012</b> , 4, 44-51		11
1639	Identification of putative candidate genes involved in cuticle formation in <i>Prunus avium</i> (sweet cherry) fruit. <b>2012</b> , 110, 101-12		55
1638	Genomic sequences of Australian bluetongue virus prototype serotypes reveal global relationships and possible routes of entry into Australia. <b>2012</b> , 86, 6724-31		48
1637	Genome sequence of the <i>Corynebacterium pseudotuberculosis</i> Cp316 strain, isolated from the abscess of a Californian horse. <b>2012</b> , 194, 6620-1		10
1636	Genome sequence of a cold-adaptable sulfamethoxazole-degrading bacterium, <i>Pseudomonas psychrophila</i> HA-4. <b>2012</b> , 194, 5721		9
1635	Dynamic viral populations in hypersaline systems as revealed by metagenomic assembly. <b>2012</b> , 78, 6309-20		63
1634	Analysis of <i>Arabidopsis</i> genome-wide variations before and after meiosis and meiotic recombination by resequencing <i>Landsberg erecta</i> and all four products of a single meiosis. <i>Genome Research</i> , <b>2012</b> , 22, 508-18	9.7	89
1633	Complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> strain Cp267, isolated from a llama. <b>2012</b> , 194, 3567-8		13
1632	Draft genome sequence of <i>Pseudomonas fuscovaginae</i> , a broad-host-range pathogen of plants. <b>2012</b> , 194, 2765-6		10
1631	Genome sequence of <i>Pseudomonas putida</i> S12, a potential platform strain for industrial production of valuable chemicals. <b>2012</b> , 194, 5985-6		11
1630	Genome sequence of a highly efficient aerobic denitrifying bacterium, <i>Pseudomonas stutzeri</i> T13. <b>2012</b> , 194, 5720		29
1629	Genome sequence of the halotolerant bacterium <i>Imtechella halotolerans</i> K1T. <b>2012</b> , 194, 3731		3
1628	Complete genome sequence of the dairy isolate <i>Streptococcus macedonicus</i> ACA-DC 198. <b>2012</b> , 194, 1838-9		25
1627	Genome sequence and comparative pathogenomics analysis of a <i>Salmonella enterica</i> Serovar Typhi strain associated with a typhoid carrier in Malaysia. <b>2012</b> , 194, 5970-1		18
1626	Insights from the genome sequence of a <i>Salmonella enterica</i> serovar Typhi strain associated with a sporadic case of typhoid fever in Malaysia. <b>2012</b> , 194, 5124-5		7
1625	Whole-genome sequence of <i>Staphylococcus hominis</i> , an opportunistic pathogen. <b>2012</b> , 194, 4761-2		18
1624	Genome sequence of the marine bacterium <i>Marinilabilia salmonicolor</i> JCM 21150T. <b>2012</b> , 194, 3746		5

1623	Genome sequences of the primary endosymbiont "Candidatus Portiera aleyrodidarum" in the whitefly <i>Bemisia tabaci</i> B and Q biotypes. <b>2012</b> , 194, 6678-9	22
1622	Comparative genome analysis between <i>Aspergillus oryzae</i> strains reveals close relationship between sites of mutation localization and regions of highly divergent genes among <i>Aspergillus</i> species. <b>2012</b> , 19, 375-82	21
1621	Genome sequence of <i>Parascardovia denticolens</i> IPLA 20019, isolated from human breast milk. <b>2012</b> , 194, 4776-7	9
1620	Genome sequence of <i>Staphylococcus capitis</i> QN1, which causes infective endocarditis. <b>2012</b> , 194, 4469-70	8
1619	Espirito Santo virus: a new birnavirus that replicates in insect cells. <b>2012</b> , 86, 2390-9	19
1618	Genome sequence of the lactate-utilizing <i>Pseudomonas aeruginosa</i> strain XMG. <b>2012</b> , 194, 4751-2	13
1617	Complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> strain 1/06-A, isolated from a horse in North America. <b>2012</b> , 194, 4476	13
1616	Genome sequences of two thermophilic <i>Bacillus licheniformis</i> strains, efficient producers of platform chemical 2,3-butanediol. <b>2012</b> , 194, 4133-4	14
1615	Genetic fine structure of a <i>Salmonella enterica</i> serovar Typhi strain associated with the 2005 outbreak of typhoid fever in Kelantan, Malaysia. <b>2012</b> , 194, 3565-6	16
1614	Genome sequence of <i>Stenotrophomonas maltophilia</i> PML168, which displays Baeyer-Villiger monooxygenase activity. <b>2012</b> , 194, 4753-4	4
1613	Draft genome sequence of the nitrogen-fixing symbiotic bacterium <i>Bradyrhizobium elkanii</i> 587. <b>2012</b> , 194, 3547-8	15
1612	Host RNAs, including transposons, are encapsidated by a eukaryotic single-stranded RNA virus. <b>2012</b> , 109, 1907-12	85
1611	Genome sequence of the welan gum-producing strain <i>Sphingomonas</i> sp. ATCC 31555. <b>2012</b> , 194, 5989-90	20
1610	Draft genome sequence of <i>Alicyclobacillus hesperidum</i> strain URH17-3-68. <b>2012</b> , 194, 6348	4
1609	Genome sequence of <i>Stenotrophomonas maltophilia</i> RR-10, isolated as an endophyte from rice root. <b>2012</b> , 194, 1280-1	49
1608	Draft genome sequence of <i>Clostridium sporogenes</i> PA 3679, the common nontoxigenic surrogate for proteolytic <i>Clostridium botulinum</i> . <b>2012</b> , 194, 1631-2	23
1607	RNA-Seq mapping and detection of gene fusions with a suffix array algorithm. <b>2012</b> , 8, e1002464	40
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1605	Genomic comparison of <i>Escherichia coli</i> O104:H4 isolates from 2009 and 2011 reveals plasmid, and prophage heterogeneity, including shiga toxin encoding phage stx2. <b>2012</b> , 7, e48228	94
1604	Genome sequence of herpes simplex virus 1 strain McKrae. <b>2012</b> , 86, 9540-1	31
1603	Draft genome sequence of <i>Pseudomonas syringae</i> pathovar <i>syringae</i> strain FF5, causal agent of stem tip dieback disease on ornamental pear. <b>2012</b> , 194, 3733-4	8
1602	Genome update of <i>Botrytis cinerea</i> strains B05.10 and T4. <b>2012</b> , 11, 1413-4	99
1601	Draft genome sequence of <i>Rhizobium</i> sp. strain PDO1-076, a bacterium isolated from <i>Populus deltoides</i> . <b>2012</b> , 194, 2383-4	15
1600	AN EFFICIENT ALGORITHM FOR CHINESE POSTMAN WALK ON BI-DIRECTED DE BRUIJN GRAPHS. <b>2012</b> , 04, 1250019	2
1599	Genome sequence of <i>Exiguobacterium antarcticum</i> B7, isolated from a biofilm in Ginger Lake, King George Island, Antarctica. <b>2012</b> , 194, 6689-90	39
1598	Complete genome sequences of <i>Corynebacterium pseudotuberculosis</i> strains 3/99-5 and 42/02-A, isolated from sheep in Scotland and Australia, respectively. <b>2012</b> , 194, 4736-7	12
1597	Complete genome sequence of <i>Rahnella</i> sp. strain Y9602, a gammaproteobacterium isolate from metal- and radionuclide-contaminated soil. <b>2012</b> , 194, 2113-4	9
1596	The transcriptome of <i>Verticillium dahliae</i> -infected <i>Nicotiana benthamiana</i> determined by deep RNA sequencing. <b>2012</b> , 7, 1065-9	33
1595	Genome sequence of herpes simplex virus 1 strain KOS. <b>2012</b> , 86, 6371-2	53
1594	Draft genome sequence of <i>Herbaspirillum lusitanum</i> P6-12, an endophyte isolated from root nodules of <i>Phaseolus vulgaris</i> . <b>2012</b> , 194, 4136-7	18
1593	Complete genome sequence of <i>Mycobacterium xenopi</i> type strain RIVM700367. <b>2012</b> , 194, 3282-3	3
1592	Genome sequence of <i>Klebsiella pneumoniae</i> LZ, a potential platform strain for 1,3-propanediol production. <b>2012</b> , 194, 4457-8	6
1591	Complete genome sequence of <i>Desulfurococcus fermentans</i> , a hyperthermophilic cellulolytic crenarchaeon isolated from a freshwater hot spring in Kamchatka, Russia. <b>2012</b> , 194, 5703-4	11
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1588	Managing and mining large graphs. <b>2012</b> ,	28

1587	Comparative genomics of vancomycin-resistant <i>Staphylococcus aureus</i> strains and their positions within the clade most commonly associated with Methicillin-resistant <i>S. aureus</i> hospital-acquired infection in the United States. <b>2012</b> , 3,	97
1586	Complete genome sequence of <i>Celeribacter bacteriophage</i> P12053L. <b>2012</b> , 86, 8339-40	26
1585	High-Throughput Transcriptome Sequencing for Snp and Gene Discovery in a Moth. <b>2012</b> , 41, 997-1007	5
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1583	Complete genome sequence of a variant of <i>Campylobacter jejuni</i> NCTC 11168. <b>2012</b> , 194, 6298-9	10
1582	Draft genome sequence of <i>Pantoea ananatis</i> B1-9, a nonpathogenic plant growth-promoting bacterium. <b>2012</b> , 194, 729	24
1581	A de Bruijn graph approach to the quantification of closely-related genomes in a microbial community. <b>2012</b> , 19, 814-25	11
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1576	Theoretical Basis of a New Method for DNA Fragment Assembly in k-mer Graphs. <b>2012</b> ,	2
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1573	Complete genome sequence of <i>Rahnella aquatilis</i> CIP 78.65. <b>2012</b> , 194, 3020-1	16
1572	Genome sequence of <i>Aerococcus viridans</i> LL1. <b>2012</b> , 194, 4143	4
1571	Draft genome sequences for two metal-reducing <i>Pelosinus fermentans</i> strains isolated from a Cr(VI)-contaminated site and for type strain R7. <b>2012</b> , 194, 5147-8	17
1570	Biological characterization and next-generation genome sequencing of the unclassified <i>Cotia</i> virus SPAn232 (Poxviridae). <b>2012</b> , 86, 5039-54	24

1569	Complete genome sequence of <i>Pasteurella multocida</i> HN06, a toxigenic strain of serogroup D. <b>2012</b> , 194, 3292-3	30
1568	Draft genome sequence of <i>Pelosinus fermentans</i> JBW45, isolated during in situ stimulation for Cr(VI) reduction. <b>2012</b> , 194, 5456-7	14
1567	Complete genome sequence of <i>Marinomonas bacteriophage</i> P12026. <b>2012</b> , 86, 8909-10	9
1566	Genome sequence of the pathogenic <i>Herbaspirillum seropedicae</i> strain Os34, isolated from rice roots. <b>2012</b> , 194, 6993-4	10
1565	Genome sequence of <i>Kingella kingae</i> septic arthritis isolate PYKK081. <b>2012</b> , 194, 3017	15
1564	Complete genome sequence of <i>Clostridium</i> sp. strain BNL1100, a cellulolytic mesophile isolated from corn stover. <b>2012</b> , 194, 6982-3	8
1563	Draft genome sequence of a nonhemolytic fish-pathogenic <i>Streptococcus agalactiae</i> strain. <b>2012</b> , 194, 6341-2	15
1562	FSL J1-208, a virulent uncommon phylogenetic lineage IV <i>Listeria monocytogenes</i> strain with a small chromosome size and a putative virulence plasmid carrying internalin-like genes. <b>2012</b> , 78, 1876-89	31
1561	Genome sequence of the thermophile <i>Bacillus coagulans</i> Hammer, the type strain of the species. <b>2012</b> , 194, 6294-5	9
1560	Genes involved in the evolution of herbivory by a leaf-mining, <i>Drosophilid</i> fly. <b>2012</b> , 4, 900-16	49
1559	Genome sequence of <i>Blattabacterium</i> sp. strain BGIGA, endosymbiont of the <i>Blaberus giganteus</i> cockroach. <b>2012</b> , 194, 4450-1	20
1558	Genome sequence of <i>Enterobacter</i> sp. strain SP1, an endophytic nitrogen-fixing bacterium isolated from sugarcane. <b>2012</b> , 194, 6963-4	20
1557	Whole-genome sequences and comparative genomics of <i>Salmonella enterica</i> serovar Typhi isolates from patients with fatal and nonfatal typhoid fever in Papua New Guinea. <b>2012</b> , 194, 5122-3	10
1556	Complete genome sequence of <i>Mycobacterium vaccae</i> type strain ATCC 25954. <b>2012</b> , 194, 6339-40	7
1555	Draft genome sequence of <i>Virgibacillus halodenitrificans</i> 1806. <b>2012</b> , 194, 6332-3	7
1554	Complete genome sequence of <i>Mycobacterium fortuitum</i> subsp. <i>fortuitum</i> type strain DSM46621. <b>2012</b> , 194, 6337-8	5
1553	Draft genome sequence of the plant growth-promoting bacterium <i>Bacillus siamensis</i> KCTC 13613T. <b>2012</b> , 194, 4148-9	29
1552	Draft genome sequence of the nontoxigenic <i>Clostridium difficile</i> strain CD37. <b>2012</b> , 194, 2125-6	24

1551	Draft genome sequence of <i>Leucobacter chromiirens</i> , an extremely chromium-tolerant strain. <b>2012</b> , 194, 540-1	12
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1549	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <b>2012</b> , 109, 4550-5	195
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1546	Genome sequence of a novel nicotine-degrading strain, <i>Pseudomonas geniculata</i> N1. <b>2012</b> , 194, 3553-4	9
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1544	Characterization of a verocytotoxin-producing enteroaggregative <i>Escherichia coli</i> serogroup O111:H21 strain associated with a household outbreak in Northern Ireland. <b>2012</b> , 50, 4116-9	42
1543	Short-read sequencing for genomic analysis of the brown rot fungus <i>Fibroporia radiculosa</i> . <b>2012</b> , 78, 2272-81	25
1542	Towards effective partition management for large graphs. <b>2012</b> ,	84
1541	Genome sequence of "Candidatus <i>Microthrix parvicella</i> " Bio17-1, a long-chain-fatty-acid-accumulating filamentous actinobacterium from a biological wastewater treatment plant. <b>2012</b> , 194, 6670-1	25
1540	Efficient de novo assembly of large genomes using compressed data structures. <i>Genome Research</i> , <b>2012</b> , 22, 549-56	9.7 501
1539	Complete genome sequence of <i>Bacillus subtilis</i> strain QB928, a strain widely used in <i>B. subtilis</i> genetic studies. <b>2012</b> , 194, 6308-9	7
1538	Direct comparisons of Illumina vs. Roche 454 sequencing technologies on the same microbial community DNA sample. <b>2012</b> , 7, e30087	305
1537	Draft genome sequence of <i>Staphylococcus aureus</i> 118 (ST772), a major disease clone from India. <b>2012</b> , 194, 3727-8	13
1536	Draft genome sequences of the <i>Pseudomonas fluorescens</i> biocontrol strains Wayne1R and Wood1R. <b>2012</b> , 194, 724-5	9
1535	Molecular characterization of the 2011 Hong Kong scarlet fever outbreak. <b>2012</b> , 206, 341-51	72
1534	Complete genome sequence of <i>Liberibacter crescens</i> BT-1. <b>2012</b> , 7, 271-83	74

1533	Next generation sequencing technologies and the changing landscape of phage genomics. <b>2012</b> , 2, 190-199	44
1532	Metabolic routes affecting rubber biosynthesis in <i>Hevea brasiliensis</i> latex. <b>2012</b> , 63, 1863-71	88
1531	A next-generation sequencing approach to study the transcriptomic changes during the differentiation of <i>Physarum</i> at the single-cell level. <b>2012</b> , 6, 127-37	7
1530	Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium <i>Thermovirga lienii</i> type strain (Cas60314(T)). <b>2012</b> , 6, 230-9	21
1529	Gossamer--a resource-efficient de novo assembler. <b>2012</b> , 28, 1937-8	16
1528	Identification and characterization of a kunzeaol synthase from <i>Thapsia garganica</i> : implications for the biosynthesis of the pharmaceutical thapsigargin. <b>2012</b> , 448, 261-71	44
1527	Reference-independent comparative metagenomics using cross-assembly: crAss. <b>2012</b> , 28, 3225-31	52
1526	Iodide oxidation by a novel multicopper oxidase from the alphaproteobacterium strain Q-1. <b>2012</b> , 78, 3941-9	27
1525	Complete mitochondrial and plastid genomes of the green microalga <i>Trebouxioophyceae</i> sp. strain MX-AZ01 isolated from a highly acidic geothermal lake. <b>2012</b> , 11, 1417-8	16
1524	Genome sequence of <i>Sphingomonas wittichii</i> DP58, the first reported phenazine-1-carboxylic acid-degrading strain. <b>2012</b> , 194, 3535-6	12
1523	Complete genome sequence of the strong mutator <i>Salmonella enterica</i> subsp. <i>enterica</i> serotype Heidelberg strain B182. <b>2012</b> , 194, 3537-8	8
1522	Draft genome sequences of two <i>Campylobacter jejuni</i> clinical isolates, NW and D2600. <b>2012</b> , 194, 5707-8	1
1521	Genome sequence of a nicotine-degrading strain of <i>Arthrobacter</i> . <b>2012</b> , 194, 5714-5	9
1520	Draft genome sequence of <i>Lactobacillus gigeriorum</i> CRBIP 24.85T, isolated from a chicken crop. <b>2012</b> , 194, 5973	
1519	Draft genome sequence of <i>Bacillus oceanisediminis</i> 2691. <b>2012</b> , 194, 6351-2	6
1518	Genome sequence of <i>Rhizobium grahamii</i> CCGE502, a broad-host-range symbiont with low nodulation competitiveness in <i>Phaseolus vulgaris</i> . <b>2012</b> , 194, 6651-2	5
1517	Complete sequence of the first chimera genome constructed by cloning the whole genome of <i>Synechocystis</i> strain PCC6803 into the <i>Bacillus subtilis</i> 168 genome. <b>2012</b> , 194, 7007	14
1516	Draft genome sequence of <i>Staphylococcus aureus</i> ST672, an emerging disease clone from India. <b>2012</b> , 194, 6946-7	5

1515	Genome sequences of two multidrug-resistant <i>Acinetobacter baumannii</i> strains isolated from a patient before and after treatment with tigecycline. <b>2012</b> , 194, 6979-80	9
1514	Genome sequence of OXA-48 carbapenemase-producing <i>Klebsiella pneumoniae</i> KpO3210. <b>2012</b> , 194, 6981	8
1513	Draft genome sequences of the biocontrol bacterium <i>Mitsuaria</i> sp. strain H24L5A. <b>2012</b> , 194, 734-5	8
1512	Genome sequence of <i>Staphylococcus aureus</i> strain 11819-97, an ST80-IV European community-acquired methicillin-resistant isolate. <b>2012</b> , 194, 1625-6	28
1511	Complete genome sequence of the beer spoilage organism <i>Pediococcus clausenii</i> ATCC BAA-344T. <b>2012</b> , 194, 1271-2	31
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1509	Expression dynamics of the <i>Medicago truncatula</i> transcriptome during the symbiotic interaction with <i>Sinorhizobium meliloti</i> : which role for nitric oxide?. <b>2013</b> , 161, 425-39	73
1508	Genome sequence of <i>Amycolatopsis</i> sp. strain ATCC 39116, a plant biomass-degrading actinomycete. <b>2012</b> , 194, 2396-7	31
1507	Genome sequence of <i>Klebsiella oxytoca</i> 11492-1, a nosocomial isolate possessing a FOX-5 AmpC $\beta$ -lactamase. <b>2012</b> , 194, 3028-9	7
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1505	Genome sequence of the orange-pigmented seawater bacterium <i>Owenweeksia hongkongensis</i> type strain (UST20020801(T)). <b>2012</b> , 7, 120-30	11
1504	Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute <i>Sulfobacillus acidophilus</i> type strain (NAL(T)). <b>2012</b> , 6, 1-13	20
1503	Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1(T)), reclassification in the genus <i>Sphaerochaeta</i> as <i>Sphaerochaeta coccoides</i> comb. nov. and emendations of the family Spirochaetaceae and the genus <i>Sphaerochaeta</i> . <b>2012</b> , 6, 194-209	46
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1500	Complete genome sequence of the melanogenic marine bacterium <i>Marinomonas mediterranea</i> type strain (MMB-1(T)). <b>2012</b> , 6, 63-73	18
1499	Complete genome sequence of <i>Treponema pallidum</i> strain DAL-1. <b>2012</b> , 7, 12-21	32
1498	Genome sequence of the soil bacterium <i>Saccharomonospora azurea</i> type strain (NA-128(T)). <b>2012</b> , 6, 220-9	10

1497	Complete genome sequence of the facultatively anaerobic, appendaged bacterium <i>Muricauda ruestringensis</i> type strain (B1(T)). <b>2012</b> , 6, 185-93	8
1496	Efficient assembly and annotation of the transcriptome of catfish by RNA-Seq analysis of a doubled haploid homozygote. <b>2012</b> , 13, 595	102
1495	Complete genome sequence of <i>Dehalogenimonas lykanthroporepellens</i> type strain (BL-DC-9(T)) and comparison to "Dehalococcoides" strains. <b>2012</b> , 6, 251-64	45
1494	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1(T)) from a deep-sea hydrothermal vent chimney. <b>2012</b> , 6, 21-30	6
1493	Complete genome sequence of the aquatic bacterium <i>Runella slithyformis</i> type strain (LSU 4(T)). <b>2012</b> , 6, 145-54	16
1492	Genome sequence of the ocean sediment bacterium <i>Saccharomonospora marina</i> type strain (XMU15(T)). <b>2012</b> , 6, 265-75	3
1491	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfatator indicus</i> type strain (CIR29812(T)). <b>2012</b> , 6, 155-64	9
1490	Complete genome sequence of <i>Serratia plymuthica</i> strain AS12. <b>2012</b> , 6, 165-73	15
1489	Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4(T)). <b>2012</b> , 6, 174-84	23
1488	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRP(T)). <b>2012</b> , 6, 240-50	7
1487	Complete genome sequence of <i>Thermovibrio ammonificans</i> HB-1(T), a thermophilic, chemolithoautotrophic bacterium isolated from a deep-sea hydrothermal vent. <b>2012</b> , 7, 82-90	8
1486	Complete genome sequence of the plant-associated <i>Serratia plymuthica</i> strain AS13. <b>2012</b> , 7, 22-30	16
1485	Complete genome sequence of <i>Marinomonas posidonica</i> type strain (IVIA-Po-181(T)). <b>2012</b> , 7, 31-43	5
1484	Genome sequence of the flexirubin-pigmented soil bacterium <i>Niabella soli</i> type strain (JS13-8(T)). <b>2012</b> , 7, 210-20	0
1483	Genome sequence of the Antarctic rhodopsins-containing flavobacterium <i>Gillisia limnaea</i> type strain (R-8282(T)). <b>2012</b> , 7, 107-19	9
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1481	Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6(T)). <b>2012</b> , 6, 31-42	7
1480	Complete Genome Sequence of <i>Clostridium clariflavum</i> DSM 19732. <b>2012</b> , 6, 104-15	40

1479	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093(T)). <b>2012</b> , 7, 44-58	12
1478	Complete genome sequence of <i>Terriglobus saanensis</i> type strain SP1PR4(T), an Acidobacteria from tundra soil. <b>2012</b> , 7, 59-69	16
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1472	SLIQ: simple linear inequalities for efficient contig scaffolding. <b>2012</b> , 19, 1162-75	6
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1469	Extensive variation in surface lipoprotein gene content and genomic changes associated with virulence during evolution of a novel North American house finch epizootic strain of <i>Mycoplasma gallisepticum</i> . <b>2012</b> , 158, 2073-2088	37
1468	SpolPred: rapid and accurate prediction of <i>Mycobacterium tuberculosis</i> spoligotypes from short genomic sequences. <b>2012</b> , 28, 2991-3	74
1467	Draft genome sequence of high-melanin-yielding <i>Aeromonas media</i> strain WS. <b>2012</b> , 194, 6693-4	23
1466	Transcriptional reprogramming by root knot and migratory nematode infection in rice. <b>2012</b> , 196, 887-900	117
1465	Making next-generation sequencing work for you: approaches and practical considerations for marker development and phylogenetics. <b>2012</b> , 5, 427-450	27
1464	Genome sequence of the immunomodulatory strain <i>Bifidobacterium bifidum</i> LMG 13195. <b>2012</b> , 194, 6997	2
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1462	Targeted genome enrichment for efficient purification of endosymbiont DNA from host DNA. <b>2012</b> , 58, 201-207	27

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1444	Complete nucleotide sequence of a new strain of grapevine leafroll-associated virus 3 in South Africa. <b>2012</b> , 157, 1815-9	25

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1442	Evolution of three Pyrenophora cereal pathogens: recent divergence, speciation and evolution of non-coding DNA. <b>2012</b> , 49, 825-9	36
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1428	A Multi-objective Optimisation Approach to the Design of Experiment in De Novo Assembly Projects. <b>2012</b> ,	
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1423	A physical, genetic and functional sequence assembly of the barley genome. <b>2012</b> , 491, 711-6	1124
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1413	Methods and software in NGS for TE analysis. <b>2012</b> , 859, 105-14	6
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1410	Detection of Viruses in Sweetpotato from Honduras and Guatemala Augmented by Deep-Sequencing of Small-RNAs. <b>2012</b> , 96, 1430-1437	55
1409	The core stimulon of <i>Corynebacterium pseudotuberculosis</i> strain 1002 identified using ab initio methodologies. <b>2012</b> , 4, 789-94	10
1408	Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. <b>2012</b> , 158, 1005-1015	325

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1404	Scaling metagenome sequence assembly with probabilistic de Bruijn graphs. <b>2012</b> , 109, 13272-7	177
1403	Rapid development of molecular resources for a freshwater mussel, <i>Villosa lienosa</i> (Bivalvia:Unionidae), using an RNA-seq-based approach. <b>2012</b> , 31, 695-708	22
1402	Fermentation, hydrogen, and sulfur metabolism in multiple uncultivated bacterial phyla. <b>2012</b> , 337, 1661-5	464
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1400	Parallel molecular evolution in an herbivore community. <b>2012</b> , 337, 1634-7	179
1399	Detection and identification of plasma bacterial and viral elements in HIV/AIDS patients in comparison to healthy adults. <b>2012</b> , 18, 1126-33	44
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1397	Endosymbiotic bacteria as a source of carotenoids in whiteflies. <b>2012</b> , 8, 986-9	113
1396	Intracontinental spread of human invasive <i>Salmonella</i> Typhimurium pathovariants in sub-Saharan Africa. <b>2012</b> , 44, 1215-21	279
1395	A Parameterization Study of Short Read Assembly Using the Velvet Assembler. <b>2012</b> , 179-186	
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1393	Succinct de Bruijn Graphs. <b>2012</b> , 225-235	82
1392	Strategies for transcriptome analysis in nonmodel plants. <b>2012</b> , 99, 267-76	103
1391	Massively parallel sequencing technology in pathogenic microbes. <b>2012</b> , 835, 271-94	5
1390	Rainbow: an integrated tool for efficient clustering and assembling RAD-seq reads. <b>2012</b> , 28, 2732-7	78

1389	Full-genome dissection of an epidemic of severe invasive disease caused by a hypervirulent, recently emerged clone of group A <i>Streptococcus</i> . <b>2012</b> , 180, 1522-34	63
1388	Molecular cloning and characterization of (+)-epi- $\beta$ -isabolol synthase, catalyzing the first step in the biosynthesis of the natural sweetener, hernandulcin, in <i>Lippia dulcis</i> . <b>2012</b> , 527, 37-44	35
1387	A new vesicular compartment in <i>Encephalitozoon cuniculi</i> . <b>2012</b> , 14, 324-8	4
1386	Phylogenetic, genomic organization and expression analysis of hydrophobin genes in the ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> . <b>2012</b> , 49, 199-209	40
1385	The genome of the xerotolerant mold <i>Wallemia sebi</i> reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. <b>2012</b> , 49, 217-26	83
1384	Characterization of telomeres and telomerase expression in <i>Xiphophorus</i> . <b>2012</b> , 155, 89-94	8
1383	Effects of short read quality and quantity on a de novo vertebrate transcriptome assembly. <b>2012</b> , 155, 95-101	17
1382	Mutation hot spots in yeast caused by long-range clustering of homopolymeric sequences. <b>2012</b> , 1, 36-42	21
1381	RNA-seq analysis of mucosal immune responses reveals signatures of intestinal barrier disruption and pathogen entry following <i>Edwardsiella ictaluri</i> infection in channel catfish, <i>Ictalurus punctatus</i> . <b>2012</b> , 32, 816-27	164
1380	The mitochondrial genome of <i>Moniliophthora roreri</i> , the frosty pod rot pathogen of cacao. <b>2012</b> , 116, 551-62	19
1379	Quality of prokaryote genome assembly: indispensable issues of factors affecting prokaryote genome assembly quality. <b>2012</b> , 505, 365-7	9
1378	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <b>2012</b> , 6, 1715-27	420
1377	Application of metatranscriptomics to soil environments. <b>2012</b> , 91, 246-51	107
1376	<i>Rhizobium grahamii</i> sp. nov., from nodules of <i>Dalea leporina</i> , <i>Leucaena leucocephala</i> and <i>Clitoria ternatea</i> , and <i>Rhizobium mesoamericanum</i> sp. nov., from nodules of <i>Phaseolus vulgaris</i> , siratro, cowpea and <i>Mimosa pudica</i> . <b>2012</b> , 62, 2264-2271	59
1375	Posttraumatic regeneration involves differential expression of long terminal repeat (LTR) retrotransposons. <b>2012</b> , 241, 1625-36	14
1374	Computational analysis of noncoding RNAs. <b>2012</b> , 3, 759-78	44
1373	ParticleCall: a particle filter for base calling in next-generation sequencing systems. <b>2012</b> , 13, 160	9
1372	Optimization of de novo transcriptome assembly from high-throughput short read sequencing data improves functional annotation for non-model organisms. <b>2012</b> , 13, 170	26

1371	AGORA: Assembly Guided by Optical Restriction Alignment. <b>2012</b> , 13, 189	32
1370	CaPSID: a bioinformatics platform for computational pathogen sequence identification in human genomes and transcriptomes. <b>2012</b> , 13, 206	34
1369	De novo sequencing and characterization of <i>Picrohiza kurrooa</i> transcriptome at two temperatures showed major transcriptome adjustments. <b>2012</b> , 13, 126	107
1368	Genomic characterization of the conditionally dispensable chromosome in <i>Alternaria arborescens</i> provides evidence for horizontal gene transfer. <b>2012</b> , 13, 171	63
1367	Transcriptome of the adult female malaria mosquito vector <i>Anopheles albimanus</i> . <b>2012</b> , 13, 207	31
1366	IS-seq: a novel high throughput survey of in vivo IS6110 transposition in multiple <i>Mycobacterium tuberculosis</i> genomes. <b>2012</b> , 13, 249	22
1365	On the origin of <i>Mycobacterium ulcerans</i> , the causative agent of Buruli ulcer. <b>2012</b> , 13, 258	111
1364	The immune gene repertoire of an important viral reservoir, the Australian black flying fox. <b>2012</b> , 13, 261	80
1363	Genome characterisation of the genus <i>Francisella</i> reveals insight into similar evolutionary paths in pathogens of mammals and fish. <b>2012</b> , 13, 268	101
1362	RAD tag sequencing as a source of SNP markers in <i>Cynara cardunculus</i> L. <b>2012</b> , 13, 3	70
1361	The venom-gland transcriptome of the eastern diamondback rattlesnake ( <i>Crotalus adamanteus</i> ). <b>2012</b> , 13, 312	197
1360	Development and validation of genic-SSR markers in sesame by RNA-seq. <b>2012</b> , 13, 316	97
1359	Genome-wide SNP discovery in walnut with an AGSNP pipeline updated for SNP discovery in allogamous organisms. <b>2012</b> , 13, 354	34
1358	Sequencing the genome of <i>Marssonina brunnea</i> reveals fungus-poplar co-evolution. <b>2012</b> , 13, 382	37
1357	De novo sequence assembly and characterisation of a partial transcriptome for an evolutionarily distinct reptile, the tuatara ( <i>Sphenodon punctatus</i> ). <b>2012</b> , 13, 439	33
1356	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnosae</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. <b>2012</b> , 13, 444	97
1355	High depth, whole-genome sequencing of cholera isolates from Haiti and the Dominican Republic. <b>2012</b> , 13, 468	7
1354	RNA-Seq reveals complex genetic response to Deepwater Horizon oil release in <i>Fundulus grandis</i> . <b>2012</b> , 13, 474	63

1353	De novo assembly of highly diverse viral populations. <b>2012</b> , 13, 475	147
1352	Transcriptome-scale homoeolog-specific transcript assemblies of bread wheat. <b>2012</b> , 13, 492	33
1351	Comparative genomic analysis of human infective <i>Trypanosoma cruzi</i> lineages with the bat-restricted subspecies <i>T. cruzi marinkellei</i> . <b>2012</b> , 13, 531	45
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1348	De novo assembly of the pepper transcriptome ( <i>Capsicum annuum</i> ): a benchmark for in silico discovery of SNPs, SSRs and candidate genes. <b>2012</b> , 13, 571	93
1347	Toward understanding the genetic basis of adaptation to high-elevation life in poikilothermic species: a comparative transcriptomic analysis of two ranid frogs, <i>Rana chensinensis</i> and <i>R. kukunoris</i> . <b>2012</b> , 13, 588	47
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1345	Next generation sequencing and de novo transcriptome analysis of <i>Costus pictus</i> D. Don, a non-model plant with potent anti-diabetic properties. <b>2012</b> , 13, 663	56
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1343	Cutoffs and k-mers: implications from a transcriptome study in allopolyploid plants. <b>2012</b> , 13, 92	47
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1336	Next-generation sequencing of cervical DNA detects human papillomavirus types not detected by commercial kits. <b>2012</b> , 9, 164	55

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1334	Arapan-S: a fast and highly accurate whole-genome assembly software for viruses and small genomes. <b>2012</b> , 5, 243	3
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1328	Analysis of global transcriptional profiles of enterotoxigenic <i>Escherichia coli</i> isolate E24377A. <b>2012</b> , 80, 1232-42	38
1327	Fighting outbreaks with bacterial genomics: case review and workflow proposal. <b>2012</b> , 15, 341-51	10
1326	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. <b>2012</b> , 10, 599-606	326
1325	Small World Asynchronous Parallel Model for Genome Assembly. <b>2012</b> , 145-155	8
1324	A Galaxy Workflow for the Functional Annotation of Metagenomic Samples. <b>2012</b> , 247-253	2
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1322	FinIS: Improved in silico Finishing Using an Exact Quadratic Programming Formulation. <b>2012</b> , 314-325	14
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1320	Whole genome sequencing and future breeding of rice. <b>2012</b> , 21, 10-14	1
1319	From de Bruijn Graphs to Rectangle Graphs for Genome Assembly. <b>2012</b> , 249-261	7
1318	Clinical integration of next-generation sequencing technology. <b>2012</b> , 32, 585-99	49

1317	An efficient algorithm for DNA fragment assembly in MapReduce. <b>2012</b> , 426, 395-8	11
1316	Mitogenome polymorphism in a single branch sample revealed by SOLiD deep sequencing of the <i>Lophelia pertusa</i> coral genome. <b>2012</b> , 506, 344-9	15
1315	Review of general algorithmic features for genome assemblers for next generation sequencers. <b>2012</b> , 10, 58-73	27
1314	Beyond the Pipelines: Cloud Computing Facilitates Management, Distribution, Security, and Analysis of High-Speed Sequencer Data. <b>2012</b> , 449-468	3
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1312	Allele identification in assembled genomic sequence datasets. <b>2012</b> , 888, 197-211	1
1311	A survey of copy-number variation detection tools based on high-throughput sequencing data. <b>2012</b> , Chapter 7, Unit7.19	18
1310	Sequence and analysis of the genome of the pathogenic yeast <i>Candida orthopsilosis</i> . <b>2012</b> , 7, e35750	47
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1308	Complete genome sequence of the rapeseed plant-growth promoting <i>Serratia plymuthica</i> strain AS9. <b>2012</b> , 6, 54-62	25
1307	Next generation sequencing in clinical medicine: Challenges and lessons for pathology and biomedical informatics. <b>2012</b> , 3, 40	106
1306	Definition of PromotomeTranscriptome Architecture Using CAGEscan. <b>2012</b> , 47-61	
1305	Library preparation and data analysis packages for rapid genome sequencing. <b>2012</b> , 944, 1-22	16
1304	Global gene expression analysis of gill tissues from normal and thermally selected strains of rainbow trout. <b>2012</b> , 78, 1041-1049	16
1303	Insights into the bovine rumen plasmidome. <b>2012</b> , 109, 5452-7	96
1302	Homology-independent discovery of replicating pathogenic circular RNAs by deep sequencing and a new computational algorithm. <b>2012</b> , 109, 3938-43	141
1301	MetaVelvet: an extension of Velvet assembler to de novo metagenome assembly from short sequence reads. <b>2012</b> , 40, e155	453
1300	High-temperature sorbose fermentation with thermotolerant <i>Gluconobacter frateurii</i> CHM43 and its mutant strain adapted to higher temperature. <b>2012</b> , 95, 1531-40	17

1299	De Novo Assembly of High-Throughput Sequencing Data with Cloud Computing and New Operations on String Graphs. <b>2012</b> ,	5
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1292	Identification of Splicing Factor Target Genes by High-Throughput Sequencing. <b>2012</b> , 556-564	
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911	Global transcriptome profiling reveals molecular mechanisms of metal tolerance in a chronically exposed wild population of brown trout. <b>2013</b> , 47, 8869-77	64
910	The genome of the platyfish, <i>Xiphophorus maculatus</i> , provides insights into evolutionary adaptation and several complex traits. <b>2013</b> , 45, 567-72	201
909	CathaCyc, a metabolic pathway database built from <i>Catharanthus roseus</i> RNA-Seq data. <b>2013</b> , 54, 673-85	95
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906	A targeted enrichment strategy for massively parallel sequencing of angiosperm plastid genomes. <b>2013</b> , 1, 1200497	82
905	The perfect neuroimaging-genetics-computation storm: collision of petabytes of data, millions of hardware devices and thousands of software tools. <b>2014</b> , 8, 311-22	15
904	The genome sequence of <i>Leishmania (Leishmania) amazonensis</i> : functional annotation and extended analysis of gene models. <b>2013</b> , 20, 567-81	79

903	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. <b>2013</b> , 7, 2287-300		83
902	Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. <i>Genome Research</i> , <b>2013</b> , 23, 111-20	9-7	324
901	Candidate phylum TM6 genome recovered from a hospital sink biofilm provides genomic insights into this uncultivated phylum. <b>2013</b> , 110, E2390-9		144
900	Draft Genome Sequences for Ten <i>Salmonella enterica</i> Serovar Typhimurium Phage Type 135 Variants. <b>2013</b> , 1,		3
899	PRICE: software for the targeted assembly of components of (Meta) genomic sequence data. <b>2013</b> , 3, 865-80		186
898	Genome Sequence of the "Indian Bison Type" Biotype of <i>Mycobacterium avium</i> subsp. paratuberculosis Strain S5. <b>2013</b> , 1,		9
897	Draft Genome Sequence of Fructophilic <i>Lactobacillus florum</i> . <b>2013</b> , 1,		8
896	Complete genome sequence of the avian pathogenic <i>Escherichia coli</i> strain APEC O78. <b>2013</b> , 1, e0002613		26
895	Genome Sequence of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Strain Xca5. <b>2013</b> , 1,		17
894	Draft Genome Sequence of the <i>Wolbachia</i> Endosymbiont of <i>Drosophila suzukii</i> . <b>2013</b> , 1,		33
893	Draft Genome Sequence of the Methicillin-Resistant <i>Staphylococcus aureus</i> Isolate MRSA-M2. <b>2013</b> , 1,		16
892	Genome sequence of a novel archaeal rudivirus recovered from a mexican hot spring. <b>2013</b> , 1,		10
891	Draft Genome Sequence of <i>Escherichia coli</i> Strain ATCC 23502 (Serovar O5:K4:H4). <b>2013</b> , 1, e0004613		8
890	Draft genome sequences of five strains in the genus <i>thauera</i> . <b>2013</b> , 1,		13
889	Draft Genome Sequence of <i>Methylobacterium buryatense</i> Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium. <b>2013</b> , 1,		34
888	Draft Genome Sequence of the First Isolate of Extensively Drug-Resistant (XDR) <i>Mycobacterium tuberculosis</i> in Malaysia. <b>2013</b> , 1,		6
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886	Whole-Genome Sequences of an Aerobic Anoxygenic Phototroph, <i>Blastomonas</i> sp. Strain AAP53, Isolated from a Freshwater Desert Lake in Inner Mongolia, China. <b>2013</b> , 1, e0007113		7

885	Genome Sequence of <i>Chlamydia psittaci</i> Strain 01DC12 Originating from Swine. <b>2013</b> , 1,	7
884	Draft genome sequence of <i>Frankia</i> sp. strain QA3, a nitrogen-fixing actinobacterium isolated from the root nodule of <i>Alnus nitida</i> . <b>2013</b> , 1, e0010313	35
883	Complete Genome Sequence of <i>Wohlfahrtiimonas chitiniclastica</i> Strain SH04, Isolated from <i>Chrysomya megacephala</i> Collected from Pudong International Airport in China. <b>2013</b> , 1, e0011913	16
882	Complete Genome Sequence of <i>Serratia marcescens</i> WW4. <b>2013</b> , 1, e0012613	24
881	Genome Sequence of the Pathogenic Bacterium <i>Vibrio vulnificus</i> Biotype 3. <b>2013</b> , 1, e0013613	12
880	Whole-Genome Shotgun Assembly and Analysis of the Genome of <i>Streptomyces mobaraensis</i> DSM 40847, a Strain for Industrial Production of Microbial Transglutaminase. <b>2013</b> , 1, e0014313	13
879	Draft Genome Sequence for <i>Desulfovibrio africanus</i> Strain PCS. <b>2013</b> , 1, e0014413	5
878	Draft Genome Sequence of MKD8, a Conjugal Recipient <i>Mycobacterium smegmatis</i> Strain. <b>2013</b> , 1, e0014813	4
877	Draft genome sequence of <i>Bacillus thuringiensis</i> strain DAR 81934, which exhibits molluscicidal activity. <b>2013</b> , 1, e0017512	11
876	Genome Sequence of <i>Burkholderia pseudomallei</i> NCTC 13392. <b>2013</b> , 1,	6
875	Genome Sequence of <i>Campylobacter showae</i> UNSWCD, Isolated from a Patient with Crohn's Disease. <b>2013</b> , 1,	2
874	Draft Genome Sequence of <i>Erwinia toletana</i> , a Bacterium Associated with Olive Knots Caused by <i>Pseudomonas savastanoi</i> pv. <i>Savastanoi</i> . <b>2013</b> , 1,	8
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872	Genome Sequence of <i>Mycoplasma feriruminatoris</i> sp. nov., a Fast-Growing <i>Mycoplasma</i> Species. <b>2013</b> , 1,	10
871	Draft Genome Sequence of <i>Herbaspirillum huttiense</i> subsp. <i>putei</i> IAM 15032, a Strain Isolated from Well Water. <b>2013</b> , 1,	4
870	Complete Genome of a <i>Methanosarcina mazei</i> Strain Isolated from Sediment Samples from an Amazonian Flooded Area. <b>2013</b> , 1,	8
869	Draft Genome Sequence of the Antarctic Psychrophilic Bacterium <i>Pseudomonas syringae</i> Strain Lz4W. <b>2013</b> , 1,	7
868	Draft Genome Sequence of the Moderately Halophilic Bacterium <i>Marinobacter lipolyticus</i> Strain SM19. <b>2013</b> , 1,	8

867	Draft Genome Sequence of <i>Pseudomonas fluorescens</i> LMG 5329, a White Line-Inducing Principle-Producing Bioindicator for the Mushroom Pathogen <i>Pseudomonas tolaasii</i> . <b>2013</b> , 1,	2
866	Genome Sequence of the Vancomycin-Producing <i>Amycolatopsis orientalis</i> subsp. <i>orientalis</i> Strain KCTC 9412T. <b>2013</b> , 1,	12
865	The Draft Genome Sequence of <i>Nocardioides</i> sp. Strain CF8 Reveals the Scope of Its Metabolic Capabilities. <b>2013</b> , 1,	6
864	Genome Sequences of Three Atypical <i>Xanthomonas campestris</i> pv. <i>campestris</i> Strains, CN14, CN15, and CN16. <b>2013</b> , 1,	8
863	Draft Genome Sequence of <i>Frankia</i> sp. Strain BMG5.12, a Nitrogen-Fixing Actinobacterium Isolated from Tunisian Soils. <b>2013</b> , 1,	33
862	Draft Genome Sequences of <i>Porphyromonas crevioricanis</i> JCM 15906T and <i>Porphyromonas cansulci</i> JCM 13913T Isolated from a Canine Oral Cavity. <b>2013</b> , 1,	2
861	Draft Genome Sequences of Three O157 Enteropathogenic <i>Escherichia coli</i> Isolates. <b>2013</b> , 1,	5
860	Draft Genome Sequence of an Oscillatorian Cyanobacterium, Strain ESFC-1. <b>2013</b> , 1,	5
859	Genome Sequence of <i>Clostridium diolis</i> Strain DSM 15410, a Promising Natural Producer of 1,3-Propanediol. <b>2013</b> , 1,	6
858	Genome Sequence of <i>Klebsiella pneumoniae</i> Strain ATCC 25955, an Oxygen-Insensitive Producer of 1,3-Propanediol. <b>2013</b> , 1,	2
857	Genome Sequence of the 2,4,5-Trichlorophenoxyacetate-Degrading Bacterium <i>Burkholderia phenoliruptrix</i> Strain AC1100. <b>2013</b> , 1,	3
856	Draft Genome Sequence of <i>Clostridium tyrobutyricum</i> Strain UC7086, Isolated from Grana Padano Cheese with Late-Blowing Defect. <b>2013</b> , 1,	14
855	Genome Sequence of a Novel Polymer-Grade L-Lactate-Producing Alkaliphile, <i>Exiguobacterium</i> sp. Strain 8-11-1. <b>2013</b> , 1,	12
854	Draft Genome Sequences of Five Strains of <i>Lactobacillus acidophilus</i> , Strain CIP 76.13T, Isolated from Humans, Strains CIRM-BIA 442 and CIRM-BIA 445, Isolated from Dairy Products, and Strains DSM 20242 and DSM 9126 of Unknown Origin. <b>2013</b> , 1,	3
853	Draft Genome Sequence of <i>Lactobacillus hominis</i> Strain CRBIP 24.179T, Isolated from Human Intestine. <b>2013</b> , 1,	
852	Genome sequences of six wheat-infecting <i>fusarium</i> species isolates. <b>2013</b> , 1,	23
851	High-Quality Draft Genome Sequences of Two <i>Xanthomonas citri</i> pv. <i>malvacearum</i> Strains. <b>2013</b> , 1,	6
850	Draft Genome Sequence of the <i>Xanthomonas cassavae</i> Type Strain CFBP 4642. <b>2013</b> , 1,	4

849	Whole-Genome Sequence of <i>Mycobacterium abscessus</i> Clinical Strain V06705. <b>2013</b> , 1,	4
848	Genome Sequence of the Bacterium <i>Bifidobacterium longum</i> Strain CMCC P0001, a Probiotic Strain Used for Treating Gastrointestinal Disease. <b>2013</b> , 1,	11
847	Genome Sequence of <i>Dehalobacter UNSWDHB</i> , a Chloroform-Dechlorinating Bacterium. <b>2013</b> , 1,	19
846	Draft Genome Sequence of the Earliest <i>Cronobacter sakazakii</i> Sequence Type 4 Strain, NCIMB 8272. <b>2013</b> , 1,	8
845	Draft Genome Sequences of Three Newly Identified Species in the Genus <i>Cronobacter</i> , <i>C. helveticus</i> LMG23732T, <i>C. pulveris</i> LMG24059, and <i>C. zurichensis</i> LMG23730T. <b>2013</b> , 1,	11
844	Draft Genome Sequence of a Meningitic Isolate of <i>Cronobacter sakazakii</i> Clonal Complex 4, Strain 8399. <b>2013</b> , 1,	4
843	Draft Genome Sequences of <i>Bordetella hinzii</i> and <i>Bordetella trematum</i> . <b>2013</b> , 1,	5
842	Draft Genome Sequences of Multidrug-Resistant <i>Acinetobacter</i> sp. Strains from Colombian Hospitals. <b>2013</b> , 1,	2
841	Draft Genome Sequence of the Hydrogen- and Ethanol-Producing Bacterium <i>Clostridium intestinale</i> Strain URNW. <b>2013</b> , 1,	4
840	Draft Genome Sequence of the Biosurfactant-Producing Bacterium <i>Gordonia amicalis</i> Strain CCMA-559, Isolated from Petroleum-Impacted Sediment. <b>2013</b> , 1,	4
839	Draft Genome Sequence of <i>Pseudozyma brasiliensis</i> sp. nov. Strain GHG001, a High Producer of Endo-1,4-Xylanase Isolated from an Insect Pest of Sugarcane. <b>2013</b> , 1,	9
838	Genome Sequence of <i>Dyella ginsengisoli</i> Strain LA-4, an Efficient Degradator of Aromatic Compounds. <b>2013</b> , 1,	9
837	Complete Genome Sequence of <i>Streptococcus pneumoniae</i> Strain A026, a Clinical Multidrug-Resistant Isolate Carrying Tn2010. <b>2013</b> , 1,	4
836	High-Quality Draft Genome Sequence of <i>Xanthomonas alfalfae</i> subsp. <i>alfalfae</i> Strain CFBP 3836. <b>2013</b> , 1,	5
835	Genome Sequence of Strain MOLA814, a Proteorhodopsin-Containing Representative of the Betaproteobacteria Common in the Ocean. <b>2013</b> , 1,	2
834	Draft Genome Sequence of NDM-1-Producing <i>Klebsiella pneumoniae</i> Clinical Isolate 303K. <b>2013</b> , 1,	1
833	Genome Sequences of 28 <i>Bordetella pertussis</i> U.S. Outbreak Strains Dating from 2010 to 2012. <b>2013</b> , 1,	13
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831	Draft Genome Sequence of <i>Shewanella decolorationis</i> S12, a Dye-Degrading Bacterium Isolated from a Wastewater Treatment Plant. <b>2013</b> , 1,	7
830	Genome Sequence of Growth-Improving <i>Paenibacillus mucilaginosus</i> Strain KNP414. <b>2013</b> , 1,	3
829	Livestock origin for a human pandemic clone of community-associated methicillin-resistant <i>Staphylococcus aureus</i> . <b>2013</b> , 4,	132
828	Genome Sequencing of <i>Ralstonia solanacearum</i> FQY_4, Isolated from a Bacterial Wilt Nursery Used for Breeding Crop Resistance. <b>2013</b> , 1,	17
827	Proteomic and genetic analyses demonstrate that <i>Plasmodium berghei</i> blood stages export a large and diverse repertoire of proteins. <b>2013</b> , 12, 426-48	52
826	A Sensitive and Accurate protein domain cLassification Tool (SALT) for short reads. <b>2013</b> , 29, 2103-11	10
825	Piliation of invasive <i>Streptococcus pneumoniae</i> isolates in the era before pneumococcal conjugate vaccine introduction in Malawi. <b>2013</b> , 20, 1729-35	9
824	Genome Sequences and Photosynthesis Gene Cluster Composition of a Freshwater Aerobic Anoxygenic Phototroph, <i>Sandarakinorhabdus</i> sp. Strain AAP62, Isolated from the Shahu Lake in Ningxia, China. <b>2013</b> , 1,	2
823	Draft Genome Sequence of <i>Escherichia coli</i> Strain ATCC 23506 (Seroovar O10:K5:H4). <b>2013</b> , 1, e0004913	8
822	Genome Sequence of <i>Klebsiella oxytoca</i> M5a1, a Promising Strain for Nitrogen Fixation and Chemical Production. <b>2013</b> , 1,	10
821	Draft Genome Sequence of Dihydroxyacetone-Producing <i>Gluconobacter thailandicus</i> Strain NBRC 3255. <b>2013</b> , 1, e0011813	7
820	Draft Genome Sequence of <i>Rhodococcus qingshengii</i> Strain BKS 20-40. <b>2013</b> , 1, e0012813	2
819	Draft Genome Sequence of <i>Rhodococcus triatomae</i> Strain BKS 15-14. <b>2013</b> , 1, e0012913	3
818	Draft Genome Sequence of <i>Acinetobacter baumannii</i> Strain MSP4-16. <b>2013</b> , 1, e0013713	1
817	Draft Genome Sequence of <i>Herpotrichiellaceae</i> sp. UM238 Isolated from Human Skin Scraping. <b>2013</b> , 1,	1
816	Draft Genome Sequence of Medium-Chain-Length Polyhydroxyalkanoate-Producing <i>Pseudomonas putida</i> Strain LS46. <b>2013</b> , 1, e0015113	6
815	Genome sequence of a novel archaeal fusellovirus assembled from the metagenome of a mexican hot spring. <b>2013</b> , 1, e0016413	10
814	Draft Genome Sequence of <i>Meiothermus ruber</i> H328, Which Degrades Chicken Feathers, and Identification of Proteases and Peptidases Responsible for Degradation. <b>2013</b> , 1,	14

813	Draft Genome Sequence of a Thermophilic Member of the Bacillaceae, <i>Anoxybacillus flavithermus</i> Strain Kn10, Isolated from the Kan-nawa Hot Spring in Japan. <b>2013</b> , 1,	6
812	Draft Genome Sequence of <i>Methylobacterium mesophilicum</i> Strain SR1.6/6, Isolated from <i>Citrus sinensis</i> . <b>2013</b> , 1,	7
811	Genome Sequence of the Multiple-β-Lactam-Antibiotic-Resistant Bacterium <i>Acidovorax</i> sp. Strain MR-S7. <b>2013</b> , 1,	11
810	Genome Sequence of <i>Streptococcus agalactiae</i> Strain 09mas018883, Isolated from a Swedish Cow. <b>2013</b> , 1,	8
809	Genome Sequence of <i>Thermus thermophilus</i> ATCC 33923, a Thermostable Trehalose-Producing Strain. <b>2013</b> , 1,	6
808	Draft Genome Sequence of the Brazilian Toxic Bloom-Forming Cyanobacterium <i>Microcystis aeruginosa</i> Strain SPC777. <b>2013</b> , 1,	11
807	Complete Genome Sequence of <i>Clostridium</i> sp. Strain DL-VIII, a Novel Solventogenic <i>Clostridium</i> Species Isolated from Anaerobic Sludge. <b>2013</b> , 1,	4
806	Genome Sequence of an Epidemic Isolate of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> from Rio de Janeiro, Brazil. <b>2013</b> , 1,	9
805	Complete Genome Sequence of the Encephalomyelitic <i>Burkholderia pseudomallei</i> Strain MSHR305. <b>2013</b> , 1,	6
804	Draft Genome Sequence of <i>Bacillus pumilus</i> CCMA-560, Isolated from an Oil-Contaminated Mangrove Swamp. <b>2013</b> , 1,	7
803	Draft Genome Sequence of <i>Cryptococcus flavescens</i> Strain OH182.9_3C, a Biocontrol Agent against <i>Fusarium</i> Head Blight of Wheat. <b>2013</b> , 1,	5
802	Draft Genome Sequence of <i>Pseudomonas azotifigens</i> Strain DSM 17556T (6H33bT), a Nitrogen Fixer Strain Isolated from a Compost Pile. <b>2013</b> , 1,	3
801	Complete Genome Sequence of <i>Bacillus thuringiensis</i> Serovar <i>Israelensis</i> Strain HD-789. <b>2013</b> , 1,	26
800	Pan-genome and comparative genome analyses of <i>propionibacterium acnes</i> reveal its genomic diversity in the healthy and diseased human skin microbiome. <b>2013</b> , 4, e00003-13	110
799	Within-host evolution of <i>Burkholderia pseudomallei</i> over a twelve-year chronic carriage infection. <b>2013</b> , 4,	80
798	Genomic insights to control the emergence of vancomycin-resistant enterococci. <b>2013</b> , 4,	112
797	Genome Sequence of <i>Klebsiella oxytoca</i> SA2, an Endophytic Nitrogen-Fixing Bacterium Isolated from the Pioneer Grass <i>Psammochloa villosa</i> . <b>2013</b> , 1,	8
796	Draft Genome Sequence of <i>Pseudomonas veronii</i> Strain 1YdBTEX2. <b>2013</b> , 1,	10

795	Complete Genome of <i>Serratia</i> sp. Strain FGI 94, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. <b>2013</b> , 1, e0023912		13
794	Draft Genome Sequence of <i>Frankia</i> sp. Strain BCU110501, a Nitrogen-Fixing Actinobacterium Isolated from Nodules of <i>Discaria trinevis</i> . <b>2013</b> , 1,		34
793	Draft Genome Sequence of Vancomycin-Heteroresistant <i>Staphylococcus epidermidis</i> Strain UC7032, Isolated from Food. <b>2013</b> , 1,		3
792	Draft Genome Sequences of Strains of <i>Pasteurella multocida</i> Isolated from the United Kingdom and the United States. <b>2013</b> , 1,		
791	A second-generation assembly of the <i>Drosophila simulans</i> genome provides new insights into patterns of lineage-specific divergence. <i>Genome Research</i> , <b>2013</b> , 23, 89-98	9.7	120
790	Full-genome deep sequencing and phylogenetic analysis of novel human betacoronavirus. <b>2013</b> , 19, 736-42B		117
789	Application of a MAX-CUT Heuristic to the Contig Orientation Problem in Genome Assembly. <b>2013</b> ,		
788	Suffix-Tree Based Error Correction of NGS Reads Using Multiple Manifestations of an Error. <b>2013</b> ,		3
787	Draft genome sequence of <i>Frankia</i> sp. strain CN3, an atypical, noninfective (Nod-) ineffective (Fix-) isolate from <i>Coriaria nepalensis</i> . <b>2013</b> , 1, e0008513		46
786	The epidemic of extended-spectrum-βactamase-producing <i>Escherichia coli</i> ST131 is driven by a single highly pathogenic subclone, H30-Rx. <b>2013</b> , 4, e00377-13		288
785	Evolutionary dynamics of <i>Vibrio cholerae</i> O1 following a single-source introduction to Haiti. <b>2013</b> , 4,		106
784	Complete Genome Sequence of the Hyperthermophilic Sulfate-Reducing Bacterium <i>Thermodesulfobacterium geofontis</i> OPF15T. <b>2013</b> , 1, e0016213		4
783	Draft Genome Sequence of Uropathogenic <i>Escherichia coli</i> Strain J96. <b>2013</b> , 1,		3
782	Inbreeding depression in urban environments of the bird's nest fungus <i>Cyathus stercoreus</i> (Nidulariaceae: Basidiomycota). <b>2013</b> , 110, 355-62		5
781	Memory efficient minimum substring partitioning. <b>2013</b> , 6, 169-180		25
780	Phylogenomics and taxonomy of <i>Lecomtelleae</i> (Poaceae), an isolated panicoid lineage from Madagascar. <b>2013</b> , 112, 1057-66		42
779	Sequence comparative analysis using networks: software for evaluating de novo transcript assembly from next-generation sequencing. <b>2013</b> , 30, 1975-86		11
778	Genome Sequence of a Plant-Associated Bacterium, <i>Bacillus amyloliquefaciens</i> Strain UCMB5036. <b>2013</b> , 1, e0011113		13

777	Investigating the beneficial traits of <i>Trichoderma hamatum</i> GD12 for sustainable agriculture-insights from genomics. <b>2013</b> , 4, 258		62
776	DDBJ read annotation pipeline: a cloud computing-based pipeline for high-throughput analysis of next-generation sequencing data. <b>2013</b> , 20, 383-90		63
775	Mutualistic co-evolution of type III effector genes in <i>Sinorhizobium fredii</i> and <i>Bradyrhizobium japonicum</i> . <b>2013</b> , 9, e1003204		52
774	Extensive chromosomal reshuffling drives evolution of virulence in an asexual pathogen. <i>Genome Research</i> , <b>2013</b> , 23, 1271-82	9.7	221
773	Draft Genome Sequence and Description of <i>Janthinobacterium</i> sp. Strain CG3, a Psychrotolerant Antarctic Supraglacial Stream Bacterium. <b>2013</b> , 1,		8
772	Draft Genome Sequence of <i>Escherichia coli</i> Strain Nissle 1917 (Serovar O6:K5:H1). <b>2013</b> , 1, e0004713		25
771	Genome of the pathogen <i>Porphyromonas gingivalis</i> recovered from a biofilm in a hospital sink using a high-throughput single-cell genomics platform. <i>Genome Research</i> , <b>2013</b> , 23, 867-77	9.7	51
770	De Novo transcriptome sequencing reveals important molecular networks and metabolic pathways of the plant, <i>Chlorophytum borivillianum</i> . <b>2013</b> , 8, e83336		55
769	Dominant role of nucleotide substitution in the diversification of serotype 3 pneumococci over decades and during a single infection. <b>2013</b> , 9, e1003868		58
768	In vitro evolution of an archetypal enteropathogenic <i>Escherichia coli</i> strain. <b>2013</b> , 195, 4476-83		8
767	The fungus-growing termite <i>Macrotermes natalensis</i> harbors bacillaene-producing <i>Bacillus</i> sp. that inhibit potentially antagonistic fungi. <b>2013</b> , 3, 3250		78
766	Transmission of Hypervirulence traits via sexual reproduction within and between lineages of the human fungal pathogen <i>Cryptococcus gattii</i> . <b>2013</b> , 9, e1003771		37
765	Whole genome sequence of the <i>Treponema</i> Fribourg-Blanc: unspecified simian isolate is highly similar to the yaws subspecies. <b>2013</b> , 7, e2172		45
764	Combinatorial pooling enables selective sequencing of the barley gene space. <b>2013</b> , 9, e1003010		15
763	Detection of mixed infection from bacterial whole genome sequence data allows assessment of its role in <i>Clostridium difficile</i> transmission. <b>2013</b> , 9, e1003059		65
762	The genome and development-dependent transcriptomes of <i>Pyronema confluens</i> : a window into fungal evolution. <b>2013</b> , 9, e1003820		65
761	Improving genome assemblies and annotations for nonhuman primates. <b>2013</b> , 54, 144-53		20
760	Detecting and comparing non-coding RNAs in the high-throughput era. <b>2013</b> , 14, 15423-58		16

759	Comparative genome structure, secondary metabolite, and effector coding capacity across <i>Cochliobolus</i> pathogens. <b>2013</b> , 9, e1003233	161
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