

cDNA consensus sequence derived from four bi-directionally sequenced cDNA clones
Source Tissue: Whole lung homogenate

cgtgtctggagcggcctggccagtgtctctctgcagctcagcagacgccagcagctgccttcacatggacagcataagcacagccatctta
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ttttgtatccacagagctgttctatggcacgccctttctgggctttttgtatcattcttagtacattgtaaatagattcaaaaaaaaaaaaa
aaaaaaaa

ORF Translation

mdsistaillllalvcllltsrsk*klppgprplplgnlllrsqnmlltqlskeygsvytvhlgprrvvvlsgyqavkealvdqgeef
sgrgdyvffnftkngiafsngdrwkvllrrfsiqilrnfgmgrksieerileegsflaelrktegepfdptfvlsrsvsniicsvlfgrfdy
dderlltvirlindnfqimsspwgelynifpslldwvpghqrfiqnfkrlrdliahrvhdqasldprsprdfidcfltkmaeedpls
hfhmdtllmtthnllfggtetvgttlrhafalmkypkvqarvqeeidlvvgrtrlptledraampytavihevqrfadiipmnlphrvir
dtafrgflipkgtdiitllntvhydpsqflmpqefnpehfdanqsfkksfafmpfsagrrlclgeslarmelflyltailqsfsllqplgaped
idltplssglnlprpfqlcpr*

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+1 Met Asp Ser Ile Ser Thr Ala Ile Leu Leu Leu Leu Leu Ala Leu Val Cys Leu Leu Leu Thr Leu Ser Ser
1 ATGGACAGCA TAAGCACAGC CATCTTACTC CTGCTCCTGG CTCTCGTCTG TCTGCTCCTG ACCCTAAGCT
+1 .Ser Arg Asp Lys Xxx Lys Leu Pro Pro Gly Pro Arg Pro Leu Pro Leu Leu Gly Asn Leu Leu Leu Leu Arg
71 CAAGAGATAA GYGA AAGCTG CCTCCAGGAC CTAGACCCCT CCCACTCCTG GGAAACCTGC TGCTGCTTCG
+1 .Arg Ser Gln Asn Met Leu Thr Ser Leu Thr Gln Leu Ser Lys Glu Tyr Gly Ser Val Tyr Thr Val His Leu
141 CTCCCAAAC ATGCTGACTT CTCTCACTCA GCTGAGCAAG GAGTATGGCT CTGTGTACAC AGTGCACCTG
+1 Gly Pro Arg Arg Val Val Val Leu Ser Gly Tyr Gln Ala Val Lys Glu Ala Leu Val Asp Gln Gly Glu Glu
211 GGGCCAGGC GGGTGGTGGT CCTCAGCGGG TACCAAGCCG TGAAGGAGGC CCTGGTGGAC CAGGGAGAGG
+1 .Glu Phe Ser Gly Arg Gly Asp Tyr Pro Val Phe Phe Asn Phe Thr Lys Gly Asn Gly Ile Ala Phe Ser Asn
281 AGTTTAGTGG CCGCGGTGAC TACCCTGTCT TTTTCAACTT TACCAAGGGC AATGGCATCG CCTTCTCCAA
+1 .Asn Gly Asp Arg Trp Lys Val Leu Arg Arg Phe Ser Ile Gln Ile Leu Arg Asn Phe Gly Met Gly Lys Arg
351 TGGGGATCGA TGAAGGTGC TGAGACGGTT CTCTATCCAG ATTCTACGGA ATTTCCGGGAT GGGGAAGAGA
+1 Ser Ile Glu Glu Arg Ile Leu Glu Glu Gly Ser Phe Leu Leu Ala Glu Leu Arg Lys Thr Glu Gly Glu Pro
421 AGCATCGAGG AGCGGATCCT AGAGGAGGGC AGCTTCCTGC TGGCAGAGCT GCGGAAACT GAAGGCGAGC
+1 .Pro Phe Asp Pro Thr Phe Val Leu Ser Arg Ser Val Ser Asn Ile Ile Cys Ser Val Leu Phe Gly Ser Arg
491 CCTTTGACCC CACGTTTGTG CTGAGTCGCT CAGTGTCCAA CATTATCTGT TCCGTGCTCT TCGGCAGCCG
+1 .Arg Phe Asp Tyr Asp Asp Glu Arg Leu Leu Thr Val Ile Arg Leu Ile Asn Asp Asn Phe Gln Ile Met Ser
561 CTTCGACTAC GATGATGAGC GTCTGCTCAC CGTTATCCGC CTTATCAATG ACAACTTCCA AATCATGAGC
+1 Ser Pro Trp Gly Glu Leu Tyr Asn Ile Phe Pro Ser Leu Leu Asp Trp Val Pro Gly Pro His Gln Arg Ile
631 AGCCCCGCG GCGAGTTGTA CAACATCTTC CCGAGCCTCC TGGACTGGGT GCCCGGGCCG CACCAACGCA
+1 .Ile Phe Gln Asn Phe Lys Arg Leu Arg Asp Leu Ile Ala His Xxx Val His Asp Gln Gln Ala Ser Leu Asp
701 TCTTCCAGAA CTCAAGCGC CTGAGAGACC TCATCGCCA CAGMTCCAC GACCAGCAGG CCTCTCTAGA
+1 .Asp Pro Arg Ser Pro Arg Asp Phe Ile Asp Cys Phe Leu Thr Lys Met Ala Glu Glu Lys Glu Asp Pro Leu
771 CCCCAGATCT CCCCGGGACT TCATCGACTG CTTCTCACC AAGATGGCAG AGGAGAAGGA GGACCCACTG
+1 Ser His Phe His Met Asp Thr Leu Leu Met Thr Thr His Asn Leu Leu Phe Gly Gly Thr Glu Thr Val Gly
841 AGCCACTTCC ACATGGATAC CCTGCTGATG ACCACACATA ACCTGCTCTT TGGCGGCACC GAGACGGTGG
+1 .Gly Thr Thr Leu Arg His Ala Phe Leu Ala Leu Met Lys Tyr Pro Lys Val Gln Ala Arg Val Gln Glu Glu
911 GCACCACGCT GCGCCACGCC TTCCTGGCAC TCATGAAGTA CCCGAAAGTT CAAGCCCGCG TGCAGGAGGA
+1 .Glu Ile Asp Leu Val Val Gly Arg Thr Arg Leu Pro Thr Leu Glu Asp Arg Ala Ala Met Pro Tyr Thr Asp
981 GATCGACCTC GTGGTGGGAC GCACGCGGTT GCCGACGCTG GAGGACCGCG CGGCCATGCC TTACACAGAT
+1 Ala Val Ile His Glu Val Gln Arg Phe Ala Asp Ile Ile Pro Met Asn Leu Pro His Arg Val Ile Arg Asp
1051 GCTGTGATCC ACGAGGTGCA GCGCTTTGCA GACATCATCC CCATGAACTT GCCGCACCGC GTCATTCCGG
+1 .Asp Thr Ala Phe Arg Xxx Phe Leu Ile Pro Lys Gly Thr Asp Ile Ile Thr Leu Leu Asn Thr Val His Tyr
1121 ACACGGCCTT TCGC RGC TTC CTGATACCCA AGGGCACCGA TATCATCACC CTCCTTAACA CCGTCCACTA
+1 .Tyr Asp Pro Ser Gln Phe Leu Xxx Pro Gln Glu Phe Asn Pro Glu His Phe Leu Asp Ala Asn Gln Ser Phe
1191 CGACCCCAGC CAGTTCTGA YGCCCCAGGA GTTCAACCCT GAGCATT TTTT TGGATGCCAA TCAGTCTTCT
+1 Lys Lys Ser Pro Ala Phe Met Pro Phe Ser Ala Gly Arg Arg Leu Cys Leu Gly Glu Ser Leu Ala Arg Met
1261 AAGAAGAGCC CAGCCTTTAT GCCCTTCTCA GCTGGGCGCC GTCTGTGCCT GGGCGAGTCG CTGGCGCGCA
+1 .Met Glu Leu Phe Leu Tyr Leu Thr Ala Ile Leu Gln Ser Phe Ser Leu Gln Pro Leu Gly Ala Pro Glu Asp
1331 TGGAGCTCTT TCTGTACCTC ACCGCCATCC TSCAGAGCTT CTCGCTGCAG CCGCTGGGTG CGCCCCAGGA
+1 .Asp Ile Xxx Leu Thr Pro Leu Ser Ser Gly Leu Gly Asn Leu Pro Arg Xxx Phe Gln Leu Cys Leu Cys Pro
1401 CATC KACTG ACCCCGCTCA GCTCAGGT CT SGGCAATTG CCGCGGYCT TCCAGCTGTG YCTGTGCCG
+1 Arg ***
1471 CGCTAA

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2FM ORF SNPs

Nucleotides numbered from ATG

Tissue Sources

Rhesus macaque lung (n=2)

Rhesus macaque nasal ethmoturbinates (n=14)

Position	Lung Clones	Ethmoid Clones	Baylor Data*	Translation
82	C / T	C / T	C (1)	Arg v. Stop
744	A / C	A / C	A (1) / C (2)	Arg v. Ser
1135	G	A / G	G (2)	Ser v. Gly
1211	C / T	C / T	C (1) / T (1)	Thr v. Met
1362	C / G	C / G	C (1) / G (4)	Silent (Leu)
1405	G	T / G	G (2)	Tyr v. Asp
1431**	G / C	C	C (1) / T (1)	Silent (Leu)**
1447	T / C	T / C	T (1) / C (1)	Ser v. Pro
1461	T / C	T / C	C (1)	Silent (Cys)

*(number of Blast hits against Baylor data 022605)

** G / C SNP and Baylor T / C SNP both yield Leu