

Sequence Report

Organism Name : Brg1 4340-end pET28C

Sequence length : 5998 bp

Base Count : 1449 A 1605 C 1590 G 1354 T

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1   TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG
51  TGGTTACGCG CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT
101 CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GCTTTCCCCG
151 TCAAGCTCTA AATCGGGGGC TCCCTTTAGG GTTCCGATTT AGTGCTTTAC
201 GGCACCTCGA CCCCAAAAAA CTTGATTAGG GTGATGGTTC ACGTAGTGGG
251 CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT
301 CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACTC AACCCTATCT
351 CGGTCTATTC TTTTGATTTA TAAGGGATTT TGCCGATTTT GGCTATTGG
401 TTAATAAATG AGCTGATTTA AAAAAATTT AACGCGAATT TTAACAAAAT
451 ATTAACGTTT ACAATTTT CAG 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 AGACTTGTTT
851 AACAGGCCAG CCATTACGCT CGTCATCAA ATCACTCGCA TCAACCAAAC
901 CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG
951 TAAAAGGAC AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC
1001 TGCCAGCGCA TCAACAATAT TTTACCTGA ATCAGGATAT TCTTCTAATA

                               SmaI(1070)
1051 CCTGGAATGC TGTTTTCCCG GGGATCGCAG TGGTGAGTAA CCATGCATCA
1101 TCAGGAGTAC GGATAAATG CTTGATGGTC GGAAGAGGCA TAAATTCCGT
1151 CAGCCAGTTT AGTCTGACCA TCTCATCTGT AACATCATTG GCAACGCTAC
1201 CTTTGCCATG TTTCAGAAAC AACTCTGGCG CATCGGGCTT CCCATACAAT

                               ClaI(1251)
1251 CGATAGATTG TCGCACCTGA TTGCCCGACA TTATCGCGAG CCCATTTATA
1301 CCCATATAAA TCAGCATCCA TGTTGGAATT TAATCGCGGC CTAGAGCAAG
1351 ACGTTTCCCG TTGAATATGG CTCATAACAC CCCTTGATTT ACTGTTTATG
1401 TAAGCAGACA GTTTTATTGT TCATGACCAA AATCCCTTAA CGTGAGTTTT
1451 CGTTCCTACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA
1501 GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC
1551 GCTACCAGCG GTGGTTTGTT 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 GCTTGGAGCG
1851 AACGACCTAC ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG
1901 CCACGCTTCC CGAAGGGAGA AAGGCGGACA GGTATCCGGT AAGCGGCAGG
1951 GTCGGAACAG GAGAGCGCAC GAGGGAGCTT CCAGGGGGAA ACGCCTGGTA
2001 TCTTTATAGT CCTGTCGGGT TTCGCCACCT CTGACTTGAG CGTCGATTTT
2051 TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACCGG
2101 GCCTTTTTTAC GGTTCCTGGC CTTTTGCTGG CTTTTTGCTC ACATGTTCTT
2151 TCCTGCGTTA TCCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT
2201 GAGCTGATAC CGCTCGCCGC AGCCGAACGA CCGAGCGCAG CGAGTCAGTG
2251 AGCGAGGAAG CGGAAGAGCG CCTGATGCGG TATTTTCTCC TTACGCATCT

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2301	GTGCGGTATT	TCACACCGCA	TATATGGTGC	ACTCTCAGTA	CAATCTGCTC
2351	TGATGCCGCA	TAGTTAAGCC	AGTATACACT	CCGCTATCGC	TACGTGACTG
2401	GGTCATGGCT	GCGCCCCGAC	ACCCGCCAAC	ACCCGCTGAC	GCGCCCTGAC
2451	GGGCTTGTCT	GCTCCCCGCA	TCCGCTTACA	GACAAGCTGT	GACCGTCTCC
2501	GGGAGCTGCA	TGTGTCAGAG	GTTTTCACCG	TCATCACCGA	AACGCGCGAG
2551	GCAGCTGCGG	TAAAGCTCAT	CAGCGTGGTC	GTGAAGCGAT	TCACAGATGT
2601	CTGCCTGTTC	ATCCGCGTCC	AGCTCGTTGA	GTTTCTCCAG	AAGCGTTAAT
2651	GTCTGGCTTC	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	TGCGATGCAG
2951	ATCCGGAACA	TAATGGTGCA	GGGCGCTGAC	TTCGCGGTTT	CCAGACTTTA
3001	CGAAACACGG	AAACCGAAGA	CCATTCATGT	TGTTGCTCAG	GTCGCAGACG
3051	TTTTGCAGCA	GCAGTCGCTT	CACGTTGCTT	CGCGTATCGG	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	AAGCGGTCTT	CGCCGAAAAT	GACCCAGAGC	GCTGCCGGCA
3351	CCTGTCCTAC	GAGTTGCATG	ATAAAGAAGA	CAGTCATAAG	TGCGGCGACG
3401	ATAGTCATGC	CCCGCGCCCA	CCGGAAGGAG	CTGACTGGGT	TGAAGGCTCT
3451	CAAGGGCATC	GGTCGAGATC	CCGGTGCCTA	ATGAGTGAGC	TAACCTACAT
3501	TAATTGCGTT	GCGCTCACTG	CCCGCTTTCC	AGTCGGGAAA	CCTGTCGTGC
3551	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	GTTTGCGTAT
3601	TGGGCGCCAG	GGTGGTTTTT	CTTTTCACCA	GTGAGACGGG	CAACAGCTGA
3651	TTGCCCTTCA	CCGCCTGGCC	CTGAGAGAGT	TGCAGCAAGC	GGTCCACGCT
3701	GGTTTGCCCC	AGCAGGCGAA	AATCCTGTTT	GATGGTGGTT	AACGGCGGGA
					<i>EcoRV(3797)</i>
3751	TATAACATGA	GCTGTCTTCG	GTATCGTCGT	ATCCCACTAC	CGAGATATCC
3801	GCACCAACGC	GCAGCCCGGA	CTCGGTAATG	GCGCGCATTG	CGCCCAGCGC
3851	CATCTGATCG	TTGGCAACCA	GCATCGCAGT	GGGAACGATG	CCCTCATTCA
3901	GCATTTGCAT	GGTTTGTGTA	AAACCGGACA	TGGCACTCCA	GTCGCCTTCC
3951	CGTTCCGCTA	TCGGCTGAAT	TTGATTGCGA	GTGAGATATT	TATGCCAGCC
					<i>ApaI(4040)</i>
4001	AGCCAGACGC	AGACGCGCCG	AGACAGAACT	TAATGGGCCC	GCTAACAGCG
4051	CGATTTGCTG	GTGACCCAAT	GCGACCAGAT	GCTCCACGCC	CAGTCGCGTA
4101	CCGTCTTCAT	GGGAGAAAAT	AATACTGTTG	ATGGGTGTCT	GGTCAGAGAC
4151	ATCAAGAAAT	AACGCCGGAA	CATTAGTGCA	GGCAGCTTCC	ACAGCAATGG
					<i>MluI(4243)</i>
4201	CATCCTGGTC	ATCCAGCGGA	TAGTTAATGA	TCAGCCCACT	GACGCGTTGC
4251	GCGAGAAGAT	TGTGCACCGC	CGCTTTACAG	GCTTCGACGC	CGCTTCGTTT
4301	TACCATCGAC	ACCACCACGC	TGGCACCCAG	TTGATCGGCG	CGAGATTTAA
4351	TCGCCGCGAC	AATTTGCGAC	GGCGCGTGCA	GGGCCAGACT	GGAGGTGGCA
4401	ACGCCAATCA	GCAACGACTG	TTTGCCCGCC	AGTTGTTGTG	CCACGCGGTT
4451	GGGAATGTAA	TTCAGTCCG	CCATCGCCGC	TTCCACTTTT	TCCCGCGTTT
4501	TCGCAGAAAC	GTGGCTGGCC	TGGTTCACCA	CGCGGGAAAC	GGTCTGATAA
4551	GAGACACCGG	CATACTCTGC	GACATCGTAT	AACGTTACTG	GTTTCACATT
4601	CACCACCCTG	AATTGACTCT	CTTCCGGGCG	CTATCATGCC	ATACCGCGAA

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4651  AGGTTTTGCG CCATTCGATG GTGTCCGGGA TCTCGACGCT CTCCCTTATG
4701  CGACTCCTGC ATTAGGAAGC AGCCCAGTAG TAGGTTGAGG CCGTTGAGCA
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
          NcoI(5070)
5051  CTTTAAGAAG GAGATATAAC ATGGGCAGCA GCCATCATCA TCATCATCAC
          NheI(5135)
          NdeI(5130)
5101  AGCAGCGGCC TGGTGCCCGC CGGCAGCCAT ATGGCTAGCA TGACTGGTGG
          HindIII(5191)
          EcoRI(5172)
          BamHI(5166)
          Sall(5185)
          NotI(5198)
5151  ACAGCAAATG GGTCGGATCC GAATTCGAGC TCCGTCGACA AGCTTGCGGC
5201  CGCCTGCCGA GAAACTCTCC CTAACCCAC CCAACCTCAC CAAGAAGATG
5251  AAGAAGATTG TGGATGCCGT GATCAAGTAC AAGGACAGCA GCAGTGGACG
          AatII(5302)
5301  TCAGCTCAGC GAGGTCTTCA TCCAGCTGCC CTCGCGAAAG GAGCTGCCCCG
          SacI(5364)
5351  AGTACTACGA GCTCATCCGC AAGCCCGTGG ACTTCAAGAA GATAAAGGAG
5401  CGCATTCGCA ACCACAAGTA CCGCAGCCTC AACGACCTAG AGAAGGACGT
          AatII(5451)
5451  CATGCTCCTG TGCCAGAACG CACAGACCTT CAACCTGGAG GGCTCCCTGA
5501  TCTATGAAGA CTCCATCGTC TTGCAGTCGG TCTTCACCAG CGTGCGGCAG
5551  AAAATCGAGA AGGAGGATGA CAGTGAAGGC GAGGAGAGTG AGGAGGAGGA
5601  AGAGGGCGAG GAGGAAGGCT CCGAATCCGA ATCTCGGTCC GTCAAAGTGA
          HindIII(5657)
5651  AGATCAAGCT TGGCCGGAAG GAGAAGGCAC AGGACCGGCT GAAGGGCGGC
5701  CGGCGGCGGC CGAGCCGAGG GTCCCGAGCC AAGCCGGTCG TGAGTGACGA
5751  TGACAGTGAG GAGGAACAAG AGGAGGACCG CTCAGGAAGT GGCAGCGAAG
5801  AAGACGACTA CAAGGACGAC GATGACAAAT GATAAGTCGA GCACCACCAC
5851  CACCACCACT GAGATCCGGC TGCTAACAAA GCCCGAAAGG AAGCTGAGTT
5901  GGCTGCTGCC ACCGCTGAGC AATAACTAGC ATAACCCCTT GGGGCCTCTA
5951  AACGGGTCTT GAGGGGTTTT TTGCTGAAAG GAGGAACTAT ATCCGGAT

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