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

WARNING
Groups G16B 5/00, G16B 5/10, G16B 5/20, G16B 5/30 are incomplete pending reclassification of documents from group G16B 99/00.
Group G16B 5/00 is also impacted by reclassification into groups G16B 5/10, G16B 5/20, and G16B 5/30.
All groups listed in this Warning should be considered in order to perform a complete search.

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

WARNING
Group G16B 10/00 is incomplete pending reclassification of documents from group G16B 99/00.
Groups G16B 99/00 and G16B 10/00 should be considered in order to perform a complete search.

15/00 ICT specially adapted for analysing two-dimensional or three-dimensional molecular structures, e.g. structural or functional relations or structure alignment

WARNING
Groups G16B 15/00, G16B 15/10, G16B 15/20, G16B 15/30 are incomplete pending reclassification of documents from group G16B 99/00.
Group G16B 15/00 is also impacted by reclassification into groups G16B 15/10, G16B 15/20, and G16B 15/30.
All groups listed in this Warning should be considered in order to perform a complete search.

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

WARNING
Groups G16B 20/00, G16B 20/10, G16B 20/20, G16B 20/30, G16B 20/40, G16B 20/50 are incomplete pending reclassification of documents from group G16B 99/00.
Group G16B 20/00 is also impacted by reclassification into groups G16B 20/10, G16B 20/20, G16B 20/30, G16B 20/40, and G16B 20/50.
All groups listed in this Warning should be considered in order to perform a complete search.

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

WARNING
Groups G16B 25/00, G16B 25/10, G16B 25/20, G16B 25/30 are incomplete pending reclassification of documents from group G16B 99/00.
Group G16B 25/00 is also impacted by reclassification into groups G16B 25/10, G16B 25/20, and G16B 25/30.
All groups listed in this Warning should be considered in order to perform a complete search.

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

**WARNING**

Groups **G16B 30/00, G16B 30/10, G16B 30/20** are incomplete pending reclassification of documents from group **G16B 99/00**.

Group **G16B 30/00** is also impacted by reclassification into groups **G16B 30/10** and **G16B 30/20**.

All groups listed in this Warning should be considered in order to perform a complete search.

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

**WARNING**

Groups **G16B 35/00, G16B 35/10, G16B 35/20** are incomplete pending reclassification of documents from group **G16B 99/00**.

Group **G16B 35/00** is also impacted by reclassification into groups **G16B 35/10** and **G16B 35/20**.

All groups listed in this Warning should be considered in order to perform a complete search.

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

**WARNING**

Groups **G16B 40/00, G16B 40/10, G16B 40/20, G16B 40/30** are incomplete pending reclassification of documents from group **G16B 99/00**.

Group **G16B 40/00** is also impacted by reclassification into groups **G16B 40/10, G16B 40/20**, and **G16B 40/30**.

All groups listed in this Warning should be considered in order to perform a complete search.

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

**WARNING**

Groups **G16B 50/00, G16B 50/10, G16B 50/20, G16B 50/30, G16B 50/40, G16B 50/50** are incomplete pending reclassification of documents from group **G16B 99/00**.

Group **G16B 50/00** is also impacted by reclassification into groups **G16B 50/10, G16B 50/20, G16B 50/30, G16B 50/40 and G16B 50/50**.

All groups listed in this Warning should be considered in order to perform a complete search.

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

**WARNING**


All groups listed in this Warning should be considered in order to perform a complete search.