

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 herpesviridae, 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 transferring (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	. . Denaturing 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. T_m
- 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	<ul style="list-style-type: none"> the purpose being to increase the length of an oligonucleotide strand (ligase detection reaction, LDR C12Q 2561/125)
C12Q 2533/101	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Primer extension (see also codes C12Q 2535/125, C12Q 2565/537)
C12Q 2533/107	<ul style="list-style-type: none"> <ul style="list-style-type: none"> 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	<ul style="list-style-type: none"> the purpose being to determine the identity or sequence oligonucleotides characterised by (Not used)
C12Q 2535/101	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Sanger sequencing method, i.e. oligonucleotide sequencing using primer elongation and dideoxynucleotides as chain terminators
C12Q 2535/107	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Maxam and Gilbert method, i.e. sequential release and detection of nucleotides
C12Q 2535/113	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Cycle sequencing
C12Q 2535/119	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Double strand sequencing
C12Q 2535/122	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Massive parallel sequencing
C12Q 2535/125	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Allele specific primer extension
C12Q 2535/131	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Allele specific probes
C12Q 2535/137	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Amplification Refractory Mutation System [ARMS]
C12Q 2535/138	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Amplified fragment length polymorphism [AFLP]
C12Q 2535/139	<ul style="list-style-type: none"> <ul style="list-style-type: none"> 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	<ul style="list-style-type: none"> the purpose or use of
C12Q 2537/101	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Homogeneous assay format, e.g. one pot reaction
C12Q 2537/107	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Homoduplex formation
C12Q 2537/113	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Heteroduplex formation
C12Q 2537/119	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Triple helix formation
C12Q 2537/125	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Sandwich assay format
C12Q 2537/137	<ul style="list-style-type: none"> <ul style="list-style-type: none"> a displacement step (Not used with code C12Q 2531/119)
C12Q 2537/1373	<ul style="list-style-type: none"> <ul style="list-style-type: none"> <ul style="list-style-type: none"> Displacement by a nucleic acid
C12Q 2537/1376	<ul style="list-style-type: none"> <ul style="list-style-type: none"> <ul style="list-style-type: none"> Displacement by an enzyme
C12Q 2537/143	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Multiplexing, i.e. use of multiple primers or probes in a single reaction, usually for simultaneously analyse of multiple analysis
C12Q 2537/149	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Sequential reactions (Not used with reactions implicitly known to be sequential, e.g. amplification reactions)
C12Q 2537/155	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Cyclic reactions (Not used with codes C12Q 2531/101 to C12Q 2531/149)
C12Q 2537/157	<ul style="list-style-type: none"> <ul style="list-style-type: none"> A reaction step characterised by the number of molecules incorporated or released
C12Q 2537/159	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Reduction of complexity, e.g. amplification of subsets, removing duplicated genomic regions
C12Q 2537/16	<ul style="list-style-type: none"> <ul style="list-style-type: none"> Assays for determining copy number or wherein the copy number is of special importance
C12Q 2537/161	<ul style="list-style-type: none"> <ul style="list-style-type: none"> 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 than 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
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- 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 . . characterised 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