

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.

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	
	NOTE	
	{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 .}	
	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
- 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 . . DNase
- 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]	2547/101	by confinement to a single tube/container
		2547/107	Use of permeable barriers, e.g. waxes
2537/00	Reactions characterised by the reaction format or use of a specific feature	2549/00	Reactions characterised by the features used to influence the efficiency or specificity
2537/10	the purpose or use of	2549/10	the purpose being that of reducing false positive or false negative signals
2537/101	Homogeneous assay format, e.g. one pot reaction	2549/101	Hot start
2537/107	Homoduplex formation	2549/107	Cold start
2537/113	Heteroduplex formation	2549/113	using nested probes
2537/119	Triple helix formation	2549/119	using nested primers
2537/125	Sandwich assay format	2549/125	using sterilising/blocking agents, e.g. albumin
2537/137	a displacement step	2549/126	using oligonucleotides as clamps
2537/1373	Displacement by a nucleic acid		
2537/1376	Displacement by an enzyme	2560/00	Nucleic acid detection
2537/143	Multiplexing, i.e. use of multiple primers or probes in a single reaction, usually for simultaneously analyse of multiple analysis	2561/00	Nucleic acid detection characterised by assay method
2537/149	Sequential reactions	2561/101	Taqman
2537/155	Cyclic reactions	2561/107	Enzyme complementation
2537/157	A reaction step characterised by the number of molecules incorporated or released	2561/108	Hybridisation protection assay [HPA]
2537/159	Reduction of complexity, e.g. amplification of subsets, removing duplicated genomic regions	2561/109	Invader technology
2537/16	Assays for determining copy number or wherein the copy number is of special importance	2561/113	Real time assay
2537/161	A competitive reaction step	2561/119	Fluorescence polarisation
2537/162	Helper probe	2561/12	Fluorescence lifetime measurement
2537/163	blocking probe	2561/125	Ligase Detection Reaction [LDR]
2537/164	Methylation detection other than bisulfite or methylation sensitive restriction endonucleases	2561/127	Protein truncation assay
2537/165	Mathematical modelling, e.g. logarithm, ratio		
2539/00	Reactions characterised by analysis of gene expression or genome comparison	2563/00	Nucleic acid detection characterized by the use of physical, structural and functional properties
2539/10	The purpose being sequence identification by analysis of gene expression or genome comparison characterised by	2563/101	radioactivity, e.g. radioactive labels
2539/101	Subtraction analysis	2563/103	luminescence
2539/103	Serial analysis of gene expression [SAGE]	2563/107	fluorescence
2539/105	Involving introns, exons, or splice junctions	2563/113	the label being electroactive, e.g. redox labels
2539/107	Representational Difference Analysis [RDA]	2563/116	electrical properties of nucleic acids, e.g. impedance, conductivity or resistance
2539/113	Differential Display Analysis [DDA]	2563/119	the label being proteinic
2539/115	Comparative genomic hybridisation [CGH]	2563/125	the label being enzymatic, i.e. proteins, and non proteins, such as nucleic acid with enzymatic activity
2541/00	Reactions characterised by directed evolution	2563/131	the label being a member of a cognate binding pair, i.e. extends to antibodies, haptens, avidin
2541/10	the purpose being the selection or design of target specific nucleic acid binding sequences	2563/137	Metal/ion, e.g. metal label
2541/101	Selex	2563/143	Magnetism, e.g. magnetic label
2543/00	Reactions characterised by the reaction site, e.g. cell or chromosome	2563/149	Particles, e.g. beads
2543/10	the purpose being " <u>in situ</u> " analysis	2563/155	Particles of a defined size, e.g. nanoparticles
2543/101	<u>in situ</u> amplification	2563/157	Nanotubes or nanorods
2545/00	Reactions characterised by their quantitative nature	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
2545/10	the purpose being quantitative analysis	2563/161	Vesicles, e.g. liposome
2545/101	with an internal standard/control	2563/167	Mass label
2545/107	with a competitive internal standard/control	2563/173	staining/intercalating agent, e.g. ethidium bromide
2545/113	with an external standard/control, i.e. control reaction is separated from the test/target reaction	2563/179	the label being a nucleic acid
2545/114	involving a quantitation step	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
2547/00	Reactions characterised by the features used to prevent contamination	2565/00	Nucleic acid analysis characterised by mode or means of detection
2547/10	the purpose being preventing contamination	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