

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

5/00	ICT specially adapted for modelling or simulations in systems biology, e.g. gene-regulatory networks, protein interaction networks or metabolic networks	40/00	ICT specially adapted for biostatistics; ICT specially adapted for bioinformatics-related machine learning or data mining, e.g. knowledge discovery or pattern finding
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
10/00	ICT specially adapted for evolutionary bioinformatics, e.g. phylogenetic tree construction or analysis	45/00	ICT specially adapted for bioinformatics-related data visualisation, e.g. displaying of maps or networks
15/00	ICT specially adapted for analysing two-dimensional [2D] or three-dimensional [3D] molecular structures, e.g. structural or functional relations or structure alignment	50/00	ICT programming tools or database systems specially adapted for bioinformatics
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
20/00	ICT specially adapted for functional genomics or proteomics, e.g. genotype-phenotype associations	99/00	Subject matter not provided for in other groups of this subclass
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		
25/00	ICT specially adapted for hybridisation; ICT specially adapted for gene or protein expression		
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		
30/00	ICT specially adapted for sequence analysis involving nucleotides or amino acids		
30/10	. Sequence alignment; Homology search		
30/20	. Sequence assembly		
35/00	ICT specially adapted for <u>in silico</u> combinatorial libraries of nucleic acids, proteins or peptides		
35/10	. Design of libraries		
35/20	. Screening of libraries		