

# 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  | <p><b>ICT specially adapted for modelling or simulations in systems biology, e.g. gene-regulatory networks, protein interaction networks or metabolic networks</b></p> <p><b>WARNING</b></p> <p>Groups <a href="#">G16B 5/00</a>, <a href="#">G16B 5/10</a>, <a href="#">G16B 5/20</a>, <a href="#">G16B 5/30</a> are incomplete pending reclassification of documents from group <a href="#">G16B 99/00</a>.</p> <p>Group <a href="#">G16B 5/00</a> is also impacted by reclassification into groups <a href="#">G16B 5/10</a>, <a href="#">G16B 5/20</a>, and <a href="#">G16B 5/30</a>.</p> <p>All groups listed in this Warning should be considered in order to perform a complete search.</p>              | 15/30 | <ul style="list-style-type: none"> <li>. Drug targeting using structural data; Docking or binding prediction</li> </ul>  |
| 5/10  | <ul style="list-style-type: none"> <li>. Boolean models</li> </ul>   | 20/00 | <p><b>ICT specially adapted for functional genomics or proteomics, e.g. genotype-phenotype associations</b></p> <p><b>WARNING</b></p> <p>Groups <a href="#">G16B 20/00</a>, <a href="#">G16B 20/10</a>, <a href="#">G16B 20/20</a>, <a href="#">G16B 20/30</a>, <a href="#">G16B 20/40</a>, <a href="#">G16B 20/50</a> are incomplete pending reclassification of documents from group <a href="#">G16B 99/00</a>.</p> <p>Group <a href="#">G16B 20/00</a> is also impacted by reclassification into groups <a href="#">G16B 20/10</a>, <a href="#">G16B 20/20</a>, <a href="#">G16B 20/30</a>, <a href="#">G16B 20/40</a>, and <a href="#">G16B 20/50</a>.</p> <p>All groups listed in this Warning should be considered in order to perform a complete search.</p> |
| 5/20  | <ul style="list-style-type: none"> <li>. Probabilistic models</li> </ul>   | 20/10 | <ul style="list-style-type: none"> <li>. Ploidy or copy number detection</li> </ul>  |
| 5/30  | <ul style="list-style-type: none"> <li>. Dynamic-time models</li> </ul>  | 20/20 | <ul style="list-style-type: none"> <li>. Allele or variant detection, e.g. single nucleotide polymorphism [SNP] detection</li> </ul>   |
| 10/00 | <p><b>ICT specially adapted for evolutionary bioinformatics, e.g. phylogenetic tree construction or analysis</b></p> <p><b>WARNING</b></p> <p>Group <a href="#">G16B 10/00</a> is incomplete pending reclassification of documents from group <a href="#">G16B 99/00</a>.</p> <p>Groups <a href="#">G16B 99/00</a> and <a href="#">G16B 10/00</a> should be considered in order to perform a complete search.</p>  | 20/30 | <ul style="list-style-type: none"> <li>. Detection of binding sites or motifs</li> </ul>   |
| 10/00 | <p><b>ICT specially adapted for evolutionary bioinformatics, e.g. phylogenetic tree construction or analysis</b></p> <p><b>WARNING</b></p> <p>Group <a href="#">G16B 10/00</a> is incomplete pending reclassification of documents from group <a href="#">G16B 99/00</a>.</p> <p>Groups <a href="#">G16B 99/00</a> and <a href="#">G16B 10/00</a> should be considered in order to perform a complete search.</p>  | 20/40 | <ul style="list-style-type: none"> <li>. Population genetics; Linkage disequilibrium</li> </ul>  |
| 10/00 | <p><b>ICT specially adapted for evolutionary bioinformatics, e.g. phylogenetic tree construction or analysis</b></p> <p><b>WARNING</b></p> <p>Group <a href="#">G16B 10/00</a> is incomplete pending reclassification of documents from group <a href="#">G16B 99/00</a>.</p> <p>Groups <a href="#">G16B 99/00</a> and <a href="#">G16B 10/00</a> should be considered in order to perform a complete search.</p>  | 20/50 | <ul style="list-style-type: none"> <li>. Mutagenesis</li> </ul>  |
| 15/00 | <p><b>ICT specially adapted for analysing two-dimensional or three-dimensional molecular structures, e.g. structural or functional relations or structure alignment</b></p> <p><b>WARNING</b></p> <p>Groups <a href="#">G16B 15/00</a>, <a href="#">G16B 15/10</a>, <a href="#">G16B 15/20</a>, <a href="#">G16B 15/30</a> are incomplete pending reclassification of documents from group <a href="#">G16B 99/00</a>.</p> <p>Group <a href="#">G16B 15/00</a> is also impacted by reclassification into groups <a href="#">G16B 15/10</a>, <a href="#">G16B 15/20</a>, and <a href="#">G16B 15/30</a>.</p> <p>All groups listed in this Warning should be considered in order to perform a complete search.</p> | 25/00 | <p><b>ICT specially adapted for hybridisation; ICT specially adapted for gene or protein expression</b></p> <p><b>WARNING</b></p> <p>Groups <a href="#">G16B 25/00</a>, <a href="#">G16B 25/10</a>, <a href="#">G16B 25/20</a>, <a href="#">G16B 25/30</a> are incomplete pending reclassification of documents from group <a href="#">G16B 99/00</a>.</p> <p>Group <a href="#">G16B 25/00</a> is also impacted by reclassification into groups <a href="#">G16B 25/10</a>, <a href="#">G16B 25/20</a>, and <a href="#">G16B 25/30</a>.</p> <p>All groups listed in this Warning should be considered in order to perform a complete search.</p>   |
| 15/10 | <ul style="list-style-type: none"> <li>. Nucleic acid folding</li> </ul>   | 25/10 | <ul style="list-style-type: none"> <li>. Gene or protein expression profiling; Expression-ratio estimation or normalisation</li> </ul>   |
| 15/20 | <ul style="list-style-type: none"> <li>. Protein or domain folding</li> </ul>  | 25/20 | <ul style="list-style-type: none"> <li>. Polymerase chain reaction [PCR]; Primer or probe design; Probe optimisation</li> </ul>  |
|       |  | 25/30 | <ul style="list-style-type: none"> <li>. Microarray design</li> </ul>  |

**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.