

CPC COOPERATIVE PATENT CLASSIFICATION

C CHEMISTRY; METALLURGY

(NOTES omitted)

CHEMISTRY

C12 BIOCHEMISTRY; BEER; SPIRITS; WINE; VINEGAR; MICROBIOLOGY; ENZYMOLOGY; 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 ENZYMOLOGICAL 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. In this subclass, it is desirable to add the indexing codes of subclass [C12R](#).
6. {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.}
7. {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](#).}
8. {In groups [C12Q 1/6876](#) - [C12Q 1/6895](#) and [C12Q 1/701](#) - [C12Q 1/708](#) it is compulsory 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 document relates to products.}
9. {In this subclass, combination sets [C-Sets] are used. The detailed information about the C-Sets construction and the associated syntax rules is present in the definitions of [C12Q](#).}

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.

<p>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</p> <p>NOTE</p> <p>{In this group, C-Sets are used for classification. The detailed information about the C-Sets construction and the associated syntax rules are found in the Definitions of C12Q.}</p> <p>1/001 . {Enzyme electrodes}</p> <p>1/002 . . {Electrode membranes}</p> <p>1/003 . . . {Functionalisation}</p> <p>1/004 . . {mediator-assisted}</p>	<p>1/005 . . {involving specific analytes or enzymes (including groups of enzymes, e.g. oxydases; C12Q 1/004 takes precedence)}</p> <p>1/006 . . . {for glucose}</p> <p>1/007 . {involving isoenzyme profiles (for detection of an individual isoenzyme C12Q 1/25 - C12Q 1/66)}</p> <p>1/008 . {for determining co-enzymes or co-factors, e.g. NAD, ATP}</p> <p>1/02 . involving viable microorganisms</p> <p>1/025 . . {for testing or evaluating the effect of chemical or biological compounds, e.g. drugs, cosmetics (antimicrobial activity C12Q 1/18)}</p> <p>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)}</p>
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- 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, thromboplastin, 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
- NOTES**
1. In this group, classification is made according to the most relevant feature irrespective of the last place priority rule.
 2. {In groups [C12Q 1/68](#) - [C12Q 1/6874](#), and [C12Q 1/6897](#), C-Sets are used for classification. The detailed information about the C-Sets construction and the associated syntax rules are found in the Definitions of [C12Q](#).}
- 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](#)}
- 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 adaptors
- 1/6858 . . . Allele-specific amplification
- 1/686 . . . Polymerase 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 . . . Replicase-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 {([immunoassay for viruses G01N 33/56983](#))}
- NOTES**
1. {In this group, classification is made according to the most relevant feature irrespective of the last place priority rule.}
 2. {In this group, C-Sets are used for classification. The detailed information about the C-Sets

C12Q

C12Q 1/70
(continued)

construction and the associated syntax rules are found in the Definitions of [C12Q](#).)

- 1/701 . . {Specific hybridization probes}
- 1/702 . . . {for retroviruses}
- 1/703 {Viruses associated with AIDS}
- 1/705 . . . {for herpesviridae, 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'-diamine)
- 2326/20 . Ortho-Phenylenediamine
- 2326/30 . 2,2'-Azinobis (3-ethylbenzothiazoline-6-sulfonic acid), i.e. ABTS
- 2326/32 . 3-Methyl-2-benzothiazolinone hydrazone hydrochloride hydrate, i.e. MBTH
- 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-antipyrine

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-methylumbelliferone, 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**

NOTE

Indexing codes [C12Q 2500/00](#) - [C12Q 2565/634](#) are only used as subsequent symbols in C-Sets and are not allocated as single symbols. The detailed information about the C-Sets construction and the associated syntax rules is present in the Definitions of [C12Q](#).

2520/00 **Reactions involving nucleic acids**

2521/00 **Reaction characterised by the enzymatic activity**

- 2521/10 . Nucleotidyl transferring
- 2521/101 . . DNA polymerase
- 2521/107 . . RNA dependent DNA polymerase, (i.e. reverse transcriptase)
- 2521/113 . . Telomerase
- 2521/119 . . RNA polymerase
- 2521/125 . . Methyl transferase, i.e. methylase
- 2521/131 . . Terminal transferase
- 2521/30 . Phosphoric diester hydrolysing, i.e. nuclease
- 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
- 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
- 2521/531 . . Glycosylase
- 2521/537 . . Protease
- 2521/539 . . Deaminase
- 2521/543 . . Immobilised enzyme(s)

- 2522/00** **Reaction characterised by the use of non-enzymatic proteins**
- 2522/10 . Nucleic acid binding proteins
- 2522/101 . . Single or double stranded nucleic acid binding proteins
- 2523/00** **Reactions characterised by treatment of reaction samples**
- 2523/10 . Characterised by chemical treatment
- 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 . . Bisulfite(s)
- 2523/30 . Characterised by physical treatment
- 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, photoactivation
- 2523/32 . . Centrifugation
- 2525/00** **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
- 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. polyAs, 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. T_m
- 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
- 2531/113 . . 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 dideoxynucleotides 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
- 2537/155 . . 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 than bisulfite or methylation sensitive restriction endonucleases
- 2537/165 . . Mathematical modelling, e.g. logarithm, ratio
- 2539/00 Reactions characterised by analysis of gene expression or genome comparison**
- 2539/10 . The purpose being sequence identification by analysis of gene expression or genome comparison characterised by
- 2539/101 . . Subtraction analysis
- 2539/103 . . Serial analysis of gene expression [SAGE]
- 2539/105 . . Involving introns, exons, or splice junctions
- 2539/107 . . Representational Difference Analysis [RDA]
- 2539/113 . . Differential Display Analysis [DDA]
- 2539/115 . . Comparative genomic hybridisation [CGH]
- 2541/00 Reactions characterised by directed evolution**
- 2541/10 . the purpose being the selection or design of target specific nucleic acid binding sequences
- 2541/101 . . Selex
- 2543/00 Reactions characterised by the reaction site, e.g. cell or chromosome**
- 2543/10 . the purpose being "in situ" analysis
- 2543/101 . . in situ amplification
- 2545/00 Reactions characterised by their quantitative nature**
- 2545/10 . the purpose being quantitative analysis
- 2545/101 . . with an internal standard/control
- 2545/107 . . with a competitive internal standard/control
- 2545/113 . . with an external standard/control, i.e. control reaction is separated from the test/target reaction
- 2545/114 . . involving a quantitation step
- 2547/00 Reactions characterised by the features used to prevent contamination**
- 2547/10 . the purpose being preventing contamination
- 2547/101 . . by confinement to a single tube/container
- 2547/107 . . Use of permeable barriers, e.g. waxes
- 2549/00 Reactions characterised by the features used to influence the efficiency or specificity**
- 2549/10 . the purpose being that of reducing false positive or false negative signals
- 2549/101 . . Hot start
- 2549/107 . . Cold start
- 2549/113 . . using nested probes
- 2549/119 . . using nested primers
- 2549/125 . . using sterilising/blocking agents, e.g. albumin
- 2549/126 . . using oligonucleotides as clamps
- 2560/00 Nucleic acid detection**
- 2561/00 Nucleic acid detection characterised by assay method**
- 2561/101 . Taqman
- 2561/107 . Enzyme complementation
- 2561/108 . Hybridisation protection assay [HPA]
- 2561/109 . Invader technology
- 2561/113 . Real time assay
- 2561/119 . Fluorescence polarisation
- 2561/12 . Fluorescence lifetime measurement
- 2561/125 . Ligase Detection Reaction [LDR]
- 2561/127 . Protein truncation assay
- 2563/00 Nucleic acid detection characterized by the use of physical, structural and functional properties**
- 2563/101 . radioactivity, e.g. radioactive labels
- 2563/103 . luminescence
- 2563/107 . fluorescence
- 2563/113 . the label being electroactive, e.g. redox labels
- 2563/116 . electrical properties of nucleic acids, e.g. impedance, conductivity or resistance
- 2563/119 . the label being proteinic
- 2563/125 . the label being enzymatic, i.e. proteins, and non proteins, such as nucleic acid with enzymatic activity
- 2563/131 . the label being a member of a cognate binding pair, i.e. extends to antibodies, haptens, avidin
- 2563/137 . Metal/ion, e.g. metal label
- 2563/143 . Magnetism, e.g. magnetic label
- 2563/149 . Particles, e.g. beads
- 2563/155 . Particles of a defined size, e.g. nanoparticles
- 2563/157 . Nanotubes or nanorods
- 2563/159 . 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
- 2563/161 . Vesicles, e.g. liposome
- 2563/167 . Mass label
- 2563/173 . staining/intercalating agent, e.g. ethidium bromide
- 2563/179 . the label being a nucleic acid
- 2563/185 . Nucleic acid dedicated to use as a hidden marker/bar code, e.g. inclusion of nucleic acids to mark art objects or animals
- 2565/00 Nucleic acid analysis characterised by mode or means of detection**
- 2565/10 . Detection mode being characterised by the assay principle
- 2565/101 . . Interaction between at least two labels
- 2565/1015 . . . labels being on the same oligonucleotide

- 2565/102 . . Multiple non-interacting labels
 - 2565/1025 . . . labels being on the same oligonucleotide
 - 2565/107 . . Alteration in the property of hybridised versus free label oligonucleotides
 - 2565/113 . . based on agglutination/precipitation
 - 2565/119 . . based on extraction of label to an organic phase, i.e. partitioning of label between different organic phases
 - 2565/125 . . Electrophoretic separation
 - 2565/131 . . Single/double strand conformational analysis, i.e. SSCP/DSCP
 - 2565/133 . . conformational analysis
 - 2565/137 . . Chromatographic separation
 - 2565/20 . . Detection means characterised by being a gene reporter based analysis
 - 2565/201 . . Two hybrid system
 - 2565/207 . . Three hybrid system
 - 2565/30 . . Detection characterised by liberation or release of label
 - 2565/301 . . Pyrophosphate (PPi)
 - 2565/40 . . Detection characterised by signal amplification of label
 - 2565/401 . . Signal amplification by chemical polymerisation
 - 2565/50 . . Detection characterised by immobilisation to a surface
 - 2565/501 . . being an array of oligonucleotides
 - 2565/507 . . characterised by the density of the capture oligonucleotide
 - 2565/513 . . characterised by the pattern of the arrayed oligonucleotides
 - 2565/514 . . characterised by the use of the arrayed oligonucleotides as identifier tags, e.g. universal addressable array, anti-tag or tag complement array
 - 2565/515 . . characterised by the interaction between or sequential use of two or more arrays
 - 2565/518 . . characterised by the immobilisation of the nucleic acid sample or target
 - 2565/519 . . characterised by the capture moiety being a single stranded oligonucleotide
 - 2565/525 . . characterised by the capture oligonucleotide being double stranded
 - 2565/531 . . characterised by the capture moiety being a protein for target oligonucleotides
 - 2565/537 . . characterised by the capture oligonucleotide acting as a primer
 - 2565/543 . . characterised by the use of two or more capture oligonucleotide primers in concert, e.g. bridge amplification
 - 2565/549 . . characterised by the capture oligonucleotide being a reporter labelled capture oligonucleotide
 - 2565/60 . . Detection means characterised by use of a special device
 - 2565/601 . . being a microscope, e.g. atomic force microscopy [AFM]
 - 2565/607 . . being a sensor, e.g. electrode
 - 2565/619 . . being a video camera
 - 2565/625 . . being a nucleic acid test strip device, e.g. dipsticks, strips, tapes, CD plates
 - 2565/626 . . being a flow cytometer
 - 2565/627 . . being a mass spectrometer
 - 2565/628 . . being a surface plasmon resonance spectrometer
 - 2565/629 . . being a microfluidic device
 - 2565/631 . . being a biochannel or pore
 - 2565/632 . . being a surface enhanced, e.g. resonance, Raman spectrometer
 - 2565/633 . . NMR
 - 2565/634 . . being an acoustic wave sensor
- 2600/00 Oligonucleotides characterized by their use**
- 2600/106 . . Pharmacogenomics, i.e. genetic variability in individual responses to drugs and drug metabolism
 - 2600/112 . . Disease subtyping, staging or classification
 - 2600/118 . . Prognosis of disease development
 - 2600/124 . . Animal traits, i.e. production traits, including athletic performance or the like
 - 2600/13 . . Plant traits
 - 2600/136 . . Screening for pharmacological compounds
 - 2600/142 . . Toxicological screening, e.g. expression profiles which identify toxicity
 - 2600/148 . . Screening for cosmetic compounds
 - 2600/154 . . Methylation markers
 - 2600/156 . . Polymorphic or mutational markers
 - 2600/158 . . Expression markers
 - 2600/16 . . Primer sets for multiplex assays
 - 2600/166 . . Oligonucleotides used as internal standards, controls or normalisation probes
 - 2600/172 . . Haplotypes
 - 2600/178 . . miRNA, siRNA or ncRNA