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**
5/10 . Boolean models
5/20 . Probabilistic models
5/30 . Dynamic-time models

10/00 **ICT specially adapted for evolutionary bioinformatics, e.g. phylogenetic tree construction or analysis**

15/00 **ICT specially adapted for analysing two-dimensional or three-dimensional molecular structures, e.g. structural or functional relations or structure alignment**
15/10 . Nucleic acid folding
15/20 . Protein or domain folding
15/30 . Drug targeting using structural data; Docking or binding prediction

20/00 **ICT specially adapted for functional genomics or proteomics, e.g. genotype-phenotype associations**
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 in silico combinatorial libraries of nucleic acids, proteins or peptides**
35/10 . Design of libraries
35/20 . Screening of libraries

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**
40/10 . Signal processing, e.g. from mass spectrometry [MS] or from PCR
40/20 . Supervised data analysis
40/30 . Unsupervised data analysis

45/00 **ICT specially adapted for bioinformatics-related data visualisation, e.g. displaying of maps or networks**

50/00 **ICT programming tools or database systems specially adapted for bioinformatics**
50/10 . Ontologies; Annotations
50/20 . Heterogeneous data integration
50/30 . Data warehousing; Computing architectures
50/40 . Encryption of genetic data
50/50 . Compression of genetic data

99/00 **Subject matter not provided for in other groups of this subclass**