CPC COOPERATIVE PATENT CLASSIFICATION

C12Q MEASURING OR TESTING PROCESSES INVOLVING ENZYMES OR MICRO-ORGANISMS (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 to 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 to C12Q 1/70 it is desirable to classify with symbols from groups C12Q 2500/00 to 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 to C12Q 2600/178 which reflect the use of the product in combination with the virus groups only if the application refers to products.

C12Q 1/00 Measuring or testing processes involving enzymes, {nucleic acids} or micro-organisms (measuring or testing apparatus with condition measuring or sensing means, e.g. colony counters C12M 1/34); Compositions therefor; Processes of preparing such compositions

C12Q 1/001 . {Enzyme electrodes}

C12Q 1/002 . . {Electrode membranes}

C12Q 1/003 . . . {Functionalisation}

C12Q 1/004 . . {mediator-assisted}

C12Q 1/005 . . {involving specific analytes or enzymes (including groups of enzymes, e.g. oxydases; C12Q 1/004 takes precedence)}

C12Q 1/006 . . . {for glucose}

C12Q 1/007 . {involving isoenzyme profiles (for detection of an individual isoenzyme C12Q 1/25 to C12Q 1/66)}

C12Q 1/008 . {for determining co-enzymes or co-factors, e.g. NAD, ATP}

C12Q 1/02 . involving viable micro-organisms

C12Q 1/025 . . {for testing or evaluating the effect of chemical or biological compounds, e.g. drugs, cosmetics (antimicrobial activity C12Q 1/18)}

C12Q 1/04 . . Determining presence or kind of micro-organism; Use of selective media for testing antibiotics or bacteriocides; Compositions containing a chemical indicator therefor {(C12Q 1/6897 takes precedence)}

C12Q 1/045 . . . {Culture media therefor}

C12Q 1/06 . . . Quantitative determination

C12Q 1/08 . . . . using multifield media

C12Q 1/10 . . . Enterobacteria

C12Q 1/12 . . . Nitrate to nitrite reducing bacteria

C12Q 1/14 . . . Streptococcus; Staphylococcus

C12Q 1/16 . . . using radioactive material

C12Q 1/18 . . Testing for antimicrobial activity of a material

C12Q 1/20 . . . using multifield media

C12Q 1/22 . . Testing for sterility conditions

C12Q 1/24 . . Methods of sampling, or inoculating or spreading a sample; Methods of physically isolating an intact micro-organisms

C12Q 1/25 . involving enzymes not classifiable in groups C12Q 1/26 {to C12Q 1/66}

C12Q 1/26 . involving oxidoreductase

C12Q 1/28 . . involving peroxidase

C12Q 1/30 . . involving catalase

C12Q 1/32 . . involving dehydrogenase

C12Q 1/34 . involving hydrolase

C12Q 1/37 . . involving peptidase or proteinase

C12Q 1/40 . . involving amylase

C12Q 1/42 . . involving phosphatase

C12Q 1/44 . . involving esterase

C12Q 1/46 . . . involving cholinesterase

C12Q 1/48 . involving transferase

C12Q 1/485 . . {involving kinase}

C12Q 1/50 . . involving creatine phosphokinase

C12Q 1/52 . . involving transaminase

C12Q 1/527 . involving lyase

C12Q 1/533 . involving isomerase

C12Q 1/54 . involving glucose or galactose

C12Q 1/56 . involving blood clotting factors, e.g. involving thrombin, thromboplastin, fibrinogen

C12Q 1/58 . involving urea or urease

C12Q 1/60 . involving cholesterol

C12Q 1/61 . involving triglycerides

C12Q 1/62 . involving uric acid

C12Q 1/64 . Geomicrobiological testing, e.g. for petroleum

C12Q 1/66 . involving luciferase

C12Q 1/68 . involving nucleic acids

NOTE

In subgroups of C12Q 1/68, classification is made according to the most relevant feature rather than according to the last-place-rule

C12Q 1/6802 . . {General aspects (not used, see subgroups)}

C12Q 1/6804 . . . {Nucleic acid analysis utilising immunogens}

C12Q 1/6806 . . . {Preparing nucleic acids for analysis, e.g. for PCR assay (C12Q 1/6804 takes precedence)}

C12Q 1/6809 . . . {Sequence identification involving differential detection}

C12Q 1/6811 . . . {Selection methods for production or design of target specific oligonucleotide or binding molecules}

C12Q 1/6813 . . {Hybridisation assays}

C12Q 1/6816 . . . {characterised by the means of detection (C12Q 1/6804 takes precedence)}

C12Q 1/6818 . . . . {involving interaction of at least two labels, e.g. resonant energy transfer}

C12Q 1/682 . . . . {Signal amplification}

C12Q 1/6823 . . . . {Release of bound marker}

C12Q 1/6825 . . . . {Nucleic acid detection involving sensors}

C12Q 1/6827 . . . {for mutation or polymorphism detection}

C12Q 1/683 . . . . {involving restriction enzymes, e.g. RFLP}

C12Q 1/6832 . . . {Enhancement of hybridisation reaction}

C12Q 1/6834 . . . {Nucleic acid analysis involving immobilisation; Immobilisation characterised by the carrier or coupling agent}

C12Q 1/6837 . . . . {characterised by the use of probe arrays or probe chips (C12Q 1/6874 takes precedence)}

C12Q 1/6839 . . . {Triple helix formation in hybridisation assays}

C12Q 1/6841 . . . {"In-situ" hybridisation}

C12Q 1/6844 . . {Nucleic acid amplification reactions}

C12Q 1/6846 . . . {Common amplification features}

C12Q 1/6848 . . . . {preventing contamination}

C12Q 1/6851 . . . . {Quantitative amplification}

C12Q 1/6853 . . . . {using modified primers or templates}

C12Q 1/6855 . . . . . {Ligating adaptors}

C12Q 1/6858 . . . . {Allele specific amplification}

C12Q 1/686 . . . {Polymerase Chain Reaction [PCR]}

C12Q 1/6862 . . . {Ligase Chain Reaction [LCR]}
C12Q 1/6865 . . . {Promoter based amplification, e.g. NASBA, 3SR, TAS}
C12Q 1/6867 . . . {Replicase based amplifications, e.g. Q-beta replicase}
C12Q 1/6869 . . {Methods for sequencing}
C12Q 1/6872 . . . {involving mass spectrometry}
C12Q 1/6874 . . . {involving nucleic acid arrays, e.g. Sequencing By Hybridisation [SBH]}
C12Q 1/6876 . . {Hybridisation probes}
C12Q 1/6879 . . . {for sex determination}
C12Q 1/6881 . . . {for tissue and cell typing, e.g. HLA probes}
C12Q 1/6883 . . . {for diseases caused by alterations of genetic material}
C12Q 1/6886 . . . . {for cancer}
C12Q 1/6888 . . . {for detection or identification of organisms}
C12Q 1/689 . . . . {for bacteria}
C12Q 1/6893 . . . . {for protozoa}
C12Q 1/6895 . . . . {for plants, fungi, or algae}
C12Q 1/6897 . . {involving reporter genes operably linked to promoters}
C12Q 1/70 . involving virus or bacteriophage
C12Q 1/701 . . {Specific hybridization probes}
C12Q 1/702 . . . {for retroviruses}
C12Q 1/703 . . . . {Viruses associated with AIDS}
C12Q 1/705 . . . {for herpetoviridae, e.g. herpes simplex, varicella zoster}
C12Q 1/706 . . . {for hepatitis}
C12Q 1/707 . . . . {non-A, non-B Hepatitis, excluding hepatitis D}
C12Q 1/708 . . . {for papilloma}

C12Q 3/00 **Condition responsive control processes** (apparatus therefor C12M 1/36; controlling or regulating in general G05)

C12Q 2304/00 **Chemical means of detecting micro-organisms** (hydrolase substrates C12Q 2334/00, peptidase substrates C12Q 2337/00)
C12Q 2304/10 . DNA staining
C12Q 2304/12 . . Ethidium
C12Q 2304/13 . . Propidium
C12Q 2304/16 . . Acridine orange
C12Q 2304/18 . . Thionin-type dyes, e.g. Azure, Toluidine Blue
C12Q 2304/20 . Redox indicators
C12Q 2304/22 . . Resazurin; Resorufin
C12Q 2304/24 . . Tetrazolium; Formazan
C12Q 2304/26 . . Quinone; Quinol
C12Q 2304/40 . Detection of gases
C12Q 2304/44 . . Oxygen

C12Q 2304/46 . . Carbon dioxide
C12Q 2304/48 . . Ammonia or volatile amines
C12Q 2304/60 . Chemiluminescent detection using ATP-luciferin-luciferase system
C12Q 2304/80 . Electrochemical detection via electrodes in contact with culture medium

C12Q 2326/00 Chromogens for determinations of oxidoreductase enzymes
C12Q 2326/10 . Benzidines
C12Q 2326/12 . . 3,3',5,5'-Tetramethylbenzidine, i.e. TMB
C12Q 2326/14 . . Ortho-Tolidine, i.e. 3,3'-dimethyl-(1,1'-biphenyl-4,4'-diamine)
C12Q 2326/20 . Ortho-Phenylenediamine
C12Q 2326/30 . 2,2'-Azinobis (3-ethylbenzothiazoline-6-sulfonic acid), i.e. ABTS
C12Q 2326/32 . 3-Methyl-2-benzothiazolinone hydrazone hydrochloride hydrate, i.e. MBTH
C12Q 2326/40 . Triphenylmethane dye chromogens, e.g. fluorescein derivatives
C12Q 2326/50 . Phenols; Naphthols; Catechols
C12Q 2326/90 . Developer
C12Q 2326/92 . . Nitro blue tetrazolium chloride, i.e. NBT
C12Q 2326/96 . . 4-Amino-antipyrine

C12Q 2334/00 O-linked chromogens for determinations of hydrolase enzymes, e.g. glycosidases, phosphatases, esterases
C12Q 2334/10 . p-Nitrophenol derivatives
C12Q 2334/20 . Coumarin derivatives
C12Q 2334/22 . . 4-Methylumbelliferyl, i.e. beta-methylumbelliferone, 4MU
C12Q 2334/30 . Naphthol derivatives, e.g. alpha-naphthyl-esters, i.e. alpha-NE, beta-naphthyl-esters, i.e. beta-NE
C12Q 2334/40 . Triphenylmethane dye chromogens, e.g. fluorescein derivatives
C12Q 2334/50 . Indoles
C12Q 2334/52 . . 5-Bromo-4-chloro-3-indolyl, i.e. BCI
C12Q 2334/70 . the product, e.g. phenol, naphthol being diazotised in situ, e.g. with Fast Red

C12Q 2337/00 N-linked chromogens for determinations of peptidases and proteinases
C12Q 2337/10 . Anilides
C12Q 2337/12 . . Para-Nitroanilides p-NA
C12Q 2337/20 . Coumarin derivatives
C12Q 2337/22 . . 7-Amino-4-methylcoumarin, i.e. AMC, MCA
C12Q 2337/24 . . 7-Amino-4-trifluoromethylcoumarin, i.e. AFC
C12Q 2337/30 . Naphthyl amides, e.g. beta-NA, 2-NA, 4-methoxy-beta-naphthylamine, i.e. 4MNA
C12Q 2337/40 . Rhodamine derivatives
C12Q 2337/50 . Indoles
C12Q 2337/52 . . 5-Bromo-4-chloro-3-indolyl, i.e. BCI

C12Q 2500/00 **Analytical methods involving nucleic acids** (not used)

C12Q 2520/00 **Reactions involving nucleic acids** (not used)

C12Q 2521/00 **Reaction characterised by the enzymatic activity** (not used)
C12Q 2521/10 . Nucleotidyl transfering (not used)
C12Q 2521/101 . . DNA polymerase
C12Q 2521/107 . . RNA dependent DNA polymerase,(i.e. reverse transcriptase)
C12Q 2521/113 . . Telomerase
C12Q 2521/119 . . RNA polymerase
C12Q 2521/125 . . Methyl transferase, i.e. methylase
C12Q 2521/131 . . Terminal transferase
C12Q 2521/30 . Phosphoric diester hydrolysing, i.e. nuclease (Not used)
C12Q 2521/301 . . Endonuclease
C12Q 2521/307 . . Single strand endonuclease
C12Q 2521/313 . . Type II endonucleases, i.e. cutting outside recognition site
C12Q 2521/319 . . Exonuclease
C12Q 2521/325 . . Single stranded exonuclease
C12Q 2521/327 . . RNAse, e.g. RNAseH
C12Q 2521/331 . . Methylation site specific nuclease
C12Q 2521/337 . . Ribozyme
C12Q 2521/343 . . Abzyme
C12Q 2521/345 . . DNAzyme
C12Q 2521/50 . Other enzymatic activities (Not used)
C12Q 2521/501 . . Ligase
C12Q 2521/507 . . Recombinase
C12Q 2521/513 . . Winding/unwinding enzyme, e.g. helicase
C12Q 2521/514 . . Mismatch repair protein
C12Q 2521/519 . . Topoisomerase
C12Q 2521/525 . . Phosphatase (Not used with code C12Q 2565/301)
C12Q 2521/531 . . Glycosylase
C12Q 2521/537 . . Protease
C12Q 2521/539 . . Deaminase
C12Q 2521/543 . . Immobilised enzyme(s)

C12Q 2522/00 **Reaction characterised by the use of non-enzymatic proteins** (not used)
C12Q 2522/10 . Nucleic acid binding proteins (not used)
C12Q 2522/101 . . Single or double stranded nucleic acid binding proteins

C12Q 2523/00 **Reactions characterised by treatment of reaction samples** (not used)
C12Q 2523/10 . Characterised by chemical treatment (Not used)

C12Q 2523/101 . . Crosslinking agents, e.g. psoralen
C12Q 2523/107 . . Chemical cleaving agents
C12Q 2523/109 . . chemical ligation between nucleic acids
C12Q 2523/113 . . Denaturating agents
C12Q 2523/115 . . oxidising agents
C12Q 2523/119 . . Renaturing agents
C12Q 2523/125 . . Bisulfite(s)
C12Q 2523/30 . Characterised by physical treatment (Not used)
C12Q 2523/301 . . Sonication
C12Q 2523/303 . . Applying a physical force on a nucleic acid
C12Q 2523/305 . . Denaturation or renaturation by physical action
C12Q 2523/307 . . Denaturation or renaturation by electric current/voltage
C12Q 2523/308 . . Adsorption or desorption
C12Q 2523/31 . . Electrostatic interactions, e.g. use of cationic polymers in hybridisation reactions
C12Q 2523/313 . . Irradiation, e.g. UV irradiation
C12Q 2523/319 . . Photocleavage, photolysis, photoactivation
C12Q 2523/32 . . Centrifugation

C12Q 2525/00 Reactions involving modified oligonucleotides, nucleic acids, or nucleotides
C12Q 2525/10 . Modifications characterised by
C12Q 2525/101 . . incorporating non-naturally occurring nucleotides, e.g. inosine
C12Q 2525/107 . . incorporating a peptide nucleic acid
C12Q 2525/113 . . incorporating modified backbone
C12Q 2525/117 . . incorporating modified base
C12Q 2525/119 . . incorporating abasic sites
C12Q 2525/121 . . incorporating both deoxyribonucleotides and ribonucleotides
C12Q 2525/125 . . incorporating agents resulting in resistance to degradation
C12Q 2525/131 . . incorporating a restriction site
C12Q 2525/137 . . incorporating/modifying moieties to eliminate restriction sites
C12Q 2525/143 . . incorporating a promoter sequence (Not used with code C12Q 2531/143)
C12Q 2525/149 . . incorporating a coding sequence
C12Q 2525/15 . . incorporating a consensus or conserved sequence
C12Q 2525/151 . . repeat or repeated sequences, e.g. VNTR, microsatellite, concatemer
C12Q 2525/155 . . incorporating/generating a new priming site
C12Q 2525/161 . . incorporating target specific and non-target specific sites
C12Q 2525/173 . . incorporating a polynucleotide run, e.g. polyAs, polyTs
C12Q 2525/179 . . incorporating arbitrary or random nucleotide sequences
C12Q 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)

C12Q 2525/186 . . incorporating a non-extendable or blocking moiety (not used with C12Q 2535/101)
C12Q 2525/191 . . incorporating an adaptor
C12Q 2525/197 . . incorporating a spacer/coupling moiety
C12Q 2525/203 . . incorporating a composite nucleic acid containing a polypeptide sequence other than PNA
C12Q 2525/204 . . specific length of the oligonucleotides
C12Q 2525/205 . . Aptamer
C12Q 2525/207 . . siRNA, miRNA
C12Q 2525/30 . Oligonucleotides characterised by their secondary structure
C12Q 2525/301 . . Hairpin oligonucleotides
C12Q 2525/307 . . Circular oligonucleotides
C12Q 2525/313 . . Branched oligonucleotides

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

C12Q 2531/00 **Reactions of nucleic acids characterised by**
C12Q 2531/10 . the purpose being amplify/increase the copy number of target nucleic acid (Not used)
C12Q 2531/101 . . Linear amplification, i.e. non exponential
C12Q 2531/107 . . Asymmetric PCR
C12Q 2531/113 . . PCR
C12Q 2531/119 . . Strand displacement amplification [SDA]
C12Q 2531/125 . . Rolling circle
C12Q 2531/131 . . Inverse PCR
C12Q 2531/137 . . Ligase Chain Reaction [LCR]

C12Q 2531/143 . . Promoter based amplification, e.g. NASBA, 3SR, TAS

C12Q 2531/149 . . Replicase based amplification, e.g. Q beta replicase

C12Q 2533/00 {Reactions characterised by the enzymatic reaction principle used}

C12Q 2533/10 . the purpose being to increase the length of an oligonucleotide strand (ligase detection reaction, LDR C12Q 2561/125)

C12Q 2533/101 . . Primer extension (see also codes C12Q 2535/125, C12Q 2565/537)

C12Q 2533/107 . . Probe/oligonucleotide ligation (Not used with code C12Q 2531/137, C12Q 2561/125)

C12Q 2535/00 {Reactions characterised by the assay type for determining the identity of a nucleotide base}

C12Q 2535/10 . the purpose being to determine the identity or sequence oligonucleotides characterised by (Not used)

C12Q 2535/101 . . Sanger sequencing method, i.e. oligonucleotide sequencing using primer elongation and dideoxynucleotides as chain terminators

C12Q 2535/107 . . Maxam and Gilbert method, i.e. sequential release and detection of nucleotides

C12Q 2535/113 . . Cycle sequencing

C12Q 2535/119 . . Double strand sequencing

C12Q 2535/122 . . Massive parallel sequencing

C12Q 2535/125 . . Allele specific primer extension

C12Q 2535/131 . . Allele specific probes

C12Q 2535/137 . . Amplification Refractory Mutation System [ARMS]

C12Q 2535/138 . . Amplified fragment length polymorphism [AFLP]

C12Q 2535/139 . . Random amplification polymorphism detection [RAPD] (not to be used with C12Q 2525/179)

C12Q 2537/00 {Reactions characterised by the reaction format or use of a specific feature}

C12Q 2537/10 . the purpose or use of

C12Q 2537/101 . . Homogeneous assay format, e.g. one pot reaction

C12Q 2537/107 . . Homoduplex formation

C12Q 2537/113 . . Heteroduplex formation

C12Q 2537/119 . . Triple helix formation

C12Q 2537/125 . . Sandwich assay format

C12Q 2537/137 . . a displacement step (Not used with code C12Q 2531/119)

C12Q 2537/1373 . . . Displacement by a nucleic acid

C12Q 2537/1376 . . . Displacement by an enzyme

C12Q 2537/143 . . Multiplexing, i.e. use of multiple primers or probes in a single reaction, usually for simultaneously analyse of multiple analysis

C12Q 2537/149 . . Sequential reactions (Not used with reactions implicitly known to be sequential, e.g. amplification reactions)

C12Q 2537/155 . . Cyclic reactions (Not used with codes C12Q 2531/101 to C12Q 2531/149)

C12Q 2537/157 . . A reaction step characterised by the number of molecules incorporated or released

C12Q 2537/159 . . Reduction of complexity, e.g. amplification of subsets, removing duplicated genomic regions

C12Q 2537/16 . . Assays for determining copy number or wherein the copy number is of special importance

C12Q 2537/161 . . A competitive reaction step (Not used with code C12Q 2545/107)

C12Q 2537/162 . . Helper probe

C12Q 2537/163 . . blocking probe (not used in combination with C12Q 2527/127 or C12Q 2525/186)

C12Q 2537/164 . . Methylation detection other then bisulfite or methylation sensitive restriction endonucleases

C12Q 2537/165 . . Mathematical modelling, e.g. logarithm, ratio

C12Q 2539/00 **{Reactions characterised by analysis of gene expression or genome comparison}**

C12Q 2539/10 . The purpose being sequence identification by analysis of gene expression or genome comparison characterised by

C12Q 2539/101 . . Subtraction analysis

C12Q 2539/103 . . Serial analysis of gene expression [SAGE]

C12Q 2539/105 . . Involving introns, exons, or splice junctions

C12Q 2539/107 . . Representational Difference Analysis [RDA]

C12Q 2539/113 . . Differential Display Analysis [DDA]

C12Q 2539/115 . . Comparative genomic hybridisation [CGH]

C12Q 2541/00 **{Reactions characterised by directed evolution}**

C12Q 2541/10 . the purpose being the selection/design of target specific nucleic acid binding sequences (not used)

C12Q 2541/101 . . Selex

C12Q 2543/00 **{Reactions characterised by the reaction site, e.g. cell or chromosome}**

C12Q 2543/10 . the purpose being "in situ" analysis

C12Q 2543/101 . . in situ amplification

C12Q 2545/00 **{Reactions characterised by their quantitative nature}**

C12Q 2545/10 . the purpose being quantitative analysis (Not used)

C12Q 2545/101 . . with an internal standard/control

C12Q 2545/107 . . with a competitive internal standard/control

C12Q 2545/113 . . with an external standard/control, i.e. control reaction is separated from the test/target reaction

C12Q 2545/114 . . involving a quantitation step (not to be used with C12Q 2545/101, C12Q 2545/107, C12Q 2545/113)

C12Q 2547/00 **{Reactions characterised by the features used to prevent contamination}**

C12Q 2547/10 . the purpose being preventing contamination (Not used)

C12Q 2547/101 . . by confinement to a single tube/container

C12Q 2547/107 . . Use of permeable barriers, e.g. waxes

C12Q 2549/00 **{Reactions characterised by the features used to influence the efficiency or specificity}**

C12Q 2549/10 . the purpose being that of reducing false positive/negative signals (Not used)

C12Q 2549/101 . . Hot start

C12Q 2549/107 . . Cold start

C12Q 2549/113 . . using nested probes

C12Q 2549/119 . . using nested primers

C12Q 2549/125 . . using sterilising/blocking agents, e.g. albumin

C12Q 2549/126 . . using oligonucleotides as clamps (not to be used with C12Q 2525/107)

C12Q 2560/00 **Nucleic acid detection** (not used)

C12Q 2561/00 **Nucleic acid detection characterised by assay method** (not used)

C12Q 2561/10 . Characterised by assay method (Not used)

C12Q 2561/101 . . Taqman

C12Q 2561/107 . . Enzyme complementation

C12Q 2561/108 . . Hybridisation protection assay [HPA]

C12Q 2561/109 . . Invader technology

C12Q 2561/113 . . Real time assay

C12Q 2561/119 . . Fluorescence polarisation

C12Q 2561/12 . . Fluorescence lifetime measurement

C12Q 2561/125 . . Ligase Detection Reaction [LDR]

C12Q 2561/127 . . Protein truncation assay

C12Q 2563/00 **Nucleic acid detection characterised by the use of** (not used)

C12Q 2563/101 . radioactivity, e.g. radioactive labels

C12Q 2563/103 . luminescence

C12Q 2563/107 . fluorescence

C12Q 2563/113 . the label being electroactive, e.g. redox labels

C12Q 2563/116 . electrical properties of nucleic acids, e.g. impedance, conductivity or resistance

NOTE

Not to be used with C12Q 2563/113

C12Q 2563/119 . the label being proteinic

NOTE

Not to be used with code C12Q 2565/531

C12Q 2563/125 . the label being enzymatic, i.e. proteins, and non proteins, such as nucleic acid with enzymatic activity

NOTE

This code is restricted in use to ENZYMES as a LABEL

C12Q 2563/131 . the label being a member of a cognate binding pair, i.e. extends to antibodies, haptens, avidin

C12Q 2563/137 . Metal/ion, e.g metal label

C12Q 2563/143 . Magnetism, e.g. magnetic label

C12Q 2563/149 . Particles, e.g. beads

C12Q 2563/155 . Particles of a defined size, e.g. nanoparticles

C12Q 2563/157 . Nanotubes or nanorods

C12Q 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

C12Q 2563/161 . Vesicles, e.g. liposome

C12Q 2563/167 . Mass label

C12Q 2563/173 . staining/intercalating agent, e.g. ethidium bromide

C12Q 2563/179 . the label being a nucleic acid

C12Q 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

C12Q 2565/00 Nucleic acid analysis characterised by mode or means of detection

C12Q 2565/10 . Detection mode being characterised by (Not used)

C12Q 2565/101 . . Interaction between at least two labels

C12Q 2565/1015 . . . labels being on the same oligonucleotide

C12Q 2565/102 . . Multiple non-interacting labels

C12Q 2565/1025 . . . labels being on the same oligonucleotide

C12Q 2565/107 . . Alteration in the property of hybridised versus free label oligonucleotides

C12Q 2565/113 . . based on agglutination/precipitation

C12Q 2565/119 . . based on extraction of label to an organic phase, i.e. partitioning of label between different organic phases

C12Q 2565/125 . . Electrophoretic separation

C12Q 2565/131 . . Single/double strand conformational analysis, i.e. SSCP/DSCP

C12Q 2565/133 . . conformational analysis

C12Q 2565/137 . . Chromatographic separation

C12Q 2565/20 . Detection means characterised by being a gene reporter based analysis (Not used)

C12Q 2565/201 . . Two hybrid system

C12Q 2565/207 . . Three hybrid system

C12Q 2565/30 . Detection characterised by liberation/release of label (Not used)

C12Q 2565/301 . . Pyrophosphate (PPi)

C12Q 2565/40 . Detection characterised by signal amplification of label (not used)

C12Q 2565/401	. . Signal amplification by chemical polymerisation
C12Q 2565/50	. Detection characterised by immobilisation to a surface
C12Q 2565/501	. . being on/an array of oligonucleotides
C12Q 2565/507	. . characterised by the density of the capture oligonucleotide
C12Q 2565/513	. . characterised by the pattern of the arrayed oligonucleotides
C12Q 2565/514	. . characterised by the use of the arrayed oligonucleotides as identifier tags, e.g. universal addressable array, anti-tag or tag complement array
C12Q 2565/515	. . characterised by the interaction between or sequential use of two or more arrays
C12Q 2565/518	. . characterised by the immobilisation of the nucleic acid sample or target
C12Q 2565/519	. . characteirsed by the capture moiety being a single stranded oligonucleotide
C12Q 2565/525	. . characterised by the capture oligonucleotide being double stranded
C12Q 2565/531	. . characterised by the capture moiety being a protein for target oligonucleotides
C12Q 2565/537	. . characterised by the capture oligonucleotide acting as a primer
C12Q 2565/543	. . characterised by the use of two or more capture oligonucleotide primers in concert, e.g. bridge amplification (Not used with code C12Q 2537/149)
C12Q 2565/549	. . characterised by the capture oligonucleotide being a reporter labelled capture oligonucleotide
C12Q 2565/60	. Detection means characterised by use of a special device (Not used)
C12Q 2565/601	. . being a microscope, e.g. atomic force microscopy [AFM]
C12Q 2565/607	. . being a sensor, e.g. electrode
C12Q 2565/619	. . being a video camera
C12Q 2565/625	. . being a nucleic acid test strip device, e.g. dipsticks, strips,tapes, CD plates
C12Q 2565/626	. . being a flow cytometer
C12Q 2565/627	. . being a mass spectrometer (not to be used with C12Q 2563/167)
C12Q 2565/628	. . being a surface plasmon resonance spectrometer
C12Q 2565/629	. . being a microfluidic device
C12Q 2565/631	. . being a biochannel or pore
C12Q 2565/632	. . being a surface enhanced, e.g. resonance, Raman spectrometer
C12Q 2565/633	. . NMR
C12Q 2565/634	. . being an acoustic wave sensor
C12Q 2600/00	**Oligonucleotides characterized by their use** (not used, see subgroups)
C12Q 2600/106	. Pharmacogenomics , i.e. genetic variability in individual responses to drugs and drug metabolism
C12Q 2600/112	. Disease subtyping, staging or classification
C12Q 2600/118	. Prognosis of disease development
C12Q 2600/124	. Animal traits, i.e. production traits, including athletic performance or the like
C12Q 2600/13	. Plant traits
C12Q 2600/136	. Screening for pharmacological compounds
C12Q 2600/142	. Toxicological screening, e.g. expression profiles which identify toxicity

C12Q 2600/148 . Screening for cosmetic compounds
C12Q 2600/154 . Methylation markers
C12Q 2600/156 . Polymorphic or mutational markers
C12Q 2600/158 . Expression markers
C12Q 2600/16 . Primer sets for multiplex assays
C12Q 2600/166 . Oligonucleotides used as internal standards, controls or normalisation probes
C12Q 2600/172 . Haplotypes
C12Q 2600/178 . miRNA, siRNA or ncRNA