

A computational pipeline for whole genome sequencing analysis of *Mycobacterium tuberculosis* complex isolates

TBseq

Version 1.0.0 (2017-03-22)

TBseq release

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VERSION.pdf	(v1.0.0)
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TBreads	(v1.0.0)
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samtools	(v1.3.1)
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IGV-tools	(v2.3.88)
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BWA	(v0.7.15)
GATK	(v3.6)

TBseq/var/

cat/

MTB_Gene_Categories.txt	(v1.0)
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ref/

M._abscessus_CIP-104536T_2014-02-03.fasta
M._abscessus_CIP-104536T_2014-02-03_genes.txt
M._chimaera_DSM44623_2016-01-28.fasta
M._chimaera_DSM44623_2016-01-28_genes.txt
M._fortuitum_CT6_2016-01-08.fasta
M._fortuitum_CT6_2016-01-08_genes.txt
M._tuberculosis_H37Rv_2015-11-13.fasta
M._tuberculosis_H37Rv_2015-11-13_genes.txt

res/

Base_Calibration_List.vcf	(v1.0.0)
Base_Calibration_List.vcf.idx	(v1.0.0)
MTB_Extended_Resistance_Mediating.txt	(v1.0.0)
MTB_Resistance_Mediating.txt	(v1.0.0)