

# CPC COOPERATIVE PATENT CLASSIFICATION

## G PHYSICS

(NOTES omitted)

## G16 INFORMATION AND COMMUNICATION TECHNOLOGY [ICT] SPECIALLY ADAPTED FOR SPECIFIC APPLICATION FIELDS

(NOTES omitted)

## G16B BIOINFORMATICS, i.e. INFORMATION AND COMMUNICATION TECHNOLOGY [ICT] SPECIALLY ADAPTED FOR GENETIC OR PROTEIN-RELATED DATA PROCESSING IN COMPUTATIONAL MOLECULAR BIOLOGY

|              |  |              |   |
|--------------|--|--------------|---|
| <b>5/00</b>  | <b>ICT specially adapted for modelling or simulations in systems biology, e.g. gene-regulatory networks, protein interaction networks or metabolic networks</b>      | <b>40/00</b> | <b>ICT specially adapted for biostatistics; ICT specially adapted for bioinformatics-related machine learning or data mining, e.g. knowledge discovery or pattern finding</b> |
| 5/10         | . Boolean models   | 40/10        | . Signal processing, e.g. from mass spectrometry [MS] or from PCR   |
| 5/20         | . Probabilistic models   | 40/20        | . Supervised data analysis  |
| 5/30         | . Dynamic-time models  | 40/30        | . Unsupervised data analysis  |
| <b>10/00</b> | <b>ICT specially adapted for evolutionary bioinformatics, e.g. phylogenetic tree construction or analysis</b>  | <b>45/00</b> | <b>ICT specially adapted for bioinformatics-related data visualisation, e.g. displaying of maps or networks</b>   |
| <b>15/00</b> | <b>ICT specially adapted for analysing two-dimensional or three-dimensional molecular structures, e.g. structural or functional relations or structure alignment</b> | <b>50/00</b> | <b>ICT programming tools or database systems specially adapted for bioinformatics</b>   |
| 15/10        | . Nucleic acid folding   | 50/10        | . Ontologies; Annotations   |
| 15/20        | . Protein or domain folding  | 50/20        | . Heterogeneous data integration  |
| 15/30        | . Drug targeting using structural data; Docking or binding prediction  | 50/30        | . Data warehousing; Computing architectures   |
|              |  | 50/40        | . Encryption of genetic data  |
|              |  | 50/50        | . Compression of genetic data   |
| <b>20/00</b> | <b>ICT specially adapted for functional genomics or proteomics, e.g. genotype-phenotype associations</b>   | <b>99/00</b> | <b>Subject matter not provided for in other groups of this subclass</b>   |
| 20/10        | . Ploidy or copy number detection  |              |   |
| 20/20        | . Allele or variant detection, e.g. single nucleotide polymorphism [SNP] detection   |              |   |
| 20/30        | . Detection of binding sites or motifs   |              |   |
| 20/40        | . Population genetics; Linkage disequilibrium  |              |   |
| 20/50        | . Mutagenesis  |              |   |
| <b>25/00</b> | <b>ICT specially adapted for hybridisation; ICT specially adapted for gene or protein expression</b>   |              |   |
| 25/10        | . Gene or protein expression profiling; Expression-ratio estimation or normalisation   |              |   |
| 25/20        | . Polymerase chain reaction [PCR]; Primer or probe design; Probe optimisation  |              |   |
| 25/30        | . Microarray design  |              |   |
| <b>30/00</b> | <b>ICT specially adapted for sequence analysis involving nucleotides or amino acids</b>  |              |   |
| 30/10        | . Sequence alignment; Homology search  |              |   |
| 30/20        | . Sequence assembly  |              |   |
| <b>35/00</b> | <b>ICT specially adapted for <u>in silico</u> combinatorial libraries of nucleic acids, proteins or peptides</b>   |              |   |
| 35/10        | . Design of libraries  |              |   |
| 35/20        | . Screening of libraries   |              |   |