

Psg31 (EG381852) CDS

Exon1 (L)

ATGGAAGCATCCTTTGTGCTTCCATGCAAGTGGTGTACTCACTTGCAAGGGCTTCTGCTCACAG

Exon2 (N1)

CCTCATTNTTAACTGTTGTCACCTGCCTGCCACTGCCCAAATAACCATTGAATTAGTGCCACCCCATG
TGATTGAAGGAGAAAATGTTCTCATACGTGTCAACAATCTGCCAGAGAATCTTACAACCTTAGTCTGGT
TCAGAGGAATGAGGATTAAGAGCCCTCAAATTGGACAATATACACTGGCCACTAATGTTACTGTGCTGG
GGCCTGGTACAGTGGTAGAGAACTTTGTACAGCAATGGATCCCTGCAGACTACAATGTCACCCAGG
AGGACATAGGATTTACAGCCTACGAGTCATGAATAGACATGGAAAAATTGTGTCAATAACATCCATAT
ACCTCAACGTGTACT

Exon3 (N1*)

CCTCCTTTTTAACTGCTGTCACCTGCCTACCCTGCCCAAATAACCATTGAATTAGTGCCACCCCATG
TGATTGAAGGAGAAAATGTTCTCATACGTATCAACAATCTGCCAGAGAATCTTACAACCTTAGCCTGGT
TCAGAGGAATGAGGATTAAGAGCCCTCAAATTGGACAATATACACTGGCCACTAATGTTACTGTGCTGG
GGCCTGGTACAGTGGTAGAGAACTTTGTACAGCAATGGATCCGTGCAATCTACAATGTCACCAAAG
AGGATATAGGATTTACAGCCTACGAGTCATGAATAGACATGGAGAAATTGTGTCAATAACATCCATAT
ACCTCAACGTGTACT

Exon4 (N2)

CATCTCTTTGGACATGTGAGCACCTTCTCCCCATGCCAAGCTCACCATTGAATCAGTGCCTCCCGGCA
TTTCTGAAGGGGGAAGTGTCTTCTACTGGTTAAAAATCTCCCCAAAACCTTCTATCCCTTTTCTGGT
ACAAAGGAGTTATTGCAGTGAAGAAATTTGAGTTGCCAGACACATAAAAAGCCACAAATTCAAGTGTTC
CAGGGCCTGCACACACTGGTTCGTGAGACAGTATTCAGCAATGGATCCCTTCTGCTACAGGAAGTTATGC
AGAGTGATACTGGATTCTATACTCTACGAACATGAGTACAGATCTGAAAGATGAAGTAGCACATGTGC
AGCTGTACATGGACA

Exon5 (N3)

CATCCCTTTCTACTTGCTACCAACTTTCTCAAGTCAAAATTGAATCACTTCCTCAAAAAGTTGCTGTAG
GGAAAAGTGTCTTCTTCTGGTTCACAATTTGCCTGAAGACTTTCAAGCATTTTTCTGGTACAAATCAG
CATATAGAAGAGATACATACAAAATTGTAGAATACAGCAGAGCCATGGATACCACCATCATGGGGAGTG
CATACAGTTTTAAGAGAGTTTATATACAACAATGGATCCATGCTGATAATTGATGTCACTGTGGATGATG
CAGGATTTTATGCTAGAAAATTTAAGAAAAGATTTCAAGATTGAGAAAGCCTACATTCAACTCCATG
TAAATA

Exon6 (N4)

GCTTTGTTCCAAACTCCAAGGACTTCTGGCTCCACTGCAAGGCTCAGTATAGAATCAGTGCCCCCAGCA
TTGTTGGAGGGGAAAGTGTCTTCTACTGGTTCACAATCTCCCCAAAAATCTTCAATCCCTTTTCTGGT
ACAAAGGTGTAATTGCAGAGGAGAAATCTGAGCTCATCCAACACATAATAGCCACAAGTTCAAGCTTGC
CAGGGCCTGCACACAGTGGTCGAGAAACAGTGTACAGCAATGGATCCATGCTGCTCCAGAGGGTTCATGC
ACAATGATACTGGATTCTATACTCTACGAACATAAGTACAGATCTGAAAGATGAAATAGCACATGTGC
AACTCCAGCTGGACA

Exon7 (N5)

CCTCCCTTTCTACTTGCTGTCACCATTGCAAGTCAAGATCGAATCACTTCCTCAGAATGTTGCTGTAG
GGAAAAGTGTCTTCTCCTAGTTCACAATTTGCCCTGAAGACTTTCAAGCATTTTTCTGGTACAAATCAG
CATATAGAAGAGATACATACAAAATTGCAGAATACAGCAGAGCCATGGACATCACCATTATGGGGAGTG
CATACAGTTTTAAGAGAGCTTATATACACCAATGGATCCATGGCGATGATTGATGTCACTGAGGATGATG
CAGGAATTTACATGCTAGAAAATTTAAGAGAAGACTTCAAAATTGAAAAAGCCTATGTTCAACTCCTTG
TAAATA

Exon8 (N6)

GCTTTGTTCCAAACTCCAAGGACTTCTGGCTCCACTGCAAGGTTTCAAGTATAGAATCAGTGCCACCCAGCA
TTGTTGAAGGGGAAAGTGTCTTCTACTGGTTCACAATCTCCCCAAAAATCTTCAATCCCTTTTCTGGT
ACAAAGGTGTGATTGCAGAGGAGAAATCTGAGCTCATCCAACACATAATAGCCACAAGTTCAAGCTTGC
CAGGGCCTGCACACAGTGGTCGAGAAACAGTGTACAGCAATGGATCCATGCTGCTCCAGAGGGTTCATGC
ACAATGATACTGGATTCTATACTCTACGAACATAAGTACAGATCTGAAAGATGAAATAGCACATGTGC
AACTCCAGCTGGACA

Exon9 (N7)

CTTCTACTTGCTGTAATCTTCTCAGCTCTGATCAACTCATAATTGAACCAGTGCCTTGGAAATATTGCTG
TAGGGAAAAGTGTCTTCTCCTTGTGTTGCAATGTCCAGAAGATGTTTCAGACATTTTTCTGGTACAAAT
CGGTGTATAGGACAGATATTTTTTAAAATTGCAGAATATAGCAGATCCATGGAATCCACTATCTGGGGC
TTGCACACAGTGAAGAGAGGTGGTGTACACTAATGGATCCCTGCTGATCCAGAATGTCAGTGCAGCATG
ATACAGGATTGTACATGTTAGAAATTTTACATAAGGACTTCAAACCTTGAGAGAGCACATGTGCAAGTCC
ATGTAAATA

Exon10 (A)

ACCCTGTTTCATGGCCTTTTGTGCGAGTGACTGACACCACAGTCAGAGTACAGAGCTCAGTAGTCTTCA
CTTGCTTCTCAGCTGACCCTGGAGTCTCCATCCGTTGGCTCTTCAATAAGCAGAGTCTGCAGCTCACAG
AGAGAATGACACTTTCCCTTCAAAGTGCCAACTCAGCATAGATCCCCTGCTGGAGGGAGGATGCTGGAA
AGTATCAATGTGAGGTCTACAACCCAGTCAGTTCAAAGTCCAGTCTCCAGTCTGTCTGTCTGTGATGG
AAGAGTGA

Psg31 predicted protein sequence

MEASFVLPCKWC HL |QGLLLTASFLTCCHLPATAQITIELVPPHVEGENVLIRVNNLPE
NLTTLVWFRGMRIKSPQIGQYTLATNVTVLGPGHSGRETLYSNGSLQIYNVTQEDIGFYS
LRVMNRHGKIVSITSIYLNVSFLTCCHLPPTAQITIELVPPHVEGENVLIRINNLP
NLTTLAWFRGMRIKSPQIGQYTLATNVTVLGPGHSGRETLYSNGSVQIYNVTKEDIGFYS
LRVMNRHGEIVSITSIYLNVSFLWTCHEHSPHAKLTIESVPPGISEGGSVLLLKLNLPK
NLLSLFWYKGVIAVKKFEVARHIKATNSSVPGAHTGRET VFSNGSLLLQEVMSDQTFY
TLRTMSTDLKDEVAHVQLYMDTSLSTCYQLSQVKIESLPQKVAVGKSVLLLHVHNLPEDFQ
AFFWYKSAYRRDITYKIVEYSRAMDITIMGSAYSLEFIYNNGSMLIIDVTVDAGFFMLE
ILRKDFKIEKAYIQLHVNSFVQNSKDSGSTARLSIESVPPSIVGGESVLLLHVHNLKLNQ
SLFWYKGVIAEESLQIHIATSSSLPGPAHSGRET VYSNGSMLLQRMHNDTGFYTLR
TISTDLKDEIAHVQLQDLTSLSTCCHLQVKIESLPQNVAVGKTVLLLHVHNLPEDFQAFF
WYKSAYRRDITYKIAEYSRAMDITIMGSAYSLELIYTNMAMIDVTEDDAGIYMLEILR
EDFKIEKAYVQLLVNSFVQNSKDSGSTARFSIESVPPSIVEGESVLLLHVHNLKLNQSLF
WYKGVIAEESLQIHIATSSSLPGPAHSGRET VYSNGSMLLQRMHNDTGFYTLRTIS
TDLKDEIAHVQLQDLTSTCCNLLSSDQLIEPVPWNI AVGKSVLLLVCNVPEDVQTFWY
KSVYRTDIFKIAEYSRSMESTIWGLAHSGREVYTNGLLIQNVTEHDTGLYMLEILHKD
FKLERAHVQVHVNPNVSWPFVVRVDTTTRVQSSVVFCTFSADPGVSI R WLFNKQSLQLTE
RMTLSPSKQLSIDPVWREDAGKYQCEVYNPVS KSSLPVCLSVME

Psg32 (Psg-ps1) CDS

Exon1 (L)

ATGACAGCAAATGCTGGTGCTGTGTTGGACGGGAAGTCTTCTTCTCAAAGAAAGGACAGTACAGTGA
AAGAGAGATGGAGGTGTCTTGGTGCTTCTCTACCAGGGTGTACACCCTGGCAGGGTCTTCTGCTCACA
G

Exon2 (N1)

CTTTTCTTTTAACTCTTGGTTCCTGCCACCCTGTCCAAGTCACCATTGAATTAGTGCCACCACAAG
TGGCTGAAGGAGAAAATGTCCTTATTATTGTTTACAGTCTGCCAGAGGATCTTACAGCCATAGCCTGGT
TCAAAGGAGTGACAAATATGAACCTCGGAATTGCATTGTATGCAGTGGCCTCTAACATCAGTGTGAAA
GGCCCGAACACAGTGGTAGAGAGACAGTGTTCAGCAATGGATCCCCTGTTGCTTACAATGTCACCCAGA
AGGACACAGGATCTATACTATACGGACCTTAAATAGACATGGAAAAATGTATCCACAACATCCATAT
ACCTCCACGTGTACA

Exon3 (N2)

CCTTCTTCTGGACTTGTGGACCTCTTTCCCTCTGCCAGCTCACTATTGAATCAGTGCCACCCAAAG
TTGCCGAAGGGGGAAGTGTCTTCTAGTTGTTACAATCTCCAGGGGAATCTTCGATCCCTTTCTGGT
ACAAAGGGATGATTGTGTCCAGGAACCTTGAGGTTGCAAGACACATAATAGACACAAATTTAAGTGTG
ATGGCCTTTACACAGTGGTAGAGAGACAATATACAGCAATGGATCCCCTCATGTTCTACAATGTGACAT
GGAAGGACAGTGGATTATACACCCTACGAACCTAAGTACAGATATGAAAACAGAATTAGCACATGTAC
AACTCCAGGTGGACG

Exon4 (N3)

CTTCCCTTTCTCCGTGCTGTAATCCCCTTACCTCTTCTCAACTCATGATTGAACCAGTGCCACGCTATG
CTGTTGAAGGAGAAAAGTGTCTTTTCATGGTTCATAACCTGCCAAAAGATCTTCAAACCTTTTCTCGGT
ACAAATCAGTGTATGGGGCTGAGATATTAATAATCACAGAATACAGCAGAGCCATGAGTTCCACCACAC
GTGGAAGTGAACCTAAAAGAAGAGAGCGTGTGTACACCAATGGATTCCTCCTGCTCCAGAATGCCACTG
AGAAAGATGCAGGAATGTACATACTAGAACTTTAAGCAGAGATTTCAAATTTGAAAAGCACAGGTGC
AATTATATGTAAACA

Exon5 (A)

AGCCTGTGTACAGCCCTTCATTTCGAGTCACCAACACCACGGTCACAATACAGAGTTCTGTGGTCCTCA
CCTGCCTCTCAGCTGACACTGGAATCTTCATCCATTGGATCTTCAATAACCAGAGTCTGCAGCTTACAG
AGAGGATGACACTATCCCCAACAAAGTGCCAACTCAGCATAGATCCTGTCAGGAAGGAGGATGCTGGAG
AGTACCAATGTGAGGTCTCCAACCCAGTCAGTTCACAGACCAGTCTCCAGTCAGCCTGGCTGTGACAA
ATGAGTGA

Psg32 predicted protein sequence

MTANAGAVLDGKFFFSKKGQYSEKRDGGVLGASLPGCTPWQGLLLTAFLLTSWFLPTTVQ
VTIELVPPQVAEGENVLIIVYSLPEDLTAIAWFKGVTNMNLGIALYALASNISVKGPEHS
GRETVFSNGSLLLHNVTQKDTGFYTIIRTLNRHGKIVSTTSIYLHVYTFFWTCGPLSPAQ
LTIESVPPKVAEGGSVLLVHNLQGNLRSFLWYKGMIVSRNLEVARHIIDTNLSVHGPLH
SGRETIYSNGSLMFYNVTWKDSGLYTLRTLSTDMKTELAHVQLQVDASLSPCCNPLTSSQ
LMIEPVPRYAVEGESVLFMVHNLPKDLQTFSWYKSVYGAIEILKITEYSRAMSSTTRGSEL
KRRERVYTNGLLLQNATEKDAGMYILETLRDFKIEKAQVQLYVKNPVSQPFIRVTNTT
VTIQSSVVLTCLSADTGIFIHWFNNQSLQLTERMTLSPTKQLSIDPVRKEDAGEYQCE
VSNPVSSQTSPLVSLAVTNE