

Homo sapiens c22orf15 Conceptual Translation (NM_182520.3)

```

agatgtctccgccccactgccatggagaccagcttggagcttaggggagctgctgtgg 60 5' UTR Variants
cccagggctcagtggggaggaagaggagggcaggagctctggactagctgcagggtttga 120
gctagggtgaagcagcagaaccacagaggtggctgagcaggggctggccctgggaccca 180 Upstream in-frame stop codon
gccatccacactcacacatccacttctccctccagagcccggccctgaagcaggtctctg 240
ctccacgcttttcccttagttggggaatcgagagttgggggatcaagcccccacatctc 300
cctcaccgctgcagctatgtttatcaaggtgatgtttgggctggctgctcggtgctgg 360 ex1|ex2
      M F I K V M F G A G C S V L V
      ↗
tgaacacctcttgaggctggtgaacctcaccgccacctgaggcagaaagcagggttgc 420
  N T | S C R L V N L T A H L R Q | K A G L P 35
cccagatgagaccattgctctcctggctgaggatggcaacctagtgagcctggaggagg 480 ex2|ex3
  P D A T I A L L A E D G N L V S L E E D 55 Disordered Region
acctgaaggaaggggcttccccgggcccagaccatgggcaactccctactgaaggagcgag 540
  L K E G A R A Q T M G N S L L K E R A 75
ccatataatgtcctcgttcggatcatcaagggagaggacatggcctccaccgctatgagt 600 ex3|ex4
  I Y V L V R I I K G E D M A S T R Y E S 95
ccctattggagaacctggatgaccattaccagagctggcagaggaactgcgaggctgt 660 ex4|ex5
  L L E N L D D H Y P E L A E E L [R R L S 115 Disordered Region
      ↖
caggcctcctcctctgtgggccacaactggaggaagcgtatgggcactcggcgaggccgcc 720 Disordered Region
  G L S S V G H N W R K R M ] G T {R R G R H 135
atgagcaaagccccacttcaaggcccagaaagggccctgattaaggggatggattgcaca 780 ex5|ex6
  E Q P R P R K } G P D * 148
ctgtagtgagacatccatcctgacccacctcatcagccagggagctccctgaagacagg 840 3' UTR Variants
ccatcgagagaggcacacaacaggctgtggtctaaaataaaacttttaattgcaca 895 polyA signal
                                     [Poly tail added here]

```

Key:

Protein / sequence name	Position	E-value	Sequence
c22orf15	104	{6.7}	NLDDHYPELAELRRLS + d+Y e ++e r

Conserved Amino Acids

Phosphorylation Site

O-GlcNAc Site

Sumoylation site

Position	Peptide	Score	Cutoff	P-value	Type
49 - 53	LLAEDGNLVLREDLKEGA	30.554	29.92	0.174	SUMO Interaction
84	YVLVRIIKGEDMAST	24.897	2.13	0.002	Sumoylation Consensus
145	SPTSRRKGPDP***	3.492	3.32	0.093	Sumoylation Nonconsensus

Orange vertical line: cleavage site - GvH score: -6.79 (threshold: -2.1)

Blue vertical line: R-2 motif (Gavel: prediction of cleavage sites for mitochondrial preseq)

Pat4 nuclear localization signal

Pink box: pat7 nuclear localization signal

[]: bipartite nuclear localization signal

{}: nuclear localization signal

Black underline: 2nd peroxisomal targeting signal

↗ ↖ : interleukin 2 receptor subunit gamma (IL2RG) domain