

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. Documents describing the use of an electrode for analysis of a specific analyte are classified in [C12Q 1/001](#) or subgroups and not according to the last place rule
6. Documents relating to new peptides, e.g. enzymes, or new DNA or its corresponding mRNA, encoding for the peptides, and their use in measuring or testing processes are classified in subclass [C07K](#) or in group [C12N 9/00](#) according to the peptides, with the appropriate indexing codes relating to their use in diagnostics. However where the new nucleic acids are principally used in diagnostic processes, e.g. PCR, hybridisation reactions, the documents are also classified in group [C12Q 1/68](#)
7. When classifying in groups [C12Q 1/68](#) - [C12Q 1/70](#) it is desirable to classify with symbols from groups [C12Q 2500/00](#) - [C12Q 2565/634](#), relating to relevant technical features of the invention, using Combination Sets.
8. In groups [C12Q 1/6876](#) - [C12Q 1/6895](#) and [C12Q 1/70](#) - [C12Q 1/708](#) it is desirable to add the indexing codes [C12Q 2600/00](#) - [C12Q 2600/178](#) which reflect the use of the product in combination with the virus groups only if the application refers to products.

1/00	Measuring or testing processes involving enzymes, nucleic acids or microorganisms (measuring or testing apparatus with condition measuring or sensing means, e.g. colony counters, C12M 1/34); Compositions therefor; Processes of preparing such compositions	1/04	. . 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) }
1/001	. {Enzyme electrodes}	1/045	. . . {Culture media therefor}
1/002	. . {Electrode membranes}	1/06	. . . Quantitative determination
1/003	. . . {Functionalisation}	1/08	. . . using multifield media
1/004	. . {mediator-assisted}	1/10	. . . Enterobacteria
1/005	. . {involving specific analytes or enzymes (including groups of enzymes, e.g. oxydases; C12Q 1/004 takes precedence) }	1/12	. . . Nitrate to nitrite reducing bacteria
1/006	. . . {for glucose}	1/14	. . . Streptococcus; Staphylococcus
1/007	. {involving isoenzyme profiles (for detection of an individual isoenzyme C12Q 1/25 - C12Q 1/66) }	1/16	. . . using radioactive material
1/008	. {for determining co-enzymes or co-factors, e.g. NAD, ATP}	1/18	. . Testing for antimicrobial activity of a material
1/02	. involving viable microorganisms	1/20	. . . using multifield media
1/025	. . {for testing or evaluating the effect of chemical or biological compounds, e.g. drugs, cosmetics (antimicrobial activity C12Q 1/18) }	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

NOTE

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

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

- 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
- 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	2521/119	. . RNA polymerase
2304/48	. . Ammonia or volatile amines	2521/125	. . Methyl transferase, i.e. methylase
2304/60	. Chemiluminescent detection using ATP-luciferin-luciferase system	2521/131	. . Terminal transferase
2304/80	. Electrochemical detection via electrodes in contact with culture medium	2521/30	. Phosphoric diester hydrolysing, i.e. nuclease (Not used)
2326/00	Chromogens for determinations of oxidoreductase enzymes	2521/301	. . Endonuclease
2326/10	. Benzidines	2521/307	. . Single strand endonuclease
2326/12	. . 3,3',5,5'-Tetramethylbenzidine, i.e. TMB	2521/313	. . Type II endonucleases, i.e. cutting outside recognition site
2326/14	. . Ortho-Tolidine, i.e. 3,3'-dimethyl-(1,1'-biphenyl-4,4'-diamine)	2521/319	. . Exonuclease
2326/20	. Ortho-Phenylenediamine	2521/325	. . Single stranded exonuclease
2326/30	. 2,2'-Azinobis (3-ethylbenzothiazoline-6-sulfonic acid), i.e. ABTS	2521/327	. . RNase, e.g. RNaseH
2326/32	. 3-Methyl-2-benzothiazolinone hydrazone hydrochloride hydrate, i.e. MBTH	2521/331	. . Methylation site specific nuclease
2326/40	. Triphenylmethane dye chromogens, e.g. fluorescein derivatives	2521/337	. . Ribozyme
2326/50	. Phenols; Naphthols; Catechols	2521/343	. . Abzyme
2326/90	. Developer	2521/345	. . DNase
2326/92	. . Nitro blue tetrazolium chloride, i.e. NBT	2521/50	. Other enzymatic activities (Not used)
2326/96	. . 4-Amino-antipyrine	2521/501	. . Ligase
2334/00	O-linked chromogens for determinations of hydrolase enzymes, e.g. glycosidases, phosphatases, esterases	2521/507	. . Recombinase
2334/10	. p-Nitrophenol derivatives	2521/513	. . Winding/unwinding enzyme, e.g. helicase
2334/20	. Coumarin derivatives	2521/514	. . Mismatch repair protein
2334/22	. . 4-Methylumbelliferyl, i.e. beta-methylumbelliferone, 4MU	2521/519	. . Topoisomerase
2334/30	. Naphthol derivatives, e.g. alpha-naphthyl-esters, i.e. alpha-NE, beta-naphthyl-esters, i.e. beta-NE	2521/525	. . Phosphatase (Not used with code C12Q 2565/301)
2334/40	. Triphenylmethane dye chromogens, e.g. fluorescein derivatives	2521/531	. . Glycosylase
2334/50	. Indoles	2521/537	. . Protease
2334/52	. . 5-Bromo-4-chloro-3-indolyl, i.e. BCI	2521/539	. . Deaminase
2334/70	. the product, e.g. phenol, naphthol being diazotised <u>in situ</u> , e.g. with Fast Red	2521/543	. . Immobilised enzyme(s)
2337/00	N-linked chromogens for determinations of peptidases and proteinases	2522/00	Reaction characterised by the use of non-enzymatic proteins (not used)
2337/10	. Anilides	2522/10	. Nucleic acid binding proteins (not used)
2337/12	. . Para-Nitroanilides p-NA	2522/101	. . Single or double stranded nucleic acid binding proteins
2337/20	. Coumarin derivatives	2523/00	Reactions characterised by treatment of reaction samples (not used)
2337/22	. . 7-Amino-4-methylcoumarin, i.e. AMC, MCA	2523/10	. Characterised by chemical treatment (Not used)
2337/24	. . 7-Amino-4-trifluoromethylcoumarin, i.e. AFC	2523/101	. . Crosslinking agents, e.g. psoralen
2337/30	. Naphthyl amides, e.g. beta-NA, 2-NA, 4-methoxy-beta-naphthylamine, i.e. 4MNA	2523/107	. . Chemical cleaving agents
2337/40	. Rhodamine derivatives	2523/109	. . chemical ligation between nucleic acids
2337/50	. Indoles	2523/113	. . Denaturing agents
2337/52	. . 5-Bromo-4-chloro-3-indolyl, i.e. BCI	2523/115	. . oxidising agents
2500/00	Analytical methods involving nucleic acids (not used)	2523/119	. . Renaturing agents
2520/00	Reactions involving nucleic acids (not used)	2523/125	. . Bisulfite(s)
2521/00	Reaction characterised by the enzymatic activity (not used)	2523/30	. Characterised by physical treatment (Not used)
2521/10	. Nucleotidyl transferring (not used)	2523/301	. . Sonication
2521/101	. . DNA polymerase	2523/303	. . Applying a physical force on a nucleic acid
2521/107	. . RNA dependent DNA polymerase, (i.e. reverse transcriptase)	2523/305	. . Denaturation or renaturation by physical action
2521/113	. . Telomerase	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	2531/101	. . Linear amplification, i.e. non exponential
2525/117	. . incorporating modified base	2531/107	. . Asymmetric PCR
2525/119	. . incorporating abasic sites	2531/113	. . PCR
2525/121	. . incorporating both deoxyribonucleotides and ribonucleotides	2531/119	. . Strand displacement amplification [SDA]
2525/125	. . incorporating agents resulting in resistance to degradation	2531/125	. . Rolling circle
2525/131	. . incorporating a restriction site	2531/131	. . Inverse PCR
2525/137	. . incorporating/modifying moieties to eliminate restriction sites	2531/137	. . Ligase Chain Reaction [LCR]
2525/143	. . incorporating a promoter sequence (Not used with code C12Q 2531/143)	2531/143	. . Promoter based amplification, e.g. NASBA, 3SR, TAS
2525/149	. . incorporating a coding sequence	2531/149	. . Replicase based amplification, e.g. Q beta replicase
2525/15	. . incorporating a consensus or conserved sequence	2533/00	Reactions characterised by the enzymatic reaction principle used
2525/151	. . repeat or repeated sequences, e.g. VNTR, microsatellite, concatemer	2533/10	. the purpose being to increase the length of an oligonucleotide strand (ligase detection reaction, LDR C12Q 2561/125)
2525/155	. . incorporating/generating a new priming site	2533/101	. . Primer extension (see also codes C12Q 2535/125, C12Q 2565/537)
2525/161	. . incorporating target specific and non-target specific sites	2533/107	. . Probe/oligonucleotide ligation (Not used with code C12Q 2531/137, C12Q 2561/125)
2525/173	. . incorporating a polynucleotide run, e.g. polyAs, polyTs	2535/00	Reactions characterised by the assay type for determining the identity of a nucleotide base
2525/179	. . incorporating arbitrary or random nucleotide sequences	2535/10	. the purpose being to determine the identity or sequence oligonucleotides characterised by (Not used)
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)	2535/101	. . Sanger sequencing method, i.e. oligonucleotide sequencing using primer elongation and dideoxynucleotides as chain terminators
2525/186	. . incorporating a non-extendable or blocking moiety (not used with C12Q 2535/101)	2535/107	. . Maxam and Gilbert method, i.e. sequential release and detection of nucleotides
2525/191	. . incorporating an adaptor	2535/113	. . Cycle sequencing
2525/197	. . incorporating a spacer/coupling moiety	2535/119	. . Double strand sequencing
2525/203	. . incorporating a composite nucleic acid containing a polypeptide sequence other than PNA	2535/122	. . Massive parallel sequencing
2525/204	. . specific length of the oligonucleotides	2535/125	. . Allele specific primer extension
2525/205	. . Aptamer	2535/131	. . Allele specific probes
2525/207	. . siRNA, miRNA	2535/137	. . Amplification Refractory Mutation System [ARMS]
2525/30	. Oligonucleotides characterised by their secondary structure	2535/138	. . Amplified fragment length polymorphism [AFLP]
2525/301	. . Hairpin oligonucleotides	2535/139	. . Random amplification polymorphism detection [RAPD] (not to be used with C12Q 2525/179)
2525/307	. . Circular oligonucleotides	2537/00	Reactions characterised by the reaction format or use of a specific feature
2525/313	. . Branched oligonucleotides	2537/10	. the purpose or use of
2527/00	Reactions demanding special reaction conditions (not used)	2537/101	. . Homogeneous assay format, e.g. one pot reaction
2527/10	. Reaction conditions characterised by (metal/ion C12Q 2563/137) (not used)	2537/107	. . Homoduplex formation
2527/101	. . Temperature	2537/113	. . Heteroduplex formation
2527/107	. . Temperature of melting, i.e. Tm	2537/119	. . Triple helix formation
2527/109	. . Pressure	2537/125	. . Sandwich assay format
2527/113	. . Time	2537/137	. . a displacement step (Not used with code C12Q 2531/119)
2527/119	. . pH	2537/1373	. . Displacement by a nucleic acid
2527/125	. . Specific component of sample, medium or buffer (for metal/ion use C12Q 2563/137)	2537/1376	. . Displacement by an enzyme
2527/127	. . the enzyme inhibitor or activator used	2537/143	. . Multiplexing, i.e. use of multiple primers or probes in a single reaction, usually for simultaneously analyse of multiple analysis
2527/137	. . Concentration of a component of medium	2537/149	. . Sequential reactions (Not used with reactions implicitly known to be sequential, e.g. amplification reactions)
2527/143	. . Concentration of primer/probe	2537/155	. . Cyclic reactions (Not used with codes C12Q 2531/101 - C12Q 2531/149)
2527/146	. . Concentration of target/template		
2527/149	. . Concentration of an enzyme		
2527/15	. . Gradients		
2527/153	. . Viscosity		
2527/156	. . Permeability		
2531/00	Reactions of nucleic acids characterised by		
2531/10	. the purpose being amplify/increase the copy number of target nucleic acid (Not used)		

2537/157	. . A reaction step characterised by the number of molecules incorporated or released	2549/126	. . using oligonucleotides as clamps (not to be used with C12Q 2525/107)
2537/159	. . Reduction of complexity, e.g. amplification of subsets, removing duplicated genomic regions	2560/00	Nucleic acid detection (not used)
2537/16	. . Assays for determining copy number or wherein the copy number is of special importance	2561/00	Nucleic acid detection characterised by assay method (not used)
2537/161	. . A competitive reaction step (Not used with code C12Q 2545/107)	2561/10	. Characterised by assay method (Not used)
2537/162	. . Helper probe	2561/101	. . Taqman
2537/163	. . blocking probe (not used in combination with C12Q 2527/127 or C12Q 2525/186)	2561/107	. . Enzyme complementation
2537/164	. . Methylation detection other than bisulfite or methylation sensitive restriction endonucleases	2561/108	. . Hybridisation protection assay [HPA]
2537/165	. . Mathematical modelling, e.g. logarithm, ratio	2561/109	. . Invader technology
2539/00	Reactions characterised by analysis of gene expression or genome comparison	2561/113	. . Real time assay
2539/10	. The purpose being sequence identification by analysis of gene expression or genome comparison characterised by	2561/119	. . Fluorescence polarisation
2539/101	. . Subtraction analysis	2561/12	. . Fluorescence lifetime measurement
2539/103	. . Serial analysis of gene expression [SAGE]	2561/125	. . Ligase Detection Reaction [LDR]
2539/105	. . Involving introns, exons, or splice junctions	2561/127	. . Protein truncation assay
2539/107	. . Representational Difference Analysis [RDA]	2563/00	Nucleic acid detection characterised by the use of (not used)
2539/113	. . Differential Display Analysis [DDA]	2563/101	. radioactivity, e.g. radioactive labels
2539/115	. . Comparative genomic hybridisation [CGH]	2563/103	. luminescence
2541/00	Reactions characterised by directed evolution	2563/107	. fluorescence
2541/10	. the purpose being the selection/design of target specific nucleic acid binding sequences (not used)	2563/113	. the label being electroactive, e.g. redox labels
2541/101	. . Selex	2563/116	. electrical properties of nucleic acids, e.g. impedance, conductivity or resistance
2543/00	Reactions characterised by the reaction site, e.g. cell or chromosome	NOTE	
2543/10	. the purpose being " <u>in situ</u> " analysis	Not to be used with C12Q 2563/113	
2543/101	. . <u>in situ</u> amplification	2563/119	. the label being proteinic
2545/00	Reactions characterised by their quantitative nature	NOTE	
2545/10	. the purpose being quantitative analysis (Not used)	Not to be used with code C12Q 2565/531	
2545/101	. . with an internal standard/control	2563/125	. the label being enzymatic, i.e. proteins, and non proteins, such as nucleic acid with enzymatic activity
2545/107	. . with a competitive internal standard/control	NOTE	
2545/113	. . with an external standard/control, i.e. control reaction is separated from the test/target reaction	This code is restricted in use to ENZYMES as a LABEL	
2545/114	. . involving a quantitation step (not to be used with C12Q 2545/101 , C12Q 2545/107 , C12Q 2545/113)	2563/131	. the label being a member of a cognate binding pair, i.e. extends to antibodies, haptens, avidin
2547/00	Reactions characterised by the features used to prevent contamination	2563/137	. Metal/ion, e.g. metal label
2547/10	. the purpose being preventing contamination (Not used)	2563/143	. Magnetism, e.g. magnetic label
2547/101	. . by confinement to a single tube/container	2563/149	. Particles, e.g. beads
2547/107	. . Use of permeable barriers, e.g. waxes	2563/155	. Particles of a defined size, e.g. nanoparticles
2549/00	Reactions characterised by the features used to influence the efficiency or specificity	2563/157	. Nanotubes or nanorods
2549/10	. the purpose being that of reducing false positive/negative signals (Not used)	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
2549/101	. . Hot start	2563/161	. Vesicles, e.g. liposome
2549/107	. . Cold start	2563/167	. Mass label
2549/113	. . using nested probes	2563/173	. staining/intercalating agent, e.g. ethidium bromide
2549/119	. . using nested primers	2563/179	. the label being a nucleic acid
2549/125	. . using sterilising/blocking agents, e.g. albumin	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 (Not used)
		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 ([Not used](#))
- 2565/201 . . Two hybrid system
- 2565/207 . . Three hybrid system
- 2565/30 . . Detection characterised by liberation/release of label ([Not used](#))
- 2565/301 . . Pyrophosphate (PPi)
- 2565/40 . . Detection characterised by signal amplification of label ([not used](#))
- 2565/401 . . Signal amplification by chemical polymerisation
- 2565/50 . . Detection characterised by immobilisation to a surface
- 2565/501 . . being on/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 ([Not used with code C12Q 2537/149](#))
- 2565/549 . . characterised by the capture oligonucleotide being a reporter labelled capture oligonucleotide
- 2565/60 . . Detection means characterised by use of a special device ([Not used](#))
- 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 ([not to be used with C12Q 2563/167](#))
- 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 ([not used, see subgroups](#))**
- 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