

Sequence Report

Organism Name : pET28a

Sequence length : 6663 bp

Base Count : 1494 A 1948 C 1769 G 1452 T

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1   TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG
51  TGGTTACGCG CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT
101 CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GCTTTCCCGG
151 TCAAGCTCTA AATCGGGGGC TCCCTTTAGG GTTCCGATTT AGTGCTTTAC
201 GGCACCTCGA CCCCAAAAAA CTTGATTAGG GTGATGGTTC ACGTAGTGGG
251 CCATCGCCCT GATAGACGGT TTTTTCGCCCT TTGACGTTGG AGTCCACGTT
301 CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACTC AACCCTATCT
351 CGGTCTATTC TTTTGATTTA TAAGGGATTT TGCCGATTTT GCCTATTGG
401 TTAATAAATG AGCTGATTTA AAAAAAATTT AACGCGAATT TTAACAAAAT
451 ATTAACGTTT ACAATTTTCA GTGGCACTTT TCGGGGAAAT GTGCGCGGAA
501 CCCCTATTTG TTTATTTTTT TAAATACATT CAAATATGTA TCCGCTCATG
551 AATTAATTCT TAGAAAAACT CATCGAGCAT CAAATGAAAC TGCAATTTAT
601 TCATATCAGG ATTATCAATA CCATATTTTT GAAAAAGCCG TTTCTGTAAT
651 GAAGGAGAAA ACTCACCGAG GCAGTTCAT AGGATGGCAA GATCCTGGTA
701 TCGGTCTGCG ATTCCGACTC GTCCAACATC AATACAACCT ATTAATTTCC
751 CCTCGTCAAA AATAAGGTTA TCAAGTGAGA AATCACCATG AGTGACGACT
801 GAATCCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTTCC AGACTTGTTC
851 AACAGGCCAG CCATTACGCT CGTCATCAA ATCACTCGCA TCAACCAAAC
901 CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG
951 TTAAGAGGAC AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC
1001 TGCCAGCGCA TCAACAATAT TTTACCTGA ATCAGGATAT TCTTCTAATA
1051 CCTGGAATGC TGTTTTCCCG GGGATCGCAG TGGTGAGTAA CCATGCATCA
1101 TCAGGAGTAC GGATAAAATG CTTGATGGTC GGAAGAGGCA TAAATTCGCT
1151 CAGCCAGTTT AGTCTGACCA TCTCATCTGT AACATCATTG GCAACGCTAC
1201 CTTTGCCATG TTTCAGAAAC AACTCTGGCG CATCGGGCTT CCCATACAAT
    Clal(1251)
1251 CGATAGATTG TCGCACCTGA TTGCCCGACA TTATCGCGAG CCCATTTATA
1301 CCCATATAAA TCAGCATCCA TGTTGGAATT TAATCGCGGC CTAGAGCAAG
1351 ACGTTTCCCG TTGAATATGG CTCATAACAC CCCTTGTATT ACTGTTTATG
1401 TAAGCAGACA GTTTTATTGT TCATGACCAA AATCCCTTAA CGTGAGTTTT
1451 CGTTCCTACTG AGCGTCAGAC CCGTAGAAA AGATCAAAGG ATCTTCTTGA
1501 GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC
1551 GCTACCAGCG GTGGTTTGTG TGCCGGATCA AGAGCTACCA ACTCTTTTTT
1601 CGAAGGTAAC TGGCTTCAGC AGAGCGCAGA TACCAAATAC TGTCCTTCTA
1651 GTGTAGCCGT AGTTAGGCCA CCACTTCAAG AACTCTGTAG CACCGCCTAC
1701 ATACCTCGCT CTGCTAATCC TGTTACCAGT GGCTGCTGCC AGTGGCGATA
1751 AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG
1801 CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGAGCG
1851 AACGACCTAC ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG
1901 CCACGCTTCC CGAAGGGAGA AAGGCGGACA GGTATCCGGT AAGCGGCAGG
1951 GTCGGAACAG GAGAGCGCAC GAGGGAGCTT CCAGGGGAA ACGCCTGGTA
2001 TCTTTATAGT CCTGTCGGGT TTCGCCACCT CTGACTTGAG CGTCGATTTT
2051 TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG
2101 GCCTTTTTTAC GGTTCCTGGC CTTTTGCTGG CTTTTGCTC ACATGTTCTT
2151 TCCTGCGTTA TCCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT
2201 GAGCTGATAC CGCTCGCCGC AGCCGAACGA CCGAGCGCAG CGAGTCAGTG
2251 AGCGAGGAAG CGGAAGAGCG CCTGATGCGG TATTTTCTCC TTACGCATCT
2301 GTGCGGTATT TCACACCGCA TATATGGTGC ACTCTCAGTA CAATCTGCTC

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2351 TGATGCCGCA TAGTTAAGCC AGTATACACT CCGCTATCGC TACGTGACTG
2401 GGTTCATGGCT GCGCCCCGAC ACCCGCCAAC ACCCGCTGAC GCGCCCTGAC
2451 GGGCTTGTCT GCTCCCGGCA TCCGCTTACA GACAAGCTGT GACCGTCTCC
2501 GGGAGCTGCA TGTGTCAGAG GTTTTCACCG TCATCACCGA AACGCGCGAG
2551 GCAGCTGCGG TAAAGCTCAT CAGCGTGGTC GTGAAGCGAT TCACAGATGT
2601 CTGCCTGTTC ATCCGCGTCC AGCTCGTTGA GTTTCTCCAG AAGCGTTAAT
2651 GTCGGCTTC TGATAAAGCG GGCCATGTTA AGGGCGGTTT TTTCCTGTTT
2701 GGTCACTGAT GCCTCCGTGT AAGGGGGATT TCTGTTTCATG GGGGTAATGA
2751 TACCGATGAA ACGAGAGAGG ATGCTCACGA TACGGGTTAC TGATGATGAA
2801 CATGCCCGGT TACTGGAACG TTGTGAGGGT AAACAACCTGG CGGTATGGAT
2851 GCGGCGGGAC CAGAGAAAAA TCACTCAGGG TCAATGCCAG CGCTTCGTTA
2901 ATACAGATGT AGGTGTTCCA CAGGGTAGCC AGCAGCATCC TGCAGATGCAG
2951 ATCCGGAACA TAATGGTGCA GGGCGCTGAC TTCCGCGTTT CCAGACTTTA
3001 CGAAACACGG AAACCGAAGA CCATTCATGT TGTTGCTCAG GTCGCAGACG
3051 TTTTGCAGCA GCAGTCGCTT CACGTTGCTT CCGGTATCGG TGATTCATTC
3101 TGCTAACCAG TAAGGCAACC CCGCCAGCCT AGCCGGGTCC TCAACGACAG
3151 GAGCACGATC ATGCGCACCC GTGGGGCCGC CATGCCGGCG ATAATGGCCT
3201 GCTTCTCGCC GAAACGTTTG GTGGCGGGAC CAGTGACGAA GGCTTGAGCG
3251 AGGGCGTGCA AGATTCCGAA TACCGCAAGC GACAGGCCGA TCATCGTCGC
3301 GCTCCAGCGA AAGCGTCCCT CGCCGAAAAT GACCCAGAGC GCTGCCGGCA
3351 CCTGTCTTAC GAGTTGCATG ATAAAGAAGA CAGTCATAAG TCGCGCGACG
3401 ATAGTCATGC CCCGCGCCCA CCGGAAGGAG CTGACTGGGT TGAAGGCTCT
3451 CAAGGCATC GGTGAGATC CCGGTGCCTA ATGAGTGAGC TAACTTACAT
3501 TAATTGCGTT GCGTCACTG CCCGCTTTCC AGTCGGGAAA CCTGTCTGTC
3551 CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT
3601 TGGGCGCCAG GGTGGTTTTT CTTTTACCA GTGAGACGGG CAACAGCTGA
3651 TTGCCCTTCA CCGCCTGGCC CTGAGAGAGT TGCAGCAAGC GGTCCACGCT
3701 GGTTCGCCCC AGCAGGCGAA AATCCTGTTT GATGGTGGTT AACGGCGGGA
EcoRV(3797)
3751 TATAACATGA GCTGTCTTCG GTATCGTCGT ATCCCACTAC CGAGATATCC
3801 GCACCAACGC GCAGCCCGGA CTCGGTAATG GCGCGCATTG CGCCAGCGC
3851 CATCTGATCG TTGGCAACCA GCATCGCAGT GGGAACGATG CCCTCATTC
3901 GCATTTGCAT GGTTTGTTGA AAACCGGACA TGGCACTCCA GTCGCCTTCC
3951 CGTTCGCTA TCGGCTGAAT TTGATTGCGA GTGAGATATT TATGCCAGCC
4001 AGCCAGACGC AGACGCGCCG AGACAGAACT TAATGGGCCC GCTAACAGCG
4051 CGATTTGCTG GTGACCCAAT GCGACCAGAT GCTCCACGCC CAGTCGCGTA
4101 CCGTCTTCAT GGGAGAAAAT AATACTGTTG ATGGGTGTCT GGTCCAGAGC
4151 ATCAAGAAAT AACGCCGGA CATTAGTGCA GGCAGCTTCC ACAGCAATGG
MluI(4243)
4201 CATCCTGGTC ATCCAGCGGA TAGTTAATGA TCAGCCCACT GACGCGTTGC
4251 GCGAGAAGAT TGTGCACCGC CGCTTTACAG GCTTCGACGC CGCTTCGTTT
4301 TACCATCGAC ACCACCACGC TGGCACCCAG TTGATCGGCG CGAGATTTAA
4351 TCGCCGCGAC AATTGCGGAC GGCGCGTGCA GGGCCAGACT GGAGGTGGCA
4401 ACGCCAATCA GCAACGACTG TTTGCCCGCC AGTTGTTGTG CCACGCGGTT
4451 GGGAAATGTAA TTCAGTCCG CCATCGCCGC TTCCACTTTT TCCGCGTTT
4501 TCGCAGAAAC GTGGCTGGCC TGGTTCACCA CGCGGAAAC GGTCTGATAA
4551 GAGACACCGG CATACTCTGC GACATCGTAT AACGTTACTG GTTTCACATT
4601 CACCACCCTG AATTGACTCT CTTCCGGGCG CTATCATGCC ATACCGCGAA
4651 AGGTTTTGCG CCATTCGATG GTGTCCGGGA TCTCGACGCT CTCCCTTATG
4701 CGACTCCTGC ATTAGGAAGC AGCCCAGTAG TAGGTTGAGG CCGTTGAGCA

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4751 CCGCCGCCGC AAGGAATGGT GCATGCAAGG AGATGGCGCC CAACAGTCCC
4801 CCGGCCACGG GGCTGCCAC CATAACCACG CCGAAACAAG CGCTCATGAG
4851 CCCGAAGTGG CGAGCCCGAT CTTCCCATC GGTGATGTCG GCGATATAGG
4901 CGCCAGCAAC CGCACCTGTG GCGCCGGTGA TGCCGGCCAC GATGCGTCCG
      BglII(4965)
4951 GCGTAGAGGA TCGAGATCTC GATCCCGCGA AATTAATACG ACTCACTATA
      XbaI(5031)
5001 GGGGAATTGT GAGCGGATAA CAATTCCCCT CTAGAAATAA TTTTGTTTAA
5051 CTTTAAGAAG GAGATATACC ATGGGCAGCA GCCATCATCA TCATCATCAC
      NheI(5135)
      NdeI(5130)
5101 AGCAGCGGCC TGGTGCCGCG CGGCAGCCAT ATGGCTAGCA TGACTGGTGG
      BamHI(5168)
5151 ACAGCAAATG GGTGCGGGAT CCGGTGGTGG TGCAAATCAA AGAACTGCTC
5201 CTCAGTGGAT GTTGCCTTTA CTTCTAGGCC TGTACGGAAG TGTTACTTCT
5251 GCTCTAAAAG CTGCTCTAGC CCTCGACGGC GCCGGCGGCT CCTGCAGGAG
5301 GCCACTGTCT GCAGCTCCCG TGAAGATGTC CACTCCAGAC CCACCCCTGG
5351 GCGGAACTCC TCGGCCAGGT CTTCCCGCG GCCCTGGCCC TTCCCCTGGA
5401 GCCATGCTGG GCCCTAGCCC GGGTCCCTCG CCGGGCTCCG CCCACAGCAT
5451 GATGGGGCCC AGCCAGGGC CGCCCTCAGC AGGACACCCC ATCCCCACCC
      KpnI(5518)
5501 AGGGGCCTGG AGGGTACCCT CAGGACAACA TGCACCAGAT GCACAAGCCC
5551 ATGGAGTCCA TGCATGAGAA GGGCATGTCG GACGACCCGC GCTACAACCA
5601 GATGAAAGGA ATGGGGATGC GGTCAGGGGG CCATGCTGGG ATGGGGCCCC
5651 CGCCAGCCC CATGGACCAG CACTCCCAAG GTTACCCCTC GCCCCTGGGT
5701 GGCTCTGAGC ATGCCTCTAG TCCAGTTCCA GCCAGTGGCC CGTCTTCGGG
5751 GCCCAGATG TCTTCCGGGC CAGGAGGTGC CCCGCTGGAT GGTGCTGACC
5801 CCCAGGCCTT GGGGCAGCAG AACCGGGGCC CAACCCATT TAACCAGAAC
      SacI(5872)
5851 CAGCTGCACC AGCTCAGAGC TCAGATCATG GCCTACAAGA TGCTGGCCAG
5901 GGGGCAGCCC CTCCCCGACC ACCTGCAGAT GGCGGTGCAG GGCAAGCGGC
5951 CGATGCCCGG GATGCAGCAG CAGATGCCAA CGCTACCTCC ACCCTCGGTG
6001 TCCGCAACAG GACCCGGCCC TGGCCCTGGC CCTGGCCCCG GCCCGGGTCC
6051 CGGCCCGGCA CCTCAAATT ACAGCAGGCC TCATGGTATG GGAGGGCCCA
6101 ACATGCCTCC CCCAGGACCC TCGGGCGTGC CCCCCGGGAT GCCAGGCCAG
6151 CCTCCTGGAG GGCTCCCAA GCCCTGGCCT GAAGGACCCA TGCGGAATGC
6201 TGCTGCCCCC ACGAGCACCC CTCAGAAGCT GATTCCCCCG CAGCCAACGG
6251 GCCGCCCTTC CCCCgcgccc CCTGCCGTCC CACCCGCCGC CTCGCCCGTG
6301 ATGCCACCGC AGACCCAGTC CCCCgggCAG CCGGCCCAGC CCGCGCCCAT
6351 GGTGCCACTG CACCAGAAGC AGAGCCGCAT CACCCCATC CAGAAGCCGC
6401 GGGGCCTCGA CCCTGTGGAG ATCCTGCAGG AGCGCGAGTA CAGGCTGCAG
      SacI(6478) HindIII(6487)
      EcoRI(6468) SalI(6481) NofI(6494)
6451 GCTCGCATCG CACACCGAAT TCGAGCTCCG TCGACAAGCT TGCGGCCGCA
      XhoI(6502)
6501 CTCGAGCACC ACCACCACCA CCACTGAGAT CCGGCTGCTA ACAAAGCCCC
6551 AAAGGAAGCT GAGTTGGCTG CTGCCACCGC TGAGCAATAA CTAGCATAAC
6601 CCCTTGGGGC CTCTAAACGG GTCTTGAGGG GTTTTTTGCT GAAAGGAGGA
6651 ACTATATCCG GAT

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