

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](#) - [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 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	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
1/001	. {Enzyme electrodes}	1/20	. . . using multifield media
1/002	. . {Electrode membranes}	1/22	. . Testing for sterility conditions
1/003	. . . {Functionalisation}	1/24	. . Methods of sampling, or inoculating or spreading a sample; Methods of physically isolating an intact micro-organisms
1/004	. . {mediator-assisted}		
1/005	. . {involving specific analytes or enzymes (including groups of enzymes, e.g. oxydases; C12Q 1/004 takes precedence)}	1/25	. involving enzymes not classifiable in groups C12Q 1/26 {- C12Q 1/66 }
1/006	. . . {for glucose}	1/26	. involving oxidoreductase
1/007	. {involving isoenzyme profiles (for detection of an individual isoenzyme C12Q 1/25 - C12Q 1/66)}	1/28	. . involving peroxidase
1/008	. {for determining co-enzymes or co-factors, e.g. NAD, ATP}	1/30	. . involving catalase
1/02	. involving viable micro-organisms	1/32	. . involving dehydrogenase
1/025	. . {for testing or evaluating the effect of chemical or biological compounds, e.g. drugs, cosmetics (antimicrobial activity C12Q 1/18)}	1/34	. involving hydrolase
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)}	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
1/045	. . . {Culture media therefor}	1/527	. involving lyase
1/06	. . . Quantitative determination	1/533	. involving isomerase
1/08 using multifield media	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 subgroups of [C12Q 1/68](#), classification is made according to the most relevant feature rather than according to the last-place-rule

- 1/6802 . . {General aspects (not used, see subgroups)}
- 1/6804 . . . {Nucleic acid analysis utilising immunogens}
- 1/6806 . . . {Preparing nucleic acids for analysis, e.g. for PCR assay ([C12Q 1/6804](#) takes precedence)}
- 1/6809 . . . {Sequence identification involving differential detection}
- 1/6811 . . . {Selection methods for production or design of target specific oligonucleotide or binding molecules}
- 1/6813 . . {Hybridisation assays}
- 1/6816 . . . {characterised by the means of detection ([C12Q 1/6804](#) takes precedence)}
- 1/6818 {involving interaction of at least two labels, e.g. resonant energy transfer}
- 1/682 {Signal amplification}
- 1/6823 {Release of bound marker}
- 1/6825 {Nucleic acid detection involving sensors}
- 1/6827 . . . {for mutation or polymorphism detection}
- 1/683 {involving restriction enzymes, e.g. RFLP}
- 1/6832 . . . {Enhancement of hybridisation reaction}
- 1/6834 . . . {Nucleic acid analysis involving immobilisation; Immobilisation characterised by the carrier or coupling agent}
- 1/6837 {characterised by the use of probe arrays or probe chips ([C12Q 1/6874](#) takes precedence)}
- 1/6839 . . . {Triple helix formation in hybridisation assays}
- 1/6841 . . . {"In-situ" hybridisation}
- 1/6844 . . {Nucleic acid amplification reactions}
- 1/6846 . . . {Common amplification features}
- 1/6848 {preventing contamination}
- 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. NASBA, 3SR, TAS}
- 1/6867 . . . {Replicase based amplifications, e.g. Q-beta replicase}
- 1/6869 . . {Methods for sequencing}
- 1/6872 . . . {involving mass spectrometry}
- 1/6874 . . . {involving nucleic acid arrays, e.g. Sequencing By Hybridisation [SBH]}
- 1/6876 . . {Hybridisation probes}
- 1/6879 . . . {for sex determination}
- 1/6881 . . . {for tissue and cell typing, e.g. HLA probes}

- 1/6883 . . . {for diseases caused by alterations of genetic material}
- 1/6886 {for cancer}
- 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 micro-organisms (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	2521/525	. . Phosphatase (Not used with code C12Q 2565/301)
2334/10	. p-Nitrophenol derivatives	2521/531	. . Glycosylase
2334/20	. Coumarin derivatives	2521/537	. . Protease
2334/22	. . 4-Methylumbelliferyl, i.e. beta-methylumbelliferone, 4MU	2521/539	. . Deaminase
2334/30	. Naphthol derivatives, e.g. alpha-naphthyl-esters, i.e. alpha-NE, beta-naphthyl-esters, i.e. beta-NE	2521/543	. . Immobilised enzyme(s)
2334/40	. Triphenylmethane dye chromogens, e.g. fluorescein derivatives	2522/00	Reaction characterised by the use of non-enzymatic proteins (not used)
2334/50	. Indoles	2522/10	. Nucleic acid binding proteins (not used)
2334/52	. . 5-Bromo-4-chloro-3-indolyl, i.e. BCI	2522/101	. . Single or double stranded nucleic acid binding proteins
2334/70	. the product, e.g. phenol, naphthol being diazotised in situ , e.g. with Fast Red	2523/00	Reactions characterised by treatment of reaction samples (not used)
2337/00	N-linked chromogens for determinations of peptidases and proteinases	2523/10	. Characterised by chemical treatment (Not used)
2337/10	. Anilides	2523/101	. . Crosslinking agents, e.g. psoralen
2337/12	. . Para-Nitroanilides p-NA	2523/107	. . Chemical cleaving agents
2337/20	. Coumarin derivatives	2523/109	. . chemical ligation between nucleic acids
2337/22	. . 7-Amino-4-methylcoumarin, i.e. AMC, MCA	2523/113	. . Denaturing agents
2337/24	. . 7-Amino-4-trifluoromethylcoumarin, i.e. AFC	2523/115	. . oxidising agents
2337/30	. Naphthyl amides, e.g. beta-NA, 2-NA, 4-methoxy-beta-naphthylamine, i.e. 4MNA	2523/119	. . Renaturing agents
2337/40	. Rhodamine derivatives	2523/125	. . Bisulfite(s)
2337/50	. Indoles	2523/30	. Characterised by physical treatment (Not used)
2337/52	. . 5-Bromo-4-chloro-3-indolyl, i.e. BCI	2523/301	. . Sonication
2500/00	Analytical methods involving nucleic acids (not used)	2523/303	. . Applying a physical force on a nucleic acid
2520/00	Reactions involving nucleic acids (not used)	2523/305	. . Denaturation or renaturation by physical action
2521/00	Reaction characterised by the enzymatic activity (not used)	2523/307	. . Denaturation or renaturation by electric current/voltage
2521/10	. Nucleotidyl transferring (not used)	2523/308	. . Adsorption or desorption
2521/101	. . DNA polymerase	2523/31	. . Electrostatic interactions, e.g. use of cationic polymers in hybridisation reactions
2521/107	. . RNA dependent DNA polymerase,(i.e. reverse transcriptase)	2523/313	. . Irradiation, e.g. UV irradiation
2521/113	. . Telomerase	2523/319	. . Photocleavage, photolysis, photoactivation
2521/119	. . RNA polymerase	2523/32	. . Centrifugation
2521/125	. . Methyl transferase, i.e. methylase	2525/00	Reactions involving modified oligonucleotides, nucleic acids, or nucleotides
2521/131	. . Terminal transferase	2525/10	. Modifications characterised by
2521/30	. Phosphoric diester hydrolysing, i.e. nuclease (Not used)	2525/101	. . incorporating non-naturally occurring nucleotides, e.g. inosine
2521/301	. . Endonuclease	2525/107	. . incorporating a peptide nucleic acid
2521/307	. . Single strand endonuclease	2525/113	. . incorporating modified backbone
2521/313	. . Type II endonucleases, i.e. cutting outside recognition site	2525/117	. . incorporating modified base
2521/319	. . Exonuclease	2525/119	. . incorporating abasic sites
2521/325	. . Single stranded exonuclease	2525/121	. . incorporating both deoxyribonucleotides and ribonucleotides
2521/327	. . RNase, e.g. RNaseH	2525/125	. . incorporating agents resulting in resistance to degradation
2521/331	. . Methylation site specific nuclease	2525/131	. . incorporating a restriction site
2521/337	. . Ribozyme	2525/137	. . incorporating/modifying moieties to eliminate restriction sites
2521/343	. . Abzyme	2525/143	. . incorporating a promoter sequence (Not used with code C12Q 2531/143)
2521/345	. . DNAzyme	2525/149	. . incorporating a coding sequence
2521/50	. Other enzymatic activities (Not used)	2525/15	. . incorporating a consensus or conserved sequence
2521/501	. . Ligase	2525/151	. . repeat or repeated sequences, e.g. VNTR, microsatellite, concatemer
2521/507	. . Recombinase	2525/155	. . incorporating/generating a new priming site
2521/513	. . Winding/unwinding enzyme, e.g. helicase	2525/161	. . incorporating target specific and non-target specific sites
2521/514	. . Mismatch repair protein	2525/173	. . incorporating a polynucleotide run, e.g. polyAs, polyTs
2521/519	. . Topoisomerase		

2525/179	. . incorporating arbitrary or random nucleotide sequences	2535/00	{Reactions characterised by the assay type for determining the identity of a nucleotide base}
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)	2535/10	. the purpose being to determine the identity or sequence oligonucleotides characterised by (Not used)
2525/186	. . incorporating a non-extendable or blocking moiety (not used with C12Q 2535/101)	2535/101	. . Sanger sequencing method, i.e. oligonucleotide sequencing using primer elongation and dideoxynucleotides as chain terminators
2525/191	. . incorporating an adaptor	2535/107	. . Maxam and Gilbert method, i.e. sequential release and detection of nucleotides
2525/197	. . incorporating a spacer/coupling moiety	2535/113	. . Cycle sequencing
2525/203	. . incorporating a composite nucleic acid containing a polypeptide sequence other than PNA	2535/119	. . Double strand sequencing
2525/204	. . specific length of the oligonucleotides	2535/122	. . Massive parallel sequencing
2525/205	. . Aptamer	2535/125	. . Allele specific primer extension
2525/207	. . siRNA, miRNA	2535/131	. . Allele specific probes
2525/30	. Oligonucleotides characterised by their secondary structure	2535/137	. . Amplification Refractory Mutation System [ARMS]
2525/301	. . Hairpin oligonucleotides	2535/138	. . Amplified fragment length polymorphism [AFLP]
2525/307	. . Circular oligonucleotides	2535/139	. . Random amplification polymorphism detection [RAPD] (not to be used with C12Q 2525/179)
2525/313	. . Branched oligonucleotides		
2527/00	Reactions demanding special reaction conditions (not used)	2537/00	{Reactions characterised by the reaction format or use of a specific feature}
2527/10	. Reaction conditions characterised by (metal/ion C12Q 2563/137) (not used)	2537/10	. the purpose or use of
2527/101	. . Temperature	2537/101	. . Homogeneous assay format, e.g. one pot reaction
2527/107	. . Temperature of melting, i.e. T _m	2537/107	. . Homoduplex formation
2527/109	. . Pressure	2537/113	. . Heteroduplex formation
2527/113	. . Time	2537/119	. . Triple helix formation
2527/119	. . pH	2537/125	. . Sandwich assay format
2527/125	. . Specific component of sample, medium or buffer (for metal/ion use C12Q 2563/137)	2537/137	. . a displacement step (Not used with code C12Q 2531/119)
2527/127	. . the enzyme inhibitor or activator used	2537/1373	. . . Displacement by a nucleic acid
2527/137	. . Concentration of a component of medium	2537/1376	. . . Displacement by an enzyme
2527/143	. . Concentration of primer/probe	2537/143	. . Multiplexing, i.e. use of multiple primers or probes in a single reaction, usually for simultaneously analyse of multiple analysis
2527/146	. . Concentration of target/template	2537/149	. . Sequential reactions (Not used with reactions implicitly known to be sequential, e.g. amplification reactions)
2527/149	. . Concentration of an enzyme	2537/155	. . Cyclic reactions (Not used with codes C12Q 2531/101 - C12Q 2531/149)
2527/15	. . Gradients	2537/157	. . A reaction step characterised by the number of molecules incorporated or released
2527/153	. . Viscosity	2537/159	. . Reduction of complexity, e.g. amplification of subsets, removing duplicated genomic regions
2527/156	. . Permeability	2537/16	. . Assays for determining copy number or wherein the copy number is of special importance
2531/00	Reactions of nucleic acids characterised by	2537/161	. . A competitive reaction step (Not used with code C12Q 2545/107)
2531/10	. the purpose being amplify/increase the copy number of target nucleic acid (Not used)	2537/162	. . Helper probe
2531/101	. . Linear amplification, i.e. non exponential	2537/163	. . blocking probe (not used in combination with C12Q 2527/127 or C12Q 2525/186)
2531/107	. . Asymmetric PCR	2537/164	. . Methylation detection other than bisulfite or methylation sensitive restriction endonucleases
2531/113	. . PCR	2537/165	. . Mathematical modelling, e.g. logarithm, ratio
2531/119	. . Strand displacement amplification [SDA]		
2531/125	. . Rolling circle	2539/00	{Reactions characterised by analysis of gene expression or genome comparison}
2531/131	. . Inverse PCR	2539/10	. The purpose being sequence identification by analysis of gene expression or genome comparison characterised by
2531/137	. . Ligase Chain Reaction [LCR]	2539/101	. . Subtraction analysis
2531/143	. . Promoter based amplification, e.g. NASBA, 3SR, TAS	2539/103	. . Serial analysis of gene expression [SAGE]
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 (ligase detection reaction, LDR C12Q 2561/125)		
2533/101	. . Primer extension (see also codes C12Q 2535/125, C12Q 2565/537)		
2533/107	. . Probe/oligonucleotide ligation (Not used with code C12Q 2531/137, C12Q 2561/125)		

- 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/design of target specific nucleic acid binding sequences (not used)
- 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 (Not used)
- 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 (not to be used with [C12Q 2545/101](#), [C12Q 2545/107](#), [C12Q 2545/113](#))
- 2547/00 {Reactions characterised by the features used to prevent contamination}**
- 2547/10 . the purpose being preventing contamination (Not used)
- 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/negative signals (Not used)
- 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 (not to be used with [C12Q 2525/107](#))
- 2560/00 Nucleic acid detection (not used)**
- 2561/00 Nucleic acid detection characterised by assay method (not used)**
- 2561/10 . Characterised by assay method (Not used)
- 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 characterised by the use of (not used)**
- 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
- NOTE**
- Not to be used with [C12Q 2563/113](#)
- 2563/119 . the label being proteinic
- NOTE**
- Not to be used with code [C12Q 2565/531](#)
- 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
- 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 (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