| Name | Gene Sequence | Translation |
|---|---|---|
| phiHau3 phage large terminase subunit gene | >NC_018836.1:2329-3995 Streptomyces phage phiHau3, complete genome<br>GTGAGTCCCATCTCAACCCTGACCACTGAAGAGATCGAGGCCCTGGCGCCTACGTTCCTCGGGCCTACCT<br>GGGCGAAGGATTCCCTGGGGCAGTGGAAGCTGCCGCAGCGCACGCTCGGCTGGCAGATCGCCGGCTGGTG<br>CGCGGAGTACCTGCGCGCCGAGGACGGCGGCCCGTGGAAGTTCACGCGGGAGCAGCTCCGCTTCGTCCTG<br>TGGTGGTATGCAGTCGATGAGAACGGGCGGTTCGTCTACCGCAAGGGCGTTCTTCAGCGGCTGAAGGGTT<br>GGGGC_**TTA**_**CTCCGGT**_AAGGACCCCCTCCTTGCAGTGGTCTGCATGGTCGAGTTCGTGGGGCCGTCTCGGT<br>TCTCGCACTTCGACGAGGCCGGCGATCCGGTCGGCATCCCTCACCCGCAGGCGTGGGTGCAGGTGGCCGC<br>GGTGAGCCGTGACCAGACCCGTAACACCATGACCTTGTTCCCGTCGCTGATGAGTGACCGGCTCATCGAG<br>ACGTACGGGATCAAGGCGGGAGCCGAGCTGATCCGCGCGAACGGCGGACGTCAGCGCCTTGAGGCGGTGA<br>CGAGTAGCTACCGGGCCCTTGAGGGGGCCCGGTCT_**TTA**_**ACGGTCC**_ACGTTCGTAGTGCTCAACGAAACCC<br>ATCACTGGGTGACGGGTAACAACGGCGACAAGATGTACTCGACGATCGACGGTAACGCGACCAAGAAGGA<br>CTCGCGGTACCTGGCGATCACCAACGCTTACCTGCCCGGCGAGGACAGCGTGGCCGAGCGGATGCGCGAG<br>GCGTACGACAAGATCCGCGAGGGCAAGGCCGTCGACATCGGCTTCATGTACGACAGCATCGAGGCGCATC<br>CTTCGACGCCGTTGACGGTCGAGGCGATCCGGATCGTGCTGCCGAAGATCCGCGGCGATGCCTCTTGGCT<br>GAACGTCGAGACGATCATCCAGTCCATCATGGACGCGACGATCGCTCCGTCGCGCAGCCGGCGCATGTGG<br>TTCAACCAGATCGTGGCCGAGGAAGACGCGCTGTACGGGCCTGAGCAGTGGGCGGACATCCTGCATGAGG<br>GTGCGACGCTCCAGCCGGGCGACGAGATCGTCATGGGCTTCGATGGCGGTAAGAGTGACGATGCCACGGC<br>CCTCGTTGCGATCCGCGTGCGGGACATGTGCGCGTTCGTGCTCGGCCTGTGGGAGAAGCCCGACGGCCCG<br>AAGGGTGACGGCTGGTCCGTACCTCGGGCCGAGGTCGACTCGGCCGTGCATGACGCCTTCCGCGTGTACG<br>ACGTGAAGGCGTTCTACGCCGACGTCGCCCTCTGGGAGAGCTACATCTCCGAGTGGGACGAGCTGTACGG<br>CGAGGGCCTGTCGGTGAAGTCGCCGGTCGGCAAGGACCGGATCGGCTGGGACATGCGTTCCTCGCTGAAG<br>CTGTCGACGATGGCGCACGAGCGCCTGATGCGGAGCATCTTCGACAAGAAGCTCCGGTACGACGGTGACC<br>TGACCTTGCGCCGGCACGCGCTGAACGCGCGTCGCCGGTCGAACAACTACGGCATCAGCTTCGGCAAGGA<br>GTCGCGCGAGTCGCCCCGCAAGGTCGACGCGTACGCGGCCCTGATGCTGGCGCACGAGGCGCTGTACGAC<br>CTGCGTGCGCGCGGGAAGAAGGTCCGGGCTCGCTCGGGCCGGGGTTACTTCATGTAG | >g6<br>VSPISTLTTEEIEALAPTFLGPTWAKDSLGQWKLPQRTLGWQIAGWCAEYLRAEDGGPWK<br>FTREQLRFVLWWYAVDENGRFVYRKGVLQRLKGWG<br><br>**TTA_CTCCGGT**<br><br>>g7<br>KDPLLAVVCMVEFVGPSRFSHFDEAGDPVGIPHPQAWVQVAAVSRDQTRNTMTLFPSLMS<br>DRLIETYGIKAGAELIRANGGRQRLEAVTSSYRALEGARS<br><br>**TTA_ACGGTCC**<br><br>>g8<br>TFVVLNETHHWVTGNNGDKMYSTIDGNATKKDSRYLAITNAYLPGEDSVAERMREAYDKI<br>REGKAVDIGFMYDSIEAHPSTPLTVEAIRIVLPKIRGDASWLNVETIIQSIMDATIAPSR<br>SRRMWFNQIVAEEDALYGPEQWADILHEGATLQPGDEIVMGFDGGKSDDATALVAIRVRD<br>MCAFVLGLWEKPDGPKGDGWSVPRAEVDSAVHDAFRVYDVKAFYADVALWESYISEWDEL<br>YGEGLSVKSPVGKDRIGWDMRSSLKLSTMAHERLMRSIFDKKLRYDGDLTLRRHALNARR<br>RSNNYGISFGKESRESPRKVDAYAALMLAHEALYDLRARGKKVRARSGRGYFM |
| *Streptomyces sp. C* prophage large terminase subunit gene | >ACEW01000274.1:c42728-41080 Streptomyces sp. C cont1.274<br>GTGAGTCCTATTTCAGCCCTCACAGCAGAAGAGATCGACGCCTTGGAGCCGACGTTCCTCGGCCCCGACAT<br>GGCTGCGGAACCCTGACCGGTCCTGGAAGCTGCCCGAGCACACACTCGGCTGGCAGATCGCCGGTTGGGC<br>CGCAGAGTTCCTCAAGGCGGAGGACGGCGGGCCCTGGCGCTTCACGCGCGAGCAGCTCCGCTTCGTCCTG<br>TGGTGGTACGCCGGTCGACGAGAACGGCCGCTTCGTCTACCGCAAGGGAGTTCTCCAGCGCTTGAAGGGCT<br>GGGGC_**TTA**_**CCGGC**_AAGGACCCTCTCCTCGCGGTCGTCTCGCTCGTCGAGTTCGTAGGCCCGAGCCGCTTT<br>TCCCACTGGCAGGACGGGCAGCCGGTAGGCGTCCCCCACCCCCAGGCGTGGGTACAGATCGCGGCCGTAT<br>CGCGCGACCAGACCCGCAACACCATGACCCTGATGCCGTCCCTGATGAGCGACAAGCTGATCGAGACGTA<br>CGGCATCAAGGCGGGCGCCGAGCTGATCCGTGCGAACGGTGGCCGGCAGAGACTTGAAGCGGTCACCAGC<br>TCCTTCCGTGCCCTGGAGGGCGGCCGGGTCACCTTCACCGTGCTGAACGAAACGCACCACTGGGTGACCG<br>GCAATAACGGCGATCGCATGTACGAGACGATCGACGGTAACGCCACCAAGAAGGACAGCCGTTACCTCGC<br>GATCACGAACGCCTACCTCCCCGGCGAGGATTCAGTCGCCGAGCGGATGCGCGAAGCCTTCGAGAAGATC<br>CGCGAAGGCCGGGCCTCGGACATCGGCTTCATGTACGACTCGATCGAGGCGCACCCGGCAACCCCACTGA<br>CGCCCGAGGCGATCCGGATCGTCCTGCCGAAGATCAGGGGCGACGCCGTCTGGCTCCGGGTCGAAACGAT<br>CCTTCAGTCCATCCTCGACACGACGATCGCGCCGAGCCGCTCGCGGCGTATGTGGCTGAACCAGATCGTT<br>GCCTCCGAGGATGCCCTGTACGGCCCCGGCCGAGTGGGATGTCCTGCGGCGCGATGAGCTGGAGCTGAAGC<br>CCGGCGACGAGATCGTCATGGGCTTCGATGGCGGCCGTGAGAGACGACAGCACGCCTTGATCGGGCTGCG<br>CATCTCGGACTCGTACGCCCTTCGTGATCGGCCTGTGGGAGAAGCCGGACGGCCCCGGCCGGTAAGGACTGG<br>GAAGTCCCCACGCTTGCAGGTCGACAGCGCCGTGCACGACGCCTTCAAGGTGTTCTCCGTGCAGGGCTTCT<br>ACGCCGATGTTGCCTTGTGGGAGTCGTACATCTCCGAGTGGTCGGAGACGTACGGCGAGGGCCTGGCCGT<br>GAAGGCGCCCGGCAAGGACGCGATCGGCTGGGACATGCGGTCCTCGCTGAAGGCCGCGACGATGGCGCAC<br>GAGCGCCTGATGCGCACGGTCTTCGACAAGAAGCTCGTCCACGACGGCGACCTCAAGCTCCGCCGGCACG<br>TGCTGAATGCAGTCCGGCGCACGAACAACTACGGCGTCTCCTTCGGCAAGGAAAGCCGGGAGTCGCCCCG<br>CAAGGTCGACGCCTACGCCGCGCTCATGTTGGCGCACGAGGCCCTGTTCGACCTGCGCGCCCCGAGGCAAG<br>AAGGTCCGTCAACGGTCCGGCCGAGGGTTCTTCCTGTAG | >g6<br>VSPISALTAEEIDALEPTFLGPTWLRNPDRSWKLPEHTLGWQIAGWAAEFLKAEDGGPWR<br>FTREQLRFVLWWYAVDENGRFVYRKGVLQRLKGWG<br><br>**TTA_CCGGC**<br><br>>g78<br>KDPLLAVVSLVEFVGPSRFSHWQDGQPVGVPHPQAWVQIAAVSRDQTRNTMTLMPSLMSD<br>KLIETYGIKAGAELIRANGGRQRLEAVTSSFRALEGGRVTFTVLNETHHWVTGNNGDRMY<br>ETIDGNATKKDSRYLAITNAYLPGEDSVAERMREAFEKIREGRASDIGFMYDSIEAHPAT<br>PLTPEAIRIVLPKIRGDAVWLRVETILQSILDTTIAPSRSRRMWLNQIVASEDALYGPAE<br>WDVLRRDELELKPGDEIVMGFDGGLRDDSTALIGLRISDSYAFVIGLWEKPDGPAGKDWE<br>VPRLQVDSAVHDAFKVFSVQGFYADVALWESYISEWSETYGEGLAVKAPGKDAIGWDMRS<br>SLKAATMAHERLMRTVFDKKLVHDGDLKLRRHVLNAVRRTNNYGVSFGKESRESPRKVDA<br>YAALMLAHEALFDLRARGKKVRQRSGRGFFL |