

Isolation of the gene coding for the alpha subunit of the human high affinity IgE receptorJ.Kochan, L.F.Pettine, J.Hakimi¹, K.Kishi² and J.P.Kinet³

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The receptor FcERI with high affinity for immunoglobulin E is found exclusively on mast cells, basophils, and related cells. Aggregation of this receptor triggers both the release of preformed mediators such as histamine and serotonin and the synthesis of leukotrienes (1). We have previously described the isolation of a cDNA presumptively coding for the alpha subunit of the rat FcERI (2). More recent data from our laboratories has confirmed the identity of the cDNA which was isolated (3). We now report on the isolation of a corresponding cDNA coding for the alpha subunit of the human FcERI.

A cDNA library, constructed in lambda from polyA⁺ RNA extracted from KU812 cells, was screened by in-situ hybridization with a rat alpha cDNA probe. Positively hybridizing clones were sequenced by the dideoxy chain termination method (the sequence was determined for both strands), and the nucleotide sequence as well as the corresponding amino acid sequence are presented below. (The predicted site of signal peptidase cleavage is indicated by an arrow, and the transmembrane region is underlined.) Overall, 49% of the amino acid residues of the human and rat alpha FcERI are identical. The greatest level of homology is within the transmembrane domain where 9 amino acid residues surrounding the common aspartic acid residue are identical. There is also 37% identity between the human alpha of the FcERI and the mouse FcGRI (alpha gene).

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TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCAACCGAGCATGGGCTATATTTGAAGCCTTAGATCTCTCCAGCAGATAAGCACCAGGAGTCCAT 99
GAAGAAG ATG GCT CCT GCC ATG GAA TCC CCT ACT CTA CTG TGT GTA GCC TTA CTG TTC TTC GCT CCA GAT GGC GTG 175
      MET Ala Pro Ala Met Glu Ser Pro Thr Leu Leu Cys Val Ala Leu Leu Phe Phe Ala Pro Asp Gly Val
TTA GCA1GTC CCT CAG AAA CCT AAG GTC TCC TTG AAC CCT CCA TGG AAT AGA ATA TTT AAA GGA GAG AAT GTG ACT 250
Leu Ala Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile Phe Lys Gly Glu Asn Val Thr
CTT ACA TGT AAT GGG AAC AAT TTC TTT GAA GTC AGT TCC ACC AAA TGG TTC CAC AAT GGC AGC CTT TCA GAA GAG 325
Leu Thr Cys Asn Gly Asn Asn Phe Phe Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
ACA AAT TCA AGT TTG AAT ATT GTG AAT GCC AAA TTT GAA GAC AGT GGA GAA TAC AAA TGT CAG CAC CAA CAA GTT 400
Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly Glu Tyr Lys Cys Gln His Gln Gln Glu
AAT GAG AGT GAA CCT GTG TCC GTG GAA GTC TTC AGT GAC TGG CTG CTC CTT CAG GCC TCT GCT GAG GTG GTG ATG 475
Asn Glu Ser Glu Pro Val Tyr Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val Val Met
GAG GGC CAG CCC CTC TTC CTC AGG TGC CAT GGT TGG AGG AAC TGG GAT GTG TAC AAG GTG ATC TAT TAT AAG GAT 550
Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp
GGT GAA GCT CTC AAG TAC TGG TAT GAG AAC CAC AAC ATC TCC ATT ACA AAT GCC ACA GTT GAA GAC AGT GGA ACC 625
Gly Glu Ala Leu Lys Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu Asp Ser Gly Thr
TAC TAC TGT ACG GGC AAA GTG TGG CAG CTG GAC TAT GAG TCT GAG CCC CTC AAC ATT ACT GTA ATA AAA GCT CCG 700
Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro
CGT GAG AAG TAC TGG CTA CAA TTT TTT ATC CCA TTG TTG GTG GTG ATT CTG TTT GCT GTG GAC ACA GGA TTA TTT 775
Arg Glu Lys Tyr Trp Leu Gln Phe Phe Ile Pro Leu Leu Val Val Ile Leu Phe Ala Val Asp Thr Gly Leu Phe
ATC TCA ACT CAG CAG CAG GTC ACA TTT CTC TTG AAG ATT AAG AGA ACC AGG AAA GGC TTC AGA CTT CTG AAC CCA 850
Ile Ser Thr Gln Gln Gln Val Thr Phe Leu Leu Lys Ile Lys Arg Thr Arg Lys Gly Phe Arg Leu Leu Asn Pro
CAT CCT AAG CCA AAC CCC AAA AAC TGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCAGCATCAGCAATTGCTACT 940
His Pro Lys Pro Asn Pro Lys Asn Asn
CAATTGTCAACACAGCTTGCAATATACATAGAAACGCTGTGCTCAAGGATTTATAGAAATGCTTCATTAACCTGAGTGAAGCTGGTTAAGTGCCATG 1039
TAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAAATGATAGATTCAITTTATAGCATTTGTAAAGAGATGTTCAATTTCAATAAAAA 1138
AATATAAACCACTGTAAACAGATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAA 1198

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