**EPAS1 ENSG00000116016**

**2613 nt**

ATGACAGCTGACAAGGAGAAGAAAAGGAGTAGCTCGGAGAGGAGGAAGGAGAAGTCCCGGGATGCTGCGCGGTGCCGGCGGAGCAAGGAGACGGAGGTGTTCTATGAGCTGGCCCATGAGCTGCCTCTGCCCCACAGTGTGAGCTCCCATCTGGACAAGGCCTCCATCATGCGACTGGCAATCAGCTTCCTGCGAACACACAAGCTCCTCTCCTCAGTTTGCTCTGAAAACGAGTCCGAAGCCGAAGCTGACCAGCAGATGGACAACTTGTACCTGAAAGCCTTGGAGGGTTTCATTGCCGTGGTGACCCAAGATGGCGACATGATCTTTCTGTCAGAAAACATCAGCAAGTTCATGGGACTTACACAGGTGGAGCTAACAGGACATAGTATCTTTGACTTCACTCATCCCTGCGACCATGAGGAGATTCGTGAGAACCTGAGTCTCAAAAATGGCTCTGGTTTTGGGAAAAAAAGCAAAGACATGTCCACAGAGCGGGACTTCTTCATGAGGATGAAGTGCACGGTCACCAACAGAGGCCGTACTGTCAACCTCAAGTCAGCCACCTGGAAGGTCTTGCACTGCACGGGCCAGGTGAAAGTCTACAACAACTGCCCTCCTCACAATAGTCTGTGTGGCTACAAGGAGCCCCTGCTGTCCTGCCTCATCATCATGTGTGAACCAATCCAGCACCCATCCCACATGGACATCCCCCTGGATAGCAAGACCTTCCTGAGCCGCCACAGCATGGACATGAAGTTCACCTACTGTGATGACAGAATCACAGAACTGATTGGTTACCACCCTGAGGAGCTGCTTGGCCGCTCAGCCTATGAATTCTACCATGCGCTAGACTCCGAGAACATGACCAAGAGTCACCAGAACTTGTGCACCAAGGGTCAGGTAGTAAGTGGCCAGTACCGGATGCTCGCAAAGCATGGGGGCTACGTGTGGCTGGAGACCCAGGGGACGGTCATCTACAACCCTCGCAACCTGCAGCCCCAGTGCATCATGTGTGTCAACTACGTCCTGAGTGAGATTGAGAAGAATGACGTGGTGTTCTCCATGGACCAGACTGAATCCCTGTTCAAGCCCCACCTGATGGCCATGAACAGCATCTTTGATAGCAGTGGCAAGGGGGCTGTGTCTGAGAAGAGTAACTTCCTATTCACCAAGCTAAAGGAGGAGCCCGAGGAGCTGGCCCAGCTGGCTCCCACCCCAGGAGACGCCATCATCTCTCTGGATTTCGGGAATCAGAACTTCGAGGAGTCCTCAGCCTATGGCAAGGCCATCCTGCCCCCGAGCCAGCCATGGGCCACGGAGTTGAGGAGCCACAGCACCCAGAGCGAGGCTGGGAGCCTGCCTGCCTTCACCGTGCCCCAGGCAGCTGCCCCGGGCAGCACCACCCCCAGTGCCACCAGCAGCAGCAGCAGCTGCTCCACGCCCAATAGCCCTGAAGACTATTACACATCTTTGGATAACGACCTGAAGATTGAAGTGATTGAGAAGCTCTTCGCCATGGACACAGAGGCCAAGGACCAATGCAGTACCCAGACGGATTTCAATGAGCTGGACTTGGAGACACTGGCACCCTATATCCCCATGGACGGGGAAGACTTCCAGCTAAGCCCCATCTGCCCCGAGGAGCGGCTCTTGGCGGAGAACCCACAGTCCACCCCCCAGCACTGCTTCAGTGCCATGACAAACATCTTCCAGCCACTGGCCCCTGTAGCCCCGCACAGTCCCTTCCTCCTGGACAAGTTTCAGCAGCAGCTGGAGAGCAAGAAGACAGAGCCCGAGCACCGGCCCATGTCCTCCATCTTCTTTGATGCCGGAAGCAAAGCATCCCTGCCACCGTGCTGTGGCCAGGCCAGCACCCCTCTCTCTTCCATGGGGGGCAGATCCAATACCCAGTGGCCCCCAGATCCACCATTACATTTTGGGCCCACAAAGTGGGCCGTCGGGGATCAGCGCACAGAGTTCTTGGGAGCAGCGCCGTTGGGGCCCCCTGTCTCTCCACCCCATGTCTCCACCTTCAAGACAAGGTCTGCAAAGGGTTTTGGGGCTCGAGGCCCAGACGTGCTGAGTCCGGCCATGGTAGCCCTCTCCAACAAGCTGAAGCTGAAGCGACAGCTGGAGTATGAAGAGCAAGCCTTCCAGGACCTGAGCGGGGGGGACCCACCTGGTGGCAGCACCTCACATTTGATGTGGAAACGGATGAAGAACCTCAGGGGTGGGAGCTGCCCTTTGATGCCGGACAAGCCACTGAGCGCAAATGTACCCAATGATAAGTTCACCCAAAACCCCATGAGGGGCCTGGGCCATCCCCTGAGACATCTGCCGCTGCCACAGCCTCCATCTGCCATCAGTCCCGGGGAGAACAGCAAGAGCAGGTTCCCCCCACAGTGCTACGCCACCCAGTACCAGGACTACAGCCTGTCGTCAGCCCACAAGGTGTCAGGCATGGCAAGCCGGCTGCTCGGGCCCTCATTTGAGTCCTACCTGCTGCCCGAACTGACCAGATATGACTGTGAGGTGAACGTGCCCGTGCTGGGAAGCTCCACGCTCCTGCAAGGAGGGGACCTCCTCAGAGCCCTGGACCAGGCCACCTGA

Forward (2203-2223: 20 bp) Tm: 59.90

TTGATGTGGAAACGGATGAA

Reverse（2378-2398: 20 bp）Tm: 60.00

GGAACCTGCTCTTGCTGTTC

Product: 196 bp

produced by Primer3 (version 0.4.0)

GRCh38.p13 (Ensemble Genome Browser: release 100)