

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

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|-------|--|-------|--|
| 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. | 15/30 | <ul style="list-style-type: none"> . Drug targeting using structural data; Docking or binding prediction |
| 5/10 | <ul style="list-style-type: none"> . Boolean models | 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. |
| 5/20 | <ul style="list-style-type: none"> . Probabilistic models | 20/10 | <ul style="list-style-type: none"> . Ploidy or copy number detection |
| 5/30 | <ul style="list-style-type: none"> . Dynamic-time models | 20/20 | <ul style="list-style-type: none"> . Allele or variant detection, e.g. single nucleotide polymorphism [SNP] detection |
| 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. | 20/30 | <ul style="list-style-type: none"> . Detection of binding sites or motifs |
| 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. | 20/40 | <ul style="list-style-type: none"> . Population genetics; Linkage disequilibrium |
| 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. | 20/50 | <ul style="list-style-type: none"> . Mutagenesis |
| 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. | 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. |
| 15/10 | <ul style="list-style-type: none"> . Nucleic acid folding | 25/10 | <ul style="list-style-type: none"> . Gene or protein expression profiling; Expression-ratio estimation or normalisation |
| 15/20 | <ul style="list-style-type: none"> . Protein or domain folding | 25/20 | <ul style="list-style-type: none"> . Polymerase chain reaction [PCR]; Primer or probe design; Probe optimisation |
| | | 25/30 | <ul style="list-style-type: none"> . 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**

Group [G16B 99/00](#) is impacted by reclassification into groups [G16B 5/00](#), [G16B 5/10](#), [G16B 5/20](#), [G16B 5/30](#), [G16B 10/00](#), [G16B 15/00](#), [G16B 15/10](#), [G16B 15/20](#), [G16B 15/30](#), [G16B 20/00](#), [G16B 20/10](#), [G16B 20/20](#), [G16B 20/30](#), [G16B 20/40](#), [G16B 20/50](#), [G16B 25/00](#), [G16B 25/10](#), [G16B 25/20](#), [G16B 25/30](#), [G16B 30/00](#), [G16B 30/10](#), [G16B 30/20](#), [G16B 35/00](#), [G16B 35/10](#), [G16B 35/20](#), [G16B 40/00](#), [G16B 40/10](#), [G16B 40/20](#), [G16B 40/30](#), [G16B 45/00](#), [G16B 50/00](#), [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.