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SUPPORTING INFECTIOUS DISEASE RESEARCH

Staphylococcus aureus (MRSA), Strain COL Gateway[®] Clone Set, Recombinant in *Escherichia coli*, Plate 10

Catalog No. NR-19506

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For research use only. Not for human use.

Contributor:

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

Manufacturer:

BEI Resources

Product Description:

Production in the 96-well format has increased risk of crosscontamination between adjacent wells. Individual clones should be purified (e.g. single colony isolation and purification using good microbiological practices) and sequence-verified prior to use. BEI Resources does not confirm or validate individual mutants provided by the contributor.

The methicillin-resistant *Staphylococcus aureus* (*S. aureus*), strain COL Gateway[®] clone set consists of 25 plates which contain 2343 sequence validated clones from *S. aureus* strain COL cloned in *Escherichia coli* (*E. coli*) DH10B-T1 cells. Each open reading frame was constructed in vector $pDONR^{TM}221$ (Invitrogen^{TM}) with a native start codon and no stop codon. The sequence was validated by full length sequencing of each clone with greater than 1X coverage and a mutation rate of less than 0.2%. Detailed information about each clone is shown in Table 1.

Information related to the use of Gateway[®] Clones can be obtained from InvitrogenTM. Recombination was facilitated through an *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONRTM221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 to facilitate gene transfer into a destination vector, M13 forward and reverse priming sites for sequencing and a kanamycin resistance gene for selection. Please refer to the InvitrogenTM <u>Gateway[®] Technology Manual</u> for additional details.

Material Provided:

Every inoculated well of the 96-well plate contains approximately 60 μ L of *E. coli* culture (strain DH10B-T1) in Luria Bertani (LB) broth containing 50 μ g/mL kanamycin supplemented with 15% glycerol.

Packaging/Storage:

NR-19506 was packaged aseptically in a 96-well plate. The product is provided frozen and should be stored at -80°C or

colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

Growth Conditions:

Media: LB broth or agar containing 50 µg/mL kanamycin.

Incubation:

Temperature: *E. coli*, strain DH10B-T1 clones should be grown at 37°C.

Atmosphere: Aerobic

Propagation:

- 1. Scrape top of frozen well with a pipette tip and streak onto agar plate.
- 2. Incubate the plates at 37°C for 18 to 24 hours.

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: *Staphylococcus aureus* (MRSA), Strain COL Gateway[®] Clone Set, Recombinant in *Escherichia coli*, Plate 10, NR-19506."

Biosafety Level: 1

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. <u>Biosafety in</u> <u>Microbiological and Biomedical Laboratories</u>. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see <u>www.cdc.gov/biosafety/publications/bmbl5/index.htm</u>.

Disclaimers:

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SUPPORTING INFECTIOUS DISEASE RESEARCH

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References:

 Gill, S. R., et al. "Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an Early Methicillin-Resistant *Staphylococcus aureus* Strain and a Biofilm-Producing Methicillin-Resistant *Staphylococcus epidermidis* Strain." J. Bacteriol. 187 (2005): 2426-2438. PubMed: 15774886.

ATCC[®] is a trademark of the American Type Culture Collection.



| Clone | Well | ORF | Locus ID | Description (Gene name) | Accession | Average Depth |
|-------|--------------|--------|--------------------------------------|---|-------------|---------------|
| | Position | Length | | | Number | of Coverage |
| 1917 | A01 | 589 | SACOL2275 | BioY family protein | YP_187082.1 | 3.263157895 |
| 1920 | A02 | 589 | SACOL2709 | conserved hypothetical protein | YP_187495.1 | 3.132427844 |
| 1021 | 1921 A03 592 | | capsular polysaccharide biosynthesis | VD 105040 1 | 2 126924224 | |
| 1921 | | 592 | SACULU140 | galactosyltransferase Cap5M | 1F_100040.1 | 3.130024324 |
| 1924 | A04 | 592 | SACOL0908 | hypothetical protein | YP_185779.1 | 3.527027027 |
| 1925 | A05 | 592 | SACOL1136 | conserved hypothetical protein | YP_186000.1 | 3.565878378 |
| 1927 | A06 | 592 | SACOL1587 | translation elongation factor P | YP_186427.1 | 4.297297297 |
| 1929 | A07 | 592 | SACOL1896 | conserved hypothetical protein | YP_186722.1 | 3.518581081 |
| 1931 | A08 | 592 | SACOL1990 | conserved hypothetical protein | YP_186814.1 | 3.22972973 |
| 1933 | A09 | 592 | SACOL2593 | transcriptional regulator, TetR family | YP_187384.1 | 4.22972973 |
| 1938 | A10 | 595 | SACOL0678 | integrase/recombinase, phage integrase family | YP_185561.1 | 2.416806723 |
| 1939 | A11 | 595 | SACOL1711 | DNA-3-methyladenine glycosylase | YP_186550.1 | 4.275630252 |
| 1942 | A12 | 595 | SACOL1858 | hypothetical protein | YP_186686.1 | 2.803361345 |
| 1943 | B01 | 595 | SACOL1981 | isochorismatase family protein | YP_186805.1 | 4.151260504 |
| 1945 | B02 | 595 | SACOL2066 | K+-transporting ATPase, C subunit | YP_186882.1 | 4.240336134 |
| 1947 | B03 | 595 | SACOL2667 | isochorismatase family protein | YP 187455.1 | 4.282352941 |
| 1949 | B04 | 595 | SACOL2688 | intercellular adhesion regulator | YP 187475.1 | 3.537815126 |
| 1951 | B05 | 598 | SACOL1202 | YImF protein | YP 186064.1 | 4.284280936 |
| 1953 | B06 | 598 | SACOL1485 | conserved hypothetical protein | YP 186330.1 | 3.242474916 |
| 1955 | B07 | 598 | SACOL1811 | conserved hypothetical protein | YP_186644.1 | 3.558528428 |
| 1957 | B08 | 598 | SACOL1992 | conserved hypothetical protein | YP 186816.1 | 3.52173913 |
| 1959 | B09 | 598 | SACOL2630 | conserved hypothetical protein | YP_187419.1 | 3.254180602 |
| 1961 | B10 | 601 | SACOL0410 | FMN reductase-related protein | YP 185302.1 | 2.803660566 |
| 1963 | B11 | 601 | SACOL0568 | conserved hypothetical protein | YP_185456.1 | 4.25124792 |
| 1965 | B12 | 601 | SACOL0607 | azoreductase | YP_185492.1 | 2.108153078 |
| 1969 | C02 | 601 | SACOL1081 | phosphoribosylglycinamide formyltransferase | YP_185945.1 | 3.269550749 |
| 4074 | 000 | 601 | | anthranilate synthase, glutamine | | 4.254575707 |
| 1971 | C03 | | OUT SACULI404 | amidotransferase, component II | TP_180250.1 | |
| 1974 | C04 | 601 | SACOL1870 | hypothetical protein | YP_186698.1 | 3.845257903 |
| 1975 | C05 | 604 | SACOL0452 | alkyl hydroperoxide reductase, C subunit | YP_185342.1 | 4.286423841 |
| 1977 | C06 | 604 | SACOL0580 | conserved hypothetical protein | YP_185466.1 | 3.533112583 |
| 1979 | C07 | 604 | SACOL0864 | conserved domain protein | YP_185737.1 | 4.23013245 |
| 1981 | C08 | 604 | SACOL0906 | phage terminase family protein | YP_185777.1 | 3.544701987 |
| 1983 | C09 | 604 | 04 SACOL1650 | nicotinate (nicotinamide) nucleotide | YP_186490.1 | 4.248344371 |
| | | 004 | | adenylyltransferase | | |
| 1985 | C10 | 604 | SACOL2023 | accessory gene regulator protein B | YP_186842.1 | 3.561258278 |
| 1987 | C11 | 604 | SACOL2320 | conserved hypothetical protein | YP_187127.1 | 3.627483444 |
| 1989 | C12 | 604 | SACOL2732 | transcriptional regulator, putative | YP_187518.1 | 3.541390728 |
| 1991 | D01 | 607 | SACOL0199 | conserved hypothetical protein | YP_185098.1 | 3.507413509 |
| 1993 | D02 | 607 | SACOL0444 | lipoprotein, putative | YP_185334.1 | 3.504118616 |

Table 1: Staphylococcus aureus, Strain COL Gateway[®] Clones, Plate 10 (ZSAJJ)

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Product Information Sheet for NR-19506

SUPPORTING INFECTIOUS DISEASE RESEARCH

| Position Length Position Length Position Correspendence 1995 D03 607 SACOL0546 peptidyl-IRNA hydrolase YP 185434.1 3.55022320 1999 D05 607 SACOL1512 conserved hypothetical protein YP 18560.1 2.19024 2003 D07 607 SACOL2049 | Clone | Well | ORF | Locus ID | Description (Gene name) | Accession | Average Depth |
|---|-------|----------|--------|-----------|--|-------------|---------------|
| 1995 D03 607 SACOL0646 peptidyl-RNA hydrolase YP 185689.1 3.850082272 1997 D04 607 SACOL071242 conserved hypothetical protein YP 185689.1 3.552125206 2001 D06 607 SACOL1742 conserved hypothetical protein YP 188366.1 2.71826666 2003 D07 607 SACOL1696 conserved hypothetical protein YP 188346.1 3.42916022 2006 D08 610 SACOL1696 conserved hypothetical protein YP 188346.1 3.109836666 2011 D11 610 SACOL0458 xanthine phosphorbosyltransferase YP 185706.1 3.872409836 2017 E02 613 SACOL0468 xanthine phosphorbosyltransferase YP 18616.1 3.08319739 2021 E04 613 SACOL070 imidazole glycerol-phosphate synthase, glytamine andotransferase YP 187486.1 4.254486134 2023 E06 616 SACOL0760 DAK24 coman protein YP | | Position | Length | | | Number | of Coverage |
| 1997 D04 607 SACOL1242 conserved hypothetical protein YP 186689.1 3.53212520 2001 D06 607 SACOL1512 conserved hypothetical protein YP 186336.1 2.11826655 2003 D07 607 SACOL204 3.453714992 2.053714992 2006 D08 610 SACOL1608 conserved hypothetical protein YP 186336.1 3.532768885 2007 D09 610 SACOL1608 conserved hypothetical protein YP 185306.1 3.875748923 2011 D11 610 SACOL0191 M23/M37 peptidase domain protein YP 185304.3 3.52525481 2017 E02 613 SACOL0492 pathogenicity island protein YP_185773.1 3.43230016 2019 E03 613 SACOL2699 imidazel glycorol Phosphate synthase, glutamine amidotransferase subunit YP_186154.1 3.8317329 2027 E06 616 SACOL0490 DAK2 domain protein YP_186154.1 3.8317329 2028 < | 1995 | D03 | 607 | SACOL0546 | peptidyl-tRNA hydrolase | YP_185434.1 | 3.850082372 |
| 1999 DO5 607 SACOL1242 conserved hypothetical protein YP 186102-1 4.18604612 2001 DO6 607 SACOL12049 3-lsopropylmalate dehydratase, small subunit YP 186356.1 2.718226655 2005 DO6 610 SACOL1086 conserved hypothetical protein YP 186363.4 2.49180328 2007 D09 610 SACOL10202 conserved hypothetical protein YP 185363.1 3.352786855 2014 D12 613 SACOL0459 xanthine phosphoribosyltransferase YP 185348.1 3.522285431 2017 E02 613 SACOL0200 pathogenicity lisaling protein YP 1857343 3.43220016 2019 E03 613 SACOL2090 imidazole glycerol phosphate synthase, glutamine amidornansferase subunit YP 187486.1 3.83197389 2021 E04 613 SACOL20700 imidazoleglycerol phosphate dhydratase YP 187486.1 3.84197389 2022 E06 616 SACOL14747 p | 1997 | D04 | 607 | SACOL0815 | ribosomal subunit interface protein | YP_185689.1 | 3.532125206 |
| 2001 D06 607 SACOL204 3-Isogrophymalate delytratae, small subunit YP_186356.1 2.71826655 2005 D08 610 SACOL2047 conserved hypothetical protein YP_186336.1 3.583714992 2007 D09 610 SACOL1068 conserved hypothetical protein YP_18536.1 3.583786855 2009 D10 610 SACOL1902 conserved hypothetical protein YP_18536.1 3.10933066 2011 D11 610 SACOL1902 phypothetical protein YP_18536.1 3.872540933 2015 E01 613 SACOL0902 pathogencity lead protein YP_18573.1 3.643230016 2017 E02 613 SACOL1902 CDP-tidytypeord-ghycon3-sphosphate 3- hyposphaleytransferase subunit YP_187485.1 4.264486134 2021 E04 613 SACOL2099 imidazolegycerol-phosphate 3-thypothetical protein YP_187485.1 4.264486134 2025 E06 616 SACOL1047 phosphalesythhase YP_187485.1 4.264486134 2026 E06 <td< td=""><td>1999</td><td>D05</td><td>607</td><td>SACOL1242</td><td>conserved hypothetical protein</td><td>YP_186102.1</td><td>4.196046129</td></td<> | 1999 | D05 | 607 | SACOL1242 | conserved hypothetical protein | YP_186102.1 | 4.196046129 |
| 2003 D07 607 SACOL2049 3-lsopropylmalate dehydratase, small subunit YP 186866.1 3.538714992 2007 D09 610 SACOL1086 conserved hypothetical protein YP 185950.1 3.53278685 2009 D10 610 SACOL1022 hypothetical protein YP 185346.1 3.108380666 2011 D11 610 SACOL0458 xanthine phosphoribosyltransferase YP 185348.1 3.522285481 2017 E02 613 SACOL0209 phosphatidytransferase YP 186734.1 3.54228016 2019 E03 613 SACOL2099 imidazole glycerol phosphate synthase, glutamine amidornaferase subunit YP 187486.1 3.83197399 2021 E04 613 SACOL2700 imidazoleglycerol phosphate dhydratase YP 187486.1 3.83197389 2022 E06 616 SACOL1700 DAK2 domain protein YP 185843.1 3.25245481 2023 E06 619 SACOL0769 conserved hypothetical protein <td>2001</td> <td>D06</td> <td>607</td> <td>SACOL1512</td> <td>conserved hypothetical protein</td> <td>YP_186356.1</td> <td>2.718286656</td> | 2001 | D06 | 607 | SACOL1512 | conserved hypothetical protein | YP_186356.1 | 2.718286656 |
| 2005 D08 610 SACOL0967 conserved hypothetical protein YP_185836.1 4.249180328 2007 D09 610 SACOL1502 conserved hypothetical protein YP_185950.1 3.512786885 2011 D11 610 SACOL720 hypothetical protein YP_185061.1 3.5742786885 2014 D12 613 SACOL468 xantine phosphotiosyttansferase YP_18573.1 3.543230016 2015 E01 613 SACOL4902 pathogenicity island protein YP_18573.1 3.543230016 2017 E02 613 SACOL4902 phosphatidytransferase subunit YP_187486.1 4.254486134 2021 E04 613 SACOL2700 imidazole glycerol-phosphate dhydratase YP_187486.1 3.8471139 2022 E06 616 SACOL0708 DAK2 doma protein YP_186486.1 3.13474026 2028 E08 619 SACOL0708 DAK2 doma protein YP_18648.1 3.13474026 2023 E10 619 SACOL0708 DAK2 doma protein | 2003 | D07 | 607 | SACOL2049 | 3-isopropylmalate dehydratase, small subunit | YP_186866.1 | 3.538714992 |
| 2007 D09 610 SACOL1086 conserved hypothetical protein YP_185950.1 3.532786885 2014 D11 610 SACOL2720 hypothetical protein YP_187086.1 3.875409836 2014 D12 613 SACOL0458 xanthine phosphotibosytransferase YP_18570196 3.87520901 3.518760196 2017 E02 613 SACOL0420 pathogenicity island protein YP_185731 3.54230016 2019 E03 613 SACOL2020 pathogenicity island protein YP_1867451 4.254486134 2021 E04 613 SACOL2700 imidazolegitycerol-opsphate dehytrates YP_187485.1 4.254486134 2023 E05 616 SACOL700 imidazolegitycerol-opsphate dehytrates YP_18548.1 3.831973899 2026 E06 616 SACOL706 Conserved hypothetical protein YP_185590.1 3.84431147 2023 E09 619 SACOL7076 Conserved hypothetical protein YP_185648.1 3.12762502 2034 E10 619 | 2005 | D08 | 610 | SACOL0967 | conserved hypothetical protein | YP_185836.1 | 4.249180328 |
| 2009 D10 610 SACOL1502 conserved hypothetical protein YP 186346.1 3.10933066 2011 D11 613 SACOL0191 M23M37 peptidase domain protein YP 185060.1 3.87409836 2015 E01 613 SACOL048 xanhine phosphotiobsyltransferase YP 1853481.1 3.525284841 2017 E02 613 SACOL468 xanhine phosphotibsyltransferase YP 187481.1 3.525284841 2019 E03 613 SACOL2609 imidazole glycerol-3-phosphate 3- YP_18645.1 3.083197389 2021 E04 613 SACOL2609 imidazole glycerol-phosphate synthase, YP_187486.1 4.25448134 2023 E05 616 SACOL708 DAK2 domain protein YP 187486.1 3.38197389 2024 E06 616 SACOL0708 DAK2 domain protein YP 18648.1 3.16350644 2023 E08 619 SACOL0769 conserved hypothetical protein YP 18648.1 3.1525502 2034 E10 619 SACOL0769 cons | 2007 | D09 | 610 | SACOL1086 | conserved hypothetical protein | YP_185950.1 | 3.532786885 |
| 2011 D11 610 SACOL2720 hypothetical protein YP_187506.1 3.875409836 2014 D12 613 SACOL0458 xanthine phosphoribosyttransferase YP_185248.1 3.525285481 2017 E02 613 SACOL0458 xanthine phosphoribosyttransferase YP_18573.1 3.542320016 2019 E03 613 SACOL0202 Depthosphoritytransferase YP_186159.1 3.08319739 2021 E04 613 SACOL2700 imidazole glycerol-phosphate dehydratase YP_18636.1 3.831973899 2022 E05 613 SACOL0700 imidazole glycerol-phosphate dehydratase YP_18537.1 3.86506494 2027 E06 616 SACOL0769 Conserved hydrothetical protein YP_18532.1 3.184491147 2038 E10 619 SACOL0769 conserved hydrothetical protein YP_18548.1 3.12762502 2036 E11 619 SACOL0769 conserved hydrothetical protein YP_18544.1 3.1326424379 2036 F01 622 SACOL16 | 2009 | D10 | 610 | SACOL1502 | conserved hypothetical protein | YP_186346.1 | 3.109836066 |
| 2014 D12 613 SACCL0191 M23/M37 peptidase domain protein YP_185090.1 3.518760196 2015 E01 613 SACCL0458 xanthine phosphoribosyttransferase YP_18573.1 3.543230016 2019 E03 613 SACCL1302 CDP-diacylgycerol-phycephate synthase. YP_18745.1 4.254486134 2021 E04 613 SACCL2699 limidazolegiycerol-phosphate synthase. YP_18745.1 4.254486134 2023 E06 616 SACOL147P phosphoglycerate mutase family protein YP 185337.1 3.3886506494 2027 E07 616 SACOL0708 DAX2 domain protein YP 185436.1 3.253424879 2029 E08 619 SACCL0708 DAX2 domain protein YP 185438.1 3.127625202 2034 E10 619 SACCL0469 conserved hypothetical protein YP 18543.1 2.842971 2037 E12 622 SACOL069 signal peptidase IB YP 18548.1 3.11761644 2037 E12 622 SACOL0209 | 2011 | D11 | 610 | SACOL2720 | hypothetical protein | YP_187506.1 | 3.875409836 |
| 2015 E01 613 SACCU0458 xanthine phosphoribosyttransferase YP 185348.1 3.52528441 2017 E02 613 SACCU0302 Dethogenicity island protein YP 185773.1 3.543230016 2019 E03 613 SACCU1302 Disphatidytransferase YP 18773.1 3.64323016 2021 E04 613 SACCU269 imidazole glycerol-phosphate synthase, glutamine amidotransferase subunit YP 187435.1 4.25448613 2023 E05 613 SACCU2700 imidazole glycerol-phosphate dehydratase YP 18733.1 3.886506494 2027 E07 616 SACCU0708 DAK2 domain protein YP 185429.1 3.13474026 2031 E09 619 SACCU0709 conserved hydrateirotein YP 185461.1 3.25242479 2034 E10 619 SACCU0269 conserved hydrateirotein YP 185461.1 3.127625202 2036 E11 619 SACCU1264 ATP-dependentCIp protease, proteolytic subunit | 2014 | D12 | 613 | SACOL0191 | M23/M37 peptidase domain protein | YP_185090.1 | 3.518760196 |
| 2017 E02 613 SACOL0902 pathogenicity island protein YP_185773.1 3.543230016 2019 E03 613 SACOL1302 CDP-diacylgycerol-pycerol-sphosphate 3- phosphaticyltransferase YP_187485.1 4.254486134 2021 E04 613 SACOL2699 imidazole glycerol-phosphate synthase, glutamine amidotransferase subunit YP_187485.1 4.254486134 2023 E06 616 SACOL0447 phosphoglycerate mutase family protein YP_185337.1 3.368506494 2027 E07 616 SACOL0708 DAXZ domain protein YP_185486.1 3.523424879 2031 E09 619 SACOL0708 DAXZ domain protein YP_185486.1 3.127625202 2036 E11 619 SACOL0289 conserved hypothetical protein YP_18548.1 3.127625202 2038 E11 619 SACOL0289 conserved hypothetical protein YP_18548.1 3.127865202 2039 F01 622 SACOL1649 conserved hypothetical protein YP_185451.1 3.523424879 2044 <td< td=""><td>2015</td><td>E01</td><td>613</td><td>SACOL0458</td><td>xanthine phosphoribosyltransferase</td><td>YP_185348.1</td><td>3.525285481</td></td<> | 2015 | E01 | 613 | SACOL0458 | xanthine phosphoribosyltransferase | YP_185348.1 | 3.525285481 |
| 2019 E03 613 SACOL1302 CDP-disc/glycerol-3-phosphate 3- phosphate 3- glutamine amidotransferase YP_186159.1 3.08319739 2021 E04 613 SACOL2699 imidazole glycerol phosphate synthase, glutamine amidotransferase subunit YP_187486.1 4.254486134 2023 E05 613 SACOL2700 imidazoleglycerol-phosphate dehydratase YP_187486.1 3.831973899 2025 E06 616 SACOL0447 phosphoglycerate mutase family protein YP_185493.1 3.86860434 2027 E07 616 SACOL0769 conserved hypothetical protein YP_185493.1 3.13474026 2036 E11 619 SACOL0769 conserved hypothetical protein YP_185438.1 3.12762502 2036 E11 619 SACOL069 conserved hypothetical protein YP_185481.1 2.813504823 2037 E12 622 SACOL0639 conserved hypothetical protein YP_185481.1 2.813504823 2041 F02 622 SACOL0639 conserved hypothetical protein YP_186741.1 3.122168455 | 2017 | E02 | 613 | SACOL0902 | pathogenicity island protein | YP_185773.1 | 3.543230016 |
| 2021 E04 613 SAC0L2699 imidazole glycerol phosphate synthase, glutamine amidotransferase subunit YP_187486.1 4.254486134 2023 E05 613 SAC0L2700 imidazoleglycerol-phosphate dehydratase YP_187486.1 3.831973899 2025 E06 616 SAC0L0447 phosphoglycerate mutase family protein YP_185437.1 3.868506494 2027 E07 616 SAC0L0769 conserved hypothetical protein YP_185490.1 3.84491147 2031 E10 619 SAC0L0769 conserved hypothetical protein YP_185838.1 3.127625002 2036 E11 619 SAC0L0269 signal peptidase IB YP_185846.1 2.81306423 2037 E12 622 SAC0L0269 conserved hypothetical protein YP_185846.1 3.1324762502 2034 E70 622 SAC0L0269 conserved hypothetical protein YP_185846.1 2.81306423 2037 E12 622 SAC0L0261 transcriptional regulator, TeIR family, putative YP_18671.1 3.122168495 2044 | 2019 | E03 | 613 | SACOL1302 | CDP-diacylglycerolglycerol-3-phosphate 3- phosphatidyltransferase | YP_186159.1 | 3.08319739 |
| 2023 E05 613 SACOL2700 imidazoleglycerol-phosphate dehydratese YP 187486.1 3.831973899 2025 E06 616 SACOL0589 lipporotein, putative YP 18537.1 3.86806494 2027 E07 616 SACOL0706 DAK2 domain protein YP 18542.1 3.13474026 2023 E08 619 SACOL0706 DAK2 domain protein YP 18546.1 3.522424879 2034 E10 619 SACOL0696 signal peptidase IB YP 18564.1 3.5127625202 2036 E11 619 SACOL0699 conserved hypothetical protein YP_185707.1 3.834405145 2037 E12 622 SACOL0633 ATP-dependent Clp protease, proteolytic subunit Clp YP_185707.1 3.834405145 2044 F03 622 SACOL1501 conserved hypothetical protein YP_186707.1 3.83465594 2045 F04 622 SACOL2610 transcriptional regulator. TetR family protein YP_18670.1 3.132685595 < | 2021 | E04 | 613 | SACOL2699 | imidazole glycerol phosphate synthase, glutamine amidotransferase subunit | YP_187485.1 | 4.254486134 |
| 2025 E06 616 SACOL0447 phosphoglycerate mutase family protein YP 185337.1 3.868506494 2027 E07 616 SACOL1589 lipoprotein, putative YP 186429.1 3.13474026 2029 E08 619 SACOL0706 DAK2 domain protein YP 185646.1 3.523424879 2034 E10 619 SACOL0969 conserved hypothetical protein YP 185838.1 3.127625202 2036 E11 619 SACOL089 conserved hypothetical protein YP 185481.1 2.13504823 2039 F01 622 SACOL083 ATP-dependent Clp protease, proteolytic subunit ClpP YP 185707.1 3.834405145 2041 F02 622 SACOL1602 HAM1 protein YP 186741.1 3.122166495 2044 F03 622 SACOL1686 phosphoglycerate mutase family protein YP 186741.1 3.528 2048 F06 625 SACOL1720 GTP-binding protein, putative YP 1865741.1 </td <td>2023</td> <td>E05</td> <td>613</td> <td>SACOL2700</td> <td>imidazoleglycerol-phosphate dehydratase</td> <td>YP_187486.1</td> <td>3.831973899</td> | 2023 | E05 | 613 | SACOL2700 | imidazoleglycerol-phosphate dehydratase | YP_187486.1 | 3.831973899 |
| 2027 E07 616 SACOL1589 lipoprotein, putative YP 186429.1 3.13474026 2029 E08 619 SACOL0708 DAK2 domain protein YP 185646.1 3.523424879 2034 E10 619 SACOL0769 conserved hypothetical protein YP 185838.1 3.127625202 2036 E11 619 SACOL0269 conserved hypothetical protein YP 185164.1 2.813504823 2039 F01 622 SACOL0269 conserved hypothetical protein YP 186025.1 4.263665595 2044 F02 622 SACOL1501 conserved hypothetical protein YP 186025.1 4.263665595 2044 F03 622 SACOL2610 transcriptional regulator, TetR family, putative YP 186025.1 4.25366595 2044 F06 625 SACOL2610 transcriptional regulator, TetR family, putative YP 186415.1 3.1262656 2049 F06 625 SACOL1359 conserved hypothetical protein YP | 2025 | E06 | 616 | SACOL0447 | phosphoglycerate mutase family protein | YP_185337.1 | 3.868506494 |
| 2029 E08 619 SACOL0708 DAK2 domain protein YP 185590.1 3.844911147 2031 E09 619 SACOL0769 conserved hypothetical protein YP 185638.1 3.127625202 2036 E11 619 SACOL0869 conserved hypothetical protein YP 185489.1 3.11631664 2037 E12 622 SACOL0269 conserved hypothetical protein YP 185164.1 2.813504823 2039 F01 622 SACOL0269 conserved hypothetical protein YP 185707.1 3.834405145 2041 F02 622 SACOL1610 transcriptional regulator, TeRF family, putative YP 185345.1 3.122186495 2044 F03 622 SACOL2610 transcriptional regulator, TeRF family, putative YP 185741.1 3.528 2045 F04 625 SACOL1575 hypothetical protein YP 186584.1 3.12768495 2051 F07 625 SACOL1720 GTP-binding protein, putative YP 186584.1 3.5152 2055 F09 625 SACOL2014 | 2027 | E07 | 616 | SACOL1589 | lipoprotein, putative | YP_186429.1 | 3.13474026 |
| 2031 E09 619 SACOL0769 conserved hypothetical protein YP_18546.1 3.523424879 2034 E10 619 SACOL0969 signal peptidase IB YP_18548.1 3.127625202 2036 E11 619 SACOL0269 conserved hypothetical protein YP_185164.1 2.813504823 2037 E12 622 SACOL083 ATP-dependent Clp protease, proteolytic subunit ClpP YP_18502.1 4.26366595 2041 F02 622 SACOL1501 conserved hypothetical protein YP_186402.1 4.26366595 2044 F03 622 SACOL2610 transcriptional regulator, TetR Tamily, putative YP_186415.1 3.1182186495 2045 F04 622 SACOL375 hypothetical protein YP_186415.1 3.528 2049 F06 625 SACOL1750 conserved hypothetical protein YP_186351.1 3.5263 2051 F07 625 SACOL1720 GTP-binding protein, putative YP_186384.1 3.4416 2057 F10 625 SACOL02077 | 2029 | E08 | 619 | SACOL0708 | DAK2 domain protein | YP_185590.1 | 3.844911147 |
| 2034 E10 619 SACOL0969 signal peptidase IB YP_18538.1 3.127625202 2036 E11 619 SACOL0649 conserved hypothetical protein YP_185164.1 2.813504823 2037 E12 622 SACOL0269 conserved hypothetical protein YP_185164.1 2.813504823 2039 F01 622 SACOL033 ATP-dependent Clp protease, proteolytic subunit ClpP YP_185707.1 3.834405145 2041 F02 622 SACOL1501 conserved hypothetical protein YP_186345.1 3.122186495 2044 F03 622 SACOL1501 conserved hypothetical protein YP_185741.1 3.528 2044 F05 625 SACOL1359 conserved hypothetical protein YP_185741.1 3.528 2045 F04 625 SACOL1355 chypothetical protein YP_186212.1 4.256 2051 F07 625 SACOL1375 hypothetical protein YP_18634.1 3.4416 2057 F10 625 SACOL2393 respiratyresinmisse fa | 2031 | E09 | 619 | SACOL0769 | conserved hypothetical protein | YP_185646.1 | 3.523424879 |
| 2036 E11 619 SACOL1649 conserved hypothetical protein TiGR00488 YP_186489.1 3.11631644 2037 E12 622 SACOL0269 conserved hypothetical protein YP_185164.1 2.813504823 2039 F01 622 SACOL0833 ATP-dependentClp protease, proteolytic subunit ClpP YP_185707.1 3.834405145 2041 F02 622 SACOL1501 conserved hypothetical protein YP_186345.1 3.122186495 2044 F03 622 SACOL2610 transcriptional regulator, TetR family, putative YP_186345.1 3.13265594 2048 F06 625 SACOL1359 conserved hypothetical protein YP_186415.1 3.528 2051 F07 625 SACOL1720 GTP-binding protein, putative YP_186341.1 3.4416 2057 F10 625 SACOL2014 phage terminase family protein YP_186384.1 3.4416 2057 F10 625 SACOL00773 armidotransferase, component II YP_186360.1 3.522292994 2061 F12 628< | 2034 | E10 | 619 | SACOL0969 | signal peptidase IB | YP 185838.1 | 3.127625202 |
| 2037 E12 622 SACOL0269 conserved hypothetical protein YP_185164.1 2.813504823 2039 F01 622 SACOL0833 ATP-dependent Clp protease, proteolytic subunit ClpP YP_185025.1 4.26366595 2041 F02 622 SACOL1501 conserved hypothetical protein YP_186345.1 3.12186495 2045 F04 622 SACOL2610 transcriptional regulator, TetR family, putative YP_187400.1 3.136655949 2048 F05 625 SACOL1359 conserved hypothetical protein YP_18741.1 3.528 2049 F06 625 SACOL1359 conserved hypothetical protein YP_186415.1 3.5056 2051 F07 625 SACOL1720 GTP-binding protein, putative YP_18658.1 3.5152 2055 F09 625 SACOL0214 phage terminase family protein YP_186560.1 3.522292994 2061 F12 628 SACOL0773 para-aminobenzoate synthase, glutamine YP_18560.1 3.52386535 2057 F10 628 | 2036 | E11 | 619 | SACOL1649 | conserved hypothetical protein TIGR00488 | YP 186489.1 | 3.11631664 |
| 2039 F01 622 SACOL0833 ATP-dependent Clp protease, proteolytic subunit ClpP YP_185707.1 3.834405145 2041 F02 622 SACOL1162 HAMI protein YP 186025.1 4.263665595 2044 F03 622 SACOL2610 transcriptional regulator, TetR family, putative YP 186345.1 3.122186495 2045 F04 622 SACOL2610 transcriptional regulator, TetR family, putative YP 187400.1 3.136655949 2048 F05 625 SACOL1359 conserved hypothetical protein YP 187411.3 3.528 2051 F07 625 SACOL1757 hypothetical protein YP 186415.1 3.5152 2055 F09 625 SACOL2014 phage terminase family protein YP 186834.1 3.4416 2057 F10 625 SACOL2393 respiratory nitrate reductase, delta subunit YP 18796.1 3.52289294 2061 F12 628 SACOL00773 para-aminoberozate synthase, glutamine amidotransferase, c | 2037 | E12 | 622 | SACOL0269 | conserved hypothetical protein | YP 185164.1 | 2.813504823 |
| 2041 F02 622 SACOL1162 HAM1 protein YP 186025.1 4.26366595 2044 F03 622 SACOL1501 conserved hypothetical protein YP 186345.1 3.122186495 2045 F04 622 SACOL2610 transcriptional regulator, TetR family, putative YP 185741.1 3.528 2049 F06 625 SACOL2610 transcriptional regulator, TetR family, putative YP 186212.1 4.266 2051 F07 625 SACOL20155 hypothetical protein YP 186415.1 3.5056 2053 F08 625 SACOL2014 phage terminase family protein YP 18658.1 3.5152 2055 F09 625 SACOL2014 phage terminase family protein YP 186560.1 3.522292994 2051 F10 628 SACOL00773 para-aminobenzoate synthase, glutamine YP 185650.1 3.522292994 2061 F12 628 SACOL00957 petidyl-prolyl cis-trans isomerase, cyclophilin-type 187322.1 3.863057325 2063 G01 628 SACOL0252 | 2039 | F01 | 622 | SACOL0833 | ATP-dependent Clp protease, proteolytic subunit ClpP | YP_185707.1 | 3.834405145 |
| 2044 F03 622 SACOL1501 conserved hypothetical protein YP_186345.1 3.122186495 2045 F04 622 SACOL2610 transcriptional regulator, TetR family, putative YP_187400.1 3.136655949 2048 F05 625 SACOL1359 conserved hypothetical protein YP_186212.1 4.256 2051 F07 625 SACOL1575 hypothetical protein YP_186415.1 3.5056 2053 F08 625 SACOL2014 phage terminase family protein YP_18658.1 3.5152 2057 F10 625 SACOL2014 phage terminase family protein YP_18658.1 3.52292994 2057 F10 625 SACOL0773 para-aminobenzota synthase, glutamine YP_185650.1 3.5228635 2061 F12 628 SACOL0057 peptidyl-prolyl cis-trans isomerase, cyclophilin-type_18576.1 3.845841401 2065 G02 628 SACOL0082 conserved hypothetical protein YP_185826.1 3.845841401 2065 G02 628 SACOL0082 | 2041 | F02 | 622 | SACOL1162 | HAM1 protein | YP_186025.1 | 4.263665595 |
| 2045 F04 622 SACOL2610 transcriptional regulator, TetR family, putative YP 187400.1 3.136655949 2048 F05 625 SACOL0869 phosphoglycerate mutase family protein YP 185741.1 3.528 2049 F06 625 SACOL1359 conserved hypothetical protein YP 186212.1 4.256 2051 F07 625 SACOL1720 GTP-binding protein, putative YP 186341.1 3.5152 2055 F09 625 SACOL2333 respiratory nitrate reductase, delta subunit YP 186834.1 3.4416 2057 F10 628 SACOL0773 para-aminobenzoate synthase, glutamine amidotransferase, component II YP_185650.1 3.522292994 2061 F12 628 SACOL0957 peptidyl-prolyl cis-trans isomerase, cyclophilin- type YP_185876.1 3.82388535 2063 G01 628 SACOL0082 staphylococcus tandem lipoprotein YP_185876.1 3.863057325 2067 G03 631 SACOL0082 recombination protein RecR | 2044 | F03 | 622 | SACOL1501 | conserved hypothetical protein | YP_186345.1 | 3.122186495 |
| 2048 F05 625 SACOL0869 phosphoglycerate mutase family protein YP_185741.1 3.528 2049 F06 625 SACOL1359 conserved hypothetical protein YP_186415.1 3.5056 2051 F07 625 SACOL1720 GTP-binding protein, putative YP_186415.1 3.5056 2055 F09 625 SACOL2014 phage terminase family protein YP_186434.1 3.4416 2057 F10 625 SACOL0773 para-aminobenzoate synthase, glutamine amidotransferase, component II YP_185650.1 3.522292994 2061 F12 628 SACOL00773 pertidyl-prolyl cis-trans isomerase, cyclophilin- type YP_185876.1 3.843541401 2065 G02 628 SACOL0082 etaphylococcus tandem lipoprotein YP_185876.1 3.845541401 2065 G02 628 SACOL02529 phospholipase/carboxylesterase family protein YP_185876.1 3.845541401 2065 G02 628 SACOL0252 recombination protein RecR YP_185876.1 3.849445325 2067 | 2045 | F04 | 622 | SACOL2610 | transcriptional regulator, TetR family, putative | YP_187400.1 | 3.136655949 |
| 2049 F06 625 SACOL1359 conserved hypothetical protein YP 186212.1 4.256 2051 F07 625 SACOL1575 hypothetical protein YP 186545.1 3.5056 2053 F08 625 SACOL2014 phage terminase family protein YP 18658.1 3.5152 2057 F10 625 SACOL2014 phage terminase family protein YP 18634.1 3.4416 2059 F11 628 SACOL0773 para-aminobenzoate synthase, glutamine amidotransferase, component II YP 185650.1 3.5228292994 2061 F12 628 SACOL0957 peptidyl-prolyl cis-trans isomerase, cyclophilin- type YP 185876.1 3.842541401 2063 G01 628 SACOL082 staphylococcus tandem lipoprotein YP 185876.1 3.849445325 2069 G04 631 SACOL082 recombination protein RecR YP 18502.1 3.849445325 2069 G04 631 SACOL052 recombination protein RecR YP 18502.1 3.849445325 2075 G07 634 | 2048 | F05 | 625 | SACOL0869 | phosphoglycerate mutase family protein | YP_185741.1 | 3.528 |
| 2051 F07 625 SACOL1575 hypothetical protein YP_186415.1 3.5056 2053 F08 625 SACOL1720 GTP-binding protein, putative YP_18658.1 3.5152 2055 F09 625 SACOL2393 respiratory nitrate reductase, delta subunit YP_186834.1 3.4416 2057 F10 625 SACOL2393 respiratory nitrate reductase, delta subunit YP_187196.1 4.0096 2059 F11 628 SACOL0773 para-aminobenzoate synthase, glutamine amidotransferase, component II YP_185650.1 3.52282994 2061 F12 628 SACOL0957 peptidyl-prolyl cis-trans isomerase, cyclophilin- type YP_185826.1 3.52388535 2063 G01 628 SACOL0252 phospholipase/carboxylesterase family protein YP_185876.1 3.84345325 2065 G02 628 SACOL0522 recombination protein RecR YP_185410.1 3.507131537 2071 G05 631 SACOL1792 conserved hypothetical protein YP_18625.1 4.228209192 2073 | 2049 | F06 | 625 | SACOL1359 | conserved hypothetical protein | YP_186212.1 | 4.256 |
| 2053 F08 625 SACOL1720 GTP-binding protein, putative YP_186558.1 3.5152 2055 F09 625 SACOL2014 phage terminase family protein YP_186834.1 3.4416 2057 F10 625 SACOL2033 respiratory nitrate reductase, delta subunit YP_187196.1 4.0096 2059 F11 628 SACOL0773 para-aminobenzoate synthase, glutamine amidotransferase, component II YP_185650.1 3.522292994 2061 F12 628 SACOL0957 peptidyl-prolyl cis-trans isomerase, cyclophilin- type YP_185826.1 3.52388535 2063 G01 628 SACOL0082 conserved hypothetical protein YP_185876.1 3.845541401 2065 G02 628 SACOL0082 staphylococcus tandem lipoprotein YP_184987.1 3.849445325 2069 G04 631 SACOL0522 recombination protein RecR YP_18540.1 3.507131537 2071 G05 631 SACOL1792 conserved hypothetical protein YP_18625.1 4.228209192 2075 | 2051 | F07 | 625 | SACOL1575 | hypothetical protein | YP_186415.1 | 3.5056 |
| 2055 F09 625 SACOL2014 phage terminase family protein YP_186834.1 3.4416 2057 F10 625 SACOL2393 respiratory nitrate reductase, delta subunit YP_187196.1 4.0096 2059 F11 628 SACOL0773 para-aminobenzote synthase, glutamine amidotransferase, component II YP_185650.1 3.522292994 2061 F12 628 SACOL0957 peptidyl-prolyl cis-trans isomerase, cyclophilin- type YP_185826.1 3.52388535 2063 G01 628 SACOL0088 conserved hypothetical protein YP_185876.1 3.845541401 2065 G02 628 SACOL0529 phospholipase/carboxylesterase family protein YP_187322.1 3.863057325 2067 G03 631 SACOL0522 recombination protein RecR YP_185410.1 3.507131537 2071 G05 631 SACOL0522 recombination protein RecR YP_186650.1 3.829652997 2075 G07 634 SACOL1792 conserved hypothetical protein YP_186450.1 3.835962145 2077 <td>2053</td> <td>F08</td> <td>625</td> <td>SACOL1720</td> <td>GTP-binding protein, putative</td> <td>YP_186558.1</td> <td>3.5152</td> | 2053 | F08 | 625 | SACOL1720 | GTP-binding protein, putative | YP_186558.1 | 3.5152 |
| 2057 F10 625 SACOL2393 respiratory nitrate reductase, delta subunit YP_187196.1 4.0096 2059 F11 628 SACOL0773 para-aminobenzoate synthase, glutamine amidotransferase, component II YP_185650.1 3.522292994 2061 F12 628 SACOL0957 peptidyl-prolyl cis-trans isomerase, cyclophilin- type YP_185826.1 3.52388535 2063 G01 628 SACOL2529 phospholipase/carboxylesterase family protein YP_185876.1 3.845541401 2065 G02 628 SACOL082 staphylococcus tandem lipoprotein YP_184987.1 3.849445325 2067 G03 631 SACOL0522 recombination protein RecR YP_185410.1 3.507131537 2073 G06 634 SACOL1792 conserved hypothetical protein YP_186625.1 4.228209192 2075 G07 634 SACOL1610 superoxide dismutase YP_186737.1 3.544164038 2079 G09 634 SACOL2201 conserved domain protein, putative YP_186737.1 3.544164038 2 | 2055 | F09 | 625 | SACOL2014 | phage terminase family protein | YP_186834.1 | 3.4416 |
| 2059 F11 628 SACOL0773 para-aminobenzoate synthase, glutamine amidotransferase, component II YP_185650.1 3.522292994 2061 F12 628 SACOL0957 peptidyl-prolyl cis-trans isomerase, cyclophilin- type YP_185826.1 3.52388535 2063 G01 628 SACOL1008 conserved hypothetical protein YP_185876.1 3.845541401 2065 G02 628 SACOL0822 phospholipase/carboxylesterase family protein YP_185876.1 3.845541401 2067 G03 631 SACOL082 staphylococcus tandem lipoprotein YP_185410.1 3.507131537 2071 G05 631 SACOL1792 conserved hypothetical protein YP_185022.1 3.829652997 2073 G06 634 SACOL118 superoxide dismutase YP_186450.1 3.835962145 2077 G08 634 SACOL1912 glucosamine-6-phosphate isomerase, putative YP_186737.1 3.544164038 2079 G09 634 SACOL2201 conserved domain protein, putative YP_186926.1 3.501577287 | 2057 | F10 | 625 | SACOL2393 | respiratory nitrate reductase, delta subunit | YP_187196.1 | 4.0096 |
| 2061 F12 628 SACOL0957 peptidyl-prolyl cis-trans isomerase, cyclophilin- type YP_185826.1 3.52388535 2063 G01 628 SACOL1008 conserved hypothetical protein YP_185876.1 3.845541401 2065 G02 628 SACOL2529 phospholipase/carboxylesterase family protein YP_187322.1 3.863057325 2067 G03 631 SACOL0082 staphylococcus tandem lipoprotein YP_184987.1 3.849445325 2069 G04 631 SACOL0522 recombination protein RecR YP_18502.1 3.829652997 2071 G05 631 SACOL01792 conserved hypothetical protein YP_186625.1 4.228209192 2075 G07 634 SACOL1610 superoxide dismutase YP_18650.1 3.835962145 2077 G08 634 SACOL2112 glucosamine-6-phosphate isomerase, putative YP_186737.1 3.544164038 2079 G09 634 SACOL2201 conserved domain protein, putative YP_186926.1 3.501577287 2081 G10 | 2059 | F11 | 628 | SACOL0773 | para-aminobenzoate synthase, glutamine amidotransferase, component II | YP_185650.1 | 3.522292994 |
| 2063 G01 628 SACOL1008 conserved hypothetical protein YP_185876.1 3.845541401 2065 G02 628 SACOL2529 phospholipase/carboxylesterase family protein YP_187322.1 3.863057325 2067 G03 631 SACOL082 staphylococcus tandem lipoprotein YP_184987.1 3.849445325 2069 G04 631 SACOL0522 recombination protein RecR YP_185410.1 3.507131537 2071 G05 631 SACOL0792 conserved hypothetical protein YP_186625.1 4.228209192 2073 G06 634 SACOL0118 superoxide dismutase YP_185022.1 3.829652997 2075 G07 634 SACOL1610 superoxide dismutase YP_186450.1 3.835962145 2077 G08 634 SACOL1912 glucosamine-6-phosphate isomerase, putative YP_186737.1 3.544164038 2079 G09 634 SACOL2201 conserved domain protein, putative YP_186737.1 3.501577287 2081 G10 634 SACOL | 2061 | F12 | 628 | SACOL0957 | peptidyl-prolyl cis-trans isomerase, cyclophilin- type | YP_185826.1 | 3.52388535 |
| 2065 G02 628 SACOL2529 phospholipase/carboxylesterase family protein YP_187322.1 3.863057325 2067 G03 631 SACOL0082 staphylococcus tandem lipoprotein YP_184987.1 3.849445325 2069 G04 631 SACOL0522 recombination protein RecR YP_185410.1 3.507131537 2071 G05 631 SACOL0792 conserved hypothetical protein YP_186625.1 4.228209192 2073 G06 634 SACOL0118 superoxide dismutase YP_185022.1 3.829652997 2075 G07 634 SACOL1912 glucosamine-6-phosphate isomerase, putative YP_186450.1 3.835962145 2077 G08 634 SACOL2111 thymidine kinase YP_186737.1 3.544164038 2079 G09 634 SACOL2201 conserved domain protein, putative YP_187012.1 2.823343849 2083 G11 634 SACOL2262 molybdopterin-guanine dinucleotide biosynthesis protein A YP_187069.1 3.110410095 2085 G12 63 | 2063 | G01 | 628 | SACOL1008 | conserved hypothetical protein | YP_185876.1 | 3.845541401 |
| 2067 G03 631 SACOL0082 staphylococcus tandem lipoprotein YP_184987.1 3.849445325 2069 G04 631 SACOL0522 recombination protein RecR YP_185410.1 3.507131537 2071 G05 631 SACOL1792 conserved hypothetical protein YP_186625.1 4.228209192 2073 G06 634 SACOL0118 superoxide dismutase YP_185022.1 3.829652997 2075 G07 634 SACOL1610 superoxide dismutase YP_186450.1 3.835962145 2077 G08 634 SACOL1912 glucosamine-6-phosphate isomerase, putative YP_186737.1 3.544164038 2079 G09 634 SACOL2111 thymidine kinase YP_186926.1 3.501577287 2081 G10 634 SACOL2201 conserved domain protein, putative YP_187012.1 2.823343849 2083 G11 634 SACOL2262 molybdopterin-guanine dinucleotide biosynthesis protein A YP_187069.1 3.110410095 2085 G12 634 SACOL2 | 2065 | G02 | 628 | SACOL2529 | phospholipase/carboxylesterase family protein | YP_187322.1 | 3.863057325 |
| 2069 G04 631 SACOL0522 recombination protein RecR YP_185410.1 3.507131537 2071 G05 631 SACOL1792 conserved hypothetical protein YP_186625.1 4.228209192 2073 G06 634 SACOL0118 superoxide dismutase YP_185022.1 3.829652997 2075 G07 634 SACOL1610 superoxide dismutase YP_186450.1 3.835962145 2077 G08 634 SACOL21912 glucosamine-6-phosphate isomerase, putative YP_186737.1 3.544164038 2079 G09 634 SACOL2201 conserved domain protein, putative YP_186926.1 3.501577287 2081 G10 634 SACOL2201 conserved domain protein, putative YP_187012.1 2.823343849 2083 G11 634 SACOL2262 molybdopterin-guanine dinucleotide biosynthesis protein A YP_187069.1 3.110410095 2085 G12 634 SACOL2407 lipoprotein, putative YP_187254.1 2.520504732 2089 H02 634 <td< td=""><td>2067</td><td>G03</td><td>631</td><td>SACOL0082</td><td>staphylococcus tandem lipoprotein</td><td>YP_184987.1</td><td>3.849445325</td></td<> | 2067 | G03 | 631 | SACOL0082 | staphylococcus tandem lipoprotein | YP_184987.1 | 3.849445325 |
| 2071 G05 631 SACOL1792 conserved hypothetical protein YP_186625.1 4.228209192 2073 G06 634 SACOL0118 superoxide dismutase YP_185022.1 3.829652997 2075 G07 634 SACOL1610 superoxide dismutase YP_186450.1 3.835962145 2077 G08 634 SACOL1912 glucosamine-6-phosphate isomerase, putative YP_186737.1 3.544164038 2079 G09 634 SACOL2111 thymidine kinase YP_186926.1 3.501577287 2081 G10 634 SACOL2201 conserved domain protein, putative YP_187012.1 2.823343849 2083 G11 634 SACOL2262 molybdopterin-guanine dinucleotide biosynthesis protein A YP_187069.1 3.110410095 2085 G12 634 SACOL2407 lipoprotein, putative YP_187210.1 3.522082019 2087 H01 634 SACOL2456 conserved hypothetical protein YP_18726.1 2.520504732 2089 H02 634 SACOL2570 | 2069 | G04 | 631 | SACOL0522 | recombination protein RecR | YP_185410.1 | 3.507131537 |
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| 2075 G07 634 SACOL1610 superoxide dismutase YP_186450.1 3.835962145 2077 G08 634 SACOL1912 glucosamine-6-phosphate isomerase, putative YP_186737.1 3.544164038 2079 G09 634 SACOL2111 thymidine kinase YP_186926.1 3.501577287 2081 G10 634 SACOL2201 conserved domain protein, putative YP_187012.1 2.823343849 2083 G11 634 SACOL2262 molybdopterin-guanine dinucleotide biosynthesis protein A YP_187069.1 3.110410095 2085 G12 634 SACOL2407 lipoprotein, putative YP_187210.1 3.522082019 2087 H01 634 SACOL256 conserved hypothetical protein YP_187254.1 2.520504732 2089 H02 634 SACOL2570 galactoside O-acetyltransferase YP_187362.1 3.548895899 2091 H03 637 SACOL0075 hypothetical protein YP 184980.1 4.263736264 | 2073 | G06 | 634 | SACOL0118 | superoxide dismutase | YP_185022.1 | 3.829652997 |
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| 2079 G09 634 SACOL2111 thymidine kinase YP_186926.1 3.501577287 2081 G10 634 SACOL2201 conserved domain protein, putative YP_187012.1 2.823343849 2083 G11 634 SACOL2262 molybdopterin-guanine dinucleotide biosynthesis protein A YP_187069.1 3.110410095 2085 G12 634 SACOL2407 lipoprotein, putative YP_187210.1 3.522082019 2087 H01 634 SACOL2456 conserved hypothetical protein YP_187254.1 2.520504732 2089 H02 634 SACOL2570 galactoside O-acetyltransferase YP_187362.1 3.548895899 2091 H03 637 SACOL0075 hypothetical protein YP 184980.1 4.263736264 | 2077 | G08 | 634 | SACOL1912 | glucosamine-6-phosphate isomerase, putative | YP_186737.1 | 3.544164038 |
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| 2083 G11 634 SACOL2262 molybdopterin-guanine dinucleotide biosynthesis protein A YP_187069.1 3.110410095 2085 G12 634 SACOL2407 lipoprotein, putative YP_187210.1 3.522082019 2087 H01 634 SACOL2456 conserved hypothetical protein YP_187254.1 2.520504732 2089 H02 634 SACOL2570 galactoside O-acetyltransferase YP_187362.1 3.548895899 2091 H03 637 SACOL0075 hypothetical protein YP 184980.1 4.263736264 | 2081 | G10 | 634 | SACOL2201 | conserved domain protein, putative | YP 187012.1 | 2.823343849 |
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| 2087 H01 634 SACOL2456 conserved hypothetical protein YP_187254.1 2.520504732 2089 H02 634 SACOL2570 galactoside O-acetyltransferase YP_187362.1 3.548895899 2091 H03 637 SACOL0075 hypothetical protein YP 184980.1 4.263736264 | 2085 | G12 | 634 | SACOL2407 | lipoprotein, putative | YP 187210.1 | 3.522082019 |
| 2089 H02 634 SACOL2570 galactoside O-acetyltransferase YP_187362.1 3.548895899 2091 H03 637 SACOL0075 hypothetical protein YP 184980.1 4.263736264 | 2087 | H01 | 634 | SACOL2456 | conserved hypothetical protein | YP 187254.1 | 2.520504732 |
| 2091 H03 637 SACOL0075 hypothetical protein YP 184980.1 4.263736264 | 2089 | H02 | 634 | SACOL2570 | galactoside O-acetvltransferase | YP 187362.1 | 3.548895899 |
| | 2091 | H03 | 637 | SACOL0075 | hypothetical protein | YP 184980.1 | 4.263736264 |

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Product Information Sheet for NR-19506

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| Clone | Well | ORF | Locus ID | Description (Gene name) | Accession | Average Depth |
|-------|----------|--------|-----------|---|-------------|---------------|
| | Position | Length | | | Number | of Coverage |
| 2093 | H04 | 637 | SACOL1036 | protease, putative | YP_185901.1 | 3.516483516 |
| 2095 | H05 | 637 | SACOL1355 | DNA-binding response regulator, LuxR family | YP_186207.1 | 4.20722135 |
| 2097 | H06 | 637 | SACOL1697 | Holliday junction DNA helicase RuvA | YP_186536.1 | 4.241758242 |
| 2099 | H07 | 637 | SACOL1769 | ribosomal protein S4 | YP_186603.1 | 4.233908948 |
| 2101 | H08 | 637 | SACOL1973 | conserved hypothetical protein | YP_186797.1 | 3.551020408 |
| 2103 | H09 | 637 | SACOL2587 | conserved hypothetical protein | YP_187378.1 | 3.535321821 |
| 2105 | H10 | 640 | SACOL1068 | cytochrome aa3 quinol oxidase, subunit III | YP_185932.1 | 3.7953125 |
| 2108 | H11 | 640 | SACOL2270 | molybdenum ABC transporter, ATP-binding protein ModC | YP_187077.1 | 3.8375 |
| 2109 | H12 | 640 | SACOL2638 | siroheme synthase, putative | YP_187426.1 | 4.2359375 |