(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
1 March 2007 (01.03.2007)

PCT

(10) International Publication Number
WO 2007/023461 A2

(51) International Patent Classification:
C12Q 1/68 (2006.01)

(21) International Application Number:
PCT/IB2006/052919

(22) International Filing Date: 23 August 2006 (23.08.2006)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
05107867.3 26 August 2005 (26.08.2005) EP

(71) Applicant *(for DE only)*: **PHILIPS INTELLECTUAL PROPERTY & STANDARDS GMBH** [DE/DE]; Lübeckertordamm 5, 20099 Hamburg (DE).

(71) Applicant *(for all designated States except DE, US)*: **KONINKLIJKE PHILIPS ELECTRONICS N. V.** [NL/NL]; Groenewoudseweg 1, NL-5621 BA Eindhoven (NL).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **LUEDKE, Gerd** [DE/DE]; c/o Philips Intellectual Property & Standards GmbH, Weisshausstr. 2, 52066 Aachen (DE). **BACHER, Johannes** [DE/DE]; c/o Philips Intellectual Property & Standards GmbH, Weisshausstr. 2, 52066 Aachen (DE). **SEHER, Jens-Peter** [DE/DE]; c/o Philips Intellectual Property & Standards GmbH, Weisshausstr. 2, 52066 Aachen (DE). **ENGEL, Holger** [DE/DE]; c/o Philips Intellectual Property & Standards GmbH, Weisshausstr. 2, 52066 Aachen (DE). **LAUBER, Jürgen** [DE/DE]; c/o Philips Intellectual Property & Standards GmbH, Weisshausstr. 2, 52066 Aachen (DE). **BAHR, André** [DE/DE]; c/o Philips Intellectual Property & Standards GmbH, Weisshausstr. 2, 52066 Aachen (DE). **LUBENOW, Helge** [DE/DE]; c/o Philips Intellectual Property & Standards GmbH, Weisshausstr. 2, 52066 Aachen (DE).

(74) Agent: **VOLMER, Georg**; Philips Intellectual Property & Standards GmbH, Weisshausstr. 2, 52066 Aachen (DE).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

— *with sequence listing part of description published separately in electronic form and available upon request from the International Bureau*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) **Title:** METHOD FOR DETECTION OF MICRO-ORGANISMS AND ANTIBIOTIC RESISTANCE MARKERS AND NUCLEIC ACID OLIGONUCLEOTIDES THEREFOR

(57) **Abstract:** The present invention relates to methods of detecting one or more micro¬ organisms and/or one or more antibiotic resistance markers in a sample, comprising identifying the presence of distinct nucleic acid regions. Primers and probes suitable for use in such methods are provided.

WO 2007/023461 A2

METHOD FOR DETECTION OF MICRO-ORGANISMS AND ANTIBIOTIC RESISTANCE MARKERS AND NUCLEIC ACID OLIGONUCLEOTIDES THEREFOR

Since the discovery of nucleic acids (NA), the technology relating to the detection of the presence, absence, or amount of specific DNA or RNA sequences in a sample has gained tremendous interest in academia, as well as in industry. The invention of amplification techniques, especially the Polymerase Chain Reaction (PCR) and hyridisation have contributed enormously to the development of assays of all types for the detection of the presence, absence, or amount of NA sequences. At present, it is possible to collect NA containing samples from an organism and determine the presence, absence, or amount therein of certain specific NA sequences (target sequences). Technology is available to perform such analysis for multiple target sequences at the same time, so-called multiplex detection of target sequences to thereby increase throughput as well as to improve the diagnostic significance.

At present, detection based on NA sequences is not yet performed on a routine basis, as is the case, for instance, in the measurement of blood glucose concentration of diabetics. Generally, well-equipped laboratories and well-trained staff are necessary and careful protocols have to be used in order to give reliable results. Furthermore, the present methods of analysis are not only laborious, but also time consuming. Typically, a current procedure for DNA or RNA analysis takes several days due to, amongst other thing, the requirement of various systems for the taking of samples, the culturing of samples, the isolation of DNA or RNA from the sample, the subsequent assay for the analysis of the presence, absence, or amount of the target sequences in the sample, the processing of any results obtained and the corresponding presentation of the results.

This time consuming analysis can be dramatically improved by applying highly specific hybridisation and amplification methods to the whole or parts of the target sequences so enabling the presence, absence, or amount of certain specific NA sequences to be determined. A highly sensitive and specific PCR and/or hybridisation can be applied, which in turn requires highly specific primers to certain specific NA target sequences. NA sequences of some bacterial strains are known in the art, for example, *Staphylococcus aureus*

NA sequences are disclosed in *J Clin Microbiol.* (2000), 38(2), 781-8, *Journal of Microbiological Methods* (2004), 58, 403– 411, *J Clin Microbiol.* (2004), 42(3), 1048-57, US 5,582,975, WO 90/14444, WO 03/095677, and US 5,958,679; *Staphylococcus epidermidis* NA sequences are disclosed in *Journal of Microbiological Methods* (2004), 58, 403– 411 and WO 03/095677; *Pseudomonas aeruginosa* NA sequences are disclosed in *Journal of Microbiological Methods* (2004), 58, 403– 411, *J Clin Microbiol.* (2004), 42(3), 1048-57, and WO 03/095677; *Klebsiella pneumoniae* NA sequences are disclosed in *Journal of Microbiological Methods* (2004), 58, 403– 411 and WO 03/095677; *Enterococcus faecalis* NA sequences are disclosed in *Journal of Microbiological Methods* (2004), 58, 403– 411; *Enterococcus faecium* NA sequences are disclosed in *Journal of Microbiological Methods* (2004), 58, 403– 411 and WO 03/095677; *Escherichia coli* NA sequences are disclosed in *Journal of Microbiological Methods* (2004), 58, 403– 411, *J Clin Microbiol.* (2004), 42(3), 1048-57 and WO 03/095677; *Enterobacter cloacae* NA sequences are disclosed in US 5,958,679. NA sequences of certain antibiotic resistance genes are known in the art, for example, beta lactamase SHV NA is known from J. *Clin Microbiol* (2001) 39, 3193–3196, *J. Clin Microbiol* (1998) 36, 3105–3110, J. *Clin Microbiol* (1999) 37, 4020-4027, US 2004/0002080, and US 6,242,223; beta lactamase GES-2 NA is known from *International Journal of Antimicrobial Agents* (2004) 24, 35–38 and *J. Antimicrobial Chemotherapy* (2002) 49 , 561-565; methicillin resistance *MecA* NA is known from *J Clin Microbiol.* (2002), 40(5), 1821-3, *J Clin Microbiol.* (1995), 33(11), 2864-7, *J Clin Microbiol.* 2000 Jun_38(6)_2429-33, WO02082086A2 and US 5,437,978; *spA* NA is known from *J. Clin Microbiol* (2003) 41, 5442–5448 and US 5,702,895; *vanA* NA is known from J. *Clin. Microbiol.* (1997), 703–707 and *J. Clin. Microbiol.* (2000) 3092–3095; *vanB* NA is known from J. *Clin. Microbiol.* (1997), 703–707 and *J. Clin. Microbiol.* (2000) 3092–3095; *vanC* NA is known from J. *Clin. Microbiol.* (1997), 703–707 and *J. Clin. Microbiol.* (2000) 3092–3095; beta lactamase resistance TEM-1H NA is known from *Antimicrobial Agents And Chemotherapy* (2001), 2407–2413, US 2004/0002080 and US 6,242,223.

However, a problem in the art of NA detection is providing reliable primers or probes. Particularly where multiplex detection is employed, a problem is cross-reactions and false-positive or false-negative results. The present invention aims to overcome the problems of the art by providing methods, sequences and primers which are suited to specific and reliable single mode and multiplex NA detection.

One embodiment of the present invention is a method of detecting one or more micro-organisms and/or one or more antibiotic resistance markers in a sample, comprising identifying the presence of distinct nucleic acid regions.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region of a micro-organism is in the 23S RNA gene.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region is identified using nucleic acid amplification.

Another embodiment of the present invention is a method as described above, wherein multiplex PCR is used to detect two or more distinct nucleic acid regions.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region is identified using hybridisation.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Enterobacter cloacae,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 3 and 4 or SEQ ID NOs: 5 and 6.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Enterobacter cloacae,* comprising the use of a hybridisation probe corresponding to a sequence represented by any of SEQ ID NOs: 3 to 6.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 1 or 2, and a micro-organism is *Enterobacter cloacae.*

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Enterococcus faecalis,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12, or SEQ ID NOs: 15 and 11.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Enterococcus faecalis,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 9 to 15.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 7 or 8, and a micro-organism is *Enterococcus faecalis.*

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Enterococcus faecium,* comprising the use of a pair of

amplification primers corresponding to the sequences represented by SEQ ID NOs: 18 and 19, SEQ ID NOs: 19 and 20, or SEQ ID NOs: 20 and 21.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Enterococcus faecium,* comprising the use of a probe corresponding to the sequences represented by SEQ ID NOs: 19 to 21.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 16 or 17, and a micro-organism is *Enterococcus faecium.*

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Escherichia coli,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 24 and 25, SEQ ID NOs: 24 and 26, SEQ ID NOs: 27 and 29, or SEQ ID NOs: 28 and 29.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Escherichia coli,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 24 to 29.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 22 or 23, and a micro-organism is *Escherichia coli.*

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Klebsiella pneumoniae,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36 or SEQ ID NOs: 37 and 33.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Klebsiella pneumoniae,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 32 to 37.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 30 or 31, and a micro-organism is *Klebsiella pneumoniae.*

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Pseudomonas aeruginosa,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 40 and 41 or SEQ ID NOs: 40 and 42.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Pseudomonas aeruginosa,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 40 to 42.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 38 or 39, and a micro-organism is *Pseudomonas aeruginosa.*

Another embodiment of the present invention is a method as described above, wherein a micro-organism is *Staphylococcus aureus,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, SEQ ID NOs: 50 and 51.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Staphylococcus aureus,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 45 to 51.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 43 or 44, and a micro-organism is *Staphylococcus aureus.*

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Staphylococcus epidermidis,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, or SEQ ID NOs: 63 and 61.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Staphylococcus epidermidis,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 54 to 63.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 52 or 53, and a micro-organism is *Staphylococcus epidermidis.*

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Candida albicans,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 66 and 67, SEQ ID NOs: 68 and 69, or SEQ ID NOs: 70 and 71.

Another embodiment of the present invention is a method as described above, wherein said micro-organism is *Candida albicans,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 66 to 71.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 64 or 65, and a micro-organism is *Candida albicans.*

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is $bla_{ges-2,}$ comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 74 and 75 or SEQ ID NOs: 76 and 77.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is $bla_{ges-2,}$ comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 74 to 77.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 72 or 73, and an antibiotic resistance marker is bla_{ges-2}.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is $bla_{shv,}$ comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 80 and 81 or SEQ ID NOs: 82 and 83.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is $bla_{shv,}$ comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 80 to 83.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 78 or 79, and an antibiotic resistance marker is bla_{shv}.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *mecA,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 86 and 87 or SEQ ID NOs: 88 and 89.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *mecA,* comprising the use of a probe corresponding to the sequences represented by SEQ ID NOs: 86 or 89.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 84 or 85, and an antibiotic resistance marker is *mecA*.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *spA,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 92 and 93 or SEQ ID NOs: 94 and 95.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *spA,* comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 92 to 95.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 90 or 91, and an antibiotic resistance marker is *Spa.*

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *VanA,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 98 and 99 or SEQ ID NOs: 100 and 101.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *VanA,* comprising the use of a probe corresponding to the sequences represented by SEQ ID NOs: 98 to 101.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 96 or 97, and an antibiotic resistance marker is *VanA.*

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *VanB,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 104 and 105 or SEQ ID NOs: 106 and 107.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *VanB,* comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 104 to 107.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 102 or 103, and an antibiotic resistance marker is *VanB.*

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *VanC,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 110 and 111 or SEQ ID NOs: 112 and 113.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *VanC,* comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 110 to 113.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 108 or 109, and an antibiotic resistance marker is *VanC.*

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *MDR-1,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 116 and 117 or SEQ ID NOs: 118 and 119.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *MDR-1,* comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 116 to 119.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 114 or 115, and an antibiotic resistance marker is *MDR-1.*

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *CDR-1,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 122 and 123 or SEQ ID NOs: 124 and 125.

Another embodiment of the present invention is a method as described above, wherein said antibiotic resistance marker is *CDR-1,* comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 122 to 125.

Another embodiment of the present invention is a method as described above, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 120 or 121, and an antibiotic resistance marker is *CDR-1.*

Another embodiment of the present invention is a container preloaded with one or more pairs of amplification primers, selected from the sequences represented by SEQ ID NOs: 3 and 4, SEQ ID NOs: 5 and 6,SEQ ID NOs: 9 and 10, SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12, SEQ ID NOs: 15

and 11,SEQ ID NOs: 18 and 19, SEQ ID NOs: 20 and 19, SEQ ID NOs: 20 and 21, SEQ ID NOs: 24 and 26, SEQ ID NOs: 24 and 25, SEQ ID NOs: 27 and 29, SEQ ID NOs: 28 and 29, SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36, SEQ ID NOs: 37 and 33, SEQ ID NOs: 40 and 41, SEQ ID NOs: 40 and 42, SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, SEQ ID NOs: 50 and 51, SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, SEQ ID NOs: 63 and 61, SEQ ID NOs: 66 and 67, SEQ ID NOs: 68 and 69, SEQ ID NOs: 70 and 71, SEQ ID NOs: 74 and 75, SEQ ID NOs: 76 and 77, SEQ ID NOs: 80 and 81, SEQ ID NOs: 82 and 83, SEQ ID NOs: 86 and 87, SEQ ID NOs: 88 and 89, SEQ ID NOs: 92 and 93, SEQ ID NOs: 94 and 95, SEQ ID NOs: 98 and 99, SEQ ID NOs: 100 and 101, SEQ ID NOs: 104 and 105, SEQ ID NOs: 106 and 107, SEQ ID NOs: 110 and 111, SEQ ID NOs: 112 and 113, SEQ ID NOs: 116 and 117, SEQ ID NOs: 118 and 119, SEQ ID NOs: 122 and 123, and SEQ ID NOs: 124 and 125.

Another embodiment of the present invention is a container preloaded with one or more probes, selected from the sequences represented by any of SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29, SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125.

Another embodiment of the present invention is a kit comprising one or more pairs of amplification primers, selected from the sequences represented by SEQ ID NOs: 3 and 4, SEQ ID NOs: 5 and 6,SEQ ID NOs: 9 and 10, SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12, SEQ ID NOs: 15 and 11,SEQ ID NOs: 18 and 19, SEQ ID NOs: 20 and 19, SEQ ID NOs: 20 and 21, SEQ ID NOs: 24 and 26, SEQ ID NOs: 24 and 25, SEQ ID NOs: 27 and 29, SEQ ID NOs: 28 and 29, SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36, SEQ ID NOs: 37 and 33, SEQ ID NOs: 40 and 41, SEQ ID NOs: 40 and 42, SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, SEQ ID NOs: 50 and 51, SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, SEQ ID NOs: 63 and 61, SEQ ID

NOs: 66 and 67, SEQ ID NOs: 68 and 69, SEQ ID NOs: 70 and 71, SEQ ID NOs: 74 and 75, SEQ ID NOs: 76 and 77, SEQ ID NOs: 80 and 81, SEQ ID NOs: 82 and 83, SEQ ID NOs: 86 and 87, SEQ ID NOs: 88 and 89, SEQ ID NOs: 92 and 93, SEQ ID NOs: 94 and 95, SEQ ID NOs: 98 and 99, SEQ ID NOs: 100 and 101, SEQ ID NOs: 104 and 105, SEQ ID NOs: 106 and 107, SEQ ID NOs: 110 and 111, SEQ ID NOs: 112 and 113, SEQ ID NOs: 116 and 117, SEQ ID NOs: 118 and 119, SEQ ID NOs: 122 and 123, and SEQ ID NOs: 124 and 125.

Another embodiment of the present invention is a kit comprising one or more probes selected from the sequences represented by SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29, SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125.

Another embodiment of the present invention is a kit comprising one or more containers as described above.

Another embodiment of the present invention is a device comprising one or more pairs of amplification primers selected from the sequences represented by SEQ ID NOs: 3 and 4, SEQ ID NOs: 5 and 6,SEQ ID NOs: 9 and 10, SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12, SEQ ID NOs: 15 and 11,SEQ ID NOs: 18 and 19, SEQ ID NOs: 20 and 19, SEQ ID NOs: 20 and 21, SEQ ID NOs: 24 and 26, SEQ ID NOs: 24 and 25, SEQ ID NOs: 27 and 29, SEQ ID NOs: 28 and 29, SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36, SEQ ID NOs: 37 and 33, SEQ ID NOs: 40 and 41, SEQ ID NOs: 40 and 42, SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, SEQ ID NOs: 50 and 51, SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, SEQ ID NOs: 63 and 61, SEQ ID NOs: 66 and 67, SEQ ID NOs: 68 and 69, SEQ ID NOs: 70 and 71, SEQ ID NOs: 74 and 75, SEQ ID NOs: 76 and 77, SEQ ID NOs: 80 and 81, SEQ ID NOs: 82 and 83, SEQ ID NOs: 86 and 87, SEQ ID NOs: 88 and 89, SEQ ID NOs: 92 and 93, SEQ ID NOs: 94 and 95, SEQ ID NOs: 98 and 99, SEQ ID NOs: 100 and 101, SEQ ID NOs: 104 and 105, SEQ ID NOs: 106 and 107, SEQ ID NOs: 110 and 111, SEQ ID NOs: 112 and 113, SEQ ID NOs: 116 and 117, SEQ ID NOs: 118 and 119, SEQ ID NOs: 122 and 123, SEQ ID NOs: 124 and 125.

Another embodiment of the present invention is a device comprising one or more probes, selected from the sequences represented by SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29, SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125.

Another embodiment of the present invention is a use of a container, kit or device as described above for detecting one or more micro-organisms and/or one or more antibiotic resistance markers in a sample.

Another embodiment of the present invention is a composition comprising a probe selected from the sequences represented by: SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29, SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125.

Another embodiment of the present invention is a composition comprising two or more probes selected from the sequences represented by: SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29, SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125..

Another embodiment of the present invention is a composition comprising a pair of amplification primers selected from the sequences represented by: SEQ ID NOs: 3 and 4, SEQ ID NOs: 7 and 8, SEQ ID NOs: 11 and 12, SEQ ID NOs: 15 and 16, SEQ ID NOs: 19 and 20, SEQ ID NOs: 23 and 24, SEQ ID NOs: 27 and 28, SEQ ID NOs: 31 and 32, SEQ ID NOs: 35 and 36, SEQ ID NOs: 39 and 40, SEQ ID NOs: 43 and 44, SEQ ID NOs: 47 and 48, SEQ ID NOs: 51 and 52, SEQ ID NOs: 55 and 56, and SEQ ID NOs: 59 and 60.

Another embodiment of the present invention is a composition comprising two or more pairs of amplification primers selected from the sequences represented by: SEQ ID NOs: 3 and 4, SEQ ID NOs: 7 and 8, SEQ ID NOs: 11 and 12, SEQ ID NOs: 15 and 16, SEQ ID NOs: 19 and 20, SEQ ID NOs: 23 and 24, SEQ ID NOs: 27 and 28, SEQ ID NOs: 31 and

32, SEQ ID NOs: 35 and 36, SEQ ID NOs: 39 and 40, SEQ ID NOs: 43 and 44, SEQ ID NOs: 47 and 48, SEQ ID NOs: 51 and 52, SEQ ID NOs: 55 and 56, and SEQ ID NOs: 59 and 60.

Another embodiment of the present invention is a sequence of 23S RNA gene selected from the sequences represented by SEQ ID NOs: 131 to 157.

Another embodiment of the present invention is a sequence of antibiotic resistance marker selected from the sequences represented by SEQ ID NOs: 158 to 261.

Another embodiment of the present invention is a method as described above, wherein said sequence(s) represented by said SEQ ID NO(s) is (are) the complement(s) of said SEQ ID NO(s).

Another embodiment of the present invention is a method as described above, wherein said sequence(s) represented by said SEQ ID NO(s) is (are) an homologous sequence(s) of said SEQ ID NO (s).

Another embodiment of the present invention is a container, kit, device or use as described above wherein said sequence(s) represented by said SEQ ID NO(s) is (are) the complement(s) of said SEQ ID NO(s).

Another embodiment of the present invention is a container, kit, device or use as described above wherein said sequence(s) represented by said SEQ ID NO(s) is (are) an homologous sequence(s) of said SEQ ID NO(s).

Another embodiment of the present invention is a composition as described above wherein said sequence(s) represented by said SEQ ID NO(s) is (are) the complement(s) of said SEQ ID NO(s).

Another embodiment of the present invention is a composition as described above, wherein a sequence represented by a SEQ ID NO is an homologous sequence of said SEQ ID NO.

Another embodiment of the present invention is a sequence of 23S RNA gene as described above, wherein said sequence represented by said SEQ ID NO is the complement(s) of said SEQ ID NO.

Another embodiment of the present invention is a sequence of 23S RNA gene as described above, wherein said sequence represented by said SEQ ID NO is an homologous sequence of said SEQ ID NO.

Another embodiment of the present invention is a sequence of an antibiotic resistance marker as described above, wherein said sequence(s) represented by said SEQ ID NO(s) is(are) the complement(s) of said SEQ ID NO(s).

Another embodiment of the present invention is a sequence of an antibiotic resistance marker as described above, wherein said sequence(s) represented by said SEQ ID NO(s) is(are) an homologous sequence(s) of said SEQ ID NO(s).

Figure 1: Sequences and alignments of 23S RNA sequences of micro-organisms.

Figure 2: Sequences and alignments of antibiotic resistance genes.

The present invention relates to sequences of 23S RNA genes of micro-organisms, and to antibiotic resistance genes and their use as templates for hybridisation and/or nucleic acid amplification reactions, and/or other identification methods in order to detect the presence of one or more micro-organisms and/or antibiotic resistance genes in a sample. The invention further relates to nucleic acid amplification primers and hybridisation probes suitable for amplification of and hybridisation to said sequences.

The sample may be any sample of interest. It may be derived from animals (*e.g.* human, agricultural livestock, domestic livestock, scientific livestock, zoological livestock) or non-animal (*e.g.* solid and liquid consumables, water systems, sewerage systems, soil, heating / cooling systems). Where the sample is human, it may be for example, blood, saliva, urine, faeces, any bodily fluid or tissue. The sample is any that warrants investigation, and is capable of providing template nucleic acid.

According to one embodiment of the present invention, species of micro-organisms useful according to the invention are one or more of *Staphylococcus aureus, Staphylococcus epidermidis, Enterobacter cloacae, Escherichia coli, Enterococcus faecalis, Pseudomonas aeruginosa, Enterococcus faecium, Klebsiella pneumoniae, and Candida albicans*.

According to another embodiment of the present invention, antibiotic resistance markers useful according to the invention are one or more of *mec*A (methicillin resistance gene, confers resistance to B-lactams), *van*A (vancomycin resistance gene A), *van*B (vancomycin resistance gene B), *van*C (vancomycin resistance gene C), bla_{shv} (beta-lactam resistance gene), bla_{ges-2} (beta-lactam resistance gene), spA (*Staphylococcus-aureus* protein A), MDR-1 (multi-drug resistance gene-1 in Fungi), and CDR-1 (multi-drug resistance gene-2 in Fungi).

According to the present invention, nucleic acid sequences of 23S RNA or antibiotic resistance markers serve as templates for sequence-specific nucleic acid detection

methods. A detection method involves detecting the presence of one or more distinct regions *i.e.* a region of 23S RNA gene (including 23S RNA *per se*), or a region of an antibiotic marker sufficiently distinct to enable identification of a species or an antibiotic resistance marker by detecting the presence of the region. Detection may be by amplification of at least a portion the distinct region. Alternatively, or in addition, detection may be by the use of an anti-nucleic acid antibody or sequencing. Alternatively, or in addition, detection may be by hybridisation using a probe. Detection may occur when total nucleic acid from other species or taxonomical groups is present in the sample. The distinct regions may, for example,

- comprise sequence portions which are unconserved between species,
- comprise sequence portions which are unconserved between antibiotic resistance markers,
- comprise an unconserved number of residues between conserved sequence portions, enabling identification based on product length of the amplification reaction,
- comprise certain physical properties of folding, or associated proteins particular to a species, permitting binding of primer or probe under certain conditions.

A distinct region includes homologous sequences in which one or more bases have been deleted, substituted and/or inserted. The number of substitutions, deletions and/or insertions permitted in an homologous sequence may be less than or equal to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 residues. Alternatively, the number is less than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50% of residues. An homologous sequence still permits identification of the distinct region based on some or all of the unchanged residues. A distinct region also includes the complement sequence of the distinct region.

Amplification

Where nucleic acid amplification is used (*e.g.* PCR), primers pairs are of such sequence and length to provide amplification products (amplicons) only when one or more distinct regions of the species or resistance genes are present. Alternatively, the primers may provide a product of particular length or pattern for the species of interest, distinguishable from amplification products arising from the amplification of other sequences. Alternatively,

or in addition, the amplification primers may provide a relative quantity of product, enabling identification of the species (*e.g.* one or more strong bands on a electrophoretic gel). Any method of matching the result of an amplification to the presence of the nucleic acid of interest is within the scope of the invention.

Although nucleic acid amplification methods such as the PCR process are well known in the art (see U.S. Pat. Nos. 4,683,195 and 4,683,202 which are incorporated herein by reference) and although a variety of commercial vendors, such as Roche, Invitrogen, Qiagen, Promega sell PCR reagents and publish PCR protocols, some general PCR information is provided below for purposes of clarity.

To begin the PCR process, the target nucleic acid in the sample is denatured (assuming the sample nucleic acid is double-stranded). Denaturation is typically achieved by heating the samples up to about 95°C.

Once the strands are separated, the next step in PCR involves hybridising the separated strands with primers that flank the target region or subsequence by lowering the temperature of the sample below the melting temperature T_M. The primers are then extended to form complementary copies of the target strands by increasing the sample temperature up to the temperature for optimum extension (*e.g.* 70 to 75 deg C), and the cycle of denaturation, hybridisation, and extension is repeated as many times as necessary to obtain the desired amount of amplified nucleic acid.

Template-dependent extension of primers in PCR is catalysed by a polymerising agent in the presence of adequate amounts of four deoxyribonucleotide triphosphates (dATP, dGTP, dCTP, and dTTP) in a reaction medium comprised of the appropriate salts, metal cations, and pH buffering system. Suitable polymerising agents are enzymes known to catalyse template-dependent DNA synthesis. For example, if the template is RNA, a suitable polymerising agent to convert the RNA into a complementary DNA (cDNA) sequence is reverse transcriptase (RT), such as arian myeloblastosis virus RT. Once the target for amplification is DNA, suitable polymerases include, for example, *E. coli* DNA polymerase I or its Klenow fragment, T4 DNA polymerase, and Taq polymerase, a heat stable DNA polymerase isolated from *Thermus aquaticus*. The latter enzyme, Taq DNA polymerase, is widely used in the amplification and sequencing of nucleic acids. The reaction conditions for using DNA polymerases are known in the art, and are described in, for example, the treatise Methods in Enzymology, and in Maniatis et al., Molecular Cloning: A Laboratory Manual.

During the PCR process, the temperature is carefully controlled so that strand separation and primer annealing and extension occur in equilibrium. The control of temperature is typically achieved using dry heat generated from a thermocycler.

In the preferred embodiment of the PCR process, the reaction is catalysed by a thermostable DNA polymerase enzyme, such as Taq DNA polymerase, and carried out at an elevated temperature. The preferred temperature is one at which the enzyme is thermostable, and at which the nucleic acids are in an equilibrium of single and double strands, so that sufficient primer will anneal to template strands to allow a reasonable rate of polymerisation Strand separation is achieved by heating the reaction to a sufficiently high temperature for sufficient time to cause the denaturation of the duplex, but not to cause an irreversible denaturation of the polymerase.

The PCR method can be performed in a step-wise fashion, where after each step new reagents are added, or in a fashion where all of the reagents are added after a given number of steps. For example, if strand separation is induced by heat, and the polymerase is heat-sensitive, then the polymerase will have to be added after every round of strand separation. However, if, for example, a helicase is used for denaturation, or if a thermostable polymerase is used for extension, then all of the reagents may be added initially, or, alternatively, if molar ratios of reagents are of consequence to the reaction, the reagents may be replenished periodically as they are depleted by the synthetic reaction.

Methods for detecting the presence, size and/or quantity of the PCR product are known in the art and include the use of electrophoresis, chromatography, capillary-zone electrophoresis, analytical centrifugation etc. Such method may be in combination with the use of labels (*e.g.* fluorescent, chemiluminescence, radioisotope, enzyme-labels (such as horse radish peroxidases or alkaline phosphatase), dye, antibody, etc). Detection may also be achieved by the use of hybridisation probes (mentioned below) either in solution or immobilised on a solid support or antibodies directed against the DNA to be detected.

According to one embodiment of the invention, the amplification is performed on or in a container. A container may be single sample or multiple-sample. Single sample containers include, tubes, vials, Eppendorf tubes etc., as known to the skilled person. Multi-sample containers include, but are not limited to multi-well plates, solid phase slides, solid phase membrane (*e.g.* nylon or nitrocellulose), microspheres, glass slides, microarrays, chips etc. Single sample containers may use the aforementioned substrates in a single sample mode. The multiple-sample containers permit, for example, several or a large number of PCRs to proceed simultaneously using a single thermal cycling block. The containers may be

compatible with high-throughput screening or microarray devices. One or more pairs of primers or samples may be immobilised onto the solid phase. A container may be provided which already comprises one or more pairs of primers. Such preloaded containers may comprise combinations of primers for detection of specified micro-organisms and/or resistance genes. A preloaded container may comprise a combination of primers suited for detection of a limited combination of distinct regions which are of interest to the operator (*e.g.* for the detection of just *E. coli* and *van*A or *van*B or *van*C). Several variations for the detection of particular combinations may be made available. Such preloaded containers may be available as part of a kit, or available separately.

According to one aspect of the invention, two or more pairs of amplification primers are used to detect simultaneously the presence of two or more different species, or two or more different antibiotic resistance markers, or at least one species and at least one antibiotic resistance marker. The amplification products obtained thereby are sufficiently different in property to enable identification of the presence of said species and/or antibiotic resistance marker. The simultaneous amplifications may be performed under the same temperature cycling conditions, but in different wells or spaces (*e.g.* on a microarray having separate wells for different primer pairs). Optionally, the buffers may be the same for the different pairs of amplification primers. The different primer pairs are designed of certain sequences and length, to function under identical conditions of temperature and optionally buffer.

In another aspect of the invention, the amplification primers occupy the same well or space, *i.e.* all the primers are present in the same reaction (multiplexed). The multiplex mode involves the simultaneous amplification of different target regions using more than one set of amplification primer pairs. Therefore, conditions such as temperature and optionally buffers are identical for pairs of multiplex PCR primers. The primers are thus further designed to preclude cross-reaction between primer pairs, to have similar thermal melting points, and operate in identical buffer conditions.

It is preferred that all pairs for multiplexed PCR have Tms (hybdridisation melting temperatures) within 8 deg C of each other and that the average Tm is between 45 deg C and about 70 deg C. with preference for an average Tm of between 60 deg C and 66 deg C.

Simultaneous amplification enables a range of bacterial species and/or antibiotic resistance markers to be detected on a single microarray, or in a single reaction vessel, so permitting rapid, economic and accurate screening.

The amplification primers may be completely complementary to the target *i.e.* there are no mismatches. It is also within the scope of the invention that a primer does not fully complement the target, but still allows amplification thereof. The primers may bind where there are one or more mismatches, deletions and/or insertions in the target template. The number of mismatches, deletions and/or insertions permitted in the target template may be 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues within the native complementary region, and which still allow amplification of the target region. Alternatively, the number may be less than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50% of template residues within the native complementary region. Such values depend upon the length and composition of the primers as known by the skilled person. Preferably, the mismatches, deletions and/or insertions are restricted to sequences from the middle of the complementary region towards the 3' end of a template.

The primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted. The number of substitutions, deletions and/or insertions permitted in a primer may be 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues within the native complementary region. Alternatively, the number is less than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50% of primer residues within the ends of native complementary region. Such values depend upon the length and composition of the probes as known by the skilled person. Preferably, the mismatches, deletions and/or insertions are restricted to sequences from the middle of the complementary region towards the 5' end of a primer. Furthermore, an amplification primer may be chemically modified, for example, with modified bases or backbones (*e.g.* phosphorothiates, alkylphosphorothiates, peptide nucleic acids, or may contain intercalating agents). Variations or modifications introduced may necessitate adaptations with respect to the conditions under which the oligonucleotide should be used to obtain the required specificity and sensitivity. However, the eventual results of the amplification reaction will be essentially the same.

The introduction of deletions, substitutions, insertions or modifications may be advantageous in order to positively influence characteristics such as annealing kinetics, reversibility of annealing, biological stability of oligonucleotide molecules etc.

Furthermore, an amplification primer may be extended in the 5' direction with one or more additional bases, modified bases, or chemical groups (*e.g.* tags). Such modifications are known to the skilled person and do not normally affect the amplification.

It is an aspect that identification comprises double amplification *i.e.* amplification of a region which encloses the distinct region, followed by the amplification of the distinct region *e.g.* by nested PCR. The product from the first reaction (optionally purified) may be applied as a template in the second reaction. Alternatively, the first reaction may be allowed to proceed for a limited number of cycles, before primers pertinent to the second reaction are added to the same reaction container. Such variations are known to the skilled person.

Hybridisation

Where a hybridisation probe is used, the probe may be of such sequence and length that hybridisation is indicated only when nucleic acid of a distinct region is present in the reaction. Methods and protocols to achieve selective binding of hybridisation probes are known to the skilled person. Alternatively, or in addition, the probe may provide a particular relative strength of signal to enable identification of the species against background or other hybridisation. Any method of matching the result of a hybridisation reaction to the presence of the nucleic acid of interest is within the scope of the invention.

The methods and conditions for performing a hybridisation reaction are known in the art, and can be found, for example, in Molecular Cloning: A Laboratory Manual (Third Edition) (Joseph Sambrook, Peter MacCallum, David Russell, Cold Spring Habor Laboratory Press).

For designing probes with desired characteristics, the following useful guidelines known to the person skilled in the art can be applied.

Because the extent and specificity of hybridisation reactions such as those described herein are affected by a number of factors, manipulation of one or more of those factors will determine the exact sensitivity and specificity of a particular probe, whether perfectly complementary to its target or not. The importance and effect of various assay conditions are explained further herein.

The stability of the [probe:target] nucleic acid hybrid should be chosen to be compatible with the assay conditions. This may be accomplished, for example, by avoiding long AT-rich sequences, by terminating the hybrids with G:C base pairs, and by designing the probe with an appropriate Tm. The beginning and end points of the probe should be

chosen so that the length and %GC result in a Tm about 2 to 10 deg C higher than the temperature at which the final assay is be performed. The base composition of the probe is significant because G-C base pairs exhibit greater thermal stability compared with A-T base pairs due to additional hydrogen bonding. Thus, hybridisation involving complementary nucleic acids of higher C-C content will be more stable at higher temperatures.

Conditions such as ionic strength and incubation temperature under which a probe will be used should also be taken into account when designing a probe. It is known that the degree of hybridisation will increase as the ionic strength of the reaction mixture increases, and that the thermal stability of the hybrids will increase with increasing ionic strength. On the other hand, chemical reagents, such as formamide, urea, DMSO and alcohols, which disrupt hydrogen bonds, will increase the stringency of hybridisation. Destabilisation of the hydrogen bonds by such reagents can greatly reduce the Tm. In general, optimal hybridisation for probes of about 10 to 50 bases in length occurs approximately 5 deg C below the melting temperature for a given duplex. Incubation at temperatures below the optimum may allow mismatched base sequences to hybridise and can therefore result in reduced specificity.

It is desirable to have probes which hybridise only under conditions of high stringency. Under high stringency conditions only highly complementary nucleic acid hybrids will form; hybrids without a sufficient degree of complementarity will not form or will be indicated as weaker signal. Accordingly, the stringency of the assay conditions determines the amount of complementarity needed between two nucleic acid strands forming a hybrid. The degree of stringency is chosen such as to maximize the difference in stability between the hybrid formed with the target and the non-target nucleic acid.

Regions in the target DNA or RNA which are known to form strong internal structures inhibitory to hybridisation are less preferred. Likewise, probes with extensive self-complementarity should be avoided. Hybridisation is the association of two single strands of complementary nucleic acids to form a hydrogen bonded double strand: It is implicit that if one of the two strands is wholly or partially involved in a hybrid that it will be less able to participate in formation of a new hybrid. There can be intramolecular and intermolecular hybrids formed within the molecules of one type of probe if there is sufficient self complementarity. Such structures can be avoided through careful probe design. By designing a probe so that a substantial portion of the sequence of interest is single stranded, the rate and extent of hybridisation may be greatly increased. Computer programs are available to search

for this type of interaction. However, in certain instances, it may not be possible to avoid this type of interaction.

Methods for detecting the presence of sequences may include, but are not limited to Southern blot, Northern blot, affinity chromatography and solid-phase assays. Methods may include the use of fluorescent markers, radioisotope markers, enzyme linked markers, dyes, antibodies, enzymes linked to the probe as understood by the person skilled in the art.

According to one embodiment of the invention, the analysis is performed on or in a container. A container may be single sample or multiple-sample. Single sample containers include, tubes, vials, Eppendorf tubes etc., as known to the skilled person. Multi-sample containers include, but are not limited to multi-well plates, solid-phase support, solid phase slides, solid phase membrane (*e.g.* nylon or nitrocellulose), porous structures, microspheres, glass slides, microarrays, chips etc. Single sample containers may use the aforementioned substrates in a single sample mode. Sample may be applied, for example, using an multiple applicator, soft lithography or microcontact printing, inkjet technology, etc. One or more probes or samples may be immobilised onto a container (*e.g.* onto a solid phase support). The multiple-sample solid supports permit, for example, several or a large number of hybridisations to proceed simultaneously using a single hybridisation oven or platform and/or single set of reagents. The solid support may be compatible with high-throughput screening or microarray devices. A container may be provided which already comprises one or more probes. Such preloaded containers may comprise combinations of probes for detection of specified micro-organisms and/or resistance genes. A preloaded container may comprise a combination of probes suited for detection of a limited combination of distinct regions which are of interest to the operator (*e.g.* for the detection of just *E. coli* and *van*A or *van*B or *van*C). Several variations for the detection of particular combinations may be made available. Such preloaded containers may be available as part of a kit, or separately.

According to one aspect of the invention, two or more hybridisation probes are used to detect simultaneously the presence of two or more different species, or two or more different antibiotic resistance markers, or at least one species and at least one antibiotic resistance marker. The hybridisation products obtained thereby are sufficiently different in property to enable identification of the presence of said species and/or antibiotic resistance marker. The simultaneous hybridisation may be performed under the same temperature conditions, but in different wells or spaces (*e.g.* on a microarray having separate wells for different primer pairs). Optionally, the buffers may be the same for the different probes. The

different probes are thus designed of certain sequences and length, to function under identical conditions of temperature and optionally buffer.

In another aspect of the invention, the hybridisation probes occupy the same well or space, *i.e.* all the probes are present in the same reaction. Therefore, conditions such as temperature and optionally buffers are identical for the probes. The probes are thus further designed to preclude cross-reaction, and to provide a result allowing the presence of two or more species, DNA resistance gene or both to be reliably identified.

Such simultaneous hybridisation enables detection of a range of bacterial species and/or antibiotic resistance markers on a single microarray, or in a single reaction, with the likelihood of false results from cross-binding minimized.

The hybridisation probes may be completely complementary to the target *i.e.* there are no mismatches. It is also within the scope of the invention that the probes do not fully complement the target, but still allow identification and discrimination thereof. The probe may bind when there are one or mismatches, deletions and/or insertions in the target template. The number of mismatches, deletions and/or insertions permitted in the target template may be 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues within the ends of the native complementary region. Alternatively, the number is less than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50% of template residues within the ends of the native complementary region. Such values depend upon the length and composition of the probes as known by the skilled person.

A sequence of a probe includes homologous sequences in which one or more bases have been deleted, substituted and/or inserted. The number of substitutions, deletions and/or insertions permitted in a probe may be 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues within the ends of the native complementary region. Alternatively, the number is less than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50% of primer residues within the ends of native complementary region. Such values depend upon the length and composition of the probes as known by the skilled person. Furthermore, a probe may be chemically modified, for example, with modified bases or backbones (*e.g.* phosphorothiates, alkylphosphorothiates, peptide nucleic acids, or may contain intercalating agents). Variations or modifications introduced may necessitate adaptations with respect to

the conditions under which the oligonucleotide should be used to obtain the required specificity and sensitivity. However, the eventual results of the hybridisation will be essentially the same. The introduction of these modifications may be advantageous in order to positively influence characteristics such as hybridisation kinetics, reversibility of hybridisation, biological stability of oligonucleotide molecules etc.

A hybridisation probe according to the present invention is capable of annealing to a sequence of any 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more bases of the distinct region, or the complement thereof.

It is an aspect that the template of hybridisation is an amplification product. That is to say nucleic acid enclosing a distinct region is first amplified and the hybridisation proceeds using the product of the amplification.

1. Enterobacter cloacae

According to one aspect of the invention a distinct region of *Enterobacter cloacae* 23S RNA gene comprises a nucleotide sequence (SEQ ID NOs: 1 or 2) indicated in Tables 1 and 2. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 1

```
1251(5')
|
CGGTTTAAGCATGTAGGCGGAGGTTCCAGGTAAATCCGGTACCTTTTAAC
GCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAATGCCCTG
CTTCCAGGAAAAGCCTCTAAGCATCAGGTAACAYSAAATCGTACCCCAAA
CCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGG
GTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGGCACGCTG
ATATGTAGGTGAAGCCCCTGCGGGTGGAGCTGAAATCAGTCGAAGATACC
AGCTGGCTGCAACTGTTTATTAAAAACACAGCACTGTGCAAACACGAAAG
TGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAATTGATGG
GGTTAGCGGYAACGCGAAGCTCTTGATCGAAGCCCCGGTAAACGGCGGCC
GTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCG
ACCTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCGAGACTCA
GTGAAATTGAACTCGCTGTGAAGATGCAGTGTACCCGCGGCAAGACGGAA
AGACCCCGTGAACCTTTACTATAGCTTGACACTGAACACTGGTCCTTGAT
GTGTAGGATAGGTGGGAGGCTTTGAAGCGTGGACGCCAGTCTGCGTGGAG
CCGTCCTTGAAATACCACCCTTTAATGGCTGGTGTTCTAACGTAGACCCG

TWAYCCGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGGGCGGTCT
                                                    |
                                                    2050 (3')
```

Table 1: Sequence of distinct region of 23S RNA gene of *Enterobacter cloacae*. An example of a substitution according to the invention is T1502C (underlined). W is a nucleotide with an adenine or thymine base.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO:1. Preferably, a pair of amplification primers is capable of amplifying any region between residues 1251 and 2050 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1279 and 1998 (Table 2, SEQ ID NO: 2).

SEQ ID NO: 2

1279(5')
|
GGTAAATCCGGTACCTTTTAACGCTGAGGTGTGATGACGAGGCACTACGG
TGCTGAAGTAACAAATGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGG
TAACAYSAAATCGTACCCCAAACCGACACAGGTGGTCAGGTAGAGAATAC
CAAGGCGCTTGAGAGAACTCGGGTGAAGGAACTAGGCAAAATGGTGCCGT
AACTTCGGGAGAAGGCACGCTGATATGTAGGTGAAGCCCCTGCGGGTGGA
GCTGAAATCAGTCGAAGATACCAGCTGGCTGCAACTGTTTATTAAAAACA
CAGCACTGTGCAAACACGAAAGTGGACGTATACGGTGTGACGCCTGCCCG
GTGCCGGAAGGTTAATTGATGGGGTTAGCGGYAACGCGAAGCTCTTGATC
GAAGCCCCGGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAA
ATTCCTTGTCGGGTAAGTTCCGACCTGCACGAATGGCGTAATGATGGCCA
GGCTGTCTCCACCCGAGACTCAGTGAAATTGAACTCGCTGTGAAGATGCA
GTGTACCCGCGGCAAGACGGAAAGACCCCGTGAACCTTTACTATAGCTTG
ACACTGAACACTGGTCCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGC
GTGGACGCCAGTCTGCGTGGAGCCGTCCTTGAAATACCACCCTTTAATGG
CTGGTGTTCTAACGTAGACC
|
1998 (3')

Table 2: Sequence of distinct region of 23S RNA gene of *Enterobacter cloacae*. An example of a substitution according to the invention is T1502C (underlined).

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 1279 and 1998 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 1279 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1998 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting *Enterobacter cloacae* comprise the sequences in Table 3. Combinations of forwards (F) and reverse (R) primers include SEQ ID NO: 3 (F) and SEQ ID NO: 4 (R); SEQ ID NO: 5 (F) and SEQ ID NO: 6 (R) as indicated in Table 3, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / PRIMER LENGTH	TYPE	PAIR	LEN	Tm (deg C)
SEQ ID NO: 3	GGTAAATCCGGTACCTTTTAAC / 22	F	4	331	62
SEQ ID NO: 4	GGTCTACGTTAGAACACCAGC / 21	R	3	331	64
SEQ ID NO: 5	GGAGCGTTCTGTAAGCCGTT / 20	F	6	719	62
SEQ ID NO: 6	CACACCTCAGCGTTAAAAGGTA / 22	R	5	719	64

Table 3: Amplification primer examples for amplifying distinct region of 23S RNA gene of *Enterobacter cloacae*, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 1, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 1279 and 1998 inclusive (SEQ ID NO: 2), or complement thereof. It is within the scope of the invention, that the probes are capable of binding to the region between 1279 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1998 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting *Enterobacter cloacae* comprise the sequences represented by SEQ ID NOs: 3 to 6, and the complements thereof.

Another aspect of the invention is a method for identifying *Enterobacter cloacae* by amplification of nucleic acid using primer pairs of Table 3, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 3 to 6.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 3.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

2. Enterococcus faecalis

According to one aspect of the invention a distinct region of *Enterococcus faecalis* 23S RNA gene comprises a nucleotide sequence (SEQ ID NOs: 7 or 8) indicated in

Tables 4 and 5. According to another aspect of the invention, a distinct region is an homologous sequence of said SEQ ID NOs.

SEQ ID NO: 7

```
1259(5')
|
CATGCGATTGGAAGTGCATGTCCAAGCAATGAGTCTTGAGTAGAGTTAAATGCTTTACTC
TTTAAGGACAAGTTGTGAYGGGGAGCGAAATAATAGTAGCGAAGTTCCTGATGTCACACT
GCCAAGAAAAGCTTCTAGTGAGAAAACAACTGCCCGTACCGTAAACCGACACAGGTAGTC
GAGGAGAGTATCCTAAGGTGAGCGAGCGAACTCTCGTTAAGGAACTCGGCAAAATGACCC
CGTAACTTCGGGAGAAGGGGTGCTGACTTCGGTCAGCCGCAGTGAATAGGCCCAAGCGAC
TGTTTATCAAAAACACAGGTCTCTGCAAAATCGTAAGATGAAGTATAGGGGCTGACGCCT
GCCCGGTGCTGGAAGGTTAAGAGGATGGGTTAGCTTCGGCGAAGCTCAGAATTGAAGCCC
CAGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAG
TTCCGACCCGCACGAAAGGCGTAACGATTTGGGCACTGTCTCAACGAGAGACTCGGTGAA
ATTTTAGTACCTGTGAAGATGCAGGTTACCCGCGACAGGACGGAAAGACCCCATGGAGCT
TTACTGTAGTTTGATATTGAGTGTTTGTACCACATGTACAGGATAGGTAGGAGCCGATGA
GACCGGAACGCTAGTTTCGGAGGAGGCGCTGGTGGGATACTACCCTTGTGTTATGAACCC
                                                              |
                                                          1978 (3')
```

Table 4: Sequence of distinct region of 23S RNA gene of *Enterococcus faecalis*. Examples of substitutions according to the invention are T1320Y and/or Y1337C (underlined), where Y is a nucleotide with a pyrimidine base.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 7. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1259 and 1978 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1268 and 1940 (Table 5, SEQ ID NO: 8).

SEQ ID NO: 8

```
1268(5')
|
GGAAGTGCATGTCCAAGCAATGAGTCTTGAGTAGAGTTAAATGCTTTACTC
TTTAAGGACAAGTTGTGAYGGGGAGCGAAATAATAGTAGCGAAGTTCCTGATGTCACACT
GCCAAGAAAAGCTTCTAGTGAGAAAACAACTGCCCGTACCGTAAACCGACACAGGTAGTC
GAGGAGAGTATCCTAAGGTGAGCGAGCGAACTCTCGTTAAGGAACTCGGCAAAATGACCC
CGTAACTTCGGGAGAAGGGGTGCTGACTTCGGTCAGCCGCAGTGAATAGGCCCAAGCGAC
TGTTTATCAAAAACACAGGTCTCTGCAAAATCGTAAGATGAAGTATAGGGGCTGACGCCT
GCCCGGTGCTGGAAGGTTAAGAGGATGGGTTAGCTTCGGCGAAGCTCAGAATTGAAGCCC
CAGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAG
TTCCGACCCGCACGAAAGGCGTAACGATTTGGGCACTGTCTCAACGAGAGACTCGGTGAA
ATTTTAGTACCTGTGAAGATGCAGGTTACCCGCGACAGGACGGAAAGACCCCATGGAGCT
TTACTGTAGTTTGATATTGAGTGTTTGTACCACATGTACAGGATAGGTAGGAGCCGATGA
GACCGGAACGCTAGTTTCGG
                    |
                1940(3')
```

Table 5: Sequence of distinct region of 23S RNA gene of *Enterococcus faecalis*. Examples of substitutions according to the invention are T1320Y and/or Y1337C (underlined).

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 1268 and 1940 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 1268 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1940 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting *Enterococcus faecalis* comprise the sequences in Table 6. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 9 (F) and 11 (R); SEQ ID NOs: 9 (F) and 12 (R); SEQ ID NOs: 13 (F) and 14 (R); SEQ ID NOs: 15 (F) and 12 (R); SEQ ID NOs: 15 (F) and 11 (R) as indicated in Table 6, though other primer pair combinations are possible given the similarity in melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 9	GGAAGTGCATGTCCAAGCAAT / 21	62	F	10	278
			F	11	723
			F	12	670
SEQ ID NO: 10	TATTCACTGCGGCTGACCGA / 20	62	R	9	278
SEQ ID NO: 11	GGTGCGGGTTAGAGGGTTC / 19	62	R	9	723
			R	15	479
SEQ ID NO: 12	CCGAAACTAGCGTTCCGGTC / 20	64	R	9	670
			R	15	426
SEQ ID NO: 13	GAAGGATTTGGAAAATTCCGCT / 22	62	F	14	265
SEQ ID NO: 14	CACGCCATCACTCATTAACGA / 21	62	R	13	265
SEQ ID NO: 15	GAAGGGGTGCTGACTTCGG / 19	62	F	12	426
			F	11	479

Table 6: Amplification primer examples for amplifying distinct region of 23S RNA gene of *Enterococcus faecalis*, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO:7, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 1279 and 1998 inclusive (SEQ ID NO: 8), or complement thereof. It is within the scope of the invention, that the probes are capable of binding to the region between 1279 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1998 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting *Enterococcus faecalis* comprise the sequences represented by SEQ ID NOs: 9 to 15, and the complements thereof.

Another aspect of the invention is a method for identifying *Enterococcus faecalis* by amplification of nucleic acid using primers pairs of Table 6, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 9 to 15.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 6.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

3. Enterococcus faecium

According to one aspect of the invention a distinct region of *Enterococcus faecium* 23S RNA gene comprises a nucleotide sequence (SEQ ID NOs: 16 or 17) indicated in Tables 7 and 8. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 16

```
1381(5')
|
GCCGAGAAAAGCTTCTAGTGAGAAAACAGCGGCCCGTACCGCAAACCGACACAGGTAGTC
GAGGAGAGAATCCTAAGGTGAGCGAGAGAACTCTCGTTAAGGAACTCGGCAAAATGACCC
CGTAACTTCGGGAGAAGGGGTGCTGATCATACGATCAGCCGCAGTGAATAGGCCCAAGCG
                                                             |
                                                        1560(3')
```

Table 7: Sequence of distinct region of 23S RNA gene of *Enterococcus faecium*

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 16. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1381 and 1560 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1392 and 1547 (Table 8, SEQ ID NO: 17).

SEQ ID NO: 17

```
1392(5')
|
CTTCTAGTGAGAAAACAGCGGCCCGTACCGCAAACCGACACAGGTAGTC
GAGGAGAGAATCCTAAGGTGAGCGAGAGAACTCTCGTTAAGGAACTCGGCAAAATGACCC
CGTAACTTCGGGAGAAGGGGTGCTGATCATACGATCAGCCGCAGTGA
                                                  |
                                                  1547(3')
```

Table 8: Sequence of distinct region of 23S RNA gene of *Enterococcus faecium*

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 1392 and 1547 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 1392 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1547 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting *Enterococcus faecium* comprise the sequences in Table 9. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 18 and 19; SEQ ID NOs: 19 and 20; SEQ ID NOs: 20 and 21 as indicated in Table 9, though other primer pair combinations are possible given the similarity in melting temperatures.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 18	CTTCTAGTGAGAAAACAGCGG / 21	62	F	19	155
SEQ ID NO: 19	TCACTGCGGCTGATCGTATG / 20	62	R	18	155
				20	269
SEQ ID NO: 20	CTGTCCAAGCAGTAAGTCTGA / 21	62	F	19	269
				21	62
SEQ ID NO: 21	CATCACAGCTTGTCCTTAAGAAA / 23	64	R	20	62

Table 9: Amplification primer examples for amplifying distinct region of 23S RNA gene of *Enterococcus faecium*, length and melting temperature. TYPE is either forward

(F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO:16, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 1392 and 1547 inclusive (SEQ ID NO: 17), or complement thereof. It is within the scope of the invention, that the probes are capable of binding to the region between 1392 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1547 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting *Enterococcus faecium* comprise the sequences represented by any of SEQ ID NOs: 18 to 21, and the complements thereof.

Another aspect of the invention is a method for identifying *Enterococcus faecium* by amplification of nucleic acid using primers pairs of Table 9, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 18 to 21.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 9.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

4. Escherichia coli

According to one aspect of the invention a distinct region of *Escherichia coli* 23S RNA gene comprises a nucleotide sequence (SEQ ID NOs: 22 or 23) indicated in Tables 10 and 11. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 22

```
1201(5')
|
GGGACGGAGAAGGCTATGTTGGCCGGGCGACGGTTGTCCCGGTTTAAGCGTGTAGGCTGG
TTTTCCAGGCAAATCCGGAAAACCAAGGCTGAGGCGTGATGACGAGGCACTACGGTGCTG
AAGCGACAAATGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATCAAATCGTA
CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGGGTG
AAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGGCACGCTGATATGTAGGTGAA
GCGACTTGCTCGTGGAGCTGAAATCAGTCGAAGATACCAGCTGGCTGCAACTGTTTATTA
AAAACACAGCACTGTGCAAACACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGC
CGGAAGGTTAATTGATGGGGTTAGCGGTAACGCGAAGCTCTTGATCGAAGCCCCGGTAAA
CGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGAC
                                                            |
                                                        1740(3')
```

Table 10: Sequence of distinct region of 23S RNA gene of *Escherichia coli*. An example of a deletion according to the invention is deletion of G1294 (underlined).

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 22. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1201 and 1740 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1265 and 1667 (Table 11, SEQ ID NO: 23).

SEQ ID NO: 23

```
1265(5')
|
CCAGGCAAATCCGGAAAACCAAGGCTGAGGCGTGATGACGAGGCACTACGGTGCTG
AAGCGACAAATGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATCAAATCGTA
CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGGGTG
AAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGGCACGCTGATATGTAGGTGAA
GCGACTTGCTCGTGGAGCTGAAATCAGTCGAAGATACCAGCTGGCTGCAACTGTTTATTA
AAAACACAGCACTGTGCAAACACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGC
CGGAAGGTTAATTGATGGGGTTAGCGGTAACGCGAAGCTCTTGATCG
                                                |
                                            1667(3')
```

Table 11: Sequence of distinct region of 23S RNA gene of *Escherichia coli*. An example of a deletion according to the invention is deletion of G1294 (underlined).

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 1265 and 1667 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 1265 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1667 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting *Escherichia coli* comprise the sequences in Table 12. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 24 (F) and

25 (R); SEQ ID NOs: 24 (F) and 26 (R); SEQ ID NOs: 27 (F) and 29 (R); SEQ ID NOs: 28 (F) and 29 (R) as indicated in Table 12, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 24	CCAGGCAAATCCGGAAAACC / 20	62	F	26	78
				25	402
SEQ ID NO: 25	CGATCAAGAGCTTCGCGTTAC / 21	64	R	24	402
SEQ ID NO: 26	TGGAAGCAGGGCATTTGTCG / 20	62	R	24	78
SEQ ID NO: 27	ATCAGTGTGTGTGTTAGTGGAA / 22	62	F	29	97
SEQ ID NO: 28	AAGCGTCTGGAAAGGCGCG / 19	62	F	29	77
SEQ ID NO: 29	CCTACTCATCGAGCTCACAAT / 21	62	R	27	97
				28	77

Table 12: Amplification primer examples for amplifying distinct region of 23S RNA gene of *Escherichia coli*, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO:22, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 1265 and 1667 inclusive (SEQ ID NO: 23), or complement thereof. It is within the scope of the invention, that the probes are capable of binding to the region between 1265 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1667 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting *Escherichia coli* comprise the sequences represented by SEQ ID NOs: 24 to 29, and the complements thereof.

Another aspect of the invention is a method for identifying *Escherichia coli* by amplification of nucleic acid using primers pairs of Table 12, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 24 to 29.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 12.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

5. Klebsiella pneumoniae

According to one aspect of the invention a distinct region of *Klebsiella pneumoniae* 23S RNA gene comprises a nucleotide sequence (SEQ ID NOs: 30 or 31) indicated in Tables 13 and 14. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 30
1251(5') | CGGTTGTCCCGGTTTAAGCATGTAGGCTGGTTRTCCAGGCAAATCCGGAT AATCAAGGCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAA TGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATYAAATCGTA CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAG AACTCGGGTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGG CACGCTGGTGTGTAGGTGAAGYCCCTGCGGRTGGAGCTGAGACCAGTCGA AGATACCAGCTGGCTGCAACTGTTTATTAAAAACACAGCACTGTGCAAAC | 1600(3')

Table 13: Sequence of distinct region of 23S RNA gene of *Klebsiella pneumoniae,* wherein R (underlined) is G or A and Y (underlined) is C or T. Example of a substitution according to the invention is C1354T (underlined).

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 30. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1251 and 1600 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1281and 1560 (Table 14, SEQ ID NO: 31).

SEQ ID NO: 31
1281(5') | TTRTCCAGGCAAATCCGGAT AATCAAGGCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAA TGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATYAAATCGTA CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAG AACTCGGGTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGG CACGCTGGTGTGTAGGTGAAGYCCCTGCGGRTGGAGCTGAGACCAGTCGA

```
AGATACCAGC
          |
          1560(3')
```

Table 14: Sequence of distinct region of 23S RNA gene of *Klebsiella pneumoniae,* wherein R (underlined) is any purine (G or A) and Y (underlined) is any pyrimidine (C or T). Example of a substitution according to the invention is C1354T (underlined).

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 1281 and 1560 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 1281 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1560 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting *Klebsiella pneumoniae* comprise the sequences in Table 15. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 32 (F) and 34 (R); SEQ ID NOs: 32 (F) and 33 (R); SEQ ID NOs: 35 (F) and 36 (R); SEQ ID NOs: 37 (F) and 33 (R) as indicated in Table 12, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 32	TTRTCCAGGCAAATCCGGAT / 20	60	F	34	245
				33	279
SEQ ID NO: 33	GCTGGTATCTTCGACTGGTC / 20	62	R	32	279
				37	68
SEQ ID NO: 34	AGGGRCTTCACCTACACAC / 19	60	R	32	245
SEQ ID NO: 35	GGGTGATAGTCCCGTACACC / 20	64	F	36	239
SEQ ID NO: 36	AGGTACGCAGTCACACCCG / 19	62	R	35	239
SEQ ID NO: 37	GGGAGAAGGCACGCTGGTG / 19	64	F	33	68

Table 15: Amplification primer examples for amplifying distinct region of 23S RNA gene of *Klebsiella pneumoniae*, length and temperature. Note R (underlined) is any purine (G or A)

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO:30, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 1281 and 1560 inclusive (SEQ ID NO: 31), or

complement thereof. It is within the scope of the invention, that the probes are capable of binding to the region between 1281 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1560 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting *Klebsiella pneumoniae* comprise the sequences represented by any of SEQ ID NOs: 32 to 37, and the complements thereof.

Another aspect of the invention is a method for identifying *Klebsiella pneumoniae* by amplification of nucleic acid using primers pairs of Table 15, in the combination indicated or other suitable combination of forward and reverse primers.. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 32 to 37.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 15.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

6. Pseudomonas aeruginosa

According to one aspect of the invention a distinct region of *Pseudomonas aeruginosa* 23S RNA gene comprises a nucleotide sequence (SEQ ID NOs: 38 or 39) indicated in Tables 16 and 17. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 38

51(5')
|
TCATTGATTTTAGCGGAACGCTCTGGAAAGTGCGGCCATAGTGGGTGATA
GCCCCGTACGCGAAAGGATCTTTGAAGTGAAATCGAGTAGGACGGAGCAC
GAGAAACTTTGTCTGAACATGGGGGGACCATCCTCCAAGGCTAAATACTA
CTGACTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGCGAAAAGAACC
CCGGAGAGGGGAGTGAAATAGAACCTGAAACCGTATGCGTACAAGCAGTG
GGAGCCTACTTGTTAGGTGACTGCGTACCTTTTGTATAATGGGTCAGCGA
CTTATATTCAGTGGCAAGCTTAATCGTATAGGGTAGGCGTAGCGAAAGCG
AGTCTTAATAGGGCGTTTAGTCGCTGGGTATAGACCCGAAACCGGGCGAT
CTATCCATGAGCAGGTTGAAGGTTAGGTAACACTGACTGGAGGACCGAAC
CCACTCCCGTTGAAAAGGTAGGGGATGACTTGTGGATCGGAGTGAAAGGC

```
TAATCAAGCTCGGAGATAGCTGGTTCTCCTCGAAAGCTATTTAGGTAGCG
CCTCATGTATCACTCTGGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCAT
CCCGACTTACCAAACCGATGCAAACTCCGAATACCCAGAAGTGCCGAGCA
TGGGAGACACACGGCGGGTGCTAACGTCCGTCGTGAAAAGGGAAACAACC
                                                    |
                                                    750(3')
```

Table 16: Sequence of distinct region of 23S RNA gene of *Pseudomonas aeruginosa.* Example of a substitution according to the invention is T374C (underlined).

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 38. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 51 and 750 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 104 and 704 (Table 17, SEQ ID NO: 39).

```
SEQ ID NO: 39
104(5')
|
CCGTACGCGAAAGGATCTTTGAAGTGAAATCGAGTAGGACGGAGCAC
GAGAAACTTTGTCTGAACATGGGGGGACCATCCTCCAAGGCTAAATACTA
CTGACTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGCGAAAAGAACC
CCGGAGAGGGGAGTGAAATAGAACCTGAAACCGTATGCGTACAAGCAGTG
GGAGCCTACTTGTTAGGTGACTGCGTACCTTTTGTATAATGGGTCAGCGA
CTTATATTCAGTGGCAAGCTTAATCGTATAGGGTAGGCGTAGCGAAAGCG
AGTCTTAATAGGGCGTTTAGTCGCTGGGTATAGACCCGAAACCGGGCGAT
CTATCCATGAGCAGGTTGAAGGTTAGGTAACACTGACTGGAGGACCGAAC
CCACTCCCGTTGAAAAGGTAGGGGATGACTTGTGGATCGGAGTGAAAGGC
TAATCAAGCTCGGAGATAGCTGGTTCTCCTCGAAAGCTATTTAGGTAGCG
CCTCATGTATCACTCTGGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCAT
CCCGACTTACCAAACCGATGCAAACTCCGAATACCCAGAAGTGCCGAGCA
TGGG
   |
   704(3')
```

Table 17: Sequence of distinct region of 23S RNA gene of *Pseudomonas aeruginosa.* Example of a substitution according to the invention is T374C (underlined).

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 104 and 704 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 104 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 704 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting *Pseudomonas aeruginosa* comprise the sequences in Table 18. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 40 (F) and 41 (R); SEQ ID NOs: 40 (F) and 42 (R) as indicated in Table 18, though other combinations are

possible given the similarity in melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 40	CCGTACGCGAAAGGATCTTTG / 21	64	F	41	529
				42	600
SEQ ID NO: 41	ACAGTGCTCTACCCCCCAG / 19	62	R	40	529
SEQ ID NO: 42	CCCATGCTCGGCACTTCTG / 19	62	R	40	600

Table 18: Amplification primer examples for amplifying distinct region of 23S RNA gene of *Pseudomonas aeruginosa*, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO:38, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 104 and 704 inclusive (SEQ ID NO: 39), or complement thereof. It is within the scope of the invention, that the probes are capable of binding to the region between 104 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 704 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting *Pseudomonas aeruginosa* comprise the sequences represented by any of SEQ ID NOs: 40 to 42, and the complements thereof.

Another aspect of the invention is a method for identifying *Pseudomonas aeruginosa* by amplification of nucleic acid using primers pairs of Table 18, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a sequence corresponding to any of SEQ ID NOs: 40 to 42.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 18.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

7. Staphylococcus aureus

According to one aspect of the invention a distinct region of *Staphylococcus aureus* 23S RNA gene comprises a nucleotide sequence (SEQ ID NO: 43 or 44) indicated in Tables 19 and 20. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 43

```
1021(5')
|
TAGGAGAGCGTTCTAAGGGCGTTGAAGCATGATCGTAAGGACATGTGGAGCGCTTAGAAG
TGAGAATGCCGGTGTGAGTAGCGAAAGACGGGTGAGAATCCCGTCCACCGATTGACTAAG
GTTTCCAGAGGAAGGCTCGTCCGCTCTGGGTTAGTCGGGTCCTAAGCTGAGGCCGACAGG
CGTAGGCGATGGATAACAGGTTGATATTCCTGTACCACCTATAATCGTTTTAATCGATGG
GGGGACGCAGTAGGATAGGCGAAGCGTGCGATTGGATTGCACGTCTAAGCAGTAAGGCTG
                                                          |
                                                          1320(3')
```

Table 19: Sequence of distinct region of 23S RNA gene of *Staphylococcus aureus*

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 43. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1021 and 1320 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1037 and 1263 (Table 20, SEQ ID NO: 44).

SEQ ID NO: 44

```
1037(5')
|
GGGCGTTGAAGCATGATCGTAAGGACATGTGGAGCGCTTAGAAG
TGAGAATGCCGGTGTGAGTAGCGAAAGACGGGTGAGAATCCCGTCCACCGATTGACTAAG
GTTTCCAGAGGAAGGCTCGTCCGCTCTGGGTTAGTCGGGTCCTAAGCTGAGGCCGACAGG
CGTAGGCGATGGATAACAGGTTGATATTCCTGTACCACCTATAATCGTTTTAATCGATGG
GGG
  |
  1263(3')
```

Table 20: Sequence of distinct region of 23S RNA gene of *Staphylococcus aureus*

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 1037 and 1263 inclusive. It is within the scope of the invention, that the primers are capable of amplifying

the region between residues 1037 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1263 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting *Staphylococcus aureus* comprise the sequences in Table 21. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 45 (F) and 46 (R); SEQ ID NOs: 48 (F) and 47 (R); SEQ ID NOs: 48 (F) and 49 (R); SEQ ID NOs: 48 (F) and 51 (R); SEQ ID NOs: 50 (F) and 51 (R) as indicated in Table 21, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 45	AAGCAGTAAATGTGGAGCCGT / 21	62	F	46	631
SEQ ID NO: 46	TAAGCGCTCCACATGTCCTTA / 21	62	R	45	631
SEQ ID NO: 47	GCTTAGACGTGCAATCCAATC / 21	62	R	48	273
SEQ ID NO: 48	GGGCGTTGAAGCATGATCGT / 20	62	F	47	273
				49	226
				51	409
SEQ ID NO: 49	CCCCCATCGATTAAAACGATTA / 22	62	R	48	226
SEQ ID NO: 50	TAGGATAGGCGAAGCGTGCG / 20	64	F	51	174
SEQ ID NO: 51	TGCGGTACGGGCACCTATTT / 20	62	R	50	174

Table 21: Amplification primer examples for amplifying distinct region of 23S RNA gene of *Staphylococcus aureus*, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO:43, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 1037 and 1263 inclusive (SEQ ID NO: 44), or complement thereof. It is within the scope of the invention, that the probes are capable of binding to the region between 1037 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1263 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting *Staphylococcus aureus* comprise the sequences represented by any of SEQ ID NOs: 45 to 51, and the complements thereof.

Another aspect of the invention is a method for identifying *Staphylococcus aureus* by amplification of nucleic acid using primers pairs of Table 21, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of

the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 45 to 51.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 21.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

8. Staphylococcus epidermidis

According to one aspect of the invention a distinct region of *Staphylococcus epidermidis* 23S RNA gene comprises a nucleotide sequence (SEQ ID NOs: 52 or 53) indicated in Tables 22 and 23. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 52

```
501(5')
|
CAAACTGCCCGCCTGACACTGTCTCCCACCACGATAAGTGGTGCGGGTTA
GAAAGCCAACACAGCTAGGGTAGTATCCCACCAACGCCTCCACGTAAGCT
AGCGCTCACGTTTCAAAGGCTCCTACCTATCCTGTACAAGCTGTGCCGAA
TTTCAATATCAGGCTACAGTAAAGCTCCACGGGGTCTTTCCGTCCTGTCG
CGGGTAACCTGCATCTTCACAGGTACTATGATTTCACCGAGTCTCTCGTT
GAGACAGTGCCCAAATCGTTACGCCTTTCGTGCGGGTCGGAACTTACCCG
ACAAGGAATTTCGCTACCTTAGGACCGTTATAGTTACGGCCGCCGTTTAC
TGGGGCTTTGATTCGTAGCTTCGCAGAAGCTAACCACTCCTCTTAACCTT
CCAGCACCGGGCAGGCGTCAGCCCCTATACATCACCTTACGGTTTAGCAG
AGACCTGTGTTTTTGATAAACAGTCGCTTGGGCCTATTCACTGCGGCTCT
TCTGGGCGTGAACCCTAAAGAGCACCCCTTCTCCCGAAGTTACGGGGTCA
                                                    |
                                                    1050(3')
```

Table 22: Sequence of distinct region of 23S RNA gene of *Staphylococcus epidermidis*. Example of a substitution according to the invention is T859C (underlined).

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 52 Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 501

and 1050 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1037 and 1263 (Table 23, SEQ ID NO: 53).

SEQ ID NO: 53
1037(5') | GCTAGGGTAGTATCCCACCAACGCCTCCACGTAAGCT AGCGCTCACGTTTCAAAGGCTCCTACCTATCCTGTACAAGCTGTGCCGAA TTTCAATATCAGGCTACAGTAAAGCTCCACGGGGTCTTTCCGTCCTGTCG CGGGTAACCTGCATCTTCACAGGTACTATGATTTCACCGAGTCTCTCGTT GAGACAGTGCCCAAATCGTTACGCCTTTCGTGCGGGTCGGAACTTACCCG ACAAGGAATTTCGCTACCTTAGGACCGTTATAGTTACGGCCGCCGTTTAC TGGGGCTTTGATTCGTAGCTTCGCAGAAGCTAACCACTCCTCTTAACCTT CCAGCACCGGGCAGGCGTCAGCCCCTATACATCACCTTACGGTTTAGCAG AGACCTGTGTTTTTGATAAACAGTCGCTTGGGCCTATTCACTGCGGCTCT TCTGGGCGTGAACCCTAAAGAGCACCCCT | 1263(3')

Table 23: Sequence of distinct region of 23S RNA gene of *Staphylococcus epidermidis*. Example of a substitution according to the invention is T859C (underlined).

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 1037 and 1263 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 1037 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1263 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting *Staphylococcus epidermidis* comprise the sequences in Table 24. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 54 (F) and 55 (R); SEQ ID NOs: 54 (F) and 56 (R); SEQ ID NOs: 54 (F) and 57 (R); SEQ ID NOs: 58 (F) and 57 (R); SEQ ID NOs: 58 (F) and 59 (R); SEQ ID NOs: 58 (F) and 60 (R); SEQ ID NOs: 58 (F) and 61 (R); SEQ ID NOs: 58 (F) and 62 (R); SEQ ID NOs: 63 (F) and 59 (R); SEQ ID NOs: 63 (F) and 60 (R); SEQ ID NOs: 63 (F) and 61 (R) as indicated in Table 24, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 54	GCTAGGGTAGTATCCCACCAA /21	64	F	55	465
				56	596
				57	715
SEQ ID NO: 55	AGGGGTGCTCTTTAGGGTTC / 20	62	R	54	465
SEQ ID NO: 56	AGAAAAGCCTCTAGATAGATAAC / 23	62	R	54	596

SEQ ID NO: 57	GCTGTTGGAGTGCACGTCC / 19	62	R	54	715
				58	155
SEQ ID NO: 58	CGGTACGGGCACCTGTTATC / 20	64	F	57	155
				59	170
				60	221
				61	405
				62	117
SEQ ID NO: 59	GGATAGGCGAAGCGTGCTG / 19	62	R	58	170
				63	70
SEQ ID NO: 60	TGATATTCCTGTACCACCTAGT / 22	62	R	58	221
				63	121
SEQ ID NO: 61	GGYGTCGAAGCATGATCGC / 19	62	R	58	405
				63	305
SEQ ID NO: 62	TAGGCAAATCCGGCACTCATA / 21	62	R	58	117
SEQ ID NO: 63	GAGTGCCGGATTTGCCTAAC / 20	62	F	59	70
				60	121
				61	305

Table 24: Amplification primer examples for amplifying distinct region of 23S RNA gene of *Staphylococcus epidermidis*, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO:52, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 1037 and 1263 inclusive (SEQ ID NO: 53), or complement thereof. It is within the scope of the invention, that the probes are capable of binding to the region between 1037 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 1263 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting *Staphylococcus epidermidis* comprise the sequences represented by any of SEQ ID NOs: 54 to 63, and the complements thereof.

Another aspect of the invention is a method for identifying *Staphylococcus epidermidis* by amplification of nucleic acid using primers pairs of Table 24, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the

invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 54 to 63.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 24.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

9. *Candida albicans*

According to one aspect of the invention a distinct region of *Candida albicans* 23S RNA gene comprises a nucleotide sequence (SEQ ID NOs: 64 or 65) indicated in Tables 25 and 26. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 64

181 (5')
|
TCCTTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGACCCGGGTCTG
TGTAAAGTTCCTTYGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAAT
TCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGA
TGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTT
GAGATCAGACTTGGTATTTTGCATGYTGCTCTCTCGGGGGCGGCCGCTGCGGTTTACCGG
GCCAGCATCGGTTTGGAGCGGCAGGATAATGGCGGAGGAATGTGGCACGGCTTCTGCTGT
GTGTTATAGCCTCTGACGATACTGCCAGCCTAGACCGAGGACTGCGGTTTTTXXACCTAG
GATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGT
CTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGAAGGTGGGGGC
CCATTAGGGTGCACCATCGACCGATCCTGATGTGTTCGGATGGATTTGAGTAAGAGCATA
|

778 (3')

Table 25: Sequence of distinct region of 23S RNA gene of *Candida albicans.* Y is a nucleotide with a pyrimidine base. The nucleotides "XX" may both be absent, may be "TT" or may be a single nucleotide "A".

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 64. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 181 and 778 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 214 and 739 (Table 26, SEQ ID NO: 65).

SEQ ID NO: 65

214 (5')
|
CCCGTGCGATGAGATGACCCGGGTCTG
TGTAAAGTTCCTTYGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAAT
TCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGA
TGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTT
GAGATCAGACTTGGTATTTTGCATGYTGCTCTCTCGGGGGCGGCCGCTGCGGTTTACCGG
GCCAGCATCGGTTTGGAGCGGCAGGATAATGGCGGAGGAATGTGGCACGGCTTCTGCTGT
GTGTTATAGCCTCTGACGATACTGCCAGCCTAGACCGAGGACTGCGGTTTTTXXACCTAG
GATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGT
CTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGAAGGTGGGGGC
CCATTAGGGTGCACCATCGAC
|
739 (3')

Table 26: Sequence of distinct region of 23S RNA gene of *Candida albicans*

Y is a nucleotide with a pyrimidine base. The nucleotides "XX" may both be absent, may be "TT" or may be a single nucleotide "A".

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 214 and 739 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 214 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 739 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive.

According to one aspect of the invention, amplification primers suitable for detecting *Candida albicans* comprise the sequences in Table 27. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 66 and 67; SEQ ID NOs: 68 and 69; SEQ ID NOs: 70 and 71 as indicated in Table 27, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 66	CCCGTGCGATGAGATGACC / 19	62	F	67	526
SEQ ID NO: 67	GTCGATGGTGCACCCTAATG / 20	62	R	66	526
SEQ ID NO: 68	AGACGCGGCGGTGACTGTT / 19	62	F	69	117
SEQ ID NO: 69	CTAAGTTGATCGTTAAACGTGC / 20	62	R	68	117
SEQ ID NO: 70	CGGATCGCCCAGAGGGCT / 18	62	R	71	506
SEQ ID NO: 71	GGCCGTCCGGGGCACGT / 17	62	F	70	506

Table 27 Amplification primer examples for amplifying distinct region of 23S RNA gene of *Candida albicans*, length and melting temperature. TYPE is either forward (F)

or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 64, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 214 and 739 inclusive (SEQ ID NO: 65), or complement thereof. It is within the scope of the invention, that the probes are capable of binding to the region between 214 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 739 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting *Candida albicans* comprise the sequences represented by any of SEQ ID NOs: 66 to 71, and the complements thereof.

Another aspect of the invention is a method for identifying *Candida albicans* by amplification of nucleic acid using primers pairs of Table 27, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 66 to 71.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 27.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

10. bla_{ges-2} (beta-lactam resistance gene)

According to one aspect of the invention a distinct region of a bla_{ges-2} gene comprises a nucleotide sequence (SEQ ID NOs: 72 or 73) indicated in Tables 28 and 29. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 72
1(5') | GCAATGTGCTCAACGTTCAAGTTTCCGCTAGCCGCGCTGGTCTTTGAAAG

```
AATTGACTCAGGCACCGAGCGGGGGGATCGAAAACTTTCATATGGGCCGG
ACATGATCGTCRAATGGTCTCCTGCCACGGAGCGGTTTCTAGCATCGGGA
CACATGACGGTTCTCGAGGCAGCGCAAGCTGCGGTGCAGCTTAGCGACAA
TGGGGCTACTAACCTCTTACTGAGAGAAATTGGCGGACCTGCTGCAATGA
CGCAGTATTTTCGTAAAATTGGCGACTCTGTGAGTCGGCTAGACCGGAAA
GAGCCGGAGATGRGCGACAACACACCTGGCGACCTCAGAGATACAACTAC
GCCTATTGCTATGGCACGTACTGTGGCTAAAGTCCTCTATGGCGGCGCAC
TGACGTCCACCTCGACCCACACCATTGAGAGGTGGCTGATCGGAAACCAA
ACGGGAGACGCGACACTACGAGCGGGTTTTCCTAAAGATTGGGTTGTTGG
AGAGAAAACTGGTACCTGCGCCAACGGGGGCCGGAACGACATTGGTTTTT
TTAAAGCCCAGGAGAGAGATTACGCTGTAGCGGTGTATACAACGGCCCCG
AAACTATCGGCCGTAGAACGTGACGAATTAGTTGCCTCTGTCGGTCAAGT
TAT
  |
  653(3')
```

Table 28: Sequence of distinct region of *bla*$_{ges-2}$ gene. R (underlined) is any purine (G or A). Examples of deletions according to the invention include deleting of any of R112 and/or R313.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 72. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1 and 653 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 140 and 482 (Table 26, SEQ ID NO: 73).

```
SEQ ID NO: 73
140(5')
|
TAGCATCGGGACACATGACGGTTCTCGAGGCAGCGCAAGCTGCGGTGCAGCTTAGCGACAA
TGGGGCTACTAACCTCTTACTGAGAGAAATTGGCGGACCTGCTGCAATGA
CGCAGTATTTTCGTAAAATTGGCGACTCTGTGAGTCGGCTAGACCGGAAA
GAGCCGGAGATGRGCGACAACACACCTGGCGACCTCAGAGATACAACTAC
GCCTATTGCTATGGCACGTACTGTGGCTAAAGTCCTCTATGGCGGCGCAC
TGACGTCCACCTCGACCCACACCATTGAGAGGTGGCTGATCGGAAACCAA
ACGGGAGACGCGACACTACGAGCGGGTTTTCC
                                  |
                                  482(3')
```

Table 29: Sequence of distinct region of the *bla*$_{ges-2}$ gene. Note R (underlined) is any purine (G or A). Examples of deletions according to the invention include the deleting any of R112 and/or R313.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 140 and 482 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 140 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 482 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification

primers suitable for detecting the *bla*$_{ges-2}$ gene comprise the sequences in Table 30. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 74 (F) and 75 (R); SEQ ID NOs: 76 (F) and 77 (R) as indicated in Table 30, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 74	CCTGCTGCAATGACGCAGTAT / 21	64	F	75	338
SEQ ID NO: 75	GCGTAATCTCTCTCCTGGGC / 20	64	R	74	338
SEQ ID NO: 76	TAGCATCGGGACACATGACG / 20	62	F	77	343
SEQ ID NO: 77	GGAAAACCCGCTCGTAGTGT / 20	62	R	76	343

Table 30: Amplification primer examples for amplifying a distinct region of the *bla*$_{ges-2}$ gene, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO:72, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 140 and 482 inclusive (SEQ ID NO: 73), or complement thereof. It is within the scope of the invention that the probes are capable of binding to the region between 140 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 482 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting the *bla*$_{ges-2}$ gene comprise the sequences represented by any of SEQ ID NOs: 74 to 77, and the complements thereof.

Another aspect of the invention is a method for identifying the *bla*$_{ges-2}$ gene by amplification of nucleic acid using primers pairs of Table 30, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 74 to 77.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 30.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions,

probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

11. bla_{shv} (beta-lactam resistance gene)

According to one aspect of the invention a distinct region of a *bla_{shv} gene* comprises a nucleotide sequence (SEQ ID NO: 78 or 79) indicated in Tables 31 and 32. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 78
1(5') | GTAGGCATGATAGAAATGGATCTGGCCAGCGGCCGCACGCTGACCGCCTG GCGCGCCGATGAACGCTTTCCCATGATGAGCACCTTTAAAGTAGTGCTCT GCGGCGCAGTGCTGGCGCGGGTGGATGCCGGTGACGAACAGCTGGAGCGA AAGATCCACTATCGCCAGCAGGATCTGGTGGACTACTCGCCGGTCAGCGA AAAACACCTTGCCGACGGCATGACGGTCGGCGAACTCTGYGCCGCCGCCA TTACCATGAGCGATAACAGCGCCGCCAATCTGCTGCTGGCCACCGTCGGC GGCCCCGCAGGATTGACTGCCTTTTTGCGCCAGATCGGCGACAACGTCAC CCGCCTTGACCGCTGGGAAACGGAACTGAATGAGGCGCTTCCCGGCGACG CCCGCGACACCACTACCCCGGCCAGCATGGCCGCGACCCTGCGCAAGCTG CTGACCAGCCAGCGTCTGAGCGCCCGTTCGCAACGGCAGCTGCTGCAGTG GATGGTGGACGATCGGGTCGCCGGACCGTTGATCCGCTCCGTGCTGCCGG CGGGCTGGTTTATCGCCGATAAGACCGGAGCTRGCGARCGGGGTGCGCGC GGGATTGTCGCCCTGCTTGGCCCGAATAACAAAGCAGAGCGCATTGTGGT GATTTATCTGCGGGATACSCCGGCGAGCATGGCCGAGCGAAAT | 693(3')

Table 31: Sequence of distinct region of *bla_{shv}* gene. Note Y (underlined) is any pyrimidine (C or T), R (underlined) is any purine (A or G), S is a (C or G). Examples of deletions according to the invention includes the deletion of one or more of Y240, R583, R588 and S669.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 78. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1 and 693 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 149 and 350 (Table 32, SEQ ID NO: 79).

SEQ ID NO: 79
149(5') | GAAAGATCCACTATCGCCAGCAGGATCTGGTGGACTACTCGCCGGTCAGCGA

```
AAAACACCTTGCCGACGGCATGACGGTCGGCGAACTCTGYGCCGCCGCCA
TTACCATGAGCGATAACAGCGCCGCCAATCTGCTGCTGGCCACCGTCGGC
GGCCCCGCAGGATTGACTGCCTTTTTGCGCCAGATCGGCGACAACGTCAC
                                                    |
                                                    350(3')
```

Table 32: Sequence of distinct region of the *bla*$_{shv}$ gene. Note Y (underlined) is any pyrimidine (C or T). Note Y (underlined) is any pyrimidine (C or T), R (underlined) is any purine (A or G), S is a (C or G). Examples of deletions according to the invention includes the deletion of one or more of Y240, R583, R588 and S669.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 149 and 350 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 149 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 350 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting the *bla*$_{shv}$ *gene* comprise the sequences in Table 33. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 80 and 81; SEQ ID NOs: 82 and 83 as indicated in Table 33, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 80	GAAAGATCCACTATCGCCAGC / 21	64	F	81	202
SEQ ID NO: 81	GTGACGTTGTCGCCGATCT / 19	60	R	80	202
SEQ ID NO: 82	GCTGGGAAACGGAACTGAAT / 20	60	F	83	203
SEQ ID NO: 83	GATAAACCAGCCCGCCGG / 18	60	R	82	203

Table 33: Amplification primer examples for amplifying a distinct region of the *bla*$_{shv}$ gene, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 78, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 149 and 350 inclusive (SEQ ID NO: 79), or complement thereof. It is within the scope of the invention that the probes are capable of binding to the region between residues 149 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 350 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention,

probes suitable for detecting the *bla$_{shv}$ gene* comprise the sequences represented by any of SEQ ID NOs: 80 to 83, and the complements thereof.

Another aspect of the invention is a method for identifying the *bla$_{shv}$* gene by amplification of nucleic acid using primers pairs of Table 33, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 80 to 83.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 33.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

12. mecA (methicillin resistance gene)

According to one aspect of the invention a distinct region of a *mecA gene* comprises a nucleotide sequence (SEQ ID NOs: 84 or 85) indicated in Tables 34 and 35. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 84

```
1(5')
|
AAGAGTATTTATAACAACATGAAAAATGATTATGGCTCAGGTACTGCTAT
CCACCCTCAAACAGGTGAATTATTAGCACTTGTAAGCACACCTTCATATG
ACGTCTATCCATTTATGTATGGCATGAGTAACGAAGAATATAATAAATTA
ACCGAAGATAAAAAAGAACCTCTGCTCAACAAGTTCCAGATTACAACTTC
ACCAGGTTCAACTCAAAAAATATTAACAGCAATGATTGGGTTAAATAACA
AAACATTAGACGATAAAACAAGTTATAAAATCGATGGTAAAGGTTGGCAA
AAAGATAAATCTTGGGGTGGTTACAACGTTACAAGATATGAAGTGGTAAA
TGGTAATATCGACTTAAAACAAGCAATAGAATCATCAGATAACATTTTCT
TTGCTAGAGTAGCACTCGAATTAGGCAGTAAGAAATTTGAAAAAGGCATG
AAAAAACTAGGTGTTGGTGAAGATATACCAAGTGATTATCCATTTTATAA
TGCTCAAATTTCAAACAAAAATTTAGATAATGAAATATTATTAGCTGATT
CAGGTTACGGACAAGGTGAAATACTGATTAACCCAGTACAGATCCTTTCA
ATCTATAGCGC
          |
          611(3')
```

Table 34: Sequence of distinct region of *mecA* gene.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 84. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1 and 611 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 184 and 484 (Table 35, SEQ ID NO: 85).

SEQ ID NO: 85

```
184(5')
|
TTCCAGATTACAACTTCACCAGGTTCAACTCAAAAAATATTAACAGCAATGATTGGGTTAAATAACA
AAACATTAGACGATAAAACAAGTTATAAAATCGATGGTAAAGGTTGGCAA
AAAGATAAATCTTGGGGTGGTTACAACGTTACAAGATATGAAGTGGTAAA
TGGTAATATCGACTTAAAACAAGCAATAGAATCATCAGATAACATTTTCT
TTGCTAGAGTAGCACTCGAATTAGGCAGTAAGAAATTTGAAAAAGGCATG
AAAAAACTAGGTGTTGGTGAAGATATACCAAGTG
                                    |
                                    484(3')
```

Table 35: Sequence of distinct region of the *mecA* gene.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 184 and 484 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 184 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 484 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting the *mecA gene* comprise the sequences in Table 36. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 86 (F) and 87 (R); SEQ ID NOs: 88 (F) and 89 (R) as indicated in Table 36, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 86	TGGCTCAGGTACTGCTATCCA / 21	64	F	87	297
SEQ ID NO: 87	ACGTTGTAACCACCCCAAGA / 20	60	R	86	297
SEQ ID NO: 88	TTCCAGATTACAACTTCACCAG / 22	62	F	89	301
SEQ ID NO: 89	CACTTGGTATATCTTCACCAACA / 23	64	R	88	301

Table 36: Amplification primer examples for amplifying a distinct region of the *mecA* gene, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 84, or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 149 and 349 inclusive (SEQ ID NO: 85), or complement thereof. It is within the scope of the invention that the probes are capable of binding to the region between residues 184 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 484 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting the *mecA* gene comprise the sequences represented by any of SEQ ID NOs: 86 to 89, and the complements thereof.

Another aspect of the invention is a method for identifying the *mecA* gene by amplification of nucleic acid using primers pairs of Table 36, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 86 to 89.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 36.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

13. spA (Staphylococcus-aureus protein A)

According to one aspect of the invention a distinct region of a *spA gene* comprises a nucleotide sequence (SEQ ID NOs: 90 or 91) indicated in Tables 37 and 38. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 90
1(5') | AAAACATTTATTCAATTCGTAAACTAGGTGTAGGTATTGCATCTGTAACT TTAGGTACATTACTTATATCTGGTGGCGTAACACCTGCTGCAAATGCTGC GCAACACGATGAAGCTCAACAAAATGCTTTTTATCAAGTSTTAAATATGC CTAACTTAAAYGCTGATCAACGYAATGGTTTTATCCAAAGCCTTAAAGAT GATCCAAGCCAAAGTGCTAACGTTTTAGGTGAAGCTCAAAAACTTAATGA

```
CTCTCAAGCTCCAAAAGCTGATGCGCAACAAAATAASTTCAACAAAGATC
AACAAAGCGCCTTCTATGAAATCTTGAACATGCCTAACTTAAACGAAGHG
CAACGYAAYGGYTTCATTCAAAGTCTTAAAGACGACYCAAGCCAAAGCAC
TAACGTTTTAGGTGAAGCTAAAAAATTAAACGAATCTCAAGCACCGAAAG
CTGAYAACAATTTCAACAAAGAACAACAAAATGCTTTCTATGAAATCTTGA
                                                    |
                                                    501(3')
```

Table 37: Sequence of distinct region of *spA* gene. Note S is (C or G), Y is pyrimidine (C or T), H is (A, C or T). Example of deletions according to the invention include the deletion of S140, Y161, Y173, S287, H349, Y356, Y359, Y362, Y387 and/or Y455.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 90 Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1 and 501 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 292 and 409 (Table 38, SEQ ID NO: 91).

SEQ ID NO: 91

```
292(5')
|
ACAAAGATCAACAAAGCGCCTTCTATGAAATCTTGAACATGCCTAACTTA
AACGAAGHGCAACGYAAYGGYTTCATTCAAAGTCTTAAAGACGACYCAAG
CCAAAGCACTAACGTTTT
                  |
                  409(3')
```

Table 38: Sequence of distinct region of the *spA* gene. Note Y is pyrimidine (C or T), H is (A, C or T). Example of deletions according to the invention include the deletion of H349, Y356, Y359, Y362 and/or Y387.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 292 and 409 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 292 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 409 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting the *spA gene* comprise the sequences in Table 39. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 92 (F) and 93 (R); SEQ ID NOs: 94 (F) and 95 (R) as indicated in Table 39, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 92	ACAAAGATCAACAAAGCGCCT / 21	60	F	93	118
SEQ ID NO: 93	AAAACGTTAGTGCTTTGGCTTG / 22	62	R	92	118
SEQ ID NO: 94	TTGAACATGCCTAACTTAAACGAA / 24	64	F	95	128
SEQ ID NO: 95	GCTTTCGGTGCTTGAGATTC / 20	60	R	94	128

Table 39: Amplification primer examples for amplifying a distinct region of the *spA* gene, length and melting temperature. . TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 90 or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 292 and 409 inclusive (SEQ ID NO: 46), or complement thereof. It is within the scope of the invention that the probes are capable of binding to the region between residues 292 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 409 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting the *spA* gene comprise the sequences represented by any of SEQ ID NOs: 92 to 95, and the complements thereof.

Another aspect of the invention is a method for identifying the *spA* gene by amplification of nucleic acid using primers pairs of Table 39, in the combinations indicated or other suitable combination of forward and reverse primers.. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 92 to 95.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 39.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

14. VanA (vancomycin resistance gene A)

According to one aspect of the invention a distinct region of a *VanA gene* comprises a nucleotide sequence (SEQ ID NOs: 96 or 97) indicated in Tables 40 and 41. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 96

```
1(5')
|
AAAGTTGCAATACTGTTTGGGGGTTGCTCAGAGGAGCATGACGTATCGGT
AAAATCTGCAATAGAGATAGCCGCTAACATTAATAAAGAAAAATACGAGC
CGTTATACATTGGAATTACGAAATCTGGTGTATGGAAAATGTGCGAAAAA
CCTTGCGCGGAATGGGAAAACGACAATTGCTATTCAGCTGTACTCTCGCC
GGATAAAAAAATGCACGGATTACTTGTTAAAAAGAACCATGAATATGAAA
TCAACCATGTTGATGTAGCATTTTCAGCTTTGCATGGCAAGTCAGGTGAA
GATGGATCCATACAAGGTCTGTTTGAATTGTCCGGTATCCCTTTTGTAGG
CTGCGATATTCAAAGCTCAGCAATTTGTATGGACAAATCGTTGACATACA
TCGTTGCGAAAAATGCTGGGATAGCTACTCCCGCCTTTTGGGTTATTAAT
AAAGATGATAGGCCGGTGGCAGCTACGTTTACCTATCCTGTTTTTGTTAA
GCCGGCGCGTTCAGGCTCATCCTTCGGBGTGAAAAAAGTCAATAGCGCGG
ACGAATTGGACTACGCAATTGAATCGGCAAGACAATATGACAGCAAAATC
TTAATTGAGCAGGCTGTTTCGGGCTGTGAGGTCGGTTGTGCGGTATTGGG
AAACAGTGCCGCGTTAGTTGTTGGCGAGGTGGACCAAATCAGGCTGCAGT
ACGGAATCTTTCGTATTCATCAGGAAGTCGAGCCGGAAAAAGGCTCTGAA
AACGCAGTTATAACCGTTCCCGCAGACCTTTCAGCAGAGGAGCGAGGACG
GATACAGGAAACGGCAAAAAAAATATATAAAGCGCTCGGCTGTAGAGGTC
TAGCCCGTGTGGATATGTTTTTACAAGATAACGGCCGCATTGTACTGAAC
GAAGTCAATACTCTGCCCGGTTTCACGTCATACAGTCGTTATCC
                                                    |
                                                    944(3')
```

Table 40: Sequence of distinct region of *VanA* gene. Note B is (T, C or G).

Example of a deletion according to the invention includes the deletion of B528.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 96 Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1 and 944 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 138 and 641 (Table 41, SEQ ID NO: 97).

SEQ ID NO: 97

```
138(5')
|
AATGTGCGAAAAA
CCTTGCGCGGAATGGGAAAACGACAATTGCTATTCAGCTGTACTCTCGCC
GGATAAAAAAATGCACGGATTACTTGTTAAAAAGAACCATGAATATGAAA
TCAACCATGTTGATGTAGCATTTTCAGCTTTGCATGGCAAGTCAGGTGAA
```

```
GATGGATCCATACAAGGTCTGTTTGAATTGTCCGGTATCCCTTTTGTAGG
CTGCGATATTCAAAGCTCAGCAATTTGTATGGACAAATCGTTGACATACA
TCGTTGCGAAAAATGCTGGGATAGCTACTCCCGCCTTTTGGGTTATTAAT
AAAGATGATAGGCCGGTGGCAGCTACGTTTACCTATCCTGTTTTTGTTAA
GCCGGCGCGTTCAGGCTCATCCTTCGGBGTGAAAAAAGTCAATAGCGCGG
ACGAATTGGACTACGCAATTGAATCGGCAAGACAATATGACAGCAAAATC
TTAATTGAGCAGGCTGTTTCGGGCTGTGAGGTCGGTTGTGC
                                                    |
                                                    641(3')
```

Table 41: Sequence of distinct region of the *VanA* gene. Note B is (T, C or G). Example of deletion according to the invention includes the deletion of B528.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 138 and 641 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 138 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 641 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting the *VanA gene* comprise the sequences in Table 42. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 98 (F) and 99 (R); SEQ ID NOs: 100 (F) and 101 (R) as indicated in Table 42, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 98	TTTGCATGGCAAGTCAGGTG / 20	60	F	99	501
SEQ ID NO: 99	AGGTCTGCGGGAACGGTTAT / 20	62	R	98	501
SEQ ID NO: 100	AATGTGCGAAAAACCTTGCGC / 21	62	F	101	504
SEQ ID NO: 101	GCACAACCGACCTCACAGC / 19	62	R	100	504

Table 42: Amplification primer examples for amplifying a distinct region of the *VanA* gene, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 96 or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 138 and 641 inclusive (SEQ ID NO: 97), or complement thereof. It is within the scope of the invention that the probes are capable of binding to the region between residues 138 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 641

(±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting the *VanA gene* comprise the sequences represented by any of SEQ ID NOs: 98 to 101, and the complements thereof.

Another aspect of the invention is a method for identifying the *VanA* gene by amplification of nucleic acid using primers pairs of Table 42, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 98 to 101.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 42.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

15. VanB (vancomycin resistance gene B)

According to one aspect of the invention a distinct region of a *VanB gene* comprises a nucleotide sequence (SEQ ID NOs: 102 or 103) indicated in Tables 43 and 44. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 102

1(5')
|
ATCGGAATTACAAAAAACGGTGTATGGAAGCTATGCAAGAAGCCATGTAC
GGAATGGGAAGCCGACAGTCTCCCCGCCATACTCTCCCCGGATAGGAAAA
CGCATGGGCTGCTTGTCATGAAAGAAAGCGAATACGAAACACGGCGTATT
GATGTGGCTTTCCCGGTTTTGCATGGCAAATGCGGGGAGGATGGTGCGAT
ACAGGGGCTGTTTGTATTGTCTGGTATCCCCTATGTGGGCTGTGATATTC
AAAGCTCCGCAGCTTGCATGGACAAATCACTGGCCTACATTCTTACAAAA
AATGCGGGCATCGCCGTTCCCGAATTTCAAATGATTGATAAAGGTGACAA
GCCGGAGGCGGGTGCGCTTACCTACCCTGTCTTTGTGAAGCCGGCACGGT
CAGGTTCGTCCTTTGGCBTAACCAAAGTAAACGGTACGGAAGAACTTAAC
GCTGCGATAGAAGCGGCAGGACAATATGATGGAAAAATCTTAATTGAGCA
AGCGATTTCGGGCTGTGAGGTCGGGTGTGCGGTCATGGGRAACGAGGATG
ATTTGATTGTCGGCGAAGTGGATCAAATCCGGCTGAGCCACGGTATCTTC
CGCATCCATCAGGAAAACGAGCCGGAAAAAGGCTCAGAAAATGCGATGAT
TACAGTTCCCGCAGACATTCCGGTCGAGGAACGAAATCGGGTGCARGAAA
CGGCAAAGAAAGTATATCGGGTGCTTGGATGCAGAGGGCTT

```
                                                    |
                                                    741(3')
```

Table 43: Sequence of distinct region of *VanB* gene. Note B is (T, C or G), and R is purine (G or A). Examples of deletions according to the invention include one of more of B418, R540 and R696.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 102. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1 and 741 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 126 and 574 (Table 44, SEQ ID NO: 103).

```
SEQ ID NO: 103
126(5')
|
AAGCGAATACGAAACACGGCGTATT
GATGTGGCTTTCCCGGTTTTGCATGGCAAATGCGGGGAGGATGGTGCGAT
ACAGGGGCTGTTTGTATTGTCTGGTATCCCCTATGTGGGCTGTGATATTC
AAAGCTCCGCAGCTTGCATGGACAAATCACTGGCCTACATTCTTACAAAA
AATGCGGGCATCGCCGTTCCCGAATTTCAAATGATTGATAAAGGTGACAA
GCCGGAGGCGGGTGCGCTTACCTACCCTGTCTTTGTGAAGCCGGCACGGT
CAGGTTCGTCCTTTGGCBTAACCAAAGTAAACGGTACGGAAGAACTTAAC
GCTGCGATAGAAGCGGCAGGACAATATGATGGAAAAATCTTAATTGAGCA
AGCGATTTCGGGCTGTGAGGTCGGGTGTGCGGTCATGGGRAACGAGGATG
ATTTGATTGTCGGCGAAGTGGATC
                        |
                        574(3')
```

Table 44: Sequence of distinct region of the *VanB* gene. Note B is (T, C or G), and R is purine (G or A). Examples of deletions according to the invention include one of more of B418 and R540.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 126 and 574 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 126 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 574 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting the *VanB gene* comprise the sequences in Table 45. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 104 (F) and 105 (R); SEQ ID NOs: 106 (F) and 107 (R) as indicated in Table 45, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 104	TCCCCTATGTGGGCTGTGAT / 20	62	F	105	445
SEQ ID NO: 105	GGAATGTCTGCGGGAACTGT / 20	62	R	104	445
SEQ ID NO: 106	AAGCGAATACGAAACACGGC / 20	60	F	107	449
SEQ ID NO: 107	GATCCACTTCGCCGACAATC / 20	62	R	106	449

Table 45: Amplification primer examples for amplifying a distinct region of the *VanB* gene, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 102 or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 126 and 574 inclusive (SEQ ID NO: 103), or complement thereof. It is within the scope of the invention that the probes are capable of binding to the region between residues 126 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) and 574 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues) inclusive. According to an aspect of the invention, probes suitable for detecting the *VanB* gene comprise the sequences represented by SEQ ID NOs: 102 and 103, and the complements thereof.

Another aspect of the invention is a method for identifying the *VanB* gene by amplification of nucleic acid using primers pairs of Table 45, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NOs: 104 to 107.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 45.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

16. VanC (vancomycin resistance gene C)

According to one aspect of the invention a distinct region of a *VanC gene* comprises a nucleotide sequence (SEQ ID NOs: 108 or 109) indicated in Tables 46 and 47. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

```
SEQ ID NO: 108
1(5')
|
GCTTGATACTCAAAATCAACAGTCATCAATGCATTCTCTACGGCAAAGAA
GTTTTCCTGACTCCCATTGAGTTCAAAATATTGCTTTATTTATTTGAGCA
CCAAGGATCCGTCGTCTCTTCCGAAACACTTTTCGAAGCGGTTTGGAAAG
AAAAATATTTAGATAACAATAATACTGTCATGGCACACATTGCTCGTTTA
AGAGAAAAATTGCATGAAGAACCTCGTAAACCTAAATTAATCAAAACCGT
ATGGGGGGTCGGCTATATCATTGAAAAATAGAAATCCTTTGATCCGAAAG
CTCTTGACCCAATACTTCGTCACCACTGGAATCTTGCTGGCATTCCTTGT
AATGATTCCATTAGTCATTCGCTTTATTGCCGGAACCCGGACTTGGTATG
GAACGGAACCTATCTACTATATCTTACGTTTTTTTGCG
                                        |
                                        438(3')
```

Table 46: Sequence of distinct region of *VanC* gene.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 108 Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1 and 438 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 27 and 407 (Table 47, SEQ ID NO: 109).

```
SEQ ID NO: 109
27(5')
|
CAATGCATTCTCTACGGCAAAGAA
GTTTTCCTGACTCCCATTGAGTTCAAAATATTGCTTTATTTATTTGAGCA
CCAAGGATCCGTCGTCTCTTCCGAAACACTTTTCGAAGCGGTTTGGAAAG
AAAAATATTTAGATAACAATAATACTGTCATGGCACACATTGCTCGTTTA
AGAGAAAAATTGCATGAAGAACCTCGTAAACCTAAATTAATCAAAACCGT
ATGGGGGGTCGGCTATATCATTGAAAAATAGAAATCCTTTGATCCGAAAG
CTCTTGACCCAATACTTCGTCACCACTGGAATCTTGCTGGCATTCCTTGT
AATGATTCCATTAGTCATTCGCTTTATTGCCGGAACCCGGACTTGGTATG
GAACGGA
      |
      407(3')
```

Table 47: Sequence of distinct region of the *VanC* gene.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 27 and 407 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 27 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) and 407 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting the *VanC gene* comprise the sequences in Table 48. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 110 (F) and 111 (R); SEQ ID NOs: 112 (F) and 113 (R) as indicated in Table 48, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 110	ACTCAAAATCAACAGTCATCAATG / 24	64	F	111	378
SEQ ID NO: 111	TTCCGGCAATAAAGCGAATGA / 21	60	R	110	378
SEQ ID NO: 112	CAATGCATTCTCTACGGCAAAG / 22	64	F	113	381
SEQ ID NO: 113	TCCGTTCCATACCAAGTCCG / 20	62	R	112	381

Table 48: Amplification primer examples for amplifying a distinct region of the *VanC* gene, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 108 or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 27 and 407 inclusive (SEQ ID NO: 109), or complement thereof. It is within the scope of the invention that the probes are capable of binding to the region between residues 27 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) and 407 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) inclusive. According to an aspect of the invention, probes suitable for detecting the *VanC* gene comprise the sequences represented by any of SEQ ID NOs: 110 to 113, and the complements thereof.

Another aspect of the invention is a method for identifying the *VanC* gene by amplification of nucleic acid using primers pairs of Table 48, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product

of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NO: 110 to 113.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 48.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

17. *MDR-1*

According to one aspect of the invention a distinct region of a *MDR-1* gene comprises a nucleotide sequence (SEQ ID NOs: 114 or 115) indicated in Tables 49 and 50. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 114

```
201 (5')
|
CCCTCAAAATTGGCCAACTTTACAAAAAGCATTTTTCATTTTCCAAATTT
CATTTTTGACAACTTCAGTTTATATGGGATCAGCAGTTTATACCCCTGGT
ATTGAAGAATTAATGCATGATTTTGGTATTGGAAGAGTCGTAGCTACATT
ACCTTTAACATTATTTGTTATTGGTTATGGTGTTGGCCCATTGGTTTTCA
GTCCGATGTCAGAAAATGCTATATTTGGTCGTACATCCATATATATCATA
ACATTATTTTTATTTGTCATACTACAAATYCCCACTGCTTTGGTWAATAA
TATTGCYGGTTTATGTATATTGAGATTCTTGGGTGGATTCTTTGCTAGTC
CTTGTTTGGCYACTGGTGGTGCWAGTGTTGCTGATGTGGTTAAATTTTGG
AATTTACCAGTTGGGTTAGCCGCTTGGAGTTTGGGTGCYGTTTGTGGTCC
TAGTTTTGGTCCATTCTTTGGTTCAATTTTAACTGTCAAAGCCAGTTGGA
GATGGACTTTTTGGTTCATGTGTATYATTTCTGGGTTTTCATTTGTTATG
TTGTGTTTCACTTTACCTGAAACTTTTGGCAAAACATTATTRTATCGCAA
GGCTAAAAGATTGAGAGCCATCACCGGTAACGACAGAATCACAAGTGAAG
GAGAAATTGAAAATAGCAAAATGACAAGTCATGAATTGATCATTGATACA
                                                    |
                                                850 (3')
```

Table 49: Sequence of distinct region of *MDR-1* gene. Y is any nucleotide with a pyrimidine base, R is any nucleotide with a purine base, W is any nucleotide with an adenine or thymine base.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 108. Preferably, a pair of amplification primers is a pair capable of amplifying any region between

residues 201 and 850 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 275 and 834 (Table 50, SEQ ID NO: 115).

SEQ ID NO: 115
275 (5') | TGGGATCAGCAGTTTATACCCCTGGT ATTGAAGAATTAATGCATGATTTTGGTATTGGAAGAGTCGTAGCTACATT ACCTTTAACATTATTTGTTATTGGTTATGGTGTTGGCCCATTGGTTTTCA GTCCGATGTCAGAAAATGCTATATTTGGTCGTACATCCATATATATCATA ACATTATTTTTATTTGTCATACTACAAATYCCCACTGCTTTGGTWAATAA TATTGCYGGTTTATGTATATTGAGATTCTTGGGTGGATTCTTTGCTAGTC CTTGTTTGGCYACTGGTGGTGCWAGTGTTGCTGATGTGGTTAAATTTTGG AATTTACCAGTTGGGTTAGCCGCTTGGAGTTTGGGTGCYGTTTGTGGTCC TAGTTTTGGTCCATTCTTTGGTTCAATTTTAACTGTCAAAGCCAGTTGGA GATGGACTTTTTGGTTCATGTGTATYATTTCTGGGTTTTCATTTGTTATG TTGTGTTTCACTTTACCTGAAACTTTTGGCAAAACATTATTRTATCGCAA GGCTAAAAGATTGAGAGCCATCACCGGTAACGAC | 834 (3')

Table 50: Sequence of distinct region of the *MDR-1* gene.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 275 and 834 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 275 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) and 834 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting the *MDR-1 gene* comprise the sequences in Table 51. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 116 (F) and 117 (R); SEQ ID NOs: 118 (F) and 119 (R) as indicated in Table 51, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 116	TGGGATCAGCAGTTTATACCC / 21	62	F	117	558
SEQ ID NO: 117	GTCGTTACCGGTGATGGCTC / 20	64	R	116	558
SEQ ID NO: 118	TCACTTTACCTGAAACTTTTGGC / 23	64	F	119	560
SEQ ID NO: 119	TTTGGAAAATCAAAAATGCACCAG / 24	64	R	118	560

Table 51: Amplification primer examples for amplifying a distinct region of the *MDR-1* gene, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 114 or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 275 and 834 inclusive (SEQ ID NO: 115), or complement thereof. It is within the scope of the invention that the probes are capable of binding to the region between residues 275 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) and 834 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) inclusive. According to an aspect of the invention, probes suitable for detecting the *MDR-1* gene comprise the sequences represented by any of SEQ ID NOs: 116 to 119, and the complements thereof.

Another aspect of the invention is a method for identifying the *MDR-1* gene by amplification of nucleic acid using primers pairs of Table 51, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NO: 116 to 119.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 51.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

18. CDR-1

According to one aspect of the invention a distinct region of a *CDR*-1 gene comprises a nucleotide sequence (SEQ ID NOs: 120 or 121) indicated in Tables 52 and 53. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

SEQ ID NO: 120

1 (5')
|
TCTTTTTCTATTGGTTAATGTGTRTTTGGTGTACATTTGTTATGTCCCAT
TTGTTTAGATCCATTGGTGCTGTTTCAACATCTATTKCTGGTGCYATGAC
YCCTGCTACYGTGTTGTTATTGGCTATGGTTATTTAYACTGGGTTCGTTA
TCCCAACTCCAAGTATGTTGGGTTGGTCWMGATGGATTAATTAYATYAAY
CCTGTTGGTTATGTGTTYGAAKCSCTYATGGTTAATGARTTCCAYGGTCG
TGAATTCCAATGTGCTCAATATGTTCCAAGTGGYCCAGGTTWTGAAAATR

```
TATCACGTTCRAATCAAGTGTGTACTGCAGTKGGGTCTRTTCCAGGTAAT
GAAATGGTTAGTGGTACCAATTATTTGGCTGGTGCTT
                                        |
                                       387 (3')
```

Table 52: Sequence of distinct region of *CDR*-1 gene. Y is any nucleotide with a pyrimidine base, R is any nucleotide with a purine base, K is any nucleotide with a thymine or guanine base, W is any nucleotide with an adenine or thymine base, M is any nucleotide with a cytosine or adenine base, S is any nucleotide with a cytosine or guanine base.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of SEQ ID NO: 120. Preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 1 and 387 inclusive. Even more preferably, a pair of amplification primers is a pair capable of amplifying any region between residues 111 and 178 (Table 53, SEQ ID NO: 121).

```
SEQ ID NO: 121
111 (5')
|
GTGTTGTTATTGGCTATGGTTATTTAYACTGGGTTCGTTA
TCCCAACTCCAAGTATGTTGGGTTGGT
                           |
                          178 (3')
```

Table 53: Sequence of distinct region of the *CDR*-1 gene. Sequence of distinct region of *CDR*-1 gene. Y is any nucleotide with a pyrimidine base.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying the region between residues 111 and 178 inclusive. It is within the scope of the invention, that the primers are capable of amplifying the region between residues 111 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) and 178 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) inclusive. According to a preferred aspect of the invention, amplification primers suitable for detecting the *CDR*-1 gene comprise the sequences in Table 54. Combinations of forwards (F) and reverse (R) primers include SEQ ID NOs: 122 (F) and 123 (R); SEQ ID NOs: 124 (F) and 125 (R) as indicated in Table 54, though other primer pair combinations are possible given the similarity of melting temperatures. Such combination may be present in a composition.

CODE	SEQUENCE / LENGTH	Tm (deg C)	TYPE	PAIR	LEN
SEQ ID NO: 122	TCTTTTTCTATTGGTTAATGTGT / 23	58	F	123	68
SEQ ID NO: 123	TGTTGAAACAGCACCAATGGA / 21	60	R	122	68

SEQ ID NO: 124	GTGTTGTTATTGGCTATGGTTAT / 23	62	F	125	80
SEQ ID NO: 125	GACCAACCCAACATACTTGGA / 21	62	R	124	80

Table 54: Amplification primer examples for amplifying a distinct region of the *CDR*-1 gene, length and melting temperature. TYPE is either forward (F) or reverse (R) primer, PAIR is a paired primer SEQ ID NO. for amplification, LEN is the amplification product length.

A hybridisation probe according to one aspect of the present invention is capable of annealing to SEQ ID NO: 120 or the complement thereof.

According to one embodiment of the invention, hybridisation probe is capable of hybridising to the region between residues 111 and 178 inclusive (SEQ ID NO: 121), or complement thereof. It is within the scope of the invention that the probes are capable of binding to the region between residues 111 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) and 178 (±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residue) inclusive. According to an aspect of the invention, probes suitable for detecting the *MDR-1* gene comprise the sequences represented by any of SEQ ID NOs: 122 to 125, and the complements thereof.

Another aspect of the invention is a method for identifying the *CDR*-1 gene by amplification of nucleic acid using primers pairs of Table 54, in the combination indicated or other suitable combination of forward and reverse primers. A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification; according to one embodiment of the invention, such hybridisation probe comprises a suitable sequence corresponding to any of SEQ ID NO: 122 to 125.

Another aspect of the invention is an oligonucleotide (primer or probe) corresponding to a sequence indicated in Table 54.

Homologous sequences of the above mentioned distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

Figure 1

The Figure shows an alignment of sequences 23S RNA genes of each of *Staphylococcus aureus, Staphylococcus epidermidis, Enterobacter cloacae, Escherichia coli, Enterococcus faecalis, Pseudomonas aeruginosa, Enterococcus faecium, Klebsiella pneumoniae, and Candida albicans*, and an indication of identity (marked with *).

According to one aspect of the invention a distinct region of a 23S RNA gene of a micro-organism comprises a nucleotide sequence (SEQ ID NOs: 131 to 157) indicated in

Figure 1. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. One aspect of the present invention is nucleotide acid corresponding to a sequence represented by any of SEQ ID NOs: 131 to 157 indicated in Figure 1, or complement thereof.

According to one aspect of the invention a distinct region of a 23S RNA gene of a micro-organism comprises a nucleotide sequence indicated in Figure 1, corresponding to a distinct region represented by any of SEQ ID NOs: 1 or 2 (*Enterobacter cloacae*), 7 or 8 (*Enterococcus faecalis*), 16 or 17 (*Enterococcus faecium*), 22 or 23 (*Escherichia coli*), 30 or 31 (*Klebsiella pneumoniae*), 38 or 39 (*Pseudomonas aeruginosa*), 43 or 44 (*Staphylococcus aureus*), 52 or 53 (*Staphylococcus epidermidis*), 64 and 65 (*Candida albicans*).

According to one aspect of the invention a distinct region of a 23S RNA gene of a micro-organism comprises a nucleotide sequence indicated in Figure 1, obtainable using a pair of amplification primers specific to said micro-organism. Said amplification primer are mentioned above, and are, depending on the micro-organism:

Enterobacter cloacae: SEQ ID NOs: 3 and 4, or SEQ ID NOs: 5 and 6,

Enterococcus faecalis: SEQ ID NOs: 9 and 10, SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12 or SEQ ID NOs: 15 and 11,

Enterococcus faecium: SEQ ID NOs: 18 and 19, SEQ ID NOs: 20 and 19, or SEQ ID NOs: 20 and 21,

Escherichia coli: SEQ ID NOs: 24 and 26, SEQ ID NOs: 24 and 25, SEQ ID NOs: 27 and 29, or SEQ ID NOs: 28 and 29,

Klebsiella pneumoniae: SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36, or SEQ ID NOs: 37 and 33,

Pseudomonas aeruginosa: SEQ ID NOs: 40 and 41 or SEQ ID NOs: 40 and 42,

Staphylococcus aureus: SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, or SEQ ID NOs: 50 and 51,

Staphylococcus epidermidis: SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, or SEQ ID NOs: 63 and 61,

Candida albicans: SEQ ID NOs: 66 and 67, SEQ ID NOs: 68 and 69, or SEQ ID NOs: 70 and 71.

According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of a SEQ ID NO in Figure 1, a complement thereof, or an homologous sequence of said region or complement.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying a region of a sequence listed in Figure 1 corresponding to a distinct region represented by any of SEQ ID NOs: 1 or 2 (*Enterobacter cloacae*), 7 or 8 (*Enterococcus faecalis*), 16 or 17 (*Enterococcus faecium*), 22 or 23 (*Escherichia coli*), 30 or 31 (*Klebsiella pneumoniae*), 38 or 39 (*Pseudomonas aeruginosa*), 43 or 44 (*Staphylococcus aureus*), 52 or 53 (*Staphylococcus epidermidis*), 64 and 65 (*Candida albicans*).

It is within the scope of the invention, that the primers are capable of amplifying the aforementioned corresponding region in Figure 1, ±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues from either or both ends.

A hybridisation probe according to the present invention is capable of hybridising to a region of a sequence listed in Figure 1, corresponding to a distinct region, or complement thereof, represented by any of SEQ ID NOs: 1 or 2 (*Enterobacter cloacae*), 7 or 8 (*Enterococcus faecalis*), 16 or 17 (*Enterococcus faecium*), 22 or 23 (*Escherichia coli*), 30 or 31 (*Klebsiella pneumoniae*), 38 or 39 (*Pseudomonas aeruginosa*), 43 or 44 (*Staphylococcus aureus*), 52 or 53 (*Staphylococcus epidermidis*), 64 and 65 (*Candida albicans*).

It is within the scope of the invention that the probes are capable of binding to the aforementioned corresponding sequences of Figure 1, ±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues from either or both ends.

Another aspect of the invention is a method for identifying a distinct region by amplification of nucleic acid using a pair of primers directed towards a region of a sequence in Figure 1 corresponding to a distinct region, or complement thereof, represented by any of SEQ ID NOs: 1 or 2 (*Enterobacter cloacae*), 7 or 8 (*Enterococcus faecalis*), 16 or 17 (*Enterococcus faecium*), 22 or 23 (*Escherichia coli*), 30 or 31 (*Klebsiella pneumoniae*), 38 or 39 (*Pseudomonas aeruginosa*), 43 or 44 (*Staphylococcus aureus*), 52 or 53 (*Staphylococcus epidermidis*), 64 and 65 (*Candida albicans*).

A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification.

Homologous sequences of the above mentioned regions corresponding to distinct regions, amplification primers and hybridisation probes are within the scope of the

invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

Figure 2

The Figure shows an alignment of sequenced genes of each of *mec*A, *van*A, *van*B, *van*C, bla_{shv}, bla_{ges-2}, spA, MDR-1, and CDR-1, together with a consensus sequence.

According to one aspect of the invention a distinct region of an antibiotic resistance gene of a comprises a nucleotide sequence (SEQ ID NOs: 158 to 261) indicated in Figure 2. According to another aspect of the invention, a distinct region is a complement of said SEQ ID NOs. One aspect of the present invention is nucleotide acid corresponding to a sequence represented by any of SEQ ID NOs: 158 to 261 indicated in Figure 2, or complement thereof.

According to one aspect of the invention a distinct region of an antibiotic resistance gene comprises a nucleotide sequence indicated in Figure 2, corresponding to a distinct region represented by any of SEQ ID NOs: 72 or 73 (bla_{ges-2}), 78 or 79 (bla_{shv}), 84 or 85 (*mec*A), 90 or 91 (spA), 96 or 97 (*van*A), 102 or 103 (*van*B), 108 or 109 (*van*C), 114 or 115 (MDR-1), 120 or 121 (CDR-1).

According to one aspect of the invention a distinct region of an antibiotic resistance gene comprises a nucleotide sequence indicated in Figure 2, obtainable using a pair of amplification primers specific to said micro-organism. Said amplification primer are mentioned above, and are, depending on the marker:

bla_{ges-2} marker: SEQ ID NOs: 74 and 75, or SEQ ID NOs: 76 and 77,
bla_{shv} marker: SEQ ID NOs: 80 and 81, or SEQ ID NOs: 82 and 83,
mecA marker: SEQ ID NOs: 86 and 87, or SEQ ID NOs: 88 and 89,
spA marker: SEQ ID NOs: 92 and 93, or SEQ ID NOs: 94 and 95,
VanA marker: SEQ ID NOs: 98 and 99, or SEQ ID NOs: 100 and 101,
VanB marker: SEQ ID NOs: 104 and 105, or SEQ ID NOs: 106 and 107,
VanC marker: SEQ ID NOs: 110 and 111, or SEQ ID NOs: 112 and 113,
MDR-1 marker: SEQ ID NOs: 116 and 117, or SEQ ID NOs: 118 and 119, and
CDR-1 marker: SEQ ID NOs: 122 and 123, or SEQ ID NOs: 124 and 125.

According to another aspect of the invention, a distinct region is an homologous sequence of the distinct region or complement thereof.

A pair of amplification primers according to one embodiment of the invention is a pair capable of amplifying any region of at least 30 bases of a SEQ ID NO in Figure 2, a complement thereof, or an homologous sequence of said region or complement.

A pair of amplification primers according to another embodiment of the invention, is a pair capable of amplifying a region of a sequence listed in Figure 2 corresponding to a distinct region represented by any of SEQ ID NOs: 72 or 73 (bla_{ges-2}), 78 or 79 (bla_{shv}), 84 or 85 (*mec*A), 90 or 91 (spA), 96 or 97 (*van*A), 102 or 103 (*van*B), 108 or 109 (*van*C), 114 or 115 (MDR-1), 120 or 121 (CDR-1).

It is within the scope of the invention, that the primers are capable of amplifying the aforemention corresponding region in Figure 2, ±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues from either or both ends.

A hybridisation probe according to the present invention is capable of hybridising to a region of a sequence listed in Figure 2, corresponding to a distinct region, or complement thereof, represented by any of SEQ ID NOs: 72 or 73 (bla_{ges-2}), 78 or 79 (bla_{shv}), 84 or 85 (*mec*A), 90 or 91 (spA), 96 or 97 (*van*A), 102 or 103 (*van*B), 108 or 109 (*van*C), 114 or 115 (MDR-1), 120 or 121 (CDR-1).

It is within the scope of the invention that the probes are capable of binding to the aforementioned corresponding sequences of Figure 2, ±10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 residues from either or both ends.

Another aspect of the invention is a method for identifying a distinct region by amplification of nucleic acid using a pair of primers directed towards a region of a sequence in Figure 2 corresponding to a distinct region, or complement thereof, represented by any of SEQ ID NOs: 72 or 73 (bla_{ges-2}), 78 or 79 (bla_{shv}), 84 or 85 (*mec*A), 90 or 91 (spA), 96 or 97 (*van*A), 102 or 103 (*van*B), 108 or 109 (*van*C), 114 or 115 (MDR-1), 120 or 121 (CDR-1). A further aspect of the invention is a subsequent detection step using one or more hybridisation probes specific for the product of the amplification.

Homologous sequences of the above mentioned regions corresponding to distinct regions, amplification primers and hybridisation probes are within the scope of the invention. The distinct regions, probes and primers include homologous sequences in which one or more bases have been deleted, substituted and/or inserted as mentioned above.

Combinations

As mentioned above, the present invention also relates to the simultaneous detection of two or more (*e.g.* 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) distinct regions of nucleic acid. One embodiment of the invention is a method for detection of two or more (*e.g.* 3, 4, 5, 6, 7, 8, 9 or more) of *Staphylococcus aureus, Staphylococcus epidermidis, Enterobacter cloacae, Escherichia coli, Enterococcus faecalis,*

Pseudomonas aeruginosa, Enterococcus faecium, Klebsiella pneumoniae and Candida albicans by detecting nucleic acid corresponding to distinct regions of 23S RNA therein.

Another embodiment of the invention is a method for identifying at least two micro-organisms in a sample by detecting nucleic acid corresponding to two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) of:

SEQ ID NOs: 1 or 2 (*Enterobacter cloacae*),

SEQ ID NOs: 7 or 8 (*Enterococcus faecalis*),

SEQ ID NOs: 16 or 17 (*Enterococcus faecium*),

SEQ ID NOs: 22 or 23 (*Escherichia coli*),

SEQ ID NOs: 30 or 31 (*Klebsiella pneumoniae*),

SEQ ID NOs: 38 or 39 (*Pseudomonas aeruginosa*),

SEQ ID NOs: 43 or 44 (*Staphylococcus aureus*),

SEQ ID NOs: 52 or 53 (*Staphylococcus epidermidis*), and

SEQ ID NOs: 64 and 65 (*Candida albicans*).

Another embodiment of the invention is a method for identifying at least two micro-organisms in a sample by detecting two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) of nucleic acid sequences listed in Figure 1, each sequence corresponding to the micro-organism for detection.

Another embodiment of the invention is a method for identifying at least two micro-organisms in a sample by detecting at least two (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) regions of a nucleic acid listed in Figure 1, each region corresponding a distinct region of SEQ ID NOs: 1 or 2 (*Enterobacter cloacae*), 7 or 8 (*Enterococcus faecalis*), 16 or 17 (*Enterococcus faecium*), 22 or 23 (*Escherichia coli*), 30 or 31 (*Klebsiella pneumoniae*), 38 or 39 (*Pseudomonas aeruginosa*), 43 or 44 (*Staphylococcus aureus*), 52 or 53 (*Staphylococcus epidermidis*), or 64 and 65 (*Candida albicans*).

Another embodiment of the invention is a method for identifying at least two micro-organisms in a sample by using two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) primer pairs, wherein the two or more organisms for detection and the primer pairs are selected from the following, preferably, though not necessarily, one primer pair selected for one micro-organism:

Enterobacter cloacae: SEQ ID NOs: 3 and 4, or SEQ ID NOs: 5 and 6,

Enterococcus faecalis: SEQ ID NOs: 9 and 10, SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12 or SEQ ID NOs: 15 and 11,

Enterococcus faecium: SEQ ID NOs: 18 and 19, SEQ ID NOs: 20 and 19, or SEQ ID NOs: 20 and 21,

Escherichia coli: SEQ ID NOs: 24 and 26, SEQ ID NOs: 24 and 25, SEQ ID NOs: 27 and 29, or SEQ ID NOs: 28 and 29,

Klebsiella pneumoniae: SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36, or SEQ ID NOs: 37 and 33,

Pseudomonas aeruginosa: SEQ ID NOs: 40 and 41 or SEQ ID NOs: 40 and 42,

Staphylococcus aureus: SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, or SEQ ID NOs: 50 and 51,

Staphylococcus epidermidis: SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, or SEQ ID NOs: 63 and 61,

Candida albicans: SEQ ID NOs: 66 and 67, SEQ ID NOs: 68 and 69, or SEQ ID NOs: 70 and 71.

Another embodiment of the present invention is a composition comprising two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) of the following primer pairs:

Enterobacter cloacae: SEQ ID NOs: 3 and 4,

Enterococcus faecalis: SEQ ID NOs: 9 and 12,

Enterococcus faecium: SEQ ID NOs: 18 and 19,

Escherichia coli: SEQ ID NOs: 24 and 25,

Klebsiella pneumoniae: SEQ ID NOs: 32 and 33,

Pseudomonas aeruginosa: SEQ ID NOs: 40 and 42,

Staphylococcus aureus: SEQ ID NOs: 48 and 49,

Staphylococcus epidermidis: SEQ ID NOs: 54 and 55,

Candida albicans: SEQ ID NOs: 66 and 67.

Another embodiment of the invention is a method for identifying at least two micro-organisms in a sample by using two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) single probes corresponding to said two or more organisms for detection below, preferably, though not necessarily, one probe selected for one micro-organism:

Enterobacter cloacae: any of SEQ ID NOs: 3 to 6,

Enterococcus faecalis: any of SEQ ID NOs: 9 to 15,

Enterococcus faecium: any of SEQ ID NOs: 18 to 21,

Escherichia coli: any of SEQ ID NOs: 24 to 29,

Klebsiella pneumoniae: any of SEQ ID NOs: 32 to37,

Pseudomonas aeruginosa: any of SEQ ID NOs: 40 to 42,

Staphylococcus aureus: any of SEQ ID NOs: 45 to 51,

Staphylococcus epidermidis: any of SEQ ID NOs: 54 to 63,

Candida albicans: SEQ ID NOs: any of 66 to 71.

Another embodiment of the present invention is a composition comprising two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) of the following probes, preferably, though not necessarily, one probe selected for one micro-organism:

Enterobacter cloacae: SEQ ID NOs: 3 or 4,

Enterococcus faecalis: SEQ ID NOs: 9 or 12,

Enterococcus faecium: SEQ ID NOs: 18 or 19,

Escherichia coli: SEQ ID NOs: 24 or 25,

Klebsiella pneumoniae: SEQ ID NOs: 32 or 33,

Pseudomonas aeruginosa: SEQ ID NOs: 40 or 42,

Staphylococcus aureus: SEQ ID NOs: 48 or 49,

Staphylococcus epidermidis: SEQ ID NOs: 54 or 55,

Candida albicans: SEQ ID NOs: 66 or 67.

Another embodiment of the invention is a method for detecting two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, 9, or 10) of the antibiotic resistance markers *mec*A, *SpA*, *van*A, *van*B, *van*C, bla_{shv}, bla_{ges-2}, MDR-1, CDR-1 by detecting nucleic acid corresponding to distinct regions therein.

Another embodiment of the invention is a method for identifying at least two antibiotic resistance markers in a sample by detecting nucleic acid corresponding to two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, 9, or 10) of

SEQ ID NOs: 72 or 73 (bla_{ges-2} marker),

SEQ ID NOs: 78 or 79 (bla_{shv} marker),

SEQ ID NOs: 84 or 85 (*mecA* marker),

SEQ ID NOs: 90 or 91 (*spA* marker),

SEQ ID NOs: 96 or 97 (*VanA* marker),

SEQ ID NOs: 102 or 103 (*VanB* marker),

SEQ ID NOs: 108 or 109 (*VanC* marker)

SEQ ID NOs: 114 or 115 (MDR-1 marker)

SEQ ID NOs: 120 or 121 (CDR-1 marker)

Another embodiment of the invention is a method for identifying at least two micro-organisms in a sample by detecting two or more ((*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) of nucleic acid sequences listed in Figure 2, each sequence corresponding to the micro-organism for detection.

Another embodiment of the invention is a method for identifying at least two micro-organisms in a sample by detecting at least two (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) regions of a nucleic acid listed in Figure 1, each region corresponding a distinct region of SEQ ID NOs: 72 or 73 (bla_{ges-2} marker), SEQ ID NOs: 78 or 79 (bla_{shv} marker), SEQ ID NOs: 84 or 85 (*mecA* marker), SEQ ID NOs: 90 or 91 (*spA* marker), SEQ ID NOs: 96 or 97 (*VanA* marker), SEQ ID NOs: 102 or 103 (*VanB* marker), SEQ ID NOs: 108 or 109 (*VanC* marker), SEQ ID NOs: 114 or 115 (MDR-1 marker), or SEQ ID NOs: 120 or 121 (CDR-1 marker).

Another embodiment of the invention is a method for identifying at least two antibiotic resistance markers in a sample by using two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, 9, or 10) primer pairs wherein the antibiotic resistance markers for detection and the primer pairs are selected from the following preferably, though not necessarily, one primer pair selected for one marker:

bla_{ges-2} marker: SEQ ID NOs: 74 and 75, or SEQ ID NOs: 76 and 77,
bla_{shv} marker: SEQ ID NOs: 80 and 81, or SEQ ID NOs: 82 and 83,
mecA marker: SEQ ID NOs: 86 and 87, or SEQ ID NOs: 88 and 89,
spA marker: SEQ ID NOs: 92 and 93, or SEQ ID NOs: 94 and 95,
VanA marker: SEQ ID NOs: 98 and 99, or SEQ ID NOs: 100 and 101,
VanB marker: SEQ ID NOs: 104 and 105, or SEQ ID NOs: 106 and 107,
VanC marker: SEQ ID NOs: 110 and 111, or SEQ ID NOs: 112 and 113,
MDR-1 marker: SEQ ID NOs: 116 and 117, or SEQ ID NOs: 118 and 119, and
CDR-1 marker: SEQ ID NOs: 122 and 123, or SEQ ID NOs: 124 and 125.

Another embodiment of the invention is a composition comprising two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) of the following primer pairs:

bla_{ges-2} marker: SEQ ID NOs: 76 and 77,
bla_{shv} marker: SEQ ID NOs: 80 and 81,
mecA marker: SEQ ID NOs: 88 and 89,
spA marker: SEQ ID NOs: 92 and 93,
VanA marker: SEQ ID NOs: 100 and 101,
VanB marker: SEQ ID NOs: 106 and 107,

VanC marker: SEQ ID NOs: 112 and 113,

MDR-1 marker: SEQ ID NOs: 116 and 117,

CDR-1 marker: SEQ ID NOs: 124 and 125.

Another embodiment of the invention is a method for identifying at least two antibiotic resistance markers in a sample by using two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, 9, or 10) probes wherein the antibiotic resistance markers for detection and the probes are selected from the following, preferably, though not necessarily, one probe selected for one micro-organism:

bla_{ges-2} marker: any of SEQ ID NOs: 74 to 77,

bla_{shv} marker: any of SEQ ID NOs: 80 to 83,

mecA marker: any of SEQ ID NOs: 86 to 89,

spA marker: any of SEQ ID NOs: 92 to 95,

VanA marker: any of SEQ ID NOs: 98 to 101,

VanB marker: any of SEQ ID NOs: 104 to 107,

VanC marker: any of SEQ ID NOs: 110 to 113,

MDR-1 marker: any of SEQ ID NOs: 116 to 119,

CDR-1 marker: any of SEQ ID NOs: 122 to 125.

Another embodiment of the present invention is composition comprising two or more (*e.g.* at least 3, 4, 5, 6, 7, 8, or 9) of the following probes, preferably, though not necessarily, one probe selected for one marker:

bla_{ges-2} marker: SEQ ID NOs: 76 or 77,

bla_{shv} marker: SEQ ID NOs: 80 or 81,

mecA marker: SEQ ID NOs: 88 or 89,

spA marker: SEQ ID NOs: 92 or 93,

VanA marker: SEQ ID NOs: 100 or 101,

VanB marker: SEQ ID NOs: 106 or 107,

VanC marker: SEQ ID NOs: 112 or 113,

MDR-1 marker: SEQ ID NOs: 116 or 117,

CDR-1 marker: SEQ ID NOs: 124 or 125.

Another embodiment of the invention is a method for detecting at least one (*e.g.* 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more) of the antibiotic resistance markers *mec*A, *SpA*, *van*A, *van*B, *van*C, bla_{shv}, bla_{ges-2}, MDR-1 and CDR-1 and at least one (*e.g.* 2, 3, 4, 5, 6, 7, 8 or 9 or more) of the micro-organisms *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus*

aureus, Staphylococcus epidermidis, and Candida albicans by detecting nucleic acid corresponding to distinct regions therein.

Another embodiment of the invention is a method for identifying at least one micro-organism and at least one antibiotic resistance marker in a sample, by detecting the distinct regions corresponding to the SEQ ID NOs mentioned above.

Another embodiment of the invention is a method for identifying at least one micro-organism and at least one antibiotic resistance marker in a sample, by using two or more of the primer pairs or single probes corresponding to the SEQ ID NOs mentioned above.

Another embodiment of the invention is a method for identifying one micro-organism and at least one antibiotic resistance marker in a sample, by using one of the primer pairs or single probes corresponding to the SEQ ID NOs mentioned above relating to 23S RNA and two or more (*e.g.* 3, 4, 5, 6, 7, 8, 9 or 10 or more) primer pairs or single probes corresponding to the SEQ ID NOs mentioned above relating to antibiotic resistance genes.

Another embodiment of the present invention is a composition comprising one or more (*e.g.* at least 2, 3, 4, 5, 6, 7, 8, or 9) of the following primer pairs:

Enterobacter cloacae: SEQ ID NOs: 3 and 4,
Enterococcus faecalis: SEQ ID NOs: 9 and 12,
Enterococcus faecium: SEQ ID NOs: 18 and 19,
Escherichia coli: SEQ ID NOs: 24 and 25,
Klebsiella pneumoniae: SEQ ID NOs: 32 and 33,
Pseudomonas aeruginosa: SEQ ID NOs: 40 and 42,
Staphylococcus aureus: SEQ ID NOs: 48 and 49,
Staphylococcus epidermidis: SEQ ID NOs: 54 and 55,
Candida albicans: SEQ ID NOs: 66 and 67,

and one of more (*e.g.* at least 2, 3, 4, 5, 6, 7, 8, or 9) of the following primer pairs:

bla_{ges-2} marker: SEQ ID NOs: 76 and 77,
bla_{shv} marker: SEQ ID NOs: 80 and 81,
mecA marker: SEQ ID NOs: 88 and 89,
spA marker: SEQ ID NOs: 92 and 93,
VanA marker: SEQ ID NOs: 100 and 101,
VanB marker: SEQ ID NOs: 106 and 107,
VanC marker: SEQ ID NOs: 112 and 113,

MDR-1 marker: SEQ ID NOs: 116 and 117,

CDR-1 marker: SEQ ID NOs: 124 and 125.

Another embodiment of the present invention is a composition comprising one or more (*e.g.* at least 2, 3, 4, 5, 6, 7, 8, or 9) of the following probes, preferably, though not necessarily, one probe selected for one micro-organism:

Enterobacter cloacae: SEQ ID NOs: 3 or 4,

Enterococcus faecalis: SEQ ID NOs: 9 or 12,

Enterococcus faecium: SEQ ID NOs: 18 or 19,

Escherichia coli: SEQ ID NOs: 24 or 25,

Klebsiella pneumoniae: SEQ ID NOs: 32 or 33,

Pseudomonas aeruginosa: SEQ ID NOs: 40 or 42,

Staphylococcus aureus: SEQ ID NOs: 48 or 49,

Staphylococcus epidermidis: SEQ ID NOs: 54 or 55,

Candida albicans: SEQ ID NOs: 66 or 67.

and one of more (*e.g.* at least 2, 3, 4, 5, 6, 7, 8, or 9) of the following probes, preferably though not necessarily, one probe selected for one marker:

bla_{ges-2} marker: SEQ ID NOs: 76 or 77,

bla_{shv} marker: SEQ ID NOs: 80 or 81,

mecA marker: SEQ ID NOs: 88 or 89,

spA marker: SEQ ID NOs: 92 or 93,

VanA marker: SEQ ID NOs: 100 or 101,

VanB marker: SEQ ID NOs: 106 or 107,

VanC marker: SEQ ID NOs: 112 or 113,

MDR-1 marker: SEQ ID NOs: 116 or 117,

CDR-1 marker: SEQ ID NOs: 124 or 125.

A composition according to the present invention may be a solution, a mixture, an admixture, or may constitute the components in or on a container or device of the invention.

Another embodiment of the present invention is a container comprising two or more (*e.g.* at least 2, 3, 4, 5, 6, 7, 8, or 9) primer pairs as defined in the above method and composition embodiments.

Another embodiment of the present invention is a container comprising two or more probes (*e.g.* at least 2, 3, 4, 5, 6, 7, 8, or 9) as defined in the above method and composition embodiments.

Another embodiment of the present invention is a kit comprising two or more (*e.g.* at least 2, 3, 4, 5, 6, 7, 8, or 9) primer pairs as defined in the above method and composition embodiments.

Another embodiment of the present invention is a kit comprising two or more probes (*e.g.* at least 2, 3, 4, 5, 6, 7, 8, or 9) as defined in the above method and composition embodiments.

According to an aspect of the invention, a method detects the presence of one or more antibiotic resistance genes a micro-organism. According to another aspect of the invention, a method detects the presence of one or more antibiotic resistance genes a micro-organism and also the micro-organism.

The primers advantageously permit simultaneous or multiplexed PCR of template sequences in a single reaction, without the formation of primer dimer or cross reactions. Furthermore, the length of a product is particular to a species or antibiotic resistance marker. This allows the product of an amplification reaction to be separated, for example, by electrophoresis, and identification of several genes by evaluating the length attributed to one or more bands.

Multiplex detection of target sequences not only has the benefit of increasing throughput, but also allows differential diagnosis and monitoring of therapy in clinical applications. For example, the disease of bacteraemia and septicaemia is caused by one or more different pathogens and the therapy strongly depends on the detection of the involved bacteria and involved antibiotic resistant bacterial strains, which will guide the application of the right antibiotics. Therefore, for a proper and effective therapy it is essential to very specific and sensitive detection of the presence, absence or amount of specific NA sequences of one or more pathogens and their antibiotic resistant species, - the so called panel of pathogens and antibiotic resistant species. It is well known to the person skilled in the art, that the treatment of bacteraemia and septicaemia will only be successful in a very narrow timeframe after the outbreak of the disease. Furthermore, it is also well known to the person skilled in the art, that the earlier a disease is detected, the more successful and the faster therapy will work. Furthermore it is also well known to the person skilled in the art, that the detection of pathogenicity as a whole is not only restricted to panels containing bacteria and antibiotic resistant bacterial strains, but also to panels combining fungal strains, virus strains, proteins, and/ or haptens alone or in combination with bacteria and antibiotic resistant bacterial strains.

Products

The present invention includes products comprising one or more primers or probes, suitable for use in a device enabling identification of the distinct regions mentioned herein. Such products include, for example,

- one or more containers (e.g. microarray or multi-sample container) preloaded with one or more pairs of amplification primers. A multi-sample container allows simultaneous detection of distinct regions either in the same reaction or as separate reactions,
- a kit comprising one or more pairs of primers and optionally buffers, reagents and containers for performing amplification reactions,
- a kit comprising one or more containers and optionally buffers, reagents for performing amplification reactions,
- a device comprising one or more pairs of primers for performing amplification reactions.
- one or more containers (e.g. microarray or multi-sample consumable) preloaded with one or more preloaded with one or more probes. A multi-sample container allows simultaneous detection of distinct regions either in the same reaction or as separate reactions, ,
- a kit comprising one or more probes and optionally buffers, reagents and containers for performing hybridisation,
- a kit comprising one or more containers and optionally buffers, reagents and containers for performing hybridisation,
- a device comprising one or more probes for performing hybridisation.
- a composition comprising one or more primer pairs as mentioned herein.
- a composition comprising one or more probes as mentioned herein.

EXAMPLES

The following examples are intended to illustrate the various methods and compounds of the invention

Example 1: Sample preparation

200 µl of patient's blood was pipetted into a vessel containing glass beads, acid-washed (Sigma-Aldrich) with a diameter 106 µm and finer. On a commerical IKA MS2 Minishaker the suspension was vortexed for 1 to 3 min at ambient temperature.

Example 2: Nucleic acid extraction and purification

The extraction and purification of nucleic acid was performed on a modified commercial biorobot EZ1 (Qiagen). The vortexed blood sample was incubated with lysostaphin at 37°C for 10 min. In a following reaction step the nucleic acid was immobilized on magnetic beads. By actuating the magnetic beads via external magnetic fields in different washing and rinsing solutions, the immobilized nucleic acid will be freed from cell debris and other cell proteins. In a final elution step the nucleic acid will be separated from the magnetic particles and then mixed in a separate vessel with a multiplex PCR Mastermix (Qiagen). After mixing, the solution will be distributed to strip vessels with multiplex primer pairs and human control primer pairs.

Example 3: Multiplex PCR

Multiplex PCR was performed on a commercial thermal cycler, e.g. Perkin Elmer 9700, with a Qiagen Multiplex PCR kit. Following the universal multiplex cycling protocol, a first initial activation step was performed at 95°C for 15 min. It followed a 3 step cycling with denaturing at 94°C for 30 sec, annealing at 61°C for 90 sec, and extension at 72°C for 90 sec. The cycle number was between 30 and 45, dependend on the sensitivity requirements. A final extension at 72°C for 10 min finished the amplification.

Example 4: Detection

The detection of the amplified nucleic acid was performed on a DNA 1000 kit. The chip, which is part of the kit, was read out with a 2100 bioanalyzer. Kits and Analyzer were purchased from Agilent Technologies.

According to the manufacturer's recommendation the chip was prepared and loaded with the references and amplified nucleic acids and then inserted in the 2100 bioanalyzer. After an analysis run time of 30 min, proprietary software running on a PC read out and analyzed the data from the bioanalyzer.

CLAIMS:

1. Method of detecting one or more micro-organisms and/or one or more antibiotic resistance markers in a sample, comprising identifying the presence of distinct nucleic acid regions.

2. Method according to claim 1, wherein said distinct nucleic acid region of a micro-organism is in the 23S RNA gene.

3. Method according to claims 1 or 2, wherein said distinct nucleic acid region is identified using nucleic acid amplification.

4. Method according to claims 2 or 3, wherein multiplex PCR is used to detect two or more distinct nucleic acid regions.

5. Method according to claims 1 or 2, wherein said distinct nucleic acid region is identified using hybridisation.

6. Method according to claims 3 or 4, wherein said micro-organism is *Enterobacter cloacae,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 3 and 4 or SEQ ID NOs: 5 and 6.

7. Method according to claim 5, wherein said micro-organism is *Enterobacter cloacae,* comprising the use of a hybridisation probe corresponding to a sequence represented by any of SEQ ID NOs: 3 to 6.

8. Method according to any of claims 1 to 5, wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 1 or 2, and a micro-organism is *Enterobacter cloacae*.

9. Method according to claims 3 or 4, wherein said micro-organism is *Enterococcus faecalis,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12, or SEQ ID NOs: 15 and 11.

10. Method according to claim 5, wherein said micro-organism is *Enterococcus faecalis,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 9 to 15.

11. Method according to any of claims 1 to 5 wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 7 or 8, and a micro-organism is *Enterococcus faecalis.*

12. Method according to claims 3 or 4, wherein said micro-organism is *Enterococcus faecium,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 18 and 19, SEQ ID NOs: 19 and 20, or SEQ ID NOs: 20 and 21.

13. Method according to claim 5, wherein said micro-organism is *Enterococcus faecium,* comprising the use of a probe corresponding to the sequences represented by SEQ ID NOs: 19 to 21.

14. Method according to any of claims 1 to 5 wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 16 or 17, and a micro-organism is *Enterococcus faecium.*

15. Method according to claims 3 or 4, wherein said micro-organism is *Escherichia coli,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 24 and 25, SEQ ID NOs: 24 and 26, SEQ ID NOs: 27 and 29, or SEQ ID NOs: 28 and 29.

16. Method according to claim 5, wherein said micro-organism is *Escherichia coli,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 24 to 29.

17. Method according to any of claims 1 to 5 wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 22 or 23, and a micro-organism is *Escherichia coli.*

18. Method according to claims 3 or 4, wherein said micro-organism is *Klebsiella pneumoniae,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36 or SEQ ID NOs: 37 and 33.

19. Method according to claim 5, wherein said micro-organism is *Klebsiella pneumoniae,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 32 to 37.

20. Method according to any of claims 1 to 5 wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 30 or 31, and a micro-organism is *Klebsiella pneumoniae.*

21. Method according to claims 3 or 4, wherein said micro-organism is *Pseudomonas aeruginosa,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 40 and 41 or SEQ ID NOs: 40 and 42.

22. Method according to claim 5, wherein said micro-organism is *Pseudomonas aeruginosa,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 40 to 42.

23. Method according to any of claims 1 to 5 wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 38 or 39, and a micro-organism is *Pseudomonas aeruginosa.*

24. Method according to claims 3 or 4, wherein a micro-organism is *Staphylococcus aureus,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, SEQ ID NOs: 50 and 51.

25. Method according to claim 5, wherein said micro-organism is *Staphylococcus aureus,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 45 to 51.

26. Method according to any of claims 1 to 5 wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 43 or 44, and a micro-organism is *Staphylococcus aureus.*

27. Method according to claims 3 or 4, wherein said micro-organism is *Staphylococcus epidermidis,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, or SEQ ID NOs: 63 and 61.

28. Method according to claim 5, wherein said micro-organism is *Staphylococcus epidermidis,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 54 to 63.

29. Method according to any of claims 1 to 5 wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 52 or 53, and a micro-organism is *Staphylococcus epidermidis.*

30. Method according to claims 3 or 4, wherein said micro-organism is *Candida albicans,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 66 and 67, SEQ ID NOs: 68 and 69, or SEQ ID NOs: 70 and 71.

31. Method according to claim 5, wherein said micro-organism is *Candida albicans,* comprising the use of a probe corresponding to a sequence represented by any of SEQ ID NOs: 66 to 71.

32. Method according to any of claims 1 to 5 wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 64 or 65, and a micro-organism is *Candida albicans.*

33. Method according to claims 3 or 4, wherein said antibiotic resistance marker is $bla_{ges-2,}$ comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 74 and 75 or SEQ ID NOs: 76 and 77.

34. Method according to claim 5, wherein said antibiotic resistance marker is $bla_{ges-2,}$ comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 74 to 77.

35. Method according to any of claims 1, 3 to 5, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 72 or 73, and an antibiotic resistance marker is bla_{ges-2}.

36. Method according to claims 3 or 4, wherein said antibiotic resistance marker is $bla_{shv,}$ comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 80 and 81 or SEQ ID NOs: 82 and 83.

37. Method according to claim 5, wherein said antibiotic resistance marker is $bla_{shv,}$ comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 80 to 83.

38. Method according to any of claims 1, 3 to 5, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 78 or 79, and an antibiotic resistance marker is bla_{shv}.

39. Method according to claims 3 or 4, wherein said antibiotic resistance marker is *mecA,*

comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 86 and 87 or SEQ ID NOs: 88 and 89.

40. Method according to claim 5, wherein said antibiotic resistance marker is *mecA*,

comprising the use of a probe corresponding to the sequences represented by SEQ ID NOs: 86 or 89.

41. Method according to any of claims 1, 3 to 5 wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 84 or 85, and an antibiotic resistance marker is *mecA*.

42. Method according to claims 3 or 4, wherein said antibiotic resistance marker is *spA*, comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 92 and 93 or SEQ ID NOs: 94 and 95.

43. Method according to claim 5, wherein said antibiotic resistance marker is *spA*, comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 92 to 95.

44. Method according to any of claims 1, 3 to 5, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 90 or 91, and an antibiotic resistance marker is *Spa*.

45. Method according to claims 3 or 4, wherein said antibiotic resistance marker is *VanA*,

comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 98 and 99 or SEQ ID NOs: 100 and 101.

46. Method according to claim 5, wherein said antibiotic resistance marker is *VanA*, comprising the use of a probe corresponding to the sequences represented by SEQ ID NOs: 98 to 101.

47. Method according to any of claims 1, 3 to 5, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 96 or 97, and an antibiotic resistance marker is *VanA*.

48. Method according to claims 3 or 4, wherein said antibiotic resistance marker is *VanB,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 104 and 105 or SEQ ID NOs: 106 and 107.

49. Method according to claim 5, wherein said antibiotic resistance marker is *VanB,* comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 104 to 107.

50. Method according to any of claims 1, 3 to 5, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 102 or 103, and an antibiotic resistance marker is *VanB.*

51. Method according to claims 3 or 4, wherein said antibiotic resistance marker is *VanC,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 110 and 111 or SEQ ID NOs: 112 and 113.

52. Method according to claim 5, wherein said antibiotic resistance marker is *VanC,* comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 110 to 113.

53. Method according to any of claims 1, 3 to 5, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 108 or 109, and an antibiotic resistance marker is *VanC.*

54. Method according to claims 3 or 4, wherein said antibiotic resistance marker is *MDR-1,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 116 and 117 or SEQ ID NOs: 118 and 119.

55. Method according to claim 5, wherein said antibiotic resistance marker is *MDR-1,* comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 116 to 119.

56. Method according to any of claims 1, 3 to 5, wherein said distinct nucleic acid region corresponds to SEQ ID NOs: 114 or 115, and an antibiotic resistance marker is *MDR-1.*

57. Method according to claims 3 or 4, wherein said antibiotic resistance marker is *CDR-1,* comprising the use of a pair of amplification primers corresponding to the sequences represented by SEQ ID NOs: 122 and 123 or SEQ ID NOs: 124 and 125.

58. Method according to claim 5, wherein said antibiotic resistance marker is *CDR-1,* comprising the use of a probe corresponding to the sequences represented by any of SEQ ID NOs: 122 to 125.

59. Method according to any of claims 1, 3 to 5, wherein said distinct nucleic acid region corresponds to a sequence represented by SEQ ID NOs: 120 or 121, and an antibiotic resistance marker is *CDR-1.*

60. A container preloaded with one or more pairs of amplification primers, selected from the sequences represented by SEQ ID NOs: 3 and 4, SEQ ID NOs: 5 and 6,SEQ ID NOs: 9 and 10, SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12, SEQ ID NOs: 15 and 11,SEQ ID NOs: 18 and 19, SEQ ID NOs: 20 and 19, SEQ ID NOs: 20 and 21, SEQ ID NOs: 24 and 26, SEQ ID NOs: 24 and 25, SEQ ID NOs: 27 and 29, SEQ ID NOs: 28 and 29, SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36, SEQ ID NOs: 37 and 33, SEQ ID NOs: 40 and 41, SEQ ID NOs: 40 and 42, SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, SEQ ID NOs: 50 and 51, SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, SEQ ID NOs: 63 and 61, SEQ ID NOs: 66 and 67, SEQ ID NOs: 68 and 69, SEQ ID NOs: 70 and 71, SEQ ID NOs: 74 and 75, SEQ ID NOs: 76 and 77, SEQ ID NOs: 80 and 81, SEQ ID NOs: 82 and 83, SEQ ID NOs: 86 and 87, SEQ ID NOs: 88 and 89, SEQ ID NOs: 92 and 93, SEQ ID NOs: 94 and 95, SEQ ID NOs: 98 and 99, SEQ ID NOs: 100 and 101, SEQ ID NOs: 104 and 105, SEQ ID NOs: 106 and 107, SEQ ID NOs: 110 and 111, SEQ ID NOs: 112 and 113, SEQ ID NOs: 116 and 117, SEQ ID NOs: 118 and 119, SEQ ID NOs: 122 and 123, and SEQ ID NOs: 124 and 125.

61. A container preloaded with one or more probes, selected from the sequences represented by any of SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29, SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125.

62. A kit comprising one or more pairs of amplification primers, selected from the sequences represented by SEQ ID NOs: 3 and 4, SEQ ID NOs: 5 and 6,SEQ ID NOs: 9 and 10, SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12, SEQ ID NOs: 15 and 11,SEQ ID NOs: 18 and 19, SEQ ID NOs: 20 and 19, SEQ ID NOs: 20 and 21, SEQ ID NOs: 24 and 26, SEQ ID NOs: 24 and 25, SEQ ID NOs: 27 and 29, SEQ ID NOs: 28 and 29, SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36, SEQ ID NOs: 37 and 33, SEQ ID NOs: 40 and 41, SEQ ID NOs: 40 and 42, SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, SEQ ID NOs: 50 and 51, SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, SEQ ID NOs: 63 and 61, SEQ ID NOs: 66 and 67, SEQ ID NOs: 68 and 69, SEQ ID NOs: 70 and 71, SEQ ID NOs: 74 and 75, SEQ ID NOs: 76 and 77, SEQ ID NOs: 80 and 81, SEQ ID NOs: 82 and 83, SEQ ID NOs: 86 and 87, SEQ ID NOs: 88 and 89, SEQ ID NOs: 92 and 93, SEQ ID NOs: 94 and 95, SEQ ID NOs: 98 and 99, SEQ ID NOs: 100 and 101, SEQ ID NOs: 104 and 105, SEQ ID NOs: 106 and 107, SEQ ID NOs: 110 and 111, SEQ ID NOs: 112 and 113, SEQ ID NOs: 116 and 117, SEQ ID NOs: 118 and 119, SEQ ID NOs: 122 and 123, and SEQ ID NOs: 124 and 125.

63. A kit comprising one or more probes selected from the sequences represented by SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29, SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125.

64. A kit comprising one or more containers according to claims 60 or 61.

65. A device comprising one or more pairs of amplification primers selected from the sequences represented by SEQ ID NOs: 3 and 4, SEQ ID NOs: 5 and 6,SEQ ID NOs: 9 and 10, SEQ ID NOs: 9 and 11, SEQ ID NOs: 9 and 12, SEQ ID NOs: 13 and 14, SEQ ID NOs: 15 and 12, SEQ ID NOs: 15 and 11,SEQ ID NOs: 18 and 19, SEQ ID NOs: 20 and 19, SEQ ID NOs: 20 and 21, SEQ ID NOs: 24 and 26, SEQ ID NOs: 24 and 25, SEQ ID NOs: 27 and 29, SEQ ID NOs: 28 and 29, SEQ ID NOs: 32 and 34, SEQ ID NOs: 32 and 33, SEQ ID NOs: 35 and 36, SEQ ID NOs: 37 and 33, SEQ ID NOs: 40 and 41, SEQ ID NOs: 40 and 42, SEQ ID NOs: 45 and 46, SEQ ID NOs: 48 and 47, SEQ ID NOs: 48 and 49, SEQ ID NOs: 48 and 51, SEQ ID NOs: 50 and 51, SEQ ID NOs: 54 and 55, SEQ ID NOs: 54 and 56, SEQ ID NOs: 54 and 57, SEQ ID NOs: 58 and 57, SEQ ID NOs: 58 and 59, SEQ ID NOs: 58 and 60, SEQ ID NOs: 58 and 61, SEQ ID NOs: 58 and 62, SEQ ID NOs: 63 and 59, SEQ ID NOs: 63 and 60, SEQ ID NOs: 63 and 61, SEQ ID NOs: 66 and 67, SEQ ID NOs: 68 and 69, SEQ ID NOs: 70 and 71, SEQ ID NOs: 74 and 75, SEQ ID NOs: 76 and 77, SEQ ID NOs: 80 and 81, SEQ ID NOs: 82 and 83, SEQ ID NOs: 86 and 87, SEQ ID NOs: 88 and 89, SEQ ID NOs: 92 and 93, SEQ ID NOs: 94 and 95, SEQ ID NOs: 98 and 99, SEQ ID NOs: 100 and 101, SEQ ID NOs: 104 and 105, SEQ ID NOs: 106 and 107, SEQ ID NOs: 110 and 111, SEQ ID NOs: 112 and 113, SEQ ID NOs: 116 and 117, SEQ ID NOs: 118 and 119, SEQ ID NOs: 122 and 123, SEQ ID NOs: 124 and 125.

66. A device comprising one or more probes, selected from the sequences represented by SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29, SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125.

67. Use of a container, kit or device according to any of claims 60 to 66 for detecting one or more micro-organisms and/or one or more antibiotic resistance markers in a sample.

68. Composition comprising a probe selected from the sequences represented by: SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29,

SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125.

69. Composition comprising two or more probes selected from the sequences represented by: SEQ ID NOs: 3 to 6, SEQ ID NOs: 9 to 15, SEQ ID NOs: 18 to 21, SEQ ID NOs: 24 to 29, SEQ ID NOs: 32 to 37, SEQ ID NOs: 40 to 42, SEQ ID NOs: 45 to 51, SEQ ID NOs: 54 to 63, SEQ ID NOs: 66 to 71, SEQ ID NOs: 74 to 77, SEQ ID NOs: 80 to 83, SEQ ID NOs: 86 to 89, SEQ ID NOs: 92 to 95, SEQ ID NOs: 98 to 101, SEQ ID NOs: 104 to 107, SEQ ID NOs: 110 to 113, SEQ ID NOs: 116 to 119, and SEQ ID NOs: 122 to 125..

70. Composition comprising a pair of amplification primers selected from the sequences represented by: SEQ ID NOs: 3 and 4, SEQ ID NOs: 7 and 8, SEQ ID NOs: 11 and 12, SEQ ID NOs: 15 and 16, SEQ ID NOs: 19 and 20, SEQ ID NOs: 23 and 24, SEQ ID NOs: 27 and 28, SEQ ID NOs: 31 and 32, SEQ ID NOs: 35 and 36, SEQ ID NOs: 39 and 40, SEQ ID NOs: 43 and 44, SEQ ID NOs: 47 and 48, SEQ ID NOs: 51 and 52, SEQ ID NOs: 55 and 56, and SEQ ID NOs: 59 and 60.

71. Composition comprising two or more pairs of amplification primers selected from the sequences represented by: SEQ ID NOs: 3 and 4, SEQ ID NOs: 7 and 8, SEQ ID NOs: 11 and 12, SEQ ID NOs: 15 and 16, SEQ ID NOs: 19 and 20, SEQ ID NOs: 23 and 24, SEQ ID NOs: 27 and 28, SEQ ID NOs: 31 and 32, SEQ ID NOs: 35 and 36, SEQ ID NOs: 39 and 40, SEQ ID NOs: 43 and 44, SEQ ID NOs: 47 and 48, SEQ ID NOs: 51 and 52, SEQ ID NOs: 55 and 56, and SEQ ID NOs: 59 and 60.

72. Sequence of 23S RNA gene selected from the sequences represented by SEQ ID NOs: 131 to 157.

73. Sequence of antibiotic resistance marker selected from the sequences represented by SEQ ID NOs: 158 to 261.

74. A method according to any of claims 6 to 59, wherein said sequence(s) represented by said SEQ ID NO(s) is (are) the complement(s) of said SEQ ID NO(s).

75. A method according to any of claims 6 to 59 and 74, wherein said sequence(s) represented by said SEQ ID NO(s) is (are) an homologous sequence(s) of said SEQ ID NO (s).

76. A container, kit, device or use according to any of claims 60 to 67 wherein said sequence(s) represented by said SEQ ID NO(s) is (are) the complement(s) of said SEQ ID NO(s).

77. A container, kit, device or use according to any of claims 60 to 67 and 76 wherein said sequence(s) represented by said SEQ ID NO(s) is (are) an homologous sequence(s) of said SEQ ID NO(s).

78. A composition according to claims 68 to 71 wherein said sequence(s) represented by said SEQ ID NO(s) is (are) the complement(s) of said SEQ ID NO(s).

79. A composition according to any of claims 68 to 71, and 78 wherein a sequence represented by a SEQ ID NO is an homologous sequence of said SEQ ID NO.

80. Sequence of 23S RNA gene according to claim 72 wherein said sequence represented by said SEQ ID NO is the complement(s) of said SEQ ID NO.

81. Sequence of 23S RNA gene according to claims 72 or 80 wherein said sequence represented by said SEQ ID NO is an homologous sequence of said SEQ ID NO.

82. Sequence of an antibiotic resistance marker according to claim 73 wherein said sequence(s) represented by said SEQ ID NO(s) is(are) the complement(s) of said SEQ ID NO(s).

83. Sequence of an antibiotic resistance marker according to claims 73 or 82 wherein said sequence(s) represented by said SEQ ID NO(s) is(are) an homologous sequence(s) of said SEQ ID NO(s).

FIGURE 1-1

1 *Enterobacter cloacae*

```
'07BLSU.seq' (SEQ ID NO: 130)   GAGGAAAAGAAATCAACCGAGATTCCCCCAGTAGCGGCGAGCGAACGGGG 50
'08BLSU.seq' (SEQ ID NO: 131)   GAGGAAAAGAAATCAACCGAGATTCCCCCAGTAGCGGCGAGCGAACGGGG 50
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   AGCAGCCCAGAGTCTGAATCAGCTTGTGTGTTAGTGGAAGCGTCTGGAAA 100
'08BLSU.seq' (SEQ ID NO: 131)   AGCAGCCCAGAGTCTGAATCAGCTTGTGTGTTAGTGGAAGCGTCTGGAAA 100
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GTCGCACGGTACAGGGTGAAAGTCCCGTACACGAAAACACACAGGCTGTG 150
'08BLSU.seq' (SEQ ID NO: 131)   GTCGCACGGTACAGGGTGAAAGTCCCGTACACGAAAACACACAGGCTGTG 150
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   AACTCGAAGAGTAGGGCGGGACACGTGGTATCCTGTCTGAATATGGGGGG 200
'08BLSU.seq' (SEQ ID NO: 131)   AACTCGAAGAGTAGGGCGGGACACGTGGTATCCTGTCTGAATATGGGGGG 200
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   ACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGAACCAGTAC 250
'08BLSU.seq' (SEQ ID NO: 131)   ACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGAACCAGTAC 250
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   CGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGAGTGAAAAAGAACCT 300
'08BLSU.seq' (SEQ ID NO: 131)   CGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGAGTGAAAAAGAACCT 300
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GAAACCGTGTACGTACAAGCAGTGGGAGCACCTTCGTGGTGTGACTGCGT 350
'08BLSU.seq' (SEQ ID NO: 131)   GAAACCGTGTACGTACAAGCAGTGGGAGCACCTTCGTGGTGTGACTGCGT 350
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   ACCTTTTGTATAATGGGTCAGCGACTTATATTCTGTAGCAAGGTTAACCG 400
'08BLSU.seq' (SEQ ID NO: 131)   ACCTTTTGTATAATGGGTCAGCGACTTATATTCTGTAGCAAGGTTAACCG 400
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   TATAGGGGAGCCGAAGGRAAACCGAGTCTTAACTGGGCGTTAAGTTGCAG 450
'08BLSU.seq' (SEQ ID NO: 131)   TATAGGGGAGCCGAAGGRAAACCGAGTCTTAACTGGGCGTTAAGTTGCAG 450
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGTTGAAGGTTGG 500
'08BLSU.seq' (SEQ ID NO: 131)   GGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGTTGAAGGTTGG 500
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAAATTAGCGGAT 550
'08BLSU.seq' (SEQ ID NO: 131)   GTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAAATTAGCGGAT 550
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GACCTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGATAGCTGGTTC 600
'08BLSU.seq' (SEQ ID NO: 131)   GACCTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGATAGCTGGTTC 600
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   TCCCCGAAAGCTATTTAGGTAGCGCCTCGTGAACTCATCTTCGGGGGTAG 650
'08BLSU.seq' (SEQ ID NO: 131)   TCCCCGAAAGCTATTTAGGTAGCGCCTCGTGAACTCATCTTCGGGGGTAG 650
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   AGCACTGTTTCGGCTAGGGGGCCATCCCGGCTTACCAACCCGATGCAAAC 700
'08BLSU.seq' (SEQ ID NO: 131)   AGCACTGTTTCGGCTAGGGGGCCATCCCGGCTTACCAACCCGATGCAAAC 700
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   TACGAATACCGAAGAATGTTATCACGGGAGACACACGGCGGGTGCTAACG 750
'08BLSU.seq' (SEQ ID NO: 131)   TACGAATACCGAAGAATGTTATCACGGGAGACACACGGCGGGTGCTAACG 750
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------
```

FIGURE 1-2

```
'07BLSU.seq' (SEQ ID NO: 130)   TCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAGGTCCCAAAGT 800
'08BLSU.seq' (SEQ ID NO: 131)   TCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAGGTCCCAAAGT 800
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   CATGGTTAAGTGGGAAACGATGTGGGAAGGCCCAGACAGCCAGGATGTTG 850
'08BLSU.seq' (SEQ ID NO: 131)   CATGGTTAAGTGGGAAACGATGTGGGAAGGCCCAGACAGCCAGGATGTTG 850
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GCTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTCACTGGTCGAG 900
'08BLSU.seq' (SEQ ID NO: 131)   GCTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTCACTGGTCGAG 900
'E_cloac.seq' (SEQ ID NO: 132)  ----------------CATTTAAAGAAAGCGTAATAGCTCACTGGTCGAG 34
                                                **********************************

'07BLSU.seq' (SEQ ID NO: 130)   TCGGCCTGCGCGGAAGATGTAACGGGGCTAAACCATGCACCGAAGCTGCG 950
'08BLSU.seq' (SEQ ID NO: 131)   TCGGCCTGCGCGGAAGATGTAACGGGGCTAAACCATGCACCGAAGCTGCG 950
'E_cloac.seq' (SEQ ID NO: 132)  TCGGCCTGCGCGGAAGATGTAACGGGGCTAAACCATGCACCGAAGCTGCG 84
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   GCAGCGACGCTTATGCGTTGTTGGGTAGGGGAGCGTTCTGTAAGCCGTTG 1000
'08BLSU.seq' (SEQ ID NO: 131)   GCAGCGACGCTTATGCGTTGTTGGGTAGGGGAGCGTTCTGTAAGCCGTTG 1000
'E_cloac.seq' (SEQ ID NO: 132)  GCAGCGACGCTTATGCGTTGTTGGGTAGGGGAGCGTTCTGTAAGCCGTTG 134
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   AAGGTGGCCTGTGAGGGTTGCTGGAGGTATCAGAAGTGCGAATGCTGACA 1050
'08BLSU.seq' (SEQ ID NO: 131)   AAGGTGGCCTGTGAGGGTTGCTGGAGGTATCAGAAGTGCGAATGCTGACA 1050
'E_cloac.seq' (SEQ ID NO: 132)  AAGGTGGCCTGTGAGGGTTGCTGGAGGTATCAGAAGTGCGAATGCTGACA 184
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   TAAGTAACGATAAAGCGGGTGAAARGCCCGCTCGCCGGAAGACCAAGGGT 1100
'08BLSU.seq' (SEQ ID NO: 131)   TAAGTAACGATAAAGCGGGTGAAARGCCCGCTCGCCGGAAGACCAAGGGT 1100
'E_cloac.seq' (SEQ ID NO: 132)  TAAGTAACGATAAAGCGGGTGAAARGCCCGCTCGCCGGAAGACCAAGGGT 234
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   TCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTAAGGCGAGGC 1150
'08BLSU.seq' (SEQ ID NO: 131)   TCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTAAGGCGAGGC 1150
'E_cloac.seq' (SEQ ID NO: 132)  TCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTAAGGCGAGGC 284
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   CGAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTACTTGGTGTT 1200
'08BLSU.seq' (SEQ ID NO: 131)   CGAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTACTTGGTGTT 1200
'E_cloac.seq' (SEQ ID NO: 132)  CGAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTACTTGGTGTT 334
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   ACTGCGAAGGGGGGACGGAGAAGGCTATGTTAGCCGGGCGACGGTTGTCC 1250
'08BLSU.seq' (SEQ ID NO: 131)   ACTGCGAAGGGGGGACGGAGAAGGCTATGTTAGCCGGGCGACGGTTGTCC 1250
'E_cloac.seq' (SEQ ID NO: 132)  ACTGCGAAGGGGGGACGGAGAAGGCTATGTTAGCCGGGCGACGGTTGTCC 384
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   CGGTTTAAGCATGTAGGCGGAGGTTCCAGGTAAATCCGGTACCTTTTAAC 1300
'08BLSU.seq' (SEQ ID NO: 131)   CGGTTTAAGCATGTAGGCGGAGGTTCCAGGTAAATCCGGTACCTTTTAAC 1300
'E_cloac.seq' (SEQ ID NO: 132)  CGGTTTAAGCATGTAGGCGGAGGTTCCAGGTAAATCCGGTACCTTTTAAC 434
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   GCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAATGCCCTG 1350
'08BLSU.seq' (SEQ ID NO: 131)   GCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAATGCCCTG 1350
'E_cloac.seq' (SEQ ID NO: 132)  GCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAATGCCCTG 484
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   CTTCCAGGAAAAGCCTCTAAGCATCAGGTAACAYSAAATCGTACCCCAAA 1400
'08BLSU.seq' (SEQ ID NO: 131)   CTTCCAGGAAAAGCCTCTAAGCATCAGGTAACAYSAAATCGTACCCCAAA 1400
'E_cloac.seq' (SEQ ID NO: 132)  CTTCCAGGAAAAGCCTCTAAGCATCAGGTAACAYSAAATCGTACCCCAAA 534
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   CCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGG 1450
'08BLSU.seq' (SEQ ID NO: 131)   CCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGG 1450
'E_cloac.seq' (SEQ ID NO: 132)  CCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGG 584
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   GTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGGCACGCTG 1500
'08BLSU.seq' (SEQ ID NO: 131)   GTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGGCACGCTG 1500
'E_cloac.seq' (SEQ ID NO: 132)  GTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGGCACGCTG 634
                                **************************************************

'07BLSU.seq' (SEQ ID NO: 130)   ATATGTAGGTGAAGCCCCTGCGGGTGGAGCTGAAATCAGTCGAAGATACC 1550
```

FIGURE 1-3

```
'08BLSU.seq' (SEQ ID NO: 131)   ATATGTAGGTGAAGCCCCTGCGGGTGGAGCTGAAATCAGTCGAAGATACC 1550
'E_cloac.seq' (SEQ ID NO: 132)  ACATGTAGGTGAAGCCCCTGCGGGTGGAGCTGAAATCAGTCGAAGATACC 684
                                * ********************************************

'07BLSU.seq' (SEQ ID NO: 130)   AGCTGGCTGCAACTGTTTATTAAAAACACAGCACTGTGCAAACACGAAAG 1600
'08BLSU.seq' (SEQ ID NO: 131)   AGCTGGCTGCAACTGTTTATTAAAAACACAGCACTGTGCAAACACGAAAG 1600
'E_cloac.seq' (SEQ ID NO: 132)  AGCTGGCTGCAACTGTTTATTAAAAACACAGCACTGTGCAAACACGAAAG 734
                                *********************************************

'07BLSU.seq' (SEQ ID NO: 130)   TGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAATTGATGG 1650
'08BLSU.seq' (SEQ ID NO: 131)   TGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAATTGATGG 1650
'E_cloac.seq' (SEQ ID NO: 132)  TGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAATTGATGG 784
                                *********************************************

'07BLSU.seq' (SEQ ID NO: 130)   GGTTAGCGGYAACGCGAAGCTCTTGATCGAAGCCCCGGTAAACGGCGGCC 1700
'08BLSU.seq' (SEQ ID NO: 131)   GGTTAGCGGYAACGCGAAGCTCTTGATCGAAGCCCCGGTAAACGGCGGCC 1700
'E_cloac.seq' (SEQ ID NO: 132)  GGTTAGCGGYAACGCGAAGCTCTTGATCGAAGCCCCGGTAAACGGCG--- 831
                                ******************************************

'07BLSU.seq' (SEQ ID NO: 130)   GTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCG 1750
'08BLSU.seq' (SEQ ID NO: 131)   GTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCG 1750
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   ACCTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCGAGACTCA 1800
'08BLSU.seq' (SEQ ID NO: 131)   ACCTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCGAGACTCA 1800
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GTGAAATTGAACTCGCTGTGAAGATGCAGTGTACCCGCGGCAAGACGGAA 1850
'08BLSU.seq' (SEQ ID NO: 131)   GTGAAATTGAACTCGCTGTGAAGATGCAGTGTACCCGCGGCAAGACGGAA 1850
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   AGACCCCGTGAACCTTTACTATAGCTTGACACTGAACACTGGTCCTTGAT 1900
'08BLSU.seq' (SEQ ID NO: 131)   AGACCCCGTGAACCTTTACTATAGCTTGACACTGAACACTGGTCCTTGAT 1900
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GTGTAGGATAGGTGGGAGGCTTTGAAGCGTGGACGCCAGTCTGCGTGGAG 1950
'08BLSU.seq' (SEQ ID NO: 131)   GTGTAGGATAGGTGGGAGGCTTTGAAGCGTGGACGCCAGTCTGCGTGGAG 1950
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   CCGTCCTTGAAATACCACCCTTTAATGGCTGGTGTTCTAACGTAGACCCG 2000
'08BLSU.seq' (SEQ ID NO: 131)   CCGTCCTTGAAATACCACCCTTTAATGGCTGGTGTTCTAACGTAGACCCG 2000
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   TWAYCCGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGGGCGGTCT 2050
'08BLSU.seq' (SEQ ID NO: 131)   TWAYCCGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGGGCGGTCT 2050
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   CCTCCCAAAGAGTAACGGAGGAGCACGAAGGTTAGCTAATCCTGGTCGGA 2100
'08BLSU.seq' (SEQ ID NO: 131)   CCTCCCAAAGAGTAACGGAGGAGCACGAAGGTTAGCTAATCCTGGTCGGA 2100
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   CATCAGGAGGTTAGTGCAATGGCATAAGCTAGCTTGACTGCGAGAGTGAC 2150
'08BLSU.seq' (SEQ ID NO: 131)   CATCAGGAGGTTAGTGCAATGGCATAAGCTAGCTTGACTGCGAGAGTGAC 2150
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GGCTCGAGCAGGTGCGAAAGCAGGTCATAGTGATCCGGTGGTTCTGAATG 2200
'08BLSU.seq' (SEQ ID NO: 131)   GGCTCGAGCAGGTGCGAAAGCAGGTCATAGTGATCCGGTGGTTCTGAATG 2200
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   GAAGGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAACAGGCTGA 2250
'08BLSU.seq' (SEQ ID NO: 131)   GAAGGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAACAGGCTGA 2250
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------

'07BLSU.seq' (SEQ ID NO: 130)   TACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCGATGTCGG 2300
'08BLSU.seq' (SEQ ID NO: 131)   TACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCGATGTCGG 2300
'E_cloac.seq' (SEQ ID NO: 132)  -------------------------------------------------
```

FIGURE 1-4

```
'07BLSU.seq' (SEQ ID NO: 130)   CTCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCTGTTCGCC 2350
'08BLSU.seq' (SEQ ID NO: 130)   CTCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCTGTTCGCC 2350
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------


'07BLSU.seq' (SEQ ID NO: 130)   ATTTAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGT 2400
'08BLSU.seq' (SEQ ID NO: 131)   ATTTAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGT 2400
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------


'07BLSU.seq' (SEQ ID NO: 130)   CCCTATCTGCCGTGGGCGCTGGAGAATTGAGGGGGGCTGCTCCTAGTACG 2450
'08BLSU.seq' (SEQ ID NO: 131)   CCCTATCTGCCGTGGGCGCTGGAGAATTGAGGGGGGCTGCTCCTAGTACG 2450
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------


'07BLSU.seq' (SEQ ID NO: 130)   AGAGGACCGGAGTGGACGCATCACTGGTGTTCGGGTTGTCATGCCAATGG 2500
'08BLSU.seq' (SEQ ID NO: 131)   AGAGGACCGGAGTGGACGCATCACTGGTGTTCGGGTTGTCATGCCAATGG 2500
'E_cloac.seq' (SEQ ID NO: 132)  --------------------------------------------------


'07BLSU.seq' (SEQ ID NO: 130)   CACTGCCCGGTAGCTAAATGC 2521
'08BLSU.seq' (SEQ ID NO: 131)   CACTGCCCGGTAGCTAAATGC 2521
'E_cloac.seq' (SEQ ID NO: 132)  ---------------------
```

FIGURE 1-5

2 Enterococcus faecalis

```
'12BLSU.seq' (SEQ ID NO:133) --ATTCGATTCCCTGAGTAGCGGCGAGCGAAACGGGAAGAGCCCAAACCAACAAGCTTGC 58
'11BLSU.seq' (SEQ ID NO:134) --ATTCGATTCCCTGAGTAGCGGCGAGCGAAACGGGAAGAGCCCAAACCAACAAGCTTGC 58
'10BLSU.seq' (SEQ ID NO:135) AAATTCGATTCCCTGAGTAGCGGCGAGCGAAACGGGAAGAGCCCAAACCAACAAGCTTGC 60
'Efaecl.seq' (SEQ ID NO:136) AAATTCGATTCCCTGAGTAGCGGCGAGCGAAACGGGAAGAGCCCAAACCAACAAGCTTGC 60
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TTGTTGGGGTTGTAGGACTCCAATATGGTAGTCTGTTAGTATAGTTGAAGGATTTGGAAA 118
'11BLSU.seq' (SEQ ID NO:134) TTGTTGGGGTTGTAGGACTCCAATATGGTAGTCTGTTAGTATAGTTGAAGGATTTGGAAA 118
'10BLSU.seq' (SEQ ID NO:135) TTGTTGGGGTTGTAGGACTCCAATATGGTAGTCTGTTAGTATAGTTGAAGGATTTGGAAA 120
'Efaecl.seq' (SEQ ID NO:136) TTGTTGGGGTTGTAGGACTCCAATATGGTAGTCTGTTAGTATAGTTGAAGGATTTGGAAA 120
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) ATTCCGCTAAAGAGGGTGAAAGCCCCGTAGACGAAATGCTGACAACACCTAGGAGGATCC 178
'11BLSU.seq' (SEQ ID NO:134) ATTCCGCTAAAGAGGGTGAAAGCCCCGTAGACGAAATGCTGACAACACCTAGGAGGATCC 178
'10BLSU.seq' (SEQ ID NO:135) ATTCCGCTAAAGAGGGTGAAAGCCCCGTAGACGAAATGCTGACAACACCTAGGAGGATCC 180
'Efaecl.seq' (SEQ ID NO:136) ATTCCGCTAAAGAGGGTGAAAGCCCCGTAGACGAAATGCTAACAACACCTAGGAGGATCC 180
                             ************************************* ******************

'12BLSU.seq' (SEQ ID NO:133) TGAGTACGGCGGAACACGAGAAATTCCGTCGGAATCCGCGGGGACCATCCCGCAAGGCTA 238
'11BLSU.seq' (SEQ ID NO:134) TGAGTACGGCGGAACACGAGAAATTCCGTCGGAATCCGCGGGGACCATCCCGCAAGGCTA 238
'10BLSU.seq' (SEQ ID NO:135) TGAGTACGGCGGAACACGAGAAATTCCGTCGGAATCCGCGGGGACCATCCCGCAAGGCTA 240
'Efaecl.seq' (SEQ ID NO:136) TGAGTACGGCGGAACACGAGAAATTCCGTCGGAATCCGCGGGGACCATCCCGCAAGGCTA 240
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) AATACTCCCTAGTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGTGAAAAGCACCCCG 298
'11BLSU.seq' (SEQ ID NO:134) AATACTCCCTAGTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGTGAAAAGCACCCCG 298
'10BLSU.seq' (SEQ ID NO:135) AATACTCCCTAGTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGTGAAAAGCACCCCG 300
'Efaecl.seq' (SEQ ID NO:136) AATACTCCCTAGTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGTGAAAAGCACCCCG 300
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GAAGGGGAGTGAAATAGATCCTGAAACCGTGTGCCTACAACAAGTCAAAGCTCGTTAATG 358
'11BLSU.seq' (SEQ ID NO:134) GAAGGGGAGTGAAATAGATCCTGAAACCGTGTGCCTACAACAAGTCAAAGCTCGTTAATG 358
'10BLSU.seq' (SEQ ID NO:135) GAAGGGGAGTGAAATAGATCCTGAAACCGTGTGCCTACAACAAGTCAAAGCTCGTTAATG 360
'Efaecl.seq' (SEQ ID NO:136) GAAGGGGAGTGAAATAGATCCTGAAACCGTGTGCCTACAACAAGTCAAAGCTCGTTAATG 360
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) AGTGATGGCGTGCCTTTTGTAGAATGAACCGGCGAGTTACGATTGCATGCGAGGTTAAGT 418
'11BLSU.seq' (SEQ ID NO:134) AGTGATGGCGTGCCTTTTGTAGAATGAACCGGCGAGTTACGATTGCATGCGAGGTTAAGT 418
'10BLSU.seq' (SEQ ID NO:135) AGTGATGGCGTGCCTTTTGTAGAATGAACCGGCGAGTTACGATTGCATGCGAGGTTAAGT 420
'Efaecl.seq' (SEQ ID NO:136) AGTGATGGCGTGCCTTTTGTAGAATGAACCGGCGAGTTACGATTGCATGCGAGGTTAAGT 420
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) CGAAGAGACGGAGCCGCAGCGAAAGCGAGTCTGAATAGGGCGAATGAGTATGTAGTCGTA 478
'11BLSU.seq' (SEQ ID NO:134) CGAAGAGACGGAGCCGCAGCGAAAGCGAGTCTGAATAGGGCGAATGAGTATGTAGTCGTA 478
'10BLSU.seq' (SEQ ID NO:135) CGAAGAGACGGAGCCGCAGCGAAAGCGAGTCTGAATAGGGCGAATGAGTATGTAGTCGTA 480
'Efaecl.seq' (SEQ ID NO:136) CGAAGAGACGGAGCCGCAGCGAAAGCGAGTCTGAATAGGGCGAATGAGTATGTAGTCGTA 480
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GACCCGAAACCATGTGATCTACCCATGTCCAGGTTGAAGGTGCGGTAAAACGCACTGGAG 538
'11BLSU.seq' (SEQ ID NO:134) GACCCGAAACCATGTGATCTACCCATGTCCAGGTTGAAGGTGCGGTAAAACGCACTGGAG 538
'10BLSU.seq' (SEQ ID NO:135) GACCCGAAACCATGTGATCTACCCATGTCCAGGTTGAAGGTGCGGTAAAACGCACTGGAG 540
'Efaecl.seq' (SEQ ID NO:136) GACCCGAAACCATGTGATCTACCCATGTCCAGGTTGAAGGTGCGGTAAAACGCACTGGAG 540
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GACCGAACCCACGTACGTTGAAAAGTGCGGGGATGAGGTGTGGGTAGCGGAGAAATTCCA 598
'11BLSU.seq' (SEQ ID NO:134) GACCGAACCCACGTACGTTGAAAAGTGCGGGGATGAGGTGTGGGTAGCGGAGAAATTCCA 598
'10BLSU.seq' (SEQ ID NO:135) GACCGAACCCACGTACGTTGAAAAGTGCGGGGATGAGGTGTGGGTAGCGGAGAAATTCCA 600
'Efaecl.seq' (SEQ ID NO:136) GACCGAACCCACGTACGTTGAAAAGTGCGGGGATGAGGTGTGGGTAGCGGAGAAATTCCA 600
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) AACGAACTTGGAGATAGCTGGTTCTCTCCGAAATAGCTTTAGGGCTAGCCTCGGAATTGA 658
'11BLSU.seq' (SEQ ID NO:134) AACGAACTTGGAGATAGCTGGTTCTCTCCGAAATAGCTTTAGGGCTAGCCTCGGAATTGA 658
'10BLSU.seq' (SEQ ID NO:135) AACGAACTTGGAGATAGCTGGTTCTCTCCGAAATAGCTTTAGGGCTAGCCTCGGAATTGA 660
'Efaecl.seq' (SEQ ID NO:136) AACGAACTTGGAGATAGCTGGTTCTCTCCGAAATAGCTTTAGGGCTAGCCTCGGAATTGA 660
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GAATGATGGAGGTAGAGCACTGTTTGGACTAGGGGCCCATCTCGGGTTACCGAATTCAGA 718
'11BLSU.seq' (SEQ ID NO:134) GAATGATGGAGGTAGAGCACTGTTTGGACTAGGGGCCCATCTCGGGTTACCGAATTCAGA 718
'10BLSU.seq' (SEQ ID NO:135) GAATGATGGAGGTAGAGCACTGTTTGGACTAGGGGCCCATCTCGGGTTACCGAATTCAGA 720
'Efaecl.seq' (SEQ ID NO:136) GAATGATGGAGGTAGAGCACTGTTTGGACTAGGGGCCCATCTCGGGTTACCGAATTCAGA 720
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TAAACTCCGAATGCCATTCATTTATATCCGGGAGTCAGACTGCGAGTGATAAGATCCGTA 778
'11BLSU.seq' (SEQ ID NO:134) TAAACTCCGAATGCCATTCATTTATATCCGGGAGTCAGACTGCGAGTGATAAGATCCGTA 778
```

FIGURE 1-6

```
'10BLSU.seq' (SEQ ID NO:135) TAAACTCCGAATGCCATTCATTTATATCCGGGAGTCAGACTGCGAGTGATAAGATCCGTA 780
'Efaecl.seq' (SEQ ID NO:136) TAAACTCCGAATGCCATTCATTTATATCCGGGAGTCAGACTGCGAGTGATAAGATCCGTA 780
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GTCGAAAGGGAAACAGCCCAGACCACCAGCTAAGGTCCCAAAATATATGTTAAGTGGAAA 838
'11BLSU.seq' (SEQ ID NO:134) GTCGAAAGGGAAACAGCCCAGACCACCAGCTAAGGTCCCAAAATATATGTTAAGTGGAAA 838
'10BLSU.seq' (SEQ ID NO:135) GTCGAAAGGGAAACAGCCCAGACCACCAGCTAAGGTCCCAAAATATATGTTAAGTGGAAA 840
'Efaecl.seq' (SEQ ID NO:136) GTCGAAAGGGAAACAGCCCAGACCACCAGCTAAGGTCCCAAAATATATGTTAAGTGGAAA 840
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) AGGATGTGGGGTTGCACAGACAACTAGGATGTTGGCTTAGAAGCAGCCACCATTTAAAGA 898
'11BLSU.seq' (SEQ ID NO:134) AGGATGTGGGGTTGCACAGACAACTAGGATGTTGGCTTAGAAGCAGCCACCATTTAAAGA 898
'10BLSU.seq' (SEQ ID NO:135) AGGATGTGGGGTTGCACAGACAACTAGGATGTTGGCTTAGAAGCAGCCACCATTTAAAGA 900
'Efaecl.seq' (SEQ ID NO:136) AGGATGTGGGGTTGCACAGACAACTAGGATGTTGGCTTAGAAGCAGCCACCATTTAAAGA 900
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GTGCGTAATAGCTCACTAGTCGAGTGACCCTGCGCCGAAAATGTACCGGGGCTAAACATA 958
'11BLSU.seq' (SEQ ID NO:134) GTGCGTAATAGCTCACTAGTCGAGTGACCCTGCGCCGAAAATGTACCGGGGCTAAACATA 958
'10BLSU.seq' (SEQ ID NO:135) GTGCGTAATAGCTCACTAGTCGAGTGACCCTGCGCCGAAAATGTACCGGGGCTAAACATA 960
'Efaecl.seq' (SEQ ID NO:136) GTGCGTAATAGCTCACTAGTCGAGTGACCCTGCGCCGAAAATGTACCGGGGCTAAACATA 960
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TTACCGAAGCTGTGGACTACACCATTAGGTGTAGTGGTAGGAGAGCGTTCTAAGGGCGTT 1018
'11BLSU.seq' (SEQ ID NO:134) TTACCGAAGCTGTGGACTACACCATTAGGTGTAGTGGTAGGAGAGCGTTCTAAGGGCGTT 1018
'10BLSU.seq' (SEQ ID NO:135) TTACCGAAGCTGTGGACTACACCATTAGGTGTAGTGGTAGGAGAGCGTTCTAAGGGCGTT 1020
'Efaecl.seq' (SEQ ID NO:136) TTACCGAAGCTGTGGACTACACCATTAGGTGTAGTGGTAGGAGAGCGTTCTAAGGGCGTT 1020
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GAAGGTCGATCGTGAGGACGGCTGGAGCGCTTAGAAGTGAGAATGCCGGTATGAGTAGCG 1078
'11BLSU.seq' (SEQ ID NO:134) GAAGGTCGATCGTGAGGACGGCTGGAGCGCTTAGAAGTGAGAATGCCGGTATGAGTAGCG 1078
'10BLSU.seq' (SEQ ID NO:135) GAAGGTCGATCGTGAGGACGGCTGGAGCGCTTAGAAGTGAGAATGCCGGTATGAGTAGCG 1080
'Efaecl.seq' (SEQ ID NO:136) GAAGGTCGATCGTGAGGACGGCTGGAGCGCTTAGAAGTGAGAATGCCGGTATGAGTAGCG 1080
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) AAAGACAGGTGAGAATCCTGTCCACCGTATGACTAAGGTTTCCTGGGGAAGGCTCGTCCG 1138
'11BLSU.seq' (SEQ ID NO:134) AAAGACAGGTGAGAATCCTGTCCACCGTATGACTAAGGTTTCCTGGGGAAGGCTCGTCCG 1138
'10BLSU.seq' (SEQ ID NO:135) AAAGACAGGTGAGAATCCTGTCCACCGTATGACTAAGGTTTCCTGGGGAAGGCTCGTCCG 1140
'Efaecl.seq' (SEQ ID NO:136) AAAGACAGGTGAGAATCCTGTCCACCGTATGACTAAGGTTTCCTGGGGAAGGCTCGTCCG 1140
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) CCCAGGGTTAGTCGGGACCTAAGCCGAGGCCGATAGGCGTAGGCGATGGACAACAGGTTG 1198
'11BLSU.seq' (SEQ ID NO:134) CCCAGGGTTAGTCGGGACCTAAGCCGAGGCCGATAGGCGTAGGCGATGGACAACAGGTTG 1198
'10BLSU.seq' (SEQ ID NO:135) CCCAGGGTTAGTCGGGACCTAAGCCGAGGCCGATAGGCGTAGGCGATGGACAACAGGTTG 1200
'Efaecl.seq' (SEQ ID NO:136) CCCAGGGTTAGTCGGGACCTAAGCCGAGGCCGATAGGCGTAGGCGATGGACAACAGGTTG 1200
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) ATATTCCTGTACCAGTTGTTTTTGTTTGAGCAATGGAGGGACGCAGTAGGCTAAGGAATG 1258
'11BLSU.seq' (SEQ ID NO:134) ATATTCCTGTACCAGTTGTTTTTGTTTGAGCAATGGAGGGACGCAGTAGGCTAAGGAATG 1258
'10BLSU.seq' (SEQ ID NO:135) ATATTCCTGTACCAGTTGTTTTTGTTTGAGCAATGGAGGGACGCAGTAGGCTAAGGAATG 1260
'Efaecl.seq' (SEQ ID NO:136) ATATTCCTGTACCAGTTGTTTTTGTTTGAGCAATGGAGGGACGCAGTAGGCTAAGGAATG 1260
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) CATGCGATTGGAAGTGCATGTCCAAGCAATGAGTCTTGAGTAGAGTTAAATGCTTTACTC 1318
'11BLSU.seq' (SEQ ID NO:134) CATGCGATTGGAAGTGCATGTCCAAGCAATGAGTCTTGAGTAGAGTTAAATGCTTTACTC 1318
'10BLSU.seq' (SEQ ID NO:135) CATGCGATTGGAAGTGCATGTCCAAGCAATGAGTCTTGAGTAGAGTTAAATGCTTTACTC 1320
'Efaecl.seq' (SEQ ID NO:136) CATGCGATTGGAAGTGCATGTCCAAGCAATGAGTCTTGAGTAGAGTTAAATGCTTTACTC 1320
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TTTAAGGACAAGTTGTGAYGGGGAGCGAAATAATAGTAGCGAAGTTCCTGATGTCACACT 1378
'11BLSU.seq' (SEQ ID NO:134) TYTAAGGACAAGTTGTGACGGGGAGCGAAATAATAGTAGCGAAGTTCCTGATGTCACACT 1378
'10BLSU.seq' (SEQ ID NO:135) TTTAAGGACAAGTTGTGACGGGGAGCGAAATAATAGTAGCGAAGTTCCTGATGTCACACT 1380
'Efaecl.seq' (SEQ ID NO:136) TTTAAGGACAAGTTGTGACGGGGAGCGAAATAATAGTAGCGAAGTTCCTGATGTCACACT 1380
                             * ********** ****************************************

'12BLSU.seq' (SEQ ID NO:133) GCCAAGAAAAGCTTCTAGTGAGAAAACAACTGCCCGTACCGTAAACCGACACAGGTAGTC 1438
'11BLSU.seq' (SEQ ID NO:134) GCCAAGAAAAGCTTCTAGTGAGAAAACAACTGCCCGTACCGTAAACCGACACAGGTAGTC 1438
'10BLSU.seq' (SEQ ID NO:135) GCCAAGAAAAGCTTCTAGTGAGAAAACAACTGCCCGTACCGTAAACCGACACAGGTAGTC 1440
'Efaecl.seq' (SEQ ID NO:136) GCCAAGAAAAGCTTCTAGTGAGAAAACAACTGCCCGTACCGTAAACCGACACAGGTAGTC 1440
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GAGGAGAGTATCCTAAGGTGAGCGAGCGAACTCTCGTTAAGGAACTCGGCAAAATGACCC 1498
'11BLSU.seq' (SEQ ID NO:134) GAGGAGAGTATCCTAAGGTGAGCGAGCGAACTCTCGTTAAGGAACTCGGCAAAATGACCC 1498
'10BLSU.seq' (SEQ ID NO:135) GAGGAGAGTATCCTAAGGTGAGCGAGCGAACTCTCGTTAAGGAACTCGGCAAAATGACCC 1500
'Efaecl.seq' (SEQ ID NO:136) GAGGAGAGTATCCTAAGGTGAGCGAGCGAACTCTCGTTAAGGAACTCGGCAAAATGACCC 1500
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) CGTAACTTCGGGAGAAGGGGTGCTGACTTCGGTCAGCCGCAGTGAATAGGCCCAAGCGAC 1558
'11BLSU.seq' (SEQ ID NO:134) CGTAACTTCGGGAGAAGGGGTGCTGACTTCGGTCAGCCGCAGTGAATAGGCCCAAGCGAC 1558
```

FIGURE 1-7

```
'10BLSU.seq' (SEQ ID NO:135) CGTAACTTCGGGAGAAGGGGTGCTGACTTCGGTCAGCCGCAGTGAATAGGCCCAAGCGAC 1560
'Efaecl.seq' (SEQ ID NO:136) CGTAACTTCGGGAGAAGGGGTGCTGACTTCGGTCAGCCGCAGTGAATAGGCCCAAGCGAC 1560
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TGTTTATCAAAAACACAGGTCTCTGCAAAATCGTAAGATGAAGTATAGGGGCTGACGCCT 1618
'11BLSU.seq' (SEQ ID NO:134) TGTTTATCAAAAACACAGGTCTCTGCAAAATCGTAAGATGAAGTATAGGGGCTGACGCCT 1618
'10BLSU.seq' (SEQ ID NO:135) TGTTTATCAAAAACACAGGTCTCTGCAAAATCGTAAGATGAAGTATAGGGGCTGACGCCT 1620
'Efaecl.seq' (SEQ ID NO:136) TGTTTATCAAAAACACAGGTCTCTGCAAAATCGTAAGATGAAGTATAGGGGCTGACGCCT 1620
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GCCCGGTGCTGGAAGGTTAAGAGGATGGGTTAGCTTCGGCGAAGCTCAGAATTGAAGCCC 1678
'11BLSU.seq' (SEQ ID NO:134) GCCCGGTGCTGGAAGGTTAAGAGGATGGGTTAGCTTCGGCGAAGCTCAGAATTGAAGCCC 1678
'10BLSU.seq' (SEQ ID NO:135) GCCCGGTGCTGGAAGGTTAAGAGGATGGGTTAGCTTCGGCGAAGCTCAGAATTGAAGCCC 1680
'Efaecl.seq' (SEQ ID NO:136) GCCCGGTGCTGGAAGGTTAAGAGGATGGGTTAGCTTCGGCGAAGCTCAGAATTGAAGCCC 1680
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) CAGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAG 1738
'11BLSU.seq' (SEQ ID NO:134) CAGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAG 1738
'10BLSU.seq' (SEQ ID NO:135) CAGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAG 1740
'Efaecl.seq' (SEQ ID NO:136) CAGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAG 1740
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TTCCGACCCGCACGAAAGGCGTAACGATTTGGGCACTGTCTCAACGAGAGACTCGGTGAA 1798
'11BLSU.seq' (SEQ ID NO:134) TTCCGACCCGCACGAAAGGCGTAACGATTTGGGCACTGTCTCAACGAGAGACTCGGTGAA 1798
'10BLSU.seq' (SEQ ID NO:135) TTCCGACCCGCACGAAAGGCGTAACGATTTGGGCACTGTCTCAACGAGAGACTCGGTGAA 1800
'Efaecl.seq' (SEQ ID NO:136) TTCCGACCCGCACGAAAGGCGTAACGATTTGGGCACTGTCTCAACGAGAGACTCGGTGAA 1800
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) ATTTTAGTACCTGTGAAGATGCAGGTTACCCGCGACAGGACGGAAAGACCCCATGGAGCT 1858
'11BLSU.seq' (SEQ ID NO:134) ATTTTAGTACCTGTGAAGATGCAGGTTACCCGCGACAGGACGGAAAGACCCCATGGAGCT 1858
'10BLSU.seq' (SEQ ID NO:135) ATTTTAGTACCTGTGAAGATGCAGGTTACCCGCGACAGGACGGAAAGACCCCATGGAGCT 1860
'Efaecl.seq' (SEQ ID NO:136) ATTTTAGTACCTGTGAAGATGCAGGTTACCCGCGACAGGACGGAAAGACCCCATGGAGCT 1860
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TTACTGTAGTTTGATATTGAGTGTTTGTACCACATGTACAGGATAGGTAGGAGCCGATGA 1918
'11BLSU.seq' (SEQ ID NO:134) TTACTGTAGTTTGATATTGAGTGTTTGTACCACATGTACAGGATAGGTAGGAGCCGATGA 1918
'10BLSU.seq' (SEQ ID NO:135) TTACTGTAGTTTGATATTGAGTGTTTGTACCACATGTACAGGATAGGTAGGAGCCGATGA 1920
'Efaecl.seq' (SEQ ID NO:136) TTACTGTAGTTTGATATTGAGTGTTTGTACCACATGTACAGGATAGGTAGGAGCCGATGA 1920
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GACCGGAACGCTAGTTTCGGAGGAGGCGCTGGTGGGATACTACCCTTGTGTTATGAACCC 1978
'11BLSU.seq' (SEQ ID NO:134) GACCGGAACGCTAGTTTCGGAGGAGGCGCTGGTGGGATACTACCCTTGTGTTATGAACCC 1978
'10BLSU.seq' (SEQ ID NO:135) GACCGGAACGCTAGTTTCGGAGGAGGCGCTGGTGGGATACTACCCTTGTGTTATGAACCC 1980
'Efaecl.seq' (SEQ ID NO:136) GACCGGAACGCTAGTTTCGGAGGAGGCGCTGGTGGGATACTACCCTTGTGTTATGAACCC 1980
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TCTAACCCGCACCACTAATCGTGGTGGGAGACAGTGTCAGATGGGCAGTTTGACTGGGGC 2038
'11BLSU.seq' (SEQ ID NO:134) TCTAACCCGCACCACTAATCGTGGTGGGAGACAGTGTCAGATGGGCAGTTTGACTGGGGC 2038
'10BLSU.seq' (SEQ ID NO:135) TCTAACCCGCACCACTAATCGTGGTGGGAGACAGTGTCAGATGGGCAGTTTGACTGGGGC 2040
'Efaecl.seq' (SEQ ID NO:136) TCTAACCCGCACCACTAATCGTGGTGGGAGACAGTGTCAGATGGGCAGTTTGACTGGGGC 2040
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GGTCGCCTCCTAAAAGGTAACGGAGGCGCCCAAAGGTTCCCTCAGAATGGTTGGAAATCA 2098
'11BLSU.seq' (SEQ ID NO:134) GGTCGCCTCCTAAAAGGTAACGGAGGCGCCCAAAGGTTCCCTCAGAATGGTTGGAAATCA 2098
'10BLSU.seq' (SEQ ID NO:135) GGTCGCCTCCTAAAAGGTAACGGAGGCGCCCAAAGGTTCCCTCAGAATGGTTGGAAATCA 2100
'Efaecl.seq' (SEQ ID NO:136) GGTCGCCTCCTAAAAGGTAACGGAGGCGCCCAAAGGTTCCCTCAGAATGGTTGGAAATCA 2100
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TTCGAAGAGTGTAAAGGCAGAAGGGAGCTTGACTGCGAGACCTACAAGTCGAGCAGGGAC 2158
'11BLSU.seq' (SEQ ID NO:134) TTCGAAGAGTGTAAAGGCAGAAGGGAGCTTGACTGCGAGACCTACAAGTCGAGCAGGGAC 2158
'10BLSU.seq' (SEQ ID NO:135) TTCGAAGAGTGTAAAGGCAGAAGGGAGCTTGACTGCGAGACCTACAAGTCGAGCAGGGAC 2160
'Efaecl.seq' (SEQ ID NO:136) TTCGAAGAGTGTAAAGGCAGAAGGGAGCTTGACTGCGAGACCTACAAGTCGAGCAGGGAC 2160
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GAAAGTCGGGCTTAGTGATCCGGTGGTTCCGCATGGAAGGGCCATCGCTCAACGGATAAA 2218
'11BLSU.seq' (SEQ ID NO:134) GAAAGTCGGGCTTAGTGATCCGGTGGTTCCGCATGGAAGGGCCATCGCTCAACGGATAAA 2218
'10BLSU.seq' (SEQ ID NO:135) GAAAGTCGGGCTTAGTGATCCGGTGGTTCCGCATGGAAGGGCCATCGCTCAACGGATAAA 2220
'Efaecl.seq' (SEQ ID NO:136) GAAAGTCGGGCTTAGTGATCCGGTGGTTCCGCATGGAAGGGCCATCGCTCAACGGATAAA 2220
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) AGCTACCCTGGGGATAACAGGCTTATCTCCCCCAAGAGTCCACATCGACGGGGAGGTTTG 2278
'11BLSU.seq' (SEQ ID NO:134) AGCTACCCTGGGGATAACAGGCTTATCTCCCCCAAGAGTCCACATCGACGGGGAGGTTTG 2278
'10BLSU.seq' (SEQ ID NO:135) AGCTACCCTGGGGATAACAGGCTTATCTCCCCCAAGAGTCCACATCGACGGGGAGGTTTG 2280
'Efaecl.seq' (SEQ ID NO:136) AGCTACCCTGGGGATAACAGGCTTATCTCCCCCAAGAGTCCACATCGACGGGGAGGTTTG 2280
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGTAGTCGGTCCCAAGGGTTGGGCTGT 2338
'11BLSU.seq' (SEQ ID NO:134) GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGTAGTCGGTCCCAAGGGTTGGGCTGT 2338
```

FIGURE 1-8

```
'10BLSU.seq' (SEQ ID NO:135) GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGTAGTCGGTCCCAAGGGTTGGGCTGT 2340
'Efaecl.seq' (SEQ ID NO:136) GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGTAGTCGGTCCCAAGGGTTGGGCTGT 2340
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TCGCCCATTAAAGCGGCACGCGAGCTGGGTTCAGAACGTCGTGAGACAGTTCGGTCCCTA 2398
'11BLSU.seq' (SEQ ID NO:134) TCGCCCATTAAAGCGGCACGCGAGCTGGGTTCAGAACGTCGTGAGACAGTTCGGTCCCTA 2398
'10BLSU.seq' (SEQ ID NO:135) TCGCCCATTAAAGCGGCACGCGAGCTGGGTTCAGAACGTCGTGAGACAGTTCGGTCCCTA 2400
'Efaecl.seq' (SEQ ID NO:136) TCGCCCATTAAAGCGGCACGCGAGCTGGGTTCAGAACGTCGTGAGACAGTTCGGTCCCTA 2400
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) TCCGTCGCGGGCGTTGGAAATTTGAGAGGAGCTGTCCTTAGTACGAGAGGACCGGGATGG 2458
'11BLSU.seq' (SEQ ID NO:134) TCCGTCGCGGGCGTTGGAAATTTGAGAGGAGCTGTCCTTAGTACGAGAGGACCGGGATGG 2458
'10BLSU.seq' (SEQ ID NO:135) TCCGTCGCGGGCGTTGGAAATTTGAGAGGAGCTGTCCTTAGTACGAGAGGACCGGGATGG 2460
'Efaecl.seq' (SEQ ID NO:136) TCCGTCGCGGGCGTTGGAAATTTGAGAGGAGCTGTCCTTAGTACGAGAGGACCGGGATGG 2460
                             ************************************************************

'12BLSU.seq' (SEQ ID NO:133) ACTTACCGCTGGTGTACCAGTTGTTCTGCCAAGGGCATTGCTGGGTAGCTA 2509
'11BLSU.seq' (SEQ ID NO:134) ACTTACCGCTGGTGTACCAGTTGTTCTGCCAAGGGCATTGCTGGGTAG--- 2506
'10BLSU.seq' (SEQ ID NO:135) ACTTACCGCTGGTGTACCAGTTGTTCTGCCAAGGGCATTGCTGG------- 2504
'Efaecl.seq' (SEQ ID NO:136) ACTTACCGCTGGTGTACCAGTTGTTCTGCCAAGGGCATTGCTGGGTAGCTA 2511
                             *********************************************
```

FIGURE 1-9

3 *Enterococcus faecium*

```
'Efaecm.seq' (SEQ ID NO:137)AAATTCGATTCCCTGAGTAGCGGCGAGCGAAACGGGAAAAGCCCAAACCAGCAAGCTTGC 60
'16BLSU.seq' (SEQ ID NO:138)AAATTCGATTCCCTGAGTAGCGGCGAGCGAAACGGGAAAAGCCCAAACCAGCAAGCTTGC 60
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)TTGTTGGGGTTGTAGGACTCCAATATGGTAGTTCTTTCAGATAGTCGAATGACTTGGAAA 120
'16BLSU.seq' (SEQ ID NO:138)TTGTTGGGGTTGTAGGACTCCAATATGGTAGTTCTTTCAGATAGTCGAATGACTTGGAAA 120
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)AGTCAGTCAAAGAGGGTAAAAACCCCGTAGACGAAATGTGGAAGACACCTAGGAGGATCC 180
'16BLSU.seq' (SEQ ID NO:138)AGTCAGTCAAAGAGGGTAAAAACCCCGTAGACGAAATGTGGAAGACACCTAGGAGGATCC 180
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)TGAGTACGGCGGAACACGAGAAATTCCGTCGGAATCCGGGAGGACCATCTCCCAAGGCTA 240
'16BLSU.seq' (SEQ ID NO:138)TGAGTACGGCGGAACACGAGAAATTCCGTCGGAATCCGGGAGGACCATCTCCCAAGGCTA 240
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)AATACTCCCTAGTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGTGAAAAGCACCCCG 300
'16BLSU.seq' (SEQ ID NO:138)AATACTCCCTAGTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGTGAAAAGCACCCCG 300
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GAAGGGGAGTGAAATAGAACCTGAAACCGTGTGCCTACAACAAGTCAAAGCCCGTTAATG 360
'16BLSU.seq' (SEQ ID NO:138)GAAGGGGAGTGAAATAGAACCTGAAACCGTGTGCCTACAACAAGTCAAAGCCCGTTAATG 360
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GGTGATGGCGTGCCTTTTGTAGAATGAACCGGCGAGTTACGATTGCATGCGAGGTTAAGT 420
'16BLSU.seq' (SEQ ID NO:138)GGTGATGGCGTGCCTTTTGTAGAATGAACCGGCGAGTTACGATTGCATGCGAGGTTAAGT 420
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)TGAAGAGACGGAGCCGCAGCGAAAGCGAGTCTGAATAGGGCGTTTGAGTATGTAGTCGTA 480
'16BLSU.seq' (SEQ ID NO:138)TGAAGAGACGGAGCCGCAGCGAAAGCGAGTCTGAATAGGGCGTTTGAGTATGTAGTCGTA 480
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GACCCGAAACCATGTGATCTACCCATGTCCAGGTTGAAGGTGCGGTAAAACGCACTGGAG 540
'16BLSU.seq' (SEQ ID NO:138)GACCCGAAACCATGTGATCTACCCATGTCCAGGTTGAAGGTGCGGTAAAACGCACTGGAG 540
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GACCGAACCCACGTACGTTGAAAAGTGCGGGGATGAGGTGTGGGTAGCGGAGAAATTCCA 600
'16BLSU.seq' (SEQ ID NO:138)GACCGAACCCACGTACGTTGAAAAGTGCGGGGATGAGGTGTGGGTAGCGGAGAAATTCCA 600
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)AACGAACTTGGAGATAGCTGGTTCTCTCCGAAATAGCTTTAGGGCTAGCCTCGGAATTGA 660
'16BLSU.seq' (SEQ ID NO:138)AACGAACTTGGAGATAGCTGGTTCTCTCCGAAATAGCTTTAGGGCTAGCCTCGGAATTGA 660
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GAATGATGGAGGTAGAGCACTGTTTGGACTAGGGGCCCATCTCGGGTTACCGAATTCAGA 720
'16BLSU.seq' (SEQ ID NO:138)GAATGATGGAGGTAGAGCACTGTTTGGACTAGGGGCCCATCTCGGGTTACCGAATTCAGA 720
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)TAAACTCCGAATGCCATTCATTCATATCCGGGAGTCAGACTGTGAGTGATAAGATCCATA 780
'16BLSU.seq' (SEQ ID NO:138)TAAACTCCGAATGCCATTCATTCATATCCGGGAGTCAGACTGTGAGTGATAAGATCCATA 780
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GTCGAAAGGGAAACAGCCCAGACCACCAGCTAAGGTCCCAAAATATATGTTAAGTGGAAA 840
'16BLSU.seq' (SEQ ID NO:138)GTCGAAAGGGAAACAGCCCAGACCACCAGCTAAGGTCCCAAAATATATGTTAAGTGGAAA 840
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)AGGATGTGGGGTTGCACAGACAACTAGGATGTTGGCTTAGAAGCAGCCACCATTTAAAGA 900
'16BLSU.seq' (SEQ ID NO:138)AGGATGTGGGGTTGCACAGACAACTAGGATGTTGGCTTAGAAGCAGCCACCATTTAAAGA 900
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GTGCGTAATAGCTCACTAGTCGAGTGACCCTGCGCCGAAAATGTACCGGGGCTAAACATA 960
'16BLSU.seq' (SEQ ID NO:138)GTGCGTAATAGCTCACTAGTCGAGTGACCCTGCGCCGAAAATGTACCGGGGCTAAACATA 960
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)TTACCGAAGCTGTGGAGTACACCTTTAGGTGTATTGGTAGGAGAGCGTTCTAAGGGCGTC 1020
'16BLSU.seq' (SEQ ID NO:138)TTACCGAAGCTGTGGAGTACACCTTTAGGTGTATTGGTAGGAGAGCGTTCTAAGGGCGTT 1020
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GAAGGCAGATCGTGAGGACTGCTGGAGCGCTTAGAAGTGAGAATGCCGGTATGAGTAGCG 1080
'16BLSU.seq' (SEQ ID NO:138)GAAGGCAGATCGTGAGGACTGCTGGAGCGCTTAGAAGTGAGAATGCCGGTATGAGTAGCG 1080
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)AAAGACAGGTGAGAATCCTGTCCACCGAATGACTAAGGTTTCCTGGGGAAGGCTCGTCCG 1140
'16BLSU.seq' (SEQ ID NO:138)AAAGACAGGTGAGAATCCTGTCCACCGAATGACTAAGGTTTCCTGGGGAAGGCTCGTCCG 1140
```

FIGURE 1-10

```
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)CCCAGGGTTAGTCGGGACCTAAGCCGAGGCCGACAGGCGTAGGCGATGGATAACAGGTTG 1200
'16BLSU.seq' (SEQ ID NO:138)CCCAGGGTTAGTCGGGACCTAAGCCGAGGCCGACAGGCGTAGGCGATGGATAACAGGTTG 1200
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)ATATTCCTGTACCCGTTGTTTTTGTTTGAGCAATGGAGGGACGCAGGAGGCTAAGGAATG 1260
'16BLSU.seq' (SEQ ID NO:138)ATATTCCTGTACCCGTTGTTTTTGTTTGAGCAATGGAGGGACGCAGGAGGCTAAGGAATG 1260
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)CAGACGATCGGAAATGTCTGTCCAAGCAGTAAGTCTGAAGAGGAGTCAAATGCTTCTTTT 1320
'16BLSU.seq' (SEQ ID NO:138)CAGACGATCGGAAATGTCTGTCCAAGCAGTAAGTCTGAAGAGGAGTCAAATGCTTCTTTT 1320
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)CTTAAGGACAAGCTGTGATGGGGAGGGAAATAATAGTACCGAAGTTCCTGATGTCACACT 1380
'16BLSU.seq' (SEQ ID NO:138)CTTAAGGACAAGCTGTGATGGGGAGGGAAATAATAGTACCGAAGTTCCTGATGTCACACT 1380
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GCCGAGAAAAGCTTCTAGTGAGAAAACAGCGGCCCGTACCGCAAACCGACACAGGTAGTC 1440
'16BLSU.seq' (SEQ ID NO:138)GCCGAGAAAAGCTTCTAGTGAGAAAACAGCGGCCCGTACCGCAAACCGACACAGGTAGTC 1440
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GAGGAGAGAATCCTAAGGTGAGCGAGAGAACTCTCGTTAAGGAACTCGGCAAAATGACCC 1500
'16BLSU.seq' (SEQ ID NO:138)GAGGAGAGAATCCTAAGGTGAGCGAGAGAACTCTCGTTAAGGAACTCGGCAAAATGACCC 1500
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)CGTAACTTCGGGAGAAGGGGTGCTGATCATACGATCAGCCGCAGTGAATAGGCCCAAGCG 1560
'16BLSU.seq' (SEQ ID NO:138)CGTAACTTCGGGAGAAGGGGTGCTGATCATACGATCAGCCGCAGTGAATAGGCCCAAGCG 1560
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)ACTGTTTATCAAAAACACAGGTCTCTGCAAAATCGTAAGATGAAGTATAGGGGCTGACGC 1620
'16BLSU.seq' (SEQ ID NO:138)ACTGTTTATCAAAAACACAGGTCTCTGCAAAATCGTAAGATGAAGTATAGGGGCTGACGC 1620
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)CTGCCCGGTGCTGGAAGGTTAAGAGGAGTGCTTAGCGCA-GCGGAGGTACGAATTGAAGC 1679
'16BLSU.seq' (SEQ ID NO:138)CTGCCCGGTGCTGGAAGGTTAAGAGGAGTGCTTAGCGCAAGCGAAGGTACGAATTGAAGC 1680
                          ************************************* *** ****************

'Efaecm.seq' (SEQ ID NO:137)CCCAGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTA 1739
'16BLSU.seq' (SEQ ID NO:138)CCCAGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTA 1740
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)AGTTCCGACCCGCACGAAAGGCGTAACGATTTGGGCACTGTCTCAACGAGAGACTCGGTG 1799
'16BLSU.seq' (SEQ ID NO:138)AGTTCCGACCCGCACGAAAGGCGTAACGATTTGGGCACTGTCTCAACGAGAGACTCGGTG 1800
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)AAATTTTAGTACCTGTGAAGATGCAGGTTACCCGCGACAGGACGGAAAGACCCCATGGAG 1859
'16BLSU.seq' (SEQ ID NO:138)AAATTTTAGTACCTGTGAAGATGCAGGTTACCCGCGACAGGACGGAAAGACCCCATGGAG 1860
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)CTTTACTGTAGTTTGATATTGAGTGTCTGTACCGCATGTACAGGATAGGTAGGAGCCGTA 1919
'16BLSU.seq' (SEQ ID NO:138)CTTTACTGTAGTTTGATATTGAGTGTCTGTACCGCATGTACAGGATAGGTAGGAGCCGTA 1920
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GAAATCGGAACGCTAGTTTCGATGGAGGCGCTGGTGGGATACTACCCCTGCGTTATGGCC 1979
'16BLSU.seq' (SEQ ID NO:138)GAAATCGGAACGCTAGTTTCGATGGAGGCGCTGGTGGGATACTACCCCTGCGTTATGGCC 1980
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)ACTCTAACCCGCACCACTAATCGTGGTGGGAGACAGTGTCAGATGGGCAGTTTGACTGGG 2039
'16BLSU.seq' (SEQ ID NO:138)ACTCTAACCCGCACCACTAATCGTGGTGGGAGACAGTGTCAGATGGGCAGTTTGACTGGG 2040
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GCGGTCGCCTCCTAAAAGGTAACGGAGGCGCCCAAAGGTTCCCTCAGAATGGTTGGAAAT 2099
'16BLSU.seq' (SEQ ID NO:138)GCGGTCGCCTCCTAAAAGGTAACGGAGGCGCCCAAAGGTTCCCTCAGAATGGTTGGAAAT 2100
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)CATTCGAAGAGTGTAAAGGCAGAAGGGAGCTTGACTGCGAGACCAACAAGTCGAGCAGGG 2159
'16BLSU.seq' (SEQ ID NO:138)CATTCGAAGAGTGTAAAGGCAGAAGGGAGCTTGACTGCGAGACCAACAAGTCGAGCAGGG 2160
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)ACGAAAGTCGGGCTTAGTGATCCGGTGGTTCCGCATGGAAGGGCCATCGCTCAACGGATA 2219
'16BLSU.seq' (SEQ ID NO:138)ACGAAAGTCGGGCTTAGTGATCCGGTGGTTCCGCATGGAAGGGCCATCGCTCAACGGATA 2220
                          ************************************************************

'Efaecm.seq' (SEQ ID NO:137)AAAGCTACCCTGGGGATAACAGGCTTATCTCCCCCAAGAGTCCACATCGACGGGGAGGTT 2279
'16BLSU.seq' (SEQ ID NO:138)AAAGCTACCCTGGGGATAACAGGCTTATCTCCCCCAAGAGTCCACATCGACGGGGAGGTT 2280
                          ************************************************************
```

FIGURE 1-11

```
'Efaecm.seq' (SEQ ID NO:137)TGGCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGTAGTCGGTCCCAAGGGTTGGGCT 2339
'16BLSU.seq' (SEQ ID NO:138)TGGCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGTAGTCGGTCCCAAGGGTTGGGCT 2340
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GTTCGCCCATTAAAGCGGCACGCGAGCTGGGTTCAGAACGTCGTGAGACAGTTCGGTCCC 2399
'16BLSU.seq' (SEQ ID NO:138)GTTCGCCCATTAAAGCGGCACGCGAGCTGGGTTCAGAACGTCGTGAGACAGTTCGGTCCC 2400
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)TATCCGTCGCGGGCGTTGGAAATTTGAGAGGAGCTGTCCTTAGTACGAGAGGACCGGGAT 2459
'16BLSU.seq' (SEQ ID NO:138)TATCCGTCGCGGGCGTTGGAAATTTGAGAGGAGCTGTCCTTAGTACGAGAGGACCGGGAT 2460
                            ************************************************************

'Efaecm.seq' (SEQ ID NO:137)GGACTTACCGCTGGTGTACCAGTTGTTCTGCCAAG 2494
'16BLSU.seq' (SEQ ID NO:138)GGACTTACCGCTGGTGTACCAGTTGTTCTGCCAAG 2495
                            ********************************
```

FIGURE 1-12

4 Escherichia coli

```
'22BLSU.seq' (SEQ ID NO:139)AATCAACCGAGATTCCCCCAGTAGCGGCGAGCGAACGGGGAGGAGCCCAGAGCCTGAATC 60
'21BLSU.seq' (SEQ ID NO:140)-----ACCGAGATTCCCCCAGTAGCGGCGAGCGAACGGGGAGGAGCCCAGAGCCTGAATC 55
'E_coli.seq' (SEQ ID NO:141)AATCAACCGAGATTCCCCCAGTAGCGGCGAGCGAACGGGGAGGAGCCCAGAGCCTGAATC 60
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)AGTGTGTGTGTTAGTGGAAGCGTCTGGAAAGGCGCGCGATACAGGGTGACAGCCCCGTAC 120
'21BLSU.seq' (SEQ ID NO:140)AGTGTGTGTGTTAGTGGAAGCGTCTGGAAAGGCGCGCGATACAGGGTGACAGCCCCGTAC 115
'E_coli.seq' (SEQ ID NO:141)AGTGTGTGTGTTAGTGGAAGCGTCTGGAAAGGCGCGCGATACAGGGTGACAGCCCCGTAC 120
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)ACAAAAATGCACATATTGTGAGCTCGATGAGTAGGGCGGGACACGTGGTATCCTGTCTGA 180
'21BLSU.seq' (SEQ ID NO:140)ACAAAAATGCACATATTGTGAGCTCGATGAGTAGGGCGGGACACGTGGTATCCTGTCTGA 175
'E_coli.seq' (SEQ ID NO:141)ACAAAAATGCACATATTGTGAGCTCGATGAGTAGGGCGGGACACGTGGTATCCTGTCTGA 180
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)ATATGGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGAACCAGTAC 240
'21BLSU.seq' (SEQ ID NO:140)ATATGGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGAACCAGTAC 235
'E_coli.seq' (SEQ ID NO:141)ATATGGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGAACCAGTAC 240
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)CGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGAGTGAAAAAGAACCTGAAACCGTGT 300
'21BLSU.seq' (SEQ ID NO:140)CGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGAGTGAAAAAGAACCTGAAACCGTGT 295
'E_coli.seq' (SEQ ID NO:141)CGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGAGTGAAAAAGAACCTGAAACCGTGT 300
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)ACGTACAAGCAGTGGGAGCCTCTTTATGGGGTGACTGCGTACCTTTTGTATAATGGGTCA 360
'21BLSU.seq' (SEQ ID NO:140)ACGTACAAGCAGTGGGAGCCTCTTTATGGGGTGACTGCGTACCTTTTGTATAATGGGTCA 355
'E_coli.seq' (SEQ ID NO:141)ACGTACAAGCAGTGGGAGCCTCTTTATGGGGTGACTGCGTACCTTTTGTATAATGGGTCA 360
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GCGACTTATATTCTGTAGCAAGGTTAACCGAATAGGGGAGCCGAAGGGAAACCGAGTCTT 420
'21BLSU.seq' (SEQ ID NO:140)GCGACTTATATTCTGTAGCAAGGTTAACCGAATAGGGGAGCCGAAGGGAAACCGAGTCTT 415
'E_coli.seq' (SEQ ID NO:141)GCGACTTATATTCTGTAGCAAGGTTAACCGAATAGGGGAGCCGAAGGGAAACCGAGTCTT 420
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)AACTGGGCGTTAAGTTGCAGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGT 480
'21BLSU.seq' (SEQ ID NO:140)AACTGGGCGTTAAGTTGCAGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGT 475
'E_coli.seq' (SEQ ID NO:141)AACTGGGCGTTAAGTTGCAGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGT 480
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)TGAAGGTTGGGTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAAATTAGCGGAT 540
'21BLSU.seq' (SEQ ID NO:140)TGAAGGTTGGGTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAAATTAGCGGAT 535
'E_coli.seq' (SEQ ID NO:141)TGAAGGTTGGGTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAAATTAGCGGAT 540
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GACTTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGATAGCTGGTTCTCCCCGAAAG 600
'21BLSU.seq' (SEQ ID NO:140)GACTTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGATAGCTGGTTCTCCCCGAAAG 595
'E_coli.seq' (SEQ ID NO:141)GACTTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGATAGCTGGTTCTCCCCGAAAG 600
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)CTATTTAGGTAGCGCCTCGTGAATTCATCTCCGGGGGGTAGAGCACTGTTTCGGCAAGGGG 660
'21BLSU.seq' (SEQ ID NO:140)CTATTTAGGTAGCGCCTCGTGAATTCATCTCCGGGGGGTAGAGCACTGTTTCGGCAAGGGG 655
'E_coli.seq' (SEQ ID NO:141)CTATTTAGGTAGCGCCTCGTGAATTCATCTCCGGGGGGTAGAGCACTGTTTCGGCAAGGGG 660
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GTCATCCCGACTTACCAACCCGATGCAAACTGCGAATACCGGAGAATGTTATCACGGGAG 720
'21BLSU.seq' (SEQ ID NO:140)GTCATCCCGACTTACCAACCCGATGCAAACTGCGAATACCGGAGAATGTTATCACGGGAG 715
'E_coli.seq' (SEQ ID NO:141)GTCATCCCGACTTACCAACCCGATGCAAACTGCGAATACCGGAGAATGTTATCACGGGAG 720
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)ACACACGGCGGGTGCTAACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAG 780
'21BLSU.seq' (SEQ ID NO:140)ACACACGGCGGGTGCTAACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAG 775
'E_coli.seq' (SEQ ID NO:141)ACACACGGCGGGTGCTAACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAG 780
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GTCCCAAAGTCATGGTTAAGTGGGAAACGATGTGGGAAGGCCCAGACAGCCAGGATGTTG 840
'21BLSU.seq' (SEQ ID NO:140)GTCCCAAAGTCATGGTTAAGTGGGAAACGATGTGGGAAGGCCCAGACAGCCAGGATGTTG 835
'E_coli.seq' (SEQ ID NO:141)GTCCCAAAGTCATGGTTAAGTGGGAAACGATGTGGGAAGGCCCAGACAGCCAGGATGTTG 840
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GCTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTCACTGGTCGAGTCGGCCTGCG 900
'21BLSU.seq' (SEQ ID NO:140)GCTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTCACTGGTCGAGTCGGCCTGCG 895
'E_coli.seq' (SEQ ID NO:141)GCTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTCACTGGTCGAGTCGGCCTGCG 900
                            ************************************************************
```

FIGURE 1-13

```
'22BLSU.seq' (SEQ ID NO:139)CGGAAGATGTAACGGGGCTAAACCATGCACCGAAGCTGCGGCAGCGACACTATGTGTTGT 960
'21BLSU.seq' (SEQ ID NO:140)CGGAAGATGTAACGGGGCTAAACCATGCACCGAAGCTGCGGCAGCGACACTATGTGTTGT 955
'E_coli.seq' (SEQ ID NO:141)CGGAAGATGTAACGGGGCTAAACCATGCACCGAAGCTGCGGCAGCGACACTATGTGTTGT 960
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)TGGGTAGGGGAGCGTTCTGTAAGCCTGTGAAGGTGGCCTGTGAGGGTTGCTGGAGGTATC 1020
'21BLSU.seq' (SEQ ID NO:140)TGGGTAGGGGAGCGTTCTGTAAGCCTGTGAAGGTGGCCTGTGAGGGTTGCTGGAGGTATC 1015
'E_coli.seq' (SEQ ID NO:141)TGGGTAGGGGAGCGTTCTGTAAGCCTGTGAAGGTGGCCTGTGAGGGTTGCTGGAGGTATC 1020
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)AGAAGTGCGAATGCTGACATAAGTAACGATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAG 1080
'21BLSU.seq' (SEQ ID NO:140)AGAAGTGCGAATGCTGACATAAGTAACGATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAG 1075
'E_coli.seq' (SEQ ID NO:141)AGAAGTGCGAATGCTGACATAAGTAACGATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAG 1080
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)ACCAAGGGTTCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTAAGGCGAGGCC 1140
'21BLSU.seq' (SEQ ID NO:140)ACCAAGGGTTCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTAAGGCGAGGCC 1135
'E_coli.seq' (SEQ ID NO:141)ACCAAGGGTTCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTAAGGCGAGGCC 1140
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTACTTGGTGTTACTGCGAAGGG 1200
'21BLSU.seq' (SEQ ID NO:140)GAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTACTTGGTGTTACTGCGAAGGG 1195
'E_coli.seq' (SEQ ID NO:141)GAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTACTTGGTGTTACTGCGAAGGG 1200
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GGGACGGAGAAGGCTATGTTGGCCGGGCGACGGTTGTCCCGGTTTAAGCGTGTAGGCTGG 1260
'21BLSU.seq' (SEQ ID NO:140)GGGACGGAGAAGGCTATGTTGGCCGGGCGACGGTTGTCCCGGTTTAAGCGTGTAGGCTGG 1255
'E_coli.seq' (SEQ ID NO:141)GGGACGGAGAAGGCTATGTTGGCCGGGCGACGGTTGTCCCGGTTTAAGCGTGTAGGCTGG 1260
                            ************************************************************

                                Escoli_1284f-------->
'22BLSU.seq' (SEQ ID NO:139)TTTTCCAGGCAAATCCGGAAAACCAAGGCTGAGGCGTGATGACGAGGCACTACGGTGCTG 1320
'21BLSU.seq' (SEQ ID NO:140)TTTTCCAGGCAAATCCGGAAAACCAAGGCTGAGGCGTGATGACGAGGCACTACGGTGCTG 1315
'E_coli.seq' (SEQ ID NO:141)TTTTCCAGGCAAATCCGGAAAACCAAGGCTGAG-CGTGATGACGAGGCACTACGGTGCTG 1319
                            ********************************** ************************

'22BLSU.seq' (SEQ ID NO:139)AAGCGACAAATGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATCAAATCGTA 1380
'21BLSU.seq' (SEQ ID NO:140)AAGCGACAAATGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATCAAATCGTA 1375
'E_coli.seq' (SEQ ID NO:141)AAGCGACAAATGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATCAAATCGTA 1379
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGGGTG 1440
'21BLSU.seq' (SEQ ID NO:140)CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGGGTG 1435
'E_coli.seq' (SEQ ID NO:141)CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGGGTG 1439
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)AAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGGCACGCTGATATGTAGGTGAA 1500
'21BLSU.seq' (SEQ ID NO:140)AAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGGCACGCTGATATGTAGGTGAA 1495
'E_coli.seq' (SEQ ID NO:141)AAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGGCACGCTGATATGTAGGTGAA 1499
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GCGACTTGCTCGTGGAGCTGAAATCAGTCGAAGATACCAGCTGGCTGCAACTGTTTATTA 1560
'21BLSU.seq' (SEQ ID NO:140)GCGACTTGCTCGTGGAGCTGAAATCAGTCGAAGATACCAGCTGGCTGCAACTGTTTATTA 1555
'E_coli.seq' (SEQ ID NO:141)GCGACTTGCTCGTGGAGCTGAAATCAGTCGAAGATACCAGCTGGCTGCAACTGTTTATTA 1559
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)AAAACACAGCACTGTGCAAACACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGC 1620
'21BLSU.seq' (SEQ ID NO:140)AAAACACAGCACTGTGCAAACACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGC 1615
'E_coli.seq' (SEQ ID NO:141)AAAACACAGCACTGTGCAAACACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGC 1619
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)CGGAAGGTTAATTGATGGGGTTAGCGGTAACGCGAAGCTCTTGATCGAAGCCCCGGTAAA 1680
'21BLSU.seq' (SEQ ID NO:140)CGGAAGGTTAATTGATGGGGTTAGCGGTAACGCGAAGCTCTTGATCGAAGCCCCGGTAAA 1675
'E_coli.seq' (SEQ ID NO:141)CGGAAGGTTAATTGATGGGGTTAGCGGTAACGCGAAGCTCTTGATCGAAGCCCCGGTAAA 1679
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)CGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGAC 1740
'21BLSU.seq' (SEQ ID NO:140)CGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGAC 1735
'E_coli.seq' (SEQ ID NO:141)CGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGAC 1739
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)CTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCGAGACTCAGTGAAATTGAAC 1800
'21BLSU.seq' (SEQ ID NO:140)CTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCGAGACTCAGTGAAATTGAAC 1795
'E_coli.seq' (SEQ ID NO:141)CTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCGAGACTCAGTGAAATTGAAC 1799
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)TCGCTGTGAAGATGCAGTGTACCCGCGGCAAGACGGAAAGACCCCGTGAACCTTTACTAT 1860
'21BLSU.seq' (SEQ ID NO:140)TCGCTGTGAAGATGCAGTGTACCCGCGGCAAGACGGAAAGACCCCGTGAACCTTTACTAT 1855
```

FIGURE 1-14

```
'E_coli.seq' (SEQ ID NO:141)TCGCTGTGAAGATGCAGTGTACCCGCGGCAAGACGGAAAGACCCCGTGAACCTTTACTAT 1859
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)AGCTTGACACTGAACATTGAGCCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGTGTGG 1920
'21BLSU.seq' (SEQ ID NO:140)AGCTTGACACTGAACATTGAGCCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGTGTGG 1915
'E_coli.seq' (SEQ ID NO:141)AGCTTGACACTGAACATTGAGCCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGTGTGG 1919
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)ACGCCAGTCTGCATGGAGCCGACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAACG 1980
'21BLSU.seq' (SEQ ID NO:140)ACGCCAGTCTGCATGGAGCCGACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAACG 1975
'E_coli.seq' (SEQ ID NO:141)ACGCCAGTCTGCATGGAGCCGACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAACG 1979
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)TTGGCCCGTAATCCGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGGGCGGTCTCC 2040
'21BLSU.seq' (SEQ ID NO:140)TTGGCCCGTAATCCGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGGGCGGTCTCC 2035
'E_coli.seq' (SEQ ID NO:141)TTGGCCCGTAATCCGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGGGCGGTCTCC 2039
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)TCCTAAAGAGTAACGGAGGAGCACGAAGGTTGGCTAATCCTGGTCGGACATCAGGAGGTT 2100
'21BLSU.seq' (SEQ ID NO:140)TCCTAAAGAGTAACGGAGGAGCACGAAGGTTGGCTAATCCTGGTCGGACATCAGGAGGTT 2095
'E_coli.seq' (SEQ ID NO:141)TCCTAAAGAGTAACGGAGGAGCACGAAGGTTGGCTAATCCTGGTCGGACATCAGGAGGTT 2099
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)AGTGCAATGGCATAAGCCAGCTTGACTGCGAGCGTGACGGCGCGAGCAGGTGCGAAAGCA 2160
'21BLSU.seq' (SEQ ID NO:140)AGTGCAATGGCATAAGCCAGCTTGACTGCGAGCGTGACGGCGCGAGCAGGTGCGAAAGCA 2155
'E_coli.seq' (SEQ ID NO:141)AGTGCAATGGCATAAGCCAGCTTGACTGCGAGCGTGACGGCGCGAGCAGGTGCGAAAGCA 2159
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GGTCATAGTGATCCGGTGGTTCTGAATGGAAGGGCCATCGCTCAACGGATAAAAGGTACT 2220
'21BLSU.seq' (SEQ ID NO:140)GGTCATAGTGATCCGGTGGTTCTGAATGGAAGGGCCATCGCTCAACGGATAAAAGGTACT 2215
'E_coli.seq' (SEQ ID NO:141)GGTCATAGTGATCCGGTGGTTCTGAATGGAAGGGCCATCGCTCAACGGATAAAAGGTACT 2219
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)CCGGGGATAACAGGCTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTC 2280
'21BLSU.seq' (SEQ ID NO:140)CCGGGGATAACAGGCTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTC 2275
'E_coli.seq' (SEQ ID NO:141)CCGGGGATAACAGGCTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTC 2279
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)GATGTCGGCTCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCTGTTCGCCAT 2340
'21BLSU.seq' (SEQ ID NO:140)GATGTCGGCTCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCTGTTCGCCAT 2335
'E_coli.seq' (SEQ ID NO:141)GATGTCGGCTCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCTGTTCGCCAT 2339
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)TTAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGTCCCTATCTGCCG 2400
'21BLSU.seq' (SEQ ID NO:140)TTAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGTCCCTATCTGCCG 2395
'E_coli.seq' (SEQ ID NO:141)TTAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGTCCCTATCTGCCG 2399
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)TGGGCGCTGGAGAACTGAGGGGGGCTGCTCCTAGTACGAGAGGACCGGAGTGGACGCATC 2460
'21BLSU.seq' (SEQ ID NO:140)TGGGCGCTGGAGAACTGAGGGGGGCTGCTCCTAGTACGAGAGGACCGGAGTGGACGCATC 2455
'E_coli.seq' (SEQ ID NO:141)TGGGCGCTGGAGAACTGAGGGGGGCTGCTCCTAGTACGAGAGGACCGGAGTGGACGCATC 2459
                            ************************************************************

'22BLSU.seq' (SEQ ID NO:139)ACTGGTGTTCGGGTTGTCATGCCAATGGCACTGCCCGGTAGCTAA- 2505
'21BLSU.seq' (SEQ ID NO:140)ACTGGTGTTCGGGTTGTCATGCCAATGGCACTGCCCGGTAGCTAAA 2501
'E_coli.seq' (SEQ ID NO:141)ACTGGTGTTCGGGTTGTCATGCCAATGGCACTGCCCGGTAGCTAAA 2505
                            *******************************************
```

FIGURE 1-15

5 Klebsiella pneumoniae

```
'01BLSU.seq' (SEQ ID NO:142)   CTAAGTACCCCGAGGAAAAGAAATCAACCGAGATTCCCCCAGTAGCGGCG 50
'24BLSU.seq' (SEQ ID NO:143)   ----------------------AATCAACCGAGATTCCCCCAGTAGCGGCG 29
'19BLSU.seq' (SEQ ID NO:144)   CTAAGTACCCCGAGGAAAAGAAATCAACCGAGATTCCCCCAGTAGCGGCG 50
'K_pneumon.seq' (SEQ ID NO:145)CTAAGTACCCCGAGGAAAAGAAATCAACCGAGATTCCCCCAGTAGCGGCG 50
                                                  ****************************

'01BLSU.seq' (SEQ ID NO:142)   AGCGAACGGGGAGCAGCCCAGAGTCTGAATCAGCTTGTGTGTTAGTGGAA 100
'24BLSU.seq' (SEQ ID NO:143)   AGCGAACGGGGAGCAGCCCAGAGTCTGAATCAGCTTGTGTGTTAGTGGAA 79
'19BLSU.seq' (SEQ ID NO:144)   AGCGAACGGGGAGCAGCCCAGAGTCTGAATCAGCTTGTGTGTTAGTGGAA 100
'K_pneumon.seq' (SEQ ID NO:145)AGCGAACGGGGAGCAGCCCAGAGTCTGAATCAGCTTGTGTGTTAGTGGAA 100
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   CGGTCTGGAAAGTCCGACGGTACAGGGTGATAGTCCCGTACACCAAAATG 150
'24BLSU.seq' (SEQ ID NO:143)   CGGTCTGGAAAGTCCGACGGTACAGGGTGATAGTCCCGTACACCAAAATG 129
'19BLSU.seq' (SEQ ID NO:144)   CGGTCTGGAAAGTCCGACGGTACAGGGTGATAGTCCCGTACACCAAAATG 150
'K_pneumon.seq' (SEQ ID NO:145)CGGTCTGGAAAGTCCGACGGTACAGGGTGATAGTCCCGTACACCAAAATG 150
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   CACAGGYTGTGAACTCGAAGAGTAGGGCGGGACACGTGGTATCCTGTCTG 200
'24BLSU.seq' (SEQ ID NO:143)   CACAGGTTGTGAACTCGAAGAGTAGGGCGGGACACGTGGTATCCTGTCTG 179
'19BLSU.seq' (SEQ ID NO:144)   CACAGGTTGTGAACTCGAAGAGTAGGGCGGGACACGTGGTATCCTGTCTG 200
'K_pneumon.seq' (SEQ ID NO:145)CACAGGCTGTGAACTCGAAGAGTAGGGCGGGACACGTGGTATCCTGTCTG 200
                               ****** ***************************************

'01BLSU.seq' (SEQ ID NO:142)   AATATGGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAG 250
'24BLSU.seq' (SEQ ID NO:143)   AATATGGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAG 229
'19BLSU.seq' (SEQ ID NO:144)   AATATGGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAG 250
'K_pneumon.seq' (SEQ ID NO:145)AATATGGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAG 250
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   TGAACCAGTACCGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGAGTG 300
'24BLSU.seq' (SEQ ID NO:143)   TGAACCAGTACCGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGAGTG 279
'19BLSU.seq' (SEQ ID NO:144)   TGAACCAGTACCGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGAGTG 300
'K_pneumon.seq' (SEQ ID NO:145)TGAACCAGTACCGTGAGGGAAAGGCGAAAAGAACCCCGGCGAGGGGAGTG 300
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   AAAAAGAACCTGAAACCGTGTACGTACAAGCAGTGGGAGCACCTTCGGGT 350
'24BLSU.seq' (SEQ ID NO:143)   AAAAAGAACCTGAAACCGTGTACGTACAAGCAGTGGGAGCACCTTCGGGT 329
'19BLSU.seq' (SEQ ID NO:144)   AAAAAGAACCTGAAACCGTGTACGTACAAGCAGTGGGAGCACCTTCGGGT 350
'K_pneumon.seq' (SEQ ID NO:145)AAAAAGAACCTGAAACCGTGTACGTACAAGCAGTGGGAGCACCTTCGGGT 350
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   GTGACTGCGTACCTTTTGTATAATGGGTCAGCGACTTATATTCTGTAGCA 400
'24BLSU.seq' (SEQ ID NO:143)   GTGACTGCGTACCTTTTGTATAATGGGTCAGCGACTTATATTCTGTAGCA 379
'19BLSU.seq' (SEQ ID NO:144)   GTGACTGCGTACCTTTTGTATAATGGGTCAGCGACTTATATTCTGTAGCA 400
'K_pneumon.seq' (SEQ ID NO:145)GTGACTGCGTACCTTTTGTATAATGGGTCAGCGACTTATATTCTGTAGCA 400
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   AGGTTAACCGTATAGGGGAGCCGCAGGGAAACCGAGTCTTAACTGGGCGT 450
'24BLSU.seq' (SEQ ID NO:143)   AGGTTAACCGTATAGGGGAGCCGCAGGGAAACCGAGTCTTAACTGGGCGT 429
'19BLSU.seq' (SEQ ID NO:144)   AGGTTAACCGTATAGGGGAGCCGCAGGGAAACCGAGTCTTAACTGGGCGT 450
'K_pneumon.seq' (SEQ ID NO:145)AGGTTAACCGTATAGGGGAGCCGCAGGGAAACCGAGTCTTAACTGGGCGT 450
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   TAAGTTGCAGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGT 500
'24BLSU.seq' (SEQ ID NO:143)   TAAGTTGCAGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGT 479
'19BLSU.seq' (SEQ ID NO:144)   TAAGTTGCAGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGT 500
'K_pneumon.seq' (SEQ ID NO:145)TAAGTTGCAGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGT 500
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   TGAAGGTTGGGTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAA 550
'24BLSU.seq' (SEQ ID NO:143)   TGAAGGTTGGGTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAA 529
'19BLSU.seq' (SEQ ID NO:144)   TGAAGGTTGGGTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAA 550
'K_pneumon.seq' (SEQ ID NO:145)TGAAGGTTGGGTAACACTAACTGGAGGACCGAACCGACTAATGTTGAAAA 550
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   ATTAGCGGATGACTTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGA 600
'24BLSU.seq' (SEQ ID NO:143)   ATTAGCGGATGACTTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGA 579
'19BLSU.seq' (SEQ ID NO:144)   ATTAGCGGATGACTTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGA 600
'K_pneumon.seq' (SEQ ID NO:145)ATTAGCGGATGACTTGTGGCTGGGGGTGAAAGGCCAATCAAACCGGGAGA 600
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   TAGCTGGTTCTCCCCGAAAGCTATTTAGGTAGCGCCTCGTGAAYTCATCT 650
'24BLSU.seq' (SEQ ID NO:143)   TAGCTGGTTCTCCCCGAAAGCTATTTAGGTAGCGCCTCGTGAAYTCATCT 629
'19BLSU.seq' (SEQ ID NO:144)   TAGCTGGTTCTCCCCGAAAGCTATTTAGGTAGCGCCTCGTGAATTCATCT 650
```

FIGURE 1-16

```
'K_pneumon.seq' (SEQ ID NO:145)TAGCTGGTTCTCCCCGAAAGCTATTTAGGTAGCGCCTCGTGAACTCATCT 650
                               ****************************************** ******

'01BLSU.seq' (SEQ ID NO:142)   TCGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCATCCCGACTTACCAACC 700
'24BLSU.seq' (SEQ ID NO:143)   TCGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCATCCCGACTTACCAACC 679
'19BLSU.seq' (SEQ ID NO:144)   TCGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCATCCCGACTTACCAACC 700
'K_pneumon.seq' (SEQ ID NO:145)TCGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCATCCCGACTTACCAACC 700
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   CGATGCAAACTACGAATACCGAAGAATGTTATCACGGGAGACACACGGCG 750
'24BLSU.seq' (SEQ ID NO:143)   CGATGCAAACTACGAATACCGAAGAATGTTATCACGGGAGACACACGGCG 729
'19BLSU.seq' (SEQ ID NO:144)   CGATGCAAACTACGAATACCGAAGAATGTTATCACGGGAGACACACGGCG 750
'K_pneumon.seq' (SEQ ID NO:145)CGATGCAAACTACGAATACCGAAGAATGTTATCACGGGAGACACACGGCG 750
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   GGTGCTAACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAG 800
'24BLSU.seq' (SEQ ID NO:143)   GGTGCTAACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAG 779
'19BLSU.seq' (SEQ ID NO:144)   GGTGCTAACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAG 800
'K_pneumon.seq' (SEQ ID NO:145)GGTGCTAACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAG 800
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   GTCCCAAAGTCATGGTTAAGTGGGAAACGATGTGGGAAGGCACAGACAGC 850
'24BLSU.seq' (SEQ ID NO:143)   GTCCCAAAGTCATGGTTAAGTGGGAAACGATGTGGGAAGGCACAGACAGC 829
'19BLSU.seq' (SEQ ID NO:144)   GTCCCAAAGTCATGGTTAAGTGGGAAACGATGTGGGAAGGCACAGACAGC 850
'K_pneumon.seq' (SEQ ID NO:145)GTCCCAAAGTCATGGTTAAGTGGGAAACGATGTGGGAAGGCACAGACAGC 850
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   CAGGATGTTGGCTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTC 900
'24BLSU.seq' (SEQ ID NO:143)   CAGGATGTTGGCTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTC 879
'19BLSU.seq' (SEQ ID NO:144)   CAGGATGTTGGCTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTC 900
'K_pneumon.seq' (SEQ ID NO:145)CAGGATGTTGGCTTAGAAGCAGCCATCATTTAAAGAAAGCGTAATAGCTC 900
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   ACTGGTCGAGTCGGCCTGCGCGGAAGATGTAACGGGGCTAAACCATGCAC 950
'24BLSU.seq' (SEQ ID NO:143)   ACTGGTCGAGTCGGCCTGCGCGGAAGATGTAACGGGGCTAAACCATGCAC 929
'19BLSU.seq' (SEQ ID NO:144)   ACTGGTCGAGTCGGCCTGCGCGGAAGATGTAACGGGGCTAAACCATGCAC 950
'K_pneumon.seq' (SEQ ID NO:145)ACTGGTCGAGTCGGCCTGCGCGGAAGATGTAACGGGGCTAAACCATGCAC 950
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   CGAAGCTGCGGCAGCGACACTATGTGTTGTTGGGTAGGGGAGCGTTCTGT 1000
'24BLSU.seq' (SEQ ID NO:143)   CGAAGCTGCGGCAGCGACACTATGTGTTGTTGGGTAGGGGAGCGTTCTGT 979
'19BLSU.seq' (SEQ ID NO:144)   CGAAGCTGCGGCAGCGACACTATGTGTTGTTGGGTAGGGGAGCGTTCTGT 1000
'K_pneumon.seq' (SEQ ID NO:145)CGAAGCTGCGGCAGCGACACTATGTGTTGTTGGGTAGGGGAGCGTTCTGT 1000
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   AAGCCTGCGAAGGTGWSCTGTGAGGSWTGCTGGAGGTATCAGAAGTGCGA 1050
'24BLSU.seq' (SEQ ID NO:143)   AAGCCTGCGAAGGTGWSCTGTGAGGSWTGCTGGAGGTATCAGAAGTGCGA 1029
'19BLSU.seq' (SEQ ID NO:144)   AAGCCTGCGAAGGTGGCCTGTGAGGGTTGCTGGAGGTATCAGAAGTGCGA 1050
'K_pneumon.seq' (SEQ ID NO:145)AAGCCTGCGAAGGTGTGCTGTGAGGCATGCTGGAGGTATCAGAAGTGCGA 1050
                               ***************  ********  ***********************

'01BLSU.seq' (SEQ ID NO:142)   ATGCTGACATAAGTAACGATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAG 1100
'24BLSU.seq' (SEQ ID NO:143)   ATGCTGACATAAGTAACGATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAG 1079
'19BLSU.seq' (SEQ ID NO:144)   ATGCTGACATAAGTAACGATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAG 1100
'K_pneumon.seq' (SEQ ID NO:145)ATGCTGACATAAGTAACGATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAG 1100
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   ACCAAGGGTTCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTA 1150
'24BLSU.seq' (SEQ ID NO:143)   ACCAAGGGTTCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTA 1129
'19BLSU.seq' (SEQ ID NO:144)   ACCAAGGGTTCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTA 1150
'K_pneumon.seq' (SEQ ID NO:145)ACCAAGGGTTCCTGTCCAACGTTAATCGGGGCAGGGTGAGTCGACCCCTA 1150
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   AGGCGAGGCCGAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTA 1200
'24BLSU.seq' (SEQ ID NO:143)   AGGCGAGGCCGAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTA 1179
'19BLSU.seq' (SEQ ID NO:144)   AGGCGAGGCCGAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTA 1200
'K_pneumon.seq' (SEQ ID NO:145)AGGCGAGGCCGAAAGGCGTAGTCGATGGGAAACAGGTTAATATTCCTGTA 1200
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   CTTGGTGTTACTGCGAAGGGGGGACGGAGAAGGCTATGTTAGCCGGGCGA 1250
'24BLSU.seq' (SEQ ID NO:143)   CTTGGTGTTACTGCGAAGGGGGGACGGAGAAGGCTATGTTAGCCGGGCGA 1229
'19BLSU.seq' (SEQ ID NO:144)   CTTGGTGTTACTGCGAAGGGGGGACGGAGAAGGCTATGTTAGCCGGGCGA 1250
'K_pneumon.seq' (SEQ ID NO:145)CTTGGTGTTACTGCGAAGGGGGGACGGAGAAGGCTATGTTAGCCGGGCGA 1250
                               **************************************************



'01BLSU.seq' (SEQ ID NO:142)   CGGTTGTCCCGGTTTAAGCATGTAGGCTGGTTRTCCAGGCAAATCCGGAT 1300
```

FIGURE 1-17

```
'24BLSU.seq' (SEQ ID NO:143)   CGGTTGTCCCGGTTTAAGCATGTAGGCTGGTTRTCCAGGCAAATCCGGAT 1279
'19BLSU.seq' (SEQ ID NO:144)   CGGTTGTCCCGGTTTAAGCATGTAGGCTGGTTATCCAGGCAAATCCGGAT 1300
'K_pneumon.seq' (SEQ ID NO:145)CGGTTGTCCCGGTTTAAGCATGTAGGCTGGTTGTCCAGGCAAATCCGGAT 1300
                               ******************************** *****************

'01BLSU.seq' (SEQ ID NO:142)   AATCAAGGCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAA 1350
'24BLSU.seq' (SEQ ID NO:143)   AATCAAGGCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAA 1329
'19BLSU.seq' (SEQ ID NO:144)   AATCAAGGCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAA 1350
'K_pneumon.seq' (SEQ ID NO:145)AATCAAGGCTGAGGTGTGATGACGAGGCACTACGGTGCTGAAGTAACAAA 1350
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   TGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATYAAATCGTA 1400
'24BLSU.seq' (SEQ ID NO:143)   TGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATCAAATCGTA 1379
'19BLSU.seq' (SEQ ID NO:144)   TGCCCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATTAAATCGTA 1400
'K_pneumon.seq' (SEQ ID NO:145)TGCTCTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATCAAATCGTA 1400
                               *** ********************************** ********

'01BLSU.seq' (SEQ ID NO:142)   CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAG 1450
'24BLSU.seq' (SEQ ID NO:143)   CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAG 1429
'19BLSU.seq' (SEQ ID NO:144)   CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAG 1450
'K_pneumon.seq' (SEQ ID NO:145)CCCCAAACCGACACAGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAT 1450
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   AACTCGGGTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGG 1500
'24BLSU.seq' (SEQ ID NO:143)   AACTCGGGTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGG 1479
'19BLSU.seq' (SEQ ID NO:144)   AACTCGGGTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGG 1500
'K_pneumon.seq' (SEQ ID NO:145)AACTCGGGTGAAGGAACTAGGCAAAATGGTGCCGTAACTTCGGGAGAAGG 1500
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   CACGCTGGTGTGTAGGTGAAGYCCCTGCGGRTGGAGCTGAGACCAGTCGA 1550
'24BLSU.seq' (SEQ ID NO:143)   CACGCTGGTGTGTAGGTGAAGYCCCTGCGGRTGGAGCTGAGACCAGTCGA 1529
'19BLSU.seq' (SEQ ID NO:144)   CACGCTGGTGTGTAGGTGAAGTCCCTGCGGATGGAGCTGAGACCAGTCGA 1550
'K_pneumon.seq' (SEQ ID NO:145)CACGCTGGTGTGTAGGTGAAGCCCCTGCGGGTGGAGCTGAGACCAGTCGA 1550
                               ********************* ******** ******************

'01BLSU.seq' (SEQ ID NO:142)   AGATACCAGCTGGCTGCAACTGTTTATTAAAAACACAGCACTGTGCAAAC 1600
'24BLSU.seq' (SEQ ID NO:143)   AGATACCAGCTGGCTGCAACTGTTTATTAAAAACACAGCACTGTGCAAAC 1579
'19BLSU.seq' (SEQ ID NO:144)   AGATACCAGCTGGCTGCAACTGTTTATTAAAAACACAGCACTGTGCAAAC 1600
'K_pneumon.seq' (SEQ ID NO:145)AGATACCAGCTGGCTGCAACTGTTTATTAAAAACACAGCACTGTGCAAAC 1600
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   ACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAA 1650
'24BLSU.seq' (SEQ ID NO:143)   ACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAA 1629
'19BLSU.seq' (SEQ ID NO:144)   ACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAA 1650
'K_pneumon.seq' (SEQ ID NO:145)ACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAA 1650
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   TTGATGGGGTTATCCGTAAGGAGAAGCTCTTGATCGAAGCCCCGGTAAAC 1700
'24BLSU.seq' (SEQ ID NO:143)   TTGATGGGGTTATCCGTAAGGAGAAGCTCTTGATCGAAGCCCCGGTAAAC 1679
'19BLSU.seq' (SEQ ID NO:144)   TTGATGGGGTTATCCGTAAGGAGAAGCTCTTGATCGAAGCCCCGGTAAAC 1700
'K_pneumon.seq' (SEQ ID NO:145)TTGATGGGGTTATCCGTAAGGAGAAGCTCTTGATCGAAGCCCCGGTAAAC 1700
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   GGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTA 1750
'24BLSU.seq' (SEQ ID NO:143)   GGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTA 1729
'19BLSU.seq' (SEQ ID NO:144)   GGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTA 1750
'K_pneumon.seq' (SEQ ID NO:145)GGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTA 1750
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   AGTTCCGACCTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCG 1800
'24BLSU.seq' (SEQ ID NO:143)   AGTTCCGACCTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCG 1779
'19BLSU.seq' (SEQ ID NO:144)   AGTTCCGACCTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCG 1800
'K_pneumon.seq' (SEQ ID NO:145)AGTTCCGACCTGCACGAATGGCGTAATGATGGCCAGGCTGTCTCCACCCG 1800
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   AGACTCAGTGAAATTGAACTCGCTGTGAAGATGCAGTGTACCCGCGGCAA 1850
'24BLSU.seq' (SEQ ID NO:143)   AGACTCAGTGAAATTGAACTCGCTGTGAAGATGCAGTGTACCCGCGGCAA 1829
'19BLSU.seq' (SEQ ID NO:144)   AGACTCAGTGAAATTGAACTCGCTGTGAAGATGCAGTGTACCCGCGGCAA 1850
'K_pneumon.seq' (SEQ ID NO:145)AGACTCAGTGAAATTGAACTCGCTGTGAAGATGCAGTGTACCCGCGGCAA 1850
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   GACGGAAAGACCCCGTGAACCTTTACTATAGCTTGACACTGAACATTGAG 1900
'24BLSU.seq' (SEQ ID NO:143)   GACGGAAAGACCCCGTGAACCTTTACTATAGCTTGACACTGAACATTGAG 1879
'19BLSU.seq' (SEQ ID NO:144)   GACGGAAAGACCCCGTGAACCTTTACTATAGCTTGACACTGAACATTGAG 1900
'K_pneumon.seq' (SEQ ID NO:145)GACGGAAAGACCCCGTGAACCTTTACTATAGCTTGACACTGAACATTGAG 1900
                               ************************************************

'01BLSU.seq' (SEQ ID NO:142)   CCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGCGTGGACGCCAGTCTG 1950
```

FIGURE 1-18

```
'24BLSU.seq' (SEQ ID NO:143)   CCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGCGTGGACGCCAGTCTG 1929
'19BLSU.seq' (SEQ ID NO:144)   CCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGCGTGGACGCCAGTCTG 1950
'K_pneumon.seq' (SEQ ID NO:145)CCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGCGTGGACGCCAGTCTG 1950
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   CGTGGAGCCAACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAACGT 2000
'24BLSU.seq' (SEQ ID NO:143)   CGTGGAGCCAACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAACGT 1979
'19BLSU.seq' (SEQ ID NO:144)   CGTGGAGCCAACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAACGT 2000
'K_pneumon.seq' (SEQ ID NO:145)CGTGGAGCCAACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAACGT 2000
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   TGGCCCCTKAYCGGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGG 2050
'24BLSU.seq' (SEQ ID NO:143)   TGGCCCCTKACCGGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGG 2029
'19BLSU.seq' (SEQ ID NO:144)   TGGCCCCTGACCGGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGG 2050
'K_pneumon.seq' (SEQ ID NO:145)TGGCCCCTCACCGGGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGG 2050
                               ******** * ***************************************

'01BLSU.seq' (SEQ ID NO:142)   GCGGTCTCCTCCCAAAGCGTAACGGAGGAGCACGAAGGTTAGCTAATCCT 2100
'24BLSU.seq' (SEQ ID NO:143)   GCGGTCTCCTCCCAAAGCGTAACGGAGGAGCACGAAGGTTAGCTAATCCT 2079
'19BLSU.seq' (SEQ ID NO:144)   GCGGTCTCCTCCCAAAGCGTAACGGAGGAGCACGAAGGTTAGCTAATCCT 2100
'K_pneumon.seq' (SEQ ID NO:145)GCGGTCTCCTCCCAAAGCGTAACGGAGGAGCACGAAGGTTAGCTAATCCT 2100
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   GGTCGGACATCAGGAGGTTAGTGCAATGGCATAAGCTAGCTTGACTGCGA 2150
'24BLSU.seq' (SEQ ID NO:143)   GGTCGGACATCAGGAGGTTAGTGCAATGGCATAAGCTAGCTTGACTGCGA 2129
'19BLSU.seq' (SEQ ID NO:144)   GGTCGGACATCAGGAGGTTAGTGCAATGGCATAAGCTAGCTTGACTGCGA 2150
'K_pneumon.seq' (SEQ ID NO:145)GGTCGGACATCAGGAGGTTAGTGCAATGGCATAAGCTAGCTTGACTGCGA 2150
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   GCGTGACGGCGCGAGCAGGTGCGAAAGCAGGTCATAGTGATCCGGTGGTT 2200
'24BLSU.seq' (SEQ ID NO:143)   GCGTGACGGCGCGAGCAGGTGCGAAAGCAGGTCATAGTGATCCGGTGGTT 2179
'19BLSU.seq' (SEQ ID NO:144)   GCGTGACGGCGCGAGCAGGTGCGAAAGCAGGTCATAGTGATCCGGTGGTT 2200
'K_pneumon.seq' (SEQ ID NO:145)GCGTGACGGCGCGAGCAGGTGCGAAAGCAGGTCATAGTGATCCGGTGGTT 2200
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   CTGAATGGAAGGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAAC 2250
'24BLSU.seq' (SEQ ID NO:143)   CTGAATGGAAGGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAAC 2229
'19BLSU.seq' (SEQ ID NO:144)   CTGAATGGAAGGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAAC 2250
'K_pneumon.seq' (SEQ ID NO:145)CTGAATGGAAGGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAAC 2250
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   AGGCTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCG 2300
'24BLSU.seq' (SEQ ID NO:143)   AGGCTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCG 2279
'19BLSU.seq' (SEQ ID NO:144)   AGGCTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCG 2300
'K_pneumon.seq' (SEQ ID NO:145)AGGCTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCG 2300
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   ATGTCGGCTCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCT 2350
'24BLSU.seq' (SEQ ID NO:143)   ATGTCGGCTCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCT 2329
'19BLSU.seq' (SEQ ID NO:144)   ATGTCGGCTCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCT 2350
'K_pneumon.seq' (SEQ ID NO:145)ATGTCGGCTCATCACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCT 2350
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   GTTCGCCATTTAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACA 2400
'24BLSU.seq' (SEQ ID NO:143)   GTTCGCCATTTAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACA 2379
'19BLSU.seq' (SEQ ID NO:144)   GTTCGCCATTTAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACA 2400
'K_pneumon.seq' (SEQ ID NO:145)GTTCGCCATTTAAAGTGGTACGCGAGCTGGGTTTAGAACGTCGTGAGACA 2400
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   GTTCGGTCCCTATCTGCCGTGGGCGCTGGAGAATTGAGGGGGGCTGCTCC 2450
'24BLSU.seq' (SEQ ID NO:143)   GTTCGGTCCCTATCTGCCGTGGGCGCTGGAGAATTGAGGGGGGCTGCTCC 2429
'19BLSU.seq' (SEQ ID NO:144)   GTTCGGTCCCTATCTGCCGTGGGCGCTGGAGAATTGAGGGGGGCTGCTCC 2450
'K_pneumon.seq' (SEQ ID NO:145)GTTCGGTCCCTATCTGCCGTGGGCGCTGGAGAATTGAGGGGGGCTGCTCC 2450
                               **************************************************

'01BLSU.seq' (SEQ ID NO:142)   TAGTACGAGAGGACCGGAGTGGACGCATCACTGGTGTTCGGGTTGTCATG 2500
'24BLSU.seq' (SEQ ID NO:143)   TAGTACGAGAGGACCGGAGTGGACGCATCACTGGTGTTCGGGTTGTCATG 2479
'19BLSU.seq' (SEQ ID NO:144)   TAGTACGAGAGGACCGGAGTGGACGCATCACTGGTGTTCGGGTTGTCATG 2500
'K_pneumon.seq' (SEQ ID NO:145)TAGTACGAGAGGACCGGAGTGGACGCATCACTGGTGTTCGGGTTGTCATG 2500
                               **************************************************




'01BLSU.seq' (SEQ ID NO:142)   CCAATGGCACTGCCCGGTAGCTAAATGCGGAAGAGATAAGTGCTGAAAGC 2550
'24BLSU.seq' (SEQ ID NO:143)   CCAATGGCACTGCCCGGTAGCTAA------------------------- 2503
'19BLSU.seq' (SEQ ID NO:144)   CCAATGGCACTGCCCGGTAGCTAAA------------------------ 2525
'K_pneumon.seq' (SEQ ID NO:145)CCAATGGCACTGCCCGGTAGCTAAATGCGGAAGAGATAAGTGCTGAAAGC 2550
```

FIGURE 1-19

6 *Pseudomonas aeruginosa*

```
'P_aerugin.seq' (SEQ ID NO:146)ACCGAGATTCCCTTAGTAGTGGCGAGCGAACGGGGATTAGCCCTTAAGCT 50
'23BLSU.seq' (SEQ ID NO:147)   ACCGAGATTCCCTTAGTAGTGGCGAGCGAACGGGGATTAGCCCTTAAGCT 50
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)TCATTGATTTTAGCGGAACGCTCTGGAAAGTGCGGCCATAGTGGGTGATA 100
'23BLSU.seq' (SEQ ID NO:147)   TCATTGATTTTAGCGGAACGCTCTGGAAAGTGCGGCCATAGTGGGTGATA 100
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GCCCCGTACGCGAAAGGATCTTTGAAGTGAAATCGAGTAGGACGGAGCAC 150
'23BLSU.seq' (SEQ ID NO:147)   GCCCCGTACGCGAAAGGATCTTTGAAGTGAAATCGAGTAGGACGGAGCAC 150
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GAGAAACTTTGTCTGAACATGGGGGGACCATCCTCCAAGGCTAAATACTA 200
'23BLSU.seq' (SEQ ID NO:147)   GAGAAACTTTGTCTGAACATGGGGGGACCATCCTCCAAGGCTAAATACTA 200
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CTGACTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGCGAAAAGAACC 250
'23BLSU.seq' (SEQ ID NO:147)   CTGACTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGCGAAAAGAACC 250
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CCGGAGAGGGGAGTGAAATAGAACCTGAAACCGTATGCGTACAAGCAGTG 300
'23BLSU.seq' (SEQ ID NO:147)   CCGGAGAGGGGAGTGAAATAGAACCTGAAACCGTATGCGTACAAGCAGTG 300
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GGAGCCTACTTGTTAGGTGACTGCGTACCTTTTGTATAATGGGTCAGCGA 350
'23BLSU.seq' (SEQ ID NO:147)   GGAGCCTACTTGTTAGGTGACTGCGTACCTTTTGTATAATGGGTCAGCGA 350
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CTTATATTCAGTGGCAAGCTTAATCGTATAGGGTAGGCGTAGCGAAAGCG 400
'23BLSU.seq' (SEQ ID NO:147)   CTTATATTCAGTGGCAAGCTTAACCGTATAGGGTAGGCGTAGCGAAAGCG 400
                               ********************** ************************

'P_aerugin.seq' (SEQ ID NO:146)AGTCTTAATAGGGCGTTTAGTCGCTGGGTATAGACCCGAAACCGGGCGAT 450
'23BLSU.seq' (SEQ ID NO:147)   AGTCTTAATAGGGCGTTTAGTCGCTGGGTATAGACCCGAAACCGGGCGAT 450
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CTATCCATGAGCAGGTTGAAGGTTAGGTAACACTGACTGGAGGACCGAAC 500
'23BLSU.seq' (SEQ ID NO:147)   CTATCCATGAGCAGGTTGAAGGTTAGGTAACACTGACTGGAGGACCGAAC 500
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CCACTCCCGTTGAAAAGGTAGGGGATGACTTGTGGATCGGAGTGAAAGGC 550
'23BLSU.seq' (SEQ ID NO:147)   CCACTCCCGTTGAAAAGGTAGGGGATGACTTGTGGATCGGAGTGAAAGGC 550
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)TAATCAAGCTCGGAGATAGCTGGTTCTCCTCGAAAGCTATTTAGGTAGCG 600
'23BLSU.seq' (SEQ ID NO:147)   TAATCAAGCTCGGAGATAGCTGGTTCTCCTCGAAAGCTATTTAGGTAGCG 600
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CCTCATGTATCACTCTGGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCAT 650
'23BLSU.seq' (SEQ ID NO:147)   CCTCATGTATCACTCTGGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCAT 650
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CCCGACTTACCAAACCGATGCAAACTCCGAATACCCAGAAGTGCCGAGCA 700
'23BLSU.seq' (SEQ ID NO:147)   CCCGACTTACCAAACCGATGCAAACTCCGAATACCCAGAAGTGCCGAGCA 700
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)TGGGAGACACACGGCGGGTGCTAACGTCCGTCGTGAAAAGGGAAACAACC 750
'23BLSU.seq' (SEQ ID NO:147)   TGGGAGACACACGGCGGGTGCTAACGTCCGTCGTGAAAAGGGAAACAACC 750
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CAGACCGCCAGCTAAGGTCCCAAAGTTGTGGTTAAGTGGTAAACGATGTG 800
'23BLSU.seq' (SEQ ID NO:147)   CAGACCGCCAGCTAAGGTCCCAAAGTTGTGGTTAAGTGGTAAACGATGTG 800
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GGAAGGCTTAGACAGCTAGGAGGTTGGCTTAGAAGCAGCCATCCTTTAAA 850
'23BLSU.seq' (SEQ ID NO:147)   GGAAGGCTTAGACAGCTAGGAGGTTGGCTTAGAAGCAGCCATCCTTTAAA 850
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GAAAGCGTAATAGCTCACTAGTCGAGTCGGCCTGCGCGGAAGATGTAACG 900
'23BLSU.seq' (SEQ ID NO:147)   GAAAGCGTAATAGCTCACTAGTCGAGTCGGCCTGCGCGGAAGATGTAACG 900
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GGGCTCAAACCACACACCGAAGCTGCGGGTGTCACGTAAGTGACGCGGTA 950
'23BLSU.seq' (SEQ ID NO:147)   GGGCTCAAACCACACACCGAAGCTGCGGGTGTCACGCAAGTGACGCGGTA 950
```

FIGURE 1-20

```
                                  ********************************** *************

'P_aerugin.seq' (SEQ ID NO:146)GAGGAGCGTTCTGTAAGCCTGTGAAGGTGAGTTGAGAAGCTTGCTGGAGG 1000
'23BLSU.seq' (SEQ ID NO:147)   GAGGAGCGTTCTGTAAGCCTGTGAAGGTGAGTTGAGAAGCTTGCTGGAGG 1000
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)TATCAGAAGTGCGAATGCTGACATGAGTAACGACAATGGGTGTGAAAAGC 1050
'23BLSU.seq' (SEQ ID NO:147)   TATCAGAAGTGCGAATGCTGACATGAGTAACGACAATGGGTGTGAAAAAC 1050
                               ********************************************** *

'P_aerugin.seq' (SEQ ID NO:146)ACCCACGCCGAAAGACCAAGGGTTCCTGCGCAACGTTAATCGACGCAGGG 1100
'23BLSU.seq' (SEQ ID NO:147)   ACCCACGCCGAAAGACCAAGGGTTCCTGCGCAACGTTAATCGACGCAGGG 1100
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)TTAGTCGGTTCCTAAGGCGAGGCTGAAAAGCGTAGTCGATGGGAAACAGG 1150
'23BLSU.seq' (SEQ ID NO:147)   TTAGTCGGTTCCTAAGGCGAGGCTGAAAAGCGTAGTCGATGGGAAACAGG 1150
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)TTAATATTCCTGTACTTCTGGTTACTGCGATGGAGGGGCGGAGGAGGCTA 1200
'23BLSU.seq' (SEQ ID NO:147)   TTAATATTCCTGTACTTCTGGTTACTGCGATGGAGGGACGGAGAAGGCTA 1200
                               ********************************** ***** ******

'P_aerugin.seq' (SEQ ID NO:146)GGGCCGCTTGGCCGTGGGTGGCCAAGTTTAAGGTGGTAGGCTGAAATCTT 1250
'23BLSU.seq' (SEQ ID NO:147)   GGCCAGCTTGGCGTTGGTTGTCCAAGTTTAAGGTGGTAGGCTGAAATCTT 1250
                               ** * *******  *** ** ****************************

'P_aerugin.seq' (SEQ ID NO:146)AGGTAAATCCGGGGTTTCAAGGCCGAGAGGTGATGACGAGTCGTCTTTTA 1300
'23BLSU.seq' (SEQ ID NO:147)   AGGTAAATCCGGGGTTTCAAGGCCGAGAGCTGATGACGAGTCGTCTTTTA 1300
                               ***************************** ********************

'P_aerugin.seq' (SEQ ID NO:146)GATGACGAAGTGCTTGATGCCATGCTTCCAAGAAAAGCTTCTAAGCTTCA 1350
'23BLSU.seq' (SEQ ID NO:147)   GATGACGAAGTGGTTGATGCCATGCTTCCAAGAAAAGCTTCTAAGCTTCA 1350
                               ************ ************************************

'P_aerugin.seq' (SEQ ID NO:146)GGTAACCAGGAACCGTACCCCAAACCGACACAGGTGGTCGGGTAGAGAAT 1400
'23BLSU.seq' (SEQ ID NO:147)   GGTAACCAGGAACCGTACCCCAAACCGACACAGGTGGTCGGGTAGAGAAT 1400
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)ACCAAGGCGCTTGAGAGAACTCGGGTGAAGGAACTAGGCAAAATGGCACC 1450
'23BLSU.seq' (SEQ ID NO:147)   ACCAAGGCGCTTGAGAGAACTCGGGTGAAGGAACTAGGCAAAATGGCACC 1450
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GTAACTTCGGGAGAAGGTGCGCCGGCTAGGGTGAAGGATTTACTCCGTAA 1500
'23BLSU.seq' (SEQ ID NO:147)   GTAACTTCGGGAGAAGGTGCGCCGGCTAGGGTGAAGGATTTACTCCGTAA 1500
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GCTCTGGCTGGTCGAAGATACCAGGCCGCTGCGACTGTTTATTAAAAACA 1550
'23BLSU.seq' (SEQ ID NO:147)   GCTCTGGCTGGTCGAAGATACCAGGCCGCTGCGACTGTTTATTAAAAACA 1550
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CAGCACTCTGCAAACACGAAAGTGGACGTATAGGGTGTGACGCCTGCCCG 1600
'23BLSU.seq' (SEQ ID NO:147)   CAGCACTCTGCAAACACGAAAGTGGACGTATAGGGTGTGACGCCTGCCCG 1600
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GTGCCGGAAGGTTAATTGATGGGGTTAGCGCAAGCGAAGCTCTTGATCGA 1650
'23BLSU.seq' (SEQ ID NO:147)   GTGCCGGAAGGTTAATTGATGGGGTTAGCGCAAGCGAAGCTCTTGATCGA 1650
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)AGCCCCGGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAAT 1700
'23BLSU.seq' (SEQ ID NO:147)   AGCCCCGGTAAACGGCGGCCGTAACTATAACGGTCCTAAGGTAGCGAAAT 1700
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)TCCTTGTCGGGTAAGTTCCGACCTGCACGAATGGCGTAACGATGGCGGCG 1750
'23BLSU.seq' (SEQ ID NO:147)   TCCTTGTCGGGTAAGTTCCGACCTGCACGAATGGCGTAACGATGGCGGCG 1750
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CTGTCTCCACCCGAGACTCAGTGAAATTGAAATCGCTGTGAAGATGCAGT 1800
'23BLSU.seq' (SEQ ID NO:147)   CTGTCTCCACCCGAGACTCAGTGAAATTGAAATCGCTGTGAAGATGCAGT 1800
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GTATCCGCGGCTAGACGGAAAGACCCCGTGAACCTTTACTGTAGCTTTGC 1850
'23BLSU.seq' (SEQ ID NO:147)   GTATCCGCGGCTAGACGGAAAGACCCCGTGAACCTTTACTGTAGCTTTGC 1850
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)ACTGGACTTTGAGCCTGCTTGTGTAGGATAGGTGGGAGGCTTTGAAGCGT 1900
'23BLSU.seq' (SEQ ID NO:147)   ACTGGACTTTGAGCCTGCTTGTGTAGGATAGGTGGGAGGCTTTGAAGCGT 1900
                               **************************************************
```

FIGURE 1-21

```
'P_aerugin.seq' (SEQ ID NO:146)GGACGCCAGTTCGCGTGGAGCCATCCTTGAAATACCACCCTGGCATGCTT 1950
'23BLSU.seq' (SEQ ID NO:147)   GGACGCCAGTTCGCGTGGAGCCATCCTTGAAATACCACCCTGGCATGCTT 1950
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GAGGTTCTAACTCTGGTCCGTGATCCGGATCGAGGACAGTGTATGGTGGG 2000
'23BLSU.seq' (SEQ ID NO:147)   GAGGTTCTAACTCTGGTCCGTGATCCGGATCGAGGACAGTGTATGGTGGG 2000
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CAGTTTGACTGGGGCGGTCTCCTCCTAAAGAGTAACGGAGGAGTACGAAG 2050
'23BLSU.seq' (SEQ ID NO:147)   CAGTTTGACTGGGGCGGTCTCCTCCTAAAGAGTAACGGAGGAGTACGAAG 2050
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GTGCGCTCAGACCGGTCGGAAATCGGTCGCAGAGTATAAAGGCAAAAGCG 2100
'23BLSU.seq' (SEQ ID NO:147)   GTGCGCTCAGACCGGTCGGAAATCGGTCGCAGAGTATAAAGGCAAAAGCG 2100
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CGCTTGACTGCGAGACAGACACGTCGAGCAGGTACGAAAGTAGGTCTTAG 2150
'23BLSU.seq' (SEQ ID NO:147)   CGCTTGACTGCGAGACAGACACGTCGAGCAGGTACGAAAGTAGGTCTTAG 2150
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)TGATCCGGTGGTTCTGTATGGAAGGGCCATCGCTCAACGGATAAAAGGTA 2200
'23BLSU.seq' (SEQ ID NO:147)   TGATCCGGTGGTTCTGTATGGAAGGGCCATCGCTCAACGGATAAAAGGTA 2200
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CTCCGGGGATAACAGGCTGATACCGCCCAAGAGTTCATATCGACGGCGGT 2250
'23BLSU.seq' (SEQ ID NO:147)   CTCCGGGGATAACAGGCTGATACCGCCCAAGAGTTCATATCGACGGCGGT 2250
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GTTTGGCACCTCGATGTCGGCTCATCACATCCTGGGGCTGAAGCCGGTCC 2300
'23BLSU.seq' (SEQ ID NO:147)   GTTTGGCACCTCGATGTCGGCTCATCACATCCTGGGGCTGAAGCCGGTCC 2300
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)CAAGGGTATGGCTGTTCGCCATTTAAAGTGGTACGCGAGCTGGGTTTAGA 2350
'23BLSU.seq' (SEQ ID NO:147)   CAAGGGTATGGCTGTTCGCCATTTAAAGTGGTACGCGAGCTGGGTTTAGA 2350
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)ACGTCGTGAGACAGTTCGGTCCCTATCTGCCGTGGACGTTTGAGATTTGA 2400
'23BLSU.seq' (SEQ ID NO:147)   ACGTCGTGAGACAGTTCGGTCCCTATCTGCCGTGGACGTTTGAGATTTGA 2400
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)GAGGGGCTGCTCCTAGTACGAGAGGACCGGAGTGGACGAACCTCTGGTGT 2450
'23BLSU.seq' (SEQ ID NO:147)   GAGGGGCTGCTCCTAGTACGAGAGGACCGGAGTGGACGAACCTCTGGTGT 2450
                               **************************************************

'P_aerugin.seq' (SEQ ID NO:146)TCCGGTTGTCACGCCAGTGGCATTGCCGGGTAGCTA 2486
'23BLSU.seq' (SEQ ID NO:147)   TCCGGTTGTCACGCCAGTGGCATTGCCGGGTAGCTA 2486
                               **********************************
```

FIGURE 1-22

7 Staphylococcus aureus

```
'S_aureus.seq' (SEQ ID NO:148)AGTACCCGGAGGAAGAGAAAGAAAATTCGATTCCCTTAGTAGCGGCGAGCGAAACGGGAA 60
'02BLSU.seq' (SEQ ID NO:149)  AGTACCCGGAGGAAGAGAAAGAAAATTCGATTCCCTTAGTAGCGGCGAGCGAAACGGGAA 60
'20BLSU.seq' (SEQ ID NO:150)  ----------------------AAAATTCGATTCCCTTAGTAGCGGCGAGCGAAACGGGAA 39
                                                    ************************************

'S_aure.seq' (SEQ ID NO:148)GAGCCCAAACCAACAAGCTTGCTTGTTGGGGTTGTAGGACACTCTATACGGAGTTACAAA 120
'02BLSU.seq' (SEQ ID NO:149)GAGCCCAAACCAACAAGCTTGCTTGTTGGGGTTGTAGGACACTCTATACGGAGTTACAAA 120
'20BLSU.seq' (SEQ ID NO:150)GAGCCCAAACCAACAAGCTTGCTTGTTGGGGTTGTAGGACACTCTATACGGAGTTACAAA 99
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GGACGACATTAGACGAATCATCTGGAAAGATGAATCAAAGAAGGTAATAATCCTGTAGTC 180
'02BLSU.seq' (SEQ ID NO:149)GGACGACATTAGACGAATCATCTGGAAAGATGAATCAAAGAAGGTAATAATCCTGTAGTC 180
'20BLSU.seq' (SEQ ID NO:150)GGACGACATTAGACGAATCATCTGGAAAGATGAATCAAAGAAGGTAATAATCCTGTAGTC 159
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GAAAATGTTGTCTCTCTTGAGTGGATCCTGAGTACGACGGAGCACGTGAAATTCCGTCGG 240
'02BLSU.seq' (SEQ ID NO:149)GAAAATGTTGTCTCTCTTGAGTGGATCCTGAGTACGACGGAGCACGTGAAATTCCGTCGG 240
'20BLSU.seq' (SEQ ID NO:150)GAAAATGTTGTCTCTCTTGAGTGGATCCTGAGTACGACGGAGCACGTGAAATTCCGTCGG 219
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)AATCTGGGAGGACCATCTCCTAAGGCTAAATACTCTCTAGTGACCGATAGTGAACCAGTA 300
'02BLSU.seq' (SEQ ID NO:149)AATCTGGGAGGACCATCTCCTAAGGCTAAATACTCTCTAGTGACCGATAGTGAACCAGTA 300
'20BLSU.seq' (SEQ ID NO:150)AATCTGGGAGGACCATCTCCTAAGGCTAAATACTCTCTAGTGACCGATAGTGAACCAGTA 279
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)CCGTGAGGGAAAGGTGAAAAGCACCCCGGAAGGGGAGTGAAATAGAACCTGAAACCGTGT 360
'02BLSU.seq' (SEQ ID NO:149)CCGTGAGGGAAAGGTGAAAAGCACCCCGGAAGGGGAGTGAAATAGAACCTGAAACCGTGT 360
'20BLSU.seq' (SEQ ID NO:150)CCGTGAGGGAAAGGTGAAAAGCACCCCGGAAGGGGAGTGAAATAGAACCTGAAACCGTGT 339
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GCTTACAAGTAGTCAGAGCCCGTTAATGGGTGATGGCGTGCCTTTTGTAGAATGAACCGG 420
'02BLSU.seq' (SEQ ID NO:149)GCTTACAAGTAGTCAGAGCCCGTTAATGGGTGATGGCGTGCCTTTTGTAGAATGAACCGG 420
'20BLSU.seq' (SEQ ID NO:150)GCTTACAAGTAGTCAGAGCCCGTTAATGGGTGATGGCGTGCCTTTTGTAGAATGAACCGG 399
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)CGAGTTACGATTTGATGCAAGGTTAAGCAGTAAATGTGGAGCCGTAGCGAAAGCGAGTCT 480
'02BLSU.seq' (SEQ ID NO:149)CGAGTTACGATTTGATGCAAGGTTAAGCAGTAAATGTGGAGCCGTAGCGAAAGCGAGTCT 480
'20BLSU.seq' (SEQ ID NO:150)CGAGTTACGATTTGATGCAAGGTTAAGCAGTAAATGTGGAGCCGTAGCGAAAGCGAGTCT 459
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GAATAGGGCGTTTAGTATTTGGTCGTAGACCCGAAACCAGGTGATCTACCCTTGGTCAGG 540
'02BLSU.seq' (SEQ ID NO:149)GAATAGGGCGTTTAGTATTTGGTCGTAGACCCGAAACCAGGTGATCTACCCTTGGTCAGG 540
'20BLSU.seq' (SEQ ID NO:150)GAATAGGGCGTTTAGTATTTGGTCGTAGACCCGAAACCAGGTGATCTACCCTTGGTCAGG 519
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)TTGAAGTTCAGGTAACACTGAATGGAGGACCGAACCGACTTACGTTGAAAAGTGAGCGGA 600
'02BLSU.seq' (SEQ ID NO:149)TTGAAGTTCAGGTAACACTGAATGGAGGACCGAACCGACTTACGTTGAAAAGTGAGCGGA 600
'20BLSU.seq' (SEQ ID NO:150)TTGAAGTTCAGGTAACACTGAATGGAGGACCGAACCGACTTACGTTGAAAAGTGAGCGGA 579
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)TGAACTGAGGGTAGCGGAGAAATTCCAATCGAACCTGGAGATAGCTGGTTCTCTCCGAAA 660
'02BLSU.seq' (SEQ ID NO:149)TGAACTGAGGGTAGCGGAGAAATTCCAATCGAACCTGGAGATAGCTGGTTCTCTCCGAAA 660
'20BLSU.seq' (SEQ ID NO:150)TGAACTGAGGGTAGCGGAGAAATTCCAATCGAACCTGGAGATAGCTGGTTCTCTCCGAAA 639
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)TAGCTTTAGGGCTAGCCTCAAGTGATGATTATTGGAGGTAGAGCACTGTTTGGACGAGGG 720
'02BLSU.seq' (SEQ ID NO:149)TAGCTTTAGGGCTAGCCTCAAGTGATGATTATTGGAGGTAGAGCACTGTTTGGACGAGGG 720
'20BLSU.seq' (SEQ ID NO:150)TAGCTTTAGGGCTAGCCTCAAGTGATGATTATTGGAGGTAGAGCACTGTTTGGACGAGGG 699
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GCCCCTCTCGGGTTACCGAATTCAGACAAACTCCGAATGCCAATTAATTTAACTTGGGAG 780
'02BLSU.seq' (SEQ ID NO:149)GCCCCTCTCGGGTTACCGAATTCAGACAAACTCCGAATGCCAATTAATTTAACTTGGGAG 780
'20BLSU.seq' (SEQ ID NO:150)GCCCCTCTCGGGTTACCGAATTCAGACAAACTCCGAATGCCAATTAATTTAACTTGGGAG 759
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)TCAGAACATGGGTGATAAGGTCCGTGTTCGAAAGGGAAACAGCCCAGACCACCAGCTAAG 840
'02BLSU.seq' (SEQ ID NO:149)TCAGAACATGGGTGATAAGGTCCGTGTTCGAAAGGGAAACAGCCCAGACCACCAGCTAAG 840
'20BLSU.seq' (SEQ ID NO:150)TCAGAACATGGGTGATAAGGTCCGTGTTCGAAAGGGAAACAGCCCAGCCCACCAGCTAAG 819
                            ******************************************* ************

'S_aure.seq' (SEQ ID NO:148)GTCCCAAAATATATGTTAAGTGGAAAAGGATGTGGCGTTGCCCAGACAACTAGGATGTTG 900
'02BLSU.seq' (SEQ ID NO:149)GTCCCAAAATATATGTTAAGTGGAAAAGGATGTGGCGTTGCCCAGACAACTAGGATGTTG 900
'20BLSU.seq' (SEQ ID NO:150)GTCCCAAAATATATGTTAAGTGGAAAAGGATGTGGCGTTGCCCAGACAACTAGGATGTTG 879
```

FIGURE 1-23

```
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)GCTTAGAAGCAGCCATCATTTAAAGAGTGCGTAATAGCTCACTAGTCGAGTGACACTGCG 960
'02BLSU.seq' (SEQ ID NO:149)GCTTAGAAGCAGCCATCATTTAAAGAGTGCGTAATAGCTCACTAGTCGAGTGACACTGCG 960
'20BLSU.seq' (SEQ ID NO:150)GCTTAGAAGCAGCCATCATTTAAAGAGTGCGTAATAGCTCACTAGTCGAGTGACACTGCG 939
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)CCGAAAATGTACCGGGGCTAAACATATTACCGAAGCTGTGGATTGTCCTTTGGACAATGG 1020
'02BLSU.seq' (SEQ ID NO:149)CCGAAAATGTACCGGGGCTAAACATATTACCGAAGCTGTGGATTGTCCTTTGGACAATGG 1020
'20BLSU.seq' (SEQ ID NO:150)CCGAAAATGTACCGGGGCTAAACATATTACCGAAGCTGTGGATTGTCCTTTGGACAATGG 999
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)TAGGAGAGCGTTCTAAGGGCGTTGAAGCATGATCGTAAGGACATGTGGAGCGCTTAGAAG 1080
'02BLSU.seq' (SEQ ID NO:149)TAGGAGAGCGTTCTAAGGGCGTTGAAGCATGATCGTAAGGACATGTGGAGCGCTTAGAAG 1080
'20BLSU.seq' (SEQ ID NO:150)TAGGAGAGCGTTCTAAGGGCGTTGAAGCATGATCGTAAGGACATGTGGAGCGCTTAGAAG 1059
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)TGAGAATGCCGGTGTGAGTAGCGAAAGACGGGTGAGAATCCCGTCCACCGATTGACTAAG 1140
'02BLSU.seq' (SEQ ID NO:149)TGAGAATGCCGGTGTGAGTAGCGAAAGACGGGTGAGAATCCCGTCCACCGATTGACTAAG 1140
'20BLSU.seq' (SEQ ID NO:150)TGAGAATGCCGGTGTGAGTAGCGAAAGACGGGTGAGAATCCCGTCCACCGATTGACTAAG 1119
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)GTTTCCAGAGGAAGGCTCGTCCGCTCTGGGTTAGTCGGGTCCTAAGCTGAGGCCGACAGG 1200
'02BLSU.seq' (SEQ ID NO:149)GTTTCCAGAGGAAGGCTCGTCCGCTCTGGGTTAGTCGGGTCCTAAGCTGAGGCCGACAGG 1200
'20BLSU.seq' (SEQ ID NO:150)GTTTCCAGAGGAAGGCTCGTCCGCTCTGGGTTAGTCGGGTCCTAAGCTGAGGCCGACAGG 1179
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)CGTAGGCGATGGATAACAGGTTGATATTCCTGTACCACCTATAATCGTTTTAATCGATGG 1260
'02BLSU.seq' (SEQ ID NO:149)CGTAGGCGATGGATAACAGGTTGATATTCCTGTACCACCTATAATCGTTTTAATCGATGG 1260
'20BLSU.seq' (SEQ ID NO:150)CGTAGGCGATGGATAACAGGTTGATATTCCTGTACCACCTATAATCGTTTTAATCGATGG 1239
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)GGGGACGCAGTAGGATAGGCGAAGCGTGCGATTGGATTGCACGTCTAAGCAGTAAGGCTG 1320
'02BLSU.seq' (SEQ ID NO:149)GGGGACGCAGTAGGATAGGCGAAGCGTGCGATTGGATTGCACGTCTAAGCAGTAAGGCTG 1320
'20BLSU.seq' (SEQ ID NO:150)GGGGACGCAGTAGGATAGGCGAAGCGTGCGATTGGATTGCACGTCTAAGCAGTAAGGCTG 1299
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)AGTATTAGGCAAATCCGGTACTCGTTAAGGCTGAGCTGTGATGGGGAGAAGACATTGTGT 1380
'02BLSU.seq' (SEQ ID NO:149)AGTATTAGGCAAATCCGGTACTCATTAAGGCTGAGCTGTGATGGGGAGAAGACATTGTGT 1380
'20BLSU.seq' (SEQ ID NO:150)AGTATTAGGCAAATCCGGTACTCGTTAAGGCTGAGCTGTGATGGGGAGAAGACATTGAGT 1359
                          ********************** ******************************** **

'S_aure.seq' (SEQ ID NO:148)CTTCGAGTCGTTGATTTCACACTGCCGAGAAAAGCCTCTAGATAGAAAATAGGTGCCCGT 1440
'02BLSU.seq' (SEQ ID NO:149)CTTCGAGTCGTTGATTTCACACTGCCGAGAAAAGCCTCTAGATAGAAAATAGGTGCCCGT 1440
'20BLSU.seq' (SEQ ID NO:150)CTTCGAGTCGTTGATTTCACACTGCCGAGAAAAGCCTCTAGATAGAAAATAGGTGCCCGT 1419
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)ACCGCAAACCGACACAGGTAGTCAAGATGAGAATTCTAAGGTGAGCGAGCGAACTCTCGT 1500
'02BLSU.seq' (SEQ ID NO:149)ACCGCAAACCGACACAGGTAGTCAAGATGAGAATTCTAAGGTGAGCGAGCGAACTCTCGT 1500
'20BLSU.seq' (SEQ ID NO:150)ACCGCAAACCGACACAGGTAGTCAAGATGAGAATTCTAAGGTGAGCGAGCGAACTCTCGT 1479
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)TAAGGAACTCGGCAAAATGACCCCGTAACTTCGGGAGAAGGGGTGCTCTTTAGGGTTAAC 1560
'02BLSU.seq' (SEQ ID NO:149)TAAGGAACTCGGCAAAATGACCCCGTAACTTCGGGAGAAGGGGTGCTCTTTAGGGTTAAC 1560
'20BLSU.seq' (SEQ ID NO:150)TAAGGAACTCGGCAAAATGACCCCGTAACTTCGGGAGAAGGGGTGCTCTTTAGGGTTAAC 1539
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)GCCCAGAAGAGCCGCAGTGAATAGGCCCAAGCGACTGTTTATCAAAAACACAGGTCTCTG 1620
'02BLSU.seq' (SEQ ID NO:149)GCCCAGAAGAGCCGCAGTGAATAGGCCCAAGCGACTGTTTATCAAAAACACAGGTCTCTG 1620
'20BLSU.seq' (SEQ ID NO:150)GCCCAGAAGAGCCGCAGTGAATAGGCCCAAGCGACTGTTTATCAAAAACACAGGTCTCTG 1599
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)CTAAACCGTAAGGTGATGTATAGGGGCTGACGCCTGCCCGGTGCTGGAAGGTTAAGAGGA 1680
'02BLSU.seq' (SEQ ID NO:149)CTAAACCGTAAGGTGATGTATAGGGGCTGACGCCTGCCCGGTGCTGGAAGGTTAAGAGGA 1680
'20BLSU.seq' (SEQ ID NO:150)CTAAACCGTAAGGTGATGTATAGGGGCTGACGCCTGCCCGGTGCTGGAAGGTTAAGAGGA 1659
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)GTGGTTAGCTTCTGCGAAGCTACGAATCGAAGCCCCAGTAAACGGCGGCCGTAACTATAA 1740
'02BLSU.seq' (SEQ ID NO:149)GTGGTTAGCTTCTGCGAAGCTACGAATCGAAGCCCCAGTAAACGGCGGCCGTAACTATAA 1740
'20BLSU.seq' (SEQ ID NO:150)GTGGTTAGCTTCTGCGAAGCTACGAATCGAAGCCCCAGTAAACGGCGGCCGTAACTATAA 1719
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)CGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGACCCGCACGAAAGGCGTAAC 1800
'02BLSU.seq' (SEQ ID NO:149)CGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGACCCGCACGAAAGGCGTAAC 1800
'20BLSU.seq' (SEQ ID NO:150)CGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGACCCGCACGAAAGGCGTAAC 1779
                          ************************************************************

'S_aure.seq' (SEQ ID NO:148)GATTTGGGCACTGTCTCAACGAGAGACTCGGTGAAATCATAGTACCTGTGAAGATGCAGG 1860
```

FIGURE 1-24

```
'02BLSU.seq' (SEQ ID NO:149)GATTTGGGCACTGTCTCAACGAGAGACTCGGTGAAATCATAGTACCTGTGAAGATGCAGG 1860
'20BLSU.seq' (SEQ ID NO:150)GATTTGGGCACTGTCTCAACGAGAGACTCGGTGAAATCATAGTACCTGTGAAGATGCAGG 1839
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)TTACCCGCGACAGGACGGAAAGACCCCGTGGAGCTTTACTGTAGCCTGATATTGAAATTC 1920
'02BLSU.seq' (SEQ ID NO:149)TTACCCGCGACAGGACGGAAAGACCCCGTGGAGCTTTACTGTAGCCTGATATTGAAATTC 1920
'20BLSU.seq' (SEQ ID NO:150)TTACCCGCGACAGGACGGAAAGACCCCGTGGAGCTTTACTGTAGCCTGATATTGAAATTC 1899
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GGCACAGCTTGTACAGGATAGGTAGGAGCCTTTGAAACGTGAGCGCTAGCTTACGTGGAG 1980
'02BLSU.seq' (SEQ ID NO:149)GGCACAGCTTGTACAGGATAGGTAGGAGCCTTTGAAACGTGAGCGCTAGCTTACGTGGAG 1980
'20BLSU.seq' (SEQ ID NO:150)GGCACAGCTTGTACAGGATAGGTAGGAGCCTTTGAAACGTGAGCGCTAGCTTACGTGGAG 1959
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GCGCTGGTGGGATACTACCCTAGCTGTGTTGGCTTTCTAACCCGCACCACTTATCGTGGT 2040
'02BLSU.seq' (SEQ ID NO:149)GCGCTGGTGGGATACTACCCTAGCTGTGTTGGCTTTCTAACCCGCACCACTTATCGTGGT 2040
'20BLSU.seq' (SEQ ID NO:150)GCGCTGGTGGGATACTACCCTAGCTGTGTTGGCTTTCTAACCCGCACCACTTATCGTGGT 2019
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GGGAGACAGTGTCAGGCGGGCAGTTTGACTGGGGCGGTCGCCTCCTAAAAGGTAACGGAG 2100
'02BLSU.seq' (SEQ ID NO:149)GGGAGACAGTGTCAGGCGGGCAGTTTGACTGGGGCGGTCGCCTCCTAAAAGGTAACGGAG 2100
'20BLSU.seq' (SEQ ID NO:150)GGGAGACAGTGTCAGGCGGGCAGTTTGACTGGGGCGGTCGCCTCCTAAAAGGTAACGGAG 2079
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GCGCTCAAAGGTTCCCTCAGAATGGTTGGAAATCATTCATAGAGTGTAAAGGCATAAGGG 2160
'02BLSU.seq' (SEQ ID NO:149)GCGCTCAAAGGTTCCCTCAGAATGGTTGGAAATCATTCATAGAGTGTAAAGGCATAAGGG 2160
'20BLSU.seq' (SEQ ID NO:150)GCGCTCAAAGGTTCCCTCAGAATGGTTGGAAATCATTCATAGAGTGTAAAGGCATAAGGG 2139
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)AGCTTGACTGCGAGACCTACAAGTCGAGCAGGGTCGAAAGACGGACTTAGTGATCCGGTG 2220
'02BLSU.seq' (SEQ ID NO:149)AGCTTGACTGCGAGACCTACAAGTCGAGCAGGGTCGAAAGACGGACTTAGTGATCCGGTG 2220
'20BLSU.seq' (SEQ ID NO:150)AGCTTGACTGCGAGACCTACAAGTCGAGCAGGGTCGAAAGACGGACTTAGTGATCCGGTG 2199
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)GTTCCGCATGGAAGGGCCATCGCTCAACGGATAAAAGCTACCCCGGGGATAACAGGCTTA 2280
'02BLSU.seq' (SEQ ID NO:149)GTTCCGCATGGAAGGGCCATCGCTCAACGGATAAAAGCTACCCCGGGGATAACAGGCTTA 2280
'20BLSU.seq' (SEQ ID NO:150)GTTCCGCATGGAAGGGCCATCGCTCAACGGATAAAAGCTACCCCGGGGATAACAGGCTTA 2259
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)TCTCCCCCAAGAGTTCACATCGACGGGGAGGTTTGGCACCTCGATGTCGGCTCATCGCAT 2340
'02BLSU.seq' (SEQ ID NO:149)TCTCCCCCAAGAGTTCACATCGACGGGGAGGTTTGGCACCTCGATGTCGGCTCATCGCAT 2340
'20BLSU.seq' (SEQ ID NO:150)TCTCCCCCAAGAGTTCACATCGACGGGGAGGTTTGGCACCTCGATGTCGGCTCATCGCAT 2319
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)CCTGGGGCTGTAGTCGGTCCCAAGGGTTGGGCTGTTCGCCCATTAAAGCGGTACGCGAGC 2400
'02BLSU.seq' (SEQ ID NO:149)CCTGGGGCTGTAGTCGGTCCCAAGGGTTGGGCTGTTCGCCCATTAAAGCGGTACGCGAGC 2400
'20BLSU.seq' (SEQ ID NO:150)CCTGGGGCTGTAGTCGGTCCCAAGGGTTGGGCTGTTCGCCCATTAAAGCGGTACGCGAGC 2379
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)TGGGTTCAGAACGTCGTGAGACAGTT-CGGTCCCTATCCGTCGTGGGCGTAGGAAATTTG 2459
'02BLSU.seq' (SEQ ID NO:149)TGGGTTCAGAACGTCGTGAGACAGTT-CGGTCCCTATCCGTCGTGGGCGTAGGAAATTTG 2459
'20BLSU.seq' (SEQ ID NO:150)TGGGTTCAGAACGTCGTGAGACAGTTACGGTCCCTATCCGTCGTGGGCGTAGGAAATTTG 2439
                            ************************** *********************************

'S_aure.seq' (SEQ ID NO:148)AGAGGAGCTGTCCTTAGTACGAGAGGACCGGGATGGACATACCTCTGGTGTACCAGTTGT 2519
'02BLSU.seq' (SEQ ID NO:149)AGAGGAGCTGTCCTTAGTACGAGAGGACCGGGATGGACATACCTCTGGTGTACCAGTTGT 2519
'20BLSU.seq' (SEQ ID NO:150)AGAGGAGCTGTCCTTAGTACGAGAGGACCGGGATGGACATACCTCTGGTGTACCAGTTGT 2499
                            ************************************************************

'S_aure.seq' (SEQ ID NO:148)CGTGCCAACGGCATAGCTGGGTAGCTATGTGTGGACGGGATAAGT 2564
'02BLSU.seq' (SEQ ID NO:149)CGTGCCAACGGCATAGCTGGGTAGCTATGTGTGGACGGGATAAGT 2564
'20BLSU.seq' (SEQ ID NO:150)CGTGCCAACGGCATAG---------------------------- 2515
                            ****************
```

FIGURE 1-25

8 *Staphylococcus epidermidis*

```
'S_epidermi.seq' (SEQ ID NO:150)AGCACTTATCCCGTCCATACATAGCTACCCAGCTATGCCGTTGGCACGAC 50
'06BLSU.seq' (SEQ ID NO:151)    ----------------TACATAGCTACCCAGCTATGCCGTTGGCACGAC 33
'04BLSU.seq' (SEQ ID NO:152)    AGCACTTATCCCGTCCATACATAGCTACCCAGCTATGCCGTTGGCACGAC 50
'05BLSU.seq' (SEQ ID NO:153)    -----------CGTCCATACATAGCTACCCAGCTATGCCGTTGGCACGAC 39
                                          **********************************

'S_epidermi.seq' (SEQ ID NO:150)AACTGGTACACCAGAGGTATGTCCATCCCGGTCCTCTCGTACTAAGGACA 100
'06BLSU.seq' (SEQ ID NO:151)    AACTGGTACACCAGAGGTATGTCCATCCCGGTCCTCTCGTACTAAGGACA 83
'04BLSU.seq' (SEQ ID NO:152)    AACTGGTACACCAGAGGTATGTCCATCCCGGTCCTCTCGTACTAAGGACA 100
'05BLSU.seq' (SEQ ID NO:153)    AACTGGTACACCAGAGGTATGTCCATCCCGGTCCTCTCGTACTAAGGACA 89
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)GCTCCTCTCAAATTTCCTACGCCCACGACGGATAGGGACCGAACTGTCTC 150
'06BLSU.seq' (SEQ ID NO:151)    GCTCCTCTCAAATTTCCTACGCCCACGACGGATAGGGACCGAACTGTCTC 133
'04BLSU.seq' (SEQ ID NO:152)    GCTCCTCTCAAATTTCCTACGCCCACGACGGATAGGGACCGAACTGTCTC 150
'05BLSU.seq' (SEQ ID NO:153)    GCTCCTCTCAAATTTCCTACGCCCACGACGGATAGGGACCGAACTGTCTC 139
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)ACGACGTTCTGAACCCAGCTCGCGTACCGCTTTAATGGGCGAACAGCCCA 200
'06BLSU.seq' (SEQ ID NO:151)    ACGACGTTCTGAACCCAGCTCGCGTACCGCTTTAATGGGCGAACAGCCCA 183
'04BLSU.seq' (SEQ ID NO:152)    ACGACGTTCTGAACCCAGCTCGCGTACCGCTTTAATGGGCGAACAGCCCA 200
'05BLSU.seq' (SEQ ID NO:153)    ACGACGTTCTGAACCCAGCTCGCGTACCGCTTTAATGGGCGAACAGCCCA 189
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)ACCCTTGGGACCGACTACAGCCCCAGGATGCGATGAGCCGACATCGAGGT 250
'06BLSU.seq' (SEQ ID NO:151)    ACCCTTGGGACCGACTACAGCCCCAGGATGCGATGAGCCGACATCGAGGT 233
'04BLSU.seq' (SEQ ID NO:152)    ACCCTTGGGACCGACTACAGCCCCAGGATGCGATGAGCCGACATCGAGGT 250
'05BLSU.seq' (SEQ ID NO:153)    ACCCTTGGGACCGACTACAGCCCCAGGATGCGATGAGCCGACATCGAGGT 239
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)GCCAAACCTCCCCGTCGATGTGAACTCTTGGGGGAGATAAGCCTGTTATC 300
'06BLSU.seq' (SEQ ID NO:151)    GCCAAACCTCCCCGTCGATGTGAACTCTTGGGGGAGATAAGCCTGTTATC 283
'04BLSU.seq' (SEQ ID NO:152)    GCCAAACCTCCCCGTCGATGTGAACTCTTGGGGGAGATAAGCCTGTTATC 300
'05BLSU.seq' (SEQ ID NO:153)    GCCAAACCTCCCCGTCGATGTGAACTCTTGGGGGAGATAAGCCTGTTATC 289
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CCCGGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTCCATGCGGAACCAC 350
'06BLSU.seq' (SEQ ID NO:151)    CCCGGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTCCATGCGGAACCAC 333
'04BLSU.seq' (SEQ ID NO:152)    CCCGGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTCCATGCGGAACCAC 350
'05BLSU.seq' (SEQ ID NO:153)    CCCGGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTCCATGCGGAACCAC 339
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CGGATCACTAAGTCCGTCTTTCGACCCTGCTCGACTTGTAGGTCTCGCAG 400
'06BLSU.seq' (SEQ ID NO:151)    CGGATCACTAAGTCCGTCTTTCGACCCTGCTCGACTTGTAGGTCTCGCAG 383
'04BLSU.seq' (SEQ ID NO:152)    CGGATCACTAAGTCCGTCTTTCGACCCTGCTCGACTTGTAGGTCTCGCAG 400
'05BLSU.seq' (SEQ ID NO:153)    CGGATCACTAAGTCCGTCTTTCGACCCTGCTCGACTTGTAGGTCTCGCAG 389
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TCAAGCTCCCTTATGCCTTTACACTCTATGAATGATTTCCAACCATTCTG 450
'06BLSU.seq' (SEQ ID NO:151)    TCAAGCTCCCTTATGCCTTTACACTCTATGAATGATTTCCAACCATTCTG 433
'04BLSU.seq' (SEQ ID NO:152)    TCAAGCTCCCTTATGCCTTTACACTCTATGAATGATTTCCAACCATTCTG 450
'05BLSU.seq' (SEQ ID NO:153)    TCAAGCTCCCTTATGCCTTTACACTCTATGAATGATTTCCAACCATTCTG 439
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)AGGGAACCTTTGAGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGT 500
'06BLSU.seq' (SEQ ID NO:151)    AGGGAACCTTTGAGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGT 483
'04BLSU.seq' (SEQ ID NO:152)    AGGGAACCTTTGAGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGT 500
'05BLSU.seq' (SEQ ID NO:153)    AGGGAACCTTTGAGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGT 489
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CAAACTGCCCGCCTGACACTGTCTCCCACCACGATAAGTGGTGCGGGTTA 550
'06BLSU.seq' (SEQ ID NO:151)    CAAACTGCCCGCCTGACACTGTCTCCCACCACGATAAGTGGTGCGGGTTA 533
'04BLSU.seq' (SEQ ID NO:152)    CAAACTGCCCGCCTGACACTGTCTCCCACCACGATAAGTGGTGCGGGTTA 550
'05BLSU.seq' (SEQ ID NO:153)    CAAACTGCCCGCCTGACACTGTCTCCCACCACGATAAGTGGTGCGGGTTA 539
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)GAAAGCCAACACAGCTAGGGTAGTATCCCACCAACGCCTCCACGTAAGCT 600
'06BLSU.seq' (SEQ ID NO:151)    GAAAGCCAACACAGCTAGGGTAGTATCCCACCAACGCCTCCACGTAAGCT 583
'04BLSU.seq' (SEQ ID NO:152)    GAAAGCCAACACAGCTAGGGTAGTATCCCACCAACGCCTCCACGTAAGCT 600
'05BLSU.seq' (SEQ ID NO:153)    GAAAGCCAACACAGCTAGGGTAGTATCCCACCAACGCCTCCACGTAAGCT 589
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)AGCGCTCACGTTTCAAAGGCTCCTACCTATCCTGTACAAGCTGTGCCGAA 650
'06BLSU.seq' (SEQ ID NO:151)    AGCGCTCACGTTTCAAAGGCTCCTACCTATCCTGTACAAGCTGTGCCGAA 633
```

FIGURE 1-26

```
'04BLSU.seq' (SEQ ID NO:152)    AGCGCTCACGTTTCAAAGGCTCCTACCTATCCTGTACAAGCTGTGCCGAA 650
'05BLSU.seq' (SEQ ID NO:153)    AGCGCTCACGTTTCAAAGGCTCCTACCTATCCTGTACAAGCTGTGCCGAA 639
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TTTCAATATCAGGCTACAGTAAAGCTCCACGGGGTCTTTCCGTCCTGTCG 700
'06BLSU.seq' (SEQ ID NO:151)    TTTCAATATCAGGCTACAGTAAAGCTCCACGGGGTCTTTCCGTCCTGTCG 683
'04BLSU.seq' (SEQ ID NO:152)    TTTCAATATCAGGCTACAGTAAAGCTCCACGGGGTCTTTCCGTCCTGTCG 700
'05BLSU.seq' (SEQ ID NO:153)    TTTCAATATCAGGCTACAGTAAAGCTCCACGGGGTCTTTCCGTCCTGTCG 689
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CGGGTAACCTGCATCTTCACAGGTACTATGATTTCACCGAGTCTCTCGTT 750
'06BLSU.seq' (SEQ ID NO:151)    CGGGTAACCTGCATCTTCACAGGTACTATGATTTCACCGAGTCTCTCGTT 733
'04BLSU.seq' (SEQ ID NO:152)    CGGGTAACCTGCATCTTCACAGGTACTATGATTTCACCGAGTCTCTCGTT 750
'05BLSU.seq' (SEQ ID NO:153)    CGGGTAACCTGCATCTTCACAGGTACTATGATTTCACCGAGTCTCTCGTT 739
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)GAGACAGTGCCCAAATCGTTACGCCTTTCGTGCGGGTCGGAACTTACCCG 800
'06BLSU.seq' (SEQ ID NO:151)    GAGACAGTGCCCAAATCGTTACGCCTTTCGTGCGGGTCGGAACTTACCCG 783
'04BLSU.seq' (SEQ ID NO:152)    GAGACAGTGCCCAAATCGTTACGCCTTTCGTGCGGGTCGGAACTTACCCG 800
'05BLSU.seq' (SEQ ID NO:153)    GAGACAGTGCCCAAATCGTTACGCCTTTCGTGCGGGTCGGAACTTACCCG 789
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)ACAAGGAATTTCGCTACCTTAGGACCGTTATAGTTACGGCCGCCGTTTAC 850
'06BLSU.seq' (SEQ ID NO:151)    ACAAGGAATTTCGCTACCTTAGGACCGTTATAGTTACGGCCGCCGTTTAC 833
'04BLSU.seq' (SEQ ID NO:152)    ACAAGGAATTTCGCTACCTTAGGACCGTTATAGTTACGGCCGCCGTTTAC 850
'05BLSU.seq' (SEQ ID NO:153)    ACAAGGAATTTCGCTACCTTAGGACCGTTATAGTTACGGCCGCCGTTTAC 839
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TGGGGCTTTGATTCGTAGCTTCGCAGAAGCTAACCACTCCTCTTAACCTT 900
'06BLSU.seq' (SEQ ID NO:151)    TGGGGCTTCGATTCGTAGCTTCGCAGAAGCTAACCACTCCTCTTAACCTT 883
'04BLSU.seq' (SEQ ID NO:152)    TGGGGCTTCGATTCGTAGCTTCGCAGAAGCTAACCACTCCTCTTAACCTT 900
'05BLSU.seq' (SEQ ID NO:153)    TGGGGCTTCGATTCGTAGCTTCGCAGAAGCTAACCACTCCTCTTAACCTT 889
                                ******** ****************************************

'S_epidermi.seq' (SEQ ID NO:150)CCAGCACCGGGCAGGCGTCAGCCCCTATACATCACCTTACGGTTTAGCAG 950
'06BLSU.seq' (SEQ ID NO:151)    CCAGCACCGGGCAGGCGTCAGCCCCTATACATCACCTTACGGTTTAGCAG 933
'04BLSU.seq' (SEQ ID NO:152)    CCAGCACCGGGCAGGCGTCAGCCCCTATACATCACCTTACGGTTTAGCAG 950
'05BLSU.seq' (SEQ ID NO:153)    CCAGCACCGGGCAGGCGTCAGCCCCTATACATCACCTTACGGTTTAGCAG 939
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)AGACCTGTGTTTTTGATAAACAGTCGCTTGGGCCTATTCACTGCGGCTCT 1000
'06BLSU.seq' (SEQ ID NO:151)    AGACCTGTGTTTTTGATAAACAGTCGCTTGGGCCTATTCACTGCGGCTCT 983
'04BLSU.seq' (SEQ ID NO:152)    AGACCTGTGTTTTTGATAAACAGTCGCTTGGGCCTATTCACTGCGGCTCT 1000
'05BLSU.seq' (SEQ ID NO:153)    AGACCTGTGTTTTTGATAAACAGTCGCTTGGGCCTATTCACTGCGGCTCT 989
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TCTGGGCGTGAACCCTAAAGAGCACCCCTTCTCCCGAAGTTACGGGGTCA 1050
'06BLSU.seq' (SEQ ID NO:151)    TCTGGGCGTGAACCCTAAAGAGCACCCCTTCTCCCGAAGTTACGGGGTCA 1033
'04BLSU.seq' (SEQ ID NO:152)    TCTGGGCGTGAACCCTAAAGAGCACCCCTTCTCCCGAAGTTACGGGGTCA 1050
'05BLSU.seq' (SEQ ID NO:153)    TCTGGGCGTGAACCCTAAAGAGCACCCCTTCTCCCGAAGTTACGGGGTCA 1039
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TTTTGCCGAGTTCCTTAACGAGAGTTCGCTCGCTCACCTTAGAATTCTCA 1100
'06BLSU.seq' (SEQ ID NO:151)    TTTTGCCGAGTTCCTTAACGAGAGTTCGCTCGCTCACCTTAGAATTCTCA 1083
'04BLSU.seq' (SEQ ID NO:152)    TTTTGCCGAGTTCCTTAACGAGAGTTCGCTCGCTCACCTTAGAATTCTCA 1100
'05BLSU.seq' (SEQ ID NO:153)    TTTTGCCGAGTTCCTTAACGAGAGTTCGCTCGCTCACCTTAGAATTCTCA 1089
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TCTTGACTACCTGTGTCGGTTTGCGGTACGGGCACCTGTTATCTATCTAG 1150
'06BLSU.seq' (SEQ ID NO:151)    TCTTGACTACCTGTGTCGGTTTGCGGTACGGGCACCTGTTATCTATCTAG 1133
'04BLSU.seq' (SEQ ID NO:152)    TCTTGACTACCTGTGTCGGTTTGCGGTACGGGCACCTGTTATCTATCTAG 1150
'05BLSU.seq' (SEQ ID NO:153)    TCTTGACTACCTGTGTCGGTTTGCGGTACGGGCACCTGTTATCTATCTAG 1139
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)AGGCTTTTCTCGGCAGTGTGAAATCAACGACTCGAGGAAACAATTTCCTC 1200
'06BLSU.seq' (SEQ ID NO:151)    AGGCTTTTCTCGGCAGTGTGAAATCAACGACTCGAGGAAACAATTTCCTC 1183
'04BLSU.seq' (SEQ ID NO:152)    AGGCTTTTCTCGGCAGTGTGAAATCAACGACTCGAGGAAACAATTTCCTC 1200
'05BLSU.seq' (SEQ ID NO:153)    AGGCTTTTCTCGGCAGTGTGAAATCAACGACTCGAGGAAACAATTTCCTC 1189
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TCCCCATCACAGCTCAGCCTTATGAGTGCCGGATTTGCCTAACACTCAGC 1250
'06BLSU.seq' (SEQ ID NO:151)    TCCCCATCACAGCTCAGCCTTATGAGTGCCGGATTTGCCTAACACTCAGC 1233
'04BLSU.seq' (SEQ ID NO:152)    TCCCCATCACAGCTCAGCCTTATGAGTGCCGGATTTGCCTAACACTCAGC 1250
'05BLSU.seq' (SEQ ID NO:153)    TCCCCATCACAGCTCAGCCTTATGAGTGCCGGATTTGCCTAACACTCAGC 1239
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CTTACTGCTTGGACGTGCACTCCAACAGCACGCTTCGCCTATCCTACTGC 1300
'06BLSU.seq' (SEQ ID NO:151)    CTTACTGCTTGGACGTGCACTCCAACAGCACGCTTCGCCTATCCTACTGC 1283
```

FIGURE 1-27

```
'04BLSU.seq' (SEQ ID NO:152)    CTTACTGCTTGGACGTGCACTCCAACAGCACGCTTCGCCTATCCTACTGC 1300
'05BLSU.seq' (SEQ ID NO:153)    CTTACTGCTTGGACGTGCACTCCAACAGCACGCTTCGCCTATCCTACTGC 1289
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)GTCCCCCCATCGATTAAAACGATACTAGGTGGTACAGGAATATCAACCTG 1350
'06BLSU.seq' (SEQ ID NO:151)    GTCCCCCCATCGATTAAAACGATACTAGGTGGTACAGGAATATCAACCTG 1333
'04BLSU.seq' (SEQ ID NO:152)    GTCCCCCCATCGATTAAAACGATACTAGGTGGTACAGGAATATCAACCTG 1350
'05BLSU.seq' (SEQ ID NO:153)    GTCCCCCCATCGATTAAAACGATACTAGGTGGTACAGGAATATCAACCTG 1339
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TTATCCATCGCCTACGCCTGTCGGCCTCAGCTTAGGACCCGACTAACCCA 1400
'06BLSU.seq' (SEQ ID NO:151)    TTATCCATCGCCTACGCCTGTCGGCCTCAGCTTAGGACCCGACTAACCCA 1383
'04BLSU.seq' (SEQ ID NO:152)    TTATCCATCGCCTACGCCTGTCGGCCTCAGCTTAGGACCCGACTAACCCA 1400
'05BLSU.seq' (SEQ ID NO:153)    TTATCCATCGCCTACGCCTGTCGGCCTCAGCTTAGGACCCGACTAACCCA 1389
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)GAGCGGACGAGCCTTCCTCTGGAAACCTTAGTCAATCGGTGGACGGGATT 1450
'06BLSU.seq' (SEQ ID NO:151)    GAGCGGACGAGCCTTCCTCTGGAAACCTTAGTCAATCGGTGGACGGGATT 1433
'04BLSU.seq' (SEQ ID NO:152)    GAGCGGACGAGCCTTCCTCTGGAAACCTTAGTCAATCGGTGGACGGGATT 1450
'05BLSU.seq' (SEQ ID NO:153)    GAGCGGACGAGCCTTCCTCTGGAAACCTTAGTCAATCGGTGGACGGGATT 1439
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CTCACCCGTCTTTCGCTACTCACACCGGCATTCTCACTTCTAAGCGCTCC 1500
'06BLSU.seq' (SEQ ID NO:151)    CTCACCCGTCTTTCGCTACTCACACCGGCATTCTCACTTCTAAGCGCTCC 1483
'04BLSU.seq' (SEQ ID NO:152)    CTCACCCGTCTTTCGCTACTCACACCGGCATTCTCACTTCTAAGCGCTCC 1500
'05BLSU.seq' (SEQ ID NO:153)    CTCACCCGTCTTTCGCTACTCACACCGGCATTCTCACTTCTAAGCGCTCC 1489
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)ACATGTCCTTGCGATCATGCTTCGACACCCTTAGAACGCTCTCCTACCAT 1550
'06BLSU.seq' (SEQ ID NO:151)    ACATGTCCTTGCGATCATGCTTCGACGCCCTTAGAACGCTCTCCTACCAT 1533
'04BLSU.seq' (SEQ ID NO:152)    ACATGTCCTTGCGATCATGCTTCGACGCCCTTAGAACGCTCTCCTACCAT 1550
'05BLSU.seq' (SEQ ID NO:153)    ACATGTCCTTGCGATCATGCTTCGACGCCCTTAGAACGCTCTCCTACCAT 1539
                                ************************* ***********************

'S_epidermi.seq' (SEQ ID NO:150)TGTCCAAAGGACAATCCACAGCTTCGGTAATATGTTTAGCCCCGGTACAT 1600
'06BLSU.seq' (SEQ ID NO:151)    TGTCCAAAGGACAATCCACAGCTTCGGTAATATGTTTAGCCCCGGTACAT 1583
'04BLSU.seq' (SEQ ID NO:152)    TGTCCAAAGGACAATCCACAGCTTCGGTAATATGTTTAGCCCCGGTACAT 1600
'05BLSU.seq' (SEQ ID NO:153)    TGTCCAAAGGACAATCCACAGCTTCGGTAATATGTTTAGCCCCGGTACAT 1589
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TTTCGGCGCAGTGTCACTCGACTAGTGAGCTATTACGCACTCTTTAAATG 1650
'06BLSU.seq' (SEQ ID NO:151)    TTTCGGCGCAGTGTCACTCGACTAGTGAGCTATTACGCACTCTTTAAATG 1633
'04BLSU.seq' (SEQ ID NO:152)    TTTCGGCGCAGTGTCACTCGACTAGTGAGCTATTACGCACTCTTTAAATG 1650
'05BLSU.seq' (SEQ ID NO:153)    TTTCGGCGCAGTGTCACTCGACTAGTGAGCTATTACGCACTCTTTAAATG 1639
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)ATGGCTGCTTCTAAGCCAACATCCTAGTTGTCTGGGCAACGCCACATCCT 1700
'06BLSU.seq' (SEQ ID NO:151)    ATGGCTGCTTCTAAGCCAACATCCTAGTTGTCTGGGCAACGCCACATCCT 1683
'04BLSU.seq' (SEQ ID NO:152)    ATGGCTGCTTCTAAGCCAACATCCTAGTTGTCTGGGCAACGCCACATCCT 1700
'05BLSU.seq' (SEQ ID NO:153)    ATGGCTGCTTCTAAGCCAACATCCTAGTTGTCTGGGCAACGCCACATCCT 1689
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TTTCCACTTAACATATATTTTGGGACCTTAGCTGGTGGTCTGGGCTGTTT 1750
'06BLSU.seq' (SEQ ID NO:151)    TTTCCACTTAACATATATTTTGGGACCTTAGCTGGTGGTCTGGGCTGTTT 1733
'04BLSU.seq' (SEQ ID NO:152)    TTTCCACTTAACATATATTTTGGGACCTTAGCTGGTGGTCTGGGCTGTTT 1750
'05BLSU.seq' (SEQ ID NO:153)    TTTCCACTTAACATATATTTTGGGACCTTAGCTGGTGGTCTGGGCTGTTT 1739
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CCCTTTCGAACACGGACCTTATCACCCATGTTCTGACTCCCAAGTTAAAT 1800
'06BLSU.seq' (SEQ ID NO:151)    CCCTTTCGAACACGGACCTTATCACCCATGTTCTGACTCCCAAGTTAAAT 1783
'04BLSU.seq' (SEQ ID NO:152)    CCCTTTCGAACACGGACCTTATCACCCATGTTCTGACTCCCAAGTTAAAT 1800
'05BLSU.seq' (SEQ ID NO:153)    CCCTTTCGAACACGGACCTTATCACCCATGTTCTGACTCCCAAGTTAAAT 1789
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TAATTGGCATTCGGAGTTTGTCTGAATTCGGTAACCCGAGAGGGGCCCCT 1850
'06BLSU.seq' (SEQ ID NO:151)    TAATTGGCATTCGGAGTTTGTCTGAATTCGGTAACCCGAGAGGGGCCCCT 1833
'04BLSU.seq' (SEQ ID NO:152)    TAATTGGCATTCGGAGTTTGTCTGAATTCGGTAACCCGAGAGGGGCCCCT 1850
'05BLSU.seq' (SEQ ID NO:153)    TAATTGGCATTCGGAGTTTGTCTGAATTCGGTAACCCGAGAGGGGCCCCT 1839
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CGTCCAAACAGTGCTCTACCTCCAATAATCATCACTTGAGGCTAGCCCTA 1900
'06BLSU.seq' (SEQ ID NO:151)    CGTCCAAACAGTGCTCTACCTCCAATAATCATCACTTGAGGCTAGCCCTA 1883
'04BLSU.seq' (SEQ ID NO:152)    CGTCCAAACAGTGCTCTACCTCCAATAATCATCACTTGAGGCTAGCCCTA 1900
'05BLSU.seq' (SEQ ID NO:153)    CGTCCAAACAGTGCTCTACCTCCAATAATCATCACTTGAGGCTAGCCCTA 1889
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)AAGCTATTTCGGAGAGAACCAGCTATCTCCAAGTTCGATTGGAATTTCTC 1950
'06BLSU.seq' (SEQ ID NO:151)    AAGCTATTTCGGAGAGAACCAGCTATCTCCAAGTTCGATTGGAATTTCTC 1933
```

FIGURE 1-28

```
'04BLSU.seq' (SEQ ID NO:152)    AAGCTATTTCGGAGAGAACCAGCTATCTCCAAGTTCGATTGGAATTTCTC 1950
'05BLSU.seq' (SEQ ID NO:153)    AAGCTATTTCGGAGAGAACCAGCTATCTCCAAGTTCGATTGGAATTTCTC 1939
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CGCTACCCTCAGTTCATCCGCTCACTTTTCAACGTAAGTCGGTTCGGTCC 2000
'06BLSU.seq' (SEQ ID NO:151)    CGCTACCCTCAGTTCATCCGCTCACTTTTCAACGTAAGTCGGTTCGGTCC 1983
'04BLSU.seq' (SEQ ID NO:152)    CGCTACCCTCAGTTCATCCGCTCACTTTTCAACGTAAGTCGGTTCGGTCC 2000
'05BLSU.seq' (SEQ ID NO:153)    CGCTACCCTCAGTTCATCCGCTCACTTTTCAACGTAAGTCGGTTCGGTCC 1989
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TCCATTCAGTGTTACCTGAACTTCAACCTGACCAAGGGTAGATCACCTGG 2050
'06BLSU.seq' (SEQ ID NO:151)    TCCATTCAGTGTTACCTGAACTTCAACCTGACCAAGGGTAGATCACCTGG 2033
'04BLSU.seq' (SEQ ID NO:152)    TCCATTCAGTGTTACCTGAACTTCAACCTGACCAAGGGTAGATCACCTGG 2050
'05BLSU.seq' (SEQ ID NO:153)    TCCATTCAGTGTTACCTGAACTTCAACCTGACCAAGGGTAGATCACCTGG 2039
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TTTCGGGTCTACGACCAAATACTCAACGCCCTATTCAGACTCGCTTTCGC 2100
'06BLSU.seq' (SEQ ID NO:151)    TTTCGGGTCTACGACCAAATACTCAACGCCCTATTCAGACTCGCTTTCGC 2083
'04BLSU.seq' (SEQ ID NO:152)    TTTCGGGTCTACGACCAAATACTCAACGCCCTATTCAGACTCGCTTTCGC 2100
'05BLSU.seq' (SEQ ID NO:153)    TTTCGGGTCTACGACCAAATACTCAACGCCCTATTCAGACTCGCTTTCGC 2089
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TGCGGCTCCACATTTGCTGCTTAACCTTGCATCAGATCGTAACTCGCCGG 2150
'06BLSU.seq' (SEQ ID NO:151)    TGCGGCTCCACATTTGCTGCTTAACCTTGCATCAGATCGTAACTCGCCGG 2133
'04BLSU.seq' (SEQ ID NO:152)    TGCGGCTCCACATTTGCTGCTTAACCTTGCATCAGATCGTAACTCGCCGG 2150
'05BLSU.seq' (SEQ ID NO:153)    TGCGGCTCCACATTTGCTGCTTAACCTTGCATCAGATCGTAACTYGCCGG 2139
                                ******************************************* *****

'S_epidermi.seq' (SEQ ID NO:150)TTCATTCTACAAAAGGCACGCCATCACCCATTAACGGGCTCTGACTACTT 2200
'06BLSU.seq' (SEQ ID NO:151)    TTCATTCTACAAAAGGCACGCCATCACCCATTAACGGGCTCTGACTACTT 2183
'04BLSU.seq' (SEQ ID NO:152)    TTCATTCTACAAAAGGCACGCCATCACCCATTAACGGGCTCTGACTACTT 2200
'05BLSU.seq' (SEQ ID NO:153)    TTCATTCTACAAAAGGCACGCCATCACCCATTAACGGGCTCTGACTACTT 2189
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)GTAAGCACACGGTTTCAAGTTCTCTTTCACTCCCCTTCCGGGGTACTTTT 2250
'06BLSU.seq' (SEQ ID NO:151)    GTAAGCACACGGTTTCAAGTTCTCTTTCACTCCCCTTCCGGGGTACTTTT 2233
'04BLSU.seq' (SEQ ID NO:152)    GTAAGCACACGGTTTCAAGTTCTCTTTCACTCCCCTTCCGGGGTACTTTT 2250
'05BLSU.seq' (SEQ ID NO:153)    GTAAGCACACGGTTTCAAGTTCTCTTTCACTCCCCTTCCGGGGTACTTTT 2239
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CACCTTTCCCTCACGGTACTGGTTCACTATCGGTCACTAGAGAGTATTTA 2300
'06BLSU.seq' (SEQ ID NO:151)    CACCTTTCCCTCACGGTACTGGTTCACTATCGGTCACTAGAGAGTATTTA 2283
'04BLSU.seq' (SEQ ID NO:152)    CACCTTTCCCTCACGGTACTGGTTCACTATCGGTCACTAGAGAGTATTTA 2300
'05BLSU.seq' (SEQ ID NO:153)    CACCTTTCCCTCACGGTACTGGTTCACTATCGGTCACTAGAGAGTATTTA 2289
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)GCCTTAGGAGATGGTCCTCCCAGATTCCGACGGAATTTCACGTGCTCCGT 2350
'06BLSU.seq' (SEQ ID NO:151)    GCCTTAGGAGATGGTCCTCCCAGATTCCGACGGAATTTCACGTGCTCCGT 2333
'04BLSU.seq' (SEQ ID NO:152)    GCCTTAGGAGATGGTCCTCCCAGATTCCGACGGAATTTCACGTGCTCCGT 2350
'05BLSU.seq' (SEQ ID NO:153)    GCCTTAGGAGATGGTCCTCCCAGATTCCGACGGAATTTCACGTGCTCCGT 2339
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)CGTACTCAGGATCCACTCAAGAGAGAATATGTTTTCGACTACAGGATTAT 2400
'06BLSU.seq' (SEQ ID NO:151)    CGTACTCAGGATCCACTCAAGAGAGAATATGTTTTCGACTACAGGATTAT 2383
'04BLSU.seq' (SEQ ID NO:152)    CGTACTCAGGATCCACTCAAGAGAGAATATGTTTTCGACTACAGGATTAT 2400
'05BLSU.seq' (SEQ ID NO:153)    CGTACTCAGGATCCACTCAAGAGAGAATATGTTTTCGACTACAGGATTAT 2389
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TACCTTCTTTGATTCATCTTTCCAGATGATTCGTCTAACATGTTCTTTTG 2450
'06BLSU.seq' (SEQ ID NO:151)    TACCTTCTTTGATTCATCTTTCCAGATGATTCGTCTAACATGTTCTTTTG 2433
'04BLSU.seq' (SEQ ID NO:152)    TACCTTCTTTGATTCATCTTTCCAGATGATTCGTCTAACATGTTCTTTTG 2450
'05BLSU.seq' (SEQ ID NO:153)    TACCTTCTTTGATTCATCTTTCCAGATGATTCGTCTAACATGTTCTTTTG 2439
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TAACTCCGTATAGAGTGTCCTACAACCCCAACAAGCAAGCTTGTTGGTTT 2500
'06BLSU.seq' (SEQ ID NO:151)    TAACTCCGTATAGAGTGTCCTACAACCCCAACAAGCAAGCTTGTTGGTTT 2483
'04BLSU.seq' (SEQ ID NO:152)    TAACTCCGTATAGAGTGTCCTACAACCCCAACAAGCAAGCTTGTTGGTTT 2500
'05BLSU.seq' (SEQ ID NO:153)    TAACTCCGTATAGAGTGTCCTACAACCCCAACAAGCAAGCTTGTTGGTTT 2489
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)GGGCTCTTCCCGTTTCGCTCGCCGCTACTCAGGGAATCGATTTTTCTTTC 2550
'06BLSU.seq' (SEQ ID NO:151)    GGGCTCTTCCCGTTTCGCTCGCCGCTACTCAGGGAATCGATTTTTCTTTC 2533
'04BLSU.seq' (SEQ ID NO:152)    GGGCTCTTCCCGTTTCGCTCGCCGCTACTCAGGGAATCGATTTTTCTTTC 2550
'05BLSU.seq' (SEQ ID NO:153)    GGGCTCTTCCCGTTTCGCTCGCCGCTACTCAGGGAATCGATTTTTCTTTC 2539
                                **************************************************

'S_epidermi.seq' (SEQ ID NO:150)TCTTCCTCCGGGTACT 2566
'06BLSU.seq' (SEQ ID NO:151)    TCTTCCTCCGGGTACT 2549
```

FIGURE 1-29

```
'04BLSU.seq' (SEQ ID NO:152)     TCTTCCTCCGG----- 2561
'05BLSU.seq' (SEQ ID NO:153)     TCTTCCT--------- 2546
                                 *******
```

FIGURE 2-30
9 *Candida albicans*

```
'26NLSU.seq' (SEQ ID NO:154) AAATCAGGTAGGACTWCCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCA 60
'29NLSU.seq' (SEQ ID NO:155) ------------------------------------------------------------
'C_AlbLSU.seq'(SEQ ID NO:156)AAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCA 60
'25NLSU.seq' (SEQ ID NO:157) AAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCA 60

'26NLSU.seq' (SEQ ID NO:154) ACAGGGATTGCCTCAGTAGCGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCG 120
'29NLSU.seq' (SEQ ID NO:155) ----------------------------------------------TTGAAATCTGGCG 13
'C_AlbLSU.seq'(SEQ ID NO:156)ACAGGGATTGCCTCAGTAGCGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCG 120
'25NLSU.seq' (SEQ ID NO:157) ACAGGGATTGCCTCAGTAGCGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCG 120
                                                             *************

'26NLSU.seq' (SEQ ID NO:154) TCTTTGGCGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGCCCGGCTCTTGTCTATGT 180
'29NLSU.seq' (SEQ ID NO:155) TCTTTGGCGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGCCCGGCTCTTGTCTATGT 73
'C_AlbLSU.seq'(SEQ ID NO:156)TCTTTGGCGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGCCCGGCTCTTGTCTATGT 180
'25NLSU.seq' (SEQ ID NO:157) TCTTTGGCGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGGCCCGGCTCTTGTCTATGT 180
                             ************************************************************
                                                      Calbic_232f ~~~~~~>
'26NLSU.seq' (SEQ ID NO:154) TCCTTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGACCCGGGTCTG 240
'29NLSU.seq' (SEQ ID NO:155) TCCTTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGACCCGGGTCTG 133
'C_AlbLSU.seq'(SEQ ID NO:156)TCCTTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGACCCGGGTCTG 240
'25NLSU.seq' (SEQ ID NO:157) TCCTTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGACCCGGGTCTG 240
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TGTAAAGTTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAAT 300
'29NLSU.seq' (SEQ ID NO:155) TGTAAAGTTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAAT 193
'C_AlbLSU.seq'(SEQ ID NO:156)TGTAAAGTTCCTTTGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAAT 300
'25NLSU.seq' (SEQ ID NO:157) TGTAAAGTTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAAT 300
                             ************* ********************************************

'26NLSU.seq' (SEQ ID NO:154) TCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGA 360
'29NLSU.seq' (SEQ ID NO:155) TCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGA 253
'C_AlbLSU.seq'(SEQ ID NO:156)TCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGA 360
'25NLSU.seq' (SEQ ID NO:157) TCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGA 360
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTT 420
'29NLSU.seq' (SEQ ID NO:155) TGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTT 313
'C_AlbLSU.seq'(SEQ ID NO:156)TGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTT 420
'25NLSU.seq' (SEQ ID NO:157) TGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTT 420
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GAGATCAGACTTGGTATTTTGCATGTTGCTCTCTCGGGGGCGGCCGCTGCGGTTTACCGG 480
'29NLSU.seq' (SEQ ID NO:155) GAGATCAGACTTGGTATTTTGCATGCTGCTCTCTCGGGGGCGGCCGCTGCGGTTTACCGG 373
'C_AlbLSU.seq'(SEQ ID NO:156)GAGATCAGACTTGGTATTTTGCATGCTGCTCTCTCGGGGGCGGCCGCTGCGGTTTACCGG 480
'25NLSU.seq' (SEQ ID NO:157) GAGATCAGACTTGGTATTTTGCATGCTGCTCTCTCGGGGGCGGCCGCTGCGGTTTACCGG 480
                             ************************ *********************************

'26NLSU.seq' (SEQ ID NO:154) GCCAGCATCGGTTTGGAGCGGCAGGATAATGGCGGAGGAATGTGGCACGGCTTCTGCTGT 540
'29NLSU.seq' (SEQ ID NO:155) GCCAGCATCGGTTTGGAGCGGCAGGATAATGGCGGAGGAATGTGGCACGGCTTCTGCTGT 433
'C_AlbLSU.seq'(SEQ ID NO:156)GCCAGCATCGGTTTGGAGCGGCAGGATAATGGCGGAGGAATGTGGCACGGCTTCTGCTGT 540
'25NLSU.seq' (SEQ ID NO:157) GCCAGCATCGGTTTGGAGCGGCAGGATAATGGCGGAGGAATGTGGCACGGCTTCTGCTGT 540
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GTGTTATAGCCTCTGACGATACTGCCAGCCTAGACCGAGGACTGCGGTTTTT--ACCTAG 598
'29NLSU.seq' (SEQ ID NO:155) GTGTTATAGCCTCTGACGATACTGCCAGCCTAGACCGAGGACTGCGGTTTTT--ACCTAG 491
'C_AlbLSU.seq'(SEQ ID NO:156)GTGTTATAGCCTCTGACGATACTGCCAGCCTAGACCGAGGACTGCGGTTTTTTTACCTAG 600
'25NLSU.seq' (SEQ ID NO:157) GTGTTATAGCCTCTGACGATACTGCCAGCCTAGACCGAGGACTGCGGTTTTTA-ACCTAG 599
                             ************************************************  ******

'26NLSU.seq' (SEQ ID NO:154) GATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGT 658
'29NLSU.seq' (SEQ ID NO:155) GATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGT 551
'C_AlbLSU.seq'(SEQ ID NO:156)GATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGT 660
'25NLSU.seq' (SEQ ID NO:157) GATGTTGGCATAATGATCTTAAGTCGCCCGTCTTGAAACACGGACCAAGGAGTCTAACGT 659
                             ************************************************************
```

FIGURE 2-31

```
'26NLSU.seq' (SEQ ID NO:154) CTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGAAGGTGGGGGC 718
'29NLSU.seq' (SEQ ID NO:155) CTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGAAGGTGGGGGC 611
'C_AlbLSU.seq'(SEQ ID NO:156)CTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGAAGGTGGGGGC 720
'25NLSU.seq' (SEQ ID NO:157) CTATGCGAGTGTTTGGGTGTAAAACCCGTACGCGTAATGAAAGTGAACGAAGGTGGGGGC 719
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) CCATTAGGGTGCACCATCGACCGATCCTGATGTGTTCGGATGGATTTGAGTAAGAGCATA 778
'29NLSU.seq' (SEQ ID NO:155) CCATTAGGGTGCACCATCGACCGATCCTGATGTGTTCGGATGGATTTGAGTAAGAGCATA 671
'C_AlbLSU.seq'(SEQ ID NO:156)CCATTAGGGTGCACCATCGACCGATCCTGATGTGTTCGGATGGATTTGAGTAAGAGCATA 780
'25NLSU.seq' (SEQ ID NO:157) CCATTAGGGTGCACCATCGACCGATCCTGATGTGTTCGGATGGATTTGAGTAAGAGCATA 779
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTC 838
'29NLSU.seq' (SEQ ID NO:155) GCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTC 731
'C_AlbLSU.seq'(SEQ ID NO:156)GCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTC 840
'25NLSU.seq' (SEQ ID NO:157) GCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGAAGCCAGAGGAAACTC 839
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGC 898
'29NLSU.seq' (SEQ ID NO:155) TGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGC 791
'C_AlbLSU.seq'(SEQ ID NO:156)TGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGC 900
'25NLSU.seq' (SEQ ID NO:157) TGGTGGAGGCTCGTAGCGGTTCTGACGTGCAAATCGATCGTCGAATTTGGGTATAGGGGC 899
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAG 958
'29NLSU.seq' (SEQ ID NO:155) GAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAG 851
'C_AlbLSU.seq'(SEQ ID NO:156)GAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAG 960
'25NLSU.seq' (SEQ ID NO:157) GAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGGATAGCAG 959
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) AAGCTCGTATCAGTTTTATGAGGTAAAGCGAATGATTAGAAGTCTTGGGGTTGAAATGAC 1018
'29NLSU.seq' (SEQ ID NO:155) AAGCTCGTATCAGTTTTATGAGGTAAAGCGAATGATTAGAAGTCTTGGGGTTGAAATGAC 911
'C_AlbLSU.seq'(SEQ ID NO:156)AAGCTCGTATCAGTTTTATGAGGTAAAGCGAATGATTAGAAGTCTTGGGGTTGAAATGAC 1020
'25NLSU.seq' (SEQ ID NO:157) AAGCTCGTATCAGTTTTATGAGGTAAAGCGAATGATTAGAAGTCTTGGGGTTGAAATGAC 1019
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) CTTAACTTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGA 1078
'29NLSU.seq' (SEQ ID NO:155) CTTAACTTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGA 971
'C_AlbLSU.seq'(SEQ ID NO:156)CTTAACTTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGA 1080
'25NLSU.seq' (SEQ ID NO:157) CTTAACTTATTCTCAAACTTTAAATATGTAAGAAGTCCTTGTTGCTTAATTGAACGTGGA 1079
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) CAATTGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGAT 1138
'29NLSU.seq' (SEQ ID NO:155) CAATTGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGAT 1031
'C_AlbLSU.seq'(SEQ ID NO:156)CAATTGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGAT 1140
'25NLSU.seq' (SEQ ID NO:157) CAATTGAATGAAGAGCTTTTAGTGGGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGAT 1139
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GAACCGAACGTGAAGTTAAAGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTT 1198
'29NLSU.seq' (SEQ ID NO:155) GAACCGAACGTGAAGTTAAAGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTT 1091
'C_AlbLSU.seq'(SEQ ID NO:156)GAACCGAACGTGAAGTTAAAGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTT 1200
'25NLSU.seq' (SEQ ID NO:157) GAACCGAACGTGAAGTTAAAGTGCCGGAATGCACGCTCATCAGACACCACAAAAGGTGTT 1199
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) AGTTCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAA 1258
'29NLSU.seq' (SEQ ID NO:155) AGTTCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAA 1151
'C_AlbLSU.seq'(SEQ ID NO:156)AGTTCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAA 1260
'25NLSU.seq' (SEQ ID NO:157) AGTTCATCTAGACAGCCGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGTGTGTAA 1259
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) CAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACTTAT 1318
'29NLSU.seq' (SEQ ID NO:155) CAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACTTAT 1211
'C_AlbLSU.seq'(SEQ ID NO:156)CAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACTTAT 1320
'25NLSU.seq' (SEQ ID NO:157) CAACTCACCGGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGCTACTTAT 1319
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) ACTTCACCGTGATTGCTGTTTTGACGCTTTCACGAGTAGGCAGGCGTGGAGGTCAGTGAC 1378
'29NLSU.seq' (SEQ ID NO:155) ACTTCACCGTGATTGCTGTTTTGACGCTTTCACGAGTAGGCAGGCGTGGAGGTCAGTGAC 1271
'C_AlbLSU.seq'(SEQ ID NO:156)ACTTCACCGTGATTGCTGTTTTGACGCTTTCACGAGTAGGCAGGCGTGGAGGTCAGTGAC 1380
'25NLSU.seq' (SEQ ID NO:157) ACTTCACCGTGATTGCTGTTTTGACGCTTTCACGAGTAGGCAGGCGTGGAGGTCAGTGAC 1379
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GAAGCCTTTGCTGTAAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGC 1438
'29NLSU.seq' (SEQ ID NO:155) GAAGCCTTTGCTGTAAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGC 1331
'C_AlbLSU.seq'(SEQ ID NO:156)GAAGCCTTTGCTGTAAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGC 1440
'25NLSU.seq' (SEQ ID NO:157) GAAGCCTTTGCTGTAAAGCTGGGTCGAACGGCCTCTAGTGCAGATCTTGGTGGTAGTAGC 1439
                             ************************************************************
```

FIGURE 2-32

```
'26NLSU.seq' (SEQ ID NO:154) AAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGT 1498
'29NLSU.seq' (SEQ ID NO:155) AAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGT 1391
'C_AlbLSU.seq'(SEQ ID NO:156)AAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGT 1500
'25NLSU.seq' (SEQ ID NO:157) AAATATTCAAATGAGAACTTTGAAGACTGAAGTGGGGAAAGGTTCCATGTCAACAGCAGT 1499
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TGGACATGGGTTAGTCGATCCTAAGAGATGGGGAAGCTCCGTTTCAACGTGCTTGATTTT 1558
'29NLSU.seq' (SEQ ID NO:155) TGGACATGGGTTAGTCGATCCTAAGAGATGGGGAAGCTCCGTTTCAACGTGCTTGATTTT 1451
'C_AlbLSU.seq'(SEQ ID NO:156)TGGACATGGGTTAGTCGATCCTAAGAGATGGGGAAGCTCCGTTTCAACGTGCTTGATTTT 1560
'25NLSU.seq' (SEQ ID NO:157) TGGACATGGGTTAGTCGATCCTAAGAGATGGGGAAGCTCCGTTTCAACGTGCTTGATTTT 1559
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TCAGGCCAACCATCGAAAGGGAATCCGGTTAAAATTCCGGAACTTGGATATGGATTCTTC 1618
'29NLSU.seq' (SEQ ID NO:155) TCAGGCCAACCATCGAAAGGGAATCCGGTTAAAATTCCGGAACTTGGATATGGATTCTTC 1511
'C_AlbLSU.seq'(SEQ ID NO:156)TCAGGCCAGCCATCGAAAGGGAATCCGGTTAAAATTCCGGAACTTGGATATGGATTCTTC 1620
'25NLSU.seq' (SEQ ID NO:157) TCAGGCCAGCCATCGAAAGGGAATCCGGTTAAAATTCCGGAACTTGGATATGGATTCTTC 1619
                             ******** ***************************************************

'26NLSU.seq' (SEQ ID NO:154) ACGGCAACGTAACTGAATGTGGAGACGTCGGCGTGAGCCCTGGGAGGAGTTATCTTTTCT 1678
'29NLSU.seq' (SEQ ID NO:155) ACGGCAACGTAACTGAATGTGGAGACGTCGGCGTGAGCCCTGGGAGGAGTTATCTTTTCT 1571
'C_AlbLSU.seq'(SEQ ID NO:156)ACGGCAACGTAACTGAATGTGGAGACGTCGGCGTGAGCCCTGGGAGGAGTTATCTTTTCT 1680
'25NLSU.seq' (SEQ ID NO:157) ACGGCAACGTAACTGAATGTGGAGACGTCGGCGTGAGCCCTGGGAGGAGTTATCTTTTCT 1679
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAGATGGGGTCTTATGGCTGGAAG 1738
'29NLSU.seq' (SEQ ID NO:155) TCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAGATGGGGTCTTATGGCTGGAAG 1631
'C_AlbLSU.seq'(SEQ ID NO:156)TCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAGATGGGGTCTTAGGGCTGGAAG 1740
'25NLSU.seq' (SEQ ID NO:157) TCTTAACAGCTTATCACCCTGGAATTGGTTTATCCGGAGATGGGGTCTTATGGCTGGAAG 1739
                             ************************************************* *********

'26NLSU.seq' (SEQ ID NO:154) AGCGCGGTAATTTTGCCGCGTCCGGTGCGCTTACGACGGTCCTTGAAAATCCACAGGAAG 1798
'29NLSU.seq' (SEQ ID NO:155) AGCGCGGTAATTTTGCCGCGTCCGGTGCGCTTACGACGGTCCTTGAAAATCCACAGGAAG 1691
'C_AlbLSU.seq'(SEQ ID NO:156)AGCGCGGTAATTTTGCCGCGTCCGGTGCGCTTACGACGGTCCTTGAAAATCCACAGGAAG 1800
'25NLSU.seq' (SEQ ID NO:157) AGCGCGGTAATTTTGCCGCGTCCGGTGCGCTTACGACGGTCCTTGAAAATCCACAGGAAG 1799
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GAATAGTTTTCATGCCAAGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTTAACAGCCT 1858
'29NLSU.seq' (SEQ ID NO:155) GAATAGTTTTCATGCCAAGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTTAACAGCCT 1751
'C_AlbLSU.seq'(SEQ ID NO:156)GAATAGTTTTCATGCCAAGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTTAACAGCCT 1860
'25NLSU.seq' (SEQ ID NO:157) GAATAGTTTTCATGCCAAGTCGTACTCATAACCGCAGCAGGTCTCCAAGGTTAACAGCCT 1859
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) CTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAT 1918
'29NLSU.seq' (SEQ ID NO:155) CTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAT 1811
'C_AlbLSU.seq'(SEQ ID NO:156)CTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAT 1920
'25NLSU.seq' (SEQ ID NO:157) CTAGTTGATAGAATAATGTAGATAAGGGAAGTCGGCAAAATAGATCCGTAACTTCGGGAT 1919
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) AAGGATTGGCTCTAAGGATCGGGTGTCTTGGGCCTTGTGTAGACGCGGCGGTGACTGTTG 1978
'29NLSU.seq' (SEQ ID NO:155) AAGGATTGGCTCTAAGGATCGGGTGTCTTGGGCCTTGTGTAGACGCGGCGGTGACTGTTG 1871
'C_AlbLSU.seq'(SEQ ID NO:156)AAGGATTGGCTCTAAGGATCGGGTGTCTTGGGCCTTGTGTAGACGCGGCGGTGACTGTTG 1980
'25NLSU.seq' (SEQ ID NO:157) AAGGATTGGCTCTAAGGATCGGGTGTCTTGGGCCTTGTGTAGACGCGGCGGTGACTGTTG 1979
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GCGGGCTGTTTTACGACGGACTGCTGGTGGATGCTGCTGTAGACACGCTTGGTAGGTCTT 2038
'29NLSU.seq' (SEQ ID NO:155) GCGGGCTGTTTTACGACGGACTGCTGGTGGATGCTGCTGTAGACACGCTTGGTAGGTCTT 1931
'C_AlbLSU.seq'(SEQ ID NO:156)GCGGGCTGTTTCACGACGGACTGCTGGTGGATGCTGCTGTAGACACGCTTGGTAGGTCTT 2040
'25NLSU.seq' (SEQ ID NO:157) GCGGGCTGTTTCACGACGGACTGCTGGTGGATGCTGCTGTAGACACGCTTGGTAGGTCTT 2039
                             *********** ************************************************

'26NLSU.seq' (SEQ ID NO:154) TATGGCCGTCCGGGGCACGTTTAACGATCAACTTAGAACTGGTACGGACAAGGGGAATCT 2098
'29NLSU.seq' (SEQ ID NO:155) TATGGCCGTCCGGGGCACGTTTAACGATCAACTTAGAACTGGTACGGACAAGGGGAATCT 1991
'C_AlbLSU.seq'(SEQ ID NO:156)TATGGCCGTCCGGGGCACGTTTAACGATCAACTTAGAACTGGTACGGACAAGGGGAATCT 2100
'25NLSU.seq' (SEQ ID NO:157) TATGGCCGTCCGGGGCACGTTTAACGATCAACTTAGAACTGGTACGGACAAGGGGAATCT 2099
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GACTGTCTAATTAAAACATAGCATTGTGATGGTCAGAAAGTGATGTTGACACAATGTGAT 2158
'29NLSU.seq' (SEQ ID NO:155) GACTGTCTAATTAAAACATAGCATTGTGATGGTCAGAAAGTGATGTTGACACAATGTGAT 2051
'C_AlbLSU.seq'(SEQ ID NO:156)GACTGTCTAATTAAAACATAGCATTGTGATGGTCAGAAAGTGATGTTGACACAATGTGAT 2160
'25NLSU.seq' (SEQ ID NO:157) GACTGTCTAATTAAAACATAGCATTGTGATGGTCAGAAAGTGATGTTGACACAATGTGAT 2159
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCG 2218
'29NLSU.seq' (SEQ ID NO:155) TTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCG 2111
'C_AlbLSU.seq'(SEQ ID NO:156)TTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCG 2220
'25NLSU.seq' (SEQ ID NO:157) TTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAACCAAGCGCGGGTAAACGGCG 2219
                             ************************************************************
```

FIGURE 2-33

```
'26NLSU.seq' (SEQ ID NO:154) GGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCA 2278
'29NLSU.seq' (SEQ ID NO:155) GGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCA 2171
'C_AlbLSU.seq'(SEQ ID NO:156)GGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCA 2280
'25NLSU.seq' (SEQ ID NO:157) GGAGTAACTATGACTCTCTTAAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCA 2279
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAG 2338
'29NLSU.seq' (SEQ ID NO:155) TGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAG 2231
'C_AlbLSU.seq'(SEQ ID NO:156)TGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAG 2340
'25NLSU.seq' (SEQ ID NO:157) TGAATGGATTAACGAGATTCCCACTGTCCCTATCTACTATCTAGCGAAACCACAGCCAAG 2339
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTG 2398
'29NLSU.seq' (SEQ ID NO:155) GGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTG 2291
'C_AlbLSU.seq'(SEQ ID NO:156)GGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTG 2400
'25NLSU.seq' (SEQ ID NO:157) GGAACGGGCTTGGCAGAATCAGCGGGGAAAGAAGACCCTGTTGAGCTTGACTCTAGTTTG 2399
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) ACATTGTGAAAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATAC 2458
'29NLSU.seq' (SEQ ID NO:155) ACATTGTGAAAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATAC 2351
'C_AlbLSU.seq'(SEQ ID NO:156)ACATTGTGAAAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATAC 2460
'25NLSU.seq' (SEQ ID NO:157) ACATTGTGAAAAGACATGGAGGGTGTAGAATAAGTGGGAGCTTCGGCGCCGGTGAAATAC 2459
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) CACTACCTCTATAGTTTTTTTACTTATTCAATGAAGCGGAGCTGGAGGTCAAACTCCACG 2518
'29NLSU.seq' (SEQ ID NO:155) CACTACCTCTATAGTTTTTTTACTTATTCAATGAAGCGGAGCTGGAGGTCAAACTCCACG 2411
'C_AlbLSU.seq'(SEQ ID NO:156)CACTACCTCTATAGTTTTTTTACTTATTCAATGAAGCGGAGCTGGAGGTCAAACTCCACG 2520
'25NLSU.seq' (SEQ ID NO:157) CACTACCTCTATAGTTTTTTTACTTATTCAATGAAGCGGAGCTGGAGGTCAAACTCCACG 2519
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TTCTAGCATTAAGCCCTCTGGGCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGG 2578
'29NLSU.seq' (SEQ ID NO:155) TTCTAGCATTAAGCCCTCTGGGCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGG 2471
'C_AlbLSU.seq'(SEQ ID NO:156)TTCTAGCATTAAGCCCTCTGGGCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGG 2580
'25NLSU.seq' (SEQ ID NO:157) TTCTAGCATTAAGCCCTCTGGGCGATCCGGGTTGAAGACATTGTCAGGTGGGGAGTTTGG 2579
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) CTGGGGCGGCACATCTGTTAAACGATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAAC 2638
'29NLSU.seq' (SEQ ID NO:155) CTGGGGCGGCACATCTGTTAAACGATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAAC 2531
'C_AlbLSU.seq'(SEQ ID NO:156)CTGGGGCGGCACATCTGTTAAACGATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAAC 2640
'25NLSU.seq' (SEQ ID NO:157) CTGGGGCGGCACATCTGTTAAACGATAACGCAGGTGTCCTAAGGGGGACTCATGGAGAAC 2639
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) AGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAAT 2698
'29NLSU.seq' (SEQ ID NO:155) AGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAAT 2591
'C_AlbLSU.seq'(SEQ ID NO:156)AGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAAT 2700
'25NLSU.seq' (SEQ ID NO:157) AGAAATCTCCAGTAGAACAAAAGGGTAAAAGTCCCCTTGATTTTGATTTTCAGTGTGAAT 2699
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) ACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGT 2758
'29NLSU.seq' (SEQ ID NO:155) ACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGT 2651
'C_AlbLSU.seq'(SEQ ID NO:156)ACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGT 2760
'25NLSU.seq' (SEQ ID NO:157) ACAAACCATGAAAGTGTGGCCTATCGATCCTTTAGTCCCTCGGAATTTGAGGCTAGAGGT 2759
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATT 2818
'29NLSU.seq' (SEQ ID NO:155) GCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATT 2711
'C_AlbLSU.seq'(SEQ ID NO:156)GCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATT 2820
'25NLSU.seq' (SEQ ID NO:157) GCCAGAAAAGTTACCACAGGGATAACTGGCTTGTGGCAGTCAAGCGTTCATAGCGACATT 2819
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) GCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGT 2878
'29NLSU.seq' (SEQ ID NO:155) GCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGT 2771
'C_AlbLSU.seq'(SEQ ID NO:156)GCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCGT 2880
'25NLSU.seq' (SEQ ID NO:157) GCTTTTTGATTCTTCGATGTCGGCTCTTCCTATCATACCGAAGCAGAATTCGGTAAGCG- 2878
                             ************************************************************

'26NLSU.seq' (SEQ ID NO:154) TGGAT 2883
'29NLSU.seq' (SEQ ID NO:155) TGGA- 2775
'C_AlbLSU.seq'(SEQ ID NO:156)TGGA- 2884
'25NLSU.seq' (SEQ ID NO:157) -----
```

9 Bla_{ges-2}

```
                                        10        20        30        40        50
79 AF326355 (SEQ ID NO: 158) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
80 AY219651 (SEQ ID NO: 159) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
84 AF156486 (SEQ ID NO: 160) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
81 AF355189 (SEQ ID NO: 161) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
85 AY260546 (SEQ ID NO: 162) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
86 AB116723 (SEQ ID NO: 163) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
89 AB113580 (SEQ ID NO: 164) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
90 AF329699 (SEQ ID NO: 165) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
88 AF208529 (SEQ ID NO: 166) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
83 AY494718 (SEQ ID NO: 167) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
82 AY494717 (SEQ ID NO: 168) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
87 AB116260 (SEQ ID NO: 169) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
25 AF347074 (SEQ ID NO: 170) gcaatgtgctcaacgttcaagtttccgctagccgcgctggtctttgaaag
  CONSENSUS (SEQ ID NO: 171) GCAATGTGCTCAACGTTCAAGTTTCCGCTAGCCGCGCTGGTCTTTGAAAG

                                        60        70        80        90       100
79 AF326355 (SEQ ID NO: 158) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
80 AY219651 (SEQ ID NO: 159) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
84 AF156486 (SEQ ID NO: 160) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
81 AF355189 (SEQ ID NO: 161) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
85 AY260546 (SEQ ID NO: 162) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
86 AB116723 (SEQ ID NO: 163) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
89 AB113580 (SEQ ID NO: 164) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
90 AF329699 (SEQ ID NO: 165) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
88 AF208529 (SEQ ID NO: 166) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
83 AY494718 (SEQ ID NO: 167) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
82 AY494717 (SEQ ID NO: 168) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
87 AB116260 (SEQ ID NO: 169) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
25 AF347074 (SEQ ID NO: 170) aattgactcaggcaccgagcgggggggatcgaaaactttcatatgggccgg
  CONSENSUS (SEQ ID NO: 171) AATTGACTCAGGCACCGAGCGGGGGGATCGAAAACTTTCATATGGGCCGG


                                       110       120       130       140       150
79 AF326355 (SEQ ID NO: 158) acatgatcgtcgaatggtctcctgccacggagcggtttctagcatcggga
80 AY219651 (SEQ ID NO: 159) acatgatcgtcgaatggtctcctgccacggagcggtttctagcatcggga
84 AF156486 (SEQ ID NO: 160) acatgatcgtcgaatggtctcctgccacggagcggtttctagcatcggga
81 AF355189 (SEQ ID NO: 161) acatgatcgtcgaatggtctcctgccacggagcggtttctagcatcggga
85 AY260546 (SEQ ID NO: 162) acatgatcgtcaaatggtctcctgccacggagcggtttctagcatcggga
86 AB116723 (SEQ ID NO: 163) acatgatcgtcaaatggtctcctgccacggagcggtttctagcatcggga
89 AB113580 (SEQ ID NO: 164) acatgatcgtcaaatggtctcctgccacggagcggtttctagcatcggga
90 AF329699 (SEQ ID NO: 165) acatgatcgtcgaatggtctcctgccacggagcggtttctagcatcggga
88 AF208529 (SEQ ID NO: 166) acatgatcgtcaaatggtctcctgccacggagcggtttctagcatcggga
83 AY494718 (SEQ ID NO: 167) acatgatcgtcaaatggtctcctgccacggagcggtttctagcatcggga
82 AY494717 (SEQ ID NO: 168) acatgatcgtcgaatggtctcctgccacggagcggtttctagcatcggga
87 AB116260 (SEQ ID NO: 169) acatgatcgtcaaatggtctcctgccacggagcggtttctagcatcggga
25 AF347074 (SEQ ID NO: 170) acatgatcgtcgaatggtctcctgccacggagcggtttctagcatcggga
  CONSENSUS (SEQ ID NO: 171) ACATGATCGTC-AATGGTCTCCTGCCACGGAGCGGTTTCTAGCATCGGGA

                                       160       170       180       190       200
79 AF326355 (SEQ ID NO: 158) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
80 AY219651 (SEQ ID NO: 159) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
84 AF156486 (SEQ ID NO: 160) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
81 AF355189 (SEQ ID NO: 161) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
85 AY260546 (SEQ ID NO: 162) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
86 AB116723 (SEQ ID NO: 163) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
89 AB113580 (SEQ ID NO: 164) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
90 AF329699 (SEQ ID NO: 165) cacatgacggttctcgaggcagcgcaactggcggtgcagcttagcgacaa
88 AF208529 (SEQ ID NO: 166) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
83 AY494718 (SEQ ID NO: 167) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
82 AY494717 (SEQ ID NO: 168) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
87 AB116260 (SEQ ID NO: 169) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
25 AF347074 (SEQ ID NO: 170) cacatgacggttctcgaggcagcgcaagctgcggtgcagcttagcgacaa
  CONSENSUS (SEQ ID NO: 171) CACATGACGGTTCTCGAGGCAGCGCAAGCTGCGGTGCAGCTTAGCGACAA

                                       210       220       230       240       250
79 AF326355 (SEQ ID NO: 158) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
80 AY219651 (SEQ ID NO: 159) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
84 AF156486 (SEQ ID NO: 160) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
81 AF355189 (SEQ ID NO: 161) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
85 AY260546 (SEQ ID NO: 162) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
86 AB116723 (SEQ ID NO: 163) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
89 AB113580 (SEQ ID NO: 164) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
90 AF329699 (SEQ ID NO: 165) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
88 AF208529 (SEQ ID NO: 166) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
83 AY494718 (SEQ ID NO: 167) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
```

```
82 AY494717 (SEQ ID NO: 168) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
87 AB116260 (SEQ ID NO: 169) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
25 AF347074 (SEQ ID NO: 170) tggggctactaacctcttactgagagaaattggcggacctgctgcaatga
  CONSENSUS (SEQ ID NO: 171) TGGGGCTACTAACCTCTTACTGAGAGAAATTGGCGGACCTGCTGCAATGA

                                      260        270        280        290        300
79 AF326355 (SEQ ID NO: 158) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
80 AY219651 (SEQ ID NO: 159) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
84 AF156486 (SEQ ID NO: 160) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
81 AF355189 (SEQ ID NO: 161) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
85 AY260546 (SEQ ID NO: 162) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
86 AB116723 (SEQ ID NO: 163) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
89 AB113580 (SEQ ID NO: 164) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
90 AF329699 (SEQ ID NO: 165) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
88 AF208529 (SEQ ID NO: 166) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
83 AY494718 (SEQ ID NO: 167) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
82 AY494717 (SEQ ID NO: 168) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
87 AB116260 (SEQ ID NO: 169) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
25 AF347074 (SEQ ID NO: 170) cgcagtattttcgtaaaattggcgactctgtgagtcggctagaccggaaa
  CONSENSUS (SEQ ID NO: 171) CGCAGTATTTTCGTAAAATTGGCGACTCTGTGAGTCGGCTAGACCGGAAA

                                      310        320        330        340        350
79 AF326355 (SEQ ID NO: 158) gagccggagatgaacgacaacacacctggcgacctcagagatacaactac
80 AY219651 (SEQ ID NO: 159) gagccggagatgggcgacaacacacctggcgacctcagagatacaactac
84 AF156486 (SEQ ID NO: 160) gagccggagatgggcgacaacacacctggcgacctcagagatacaactac
81 AF355189 (SEQ ID NO: 161) gagccggagatgggcgacaacacacctggcgacctcagagatacaactac
85 AY260546 (SEQ ID NO: 162) gagccggagatgggcgacaacacacctggcgacctcagagatacaactac
86 AB116723 (SEQ ID NO: 163) gagccggagatgagcgacaacacacctggcgacctcagagatacaactac
89 AB113580 (SEQ ID NO: 164) gagccggagatgggcgacaacacacctggcgacctcagagatacaactac
90 AF329699 (SEQ ID NO: 165) gagccggagatgggcgacaacacacctggcgacctcagagatacaactac
88 AF208529 (SEQ ID NO: 166) gagccggagatgggcgacaacacacctggcgacctcagagatacaactac
83 AY494718 (SEQ ID NO: 167) gagccggagatgagcgacaacacacctggcgacctcagagatacaactac
82 AY494717 (SEQ ID NO: 168) gagccggagatgagcgacaacacacctggcgacctcagagatacaactac
87 AB116260 (SEQ ID NO: 169) gagccggagatgagcgacaacacacctggcgacctcagagatacaactac
25 AF347074 (SEQ ID NO: 170) gagccggagatgaacgacaacacacctggcgacctcagagatacaactac
  CONSENSUS (SEQ ID NO: 171) GAGCCGGAGATG-GCGACAACACACCTGGCGACCTCAGAGATACAACTAC

                                      360        370        380        390        400
79 AF326355 (SEQ ID NO: 158) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
80 AY219651 (SEQ ID NO: 159) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
84 AF156486 (SEQ ID NO: 160) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
81 AF355189 (SEQ ID NO: 161) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
85 AY260546 (SEQ ID NO: 162) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
86 AB116723 (SEQ ID NO: 163) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
89 AB113580 (SEQ ID NO: 164) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
90 AF329699 (SEQ ID NO: 165) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
88 AF208529 (SEQ ID NO: 166) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
83 AY494718 (SEQ ID NO: 167) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
82 AY494717 (SEQ ID NO: 168) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
87 AB116260 (SEQ ID NO: 169) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
25 AF347074 (SEQ ID NO: 170) gcctattgctatggcacgtactgtggctaaagtcctctatggcggcgcac
  CONSENSUS (SEQ ID NO: 171) GCCTATTGCTATGGCACGTACTGTGGCTAAAGTCCTCTATGGCGGCGCAC

                                      410        420        430        440        450
79 AF326355 (SEQ ID NO: 158) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
80 AY219651 (SEQ ID NO: 159) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
84 AF156486 (SEQ ID NO: 160) tgacgtccacttcgacccacaccattgagaggtggctgatcggaaaccaa
81 AF355189 (SEQ ID NO: 161) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
85 AY260546 (SEQ ID NO: 162) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
86 AB116723 (SEQ ID NO: 163) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
89 AB113580 (SEQ ID NO: 164) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
90 AF329699 (SEQ ID NO: 165) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
88 AF208529 (SEQ ID NO: 166) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
83 AY494718 (SEQ ID NO: 167) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
82 AY494717 (SEQ ID NO: 168) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
87 AB116260 (SEQ ID NO: 169) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
25 AF347074 (SEQ ID NO: 170) tgacgtccacctcgacccacaccattgagaggtggctgatcggaaaccaa
  CONSENSUS (SEQ ID NO: 171) TGACGTCCACCTCGACCCACACCATTGAGAGGTGGCTGATCGGAAACCAA

                                      460        470        480        490        500
79 AF326355 (SEQ ID NO: 158) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
80 AY219651 (SEQ ID NO: 159) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
84 AF156486 (SEQ ID NO: 160) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
81 AF355189 (SEQ ID NO: 161) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
85 AY260546 (SEQ ID NO: 162) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
86 AB116723 (SEQ ID NO: 163) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
89 AB113580 (SEQ ID NO: 164) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
90 AF329699 (SEQ ID NO: 165) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
```

```
88 AF208529 (SEQ ID NO: 166) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
83 AY494718 (SEQ ID NO: 167) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
82 AY494717 (SEQ ID NO: 168) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
87 AB116260 (SEQ ID NO: 169) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
25 AF347074 (SEQ ID NO: 170) acgggagacgcgacactacgagcgggttttcctaaagattgggttgttgg
  CONSENSUS (SEQ ID NO: 171) ACGGGAGACGCGACACTACGAGCGGGTTTTCCTAAAGATTGGGTTGTTGG

                                      510       520       530       540       550
79 AF326355 (SEQ ID NO: 158) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
80 AY219651 (SEQ ID NO: 159) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
84 AF156486 (SEQ ID NO: 160) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
81 AF355189 (SEQ ID NO: 161) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
85 AY260546 (SEQ ID NO: 162) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
86 AB116723 (SEQ ID NO: 163) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
89 AB113580 (SEQ ID NO: 164) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
90 AF329699 (SEQ ID NO: 165) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
88 AF208529 (SEQ ID NO: 166) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
83 AY494718 (SEQ ID NO: 167) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
82 AY494717 (SEQ ID NO: 168) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
87 AB116260 (SEQ ID NO: 169) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
25 AF347074 (SEQ ID NO: 170) agagaaaactggtacctgcgccaacgggggccggaacgacattggttttt
  CONSENSUS (SEQ ID NO: 171) AGAGAAAACTGGTACCTGCGCCAACGGGGGCCGGAACGACATTGGTTTTT

                                      560       570       580       590       600
79 AF326355 (SEQ ID NO: 158) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
80 AY219651 (SEQ ID NO: 159) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
84 AF156486 (SEQ ID NO: 160) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
81 AF355189 (SEQ ID NO: 161) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
85 AY260546 (SEQ ID NO: 162) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
86 AB116723 (SEQ ID NO: 163) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
89 AB113580 (SEQ ID NO: 164) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
90 AF329699 (SEQ ID NO: 165) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
88 AF208529 (SEQ ID NO: 166) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
83 AY494718 (SEQ ID NO: 167) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
82 AY494717 (SEQ ID NO: 168) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
87 AB116260 (SEQ ID NO: 169) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
25 AF347074 (SEQ ID NO: 170) ttaaagcccaggagagagattacgctgtagcggtgtatacaacggccccg
  CONSENSUS (SEQ ID NO: 171) TTAAAGCCCAGGAGAGAGATTACGCTGTAGCGGTGTATACAACGGCCCCG

                                      610       620       630       640       650
79 AF326355 (SEQ ID NO: 158) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
80 AY219651 (SEQ ID NO: 159) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
84 AF156486 (SEQ ID NO: 160) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
81 AF355189 (SEQ ID NO: 161) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
85 AY260546 (SEQ ID NO: 162) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
86 AB116723 (SEQ ID NO: 163) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
89 AB113580 (SEQ ID NO: 164) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
90 AF329699 (SEQ ID NO: 165) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
88 AF208529 (SEQ ID NO: 166) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
83 AY494718 (SEQ ID NO: 167) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
82 AY494717 (SEQ ID NO: 168) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
87 AB116260 (SEQ ID NO: 169) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
25 AF347074 (SEQ ID NO: 170) aaactatcggccgtagaacgtgacgaattagttgcctctgtcggtcaagt
  CONSENSUS (SEQ ID NO: 171) AAACTATCGGCCGTAGAACGTGACGAATTAGTTGCCTCTGTCGGTCAAGT


79 AF326355 (SEQ ID NO: 158) tat
80 AY219651 (SEQ ID NO: 159) tat
84 AF156486 (SEQ ID NO: 160) tat
81 AF355189 (SEQ ID NO: 161) tat
85 AY260546 (SEQ ID NO: 162) tat
86 AB116723 (SEQ ID NO: 163) tat
89 AB113580 (SEQ ID NO: 164) tat
90 AF329699 (SEQ ID NO: 165) tat
88 AF208529 (SEQ ID NO: 166) tat
83 AY494718 (SEQ ID NO: 167) tat
82 AY494717 (SEQ ID NO: 168) tat
87 AB116260 (SEQ ID NO: 169) tat
25 AF347074 (SEQ ID NO: 170) tat
  CONSENSUS (SEQ ID NO: 171) TAT
```

FIGURE 2-4

10 Bla_{shv}

```
                                        10        20        30        40        50
34 KPBLASHV6(SEQ ID NO: 172) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
45 AF467948 (SEQ ID NO: 173) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
44 AF467947 (SEQ ID NO: 174) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
40 AF293345 (SEQ ID NO: 175) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
37 AF164577 (SEQ ID NO: 176) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
36 AF148851 (SEQ ID NO: 177) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
35 AF148850 (SEQ ID NO: 178) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
41 AY036620 (SEQ ID NO: 179) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
39 AF226622 (SEQ ID NO: 180) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
38 AF132290 (SEQ ID NO: 181) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
43 AY037779 (SEQ ID NO: 182) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
42 AY037778 (SEQ ID NO: 183) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
46 AY079099 (SEQ ID NO: 184) gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
32 STYBLA (SEQ ID NO: 185)   gtaggcatgatagaaatggatctggccagcggccggacgctgaccgcctg
33 KPBLA (SEQ ID NO: 186)    gtaggcatgatagaaatggatctggccagcggccgcacgctgaccgcctg
  CONSENSUS (SEQ ID NO: 187) GTAGGCATGATAGAAATGGATCTGGCCAGCGGCCGCACGCTGACCGCCTG

                                        60        70        80        90       100
34 KPBLASHV6 (SEQ ID NO: 172)gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
45 AF467948 (SEQ ID NO: 173) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
44 AF467947 (SEQ ID NO: 174) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
40 AF293345 (SEQ ID NO: 175) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
37 AF164577 (SEQ ID NO: 176) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
36 AF148851 (SEQ ID NO: 177) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
35 AF148850 (SEQ ID NO: 178) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
41 AY036620 (SEQ ID NO: 179) gcgcgccgatggacgctttcccatgatgagcacctttaaagtagtgctct
39 AF226622 (SEQ ID NO: 180) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
38 AF132290 (SEQ ID NO: 181) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
43 AY037779 (SEQ ID NO: 182) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
42 AY037778 (SEQ ID NO: 183) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
46 AY079099 (SEQ ID NO: 184) gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
32 STYBLA (SEQ ID NO: 185)   gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
33 KPBLA (SEQ ID NO: 186)    gcgcgccgatgaacgctttcccatgatgagcacctttaaagtagtgctct
  CONSENSUS (SEQ ID NO: 187) GCGCGCCGATGAACGCTTTCCCATGATGAGCACCTTTAAAGTAGTGCTCT

                                       110       120       130       140       150
34 KPBLASHV6 (SEQ ID NO: 172)gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
45 AF467948 (SEQ ID NO: 173) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
44 AF467947 (SEQ ID NO: 174) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
40 AF293345 (SEQ ID NO: 175) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
37 AF164577 (SEQ ID NO: 176) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
36 AF148851 (SEQ ID NO: 177) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
35 AF148850 (SEQ ID NO: 178) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
41 AY036620 (SEQ ID NO: 179) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
39 AF226622 (SEQ ID NO: 180) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
38 AF132290 (SEQ ID NO: 181) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
43 AY037779 (SEQ ID NO: 182) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
42 AY037778 (SEQ ID NO: 183) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
46 AY079099 (SEQ ID NO: 184) gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
32 STYBLA (SEQ ID NO: 185)   gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
33 KPBLA (SEQ ID NO: 186)    gcggcgcagtgctggcgcgggtggatgccggtgacgaacagctggagcga
  CONSENSUS (SEQ ID NO: 187) GCGGCGCAGTGCTGGCGCGGGTGGATGCCGGTGACGAACAGCTGGAGCGA


                                       160       170       180       190       200
34 KPBLASHV6 (SEQ ID NO: 172)aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
45 AF467948 (SEQ ID NO: 173) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
44 AF467947 (SEQ ID NO: 174) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
40 AF293345 (SEQ ID NO: 175) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
37 AF164577 (SEQ ID NO: 176) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
36 AF148851 (SEQ ID NO: 177) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
35 AF148850 (SEQ ID NO: 178) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
41 AY036620 (SEQ ID NO: 179) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
39 AF226622 (SEQ ID NO: 180) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
38 AF132290 (SEQ ID NO: 181) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
43 AY037779 (SEQ ID NO: 182) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
42 AY037778 (SEQ ID NO: 183) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
46 AY079099 (SEQ ID NO: 184) aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
32 STYBLA (SEQ ID NO: 185)   aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
33 KPBLA (SEQ ID NO: 186)    aagatccactatcgccagcaggatctggtggactactcgccggtcagcga
  CONSENSUS (SEQ ID NO: 187) AAGATCCACTATCGCCAGCAGGATCTGGTGGACTACTCGCCGGTCAGCGA

                                     210       220       230       240       250
34 KPBLASHV6 (SEQ ID NO: 172)aaaacaccttgccgacggcatgacggtcggcgaactctgcgccgccgcca
```

```
45 AF467948 (SEQ ID NO: 173) aaaacaccttgccgacggcatgacggtcggcgaactctgcgccgccgcca
44 AF467947 (SEQ ID NO: 174) aaaacaccttgccgacggcatgacggtcggcgaactctgtgccgccgcca
40 AF293345 (SEQ ID NO: 175) aaaacatcttgccgacggcatgacggtcggcgaactctgtgccgccgcca
37 AF164577 (SEQ ID NO: 176) aaaacaccttgccgacggcatgacggtcggcgaactctgcgccgccgcca
36 AF148851 (SEQ ID NO: 177) aaaacaccttgccgacggcatgacggtcggcgaactctgcgccgccgcca
35 AF148850 (SEQ ID NO: 178) aaaacaccttgccgacggcatgacggtcggcgaactctgcgccgccgcca
41 AY036620 (SEQ ID NO: 179) aaaacaccttgccgacggcatgacggtcggcgaactctgtgccgccgcca
39 AF226622 (SEQ ID NO: 180) aaaacaccttgccgacggcatgacggtcggcgaactctgtgccgccgcca
38 AF132290 (SEQ ID NO: 181) aaaacaccttgccgacggcatgacggtcggcgaactctgtgccgccgcca
43 AY037779 (SEQ ID NO: 182) aaaacaccttgccgacggcatgacggtcggcgaactctgtgccgccgcca
42 AY037778 (SEQ ID NO: 183) aaaacatcttgccgacggcatgacggtcggcgaactctgtgccgccgtca
46 AY079099 (SEQ ID NO: 184) aaaacaccttgccgacggcatgacggtcggcgaactctgtgccgccgcca
32 STYBLA (SEQ ID NO: 185)   aaaacaccttgccgacggcatgacggtcggcgaactctgcgccgccgcca
33 KPBLA (SEQ ID NO: 186)    aaaacaccttgccgacggcatgacggtcggcgaactctgcgccgccgcca
  CONSENSUS (SEQ ID NO: 187) AAAACACCTTGCCGACGGCATGACGGTCGGCGAACTCTG-GCCGCCGCCA

                                      260       270       280       290       300
34 KPBLASHV6 (SEQ ID NO: 172)ttaccatgagcgataacagcgccgccaatctgctactggccaccgtcggc
45 AF467948 (SEQ ID NO: 173) ttaccgtgagcgataacagcgccgccaatctgctgctggccaccgtcggc
44 AF467947 (SEQ ID NO: 174) ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
40 AF293345 (SEQ ID NO: 175) ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
37 AF164577 (SEQ ID NO: 176) ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
36 AF148851 (SEQ ID NO: 177) ttaccatgagcgataacagcgccgccaatctgctactggccaccgtcggc
35 AF148850 (SEQ ID NO: 178) ttaccatgagcgataacagcgccgccaatctgctactggccaccgtcggc
41 AY036620 (SEQ ID NO: 179) ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
39 AF226622 (SEQ ID NO: 180) ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
38 AF132290 (SEQ ID NO: 181) ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
43 AY037779 (SEQ ID NO: 182) ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
42 AY037778 (SEQ ID NO: 183) ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
46 AY079099 (SEQ ID NO: 184) ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
32 STYBLA (SEQ ID NO: 185)   ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
33 KPBLA (SEQ ID NO: 186)    ttaccatgagcgataacagcgccgccaatctgctgctggccaccgtcggc
  CONSENSUS (SEQ ID NO: 187) TTACCATGAGCGATAACAGCGCCGCCAATCTGCTGCTGGCCACCGTCGGC

                                      310       320       330       340       350
34 KPBLASHV6 (SEQ ID NO: 172)ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
45 AF467948 (SEQ ID NO: 173) ggccccgcaggattgactgccttttgcgccagatcggggacaatgtcac
44 AF467947 (SEQ ID NO: 174) ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
40 AF293345 (SEQ ID NO: 175) ggccccgcaggattgactgccttttgcgccagatcgacgacaacgtcac
37 AF164577 (SEQ ID NO: 176) ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
36 AF148851 (SEQ ID NO: 177) ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
35 AF148850 (SEQ ID NO: 178) ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
41 AY036620 (SEQ ID NO: 179) ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
39 AF226622 (SEQ ID NO: 180) ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
38 AF132290 (SEQ ID NO: 181) ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
43 AY037779 (SEQ ID NO: 182) ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
42 AY037778 (SEQ ID NO: 183) ggccccgcaggattgactgccttttgcgccagatcgacgacaacgtcac
46 AY079099 (SEQ ID NO: 184) ggccccgtaggattgactgccttttgcgccagatcggcgacaacgtcac
32 STYBLA (SEQ ID NO: 185)   ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
33 KPBLA (SEQ ID NO: 186)    ggccccgcaggattgactgccttttgcgccagatcggcgacaacgtcac
  CONSENSUS (SEQ ID NO: 187) GGCCCCGCAGGATTGACTGCCTTTTTGCGCCAGATCGGCGACAACGTCAC

                                      360       370       380       390       400
34 KPBLASHV6 (SEQ ID NO: 172)ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
45 AF467948 (SEQ ID NO: 173) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
44 AF467947 (SEQ ID NO: 174) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
40 AF293345 (SEQ ID NO: 175) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
37 AF164577 (SEQ ID NO: 176) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
36 AF148851 (SEQ ID NO: 177) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
35 AF148850 (SEQ ID NO: 178) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
41 AY036620 (SEQ ID NO: 179) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
39 AF226622 (SEQ ID NO: 180) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
38 AF132290 (SEQ ID NO: 181) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
43 AY037779 (SEQ ID NO: 182) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
42 AY037778 (SEQ ID NO: 183) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
46 AY079099 (SEQ ID NO: 184) ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
32 STYBLA (SEQ ID NO: 185)   ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
33 KPBLA (SEQ ID NO: 186)    ccgccttgaccgctgggaaacggaactgaatgaggcgcttcccggcgacg
  CONSENSUS (SEQ ID NO: 187) CCGCCTTGACCGCTGGGAAACGGAACTGAATGAGGCGCTTCCCGGCGACG

                                      410       420       430       440       450
34 KPBLASHV6 (SEQ ID NO: 172)cccgcgccaccactaccccggccagcatggccgcgaccctgcgcaagctg
45 AF467948 (SEQ ID NO: 173) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
44 AF467947 (SEQ ID NO: 174) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
40 AF293345 (SEQ ID NO: 175) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
37 AF164577 (SEQ ID NO: 176) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
36 AF148851 (SEQ ID NO: 177) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
35 AF148850 (SEQ ID NO: 178) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
```

```
41 AY036620 (SEQ ID NO: 179) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
39 AF226622 (SEQ ID NO: 180) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
38 AF132290 (SEQ ID NO: 181) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
43 AY037779 (SEQ ID NO: 182) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
42 AY037778 (SEQ ID NO: 183) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
46 AY079099 (SEQ ID NO: 184) cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
32 STYBLA (SEQ ID NO: 185)   cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
33 KPBLA (SEQ ID NO: 186)    cccgcgacaccactaccccggccagcatggccgcgaccctgcgcaagctg
  CONSENSUS (SEQ ID NO: 187) CCCGCGACACCACTACCCCGGCCAGCATGGCCGCGACCCTGCGCAAGCTG

                                        460       470       480       490       500
34 KPBLASHV6 (SEQ ID NO: 172)ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
45 AF467948 (SEQ ID NO: 173) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
44 AF467947 (SEQ ID NO: 174) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
40 AF293345 (SEQ ID NO: 175) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
37 AF164577 (SEQ ID NO: 176) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
36 AF148851 (SEQ ID NO: 177) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
35 AF148850 (SEQ ID NO: 178) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
41 AY036620 (SEQ ID NO: 179) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
39 AF226622 (SEQ ID NO: 180) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
38 AF132290 (SEQ ID NO: 181) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
43 AY037779 (SEQ ID NO: 182) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
42 AY037778 (SEQ ID NO: 183) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
46 AY079099 (SEQ ID NO: 184) ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
32 STYBLA (SEQ ID NO: 185)   ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
33 KPBLA (SEQ ID NO: 186)    ctgaccagccagcgtctgagcgcccgttcgcaacggcagctgctgcagtg
  CONSENSUS (SEQ ID NO: 187) CTGACCAGCCAGCGTCTGAGCGCCCGTTCGCAACGGCAGCTGCTGCAGTG

                                        510       520       530       540       550
34 KPBLASHV6 (SEQ ID NO: 172)gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
45 AF467948 (SEQ ID NO: 173) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
44 AF467947 (SEQ ID NO: 174) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
40 AF293345 (SEQ ID NO: 175) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
37 AF164577 (SEQ ID NO: 176) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
36 AF148851 (SEQ ID NO: 177) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
35 AF148850 (SEQ ID NO: 178) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
41 AY036620 (SEQ ID NO: 179) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
39 AF226622 (SEQ ID NO: 180) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
38 AF132290 (SEQ ID NO: 181) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
43 AY037779 (SEQ ID NO: 182) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgtcgg
42 AY037778 (SEQ ID NO: 183) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
46 AY079099 (SEQ ID NO: 184) gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
32 STYBLA (SEQ ID NO: 185)   gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
33 KPBLA (SEQ ID NO: 186)    gatggtggacgatcgggtcgccggaccgttgatccgctccgtgctgccgg
  CONSENSUS (SEQ ID NO: 187) GATGGTGGACGATCGGGTCGCCGGACCGTTGATCCGCTCCGTGCTGCCGG

                                        560       570       580       590       600
34 KPBLASHV6(SEQ ID NO: 172) cgggctggtttatcgccgataagaccggagctggcgagcggggtgcgcgc
45 AF467948 (SEQ ID NO: 173) cgggctggtttatcgccgataagaccggagctggcgaacggggtgcgcgc
44 AF467947 (SEQ ID NO: 174) cgggctggtttatcgccgataagaccggagctggcgagcggggtgcgcgc
40 AF293345 (SEQ ID NO: 175) cgggctggtttatcgccgataagaccggagctggcgagcggggtgcgcgc
37 AF164577 (SEQ ID NO: 176) cgggctggtttatcgccgataagaccggagctgccgagcggggtgcgcgc
36 AF148851 (SEQ ID NO: 177) cgggctggtttatcgccgataagaccggagctagcgagcggggtgcgcgc
35 AF148850 (SEQ ID NO: 178) cgggctggtttatcgccgataagaccggagctggcgagcggggtgcgcgc
41 AY036620 (SEQ ID NO: 179) cgggctggtttatcgccgataagaccggagctagcgaacggggtgcgcgc
39 AF226622 (SEQ ID NO: 180) cgggctggtttatcgccgataagaccggagctggcgaacggggtgcgcgc
38 AF132290 (SEQ ID NO: 181) cgggctggtttatcgccgataagaccggagctgccaaacggggtgcgcgc
43 AY037779 (SEQ ID NO: 182) cgggctggtttatcgccgataagaccggagctggcgaacggggtgcgcgc
42 AY037778 (SEQ ID NO: 183) cgggctggtttatcgccgataagaccggagctggcgagcggggtgcgcgc
46 AY079099 (SEQ ID NO: 184) cgggctggtttatcgccgataagaccggagctggcgaacggggtgcgcgc
32 STYBLA (SEQ ID NO: 185)   cgggttggtttatcgccgataagaccggagctagcgagcggggtgcgcgc
33 KPBLA (SEQ ID NO: 186)    cgggctggtttatcgccgataagaccggagctagcgagcggggtgcgcgc
  CONSENSUS (SEQ ID NO: 187) CGGGCTGGTTTATCGCCGATAAGACCGGAGCT-GCGA-CGGGGTGCGCGC

                                        610       620       630       640       650
34 KPBLASHV6(SEQ ID NO: 172) gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
45 AF467948 (SEQ ID NO: 173) gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
44 AF467947 (SEQ ID NO: 174) ggcattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
40 AF293345 (SEQ ID NO: 175) gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
37 AF164577 (SEQ ID NO: 176) gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
36 AF148851 (SEQ ID NO: 177) gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
35 AF148850 (SEQ ID NO: 178) gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
41 AY036620 (SEQ ID NO: 179) gggattgtcgccctgcttggcccgaataacaaagcagagcggattgtggt
39 AF226622 (SEQ ID NO: 180) gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
38 AF132290 (SEQ ID NO: 181) gggattgtcgccctgcttggcccgaataacaaagcagagcggattgtggt
43 AY037779 (SEQ ID NO: 182) gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
42 AY037778 (SEQ ID NO: 183) gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
46 AY079099 (SEQ ID NO: 184) gggattgtcgccctgcttggcccgaataacaaagcagagcggattgtggt
```

```
32 STYBLA (SEQ ID NO: 185)   gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
33 KPBLA (SEQ ID NO: 186)    gggattgtcgccctgcttggcccgaataacaaagcagagcgcattgtggt
  CONSENSUS (SEQ ID NO: 187) GGGATTGTCGCCCTGCTTGGCCCGAATAACAAAGCAGAGCGCATTGTGGT

                                        660       670       680       690
34 KPBLASHV6(SEQ ID NO: 172) gatttatctgcgggataccccggcgagcatggccgagcgaaat
45 AF467948 (SEQ ID NO: 173) gatttatctgcgggatacgccggcgagcatggccgagcgaaat
44 AF467947 (SEQ ID NO: 174) gatttatctgcgggatacgccggcgagcatggccgagcgaaat
40 AF293345 (SEQ ID NO: 175) gatttatctgcgggatacgccggcgagcatggccgagcgaaat
37 AF164577 (SEQ ID NO: 176) gatttatctgcgggatacgccggcgagcatggccgagcgaaat
36 AF148851 (SEQ ID NO: 177) gatttatctgcgggataccccggcgagcatggccgagcgaaat
35 AF148850 (SEQ ID NO: 178) gatttatctgcgggataccccggcgagcatggccgagcgaaat
41 AY036620 (SEQ ID NO: 179) gatttatctgcgggatacgccggcgagcatggccgagcgaaat
39 AF226622 (SEQ ID NO: 180) gatttatctgcgggatacgccggcgagcatggccgagcgaaat
38 AF132290 (SEQ ID NO: 181) gatttatctgcgggatacgccggcgagcatggccgagcgaaat
43 AY037779 (SEQ ID NO: 182) gatttatctgcgggataccccggcgagcatggccgagcgaaat
42 AY037778 (SEQ ID NO: 183) gatttatctgcgggatacgccggcgagcatggccgagcgaaat
46 AY079099 (SEQ ID NO: 184) gatttatctgcgggatacgccggcgagcatggccgagcgaaat
32 STYBLA (SEQ ID NO: 185)   gatttatctgcgggatacgccggcgagcatggccgagcgaaat
33 KPBLA (SEQ ID NO: 186)    gatttatctgcgggatacgccggcgagcatggccgagcgaaat
  CONSENSUS (SEQ ID NO: 187) GATTTATCTGCGGGATAC-CCGGCGAGCATGGCCGAGCGAAAT
```

11 *MecA*

```
                                        10        20        30        40        50
  51 SAMECAPB (SEQ ID NO:188) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
  91 SAMECAR1I (SEQ ID NO:189)aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
  93 SSK8MECA (SEQ ID NO:190) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
  92 SAPBP (SEQ ID NO:191)    aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
  99 SEMECAPB (SEQ ID NO:192) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
  94 AB033763 (SEQ ID NO:193) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
  95 AB096217 (SEQ ID NO:194) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
  97 AY271717 (SEQ ID NO:195) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
 100 AB063173 (SEQ ID NO:196) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
 101 AB037671 (SEQ ID NO:197) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
 102 AB063172 (SEQ ID NO:198) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
 103 D86934 (SEQ ID NO:199)   aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
 106 SSK3MECA2 (SEQ ID NO:200)aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
-105 AP004822 (SEQ ID NO:201) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
-104 AP003129 (SEQ ID NO:202) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
 -98 AP003358 (SEQ ID NO:203) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
 -96 AB047089 (SEQ ID NO:204) aagagtatttataacaacatgaaaaatgattatggctcaggtactgctat
     CONSENSUS(SEQ ID NO:205) AAGAGTATTTATAACAACATGAAAAATGATTATGGCTCAGGTACTGCTAT

                                        60        70        80        90       100
  51 SAMECAPB (SEQ ID NO:188) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
  91 SAMECAR1I(SEQ ID NO:189) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
  93 SSK8MECA (SEQ ID NO:190) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
  92 SAPBP (SEQ ID NO:191)    ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
  99 SEMECAPB (SEQ ID NO:192) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
  94 AB033763 (SEQ ID NO:193) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
  95 AB096217 (SEQ ID NO:194) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
  97 AY271717 (SEQ ID NO:195) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
 100 AB063173 (SEQ ID NO:196) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
 101 AB037671 (SEQ ID NO:197) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
 102 AB063172 (SEQ ID NO:198) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
 103 D86934 (SEQ ID NO:199)   ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
 106 SSK3MECA2 (SEQ ID NO:200)ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
-105 AP004822 (SEQ ID NO:201) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
-104 AP003129 (SEQ ID NO:202) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
 -98 AP003358 (SEQ ID NO:203) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
 -96 AB047089 (SEQ ID NO:204) ccacgctcaaacaggtgaattattagcacttgtaagcacaccttcatatg
    CONSENSUS (SEQ ID NO:205) CCACGCTCAAACAGGTGAATTATTAGCACTTGTAAGCACACCTTCATATG

                                       110       120       130       140       150
  51 SAMECAPB (SEQ ID NO:188) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
  91 SAMECAR1I(SEQ ID NO:189) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
  93 SSK8MECA (SEQ ID NO:190) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
  92 SAPBP (SEQ ID NO:191)    acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
  99 SEMECAPB (SEQ ID NO:192) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
  94 AB033763 (SEQ ID NO:193) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
  95 AB096217 (SEQ ID NO:194) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
  97 AY271717 (SEQ ID NO:195) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
 100 AB063173 (SEQ ID NO:196) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
 101 AB037671 (SEQ ID NO:197) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
 102 AB063172 (SEQ ID NO:198) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
 103 D86934 (SEQ ID NO:199)   acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
 106 SSK3MECA2(SEQ ID NO:200) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
-105 AP004822 (SEQ ID NO:201) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
-104 AP003129 (SEQ ID NO:202) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
 -98 AP003358 (SEQ ID NO:203) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
 -96 AB047089 (SEQ ID NO:204) acgtctatccatttatgtatggcatgagtaacgaagaatataataaatta
    CONSENSUS (SEQ ID NO:205) ACGTCTATCCATTTATGTATGGCATGAGTAACGAAGAATATAATAAATTA


                                       160       170       180       190       200
  51 SAMECAPB (SEQ ID NO:188) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
  91 SAMECAR1I(SEQ ID NO:189) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
  93 SSK8MECA (SEQ ID NO:190) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
  92 SAPBP (SEQ ID NO:191)    accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
  99 SEMECAPB (SEQ ID NO:192) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
  94 AB033763 (SEQ ID NO:193) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
  95 AB096217 (SEQ ID NO:194) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
  97 AY271717 (SEQ ID NO:195) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
 100 AB063173 (SEQ ID NO:196) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
 101 AB037671 (SEQ ID NO:197) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
 102 AB063172 (SEQ ID NO:198) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
 103 D86934 (SEQ ID NO:199)   accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
 106 SSK3MECA2(SEQ ID NO:200) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
-105 AP004822 (SEQ ID NO:201) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
```

```
-104 AP003129 (SEQ ID NO:202) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
 -98 AP003358 (SEQ ID NO:203) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
 -96 AB047089 (SEQ ID NO:204) accgaagataaaaaagaacctctgctcaacaagttccagattacaacttc
     CONSENSUS(SEQ ID NO:205) ACCGAAGATAAAAAAGAACCTCTGCTCAACAAGTTCCAGATTACAACTTC


                                        210       220       230       240       250
  51 SAMECAPB (SEQ ID NO:188) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
  91 SAMECAR1I(SEQ ID NO:189) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
  93 SSK8MECA (SEQ ID NO:190) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
  92 SAPBP (SEQ ID NO:191)    accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
  99 SEMECAPB (SEQ ID NO:192) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
  94 AB033763 (SEQ ID NO:193) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
  95 AB096217 (SEQ ID NO:194) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
  97 AY271717 (SEQ ID NO:195) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
 100 AB063173 (SEQ ID NO:196) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
 101 AB037671 (SEQ ID NO:197) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
 102 AB063172 (SEQ ID NO:198) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
 103 D86934 (SEQ ID NO:199)   accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
 106 SSK3MECA2(SEQ ID NO:200) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
-105 AP004822 (SEQ ID NO:201) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
-104 AP003129 (SEQ ID NO:202) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
 -98 AP003358 (SEQ ID NO:203) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
 -96 AB047089 (SEQ ID NO:204) accaggttcaactcaaaaaatattaacagcaatgattgggttaaataaca
     CONSENSUS(SEQ ID NO:205) ACCAGGTTCAACTCAAAAAATATTAACAGCAATGATTGGGTTAAATAACA

                                        260       270       280       290       300
  51 SAMECAPB (SEQ ID NO:188) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
  91 SAMECAR1I(SEQ ID NO:189) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
  93 SSK8MECA (SEQ ID NO:190) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
  92 SAPBP (SEQ ID NO:191)    aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
  99 SEMECAPB (SEQ ID NO:192) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
  94 AB033763 (SEQ ID NO:193) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
  95 AB096217 (SEQ ID NO:194) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
  97 AY271717 (SEQ ID NO:195) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
 100 AB063173 (SEQ ID NO:196) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
 101 AB037671 (SEQ ID NO:197) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
 102 AB063172 (SEQ ID NO:198) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
 103 D86934 (SEQ ID NO:199)   aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
 106 SSK3MECA2(SEQ ID NO:200) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
-105 AP004822 (SEQ ID NO:201) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
-104 AP003129 (SEQ ID NO:202) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
 -98 AP003358 (SEQ ID NO:203) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
 -96 AB047089 (SEQ ID NO:204) aaacattagacgataaaacaagttataaaatcgatggtaaaggttggcaa
CONSENSUS(SEQ ID NO:205)     AAACATTAGACGATAAAACAAGTTATAAAATCGATGGTAAAGGTTGGCAA

                                        310       320       330       340       350
  51 SAMECAPB (SEQ ID NO:188) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
  91 SAMECAR1I(SEQ ID NO:189) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
  93 SSK8MECA (SEQ ID NO:190) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
  92 SAPBP (SEQ ID NO:191)    aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
  99 SEMECAPB (SEQ ID NO:192) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
  94 AB033763 (SEQ ID NO:193) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
  95 AB096217 (SEQ ID NO:194) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
  97 AY271717 (SEQ ID NO:195) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
 100 AB063173 (SEQ ID NO:196) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
 101 AB037671 (SEQ ID NO:197) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
 102 AB063172 (SEQ ID NO:198) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
 103 D86934 (SEQ ID NO:199)   aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
 106 SSK3MECA2(SEQ ID NO:200) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
-105 AP004822 (SEQ ID NO:201) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
-104 AP003129 (SEQ ID NO:202) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
 -98 AP003358 (SEQ ID NO:203) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
 -96 AB047089 (SEQ ID NO:204) aaagataaatcttggggtggttacaacgttacaagatatgaagtggtaaa
     CONSENSUS(SEQ ID NO:205) AAAGATAAATCTTGGGGTGGTTACAACGTTACAAGATATGAAGTGGTAAA

                                        360       370       380       390       400
  51 SAMECAPB (SEQ ID NO:188) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
  91 SAMECAR1I(SEQ ID NO:189) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
  93 SSK8MECA (SEQ ID NO:190) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
  92 SAPBP (SEQ ID NO:191)    tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
  99 SEMECAPB (SEQ ID NO:192) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
  94 AB033763 (SEQ ID NO:193) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
  95 AB096217 (SEQ ID NO:194) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
  97 AY271717 (SEQ ID NO:195) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
 100 AB063173 (SEQ ID NO:196) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
 101 AB037671 (SEQ ID NO:197) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
 102 AB063172 (SEQ ID NO:198) tggtaatatcgacttaaaacaagcaatagaatcatcagataacattttct
```

```
 103 D86934 (SEQ ID NO:199)   tggtaatatcgacttaaaacaagcaatagaatcatcagataacatttttct
 106 SSK3MECA2(SEQ ID NO:200) tggtaatatcgacttaaaacaagcaatagaatcatcagataacatttttct
-105 AP004822 (SEQ ID NO:201) tggtaatatcgacttaaaacaagcaatagaatcatcagataacatttttct
-104 AP003129 (SEQ ID NO:202) tggtaatatcgacttaaaacaagcaatagaatcatcagataacatttttct
 -98 AP003358 (SEQ ID NO:203) tggtaatatcgacttaaaacaagcaatagaatcatcagataacatttttct
 -96 AB047089 (SEQ ID NO:204) tggtaatatcgacttaaaacaagcaatagaatcatcagataacatttttct
     CONSENSUS(SEQ ID NO:205) TGGTAATATCGACTTAAAACAAGCAATAGAATCATCAGATAACATTTTCT

                                        410        420        430        440        450
  51 SAMECAPB (SEQ ID NO:188) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
  91 SAMECAR1I(SEQ ID NO:189) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
  93 SSK8MECA (SEQ ID NO:190) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
  92 SAPBP (SEQ ID NO:191)    ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
  99 SEMECAPB (SEQ ID NO:192) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
  94 AB033763 (SEQ ID NO:193) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
  95 AB096217 (SEQ ID NO:194) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
  97 AY271717 (SEQ ID NO:195) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
 100 AB063173 (SEQ ID NO:196) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
 101 AB037671 (SEQ ID NO:197) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
 102 AB063172 (SEQ ID NO:198) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
 103 D86934 (SEQ ID NO:199)   ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
 106 SSK3MECA2(SEQ ID NO:200) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
-105 AP004822 (SEQ ID NO:201) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
-104 AP003129 (SEQ ID NO:202) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
 -98 AP003358 (SEQ ID NO:203) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
 -96 AB047089 (SEQ ID NO:204) ttgctagagtagcactcgaattaggcagtaagaaatttgaaaaaggcatg
     CONSENSUS(SEQ ID NO:205) TTGCTAGAGTAGCACTCGAATTAGGCAGTAAGAAATTTGAAAAAGGCATG

                                       460        470        480        490        500
  51 SAMECAPB (SEQ ID NO:188) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
  91 SAMECAR1I(SEQ ID NO:189) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
  93 SSK8MECA (SEQ ID NO:190) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
  92 SAPBP (SEQ ID NO:191)    aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
  99 SEMECAPB (SEQ ID NO:192) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
  94 AB033763 (SEQ ID NO:193) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
  95 AB096217 (SEQ ID NO:194) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
  97 AY271717 (SEQ ID NO:195) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
 100 AB063173 (SEQ ID NO:196) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
 101 AB037671 (SEQ ID NO:197) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
 102 AB063172 (SEQ ID NO:198) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
 103 D86934 (SEQ ID NO:199)   aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
 106 SSK3MECA2(SEQ ID NO:200) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
-105 AP004822 (SEQ ID NO:201) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
-104 AP003129 (SEQ ID NO:202) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
 -98 AP003358 (SEQ ID NO:203) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
 -96 AB047089 (SEQ ID NO:204) aaaaaactaggtgttggtgaagatataccaagtgattatccattttataa
     CONSENSUS(SEQ ID NO:205) AAAAAACTAGGTGTTGGTGAAGATATACCAAGTGATTATCCATTTTATAA

                                       510        520        530        540        550
  51 SAMECAPB (SEQ ID NO:188) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
  91 SAMECAR1I(SEQ ID NO:189)  tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
  93 SSK8MECA (SEQ ID NO:190) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
  92 SAPBP (SEQ ID NO:191)    tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
  99 SEMECAPB (SEQ ID NO:192) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
  94 AB033763 (SEQ ID NO:193) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
  95 AB096217 (SEQ ID NO:194) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
  97 AY271717 (SEQ ID NO:195) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
 100 AB063173 (SEQ ID NO:196) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
 101 AB037671 (SEQ ID NO:197) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
 102 AB063172 (SEQ ID NO:198) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
 103 D86934 (SEQ ID NO:199)   tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
 106 SSK3MECA2(SEQ ID NO:200) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
-105 AP004822 (SEQ ID NO:201) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
-104 AP003129 (SEQ ID NO:202) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
 -98 AP003358 (SEQ ID NO:203) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
 -96 AB047089 (SEQ ID NO:204) tgctcaaatttcaaacaaaaatttagataatgaaatattattagctgatt
     CONSENSUS(SEQ ID NO:205) TGCTCAAATTTCAAACAAAAATTTAGATAATGAAATATTATTAGCTGATT

                                       560        570        580        590        600
  51 SAMECAPB (SEQ ID NO:188) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  91 SAMECAR1I (SEQ ID NO:189)caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  93 SSK8MECA (SEQ ID NO:190) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  92 SAPBP (SEQ ID NO:191)    caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  99 SEMECAPB (SEQ ID NO:192) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  94 AB033763 (SEQ ID NO:193) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  95 AB096217 (SEQ ID NO:194) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  97 AY271717 (SEQ ID NO:195) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
 100 AB063173 (SEQ ID NO:196) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
```

```
  101 AB037671 (SEQ ID NO:197) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  102 AB063172 (SEQ ID NO:198) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  103 D86934 (SEQ ID NO:199)   caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  106 SSK3MECA2 (SEQ ID NO:200)caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
 -105 AP004822 (SEQ ID NO:201) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
 -104 AP003129 (SEQ ID NO:202) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  -98 AP003358 (SEQ ID NO:203) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
  -96 AB047089 (SEQ ID NO:204) caggttacggacaaggtgaaatactgattaacccagtacagatcctttca
      CONSENSUS(SEQ ID NO:205) CAGGTTACGGACAAGGTGAAATACTGATTAACCCAGTACAGATCCTTTCA

                                      610
   51 SAMECAPB (SEQ ID NO:188) atctatagcgc
   91 SAMECAR1I(SEQ ID NO:189) atctatagcgc
   93 SSK8MECA (SEQ ID NO:190) atctatagcgc
   92 SAPBP (SEQ ID NO:191)    atctatagcgc
   99 SEMECAPB (SEQ ID NO:192) atctatagcgc
   94 AB033763 (SEQ ID NO:193) atctatagcgc
   95 AB096217 (SEQ ID NO:194) atctatagcgc
   97 AY271717 (SEQ ID NO:195) atctatagcgc
  100 AB063173 (SEQ ID NO:196) atctatagcgc
  101 AB037671 (SEQ ID NO:197) atctatagcgc
  102 AB063172 (SEQ ID NO:198) atctatagcgc
  103 D86934 (SEQ ID NO:199)   atctatagcgc
  106 SSK3MECA2(SEQ ID NO:200) atctatagcgc
 -105 AP004822 (SEQ ID NO:201) atctatagcgc
 -104 AP003129 (SEQ ID NO:202) atctatagcgc
  -98 AP003358 (SEQ ID NO:203) atctatagcgc
  -96 AB047089 (SEQ ID NO:204) atctatagcgc
      CONSENSUS(SEQ ID NO:205) ATCTATAGCGC
```

FIGURE 2-12

12 *Spa*

```
                                        10        20        30        40        50
 52 STASPAA (SEQ ID NO:206)   aaaacatttattcaattcgtaaactaggtgtaggtattgcatctgtaact
112 SAV1SPA (SEQ ID NO:207)   aaaacatttattcaattcgtaaactaggtgtaggtattgcatctgtaact
111 AB050857 (SEQ ID NO:208)  aaaacatttattcaattcgtaaactaggtgtaggtattgcatctgtaact
110 SAU54636 (SEQ ID NO:209)  aaaaaatttattcaattcgtaaactaggtgtaggtattgcatctgtaact
108 STASPA (SEQ ID NO:210)    aaaacatttattcaattcgtaaactaggtgtaggtattgcatctgtaact
109 SASPAPA (SEQ ID NO:211)   aaaacatttattcaattcgtaaactaggtgtaggtattgcatctgtaact
113 AB035454 (SEQ ID NO:212)  aaaacatttattcaattcgtaaactaggtgtaggtattgcatctgtaact
107 AC025949 (SEQ ID NO:213)  aaaacatttattcaattcgtaaactaggtgtaggtattgcatctgtaact
114 SASPAX (SEQ ID NO:214)    aaaacatttattcaattcgtaaactaggtgtaggtattgcatctgtaact
    CONSENSUS (SEQ ID NO:218) AAAACATTTATTCAATTCGTAAACTAGGTGTAGGTATTGCATCTGTAACT

                                        60        70        80        90       100
 52 STASPAA (SEQ ID NO:206)   ttaggtacattacttatatctggtggcgtaacacctgctgcaaatgctgc
112 SAV1SPA (SEQ ID NO:207)   ttaggtacattacttatatctggtggcgtaacacctgctgcaaatgctgc
111 AB050857 (SEQ ID NO:208)  ttaggtacattacttatatctggtggcgtaacacctgctgcaaatgctgc
110 SAU54636 (SEQ ID NO:209)  ttaggtacattacttatatctggtggcgtaacacctgctgcaaatgctgc
108 STASPA (SEQ ID NO:210)    ttaggtacattacttatatctggtggcgtaacacctgctgcaaatgctgc
109 SASPAPA (SEQ ID NO:211)   ttaggtacattacttatatctggtggcgtaacacctgctgcaaatgctgc
113 AB035454 (SEQ ID NO:212)  ttaggtacattacttatatgtggtggcgtaacacctgctgcaaatgctgc
107 AC025949 (SEQ ID NO:213)  ttaggtacattacttatatctggtggcgtaacacctgctgcaaatgctgc
114 SASPAX (SEQ ID NO:214)    ttaggtacattacttatatctggtggcgtaacacctgctgcaaatgctgc
115 AJ606381 (SEQ ID NO:215)                                                   gc
    CONSENSUS (SEQ ID NO:218) TTAGGTACATTACTTATATCTGGTGGCGTAACACCTGCTGCAAATGCTGC

                                       110       120       130       140       150
 52 STASPAA (SEQ ID NO:206)   gcaacacgatgaagctcaacaaaatgctttttatcaagtgttaaatatgc
112 SAV1SPA (SEQ ID NO:207)   gcaacacgatgaagctcaacaaaatgctttttatcaagtgttaaatatgc
111 AB050857 (SEQ ID NO:208)  gcaacacgatgaagctcaacaaaatgctttttatcaagtgttaaatatgc
110 SAU54636 (SEQ ID NO:209)  gcaacacgatgaagctcaacaaaatgctttttatcaagtgttaaatatgc
108 STASPA (SEQ ID NO:210)    gcaacacgatgaagctcaacaaaatgctttttatcaagtcttaaatatgc
109 SASPAPA (SEQ ID NO:211)   gcaacacgatgaagctcaacaaaatgctttttatcaagtgttaaatatgc
113 AB035454 (SEQ ID NO:212)  gcaacacgatgaagctcaacaaaatgctttttatcaagtgttaaatatgc
107 AC025949 (SEQ ID NO:213)  gcaacacgatgaagctcaacaaaatgctttttatcaagtcttaaatatgc
114 SASPAX (SEQ ID NO:214)    gcaacacgatgaagctcaacaaaatgctttttatcaagtcttaaatatgc
115 AJ606381 (SEQ ID NO:215)  gcaacacgatgaagctgaacaaaatgctttttatcaagtcttaaatatgc
117 AJ606379 (SEQ ID NO:216)            tgaagctcaacaaaatgctttttatcaagtgttaaatatgc
    CONSENSUS (SEQ ID NO:218) GCAACACGATGAAGCTCAACAAAATGCTTTTTATCAAGT-TTAAATATGC

                                       160       170       180       190       200
 52 STASPAA (SEQ ID NO:206)   ctaacttaaacgctgatcaacgtaatggttttatccaaagccttaaagat
112 SAV1SPA (SEQ ID NO:207)   ctaacttaaacgctgatcaacgtaatggttttatccaaagccttaaagat
111 AB050857 (SEQ ID NO:208)  ctaacttaaacgctgatcaacgtaatggttttatccaaagccttaaagat
110 SAU54636 (SEQ ID NO:209)  ctaacttaaacgctgatcaacgtaatggttttatccaaagccttaaagat
108 STASPA (SEQ ID NO:210)    ctaacttaaatgctgatcaacgcaatggttttatccaaagccttaaagat
109 SASPAPA (SEQ ID NO:211)   ctaacttaaacgctgatcaacgtaatggttttatccaaagccttaaagat
113 AB035454 (SEQ ID NO:212)  ctaacttaaacgctgatcaacgtaatggttttatccaaagccttaaagat
107 AC025949 (SEQ ID NO:213)  ctaacttaaatgctgatcaacgcaatggttttatccaaagccttaaagat
114 SASPAX (SEQ ID NO:214)    ctaacttaaatgctgatcaacgcaatggttttatccaaagccttaaagat
115 AJ606381 (SEQ ID NO:215)  ctaacttaaatgctgatcaacgcaatggttttatccaaagccttaaagat
117 AJ606379 (SEQ ID NO:216)  ctaacttaaacgctgatcaacgtaatggttttatccaaagccttaaagat
    CONSENSUS (SEQ ID NO:218) CTAACTTAAA-GCTGATCAACG-AATGGTTTTATCCAAAGCCTTAAAGAT

                                       210       220       230       240       250
 52 STASPAA (SEQ ID NO:206)   gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
112 SAV1SPA (SEQ ID NO:207)   gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
111 AB050857 (SEQ ID NO:208)  gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
110 SAU54636 (SEQ ID NO:209)  gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
108 STASPA (SEQ ID NO:210)    gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
109 SASPAPA (SEQ ID NO:211)   gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
113 AB035454 (SEQ ID NO:212)  gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
107 AC025949 (SEQ ID NO:213)  gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
114 SASPAX (SEQ ID NO:214)    gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
115 AJ606381 (SEQ ID NO:215)  gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
117 AJ606379 (SEQ ID NO:216)  gatccaagccaaagtgctaacgttttaggtgaagctcaaaaacttaatga
    CONSENSUS (SEQ ID NO:218) GATCCAAGCCAAAGTGCTAACGTTTTAGGTGAAGCTCAAAAACTTAATGA


                                       260       270       280       290       300
 52 STASPAA (SEQ ID NO:206)   ctctcaagctccaaaagctgatgcgcaacaaaataagttcaacaaagatc
112 SAV1SPA (SEQ ID NO:207)   ctctcaagctccaaaagctgatgcgcaacaaaataagttcaacaaagatc
111 AB050857 (SEQ ID NO:208)  ctctcaagctccaaaagctgatgcgcaacaaaataacttcaacaaagatc
110 SAU54636 (SEQ ID NO:209)  ctctcaagctccaaaagctgatgcgcaacaaaataagttcaacaaagatc
108 STASPA (SEQ ID NO:210)    ctctcaagctccaaaagctgatgcgcaacaaaataacttcaacaaagatc
109 SASPAPA (SEQ ID NO:211)   ctctcaagctccaaaagctgatgcgcaacaaaataagttcaacaaagatc
113 AB035454 (SEQ ID NO:212)  ctctcaagctccaaaagctgatgcgcaacaaaataacttcaacaaagatc
```

```
107 AC025949 (SEQ ID NO:213)  ctctcaagctccaaaagctgatgcgcaacaaaataacttcaacaaagatc
114 SASPAX (SEQ ID NO:214)    ctctcaagctccaaaagctgatgcgcaacaaaataacttcgacaaagatc
115 AJ606381 (SEQ ID NO:215)  ctctcaagctccaaaagctgatgcgcaacaaaataacttcaacaaagatc
117 AJ606379 (SEQ ID NO:216)  ctctcaagctccaaaagctgatgcgcaacaaaataacttcaacaaagatc
116 AJ606380 (SEQ ID NO:217)                  tgctgcgcaacacgat**g*******aagctc
    CONSENSUS (SEQ ID NO:218) CTCTCAAGCTCCAAAAGCTGATGCGCAACAAAATAA-TTCAACAAAGATC

                                       310       320       330       340       350
 52 STASPAA (SEQ ID NO:206)   aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagag
112 SAV1SPA (SEQ ID NO:207)   aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagag
111 AB050857 (SEQ ID NO:208)  aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagcg
110 SAU54636 (SEQ ID NO:209)  aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagag
108 STASPA (SEQ ID NO:210)    aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagcg
109 SASPAPA (SEQ ID NO:211)   aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagag
113 AB035454 (SEQ ID NO:212)  aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagcg
107 AC025949 (SEQ ID NO:213)  aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagcg
114 SASPAX (SEQ ID NO:214)    aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagcg
115 AJ606381 (SEQ ID NO:215)  aacaaagcgccttctatgaaattttgaacatgcctaacttaaacgaagtg
117 AJ606379 (SEQ ID NO:216)  aacaaagcgccttctatgaaatcttgaacatgcctaacttaaacgaagcg
116 AJ606380 (SEQ ID NO:217)  aacaaaacgctttttatcaagtcttaaatatgcctaacttaaatgctgat
    CONSENSUS (SEQ ID NO:218) AACAAAGCGCCTTCTATGAAATCTTGAACATGCCTAACTTAAACGAAG-G

                                       360       370       380       390       400
 52 STASPAA (SEQ ID NO:206)   caacgcaatggtttcattcaaagtcttaaagacgatccaagccaaagcac
112 SAV1SPA (SEQ ID NO:207)   caacgcaatggtttcattcaaagtcttaaagacgatccaagccaaagcac
111 AB050857 (SEQ ID NO:208)  caacgtaacggcttcattcaaagtcttaaagacgacccaagccaaagcac
110 SAU54636 (SEQ ID NO:209)  caacgcaatggtttcattcaaagtcttaaagacgatccaagccaaagcac
108 STASPA (SEQ ID NO:210)    caacgtaacggcttcattcaaagtcttaaagacgacccaagccaaagcac
109 SASPAPA (SEQ ID NO:211)   caacgcaatggtttcattcaaagtcttaaagacgatccaagccaaagcac
113 AB035454 (SEQ ID NO:212)  caacgtaacggcttcattcaaagtcttaaagacgacccaagccaaagcac
107 AC025949 (SEQ ID NO:213)  caacgtaacggcttcattcaaagtcttaaagacgacccaagccaaagcac
114 SASPAX (SEQ ID NO:214)    caacgtaacggcttcattcaaagtcttaaagacgacccaagccaaagcac
115 AJ606381 (SEQ ID NO:215)  caacgcaatggtttcattcaaagtcttaaagacgatccaagccaaagcac
117 AJ606379 (SEQ ID NO:216)  caacgcaatggtttcattcaaagtcttaaagacgatccaagccaaagcac
116 AJ606380 (SEQ ID NO:217)  caacgcaatggttttatccaaagccttaaagatgatccaagccaaagtgc
    CONSENSUS (SEQ ID NO:218) CAACG-AA-GG-TTCATTCAAAGTCTTAAAGACGA-CCAAGCCAAAGCAC

                                       410       420       430       440       450
 52 STASPAA (SEQ ID NO:206)   taacgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
112 SAV1SPA (SEQ ID NO:207)   taacgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
111 AB050857 (SEQ ID NO:208)  taatgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
110 SAU54636 (SEQ ID NO:209)  taacgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
108 STASPA (SEQ ID NO:210)    taacgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
109 SASPAPA (SEQ ID NO:211)   taacgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
113 AB035454 (SEQ ID NO:212)  taatgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
107 AC025949 (SEQ ID NO:213)  taacgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
114 SASPAX (SEQ ID NO:214)    taacgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
115 AJ606381 (SEQ ID NO:215)  taacgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
117 AJ606379 (SEQ ID NO:216)  taacgttttaggtgaagctaaaaaattaaatgaatctcaagcaccgaaag
116 AJ606380 (SEQ ID NO:217)  taacgttttaggtgaagctaaaaaattaaacgaatctcaagcaccgaaag
    CONSENSUS (SEQ ID NO:218) TAACGTTTTAGGTGAAGCTAAAAAATTAAACGAATCTCAAGCACCGAAAG

                                       460       470       480       490       500
 52 STASPAA (SEQ ID NO:206)   ctgacaacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
112 SAV1SPA (SEQ ID NO:207)   ctgacaacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
111 AB050857 (SEQ ID NO:208)  ctgataacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
110 SAU54636 (SEQ ID NO:209)  ctgacaacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
108 STASPA (SEQ ID NO:210)    ctgataacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
109 SASPAPA (SEQ ID NO:211)   ctgacaacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
113 AB035454 (SEQ ID NO:212)  ctgataacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
107 AC025949 (SEQ ID NO:213)  ctgataacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
114 SASPAX (SEQ ID NO:214)    ctgataacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
115 AJ606381 (SEQ ID NO:215)  ctgacaacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
117 AJ606379 (SEQ ID NO:216)  ctgacaacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
116 AJ606380 (SEQ ID NO:217)  ctgacaacaatttcaacaaagaacaacaaaatgctttctatgaaatcttg
    CONSENSUS (SEQ ID NO:218) CTGA-AACAATTTCAACAAAGAACAACAAAATGCTTTCTATGAAATCTTG


 52 STASPAA (SEQ ID NO:206)   a
112 SAV1SPA (SEQ ID NO:207)   a
111 AB050857 (SEQ ID NO:208)  a
110 SAU54636 (SEQ ID NO:209)  a
108 STASPA (SEQ ID NO:210)    a
109 SASPAPA (SEQ ID NO:211)   a
113 AB035454 (SEQ ID NO:212)  a
107 AC025949 (SEQ ID NO:213)  a
114 SASPAX (SEQ ID NO:214)    a
115 AJ606381 (SEQ ID NO:215)  a
```

FIGURE 2-14

```
117 AJ606379 (SEQ ID NO:216)  a
116 AJ606380 (SEQ ID NO:217)  a
    CONSENSUS (SEQ ID NO:218) A
```

13 *VanA*

```
                                        10        20        30        40        50
 53 AE017171(SEQ ID NO:219)   aaagttgcaatactgtttgggggttgctcagaggagcatgacgtatcggt
 54 AF516335 (SEQ ID NO:220)  aaagttgcaatactgtttgggggttgctcagaggagcatgacgtatcggt
 48 EFPVANAG (SEQ ID NO:221)  aaagttgcaatactgtttgggggttgctcagaggagcatgacgtatcggt
 49 BCY15704 (SEQ ID NO:222)  aaagttgcaatattgtttgggggttgctcagaggagcatgacgtatctgt
 50 TRNVAN (SEQ ID NO:223)    aaagttgcaatactgtttgggggttgctcagaggagcatgacgtatcggt
    CONSENSUS (SEQ ID NO:225) AAAGTTGCAATACTGTTTGGGGGTTGCTCAGAGGAGCATGACGTATCGGT

                                        60        70        80        90       100
 53 AE017171(SEQ ID NO:219)   aaaatctgcaatagagatagccgctaacattaataaagaaaaatacgagc
 54 AF516335 (SEQ ID NO:220)  aaaatctgcaatagagatagccgctaacattaataaagaaaaatacgagc
 48 EFPVANAG (SEQ ID NO:221)  aaaatctgcaatagagatagccgctaacattaataaagaaaaatacgagc
 49 BCY15704 (SEQ ID NO:222)  aaaatccgcaatagaaatagccgctaacattgataaagaaaaatacgaga
 50 TRNVAN (SEQ ID NO:223)    aaaatctgcaatagagatagccgctaacattaataaagaaaaatacgagc
    CONSENSUS                 AAAATCTGCAATAGAGATAGCCGCTAACATTAATAAAGAAAAATACGAGC

                                       110       120       130       140       150
 53 AE017171(SEQ ID NO:219)   cgttatacattggaattacgaaatctggtgtatggaaaatgtgcgaaaaa
 54 AF516335(SEQ ID NO:220)   cgttatacattggaattacgaaatctggtgtatggaaaatgtgcgaaaaa
 48 EFPVANAG(SEQ ID NO:221)   cgttatacattggaattacgaaatctggtgtatggaaaatgtgcgaaaaa
 49 BCY15704(SEQ ID NO:222)   cgttatacattgggattaccaaatctggtgtatggaaaatgtgtgaaaaa
 50 TRNVAN (SEQ ID NO:223)    cgttatacattggaattacgaaatctggtgtatggaaaatgtgcgaaaaa
 55 OTPDVANA2 (SEQ ID NO:224)                cgaaatctggtgtatggaaaatgtgcgaaaaa
   CONSENSUS(SEQ ID NO:225)   CGTTATACATTGGAATTACGAAATCTGGTGTATGGAAAATGTGCGAAAAA

                                       160       170       180       190       200
 53 AE017171(SEQ ID NO:219)   ccttgcgcggaatgggaaaacgacaattgctattcagctgtactctcgcc
 54 AF516335(SEQ ID NO:220)   ccttgcgcggaatgggaaaacgacaattgctattcagctgtactctcgcc
 48 EFPVANAG(SEQ ID NO:221)   ccttgcgcggaatgggaaaacgacaattgctattcagctgtactctcgcc
 49 BCY15704(SEQ ID NO:222)   ccgtgcgtggaatgggaaaacgacaattgctgttcagcagtactctcgcc
 50 TRNVAN (SEQ ID NO:223)    ccttgcgcggaatgggaaaacgacaattgctattcagctgtactctcgcc
 55 OTPDVANA2(SEQ ID NO:224)  ccttgcgcggaatgggaaaacgacaattgctattcagctgtactctcgcc
    CONSENSUS(SEQ ID NO:225)  CCTTGCGCGGAATGGGAAAACGACAATTGCTATTCAGCTGTACTCTCGCC

                                       210       220       230       240       250
 53 AE017171(SEQ ID NO:219)   ggataaaaaaatgcacggattacttgttaaaaagaaccatgaatatgaaa
 54 AF516335(SEQ ID NO:220)   ggataaaaaaatgcacggattacttgttaaaaagaaccatgaatatgaaa
 48 EFPVANAG(SEQ ID NO:221)   ggataaaaaaatgcacggattacttgttaaaaagaaccatgaatatgaaa
 49 BCY15704(SEQ ID NO:222)   ggataaaaaaatgcacggattacttgttaaaaagaaccatgaatatgaaa
 50 TRNVAN (SEQ ID NO:223)    ggataaaaaaatgcacggattacttgttaaaaagaaccatgaatatgaaa
 55 OTPDVANA2(SEQ ID NO:224)  ggataaaaaaatgcacggattacttgttaaaaagaaccatgaatatgaaa
    CONSENSUS(SEQ ID NO:225)  GGATAAAAAAATGCACGGATTACTTGTTAAAAAGAACCATGAATATGAAA

                                       260       270       280       290       300
 53 AE017171(SEQ ID NO:219)   tcaaccatgttgatgtagcattttcagctttgcatggcaagtcaggtgaa
 54 AF516335 (SEQ ID NO:220)  tcaaccatgttgatgtagcattttcagctttgcatggcaagtcaggtgaa
 48 EFPVANAG (SEQ ID NO:221)  tcaaccatgttgatgtagcattttcagctttgcatggcaagtcaggtgaa
 49 BCY15704 (SEQ ID NO:222)  tcgaccacgttgatgtagcattttcggttttgcacggcaagtcgggtgaa
 50 TRNVAN (SEQ ID NO:223)    tcaaccatgttgatgtagcattttcagctttgcatggcaagtcaggtgaa
 55 OTPDVANA2 (SEQ ID NO:224) tcaaccatgttgatgtagcattttcagctttgcatggcaagtcaggtgaa
    CONSENSUS (SEQ ID NO:225) TCAACCATGTTGATGTAGCATTTTCAGCTTTGCATGGCAAGTCAGGTGAA

                                       310       320       330       340       350
 53 AE017171(SEQ ID NO:219)   gatggatccatacaaggtctgtttgaattgtccggtatccctttgtagg
 54 AF516335 (SEQ ID NO:220)  gatggatccatacaaggtctgtttgaattgtccggtatccctttgtagg
 48 EFPVANAG (SEQ ID NO:221)  gatggatccatacaaggtctgtttgaattgtccggtatccctttgtagg
 49 BCY15704 (SEQ ID NO:222)  gatggatccaatacaaggtctttttgaattgtccggtatccctttgtagg
 50 TRNVAN (SEQ ID NO:223)    gatggatccatacaaggtctgtttgaattgtccggtatccctttgtagg
 55 OTPDVANA2 (SEQ ID NO:224) gatggatccatacaaggtctgtttgaattgtccggtatccctttgtagg
    CONSENSUS (SEQ ID NO:225) GATGGATCCATACAAGGTCTGTTTGAATTGTCCGGTATCCCTTTTGTAGG

                                       360       370       380       390       400
 53 AE017171(SEQ ID NO:219)   ctgcgatattcaaagctcagcaatttgtatggacaaatcgttgacataca
 54 AF516335 (SEQ ID NO:220)  ctgcgatattcaaagctcagcaatttgtatggacaaatcgttgacataca
 48 EFPVANAG (SEQ ID NO:221)  ctgcgatattcaaagctcagcaatttgtatggacaaatcgttgacataca
 49 BCY15704 (SEQ ID NO:222)  ctgcgatattcaaagctcagcgatttgtatggacaaatcactgacataca
 50 TRNVAN (SEQ ID NO:223)    ctgcgatattcaaagctcagcaatttgtatggacaaatcgttgacataca
 55 OTPDVANA2 (SEQ ID NO:224) ctgcgatattcaaagctcagcaatttgtatggacaaatcgttgacataca
    CONSENSUS (SEQ ID NO:225) CTGCGATATTCAAAGCTCAGCAATTTGTATGGACAAATCGTTGACATACA

                                       410       420       430       440       450
 53 AE017171(SEQ ID NO:219)   tcgttgcgaaaaatgctgggatagctactcccgccttttgggttattaat
 54 AF516335 (SEQ ID NO:220)  tcgttgcgaaaaatgctgggatagctactcccgccttttgggttattaat
 48 EFPVANAG (SEQ ID NO:221)  tcgttgcgaaaaatgctgggatagctactcccgccttttgggttattaat
 49 BCY15704 (SEQ ID NO:222)  tcgttgcggaaaatgctggcatagctactcccgaattttgggttttaat
 50 TRNVAN (SEQ ID NO:223)    tcgttgcgaaaaatgctgggatagctactcccgccttttgggttattaat
```

```
55 OTPDVANA2 (SEQ ID NO:224) tcgttgcgaaaaatgctgggatagctactcccgccttttgggttattaat
   CONSENSUS (SEQ ID NO:225) TCGTTGCGAAAAATGCTGGGATAGCTACTCCCGCCTTTTGGGTTATTAAT

                                    460       470       480       490       500
53 AE017171(SEQ ID NO:219)   aaagatgataggccggtggcagctacgtttacctatcctgtttttgttaa
54 AF516335 (SEQ ID NO:220)  aaagatgataggccggtggcagctacgtttacctatcctgtttttgttaa
48 EFPVANAG (SEQ ID NO:221)  aaagatgataggccggtggcagctacgtttacctatcctgtttttgttaa
49 BCY15704 (SEQ ID NO:222)  aaagacgataagccgatggcagatacgtttacctatcctgtttttgttaa
50 TRNVAN (SEQ ID NO:223)    aaagatgataggccggtggcagctacgtttacctatcctgtttttgttaa
55 OTPDVANA2 (SEQ ID NO:224) aaagatgataggccggtggcagctacgtctacctatcctgtgtttggtaa
   CONSENSUS (SEQ ID NO:225) AAAGATGATAGGCCGGTGGCAGCTACGTTTACCTATCCTGTTTTTGTTAA

                                    510       520       530       540       550
53 AE017171(SEQ ID NO:219)   gccggcgcgttcaggctcatccttcggtgtgaaaaaagtcaatagcgcgg
54 AF516335 (SEQ ID NO:220)  gccggcgcgttcaggctcatccttcggtgtgaaaaaagtcaatagcgcgg
48 EFPVANAG (SEQ ID NO:221)  gccggcgcgttcaggctcatccttcggtgtgaaaaaagtcaatagcgcgg
49 BCY15704 (SEQ ID NO:222)  gcctgcgcgttcaggctcatcctttggcgtgaaaaaggtcaatggagcag
50 TRNVAN (SEQ ID NO:223)    gccggcgcgttcaggctcatccttcggtgtgaaaaaagtcaatagcgcgg
55 OTPDVANA2 (SEQ ID NO:224) gccggcgcgttcaggctcatccttcggggtgaaaaaagtcaatagcgcgg
   CONSENSUS (SEQ ID NO:225) GCCGGCGCGTTCAGGCTCATCCTTCGG-GTGAAAAAAGTCAATAGCGCGG

                                    560       570       580       590       600
53 AE017171(SEQ ID NO:219)   acgaattggactacgcaattgaatcggcaagacaatatgacagcaaaatc
54 AF516335 (SEQ ID NO:220)  acgaattggactacgcaattgaatcggcaagacaatatgacagcaaaatc
48 EFPVANAG (SEQ ID NO:221)  acgaattggactacgcaattgaatcggcaagacaatatgacagcaaaatc
49 BCY15704 (SEQ ID NO:222)  acgaattggacgccgcaattgaattggctggacaatatgacagcaaaatc
50 TRNVAN (SEQ ID NO:223)    acgaattggactacgcaattgaatcggcaagacaatatgacagcaaaatc
55 OTPDVANA2 (SEQ ID NO:224) acgaattggactacgcaattgaatcggcaagacaatatgacagcaaaatc
   CONSENSUS (SEQ ID NO:225) ACGAATTGGACTACGCAATTGAATCGGCAAGACAATATGACAGCAAAATC

                                    610       620       630       640       650
53 AE017171(SEQ ID NO:219)   ttaattgagcaggctgtttcgggctgtgaggtcggttgtgcggtattggg
54 AF516335 (SEQ ID NO:220)  ttaattgagcaggctgtttcgggctgtgaggtcggttgtgcggtattggg
48 EFPVANAG (SEQ ID NO:221)  ttaattgagcaggctgtttcgggctgtgaggtcggttgtgcggtattggg
49 BCY15704 (SEQ ID NO:222)  ttaattgagcaggctgttttgggctgtgaggtcggttgtgccgtattggg
50 TRNVAN (SEQ ID NO:223)    ttaattgagcaggctgtttcgggctgtgaggtcggttgtgcggtattggg
55 OTPDVANA2 (SEQ ID NO:224) ttaattgagcaggctgtttcgggctgtgaggtcggttgtgcggtattggg
   CONSENSUS (SEQ ID NO:225) TTAATTGAGCAGGCTGTTTCGGGCTGTGAGGTCGGTTGTGCGGTATTGGG

                                    660       670       680       690       700
53 AE017171(SEQ ID NO:219)   aaacagtgccgcgttagttgttggcgaggtggaccaaatcaggctgcagt
54 AF516335 (SEQ ID NO:220)  aaacagtgccgcgttagttgttggcgaggtggaccaaatcaggctgcagt
48 EFPVANAG (SEQ ID NO:221)  aaacagtgccgcgttagttgttggcgaggtggaccaaatcaggctgcagt
49 BCY15704 (SEQ ID NO:222)  aaacagttccgcttttgttgttggcgaggtagaccaaatcagactgcagc
50 TRNVAN (SEQ ID NO:223)    aaacagtgccgcgttagttgttggcgaggtggaccaaatcaggctgcagt
55 OTPDVANA2 (SEQ ID NO:224) aaacagtgcggcgttagttgttggcgaggtggaccaaatcaggctgcagt
   CONSENSUS (SEQ ID NO:225) AAACAGTGCCGCGTTAGTTGTTGGCGAGGTGGACCAAATCAGGCTGCAGT

                                    710       720       730       740       750
53 AE017171(SEQ ID NO:219)   acggaatctttcgtattcatcaggaagtcgagccggaaaaaggctctgaa
54 AF516335 (SEQ ID NO:220)  acggaatctttcgtattcatcaggaagtcgagccggaaaaaggctctgaa
48 EFPVANAG (SEQ ID NO:221)  acggaatctttcgtattcatcaggaagtcgagccggaaaaaggctctgaa
49 BCY15704 (SEQ ID NO:222)  acggaatctttcgtattcatcaggaagccgagccggaaaaaggctctgaa
50 TRNVAN (SEQ ID NO:223)    acggaatctttcgtattcatcaggaagtcgagccggaaaaaggctctgaa
55 OTPDVANA2 (SEQ ID NO:224) acggaatctttcgtattcatcaggaagtcgagccggaaaaaggctctgaa
   CONSENSUS (SEQ ID NO:225) ACGGAATCTTTCGTATTCATCAGGAAGTCGAGCCGGAAAAAGGCTCTGAA

                                    760       770       780       790       800
53 AE017171(SEQ ID NO:219)   aacgcagttataaccgttcccgcagacctttcagcagaggagcgaggacg
54 AF516335 (SEQ ID NO:220)  aacgcagttataaccgttcccgcagacctttcagcagaggagcgaggacg
48 EFPVANAG (SEQ ID NO:221)  aacgcagttataaccgttcccgcagacctttcagcagaggagcgaggacg
49 BCY15704 (SEQ ID NO:222)  aacgcagttataaccgttcccgcagacctgtcggcagaggagcgaggacg
50 TRNVAN (SEQ ID NO:223)    aacgcagttataaccgttcccgcagacctttcagcagaggagcgaggacg
55 OTPDVANA2 (SEQ ID NO:224) aacgcagttataaccgttcccgcagacctttcagcagaggagcgaggacg
   CONSENSUS (SEQ ID NO:225) AACGCAGTTATAACCGTTCCCGCAGACCTTTCAGCAGAGGAGCGAGGACG

                                    810       820       830       840       850
53 AE017171(SEQ ID NO:219)   gatacaggaaacggcaaaaaaaatatataaagcgctcggctgtagaggtc
54 AF516335 (SEQ ID NO:220)  gatacaggaaacggcaaaaaaaatatataaagcgctcggctgtagaggtc
48 EFPVANAG (SEQ ID NO:221)  gatacaggaaacggcaaaaaaaatatataaagcgctcggctgtagaggtc
49 BCY15704 (SEQ ID NO:222)  gatacaggaaacggcaaaaaaaatatataatgcgctcggctgtagaggtc
50 TRNVAN (SEQ ID NO:223)    gatacaggaaacggcaaaaaaaatatataaagcgctcggctgtagaggtc
55 OTPDVANA2 (SEQ ID NO:224) gatacaggaaacgggaaaaaaaatatataaagcgctcggctgtagaggtc
   CONSENSUS (SEQ ID NO:225) GATACAGGAAACGGCAAAAAAAATATATAAAGCGCTCGGCTGTAGAGGTC

                                    860       870       880       890       900
53 AE017171(SEQ ID NO:219)   tagcccgtgtggatatgtttttacaagataacggccgcattgtactgaac
54 AF516335 (SEQ ID NO:220)  tagcccgtgtggatatgtttttacaagataacggccgcattgtactgaac
```

```
48 EFPVANAG (SEQ ID NO:221)  tagcccgtgtggatatgtttttacaagataacggccgcattgtactgaac
49 BCY15704 (SEQ ID NO:222)  tagcccgtgtcgatatgtttttacaagataacggccgcattgtactgaac
50 TRNVAN (SEQ ID NO:223)    tagcccgtgtggatatgtttttacaagataacggccgcattgtactgaac
55 OTPDVANA2 (SEQ ID NO:224) tagcccgtgtggatatgtttttacaagataacggccgcattgtactgaac
   CONSENSUS (SEQ ID NO:225) TAGCCCGTGTGGATATGTTTTTACAAGATAACGGCCGCATTGTACTGAAC

                                    910       920       930       940
53 AE017171(SEQ ID NO:219)   gaagtcaatactctgcccggtttcacgtcatacagtcgttatcc
54 AF516335 (SEQ ID NO:220)  gaagtcaatactctgcccggtttcacgtcatacagtcgttatcc
48 EFPVANAG (SEQ ID NO:221)  gaagtcaatactctgcccggtttcacgtcatacagtcgttatcc
49 BCY15704 (SEQ ID NO:222)  gaagtcaataccctgcccggtttcacttcatacagccgttatcc
50 TRNVAN (SEQ ID NO:223)    gaagtcaatactctgcccggtttcacgtcatacagtcgttatcc
55 OTPDVANA2 (SEQ ID NO:224) gaag
   CONSENSUS (SEQ ID NO:225) GAAGTCAATACTCTGCCCGGTTTCACGTCATACAGTCGTTATCC
```

14 *VanB*

```
                                        10        20        30        40        50
  58 EFU81452 (SEQ ID NO:226)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  56 EFVANRES (SEQ ID NO:227)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  60 AY145441 (SEQ ID NO:228)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  64 AF310953 (SEQ ID NO:229)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
 -59 EFU94526 (SEQ ID NO:230)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
 -61 EFU94530 (SEQ ID NO:231)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  63 EFA306726 (SEQ ID NO:232) atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  31 AF550667 (SEQ ID NO:233)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  28 EFA306727 (SEQ ID NO:234) atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  30 U00456 (SEQ ID NO:235)    atcggaattacaaaaaacggcgtatggaagctatgcaagaagccatgtac
 -27 EFU94528 (SEQ ID NO:236)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  67 AF310955 (SEQ ID NO:237)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  66 AF310957 (SEQ ID NO:238)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  69 EFU72704 (SEQ ID NO:239)  atcggaattacaaaaaggggtgtatggaagctatgcaagaagccatgtac
 -72 EFU94527 (SEQ ID NO:240)  atcggaattacaaaaaacggcgtatggaagctatgcaagaagccatgtac
 -62 EFU94529 (SEQ ID NO:241)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  57 AF310956 (SEQ ID NO:242)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
  65 AF310954 (SEQ ID NO:243)  atcggaattacaaaaaacggtgtatggaagctatgcaagaagccatgtac
     CONSENSUS (SEQ ID NO:247) ATCGGAATTACAAAAAACGGTGTATGGAAGCTATGCAAGAAGCCATGTAC

                                        60        70        80        90       100
  58 EFU81452 (SEQ ID NO:226)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  56 EFVANRES (SEQ ID NO:227)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  60 AY145441 (SEQ ID NO:228)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  64 AF310953 (SEQ ID NO:229)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
 -59 EFU94526 (SEQ ID NO:230)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
 -61 EFU94530 (SEQ ID NO:231)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  63 EFA306726 (SEQ ID NO:232) ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  31 AF550667 (SEQ ID NO:233)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  28 EFA306727 (SEQ ID NO:234) ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  30 U00456 (SEQ ID NO:235)    ggaatgggaagccgatagtctccccgccatattctccccggataggaaaa
 -27 EFU94528 (SEQ ID NO:236)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  67 AF310955 (SEQ ID NO:237)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  66 AF310957 (SEQ ID NO:238)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  69 EFU72704 (SEQ ID NO:239)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
 -72 EFU94527 (SEQ ID NO:240)  ggaatgggaagccgatagtctccccgccatattctccccggataggaaaa
 -62 EFU94529 (SEQ ID NO:241)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  57 AF310956 (SEQ ID NO:242)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  65 AF310954 (SEQ ID NO:243)  ggaatgggaagccgacagtctccccgccatactctccccggataggaaaa
  70 SBVANB2 (SEQ ID NO:244)     atgggaagccgatagtctccccgccatactctccccggataggaaaa
     CONSENSUS (SEQ ID NO:247) GGAATGGGAAGCCGACAGTCTCCCCGCCATACTCTCCCCGGATAGGAAAA

                                       110       120       130       140       150
  58 EFU81452 (SEQ ID NO:226)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  56 EFVANRES (SEQ ID NO:227)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  60 AY145441 (SEQ ID NO:228)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  64 AF310953 (SEQ ID NO:229)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
 -59 EFU94526 (SEQ ID NO:230)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
 -61 EFU94530 (SEQ ID NO:231)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  63 EFA306726 (SEQ ID NO:232) cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  31 AF550667 (SEQ ID NO:233)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  28 EFA306727 (SEQ ID NO:234) cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  30 U00456 (SEQ ID NO:235)    cgcatggtctgcttgtcatgaaagaaagagaatacgaaactcggcgtatt
 -27 EFU94528 (SEQ ID NO:236)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  67 AF310955 (SEQ ID NO:237)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  66 AF310957 (SEQ ID NO:238)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  69 EFU72704 (SEQ ID NO:239)  cgcatggtctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
 -72 EFU94527 (SEQ ID NO:240)  cgcatggtctgcttgtcatgaaagaaagagaatacgaaactcggcgtatt
 -62 EFU94529 (SEQ ID NO:241)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  57 AF310956 (SEQ ID NO:242)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  65 AF310954 (SEQ ID NO:243)  cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
  70 SBVANB2 (SEQ ID NO:244)   cgcatgggctgcttgtcatgaaagaaagcgaatacgaaacacggcgtatt
     CONSENSUS (SEQ ID NO:247) CGCATGGGCTGCTTGTCATGAAAGAAAGCGAATACGAAACACGGCGTATT

                                       160       170       180       190       200
  58 EFU81452 (SEQ ID NO:226)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
  56 EFVANRES (SEQ ID NO:227)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
  60 AY145441 (SEQ ID NO:228)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
  64 AF310953 (SEQ ID NO:229)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
 -59 EFU94526 (SEQ ID NO:230)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
 -61 EFU94530 (SEQ ID NO:231)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
  63 EFA306726 (SEQ ID NO:232) gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
  31 AF550667 (SEQ ID NO:233)  gatgtagctttcccggttttgcatggcaaatgcggggaggatggtgcgat
  28 EFA306727 (SEQ ID NO:234) gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
```

```
 30 U00456 (SEQ ID NO:235)    gacgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
-27 EFU94528 (SEQ ID NO:236)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
 67 AF310955 (SEQ ID NO:237)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
 66 AF310957 (SEQ ID NO:238)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
 69 EFU72704 (SEQ ID NO:239)  gatgtggctttcccagttttgcatggcaaatgcggggaggacggtgcgat
-72 EFU94527 (SEQ ID NO:240)  gacgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
-62 EFU94529 (SEQ ID NO:241)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
 57 AF310956 (SEQ ID NO:242)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
 65 AF310954 (SEQ ID NO:243)  gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
 70 SBVANB2 (SEQ ID NO:244)   gatgtggctttcccggttttgcatggcaaatgcggggaggatggtgcgat
 29 ENEVANB2A (SEQ ID NO:245)                                    gaggatgggtgcat
    CONSENSUS (SEQ ID NO:247) GATGTGGCTTTCCCGGTTTTGCATGGCAAATGCGGGGAGGATGGTGCGAT

                                       210       220       230       240       250
 58 EFU81452 (SEQ ID NO:226)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 56 EFVANRES (SEQ ID NO:227)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 60 AY145441 (SEQ ID NO:228)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 64 AF310953 (SEQ ID NO:229)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
-59 EFU94526 (SEQ ID NO:230)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
-61 EFU94530 (SEQ ID NO:231)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 63 EFA306726(SEQ ID NO:232)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 31 AF550667 (SEQ ID NO:233)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 28 EFA306727 (SEQ ID NO:234) acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 30 U00456 (SEQ ID NO:235)    acagggtctgtttgaattgtctggtatcccctatgtaggctgcgatattc
-27 EFU94528 (SEQ ID NO:236)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 67 AF310955 (SEQ ID NO:237)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 66 AF310957 (SEQ ID NO:238)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 69 EFU72704 (SEQ ID NO:239)  acagggtttatttgaattgtctggcatcccctatgtgggctgcgatattc
-72 EFU94527 (SEQ ID NO:240)  acagggtctgtttgaattgtctggtatcccctatgtaggctgcgatattc
-62 EFU94529 (SEQ ID NO:241)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 57 AF310956 (SEQ ID NO:242)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 65 AF310954 (SEQ ID NO:243)  acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 70 SBVANB2 (SEQ ID NO:244)   acaggggctgtttgtattgtctggtatcccctatgtgggctgtgatattc
 29 ENEVANB2A (SEQ ID NO:245) ccagggactgtttgaattgtctggtatcccctatgtgggctgtgatattc
 26 ENEVANB (SEQ ID NO:246)         tctgtttgaattgtctggtatcccctatgtaggctgcgatattc
    CONSENSUS (SEQ ID NO:247) ACAGGGGCTGTTTGTATTGTCTGGTATCCCCTATGTGGGCTGTGATATTC

                                       260       270       280       290       300
 58 EFU81452 (SEQ ID NO:226)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 56 EFVANRES (SEQ ID NO:227)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 60 AY145441 (SEQ ID NO:228)  aaagctccgcagtttgcatggacaaatcactggcctacattcttacaaaa
 64 AF310953 (SEQ ID NO:229)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
-59 EFU94526 (SEQ ID NO:230)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
-61 EFU94530 (SEQ ID NO:231)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 63 EFA306726 (SEQ ID NO:232) aaagctccgcagcttgcgtggacaaatcactggcctacattcttacaaaa
 31 AF550667 (SEQ ID NO:233)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 28 EFA306727 (SEQ ID NO:234) aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 30 U00456 (SEQ ID NO:235)    aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
-27 EFU94528 (SEQ ID NO:236)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 67 AF310955 (SEQ ID NO:237)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 66 AF310957 (SEQ ID NO:238)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 69 EFU72704 (SEQ ID NO:239)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
-72 EFU94527 (SEQ ID NO:240)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
-62 EFU94529 (SEQ ID NO:241)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 57 AF310956 (SEQ ID NO:242)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 65 AF310954 (SEQ ID NO:243)  aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 70 SBVANB2 (SEQ ID NO:244)   aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 29 ENEVANB2A (SEQ ID NO:245) aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
 26 ENEVANB (SEQ ID NO:246)   aaagctccgcagcttgcatggacaaatcactggcctacattcttacaaaa
    CONSENSUS (SEQ ID NO:247) AAAGCTCCGCAGCTTGCATGGACAAATCACTGGCCTACATTCTTACAAAA

                                       310       320       330       340       350
 58 EFU81452 (SEQ ID NO:226)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 56 EFVANRES (SEQ ID NO:227)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 60 AY145441 (SEQ ID NO:228)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 64 AF310953 (SEQ ID NO:229)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
-59 EFU94526 (SEQ ID NO:230)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
-61 EFU94530 (SEQ ID NO:231)  aatgcgggcatcgccgttcccgaatttcaaattattgataaaggtgacaa
 63 EFA306726 (SEQ ID NO:232) aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 31 AF550667 (SEQ ID NO:233)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 28 EFA306727 (SEQ ID NO:234) aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 30 U00456 (SEQ ID NO:235)    aatgcgggcatcgccgtccccgaatttcaaatgattgaaaaaggtgacaa
-27 EFU94528 (SEQ ID NO:236)  aatgcgggcatcgccgttcccgaatttcaaattattgataaaggtgacaa
 67 AF310955 (SEQ ID NO:237)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 66 AF310957 (SEQ ID NO:238)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 69 EFU72704 (SEQ ID NO:239)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
-72 EFU94527 (SEQ ID NO:240)  aatgcgggcatcgccgtccccgaatttcaaatgattgaaaaaggtgacaa
-62 EFU94529 (SEQ ID NO:241)  aatgcgggcatcgccgttcccgaatttcaaattattgataaaggtgacaa
```

```
 57 AF310956 (SEQ ID NO:242)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 65 AF310954 (SEQ ID NO:243)  aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 70 SBVANB2 (SEQ ID NO:244)   aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 29 ENEVANB2A (SEQ ID NO:245) aatgcgggcatcgccgttcccgaatttcaaatgattgataaaggtgacaa
 26 ENEVANB (SEQ ID NO:246)   aatgcgggcatcgccgtccccgaatttcaaatgattgaaaaaggtgacaa
    CONSENSUS (SEQ ID NO:247) AATGCGGGCATCGCCGTTCCCGAATTTCAAATGATTGATAAAGGTGACAA

                                       360        370        380        390        400
 58 EFU81452 (SEQ ID NO:226)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 56 EFVANRES (SEQ ID NO:227)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 60 AY145441 (SEQ ID NO:228)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 64 AF310953 (SEQ ID NO:229)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
-59 EFU94526 (SEQ ID NO:230)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
-61 EFU94530 (SEQ ID NO:231)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 63 EFA306726 (SEQ ID NO:232) gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 31 AF550667 (SEQ ID NO:233)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 28 EFA306727 (SEQ ID NO:234) gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 30 U00456 (SEQ ID NO:235)    accggaggcgaggacgcttacctaccctgtctttgtgaagccggcacggt
-27 EFU94528 (SEQ ID NO:236)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 67 AF310955 (SEQ ID NO:237)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 66 AF310957 (SEQ ID NO:238)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 69 EFU72704 (SEQ ID NO:239)  gccggagacgggtgcgcttacctaccctgtctttgtgaagccggcacggt
-72 EFU94527 (SEQ ID NO:240)  accggaggcgaggacgcttacctaccctgtctttgtgaagccggcacggt
-62 EFU94529 (SEQ ID NO:241)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 57 AF310956 (SEQ ID NO:242)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 65 AF310954 (SEQ ID NO:243)  gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggg
 70 SBVANB2 (SEQ ID NO:244)   gccggaggcgggtacgcttacctaccctgtctttgtgaagccggcacggt
 29 ENEVANB2A (SEQ ID NO:245) gccggaggcgggtgcgcttacctaccctgtctttgtgaagccggcacggt
 26 ENEVANB (SEQ ID NO:246)   accggaggcgaggacgcttacctaccctgtctttgtgaagccggcacggt
    CONSENSUS (SEQ ID NO:247) GCCGGAGGCGGGTGCGCTTACCTACCCTGTCTTTGTGAAGCCGGCACGGT

                                       410        420        430        440        450
 58 EFU81452 (SEQ ID NO:226)  caggttcgtcctttggcctaaccaaagtaaacggtacggaagaacttaac
 56 EFVANRES (SEQ ID NO:227)  caggttcgtcctttggcctaaccaaagtaaacggtacggaagaacttaac
 60 AY145441 (SEQ ID NO:228)  caggttcgtcctttggcgtaaccaaagtaaacggtacggaagaacttaac
 64 AF310953 (SEQ ID NO:229)  caggttcgtcctttggcctaaccaaagtaaacggtacggaagaacttaac
-59 EFU94526 (SEQ ID NO:230)  caggttcgtcctttggcgtaaccaaagtaaacggtacggaagaacttaac
-61 EFU94530 (SEQ ID NO:231)  caggttcgtcctttggcgtaaccaaagtaaacggtacggaagaacttaac
 63 EFA306726 (SEQ ID NO:232) caggttcgtcctttggcgtaaccaaagtaaacggtacggaagaacttaac
 31 AF550667 (SEQ ID NO:233)  caggttcgtcctttggcctaaccaaagtaaacggtacggaagaacttaac
 28 EFA306727 (SEQ ID NO:234) caggttcgtcctttggcgtaaccaaagtaaacggtacggaagaacttaac
 30 U00456 (SEQ ID NO:235)    caggttcgtcctttggcgtaaccaaagtaaacagtacggaagaactaaac
-27 EFU94528 (SEQ ID NO:236)  caggttcgtcctttggcgtaaccaaagtaaacggtacggaagaacttaac
 67 AF310955 (SEQ ID NO:237)  caggttcgtcctttggcgtaaccaaagtaaacggtccggaagaacttaac
 66 AF310957 (SEQ ID NO:238)  caggttcgtcctttggcgtaaccaaagtaaacggtccggaagaacttaac
 69 EFU72704 (SEQ ID NO:239)  caggttcgtcctttggcttaaccaaagtaaacggtacggaagaacttaac
-72 EFU94527 (SEQ ID NO:240)  caggttcgtcctttggcgtaaccaaagtaaacagtacggaagaactaaac
-62 EFU94529 (SEQ ID NO:241)  caggttcgtcctttggcgtaaccaaagtaaacggtacggaagaacttaac
 57 AF310956 (SEQ ID NO:242)  caggttcgtcctttggcctaaccaaagtaaacggtacggaagaacttaac
 65 AF310954 (SEQ ID NO:243)  caggttcgtcctttggcctaaccaaagtaaacggtacggaagaacttaac
 70 SBVANB2 (SEQ ID NO:244)   caggttcgtcctttggcgtaaccaaagtaaacggtacggaagaacttaac
 29 ENEVANB2A (SEQ ID NO:245) caggttcgtcctttggcgtaaccaaagtaaacggtacggaagaacttaac
 26 ENEVANB (SEQ ID NO:246)   caggttcgtcctttggcgtaaccaaagtaaacagtacggaagaactaaac
    CONSENSUS (SEQ ID NO:247) CAGGTTCGTCCTTTGGC-TAACCAAAGTAAACGGTACGGAAGAACTTAAC

                                       460        470        480        490        500
 58 EFU81452 (SEQ ID NO:226)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 56 EFVANRES (SEQ ID NO:227)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 60 AY145441 (SEQ ID NO:228)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 64 AF310953 (SEQ ID NO:229)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
-59 EFU94526 (SEQ ID NO:230)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
-61 EFU94530 (SEQ ID NO:231)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 63 EFA306726 (SEQ ID NO:232) gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 31 AF550667 (SEQ ID NO:233)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 28 EFA306727 (SEQ ID NO:234) gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 30 U00456 (SEQ ID NO:235)    gctgcgatagaagcagcaggacaatatgatggaaaaatcttaattgagca
-27 EFU94528 (SEQ ID NO:236)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 67 AF310955 (SEQ ID NO:237)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 66 AF310957 (SEQ ID NO:238)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 69 EFU72704 (SEQ ID NO:239)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
-72 EFU94527 (SEQ ID NO:240)  gctgcgatagaagcagcaggacaatatgatggaaaaatcttaattgagca
-62 EFU94529 (SEQ ID NO:241)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 57 AF310956 (SEQ ID NO:242)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 65 AF310954 (SEQ ID NO:243)  gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 70 SBVANB2 (SEQ ID NO:244)   gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 29 ENEVANB2A (SEQ ID NO:245) gctgcgatagaagcggcaggacaatatgatggaaaaatcttaattgagca
 26 ENEVANB (SEQ ID NO:246)   gctgcgatagaagcagcaggacaatatgatggaaaaatcttaattgagca
   CONSENSUS (SEQ ID NO:247)  GCTGCGATAGAAGCGGCAGGACAATATGATGGAAAAATCTTAATTGAGCA
```

```
                                        510        520        530        540        550
 58 EFU81452 (SEQ ID NO:226)  agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 56 EFVANRES (SEQ ID NO:227)  agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 60 AY145441 (SEQ ID NO:228)  agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 64 AF310953 (SEQ ID NO:229)  agcgatttcgggctgtgaggtcgggtgtgcggtcatgggaaacgaggatg
-59 EFU94526 (SEQ ID NO:230)  agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
-61 EFU94530 (SEQ ID NO:231)  agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 63 EFA306726 (SEQ ID NO:232) agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 31 AF550667 (SEQ ID NO:233)  agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 28 EFA306727 (SEQ ID NO:234) agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 30 U00456 (SEQ ID NO:235)    agcgatttcgggctgtgaggtcggctgcgcggtcatgggaaacgaggatg
-27 EFU94528 (SEQ ID NO:236)  agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 67 AF310955 (SEQ ID NO:237)  agcgatttcgggctgtgaggtcgggtgtgcggtcatgggaaacgaggatg
 66 AF310957 (SEQ ID NO:238)  agcgatttcgggctgtgaggtcgggtgtgcggtcatgggaaacgaggatg
 69 EFU72704 (SEQ ID NO:239)  agcgatttcgggctgtgaggtcggctgtgcggttatggggaacgaggatg
-72 EFU94527 (SEQ ID NO:240)  agcgatttcgggctgtgaggtcggctgcgcggtcatgggaaacgaggatg
-62 EFU94529 (SEQ ID NO:241)  agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 57 AF310956 (SEQ ID NO:242)  agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 65 AF310954 (SEQ ID NO:243)  agcgatttcgggctgtgaggtcgggtgtgcggtcatgggaaacgaggatg
 70 SBVANB2 (SEQ ID NO:244)   agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 29 ENEVANB2A (SEQ ID NO:245) agcgatttcgggctgtgaggtcgggtgtgcggtcatggggaacgaggatg
 26 ENEVANB (SEQ ID NO:246)   agcgatttcgggctgtgaggtcggctgcgcggtcatgggaaacgaggatg
    CONSENSUS (SEQ ID NO:247) AGCGATTTCGGGCTGTGAGGTCGGGTGTGCGGTCATGGG-AACGAGGATG

                                        560        570        580        590        600
 58 EFU81452 (SEQ ID NO:226)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 56 EFVANRES (SEQ ID NO:227)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 60 AY145441 (SEQ ID NO:228)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 64 AF310953 (SEQ ID NO:229)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
-59 EFU94526 (SEQ ID NO:230)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
-61 EFU94530 (SEQ ID NO:231)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 63 EFA306726 (SEQ ID NO:232) atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 31 AF550667 (SEQ ID NO:233)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 28 EFA306727 (SEQ ID NO:234) atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 30 U00456 (SEQ ID NO:235)    atttgattgtcggcgaagtggatcaaatccggttgagccacggtatcttc
-27 EFU94528 (SEQ ID NO:236)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 67 AF310955 (SEQ ID NO:237)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 66 AF310957 (SEQ ID NO:238)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 69 EFU72704 (SEQ ID NO:239)  atttgattgtcggcgaagtggatcaaatccggctgagccatggtatcttc
-72 EFU94527 (SEQ ID NO:240)  atttgattgtcggcgaagtggatcaaatccggttgagccacggtatcttc
-62 EFU94529 (SEQ ID NO:241)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 57 AF310956 (SEQ ID NO:242)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 65 AF310954 (SEQ ID NO:243)  atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 70 SBVANB2 (SEQ ID NO:244)   atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 29 ENEVANB2A (SEQ ID NO:245) atttgattgtcggcgaagtggatcaaatccggctgagccacggtatcttc
 26 ENEVANB (SEQ ID NO:246)   atttgattgtcggcgaagtggatcaaatccggttgagccacggtatcttc
    CONSENSUS (SEQ ID NO:247) ATTTGATTGTCGGCGAAGTGGATCAAATCCGGCTGAGCCACGGTATCTTC

                                        610        620        630        640        650
 58 EFU81452 (SEQ ID NO:226)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 56 EFVANRES (SEQ ID NO:227)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 60 AY145441 (SEQ ID NO:228)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 64 AF310953 (SEQ ID NO:229)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
-59 EFU94526 (SEQ ID NO:230)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
-61 EFU94530 (SEQ ID NO:231)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 63 EFA306726 (SEQ ID NO:232) cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 31 AF550667 (SEQ ID NO:233)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 28 EFA306727 (SEQ ID NO:234) cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 30 U00456 (SEQ ID NO:235)    cgcatccatcaggaaaacgagccggaaaaaggctcagagaatgcgatgat
-27 EFU94528 (SEQ ID NO:236)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 67 AF310955 (SEQ ID NO:237)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 66 AF310957 (SEQ ID NO:238)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 69 EFU72704 (SEQ ID NO:239)  cgcatccatcaggaaaacgagccggaaaaaggatcagagaatgcgatgat
-72 EFU94527 (SEQ ID NO:240)  cgcatccatcaggaaaacgagccggaaaaaggctcagagaatgcgatgat
-62 EFU94529 (SEQ ID NO:241)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 57 AF310956 (SEQ ID NO:242)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 65 AF310954 (SEQ ID NO:243)  cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 70 SBVANB2 (SEQ ID NO:244)   cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 29 ENEVANB2A (SEQ ID NO:245) cgcatccatcaggaaaacgagccggaaaaaggctcagaaaatgcgatgat
 26 ENEVANB (SEQ ID NO:246)   cgcatccatcaggaaaacgagccggaaaaaggctcagagaatgcgatgat
    CONSENSUS (SEQ ID NO:247) CGCATCCATCAGGAAAACGAGCCGGAAAAAGGCTCAGAAAATGCGATGAT

                                        660        670        680        690        700
 58 EFU81452 (SEQ ID NO:226)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
 56 EFVANRES (SEQ ID NO:227)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
 60 AY145441 (SEQ ID NO:228)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
 64 AF310953 (SEQ ID NO:229)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaagaga
```

```
-59 EFU94526 (SEQ ID NO:230)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
-61 EFU94530 (SEQ ID NO:231)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
 63 EFA306726 (SEQ ID NO:232) tacagttcccgcagacattccggtcgaggaacgaaaacgggtgcaggaaa
 31 AF550667 (SEQ ID NO:233)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
 28 EFA306727  (SEQ ID NO:234)tacagttcccgcagacattccggtcgaggaacgaaaacgggtgcaggaaa
 30 U00456 (SEQ ID NO:235)    tatcgttccagcagacattccggtcgaggaacgaaatcgggtgcaagaaa
-27 EFU94528 (SEQ ID NO:236)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
 67 AF310955 (SEQ ID NO:237)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaagaga
 66 AF310957 (SEQ ID NO:238)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaagaga
 69 EFU72704 (SEQ ID NO:239)  taccgttcctgcagacatcccagtcggggaacgaaatcgggtgcaggaaa
-72 EFU94527 (SEQ ID NO:240)  tatcgttccagcagacattccggtcgaggaacgaaatcgggtgcaagaaa
-62 EFU94529 (SEQ ID NO:241)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
 57 AF310956 (SEQ ID NO:242)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
 65 AF310954 (SEQ ID NO:243)  tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaagaga
 70 SBVANB2 (SEQ ID NO:244)   tacagttcccgcagacattccggtcgaggaacgaaatc
 29 ENEVANB2A (SEQ ID NO:245) tacagttcccgcagacattccggtcgaggaacgaaatcgggtgcaggaaa
 26 ENEVANB (SEQ ID NO:246)   tatcgttccagcagacattccggtcgaggaacgaaatcgggtgcaagaaa
    CONSENSUS (SEQ ID NO:247) TACAGTTCCCGCAGACATTCCGGTCGAGGAACGAAATCGGGTGCA-GAAA

                                    710       720       730       740
 58 EFU81452 (SEQ ID NO:226)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 56 EFVANRES (SEQ ID NO:227)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 60 AY145441 (SEQ ID NO:228)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 64 AF310953 (SEQ ID NO:229)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
-59 EFU94526 (SEQ ID NO:230)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
-61 EFU94530 (SEQ ID NO:231)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 63 EFA306726 (SEQ ID NO:232) cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 31 AF550667 (SEQ ID NO:233)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 28 EFA306727 (SEQ ID NO:234) cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 30 U00456 (SEQ ID NO:235)    cggcaaagaaagtatatcgggtgcttggatgcagagggctt
-27 EFU94528 (SEQ ID NO:236)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 67 AF310955 (SEQ ID NO:237)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 66 AF310957 (SEQ ID NO:238)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 69 EFU72704 (SEQ ID NO:239)  cggcaaagaaagtatatcgggcgcttggatgcagagggctt
-72 EFU94527 (SEQ ID NO:240)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
-62 EFU94529 (SEQ ID NO:241)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 57 AF310956 (SEQ ID NO:242)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 65 AF310954 (SEQ ID NO:243)  cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 29 ENEVANB2A (SEQ ID NO:245) cggcaaagaaagtatatcgggtgcttggatgcagagggctt
 26 ENEVANB (SEQ ID NO:246)   cggcaaagaaagtatatcgggtgcttggatgcagagggctt
    CONSENSUS (SEQ ID NO:247) CGGCAAAGAAAGTATATCGGGTGCTTGGATGCAGAGGGCTT
```

15 *VanC*

```
                                      10        20        30        40        50
24 AF162694 (SEQ ID NO: 248) gcttgatactcaaaatcaacagtcatcaatgcattctctacggcaaagaa
   CONSENSUS (SEQ ID NO:249) GCTTGATACTCAAAATCAACAGTCATCAATGCATTCTCTACGGCAAAGAA

                                      60        70        80        90       100
24 AF162694 (SEQ ID NO:248)  gttttcctgactcccattgagttcaaaatattgctttatttatttgagca
   CONSENSUS (SEQ ID NO:249) GTTTTCCTGACTCCCATTGAGTTCAAAATATTGCTTTATTTATTTGAGCA

                                     110       120       130       140       150
24 AF162694 (SEQ ID NO:248)  ccaaggatccgtcgtctcttccgaaacacttttcgaagcggtttggaaag
   CONSENSUS (SEQ ID NO:249) CCAAGGATCCGTCGTCTCTTCCGAAACACTTTTCGAAGCGGTTTGGAAAG

                                     160       170       180       190       200
24 AF162694 (SEQ ID NO:248)  aaaaatatttagataacaataatactgtcatggcacacattgctcgttta
   CONSENSUS (SEQ ID NO:249) AAAAATATTTAGATAACAATAATACTGTCATGGCACACATTGCTCGTTTA

                                     210       220       230       240       250
24 AF162694 (SEQ ID NO:248)  agagaaaaattgcatgaagaacctcgtaaacctaaattaatcaaaaccgt
   CONSENSUS (SEQ ID NO:249) AGAGAAAAATTGCATGAAGAACCTCGTAAACCTAAATTAATCAAAACCGT

                                     260       270       280       290       300
24 AF162694 (SEQ ID NO:248)  atgggggggtcggctatatcattgaaaaatagaaatcctttgatccgaaag
   CONSENSUS (SEQ ID NO:249) ATGGGGGGTCGGCTATATCATTGAAAAATAGAAATCCTTTGATCCGAAAG

                                     310       320       330       340       350
24 AF162694 (SEQ ID NO:248)  ctcttgacccaatacttcgtcaccactggaatcttgctggcattccttgt
   CONSENSUS (SEQ ID NO:249) CTCTTGACCCAATACTTCGTCACCACTGGAATCTTGCTGGCATTCCTTGT

                                     360       370       380       390       400
24 AF162694 (SEQ ID NO:248)  aatgattccattagtcattcgctttattgccggaacccggacttggtatg
   CONSENSUS (SEQ ID NO:249) AATGATTCCATTAGTCATTCGCTTTATTGCCGGAACCCGGACTTGGTATG


                                     410       420       430
24 AF162694 (SEQ ID NO:248)  gaacggaacctatctactatatcttacgttttttgcg
   CONSENSUS (SEQ ID NO:249) GAACGGAACCTATCTACTATATCTTACGTTTTTTTGCG
```

FIGURE 2-24

17 CACDR1

```
                                        10        20        30        40        50
 1 CACDR1 (SEQ ID NO: 250)      tctttttctattggttaatgtgtatttggtgtacatttgttatgtcccat
74 CDU439074 (SEQ ID NO: 251)   tctttttctattggttaatgtgtgtttggtgtacatttgttatgtcccat
75 CDU439073 (SEQ ID NO: 252)   tctttttctattggttaatgtgtgtttggtgtacatttgttatgtcccat
   CONSENSUS (SEQ ID NO: 253)   TCTTTTTCTATTGGTTAATGTGT-TTTGGTGTACATTTGTTATGTCCCAT

                                        60        70        80        90       100
 1 CACDR1 (SEQ ID NO: 250)      ttgtttagatccattggtgctgtttcaacatctatttctggtgccatgac
74 CDU439074 (SEQ ID NO: 251)   ttgtttagatccattggtgctgtttcaacatctattgctggtgctatgac
75 CDU439073 (SEQ ID NO: 252)   ttgtttagatccattggtgctgtttcaacatctattgctggtgctatgac
   CONSENSUS (SEQ ID NO: 253)   TTGTTTAGATCCATTGGTGCTGTTTCAACATCTATT-CTGGTGC-ATGAC

                                      110       120       130       140       150
 1 CACDR1 (SEQ ID NO: 250)      tcctgctaccgtgttgttattggctatggttatttatactgggttcgtta
74 CDU439074 (SEQ ID NO: 251)   ccctgctactgtgttgttattggctatggttatttacactgggttcgtta
75 CDU439073 (SEQ ID NO: 252)   ccctgctactgtgttgttattggctatggttatttacactgggttcgtta
   CONSENSUS (SEQ ID NO: 253)   -CCTGCTAC-GTGTTGTTATTGGCTATGGTTATTTA-ACTGGGTTCGTTA

                                      160       170       180       190       200
 1 CACDR1 (SEQ ID NO: 250)      tcccaactccaagtatgttgggttggtctcgatggattaattatattaac
74 CDU439074 (SEQ ID NO: 251)   tcccaactccaagtatgttgggttggtcaagatggattaattacatcaat
75 CDU439073 (SEQ ID NO: 252)   tcccaactccaagtatgttgggttggtcaagatggattaattacatcaat
   CONSENSUS (SEQ ID NO: 253)   TCCCAACTCCAAGTATGTTGGGTTGGTC--GATGGATTAATTA-AT-AA-

                                      210       220       230       240       250
 1 CACDR1 (SEQ ID NO: 250)      cctgttggttatgtgtttgaatcccttatggttaatgaattccacggtcg
74 CDU439074 (SEQ ID NO: 251)   cctgttggttatgtgtttgaagcgctcatggttaatgagttccatggtcg
75 CDU439073 (SEQ ID NO: 252)   cctgttggttatgtgttcgaagcgctcatggttaatgagttccatggtcg
   CONSENSUS (SEQ ID NO: 253)   CCTGTTGGTTATGTGTT-GAA-C-CT-ATGGTTAATGA-TTCCA-GGTCG

                                      260       270       280       290       300
 1 CACDR1 (SEQ ID NO: 250)      tgaattccaatgtgctcaatatgttccaagtggtccaggttatgaaaata
74 CDU439074 (SEQ ID NO: 251)   tgaattccaatgtgctcaatatgttccaagtggcccaggttttgaaaatg
75 CDU439073 (SEQ ID NO: 252)   tgaattccaatgtgctcaatatgttccaagtggcccaggttttgaaaatg
   CONSENSUS (SEQ ID NO: 253)   TGAATTCCAATGTGCTCAATATGTTCCAAGTGG-CCAGGTT-TGAAAAT-

                                      310       320       330       340       350
 1 CACDR1 (SEQ ID NO: 250)      tatcacgttcaaatcaagtgtgtactgcagtggggtctgttccaggtaat
74 CDU439074 (SEQ ID NO: 251)   tatcacgttcgaatcaagtgtgtactgcagttgggtctattccaggtaat
75 CDU439073 (SEQ ID NO: 252)   tatcacgttcgaatcaagtgtgtactgcagttgggtctattccaggtaat
   CONSENSUS (SEQ ID NO: 253)   TATCACGTTC-AATCAAGTGTGTACTGCAGT-GGGTCT-TTCCAGGTAAT

                                      360       370       380
 1 CACDR1 (SEQ ID NO: 250)      gaaatggttagtggtaccaattatttggctggtgctt
74 CDU439074 (SEQ ID NO: 251)   gaaatggttagtggtaccaattatttggctggtgctt
75 CDU439073 (SEQ ID NO: 252)   gaaatggttagtggtaccaattatttggctggtgctt
   CONSENSUS (SEQ ID NO: 253)   GAAATGGTTAGTGGTACCAATTATTTGGCTGGTGCTT
```

FIGURE 2-25

18 CAY1

```
                                          10        20        30        40        50
4 CAY16396 (SEQ ID NO: 254)    gccgattacaaaccaactcttgctgatgatacaagtataaattttgaaaa
7 CAY16404 (SEQ ID NO: 255)    gccgattacaaaccaactcttgctgatgatacaagtataaattttgaaaa
5 CAY16401 (SEQ ID NO: 256)    gccgattacaaaccaactcttgctgatgatacaagtataaattttgaaaa
3 CAY16399 (SEQ ID NO: 257)    gccgattacaaaccaactcttgctgatgatacaagtataaattttgaaaa
2 CAY16408 (SEQ ID NO: 258)    gccgattacaaaccaactcttgctgatgatacaagtataaattttgaaaa
8 CAY14703 (SEQ ID NO: 259)    gccgattacaaaccaactcttgctgatgatacaagtataaattttgaaaa
6 CAY16405 (SEQ ID NO: 260)    gccgattacaaaccaactcttgctgatgatacaagtataaattttgaaaa
  CONSENSUS (SEQ ID NO: 261)   GCCGATTACAAACCAACTCTTGCTGATGATACAAGTATAAATTTTGAAAA

                                          60        70        80        90       100
4 CAY16396 (SEQ ID NO: 254)    agaagaaatagataatcaaggtgaacccaattcaagtcaatcatcatctt
7 CAY16404 (SEQ ID NO: 255)    agaagaaatagataatcaaggtgaacccaattcaagtcaatcatcatctt
5 CAY16401 (SEQ ID NO: 256)    agaagaaatagataatcaaggtgaacccaattcaagtcaatcatcatctt
3 CAY16399 (SEQ ID NO: 257)    agaagaaatagataatcaaggtgaacccaattcaagtcaatcatcatctt
2 CAY16408 (SEQ ID NO: 258)    agaagaaatagataatcaaggtgaacccaattcaagtcaatcatcatctt
8 CAY14703 (SEQ ID NO: 259)    agaagaaatagataatcaaggtgaacccaattcaagtcaatcatcatctt
6 CAY16405 (SEQ ID NO: 260)    agaagaaatagataatcaaggtgaacccaattcaagtcaatcatcatctt
  CONSENSUS (SEQ ID NO: 261)   AGAAGAAATAGATAATCAAGGTGAACCCAATTCAAGTCAATCATCATCTT

                                         110       120       130       140       150
4 CAY16396 (SEQ ID NO: 254)    ctaataacacaatagtcgacaacaacaacaataataatgataatgatgtt
7 CAY16404 (SEQ ID NO: 255)    ccaataacacaatagtcgacaacaacaacaataataatgataatgatgtt
5 CAY16401 (SEQ ID NO: 256)    ccaataacacaatagtcggaaacaacaac***aataatgataatgatgtt
3 CAY16399 (SEQ ID NO: 257)    ctgataacacaatagtcgacaacaacaacaataataatgataatgatgtt
2 CAY16408 (SEQ ID NO: 258)    ccaataacacaatagtcggaaacaacaac***aataatgataatgatgtt
8 CAY14703 (SEQ ID NO: 259)    ccaataacacaatagtcgacaacaacaacaataataatgataatgatgtt
6 CAY16405 (SEQ ID NO: 260)    ctaataacacaatagtcggaaacaacaac***aataatgataatgatgtt
  CONSENSUS (SEQ ID NO: 261)   C-AATAACACAATAGTCG--AACAACAAC---AATAATGATAATGATGTT

                                         160       170       180       190       200
4 CAY16396 (SEQ ID NO: 254)    gatggagataaaatagttgtcacttgggatggtgatgatgatcccgaaaa
7 CAY16404 (SEQ ID NO: 255)    gatggagataaaatagttgtcacttgggatggtgatgatgatcccgaaaa
5 CAY16401 (SEQ ID NO: 256)    gatggagataaaatagttgtcacttgggatggtgatgatgatcccgaaaa
3 CAY16399 (SEQ ID NO: 257)    gatggagataaaatagttgtcacttgggatggtgatgatgatcccgaaaa
2 CAY16408 (SEQ ID NO: 258)    gatggagataaaatagttgtcacttgggatggtgatgatgatcccgaaaa
8 CAY14703 (SEQ ID NO: 259)    gatggagataaaatagttgtcacttgggatggtgatgatgatcccgaaaa
6 CAY16405 (SEQ ID NO: 260)    gatggaaataaaatagttgtcacttgggatggtgatgatgatcccgaaaa
  CONSENSUS (SEQ ID NO: 261)   GATGGAGATAAAATAGTTGTCACTTGGGATGGTGATGATGATCCCGAAAA

                                         210       220       230       240       250
4 CAY16396 (SEQ ID NO: 254)    ccctcaaaattggccaactttacaaaaagcatttttcattttccaaattt
7 CAY16404 (SEQ ID NO: 255)    ccctcaaaattggccaactttacaaaaagcatttttcattttccaaattt
5 CAY16401 (SEQ ID NO: 256)    ccctcaaaattggccaactttacaaaaagcatttttcattttccaaattt
3 CAY16399 (SEQ ID NO: 257)    ccctcaaaattggccaactttacaaaaagcatttttcattttccaaattt
2 CAY16408 (SEQ ID NO: 258)    ccctcaaaattggccaactttacaaaaagcatttttcattttccaaattt
8 CAY14703 (SEQ ID NO: 259)    ccctcaaaattggccaactttacaaaaagcatttttcattttccaaattt
6 CAY16405 (SEQ ID NO: 260)    ccctcaaaattggccaactttacaaaaagcatttttcattttccaaattt
  CONSENSUS (SEQ ID NO: 261)   CCCTCAAAATTGGCCAACTTTACAAAAAGCATTTTTCATTTTCCAAATTT

                                         260       270       280       290       300
4 CAY16396 (SEQ ID NO: 254)    catttttgacaacttcagtttatatgggatcagcagtttataccccctggt
7 CAY16404 (SEQ ID NO: 255)    catttttgacaacttcagtttatatgggatcagcagtttataccccctggt
5 CAY16401 (SEQ ID NO: 256)    catttttgacaacttcagtttatatgggatcagcagtttataccccctggt
3 CAY16399 (SEQ ID NO: 257)    catttttgacaacttcagtttatatgggatcagcagtttataccccctggt
2 CAY16408 (SEQ ID NO: 258)    catttttgacaacttcagtttatatgggatcagcagtttataccccctggt
8 CAY14703 (SEQ ID NO: 259)    catttttgacaacttcagtttatatgggatcagcagtttataccccctggt
6 CAY16405 (SEQ ID NO: 260)    catttttgacaacttcagtttatatgggatcagcagtttataccccctggt
  CONSENSUS (SEQ ID NO: 261)   CATTTTTGACAACTTCAGTTTATATGGGATCAGCAGTTTATACCCCTGGT

                                         310       320       330       340       350
4 CAY16396 (SEQ ID NO: 254)    attgaagaattaatgcatgattttggtattggaagagtcgtagctacatt
7 CAY16404 (SEQ ID NO: 255)    attgaagaattaatgcatgattttggtattggaagagtcgtagctacatt
5 CAY16401 (SEQ ID NO: 256)    attgaagaattaatgcatgattttggtattggaagagtcgtagctacatt
3 CAY16399 (SEQ ID NO: 257)    attgaagaattaatgcatgattttggtattggaagagtcgtagctacatt
2 CAY16408 (SEQ ID NO: 258)    attgaagaattaatgcatgattttggtattggaagagtcgtagctacatt
8 CAY14703 (SEQ ID NO: 259)    attgaagaattaatgcatgattttggtattggaagagtcgtagctacatt
6 CAY16405 (SEQ ID NO: 260)    attgaagaattaatgcatgattttggtattggaagagtcgtagctacatt
  CONSENSUS (SEQ ID NO: 261)   ATTGAAGAATTAATGCATGATTTTGGTATTGGAAGAGTCGTAGCTACATT
```

```
                                        360       370       380       390       400
4 CAY16396 (SEQ ID NO: 254)    acctttaacattatttgttattggttatggtgttggcccattggttttca
7 CAY16404 (SEQ ID NO: 255)    acctttaacattatttgttattggttatggtgttggcccattggttttca
5 CAY16401 (SEQ ID NO: 256)    acctttaacattatttgttattggttatggtgttggcccattggttttca
3 CAY16399 (SEQ ID NO: 257)    acctttaacattatttgttattggttatggtgttggcccattggttttca
2 CAY16408 (SEQ ID NO: 258)    acctttaacattatttgttattggttatggtgttggcccattggttttca
8 CAY14703 (SEQ ID NO: 259)    acctttaacattatttgttattggttatggtgttggcccattggttttca
6 CAY16405 (SEQ ID NO: 260)    acctttaacattatttgttattggttatggtgttggcccattggttttca
  CONSENSUS (SEQ ID NO: 261)   ACCTTTAACATTATTTGTTATTGGTTATGGTGTTGGCCCATTGGTTTTCA

                                        410       420       430       440       450
4 CAY16396 (SEQ ID NO: 254)    gtccgatgtcagaaaatgctatatttggtcgtacatccatatatatcata
7 CAY16404 (SEQ ID NO: 255)    gtccgatgtcagaaaatgctatatttggtcgtacatccatatatatcata
5 CAY16401 (SEQ ID NO: 256)    gtccgatgtcagaaaatgctatatttggtcgtacatccatatatatcata
3 CAY16399 (SEQ ID NO: 257)    gtccgatgtcagaaaatgctatatttggtcgtacatccatatatatcata
2 CAY16408 (SEQ ID NO: 258)    gtccgatgtcagaaaatgctatatttggtcgtacatccatatatatcata
8 CAY14703 (SEQ ID NO: 259)    gtccgatgtcagaaaatgctatatttggtcgtacatccatatatatcata
6 CAY16405 (SEQ ID NO: 260)    gtccgatatcagaaaatgctatatttggtcgtacatccatatatatcata
  CONSENSUS (SEQ ID NO: 261)   GTCCGATGTCAGAAAATGCTATATTTGGTCGTACATCCATATATATCATA

                                        460       470       480       490       500
4 CAY16396 (SEQ ID NO: 254)    acattatttttatttgtcatactacaaattcccactgctttggttaataa
7 CAY16404 (SEQ ID NO: 255)    acattatttttatttgtcatactacaaattcccactgctttggttaataa
5 CAY16401 (SEQ ID NO: 256)    acattatttttatttgtcatactacaaatccccactgctttggtaaataa
3 CAY16399 (SEQ ID NO: 257)    acattatttttatttgtcatactacaaattcccactgctttggttaataa
2 CAY16408 (SEQ ID NO: 258)    acattatttttatttgtcatactacaaatccccactgctttggtaaataa
8 CAY14703 (SEQ ID NO: 259)    acattatttttatttgtcatactacaaattcccactgctttggttaataa
6 CAY16405 (SEQ ID NO: 260)    acattatttttatttgtcatactacaaatccccactgctttggtaaataa
  CONSENSUS (SEQ ID NO: 261)   ACATTATTTTTATTTGTCATACTACAAAT-CCCACTGCTTTGGT-AATAA

                                        510       520       530       540       550
4 CAY16396 (SEQ ID NO: 254)    tattgctggtttatgtatattgagattcttgggtggattctttgctagtc
7 CAY16404 (SEQ ID NO: 255)    tattgctggtttatgtatattgagattcttgggtggattctttgctagtc
5 CAY16401 (SEQ ID NO: 256)    tattgccggtttatgtatattgagattcttgggtggattctttgctagtc
3 CAY16399 (SEQ ID NO: 257)    tattgctggtttatgtatattgagattcttgggtggattctttgctagtc
2 CAY16408 (SEQ ID NO: 258)    tattgccggtttatgtatattgagattcttgggtggattctttgctagtc
8 CAY14703 (SEQ ID NO: 259)    tattgctggtttatgtatattgagattctcgggtggattctttgctaatc
6 CAY16405 (SEQ ID NO: 260)    tattgccggtttatgtatattgagattcttgggtggattctttgctagtc
  CONSENSUS (SEQ ID NO: 261)   TATTGC-GGTTTATGTATATTGAGATTCTTGGGTGGATTCTTTGCTAGTC

                                        560       570       580       590       600
4 CAY16396 (SEQ ID NO: 254)    cttgtttggctactggtggtgcaagtgttgctgatgtggttaaattttgg
7 CAY16404 (SEQ ID NO: 255)    cttgtttggctactggtggtgcaagtgttgctgatgtggttaaattttgg
5 CAY16401 (SEQ ID NO: 256)    cttgtttggccactggtggtgctagtgttgctgatgtggttaaattttgg
3 CAY16399 (SEQ ID NO: 257)    cttgtttggctactggtggtgcaagtgttgctgatgtggttaaattttgg
2 CAY16408 (SEQ ID NO: 258)    cttgtttggccactggtggtgctagtgttgctgatgtggttaaattttgg
8 CAY14703 (SEQ ID NO: 259)    cttgtttggctactggtggtgcaagtgttgctgatgtggttaaattttgg
6 CAY16405 (SEQ ID NO: 260)    cttgtttggccactggtggtgctagtgttgctgatatggttaaattttgg
  CONSENSUS (SEQ ID NO: 261)   CTTGTTTGGC-ACTGGTGGTGC-AGTGTTGCTGATGTGGTTAAATTTTGG

                                        610       620       630       640       650
4 CAY16396 (SEQ ID NO: 254)    aatttaccagttgggttagccgcttggagtttgggtgccgtttgtggtcc
7 CAY16404 (SEQ ID NO: 255)    aatttaccagttgggttagccgcttggagtttgggtgccgtttgtggtcc
5 CAY16401 (SEQ ID NO: 256)    aatttaccagttgggttagccgcttggagtttgggtgctgtttgtggtcc
3 CAY16399 (SEQ ID NO: 257)    aatttaccagttgggttagccgcttggagtttgggtgccgtttgtggtcc
2 CAY16408 (SEQ ID NO: 258)    aatttaccagttgggttagccgcttggagtttgggtgctgtttgtggtcc
8 CAY14703 (SEQ ID NO: 259)    aatttaccagttgggttagccgcttggagtttgggtgccgtttgtggtcc
6 CAY16405 (SEQ ID NO: 260)    aatttaccagttgggttagccgcttggagtttgggtgctgtttgtggtcc
  CONSENSUS (SEQ ID NO: 261)   AATTTACCAGTTGGGTTAGCCGCTTGGAGTTTGGGTGC-GTTTGTGGTCC

                                        660       670       680       690       700
4 CAY16396 (SEQ ID NO: 254)    tagttttggtccattctttggttcaattttaactgtcaaagccagttgga
7 CAY16404 (SEQ ID NO: 255)    tagttttggtccattctttggttcaattttaactgtcaaagccagttgga
5 CAY16401 (SEQ ID NO: 256)    tagttttggtccattctttggttcaattttaactgtcaaagccagttgga
3 CAY16399 (SEQ ID NO: 257)    tagttttggtccattctttggttcaattttaactgtcaaagccagttgga
2 CAY16408 (SEQ ID NO: 258)    tagttttggtccattctttggttcaattttaactgtcaaagccagttgga
8 CAY14703 (SEQ ID NO: 259)    tagttttggtccattctttggttcaattttaactgtcaaagccagttgga
6 CAY16405 (SEQ ID NO: 260)    tagttttggtccattctttggttcaattttaactgtcaaagccagttgga
  CONSENSUS (SEQ ID NO: 261)   TAGTTTTGGTCCATTCTTTGGTTCAATTTTAACTGTCAAAGCCAGTTGGA
```

```
                                        710       720       730       740       750
4 CAY16396 (SEQ ID NO: 254)    gatggacttttttggttcatgtgtatcatttctgggttttcatttgttatg
7 CAY16404 (SEQ ID NO: 255)    gatggacttttttggttcatgtgtatcatttctgggttttcatttgttatg
5 CAY16401 (SEQ ID NO: 256)    gatggacttttttggttcatgtgtattatttctgggttttcatttgttatg
3 CAY16399 (SEQ ID NO: 257)    gatggacttttttggttcatgtgtatcatttctgggttttcatttgttatg
2 CAY16408 (SEQ ID NO: 258)    gatggacttttttggttcatgtgtattatttctgggttttcatttgttatg
8 CAY14703 (SEQ ID NO: 259)    gatggacttttttggttcatgtgtatcatttctgggttttcatttgttatg
6 CAY16405 (SEQ ID NO: 260)    gatggacttttttggttcatgtgtattatttctgggttttcatttgttatg
  CONSENSUS (SEQ ID NO: 261)   GATGGACTTTTTGGTTCATGTGTAT-ATTTCTGGGTTTTCATTTGTTATG

                                        760       770       780       790       800
4 CAY16396 (SEQ ID NO: 254)    ttgtgtttcactttacctgaaacttttggcaaaacattattatatcgcaa
7 CAY16404 (SEQ ID NO: 255)    ttgtgtttcactttacctgaaacttttggcaaaacattattgtatcgcaa
5 CAY16401 (SEQ ID NO: 256)    ttgtgtttcactttacctgaaacttttggcaaaacattattgtatcgcaa
3 CAY16399 (SEQ ID NO: 257)    ttgtgtttcactttacctgaaacttttggcaaaacattattatatcgcaa
2 CAY16408 (SEQ ID NO: 258)    ttgtgtttcactttacctgaaacttttggcaaaacattattgtatcgcaa
8 CAY14703 (SEQ ID NO: 259)    ttgtgtttcactttacctgaaacttttggcaaaacattattatatcgcaa
6 CAY16405 (SEQ ID NO: 260)    ttgtgtttcactttacctgaaacttttggcaaaacattattgtatcgcaa
  CONSENSUS (SEQ ID NO: 261)   TTGTGTTTCACTTTACCTGAAACTTTTGGCAAAACATTATT-TATCGCAA

                                        810       820       830       840       850
4 CAY16396 (SEQ ID NO: 254)    ggctaaaagattgagagccatcaccggtaacgacagaatcacaagtgaag
7 CAY16404 (SEQ ID NO: 255)    ggctaaaagattgagagccatcaccggtaacgacagaatcacaagtgaag
5 CAY16401 (SEQ ID NO: 256)    ggctaaaagattgagagccatcaccggtaacgacagaatcacaagtgaag
3 CAY16399 (SEQ ID NO: 257)    ggctaaaagattgagagccatcaccggtaacgacagaatcacaagtgaag
2 CAY16408 (SEQ ID NO: 258)    ggctaaaagattgagagccatcaccggtaacgacagaatcacaagtgaag
8 CAY14703 (SEQ ID NO: 259)    ggctaaaagattgagagccatcaccggtaacgacagaatcacaagtgaag
6 CAY16405 (SEQ ID NO: 260)    ggctaaaagattgagagccatcaccggtaacgacagaatcacaagtgaag
  CONSENSUS (SEQ ID NO: 261)   GGCTAAAAGATTGAGAGCCATCACCGGTAACGACAGAATCACAAGTGAAG

                                        860       870       880       890       900
4 CAY16396 (SEQ ID NO: 254)    gagaaattgaaaatagcaaaatgacaagtcatgaattgatcattgataca
7 CAY16404 (SEQ ID NO: 255)    gagaaattgaaaatagcaaaatgacaagtcatgaattgatcattgataca
5 CAY16401 (SEQ ID NO: 256)    gagaaattgaaaatagcaaaatgacaagtcatgaattgatcattgataca
3 CAY16399 (SEQ ID NO: 257)    gagaaattgaaaatagcaaaatgacaagtcatgaattgatcattgataca
2 CAY16408 (SEQ ID NO: 258)    gagaaattgaaaatagcaaaatgacaagtcatgaattgatcattgataca
8 CAY14703 (SEQ ID NO: 259)    gagaaattgaaaatagcaaaatgacaagtcatgaattgatcattgataca
6 CAY16405 (SEQ ID NO: 260)    gagaaattgaaaatagcaaaatgacaagtcatgaattgatcattgataca
  CONSENSUS (SEQ ID NO: 261)   GAGAAATTGAAAATAGCAAAATGACAAGTCATGAATTGATCATTGATACA

                                        910       920       930       940       950
4 CAY16396 (SEQ ID NO: 254)    ttatggaggccattagaaatcaccgttatggaaccagttgttctttttaat
7 CAY16404 (SEQ ID NO: 255)    ttatggagaccattagaaatcaccgttatggaaccagttgttctttttgat
5 CAY16401 (SEQ ID NO: 256)    ttatggagaccattagaaatcaccgttatggaaccagttgttctttttgat
3 CAY16399 (SEQ ID NO: 257)    ttatggaggccattagaaatcaccgttatggaaccagttgttctttttgat
2 CAY16408 (SEQ ID NO: 258)    ttatggagaccattagaaatcaccgttatggaaccagttgttctttttgat
8 CAY14703 (SEQ ID NO: 259)    ttatggaggccattagaaatcaccgttatggaaccagttgttctttttgat
6 CAY16405 (SEQ ID NO: 260)    ttatggagaccattagaaatcaccgttatggaaccagttgttctttttgat
  CONSENSUS (SEQ ID NO: 261)   TTATGGAG-CCATTAGAAATCACCGTTATGGAACCAGTTGTTCTTTTGAT

                                        960       970       980       990      1000
4 CAY16396 (SEQ ID NO: 254)    taacatttacattgccatggtgtacagtattctttacttgtttttcgaag
7 CAY16404 (SEQ ID NO: 255)    taacatttacattgccatggtgtacagtattctttacttgtttttcgaag
5 CAY16401 (SEQ ID NO: 256)    taacatttacattgccatggtgtacagtattctttacttgtttttcgaag
3 CAY16399 (SEQ ID NO: 257)    taacatttacattgccatggtgtacagtattctttacttgtttttcgaag
2 CAY16408 (SEQ ID NO: 258)    taacatttacattgccatggtgtacagtattctttacttgtttttcgaag
8 CAY14703 (SEQ ID NO: 259)    taacatttacattgccatggtgtacagtattctttacttgtttttcgaag
6 CAY16405 (SEQ ID NO: 260)    taacatttacattgccatggtgtacagtattctttacttgtttttcgaag
  CONSENSUS (SEQ ID NO: 261)   TAACATTTACATTGCCATGGTGTACAGTATTCTTTACTTGTTTTTCGAAG

                                       1010      1020      1030      1040      1050
4 CAY16396 (SEQ ID NO: 254)    ttttcccaatttatttcgttggagttaaacatttcaccctcgttgaattg
7 CAY16404 (SEQ ID NO: 255)    ttttcccaatttatttcgttggagttaaacatttcaccctcgttgaattg
5 CAY16401 (SEQ ID NO: 256)    ttttcccaatttatttcgttggagttaaacatttcaccctcgttgaattg
3 CAY16399 (SEQ ID NO: 257)    ttttcccaatttatttcgttggagttaaacatttcaccctcgttgaattg
2 CAY16408 (SEQ ID NO: 258)    ttttcccaatttatttcgttggagttaaacatttcaccctcgttgaattg
8 CAY14703 (SEQ ID NO: 259)    ttttcccaatttatttcgttggagttaaacatttcaccctcgttgaattg
6 CAY16405 (SEQ ID NO: 260)    ttttcccaatttatttcgttggagttaaacatttcaccctcgttgaattg
  CONSENSUS (SEQ ID NO: 261)   TTTTCCCAATTTATTTCGTTGGAGTTAAACATTTCACCCTCGTTGAATTG
```

```
                                        1060      1070      1080      1090      1100
4 CAY16396 (SEQ ID NO: 254)    ggtaccacatatatgtcgattgttattggtattgtcattgctgccttcat
7 CAY16404 (SEQ ID NO: 255)    ggtaccacatatatgtcgattgttattggtattgtcattgctgcctttat
5 CAY16401 (SEQ ID NO: 256)    ggtaccacatatatgtcgattgttattggtattgtcattgctgcctttat
3 CAY16399 (SEQ ID NO: 257)    ggtaccacatatatgtcgattgttattggtattgtcattgctgcctttat
2 CAY16408 (SEQ ID NO: 258)    ggtaccacatatatgtcgattgttattggtattgtcattgctgcctttat
8 CAY14703 (SEQ ID NO: 259)    ggtaccacatatatgtcgattgttattggtattgtcattgctgcctttat
6 CAY16405 (SEQ ID NO: 260)    ggtaccacatatatgtcgattgttattggtattgtcattgctgcctttat
  CONSENSUS (SEQ ID NO: 261)   GGTACCACATATATGTCGATTGTTATTGGTATTGTCATTGCTGCCTTTAT

                                        1110      1120      1130      1140      1150
4 CAY16396 (SEQ ID NO: 254)    ttatattccagttattagacaaaaattcaccaaaccaattttgcgtcaag
7 CAY16404 (SEQ ID NO: 255)    ttatattccagttattagacaaaaattcaccaaaccaattttgcgtcaag
5 CAY16401 (SEQ ID NO: 256)    ttatattccagttattagacaaaaattcaccaaaccaattttgcgtcaag
3 CAY16399 (SEQ ID NO: 257)    ttatattccagttattagacaaaaattcaccaaaccaattttgcgtcaag
2 CAY16408 (SEQ ID NO: 258)    ttatattccagttattagacaaaaattcaccaaaccaattttgcgtcaag
8 CAY14703 (SEQ ID NO: 259)    ttatattccagttattagacaaaaattcaccaaaccaattttgcgtcaag
6 CAY16405 (SEQ ID NO: 260)    ttatattccagttattagacaaaaattcaccaaaccaattttgcgtcaag
  CONSENSUS (SEQ ID NO: 261)   TTATATTCCAGTTATTAGACAAAAATTCACCAAACCAATTTTGCGTCAAG

                                        1160      1170      1180      1190      1200
4 CAY16396 (SEQ ID NO: 254)    aacaggttttccccgaagtgtttattccaattgccattgttggtggtatc
7 CAY16404 (SEQ ID NO: 255)    aacaggttttccccgaagtatttattccaattgccattgttggtggtatc
5 CAY16401 (SEQ ID NO: 256)    aacaggttttccccgaagtntttattccaatngccattgttggtggtatc
3 CAY16399 (SEQ ID NO: 257)    aacaggttttccccgaagtgtttattccaattgccattgttggtggtatc
2 CAY16408 (SEQ ID NO: 258)    aacaggttttccccgaagtgtttattccaattgccattgttggtggtatc
8 CAY14703 (SEQ ID NO: 259)    aacaggttttccccgaagtgtttattccaattgccattgttggtggtatc
6 CAY16405 (SEQ ID NO: 260)    aacaggttttccccgaagtgtttattccaattgccattgttggtggtatc
  CONSENSUS (SEQ ID NO: 261)   AACAGGTTTTCCCCGAAGTGTTTATTCCAATTGCCATTGTTGGTGGTATC

                                        1210      1220      1230      1240      1250
4 CAY16396 (SEQ ID NO: 254)    ttgttaacttcaggtcttttcatttttggttggtcagcaaatagaaccac
7 CAY16404 (SEQ ID NO: 255)    ttgttaacttcaggtctctccatttatggttggtcagcaaataaaaccac
5 CAY16401 (SEQ ID NO: 256)    ttgttaacttcaggtcttttcatttttggttgggcagcaaatagaaccac
3 CAY16399 (SEQ ID NO: 257)    ttgttaacttcaggtcttttcatttttggttggtcagcaaatagaaccac
2 CAY16408 (SEQ ID NO: 258)    ttgttaacttcaggtcttttcatttttggttgggcagcaaatagaaccac
8 CAY14703 (SEQ ID NO: 259)    ttgttaacttcaggtcttttcatttttggttggtcagcaaatagaaccac
6 CAY16405 (SEQ ID NO: 260)    ttgttaacttcaggtcttttcatttttggttggtcagcaaatagaaccac
  CONSENSUS (SEQ ID NO: 261)   TTGTTAACTTCAGGTCTTTTCATTTTTGGTTGG-CAGCAAATAGAACCAC

                                        1260      1270      1280      1290      1300
4 CAY16396 (SEQ ID NO: 254)    tcattgggtgggtccattgtttggtgctgctactactgcttctggtgcat
7 CAY16404 (SEQ ID NO: 255)    tcattgggtgggtccattgtttggtgctgctactactgcttctggtgcat
5 CAY16401 (SEQ ID NO: 256)    tcattgggtgggtccattgtttggtgctgctactactgcttctggtgcat
3 CAY16399 (SEQ ID NO: 257)    tcattgggtgggtccattgtttggtgctgctactactgcttctggtgcat
2 CAY16408 (SEQ ID NO: 258)    tcattgggtgggtccattgtttggtgctgctactactgcttctggtgcat
8 CAY14703 (SEQ ID NO: 259)    tcattgggtgggtccattgtttggtgctgctactactgcttctggtgcat
6 CAY16405 (SEQ ID NO: 260)    tcattgggttggtccattgtttggtgctgccactactgcttctggtgcat
  CONSENSUS (SEQ ID NO: 261)   TCATTGGGTGGGTCCATTGTTTGGTGCTGCTACTACTGCTTCTGGTGCAT

                                        1310      1320      1330      1340      1350
4 CAY16396 (SEQ ID NO: 254)    ttttgattttccaaacattattcaatttcatgggtgcttcatttaagcct
7 CAY16404 (SEQ ID NO: 255)    ttttgattttccaaacattattcaatttcatgggtgcttcatttaagcct
5 CAY16401 (SEQ ID NO: 256)    ttttgattttccaaacattattcaatttcatgggtgcttcatttaagcct
3 CAY16399 (SEQ ID NO: 257)    ttttgattttccaaacattattcaatttcatgggtgcttcatttaagcct
2 CAY16408 (SEQ ID NO: 258)    ttttgattttccaaacattattcaatttcatgggtgcttcatttaagcct
8 CAY14703 (SEQ ID NO: 259)    ttttgattttccaaacattattcaatttcatgggtgcttcatttaagcct
6 CAY16405 (SEQ ID NO: 260)    ttttgattttccaaacattattcaatttcatgggtgcttcatttaagcct
  CONSENSUS (SEQ ID NO: 261)   TTTTGATTTTCCAAACATTATTCAATTTCATGGGTGCTTCATTTAAGCCT

                                        1360      1370      1380      1390      1400
4 CAY16396 (SEQ ID NO: 254)    cattatattgcttcagtttttgcatcaaatgatttgttcagatcagtcat
7 CAY16404 (SEQ ID NO: 255)    cattatattgcttcagtttttgcatcaaatgatttgttcagatcagtcat
5 CAY16401 (SEQ ID NO: 256)    cattatattgcttctgtttttgcatcaaatgatttgttcagatcagtcat
3 CAY16399 (SEQ ID NO: 257)    cattatattgcttcagtttttgcatcaaatgatttgttcagatcagtcat
2 CAY16408 (SEQ ID NO: 258)    cattatattgcttctgtttttgcatcaaatgatttgttcagatcagtcat
8 CAY14703 (SEQ ID NO: 259)    cattatattgcttcagtttttgcatcaaatgatttgttcagatcagtcat
6 CAY16405 (SEQ ID NO: 260)    cactatattgcttcagtttttgcatcaaatgatttgttcagatcagtcat
  CONSENSUS (SEQ ID NO: 261)   CATTATATTGCTTC-GTTTTTGCATCAAATGATTTGTTCAGATCAGTCAT
```

FIGURE 2-29

```
                                        1410      1420      1430      1440      1450
4 CAY16396 (SEQ ID NO: 254)    tgcatcagtgttcccattatttggtgctcctttgtttgacaatttggcta
7 CAY16404 (SEQ ID NO: 255)    tgcatcagtgttcccattatttggtgctcctttgtttgacaatttggcta
5 CAY16401 (SEQ ID NO: 256)    tgcttcagtgttcccattatttggtgctcctttgtttgacaatttggcta
3 CAY16399 (SEQ ID NO: 257)    tgcatcagtgttcccattatttggtgctcctttgtttgacaatttggcta
2 CAY16408 (SEQ ID NO: 258)    tgcttcagtgttcccattatttggtgctcctttgtttgacaatttggcta
8 CAY14703 (SEQ ID NO: 259)    tgcatcagtgttcccattatttggtgctcctttgtttgacaatttggcta
6 CAY16405 (SEQ ID NO: 260)    tgcatcagtgttcccattatttggtgctcctttgtttgacaatttggcca
  CONSENSUS (SEQ ID NO: 261)   TGC-TCAGTGTTCCCATTATTTGGTGCTCCTTTGTTTGACAATTTGGCTA

                                        1460      1470      1480      1490      1500
4 CAY16396 (SEQ ID NO: 254)    cccctgaatatccagttgcttggggtagttccgtgttgggtttcatcacc
7 CAY16404 (SEQ ID NO: 255)    cccctgaatatccagttgcttggggtagttccgtgttgggtttcatcacc
5 CAY16401 (SEQ ID NO: 256)    cccctgaatatccagttgcttggggtagttccgtgttgggtttcatcacc
3 CAY16399 (SEQ ID NO: 257)    cccctgaatatccagttgcttggggtagttccgtgttgggtttcatcacc
2 CAY16408 (SEQ ID NO: 258)    cccctgaatatccagttgcttggggtagttccgtgttgggtttcatcacc
8 CAY14703 (SEQ ID NO: 259)    cccctgaatatccagttgcttggggtagttccgtgttgggtttcatcacc
6 CAY16405 (SEQ ID NO: 260)    cccctgaatatccagttgcttggggtagttccgtgttgggtttcatcacc
  CONSENSUS (SEQ ID NO: 261)   CCCCTGAATATCCAGTTGCTTGGGGTAGTTCCGTGTTGGGTTTCATCACC

                                        1510      1520      1530      1540      1550
4 CAY16396 (SEQ ID NO: 254)    cttgttatgattgctattccagttttgttttacttgaacggaccaaaatt
7 CAY16404 (SEQ ID NO: 255)    cttgttatgattgctattccagttttgttttacttgaacggaccaaaatt
5 CAY16401 (SEQ ID NO: 256)    cttgttatgattgctattccagttttgttttacttgaacggaccaaaatt
3 CAY16399 (SEQ ID NO: 257)    cttgttatgattgctattccagttttgttttacttgaacggaccaaaatt
2 CAY16408 (SEQ ID NO: 258)    cttgttatgattgctattccagttttgttttacttgaacggaccaaaatt
8 CAY14703 (SEQ ID NO: 259)    cttgttatgattgctattccagttttgttttacttgaacggaccaaaatt
6 CAY16405 (SEQ ID NO: 260)    cttgttatgattgctattccagttttgttttacttgaacggaccaaagtt
  CONSENSUS (SEQ ID NO: 261)   CTTGTTATGATTGCTATTCCAGTTTTGTTTTACTTGAACGGACCAAAATT
```