UniSTS – SNPs

- 1. Report the following features of the human gene TSC1:
 - a. The gene id;
 - b. The function and the associated disease;
 - c. The accession code and the length of the possible isoforms;
 - d. The accession code and the original name of a unique marker common to *Homo* Sapiens, Macaca Mulatta and Pan Troglodytes.
 - i. For each organism report:
 - 1. Chromosomal location and genomic location (bp);
 - 2. The accession code of the corresponding contig;
 - 3. The accession codes of the corresponding mRNAs.
- 2. In the UniSTS data base find the record RH68414 and report
 - a. the position of the marker in the HuRef and Celera chromosomes;
 - b. the code id, names and functions of the associated genes;
 - c. the marker position in the corresponding mRNAs.
- 3. Among the SNPs associated with the human TSC1 gene report those with PubMed references and write the most recent reference.
 - a. Of the first reference cluster report:
 - i. The accession code and the mutation;
 - ii. The accession codes of mRNAs and contig in GRCh37 assembly where it maps to;
 - iii. The accession code of the submitted record which reports the SNP frequency in samples from Europe, Asia e Africa;
 - 1. The related allelic and genotipic frequencies.
- 4. Report the following features of the human gene SNTB2:
 - a. The gene id, chromosomal location, map position in bp;
 - b. The gene function and the associated disease;
 - c. The accession codes and length of mRNAs, proteins and contig in GRCh37 assembly where it maps to;
 - d. The number of exons in the Consensus CDS database and amino acids and corresponding codons across splice junctions;
 - a. mutation and alleles of rs78009624 marker;
 - i. the accession code and position in contig, mRNA and protein;
 - ii. the allele frequency in the examined samples.
- 5. For the homologous genes in mouse and rat, report:
 - a. the accession code and map position of del contig;
 - b. the accession code and map position of the UniSTS markers;
 - c. the accession code and map position of the SNP reference clusters.