**Bag-1 internal ribosome entry site (IRES)**

The bag-1 internal ribosome entry site (IRES) is a cis-acting element located in the 5 ' untranslated region of the BAG-1 protein mRNA. Its effects apoptosis through IRES mediated translation of the BAG-1 protein.

When expressed, the BAG-1 protein is known to enhance the anti-apoptotic properties of the Bcl-2 protein. Although bag-1 translation usually occurs via a cap-dependent mechanism it has been found to contain an IRES in its 5' UTR. Translation via the IRES has been found to be common following heat shock when cap-dependent scanning is compromised.

>**AF022224.1** Homo sapiens Bcl-2-binding protein (BAG-1) mRNA, complete cds.

ACGCCGCGCTCAGCTTCCATCGCTGGGCGGTCAACAAGTGCGGGCCTGGCTCAGCGCGGG

GGGGCGCGGAGACCGCGAGGCGACCGGGAGCGGCTGGGTTCCCGGCTGCGCGCCCTTCGG

CCAGGCCGGGAGCCGCGCCAGTCGGAGCCCCCGGCCCAGCGTGGTCCGCCTCCCTCTCGG

CGTCCACCTGCCCGGAGTACTGCCAGCGGGCATGACCGACCCACCAGGGGCGCCGCCGCC

GGCGCTCGCAGGCCGCGGATGAAGAAGAAAACCCGGCGCCGCTCGACCCGGAGCGAGGAG

TTGACCCGGAGCGAGGAGTTGACCCTGAGTGAGGAAGCGACCTGGAGTGAAGAGGCGACC

CAGAGTGAGGAGGCGACCCAGGGCGAAGAGATGAATCGGAGCCAGGAGGTGACCCGGGAC

GAGGAGTCGACCCGGAGCGAGGAGGTGACCAGGGAGGAAATGGCGGCAGCTGGGCTCACC

GTGACTGTCACCCACAGCAATGAGAAGCACGACCTTCATGTTACCTCCCAGCAGGGCAGC

AGTGAACCAGTTGTCCAAGACCTGGCCCAGGTTGTTGAAGAGGTCATAGGGGTTCCACAG

TCTTTTCAGAAACTCATATTTAAGGGAAAATCTCTGAAGGAAATGGAAACACCGTTGTCA

GCACTTGGAATACAAGATGGTTGCCGGGTCATGTTAATTGGGAAAAAGAACAGTCCACAG

GAAGAGGTTGAACTAAAGAAGTTGAAACATTTGGAGAAGTCTGTGGAGAAGATAGCTGAC

CAGCTGGAAGAGTTGAATAAAGAGCTTACTGGAATCCAGCAGGGTTTTCTGCCCAAGGAT

TTGCAAGCTGAAGCTCTCTGCAAACTTGATAGGAGAGTAAAAGCCACAATAGAGCAGTTT

ATGAAGATCTTGGAGGAGATTGACACACTGATCCTGCCAGAAAATTTCAAAGACAGTAGA

TTGAAAAGGAAAGGCTTGGTAAAAAAGGTTCAGGCATTCCTAGCCGAGTGTGACACAGTG

GAGCAGAACATCTGCCAGGAGACTGAGCGGCTGCAGTCTACAAACTTTGCCCTGGCCGAG

TGAGGTGTAGCAGAAAAAGGCTGTGCTGCCCTGAAGAATGGCGCCACCAGCTCTGCCGTC

TCTGGATCGGAATTTACCTGATTTCTTCAGGGCTGCTGGGGGCAACTGGCCATTTGCCAA

TTTTCCTACTCTCACACTGGTTCTCAATGAAAAATAGTGTCTTTGTGATTTGAGTAAAGC

TCCTATTCTGTTTTTCACAAAAAAAAAAAAA

>**U46917.1** Human Bcl-2 associating athanogene-1 protein (hBAG-1) mRNA, complete cds.

TGGGCGGTCAACAAGTGCGGGCCTGGCTCAGCGCGGGGGGGCGCGGAGACCGCGAGGCGACCGGGAGCGGCTGGGTTCCCGGCTGCCCCCCCTTCGCCCAGCCCGGGAGCCGCCCCAGTCGGAGCCTCCGGCCCAGCGTGGTCCGCCTCCCTCTCGGCGTCCACCTGCCCGGAGTACTGCCAGCGGGCATGACCGACCCACCAGGGGCGCCGCCGCCGGCGCTCGCAGGCCGCGGATGAAGAAGAAAACCCGGCGCTTCTCGACCCGGAGCAAGGAGTTGACCCGGAGCAAGGAGTTGACCCTGAGTGAGGAAGCGACCTGGAGTGAAGAGGCGACCCAGAGTGAGGAGGCGACCCAGGGCGAAGAGATG

>**Z35491.1** H.sapiens mRNA for novel glucocorticoid receptor-associated protein

TGGGCGGTCAACAAGTGCGGGCCTGGCTCAGCGCGGGGGGGCGCGGAGACCGCGAGGCGACCGGGAGCGGCTGGGTTCCCGGCTGCGCGCCCTTCGGCCAGGCCGGGAGCCGCGCCAGTCGGAGCCCCCGGCCCAGCGTGGTCCGCCTCCCTCTCGGCGTCCACCTGCCCGGAGTACTGCCAGCGGGCATGACCGACCCACCAGGGGCGCCGCCGCCGGCGCTCGCAGGCCGCGGATGAAGAAGAAAACCCGGCGCCGCTCGACCCGGAGCGAGGAGTTGACCCGGAGCGAGGAGTTGACCCTGAGTGAGGAAGCGACCTGGAGTGAAGAGGCGACCCAGAGTGAGGAGGCGACCCAGGGCGAAGAGATG

>**AF116273.1** Homo sapiens Bag1 protein variant mRNA, complete cds.

TCAACAAGTGCGGGCCTGGCTCAGCGCGGGGGGGCGCGGAGACCGCGAGGCGACCGGGAGCGGCTGGGTTCCCGGCTGCGCGCCCTTCGGCCAGGCCGGGAGCCGCGCCAGTCGGAGCCCCCGGCCCAGCGTGGTCCGCCTCCCTCTCGGCGTCCACCTGCCCGGAGTACTGCCAGCGGGCATGACCGACCCACCAGGGGCGCCGCCGCCGGCGCTCGCAGGCCGCGGATGAAGAAGAAAACCCGGCGCCGCTCGACCCGGAGCGAGGAGTTGACCCGGAGCGAGGAGTTGACCCTGAGTGAGGAAGCGACCTGGAGTGAAGAGGCGACCCAGAGTGAGGAGGCGACCCAGGGCGAAGAGATG

**Antizyme RNA frameshifting stimulation element**

Antizyme RNA frameshifting stimulation element is a structural element which is found in antizyme mRNA and is known to promote frameshifting. Antizyme genes have two partially overlapping open reading frames, the second, which encodes the functional (antizyme) protein requires +1 translational frameshifting. This frameshift is stimulated by a pseudoknot present 3' of the frameshift site in the antizyme mRNA. The frameshifting efficiency is dependent on the concentration of polyamines in the cell, when the polyamine concentration is high frameshifting is more likely to occur which leads to an increase in the quantity of functional antizyme produced. The functional antizyme acts to reduce ornithine decarboxylase (ODC) activity which leads to a drop in polyamines present in the cell. Therefore, this family can be thought of as a biosensor for intracellular free polyamines that functions via a negative feedback loop.

>**AF293339.1** - Homo sapiens ornithine decarboxylase antizyme 4 mRNA, complete cds.

TGATGTCCCTCACCCACCCCTGAAGATCCCAGGTGGGCGAGGGGATAGCCAGAGGGATC

>**AC004152.1**/16641-16699 - Homo sapiens chromosome 19, fosmid 37308, complete sequence.

TGATGCCCCTCACCCACCCCTGAAGATCCCAGGTGGGCGAGGGAATAGTCAGAGGGATC

>**AF242520.1**/225-280 - Homo sapiens ornithine decarboxylase antizyme silent variant sequence.

TGATGCCCCTCACCCACTGTCGAAGATCCCCGGTGGGCGAGGGGGCGGCAGGGATC

**APC internal ribosome entry site (IRES)**

The APC internal ribosome entry site (IRES) is an RNA element which is located in the coding sequence of the APC gene. APC is a tumour suppressor gene which is associated with the inherited disease adenomatous polyposis coli (APC). It is thought that IRES-mediated translation of APC is important for an apoptotic cascade.

> **M74088.1** - Human APC gene mRNA, complete cds.

AGTCTTCCTTTAACTGAAAATTTTTCCTTACAAACAGATATGACCAGAAGGCA

> **M73548.1** - Human polyposis locus (DP2.5 gene) mRNA, complete cds.

AGTCTTCCTTTAACTGAAAATTTTTCCTTACAAACAGATTTGACCAGAAGGCA

**Apolipoprotein B (apoB) 5' UTR cis-regulatory element**

The apolipoprotein B (apoB) 5′ UTR cis regulatory element is an RNA element located in the 5′ UTR of the human apoB mRNA. This structured element increases translation of the apoB protein or a reporter gene.

>**X04714.1**/1-127 Human mRNA for apolipoprotein B-100 (apoB-100)

ATTCCCACCGGGACCTGCGGGGCTGAGTGCCCTTCTCGGTTGCTGCCGCTGAGGAGCCCGCCCAGCCAGCCAGGGCCGCGAGGCCGAGGCCAGGCCGCAGCCCAGGAGCCGCCCCACCGCAGCTGGC

>**X16152.1**/899-1020 Human apoB gene 5' regulatory region (apolipoprotein B)

ATTCCCACCGGGACCTGCGGGGCTGAGTGCCCTTCTCGGTTGCTGCCGCTGAGGAGCCCGCCCAGCCAGCCAGGGCCGCGAGGCCGAGGCCAGGCCGCAGCCCAGGAGCCGCCCCACCGCAG

>**AJ331299.1**/203-76 Homo sapiens genomic sequence surrounding NotI site, clone NL4-AK2RS.

ATTCCCCCCGATAGATACGGGGTTTAGTGCCCTTATCGGTTCCGGCCGATCAGCAGACCGGGCTTCCAGACAGGGCCGGGTGGCAGAGGCCAGGCCGCACGCCCTGGAGCCGCGCCACCGCAGCTGGT

**AU-rich elements**

Adenylate-uridylate-rich elements (AU-rich elements; AREs) are found in the 3' untranslated region (UTR) of many messenger RNAs (mRNAs) that code for proto-oncogenes, nuclear transcription factors, and cytokines. AREs are one of the most common determinants of RNA stability in mammalian cells.[1]

AREs are defined as a region with frequent adenine and uridine bases in a mRNA. They usually target the mRNA for rapid degradation.

The best characterised adenylate uridylate (AU)-rich Elements have a core sequence of AUUUA within U-rich sequences (for example WWWU(AUUUA)UUUW where W is A or U)

**ctgf/hcs24 CAESAR**

ctgf/hcs24 CAESAR is the name given to the cis-acting RNA element identified in the 3' untranslated region (3'UTR) of the human connective tissue growth factor (CTGF) messenger RNA. This gene is also known as hypertrophic chondrocyte specific 24 (hcs24).

The importance of the 3'UTR in repressing ctgf gene expression was initially characacterised and subsequently the minimal RNA element responsible for repression was identified This element was predicted to form a stable secondary structure, which acts as a post-transcriptional cis-acting element of structure-anchored repression (CAESAR).

>**X78947.1**/1179-1258 H.sapiens mRNA for connective tissue growth factor

ACGGAGACATGGCATGAAGCCAGAGAGTGAGAGACATTAACTCATTAGACTGGAACTTGAACTGATTCACATCTCATTTT

**G-CSF factor stem-loop destabilising element (SLDE)**

The G-CSF factor stem-loop destabilising element (SLDE) is an RNA element secreted by fibroblasts and endothelial cells in response to the inflammatory mediators interleukin-1 (IL-1) and tumour necrosis factor-alpha and by activated macrophages. The synthesis of G-CSF is regulated both transcriptionally and through control of mRNA stability. In unstimulated cells G-CSF mRNA is unstable but becomes stabilised in response to IL-1 or tumour necrosis factor alpha, and also in the case of monocytes and macrophages, in response to lipopolysaccharide. It is likely that the presence of the SLDE in the G-CSF mRNA contributes to the specificity of regulation of G-CSF mRNA and enhances the rate of shortening of the poly(A) tail.

>**X03655.1**/931-1023 Human mRNA for granulocyte colony-stimulating factor (G-CSF) (pBRV-2)

CTGAGGGTCCCCACCTGGGACCCTTGAGAGTATCAGGTCTCCCACGTGGGAGACAAGAAATCCCTGTTTAATATTTAAACAGCAGTGTTCCCC

**Heat shock protein 70 (Hsp70) internal ribosome entry site (IRES)**

The heat shock protein 70 (Hsp70) internal ribosome entry site (IRES) is an RNA element that allows cap independent translation during conditions such as heat shock and stress. It has been shown that the 216 nucleotide long 5' UTR contains internal ribosome entry site activity.

>GL000250.2/3160362-3160579 Homo sapiens chromosome 6 genomic contig, GRCh38 reference assembly alternate locus group ALT\_REF\_LOCI\_1.

AAAACGGCCAGCCTGAGGAGCTGCTGCGAGGGTCCGCTTCGTCTTTCGAGAGTGACTCCCGCGGTCCCAAGGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCCGAAGGACTGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCGGAGCCCACAGAGCAGGGCACCGGCATGG

>CM000668.2/31815541-31815760 Homo sapiens chromosome 6, GRCh38 reference primary assembly.

ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCGGAGCCGACAGAGAGCAGGGAACCGGCATGG

>BC057397.1/1-196 Homo sapiens heat shock 70kDa protein 1B, mRNA (cDNA clone MGC:60385 IMAGE:6188453), complete cds.

GCTGCGAGGGTCCGTTTCGTCTTTCGAGAGTGACTCCCGCGGTCCCAAGGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCCGAAGGACTGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCGGAGCCCACAGAGCAGGGCACCGGCATGG

>M11717.1/274-492 Human heat shock protein (hsp 70) gene, complete cds.

ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGCATGG

>X04676.1/269-487 Human hsp 70 gene 5' region for 70 kDa heat shock protein

ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCGGAGCCGACAGAGAGCAGGGAACCGCATGG

>AB018045.1/2322-2530 Homo sapiens HSP70-1 gene for heat shock protein 72, spliced variant, partial cds.

ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGCGGACACCGAGCGGCTCATCGGGG

>AL662834.8/79426-79645 Human DNA sequence from clone CH502-40G17 on chromosome 6

ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGGCATGG

>BC063507.1/1-202 Homo sapiens heat shock 70kDa protein 1B, mRNA (cDNA clone MGC:74463 IMAGE:4153196), complete cds.

GGAGCTGCTGCGAGGGTCCGCTTCGTCTTTCGAGAGTGACTCCCGCGGTCCCAAGGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCCGAAGGACTGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCGGAGCCCACAGAGCAGGGCACCGGCATGG

>S52686.1/274-482 HLA class III polymorphic region: HSP70-1=heat shock protein 70 {5' region} [human, PGF, WT49, WT51, Genomic, 488 nt].

ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTYCCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACAGAGAGCAGGG

**Mnt IRES**

The Mnt internal ribosome entry site (IRES) is an RNA element. Mnt is a transcriptional repressor related to the Myc/Mad family of transcription factors. It is thought that this IRES allows efficient Mnt synthesis when cap-dependent translation initiation is reduced.

>**X96401.1**/13-215 H.sapiens mRNA for ROX protein

TTATATTTTGCAAATATTTTGAGAGACATTGATTTTTCTCCCCGTGCTCCCCCGTTCTTCCCTGCGGAGTGCGCTGCGCCGCCCAGCCCTGTCGCCCCCCGGAGGTGATCCCTCCCTCCTGCCTGCCCGCCAGCCTGACCTGTGCCCGGCTCGCGGGCCGCAGCCTCGGCCCCGGCGCGCCCCCGGCAGCTCTCGGCGCGATG

**n-myc internal ribosome entry site (IRES)**

The N-myc internal ribosome entry site (IRES) is an RNA element found in the n-myc gene. The myc family of genes when expressed are known to be involved in the control of cell growth, differentiation and apoptosis. n-myc mRNA has an alternative method of translation via an internal ribosome entry site where ribosomes are recruited to the IRES located in the 5' UTR thus bypassing the typical eukaryotic cap-dependent translation pathway.

**>AC010145.10/67113-67436 Homo sapiens BAC clone RP11-355H10 from 2, complete sequence.**

CACAAAAGGAGGGCGGGAGGGAGGGAGCGAGAGGCACAACTTCCTCCACCTTCGGGAGCAGTGGGCAGAGTGGGGGGCTTGGAGGGAAGATTGGGGAACCTGGTTAGAGGGGGCGCCCATTGCCTATCCCCTCGGTCTGCCCCGTTTGCCCACCCTCTCCGGTGTGTCTGTCGGTTGCAGTGTTGGAGGTCGGCGCCGGCCCCCGCCTTCCGCGCCCCCCACGGGAAGGAAGCACCCCCGGTATTAAAACGAACGGGGCGGAAAGAAGCCCTCAGTCGCCGGCCGGGAGGCGAGCCGATGCCGAGCTGCTCCACGTCCACCATG

>**AF320053.1/5-324 Homo sapiens N-MYC mRNA, complete cds.**

GTCTGGACGCGCTGGGTGGATGCGGGGGGCTCCTGGGAACTGTGTTGGAGCCGAGCAAGCGCTAGCCAGGCGCAAGCGCGCACAGACTGTAGCCATCCGAGGACACCCCCGCCCCCCCGGCCCACCCGGAGACACCCGCGCAGAATCGCCTCCGGATCCCCTGCAGTCGGCGGGAGTGTTGGAGGTCGGCGCCGGCCCCCGCCTTCCGCGCCCCCCACGGGAAGGAAGCACCCCCGGTATTAAAACGAACGGGGCGGAAAGAAGCCCTCAGTCGCCGGCCGGGAGGCGAGCCGATGCCGAGCTGCTCCACGTCCACCATG

**>CM000664.2/15940568-15940760 Homo sapiens chromosome 2, GRCh38 reference primary assembly.**

GTCTGGACGCGCTGGGTGGATGCGGGGGGCTCCTGGGAACTGTGTTGGAGCCGAGCAAGCGCTAGCCAGGCGCAAGCGCGCACAGACTGTAGCCATCCGAGGACACCCCCGCCCCCCCGGCCCACCCGGAGACACCCGCGCAGAATCGCCTCCGGATCCCCTGCAGTCGGCGGGAGGTAAGGAGCAGGGCTTG

**p27 cis-regulatory element**

The p27 cis-regulatory element is a structured G/C rich RNA element which is involved in controlling cell cycle regulated translation of the p27 protein in human cells.

The p27 protein is involved in cell cycle regulation and belongs to the Cip/Kip family of cyclin dependent kinase(CDK)inhibitors. These inhibitors possess an N-terminal CDK-inhibitory domain which binds to the ATP binding pocket of the kinase and modulates its function.

This p27 cis-regulatory element is 114 nucleotides in length and is located at the very 5' end of the 5'UTR of the p27 mRNA. It contains a small open reading frame (ORF) of 29 amino acids which is preceded by and overlaps with a G/C-rich hairpin domain. This hairpin domain is predicted to form multiple stable stem loops with similar free energy. Both the open reading frame and the stem loop elements contribute to cell cycle-regulated translation of the p27 mRNA.

The structure of the G/C rich element appears to be important to its regulatory function as replacement of the G/C rich region with an unstructured sequence has a greater effect on regulation of translation than a simple deletion of part of the G/C rich region. It has been suggested that cell cycle specific binding proteins may favour one of the predicted structures in the G/C region thereby promoting conformational states which could regulate downstream translation.

This element was initially characterized in human cells but has predicted homologs in mice and chickens.

>AB005590.1/2427-2485 Homo sapiens p27kip1 gene, 5' upstream region and partial cds.

CCACCTTAAGGCCGCGCTCGCCAGCCTCGGCGGGGCGGCTCCCGCCGCCGCAACCAATG

**Potassium channel RNA editing signal**

The potassium channel RNA editing signal is an RNA element found in human Kv1.1 and its homologues which directs the efficient modification of an adenosine to inosine by an adenosine deaminase acting on RNA (ADAR). The ADAR modification causes an isoleucine/valine recoding event which lies in the ion-conducting pore of the potassium channel. It is thought that this editing event targets the process of fast inactivation and allows a more rapid recovery from inactivation at negative potentials.

>CM000663.2/110603660-110603547 Homo sapiens chromosome 1, GRCh38 reference primary assembly.

GTAGGCTATGGAGACATGGTTCCGACTACCATTGGGGGAAAGATAGTGGGTTCCCTATGTGCGATTGCAGGTGTGTTAACTATTGCCTTACCGGTCCCTGTCATTGTGTCCAAT

>CM000674.2/5045588-5045701 Homo sapiens chromosome 12, GRCh38 reference primary assembly.

GTGGGCTACGGGGACATGAGGCCCATCACTGTTGGGGGCAAGATCGTGGGCTCGCTGTGTGCCATCGCCGGGGTCCTCACCATTGCCCTGCCTGTGCCCGTCATCGTCTCCAAC

>CM000670.2/72936499-72936612 Homo sapiens chromosome 8, GRCh38 reference primary assembly.

GTTGGCTATGGTGACATTTACCCTAAAACATTACTAGGGAAAATTGTGGGAGGTCTGTGCTGTATTGCTGGGGTTCTGGTTATTGCCCTTCCTATCCCAATTATTGTGAACAAT

>CM000681.2/49070359-49070246 Homo sapiens chromosome 19, GRCh38 reference primary assembly.

GTTGGCTATGGAGACATGGCACCCGTCACTGTGGGTGGCAAGATAGTGGGCTCTCTGTGTGCCATTGCGGGCGTGCTGACTATTTCCCTGCCAGTGCCCGTCATTGTCTCCAAT

>CM000674.2/75050693-75050580 Homo sapiens chromosome 12, GRCh38 reference primary assembly.

CTGGGTTATGGGGATATGTACCCCCAAACATGGTCAGGCATGCTGGTGGGAGCCCTGTGTGCTCTGGCTGGAGTGCTGACAATAGCCATGCCAGTGCCTGTCATTGTCAATAAT

>CM000663.2/111787111-111786998 Homo sapiens chromosome 1, GRCh38 reference primary assembly.

CTCAGATACGGAGACATGGTGCCTAAGACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTGCCAGTCCCTGTGATTGTTTCCAAC

>CM000685.2/48967112-48966998 Homo sapiens chromosome X, GRCh38 reference primary assembly.

CTCCAGCTACGGAGACATGGTGCCCAGCACCATTGCTGGCAAGATTTTCGGGTCCATCTGCTCACTCAGTGGCGTCTTGGTCATTGCCCTGCCTGTGCCAGTCATTGTGTCCAAC

**>CM000682.2/49374428-49374315 Homo sapiens chromosome 20, GRCh38 reference primary assembly.**

GTTGGGTATGGAGACATCTACCCCAAGACTCTCCTGGGGAAAATTGTTGGGGGACTCTGCTGCATTGCAGGAGTCCTGGTGATTGCTCTTCCCATCCCCATCATCGTCAATAAC

>CM000674.2/4912495-4912608 Homo sapiens chromosome 12, GRCh38 reference primary assembly.

GTAGGATACGGTGACATGTACCCTGTGACAATTGGAGGCAAGATCGTGGGCTCCTTGTGTGCCATCGCTGGTGTGCTAACAATTGCCCTGCCCGTACCTGTCATTGTGTCCAAT

**>U96110.1/1273-1386 Homo sapiens cyclic GMP gated potassium channel (Kcn1) gene, complete cds.**

GTAGGCTATGGGGACATGTGCCCGACCACCCCAGGGGGGAAGATTGTGGGCACTCTGTGTGCCATTGCAGGGGTCCTCACCATTGCCCTCCCTGTGCCTGTCATTGTCTCCAAC

>BX537638.1/3883-3996 Homo sapiens mRNA; cDNA DKFZp686F1444 (from clone DKFZp686F1444)

CTGGGCTACGGAGACATGTACCCCAAGACGTGGTCAGGCATGCTGGTAGGGGCACTGTGTGCACTGGCTGGCGTGCTCACCATCGCCATGCCGGTGCCTGTCATCGTCAACAAC

**>CM000681.2/50323443-50323330 Homo sapiens chromosome 19, GRCh38 reference primary assembly.**

CTGGGCTATGGAGACATGTACCCCAAGACGTGGTCGGGGATGCTGGTCGGGGCGCTGTGTGCCCTGGCGGGGGTGCTGACCATCGCCATGCCTGTGCCCGTCATTGTCAACAAC

>AF205856.1/1102-1215 Homo sapiens potassium ionic channel Kv4.3 short isoform mRNA, complete cds.

CTGGGATACGGAGACATGGTGCCTAAGACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTGCCAGTCCCTGTGATTGTTTCCAAC

**>AF166008.1/340-453 Homo sapiens voltage-gated potassium channel Kv4.2 (KCND2) gene, exons 2 through** 6; and complete cds.

CTCAGGTATGGTGACATGGTGCCAAAAACCATAGCAGGGAAGATTTTTGGTTCTATCTGTTCGCTGAGTGGGGTCTTGGTCATTGCTCTACCTGTTCCGGTGATTGTATCCAAC

>AF048712.1/1102-1215 Homo sapiens Kv4.3 potassium channel short splice variant (Kv4.3) mRNA, complete cds.

CTGGGGTACGGAGACATGGTGCTTAAGACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTGCCAGTCCCTGTGATTGTTTCCAAC

>M38217.1/1195-1308 Homo sapiens voltage-gated potassium channel (HGK5) gene, complete cds.

GTGGGTTACGGCGATATGCACCCAGTGACCATAGGGGGCAAGATTGTGGGATCTCTCTGTGCCATCGCCGGTGTCTTGACCATCGCATTGCCAGTTCCCGTGATTGTTTCCAAC

>AF166003.1/1167-1280 Homo sapiens voltage-gated potassium channel Kv4.1 (KCND1) mRNA, complete cds.

CTTGGCTACGGAGACATGGTGCCCAGCACCATTGCTGGCAAGATTTTCGGGTCCATCTGCTCACTCAGTGGCGTCTTGGTCATTGCCCTGCCTGTGCCAGTCATTGTGTCCAAC

>M96747.1/472-585 Human KCNC1 gene, partial cds.

CTGGGCTATGGAGACATGTACCCGCAGACGTGGTCCGGCATGCTGGTGGGGGCTCTGTGTGCGCTGGCGGGCGTGCTCACCATCGCCATGCCCGTGCCCGTCATCGTGAACAAT

>M55514.1/2727-2840 Human potassium channel (HPCN2) mRNA, complete cds.

GTGGGCTATGGGGACATGAAGCCCATCACTGTAGGGGGCAAGATTGTCGGGGTCCTGTGTGCCATTGCGGGTGTCTTAACCATTGCTTTGCCAGTGCCAGTGATTGTCTCTAAC

>L02751.1/1573-1686 Human potassium channel mRNA, complete cds.

GTGGGCTATGGGGACATGAAGCCCATCACTGTAGGGGGCAAGATTGTCGGGTCCCTGTGTGCCATTGCGGGTGTCTTAACCATTGCTTTGCCAGTGCCAGTGATTGTCTCTAAC

>X17622.1/2129-2242 Human HBK2 mRNA for potassium channel protein

GTAGGTTACGGGGACATGTACCCCATGACTGTGGGGGGAAAGATCGTGGGCTCGCTGTGTGCCATCGCTGGGGTCCTCACCATTGCCCTGCCTGTGCCCGTCATCGTCTCCAAC

>M55515.1/1302-1415 Human potassium channel protein (HPCN3) gene, complete cds.

GTGGGTTACGGCGATATGCACCCAGTGACCATAGGGGGGAAGATTGTGGGATCTCTCTGTGCCATCGCCGGTGTCTTGTCCATCGCATTGCCAGTTCCCGTGATTGTTTCCAAC

**Prion pseudoknot**

The prion pseudoknot is predicted RNA pseudoknot structure found in prion protein mRNA. It has been suggested that this element has a possible effect in prion protein translation. The human prion protein contains 5 copies of a 24 nucleotide repeat that contains this structure.

>CM000676.2/98055276-98055236 Homo sapiens chromosome 14, GRCh38 reference primary assembly.

CCAAGATGTGGAGGCTGGGGTCAGCCCTTGGTGGAGGTTGC

>S80743.1/84-123 Homo sapiens prion protein (PRNP) gene, partial cds.

CCATGGTGGTGGCTGGGGACAGCCTCATGGTGGTGGCTGG

>S80743.1/33-75 Homo sapiens prion protein (PRNP) gene, partial cds.

TCAGGGCGGTGGTGGCTGGGGGCAGCCTCATGGTGGTGGCTGG

**>U29185.1/25677-25716 Homo sapiens prion protein (PrP) gene, complete cds.**

TCATGGTGGTGGCTGGGGGCAGCCCCATGGTGGTGGCTGG

>S80539.1/54-93 PRNP=PrP amyloid [human, Genomic Mutant, 291 nt].

TCATGGCGGTGGCTGGGGGCAGCCCCATGGTGGTGGCTGG

**Spi-1 (PU.1) 5' UTR regulatory element**

The Spi-1 (PU.1) 5′ UTR regulatory element is an RNA element found in the 5′ UTR of Spi-1 mRNA which is able to inhibit the translation Spi-1 transcripts by 8-fold. Spi-1 regulates myeloid gene expression during haemopoietic development. Mutations in this regulatory region of the 5′ UTR can lead to overexpression of Spi-1 which has been linked to development of leukemia.

>U34046.1/345-511 Human transcription factor PU.1 (Spi-1) gene, promoter region and partial cds.

CTCACCCAGGGCTCCTGTAGCTCAGGGGGCAGGCCTGAGCCCTGCACCCGCCCCACGACCGTCCAGCCCCTGACGGGCACCCCATCCTGAGGGGCTCTGCATTGGCCCCCACCGAGGCAGGGGATCTGACCGACTCGGAGCCCGGCTGGATGTTACAGGCGTGCAAA

>CM000673.2/47378503-47378336 Homo sapiens chromosome 11, GRCh38 reference primary assembly.

CTCACCCAGGGCTCCTGTAGCTCAGGGGGCAGGCCTGAGCCCTGCACCCGCCCCACGACCGTCCAGCCCCTGACGGGGCACCCCATCCTGAGGGGCTCTGCATTGGCCCCCACCGAGGCAGGGGATCTGACCGACTCGGAGCCCGGCTGGATGTTACAGGCGTGCAAA

>AC090582.9/66882-66715 Homo sapiens chromosome 11, clone RP11-125F14, complete sequence.

CTCACCCAGGGCTCCTGTAGCTCAAGGGGCAGGCCTGAGCCCTGCACCCGCCCCACGACCGTCCAGCCCCTGACGGGGCACCCCATCCTGAGGGGCTCTGCATTGGCCCCCACCGAGGCAGGGGATCTGACCGACTCGGAGCCCGGCTGGATGTTACAGGCGTGCAAA

**TrkB IRES**

The TrkB internal ribosome entry site (IRES) is an RNA element which is present in the 5' UTR sequence of the mRNA. TrkB is a neurotrophin receptor which is essential for the development and maintenance of the nervous system. The internal ribosome entry site IRES element allows cap-independent translation of TrkB which may be needed for efficient translation in neuronal dendrites.

**>BC031835.1/57-409 Homo sapiens neurotrophic tyrosine kinase, receptor, type 2, mRNA (cDNA clone MGC:24881 IMAGE:4941763), complete cds.**

CCCCCATTCGCATCTAACAAGGAATCTGCGCCCCAGAGAGTCCCGGGAGCGCCGCCGGTCGGTGCCCGGCGCGCCGGGCCATGCAGCGACGGCCGCCGCGGAGCTCCGAGCAGCGGTAGCGCCCCCCTGTAAAGCGGTTCGCTATGCCGGGGCCACTGTGAACCCTGCCGCCTGCCGGAACACTCTTCGCTCCGGACCAGCTCAGCCTCTGATAAGCTGGACTCGGCACGCCCGCAACAAGCACCGAGGAGTTAAGAGAGCCGCAAGCGCAGGGAAGGCCTCCCGGCACGGGTGGGGGAAAGCGGCCGGTGCAGCGCGGGGACAGGCACTCGGGCTGGCACTGGCTGCTAGGG

**>U12140.1/1-351 Human tyrosine kinase receptor p145TRK-B (TRK-B) mRNA, complete cds.**

CCCCCATTCGCATCTAACAAGGAATCTGCGCCCCAGAGAGTCCCGGACGCCGCCGGTCGGTGCCCGGCGCGCCGGGCCATGCAGCGACGGCCGCCGCGGAGCTCCGAGCAGCGGTAGCGCCCCCCTGTAAAGCGGTTCGCTATGCCGGGACCACTGTGAACCCTGCCGCCTGCCGGAACACTCTTCGCTCCGGACCAGCTCAGCCTCTGATAAGCTGGACTCGGCACGCCCGCAACAAGCACCGAGGAGTTAAGAGAGCCGCAAGCGCAGGGAAGGCCTCCCCGCACGGGTGGGGGAAAGCGGCCGGTGCAGCGCGGGGACAGGCACTCGGGCTGGCACTGGCTGCTAGGG

**>AF410902.1/3685-4037 Homo sapiens neurotrophin receptor tyrosine kinase type 2 (NTRK2) gene, promoter region and partial cds; alternatively spliced.**

CCCCCATTCGCATCTAACAAGGAATCTGCGCCCCAGAGAGTCCCGGGAGCGCCGCCGGTCGGTGCCCGGCGCGCCGGGCCATGCAGCGACGGCCGCCGCGGAGCTCCGAGCAGCGGTAGCGCCCCCCTGTAAAGCGGTTCGCTATGCCGGGGCCACTGTGAACCCTGCCGCCTGCCGGAACACTCTTCGCTCCGGACCAGCTCAGCCTCTGATAAGCTGGACTCGGCACGCCCGCAACAAGCACCGAGGAGTTAAGAGAGCCGCAAGCGCAGGGAAGGCCTCCCCGCACGGGTGGGGGAAAGCGGCCGGTGCAGCGCGGGGACAGGCACTCGGGCTGGCACTGGCTGCTAGGG

**U1A polyadenylation inhibition element (PIE)**

The U1A polyadenylation inhibition element (PIE) is an RNA element which is responsible for the regulation of the length of the polyA tail of the U1A protein pre-mRNA. The PIE is located in the U1A mRNA 3' UTR. PIE adopts a U-shaped structure, with binding sites for a single U1A protein at each bend and when complexed with the two proteins it blocks activity of poly(A) polymerase (PAP), and inhibits its activity.

>BC000405.2/1511-1584 Homo sapiens small nuclear ribonucleoprotein polypeptide A, mRNA (cDNA clone MGC:8567 IMAGE:2822987), complete cds.

CCACACAGCATTGTACCCAGAGTCTGTCCCCAGACATTGCACCTGGCGCTGTTAGGCCGGAATTAAAGTGGCTT

**Vimentin 3' UTR protein-binding region**

The vimentin 3′ UTR protein-binding region is an RNA element that contains a Y shaped structure which has been shown to have protein binding activity. The same region has been implicated in the control of mRNA localization to the perinuclear region of the cytoplasm, possibly at sites of intermediate filament assembly. The identity of the proteins involved and the localization mechanism are not known.

>CM000668.2/126602298-126602234 Homo sapiens chromosome 6, GRCh38 reference primary assembly.

ACTACATCTTAAAGAAACAGCCTTCAAATGCCCCTCTACAGCTTTTCAGTAGCATAAGATAAATT

>CM000672.2/17237325-17237389 Homo sapiens chromosome 10, GRCh38 reference primary assembly.

TCCATATCTTAAAGAAACAGCTTTCAAGTGCCTTTCTGCAGTTTTTCAGGAGCGCAAGATAGATT

>M18895.1/303-367 Homo sapiens vimentin (VIM) gene, exon 9 and partial cds.

TCCATATCTTAAAGAAACAGCTTTCAAGTGCCTTTCTGCAGTTTTTCAGGAGCGCAAGGAATTAA

**Voltage-gated potassium-channel Kv1.4 IRES**

This family represents the Kv1.4 voltage-gated potassium channel internal ribosome entry site (IRES). This region has been shown to mediate internal ribosome entry in cells derived from brain, heart, and skeletal muscle; tissues known to express Kv1.4 mRNA species.

>CM000673.2/30012935-30012676 Homo sapiens chromosome 11, GRCh38 reference primary assembly.

TAGTCTTGAGAGTGCCAGGCTATTTATCTCGACCAGCCAAGCTCTGGAGAGCAATGTTGAATCCCTGAGAAGAGAGAGCATGGGGCGTGCTGATTTAAAAACAGAAAATGCAAAGTTGGACTGAAAATATCCTTAGTCTTCCAAGCAATCTGCTTAAGGGTTCCAAACTTACCTTAATTTGGTGAGAAAAGAAGCTGCCCTATTTTTCTTTCTTCTTCTTCTACAACTGGAACCAGCCATTTCCGAAAACCACCACCATG

>M55514.1/896-1157 Human potassium channel (HPCN2) mRNA, complete cds.

TAGTCTTGAGAGTGCCAGGCTATTTATCTCGACCAGCCAAGCTCTGGAGAGCAATGTTGAATCCCTGAGAAGAGAGAGGCATGGGGCGTGCTGATTTAAAAACAGAAAATGCAAAGTTGGAGCTGAAAATATCCTTAGTCTTCCAAGCAATCTGCTTAAGGGTTCCAAACTTACCTTAATTTGGTGAGAAAAGAAGCTGCCCTATTTTTCTTTCTTCTTCTTCTACAACTGGAACCAGCCATTTCCGAAAACCACCACCATG

**#For now lets just use this list. There will always be more.**

https://rfam.org/search?q=TAXONOMY:%229606%22%20AND%20rna\_type:%22Cis-reg%22