**Comparative Genomic Studies of ORFan genes in Mammalian Genomes**

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| Purpose |
| Investigate the function/s, if any, of the ORFan gene sequences identified in previous studies from the literature, with a special focus of Clamp *at el* study. |

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| Method |
| There are three main phases of this proposed investigation   1. Find ORFan genes from the ORFanFinder online tool 2. Results Validation 3. Determine the function/s, if any, of the ORFan genes   ***Find ORFan genes from the ORFanFinder online tool***  Step 1: Find all genes of the chromosome  Ensembl BioMart[[1]](#footnote-1) online tool will be used to retrieve all the genes. Following parameters will be used in the BioMart search:  *Dataset*: Homo sapiens genes (GRCh38.p7)  *Filters*: Chromosome: 1-22 and X  *Attributes*: Peptide, Ensembl Gene ID, Ensembl Transcript ID  Step 2: Remove non-coding genes  Genes that do not contain a protein sequence will be removed from the output file.  Step 3: Find orphan genes  Sequences of all the genes will be input into the ORFanFinder online tool[[2]](#footnote-2) to find orphan genes. Following parameters were used for the analysis:  *NCBI Taxonomy ID*: 9606  *Program*: blastp  *Use Premade Database*: nr  *E-value*: 1e-3  **Results Validation**  The orphan genes reported from the ORFanFinder can be compared against Clamp *at*. el study results. Further, each gene found as an orphan gene can be viewed in UCSC Brower for further validation such as:   * Retroposon/ Pseudogenes (RetroGenes V9 Track) * Pfam Domain (Pfam in UCSC Gene Track) * Repeating Elements (RepeatMasker Track) * Compare with mouse and dog sequence (Conservation Track)   **Determine the function of the ORFan genes**  Gene Ontology[[3]](#footnote-3) and GeneCard[[4]](#footnote-4) tools can be used to find the known functions of these genes |

1. http://asia.ensembl.org/biomart/martview [↑](#footnote-ref-1)
2. http://cys.bios.niu.edu/orfanfinder/index.php [↑](#footnote-ref-2)
3. http://www.geneontology.org [↑](#footnote-ref-3)
4. http://www.genecards.org [↑](#footnote-ref-4)