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.

WARNING
In this subclass non-limiting references (in the sense of paragraph 39 of the Guide to the IPC) may still be displayed in the scheme.

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

1/001  .  (Enzyme electrodes)
1/002  .  (Electrode membranes)
1/003  .  .  (Functionalisation)
1/004  .  .  (mediator-assisted)
1/005  .  .  (involving specific analytes or enzymes (including groups of enzymes, e.g. oxydases; C12Q 1/004 takes precedence))
1/006  .  .  {for glucose}
1/007  .  .  (involving isoenzyme profiles (for detection of an individual isoenzyme C12Q 1/25 - C12Q 1/66))
1/008  .  .  (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
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 [Common amplification features]
1/6848 characterised by the means for preventing contamination or increasing the specificity or sensitivity of an amplification reaction
1/6851 Quantitative amplification
1/6853 using modified primers or templates
1/6855 Ligating adapters
1/6858 Allele-specific amplification
1/686 Polyamide chain reaction [PCR]
1/6862 Ligase chain reaction [LCR]
1/6865 Promoter-based amplification, e.g. nucleic acid sequence amplification [NASBA], self-sustained sequence replication [3SR] or transcription-based amplification system [TAS]
1/6867 Replicate-based amplification, e.g. using Q-beta replicase
1/6869 Methods for sequencing
1/6872 involving mass spectrometry
1/6874 involving nucleic acid arrays, e.g. sequencing by hybridisation
1/6876 Nucleic acid products used in the analysis of nucleic acids, e.g. primers or probes
1/6879 for sex determination
1/6881 for tissue or cell typing, e.g. human leukocyte antigen [HLA] probes
1/6883 for diseases caused by alterations of genetic material
1/6886 for cancer (immunoassay for cancer G01N 33/574)
1/6888 for detection or identification of organisms
1/689 for bacteria
1/6893 for protozoa
1/6895 for plants, fungi or algae
1/6897 involving reporter genes operably linked to promoters
1/70 involving virus or bacteriophage
1/701 [Specific hybridization probes]
1/702 [for retroviruses]
1/703 [Viruses associated with AIDS]
1/705 [for herpetoviridae, e.g. herpes simplex, varicella zoster]
1/706 [for hepatitis]
1/707 [non-A, non-B Hepatitis, excluding hepatitis D]
1/708 [for papilloma]
3/00 Condition responsive control processes (apparatus therefor C12M 1/36; controlling or regulating in general G05)
2304/00 Chemical means of detecting microorganisms (hydrolase substrates C12Q 2334/00; peptidase substrates C12Q 2337/00)
2304/10 DNA staining
2304/12 Ethidium
2304/13 Propidium
2304/16 Acridine orange
2304/18 Thionin-type dyes, e.g. Azure, Toluidine Blue
2304/20 . Redox indicators
2304/22 . Resazurin; Resorufin
2304/24 . Tetrazolium; Formazan
2304/26 . Quinone; Quinol
2304/40 . Detection of gases
2304/44 . Oxygen
2304/46 . Carbon dioxide
2304/48 . Ammonia or volatile amines
2304/60 . Chemiluminescent detection using ATP-luciferin-luciferase system
2304/80 . Electrochemical detection via electrodes in contact with culture medium

2326/00 Chromogens for determinations of oxidoreductase enzymes
2326/10 . Benzidines
2326/12 . 3,3',5,5'-Tetramethylbenzidine, i.e. TMB
2326/14 . Ortho-Tolidine, i.e. 3,3'-dimethyl-(1,1'-biphenyl-4,4'-diame)
2326/20 . Ortho-Phenylenediamine
2326/30 . 2,2'-Azinobis (3-ethylbenzothiazoline-6-sulfonic acid), i.e. ABTS
2326/32 . 3-Methyl-2-benzothiazolinone hydrazone
2326/40 . Triphenylmethane dye chromogens, e.g. fluorescein derivatives
2326/50 . Phenols; Naphthols; Catechols
2326/90 . Developer
2326/92 . Nitro blue tetrazolium chloride, i.e. NBT
2326/96 . 4-Amino-anthpyrine

2334/00 O-linked chromogens for determinations of hydrolase enzymes, e.g. glycosidases, phosphatases, esterases
2334/10 . p-Nitrophenol derivatives
2334/20 . Coumarin derivatives
2334/22 . 4-Methylumbelliferyl, i.e. beta-methylumbellifereone, 4MU
2334/30 . Naphthol derivatives, e.g. alpha-naphthyl-esters, i.e. alpha-NE, beta-naphthyl-esters, i.e. beta-NE
2334/40 . Triphenylmethane dye chromogens, e.g. fluorescein derivatives
2334/50 . Indoles
2334/52 . 5-Bromo-4-chloro-3-indolyl, i.e. BCI
2334/70 . the product, e.g. phenol, naphthol being diazotised in situ, e.g. with Fast Red

2337/00 N-linked chromogens for determinations of peptidases and proteinases
2337/10 . Anilides
2337/12 . Para-Nitroanilides p-NA
2337/20 . Coumarin derivatives
2337/22 . 7-Amino-4-methylcoumarin, i.e. AMC, MCA
2337/24 . 7-Amino-4-trifluoromethylcoumarin, i.e. AFC
2337/30 . Naphthyl amides, e.g. beta-NA, 2-NA, 4-methoxy-beta-naphthylamine, i.e. 4MNA
2337/40 . Rhodamine derivatives
2337/50 . Indoles
2337/52 . 5-Bromo-4-chloro-3-indolyl, i.e. BCI

2500/00 Analytical methods involving nucleic acids
2520/00 Reactions involving nucleic acids
2521/00 Reaction characterised by the enzymatic activity
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
2525/149 . incorporating a coding sequence
2525/15 . incorporating a consensus or conserved sequence
2525/151 . repeat or repeated sequences, e.g. VNTR, microsatellite, concatemer
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. polyA, polyTs
2525/179 . incorporating arbitrary or random nucleotide sequences
2525/185 . incorporating bases where the precise position of the bases in the nucleic acid string is important
2525/186 . incorporating a non-extendable or blocking moiety
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
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
2527/127 . the enzyme inhibitor or activator used
2527/137 . Concentration of a component of medium
2527/143 . Concentration of primer or probe
2527/146 . Concentration of target or 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
2531/101 . Linear amplification, i.e. non exponential
2531/107 . Probe or oligonucleotide ligation
2531/109 . Amplified fragment length polymorphism [AFLP]
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
2533/101 . Primer extension
2533/107 . Probe or oligonucleotide ligation

2535/00 Reactions characterised by the assay type for determining the identity of a nucleotide base or a sequence of oligonucleotides
2535/101 . Sanger sequencing method, i.e. oligonucleotide sequencing using primer elongation and deoxyribonucleotides 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]

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
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
2537/151 . Cyclic reactions
2537/157 . A reaction step characterised by the number of molecules incorporated or released
2537/159 . Reduction of complexity, e.g. amplification of subsets, removing duplicated genomic regions
2537/16 . Assays for determining copy number or wherein the copy number is of special importance
2537/161 . A competitive reaction step
2537/162 . Helper probe
2537/163 . blocking probe
2537/164 . Methylation detection other then bisulfite or methylation sensitive restriction endonucleases
2537/165 . Mathematical modelling, 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 or design of target specific nucleic acid binding sequences
- 
- 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
- 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

Reactions characterised by the features used to prevent contamination

- The purpose being preventing contamination
- 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 or false negative signals
- Hot start
- Cold start
- using nested probes
- using nested primers
- using sterilising/blocking agents, e.g. albumin
- using oligonucleotides as clamps

Nucleic acid detection

Nucleic acid detection characterised by assay method

- Taqman
- 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 physical, structural and functional properties

- 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
- the label being proteinic
- the label being enzymatic, i.e. proteins, and non proteins, such as nucleic acid with enzymatic activity
- the label being a member of a cognate binding pair, i.e. extends to antibodies, haptons, avidin
- Metal/ion, e.g. metal label
- Magnetism, e.g. magnetic label
- Particles, e.g. beads
- Particles of a defined size, e.g. nanoparticles
- Nanotubes or nanorods
- Microreactors, e.g. emulsion PCR or sequencing, droplet PCR, microcapsules, i.e. non-liquid containers with a range of different permeability's for different reaction components
- Vesicles, e.g. liposome
- Mass label
- staining/intercalating agent, e.g. ethidium bromide
- the label being a nucleic acid
- Nucleic acid dedicated to use as a hidden marker/bar code, e.g. inclusion of nucleic acids to mark art objects or animals

Nucleic acid analysis characterised by mode or means of detection

Detection mode being characterised by the assay principle

- Interaction between at least two labels
- . . . labels being on the same oligonucleotide
- . . . Multiple non-interacting labels
- . . . labels being on the same oligonucleotide
- . . . Alteration in the property of hybridised versus free label oligonucleotides
- 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
- Two hybrid system
- Three hybrid system
- Detection characterised by liberation or release of label
- Pyrophosphate (PPi)
- Detection characterised by signal amplification of label
- Signal amplification by chemical polymerisation
- Detection characterised by immobilisation to a surface
- being 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

. characterised by the capture oligonucleotide being a reporter labelled capture oligonucleotide

. Detection means characterised by use of a special device

. 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

. being a surface plasmon resonance spectrometer

. being a microfluidic device

. being a biochannel or pore

. being a surface enhanced, e.g. resonance, Raman spectrometer

. NMR

. being an acoustic wave sensor

Oligonucleotides characterized by their use

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