

# 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

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