SEQUENCE LISTING

<110> Japan Tobacco Inc.
Virus Ikagaku kenkyusho Inc.

<120> Method for detecting a substance in a biological sample

<130> FA0392-09156

<140> PCT/JP2010/055887
<141> 2010-03-31

<150> JP 2009-087839
<151> 2009-03-31

<160> 11
<170> PatentIn version 3.1

<210> 1
<211> 159
<212> PRT
<213> Human herpesvirus 6

<400> 1

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Ile Leu Ala Cys Leu Ile Val Leu Ile Leu Ala Ala Ala Ile Thr Met
20 25 30

Leu Thr Leu Glu Ile Ile Ser Asn Gln Lys Arg Thr Thr Thr Asp Leu
35 40 45

Glu Ala Val Thr Val Ala Leu Lys His Val Ser Thr Ser Leu Ala Ser
50 55 60

Cys Thr Glu Ser Thr Thr Ser Val His Thr Asp Ser Val Thr Ser Gln
65 70 75 80

Pro Thr Lys Asn Lys Glu Ser Arg Lys Lys Ile Glu Gly Lys Ser Pro
85 90 95

Ser Trp Val Gln Ala Leu Thr Thr Ala Ser Gly Ile Ile Leu Leu Phe
100 105 110

Cys Ile Met Met Ile Phe Ile Thr Cys Ser Trp Thr Thr Glu Lys Asp
115 120 125

Thr Glu Lys Ser Glu Val Gln Ser Tyr Ala Ser Ser Val Glu Thr Leu
130 135 140

Asp Ser Leu Asn Glu Ala Ile Ile Pro Lys Thr Glu Met Asn Val
145 150 155

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<212> DNA
<213> Human herpesvirus 6

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tgttcctgga ccacagaaaa agatacagag aagagtgaag tgcaatctta tgcttcttca 420
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<210> 3
<211> 1795
<212> DNA
<213> Human herpesvirus 6

<400> 3
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<211> 432
<212> DNA
<213> Pleurotus cornucopiae

<220>
<221> CDS
<222> (1)..(432)
<223>

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1 5 10 15

ggc tca aca atg aat ttg act gca aat aaa gac ggt tcg ctc acc gga 96
Gly Ser Thr Met Asn Leu Thr Ala Asn Lys Asp Gly Ser Leu Thr Gly
20 25 30

acg tac cac tcc aac gtc ggc gag gtt ccc cca act tat cac ctt tct 144
Thr Tyr His Ser Asn Val Gly Glu Val Pro Pro Thr Tyr His Leu Ser
35 40 45

ggc cgg tac aac ctc cag ccc ccc tcg ggt caa ggc gtt act ctg gga 192
Gly Arg Tyr Asn Leu Gln Pro Pro Ser Gly Gln Gly Val Thr Leu Gly
50 55 60

tgg gcg gtg tct ttc gaa aac act agt gcg aat gtt cat tct gtc tca 240
Trp Ala Val Ser Phe Glu Asn Thr Ser Ala Asn Val His Ser Val Ser
65 70 75 80

aca tgg agc ggg cag tac ttc tct gaa ccc gcc gag gtg atc ctc acc 288
Thr Trp Ser Gly Gln Tyr Phe Ser Glu Pro Ala Glu Val Ile Leu Thr
85 90 95

cag tgg ctg ttg tca agg agc tct gag cgc gaa gat ttg tgg cag tcc 336
Gln Trp Leu Leu Ser Arg Ser Ser Glu Arg Glu Asp Leu Trp Gln Ser
100 105 110

acc cat gtg ggg cat gat gag ttc agc aag aca aag cca acc aag gag 384
Thr His Val Gly His Asp Glu Phe Ser Lys Thr Lys Pro Thr Lys Glu
115 120 125

aag att gcc cag gct caa ctc ctt cgt cgc ggg ttg aag ttc gag tga 432
Lys Ile Ala Gln Ala Gln Leu Leu Arg Arg Gly Leu Lys Phe Glu
130 135 140

<210> 5
<211> 143
<212> PRT
<213> Pleurotus cornucopiae

<400> 5
Met Lys Asp Val Gln Ser Leu Leu Thr Gly Thr Trp Tyr Asn Glu Leu
1 5 10 15

Gly Ser Thr Met Asn Leu Thr Ala Asn Lys Asp Gly Ser Leu Thr Gly
20 25 30

Thr Tyr His Ser Asn Val Gly Glu Val Pro Pro Thr Tyr His Leu Ser
35 40 45

Gly Arg Tyr Asn Leu Gln Pro Pro Ser Gly Gln Gly Val Thr Leu Gly
50 55 60

Trp Ala Val Ser Phe Glu Asn Thr Ser Ala Asn Val His Ser Val Ser
65 70 75 80

Thr Trp Ser Gly Gln Tyr Phe Ser Glu Pro Ala Glu Val Ile Leu Thr
85 90 95

Gln Trp Leu Leu Ser Arg Ser Ser Glu Arg Glu Asp Leu Trp Gln Ser
100 105 110

Thr His Val Gly His Asp Glu Phe Ser Lys Thr Lys Pro Thr Lys Glu
115 120 125

Lys Ile Ala Gln Ala Gln Leu Leu Arg Arg Gly Leu Lys Phe Glu
130 135 140

<210> 6
<211> 426
<212> DNA
<213> Pleurotus cornucopiae

<220>
<221> CDS
<222> (1)..(426)
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<400> 6
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1 5 10 15

aac tcc aag atg gaa ttg act gca aac aaa gac ggt act ctc act gga 96
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30

aag tac ctc tcc aaa gtt ggg gat gtc tac gtg ccc tac cca ctc tct 144
Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45

ggt cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg 192
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60

tgg gcg gta tcc tgg gag aac agt aaa att cat tcc gct acg aca tgg 240
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80

agc gga cag ttc ttc tct gag tcg tct cca gtg att ctt act cag tgg 288
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95

ttg ttg tca tcg agc act gcg cgt ggg gac gta tgg gaa tcc aca ctt 336
Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
100 105 110

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gtg ggg aat gat tcg ttt aca aag acg gcg ccg act gag cag cag atc      384
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
   115                 120                 125

gct cat gct caa ctc cat tgt cgc gca ccg agg ttg aag taa              426
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
    130                 135                 140
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〈210〉 7
〈211〉 141
〈212〉 PRT
〈213〉 Pleurotus cornucopiae

〈400〉 7

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Met Ser Asp Val Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu
1               5                   10                  15

Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
       20                  25                  30

Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
   35                  40                  45

Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
    50                  55                  60

Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65                  70                  75                  80

Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
            85                  90                  95

Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
       100                 105                 110

Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
   115                 120                 125

Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
    130                 135                 140
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〈210〉 8
〈211〉 271
〈212〉 PRT
〈213〉 Artificial Sequence

〈220〉
〈223〉 Fusion protein BioEase Tag-SITH-1

〈400〉 8

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  1               5                  10                  15
Thr Pro Val Thr Ala Pro Leu Ala Gly Thr Ile Trp Lys Val Leu Ala
            20                  25                  30
Ser Glu Gly Gln Thr Val Ala Ala Gly Glu Val Leu Leu Ile Leu Glu
        35                  40                  45
Ala Met Lys Met Glu Thr Glu Ile Arg Ala Ala Gln Ala Gly Thr Val
    50                  55                  60
Arg Gly Ile Ala Val Lys Ala Gly Asp Ala Val Ala Val Gly Asp Thr
65                  70                  75                  80
Leu Met Thr Leu Ala Gly Ser Gly Ser Asp Leu Tyr Asp Asp Asp Asp
                85                  90                  95
Lys Gly Ile Ile Thr Ser Leu Tyr Lys Lys Ala Gly Ser Glu Phe Ala
            100                 105                 110
Leu Gly Tyr Glu Glu Lys Val Ser Ala Thr Gly Lys Thr Arg Leu Lys
        115                 120                 125
Ile Leu Ala Cys Leu Ile Val Leu Ile Leu Ala Ala Ala Ile Thr Met
    130                 135                 140
Leu Thr Leu Glu Ile Ile Ser Asn Gln Lys Arg Thr Thr Thr Asp Leu
145                 150                 155                 160
Glu Ala Val Thr Val Ala Leu Lys His Val Ser Thr Ser Leu Ala Ser
                165                 170                 175
Cys Thr Glu Ser Thr Thr Ser Val His Thr Asp Ser Val Thr Ser Gln
            180                 185                 190
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Pro Thr Lys Asn Lys Glu Ser Arg Lys Lys Ile Glu Gly Lys Ser Pro
        195                 200                 205
Ser Trp Val Gln Ala Leu Thr Thr Ala Ser Gly Ile Ile Leu Leu Phe
    210                 215                 220
Cys Ile Met Met Ile Phe Ile Thr Cys Ser Trp Thr Thr Glu Lys Asp
225                 230                 235                 240
Thr Glu Lys Ser Glu Val Gln Ser Tyr Ala Ser Ser Val Glu Thr Leu
                245                 250                 255
Asp Ser Leu Asn Glu Ala Ile Ile Pro Lys Thr Glu Met Asn Val
            260                 265                 270 271
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〈210〉 9
〈211〉 816
〈212〉 DNA
〈213〉 Artificial Sequence

〈220〉
〈223〉 DNA encoding fusion protein BioEase Tag-SITH-1

〈400〉 9

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gccccgctgg cgggcactat ctggaaggtg ctggccagcg aaggccagac ggtggccgca    120
ggcgaggtgc tgctgattct ggaagccatg aagatggaaa ccgaaatccg cgccgcgcag    180
gccgggaccg tgcgcggtat cgcggtgaaa gccggcgacg cggtggcggt cggcgacacc    240
ctgatgaccc tggcgggctc tggatccgat ctgtacgacg atgacgataa gggaattatc    300
acaagtttgt acaaaaaagc aggctccgaa ttcgcccttg gatatgaaga aaaagtgtca    360
gctactggaa agactcgttt aaagatactg gcatgtctga tcgttttaat actagctgcg    420
gcaataacta tgttaacgct ggaaattata tcgaaccaaa aacgtaccac tactgatctc    480
gaagctgtga ctgtggcgct gaagcatgta agcacatctc ttgccagctg cactgaatcc    540
actacttctg tacataccga ttctgtgacg agccaaccca cgaaaaacaa agaatcgagg    600
aaaaaaattg aagggaaatc tccaagttgg gttcaggctt taactacagc atctggaatt    660
atcctactgt tttgtataat gatgatattc attacatgtt cctggaccac agaaaaagat   720
acagagaaga gtgaagtgca atcttatgct tcttcagtag agactttaga ctctttaaat   780
gaggctatta taccgaaaac tgaaaatgaat gtgtaa                             816
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〈210〉 10
〈211〉 20
〈212〉 DNA
〈213〉 Artificial Sequence

〈220〉
〈223〉 primer SITH1NtermGW-F

〈400〉 10

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ggatatgaag aaaaagtgtc     20
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〈210〉 11
〈211〉 20
〈212〉 DNA
〈213〉 Artificial Sequence

〈220〉
〈223〉 primer SITH1CtermGW-R

〈400〉 11

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ttacacattc atttcagttt     20
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