NCBI ID: NG\_012575.2

Description: Homo sapiens angiotensin I converting enzyme 2 (ACE2), RefSeqGene on chromosome X

Localization: 6199..46126 in Chromosome X of homo sapiens

Gene ID: 59272/ HGNC:HGNC:13557/ MIM:300335 (HGNC-HUGO gene nomenclature committee/ Mim- Mendelian Inheritance in Man

Synonim Gene: ACEH

Gene size: 39928 bp(base pair)

Organism: Homo sapiens

Taxonomy Homo sapiens: ['Eukaryota', 'Metazoa', 'Chordata', 'Craniata', 'Vertebrata', 'Euteleostomi', 'Mammalia', 'Eutheria', 'Euarchontoglires', 'Primates', 'Haplorrhini', 'Catarrhini', 'Hominidae', 'Homo']

Protein: angiotensin-converting enzyme 2 isoform 1 precursor

Protein ID: NP\_001358344.1

Transcript ID: NM\_001371415.1

Gene translation: MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENPYASIDISKGENNPGFQNTDDVQTSF (O codão de Stop nunca aparece mas é como se tivesse lá)

Because of the qualifiers we notice that our protein is subdivided in 3 parts, the first one is sig\_peptide: is a signal peptide coding sequence; coding sequence for an N-terminal domain of a secreted protein; this domain is involved in attaching nascent polypeptide to the membrane leader sequence. This sig\_peptide starts in the first amino acid and finish in the 17 amino acid. The last 2 are mat\_peptide: mature peptide or protein coding sequence; coding sequence for the mature or final peptide or protein producte following post-translational modification; the location does not include the stop codon. The first peptide is a Angiotensin-converting enzyme 2 with the ID: PRO\_ 0000028570. The second peptide is a Processed angiotensin-converting enzyme 2 with the ID: PRO\_ 0000292268.

<https://www.uniprot.org/uniprot/Q9BYF1> (Decher até a parte que diz PTM/Processing)

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In these qualifiers we have a lot of misc\_features: Regions of biological interest witch can not be described by any other feature Key; a new or a rare feature.

The 1st feature gives us Region: Interaction with SARS-CoV spike glycoprotein. This feature gives us a Pubmed article <https://pubmed.ncbi.nlm.nih.gov/15791205/>

(In particular, residues along the first α-helix, and lysine 353 and proximal residues at the N-terminus of β-sheet 5, participate in S-protein binding and in infection) # A posição onde da binding se quisermos mostrar.

(This S-protein-binding region of ACE2 remains intact in the presence of an inhibitor that dramatically alters the overall conformation of ACE2)

Resumo: Este artigo fala o surto de Sars Covid, que acontceu em 2005, onde foram infetadas cerca de 100 pessoas onde ocorreu a morte de 10%, onde foram estudar o virus e repararam que o Gene S do virus dava bind com o gene ACE2 do ser humano e de outro animais, mas repararam que teria de ocorrer umas alterações no Gene S para que este podesse ter uma afinidade alta com o gene humano ACE2 repararam tb que não era por alterarem a estrutrura da proteina com inibidor que esta iria fazer diferença na infeção. <http://europepmc.org/article/MED/15791205> # O link do artigo completo

The 2nd one gives us a Pubmed article <https://pubmed.ncbi.nlm.nih.gov/14754895/>

<https://www.jbc.org/content/279/17/17996.long> # link do artigo completo

resumo: Este artigo fala sobre a fromação do ACE2 e de todas as suas substruturas e crescimento em meio de iniibição quais as diferenças.

The 3rd one gives us a Pubmed article <https://pubmed.ncbi.nlm.nih.gov/15084671/>

Resumo: (enzima encontrada no na bilis, durante o cancro desta mesma)

<https://www.mcponline.org/content/3/7/715.long> # link do artigo completo

The 4th one gives us a Pubmed article <https://pubmed.ncbi.nlm.nih.gov/19159218/>

Resumo: Artigo que deteta glicoproteins, com enzimas de digestão devido ao facto de a proteomica não ter maneira de o fazer.

<https://pubs.acs.org/doi/abs/10.1021/pr8008012> # link do artigo completo

The 5th one gives us a Region: Essential for cleavage by ADAM17. This feature gives a Pubmed article <https://pubmed.ncbi.nlm.nih.gov/24227843/>

(Thus, TMPRSS2 expression increases uptake of SARS-S1-Fc and potentially authentic SARS-CoV, which might account for increased SARS-S-driven entry into TMPRSS2-positive cells.)

(Thus, TMPRSS2 expression increases uptake of SARS-S1-Fc and potentially authentic SARS-CoV, which might account for increased SARS-S-driven entry into TMPRSS2-positive cells.)

Resumo: TMPRSS2 ajuda na infeção do COVID fazendo a clivagem do ACE2 e da spike glicoprotein, fazendo com que a infeção seja aumentada, mas sem o TMPRSS2 o virus consegue infetar na mesma.

<http://europepmc.org/article/MED/24227843> #link do artigo completo