

使用生物数据库

截止日期：2022年3月21日

总分: 20

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Q1: A mitosis-associated gene *X* was experimentally identified in *Mus musculus*. By DNA sequencing, a partial sequence was obtained as below:

GATGAGCTGCTTATCCTACAACGAG
AAGTCGGACATCTGGTCCTTG
GGCTGCCTGCTGTATGAGCTGTGTG
CACTAATGCCTCCCTTTACAG
CTTTCAACCAAAAAGAGCTAGCTGG
GAAAATCAGGGGAAGGGAGGT
TCAGGCGCATCCCCTACCGCTACTC
TGATGGCTTGAATGACCTCAT
CACTCGGATGCTGAATTAAAGGAC
TACCATCGACCTTCAGTGGAA
GAAATTCTGGAGAGCCCTTTGATAG
CAGACTTGGTTGCAGAAGAGC
AAAGGAGAAATCTGGAGAGGAGAG
GACGGCGCTCAGGCGAGCCT
TCGAAGCTGCCGGACTCCAGCCCT
GTGCTGAGCGAGCTCAAGTTG
AAGGAAAGGCAACTGCAGGATCGA
GAGCAAGCACTCAGAGCTCGG
GAGGACATCCT

- 1. What's the name of gene *X* in *Mus musculus*? Its accession number in GenBank database and coordinates of mouse genome.**
- 2. The homolog of gene *X* in human, and its accession number.**
- 3. In human, the protein product of this gene. Its functions, sub-cellular localizations. Whether it's an enzyme? If so, does it have a conserved functional domain?**
- 4. Whether this gene is conserved in yeast? If so, identify its potential homolog.**
- 5. The 3D structural information of gene *X* in human, but not mouse. Its accession number in PDB.**

Q2:

(1)Randomly select (by writing a program) 10 proteins from the PDB entry list (exclude those with nuc only): (ftp://ftp.wwpdb.org/pub/pdb/derived_data/pdb_entry_type.txt)

(2)Give the mapping of the PDB ID to the UniProt ID, and GenBank ID (if available); Provide the function description of these proteins.

(3)Manually collect the SCOP fold and CATH fold information and compare their difference; Draw the two set of fold structures with RasMol or PyMOL; Put these figures together with some software such as Photoshop, CoreDraw.