

# 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		