Uniprot

1) Search in UniprotKB the records regarding insulin and report:
    a) how many record are found;
    b) how many entries are from Swiss-Prot?
    c) the accession code for the human protein (INS gene);
    d) the number of the references inside the previous record;
    e) where in the cell/outside the cell you can find insulin;
    f) the length of the signal peptide and the propeptide, respectively;
    g) which type of variants (mutations) of insulin have been described ;
    h) which variant is related to diabetes mellitus type-II and the references that have been published on it.

2) Find the human muscle 6-phosphofructokinase in Uniprot and, of this protein report:
    a) the gene name and its accession code;
    b) how many alternative products are present and their lengths;
    c) how many references regards this protein;
    d) the accession code of the mRNA and protein reference sequences;
    e) the length of the mRNA and coding reference sequences.

3) Explain the differences between the previous records found in RefSeq and in Uniprot. Moreover, defects in the previous protein cause a human disease of which report:
    a) the accession number of the OMIM record;
    b) the inheritance transmission;
    c) the MIM number, name and the chromosomal localization of the related gene;
    d) the number and the type of allelic variants associated to that disease.

3) Using UniprotKB, find the records regarding human Bombesin receptor subtype 3. Report:
    a) how many records you find;
    b) their accession codes;
    c) the different kind of information you expect to find inside the record;
    d) the accession code of the mRNA and protein reference sequences of the reviewed protein.

4) Report how many records are present in UniprotKB/SwissProt regarding Aurora kinase A. Restrict the data base sequence redundancy at 50% and reviewed sequences and report the cluster accession code, the accession code and organisms of the sequences grouped inside the cluster.