CPC  COOPERATIVE PATENT CLASSIFICATION

C  CHEMISTRY; METALLURGY
   (NOTES omitted)

CHEMISTRY

C12  BIOCHEMISTRY; BEER; SPIRITS; WINE; VINEGAR; MICROBIOLOGY; ENZYMEOLOGY; MUTATION OR GENETIC ENGINEERING
   (NOTES omitted)

C12Q  MEASURING OR TESTING PROCESSES INVOLVING ENZYMES, NUCLEIC ACIDS OR MICROORGANISMS (immunoassay G01N 33/53); COMPOSITIONS OR TEST PAPERS THEREFOR; PROCESSES OF PREPARING SUCH COMPOSITIONS; CONDITION-RESPONSIVE CONTROL IN MICROBIOLOGICAL OR ENZYMEOLOGICAL PROCESSES

NOTES
1. This subclass does not cover the observation of the progress or of the result of processes specified in this subclass by any of the methods specified in groups G01N 3/00 - G01N 29/00, which is covered by subclass G01N.
2. In this subclass, the following expression is used with the meaning indicated:
   "involving", when used in relation to a substance, includes the testing for the substance as well as employing the substance as a determinant or reactant in a test for a different substance.
3. Attention is drawn to Notes (1) to (3) following the title of class C12.
4. In this subclass, test media are classified in the appropriate group for the relevant test process.
5. Documents describing the use of an electrode for analysis of a specific analyte are classified in C12Q 1/001 or subgroups and not according to the last place rule.
6. Documents relating to new peptides, e.g. enzymes, or new DNA or its corresponding mRNA, encoding for the peptides, and their use in measuring or testing processes are classified in subclass C07K or in group C12N 9/00 according to the peptides, with the appropriate indexing codes relating to their use in diagnostics. However where the new nucleic acids are principally used in diagnostic processes, e.g. PCR, hybridisation reactions, the documents are also classified in group C12Q 1/68.
7. When classifying in groups C12Q 1/68 - C12Q 1/70 it is desirable to classify with symbols from groups C12Q 2500/00 - C12Q 2565/634, relating to relevant technical features of the invention, using Combination Sets.
8. In groups C12Q 1/6876 - C12Q 1/6895 and C12Q 1/70 - C12Q 1/708 it is desirable to add the indexing codes C12Q 2600/00 - C12Q 2600/178 which reflect the use of the product in combination with the virus groups only if the application refers to products.

| 1/00 | Measuring or testing processes involving enzymes, nucleic acids or microorganisms (measuring or testing apparatus with condition measuring or sensing means, e.g. colony counters, C12M 1/34); Compositions therefor; Processes of preparing such compositions |
| 1/01 | .  (Enzyme electrodes) |
| 1/02 | .  (Electrode membranes) |
| 1/03 | .  (Functionalisation) |
| 1/04 | .  (mediator-assisted) |
| 1/05 | .  (involving specific analytes or enzymes (including groups of enzymes, e.g. oxidases; C12Q 1/004 takes precedence)) |
| 1/06 | .  (for glucose) |
| 1/07 | .  (involving isoenzyme profiles (for detection of an individual isoenzyme C12Q 1/25 - C12Q 1/66)) |
| 1/08 | .  (for determining co-enzymes or co-factors, e.g. NAD, ATP) |
| 1/02 | .  involving viable microorganisms |
| 1/025 | .  (for testing or evaluating the effect of chemical or biological compounds, e.g. drugs, cosmetics (antimicrobial activity C12Q 1/18)) |
| 1/04 | .  Determining presence or kind of microorganism; Use of selective media for testing antibiotics or bacteriocides; Compositions containing a chemical indicator therefor (C12Q 1/6897 takes precedence)) |
| 1/045 | .  (Culture media therefor) |
| 1/06 | .  Quantitative determination |
| 1/08 | .  using multifield media |
| 1/10 | .  Enterobacteria |
| 1/12 | .  Nitrate to nitrite reducing bacteria |
| 1/14 | .  Streptococcus; Staphylococcus |
| 1/16 | .  using radioactive material |
| 1/18 | .  Testing for antimicrobial activity of a material |
| 1/20 | .  using multifield media |
| 1/22 | .  Testing for sterility conditions |
| 1/24 | .  Methods of sampling, or inoculating or spreading a sample; Methods of physically isolating an intact microorganisms |
| 1/25 | .  involving enzymes not classifiable in groups C12Q 1/26 - C12Q 1/66 |
| 1/26 | .  involving oxidoreductase |
| 1/28 | .  involving peroxidase |
1/30 . . involving catalase
1/32 . . involving dehydrogenase
1/34 . . involving hydrolase
1/37 . . involving peptidase or proteinase
1/40 . . involving amylase
1/42 . . involving phosphatase
1/44 . . involving esterase
1/46 . . . involving cholinesterase
1/48 . . involving transferase
1/485 . . . {involving kinase}
1/50 . . involving creatine phosphokinase
1/52 . . involving transaminase
1/527 . . involving lyase
1/533 . . involving isomerase
1/54 . . involving glucose or galactose
1/56 . . involving blood clotting factors, e.g. involving thrombin, thromboplatin, fibrinogen
1/58 . . involving urea or urease
1/60 . . involving cholesterol
1/61 . . involving triglycerides
1/62 . . involving uric acid
1/64 . . Geomicrobiological testing, e.g. for petroleum
1/66 . . involving luciferase
1/68 . . involving nucleic acids

**NOTE**

In this group, classification is made according to the most relevant feature irrespective of the last place priority rule.

1/6804 . . Nucleic acid analysis using immunogens
   (immunoassay G01N 33/53)
1/6806 . . Preparing nucleic acids for analysis, e.g. for polymerase chain reaction [PCR] assay
   (C12Q 1/6804 takes precedence)
1/6809 . . Methods for determination or identification of nucleic acids involving differential detection
1/6811 . . Selection methods for production or design of target specific oligonucleotides or binding molecules
1/6813 . . Hybridisation assays
1/6816 . . . characterised by the detection means
   (C12Q 1/6804 takes precedence)
1/6818 . . . involving interaction of two or more labels, e.g. resonant energy transfer
1/682 . . . Signal amplification
1/6823 . . . Release of bound markers
1/6825 . . . Nucleic acid detection involving sensors
1/6827 . . . for detection of mutation or polymorphism
1/683 . . . involving restriction enzymes, e.g. restriction fragment length polymorphism [RFLP]
1/6832 . . . Enhancement of hybridisation reaction
1/6834 . . . Enzymatic or biochemical coupling of nucleic acids to a solid phase
1/6837 . . . using probe arrays or probe chips
   (C12Q 1/6874 takes precedence)
1/6839 . . . Triple helix formation or other higher order conformations in hybridisation assays
1/6841 . . . In situ hybridisation
1/6844 . . . Nucleic acid amplification reactions
1/6846 . . . {Common amplification features}
Reactions involving nucleic acids

Analytical methods involving nucleic acids (not used)

Reactions involving nucleic acids (not used)

Reaction characterised by the enzymatic activity (not used)

2521/119 . . . RNA polymerase
2521/125 . . . Methyl transferase, i.e. methylase
2521/131 . . . Terminal transferase
2521/30 . . . Phosphoric diester hydrolysing, i.e. nuclease (Not used)
2521/301 . . . Endonuclease
2521/307 . . . Single strand endonuclease
2521/313 . . . Type II endonucleases, i.e. cutting outside recognition site
2521/319 . . . Exonuclease
2521/325 . . . Single stranded exonuclease
2521/327 . . . RNAse, e.g. RNAseH
2521/331 . . . Methylation site specific nuclease
2521/337 . . . Ribozyme
2521/343 . . . Abzyme
2521/345 . . . DNAzyme
2521/50 . . . Other enzymatic activities (Not used)
2521/501 . . . Ligase
2521/507 . . . Recombinase
2521/513 . . . Winding/unwinding enzyme, e.g. helicase
2521/514 . . . Mismatch repair protein
2521/519 . . . Topoisomerase
2521/525 . . . Phosphatase (Not used with code C12Q 2565/301)
2521/531 . . . Glycosylase
2521/537 . . . Protease
2521/539 . . . Deaminase
2521/543 . . . Immobilised enzyme(s)

Reactions characterised by treatment of reaction samples (not used)

2523/10 . . . Characterised by chemical treatment (Not used)
2523/101 . . . Crosslinking agents, e.g. psoralen
2523/107 . . . Chemical cleaving agents
2523/109 . . . chemical ligation between nucleic acids
2523/113 . . . Denaturing agents
2523/115 . . . oxidising agents
2523/119 . . . Renaturing agents
2523/125 . . . Bisulphite(s)
2523/30 . . . Characterised by physical treatment (Not used)
2523/301 . . . Sonication
2523/303 . . . Applying a physical force on a nucleic acid
2523/305 . . . Denaturation or renaturation by physical action
2523/307 . . . Denaturation or renaturation by electric current/voltage
2523/308 . . . Adsorption or desorption
2523/31 . . . Electrostatic interactions, e.g. use of cationic polymers in hybridisation reactions
2523/313 . . . Irradiation, e.g. UV irradiation
2523/319 . . . Photocleavage, photolysis, photoproduction
2523/32 . . . Centrifugation

Reactions involving modified oligonucleotides, nucleic acids, or nucleotides

2525/10 . . . Modifications characterised by
2525/101 . . . incorporating non-naturally occurring nucleotides, e.g. inosine
2525/107 . . . incorporating a peptide nucleic acid
2525/113 . . incorporating modified backbone
2525/117 . . incorporating modified base
2525/119 . . incorporating abasic sites
2525/121 . . incorporating both deoxyribonucleotides and ribonucleotides
2525/125 . . incorporating agents resulting in resistance to degradation
2525/131 . . incorporating a restriction site
2525/137 . . incorporating/modifying moieties to eliminate restriction sites
2525/143 . . incorporating a promoter sequence (Not used with code C12Q 2531/143)
2525/149 . . incorporating a coding sequence
2525/15 . . incorporating a consensus or conserved sequence
2525/151 . . repeat or repeated sequences, e.g. VNTR, microsatellite, concatamer
2525/155 . . incorporating/generating a new priming site
2525/161 . . incorporating target specific and non-target specific sites
2525/173 . . incorporating a polynucleotide run, e.g. polyAs, polyTs
2525/179 . . incorporating arbitrary or random nucleotide sequences
2525/185 . . incorporating base(s) where the precise position of the base(s) in the nucleic acid string is important (Not to be used for 3'-end base)
2525/186 . . incorporating a non-extendable or blocking moiety (not used with C12Q 2535/101)
2525/191 . . incorporating an adaptor
2525/197 . . incorporating a spacer/coupling moiety
2525/203 . . incorporating a composite nucleic acid containing a polypeptide sequence other than PNA
2525/204 . . specific length of the oligonucleotides
2525/205 . . Aptamer
2525/207 . . siRNA, miRNA
2525/30 . . Oligonucleotides characterised by their secondary structure
2525/301 . . Hairpin oligonucleotides
2525/307 . . Circular oligonucleotides
2525/313 . . Branched oligonucleotides

2527/00 Reactions demanding special reaction conditions (not used)
2527/10 . . Reaction conditions characterised by (metal/ion C12Q 2563/137) (not used)
2527/101 . . Temperature
2527/107 . . Temperature of melting, i.e. Tm
2527/109 . . Pressure
2527/113 . . Time
2527/119 . . pH
2527/125 . . Specific component of sample, medium or buffer (for metal/ion use C12Q 2563/137)
2527/127 . . the enzyme inhibitor or activator used
2527/137 . . Concentration of a component of medium
2527/143 . . Concentration of primer/probe
2527/146 . . Concentration of target/template
2527/149 . . Concentration of an enzyme
2527/15 . . Gradients
2527/153 . . Viscosity
2527/156 . . Permeability

2531/00 Reactions of nucleic acids characterised by
2531/10 . . the purpose being amplify/increase the copy number of target nucleic acid (Not used)
2531/101 . . Linear amplification, i.e. non exponential
2531/107 . . Asymmetric PCR
2531/113 . . PCR
2531/119 . . Strand displacement amplification [SDA]
2531/125 . . Rolling circle
2531/131 . . Inverse PCR
2531/137 . . Ligase Chain Reaction [LCR]
2531/143 . . Promoter based amplification, e.g. NASBA, 3SR, TAS
2531/149 . . Replicase based amplification, e.g. Q beta replicase

2533/00 Reactions characterised by the enzymatic reaction principle used
2533/10 . . the purpose being to increase the length of an oligonucleotide strand (ligase detection reaction, LDR C12Q 2561/125)
2533/101 . . Primer extension (see also codes C12Q 2535/125, C12Q 2565/537)
2533/107 . . Probe/oligonucleotide ligation (Not used with code C12Q 2531/137, C12Q 2561/125)

2535/00 Reactions characterised by the assay type for determining the identity of a nucleotide base
2535/10 . . the purpose being to determine the identity or sequence oligonucleotides characterised by (Not used)
2535/101 . . Sanger sequencing method, i.e. oligonucleotide sequencing using primer elongation and deoxynucleotides as chain terminators
2535/107 . . Maxam and Gilbert method, i.e. sequential release and detection of nucleotides
2535/113 . . Cycle sequencing
2535/119 . . Double strand sequencing
2535/122 . . Massive parallel sequencing
2535/125 . . Allele specific primer extension
2535/131 . . Allele specific probes
2535/137 . . Amplification Refractory Mutation System [ARMS]
2535/138 . . Amplified fragment length polymorphism [AFLP]
2535/139 . . Random amplification polymorphism detection [RAPD] (not to be used with C12Q 2525/179)

2537/00 Reactions characterised by the reaction format or use of a specific feature
2537/10 . . the purpose or use of
2537/101 . . Homogeneous assay format, e.g. one pot reaction
2537/107 . . Homoduplex formation
2537/113 . . Heteroduplex formation
2537/119 . . Triple helix formation
2537/125 . . Sandwich assay format
2537/137 . . a displacement step (Not used with code C12Q 2531/119)
2537/1373 . . Displacement by a nucleic acid
2537/1376 . . Displacement by an enzyme
2537/143 . . Multiplexing, i.e. use of multiple primers or probes in a single reaction, usually for simultaneously analyse of multiple analysis
2537/149 . . Sequential reactions (Not used with reactions implicitly known to be sequential, e.g. amplification reactions)
2537/155 . . Cyclic reactions (Not used with codes C12Q 2531/101 - C12Q 2531/149)
A reaction step characterised by the number of molecules incorporated or released

Reduction of complexity, e.g. amplification of subsets, removing duplicated genomic regions

Assays for determining copy number or wherein the copy number is of special importance

A competitive reaction step (Not used with code C12Q 2545/101)

Helper probe

Blocking probe (not used in combination with C12Q 2527/127 or C12Q 2525/186)

Methylation detection other than bisulphite or methylation sensitive restriction endonucleases

Mathematicalmodelling, e.g. logarithm, ratio

Reactions characterised by analysis of gene expression or genome comparison

The purpose being sequence identification by analysis of gene expression or genome comparison characterised by

Subtraction analysis

Serial analysis of gene expression [SAGE]

Involving introns, exons, or splice junctions

Representational Difference Analysis [RDA]

Differential Display Analysis [DDA]

Comparative genomic hybridisation [CGH]

Reactions characterised by directed evolution

the purpose being the selection/design of target specific nucleic acid binding sequences (not used)

Selex

Reactions characterised by the reaction site, e.g. cell or chromosome

the purpose being "in situ" analysis

in situ amplification

Reactions characterised by their quantitative nature

the purpose being quantitative analysis (Not used)

with an internal standard/control

with a competitive internal standard/control

with an external standard/control, i.e. control reaction is separated from the test/target reaction

involving a quantitation step (not to be used with C12Q 2545/101, C12Q 2545/107, C12Q 2545/113)

Reactions characterised by the features used to prevent contamination

the purpose being preventing contamination (Not used)

by confinement to a single tube/container

Use of permeable barriers, e.g. waxes

Reactions characterised by the features used to influence the efficiency or specificity

the purpose being that of reducing false positive/negative signals (Not used)

Hot start

Cold start

using nested probes

using nested primers

using sterilising/blocking agents, e.g. albumin

using oligonucleotides as clamps (not to be used with C12Q 2525/107)

Nucleic acid detection (not used)

Nucleic acid detection characterised by assay method (not used)

Characterised by assay method (Not used)

Taquin

Enzyme complementation

Hybridisation protection assay [HPA]

Invader technology

Real time assay

Fluorescence polarisation

Fluorescence lifetime measurement

Ligase Detection Reaction [LDR]

Protein truncation assay

Nucleic acid detection characterised by the use of (not used)

radioactivity, e.g. radioactive labels

luminescence

fluorescence

the label being electroactive, e.g. redox labels

electrical properties of nucleic acids, e.g. impedance, conductivity or resistance

Nucleic acid detection characterised by assay method (not used)

Radioisotopes

Luminescence

Radioactivity

Fluorescence

Nucleic acid detection characterised by mode or means of detection

Detection mode being characterised by (Not used)

Interaction between at least two labels

labels being on the same oligonucleotide

C12Q
Multiple non-interacting labels

Based on agglutination/precipitation

Based on extraction of label to an organic phase, i.e. partitioning of label between different organic phases

Electrophoretic separation

Single/double strand conformational analysis, i.e. SSCP/DSCP

Conformational analysis

Chromatographic separation

Detection means characterised by being a gene reporter based analysis (Not used)

Two hybrid system

Three hybrid system

Detection characterised by liberation/release of label (Not used)

Pyrophosphate (PPi)

Detection characterised by signal amplification of label (not used)

Signal amplification by chemical polymerisation

Detection characterised by immobilisation to a surface

being on/an array of oligonucleotides

characterised by the density of the capture oligonucleotide

characterised by the pattern of the arrayed oligonucleotides

characterised by the use of the arrayed oligonucleotides as identifier tags, e.g. universal addressable array, anti-tag or tag complement array

characterised by the interaction between or sequential use of two or more arrays

characterised by the immobilisation of the nucleic acid sample or target

characterised by the capture moiety being a single stranded oligonucleotide

characterised by the capture oligonucleotide being double stranded

characterised by the capture moiety being a protein for target oligonucleotides

characterised by the capture oligonucleotide acting as a primer

characterised by the use of two or more capture oligonucleotide primers in concert, e.g. bridge amplification (Not used with code C12Q 2537/149)

characterised by the capture oligonucleotide being a reporter labelled capture oligonucleotide

Detection means characterised by use of a special device (Not used)

being a microscope, e.g. atomic force microscopy [AFM]

being a sensor, e.g. electrode

being a video camera

being a nucleic acid test strip device, e.g. dipsticks, strips, tapes, CD plates

being a flow cytometer

being a mass spectrometer (not to be used with C120 2563/167)

being a surface plasmon resonance spectrometer

Oligonucleotides characterized by their use (not used, see subgroups)

Pharmacogenomics, i.e. genetic variability in individual responses to drugs and drug metabolism

Disease subtyping, staging or classification

Prognosis of disease development

Animal traits, i.e. production traits, including athletic performance or the like

Plant traits

Screening for pharmacological compounds

Toxicological screening, e.g. expression profiles which identify toxicity

Screening for cosmetic compounds

Methylation markers

Polymorphic or mutational markers

Expression markers

Primer sets for multiplex assays

Oligonucleotides used as internal standards, controls or normalisation probes

Haplotypes

miRNA, siRNA or ncRNA