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Genome sequence of *Frateuria aurantia* type strain (Kondô 67\(^T\)), a xanthomonade isolated from *Lilium auratium* Lindl.

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† In Memoriam of our colleague and friend Iain Anderson who prematurely passed away on Oct 14th 2012. Iain launched the archaeal tree of life sequencing program at the Joint Genome Institute and he was a key member of the team of scientists and engineers that developed IMG

**Keywords:** strictly aerobic, motile, rod-shaped, acetogenic, mesophilic, ‘*Acetobacter aurantius*’, Xanthomonadaceae, GEBA

*Frateuria aurantia* (ex Kondô and Ameyama 1958) Swings et al. 1980 is a member of the bispecific genus *Frateuria* in the family Xanthomonadaceae, which is already heavily targeted for non-type strain genome sequencing. Strain Kondô 67\(^T\) was initially (1958) identified as a member of 'Acetobacter aurantius', a name that was not considered for the approved list. Kondô 67\(^T\) was therefore later designated as the type strain of the newly proposed acetogenic species *Frateuria aurantia*. The strain is of interest because of its triterpenoids (hopane family). *F. aurantia* Kondô 67\(^T\) is the first member of the genus *Frateura* whose genome sequence has been deciphered, and here we describe the features of this organism, together with the complete genome sequence and annotation. The 3,603,458-bp long chromosome with its 3,200 protein-coding and 88 RNA genes is a part of the *Genomic Encyclopedia of Bacteria and Archaea* project.
Introduction

Strain Kondô 67T, also known as G-6T and as IFO 3245T (= DSM 6220 = ATCC 33424 = NBRC 3245) is the type strain of the species *Frateria aurantia* [1], the type species in the bispecific genus *Frateria* [1]. Kondô 67T was originally isolated from *Lilium auratum* Lindl and classified as a member of *Acetobacter aurantius* from which it was reclassified 22 years later as the type strain of the type species of *Frateria* [1]. The genus was named after the Belgian microbiologist Joseph Frateur (1903-1974) [1]; the species epithet is derived from the Neo-Latin adjective *aurantia*, referring to the gold-yellow color of the strain on MYP agar [1]. Strain Kondô 67T was characterized as 'acetogenic' [2] and as containing triterpenoids of the hopane family [3]. Here we present a summary classification and a set of features for *F. aurantia* Kondô 67T, together with the description of the genomic sequencing and annotation.

Classification and features

A representative genomic 16S rRNA gene sequence of strain Kondô 67T was compared using NCBI BLAST [4,5] under default settings (e.g., considering only the high-scoring segment pairs (HSPs) from the best 250 hits) with the most recent release of the Greengenes database [6] and the relative frequencies of taxa and keywords (reduced to their stem) [7] were determined, weighted by BLAST scores. The most frequently occurring genera were *Dyella* (34.3%), *Rhodanobacter* (24.0%), *Frateria* (19.6%), *Luteibacter* (11.9%) and 'Luteibactor' (3.7%) (105 hits in total). Regarding the eleven hits to sequences from members of the species, the average identity within HSPs was 99.6%, whereas the average coverage by HSPs was 100.0%. Among all other species, the one yielding the highest score was *Dyella ginsengisoli* (EF191354), which corresponded to an identity of 98.2% and an HSP coverage of 99.0%. (Note that the Greengenes database uses the INSDC (= EMBL/NCBI/DDBJ) annotation, which is not an authoritative source for nomenclature or classification.) The highest-scoring environmental sequence was HM556321 ('insect herbivore microbiome plant biomass-degrading capacity *Atta colombica* colony N1 fungus garden top clone TIBW663'), which showed an identity of 99.7% and an HSP coverage of 97.2%. The most frequently occurring keywords within the labels of all environmental samples which yielded hits were 'soil' (5.9%), 'sediment' (2.5%), 'microbi' (1.8%), 'enrich' (1.5%) and 'vent' (1.3%) (145 hits in total). The most frequently occurring keyword within the labels of those environmental samples which yielded hits of a higher score than the highest scoring species was 'atta, biomass-degrad, capac, colombica, coloni, fungu, garden, herbivor, insect, microbiom, plant, top' (8.3%) (6 hits in total), reflecting some of the known features of the strain's origin.

Figure 1 shows the phylogenetic neighborhood of *F. aurantia* in a 16S rRNA based tree. The sequences of the four identical 16S rRNA gene copies in the genome differ by one nucleotide from the previously published 16S rRNA sequence (AB091194).

*F. aurantia* Kondô 67T cells stain Gram-negative [1], were straight rod shaped, 0.5-0.7 μm in width and 0.7-3.5 μm in length (Figure 2) [1] and motile via polar flagella [1] (not visible in Figure 2). Cells occur singly or in pairs, rarely in filaments [1]. Cultures grow in dark, glistening, flat colonies with a soluble brown pigment [1]. They are oxidase positive and catalase negative [1]; physiological features and antibiotic susceptibilities were reported in great detail in [1]. Cells grow well at pH 3.6 and 34°C [1].

Chemotaxonomy

Besides trace amounts of diploptene and rearranged compounds like fern-7-ene [3], the main lipids isolated from DSM 6220T are *iso*-branched fatty acids and triterpenoids of the hopane family, such as bacteriohopanetetrol and derived hopanoid. The organism also produces ubiquinone Q8 [27].

Genome sequencing and annotation

Genome project history

This organism was selected for sequencing on the basis of its phylogenetic position [28], and is part of the *Genomic Encyclopedia of Bacteria and Archaea* project [29]. The genome project is deposited in the Genomes On Line Database [14] and the complete genome sequence is deposited in GenBank. Sequencing, finishing and annotation were performed by the DOE Joint Genome Institute (JGI) using state of the art sequencing technology [30]. A summary of the project information is shown in Table 2.
Figure 1. Phylogenetic tree highlighting the position of *F. aurantia* relative to the type strains of the other species within the family *Xanthomonadaceae*. The tree was inferred from 1,431 aligned characters [8,9] of the 16S rRNA gene sequence under the maximum likelihood (ML) criterion [10]. Rooting was done initially using the midpoint method [11] and then checked for its agreement with the current classification (Table 1). The branches are scaled in terms of the expected number of substitutions per site. Numbers adjacent to the branches are support values from 750 ML bootstrap replicates [12] (left) and from 1,000 maximum-parsimony bootstrap replicates [13] (right) if larger than 60%. Lineages with type strain genome sequencing projects registered in GOLD [14] are labeled with one asterisk, those also listed as 'Complete and Published' with two asterisks.

Figure 2. Scanning electron micrograph of *F. aurantia* Kondô 67T
Table 1. Classification and general features of *F. aurantia* Kondô 67T according to the MIGS recommendations [15] (published by the Genome Standards Consortium [16]) and NamesforLife [17].

| MIGS ID | Property                      | Term                                      | Evidence code |
|---------|-------------------------------|-------------------------------------------|---------------|
|         | Current classification        | Species *Frateuria aurantia*              | TAS [1]       |
|         | Type strain Kondô 67 = G-6 = IFO 3245 |                            | TAS [1]       |
|         | Gram stain                    | negative                                  | TAS [1]       |
|         | Cell shape                    | rod-shaped, mostly strait                 | TAS [1]       |
|         | Motility                      | motile                                    | TAS [1]       |
|         | Sporulation                   | not reported                              |               |
|         | Temperature range             | mesophile                                 | TAS [1]       |
|         | Optimum temperature           | 30°C                                      | TAS [1]       |
|         | Salinity                      | 0.2 - 2% NaCl (w/v)                       | TAS [1]       |
| MIGS-22 | Oxygen requirement            | aerobe                                    | TAS [1]       |
|         | Carbon source                 | glucose, yeast extract, mannitol, peptone | TAS [1]       |
|         | Energy metabolism             | organoheterotroph                         | TAS [1]       |
| MIGS-6  | Habitat                       | *Lilium auratum*                          | TAS [1]       |
| MIGS-15 | Biotic relationship           | host-associated                           | TAS [1]       |
| MIGS-14 | Pathogenicity                 | none                                      | NAS           |
|         | Biosafety level               | 1                                         | TAS [24]      |
| MIGS-23.1| Isolation                    | from *Lilium auratum* Lindl               | TAS [25]      |
| MIGS-4  | Geographic location           | Kawasaki, Japan                           | TAS [1]       |
| MIGS-5  | Sample collection time        | 1958 or before                            | TAS [25]      |
| MIGS-4.1| Latitude                      | 35.50                                     | TAS [1]       |
| MIGS-4.2| Longitude                     | 139.77                                    | TAS [1]       |
| MIGS-4.3| Depth                        | not reported                              |               |
| MIGS-4.4| Altitude                     | not reported                              |               |

Evidence codes - TAS: Traceable Author Statement (i.e., a direct report exists in the literature); NAS: Non-traceable Author Statement (i.e., not directly observed for the living, isolated sample, but based on a generally accepted property for the species, or anecdotal evidence). Evidence codes are from the Gene Ontology project [26].
Table 2. Genome sequencing project information

| MIGS ID | Property                | Term                                                                 |
|---------|-------------------------|----------------------------------------------------------------------|
| MIGS-31 | Finishing quality       | Finished                                                              |
| MIGS-28 | Libraries used          | Two genomic libraries: one 454 PE library (7.5 kb insert size), one Illumina library |
| MIGS-29 | Sequencing platforms    | Illumina GAii, 454 GS FLX Titanium                                    |
| MIGS-31.2 | Sequencing coverage    | 537.4 × Illumina; 8.6 × pyrosequence                                |
| MIGS-30 | Assemblers              | Newbler version 2.3-PreRelease-6/30/2009, Velvet 1.0.13, phrap version SPS - 4.24 |
| MIGS-32 | Gene calling method     | Prodigal                                                              |

INSDC ID CP003350
GenBank Date of Release June 14, 2012
GOLD ID Gc02155
NCBI project ID 64505
Database: IMG 2509601034

MIGS-13 Source material identifier DSM 6220
Project relevance Tree of Life, GEBA

Growth conditions and DNA isolation

F. aurantia strain Kondô 67°, DSM 6220, was grown in DSMZ medium 360 (YPM medium) [31] at 30°C. DNA was isolated from 0.5-1 g of cell paste using standard procedures at the DSMZ DNA laboratory and quality control processes requested by the sequencing center (JGI). DNA is available through the DNA Bank Network [32].

Genome sequencing and assembly

The genome was sequenced using a combination of Illumina and 454 sequencing platforms. All general aspects of library construction and sequencing can be found at the JGI website [33]. Pyrosequencing reads were assembled using the Newbler assembler (Roche). The initial Newbler assembly consisting of 36 contigs in one scaffold was converted into a phrap [34] assembly by making fake reads from the consensus, to collect the read pairs in the 454 paired end library. Illumina GAii sequencing data (2,074.3 Mb) was assembled with Velvet [35] and the consensus sequences were shredded into 1.5 kb overlapped fake reads and assembled together with the 454 data. The 454 draft assembly was based on 63.7Mb 454 draft data. Newbler parameters are -consed -a 50 -l 350 -g -m -ml 20. The Phred/Phrap/Consed software package [34] was used for sequence assembly and quality assessment in the subsequent finishing process. After the shotgun stage, reads were assembled with parallel phrap (High Performance Software, LLC). Possible mis-assemblies were corrected with gapResolution [33], Dupfinisher [36], or sequencing cloned bridging PCR fragments with subcloning. Gaps between contigs were closed by editing in Consed, by PCR and by Bubble PCR primer walks (J.-F. Chang, unpublished). A total of 43 additional reactions and one shatter library were necessary to close gaps and to raise the quality of the final sequence. Illumina reads were also used to correct potential base errors and increase consensus quality using a software Polisher developed at JGI [37]. The error rate of the final genome sequence is less than 1 in 100,000.
Together, the combination of the Illumina and 454 sequencing platforms provided 546.0 × coverage of the genome. The final assembly contained 163,130 pyrosequence and 25,455,174 Illumina reads.

**Genome annotation**

Genes were identified using Prodigal [38] as part of the DOE-JGI [39] genome annotation pipeline, followed by a round of manual curation using the JGI GenePRIMP pipeline [40]. The predicted CDSs were translated and used to search the National Center for Biotechnology Information (NCBI) non-redundant database, UniProt, TIGRFam, Pfam, PRIAM, KEGG, COG, and InterPro databases. These data sources were combined to assert a product description for each predicted protein. Additional gene prediction analysis and functional annotation were performed within the Integrated Microbial Genomes - Expert Review (IMG-ER) platform [41].

**Genome properties**

The genome consists of a 3,603,458 bp long circular chromosome with a G+C content of 63.4% (Table 3 and Figure 3). Of the 3,288 genes predicted, 3,200 were protein-coding genes, and 88 RNAs; 99 pseudogenes were also identified. The majority of the protein-coding genes (79.6%) were assigned a putative function while the remaining ones were annotated as hypothetical proteins. The distribution of genes into COGs functional categories is presented in Table 4.

### Table 3. Genome Statistics

| Attribute                        | Value   | % of Total |
|----------------------------------|---------|------------|
| Genome size (bp)                 | 3,603,458 | 100.00%   |
| DNA coding region (bp)           | 3,189,580 | 88.51%    |
| DNA G+C content (bp)             | 2,284,441 | 63.40%    |
| Number of replicons              | 1       |            |
| Extrachromosomal elements        | 0       |            |
| Total genes                      | 3,288   | 100.00%    |
| RNA genes                        | 88      | 2.68%      |
| rRNA operons                     | 4       |            |
| tRNA genes                       | 73      | 2.22%      |
| Protein-coding genes             | 3,200   | 97.32%     |
| Pseudo genes                     | 99      | 3.01%      |
| Genes with function prediction (proteins) | 2,616 | 79.56%    |
| Genes in paralog clusters        | 1,350   | 41.06%     |
| Genes assigned to COGs           | 2,610   | 79.38%     |
| Genes assigned Pfam domains      | 2,724   | 82.85%     |
| Genes with signal peptides       | 313     | 9.52%      |
| Genes with transmembrane helices | 722     | 21.96%     |
| CRISPR repeats                   | 1       |            |
Figure 3. Graphical map of the chromosome. From outside to center: Genes on forward strand (colored by COG categories), Genes on reverse strand (colored by COG categories), RNA genes (tRNAs green, rRNAs red, other RNAs black), GC content(black), GC skew (purple/olive).
Table 4. Number of genes associated with the general COG functional categories

| Code | value | %age | Description                                                      |
|------|-------|------|------------------------------------------------------------------|
| J    | 167   | 5.7  | Translation, ribosomal structure and biogenesis                  |
| A    | 1     | 0.0  | RNA processing and modification                                  |
| K    | 192   | 6.6  | Transcription                                                    |
| L    | 145   | 5.0  | Replication, recombination and repair                             |
| B    | 1     | 0.0  | Chromatin structure and dynamics                                  |
| D    | 30    | 1.0  | Cell cycle control, cell division, chromosome partitioning      |
| Y    | 0     | 0.0  | Nuclear structure                                                |
| V    | 56    | 1.9  | Defense mechanisms                                               |
| T    | 129   | 4.4  | Signal transduction mechanisms                                   |
| M    | 214   | 7.3  | Cell wall/membrane biogenesis                                    |
| N    | 92    | 3.1  | Cell motility                                                    |
| Z    | 0     | 0.0  | Cytoskeleton                                                     |
| W    | 0     | 0.0  | Extracellular structures                                         |
| U    | 112   | 3.8  | Intracellular trafficking and secretion, and vesicular transport |
| O    | 133   | 4.5  | Posttranslational modification, protein turnover, chaperones     |
| C    | 186   | 6.4  | Energy production and conversion                                 |
| G    | 170   | 5.8  | Carbohydrate transport and metabolism                            |
| E    | 209   | 7.1  | Amino acid transport and metabolism                              |
| F    | 68    | 2.3  | Nucleotide transport and metabolism                              |
| H    | 143   | 4.9  | Coenzyme transport and metabolism                                |
| I    | 101   | 3.5  | Lipid transport and metabolism                                   |
| P    | 146   | 5.0  | Inorganic ion transport and metabolism                           |
| Q    | 63    | 2.2  | Secondary metabolites biosynthesis, transport and catabolism     |
| R    | 323   | 11.0 | General function prediction only                                  |
| S    | 246   | 8.4  | Function unknown                                                 |
| -    | 678   | 20.6 | Not in COGs                                                      |

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References

1. Swings J, Gillis M, Kersters K, De Vos P, Gosselé F, de Ley J. *Frateuria*, a new genus for *"Acetobacter aurantius"*. *Int J Syst Bacteriol* 1980; 30:547-556. [http://dx.doi.org/10.1099/00207713-30-3-547](http://dx.doi.org/10.1099/00207713-30-3-547)

2. Johnson DB, Rolfe S, Hallberg KB, Iversen E. Isolation and phylogenetic characterization of aci-dophilic microorganisms indigenous to acidic drainage waters at an abandoned Norwegian copper mine. *Environ Microbiol* 2001; 3:630-637.
3. Joyceux C, Fouchard S, Llopiz P, Neunlist S. Influence of the temperature and the growth phase on the hopanoids and fatty acids content of Frateuria aurantia (DSMZ 6220). FEMS Microbiol Ecol 2004; 47:371-379. PubMed http://dx.doi.org/10.1016/S0168-6496(03)00302-7

4. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. J Mol Biol 1990; 215:403-410. PubMed http://dx.doi.org/10.1012/AEM.03006-05

5. Korf I, Yandell M, Bedell J. BLAST, O'Reilly, Sinauer Associates, Sunderland, 2002.

6. DeSantis TZ, Hugenholtz P, Larsen N, Rojas M, Brodie EL, Keller K, Huber T, Dalevi D, Hu P, Andersen GL. Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. Appl Environ Microbiol 2006; 72:5069-5072. PubMed http://dx.doi.org/10.1099/ijs.0.64108-0

7. Porter MF. An algorithm for suffix stripping. Program: electronic library and information systems 1980; 14:130-137.

8. Lee C, Grasso C, Sharlow MF. Multiple sequence alignment using partial order graphs. Bioinformatics 2002; 18:452-464. PubMed http://dx.doi.org/10.1093/bioinformatics/18.3.452

9. Castresana J. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. Mol Biol Evol 2000; 17:540-552. PubMed http://dx.doi.org/10.1093/oxfordjournals.molbev.a026334

10. Stamatakis A, Hoover P, Rougemont J. A rapid bootstrap algorithm for the RAxML web servers. Syst Biol 2008; 57:578-771. PubMed http://dx.doi.org/10.1080/10635150802429642

11. Hess PN, De Moraes Russo CA. An empirical test of the midpoint rooting method. Biol J Linn Soc Lond 2007; 92:669-674. http://dx.doi.org/10.1111/j.1095-8312.2007.00864.x

12. Pattengale ND, Alipour M, Bininda-Emonds ORP, Moret BME, Stamatakis A. How many bootstrap replicates are necessary? Lect Notes Comput Sci 2009; 5541:184-200. http://dx.doi.org/10.1007/978-3-642-02008-7_13

13. Swofford DL. PAUP*: Phylogenetic Analysis Using Parsimony (*and Other Methods), Version 4.0 b10. Sinauer Associates, Sunderland, 2002.

14. Pagani I, Liolios K, Jansson J, Chen IM, Smirnova T, Nosrat B, Markowitz VM, Kyrpides NC. The Genomes OnLine Database (GOLD) v.4: status of genomic and metagenomic projects and their associated metadata. Nucleic Acids Res 2012; 40:D571-D579. PubMed http://dx.doi.org/10.1093/nar/gkr1100

15. Field D, Garrity G, Gray T, Morrison N, Selengut J, Sterk P, Tatusova T, Thomson N, Allen MJ, Angiuoli SV, et al. The minimum information about a genome sequence (MIGS) specification. Nat Biotechnol 2008; 26:541-547. PubMed http://dx.doi.org/10.1038/nbt1360

16. Field D, Amaral-Zettler L, Cochrane G, Cole JR, Dwyndt P, Garrity GM, Gilbert J, Glöckner FO, Hirschman L, Karsch-Mizrachi I, et al. PLoS Biol 2011; 9:e1001088. PubMed http://dx.doi.org/10.1371/journal.pbio.1001088

17. Garrity G. NamesforLife. BrowserTool takes expertise out of the database and puts it right in the browser. Microbiol Today 2010; 37:9.

18. Woese CR, Kandler O, Wheelis ML. Towards a natural system of organisms. Proposal for the domains Archaea and Bacteria. Proc Natl Acad Sci USA 1990; 87:4576-4579. PubMed http://dx.doi.org/10.1073/pnas.87.12.4576

19. Garrity GM, Bell JA, Lilburn T. Phylum XIV. Proteobacteria phyl. nov. In: Garrity GM, Brenner DJ, Krieg NR, Staley JT (eds), Bergey's Manual of Systematic Bacteriology, Second Edition, Volume 2, Part B, Springer, New York, 2005, p. 1.

20. Validation of publication of new names and new combinations previously effectively published outside the IJSEM. List no. 106. Int J Syst Evol Microbiol 2005; 55:2235-2238. http://dx.doi.org/10.1099/ijs.0.64108-0

21. Garrity GM, Bell JA, Lilburn T. Class III. Gammaproteobacteria class. nov. In: Garrity GM, Brenner DJ, Krieg NR, Staley JT (eds), Bergey's Manual of Systematic Bacteriology, Second Edition, Volume 2, Part B, Springer, New York, 2005, p. 1.

22. Saddler GS, Bradbury JF. Order III. Xanthomonadales ord. nov. In: Garrity GM, Brenner DJ, Krieg NR, Staley JT (eds), Bergey's Manual of Systematic Bacteriology, Second Edition, Volume 2, Part B, Springer, New York, 2005, p. 63.

23. Zhang JY, Liu XY, Liu SJ. Frateuria terrea sp. nov., isolated from forest soil, and emended description of the genus Frateuria. Int J Syst Evol Microbiol
24. B. A. Kondo 2010, Classification of bacteria and archaea in risk groups. http://www.baua.de TRBA 466, p. 89.

25. Kondô K, Ameyama M. Carbohydrate metabolism by Acetobacter species. I. Oxidative activity for various carbohydrates. Bull Agric Chem Soc Jpn 1958; 22:369-372. http://dx.doi.org/10.1271/bbb1924.22.369

26. Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, Davis AP, Dolinski K, Dwight SS, Eppig JT, et al. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. Nat Genet 2000; 25:25-29. PubMed http://dx.doi.org/10.1038/75556

27. Yamada Y, Okada Y, Kondô K. Isolation and characterization of “polarly flaggellated intermediate strains” in acetic bacteria. J Gen Appl Microbiol 1976; 22:237-245. http://dx.doi.org/10.2323/jgam.22.237

28. Klenk HP, Göker M. En route to a genome-based classification of Archaea and Bacteria? Syst Appl Microbiol 2010; 33:175-182. PubMed http://dx.doi.org/10.1016/j.syapm.2010.03.003

29. Wu D, Hugenholtz P, Mavromatis K, Pukall R, Dalin E, Ivanova NN, Kunin V, Goodwin L, Wu M, Tindall BJ, et al. A phylogeny-driven Genomic Encyclopedia of Bacteria and Archaea. Nature 2009; 462:1056-1060. PubMed http://dx.doi.org/10.1038/nature08656

30. Mavromatis K, Land ML, Brettin TS, Quest DJ, Copeland A, Clum A, Goodwin L, Woyke T, Lapidus A, Klenk HP, et al. The fast changing landscape of sequencing technologies and their impact on microbial genome assemblies and annotation. PloS ONE 2012; 7:e48837. PubMed http://dx.doi.org/10.1371/journal.pone.0048837

31. List of growth media used at DSMZ: http://www.dsmz.de/catalogues/catalogue-microorganisms/culture-technology/list-of-media-for-microorganisms.html.

32. Gemeinholzer B, Dröge G, Zetzsche H, Haszprunar G, Klenk HP, Güntsch A, Berendsohn WG, Wägele JW. The DNA Bank Network: the start from a German initiative. Biopreserv Biobank 2011; 9:51-55. http://dx.doi.org/10.1089/bio.2010.0029

33. The DOE Joint Genome Institute. www.jgi.doe.gov

34. Phrap and Phred for Windows. MacOS, Linux, and Unix. www.phrap.com

35. Zerbino DR, Birney E. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res 2008; 18:821-829. PubMed http://dx.doi.org/10.1101/gr.074492.107

36. Han C, Chain P. Finishing repeat regions automatically with Dupfinisher. In: Proceedings of the 2006 international conference on bioinformatics & computational biology. Arabnia HR, Valafar H (eds), CSREA Press. June 26-29, 2006: 141-146.

37. Lapidus A, LaButti K, Foster B, Lowry S, Trong S, Goltzman E. POLISHER: An effective tool for using ultra short reads in microbial genome assembly and finishing. AGBT, Marco Island, FL, 2008.

38. Hyatt D, Chen GL, Locascio PF, Land ML, Larimer FW, Hauser LJ. Prodigal Prokaryotic Dynamic Programming Genefinding Algorithm. BMC Bioinformatics 2010; 11:119. PubMed http://dx.doi.org/10.1186/1471-2105-11-119

39. Mavromatis K, Ivanova NN, Chen IM, Szeto E, Markowitz VM, Kyrpides NC. The DOE-JGI Standard operating procedure for the annotations of microbial genomes. Stand Genomic Sci 2009; 1:63-67. PubMed http://dx.doi.org/10.4056/sigs.632

40. Pati A, Ivanova N, Mikhailova N, Ovchinkova G, Hooper SD, Lykidis A, Kyrpides NC. GenePRIMP: A Gene Prediction Improvement Pipeline for microbial genomes. Nat Methods 2010; 7:455-457. PubMed http://dx.doi.org/10.1038/nmeth.1457

41. Markowitz VM, Ivanova NN, Chen IM, Chu K, Kyrpides NC. IMG ER: a system for microbial genome annotation expert review and curation. Bioinformatics 2009; 25:2271-2278. PubMed http://dx.doi.org/10.1093/bioinformatics/btp393