Biofilm formation (slime production) plays an important role in the pathogenesis of infections caused by different microorganisms . Samples collected from denture and orthodontic devices were diagnosed genetically after cultured and diagnostic microscopy using 16SrDNA sequencing from both devices. 16SrDNA sequence database provides high quality excellent identification at the species and subspecies levels. Screened these bacterial isolates for ability to form biofilm formation using CRA test, TCP test and icaAD gene test found gene test 100% was the best test for identified bacterial species to form biofilm for both devices . Moreover, in the present study four bacterial strains were recorded in European Nucleotide Archive (ENA), National Centre for Biotechnology (NCBI) and GeneBank as new strains in world and registered in the name of Iraq / Basrah.

Lecturer Kholoud Abdul Kareem Hussein has obtained her M.Sc. degree in Molecular Genetic of Medical Microbiology in 2013 from Basrah University , Science college, Biology department.

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Genetic Study of Biofilm Forming Bacteria

Hussein

Kholoud Abdul Kareem Hussein

Study Biofilm of Bacteria Isolates, Identified by16srRNA Gene Sequencing

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Kholoud

Summary

One hundred samples were collected from patients wearing dentures (n=50) using sterile cotton swabs and orthodontic devices (n=50) using sterile needle Under the supervision of a specialist doctor from the center of Al-shaheed Qais dental and private clinics in Basrah. All samples were collected randomly from both genders aged between 12-70 years.

The bacterial species were identified by molecular diagnosis using *16SrDNA* sequencing for only 94 bacterial samples from patient wearing denture (n=47) and orthodontic devices (n=47) revealing the following species in patient wearnig denture : *Klebsiella pneumoniae* [8(40%)], *Proteus mirabilis* [7(35%)] , *Proteus penneri* [5(25%)] , *Enterobacter cloacae* [3(15%)], *morganella morganii* [2(10%)], *Hafnia alvei* [2(10%)], *Enterobacter aerogenes* [2(10%)],*Enterococcus faecalis* [1(5%)] , *Enterobacter faecium* [1(5%)], *Bacillus cereus*[1(5%)], *Enterobacter mori* [1(5%)] and *Citrobacter freundii* [1(5%)],Some of these bacterial species were isolated at first time in the world from patient wearing denture as : *Proteus houseri* [1(5%)], *Klebsiella variicala* [1(5%)], *Lactococcus lactis* [1(5%)], *Streptococcus equinus* [1(5%)], *Acinetobacter baumannii* [1(5%1)], *Chryseobacterium vietnamense* [1(5%)], *Klebsiella oxytoca* [1(5%)], and *Staphylococcus hominis* [1(5%)]. But the following species from patient wearing orthodontic devices : *Klebsiella pneumoniae* [8(40%)] , *Staphylocpccus aureus* [7 (35%)], *Bacillus cereus*[4(20%)], *Enterobacter cloacae* [3(15%)], *Enterococcus faecalis* [3(15%)], *Staphylococcus epidremidis* [2(10%)], *Proteus penneri* [2(10%)], *Enterobacter faecium* [2(10%)], *Enterobacter mori* [1(5%)], *Citrobacter freundii* [1(5%)], *Staphylococcus worneri* [1(5%)] and

Serratia marcescens [1(5%)].Some of these bacterial species were isolated at first time in the world from patient wearing orthodontic devices as: *Staphylococcus pasteuri* [1(5%)], *Enerobacter ludwigii* [1(5%)], *Lactobacillus plantarum* [2(10%)], *Streptococcus anginosus* [2(10%)], *Pediococcus acidilactici* [1(5%)], *Bacillus subtilis* [2(10%)], *Escherichia fergusonii* [1(5%)], and *Proteus mirabilis* [1(5%)]. Furthermore, *Proteus penneri, Enterobacter mori* and *Citrobacter freundii* in both patient wearing denture and orthodontic devices were isolated at the first time.

The rooted neighbour joining (NJ) phylogenetic tree of isolates from present study (n=28) with 28 type strains from GeneBank showed that *Enterobacter cloacae* is the out group (root).Moreover, four bacterial strains were recorded in European Nucleotide Archive (ENA),National Centre for Biotechnology Information (NCBI) and Gene Bank as new strains in the world, these are: 71-*Chryseobacterium vietnamense* "IRQBAS3" (HG003648) and 74-*Morganella morganii* "IRQBAS4" (HG003649) isolated from patient wearing dentures, and 7-*Enterobacter ludwigii* "IRQBAS1" (HG003646), and 34-*Enterobacter cloacae* "IRQBAS2" (HG003647) isolated from patient wearing orthodontic devices . All these strains showed 99% sequence identity with their reference due to occur of point or frame shift mutation.

Biofilm formation of bacterial isolates from patient wearing dentures (n=47) and patient wearing orthodontic devices (n=47) were screened by Congo red agar (CRA) ,tissue culture plate (TCP) and *icaAD* gene method. In patient wearing dentures, CRA method appeared the frequency of negative isolates 37(78.7%) of 47 isolates was higher than positive isolates 8(17.02%) of 47 isolates with high significant ($p \leq 0.01$) , and higher than intermediate 2(4.3%) of 47 isolates with high

significant (p≤ 0.01), while frequency of positive isolates was higher than intermediate isolates with high significant (p ≤0.01).

The frequency in patient wearing orthodontic devices recovered very different results : 4(8.5%) of 47 isolates appeared positive result , 2(4.3%) of 47 isolates appeared intermediate result. In contrast, frequency of positive results was higher than intermediate with high significant (p≤0.01). 41(87.2%) of 47 isolates appeared negative results and frequency of this result was higher than positive and intermediate with high significant (p≤0.01). No significant differences were appeared between patient wearing dentures and orthodontic devices results for each test (positive, intermediate and negative) .

TCP method was recovered in patient wearing dentures, frequency of weak positive results [29(61.7%) of 47 isolate] appeared to be higher than high [8(17.02%) of 47 isolates] and moderate [7(14.9%) of 47 isolates] positive results with high significant difference (p≤0.01) , 3(6.4%) of 47 isolates showed negative results . However , the frequency of positive isolates 44(94%) of 47 isolates (high, moderate ,and weak) was higher (p≤0.01) than negative results.

The TCP method for patient wearing orthodontic devices , recovered that the weak positive [9(19.2%) of 47 isolates] result is higher than positive[2(4.3%) of 47 isolates] with high significant difference (p≤0.01). Furthermore, 36(76.6%) of 47 isolates showed negative results with high significant (p≤0.01) than positive (high, moderate and weak) results. However, frequency of positive result (high, moderate and weak) in patient wearing dentures was higher (p≤0.01) than in patient wearing orthodontic devices . Following, the frequency of negative result in patient wearing orthodontic devices is higher (p≤0.01) than inpatient wearing dentures .

icaAD gene method for isolates of patient wearing dentures showed that the present of *icaA* [37(78.7%) of 47 isolates] results was higher than the absent of *icaA* [10(21.3%) of 47 isolates] gene with high significant difference ($p \leq 0.01$). *icaD* gene was recovered 40(85.1%) of 47 isolates as positive results with high significant difference ($p \leq 0.01$) than negative results 7(14.9%) of 47 isolates.

In patient wearing orthodontic devices , the frequency of *icaA*[2(4.3%) of 47 isolates] gene negative results was higher than *icaA*[45 (95.8%) of 47 isolates] gene positive results with high significant difference ($p \leq 0.01$). While, the *icaD* gene was recovered 24(51.1%) of 47 isolates as positive results and 23(48.9%) of 47 isolates as negative results but without significant difference . Comparing ,in patient wearing dentures, TCP 44(93.6) and *icaA* and /or *icaD* gene 47(100%) are the best methods for detection of biofilm formation (no significant differences between these results), on the other hands, *icaA* and /or *icaD* gene were only the best method for detection biofilm formation in patient wearing orthodontic devices .

The frequency of bacteria was higher ($p \leq 0.01$) with patients aged >35 (70.1%), denture washing (in day) < 2 time (61.7%), without tonsillitis (100%), without gingivitis (100%), no cigarettes smoking (95.7%) and without dental caries (95.7%), but no significant difference with date of denture wearer (year). In orthodontic , the frequency of bacteria was higher ($p \leq 0.01$) in patients aged <18 (78.7%) , orthodontic washing > 2(68.1%),tonsillitis (100%) , gingivitis (70.2%) , no cigarettes smocking (100%),without dental caries (100%), but no significant differences in patients with date of orthodontic insertion factor.

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Abbreviations

Bp	Base pair
C	Celsius
CRA	Congo Red Agar
D.W.	Distal water
DNA	Deoxy ribonucleic acid

dNTPs	Deoxy ribonucleotide triphosphate
EDTA	Ethylene Diamine Tetra Acetic acid
ELISA	Enzyme Linked Immunosorbent Assay test
F	Forward
hr	Hour
Kb	Kilobase
min	Minute
ml	milliliter
NCBI	National Center for Biotechnology
Ng	Nanogram
No.	Number
OD	Optical density
PBS	Phosphate buffer Saline
PCR	Polymerase Chain Reaction
PEG	Poly Ethylene Glycol
pH	Power of hydrogen
pmol	Pico mole
R	Reverse
Sec	Second
TCP	Tissue Culture Plate
Tm	Melting temperature
µl	Microliter

µm	Micrometer
UV	Ultraviolet
V	Volt
µg	Microgram
ica	Intra cellular adhesion
16S rDNA	Sixteen subunit ribosomal deoxyribonucleic acid

Chapter one

Introduction

Oral cavity is one of the most complex microbial habitats in the human body that comprises of more than 600 diverse arrays of bacterial species (Kazor *et al*., 2003). Oral microbiota beside its importance in oral health reflects the health and disease status of the host as it effects many other systemic diseases like bacterial endocarditis, pneumonia, preterm low birth weight and coronary heart disease gastrointestinal infection and chronic obstructive pulmonary (Thean *et al*., 2007). Among many oral the dental caries and periodontal disease are the most common causes of tooth loss (Bowley, 2002 ; Petersen *et al*., 2005). Tooth loss can result in diminished function, unbalanced diet, malnutrition,(Wöstman *et al*., 2005), as well as loss of self-esteem(Jones *et al*., 2003).Furtheremore, dental caries and periodontal diseases have been historically considered the most important global oral health burdens, at present, the distribution and severity of oral diseases vary in different parts of the world and within the same country or region (Moimaz *et al*., 2006).

Dental caries are commonly known as tooth decay However, it has been known for over 100 years that dental decay is caused by bacteria fermenting foods, producing acids and dissolving tooth mineral (Featherstone, 2008). At least two major groups of bacteria, namely the mutans streptococci and the lactobacilli species, are able to produce organic acids during metabolism of fermentable carbohydrates by these bacteria (Loesche, 1986; Marsh,1994) Furthermore, *Lactobacillus acidophilus* , and *Actinomyces viscosus* may be considered the main pathogenic species

involved in the initiation and development of dental caries (Shivakumar *et al*., 2009).Periodontal disease is one of the most Common diseases of man and is responsible for most of the tooth loss in adults, bacterial species associated with periodontitis are *Porphyromonas gingivalis* , *Tannerella forsythia* and *Treponema denticola , Aggregatibacter actinomycetemcomitans*, associated with localized aggressive periodontitis, some Gram-positive species, such as *Peptostreptococcus micros* (Socransky *et al.*, 1998).

Oral health status declines with age and as a result the need for removable prostheses increases, denture usually made from poly methylmethacrylate (PMMA) materials called resin , these prostheses are generally attached to the remaining natural teeth by clasps that hold the denture in place (Jagger, 2002).Wearing removable dental prosthesis causes an alteration in the oral micro flora (Girard *et al*., 1996). and dentures offer a reservoir for microorganisms associated with more systematic disease infections (Li *et al*., 2000). There are three types of denture these are: Removable partial dentures, Removable complete dentures , Implant over denture (Pahlevan, 2005 ; Singla, 2007 ;Vecchiatini *et al.*, 2009). Oral cavity health is closely related with the dentures the patient wears, the latter cause retention of food particles,

formation of plague, as well as inflammation of oral cavity and periodontium, both, removable and fixed dentures, may to a great extent cause problems of bad breath, although the source of unpleasant breath is commonly related to location of bacteria colonies on the tongue, in pathological gingival pockets, on teeth and adjacent tissue (Jeng *et al*., 1999) . The amount of cariogenic bacteria in persons with fixed prostheses is different from that of elderly persons with removable dentures (Tanaka

et al., 2003) There is an increase in the number of risk factors of oral diseases and missing teeth MT in the elderly, the type of prosthesis was decided by the number of MT in most cases, on the other hands , orthodontic treatment with fixed appliances resistance to undesirable tooth movement leads to increase biofilm accumulation and elevated levels of cariogenic and periodontal bacteria , the microbiological changes after bracket placement became a topic of interest during the late 1980, mainly because orthodontic brackets make good oral hygiene difficult, resulting in plaque accumulation and significantly increased risks for enamel demineralization or periodontal disease (Pellegrini *et al*., 2009).Initially cariogenic species such as Streptococcus mutans and Lactobacillus species and the subsequent decalcification of enamel were the main fields of interest among investigators (Forsberg *et al*., 1991; Rosenbloom and Tinanoff, 1991). Later on, the more complex system of periodontopathogenic microbes and the changes after bracket placement became the main topics of interest (Paolantonio *et al*., 1996; Paolantonio *et al*., 1999; Petti *et al*., 1997). Naranjo *et al*., (2006) observed a transition in subgingival dental plaque after the placement of brackets, the plaque index and gingivitis index increased significantly (Papaioannou *et al* ., 2007 ; . Pandis *et al*., 2008).The presence of denture and orthodontic in mouth may lead to increase denture and dental plaque **,** dental plaque is a highly complex biofilm ,biofilm formation capacity is associated with antimicrobial resistance, and considered widely as a virulence factor (Forsberg *et al*., 1991 ; Nikawa *et al*., 1998 ; Marsh, 2005). Invasive isolates are more prone to produce biofilm than carriage isolates of healthy individuals (de Silva *et al*.,2002 ; Peetermans *et al*., 2003).The principal component of biofilm is a polysaccharide intercellular adhesin {PIA} (Ziebuhr *et al*., 1997; Lappin-Scott *et al*., 2001). PIA is composed of a beta-1,6-N-acetylglucosamine polymer synthesized by an enzyme

codified by the *ica* operon found on the bacterial chromosome, that includes a regulating element of four genes "*A*, *B*, *C*, and *D* " (Kozitskaya *et al*., 2004). It is known that the *icaA* gene codifies the N-acetylglucosamyl transferase enzyme responsible for synthesizing PIA, this enzyme is not very active *in vitro*, but co-expression of the *icaD* gene increases the activity, *IcaB* is the deacetylase responsible for the deacetylation of mature PIA and the transmembrane protein *IcaC* seems to be involved in externalization and elongation of the growing polysaccharide (Gerke *et al*.,1998 ; Scott *et al*., 2001).

Since the discovery of the polymerase chain reaction (PCR) and DNA sequencing, comparisons of the gene sequences of bacterial species have shown that the 16S ribosomal RNA (rRNA) gene has been widely used to study prokaryote diversity and allows for the identification and prediction
of phylogenetic relationships (Weisburg *et al*., 1999).

1-2- Aims of the study

Because of increased the problems of bacteria associated with presence of denture and orthodontic in mouth and causes other systematic diseases, the present study was designed to achieve the following aims**:**

- Genetic identification all different bacterial species from denture and orthodontic without focusing on a limited type listed in previous studies .
- Comparison between the bacterial species and their frequencies in dentures and orthodontic sources.
- Looking for new strains in these two sources , as a result of the limited precise identification methods in previous studies especially in Iraq.
- detection the ability of bacteria to produce biofilm and thus ability. on adhesion . Furthermore, which the best type for biofilm forming test.
- comparison among the best test to detect biofilm formation.
- Detect which the best test for biofilm formation to each identified species.

Chapter two

Literature Review

2-1- The role of oral cavity in disease:-

The oral cavity as an integral part of the digestive system has various specific functions , the impact of common oral diseases extends beyond the oral cavity (Thorstensson and Johansson, 2009). Oral infection has been found to be associated with death risk in studies among middle-aged individuals (Soikkonen *et al*., 2000; Jansson *et al*., 2002). The relative importance of oral health as a predictor of survival has also been analyzed and the common oral diseases have shown significant influence on survival (Semba *et al*., 2006; Morita *et al*., 2006).

2-2- Common oral diseases:-

Dental caries and periodontal disease are the most common bacterial diseases of man which result from an interaction between a susceptible host, commensal microbiota and the environment, Although some specific microorganisms have been implicated in the pathogenesis of these conditions, it is now recognized that they are not classical infectious diseases but rather a complex of diseases resulting from a breakdown in the homeostasis between the human host and microbiota (Stamatova, 2010).

2-2-1- Dental caries :-

Dental caries can be defined as localised destruction of the tissues of the tooth by acids generated from bacterial fermentation of dietary carbohydrates

(Marsh,1994). Caries is a result of the complex interaction between carbohydrates in food and cariogenic microorganisms in oral biofilms, influenced by the quality and quantity of saliva and clinically manifested by demineralization and destruction of dental hard tissues(Stamatova , 2010). The development in molecular analyses have shown that all the bacteria that have been associated with caries belong to the normal microbiota of the oral cavity and dental caries is regarded as an endogenous infection (Takahashi and Nyvad , 2008).

The ecological plaque hypothesis caries is a result of a shift in the balance of resident microbiota driven by changes in local environmental conditions, it is generally believed that all three parameters (microorganisms, host and environment) must "act" simultaneously for carious lesions to develop and progress to become visually detectable (Aas *et al*., 2008). Wide group of microorganisms are identified from carious lesions of which *Streptococcus mutans* , *Lactobacillus acidophilus* and *Actinomyces viscosus* may be considered the main pathogenic species involved in the initiation and development of dental caries (Shivakumar *et al*., 2009). *Streptococcus mutans*, initially isolated in 1924,has been primarily implicated in this disease and extensively studied throughout several decades (Loesche, 1986) .According to (Belli and Marquis, 1991; Li and Burne, 2001; Kuramitsu, 2003; Scheie and Petersen, 2004) Some significant virulent traits of *S.mutans* that contribute to caries initiation and progression are :-

A- Initiation of biofilm formation by adherence and accumulation on the tooth surface that is promoted by its synthesis of insoluble, extracellular polysaccharides.

B- Production of numerous bacteriocins that kill other species, favouring its competition in dental biofilms.

C- High efficiency in catabolizing carbohydrates and producing acids.

D- The ability to tolerate low pH . fig.(2-1)**.**

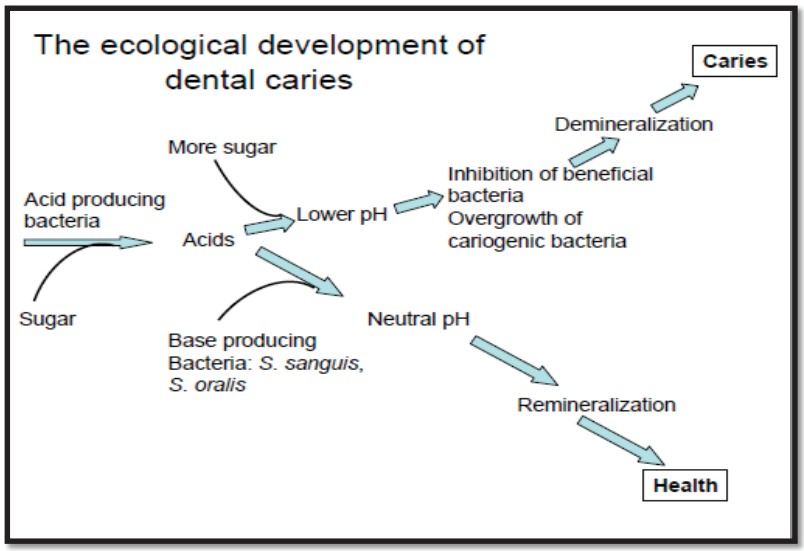


Figure (2-1): Development Schematic representation of ecological dental caries (March ,2004).

Molecular biology techniques have shown that more than 50% of the oral species are uncultivable by conventional methods, researches recognized that caries results not solely because of the presence of *S.mutans* or any single organism in dental plaque, but it is rather the interaction of multiple acid-producing organisms such as low-pH non-mutans streptococci, *Veilonella*, *Lactobacillus, Propionibacterium,*

Bifidobacterium that may be involved in the initiation of the disease (Aas *et al*., 2008; He *et al*., 2009; Mantzourani *et al*., 2009).

2-2-2-Periodontal diseases :-

Gingivitis and periodontitis are the most common diseases with a microbial etiology affecting the periodontium ,the gingivitis is an inflammation of the marginal periodontal tissues associated with an accumulation of dental plaque, the inflammation is reversible and there is
no destruction of the periodontal attachment of the teeth, although inflammation may be found at sites with a prior attachment loss, in contrast to gingivitis, periodontitis is characterized by a progressive destruction of the supporting structures of the teeth (Haukioja *et al.*, 2008). Bacteria may also directly cause tissue damage due to virulence factors, such as toxins and enzymes (Smalley, 1994). Furthermore, the capacity of micro-organisms to induce the production and / or activation of matrix metalloproteinase in host tissues is important in the pathogenesis of periodontitis (Okamoto *et al.*, 1997). The inflammatory response including an increased flow of gingival crevice fluid (GCF), a rise in pH favours the Gram-negative and proteolytic species which leading to an ecological shift as suggested by the ecological plaque hypothesis (Marsh, 2005).

Most bacterial species associated with periodontitis are Gram - negative, obligate anaerobes : *Porphyromonas gingivalis* , *Tannerella forsythia* and *Treponema denticola* form the red complex of bacteria associated with increased pocket depth and bleeding on probing (Socransky *et al.*, 1998). *Aggregatibacter actinomycetemcomitans*, associated with localised aggressive periodontitis is a

facultative anaerobe , some Gram-positive species, such as *Parvimonas micra* (*Peptostreptococcus micros*) (Socransky *et al.*, 1998), and viruses, such as *Epstein-Barr* virus, are also associated with this disease (Slots, 2007).

2-3-Dentures:-

Dentures, artificial teeth, are prosthetic devices constructed to replace missing teeth , which are supported by surrounding soft and hard tissues of the oral cavity, usually made from polymethylmethacrylate (PMMA) materials called resin, these materials are the most widely used non-metallic denture base materials (Price, 1994 ; Jagger, 2002).

2-3-1-Type of denture :-

2-3-1-1-Removable partial dentures :

Removable partial dentures are removable appliances used for the person missing some of the teeth but still having a number of natural teeth (Pahlevan, 2005). As figure (2-2)

Figure (2-2): Removable partial dentures. (Pahlevan , 2005)

2-3-1-2-Removable complete dentures(full dentures):-

Removable complete dentures or known as a full dentures are removable appliances used for a person missing all teeth (Singla, 2007).As figure (2-3)

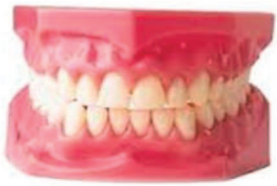


Figure (2-3): Removable complete dentures . (Singla , 2007).

2-3-1-3- Implant over denture:-Implant over denture is a denture of precision dental attachment of cylindrically shape of pore titanium that can be placed in tooth roots by surgically method (Vecchiatini *et al.*, 2009).As figure (2-4).

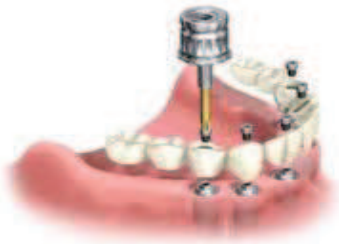


Figure (2-4): Implant over denture .(Vecchiatini *et al.*, 2009).

2-3-2-Oral environment with denture wearer:-

The adherence of microbial species to denture and other dental restorative materials ,furthermore , subsequent formation of biofilms on these surfaces are contributory factors to plaque-related oral and systemic disease, the mouth of the denture wearer presents additional hard, non-shedding areas and new environments (tissue-fitting surfaces) to support the growth of microorganisms and the development of plaque, denture may also act as a reservoir of infection for respiratory and systemic opportunistic pathogens (Sumi *et al*., 2003), and presents a niche for antibiotic-resistant bacteria(Smith *et al*., 2003). Literature review Sumi *et al*.,(2003) suggests respiratory pathogens preferentially colonies teeth or dentures, rather than soft tissue. The oral flora comprises a diverse group of microorganisms including bacteria, fungi, mycoplasmas, protozoa, viruses and bacteria predominate with an estimate of over 600 different species present in the oral cavity(Kazor *et el*., 2003). However, only half of these species can be cultured in the laboratory(Wade *et al*.,1997).

Denture plaque is a dense, complex heterogeneous layer of microorganisms and their metabolites(Nikawa *et el*., 1998). Denture plaque develops from adherence, aggregation and growth of microbes from saliva, oral mucosa and possibly fingers in the absence of denture hygiene (Theilade *et al*., 1988),plaque accumulates preferentially at stagnant sites offering protection from flow and mechanical removal forces in the mouth (March, 2004).There is general agreement that denture plaque composition is broadly similar to that of dental plaque (Theilade *et al*., 1983),with Gram positive cocci and short rods predominating (Koopmans *et al*., 1988) whereas Gram-negative rods are relatively few in number (Budtz-Jorgensen *et*

al., 1988). Plaque microflora varies between individuals and sites in the mouth and on the denture, where differences between the flange, denture tooth, tooth gum interface and the fitting surface have been identified (Budtz-Jorgensen *et al*., 1983).

The predominant cultivable microflora of denture plaque includes *Streptococcus spp*. (*S. sanguinis* [formerly *S. sanguis*], *S. oralis, S. anginosus, S. salivarius*), *Staphylococcus spp*. (*S. aureus, S. epidermidis*),
Gram-positive rods (*Actinomyces spp*. [*A. israelii, A. naeslundii, A. odontolyticus*], lactobacilli, *Propionibacterium spp*.), *Veillonella spp*., Gram-negative rods and yeasts (Budtz-Jorgensen *et al*., 1983). In addition, a higher nutrient concentration, low salivary flow rates and roughened topography support and protect plaque (Verran, 2005), Denture plaque in comparison to dental plaque was reported to have a large proportion of obligate anaerobic *Actinomyces spp*. (*A. israelii*), low proportions of Gram negative rods and the regular presence of the skin bacterium *Staphylococcus aureus* (Theilade *et al*.,1983).

2-3-3- Problems associated with denture plaque:-

2-3-3-1- Stomatitis and oral candidosis:-

Most of the literature on denture plaque focuses on *Candida Spp*. and its association with denture stomatitis, Candida is isolated more frequently from denture plaque than from dental plaque (Davenport, 1970).

2-3-3-2 Malodor:-

Oral malodor is a common and often distressing condition which is poorly explored in denture wearers, due to the artificial nature of the denture, many edentulous patients express concern that they may produce a distinct malodor (Fiske *et al*.,1995), dirty dentures contribute to malodor (Neill, 1968), which is generally acknowledged in the dentate to be caused in part by volatile sulphur compounds (VSCs), including hydrogen sulphide, methyl mercaptan and dimethyl sulphide (Tonzetich, 1977). These VSCs cause a fetid or putrid odour producing by Gram negative bacteria, particularly anaerobic species such as *Porphyromonas spp*., *Prevotella spp*. and *Fusobacterium spp*. (Rolla *et al*.,1999), by proteolytic degradation of sulphur-containing peptides and amino acids present in saliva , shed

epithelium, food debris, gingival crevicular fluid (GCF), plaque and blood, these bacteria also have an association with periodontal disease (Tonzetich ,1977), other Gram negative bacteria found in denture plaque, such as *Klebsiella spp*., may be potential pathogens in respiratory or systemic diseases arising from the oral reservoir of microorganisms (Verran,2005).

2-3-3-3-Reservoir of infection :-

There has been an increase in the number of studies investigating the link between oral and systemic diseases in the dentate (Sumi *et al*., 2007) and edentate (Senpuku *et al*., 2003) .Oral bacteria have been implicated in bacterial endocarditis (Berbari *et al*., 1997) , aspiration pneumonia(Scannapieco, 2006), gastrointestinal infection (Sumi *et al*., 2003), and chronic obstructive pulmonary disease (Thean *et*

al., 2007), among others, dentures offer a reservoir for microorganisms associated with these infections, dentures may spend time in a non-hygienic environment when out of the mouth and may also harbor microorganisms not normally associated with the oral flora, including *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Neisseria meningitidis*, certain Enterobacteriaceae including *E. coli, Klebsiella* spp. (Sumi *et al*., 2002), *Pseudomonas* spp., and staphylococci including, but rarely, MRSA (Smith *et al*., 2003), Such organisms may be considered respiratory pathogens and have been reported to colonise the denture plaque in 46% of the dependent elderly (Sumi *et al*., 2002),

2-4-Orthodontic:-

Orthodontic anchorage can be defined as resistance to undesirable tooth movement, traditional metal wired braces are stainless steel and sometimes in combination with titanium are the most widely used (Freitas *et al*, 2012),figure(2-5). The placement of orthodontic appliances is known to create a favourable environment for the accumulation of microbiota and food residues which in time, may cause caries or exacerbate any preexisting periodontal disease (Ristic et al., 2007). The microbiological changes after bracket placement became a topic of interest during the late 1980's, initially cariogenic species such as *Streptococcus mutans* , *Lactobacillus* species and the subsequent decalcification of enamel were the main fields of interest among investigators (Forsberg *et al*., 1991). Later on, the more complex system of periodontopathogenic microbes and the changes after bracket placement became the main topics of interest (Petti *et al.,* 1997).

Naranjo *et al.*, (2006) observed a transition in subgingival dental plaque after the placement of brackets, the plaque index and gingivitis index increased significantly *Porphyromonas gingivalis*, *Prevotella intermedia, Prevotella nigrescens, Tannerella forsythia* and *Fusobacterium* species were significantly elevated in the experimental group after bracket placement compared with the control group without orthodontic therapy, including superinfecting microorganisms such as *Enterobacter cloacae, Klebsiella oxytoca, Klebsiella pneumonia* and *Serratia marcescens* were also found (Naranjo *et al*., 2006). Lee *et al*.,(2005) succeeded in detecting significant differences in the subgingival dental plaque retrieved from gingivitis lesions in patients with and without orthodontic fixed appliances, *Tannerella forsythia, Treponema denticola, and Prevotella nigrescens* were significantly more common in the samples obtained from the orthodontic patients than in the samples obtained from the non orthodontic control patients (Lee *et al*., 2005) . The presence of orthodontic bands and brackets, therefore, cannot affect on the microbiologic condition of the whole mouth (Naranjo *et al*., 2006).

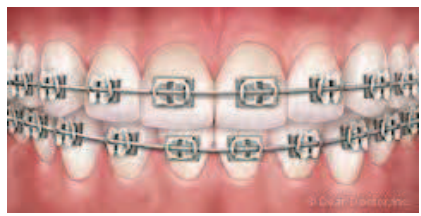


Figure (2-5): Orthodontic.(Freitas *et al*, 2012).

2-5-Dental plaque:-

Dental plaque is a highly complex biofilm that provides nutrients and protection for periodontopathogenic bacteria (Marsh, 2005). It is the primary cause of gingivitis and the possible transition to periodontitis (Löe, 1965). The Gram positive and mostly aerobic microorganisms that initially colonize intra-oral hard surfaces are replaced by predominantly Gram negative and anaerobic microorganisms (Socransky and Haffajee, 2005). *Tannerella forsythia*,*Porphyromonas gingivalis*, *Actinobacillus Actinomycetemcomitans* and *Prevotella intermedia* are found more frequently in patients with gingivitis and periodontitis than in healthy subjects (Darveau *et al*., 1997). Thus both the quantity as well as the quality of plaque , are important factors in the onset of periodontal disease and are influenced by many factors including surface characteristics (Quirynen *et al*., 1990).

Especially surface roughness and surface free energy were found to be positively correlated with the plaque growth rate (Quirynen & Bollen, 1995), additionally, the presence of gingival inflammation will further increase plaque growth (Ramberg *et al* ., 1995).

2-6-Biofilm:-

A biofilm is a community of cells attached to either a biotic or abiotic surface enclosed in a complex exopolymeric substance (EPS) (Mah& O'Toole, 2001). The oral cavity is constantly contaminated by a complex diversity of microbial species that have a strong tendency to colonize surfaces, however, the major components involved in biofilm formation are bacterial cells, a solid surface, and a fluid medium biofilm formation occurs on all hard surfaces, e.g. the tooth surface,

restorative materials and implant components. In the formation of a biofilm to a non-shedding surface the following stages have been described according to (Scheie,1994; . Bos *et al*.,1999) :-

- **Stage 1: Conditioning layer formation:-**

The first stage in the development of biofilm is the adsorption of organic and inorganic molecules to the solid surface, this conditioning layer in the oral cavity, called pellicle, consists of numerous components including glycoproteins, proline-rich proteins, phosphoproteins, histidine-rich proteins, enzymes, and other molecules that can function as receptors for bacteria.

- **Stage 2: Transport of bacteria to the substrate surface:-**

The initial transport of microbes to the substrate may occur through brownian motion, through liquid flow, or through active bacterial movement (chemotactic activity) which may be influenced by many factors include pH, temperature, flow rate of the fluid, surface energy of the substrate, bacterial growth stage, surface hydrophobicity.

- **Stage 3: Bacterial adhesion :-**

The next step in biofilm formation is the adhesion of microbial cells to the conditioning layer by the following phase:

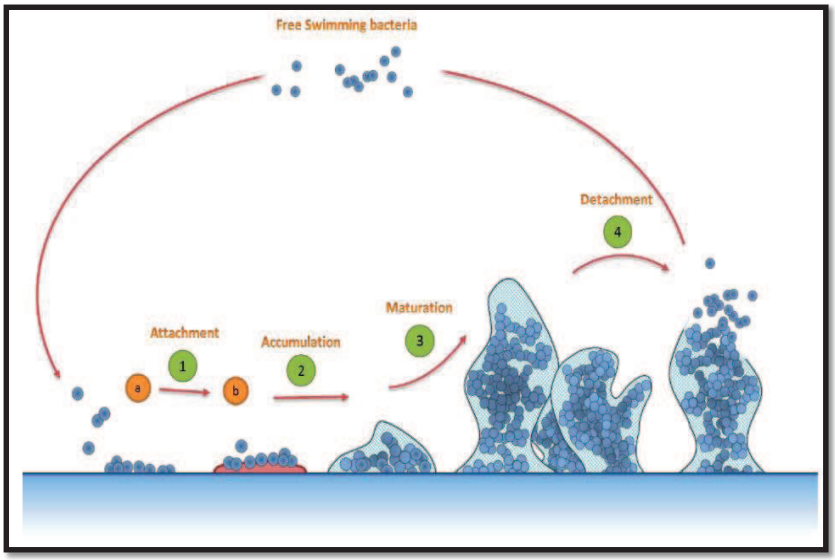
❖ **Phase 1:** Initial non-specific microbial-substrate adhesion,the bacterial surface structures form bridges between the bacteria and the conditioning layer (Grenier and Mayrand, 1986). Initially, these bridges may not be strong, however with time the bacteria-substrate bonds gains in strength.

- **Phase 2:** Specific microbial-substrate adhesion, in this phase polysaccharide adhesion or ligand on the bacterial cell surface bind to receptors on the substrates (Miron *et al*., 2001).

- **Stage 4: Bacterial colonization and biofilm maturation:-**

In this stage, the monolayer of microbes attracts secondary colonizers forming microcolony (Costerton *et al*., 1999), the firmly attached microorganisms start growing, newly formed cells remain attached and biofilms can develop, the physicochemical surface properties of a pellicle are largely dependent on the physical and chemical nature of the underlying hard surface (Sipahi *et al*., 2001). Thus, the characteristics of the underlying hard surface will influence on the initial bacterial adhesion.(figure 2-6) .

It is known from in vitro studies that monolayer of oral bacteria release enzymes that mediate their detachment (Lee *et al*., 1996). It is likely that localized detachment of microorganisms starts after initial adhesion and increases with time as it is related to the number of microorganisms present in the biofilms, the fact that microorganisms detach regularly has implications for their spreading and colonization to other sites (Auschill *et al*., 2001)



Figuer (2-6) : Steps of biofilm formation. Biofilm formation is divided into four steps: 1)initial adhesion of bacterial cells to surfaces, a) attachment to biomaterial surfaces, b)attachment to host matrix proteins coated the surfaces, 2) aggregation into multicellularstructures, 3) formation of mature stable biofilms, and 4) dispersal of bacterial cells from the biofilms (Otto *et al.,* 2009) .

2-7-Methods for the detection of bacterial forming biofilms:-

There are two methods for the detection of bacterial forming biofilms:

1. The Phenotypic method:-

Qualitative methods, such as the tube adherence (TM) test described by Christensen *et al*., (1982) , Congo red agar (CRA) method described by Freeman *et*

al., (1989), and quantitative methods, such as the tissue culture plate (TCP) assay described by Christensen *et al*.,(1985) are used in routine laboratories

2. The Genotypic method:-

PCR amplification methods have been shown to improve the detection of biofilms , biofilm non producers are negative for *icaA* and *icaD* and lack the entire *icaADBC* operon , but this requires specialized equipments and techniques (Arciola *et al*., 2001; O' Gara *et al*., 2001**).**

2-8-Genes responsible for synthesis biofilm:-

After the initial adhesion, cell-cell interaction prevents the dissemination of the initial colonizing bacteria and facilitates the formation of mature biofilms, *S. epidermidis* releases various surface macromolecules and proteins that facilitate the intercellular aggregation , polysaccharide intercellular adhesin (PIA) is involved in the cell-to-cell adhesion during *S. epidermidis* biofilm formation (Mack *et al*.,1994).PIA is a linear homoglycan composed of β-1,6-linked N-acetylglucosamine residues and carries up to 15% deacetylated amino groups, the positive and negative charges can be simultaneously introduced to the polysaccharide by substitution with ester-linked succinate and phosphate residues, then the ionic interaction caused by these positive and negative charges within the polysaccharide could explain its function in linking different cells within the biofilm (Mack *et al* .,1996), PIA biosynthesis is directed by enzymes encoded by the *icaADBC* gene operon, the intercellular adhesion (*ica*) locus is composed of four open reading

frames (ORFs) *icaA*, *icaD*, *icaB* and *icaC* in an operon (Heilmann *et al*., 1996 ; Gerke *et al*., 1998), Figure (2-7)

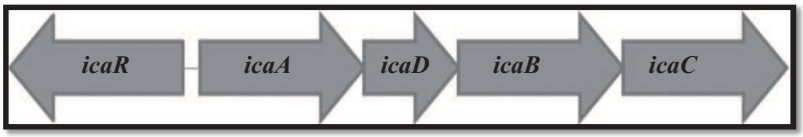


Figure (2-7): Map of genomic organization of the *icaRADBC* gene cluster from *S. epidermidis* (O'Gara & Humphreys, 2001).

IcaA and *IcaD* are transmembrane proteins involved in the synthesis of N-acetylglucosamine (GlcNAc) polymers, while elongation and export of the resultant polymers is believed to be controlled by the *IcaC* membrane protein, after export, the *IcaB* deacetylase enzyme is responsible for de-acetylation of some of the GlcNAc residues needed to provide the polymer with the cationic character that is essential for surface attachment (Rohde *et al*., 2007), In addition, it has been demonstrated that *IcaR* represses *ica* expression by binding to the *icaA* promoter region (Jefferson *et al*., 2004), as Figure (2-8).

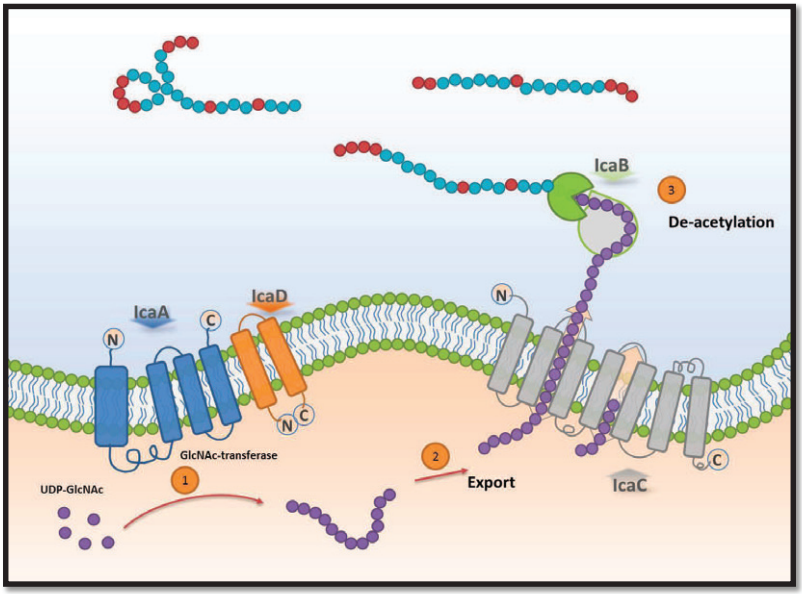


Figure.(2-8): Biosynthesis of the exopolysacharide poly-N-acetyleglucosamine (PIA). *IcaA* and *IcaD* are trans-membrane proteins involved in the synthesis of N-acetylglucosamine (GlcNAc) polymers (1). The *IcaC* membrane protein controls the elongation and export of the polymer (2). The *IcaB* protein is responsible for de-acetylation of GlcNAc residues (3), (Otto., 2009) .

2-9-Molecular genetic:-

2-9-1-Identification of bacterial species by *16SrDNA* sequencing:-

Within the biological world, ribosome share many similarities, indicating the conservative nature of its structure in prokaryotic ribosomes contain three types of RNA :(5S, 16S, and 23S) (Harmsen and Karch, 2004). Both 5S and *16SrDNA* have

been used to determine relatedness, since the 16S molecule is large (with about 1500 bases), it contains more information and the smaller 5S molecule with only 120 bases, where as little work has been done on the 23S molecule because it's so longer (about 3000 nucleotides) and it's therefore more difficult to study, thus, scientists interested in the classification and evolution of bacteria has concentrated on the 5S and 16S (Mendoza *et al.*, 1998). The more highly conserved region permit one to compare distantly related organisms and the more variable domains are used to examine the more closely related organisms (Harmsen and Karch, 2004). In previous studies, polymerase chain reaction (PCR) analysis was used to detect pathogens and many primers have been developed to detect species-species genes (Skow *et al*., 2005).The different primers for different species is impractical for routine analysis of cultures that may contain one or more of many possible pathogens, but this can be avoided by using a single pair of universal primers designed to amplify conserved stretches of *16SrDNA* from any bacterium (Khamis *et al*., 2005) .

2-9-2-Phylogenetic tree:-

The discovery of the polymerase chain reaction (PCR) and DNA sequencing, comparisons of the gene sequences of bacterial species have shown that the 16S ribosomal RNA (rRNA) gene is highly conserved within

a species and among species of the same genus, hence can be used as the new gold standard for the speciation of bacteria, using this new standard, phylogenetic trees, based on base differences between species, are constructed and bacteria are classified and reclassified into new genera (Olsen and Woese,1993; Schmidt and Relman 1994).Phylogeny is the study of the evolutionary history of organisms (Delsuc *et al*.,

2005). Cladistic relationships indicate the degree of relatedness between microorganisms as shown by pathways of ancestry (Cain & Harrison, 1960). Consequently, classifications which are based on perceived evolutionary relationships between organisms reflect the extent of change over time, therefore , Phylogenetic relationships between organisms are represented by evolutionary trees and are inferred from various types of phonetic relationships based on assumptions of how evolution occurs ,although, evolutionary systems are sometimes seen merely as simple branching over time but this is an oversimplification as *in vivo* hybridisation and lateral gene transfer lead to conceptual as well as to computational difficulties (Maynard , 1990). Bacterial systematics is increasingly being based on phylogenetic information, notably that derived from macromolecules such as DNA, RNA and proteins (Olsen *et al.*, 1994). Classification, the one of basic disciplines of bacterial systematic , is becoming increasingly dependent on the use of molecular sequence data, notably on information generated from 16S rRNA analyses (Woese *et al*., 1991).

2-10-Bacterial species isolated in dentures and orthodontic:-

Bacterial species isolated from denture and orthodontic are *Staphylococcus aureus Staphylococcus epidermidis*, *Staphylococcus hominis*, *Staphylococcus warneri* normally found on the skin of humans and animals (Cimiotti *et al*., 2007), in nasal cavities (Rasmussen *et al*.,2000) and in the mouth (Ohara-Nemoto *et al*., 2008).

Staphylococcus pasteuri is a Gram positive organism which is emerging as an agent of nosocomial infections and a blood derivatives contaminant, though its role in causing human disease mostly remains controversial (Savini *et al*., 2009).

Staphylococcus hominis is one of the major staphylococcal species inhabiting the skin of humans and on most of the people that have been examined, it produces large populations in the axillae and inguinal and perineal areas(Kloos, 1986).

Staphylococcus warnerii found as part of the skin flora on humans , animals and cause infection in patients whose immune system is compromised (Barigye *et al*., 2007) and in the mouth (Ohara-Nemoto *et al*., 2008).

Morganella morganii is a gram-negative rod commonly found in the environment and in the intestinal tracts of humans, mammals, and reptiles as normal flora.(Samonis *et al*., 2001).

Klebsiella pneumoniae is a Gram-negative found in the normal flora of the mouth, skin, and intestines, it can cause destructive changes to human lungs if aspirated (Tu *et al*., 2009).

Klebsiella oxytoca is a Gram-negative found opportunistic in nature this specie tends to colonize along the mucosa membranes of the colon and nasopharynx , and skin; however, they can be found colonizing on all parts of the body (Ménard *et al*., 2010).

Klebsiella variicola as a new species isolated in Mexico from plants (rice, maize, sugar cane and banana) and hospitals (Rosenblueth *et al*., 2004) .

Serratia marcescens is involved in nosocomial infections, particularly catheter-associated bacteremia, urinary tract infections and wound infections, and is responsible for 1.4% of nosocomial bacteremia cases in the United States ,it is commonly found in the respiratory and urinary tracts of hospitalized adults and in the gastrointestinal system of children **(** Hejazi and Falkine 1997) .

Proteus hauseri exist in manure, soil, polluted water, and in intestines of human and wide variety of animals (Garrity *et al*., 2005).

Proteus mirabilis is one of the most common gram-negative pathogens encountered in clinical specimens and can cause a variety of community- or hospital-acquired illnesses, including urinary tract, wound, and blood stream infections "BSI" (O'Hara *et al*.,2000).

Proteus penneri usually infects urinary tract, blood, abdominal wound, groin, neck and ankle and has been isolated mostly from urine (50%), wound and soft tissue exudates (25%), and blood cultures (15%) (O'Hara *et al*., 2000 ; Cantón *et al*., 2006).

Enterococcus faecalis is a gram-positive bacterium that can cause a variety of nosocomial infections of which urinary tract infections are the most common , these

infections can be exceptionally difficult to treat because of drug resistance of many *Enterococcus faecalis* isolates (Kau *et al*., 2005).

Enterococcus faecium causes nosocomial bacteremia, surgical wound infection, endocarditis, and urinary tract infections (Paulsen *et al*., 2003).

Escherichia fergusonii is belong to Enterobacteriaceae, infect open wounds in humans and may also cause bacteraemia or urinary tract infections (Mahapatra *et al*., 2005).

Bacillus cereus, which is a well-known cause of food poisoning and a dreaded cause of posttraumatic endophthalmitis ,and can also cause opportunistic infections, mainly in the immunocompromised host (Drobniewski,1993).

Bacillus subtilis is non-pathogenic , they can contaminate food and caused food poisoning (Perez, 2000).

Enterobacter aerogenes is found in soil, water, dairy products and inhabits a natural flora in the gastrointestinal tract of animals as well as humans and causes disease in humans through inadvertent bacteria transfer in hospital settings ((Burchard *et al*.,1986 ; Janda *et al*., 2006).

Enterobacter cloacae has emerged as an important nosocomial pathogen which could cause a wide spectrum of infections including respiratory system disease,

urinary tract infections, involving mostly patients with impaired host deficiency, and bacteremia (Wisplinghoff *et al*., 2004; Galani *et al*., 2005) .

Enterobacter mori is plant-pathogenic enterobacterium responsible for the bacterial wilt of *Morus alba* L. (Li *et al*., 2010) .

Enterobacter ludwigii is gram-negative, fermentative, motile rods which were isolated from clinical specimens (Hoffmann *et al*., 2005) .

Hafnia alvei can be isolated from various anatomical sites in humansand from various environmental sources and not normally pathogenic, but may cause disease in immunocompromised patients (Janda *et al* ., 2006).

Citrobacter freundii is an opportunistic pathogen cause of a variety of nosocomial infections of the respiratory tract, urinary tract, blood and several other normally sterile sites in patients (Whalen *et al*., 2007).

Lactobacilius plantarum is found in dairy, meat and much vegetable fermentations, it is also found in the human gastrointestinal tract (De Vries *et al*., 2006).

Lactococcus lactis is nonpathogenic bacteria used widely for industrial production of fermented dairy products such as milk, cheese and yogurt, however, is nonpathogenic bacteria (Tanous *et al*., 2007).

Streptococcus anginosus is part of the human bacterial flora, but can cause diseases including brain and liver abscesses under certain circumstances, the habitat of *S. anginosus* is a wide variety of sites inside the human body such as mouth, throat, feces, and vagina (Ruoff *et al*., 1988).

Streptococcus equinus makes up the majority of the bacterial flora in horse feces (Boone *et al*., 1991) and is seldom found in humans(Noble, 1978).

Acinetobacter baumanni is an opportunistic pathogen which has caused nosocomial infections as its ability of to live on a variety of hospital surfaces (Franco *et al*., 2004), commonly found in fermented vegetables, fermented dairy products and meat (Barros *et al* ., 2001).

Chryseobacterium vietnamense was isolated only from a forest soil sample in Vietnam (Li and Zhu, 2011).

Chapter three
Materials and Methods

3-1- Equipments and materials:-

The equipments used in this study are described in Table (3-1).

Table (3-1) : Equipments

No.	Equipments	Company	Country
1	Autoclave	Tuttnauer Brinkama	USA
2	Centrifuge	Human	Germany
3	Cooling incubator	Binder	Germany
4	Deep freezer (-18°C)	Nuair	Japan
5	Digital balance	Mettlertoledo	Swistezerland
6	Distillatory	GFL	Germany
7	Electrophoresis system (mini horizontal unit)	Fisher scientific	USA
8	ELISA microplate reader	Human	Germany
9	Eppendorf tubes	Eppendorf	Germany
10	Finn tips , 100µl , 500µl , 1000µl	Fisher	USA
11	Light microscope	Human	Germany
12	Micropipettes , 0.5 - 10µl 10 - 100µl , 100 - 1000µl	Fisher scientific	USA
13	Microplate titter (96 well – flatbottom)	Himedia	India

No.	Equipments	Company	Country
14	Mini vortex	Fisher scientific	USA
15	Minifuge	Fisher scientific	USA
16	Oven	Memmert	Germany
17	PCR sprint thermal cycler	Thermo	USA
18	PCR tubes	Fisher	USA
19	pH meter	Thermo	USA
20	Platinum wire loop	Himedia	India
21	Stirrer/hotplate	Coming	USA
22	Ultra centrifuge	Thermo	USA
23	U.V transilluminator	Velber Lourmat	EEC France
24	Water bath	Memmert	Germany
25	Eppendorf concentrator 5301	Hamburg	Germany

3-2- Chemicals and dyes:-

The Chemical and dyes used in this study are described in Table (3-2)

Table (3-2): Chemicals and dyes

No.	Chemicals	Company	Country
1	Agarose	Promega	USA
2	Absolute ethanol	Lab M	UK
3	Boric acid	Fisher	USA
4	DNAladder 100 bases	BIONEER	Korea
5	DNA ladder 1kb	Promega	USA
6	EDTA (ethylene diamine tetra acetate)	BDH	England
7	Ethanol (96%)	AL-Tharthar	Iraq
8	Formalin	BDH	England
9	Lysozym	Promega	USA
10	Master mix	Promega	USA
11	Phosphate buffers saline	Oxoid	England
12	Primers	BIONEER	Korea
13	Sucrose	Merck	Germany
14	Tris – HCl	Fisher	USA
15	Tris base	Fisher	USA
16	Triton X–100	Fisher	USA
17	Bromophenol blue	Fisher	USA
18	Congo red	DAB.6	Germany
19	Ethedium bromide	Fisher	USA

No.	Chemicals	Company	Country
20	Gram's stain	Fara	Iran
21	Genomic DNA mini kit (blood /cultured cell)	Geneaid	Taiwan

3-3-Prepared media:-

The media using in this study were prepared according to their companies are described in Table (3-3)

Table (3 -3) : Prepared media

No.	Media	Company	Country
1	Blood agar base	Himedia	India
2	Brain heart infusion broth	Oxoid	England
3	Nutrient agar	LAB	UK
4	Tryptic soy broth	Alpha	USA
5	Congo red agar	prepared media	

3-4- Preparation of chemical solutions:-

3-4-1- Tris Borate – EDTA.(TBE) buffer preparation 5x:-

1. EDTA (1.86 gm) was dissolved in 20ml of distilled water pH :8 .

2. Tris base (45 gm) .

3. Baric acid (27.5 gm) .

The mixture was dissolved in distilled water and completes the volume to 1 liter. The pH was adjusted to 8 , autoclaved at 121°C for 15min , and stored at 4°C (Sambrook and Rusell , 2001) .

3-4-2-Tris EDTA (TE) buffer preparation :-

TE buffer it consists of :-

A. 1.214 gm of Tris – HCL in 10ml distilled water , (1M) as astock .

B. 1.861 gm of EDTA in 10ml distilled water (0.5M) as astock and dissolved by heating .

TE buffer was prepared by mixing 1ml of solution (A) and 0.2 ml of solution (B) the volume was completed to 100 ml with distilled water and the pH was adjusted to 8 , autoclaved at 121°C for 15 min and stored at 4°Cto be use later . (Sambrook and Rusell , 2001) .

3-4-3-Ethidium bromide dye solution:-

Dissolving 0.05 gm of Ethidium bromide in 10 ml distilled water (stirred until dissolved) , and stored in a dark reagent bottle or folded by aluminum foil sheet – at 4°C (Sambrook and Rusel , 2001) .

3-4-4-Bromophenol blue dye solution:-

It is prepared of the following :

A. Bromophenol blue 0.25% (w/v) .

B. Sucrose in H_2O 40% (w/v) .

Store at 4°C .

3-4-5- Phosphate buffer saline:-

Dissolving one tablet of PBS in 100 ml distilled water and pH was adjusted to 7.2 .

3-4-6- Preparation of commercial culture media:-

Blood agar base , NA , BHIB , tryptic soy broth were prepared according to manufacturer and sterilized by autoclaving at 121°C for 15 min .

3-5- Methods:-

3-5-1-Sample collection:-

One hundred sample were collected from patients dentures (n=50) using sterile cotton swabs and from orthodontic (n=50) using sterile needle from Al-shaheed Qais center in Basrah after confirm from patient's denture and orthodontic washing. All samples were from both genders aged between 12-70 years (Figure 3- 1). Collected samples were placed in sterile tubes containing (5ml) brain heart infusion broth (BHIB) and transferred to the laboratory (Talan *et al* . , 1989) , to incubate at 37°C for 12 – 24 hr then streaked onto blood agar using a loop and incubated at 37°C for 24 hr. All colonies that appeared were gram stained and detected by light microscope ,then subcultured onto nutrient agar plate (for biological studies) and nutrient agar slants (as stock) then incubated at 37°C for 24 – 48 hr .

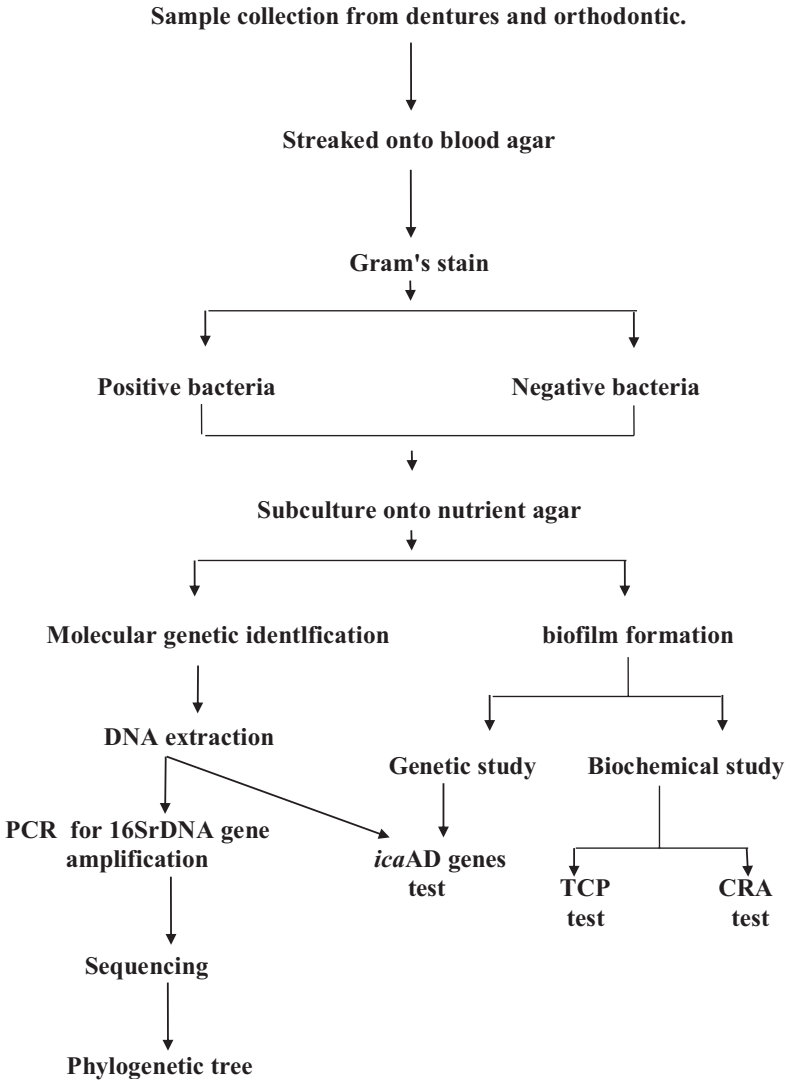


Figure: (3 - 1) : General layout of the study.

3-5-2-Examination of specimen:-

3-5-2-1-laboratory diagnosis:-

All Gram negative and positive cocci and Gram negative and positive rod bacteria were identified according to molecular study.

3-5-3- Molecular genetic identification:-

3-5-3-1-DNA extraction from bacteria :-

DNA was extracted by genomic DNA mini kit (blood /cultured cell) Geneaid ,according to the manufactured instruction as follow:

1. Cultur bacterial cells from BHIB tube containing activated bacteria was transferred to a 1.5 ml microcntrifuge tube .

2. 200 µl of lysozyme buffer (20 mg / ml lysozyme , 20mM Tris-Hcl , 20mM EDTA , 1% Triton x-100 , pH 8.0 , prepare fresh lysozyme buffer immediately prior to use) was added to the tube above and resuspend the cell pellet by shaking with pipet

3. Incubated at room temperature for 10 min . During incubation the tube was inverted every 2-3 min .

4. 200 µl of GB buffer was added to the sample and mixed by shaking vigorously for 5 sec **.**

5. Incubated at 70°C for 10 min or until the sample lysate is clear . During incubation , the tube was inverted every 3 min , At this time , the required elution Buffer (200 µl per sample) was incubated at 70˚C (for step 19 DNA elution) .

6. After 70°C incubation ,200 µl of absolute ethanol was added to the sample lysate and immediately mixed by shaking vigorously . when precipitate appears , breaked it up by pipetting .

7. The mixture (including any precipitate) was transferred to the GD column .

8. GD column was placed in a 2 ml collection tube .

9. Centrifuged at 12,000 xg for 5 minutes .

10. The 2 ml collection tube containing the flow through was discarded and the GD column was placed in a new 2 ml collection tube .

11. 400 µl of W1 buffer was Added to the GD column .

12. Centrifuged at 12,000 xg for 3 min .

13. The flow through was discarded and the GD column was placed again in the 2 ml collection tube .

14. 600 µl of wash buffer (absolute ethanol added) was added to the GD column .

15. centrifuged at 12,000 xg for 3 min .

16. The flow through was discarded and the GD column was plased again in the 2 ml collection tube .

17. Centrifuged for 5 min at 12,000 xg to dry the column matrix .

18. The dried GD column was transferred to a clean 1.5 ml microcentrifuge tube .

19. 100 µl of preheated elution buffer was added to the center of the colum matrix .

20. The column was left stand for 3.5 min or until the elution buffer was absorbed by the matrix .

21. centrifuged at 12,000 xg for 7 min . to elute the purified DNA .(DNA was stored at - 20˚ C) .

3-5-3-2-Examination of genomic DNA by agarose gel electrophoresis:-

DNA was visualized by agarose gel electrophoresis (Sambrook and russel , 2001) .

Agarose gel was prepared as follow:

1. 0.2 gm agarose was dissolved with 25 ml of TBE buffer (1 X) in a beaker , the mixture was melting by hot plate agarose ,then 0.2 µl of ethedium promide was added , and mixture was left to cool for 50 - 60˚C.

2. Melted agarose gel was poured into the casting tray of the electrophoresis apparatus and the comb was placed at one end of the tray to form wells for loading .

3. After the agarose solidified at room temperature , the cast was pushed gently upwards out of the tray , and the comb was lifted up out of the gel . the gel was gently replaced on the electrophoresis tray.

4. The electrophoresis apparatus was filled with TBE buffer until the entire gel surface was covered with the buffer .

5. 9 µl of DNA sample was mixed with 3 µl of bromophenol blue and the mixture was transferre carefully in the wells of agarose gel .

6. The gel was subjected to equal electric current by connecting to a power supplier .

7. The cathode was connected to the well sides of the tray while the anode on the other side and the gel was run at 60V until the promophenol blue tracking dye migrated to the end of the gel .

8. DNA bands were detected and examined under UV. Transilluminator.

3-5-3-3-Polymerase Chain Reaction (PCR) technique :-

PCR method for amplification the universal *16SrDNA* gene were accomplished according to Miyoshiey *et al*.(2005).

3-5-3-4-Universal *16SrDNA* gene primers:-

The bacteria in the clinical specimens were identified by using PCR in order to amplify universal bacterial *16SrDNA* gene which is listed in table (3 -4) .

Table (3-4): Universal *16SrDNA* primers used in PCR amplification

Gene	Primer type	Primer sequence (5'-3')	Size of product bp	TM	TA
Universal bacterial *16SrDNA*	B 27 F	5'-AGAGTTTG ATCCTGGC-3'	1500bp	48˚C	51.8˚C
	U 1492R	5'-GGTTACCT TGTTACGACTT-3'		42˚C	51.8˚C

*** TM=Melting temperature**

*** TA=Annealing temperature**

3-5-3-5- Reagents:-

The reagents and their volumes were used for PCR amplification are described in table (3-5) .

Table (3 -5): Reagents and volume (25µl) used in PCR amplification or *16SrDNA* gene

No	Reagent	Volume
1	DNA template	5 µl
2	Forward primer	1 µl (10 pmol)
3	Reverse primer	1 µl (10 pmol)

No	Reagent	Volume
4	Master mix	12.5 µl
5	Nuclease free water	5.5 µl
Volumes		25 µl

3-5-3-6 -Thermal cycling condition :-

The program is described in table (3-6) .

Table (3-6): Program used in PCR amplification for *16SrDNA* gene

Steps	Temperature	Time	No . Of cycles
Initial denaturation	92˚C	2min	1
Denaturation	94˚C	30 sec	30
Annealing	51.8˚C	45 sec	
Extension	72˚C	1.5 min	
Final extension	72˚C	5 min	1

3-5-3-7-Detection of PCR product by agarose gel electrophoresis :-

The solution, procedure and viewing were identical to those for the detection of DNA bands. However, there are few exceptions:

1- 0.5 gm agarose was dissolved in 25 ml from TBF buffer (5 X)

2-Without using promophenol blue .

3-10µl of PCR product was transferred into the wells of agarose gel, and in the first well was for 10µl DNA ladder (1kb).

3-5-3-8- *16 SrDNA* gene sequences:-

A-Purification of DNA product:-

Purification of PCR products was carried out to remove any unreacted primers and/or leftover dNTPs (Embley, 1991).

Procedure:-

1-20 µl of PCR product (*16SrDNA*) was transferred from the PCR tube to eppendorf tube 1.5 ml.

2-60 µl of 20% PEG was added to each tube and mixed by Vortex.

3-Tubes were incubated at room temperature for 3-4hr or overnight at 4°C.

4-The precipitated PCR product was pelleted by centrifugation at 12000 rpm for 20 min.

5-The supernatant was carefully removed by a micropipette leaving some solution in the eppendorf tube, as the DNA is gelatinous at this stage and could easily be removed accidentally.

6-0.5 ml of 70% chilled ethanol was added, and centrifuged at 12000 rpm for 10 min.

7-The supernatant was removed by a micropipette and ethanol precipitation was repeated by addition of 0.5 ml of 70% chilled ethanol and centrifuged at 12000 rpm for further 10 min.

8-The supernatant was removed from each tube by a micropipette and

precipitated DNA was dried in a vacuum drier for 30 min.

9-Pellet was resuspended in 15 µl (depending on the brightness of the band on the gel) of free nuclease water, then left overnight at 4◦C.

B-**Agarose gel electrophoresis:-**

The electrophoresis was similar to its solutions and procedure to that of *16SrDNA* produced (previously) from PCR, the electrophoresis was important to ensure that PCR product is pure after purification

C-Sending to BIONEER:-

The *16SrDNA* products sequencing and its preparation were done according to BIONEER Co.DNA concentration [45 ng/ul] and sample volume [15 ul] and for primer (for each) concentration(5pmol/ul(5uM) and volum (5ul) then sending to BIONEER for sequencing .

3-5-3-9-Identification of bacteria:-

All bacterial species were identified (using the 16SrDNA sequencing products) in " BLAST " provided by the National Center for Biotechnology Information Service (NCBI) http://www.ncbi.nlm.nih.gov after treatment and recorrection (Kerbauy *et al*., 2011).

3-5-3-10- Phylogenetic tree:-

The sequences data obtained from the present study and from type strains by Gen Bank (Sung *et al*., 2006) were aligned and concatenated at least in 893 bp and

compared to assign the differences using "CLUSTALW" http://www .ebi. ac.uk / clustalw/ (Kerbauy *et al*., 2011) (appendix-1), then a phylogenetic tree by Neighbour Joining method was constracted using MAFFT(Multiple Alignment using Fast Fourier Transform) viewed by (Kazutaka *et al*., 2005) and " forester "(Zmasek and Eddy ,2001).

3-5-4-Detection the ability of adherence:-

3-5-4-1-Congo Red Agar (CRA) method:-

This agar was prepared by blood agar base suppliemented with 0.8 gm congo red and 50 gm sucrose dissolved in 1 litter distilled water and adjusted pH to 8 , autoclaved at 121˚C for 15 min , a positive results are black colonies with a dry crystalline (slime producers), intermediate results are dark- pink colonies (weak slime producers) , and negative results are pink-wite (not slime producers) (Freeman *et al* .,1989).

3-5-4-2-Preparation of Tissue Culture Plate (TCP) method :-

A log-phase culture (18-24hr) of the isolates were inoculated into tryptic soy broth was placed in the wells of micro ELISA auto reader sterilized plate and incubated overnight at 37C°.The content of each well was gently removed by discarded .The wells were washed four times with phosphate buffer saline to remove free floating "planktonic" bacteria. Biofilms formed by adherent "sessile" bacteria in plate were fixed with 25% formalin and stained with crystal violet (0.1% w/v) . Excess stain was rinsed off through washing with deionized water plates were kept for drying

.Optical density (OD) of stained adherent bacteria were determined with micro ELISA auto reader at wavelength of 490nm (OD) These OD values were considered as an index of bacteria adhering to surface and forming biofilms (Christensen *et al*.,1985).

3-5-4-3- *icaAD* gene primers:-

The PCR method for amplification of *icaA* and *icaD* to detect the biofilm (as slim formation) were done according to Arciola *et al*. (2001) as in table (3 - 7).

Table (3 - 7): *icaAD* primers sequence.

Gene	Primer sequence (5'-3')		Size of product bp	TM	TA
IcaA gene	F	5'-TCTCTTGCAGGAGCAAT CAA-3'	188bp	58°C	55.5˚C
	R	5'-TCAGGCACTAACATCC AGCA-3'		60°C	
IcaD gene	F	5'-ATGGTCAAGCCCAGAC AGAG-3'	198bp	62°C	55.5˚C
	R	5'CGTGTTTTCAACATTTAA TGCAA-3'		60°C	

3-5-4-3-1- Reagents:-

The reagents and their volumes were used for PCR amplification are described in table (3- 8)**.**

Table (3 - 8): Reagents and volume (25µl) used in PCR amplification for *icaA* or *icaD* gene

No	Reagent	Volume
1	DNA template	5 µl
2	Forward primer	1 µl (10 pmol)
3	Reverse primer	1 µl (10 pmol)
4	Master mix	12.5 µl
5	Nuclease free water	5.5 µl
Volumes		25 µl

3-5-6-2 -Thermal cycling condition :-

The program was described in table (3 - 9) .

Table (3 - 9): Program use in PCR amplification for *icaA* or *icaD* gene

Steps	Temperature	Time	No . Of cycles
Initial denaturation	94˚C	5min	1
Denaturation	94˚C	30 sec	50
Annealing	55.5˚C	30 sec	
Extension	72˚C	30 sec	
Final extension	72˚C	1 min	1

3-5-6-3-Detection of PCR product by agarose gel electroforiasis :-

The solution, procedure and viewing were identical to those for the

detection of universal *16srDNA* bands . However there are few exceptions using 100 bp DNA ladder .

3-5-7-Statistical analysis:-

Statistical analysis was performed by Chi-square (X^2) test. P-value less than 0.05 was considered as statistically significant and P-value less than 0.01 considered as highly significant (Al-Mohammed *et al*., 1980).

Chapter four
Results

4-1- Molecular Genetic Study:-

4-1-1-DNA extraction:-

The DNA from 94 isolates (47 from dentures and 47 from orthodontic) was extracted and examined by agarose gel electrophoresis (Figure 4-1).

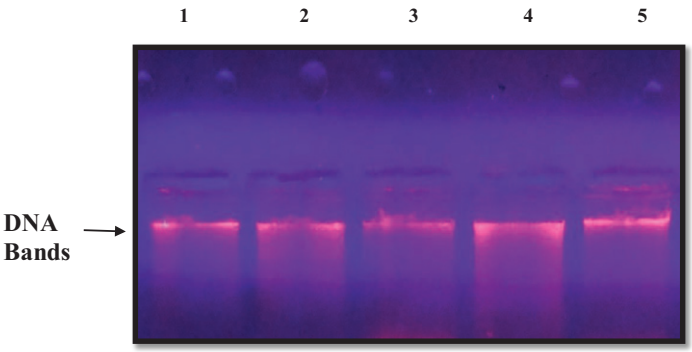


Figure (4 - 1) : Agarose (0.8%) gel electrophoresis for DNA bands (1-5) of random bacterial isolates from dentures and orthodontic under UV transilluminator .

4-1-2- Universal *16SrDNA* gene detection by PCR:-

The extracted DNA for all isolates was subjected to PCR for amplifying universal *16SrDNA* gene .PCR products for the universal *16SrDNA* primers gave bands on agarose gel at the position 1500bp when compared with standard molecular DNA ladder (Figure 4 - 2 to 4

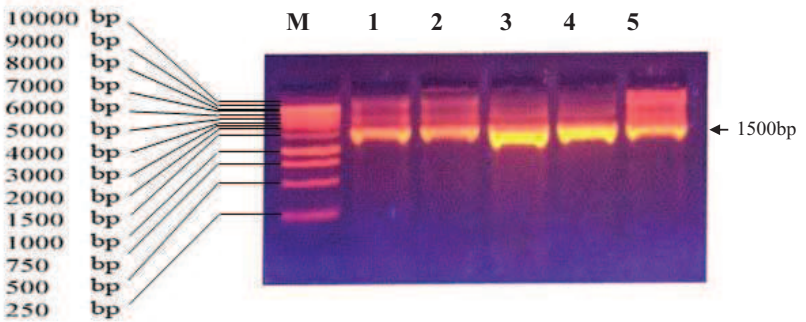


Figure (4 - 2) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and orthodontic under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. Lane 2-6: 1to5 of 1*6SrDNA* bands(1500bp) for bacterial isolates .

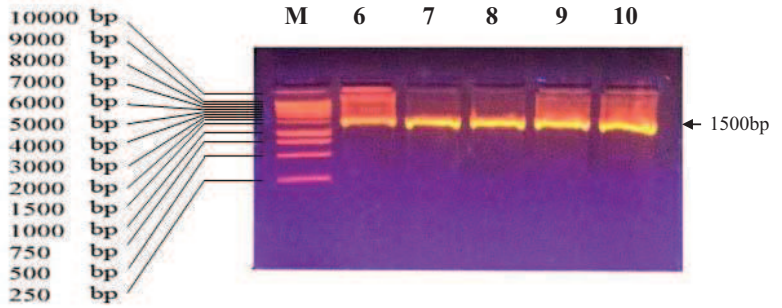


Figure (4 - 3) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and orthodontic under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. Lane 2-6: 6 to 10 of *16SrDNA* bands (1500bp) for bacterial isolates .

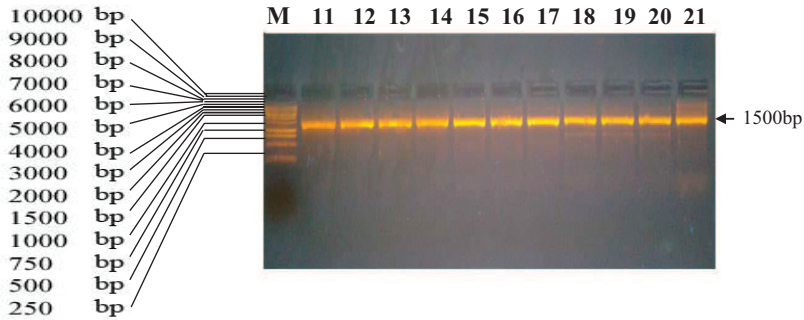


Figure (4 - 4) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and orthodontic under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. Lane 2-12: 11 to 21 of *16SrDNA* bands (1500bp) for bacterial isolates .

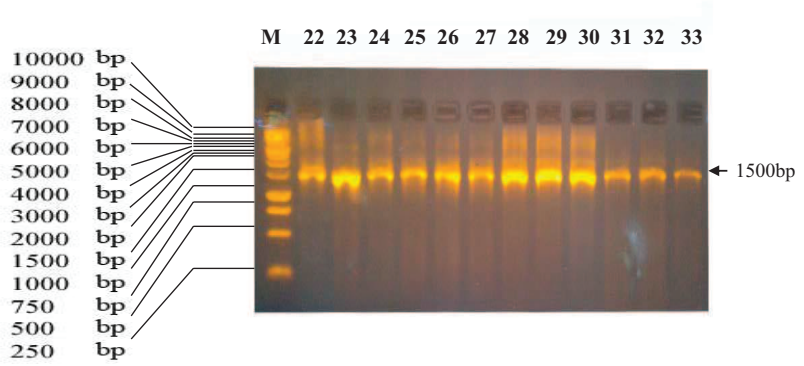


Figure (4 - 5) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and orthodontic under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. Lane 2-13: 22 to 33 of *16SrDNA* bands (1500bp) for bacterial isolates .

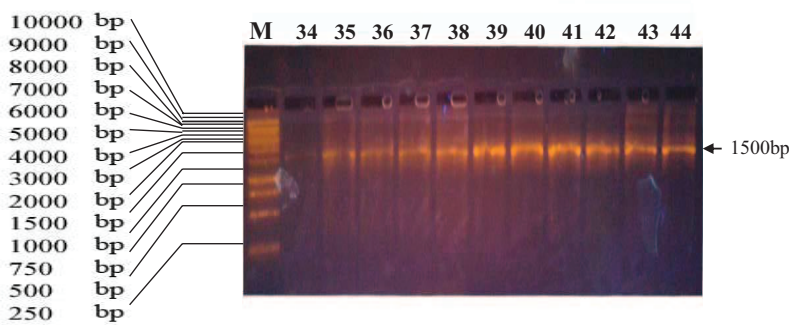


Figure (4 - 6) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and orthodontic under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. Lane 2-12: 34 to 44 of *16SrDNA* bands (1500bp) for bacterial isolates .

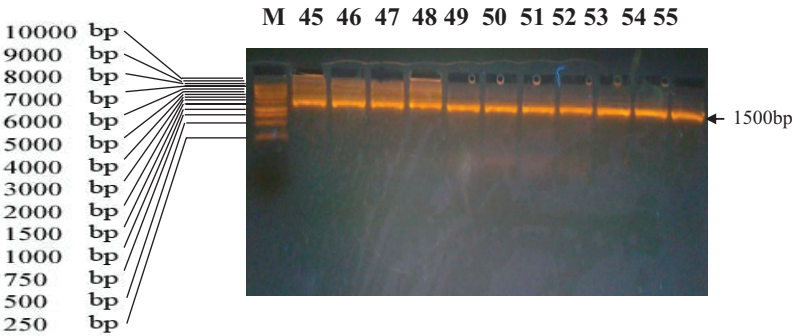


Figure (4 - 7) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and orthodontic under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. Lane 2-12: 45 to 55 of *16SrDNA* bands (1500bp) for bacterial isolates .

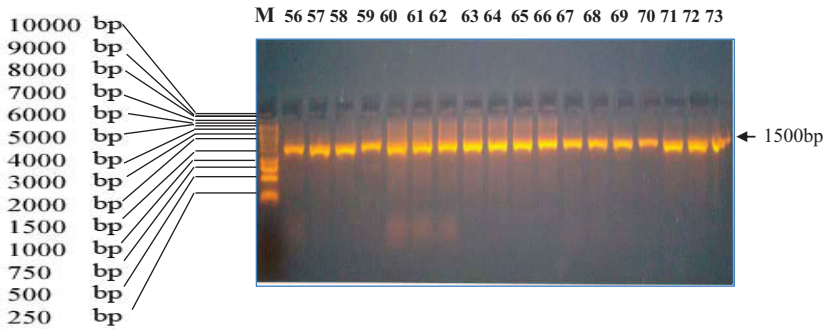


Figure (4 - 8) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and orthodontic under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. Lane 2-19: 56 to 73 of *16SrDNA* bands (1500bp) for bacterial isolates .

.

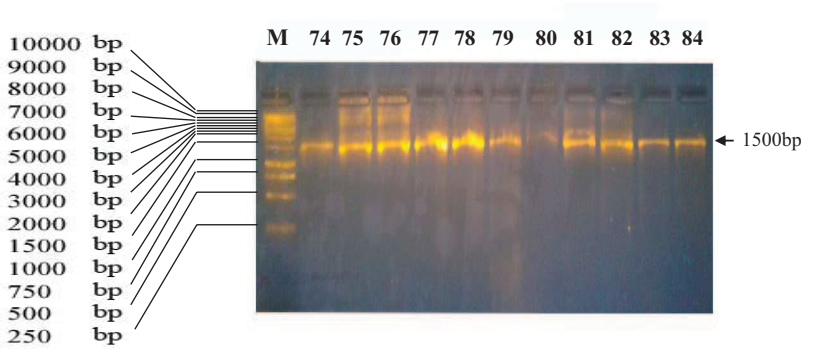


Figure (4 - 9) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and orthodontic under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. Lane 2-12: (74 to 84 of *16SrDNA* bands (1500bp) for bacterial isolates

.

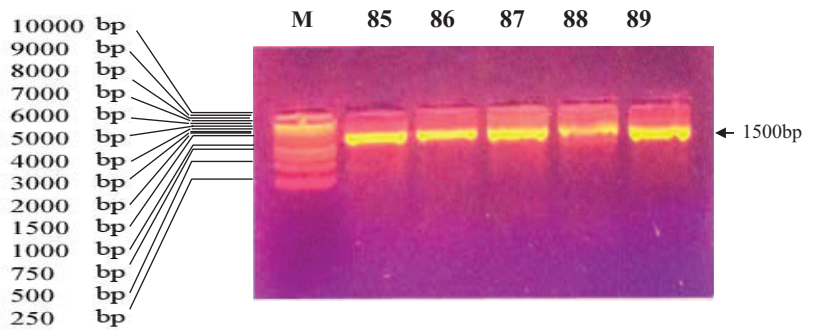


Figure (4 - 10) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and orthodontic under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. Lane 2-6: 85 to 89 of *16SrDNA* bands (1500bp) for bacterial isolates.

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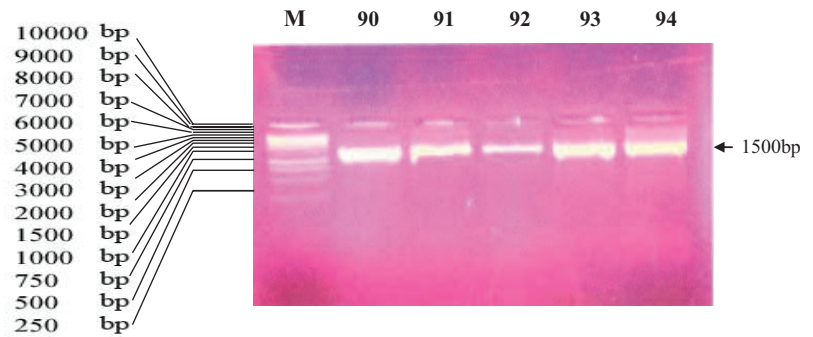


Figure (4 - 11) : Agarose (1%) gel electrophoresis of universal *16SrDNA* PCR products for bacterial isolates from denture and under UV transilluminator.Lane 1: (M) : 1Kb (250 bp – 10000bp) DNA ladder. orthodontic Lane 2-6: 90 to 94 of *16SrDNA* bands (1500bp) for bacterial isolates

4-1-3- Sequencing for universal *16S rDNA* gene:-

Table (4-1) showed out of 94 alignments *16SrDNA* gene sequences for all isolates,31 species of bacterial isolates were identified by *16SrDNA* gene sequencing (comparing with identical reference strain) from denture and orthodontic. These are*: Klebsiella pneumoniae* (n=16), *Proteus mirabilis* (n=8) , *Proteus penneri* (n=7), *Staphylocpccus aureus* (n=7)*, Enterobacter cloacae* (n=6)*, Bacillus cereus* (n=5), *Enterococcus faecalis* (n=4), *Enterobacter faecium* (n=3), *morganella morganii* (n=2), *Hafnia alvei* (n=2), *Enterobacter aerogenes* (n= 2)*, Enterobacter mori* (n=2), *Citrobacter freundii* (n=2)*, Staphylococcus epidremidis* (n=2)*, Bacillus subtilis* (n=2)*, Lactobacillus plantarum* (n= 2)*, Streptococcus anginosus* (n= 2),*Proteus houseri* (n=1),*Acinetobacter baumannii* (n=1), *Klebsiella oxytoca* (n=1)*, Lactococcus lactis* (n=1), ,*Chryseobacterium vietnamense*(n=1), *streptococcus equinus* (n=1), *Klebsiella variicala* (n=1), *Escherichia fergusonii* (n=1), *Pediococcus acidilactici* (n=1), *Staphylococcus pasteuri* (n=1), staphylococcus worneri (n=1), *Serratia marcescens* (n= 1), *Enerobacter ludwigii* (n=1), *Staphylococcus hominis*(n=1).other isolates (n=6) were fail sequencing but recognized only by morphological and gram's stain .these are: *Streptococcus* spp. (n=2) ,*Bacillus* spp.(n=1),*Staphylococcus* ssp.(n=3) .

4-1-4- Phylogenetic tree of bacterial species:-

The resultant tree rooted with *Enterobacter cloacae* as the out group, is presented in figure (4-13). This tree shows the distribution and phylogenetic relationships among the studied species and type strains.

Table (4 -1): Bacterial Species Identified By Sequencing Of Universal *16SrDNA* For Isolates From Dentures.

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
1	93	***Klebsiella pneumoniae***	GGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCC GGGAACGTATTCACCGTAGCATTCTGATCTACGATTACTAGCGATTCCGACTTCATGGAGTCGA GTTGCAGACTCCAATCCGGACTACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTT CTCTTTGTATATGCCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGATGACTTGACGT CATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCTAACCGCTGGCAA CAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGAC AGCCATGCAGCACCTGTCTCACAGTTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCTGTGGAT GTCAAGACCAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCG GGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAATCGACATCGTTTACAGCGTGGAC TACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGG GGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCT ACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATT TCACATCCGACTTGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCA CCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAA TCGATGAGGTTATTAACCTCACCGCCTTCCTCCCCGCTGAAAGTGCTTTACAACCCGAAGGCCTT CTTCACACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCT CCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCAGCTAGG GATCGTCGCCTAGGTGAGCCGTTACCCCACCTACCAGCTAATCCCATCTGGGCACATCTGATGGC ATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGCGACGTTATGCGGTATTAGCTACCGTTTCCAGT AGTTATCCCCCTCCATCAGGCAGTTTCCCAGACATTACTCACCCGTCCGCCGCTCGTCACCCGAG AGCAAGCTCTCTGTGCTACCGCTCGACTTGCATGTGT	**D***	**SY-1T 100%**	**1419bp**
2	48	***Klebsiella pneumoniae***	CAAAGATCAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCC ATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTT ATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAGC CCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGT CTCCTTTGAGTTCCCGGCCGAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAA GGCACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCA TCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACA ACCTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTC GAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGC TTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGT TAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGCCAAGGTTATTAACCTTAACGCCTTCCTCCC CGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTTG CGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAG TGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTA CTAGCTAATCCCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGC GACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGAC ATTACTCACCCGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTTGCAT GTGTAGCTGCGCCTGCCC	**D**	**DM-8T 100%**	**1419bp**
3	57	***Klebsiella pneumoniae***	CAAAGATCAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCACCCACTCCCA TGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGAT TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTTAT GAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAGCCC TGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCT CCTTTGAGTTCCCGGCCGGACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTA ACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAAGG CACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCATCG AATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCG GCCGTACTCCCCAGGCGGtCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAAC CTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCT TTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTAtTCCTCCAGATCTC TACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGA ATGCAGtTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGCTTT ACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGTcGCTGGCACGGAGTTAG CCGGTGCTTCTTCTGCGGGTAACGTCAATCGCCAAGGTTATTAACCTTAACGCCTTCCTCCCCGCT GAAAGTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTTGCGCC CATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTcTCAGTTCCAGTGTG GCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTACTAG CTAATTCCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGCGACA TTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGACATTAC TCACCCGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTTGCATGGTAG ACCGCCGCATTGCCT	**D**	**sks1T 100%**	**1411bp**
4	61	***Klebsiella pneumoniae***	CCCATGTATCACGTAGGCGCGCCGTCCGAAGGGTAACCTAACTACTTTCTTTGGTCCCAATCCCA TGGTGTGACGGGCGGTGTGGTAAAGGCCGGGAAACTATTCAACGGAGCATTGCGATCCCGATT ACTAACGAATCCCACTTCATGGAATCCAATTGGCAACTCCAATCCGGACTAGAAAGACTTTATGA AGATTGCTTGGACTCCCGAGGCCACTTCTCCTTGGAACTGCCCTTGGAACCCGTGGGGAACCCC AGGCCATAGGGGCATGGAGAATTGACGTCCTCCCCCCCTTCCTCCCGGTTAGCCCTGGGAGTCT CCTTTGAATTGCCCACCGAAATGATGGGCAACTAAGGAAAAGGGTTGCGCTCGTTGCGGGGAC TTTACCCCAACATTTTCACGACACGAGCTGACGACAACCCATGCACCACCCTGGTCTTTTAGTTCC CGAAGGCAAAGCTCTATCTCTGAGTGTTCAAAGGGATGTCAAAGACCTAGGTAAGGTTCTTCGC GTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTA ACCTTGCGGTCGTACTCCCCAGGCGGAGTGACTTAATGCGTTAGCTCCGGAAGCCAAGGGCGG AGGGCACAACCCTCCTTATCACTCTTCGTTTACGGCGTGGAACTACAAGGTATTCAATCCTTGTTT GGTCCCCCAGCCTTTCGCACCTGAGCGGTCAGTCTATGTACAAGAGAGCCGCCTCGCCACCGGG AGTCCTTCAGATCTCTTACGGCATTTTCACCGGCTACAACATGGAAATTCCCACCTCCTCCTTCTA TCATGAACTCCAAGCTCTGCCCAGGTTTCGCGAATGCACCTCTCCCACGGTTGGAGCCCGGGGG GACTTTCACACAATCAGAACTTGAACGAGACCGCCTGCGTGTCGCTTTAACGCCCAGATAATTTC GAGATAAACGCTTGGCACACCTACGTATTACCGCGGCTGCTGGGCACGGTAGTTAGCCGGTGCT TCTTCGGT	**D**	**KSST 100%**	**1030bp**
5	62	***Klebsiella pneumoniae***	GGCAATATCAAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTC CCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTAC GATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTT TATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAG CCCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAG TCTCCTTTGAGTTCCCGGCCGGACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGAC TTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAA GGCACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCA TCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACA ACCTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTC GAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGC TTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGT TAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGCCAAGGTTATTAACCTTAACGCCTTCCTCCC CGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTTG CGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAG TGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTA CTAGCTAATCCCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGC GACATTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGAC ATTACTCACCCGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTTGCAT GTGTTAGGCCTGCCGCCATGCT	**D**	**KST 100%**	**1435bp**

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
6	78	*Klebsiella pneumoniae*	GACAATATCAAGTGGTGATAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCC ATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTATT ATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATCCGCATTGTAGCACGTGTGTAGC CCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGT CTCCTTTGAGTTCCCGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTT AACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAA GGCACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCA TCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACA ACCTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TCTACGCATTTCACCGCTACACCTGGAATTCTACTCTCCTCTACTAGACTCTAGTCTGCGAGTTCG AATGCAGTCCCAGGTTGACCCCGGCGATTTCACATCCAGACTTGACAGACGCGCGTGCTGCGTGCG CTTTACGCCCAAGTAATTCCGAATAAGCGCTTGCACCCTCCGTA	D	AUH-BG208 100%	1421bp
7	80	*Klebsiella pneumoniae*	ACAATGATCATGTGTATAGGCGCCCTCCCGAACGTTAAGCTACCTACTTCTTTTGCACCCACTCCCA TGGTGGGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGA TTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTATTA TGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATCCGCATTGTAGCACGTGTGTAGCC CTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTC TCCTTTGAGTTCCCGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTA ACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCAAAG GGACCAATCGATCTCTGAAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCATC GAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCGTCAATTCATTTGAGTTTTAACCTTGCG GCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAAC CTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGC TTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCT CTACGCATTTCACCGCTACACCTGGAATTCTACTCTCCTCTACTAGACTCTAGTCTGCGAGTTCG AATGCAGTCCCAGGTTGACCCCGGCGATTTCACATCCAGACTTGACAGACGCGCGTGCTGCGTGCG CTTTACGCCCAAGTAATTCCGAATAAGCGCTTGCACCCTCCGTA	D	DSM:30104T 100%	938bp
8	89	*Klebsiella pneumoniae*	CCTATCAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCAT GGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGATT ACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTTATG AGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATCCGCATTGTAGCACGTGTGTAGCCC GGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTC CTTTGAGTTCCCGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAA CCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAAGGG ACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCATCG AATTAAACCACATGCTCACCGCTTGTGCGGGCCCCGTCAATTCATTTGAGTTTTAACCTTGCGG CCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAAC CTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGC TTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TACGCATTTCACCGCTACACCTGGAATTCTACTCTCCTCTACTAGACTCTAGTCTGCGAGTTCGA ATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGCTT TACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTA GCCGGTGCTTCTTCTGCGGTAACGTCAATCGCTAAGGTTATTAACCTTACGCCTTCCTCCTCGC TGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGC CCATTGTCCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGT GGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCATTACCCCACCTACTA GCTAATCCGACATGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTGATTTATCCTGA CGTTATCGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGACATT ACTCACCCGTCCGCCGCTGTCACCGAGAGCAAGCTCTCTGTGTACCGCTCGACTGCATGTGT AGCTGCCGCCATTGCCT	D	MGH 78578T 100%	1433bp
9	2	*Klebsiella pneumoniae*	GCCTAACACATGCAAGTCGAGCGGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGCGGCGGAC GGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAAT ACCGCATAATGTCGAAGACCAAAGTGGGGGACCTTCGGGCCTCATGCATGAGATTGGCCATG ATGGAATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGA GGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGG AATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTGTGAAGAAGGCCTTCGGG TTGTAAAGCACTTTCAGCGGGGAGGAAGGCGTTAAGGTTAATAACCTTGGCGATTGACGTTACC CGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTT AATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCG GGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTTGAGTCTTGTAGAGGGGGTAGAATT CCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCT GGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTA GTCCACGCCGTAAACGATGTCGATTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAAC GCGTTAAATCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGG CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTG ACATCCACAGAACTTAGCAGAGATGCTTTGGTGCTTCGGGAACTGTGAGACAGGTGCTGCATG GCTGTCGTCAGCTCGTGTTGTGAAATTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCTT GTTGCAGCGGTTCGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGG GATGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCATATACA AAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTATGTCGTAGTCCGGATTGGAGT CTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGCTAGATCAGAATGCTACGGTGAATA CGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGT AGCTTAACCTTCGGGAGGGGCTTACCACTTTGTATACTTGCG	OR	ATCC 700721T 100%	1427bp
10	12	*Klebsiella pneumoniae*	CACCACCGATCcAaGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTC CCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTAC GATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTT TATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATCCGCATTGTAGCACGTGTGTAG CCCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAG TCTCCTTTGAGTTCCCGGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGAC TTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAA GGGACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCA TCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACA ACCTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCGAGTTC GAATGCAGTTCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGC TTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGT TAGCCGCCTGCTTCTTCTGCGGGTAACGTCAATCGCAAGGTTATTAACCTCACGCCTTCCTCC CGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTG CGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAG TGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCATTACCCCACCTA CTAGCTAATCCCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGC GACATTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGAC ATTACTCACCCGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTTGCAT GTGTTAAGCCGCCGCCAATGCCCC	OR	4T 100%	1436 bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
11	19	***Klebsiella pneumoniae***	CACCACCGATCcAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACT CCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTA CGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACT TTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTA GCCCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCA GTCTCCTTTGAGTTCCCGGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGA CTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGA AGGCACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGC ATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTT GCGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCAC AACCTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCAC GCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGAT CTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTT CGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCG CTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAG TTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTATTAACCTCACCGCCTTCCTCC CCGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTT GCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCA GTGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCT ACTAGCTAATCCCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTG CGACATTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGA CATTACTCACCCGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTTGCA TGTGTTAGCCGCCGCCAATGCCCC	OR	4T 100%	1436 bp
12	20	***Klebsiella pneumoniae***	AAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTG ACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGATTACTAGC GATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTTATGAGGTCC GCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAGCCCTGGTCGT AAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGA GTTCCCGGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAAC ATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAAGGCACCAAT CCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCATCGAATTAA ACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTA CTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAA ATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCA CCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCA TTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGAATGCAG TTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGCTTTACGCCC AGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGT GCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTATTAACCTTATCGCCTTCCTCCCCGCTGAAA GTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTG TGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGG TCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTACTAGCTAATC CCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGCGACGTTATG CGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGACATTACTCACC CGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTTGCATGTGTAGGCT GCCCCATGCG	OR	SDM45T 100%	1430 bp
13	28	***Klebsiella pneumoniae***	CACAATAATCAAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACT CCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTA CGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACT TTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTA GCCCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCA GTCTCCTTTGAGTTCCCGGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGA CTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGA AGGCACCAAAGCATCTCTGCTAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGC ATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTT GCGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCAC AACCTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCAC GCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGAT CTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTT CGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCG CTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAG TTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTATTAACCTTATCGCCTTCCTCCC CGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTTG CGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAG TGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTA CTAGCTAATCCCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGC GACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGAC ATTACTCACCCGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTTGCAT GTGTAGCTGCCCGCCTTGCCC	OR	NBRC 105 682T 100%	1465bp
14	36	***Klebsiella pneumoniae***	CACTGATCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCA TGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGAT TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTTAT GAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAGCCC TGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCT CCTTTGAGTTCCCGGCCGAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTA ACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAAGG CACCAAAGCATCTCTGCTAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCATCG AATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCG GCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAAC CTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCT TTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTC TACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGA ATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGCTT TACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTA GCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTATTAACCTTATCGCCTTCCTCCCCG CTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTTGCG CCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTG TGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTACTA GCTAATCCCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGCGA CGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGACATT ACTCACCCGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTGCATGTGT AGGCTGCGCCATGCCG	OR	9T 100%	1429bp
15	39	***Klebsiella pneumoniae***	ACAATTGATCACGTGCGTCGCGCCCTCCTAAAGGGTAACCTACCTACTTCTTTTGGACCCACTCC CATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAAACTATTCAACGTAACATTCTGATCTACG ATTACTAACGATTCCGACTTCATGGAATCCAATTGCAAAATCCAATCCGGACTAGAAAATACTTT ATGAGGACTGCTTGGTCTCCCGAGGTCCCTTCTCTTTGTATATGCCATTGGAACACGTGTGTAAC CCTGGTCCTAAGGGCCATGAAGACTTGACCTCCTCCCCCCCTTCCTCCAGTTTATCACTGGCAGTC TCCTTTGAATTGCCGGCCTAACCGATGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTT AACCCAACATTTCACAACACGAGCTGACGACAACCATGCACCACCTGTCTCATAGTTCCCGAAAG GACAAAGCCATCTCTGTAAAGTTCTGTGGATGTCAAAACAATGTAAAGTGCTTCTCGTTGCATCG AATTAAACCACATGCGCCACCGCTTGTGCGGGCCCCCGCCAATTCATTTGAGTTTTAACCTTGCG GCCGTACTCCCCAGGCGGTCAATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAAC CTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCT TTCGCACCTGATCGTCAGTCTTTGTCCAGGGGGCCGCCTTCTTCACCGGTATTCCTCCAGATCTCT ACGCATTTCACCGCTACACCTGGAATTCTACCCCCTTCTACAAGACTCTAGCCTGTCAGCTTCGAA TGCTGATCCCACGTTGAGCCCGGGG	OR	CICR-GV4T 100%	852bp
16	42	***Klebsiella pneumoniae***	ACAAGGATCAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCC CATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTT ATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAGC CCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGT CTCCTTTGAGTTCCCGGCCGGACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAA GGCACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCA TCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACA ACCTCCAAATCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTC GAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGC TTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGT TAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAAGGTTATTAACCTTAACGCCTTCCTCCC CGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTTG CGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAG TGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTA CTAGCTAATCCCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGC GACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGAC ATTACTCACCCGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTTGCAT GTGTAGCTGCGCAAGCG	OR	TR17T 100%	1419bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
17	50	*Proteus mirabilis*	ACCCGATCAAGTGGTAGCGGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCA TGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGAT TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTAT GAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGCCC TACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCT CCTTTGAGTTCCCACCATTACGTCTGGCGACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTT AACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAAG GCACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATC GAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGC GGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAATCCACGGTTCCAAGACCACAA CCTCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGC TTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCT CTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTCA GATGCAATTCCCGACTTAAGTCCGGAGCTTTCACATCTGACTTAATTGACGCGCGTCGCGTGCGTT TACGCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTA GCCGGTGCTTCTTCTGCGGGTAACGTCAATTGACAAGGGTATTAACCTTATCACCTTCCTCCCCG CTGAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGC CCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGT GGCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTACCCACCTACTAG CTAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGAC ATTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATTA CTCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGTG TAGCTGCCGCAACGC	D	ALK419T 100%	1434 bp
18	51	*Proteus mirabilis*	CCATTTATCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCA TGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGAT TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTAT GAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGCCC TACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCT CCTTTGAGTTCCCACCATTACGTCTGGCGACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTT AACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAAG GCACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATC GAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGC GGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAATCCACGGTTCCAAGACCACAA CCTCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGC TTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCT CTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTCA GATGCAATTCCCGACTTAAGTCCGGAGCTTTCACATCTGACTTAATTGACGCGCTGCGTGCGGCT TTACGCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTA GCCGGTGCTTCTTCTGCGGGTAACGTCAATTGACAAGGGTATTAACCTTATCACCTTCCTCCCCG CTGAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGC CCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGT GGCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTACCCACCTACTAG CTAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGAC ATTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATTA CTCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGTG TAGCTGCCGCAACGC	D	ALK419T 100%	917bp
19	52	*Proteus mirabilis*	GTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGC GGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCCTGATCTACGATTACTAGCGATTCC GACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTATGAGTTCCGCTTG CTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGG CCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCTCCTTTGAGTTCCC ACCATTACGTCTGGCGACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTC ACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAAGGCACTCCTCTATCT CTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACA TGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCA GGCGGTCGATTTAACGCGTTAGCTCCAGAATCCACGGTTCCAAGACCACAACCTCTAAATCGACA TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGC GTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCAC CGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTCAGATGCAATTCCCA GCTACACATCCGACTTAAGTCCGGAGCTTTCACATCTGACTTAATTGACGCCTGCGTGCGGCTTT ACGCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGC CGGTGCTTCTTCTGCGGGTAACGTCAATTGACAAGGGTATTAACCTTATCACCTTCCTCCCCGCT GAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCC ATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTG GCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTACCCACCTACTAGC TAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGACA TTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATTA CTCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGT GTAGCTGCCGCCCATGCT	D	D27T 100%	1427bp
20	54	*Proteus mirabilis*	GACATATCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCA TGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGAT TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTAT GAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGCCC TACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCT CCTTTGAGTTCCCACCATTACGTCTGGCGACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTT AACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAAG GCACTC	D	ALK428T 100%	454bp
21	58	*Proteus mirabilis*	GACAGAGAATCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCC CATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTT ATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGC CCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGT CTCCTTTGAGTTCCCACCATTACGTCTGGCGACAAAGGATAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAA GGCACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCAT CGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCCAAGACCACA ACCTCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TCTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTC AGATGCAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACGCCTGCGTGCGCT TTACGCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTT AGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGACAAGGGTATTAACCTTATCACCTTCCTCCCC GCTGAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCG CCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTG TGGCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTACCCACCTACTA GCTAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGA CATTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATT ACTCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGT GTAGCTGCCGCCCATGCT	D	ALK419T 100%	1434bp
22	83	*Proteus mirabilis*	CCTATCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATG GTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGATTA CTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTATG AGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGCCCT ACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCTCC TTTGAGTTCCCACCATTACGTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAA CCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAAGGC ACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGA ATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGG CCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCAAGACCACAACC TCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTT CGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTA CGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTCAGAT GCAATTCCCAAGTTAAGCCTCGGGGCTTTCACATCTGACTTAATTGACCGCCTGCGTGCGGCTTTA CGCCCAGTA	D	ALK428T 99%	917bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
23	84	***Proteus mirabilis***	CGACACATCCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCC CATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACAGACTTT ATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGC CCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGT CTCCTTTGAGTTCCCACCATtACGTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAA GGCACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCAT CGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCAAGACCACA ACCTCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCACATC TCTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTC AGATGCAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCCTGCGTGCGCT TTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTT AGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGACAAGGGTATTAACCTTATCACCTTCCTCCCC GCTGAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCG CCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTG TGGCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTTACCCCACCTACTA GCTAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGA CATTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATT ACTCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGT GTAGCTGCGCATGCT	**D**	**ALK 419T 100%**	**1427bp**
24	46	***Proteus mirabilis***	AGGGTCTAAATAAAATCTATTAAAATGCATCTCGAACGTTAACCTAACAAATTTTTTTTTGCTTCC ACACCCACGGGGGGACGGGGAGTGTGTATGGGGCCCGGCCCGAAATAGGGGGATCATTACTG AATACGATGACTAACGATTCCTAATTCCTGGAACCAGTTTCGACTCCTACCCACCTTACACTATCC TTTAAACCCATTTCTTGCTCTTCGAGTCGGGGTAAAGGCCCTCTAGGTTGTAATCCCTGTGTGGC CCTAAAGGATGAGGGGCGATGGGGACTGAAATCGGCCCTTTCCCTACTTAAGACCGCCAGGGC ATTTTTTTCCCACCCCCCAAGCCGGATGAAAAAGGAAAGGGGTTACGCCAATTGCCGGAGGTTT TAAATACTTTCTCCCCCGGGGAAGGTAATAACGTTAATAACCTTTCTGATTGATCTTAACCGCAG AAAAATATCCCTAAAAGACTGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCCAAT TTTAACACAGGCTCAGGGCTTGTGCGGGCCACCGTCAATTCATTTGAGATTAACCTTGCTACCTT ACTCCCCAGCCGGC	**OR**	**SPK CZT 100%**	**122 bp**
25	9	***Staphyloc- occus aureus***	CACTTTTGTCACCTTCGACGGCTAGCTCCTAAAAGGTTACTCCACCGGCTTCGGGTGTTACAAAC TCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCT ACGATTACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAA CTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGT AGCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGC AGTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGA CTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCCG AAGGGGAAGGCTCTATCTCTAGAGTTGTCAAAGGATGTCAAGATTTGGTAAGGTTCTTCGCGTT GCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACC TTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAAC CCCCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCC CCACGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCC ATATCTCTGCGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAG TTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTACGCG CGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGT AGTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGATGTGCACAGTTACTTACACATATGTTCTT CCCTAATAACAGAGTTTTACGATCCGAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCT TTCGCCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCC AGTGTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTTGCCTTGGTAAGCCGTTACCTTACCA ACTAGCTAATGCAGCGCGGATCCATCTATAAGTGACAGCAAGACCGTCTTTCACTTTTGAACCAT GCGGTTCAAAATATTATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGG TTATCCACGTGTTACTCACCCGTCCGCCGCTAACATCAGAGAAGCAAGCTTCTCGTCCGTTCGCT CGACTTGCATGTATTAG	**OR**	**SR-05-03T 100%**	**1436bp**
26	14	***Staphyloc- occus aureus***	CACTCTGTCACTTCGACGGCTAGCTCCTAAAAGGTTACTCCACCGGCTTCGGGTGTTACAAACTC TCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCTAC GATTACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAACTT TATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGTAG CCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAG TCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCCGAA GGGGAAGGCTCTATCTCTAGAGTTGTCAAAGGATGTCAAGATTTGGTAAGGTTCTTCGCGTTGC TTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTT GCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCC CCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCC ACGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCAT ATCTCTGCGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAGTT TCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTACGCGC GCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTA GTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGATGTGCACAGTTACTTACACATATGTTCTTC CCTAATAACAGAGTTTTACGATCCGAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCTT TCGCCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCA GTGTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTTGCCTTGGTAAGCCGTTACCTTACCAA CTAGCTAATGCAGCGCGGATCCATCTATAAGTGACAGCAAGACCGTCTTTCACTTTTGAACCATG CGGTTCAAAATATTATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGGT TATCCACGTGTTACTCACCCGTCCGCCGCTAACATCAGAGAAGCAAGCTTCTCGTCCGTTCGCTC GACTTGCATGTATTAGGG	**OR**	**NBRC 12712 T 100%**	**1434 bp**
27	15	***Staphyloc- occus aureus***	CACTTCCTGTCCCACCTTCGACGGCTAGCTCCTAAAAGGTTACTCCACCGGCTTCGGGTGTTACA AACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCTG ATCTACGATTACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAA CAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTTTGTATTGTCCATTGTAGCACGTG TGTAGCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACC GGCAGTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCG GGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCC CCGAAGGGGAAGGCTCTATCTCTAGAGTTGTCAAAGGATGTCAAGATTTGGTAAGGTTCTTCGC GTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCA ACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGA AACCCCCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGA TCCCCACGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCC TCCATATCTCTGCGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTTC CAGTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTAC GCGCGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCA CGTAGTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGATGTGCACAGTTACTTACACATATGTT CTTCCCTAATAACAGAGTTTTACGATCCGAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAG GCTTTCGCCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGT TCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTTGCCTTGGTAAGCCGTTACCTTA CCAACTAGCTAATGCAGCGCGGATCCATCTATAAGTGACAGCAAGACCGTCTTTCACTTTTGAAC CATGCGGTTCAAAATATTATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGT AGGTTATCCACGTGTTACTCACCCGTCCGCCGCTAACATCAGAGAAGCAAGCTTCTCGTCCGTTC GCTCGACT	**OR**	**NBRC 12712T 100%**	**1429 bp**
28	22	***Staphyloc- occus aureus***	AACTCTGTCACTTCGACGGCTAGCTCCTAAAAGGTTACTCCACCGGCTTCGGGTGTTACAAACTC TCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCTAC GATTACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAACTT TATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGTAG CCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAG TCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCCGAA GGGGAAGGCTCTATCTCTAGAGTTGTCAAAGGATGTCAAGATTTGGTAAGGTTCTTCGCGTTGC TTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTT GCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCC CCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCC ACGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCAT ATCTCTGCGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAGTT TCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTACGCGC GCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTA GTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGATGTGCACAGTTACTTACACATATGTTCTTC CCTAATAACAGAGTTTTACGATCCGAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCTT TCGCCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCA GTGTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTTGCCTTGGTAAGCCGTTACCTTACCAA CTAGCTAATGCAGCGCGGATCCATCTATAAGTGACAGCAAGACCGTCTTTCACTTTTGAACCATG CGGTTCAAAATATTATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGGT TATCCACGTGTTACTCACCCGTCCGCCGCTAACATCAGAGAAGCAAGCTTCTCGTCCGTTCGCTC GACTTGCATGTAT	**OR**	**NBRC 12712T 100%**	**1430 bp**

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
29	29	***Staphyloc-occus aureus***	CTAATACATGCAAGTCGAGCGAACGGACGAGAAGCTTGCTTCTCTGATGTTAGCGGCGGACGG GTGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATAC CGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGTCTTGCTGTCACTTATAGATGG ATCCGCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGCATAGCCGACC TGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGT AGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTCTT CGGATCGTAAAACTCTGTTATTAGGGAAGAACATATGTGTAAGTAACTGTGCACATCTTGACGG TACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAG CGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCC CACGGCTCAACCGTGGAGGGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGG AATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTT TCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGT AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTA ACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGG GACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAATCT TGACATCCTTTGACAACTCTAGAGATAGAGCCTTCCCCTTCGGGGGACAAAGTGACAGGTGGTG CATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTA AGCTTAGTTGCCATCATTAAGTTGGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGG TGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGACAA TACAAAGGGCAGCGAAACCGCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGT AGTCTGCAACTCGACTACATGAAGCTGGAATCGCTAGTAATCGTAGATCAGCATGCTACGGTGA ATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGCCG GTGGAGTAACCTTTTAGGAGCTAGCCGTCGAAGG	OR	SR-05-03T 100%	1434bp
30	38	***Staphyloc-occus aureus***	ACCAATTGTCACTTCGACGGCTAGCTCCTAAAAGGTTACTCCACCGGCTTCGGGTGTTACAAACT CTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCTA CGATTACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAACT TTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGTA GCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCA GTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGAC TTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCCGA AGGGGAAGGCTCTATCTCTAGAGTTGTCAAAGGATGTCAAGATTTGGTAAGGTTCTTCGCGTTG CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCT TGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACC CCCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCC CACGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCA TATCTCTGCGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAGT TTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTACGCGC GCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTA GTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGATGTGCACAGTTACTTACACATATGTTCTTC CCTAATAACAGAGTTTTACGATCCGAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCTT TCGCCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCA GTGTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTTGCCTTGGTAAGCCGTTACCTTACCAA CTAGCTAATGCAGCGCGGATCCATCTATAAGTGACAGCAAGACCGTCTTTCACTTTTGAACCATG CGGTTCAAAATATTATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGGT TATCCACGTGTTACTCACCCGTCCGCCGCTAACATCAGAGAAGCAAGCTTCTCGTCCGTTCGCTC GACTTGCATGTATTAGGCACGCCGCCAATGCCC	OR	NBRC 12712T 100%	1444bp
31	45	***Staphyloc-occus aureus***	GTGCTATACATGCAGTCGAGCGAACGGACGAGAAGCTTGCTTCTCTGATGTTAGCGGCGGACG GGTGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAAT ACCGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGTCTTGCTGTCACTTATAGAT GGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGCATAGCCG ACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGC AGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTGATGAAGG TCTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACATATGTGTAAGTAACTGTGCACATCTTGA CGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGC AAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAA GCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGT GGAATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGA CTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCT GGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAG CTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGAC GGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAA ATCTTGACATCCTTTGACAACTCTAGAGATAGAGCTTTCCCCTTcGGGGGACAAAGTGACAGGTG GTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC TTAAGCTTAGTTGCCATCATTAAGTTGGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGA AGGTGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGA CAATACAAAGGGCAGCGAAACCGCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGAT TGTAGTCTGCAACTCGACTACATGAAGCTGGAATCGCTAGTAATCGTAGATCAGCATGCTACGG TGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAG CCGGTGGAGTAACCTTTTAGGAGCTAGCCGTCGAAGTGACAGAATTA	OR	SC01T 100%	1432bp
32	53	***Proteus penneri***	CACAACATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCC CATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACAGACTTT ATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGC CCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGT CTCCTTTGAGTTCCCACCATtACGTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAA GGCACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCAT CGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCAAGACCACA ACCTCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCACATC TCTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTC AGATGCAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCCTGCGTGCGCT TTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTT AGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGATAAGGGTATTAACCTTATCACCTTCCTCCCC GCTGAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCG CCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTG TGGCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTTACCCCACCTACTA GCTAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGA CATTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATT ACTCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGT GTAGCTGCCGCCATGCCCG	D	Z2T 100%	1434bp
33	85	***Proteus penneri***	ACCTATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCA TGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGAT TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACAGACTTTAT GAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGCCC TACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCT CCTTTGAGTTCCCACCATTACGTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTT AACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAAG GCACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATC GAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGC GGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCAAGACCACAA CCTCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGC TTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCACATCT CTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTCA GATGCAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCCTGCGTGCGCTT TACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTA GCCGGTGCTTCTTCTGCGGGTAACGTCAATTGAtAAGGGTATTAACCTTATCACCTTCCTCCCCGC TGAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCC CATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTG GCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTTACCCCACCTACTAGC TAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGACA TTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATTAC TCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGTGT AGCTGCCGCCATGCT	D	Z2T 100%	1434bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
34	86	***Proteus penneri***	CTATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATG GTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGATTA CTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACAGACTTTATG AGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGCCCTA CTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCTCC TTTGAGTTCCCACCATTACGTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAA CCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAAGGC ACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGA ATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGG CCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCAAGACCACAACC TCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTT CGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCACATCTCTA CGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTCAGAT GCAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCCTGCGTGCGCTTTAC GCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCC GGTGCTTCTTCTGCGGGTAACGTCAATTGAtAAGGGTATTAACCTTATCACCTTCCTCCCCGCTGA AAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCAT TGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCT GATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTTACCCCACCTACTAGCTAA TCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGACATTAT GCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATTACTCAC CCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGTGTAGCT GCCGCCCCTGCT	**D**	**Z2T 100%**	**1435bp**
35	87	***Proteus penneri***	AAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGA CGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGATTACTAGCG ATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACAGACTTTATGAGTTCCG CTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGCCCTACTCGTAA GGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCTCCTTTGAGTT CCCACCATTACGTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACAT TTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAAGGCACTCCTCTA TCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACC ACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTC CCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCAAGACCACAACCTCTAAATC GACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCT GAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCACATCTCTACGCATTT CACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTCAGATGCAATT CCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCCTGCGTGCGCTTTACGCCCAG TAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCT TCTTCTGCGGGTAACGTCAATTGACAAGGGTATTAACCTTATCACCTTCCTCCCCGCTGAAAGTA CTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGC AATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCTGATCA TCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTTACCCCACCTACTAGCTAATCCCA TATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGACATTATGCGG TATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATTACTCACCCGT CCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGTGTAGCTGCCG CACGGC	**D**	**ALK 419T 100%**	**1429bp**
36	88	***Proteus penneri***	GCCATGATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCC CATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACAGACTTT ATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGC CCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGT CTCCTTTGAGTTCCCACCATTACGTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGAC TTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGAA GGCACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCAT CGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCAAGACCACA ACCTCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCACATC TCTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTTC AGATGCAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCCTGCGTGCGCT TTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTT AGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGATAAGGGTATTAACCTTATCACCTTCCTCCCC GCTGAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCG CCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTG TGGCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTTACCCCACCTACTA GCTAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGA CATTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATT ACTCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGT GTAGC	**D**	**Z2T 100%**	**1433bp**
37	32	***Proteus penneri***	GCACTTAATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTC CCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTAC GATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACAGACT TTATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAG CCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAG TCTCCTTTGAGTTCCCACCATTACGTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGA CTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCCCGA AGGCACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGC ATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTT GCGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCAAGACCAC AACCTCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCAC GCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCACAT CTCTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCAGTTT CAGATGCAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCCTGCGTGCGC TTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGT TAGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGATAAGGGTATTAACCTTATCACCTTCCTCCCC GCTGAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCG CCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTG TGGCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTTACCCCACCTACTA GCTAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCGTAGA CATTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCATACATT ACTCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTGCATGT GTAG	**OR**	**Z2T 100%**	**1426bp**
38	47	***Proteus penneri***	AGGACCAGCAATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCA CTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATC TACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACAG ACTTTATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTG TAGCCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGG CAGTCTCCTTTGAGTTCCCACCATTACGTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCG GGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGCGTTCC CGAAGGCACTCCTCTATCTCTAAAGGATTCGCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGT TGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAA CCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCAGAAGCCACGGTTCAAGA CCACAACCTCTAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCC CCACGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCC ACATCTCTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCCAACCA GTTTCAGATGCAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCCTGCGT GCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACG GAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGATAAGGGTATTAACCTTATCACCTTCC TCCCCGCTGAAAGTACTTTACAACCCTAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGC TTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCC CAGTGTGGCTGATCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCTTTACCCCACC TACTAGCTAATCCCATATGGGTTCATCCGATAGTGCAAGGTCCGAAGAGCCCCTGCTTTGGTCCG TAGACATTATGCGGTATTAGCCACCGTTTCCAGTAGTTATCCCCCTCTATCGGGCAGATCCCCAT ACATTACTCACCCGTCCGCCGCTCGTCAGCAAGAAAGCAAGCTTTCTCCTGTTACCGCTCGACTG CATGTGTAGCTGCCGCTCCTGCAG	**OR**	**Z2T 100%**	**1433bp**

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
39	92	*Enterobacter cloacae*	CCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACT GGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGG AACTGCATTCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGG TGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGA CGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA CGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACC GCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGT GGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAACTT TCCAGAGATGGATTGGTGCCTTCGGGAACTCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCG TGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTTA GGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGT CATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGAC CTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACT CCATGAAGTCGGAATCGCTAGTAATCGTAGATCAGAATGCTACGGTGAATACGTTCCCGGGCCT TGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGG GAGGGCGCTACCACT	D	478T 100%	967bp
40	55	*Enterobacter cloacae*	CAGGTATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCC ATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTT ATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATGCGCCATTGTAGCACGTGTGTAGC CCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCaGTTTATCACTGGCAGT CTCCTTTGAGTTCCCGGCCTAACCG	D	Bio103T 100%	341bp
41	73	*Enterobacter cloacae*	AACATGATCACGTGGTAGGCGCCCTCCGAAAGGTAACCTACCTACTTCTTTTGGACCCACTCCCA TGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGAT TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTAT GAAGTCCGCTTGGTCTCCCGAGGTCCCTTCTCTTTGTATGCGCCATTGGAACACGTGTGTAACCC TGGGCCTAAGGGGCATGAAGAATTGAAGTCCTCCCCACCTTCCTCCAGTTTATCACCGGCAGTCT CCTTTGAATTGCCGGCCTAACCGATGGCAACTAAGGATAAGGGTTGCGCTCGTTGCGGGACTTA ACCCAACATTTCACAACACGAGCTGACGACAACCATGCACCACCTGTCTCCCATGTTCCGAAGAA ACCTCCTATTCCCAGGAAAGTTCTGTGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGA ATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTTAACCTTGCGG CCGTACTCCCCAGGCGGACTATTTAACGCGTTAGCTGCGGAACCCACCCCTCAAAGGCACAACC TCCAAATCGACATCCGTTTACGGCTGGAACTACCAGGGAATCTAATCTGTGTTGCTCCCCACACG CTTTCGAGCTGAGCGTCAGTCTTTGTACAGGGAGAGCCCCTTTCGCCACCGTAGTTCTCCAGATC TCTCACGGCATTCAACGGTACACACTGGGAATTTCACCCCCTCTCTATCTGACTCTCAACCTCTAA CAGTTCCCATAGGCAGTTCCCATGGGTTGAGCCCACTGGCATTTCAACATCAGACTTTATTAGAC CGCCTGC	D	AB2T 89%	914bp
42	5	*Enterobacter cloacae*	GACCCGATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCC CATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTT ATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATGCGCCATTGTAGCACGTGTGTAGC CCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGT CTCCTTTGAGTTCCCGGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGAA GGCACCAATCCATCTCTGGAAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCA TCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACA ACCTCCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTC GAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGC TTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGT TAGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGCTGCGGTTATTAACCACAACACCTTCCTCCC CGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTG CGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAG TGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCATTACCCCACCTAC TAGCTAATCCCATCTGGGCACATCTGATGGCAAGAGGCCCGAAGGTCCCCCTCTTTGGTCTTGC GACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGAC ATTACTCACCCGTCCGCCACTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGTCGACTGCATGT GTAGCTGCCGCATGCCC	OR	478T 99%	1430bp
43	6	*Enterobacter cloacae*	GCCTAACACATGCAAGTCGAACGGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGTGGCGGAC GGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAAT ACCGCATAACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCAGATGTGCCCA GATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAG AGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGG GAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGG GTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGATAAGGTTAATAACCTTGTCGATTGACGTTAC CCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGT TAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATC CCCGGGCTCAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAG AATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCC CCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTG GTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCT AACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGG GGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTaCTC TTGACATCCAGAGAACTTAGCAGAGATGCTTTGGTGCCTTCGGGAACTCTGAGACAGGTGCTGC ATGGCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAT CCTTTGTTGCCAGCGGTTAGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAG GTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCG CATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGAT TGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGG TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAG TAGGTAGCTTAACCTTCGGGAGGGCGCTTACCA	OR	SN19T 100%	1393bp
44	34	*Enterobacter cloacae*	GACACTATCAAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTC CCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATTCTGATCCAC GATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACT TTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATGCGCCATTGTAGCACGTGTGTA GCCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCA GTCTCCTTTGAGTTCCCGGCCGGACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGG ACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCG AAGGCACCAAAGCATCTCTGCTAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCT TGCGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCA CAACCTCCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCA CGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGA TCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTT TCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGC GCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGA GTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGACAGGGTTATTAACCCTGTCGCCTTCCTC CCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTT GCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCA GTGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCT ACTAGCTAATCCCATCTGGGCACATCCGATGGCAAGAGGCCCGAAGGTCCCCCTCTTTGGTCTT GCGACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAG ACATTACTCACCCGTCCGCCACTCGTCAGCGAAGCAGCAAGCTGCTTCCTGTTACCGTTCGACTT GCATGTG	OR	Nr. 3T 99%	1422bp
45	56	*Bacillus cereus*	ACTCTGTCACCTTAGGCGGCTGGCTCCAAAAAGGTTACCCCACCGACTTCGGGTGTTACAAACTC TCGGGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATCCG CGATTACTAGCGATTCCAGCTTCATGTAGGCAAGTTGCAGCCTACAATCCGAACTGAAAACGGT TTTATGAAATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCGTCCATTGTAGCACGTGTGTA GCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCA GTCACCTTAAAGTGCCCAACTAAATGATGGCAACTAAAATCAAGGGTTGCGCTCGTTGCGGGAC TTAACCCAACATCTCACGACACGAGCTGACaACAACCATGCACCACCTGTCACTCTGCTCCCGAA GGAAAAGCCCTATCTCTAGGGTTGTCAAAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCT TCAAATTAAACCACATGCTCCACCGCTGGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTT GCGGCCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCT CTAACACTTAGCACTCATCGTTTACGGCGTGAACTACCAGGGTATCTAATCCTGTTTGCTCCCCAC GCTTTCGCGCCTCAGTGTCAGTTACAGACCAGAAAAGTCGCCTTCGCCACTGGTGTTCCTCCATA TCTCTACGCATTTCACCGCTACACATGGAATTCCACTTTCcTCTTCTGCACTCAAGTCTCCCAGTTT CCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAACCACCTGCGCGCG CTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAG TTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGTGCCAGCTTATTCAACTAGCACTTGTTCTTCC CTAACAACAGAGTTTTACGACCCGAAAGCCTTCATCACTCACGCGGCGTTGCTCCGTCAGACTTT CGTCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG TGTGGCCGATCACCCTCTCAGGTCGGCTACGCATCGTTGCCTTGGTGAGCCGTTACCTCACCAAC TAGCTAATGCGACGCGGGTCCATCCATAAGTGACAGCCGAAGCCGCCTTTCAATTTCGAACCAT GCGGTTCAAAATGTTATCCGGTATTAGCCCCGGTTTCCCGGAGTTATCCCAGTCTTATGGGCAGG TTACCCACGTGTTACTCACCCGTCCGCCGCTAACTTCATAAGAGCAAGCTCTTAATCCAT	D	B1T 100%	1415bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
46	66	***Bacillus cereus***	TGTCACTTAGGCGGCTGGCTCCAAAAAGGTTACCCCACCGACTTCGGGTGTTACAAACTCTCGT GGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATCCGCGAT TACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAACGGTTTTAT GAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCGTCCATTGTAGCACGTGTGTAGCCC AGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCA CCTTAGAGTGCCCAACTtAATGATGGCAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAA CCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGA GAAGCCCTATCTCTAGGGTTGTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCG AATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCG GCCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTA ACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGC TTTCGCGCCTCAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCT CTACGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTCTCCCAGTTTCCA ATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAACCACCTGCGCGCGCTTT ACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTTA GCCGTGGCTTTCTGGTTAGGTACCGTCAAGGTGCCAGCTTATTCAACTAGCACTTGTTCTTCCCT AACAACAGAGTTTTACGACCCGAAAGCCTTCATCACTCACGCGGCGTTGCTCCGTCAGACTTTCG TCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTG TGGCCGATCACCCTCTCAGGTCGGCTACGCATCGTTGCCTTGGTGAGCCGTTACCTCACCAACTA GCTAATGCGACGCGGGTCCATCCATAAGTGACAGCCGAAGCCGCCTTTCAATTTCGAACCATGC GGTTCAAAATGTTATCCGGTATTAGCCCCGGTTTCCCGGAGTTATCCCAGTCTTATGGGCAGGTT ACCCACGTGTTACTCACCCGTCCGCCGCTAACTTCATAAGAGCAAGCTCTTAATCCATTCGCTCG ACTGCATGTATAGCACGCCGCAATTGCAT	D	JY7T 100%	1444bp
47	67	***Bacillus cereus***	GGCATGCGGCAGCTACACTGCAGTCGAGCGGATGGAATAAGAGCTTGCTCTTATGTAACTAGC GGCGGACGGGTGAGTAATGTCTGGGTAACTGGCCGATGGAACTGGAATAATTCCGGGAACGG TAGGCTAAAACCCGATAAGTTTTTGAACCGCATGGTTCGAACTTGAAAGGTCGTTTCATCTGACG CTTATGGATGGAACCGCGTCGCATTAGCTAGTTGGTGACGTAACGGCTCCCATCCGTAACTATG CTTAGACGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACCGCCCAGACTCCTACGG GAGGCAACATTAGGGAATCTTCCCCAATGGACGAAAGTCTGACGGAGCGACGCCGCGTGAGTG ATGAATGCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAAGAACAAGTGCTAGTTGAAAATGCTG GCACCTTGACGGTACCTAACCACAAAGCCCCGGCTAACTACGTGCCAACAACCGCGGTAATACG TATGTGGCAAACGTTATCCGGAATTATTGGGCGTAAAGCGCGCGCAGGTGGTTTCTTAAGTCTG ATGTGATCGCCCACGGATCTGCCGTGGAGGGTGATTGGAAACTGTCTAGACTTGAGTGCGTAA AAGGAAAGTGGAATTCCATGTGTGCCGGTGAATATGCGAAGAGATATGGAGGAGCACGAGTG CCGAAGGCGACTTTCTGGTCTGTAACTGACACTGAGGCGCGAAAGCGTGGGATAGCATACAGG ATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCT CTAGTGCTGAAGTTCACGCACTAGGCGCTCAGCCTGGGGAGTACAGCCGCAAGGCTGATACTC GGAGGAACTCGACGGGCGGCCCGGCACAAGCGGGTGTAT	D	DZ4T 90%	921bp
48	70	***Bacillus cereus***	AAAACTGTCACGTTAGGCGGCTGGCTCCTTAAGGTTACCCCACCGACTTCGGGTGTTACAAACTC TCTGGGGGTGACGGGCGGTGTGTACAGGGCCCGGGAAGTATTTCACCGCGGCAGGCTGATCCG CGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACAATCCAAACTGAAAACGGT TTTATGAGATTAGCTCCACCTCGCGGTCTTGCACCTCTTTGTACCGTCCATTGTAGCACGTGTGTA GCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCA GTCACCTTAAAGTGCCCAACTAAATGATGGCAACTAAAATCAAGGGTTGCGCTCGTTGCGGGAC TTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTCTGCTCCCGAA GGAAAAGCCCTATCTCTAGGGTTTTCAAAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTT CGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTG CGGCCGTACTCCCCAGGCGGACTGCTTATTGCGTTAACTTCACCACTAAAGGGCGGAAAGCCTC TACCACTTAGCACTCTTCGTTAACGGCGGGAACTACCAGGGAACCTAATCTGGTTTGCTCCCCAC GCTTTCGCGCTTCACTGTCAGTTAAAGACAAAAAGAGTCGCCTCCGCCATCTGGTAGTCCTTCCA ATATCTTCTACGGCATTTCACCCGCTACCACATGGAATTCCACTTTCCTTCTTCAGCACTCTAGCTC TCCCAGTATCCCAATGCACCTCTCCCACAGGTTGAGCTCGTGGGACTTTCACATCAGACTTAAGA AACCACCTAGCGCGCGCTTTACGCCCAATAATCCGGATA	D	TCCC1 1331T1 94%	942bp
49	23	***Bacillus cereus***	GCGGCTATAATGCAGTCGAGCGAATGGATTAAGAGCTTGCTCTTATGAAGTTAGCGGCGGACG GGTGAGTAACACGTGGGTAACCTGCCCATAAGACTGGGATAACTCCGGGAAACCGGGGCTAAT ACCGGATAACATTTTGAACCGCATGGTTCGAAATTGAAAGGCGGCTTCGGCTGTCACTTATGGA TGGACCCGCGTCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACGATGCGTAGCC GACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCA GCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAG GCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAAGAACAAGTGCTAGTTGAATAAGCTGGCACCT TGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGT GGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGCAGGTGGTTTCTTAAGTCTGATGTG AAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGA AAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAG GCGACTTTCTGGTCTGTAACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGAT ACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTT	OR	UAC-31T 100%	794bp
50	69	***Enterococcus faecalis***	AACTCAATGACCTTAGGCGGCTGGCTCCAAAAAGGTTACCTCACCGACTTCGGGTGTTACAAAC TCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATC CGCGATTACTAGCGATTCCGGCTTCATGCAGGCGAGTTGCAGCCTGCAATCCGAACTGAGAGAA GCTTTAAGAGATTTGCATGACCTCGCGGTCTAGCGACTCGTTGTACTTCCCATTGTAGCACGTGT GTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCG GCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGG GACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCC GAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTT GCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAAC CTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTTGCTGCAGCACTGAAGGGCGGAAAC CCTCCAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCC CACGCTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGAGCCGCCTTCGCCACTGGTGTTCCTCCA TATATCTACGCATTTCACCGCTACACATGGAATTCCACTCTCCTCTTCTGCACTCAAGTCTCCCAG TTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCCTGCGCT CGCTTTACGCCCAATAAATCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGT AGTTAGCCGTGGCTTTCTGGTTAGATACCGTCAGGGGACGTTCAGTTACTAACGTCCTtGTTCTT CTCTAACAACAGAGTTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGTTGCTCGGTCAGACT TTCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCC AGTGTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTGGCCTTGGTGAGCCGTTACCTCACC AACTAGCTAATGCACCGCGGGTCCATCCATCAGCGACACCCGAAAGCGCCTTTCACTCTTATGCC ATGCGGCATAAACTGTTATGCGGTATTAGCACCTGTTTCCAAGTGTTATCCCCCTCTGATGGGTA GGTTACCCACGTGTTACTCACCCGTCCGCCACTCCTCTTTCCAATTGAGTGCAAGCACTCGGGAG GAAAGAAGCGTTCGACTGCATGTATAGCACCCGCCCTGCCT	D	XR7T 100%	1451 bp
51	17	***Enterococcus faecalis***	AACTTCCATCACCTTAGGCGGCTGGCTCCAAAAAGGTTACCTCACCGACTTCGGGTGTTACAAAC TCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATC CGCGATTACTAGCGATTCCGGCTTCATGCAGGCGAGTTGCAGCCTGCAATCCGAACTGAGAGAA GCTTTAAGAGATTTGCATGACCTCGCGGTCTAGCGACTCGTTGTACTTCCCATTGTAGCACGTGT GTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCG GCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGG GACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCC GAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTT GCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAAC CTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTTGCTGCAGCACTGAAGGGCGGAAAC CCTCCAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCC CACGCTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGAGCCGCCTTCGCCACTGGTGTTCCTCCA TATATCtACGCATTTCACCGCTACACATGGAATTCCACTCTCCTCTTCTGCACTCAAGTCTCCCAGT TTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCCTGCGCTC GCTTTACGCCCAATAAATCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTA GTTAGCCGTGGCTTTCTGGTTAGATACCGTCAGGGGACGTTCAGTTACTAACGTCCTTGTTCTTC TCTAACAACAGAGTTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGTTGCTCGGTCAGACTT TCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCA GTGTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTGGCCTTGGTGAGCCGTTACCTCACCA ACTAGCTAATGCACCGCGGGTCCATCCATCAGCGACACCCGAAAGCGCCTTTCACTCTTATGCCA TGCGGCATAAACTGTTATGCGGTATTAGCACCTGTTTCCAAGTGTTATCCCCCTCTGATGGGTAG GTTACCCACGTGTTACTCACCCGTCCGCCACTCCTCTTTCCAATTGAGTGCAAGCACTCGGGAGG AAAGAAGCGTTCGACTTGCATGTATAGCACGCCGACTGCAC	OR	KLDS 4.0341 100%	1449bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
52	40	***Enterococcus faecalis***	GCCAATTCGCCCGTCCTAAACTGGCAGTCCAAAGGTTCACTCCCCCCGATTGCTTGCGCTCACTT GCAAGGGGAGTGGGGGAGGGGGGAGTAAACCCGGAAAACCAACCCCTCAGAAGTGGATTCTA CTGATAAAACGGGATTATTCTTCTAGGAGGTGTATGCCAAACTTCAAACCGGAGTTCAACGCTTT CTTGAAGTTTTATTGATCGACCCGGGGTGCTTTACCTTGTTGGTGACGTAACGGCTCACGAGGG CCACCATGCATAAGGGACCTGAGGGGTTGATCGGCCCCCCTGCTACTTCCACTTTGTCCCGACTC CTATCGGTGGAATTCCCGCCCAATCtTCGGCAATGGACGAAAGTCTGACCGAGCAACGCCGCGT GAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGAACAAGGACGTTAGTAACT GAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAA TACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAA GTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGAGACTTGAGTGC AGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCA GTGGCGAAGGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACA GGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCC CTTCAGTGCTGCAGCAAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACT CAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGA AGAACCTTACCAGGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGACAA AGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAAC GAGCGCAACCCTTATTGTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGACTGCCGGTGAC AAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACG TGCTACAATGGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGCAAATCTCTTAAAGCTTCT CTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGCGGATC AGCACGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTG TAACACCCGAAGTCGGTGAGGTAACCTTTTTGGAGCCAGCCGCCTAAGTGATGAAGTT	OR	OG1 RFT 97%	1246bp
53	41	***Enterococcus faecalis***	ACTTTATTCACCTTAGGCGGCTGGCTCCAAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACT CTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCC GCGATTACTAGCGATTCCGGCTTCATGCAGGCGAGTTGCAGCCTGCAATCCGAACTGAGAGAA GCTTTAAGAGATTTGCATGACCTCGCGGTCTAGCGACTCGTTGTACTTCCCATTGTAGCACGTGT GTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCG GCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGG GACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCC GAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTT GCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAAC CTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTTGCTGCAGCACTGAAGGGCGGAAAC CCTCCAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCC CACGCTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGAGCCGCCTTCGCCACTGGTGTTCCTCCA TATATCTACGCATTTCACCGCTACACATGGAATTCCACTCTCCTCTTCTGCACTCAAGTCTCCCAG TTTCCAATGACCCTCCCCGGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCCTGCG CTCGCTTTACGCCCAATAAATCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCAC GTAGTTAGCCGTGGCTTTCTGGTTAGATACCGTCAGGGGACGTTCAGTTACTAACGTCCTTGTTC TTCTCTAACAACAGAGTTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGTTGCTCGGTCAGA CTTTCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTC CCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGtGGCCTTGGTGAGCCGTTACCTCAC CAACTAGCTAATGCACCGCGGGTCCATCCATCAGCGACACCCGAAAGCGCCTTTCACTCTTATGC CATGCGGCATAAACTGTTATGCGGTATTAGCACCTGTTTCCAAGTGTTATCCCCCTCTGATGGGT AGGTTACCCACGTGTTACTCACCCGTCCGCCACTCCTCTTTCCAATTGAGTGCAAGCACTCGGGA GGAAAGAAGCGTTCGACTGCATGTATAGCACGCCCCCAATGGCC	OR	KLDS 6.0639T 100%	1632bp
54	90	***Enterococcus faecium***	GGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCC CGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGCAGGCG AGTTGCAGCCTGCAATCCGAACTGAGAGAAGCTTTAAGAGATTAGCTTAGCCTCGCGACTTCGC AACTCGTTGTACTTCCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGA CGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTTGCTAGAGTGCCCAACTGAATGATGG CAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGAC GACAACCATGCACCACCTGTCACTTTGCCCCCGAAGGGGAAGCTCTATCTCTAGAGTGGTCAAA GGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT GCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAA TGCGTTAGCTGCAGCACTGAAGGGCGGAAACCCTCCAACACTTAGCACTCATCGTTTACGGCGT GGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGAGCCTCAGCGTCAGTTACAGAC CAGAGAGCCGCCTTCGCCACTGGTGTTCCTCCATATATCTACGCATTTCACCGCTACACATGGAA TTCCACTCTCCTCTTCTGCACTCAAGTCTCCCAGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGG CTTTCACATCAGACTTAAGAAACCGCCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTT GCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTGGTTAGATACCGTC AAGGGATGAACAGTTACTCTCATCCTTGTTCTTCTCTAACAACAGAGTTTTACGATCCGAAAACC TTCTTCACTCACGCGGCGTTGCTCGGTCAGACTTTCGTCCATTGCCGAAGATTCCCTACTGCTGCC TCCCGTAGGAGTTTGGGCCGTGTCTCAGTCCCAATGTGGCCGATCACCCTCTCAGGTCGGCTAT GCATCGTGGCCTTGGTGAGCCGTTACCTCACCAACTAGCTAATGCACCGCGGGTCCATCCATCA GCGACACCCGAAAGCGCCTTTCAAATCAAAACCATGCGGTTTTGATTGTTATACGGTATTAGCAC CTGTTTCCAAGTGTTATCCCCTTCTGATGGGCAGGTTACCCACGTGTTACTCACCCGTTCGCCACT CCTCTTTTTCCGGTGGAGCAAGCTCCGGTGGAAAAAGAAGCGTTCGACTTGCA	D	044T 100%	1431bp
55	35	***Enterococcus faecium***	ATCCACCTTAGGCGGCTGGCTCCAAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGT GGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGAT TACTAGCGATTCCGGCTTCATGCAGGCGAGTTGCAGCCTGCAATCCGAACTGAGAGAAGCTTTA AGAGATTTGCATGACCTCGCGGTCTAGCGACTCGTTGTACTTCCCATTGTAGCACGTGTGTAGCC CAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTC TCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTA ACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGG GAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTC GAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGC GGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTTGCTGCAGCACTGAAGGGCGGAAACCCTCC AACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGAGCCGCCTTCGCCACTGGTGTTCCTCCATATA TCTACGCATTTCACCGCTACACATGGAATTCCACTCTCCTCTTCTGCACTCAAGTCTCCCAGTTTCC AATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCCTGCGCTCGCT TTACGCCCAATAAATCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTT AGCCGTGGCTTTCTGGTTAGATACCGTCAGGGGACGTTCAGTTACTAACGTCCTTGTTCTTCTCT AACAACAGAGTTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGTTGCTCGGTCAGACTTTCG TCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTG TGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTGGCCTTGGTGAGCCGTTACCTCACCAACTA GCTAATGCACCGCGGGTCCATCCATCAGCGACACCCGAAAGCGCCTTTCACTCTTATGCCATGCG GCATAAACTGTTATGCGGTATTAGCACCTGTTTCCAAGTGTTATCCCCCTCTGATGGGTAGGTTA CCCACGTGTTACTCACCCGTCCGCCACTCCTCTTTCCAATTGAGTGCAAGCACTCGGGAGGAAAG AAGCGTTCGACTTGCATGTATAGCACCC	OR	IB1T 100%	1450bp
56	43	***Enterococcus faecium***	AAATCATCCACTTAGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTC GTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCG ATTACTAGCGATTCCGGCTTCATGCAGGCGAGTTGCAGCCTGCAATCCGAACTGAGAGAAGCTT TAAGAGATTAGCTTAGCCTCGCGACTTCGCAACTCGTTGTACTTCCCATTGTAGCACGTGTGTAG CCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAG TCTTGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGCCCCCGAAG GGGAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTT CGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTG CGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTGAAGGGCGGAAACCCT CCAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCA CGCTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACTGGTGTTCCTCCATA TATCTACGCATTTCACCGCTACACATGGAATTCCACTCTCCTCTTCTGCACTCAAGTCTCCCAGTTT CCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCCTGCGCTCG CTTTACGCCCAATAAATCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAG TTAGCCGTGGCTTTCTGGTTAGATACCGTCAAGGGATGAACAGTTACTCTCATCCTTGTTCTTCTC TAACAACAGAGTTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGTTGCTCGGTCAGACTTTC GTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTTTGGGCCGTGTCTCAGTCCCAAT GTGGCCGATCACCCTCTCAGGTCGGCTATGCATCGTGGCCTTGGTGAGCCGTTACCTCACCAACT AGCTAATGCACCGCGGGTCCATCCATCAGCGACACCCGAAAGCGCCTTTCAAATCAAAACCATG CGGTTTTGATTGTTATACGGTATTAGCACCTGTTTCCAAGTGTTATCCCCTTCTGATGGGCAGGTT ACCCACGTGTTACTCACCCGTTCGCCACTC	OR	044T 99%	1385bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
57	91	*Morganella morganii*	GGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCC GGGAACGTATTCACCGTAGCATTCTGATCTACGATTACTAGCGATTCCGACTTCATGGAGTCGA GTTGCAGACTCCAATCCGGACTACGACGTACTTTATGAGTTCCGCTTGCCCTCGCGGGGTCGCTT CCCTTTGTATACGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGT CATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCTCCTTTGAGTTCCCGCCATCACGCGCTGGCA ACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGA CAGCCATGCAGCACCTGTCTCAGAGTTCCCGAAGGCACCAAAGCATCTCTGCTAAGTTCTCTGGA TGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCG GGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAGTCGACATCGTTTACAGCGTGGAC TACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGG GGGCCGCCTTCGCCACCGGTATTCCTCCACATCTCTACGCATTTCACCGCTACACATGGAATTCTA CCCCCCTCTACAAGACTCTAGCTGACCAGTATCAGATGCAATTCCCGGGTTAAGCCCGGGGATTT CACATCTGACTCAATCAACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCAC CCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGTCGGTAACGTCAATT GATAAGGTTATTAACCTTACCACCTTCCTCCCGACTGAAAGTACTTTACAACCCGAAGGCCTTCTT CATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCC GTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCTGATCATCCTCTCAGACCAGCTAGGGAT CGTCGCCTAGGTGAGCCGTTACCTCACCTACAAGCTAATCCCATATGGGTTCATCTGATGGCGCG AGGCCCGAAGGTCCCCCGCTTTGGTCCGAAGACATTATGCGGTATTAGCTACCGTTTCCAGTAG TTATCCCCCGCCATCAGGCAGATCCCCATACATTACTCACCCGTCCGCCGCTCGTCAGCAGAGAA GCAAGCTTCTCCCTGTTACCGCCCGACTTGCA	D	MFS 05T 99%	1414bp
58	74	*Morganella morganii*	CACAATTATCAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTC CCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTAC GATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGTACTT TATGAGTTCCGCTTGCCCTCGCGGGGTCGCTTCCCTTTGTATACGCCATTGTAGCACGTGTGTAG CCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAG TCTCCTTTGAGTTCCCGCCATCACGCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGA CTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGA AGGCACCAAAGCATCTCTGCTAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGC ATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTT GCGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCA CAACCTCCAAGTCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCA CGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCACA TCTCTACGCATTTCACCGCTACACATGGAATTCTACCCCCCTCTACAAGACTCTAGCTGACCAGTA TCAGATGCAATTCCCGGGTTAAGCCCGGGGATTTCACATCTGACTCAATCAACCGCCTGCGTGC GCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGA GTTAGCCGGTGCTTCTTCTGTCGGTAACGTCAATTGATAAGGTTATTAACCTTACCACCTTCCTCC CGACTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTT GCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCA GTGTGGCTGATCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCTCACCT ACAAGCTAATCCCATATGGGTTCATCTGATGGCGCGAGGCCCGAAGGTCCCCCGCTTTGGTCCG AAGACATTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCGCCATCAGGCAGATCCCCAT ACATTACTCACCCGTCCGCCGCTCGTCAGCAGAGAAGCAAGCTTCTCCCTGTTACCGCCCGACTT GCATGTGTTAGGCCTGCCGCCCTGCCT	D	MFS 05T 99%	1438bp
59	94	*Hafnia alvei*	TAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGG GAACGTATTCACCGTAGCATTCTGATCTACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTT GCAGACTCCAATCCGGACTACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGTTCGCTTCTC TTTGTATATGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGTCAT CCCCACCTTCCTCCGGTTTATCACCGGCAGTCTCCTTTGAGTTCCCACCATTACGTGCTGGCAACA AAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAG CCATGCAGCACCTGTCTCAGAGTTCCCGAAGGCACTAAGCTATCTCTAGCAAATTCTCTGGATGT CAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTcCACCGCTTGTGCGGG CCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGCGT TAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAGTCGACATCGTTTACAGCGTGGACTA CCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG GCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACC CCCCTCTACAAGACTCTAGCTTGCCAGTTTCAAATGCAGTTCCCAAGTTAAGCTCGGGGATTTCA CATCTGACTTAACAAACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCC TCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGAGTAACGTCAATCA CTAAGGTTATTAACCTTAATGCCTTCCTCCTCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTC ATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCG TAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCAGCTAGAGATC GTCGCCTAGGTGAGCCATTACCCCACCTACTAGCTAATCCCATCTGGGCACATCTGATGGCGTGA GGCCCGAAGGTCCCCCACTTTGGTCCGAAGACGTCATGCGGTATTAGCTACCGTTTCCAGTAGTT ATCCCCCTCCATCAGGCAGTTTCCCAGACATTACTCACCCGTCCGCCGCTCGTCACCCAGAGAGC AAGCTCTCTTGTGCTACCGCTCGACTTGCATGTGTTAGGCCTGCCG	D	E117T 100%	1408bp
60	77	*Hafnia alvei*	CACATATCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCA TGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGAT TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTTAT GAGGTCCGCTTGCTCTCGCGAGTTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAGCCC TACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCT CCTTTGAGTTCCCACCATTACTTGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTT AACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGAAG GCACTAAGCTATCTCTAGCAAATTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATC GAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGC GGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA CCTCCAAGTCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGC TTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCT CTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCTTGCCAGTTTCA AATGCAGTTCCCAAGTTAAGCTCGGGGATTTCACATCTGACTTAACAAACCGCCTGCGTGCGCTT TACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTA GCCGGTGCTTCTTCTGCGAGTAACGTCAATCACtAAGGTTATTAACCTTAATGCCTTCCTCCTCGC TGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGC CCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGT GGCTGGTCATCCTCTCAGACCAGCTAGAGATCGTCGCCTAGGTGAGCCATTACCCCACCTACTA GCTAATCCCATCTGGGCACATCTGATGGCGTGAGGCCCGAAGGTCCCCCACTTTGGTCCGAAGA CGTCATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGACATT ACTCACCCGTCCGCCGCTCGTCACCCAGAGAGCAAGCTCTCTTGTGCTACCGCTCGACTGCATGG TAGCTGCCGCATGCG	D	M3-32T 100%	1421bp
61	65	*Enterobacter aerogenes*	GACATTGATCACGTGAGTAGCGCGCTCCCGAAGGTTAACCTACCTACTTCTTTTGGACCCACTCC CATGGTGTGACGGGCGGTGTGTACAAGGGCCGGGAACGTATTCACCGTGGCATTCTGATCCAC GATTACTAACGATTCCGACTTCATGGAGTCGAATTGCAGACTCCAATCCGGACTACGAAACACTT TATGAAGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCCGCCATTGTAACACGTGTGTAA CCCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAG TCTCCTTTGAGTTCCCGGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGAC TTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAA GGCACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCA TCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGACTGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAAGGCAC CAACTCCTTATCGACATCGTTTACGGCGTGGAATACCAGGGTATCTAATCCTGGTTGCTCCCCAC GCTTTCGCACCTGCGCGTCAGTCTATGTCCAGGAGGGCCGCCTTCGCCACCGGGTAGTCCTCCA GATCTCTACGCATTTCACCGCTACACCATGGAAT	D	KNUC 5001T 82%	957bp
62	81	*Enterobacter aerogenes*	GTGCATGCGGGCAGCTACACATGCAGTCGAGCGGTTGCACTTAGAGCTTGCTCTCGTGTGACTA GCGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAAC GGTAGCTAATACCCCATAAAGTCTCTGAACCAAATGGGGGGACCTTCGGGCCTCTTTTCATCTGA TGTGCCCGGATGGGATTAGCTAGTATGTGGGGTAAGGGCTCACCTAGGCGACCATCCCTAACTG GGCTGAGAGGATGACCAGCCACACTGGAACTGACACACGGTCCACACTCCTACGGGAGGCAGC AGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAAAAGGC CTTCGGGTTGTAAAGTACTTTCTCCGAGGAGGAAGGCGTTTAGGTTAATAACCTTTGCGATTGA CGTTACTCGCAGAAAAAGCACCGGCTAACTCCGTGCCAACTACCGCGGTAATACGGAGGGTGC ACGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAA ATCCCCGGGCTCAACCTGGGAACTGCCTTCGAAACTGGCTGGCTACAGTCTTGACTTAGAGGGG GTAGAATTCCAGTGTATCGGTGAAATGCGTAGTAGATCTGCGAGGAGTACCGGTGGAGAACGC GGGCCCCTGGACACATACTGACGCTCAAGTGCGACAGCGTGCGCGAACGCACAGGATTAGATA CCCTGGTAGATCCACGCGCGTAAACGATGTCGTACATGGAGGATTGTGCGCTGGAGGCGTGGT CTTCCGCGATCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGCCTCGCGAGGATAGACTCAAA TGAGATTGACAGGGGCCCTCACAGGCGGTCGAGCATGTGGTTGTATTTGATGGTACACTGAGA ACATTCACTAGTACTCGTCACACGCTCGAGCACTCCTCAGATGATCTGAGACCTTCGGGAACTCT GTCAGAAGTGCTGTGTGGGTGTCTCAGCTCTGCTGTGAATCGTGCGTAAATCTGCAACAGCCAC CACTATCCTATGCCTGTCGATCGTTCTGGCTGGATTCATAGGAACTGCCAGGATCAGCGGAGAA AGCGGGAAGAAGGTGAGATACTGCACTTACTAGACGTCTTCACCAGTGCTCAAGCGCTAACAG GACGAGGTCAAATGCCGCATAATCTCGCAACGCT	D	LCR 83T 89%	1051bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
63	75	***Enterobacter mori***	CACAAAGATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATGCGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCGAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCAC	**D**	**R3-3T 100%**	**962bp**
64	25	***Enterobacter mori***	ATCAAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATGCGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCGAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTT	**OR**	**R3-3T 100%**	**730bp**
65	82	***Citrobacter freundii***	AAGTGGTAGCGCCCTCCCGAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATTCTGATCCACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGAAGGCACCAAAGCATCTCTGCTAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGGATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGAGTAACGTCAATTGCTGCGGTTATTAACCACAACACCTTCCTCCTCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTACTAGCTAATCCCATCTGGGCACATCCGATGGCAAGAGGCCCGAAGGTCCCCCTCTTTGGTCTTGCGACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCGGGCAGTTTCCCAGACATTACTCACCCGTCCGCCACTCGTCACCCAAGGAGCAAGCTCCTCTGTGCTACCGTCGACTGCATGGTAGCTGCCTCATGCC	**D**	**S5-19T 100%**	**1415bp**
66	27	***Citrobacter freundii***	AAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATTCTGATCCACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCGAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGAAGGCACCAAAGCATCTCTGCTAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGGATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGAGTAACGTCAATCGTTGCGGTTATTAACCACAACGCCTTCCTCCTCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTACTAGCTAATCCCATCTGGGCACATCCGATGGCAAGAGGCCCGAAGGTCCCCCTCTTTGGTCTTGCGACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCGGGCAGTTTCCCAGACATTACTCACCCGTCCGCCACTCGTCACCCAAGGAGCAAGCTCCTCTGTGCTACCGTTCGACTTGCATGTGT	**OR**	**MRB07 0408-2T 100%**	**1422bp**
67	1	***Staphylococcus epidermidis***	ACTCTGTCACTTCGACGGCTAGCTCCAATGGTTACTCCACCGGCTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCTACGATTACTAGCGATTCCAGCTTCATATAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTCTGTCCCCCGAAGGGGAAAACTCTATCTCTAGAGGGGTCAGAGGATGTCAAGATTTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCCACGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAGTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTACGCGCGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGACGTGCATAGTTACTTACACATTTGTTCTTCCCTAATAACAGAGTTTTACGATCCGAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCTTTCGCCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTACGCATCGTTGCCTTGGTAAGCCGTTACCTTACCAACTAGCTAATGCGGCGCGGATCCATCTATAAGTGACAGCAAAACCGTCTTTCACTATTGAACCATGCGGTTCAATATATTATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGGTTATCCACGTGTTACTCACCCGTCCGCCGCTAACGTCAGAGGAGCAAGCTCCTCGTCTGTTCGCTCGA	**OR**	**BBN1B -03DT 100%**	**1422bp**
68	16	***Staphylococcus epidermidis***	ACTTGTCACTTCGACGGCTAGCTCCAATGGTTACTCCACCGGCTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCTACGATTACTAGCGATTCCAGCTTCATATAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTCTGTCCCCCGAAGGGGAAAACTCTATCTCTAGAGGGGTCAGAGGATGTCAAGATTTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCCACGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAGTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTACGCGCGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGACGTGCATAGTTACTTACACATTTGTTCTTCCCTAATAACAGAGTTTTACGATCCGAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCTTTCGCCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTACGCATCGTTGCCTTGGTAAGCCGTTACCTTACCAACTAGCTAATGCGGCGCGGATCCATCTATAAGTGACAGCAAAACCGTCTTTCACTATTGAACCATGCGGTTCAATATATTATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGGTTATCCACGTGTTACTCACCCGTCCGCCGCTAACGTCAGAGGAGCAAGCTCCTCGTCTGTTCGCTCGACTTGCATGTATAGCA	**OR**	**BBN1B -03DT 100%**	**1436 bp**

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
69	13	***Bacillus subtilis***	CACCTCCTGTCACCTTCGGCGGCTGGCTCCTAAAGGTTACCTCACCGACTTCGGGTGTTACAAAC TCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATC CGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGAACTGAGAACA GATTTGTGGGATTGGCTTAACCTCGCGGTTTCGCTGCCCTTTGTTCTGTCCATTGTAGCACGTGT GTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCG GCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTAAGATCAAGGGTTGCGCTCGTTGCGG GACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTCTGCCCCC GAAGGGGACGTCCTATCTCTAGGATTGTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTT GCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGT CTTGCGACCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAA CCCCCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTC CCCACGCTTTCGCTCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTC CACATCTCTACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTCCCC AGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCCTGC GAGCCCTTTACGCCCAATAATTCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCA CGTAGTTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGTACCGCCCTATTCGAACGGTACTTGT TCTTCCCTAACAACAGAGCTTTACGATCCGAAAACCTTCATCACTCACGCGGCGTTGCTCCGTCA GACTTTCGTCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAG TCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTACGCATCGTTGCCTTGGTGAGCCGTTACCTC ACCAACTAGCTAATGCGCCGCGGGTCCATCTGTAAGTGGTAGCCGAAGCCACCTTTTATGTTTG AACCATGCGGTTCAAACAACCATCCGGTATTAGCCCCGGTTTCCCGGAGTTATCCCAGTCTTACA GGCAGGTTACCCACGTGTTACTCACCCGTCCGCCGCTAACATCAGGGAGCAAGCTCCCATCTGT CCGCTCGACTTGCATGTATAGCACCCCCATGCC	OR	N11T 100%	1444 bp
70	44	***Bacillus subtilis***	TAAAAATGCGGGAGACTAATAATGCAAGTCGAACGAGTGAACCATAGCTTGCTCTTTTGCCATT AGCTGCGGACGGGTGAGTAACTCGTTAGTAACCTGCCCATATGACTGGCATAACTCCAGGAAAC CTGGACTAATACCGGATAACATTTTAAACCGCATGGTTCGAAATTGAAAGGGGGATTCGGCTGA CACTTATGGATGGACCCTGGTCTTATTAGGTAGTTGGTGTTGTTACGGCTCACCAACGCAACGGT GCGGACCCGACCTGAAAGGGAGATCGGACTCAGTGGCACTGAGACCGCGCCCAGACTCATACG CGGCGCAGAAGTAGGAAATCGTCCCCTTTGGAAAAGAGTCAAACAGAGACGCGCCGCGTGAGT GATAAGGGCTTTCGTGTCCTAAAACTCTGGTGCTGGGGAAAAACAAGAGCTAGTGGAATAAGG TGGCACTTTGACGGTAACTAACCAGAACCCCACGGGTAACTATGTCCCCGCGCCCGCAGGAGCA CGAATGTGTAGGGCGTTATCGGTGTTTAGTGTTCGTAGGGCTCGCGCGAGCGCATTCGTATATA TGATGTTAAAGCCCACGGCTCTGCCTTGGAGGGTCTTTGGATTGTGAAAGACTTGAGTGCAGAA GAGGAGGGGAGAATTCCATGTCTAGCGAAGAAGTGCAATGAGTAAAGAATGAGCAGAAGTGG CGAAGGACACTCTGTGCTCTGTAAGTGACATTGCGGCGAGGATCCGAGGGGTGCAACAGTATT AGATACCCTGGTACTCCACTCCGCACATTATGCGTGCAGTGTGAGGTGTGGTCTCCGCCCCTGA GCGCTGAAGCTACACGCATTCAACTCTCCCACCTGGGGAGTACTAGCACCAACGCTAAAACTGA AAGGAATTGGACGGGGGCGCGGCCTGCGTAGTAGTATTTGTTTTTATTTAATCTTCTCTAAATAT CTTT	OR	BETS 11T 84%	269bp
71	24	***Lactobacillus plantarum***	CTTAGGCGGCTGGTTCCTAAAAGGTTACCCCACCGACTTTGGGTGTTACAAAC TCTCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCG GCATGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAG CCTACAATCCGAACTGAGAATGGCTTTAAGAGATTAGCTTACTCTCGCGAGTT CGCAACTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGG GCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCT CACCAGAGTGCCCAACTTAATGCTGGCAACTGATAATAAGGGTTGCGCTCGT TGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACC ACCTGTATCCATGTCCCCGAAGGGAACGTCTAATCTCTTAGATTTGCATAGTA TGTCAAGACCTGGTAAGGTTCTTCGCGTAGCTTCGAATTAAACCACATGCTCC ACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTA CTCCCCAGGCGGAATGCTTAATGCGTTAGCTGCAGCACTGAAGGGCGGAAAC CCTCCAACACTTAGCATTCATCGTTTACGGTATGGACTACCAGGGTATCTAAT CCTGTTTGCTACCCATACTTTCGAGCCTCAGCGTCAGTTACAGACCAGACAGC CGCCTTCGCCACTGGTGTTCTTCCATATATCTACGCATTTCACCGCTACACATG GAGTTCCACTGTCCTCTTCTGCACTCAAGTTTCCCAGTTTCCGATGCACTTCTT CGGTTGAGCCGAAGGCTTTCACATCAGACTTAAAAAACCGCCTGCGCTCGCTT tACGCCCAATAAATCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCT GGCACGTAGTTAGCCGTGGCTTTCTGGTTAAATACCGTCAATACCTGAACAGT TACTCTCAGATATGTTCTTCTTTAACAACAGAGTTTTACGAGCCGAAACCCTT CTTCACTCACGCGGCGTTGCTCCATCAGACTTTCGTCCATTGTGGAAGATTCC CTACTGCTGCCTCCCGTAGGAGTTTGGGCCGTGTCTCAGTCCCAATGTGGCCG ATTACCCTCTCAGGTCGGCTACGTATCATTGCCATGGTGAGCCGTTACCCCAC CATCTAGCTAATACGCCGCGGGACCATCCAAAAGTGATAGCCGAAGCCATCT TTCAAACTCGGACCATGCGGTCCAAGTTGTTATGCGGTATTAGCATCTGTTTC CAGGTGTTATCCCCCGCTTCTGGGCAGGTTTCCCACGTGTTACTCACCAGTTC GCCACTCACTCAAATGTAAATCATGATGCAAGCACCAATCAATACCAGAGTT CGTTCGACTGCATGTATAGCACGCC	OR	KLDS 1.0610T 100%	1452 bp
72	26	***Lactobacillus plantarum***	CCACTCTGTCACCTTAGGCGGCTGGTTCCTAAAAGGTTACCCCACCGACTTTG GGTGTTACAAACTCTCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAAC GTATTCACCGCGGCATGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTA GGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGATTAGCTT ACTCTCGCGAGTTCGCAACTCGTTGTACCATCCATTGTAGCACGTGTGTAGCC CAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTG TCACCGGCAGTCTCACCAGAGTGCCCAACTTAATGCTGGCAACTGATAATAA GGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACG ACAACCATGCACCACCTGTATCCATGTCCCCGAAGGGAACGTCTAATCTCTTA GATTTGCATAGTATGTCAAGACCTGGTAAGGTTCTTCGCGTAGCTTCGAATTA AACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAG CCTTGCGGCCGTACTCCCCAGGCGGAATGCTTAATGCGTTAGCTGCAGCACTG AAGGGCGGAAACCCTCCAACACTTAGCATTCATCGTTTACGGTATGGACTAC CAGGGTATCTAATCCTGTTTGCTACCCATACTTTCGAGCCTCAGCGTCAGTTA CAGACCAGACAGCCGCCTTCGCCACTGGTGTTCTTCCATATATCTACGCATTT CACCGCTACACATGGAGTTCCACTGTCCTCTTCTGCACTCAAGTTTCCCAGTTT CCGATGCACTTCTTCGGTTGAGCCGAAGGctTTCACATCAGACTTAAAAAACC GCCTGCGCTCGCTTTACGCCCAATAAATCCGGACAACGCTTGCCACCTACGTA TTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTGGTTAAATACCGTC AATACCTGAACAGTTACTCTCAGATATGTTcTTCTTTAACAACAGAGTTTTACG AGCCGAAACCCTTCTTCACTCACGCGGCGTTGCTCCATCAGACTTTCGTCCAT TGTGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTTTGGGCCGTGTCTCAGT CCCAATGTGGCCGATTACCCTCTCAGGTCGGCTACGTATCATTGCCATGGTGA GCCGTTACCCCACCATCTAGCTAATACGCCGCGGGACCATCCAAAAGTGATA GCCGAAGCCATCTTTCAAGCTCGGACCATGCGGTCCAAGTTGTTATGCGGTAT TAGCATCTGTTTCCAGGTGTTATCCCCCGCTTCTGGGCAGGTTTCCCACGTGTT ACTCACCAGTTCGCCACTCACTCAAATGTAAATCATGATGCAAGCACCAATC AATACCAGAGTTCGTTCGACtGCAtGtATAGGCTGGCGCGCTTCCGCTTT	OR	SCP21 T 100%	1454bp
73	18	***Streptococcus anginosus***	ACTCATCACTTACGCGGCTGGCTCCTAAAGGTTACCTCACCGACTTCGGTGTACAAACTCTCTGG GTGTGACGGCGGGGGTGTACAGGGCCGGGAAACGTATTCCCGCGGCGTGCTGATCCGCGATTA CTAACGATTTCCACTTTCTGGTAGCGAGTTGCAACCCTACATCCCGACTGGAAATGGCTTTTAAA GAATTACTTGGCGTCCCCGGATTGCGAACCCTTTGTACAGCCCTTGGAACACGTGGGGTACCCC AGGTCTAAAGGGGCTGGAGGATTTGACTCCTCCCCCCCTTTCTCCGGGTTATTACCGGGAGTCCC CCTAAAATGGCCCACTTAATGGAGGGAAATAAAAATAAGGGTTGGCCCTCTTGGGGGAATTAA CCCCACATCCCCCCAAACGAACTGGAGAACACCCTGGCCCACCTGGTCCCGTTGGTCCCAAAAG AATTCCTATCTCTAAAAATAGCCTCAGGATGTCCAAAACTGGTAAGGGTCTTCCCGTTGCTTCCA AATAAAACACATGGTCCACCGCCTGTGGGGGGCCCCCGCCATTTCTTTTGATTTCCACCCTGCGG GCGTACTCCCCCAGGCGGAATGGTTTATGGCGTAACTGGCGGAACTGATCCCGGAAAAGACCT AACAACCTAGCACTCATCGTTTAACGGCGTGGACTACCAAGGGTATCTAATCCTGGTTTGCTCCC CACGGCTTTTCGAGCCTCAGCGTCAGTTTACAGACAGAAAGCCGCTTTCGCCCACCGGTGTTCCT CCATATATCCTACGCATTTCACGCTACACATGGGAATTCCACTCTCCCCTCTGCACTCAGGTTAAC AGTTTCACAGCGTACCATGGTTGAAGCCACAGGCGTTTCACTTCAGACTTATTCTAACCGCCTGC GCTCGCTTTACGCCAATAATCCGGATACGCTCGGGACCTACGTATACCGCGGCTGCTGCACGTA GTAGCCGTCCCTTTCTGTTAAGTAACGTCACAGTGTGACTTCCATCTCCACATCGTCTTCCTACAA CAGAGCATTACGATCCGAACATCTCATCATGCGGCGTGCTCGGTCAGCTCGTCATGCGAGATCC TACTGCTGCTCGTAGATCTGGACAGGTTCCAGTCCATGCCGATACCTTCAGTCGCTATGTATCGT GCATGTAGCATTACTTACTGAT	OR	ATCC: 33397T 100%	1110 bp
74	37	***Streptococcus anginosus***	GGCAGTGCGGCGTGCTATACATGCaAGTAGGACGCACAGTCTATACCGTAGCTTGCTACACCAT AGGCTGTGAGTTGCGAACGGGTGAGTAACGCGTAGGTAACCTGCCTATTAGAGGGGGATAACT ATTGGAAACGATAGCTAATACCGCATAACAGTATGTAACACATGTTAGATGCTTGAAAGATGCA ATTGCATCGCTAGTAGATGGACCTGCGTTGTATTAGCTAGTAGGTAGGGTAATGGCCTACCTAG GCGACGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGA CTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGGAACCCTGACCGAGCAACGCC GCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAAGGAAGAACGAGTGTGAGAA TGGAAAGTTCATACTGTGACGGTACTTAACCAGAAAGGGACGGCTAACTACGTGCCAGCAGCC GCGGTAATACGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGT TAGAAAAGTCTGAAGTGAAAGGCAGTGGCTCAACCATTGTAGGCTTTGGAAACTGTTTAACTTG AGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAA CACCGGTGGCGAAAGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGC GAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGGTCCTTT CCGGGACTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTT GAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCA ACGCGaAGAACCTTACCAGGTCTTGACATCCCGATGCTATTTCTAGAGATAGGAAGTTTCTTCGG AACATCGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC CGCAACGAGCGCAACCCTTATTGTTAGTTGCCATCATTGAGTTGGGCACTCTAGCGAGACTGCC GGTAATAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTA CACACGTGCTACAATGGCTGGTACAACGAGTCGCAAGCCGGTGACGGCAAGCTAATCTCTGAA AGCCAGTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGTCGGAATCGCTAGTAATC GCGGATCAGCACGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGA GAGTTTGTAACACCCGAAGTCGGTGAGGTAACCGTAAGGAGCCAGCCGCCTAAGTGATAAGT	OR	PG18T 100%	1437bp

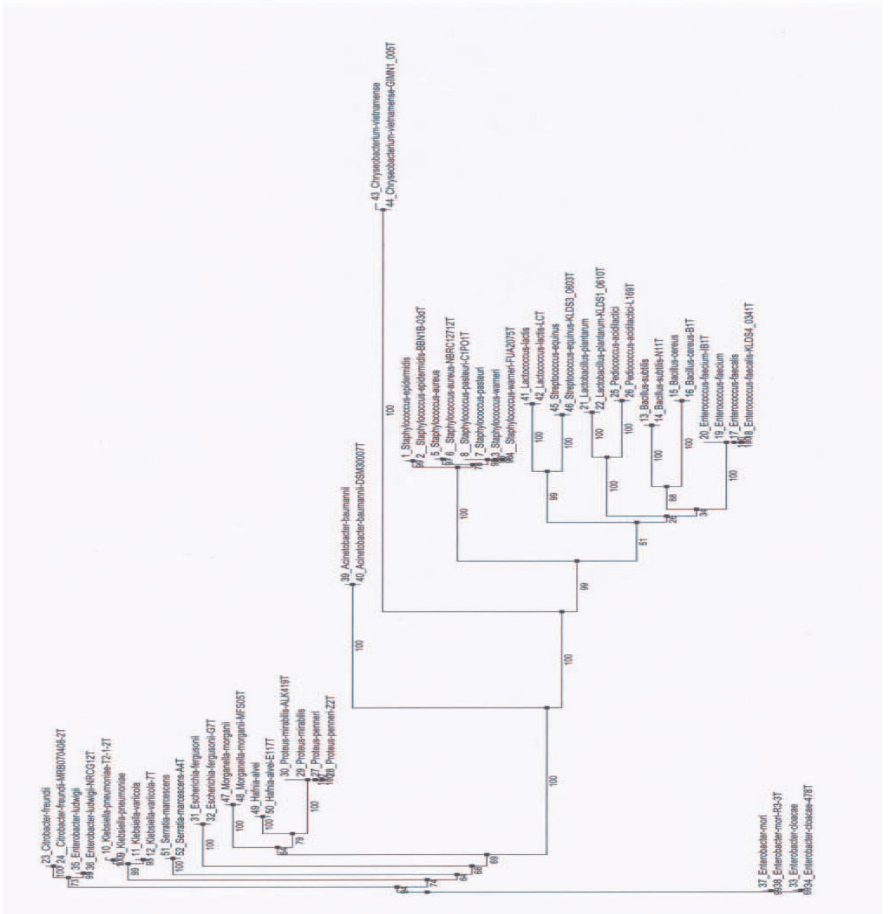
No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
75	49	***Proteus hauseri***	CGCGTAAAACACGTGCTTTATCTGACTTAGAGCTAAGCCTCCTACTTTCTGTGGACCCACTCCCCT GGTGGGGCGGGCGGTGTGTACAAGGcCCGGGAACGTATTCACCGTAGCATTCTGATCTACGAT TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACAGACTTTAT GAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATCTGCCATTGTAGCACGTGTGTAGCCC TACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTCT CCTTTGAGTTCCCACCATAAcGtGCtGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTA ACCCAACATTTCACAACACGAGTTGACAACACCCTGGCACCACCGGTCTCAGAGTTCCCAAAGG CACTCCTCTATCTCGAAAAGATTCTATGGATGTCAAGACTAGGTAAGGTTCTTCCCGTTGCATCA AATTAAACCACTGGCTCAACGGCTGGTGCGGCCCCCCGCCAATTCATTTGATTTTTATCCTGGCA GCCGTACTCCCCAGGCGG	D	S3-4T 95%	547bp
76	59	***Acinetobacter baumannii***	AGCGATAGCTACGCTGCGTGAGCCcTCTTTGCAGTTAGGCTAGCTACTTCTGGTGCAACAAACTC CCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATTCTGATCCG CGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGATCGGC TTTTTGAGATTAGCATCACATCGCTGTGTAGCAACCCTTTGTACCGACCATTGTAGCACGTGTGT AGCCCTGGCCGTAAGGGCCATGATGACTTGACGTCGTCCCCGCCTTCCTCCAGTTTGTCACTGGC AGTATCCTTAAAGTTCCCATCCGAAATGCTGGCAAGTAAGGAAAAGGGTTGCGCTCGTTGCGGG ACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTATCTAGATTCCCG AAGGCACCAATCCATCTCTGGAAAGTTTCTAGTATGTCAAGGCCAGGTAAGGTTCTTCGCGTTG CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAGTCT TGCGACCGTACTCCCCAGGCGGTCTACTTATCGCGTTAGCTGCGCCACTAAAGCCTCAAAGGCC CCAACGGCTAGTAGACATCGTTTACGGCATGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCA TGCTTTCGTACCTCAGCGTCAGTATTAGGCCAGATGGCTGCCTTCGCCATCGGTATTCCTCCAGA TCTCTACGCATTTCACCGCTACACCTGGAATTCTACCATCCTCTCCCATACTCTAGCTCACCAGTAT CGAATGCAATTCCCAAGTTAAGCTCGGGGATTTCACATCCGACTTAATAAGCCGCCTACGCACGC TTTACGCCCAGTAAATCCGATTAACGCTCGCACCCTCTGTATTACCGCGGCTGCTGGCACAGAGT TAGCCGGTGCTTATTCTGCGAGTAACGTCCACTATCTCTAGGTATTAACTAAAGTAGCCTCCTCCT CGCTTAAAGTGCTTTACAACCATAAGGCCTTCTTCACACACGCGGCATGGCTGGATCAGGGTTCC CCCCATTGTCCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGT GTGGCGGATCATCCTCTCAGACCCGCTACAGATCGTCGCCTTGGTAGGCCTTTACCCCACCAACT AGCTAATCCGACTTAGGCTCATCTATTAGCGCAAGGTCCGAAGATCCCCTGCTTTCTCCCGTAGG ACGTATGCGGTATTAGCATCCCTTTCGAGATGTTGTCCCCCACTAATAGGCAGATTCCTAAGCAT TACTCACCCGTCCGCCGCTAGGTCCGGTAGCAAGCTACCTTCCCCCGCTCGACTTGCATGTGTTA AGCCTGCCGCCATGCC	D	DSM 30007T 100%	1419bp
77	60	***Klebsiella oxytoca***	CAACATTTAATCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACT CCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATTCTGATCCA CGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACT TTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTA GCCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCA GTCTCCTTTGAGTTCCCGACCGAATCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGA CTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGA AGGCACCAAAGCATCTCTGCTAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGC ATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTT GCGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACTCCTCAAGGGAAC AACCTCCAAGTCGACATCGTTTACAGCGTGGACTACCAGGGGGAAA	D	NF9039 66T 100%	677bp
78	68	***Lactococcus lactis***	CCAATGGTCTACTTAGGAGCGCCCTCCTTGCGGTTAGGCAACCTACTTCGGGTACTCCCAACTCC CGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGC GATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGTT TTAAGAGATTAGCTAAACATCACTGTCTCGCGACTCGTTGTACCATCCATTGTAGCACGTGTGTA GCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCA GTCTCGTTAGAGTGCCCAACTTAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGAC TTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTATCCCGTGTCCCGAA GGAACTTCCTATCTCTAGGAATAGCACGAGTATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTT CGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTG CGGTCGTACTCCCCAGGCGGAGTGCTTATTGCGTTAGCTGCGATACAGAGAACTTATAGCTCCC TACATCTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGAGCCTCAGTGTCAGTTACAGGCCAGAGAGCCGCTTTCGCCACCGGTGTTCCTCCATATA TCTACGCATTTCACCGCTACACATGGAATTCCACTCTCCTCTCCTGCACTCAAGTCTACCAGTTTC CAATGCATACAATGGTTGAGCCACTGCCTTTTACACCAGACTTAATAAACCACCTGCGCTCGCTT TACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGGCTGCTGGCACGTAGTT AGCCGTCCCTTTCTGGGTAGTTACCGTCACTTGATGAGCTTTCCACTCTCACCAACGTTCTTCTCT ACCAACAGAGTTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGTTGCTCGGTCAGACTTTCG TCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTTTGGGCCGTGTCTCAGTCCCAATG TGGCCGATCACCCTCTCAGGTCGGCTATGTATCATCGCCTTGGTGAGCCTTTACCTCACCAACTA GCTAATACAACGCGGGATCATCTTTGAGTGATGCAATTGCATCTTTCAAACTTAAAACTTGTGTT TAAAGTTTTTATGCGGTATTAGCATTCGTTTCCAAATGTTGTCCCCCGCTCAAAGGCAGATTCCCC ACGCGTTACTCACCCGTTCGCTGCTCATCCAGT	D	LCT 100%	1391bp
79	29	***Chryseobact-erium vietnamense***	CGGCATGCTTACCTACGCAGCTCCTGTTACGGTCACCGACTTCAGGTACCCCAGACTTCCATGGC TTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGCCATGGCTGATGCGCGATTA CTAGCGATTCCAGCTTCATAGAGTCGAGTTGCAGACTCCAATCCGAACTGAGACCGGCTTTCGA GATTTGCATCACATCACTGTGTAGCTGCCCTCTGTACCGGCCATTGTATTACGTGTGTGGCCCAA GGCGTAAGGGCCGTGATGATTTGACGTCATCCCCACCTTCCTCTCTACTTGCGTAGGCAGTCTCA CTAGAGTCCCCAACTTAATGATGGCAACTAGTGACAGGGGTTGCGCTCGTTGCAGGACTTAACC TAACACCTCACGGCACGAGCTGACGACAACCATGCAGCACCTTGAAAAATGTCCGAAGAAAAGT CTATTTCTAAACCTGTCATTTCCCATTTAAGCCTTGGTAAGGTTCCTCGCGTATCATCGAATTAAA CCACATAATCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAAACTTGCGTTCGTACT CCCCAGGTGGCTAACTTATCACTTTCGCTTAGTCTCTGAATCCGAAAACCCAAAAACGAGTTAGC ATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGTCCATCAG CGTCAGTTGTTGCTTAGTAACCTGCCTTCGCAATTGGTGTTCTAAGTAATATCTATGCATTTCACC GCTACACTACTTATTCCAGCTACTTCAACAACACTCAAGACTTGCAGTATCAATGGCAGTTTCACA GTTAAGCTGTGAGATTTCACCACTGACTTACAAATCAGCCTACGGACCCTTTAAACCCAATAAAT CCGGATAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTATT CGTATAGTACCTTCAGCTAGATACACGTATCTAGGTTTATCCCTATACAAAAGAAGTTTACAACC CATAGGGCCGTCGTCCTTCACGCGGGATGGCTGGATCAGGCTCTCACCCATTGTCCAATATTCCT CACTGCTGCCTCCCGTAGGAGTCTGGTCCGTGTCTCAGTACCAGTGTGGGGGATCACCCTCTCA GGCCCCCTAAAGATCGTAGACTTGGTGAGCCGTTACCTCACCAACTATCTAATCTTGCGCGTGCC CATCTCTATCCACCGGAGTTTTCAATACCAGATGATGCCATCCAATATATTATGGGGTATTAATCT TCCTTTCGAAAGGCTATCCCCCAGATAAAGGCAGGTTGCACACGTGTTCCGCACCCGT	D	GIMN 1.005T 99%	1389bp
80	72	***Streptococcus equinus***	ACTTATCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCT CGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGC GATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCT TTAAGAGATTTGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTA GCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATTACCGGCA GTCTCGCTAGAGTGCCCAACTTAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGAC TTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTTCCGAA GAAACTTCCTATCTCTAGGAATAGCATCGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTT CGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTG CGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCGGCACTAAGCCCCGGAAAGGGC CTAACACCTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCA CGCTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCCTCCATA TATCTACGCATTTCACCGCTACACATGGAATTCCACTCTCCCCTTCTGCACTCAAGTCTAACAGTT TCCAAAGCGAACAATGGTTAAGCCACTGCCTTTAACTTCAGACTTATTAAACCGCCTGCGCTCGC TTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGGCTGCTGGCACGTAG TTAGCCGTCCCTTTCTGGTAAGTTACCGTCACTGTGTGAACTTTCCACTCTCACACACGTTCTTCTC TTACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGTTGCTCGGTCAGGGTTGC CCCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGT GTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGTCGCCTTGGTGAGCCGTTACCTCACCAACT AGCTAATACAACGCAGGTCCATCTACTAGTGAAGCAATTGCTCCTTTCAAGCATCTAACATGGGT TAAATGCTGTTATGCGGTATTAGCTATCGTTTCCAATAGTTATCCCCCGCTAGTAGGCAGGTTAC CTACGCGTTACTCACCCGTTCGCAACTCTTCCAACTTTAGCAAGCTAAAGTCTTCAGCGTTCTACT TGCATGTATAGCACCCCGCCACTGCG	D	KLDS 3.0603T 100%	1438bp
81	31	***Staphylococcus pasteuri***	CATTCTGTTCACTTCGACGGCTAGCTCCATAAATGGTTACTCCACCGGCTTCGGGTGTTACAAAC TCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCT ACGATTACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAA CTTTATGGGATTTGCTTGACCTCGCGGTTTAGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGT AGCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGC AGTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGA CTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCCG AAGGGGAAGACTCTATCTCTAGAGCGGTCAAAGGATGTCAAGATTTGGTAAGGTTCTTCGCGTT GCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACC TTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAAC CCCCTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCC CCACGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCC ATATCTCTGCGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAG TTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTACGCG CGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGT AGTTAGCCGTGGCTTTCTGATCAGTACCGTCAGATGTGCACAGTTACTTACACATTTGTTCTTCCC TGATAACAGAGTTTTACGAT	OR	C1P O1T 100%	1051 bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
82	76	***Klebsiella variicola***	GGCAAGATCCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCC CATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCTACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACATACTTT ATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATATGCCATTGTAGCACGTGTGTAGC CCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGT CTCCTTTGAGTTCCCGGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAA GGCACCAATCCATCTCTGGAAAGTTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCA TCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACA ACCTCCAAATCGACATCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTC GAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGC TTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGT TAGCCGGTGCTTCTTCTGCGGGTAACGTCAATCGATGAGGTTATTAACCTCACCGCCTTCCTCCC CGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTTG CGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAG TGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTA CCAGCTAATCCCATCTGGGCACATCTGATGGCATGAGGCCCGAAGGTCCCCCACTTTGGTCTTGC GACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGAC ATTACTCACCCGTCCGCCGCTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGCTCGACTGCATG TGTAGCTGCGCATGCA	D	7T 100%	1428bp
83	79	***Staphylococcus hominis***	ACCGCTAGCAGACGTTCAAGGCTATCTCGAGTGGTTACTCCAACGGCTTTTTGTGTTACAAACTC TCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTCACTCGCTGATCTAC GATTACTAGCGATTCCCTGTTCGTGTACTCGAGTTGGCCACTACAATCCGAACTGACAACAACTT TATGGGAGTTGCTTGACCTCGCGGGTTCTCTGCCCTTTGTATTGTCCATTGTACCACGTGTGTAG CCCAAATCATAAGGGGCATGATGATTTGGCGTCCTCCCCACCTTCCTCCGGTTTGTCACCGGGGG TCAACTTAGAGTGCCGAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATCTCACGACACGAACTGACGACAACCATGCACCACCTGTCACTTTGTCCCCCGAA GGGGAAACTTCTATCTCTAGAAGGGTCAAAGGATGTCAAGATTTGGTAAGGTTCTTCGCGTTGC TTCGAATTAAACCAGATGCTCCACCGCTTGGGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCT TGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACC CCCTAACACTTATCACTCATCGTTTACGGAGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCC ACGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAAGTCGCCTTCGCCACTGGTGTTCCTCCA TATCTCTGCGCATTTCAACGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTCCAGTT TCCAATGACCCTCCACGGTTGATCCGTGGGCTTTCACATCACACTTAAAAAACCGCCTACGCGCG CTTTACGTCCAATAATTCCGGATAACGCATTGCCACCTACGTATTACCGCGGCTGCTGGCACGTA GTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGACGTGCACAGTTACTTACACGTTTGTTCTTC CCTAATAACAGAGTTTTACGATCCGAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCTT TCGCCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCA GTGTGGCCGATCACCCTCTCAGGTCGGCTACGTATCGTTGCCTTGGTAAGCCGTTACCTTACCAA CTAGCTAATACGGCGCAGGTCCATCTATAAGTGATAGCAAAGCCATCTTTCACTATCGAACCATG CGGTTCGAAATATTATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGGT TACCTACGTGTTACTCACCCGTCCGCCGCTAACGTCAAAGGAGCAAGCTCCTCGTCTGTTCGCTC TGAGATGCACGTCTATACTCCTGCCCTGTTTCCG	D	L5-285T 97%	1411bp
84	75	***Escherichia fergusonii***	GCAATTATCAAGTGGTAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCC ATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATTCTGATCCACG ATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTT ATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATGCGCCATTGTAGCACGTGTGTAGC CCTGGTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGT CTCCTTTGAGTTCCCGGCCGGACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCACGGTTCCCGAA GGCACATTCTCATCTCTGAAAACTTCCGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCAT CGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTG CGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACA ACCTCCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG CTTTCGCACCTGAGCGTCAGTCTTCGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATC TCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACGAGACTCAAGCTTGCCAGTATC AGATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCTGACTTAACAAACCGCCTGCGTGCGC TTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGT TAGCCGGTGCTTCTTCTGCGGGTAACGTCAATGAGCAAAGGTATTAACTTTACTCCCTTCCTCCC CGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTG CGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAG TGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCCACCTA CTAGCTAATCCCATCTGGGCACATCCGATGGCAAGAGGCCCGAAGGTCCCCCTCTTTGGTCTTGC GACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGAC ATTACTCACCCGTCCGCCACTCGTCAGCGAAGAAGCAAGCTGTTTCCTGTTACCGTTCGACTTGC ATGTGTAGCTGCCGCATGCCC	D	G7T 100%	1430bp
85	30	***Pediococcus acidilactici***	CCAATCTGTCCACCTTAGACGGCTAGCTCCTAAAAGGTTACCCCACCGGCTTTGGGTGTTACAAA CTCTCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGAT CCGCGATTACTAGCGATTCCGACTTCGTGTAGGCGAGTTGCAGCCTACAGTCCGAACTGAGAAT GGTTTTAAGAGATTAGCTAAACCTCGCGGTTTCGCAACTCGTTGTACCATCCATTGTAGCACGTG TGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCGTCCCCACCTTCCTCCGGTTTGTCACC GGCAGTCTCACTAGAGTGCCCAACTGAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCG GGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCATTCTGTCCC CGAAGGGAACGCCTAATCTCTTAGGTTGGCAGAAGATGTCAAGACCTGGTAAGGTTCTTCGCGT AGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCTTTTGAGTTTCAA CCTTGCGGTCGTACTCCCCAGGCGGATTACTTAATGCGTTAGCTGCAGCACTGAAGGGCGGAAA CCCTCCAACACTTAGTAATCATCGTTTACGGCATGGACTACCAGGGTATCTAATCCTGTTCGCTA CCCATGCTTTCGAGCCTCAGCGTCAGTTACAGACCAGACAGCCGCCTTCGCCACTGGTGTTCTTC CATATATCTACGCATTTCACCGCTACACATGGAGTTCCACTGTCCTCTTCTGCACTCAAGTCTCCC AGTTTCCAATGCACTTCTTCGGTTGAGCCGAAGGCTTTCACATTAGACTTAAAAGACCGCCTGCG CTCGCTTTACGCCCAATAAATCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCAC GTAGTTAGCCGTGGCTTTCTGGTTAAATACCGTCACTGGGTGAACAGTTACTCTCACCCACGTTC TTCTTTAACAACAGAGCTTTACGAGCCGAAACCCTTCTTCACTCACGCGGCGTTGCTCCATCAGA CTTGCGTCCATTGTGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTC CCAATGTGGCCGATTACCCTCTCAGGTCGGCTACGCATCATCGCCTTGGTGAGCCGTTACCTCAC CAACTAGCTAATGCGCCGCGGGTCCATCCAGAAGTGATAGCAGAGCCATCTTTTAAAAGAAAAC CAGGCGGTTTTCTCTGTTATACGGTATTAGCATCTGTTTCCAGGTGTTATCCCCTGCTTCTGGGCA GGTTACCCACGTGTTACTCACCCGTCCGCCACTCACTTCGTGTTAAAATCTCATTCAGTGCAAGC ACGTCATAATCAATTAACGGAAGTTCGTTCGACTTGCATTATAGCACCCCCCCAACGCCC	OR	BFE 8260T 100%	1472 bp
86	11	***Staphylococcus warneri***	ACTTCGTCACTTCGACGGCTAGCTCCATAAATGGTTACTCCACCGGCTTCGGGTGTTACAAACTC TCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCTAC GATTACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAACTT TATGGGATTTGCTTGACCTCGCGGTTTAGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGTAG CCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAG TCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGACT TAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCCGAA GGGGAAGACTCTATCTCTAGAGCGGTCAAAGGATGTCAAGATTTGGTAAGGTTCTTCGCGTTGC TTCGAATTAAACCACATGCTCCACCGCTTGtGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTT GCGGTCGTACTCCCCAGGCGGAGTGCTTAAGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCC CTAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCCA CGCTTTCGCACATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATA TCTCTGCGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAGTTT CCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTACGCGCG CTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAG TTAGCCGTGGCTTTCTGATCAGGTACCGTCAAGATGTGCACAGTTACTTACACATTTGTTCTTCCC TGATAACAGAGTTTTACGATCCGAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCTTTC GCCCATTGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGT GTGGCCGATCACCCTCTCAGGTCGGCTACGTATCGTTGCCTTGGTAAGCCGTTACCTTACCAACT AGCTAATACGGCGCGGATCCATCTATAAGTGACAGCAAAGCCGCCTTTCACTATTGAACCATGC GGTTCAATATGTTATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGGTT ATCCACGTGTTACTCACCCGTCCGCCGCTAACGTCAAAGGAGCAAGCTCCTTATCTGTTCGCTCG ACTTGCATGTATAGCAC	OR	FUA 2 075 100%	1433bp

No.	No. of isolate	Bacterial species	Nucleotide sequence	source	Identical with Strain	Length (bp)
87	7	*Enterobacter ludwigii*	CAGCAATCAAAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATTCTGATCCACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTATGAGGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATGCGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCTAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCGAAGGCACCAAAGCATCTCTGCTAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGAATGCAGTTCCCAGGCTTGAGCCCGGGATTTCACATCCGACTTGACAGACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATTGCTCAATCGACAAGGTTATTAACCTTATCGACTTTCCTCCCCGCTGAAAGTACTTTACAACCCGAAGGCCTTCTTCATACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCACCTACTAGCTAATCCCATCTGGGCACATCTGATGGCAAGAGGCCCGAAGGTCCCCCTCTTTGGTCTTGCGACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGACATTACTCACCCGTCCGCCACTCGTCACCCGAGAGCAAGCTCTCTGTGCTACCGTTCGACTTGCATGTGTAAGCTGCCCCACGCC	OR	NRC G12T 99%	1420bp
88	8	*Serratia marcescens*	CACCGATCAAAGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATTCTGATCCACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTATGAGGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTATGCGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCGAACCGCTGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCGAAGGCACCAATCCATCTCTGGAAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTGAGCGTCAGTCTTCGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTAGGAAGCTCTAGCTTGCCAGTTTCGAATGCAGTTCCCAGGCTTGAGCCCGGGGATTTCACATCTGACTTAACAAACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCGGCAGGGAGTTAGCTGGTGCTTCTTCTGCGAGTAACGTCAATTGATGAACGTATTAAGTTCACCACCTTCCTCCTCCTGCTGAAAGTGCTTTACAACCCGAAGGCCTTCTTCACACACGCGGCATGGCTGCATCAGGCTTGCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCCAGTGTGGCTGGTCATCCTCTCAGACCAGCTAGGGATCGTCGCCTAGGTGAGCCGTTACCCACCTACTAGCTAATCCCATCTGGGCACATCTGATGGCAAGAGGCCCGAAGGTCCCCCTCTTTGGTCTTGCGACGTTATGCGGTATTAGCTACCGTTTCCAGTAGTTATCCCCCTCCATCAGGCAGTTTCCCAGACATTACTCACCCGTCCGCCACTCGTCACCCGAGGAGCAAGCTC	OR	A4T 100%	1397bp
89	3	*Staphylocpccus Spp.*	**Failed to sequencing**	OR	—	—
90	4	*Staphylocpccus Spp*	**Failed to sequencing**	OR	—	—
91	10	*Staphylocpccus Spp*	**Failed to sequencing**	OR	—	—
92	21	*Streptococcus Spp.*	**Failed to sequencing**	OR	—	—
93	63	*Streptococcus spp*	**Failed to sequencing**	D	—	—
94	64	*Bacillus spp*	**Failed to sequencing**	D	—	—

* D : Denture

** OR : Orthodontic



T: type strain, the sequence of each is available from http://blast .ncbi. nlm.nih.gov.

Figure (4 -12): Rooted neighbor joining phylogenetic tree constructed from concatenated sequences of (893bp)for bacterial species (derived from an alignment of *16SrDNA* gene sequences) then produced by (MAFFT)multiple alignment program for amino acid or nucleotide sequences and visualized using" forester" software. This NJ tree showing the distribution and phylogenetic relationships of 28 different species identified in this study and their reference strains (T). The tree has been rooted with *Enterobacter cloacae* or

4-1-5-Detection of new bacterial strain from denture and orthodontic isolates:-

In the present study four bacterial strains were identified and recorded to be new in the world . Therefore, they were tested in European Nucleotide Archive (ENA),National Centre for Biotechnology Information (NCBI) and Gene Bank (appendix-2) . These are 7-*Enterobacter ludwigii* "IRQBAS1" (HG003646), 34-*Enterobacter cloacae* "IRQBAS2" (HG003647) isolated from orthodontic , 71-*Chryseobacterium vietnamense* "IRQBAS3" (HG003648) and 74-*Morganella morganii* "IRQBAS4" (HG003649) isolated from dentures, showed 99% sequence identity with reference strains NRCG12 , Nr.3, GIMM1.005 and MFS05 respectively . 7- *Enterobacter ludwigii* was different from strain NRCG12 as a result to a frame shift mutation (deletion of base C) from the sequence at position 453 bp changing all the following amino acids , (Figure 4-13). While,34-*Enterobacter cloacae* was different from strain Nr.3 in two positions of nucleotide sequences; the first one was by point mutation (transversion) of base G instead of C at position 462 bp changing the amino acid Thr (ACC) to Ser (AGC) , and the second was point mutation (transversion) of base C instead of G at position 471bp changing the amino acid Gly (GCT) to Ala (GGT), (Figure 4 -14) .

On the other hand , 71- *Chryseobacterium vietnamense* was different from strain GIMN1.005 in eight positions of nucleotide sequences, the first one was point mutation (transition) of base A instead of G at position 208bp changing the amino acid Arg (CGC) to His (CAC) as Figure (4 - 15), the second was point mutation (trransversion) of base T instead of A at position 102bp changing the amino acid

Gln (CAG) to Leu (CTG), the third was point mutation (transition) of base G instead of A at position 149bp changing amino acid Asn (TAG) to Asp (TGG) , the fourth was point mutation (transition) of base C instead of T at position 160bp changing stop codon (TTT) to amino acid Trp (TCT) ,the fifth and sixth were mutation changing of base G instead of A at position 163bp and A instead C at position 341bp respectively, but without changing the type of amino acids Tyr (GGT) or (GAT) and Arg (CGA) or (AGA) respectively (Figure 4-16 and 4-17), the seventh mutation was point mutation (transversion) of base T instead of G changing amino acid Gly (GGA) to stop codon (TGA) figure (4-18), the last mutation was point mutation (transition) of base C instead of T at position 361bp changing amino acid Pro (TCC) to Ser (CCC), as Figure (4 -19). While 74-*Morganella morganii* was different from strain MFS05 in three positions of nucleotide sequences ,all of them were frame shift mutation (deletion of base G , C and T) from the sequence position 534bp , 58 bp and 712bp respectively, changing all the following amino acids (Figure 4 – 20 , 4 – 21 and 4-22) respectively .

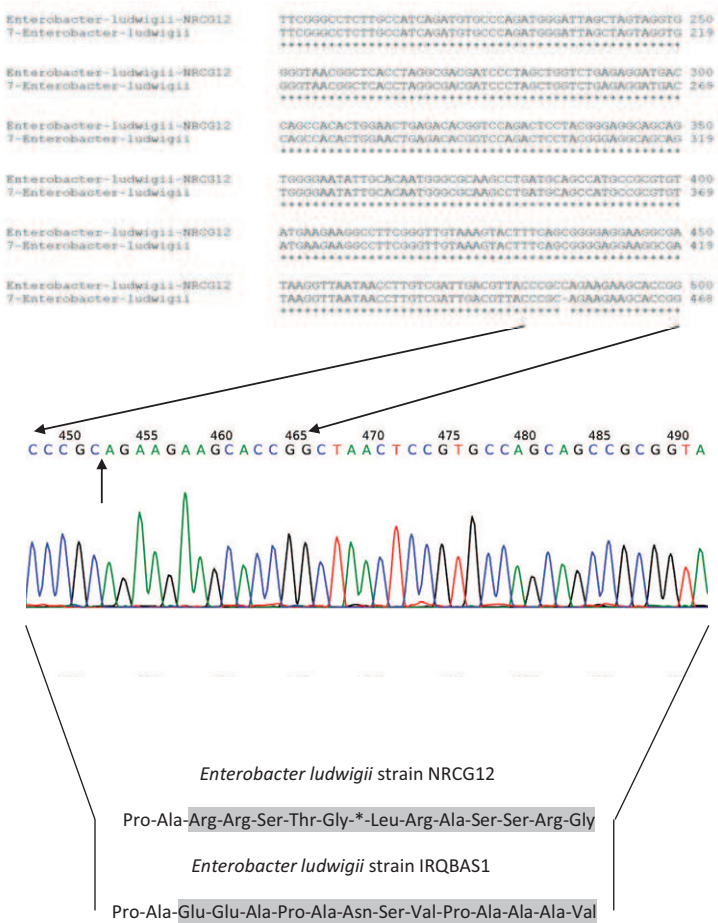


Figure (4 - 13): CLUSTALW for comparison of nucleotide sequences alignment for *16SrDNA* gene of 7-*Enterobacter ludwigii* identical (99%) to strain NRCG12 showed frame shift mutation (deletion nucleotide C) at the position 453bp changing all the following amino acid

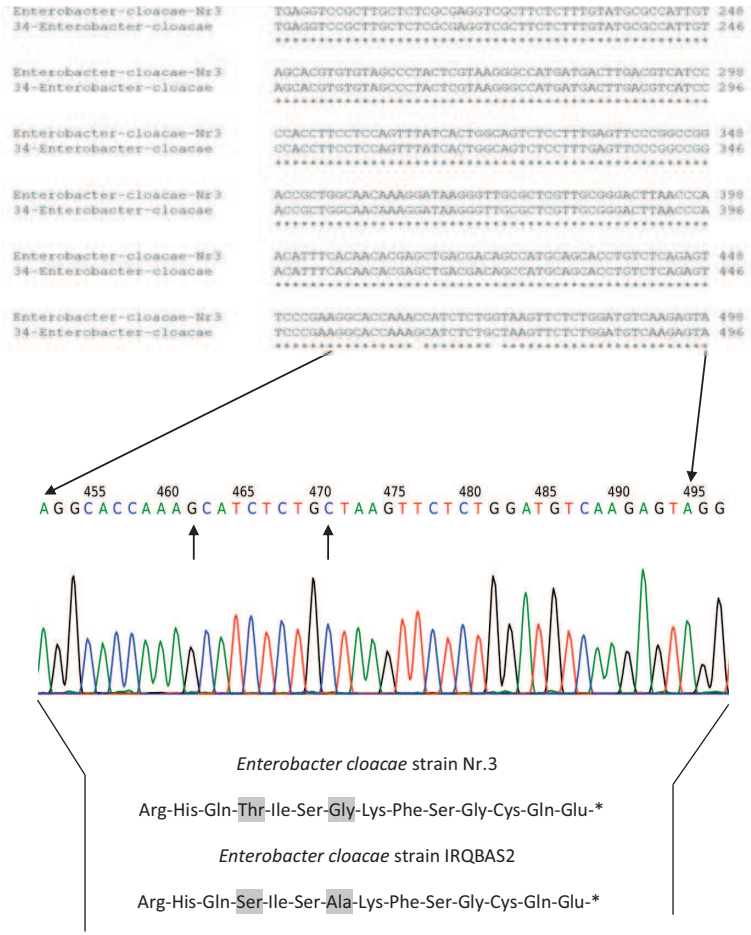


Figure (4 -14): CLUSTALW for comparison of nucleotide sequences alignment for *16SrDNA* gene of 34- *Enterobacter cloacae* identical (99%) to strain Nr.3 showed two point mutation type Transversion : G instead of C at the position 462bp changing the amino acid Thr (ACC) to Ser (AGC) and C instead of G at the position 471bp changing the amino acid Gly (GGT) to Ala (GCT).

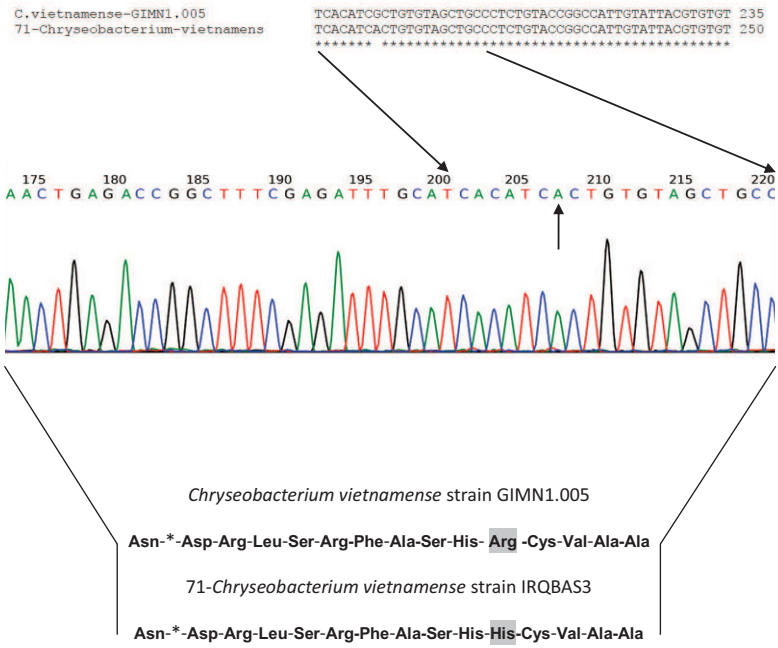


Figure (4 - 15): CLUSTALW for comparison of nucleotide sequences alignment for *16SrDNA* gene of 71- *Chryseobacterium vietnamense* identical (99%) to strain GIMN1.005; showed point mutation type transversion A instead of G at the position 207bp changing the amino acid Arg(CGC) to His (CAC).

Figure (4 – 16): CLUSTALW for comparison of nucleotide sequences alignment for *16SrDNA* gene of 71- *Chryseobacterium vietnamense* identical (99%) to strain GIMN1.005; showed point mutation type transversion T instead of A at the position 102bp changing the amino acid Gln (CAG) to Lus(CTC),and point mutation type transition G instead of A at the position 149bp changing amino acid Asn (AAT) TO Asp (GAT),and point mutation type transition C instead of T at the position 160bp changing the stop codon (ATT) to Trp (ATC),and point mutation type transition G instead of A at position 163bp without changing the type of amino acid .

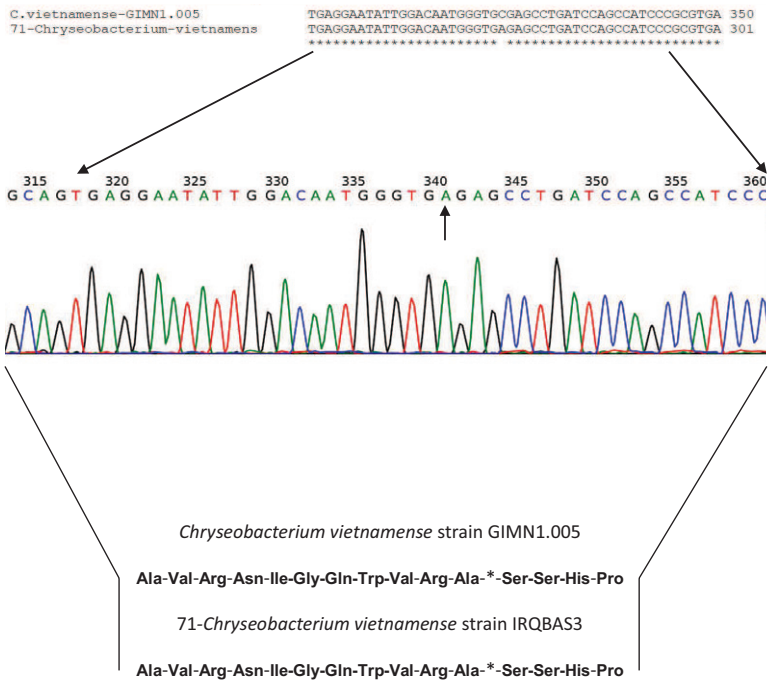


Figure (4 – 17): CLUSTALW for comparison of nucleotide sequences alignment for *16SrDNA* gene of 71- *Chryseobacterium vietnamense* identical (99%) to strain GIMN1.005; showed point mutation type transversion A instead of C at the position 341bp without changing the type of amino acid .

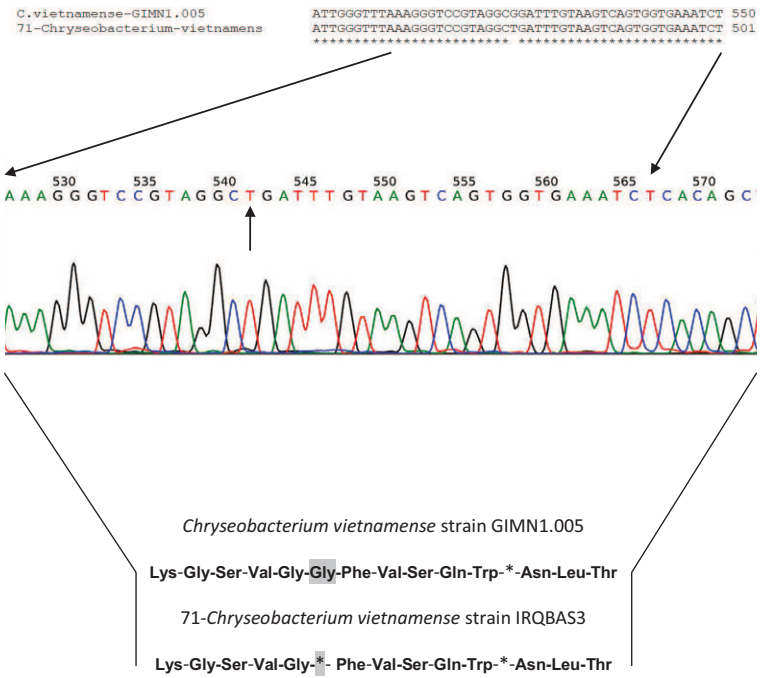


Figure (4 – 18): CLUSTALW for comparison of nucleotide sequences alignment for *16SrDNA* gene of 71- *Chryseobacterium vietnamense* identical (99%) to strain GIMN1.005; showed point mutation type transversion T instead of G at the position 542bp changing the amino acid Gly (GGA) to stop codon (TGA)

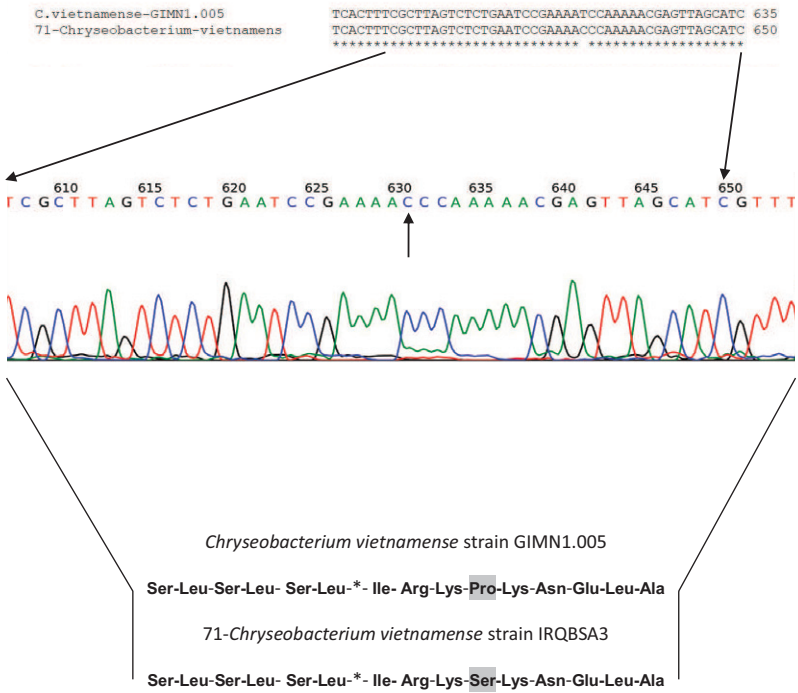


Figure (4 -19): CLUSTALW for comparison of nucleotide sequences alignment for *16SrDNA* gene of 71- *Chryseobacterium vietnamense* identical (99%) to strain GIMN1.005; showed point mutation type transversion C instead of T at the position 631bp changing the amino acid Pro (TCC) to Ser(CCC).

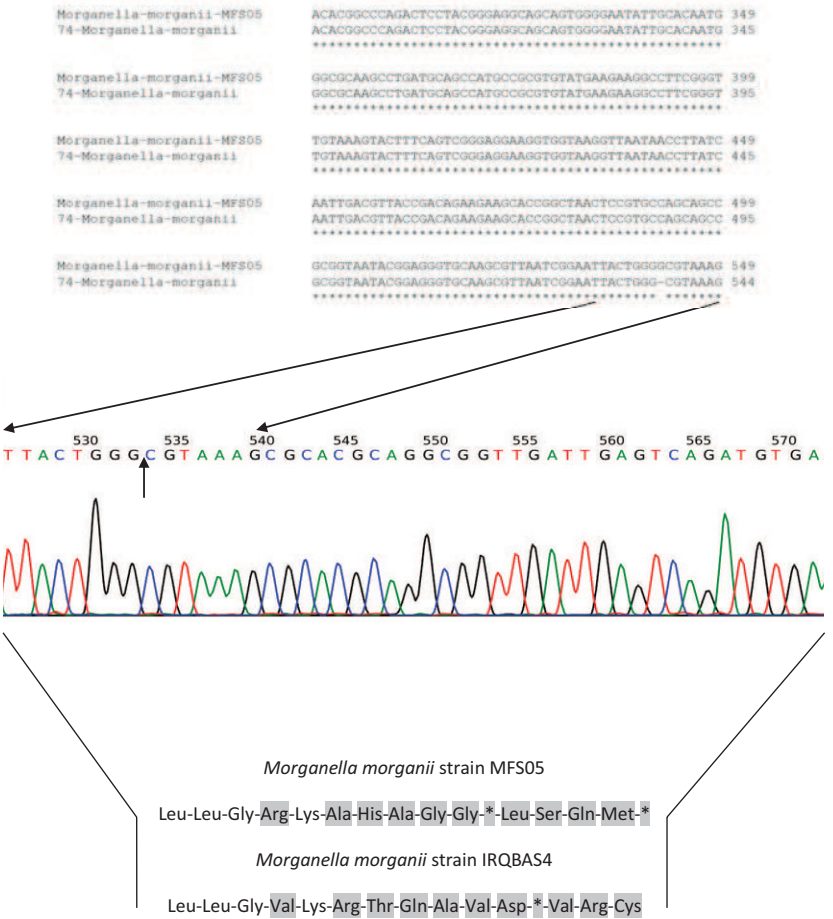


Figure (4 -20). CLUSTALW for comparison of nucleotide sequences alignment for *16SrDNA* gene of 74- *Morganella morganii* identical (99%) to strain MFS05 show frame shift mutation (deletion nucleotide G) at the position 554bp changing all following amino acids

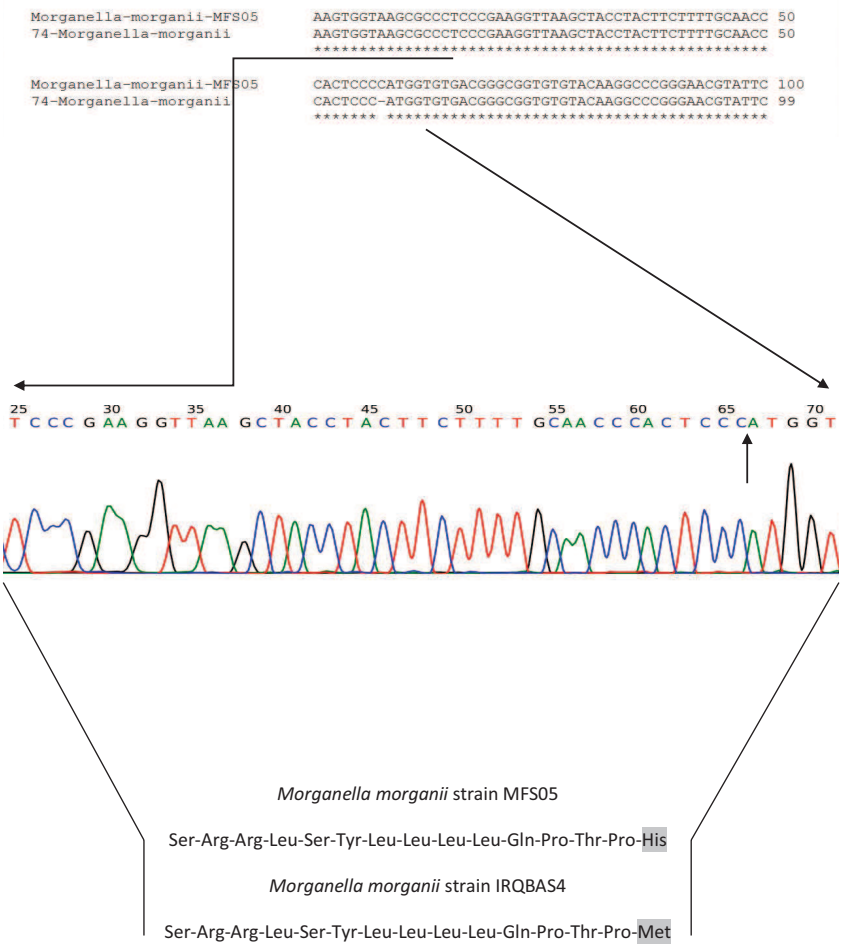


Figure (4 -21): CLUSTALW for comparison of nucleotide sequences alignment for *16SrDNA* gene of 47-*Morganella morganii* identical (99%) to strain MFS05 show frame shift mutation (deletion nucleotide C) at the position 58bp changing all the following amino acids

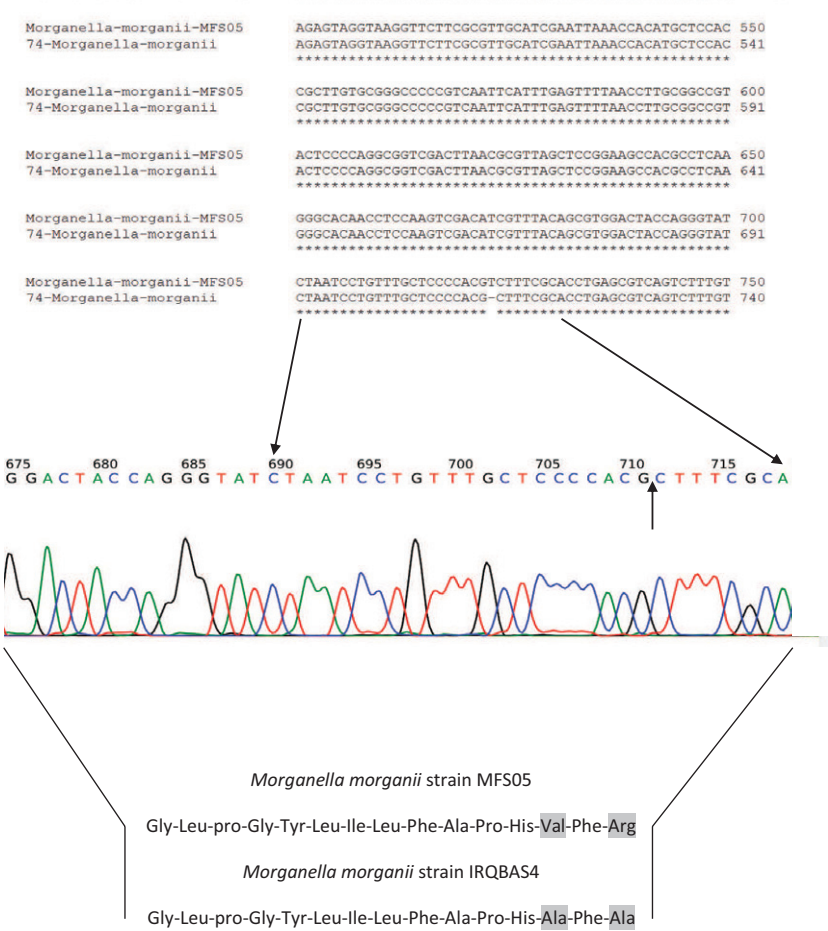


Figure (4 -22): CLUSTALW for comparison of nucleotide sequences alignment for 16SrDNA gene of 47- *Morganella morganii* identical (99%) to strain MFS05 show frame shift mutation (deletion nucleotide T) at the position 712bp changing all the following amino acids.

4-2- Detection of biofilm formation:-

4-2-1- Congo Red Agar (CRA) method:-

CRA method showed very different results. In dentures 8(17.02%)of 47 isolates showed black colonies with a dry crystalline as positive results(slime producers) as Figure (4- 23). 2(4.3%) of 47 isolates showed dark- pink colonies as intermediate results (weak slime producers) , and 37(78.7%)of 47 isolates showed pink-white as negative results (not slime producers). Frequency of negative isolates was higher than positive isolates with high significant ($p \leq 0.01$) , and higher than intermediate with high significant ($p \leq 0.01$), while frequency of positive isolates was higher than intermediate isolates with high significant ($p \leq 0.01$) , As summarized in Table (4 -2). In orthodontic recovered very different results , 4(8.5%) of 47 isolates appeared positive result , 2(4.3%) of 47 isolates appeared intermediate result. In contrast, frequency of positive results was higher than intermediate with high significant ($p \leq 0.01$).41(87.2%) of 47 isolates appeared negative results and frequency of this result was higher than positive and intermediate with high significant ($p \leq 0.01$). No significant differences appeared between denture and orthodontic results for each test (positive, intermediate, negative) .

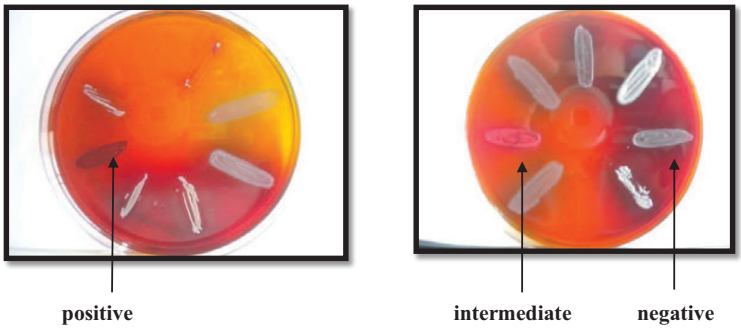


Figure (4-23): Congo Red Agar (CRA) assay for bacterial isolates from dentures and orthodontics . Positive is black colonies with dry crystalline (slime producers) , intermediate is dark- pink colonies (weak slime producers), negative is pink-wite as (not slime producers)

Table (4-2) Comparison of Congo Red Agar (CRA) assay for bacterial isolates from denture and orthodontic

source of bacterial isolates	Positive n(%)	Intermediate n(%)	Negative n(%)
Denture	8(17.02%)	2(4.3%)	37(78.7%)
Orthodontic	4(8.5%)	2(4.3%)	41(87.2%)

($p \leq 0.01$)

4-2-2-Tissue Culture Plate (TCP) method:-

TCP method Figure (4 -24) was recovered in denture, 8(17.02%) of 47 isolates showed high positive results for slime producing ,7(14.9%) of 47 isolates showed moderate positive results and 29(61.7%) of 47 isolate showed weak positive results (Table 4-3). Frequency of weak positive results appeared to be higher than high and moderate positive results with high significant difference ($p \leq 0.01$) , 3(6.4%) of 47 isolates showed negative results , However , the frequency of positive isolates 44(94%) of 47 isolates (high, moderate ,and weak) was higher ($p \leq 0.01$) than negative results . In orthodontic TCP method recovered 2(4.3%) of 47 isolates showed high positive results ,and 9(19.2%) of 47 isolates showed weak positive results, with high significant difference ($p \leq 0.01$). 36(76.6%) of 47 isolates showed negative results with high significant ($p \leq 0.01$) than positive (high, moderate and weak) results . Frequency of positive result (high, moderate and weak) in denture was higher ($p \leq 0.01$) than in orthodontic . Following, the frequency of negative result in orthodontic is higher ($p \leq 0.01$) than in denture .

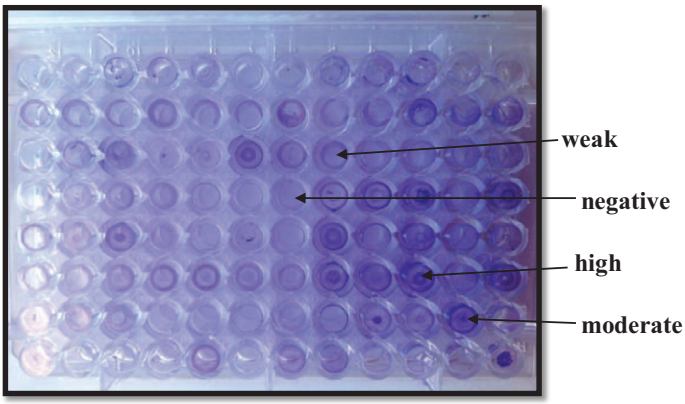


Figure (4 - 24): Tissue Culture Plate(TCP) assay of bacterial isolates from dentures and orthodontic . High: dark color, weak: poor color , moderate: medial color and negative : colorless

Table (4 -3): Comparison of Tissue Culture Plate (TCP) assay for bacterial isolates from denture and orthodontic

Sources of bacterial isolates	High OD[a] ≥0.131 n(%)	Moderate OD= 0.0655 0.0983 n(%)	Weak OD ≤0.0655 n(%)	Negative OD= 0 n(%)
Dentures	*8(17%)	*7(14.9%)	*29(61.7)	3(6.4%)
Orthodontic	2(4.3%)	Zero	9(19.2%)	*36(76.6%)

*($p \leq 0.01$)

a:Optical Density(OD

4-2-3-Detection of *icaA* and *icaD* genes in denture and orthodontic:-

PCR products for *icaA* and *icaD* genes were gave bands on agarose gel electrophoresis at 188bp and 198bp (respectively) position when compared with standard molecular DNA ladder (100 – 1000 base pair) as in figure (4 -26 and 4 -27) respectively.

4-2-3-1- *icaAD* gene for adherence :-

icaAD gene assay in denture showed that *icaA* gene showed 37(78.7%) of 47 isolates as positive results and 10(21.3%) of 47 isolates as negative results ,(Table 4-4) .Frequency of *icaA* gene positive was higher than *icaA* gene negative with high significant difference ($p \leq 0.01$). *icaD* gene was showed 40(85.1%) of 47 isolates as positive results and 7(14.9%) of 47 isolates as negative with high significant ($p \leq 0.01$) .

In orthodontic ,the *icaA* gene was showed 45 (95.8%) of 47 isolates was positive results , and only 2(4.3%) of 47 isolates was negative with high significant difference ($p \leq 0.01$). While, the *icaD* gene was showed 24(51.1%) of 47 isolates as positive results and 23(48.9%) of 47 isolates as negative results but without significant difference .

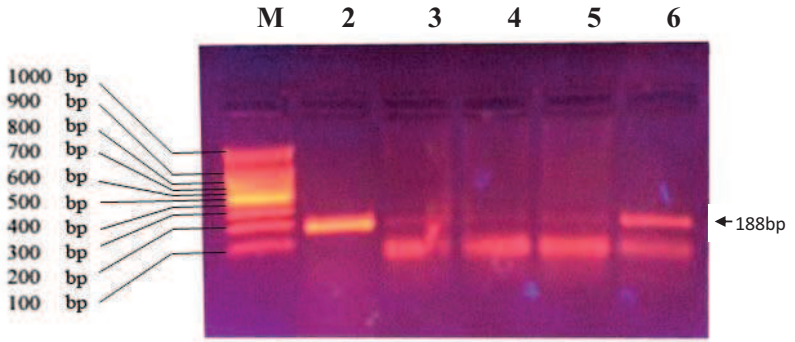


Figure (4- 25): Agarose (1%)gel electrophoresis showed PCR product of *icaA* gene for denture and orthodontic isolates. Lane 1: (100bp-1000bp) DNA ladder, Lane 2 to 6: *icaA* bands (188bp) of different isolates.

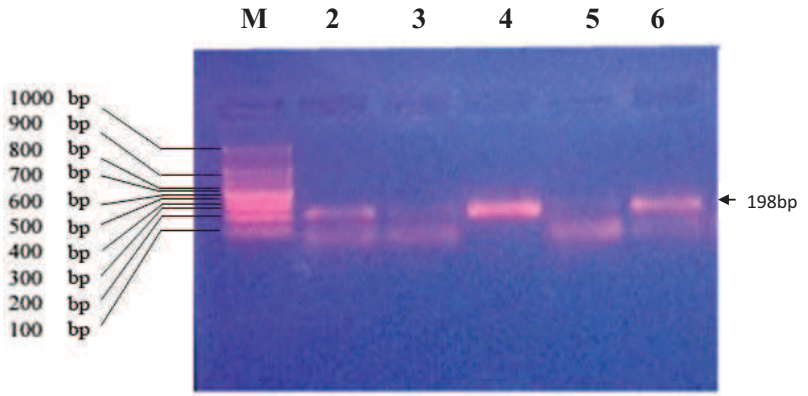


Figure (4 -26): Agarose (1%) gel electrophoresis showed PCR product of *icaD* gene to denture and orthodontic isolates. Lane 1: 1Kb (100bp-1000bp) DNA ladder (DNA marker).Lane 2 to 6: *icaD* bands(198bp) of different isolates

Table (4 - 4) : Comparison of *icaAD* genes for bacterial species from denture and orthodontic.

source of bacterial isolates	*Ica A*		*Ica D*	
	Positive n(%)	**Negative n(%)**	**Positive n(%)**	**Negative n(%)**
Denture	**37 (78.7%)**	**10 (21.3%)**	**40* (85.1%)**	**7 (14.9%)**
Orthodontic	**45* (95.8%)**	**2 (4.3%)**	**24 (51.1%)**	**23* (48.9%)**

***(p ≤ 0.01)**

discrimination between these method (CRA,TCP, *icaAD* genes) for detection biofilm formation in denture isolates showed that the frequency of *icaAD* genes and TCP results were higher than positive CRA with high significant difference ($p \leq 0.01$) and no significant difference between the results of TCP and *icaAD* genes .In orthodontic isolates the frequency of *icaAD* genes was higher than both CRA and TCP results with high significant difference ($p \leq 0.01$), but no significant difference was found between TCP and CRA results .

4-3-The effectiveness of different bacterial species towards CRA , TCP, and *icaAD* genes Assays:-

Table (4 - 5) and (4-6) showed the effectiveness of each bacterial species isolated from denture and orthodontic respectively , toward congo red agar , tissue

culture plate and *icaAD* genes assays with which the best assay for each species to detect the ability of adherence .

In denture (Table 4-5) , TCP and *icaAD* assay were the best assays for *Klebsiella Pneumoniae* (100%,100%), *Proteus mirabilis* (100%,100%), *Proteus penneri* (100%,100%) , *Bacillus cereus* (100%,100%), *Enterobacter cloacae* (100%,100%), *Enterobacter aerogenes* (100%,100%) ,*Acinetobacter baumanni* (100%,100%), *Proteus houseri* (100%,100%) , *Enterobacter mori* (100%,100%), *Klebsiella variicala* (100%,100%) and *Staphylococcus hominis* (100%,100%) respectively comparing to CRA with high significant difference ($p \leq 0.01$), while *icaAD* genes were the best assay for *Morganella morganii* (100%) ,*Hafnia alvei* (100%), *Enterococcus faecium* (100%) than TCP and CRA assays with high significant difference ($p \leq 0.01$), no significant difference ($P \leq 0.01$) between CRA TCP ,and *icaAD* genes for *Klebsiella oxytocat* (100%,100%,100%), *Lactococcus lactis* (100%,100%,100%) *Enterococcus faecalis* (100%,100%,100%), *Chryseobacterium vietnamense* (100%,100%,100%), *Streptococcus equines* (100%,100%,100%), *Citrobacter freundii* (100%,100%,100%), *Bacillus spp.* (100%,100%,100%), *Streptococcus spp*. (100%,100%,100%) respectively , all different bacterial species from denture showed *icaAD* 46(97.9%) gene and TCP 44(93.6%) are the best assays for detection biofilm formation with higher significant ($p \leq 0.01$) than CRA but no significant difference between *icaAD* genes and TCP assays.

Table (4 - 5): Effectiveness of bacterial species from dentures toward slim formation assays.

No.	Isolate No.	Bacterial species In denture	(CRA)**	(TCP)***	*IcaA* and/or *icaD* genes
1	93	*Klebsiella pneumoniae*	−	+	+
2	48	*Klebsiella pneumoniae*	−	+	+
3	57	*Klebsiella pneumoniae*	−	+	+
4	61	*Klebsiella pneumoniae*	−	+	+
5	62	*Klebsiella pneumoniae*	−	+	+
6	78	*Klebsiella pneumoniae*	−	+	+
7	80	*Klebsiella pneumoniae*	−	+	+
8	89	*Klebsiella pneumoniae*	−	+	+
n(%)		8(17%)	0	8(100%)	8(100%)
9	50	*Proteus mirabilis*	−	+	+
10	51	*Proteus mirabilis*	−	+	+
11	52	*Proteus mirabilis*	−	+	+
12	54	*Proteus mirabilis*	−	+	+
13	58	*Proteus mirabilis*	−	+	+
14	83	*Proteus mirabilis*	−	+	+
15	84	*Proteus mirabilis*	−	+	+
n(%)		7(14.9%)	0	7(100%)	7(100%)
16	53	*Proteus penneri*	−	+	+
17	85	*Proteus penneri*	−	+	+
18	86	*Proteus penneri*	−	+	+
19	87	*Proteus penneri*	−	+	+
20	88	*Proteus penneri*	−	+	+
n(%)		5(10.6%)	0	5(100%)	5(100%)
21	56	*Bacillus cereus*	−	+	+
22	66	*Bacillus cereus*	−	+	+
23	67	*Bacillus cereus*	−	+	+
24	70	*Bacillus cereus*	+	+	+
n(%)		4(8.5%)	1(25%)	4(100%)	4(100%)
25	92	*Enterobacter cloacae*	−	+	+
26	55	*Enterobacter cloacae*	−	+	+

No.	Isolate No.	Bacterial species In denture	(CRA)**	(TCP)***	*IcaA* and/or *icaD* genes
27	73	*Enterobacter cloacae*	−	+	+
n(%)		3(6.4%)	0	3(100%)	3 (100%)
28 29	91 74	*Morganella morganii* *Morganella morganii*	+ −	− +	+ +
n(%)		2(4.3%)	1(50%)	1(50%)	2(100%)
30 31	94 77	*Hafnia alvei* *Hafnia alvei*	− −	− +	+ +
n(%)		2(4.3%)	0	50%	2(100%)
32 33	65 81	*Enterobacter aerogenes* *Enterobacter aerogenes*	− −	+ +	+ +
n(%)		2(4.3%)	0	2(100%)	2(100%)
34	59	*Acinetobacter baumanni*	−	+	+
n(%)		1(2.1%)	0	1(100%)	1(100%)
35	60	*Klebsiella oxytoca*	+	+	+
n(%)		1(2.1%)	1(100%)	1(100%)	1(100%)
36	49	*Proteus houseri*	−	+	+
n(%)		1(2.1%)	0	1(100%)	1(100%)
37	68	*Lactococcus lactis*	+	+	+
n(%)		1(2.1%)	1(100%)	1(100%)	1(100%)
38	69	*Enterococcus faecalis*	+	+	+
n(%)		1(2.1%)	1(100%)	1(100%)	1(100%)

No.	Isolate No.	Bacterial species In denture	(CRA)**	(TCP)***	*IcaA* and/or *icaD* genes
39	71	*Chryseobacterium vietnamense*	+	+	+
n(%)		1(2.1%)	1(100%)	1(100%)	1(100%)
40	72	*Streptococcus equines*	+	+	+
n(%)		1(2.1%)	1(100%)	1(100%)	1(100%)
41	75	*Enterobacter mori*	−	+	+
n(%)		1(2.1%)	0	1(100%)	1(100%)
42	76	*Klebsiella variicala*	−	+	+
n(%)		1(2.1%)	0	1(100%)	1(100%)
43	74	*Staphylococcus hominis*	−	+	+
n(%)		1(2.1%)	0	1(100%)	1(100%)
44	82	*Citrobacter freundii*	+	+	+
n(%)		1(2.1%)	1(100%)	1(100%)	1(100%)
45	90	*Enterococcus faecium*	−	−	+
n(%)		1(2.1%)	0	0	1(100%)
46	64	*Bacillus spp*	+	+	+
n(%)		1(2.1%)	1(100%)	1(100%)	1(100%)
47	63	*Streptococcus spp*	+	+	+
n(%)		1(2.1%)	1(100%)	1(100%)	1(100%)
total n(%)		47(50%)	10(21.3%)	44(93.6)*	47(100%)*

*(p≤0.01)

**CRA:Congo Red Agar assay (positive and intermediate

***TCP:Tissue Culture Plate assay (high , moderate and weak)

In orthodontic (Table 4-6), *icaAD* genes were the best assay for *Klebsiella pneumoniae* (100%) , *Staphylocpccus aureus* (100%) , *Enterobacter cloacae* (100%), *Enterococcus faecalis* (100%) , *Staphylococcus epidermidis* (100%) , *Bacillus subtilis* (100%) , *Lactobacillus plantarum* (100%) , *Proteus penneri* (100%) , *Enterococcus faecium* (100%) , *Sterptococcus anginosus* (100%) , *Escherichia fergusonii* (100%) , *Proteus mirabilis* (100%) , *Pediococcus acidilactici* (100%) , *Citrobacter freundii* (100%) , *Enterobacter mori* (100%) ,*Staphylococcus pasteuri* (100%) , *Staphylococcus worneri* (100%) , *Enterobacter ludwigii* (100%) , *Staphylocpccus Spp.* (100%) , *Streptococcus Spp.* (100%) , than TCP and CRA assays with high significant difference ($p \leq 0.01$),while *icaAD* genes and TCP were the best assay for *Serratia marcescens* (100%,100%) and *cereus* (100%,100%,) respectively than CRA with high significant ($p \leq 0.01$). All different bacterial species in orthodontic showed that *icaAD* genes were the best assay for detection biofilm formation against to TCP and CRA assays with high significant ($p \leq 0.01$) .

Table (4 - 6): Effectiveness of bacterial species from orthodontic toward slim formation assays

No.	Isolate No.	Bacterial species In orthodontic	(CRA)**	(TCP)***	*IcaA* and/or *icaD* genes
1	2	*Klebsiella pneumoniae*	–	+	+
2	12	*Klebsiella pneumoniae*	–	–	+
3	19	*Klebsiella pneumoniae*	–	–	+
4	20	*Klebsiella pneumoniae*	–	+	+
5	28	*Klebsiella pneumoniae*	–	–	+
6	36	*Klebsiella pneumoniae*	–	–	+
7	39	*Klebsiella pneumoniae*	–	+	+
8	42	*Klebsiella pneumoniae*	+	–	+
n(%)		8(17%)	1(12.5%)	3(37.5%)	8(100%)
9	9	*Staphylococcus aureus*	–	–	+
10	14	*Staphylococcus aureus*	–	–	+
11	15	*Staphylococcus aureus*	–	–	+
12	22	*Staphylococcus aureus*	+	–	+
13	29	*Staphylococcus aureus*	–	–	+
14	38	*Staphylococcus aureus*	–	+	+
15	45	*Staphylococcus aureus*	+	–	+
n(%)		7(14.9%)	2(28.6%)	1(14.3%)	7(100%)
16	5	*Enterobacter cloacae*	–	+	+
17	6	*Enterobacter cloacae*	–	+	+
18	34	*Enterobacter cloacae*	–	–	+
n(%)		3(6.3%)	0	2(66.7%)	3(100%)
19	17	*Enterococcus faecalis*	–	–	+
20	40	*Enterococcus faecalis*	–	–	+
21	41	*Enterococcus faecalis*	–	–	+
n(%)		3(6.3%)	0	0	3(100%)
22	1	*Staphylococcus epidermidis*	–	–	+
23	16	*Staphylococcus epidermidis*	–	–	+
n(%)		2(4.2%)	0	0	2(100%)
24	13	*Bacillus subtilis*	–	–	+
25	44	*Bacillus subtilis*	+	–	+
n(%)		2(4.2%)	1(50%)	0	2(100%)

No.	Isolate No.	Bacterial species In orthodontic	(CRA)**	(TCP)***	*IcaA* and/or *icaD* genes
26	24	*Lactobacillus plantarum*	+	–	+
27	26	*Lactobacillus plantarum*	–	–	+
n(%)		2(4.2%)	1(50%)	0	2(100%)
28	32	*Proteus penneri*	–	–	+
29	47	*Proteus penneri*	+	–	+
n(%)		2(4.2%)	1(50%)	0	2(100%)
30	35	*Enterococcus faecium*	–	–	+
31	43	*Enterococcus faecium*	–	–	+
n(%)		2(4.2%)	0	0	2(100%)
32	18	*Sterptococcus anginosus*	–	+	+
33	37	*Sterptococcus anginosus*	–	–	+
n(%)		2(4.2%)	0	1(50%)	2(100%)
34	33	*Escherichia fergusonii*	–	–	+
n(%)		1(2.1%)	0	0	1(100%)
35	46	*Proteus mirabilis*	–	–	+
n(%)		1(2.1%)	0	0	1(100%)
36	30	*Pediococcus acidilactici*	–	–	+
n(%)		1(2.1%)	0	0	1(100%)
37	27	*Citrobacter freundii*	–	–	+
n(%)		1(2.1%)	0	0	1(100%)
38	25	*Enterobacter mori*	–	–	+
n(%)		1(2.1%)	0	0	1(100%)

No.	Isolate No.	Bacterial species In orthodontic	(CRA)**	(TCP)***	*IcaA* and/or *icaD* genes
39	23	*Bacillus cereus*	–	+	+
n(%)		1(2.1%)	0	1(100%)	1(100%)
40	31	*Staphylococcus pasteuri*	–	–	+
n(%)		1(2.1%)	0	0	1(100%)
41	11	*Staphylococcus worneri*	–	–	+
n(%)		1(2.1%)	0	0	1(100%)
42	8	*Serratia marcescens*	–	+	+
n(%)		1(2.1%)	0	1(100%)	1(100%)
43	7	*Enterobacter ludwigii*	–	–	+
n(%)		1(2.1%)	0	0	1(100%)
44 45 46	3 4 10	*Staphylococcus Spp.* *Staphylococcus Spp.* *Staphylococcus Spp.*	– – –	– + +	+ + +
n(%)		3(6.3%)	0	2(66.7%)	3(100%)
47	21	*Streptococcus Spp.*	–	–	+
n(%)		1(2.1%)	0	0	1(100%)
total n(%)		47(50%)	6(12.8%)	11(23.4%)	47(100%)*

*(p≤0.01)

**CRA: Congo Red Agar assay (positive and intermediate)

***TCP: Tissue Culture Plate assay (high , moderate and weak)

4-4-Distribution of the bacterial species between denture and orthodontic devices :-

Nine species were found in both denture and orthodontic sources : *Klebsiella pneumonia*e [8(40%) and 8(40%)] , *Proteus mirabilis* [7(35%) and 1(5%)] , *Proteus penneri* [5(25%) and 2(10%)] , *Enterobacter cloacae* [3(15%) and 3(15%)], *Enterococcus faecalis* [1(5%) and 3(15%)] , *Enterobacter faecium* [1(5%) and 2(10%)], *Bacillus cereus*[1(5%) and 4(20%)], *Enterobacter mori* [1(5%) and (5%)], *Citrobacter freundii* [1(5%) and 1(5%)] respectively. While there were 11 species in denture only : *morganella morganii* [2 (10%)], *Hafnia alvei* [2(10%)], *Enterobacter aerogenes* [2(10%)], *Proteus houseri* [1(5%)], *Acinetobacter baumannii* [1(5%)], *Klebsiella oxytoca*[1(5%)], *Lactococcus lactis* [1(5%)], ,*Chryseobacterium vietnamense* [1(5%)], *Streptococcus equines* [1(5%)], *Klebsiella variicala* [1(5%)], *Staphylococcus hominis* [1(5%)] . In contrast, there were 11 species in orthodontic only : *Staphylocpccus aureus* [7 (35%)], *Staphylococcus epidremidis* [2(10%)], *Bacillus subtilis* [2(10%)], *Lactobacillus plantarum* [2(10%)], *Streptococcus anginosus* [2(10%)], *Escherichia fergusonii* [1(5%)], *Pediococcus acidilactici* [1(5%)], *Staphylococcus pasteuri* [1(5%)], *Staphylococcus worneri* [1(5%)], *Serratia marcescens* [1(5%)], *Enerobacter ludwigii* [1(5%)].As summarized in Figure (4-27).

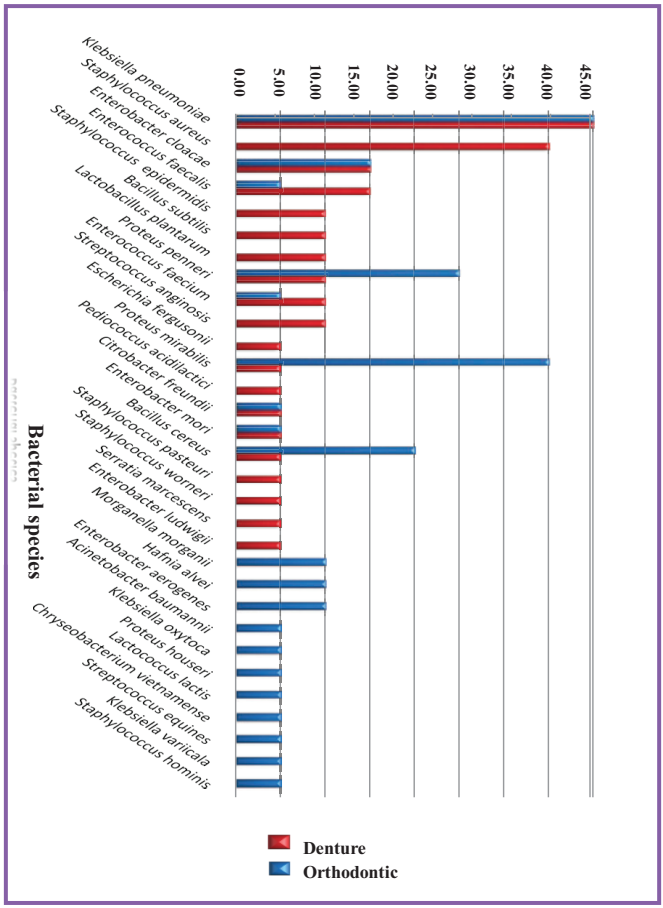


Figure (4-27) percentage of bacterial species in denture and orthodontic

4-5- detection of bacterial species isolates at first time from denture and orthodontic:-

Some bacterial species were detected and recorded from denture and orthodontic at the first time in world these are: *Proteus penneri, Enterobacter mori* and *Citrobacter freundii* found in both denture and orthodontic .While *Proteus houser*, *Klebsiella variicala*, *Lactococcus lactis*, *,streptococcus equinus ,Acinetobacter baumannii* , *Chryseobacterium vietnamense*, *Klebsiella oxytoca* and *Staphylococcus hominis* found in denture only. But *Staphylococcus pasteuri* , *Enerobacter ludwigii*, *Lactobacillus plantarum*, *Streptococcus anginosus*, *Pediococcus acidilactici* , *Bacillus subtilis*, *Escherichia fergusonii* and *Proteus mirabilis* found in orthodontic only.

4-6-The frequency of bacterial species according to some factors:-

In denture (Table 4-7), the frequency of bacteria was higher ($p \leq 0.01$) with patients aged > 35 (70.1%) denture washing (in day) < 2 time (61.7%), without tonsillitis (100%), without gingivitis (100%), no cigarettes smoking (95.7%) and without dental caries (95.7%), no significant difference with date of denture wearer (year). In orthodontic , (Table 4-8), the frequency of bacteria was higher ($p \leq 0.01$) with patients aged < 18 (78.7%) , orthodontic washing > 2(68.1%),tonsillitis (100%) , gingivitis (70.2%) , no cigarettes smocking (100%),without dental caries (100%), but there was no significant differences in patients with date of orthodontic insertion factor .

Table (4 -7): frequency of bacterial species from denture according to some factors

Bacterial Isolates from denture n(%)	Age n(%)		Date of denture wearer (year) n(%)		Times of Denture washing (in day) n(%)		Dental caries n(%)		Smoking cigarettes n(%)		Gingivitis n(%)		Tonsillitis n(%)	
	35 < 35		3 < 3		2 < 2		Yes	NO	Yes	NO	Yes	NO	Yes	NO
Klebsiella pneumonia 8(17%)	3 37.5%	5 62.5%	7 87.5%	1 12.5%	6 75%	2 25%	0	8 100%	0	8 100%	0	8 100%	0	8 100%
Proteus mirabilis 7(14.9%)	2 28.6%	5 71.2%	4 57.1%	3 42.9%	6 85.7%	1 14.3%	0	7 100%	0	7 100%	0	7 100%	0	7 100%
Proteus penneri 5(10.6%)	1 20%	4 80%	4 80%	1 20%	3 60%	2 40%	0	5 100%	0	5 100%	0	5 100%	0	5 100%
Bacillus cereus 4(8.5%)	1 25%	3 75%	2 50%	2 50%	0	4 100%	0	4 100%	0	4 100%	0	4 100%	0	4 100%
Enterobacter cloacae 3(6.4%)	1 33.3%	2 66.7%	0	3 100%	1 33.3%	2 66.7%	0	3 100%	0	3 100%	0	3 100%	0	3 100%
Morganella morganii 2(4.3%)	0	2 100%	2 100%	0	1 50%	1 50%	0	2 100%	0	2 100%	0	2 100%	0	2 100%
Hafnia alvei 2(4.3%)	0	2 100%	0	2 100%	2 100%	0	0	2 100%	0	2 100%	0	2 100%	0	2 100%
Enterobacter aerogenes 2(4.3%)	0	2 100%	2 100%	0	1 50%	1 50%	0	2 100%	0	2 100%	0	2 100%	0	2 100%
Acinetobacter baumannii 1(2.1%)	0	1 100%	0	1 100%	1 100%	0	1 100%	0	0	1 100%	0	1 100%	0	1 100%
Klebsiella oxytoca 1(2.1%)	0	1 100%	0	1 100%	1 100%	0	0	1 100%	1 100%	0	0	1 100%	0	1 100%
Proteus houseri 1(2.1%)	1 100%	0	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Lactococcus lactis 1(2.1%)	0	1 100%	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Enterococcus faecalis 1(2.1%)	1 100%	0	1 100%	0	0	1 100%	1 100%		0	1 100%	0	1 100%	0	1 100%
Staphylococcus hominis 1(2.1%)	0	1 100%	0	1 100%	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Chryseobacterium vietnamense 1(2.1%)	0	1 100%	0	1 100%	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Streptococcus equines 1(2.1%)	1 100%	0	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Enterobacter mori 1(2.1%)	1 100%	0	1 100%	0	0	1 100%	0	1 100%	1 100%	0	0	1 100%	0	1 100%

Bacterial Isolates from denture n(%)	Age n(%)		Date of denture wearer (year) n(%)		Times of Denture washing (in day) n(%)		Dental caries n(%)		Smoking cigarettes n(%)		Gingivitis n(%)		Tonsillitis n(%)	
	35 < 35		3 < 3		2 < 2		Yes	NO	Yes	NO	Yes	NO	Yes	NO
Klebsiella variicala 1(2.1%)	1 100%	0	1 100%	0	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Staphylococcus hominis 1(2.1%)	0	1 100%	0	1 100%	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Citrobacter freundii 1(2.1%)	0	1 100%	0	1 100%	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Bacillus spp. 1(2.1%)	0	1 100%	0	1 100%	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Streptococcus spp.	1 100%	0	0	1 100%	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Total	14 29.9%	33* 70.1%	27 57.4%	20 42.6%	29** 61.7%	18 38.3%	2 4.3%	45* 95.7%	2 4.3%	45* 95.7%	0	47* 100%	0	47* 100%

***p≤0.01**
****p≤0.05**

Table (4 -8): frequency of bacterial species from orthodontic according to some factors

Bacterial Isolates from denture n(%)	Age n(%)		Date of orthodontic wearer (year) n(%)		Times of orthodontic washing (in day) n(%)		Dental caries n(%)		Smoking cigarettes n(%)		Gingivitis n(%)		Tonsillitis n(%)	
	18 < 18		1.5 < 1.5		2 < 2		Yes	NO	Yes	NO	Yes	NO	Yes	NO
Klebsiella pneumonia 8(17%)	5 62.5%	3 37.5%	4 50%	4 50%	3 37.5%	5 62.5%	0	8 100%	0	8 100%	6 75%	2 25%	0	8 100%
Staphylocpccus aureus 7(14.9%)	6 85.7%	1 14.3%	4 57.1%	3 42.9%	2 28.5%	5 71.4%	0	7 100%	0	7 100%	4 57.1%	3 42.9%	0	7 100%
Enterobacter cloacae 3(6.3%)	2 66.7%	1 33.3%	3 100%	0	1 33.3%	2 66.6%	0	3 100%	0	3 100%	2 66.7%	1 33.3%	0	3 100%
Enterococcus faecalis 3(6.3%)	2 66.7%	1 33.3%	0	3 100%	0	3 100%	0	3 100%	0	3 100%	3 100%	0	0	3 100%
Staphelococcus epidermidis 2(4.2%)	2 100%	0	0	2 100%	1 50%	1 50%	0	2 100%	0	2 100%	2 100%	0	0	2 100%
Bacillus subtilis 2(4.2%)	2 100%	0	0	2 100%	2 100%	0	0	2 100%	0	2 100%	2 100%	0	0	2 100%
Lactobacillus plantarum 2(4.2%)	2 100%	0	2 100%	0	0	2 100%	0	2 100%	0	2 100%	1 50%	1 50%	0	2 100%
Proteus penneri 2(4.2%)	2 100%	0	2 100%	0	1 50%	1 50%	0	2 100%	0	2 100%	0	2 100%	0	2 100%
Enterococcus faecium 2(4.2%)	2 100%	0	1 50%	1 50%	1 50%	1 50%	0	2 100%	0	2 100%	2 100%	0	0	2 100%
Sterptococcus anginosus 2(4.2%)	2 100%	0	1 50%	1 50%	0	2 100%	0	2 100%	0	2 100%	1 50%	1 50%	0	2 100%
Enterococcus fergusonii 1(2.1%)	1 100%	0	1 100%	0	0	1 100%	0	1 100%	0	1 100%	1 100%	0	0	1 100%
Proteus mirabilis 1(2.1%)	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%	1 100%	0	0	1 100%
Pediococcus acidilactici 1(2.1%)	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%	1 100%	0	0	1 100%
Citrobacter freundii 1(2.1%)	1 100%	0	1 100%	0	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Enterobacter mori 1(2.1%)	1 100%	0	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Bacillus cereus 1(2.1%)	1 100%	0	0	1 100%	1 100%	0	0	1 100%	0	1 100%	1 100%	0	0	1 100%
Staphylococcus pasteuri 1(2.1%)	0	1 100%	0	1 100%	1 100%	0	0	1 100%	0	1 100%	1 100%	0	0	1 100%
Staphylococcus worneri 1(2.1%)	0	1 100%	0	1 100%	0	1 100%	0	1 100%	0	1 100%	0	1 100%	0	1 100%

Bacterial Isolates from denture n(%)	Age n(%)		Date of orthodontic wearer (year) n(%)		Times of orthodontic washing (in day) n(%)		Dental caries n(%)		Smoking cigarettes n(%)		Gingivitis n(%)		Tonsillitis n(%)	
	18 < 18		1.5 < 1.5		2 < 2		Yes	NO	Yes	NO	Yes	NO	Yes	NO
Serratia marcescens 1(2.1%)	0	1 100%	0	1 100%	0	1 100%	0	1 100%	0	1 100%	1 100%	0	0	1 100%
Enterobacter ludwigii 1(2.1%)	1 100%	0	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%	0	1 100%
Staphylocpccus Spp. 3(6.4%)	2 66.7%	1 33.3%	2 66.7%	1 33.3%	1 33.3%	2 66.7%	0	3 100%	0	3 100%	3 100%	0	0	3 100%
Streptococcus Spp. 1(2.1%)	1 100%	0	0	1 100%	0	1 100%	0	1 100%	0	1 100%	1 100%	0	0	1 100%
Total	37* 78.7%	10 21.3%	23 48.9%	24 51.1%	15 31.9%	32* 68.1	0	47 100%	0	47 100%	33* 70.2%	14 29.8	0	47 100%

***p≤0.01**

Chapter Five

Discussion

5-1-primer for *16SrDNA* gene:-

In the present study, DNA of all bacterial isolates from denture (n=47) and orthodontic (n=47) were extracted and electrophoreses (Figure 4-1), then subjected to PCR for amplifying their *16S rDNA* gene with universal primers (F27 and R1492). Since, the primer amplify the *16SrDNA* (16S ribosomal RNA) gene for all bacteria species preventing to lose any possible or new species (Mellmann *et al*., 206), as Figures (4-2 to 4-11). The use of *16SrDNA* gene to study bacterial phylogeny and taxonomy has been the most common genetic marker because : Its presence in almost all bacteria, often existing as a multigene family, or operon , the function of the *16SrDNA* gene over time has not changed, suggesting that random sequence changes are more accurate measure of time (evolution) and the *16SrDNA* gene (1,500 bp) is large enough for informatics purposes (Patel, 2001 ;Janda and Abbott, 2007).

5-2-Sequncing of *16SrDNA* gene and phylogenetic tree:-

The amplified *16SrDNA* gene was purified , it was important to obtain a clear single band and because the unpurified gene will cause problems during sequencing (Barker, 2006). Sequencing of the *16SrDNA* gene has served as an important tool for identifying and determining phylogenetic relationships between bacterial species from dentures and orthodontic (figure 4-12) .Since features of this molecular target (*16SrDNA* gene sequencing) that make it useful for phylogenetic tool , also make it useful for bacterial detection and identification in the clinical laboratory, sequence analysis of the *16SrDNA* gene is a powerful mechanism for identifying new

pathogens in patients with suspected bacterial disease and more recently this technology is being applied in the clinical laboratories for routine identification of bacterial isolates, on the other hand, several studies have shown that sequence identification is useful for slow-growing, unusual, and fastidious bacteria as well as for bacteria that are poorly differentiated by conventional methods (Patel, 2001).

Furthermore, Conventional biochemical tests and commercial identification system as well as phenotypic variants are not included in the level of subspecies and often miss identified (Seifert *et al*., 2003). In contrast, the high quality of *16SrDNA* sequence database provides excellent identification at the species and subspecies levels; moreover, it can lead to the recognition of novel pathogens and non cultured bacteria (Clarridge, 2004; Mellmann *et al*., 2006). Nucleotide sequences of the *16SrDNA* gene of the 28 different species identified in this study with their reference strains from Gene were concatenated in at least length 898bp depending on the shorter sequence exhibited when aligned using CLASTALW "http://www .ebi. ac.uk/clustalw/" (Kerbauy *et al*., 2011), then compared phylogenetically based on phylogenetic tree analysis. the phylogenetic tree in the present study rooted with *Enterobacter cloacae* as the out group, conserved with its genetic characteristics (Barker, 2006).

5-3- The new recording of bacterial strain from denture and orthodontic:-

The present study recorded four new bacterial strains in orthodontic [7- *Enterobacter ludwigii* (HG003646)"IRQBAS1" , 34- *Enterobacter cloacae*

(HG003647)"IRQBAS2"] and in denture [71-*Chryseobacterium vietnamense* (HG003648) "IRQBAS3" , 74-*Morganella morganii* (HG003649)"IRQBAS4"] as in Figures (4-13 to 4-22) .These strains were identical with each their reference strains at 99% (1% difference with reference strain for each) because the occurance of mutation changing nucleotide sequence of genome of an organism, mutations are caused by either unrepaired damage to DNA or to RNA genomes (typically caused by radiation or chemical mutagens),errors in the process of replication or insertion or deletion of segments of DNA by mobile genetic elements (Bertram , 2000 ; Burrus and Waldor , 2004 ; Aminetzach *et al* ., 2005) , these mutations are : point mutation often caused by chemicals or malfunction of DNA replication, exchange a single nucleotide for another , these changes are classified as 1- transitions or 2-transversions , most common is the transition that exchanges a purine to a purine (A ↔ G) or a pyrimidine to a pyrimidine, (C ↔ T) ,less common is a transversion, which exchanges a purine to a pyrimidine or a pyrimidine to a purine (C/T ↔ A/G) and 3-frame shiffet mutation which is caused by insertion or deletion of a number of nucleotides, the insertion or deletion can disrupt the reading frame, or the grouping of the codons, resulting in a completely different translation from the original (Dunnen , 2000; Ernst, 1959). Since, according to some guidelines, a range of about a 0.5% to 1% difference (99.5 to 99% similarity) is often used for classification (Song *et al*., 2003). Bosshard *et al*. (2003) used ≥ 99% similarity to define species and ≥ 95 to < 99% to define a genus whereas, Hall *et al*. (2003) adopted a distance score of 0.00 to less than 1% as the criterion for species identity. While, Tang *et al*. (1998, 2000), suggested a 0.5% difference as the limit for species designation. Furthermore, a strain with a small genotypic difference (less than 0.5%) has been considered as subspecies (Chen *et al*., 2002) . When there is a clear phenotypic

uniqueness, genogroups with less than 1% differences in sequence have in fact been named as a new species (Kattar *et al*., 2001; Roth *et al*., 2003; Tortoli, 2003). However, a comparison of sequences for several subspecies shows differences from 1 to 14 bp (Clarridge , 2004). bacterial isolates at the first time in the world me be due to a change in the Iraqi environment or may be due to the quality of feed person.

5-4- Detection of biofilm formation:-

Biofilm formation (slime production) plays an important role in the pathogenesis of infections caused by different microorganisms (Hall-Stoodley *et al*., 2004 ; Aparna *et al*., 2008). The major virulence factor is that they can form biofilm on polymeric surfaces and adherence to catheters and other artificial materials during the early phase of biofilm development (Chaieb *et al* ., 2005) . Further more, investigations to understand the pathogenesis of these infections have focused upon the process of adherence of these microorganisms on biomedical devices, using various methods of quantify number of microorganisms adhering to surfaces (Donlan , 2001; Donlan *et al*., 2001) .

Tested 94 clinical isolates n=47 from denture and n=47 from orthodontic by three *in vitro* screening procedures for their ability to form biofilm ,these are Congo Red Agar (CRA), Tissue Cultur Plate (TCP), *icaAD* genes methods in denture and orthodontic . Congo Red Agar was simple and reliable to determine whether an isolate has the potential for biofilm production or not (Jain and Agarwal, 2009). Tissue Cultur Plate has been determined according to well-established protocols

and can be modified for various biofilm formation assays,this test is fast, efficient, reliable, and reproducible method and it gives a cantitative result (Djordjevic *et al*., 2002; Tumbarello *et al*., 2007). Other investigators also reported PCR to be an important tool for the identification of *ica* genes since the technique is simple, rapid and reliable and only requires minimal amounts of DNA (Cafiso *et al*., 2004 ; Arciola *et al*., 2001). PCR was used in this study as a reference for the phenotypic method based on several studies (Cafiso *et al*., 2004 ; Arciola *et al*., 2001; Gad *et al*., 2009) that demonstrated the efficiency of this technique in detecting the genes of the *ica* operon.

By Congo red agar method we obtained very different results as Table (4-2) and Figure (4-23) most of bacterial isolates displayed in denture and orthodontic positive [8(17.02%) and 4(8.5%)] intermediate [2(4.3%) and 2(4.3%)] and negative isolates [37(78.7%) and 41(87.2%)] ,based on the observations in the present results don't recommend the CRA method as a suitable method for detection of biofilm formation, these results are in agreement with Knobloch *et al*., (2002). By tissue culture plate most of bacterial isolates as Table (4-3) and Figure (4-24) displayed in denture and orthodontic positive [8(17%) and 2(43%)] , moderate [7(14.9%) and zero], weak [29(61.7%) and 9(19.2%)] and negative [3(6.4%) and 36(76.6%)]. In denture results correlate well with those reported by Gökçe *et al*., (2007) but in orthodontic results are in disagreement with Gökçe *et al*., (2007) but they are in agreement with Oliveira and Cunha, (2010) demonstrated the tube adherence test can be indicated for the routine detection of biofilm production in CNS, because the strongly adherent is very weak when comparison TCP results assay with *icaA* and *icaD* results assay . The relationship between strongly adherent for bacterial isolates and the concomitant presence of *icaA*, and *icaD* detected by PCR , because of the slime production

increase depended on co-expression of *icaA* with *icaD* gene (Cafiso *et al*., 2004) ,in denture no significant difference between *icaA* and *icaD* gene positive but in orthodontic high significant difference between *icaA* and *icaD* gene positive as Table (4-4),this confirming the results in orthodontic and to determine the reliability of the TCP method in terms of the quantification of biofilm production.

5-5-The effectiveness of different bacterial species towared CRA, TCP and icaAD genes assays:-

The results showed CRA assay as Table (4-5 and 4-6) very little correlation [10 (21.3%) and 6 (12.8%) respectively] with corresponding methods *icaAD* genes [47(100%) and 47(100%) respectively], these results are in agreement with Arciola *et al*., (2002); Cafiso *et al*., (2004); Arciola *et al*., (2005) when Compared between the CRA test results and PCR (*icaAD* genes) showed only [10(21.3%),6(12.8%)] isolates respectively in denture and orthodontic were positive results and revealed 37(78.7%) isolates in denture and 41(87.2%) isolates in orthodontic were forming bordeaux colonies (negative results) toward CRA, while they tested positive for the concomitant presence of the *icaAD* genes, with these results, isolates by CRA being false-negative when compared to PCR , furthermore , these isolates contained complete *IcaA* and/or *icaD* genes .On the other hand, the present study showed in denture with TCP results [44(93.6%)] high significant differences than CRA results [10(21.3%)] , the TCP method was found to be most sensitive, accurate and reproducible screening method for the detection of biofilm formation. However these results were in agreement with Mathur *et al*., (2006) .No significant difference between *icaAD* gene and TCP results [47 (100%) and 44(93.6%) respectively] ,

Similar results have been reported by Arciola *et al*., (2006). However, in orthodontic, no significant differences were found between CRA results [6(12.8%)] TCP results [11(23.4%)] , while high significant differences were found between *icaAD* gene results [47(100%)] and TCP results , these results were in agreement with Oliveira and Cunha, (2010), could be due to the fact that denture is made from polymethylmethaacrylate resin (plastic) and the rough surface not only permit the bacteria attach to the surface but also to penetrate deep into the porous denture or appliance lead to be adhesion stronger than orthodontic . Based on the present results, the study is unable to recommend the CRA method for the detection of biofilm formation, in contrast, probably to recommend TCP method for detection of biofilm formation. But full accreditation on the *icaAD* genes method for detection of biofilm formation in denture and orthodontic bacterial species . Slime production depends on the presence of both/or *icaD* and *icaA*. Nevertheless, the reason for the absence of biofilm production in some *icaA* and *icaD* positive isolates in the present study may be the lack of *icaC* (Ziebuhr *et al*., 1999). In other evidences, the biofilm accumulation is mediated by certain genes, such as *icaA, icaB, icaC, icaD* and *icaR*(Begun *et al*., 2007; O'Gara *et al*., 2007). The recent findings point to an important role of the *icaA and icaD* due to their ability to produce slime strongly in a high percentage of clinical isolates collected from patients with catheters associated infection (El-Mahallawy *et al*., 2009) .

5-6-Type of bacteria have the ability to produce slime:-

The purpose of this study was to observe the ability of bacteria to produce slime and formation of biofilm, an important virulence factor, by bacterial isolates, among the

bacterial isolates in present study produce slime and form biofilm confirm this all bacterial isolates in present study when conducted tests *icaAD* gene the result are [47(100%) and 47(100%)] as Figure (4-5 and 4-6) . The results showed that these bacteria produce slime and forming biofilm in diverse environments from aquatic conditions to indwelling devices "vascular access ports/hemasites, scleral buckles, ureteral stents, urethral catheters and tracheesophageal voice prostheses (Provox2)" , furthermore, these bacteria can produce biofilms on nonliving surfaces including polystyrene, glass, latex and silicone and on biological surfaces (Reed *et al*., 1986 ; Reid *et al*., 1992 ; Inbakandan *et al*., 2010 ; Tićac *et al*., 2010).These bacteria are:*Klebsiella pneumonia* in agreement with (Maki and Tambyah, 2001; Stewart and Costerton, 2001; Donlan and Costerton, 2002) ,*Staphylocpccus aureus* in agreement with (Leid *et al*., 2002 ; Patel, 2005) , *Proteus mirabilis* in agreement with (Stickler *et al*., 1993), *Proteus penneri* in agreement with (Rózalski *et al*., 2007) , *Enterococcus faecalis* in agreement with (Baldassarri *et al*., 2001 ; Sandoe *et al*., 2003) , *Enterobacter cloacae* in agreement with (Kim *et al*., 2012), *Enterococcus faecium* in agreement with (Van Wamel *et al*., 2007) , *Bacillus cereus* in agreement with (Peng *et al*., 2001), *Citrobacter freundii* in agreement with (Pereira *et al*., 2010), *morganella morganii* in agreement with (Zubair *et al*., 2011) , *Hafnia alvei* in agreement with (Vivas *et al*., 2008), *Enterobacter aerogenes* in agreement with (Donlan &Costerton, 2002) , *Acinetobacter baumanni* in agreement with (Gaddy and Actis, 2009) , *Klebsiella oxytoca* in agreement with (Zubair *et al*., 2011), *Lactococcus lactis* in agreement with (Zaidi *et al*., 2011) , *Staphylococcus hominis* in agreement with (Krolasik *et al*., 2010), *Staphylococcus epidremidis* agreement with (Fey and Olson, 2010) , *Bacillus subtilis* in agreement with (Hamon and Lazazzera, 2001) , *Lactobacillus plantarum* in agreement with (Kubota *et al.*, 2008),*Streptococcus*

anginosus in agreement with (Petersen *et al*., 2006) , *Escherichia fergusonii* in agreement with (Ingle *et al*., 2011), *Pediococcus acidilactici* in agreement with (Kawarai *et al*., 2007) , *Staphylococcus pasteuri* and *staphylococcus worneri* in agreement with (Marino *et al*., 2011) and *Serratia marcescens* in agreement with (Rice *et al*., 2005). *Enerobacter ludwigii* , *Klebsiella variicala*, *Chryseobacterium vietnamense* and *Enterobacter mori* are new species (Hoffmann *et al*., 2005 ; Rosenblueth *et al*., 2004 ; Li and Zhu , 2012 ; Zhu *et al*., 2011). On the other hands information and research for *streptococcus equines* and *Proteus houseri* are very few, furthermore, in the present study these bacteria were tested on containment adherence gene (*icaAD* gene) this confirmsthese bacteria produces slime and formed biofilm .

5-7-Distribution of the bacterial species between denture and orthodontic :-

The presence of a denture or orthodontic in the oral mucosa alters the local environmental conditions to lead increase of bacteria formed biofilm causing infection and systematic disease (Hagg *et al*., 2004 ; Daniluk *et al*., 2006) . Dentures offer a reservoir for microorganisms associated with endocarditis, aspiration pneumonia, gastrointestinal infection and chronic obstructive pulmonary disease (Li *et al*., 2000 ; Falah-Tafti *et al*., 2008). Orthodontic treatment with fixed appliances leads to increase biofilm accumulation and elevated levels of cariogenic and periodontal bacteria ,furthermore, because orthodontic brackets make good oral hygiene difficult, resulting plaque accumulation and significantly increase risks of enamel demineralization or periodontal disease (Papaioannou *et al*., 2007 ; Pandis *et*

al., 2008 ; Pellegrini *et al*., 2009). In the present study there are 31(Three identified morphologically) species were isolated from denture and /or orthodontic.

5-8-Species isolated from denture and orthodontic:-

Klebsiella pneumonia isolate in both denture and orthodontic which is in agreement with (Goldberg *et al*., 1997; Naranjo *et al*., 2006). *klebsiellae* have become important pathogens in nosocomial infections can cause the *Klebsiella pneumonia* disease, human lungs inflammation and necrosis that sometimes produces a thick, bloody, mucoid sputum as currant jelly sputum (Chien-Ko *et al*., 2002) *Klebsiella pneumonia* infections are mostly seen in people with a weakened immune system, this patient is believed to have impaired respiratory host defenses including persons with, liver disease, alcoholism, malignancy, diabetes , Chronic obstructive pulmonary diseases ,glucocorticoid therapy, renal failure and certain occupational exposures, many of these infections are obtained when a person is in the hospital for some other disease (Podschun *et al* ., 1998; Kabra *et al*., 2001) common infection caused by *Klebsiella* bacteria outside the hospital is pneumonia (Schwaber and Carmeli , 2008).

Proteus mirabilis was isolated from which denture agreements with Goldberg *et al* 1997, Sumi *et al* (2002), Jass *et al* (2003), Tyrell *et al* (2003), Senpuku *et al* (2003). *Proteus mirabilis* infection can spread to other parts of the body (Coker *et al*., 2000) and *Proteus penneri* isolate from stool (O'Hara *et al*.,2000 a and b). Furthermore ,these bacteria formed biofilm (Coker *et al*., 2000; Rózalski *et al*., 2007), could be entire through the speaking of person wearer denture or insertion

orthodontic Providing a favorable environment for the growth of bacteria , or oral fecal contamination .Isolated in orthodontic at the first time.

Enterococcus faecalis has been frequently found in root canal-treated teeth in prevalence values ranging from 30% to 90% of the cases (Molander *et al*.,1998), resulting biofilm formation (Singh *et al*., 2007) , perhaps that's causes may be done when the persons sick with these disease at the same time of those persons wearer these devices leading to transfer this bacteria and formed biofilm and adhesive.

Enterococcus faecium found in the oral cavity (Donelli *et al*., 2004). Furthermore, the virulence factor of *E. faecium* is the enterococcal surface protein (Esp) , this protein allows the bacteria to aggregate and form biofilms (Willem *et al*., 2007) , which may allow the bacteria to colonies the devices .

Bacillus cereus can spread easily to many types of foods such as plants, eggs, meat, and dairy products causing periodontal diseases and other more serious infections , furthermore, forming biofilm on various surfaces (Hoffmaster *et al*., 2006; Oosthuizen *et al*., 2002), all of these reasons confirm the adhesion of this bacteria in people with denture wearer or orthodontic insertion ,or the other way, may be the person suffers from periodontal diseases when this bacteria is found before insertion the devices ,after insertion, this bacteria formed biofilm and adhere on these devices .

Enterobacter mori is plant-pathogenic enterobacterium responsible for the bacterial wilt of mulberry plants (Zhu *et al*., 2011). May be for this reasons, the

above plant, is the source of its existence in mouth . However, because this bacteria is new species there isn't any research confirms that the *Enterobacter mori* has the ability to form biofilm because of the lack of research dealing with this bacteria ,but only Zogaj *et al*., (2003) says that genus *Enterobacter* spp. forming biofilm. On the other hands , the pre study recovered *Enterobacter mori* contain *icaAD* genes with rate 100% in denture and orthodontic offering a favorable circumstance for adhesion. This bacteria is recorded that isolated in denture and orthodontic at the first time.

Citrobacter freundii isolated from denture and orthodontic was in agreement with Daniluk *et al* (2006) when isolated it from denture. However , this bacteria habitat include the environment (soil, water, sewage), food and forming biofilm (Wang *et al*., 2000; Pereira *et al*., 2010).Therefore, it could entire into the mouth and adhesion on to orthodontic. the first recorded in orthodontic.

Enterobacter cloacae was isolated in both from denture and orthodontic , this results is in agreement with Naranjo *et al* (2006) and Daniluk *et al* (2006).Moreover, this strain is recovered at the first time in denture named "IRQBAS2" with ID number "HG003647".

5-9-species isolated from denture only :-

morganella morganii was isolated from denture which in agreement with Daniluk *et al* (2006).Moreover, this strain the first recovered in present study named "IRQBAS4" with number ID "HG003649"

Enterobacter aerogenes isolated from denture as recorded previously by Gomaa and Helal (2010).

Hafnia alvei causing skin infection, soft tissue infections such as sputum ,tracheal, bronchial aspirates, nasal smears, bronchoalveolar lavage fluid, mouth and throat infection (Janda *et al* .,2006) .most of these infections could occur when *Hafnia alvei* is coming from denture.

Proteus houseri found in manure, soil, polluted water, and in intestines of human and wide variety of animals (Garrity *et al*., 2005), *Acinetobacter baumannii* isolated from soil and water samples in the environment (Yeom, *et al*., 2013 a and b). Furthermore, isolat *A. baumanni* among service members of the Iraq and Afghanistan military operations: Operation Iraqi Freedom and Operation Enduring Freedom, respectively (Hujer *et al*., 2006). These sources can play a role to export the bacteria to human mouth or oral fecal contamination .Isolates of these bacteria adhere in denture at the first time in the present study.

Klebsiella oxytoca can be found in a wide range of environments and this specie tends to colonize along the mucosa membranes of the colon and nasopharynx, urine and skin, however, they can colonize on all parts of the body (Ménard *et al* ., 2010). This bacteria isolated from orthodontic (Naranjo *et al*., 2006) .Recorded adhere this bacteria to denture at the first time ,may be found in mouth and adhere to denture or transfer from nasopharynx to mouth for adhering.

Lactococcus lactis is widely used for industrial production of fermented dairy products such as milk, cheese, and yogurt (Tanous *et al*., 2007).Therefore ,these sources are good origin for this bacteria to transfer to adhere the denture and recorded this bacteria at the first time adhere to denture.

Chryseobacterium vietnamense strain GIMN1.005T isolated from a forest soil sample in Vietnam at first time in 2011 (Li and Zhu, 2011).However, from that time , this bacteria contain only one strain. But in the present study, an isolate was recovered from denture at the first time as new strain named "IRQBAS3" with ID number "HG003648" .

streptococcus equines was isolated from cow , human and horses (Hodge *et al*., 1937 ; Hagan , 1988). may be source infected is oral fecal contamination. But this is the first isolation from the denture .

Klebsiella variicala was isolated in Mexico (2004) is a new species from plants (rice, maize, sugar ,cane and banana) and hospitals ,(Rosenblueth *et al* .,2004) these sources could be the origin to isolate this bacteria at the first time from mouth adhere on denture

Staphylococcus hominis is commonly as a harmless commensal on human and animal skin (Kloos and Schleifer,1975) , may be this bacteria is transfer from skin into mouth and adhere. However, no previous study confirms the presence of this bacteria in denture.

5-10-Species isolated from orthodontic only:-

Staphylocpccus aureus was isolated from orthodontic as with Al Groosh *et al*., (2011) and Soomro *et al*., (2012). *Staphylococcus epidremidis* was isolated from orthodontic as with Soomro *et al*., (2012) . *Streptococcus anginosus* cultures have been taken from the mouth, throat and poor oral hygiene (Ruoff *et al*., 1988 ; Yilmaz *et al* ., 2012). *Serratia marcescens* isolated from denture as the of result with Naranjo *et al*., (2006).

Bacillus subtilis can contaminate food (Perez, 2000). *Lactobacillus plantarum* and *Pediococcus acidilactici* founds in dairy, meat, and much vegetable fermentations, (Barros *et al*., 2001 ; De Vries *et al*., 2006). However , these bacteria may be entire with food through the eating into the gap between the enamel surface and device and adhere. isolated these bacteria at first time in orthodontic.

Escherichia fergusonii is the infected open wounds in humans and may also cause bacteraemia or urinary tract infections **(** Mahapatra *et al*.,2005). As a first isolated from orthodontic, this bacteria may be cross-contamination from urinary tract infected into hand through urine and transfer into the mouth in gap between enamel and orthodontic through eating .

Staphylococcus pasteuri ,a poor data of the literature about epidemiology and natural habitat of *S. pasteuri*, and no systematic environmental surveys on this species have been published, five among the seven strains were from human

specimens (vomit, urine, and blood), while two of them were collected from mixed vegetables and goat's milk. Anyway, natural habitat of the organism actually remained uncertain (Bjorland *et el*., 2005). This bacteria isolated at the first time in mouth ,may be found this bacteria in the vegetables and goat's milk are good origin to transefer and adhere into orthodontic

Staphylococcus worneri is found in the mouth (Ohara-Nemoto *et al*., 2008) and they are able to produce biofilms on the surface of various materials, some of them of medical importance,(Gotz, 2002) .Therefore, all of these reasons confirm to adhere in orthodontic .

Enerobacter ludwigii a new species,(Hoffmann *et al*., 2005). information on these bacteria are very few. Therefore, in the present study the presence of this bacteria adhere on the orthodontic the first recovered as a new strain named" IRQBAS1" with ID number "HG003648" .

The results showed the presence of some bacterial in denture and orthodontic ,on the other hands, some of these bacterial isolates are found only in denture and verse versa. Furthermore, since the presence of orthodontic or denture is to treat the persons' alteration of local environment, these devices provide favorable condition due to the inaccessibility of saliva and lack of mechanical cleaning by the tongue (Daniluk *et al*., 2006). Hence, these devices act as reservoirs that harbor a mixed species of bacterial biofilm (biofilms on dental hard and soft tissues) following a variety of these organisms can cause of a potential respiratory infection and other

systematic diseases because the denture is made of acrylic resin ,acrylic denture is one of the main clinical problems (Ramage *et al* ., 2004). Surface deterioration of resin composites has been demonstrated by increased roughness, effects on filler particle exposure, and sometimes by a decreased microhardness of the materials upon exposure to biofilms *in vitro* (Beyth *et al*., 2008). Moreover , orthodontic appliances severely hamper the efficacy of toothbrushing (Schatzle *et al*., 2010), reducing the self-clearance by saliva (Ogaard *et al*., 2008) , changing the composition of the oral flora (Badawi *et al*., 2003) , increasing the amount of oral biofilm formed (Hagg *et al*., 2004) ,colonizing of oral surfaces by cariogenic(Al Mulla *et al*., 2009) and periodontopathogenic bacteria(Naranjo *et al*., 2006) . Orthodontic composed of (A): adhesive; (B): bracket; (C): ligating with elastomeric ring; (D): ligating with steel ligature; (E): self-ligating bracket with the clip open; (F): self-ligating bracket with a closed clip; (G): arch wire; and (H): bonded retainer (Gameiro *et al*., 2009 ; Pellegrini *et al*., 2009 ;Van der Veen *et al*., 2010). Adhesives, Composite resins for orthodontic bonding are in direct contact with the vulnerable enamel surface and their properties with respect to bacterial adhesion may be more important than other orthodontic materials, in general, excessive composite resin at the bracket-enamel-adhesive junction is prone to bacterial adhesion, especially since polymerization shrinkage may yield a gap with a width of up to 10 µm at the adhesive-enamel interface where bacteria find themselves protected against oral cleaning forces and antibacterial components of toothpastes and mouth rinses (Sukontapatipark *et al*., 2001).

However , since in denture and orthodontic adhesive part made from the same article (Resin) and this article presence in mouth appropriate environment to form biofilm and adhesion of bacteria , on the other hand, this confirms the presence of

some bacterial species in denture such as *Staphylocpccus aureus* , *Staphylococcus epidremidis* , *Bacillus subtilis* , *Streptococcus anginosus* (Budtz-Jorgensen *et al*., 1983) ,in the present study this bacteria were isolated from orthodontic, but *Klebsiella oxytoca* isolated from denture other studies isolates from orthodontic (Naranjo *et al*., 2006). However , this study confirms that too bacterial species which were isolated from these devices at the same time ,but these may depend on adhesion strength of bacterial species on these devices or may depend on oral hygiene or coincided with the presence of these bacteria with another mouth or systematic disease increases the presence of these bacteria .

5-11-Frequency of bacterial species from denture and orthodontic according to some factors:-

The results in this study showed that some factors are closely related with people who wear denture and the presence of some species .However, observed in denture (Table 4-7), that the presence of bacteria in individuals aged 35> (elderly people) more than the aged < 35, this relationship between elderly person with denture and bacteria ,due to the decrease in immune function associated with ageing (Tada *et al*., 2006), Furthermore, Saltzman and Peterson, (1987) reported that changes in the oral bacterial flora occur in individuals aged >70 years, leading to opportunistic infections associated with a decrease in immune function .On the other hands , there was a statistically significant relationship between bacterial presence and lack denture with cleanliness, this result is in agreement with De Visschere *et al*., (2006) and no statistically significant relationship was between bacterial presence and date denture wearer , dental caries, gingivitis ,tonsillitis and smoking cigarettes in the present

study may be do to sample collected from persons without severing of this disease and no cigarettes smoking, Furthermore, the presence of bacteria in denture not depending on date of denture wearer.

In orthodontic the results showed the presence of bacteria with adolescent aged <18 more than >18 (Table 4-8) , Furthermore , statistically significant relationship was between the increase bacterial on orthodontic and gingivitis , on the other hands , no significant difference in date of orthodontic insertion , this result is in agreement with Ristic *et al*., (2007). However statistically significant relationship between the increase of bacteria with time of orthodontic washing in day , could be due to the method of brushing teeth is incorrect leading to increase bacterial species in mouth. No statistically significant relationship was found between increase bacteria with dental caries ,tonsillitis and cigarettes smoking, because all sample were collected tack from non- smoking adolescent and without severing of this disease.

Conclusions and Recommendations

6-1-Conclusions:-

- Identification of bacterial species in denture and/or orthodontic which not found in previous studies of these two sources.
- Identification of bacterial species in dentures which is not found in orthodontic and the vice versa is right.
- Identification of new four bacterial strains as a first recording internationally with European nucleotide archive (ENA).
- The study showed that the best test to determine the ability of adherence is the genetic test.
- *Klebsiella pneumoniae has* the higher frequency in dentures and orthodontic among the other bacterial species.

6-2-Recommendations:-

- Use the PCR nucleotide sequences as the best test for diagnosing the bacterial species among the other assays .Since , different bacterial species were recognized in the present study .
- Use the genetic method for determining the ability of bacteria to adherence .
- other study should be accomplished to determine the sensitivity of the bacteria under the study toward antibiotics ,toothpastes and other medical solution .

- Several studies should be taken to show the direct relationship between the adherent bacteria from denture and orthodontic with lower respiratory and digestive system diseases.
- More studies should be performed from the same sources but with yeast , fungi and viruses.

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Appendix

❖ Appendix-1:-Alignment and concatenating of bacterial species obtained from the present study after sequencing data and reference strain by GeneBank using "CLUSTALW"

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Bacillus-cereus                 TACC-CCACCGACTTCGGGTGTTACAAACTCTC-GGGGTGTGACGGGCGG 48
Streptococcus-equinus           TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Bacillus-cereus-B1T             TACC-CCACCGACTTCGGGTGTTACAAACTCTC-GGGGTGTGACGGGCGG 48
Streptococcus-equinus-KLDS3.06  TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Enterococcus-faecalis           TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Lactococcus-lactis              TAGG-CAACCTACTTCGGGTACTCCCAACTCCC-GTGGTGTGACGGGCGG 48
Enterococcus-faecium            TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Enterococcus-faecalis-KLDS4.03  TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Lactococcus-lactis-LCT          TAGG-CAACCTACTTCGGGTACTCCCAACTCCC-GTGGTGTGACGGGCGG 48
Enterococcus-faecium-IB1T       TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Pediococcus-acidilactici        TACC-CCACCGGCTTTGGGTGTTACAAACTCTC-ATGGTGTGACGGGCGG 48
Proteus-mirabilis               TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Lactobacillus-plantarum         TACC-CCACCGACTTTGGGTGTTACAAACTCTC-ATGGTGTGACGGGCGG 48
Morganella-morganii             TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Bacillus-subtilis               TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Hafnia-alvei                    TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Chryseobacterium-vietnamense    TACGGTCACCGACTTCAGGTACCCCAGACTTCC-ATGGCTTGACGGGCGG 49
Streptococcus-anginosus         TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Bacillus-subtilis-N11T          TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Hafnia-alvei-E117T              TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Staphylococcus-aureus           TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Escherichia-fergusonii          TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Enterobacter-mori-R3-3T         TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Staphylococcus-aureus-NBRC1271  TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Escherichia-fergusonii-G7T      TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Enterobacter-ludwigii-NRCG12T   TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Staphylococcus-epidermidis-BBN  TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Enterobacter-cloacae-478T       TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Staphylococcus-warneri          TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Klebsiella-variicola            TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Citrobacter-freundii            TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Staphylococcus-warneri-FUA2075  TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Klebsiella-variicola-7T         TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Enterobacter-mori               TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Staphylococcus-epidermidis      TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Enterobacter-cloacae            TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Serratia-marcescens-A4T         TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Staphylococcus-pasteuri         TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Acinetobacter-baumannii         TAGG-CTAGCTACTTCTGGTGCAACAAACTCCC-ATGGTGTGACGGGCGG 48
Staphylococcus-pasteuri-C1PO1T  TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Acinetobacter-baumannii-DSM300  TAGG-CTAGCTACTTCTGGTGCAACAAACTCCC-ATGGTGTGACGGGCGG 48
Klebsiella-pneumoniae           TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGACGG 48
Staphylococcus-hominis-S9-624T  TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Klebsiella-pneumoniae-SDM45T    TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGACGG 48
Serratia-marcescens             TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Staphylococcus-hominis          TACT-CCACCGGCTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Citrobacter-freundii-MRB070408  TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Proteus-penneri                 TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Morganella-morganii-MFS05T      TAAG-CTACCTACTTCTTTTGCAACCCACTCCCCATGGTGTGACGGGCGG 49
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Enterobacter-ludwigii                TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Lactobacillus-plantarum-KLDS1.       TACC-CCACCGACTTTGGGTGTTACAAACTCTC-ATGGTGTGACGGGCGG 48
Proteus-penneri-Z2T                  TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
Chryseobacterium-vietnamense-G       TACGGTCACCGACTTCAGGTACCCCAGACTTCC-ATGGCTTGACGGGCGG 49
Streptococcus-anginosus-CO2T         TACC-TCACCGACTTCGGGTGTTACAAACTCTC-GTGGTGTGACGGGCGG 48
Pediococcus-acidilactici-L169T       TACC-CCACCGGCTTTGGGTGTTACAAACTCTC-ATGGTGTGACGGGCGG 48
Proteus-mirabilis-ALK419T            TAAG-CTACCTACTTCTTTTGCAACCCACTCCC-ATGGTGTGACGGGCGG 48
                                     **     * *  ***    *    *  ***  *   **  ****** ***

Bacillus-cereus                      TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATG-CTGATCCGCGAT 97
Streptococcus-equinus                TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Bacillus-cereus-B1T                  TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATG-CTGATCCGCGAT 97
Streptococcus-equinus-KLDS3.06       TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Enterococcus-faecalis                TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Lactococcus-lactis                   TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Enterococcus-faecium                 TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Enterococcus-faecalis-KLDS4.03       TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Lactococcus-lactis-LCT               TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Enterococcus-faecium-IB1T            TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Pediococcus-acidilactici             TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATG-CTGATCCGCGAT 97
Proteus-mirabilis                    TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Lactobacillus-plantarum              TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATG-CTGATCCGCGAT 97
Morganella-morganii                  TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Bacillus-subtilis                    TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATG-CTGATCCGCGAT 97
Hafnia-alvei                         TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Chryseobacterium-vietnamense         TGTGTACAAGGCCCGGGAACGTATTCACCGCGCCATGGCTGATGCGCGAT 99
Streptococcus-anginosus              TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Bacillus-subtilis-N11T               TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATG-CTGATCCGCGAT 97
Hafnia-alvei-E117T                   TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Staphylococcus-aureus                TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Escherichia-fergusonii               TGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATT-CTGATCCACGAT 97
Enterobacter-mori-R3-3T              TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Staphylococcus-aureus-NBRC1271       TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Escherichia-fergusonii-G7T           TGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATT-CTGATCCACGAT 97
Enterobacter-ludwigii-NRCG12T        TGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATT-CTGATCCACGAT 97
Staphylococcus-epidermidis-BBN       TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Enterobacter-cloacae-478T            TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Staphylococcus-warneri               TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Klebsiella-variicola                 TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Citrobacter-freundii                 TGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATT-CTGATCCACGAT 97
Staphylococcus-warneri-FUA2075       TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Klebsiella-variicola-7T              TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Enterobacter-mori                    TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Staphylococcus-epidermidis           TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Enterobacter-cloacae                 TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Serratia-marcescens-A4T              TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Staphylococcus-pasteuri              TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Acinetobacter-baumannii              TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATT-CTGATCCGCGAT 97
Staphylococcus-pasteuri-C1P01T       TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Acinetobacter-baumannii-DSM300       TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATT-CTGATCCGCGAT 97
Klebsiella-pneumoniae                TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Staphylococcus-hominis-S9-624T       TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Klebsiella-pneumoniae-SDM45T         TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Serratia-marcescens                  TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Staphylococcus-hominis               TGTGTACAAGACCCGGGAACGTATTCACCGTAGCATG-CTGATCTACGAT 97
Citrobacter-freundii-MRB070408       TGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATT-CTGATCCACGAT 97
Proteus-penneri                      TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Morganella-morganii-MFS05T           TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 98
Enterobacter-ludwigii                TGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATT-CTGATCCACGAT 97
Lactobacillus-plantarum-KLDS1.       TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATG-CTGATCCGCGAT 97
Proteus-penneri-Z2T                  TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
Chryseobacterium-vietnamense-G       TGTGTACAAGGCCCGGGAACGTATTCACCGCGCCATGGCTGATGCGCGAT 99
Streptococcus-anginosus-CO2T         TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTG-CTGATCCGCGAT 97
Pediococcus-acidilactici-L169T       TGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATG-CTGATCCGCGAT 97
Proteus-mirabilis-ALK419T            TGTGTACAAGGCCCGGGAACGTATTCACCGTAGCATT-CTGATCTACGAT 97
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Bacillus-cereus                 TACTAGCGATTCCAGCTTCATGTAGGCAAGTTGCAGCCTACAATCCGAAC 147
Streptococcus-equinus           TACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAAC 147
Bacillus-cereus-B1T             TACTAGCGATTCCAGCTTCATGTAGGCAAGTTGCAGCCTACAATCCGAAC 147
Streptococcus-equinus-KLDS3.06  TACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAAC 147
Enterococcus-faecalis           TACTAGCGATTCCGGCTTCATGCAGGCGAGTTGCAGCCTGCAATCCGAAC 147
Lactococcus-lactis              TACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAAC 147
Enterococcus-faecium            TACTAGCGATTCCGGCTTCATGCAGGCGAGTTGCAGCCTGCAATCCGAAC 147
Enterococcus-faecalis-KLDS4.03  TACTAGCGATTCCGGCTTCATGCAGGCGAGTTGCAGCCTGCAATCCGAAC 147
Lactococcus-lactis-LCT          TACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAAC 147
Enterococcus-faecium-IB1T       TACTAGCGATTCCGGCTTCATGCAGGCGAGTTGCAGCCTGCAATCCGAAC 147
Pediococcus-acidilactici        TACTAGCGATTCCGACTTCGTGTAGGCGAGTTGCAGCCTACAGTCCGAAC 147
Proteus-mirabilis               TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Lactobacillus-plantarum         TACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAAC 147
Morganella-morganii             TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Bacillus-subtilis               TACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGAAC 147
Hafnia-alvei                    TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Chryseobacterium-vietnamense    TACTAGCGATTCCAGCTTCATAGAGTCGAGTTGCAGACTCCAATCCGAAC 149
Streptococcus-anginosus         TACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAAC 147
Bacillus-subtilis-N11T          TACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGAAC 147
Hafnia-alvei-E117T              TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-aureus           TACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAAC 147
Escherichia-fergusonii          TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Enterobacter-mori-R3-3T         TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-aureus-NBRC1271  TACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAAC 147
Escherichia-fergusonii-G7T      TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Enterobacter-ludwigii-NRCG12T   TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-epidermidis-BBN  TACTAGCGATTCCAGCTTCATATAGTCGAGTTGCAGACTACAATCCGAAC 147
Enterobacter-cloacae-478T       TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-warneri          TACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAAC 147
Klebsiella-variicola            TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Citrobacter-freundii            TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-warneri-FUA2075  TACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAAC 147
Klebsiella-variicola-7T         TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Enterobacter-mori               TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-epidermidis      TACTAGCGATTCCAGCTTCATATAGTCGAGTTGCAGACTACAATCCGAAC 147
Enterobacter-cloacae            TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Serratia-marcescens-A4T         TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-pasteuri         TACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAAC 147
Acinetobacter-baumannii         TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-pasteuri-C1PO1T  TACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAAC 147
Acinetobacter-baumannii-DSM300  TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Klebsiella-pneumoniae           TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-hominis-S9-624T  TACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAAC 147
Klebsiella-pneumoniae-SDM45T    TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Serratia-marcescens             TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Staphylococcus-hominis          TACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAAC 147
Citrobacter-freundii-MRB070408  TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Proteus-penneri                 TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Morganella-morganii-MFS05T      TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 148
Enterobacter-ludwigii           TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Lactobacillus-plantarum-KLDS1.  TACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAAC 147
Proteus-penneri-Z2T             TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
Chryseobacterium-vietnamense-G  TACTAGCGATTCCAGCTTCATAGAGTCGAGTTGCAGACTCCAATCCGAAC 149
Streptococcus-anginosus-CO2T    TACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAAC 147
Pediococcus-acidilactici-L169T  TACTAGCGATTCCGACTTCGTGTAGGCGAGTTGCAGCCTACAGTCCGAAC 147
Proteus-mirabilis-ALK419T       TACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGAC 147
                                ************  ****    ** * ******** ** *  **** **

Bacillus-cereus                 T-GAAAACGGTTTTATGAAATTAGCTCCACCTCGCGGTCTTGCAGCTCTT 196
Streptococcus-equinus           T-GAGATTGGCTTTAAGAGATTTGCTTGCCGTCACCGACTCGCGACTCGT 196
Bacillus-cereus-B1T             T-GAAAACGGTTTTATGAAATTAGCTCCACCTCGCGGTCTTGCAGCTCTT 196
Streptococcus-equinus-KLDS3.06  T-GAGATTGGCTTTAAGAGATTTGCTTGCCGTCACCGACTCGCGACTCGT 196
Enterococcus-faecalis           T-GAGAGAAGCTTTAAGAGATTTGCATGACCTCGCGGTCTAGCGACTCGT 196
Lactococcus-lactis              T-GAGAATGGTTTTAAGAGATTAGCTAAACATCACTGTCTCGCGACTCGT 196
Enterococcus-faecium            T-GAGAGAAGCTTTAAGAGATTTGCATGACCTCGCGGTCTAGCGACTCGT 196
Enterococcus-faecalis-KLDS4.03  T-GAGAGAAGCTTTAAGAGATTTGCATGACCTCGCGGTCTAGCGACTCGT 196
Lactococcus-lactis-LCT          T-GAGAATGGTTTTAAGAGATTAGCTAAACATCACTGTCTCGCGACTCGT 196
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Enterococcus-faecium-IB1T           T-GAGAGAAGCTTTAAGAGATTTGCATGACCTCGCGGTCTAGCGACTCGT 196
Pediococcus-acidilactici            T-GAGAATGGTTTTAAGAGATTAGCTAAACCTCGCGGTTTCGCAACTCGT 196
Proteus-mirabilis                   T-ACGACAGACTTTATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Lactobacillus-plantarum             T-GAGAATGGCTTTAAGAGATTAGCTTACTCTCGCGAGTTCGCAACTCGT 196
Morganella-morganii                 T-ACGACGTACTTTATGAGTTCCGCTTGCCCTCGCGGGGTCGCTTCCCTT 196
Bacillus-subtilis                   TGAGAACAGA-TTTGTGGGATTGGCTTAACCTCGCGGTTTCGCTGCCCTT 196
Hafnia-alvei                        T-ACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGTTCGCTTCTCTT 196
Chryseobacterium-vietnamense        TGA-GACCGGCTTTC-GAGATTTGCATCACATCACTGTGTAGCTGCCCTC 197
Streptococcus-anginosus             TGA-GACTGGCTTTCAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGT 196
Bacillus-subtilis-N11T              TGAGAACAGA-TTTGTGGGATTGGCTTAACCTCGCGGTTTCGCTGCCCTT 196
Hafnia-alvei-E117T                  T-ACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGTTCGCTTCTCTT 196
Staphylococcus-aureus               T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTT 196
Escherichia-fergusonii              T-ACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Enterobacter-mori-R3-3T             T-ACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Staphylococcus-aureus-NBRC1271      T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTT 196
Escherichia-fergusonii-G7T          T-ACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Enterobacter-ludwigii-NRCG12T       T-ACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Staphylococcus-epidermidis-BBN      T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTT 196
Enterobacter-cloacae-478T           T-ACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Staphylococcus-warneri              T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTAGCTGCCCTT 196
Klebsiella-variicola                T-ACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Citrobacter-freundii                T-ACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Staphylococcus-warneri-FUA2075      T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTAGCTGCCCTT 196
Klebsiella-variicola-7T             T-ACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Enterobacter-mori                   T-ACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Staphylococcus-epidermidis          T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTT 196
Enterobacter-cloacae                T-ACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Serratia-marcescens-A4T             T-ACGACGTACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Staphylococcus-pasteuri             T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTAGCTGCCCTT 196
Acinetobacter-baumannii             T-ACGATCGGCTTTTTGAGATTAGCATCACATCGCTGTGTAGCAACCCTT 196
Staphylococcus-pasteuri-C1P01T      T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTAGCTGCCCTT 196
Acinetobacter-baumannii-DSM300      T-ACGATCGGCTTTTTGAGATTAGCATCACATCGCTGTGTAGCAACCCTT 196
Klebsiella-pneumoniae               T-ACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Staphylococcus-hominis-S9-624T      T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTT 196
Klebsiella-pneumoniae-SDM45T        T-ACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Serratia-marcescens                 T-ACGACGTACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Staphylococcus-hominis              T-GAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTT 196
Citrobacter-freundii-MRB070408      T-ACGACATACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Proteus-penneri                     T-ACGACAGACTTTATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Morganella-morganii-MFS05T          T-ACGACGTACTTTATGAGTTCCGCTTGCCCTCGCGGGGTCGCTTCCCTT 197
Enterobacter-ludwigii               T-ACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Lactobacillus-plantarum-KLDS1.      T-GAGAATGGCTTTAAGAGATTAGCTTACTCTCGCGAGTTCGCAACTCGT 196
Proteus-penneri-Z2T                 T-ACGACAGACTTTATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
Chryseobacterium-vietnamense-G      T-GAGACCGGCTTTC-GAGATTTGCATCACATCGCTGTGTAGCTGCCCTC 197
Streptococcus-anginosus-CO2T        T-GAGACTGGCTTTCAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGT 196
Pediococcus-acidilactici-L169T      T-GAGAATGGTTTTAAGAGATTAGCTAAACCTCGCGGTTTCGCAACTCGT 196
Proteus-mirabilis-ALK419T           T-ACGACAGACTTTATGAGTTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT 196
                                    *   *     ***  *   *  **      ** *   * **  * *

Bacillus-cereus                     TGTACCGT-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Streptococcus-equinus               TGTACCAA-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Bacillus-cereus-B1T                 TGTACCGT-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Streptococcus-equinus-KLDS3.06      TGTACCAA-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Enterococcus-faecalis               TGTACTTC-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Lactococcus-lactis                  TGTACCAT-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Enterococcus-faecium                TGTACTTC-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Enterococcus-faecalis-KLDS4.03      TGTACTTC-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Lactococcus-lactis-LCT              TGTACCAT-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Enterococcus-faecium-IB1T           TGTACTTC-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Pediococcus-acidilactici            TGTACCAT-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Proteus-mirabilis                   TGTATCTG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Lactobacillus-plantarum             TGTACCAT-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Morganella-morganii                 TGTATACG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Bacillus-subtilis                   TGT-TCTGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Hafnia-alvei                        TGTATATG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Chryseobacterium-vietnamense        TGTACCGG-CCATTGTATTACGTGTGTGGCCCAAGGCGTAAGGGCCGTGA 246
Streptococcus-anginosus             TGTACCAG-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
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Bacillus-subtilis-N11T              TGT-TCTGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Hafnia-alvei-E117T                  TGTATATG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Staphylococcus-aureus               TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Escherichia-fergusonii              TGTATGCG-CCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGA 245
Enterobacter-mori-R3-3T             TGTATGCG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Staphylococcus-aureus-NBRC1271      TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Escherichia-fergusonii-G7T          TGTATGCG-CCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGA 245
Enterobacter-ludwigii-NRCG12T       TGTATGCG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Staphylococcus-epidermidis-BBN      TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Enterobacter-cloacae-478T           TGTATGCG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Staphylococcus-warneri              TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Klebsiella-variicola                TGTATATG-CCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGA 245
Citrobacter-freundii                TGTATATG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Staphylococcus-warneri-FUA2075      TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Klebsiella-variicola-7T             TGTATATG-CCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGA 245
Enterobacter-mori                   TGTATGCG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Staphylococcus-epidermidis          TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Enterobacter-cloacae                TGTATGCG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Serratia-marcescens-A4T             TGTATACG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Staphylococcus-pasteuri             TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Acinetobacter-baumannii             TGTACCGA-CCATTGTAGCACGTGTGTAGCCCTGGCCGTAAGGGCCATGA 245
Staphylococcus-pasteuri-C1P01T      TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Acinetobacter-baumannii-DSM300      TGTACCGA-CCATTGTAGCACGTGTGTAGCCCTGGCCGTAAGGGCCATGA 245
Klebsiella-pneumoniae               TGTATATG-CCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGA 245
Staphylococcus-hominis-S9-624T      TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Klebsiella-pneumoniae-SDM45T        TGTATATG-CCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGA 245
Serratia-marcescens                 TGTATACG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Staphylococcus-hominis              TGTATTGT-CCATTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGA 245
Citrobacter-freundii-MRB070408      TGTATATG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Proteus-penneri                     TGTATCTG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Morganella-morganii-MFS05T          TGTATACG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 246
Enterobacter-ludwigii               TGTATGCG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Lactobacillus-plantarum-KLDS1.      TGTACCAT-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Proteus-penneri-Z2T                 TGTATCTG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
Chryseobacterium-vietnamense-G      TGTACCGG-CCATTGTATTACGTGTGTGGCCCAAGGCGTAAGGGCCGTGA 246
Streptococcus-anginosus-CO2T        TGTACCAG-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Pediococcus-acidilactici-L169T      TGTACCAT-CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGA 245
Proteus-mirabilis-ALK419T           TGTATCTG-CCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGA 245
                                    ***      ********  ******** ****    * ****** * ***

Bacillus-cereus                     TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCACC 294
Streptococcus-equinus               TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTATTACCGGCAGTCTCG 294
Bacillus-cereus-B1T                 TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCACC 294
Streptococcus-equinus-KLDS3.06      TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTATTACCGGCAGTCTCG 294
Enterococcus-faecalis               TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCTCG 294
Lactococcus-lactis                  TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCG 294
Enterococcus-faecium                TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCTCG 294
Enterococcus-faecalis-KLDS4.03      TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCTCG 294
Lactococcus-lactis-LCT              TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCG 294
Enterococcus-faecium-IB1T           TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCTCG 294
Pediococcus-acidilactici            TGATTTGACGTCGTCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCTCA 294
Proteus-mirabilis                   TGACTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCC 294
Lactobacillus-plantarum             TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCTCA 294
Morganella-morganii                 TGACTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCC 294
Bacillus-subtilis                   TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCACC 294
Hafnia-alvei                        TGACTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCC 294
Chryseobacterium-vietnamense        TGATTTGACGTCATCCCCACCTTCCTCTCTACTTGC-GTAGGCAGTCTCA 295
Streptococcus-anginosus             TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTATTACCGGCAGTCTCG 294
Bacillus-subtilis-N11T              TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCACC 294
Hafnia-alvei-E117T                  TGACTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCC 294
Staphylococcus-aureus               TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
Escherichia-fergusonii              TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Enterobacter-mori-R3-3T             TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Staphylococcus-aureus-NBRC1271      TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
Escherichia-fergusonii-G7T          TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Enterobacter-ludwigii-NRCG12T       TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Staphylococcus-epidermidis-BBN      TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
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Enterobacter-cloacae-478T            TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Staphylococcus-warneri               TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
Klebsiella-variicola                 TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Citrobacter-freundii                 TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Staphylococcus-warneri-FUA2075       TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
Klebsiella-variicola-7T              TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Enterobacter-mori                    TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Staphylococcus-epidermidis           TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
Enterobacter-cloacae                 TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Serratia-marcescens-A4T              TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Staphylococcus-pasteuri              TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
Acinetobacter-baumannii              TGACTTGACGTCGTCCCCGCCTTCCTC-CAGTTTGTCACTGGCAGTATCC 294
Staphylococcus-pasteuri-C1PO1T       TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
Acinetobacter-baumannii-DSM300       TGACTTGACGTCGTCCCCGCCTTCCTC-CAGTTTGTCACTGGCAGTATCC 294
Klebsiella-pneumoniae                TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Staphylococcus-hominis-S9-624T       TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
Klebsiella-pneumoniae-SDM45T         TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Serratia-marcescens                  TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Staphylococcus-hominis               TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCAAC 294
Citrobacter-freundii-MRB070408       TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Proteus-penneri                      TGACTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCC 294
Morganella-morganii-MFS05T           TGACTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCC 295
Enterobacter-ludwigii                TGACTTGACGTCATCCCCACCTTCCTC-CAGTTTATCACTGGCAGTCTCC 294
Lactobacillus-plantarum-KLDS1.       TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCTCA 294
Proteus-penneri-Z2T                  TGACTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCC 294
Chryseobacterium-vietnamense-G       TGATTTGACGTCATCCCCACCTTCCTCTCTACTTGC-GTAGGCAGTCTCA 295
Streptococcus-anginosus-CO2T         TGATTTGACGTCATCCCCACCTTCCTC-CGGTTTATTACCGGCAGTCTCG 294
Pediococcus-acidilactici-L169T       TGATTTGACGTCGTCCCCACCTTCCTC-CGGTTTGTCACCGGCAGTCTCA 294
Proteus-mirabilis-ALK419T            TGACTTGACGTCATCCCCACCTTCCTC-CGGTTTATCACCGGCAGTCTCC 294
                                     *** ******** ***** ******** *   **      ******

Bacillus-cereus                      TTAAAGTGCCCA--ACTAAAT--GA--TGGCAACTAAAATCAAGGGTTGC 338
Streptococcus-equinus                CTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAACAATAGGGGTTGC 338
Bacillus-cereus-B1T                  TTAAAGTGCCCA--ACTAAAT--GA--TGGCAACTAAAATCAAGGGTTGC 338
Streptococcus-equinus-KLDS3.06       CTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAACAATAGGGGTTGC 338
Enterococcus-faecalis                CTAGAGTGCCCA--ACTAAAT--GA--TGGCAACTAACAATAAGGGTTGC 338
Lactococcus-lactis                   TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAACAATAGGGGTTGC 338
Enterococcus-faecium                 CTAGAGTGCCCA--ACTAAAT--GA--TGGCAACTAACAATAAGGGTTGC 338
Enterococcus-faecalis-KLDS4.03       CTAGAGTGCCCA--ACTAAAT--GA--TGGCAACTAACAATAAGGGTTGC 338
Lactococcus-lactis-LCT               TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAACAATAGGGGTTGC 338
Enterococcus-faecium-IB1T            CTAGAGTGCCCA--ACTAAAT--GA--TGGCAACTAACAATAAGGGTTGC 338
Pediococcus-acidilactici             CTAGAGTGCCCA--ACTGAAT--GC--TGGCAACTAGTAATAAGGGTTGC 338
Proteus-mirabilis                    TTTGAGTTCCCACCATTACGT--GC--TGGCAACAAAGGATAAGGGTTGC 340
Lactobacillus-plantarum              CCAGAGTGCCCA--ACTTAAT--GC--TGGCAACTGATAATAAGGGTTGC 338
Morganella-morganii                  TTTGAGTTCCCG--CCATCAC--GCGCTGGCAACAAAGGATAAGGGTTGC 340
Bacillus-subtilis                    TTAGAGTGCCCA--ACTGAAT--GC--TGGCAACTAAGATCAAGGGTTGC 338
Hafnia-alvei                         TTTGAGTTCCCACCATTACGT--GC--TGGCAACAAAGGATAAGGGTTGC 340
Chryseobacterium-vietnamense         CTAGAGTCCCCA--ACTTAAT--GA--TGGCAACTAGTGACAGGGGTTGC 339
Streptococcus-anginosus              CTAGAGTGCCCA--ACTCAAT--GA--TGGCAACTAACAATAAGGGTTGC 338
Bacillus-subtilis-N11T               TTAGAGTGCCCA--ACTGAAT--GC--TGGCAACTAAGATCAAGGGTTGC 338
Hafnia-alvei-E117T                   TTTGAGTTCCCACCATTACGT--GC--TGGCAACAAAGGATAAGGGTTGC 340
Staphylococcus-aureus                TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAAGCTTAAGGGTTGC 338
Escherichia-fergusonii               TTTGAGTTCCCG--GCCGGAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Enterobacter-mori-R3-3T              TTTGAGTTCCCG--GCCGAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Staphylococcus-aureus-NBRC1271       TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAAGCTTAAGGGTTGC 338
Escherichia-fergusonii-G7T           TTTGAGTTCCCG--GCCGGAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Enterobacter-ludwigii-NRCG12T        TTTGAGTTCCCG--GCCTAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Staphylococcus-epidermidis-BBN       TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAAGCTTAAGGGTTGC 338
Enterobacter-cloacae-478T            TTTGAGTTCCCG--GCCTAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Staphylococcus-warneri               TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAAGCTTAAGGGTTGC 338
Klebsiella-variicola                 TTTGAGTTCCCG--GCCTAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Citrobacter-freundii                 TTTGAGTTCCCG--GCCGAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Staphylococcus-warneri-FUA2075       TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAAGCTTAAGGGTTGC 338
Klebsiella-variicola-7T              TTTGAGTTCCCG--GCCTAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Enterobacter-mori                    TTTGAGTTCCCG--GCCGAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Staphylococcus-epidermidis           TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAAGCTTAAGGGTTGC 338
Enterobacter-cloacae                 TTTGAGTTCCCG--GCCTAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
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Serratia-marcescens-A4T             TTTGAGTTCCCG--GCCGAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Staphylococcus-pasteuri             TTAGAGTGCCCA--ACTTAA--TGA--TGGCAACTAAGCTTAAGGGTTGC 338
Acinetobacter-baumannii             TTAAAGTTCCCA--TCCGAAA-TGC--TGGCAAGTAAGGAAAAGGGTTGC 339
Staphylococcus-pasteuri-C1PO1T      TTAGAGTGCCCA--ACTTAA--TGA--TGGCAACTAAGCTTAAGGGTTGC 338
Acinetobacter-baumannii-DSM300      TTAAAGTTCCCA--TCCGAAA-TGC--TGGCAAGTAAGGAAAAGGGTTGC 339
Klebsiella-pneumoniae               TTTGAGTTCCCG--GCCGGAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Staphylococcus-hominis-S9-624T      TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAAGCTTAAGGGTTGC 338
Klebsiella-pneumoniae-SDM45T        TTTGAGTTCCCG--GCCGGAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Serratia-marcescens                 TTTGAGTTCCCG--GCCGAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Staphylococcus-hominis              TTAGAGTGCCCA--ACTTAAT--GA--TGGCAACTAAGCTTAAGGGTTGC 338
Citrobacter-freundii-MRB070408      TTTGAGTTCCCG--GCCGAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Proteus-penneri                     TTTGAGTTCCCA--CCATTACGTGC--TGGCAACAAAGGATAAGGGTTGC 340
Morganella-morganii-MFS05T          TTTGAGTTCCCG--CCATCACGCGC--TGGCAACAAAGGATAAGGGTTGC 341
Enterobacter-ludwigii               TTTGAGTTCCCG--GCCTAAC-CGC--TGGCAACAAAGGATAAGGGTTGC 339
Lactobacillus-plantarum-KLDS1.      CCAGAGTGCCCA--AC-TTA-ATGC--TGGCAACTGATAATAAGGGTTGC 338
Proteus-penneri-Z2T                 TTTGAGTTCCCA--CCATTACGTGC--TGGCAACAAAGGATAAGGGTTGC 340
Chryseobacterium-vietnamense-G      CTAGAGTCCCCA--ACTTAAT--GA--TGGCAACTAGTGACAGGGGTTGC 339
Streptococcus-anginosus-CO2T        CTAGAGTGCCCA--ACTCAAT--GA--TGGCAACTAACAATAAGGGTTGC 338
Pediococcus-acidilactici-L169T      CTAGAGTGCCCA--ACTGAAT--GC--TGGCAACTAGTAATAAGGGTTGC 338
Proteus-mirabilis-ALK419T           TTTGAGTTCCCACCATTACGT--GC--TGGCAACAAAGGATAAGGGTTGC 340
                                        *** ***           *   ******       * *******

Bacillus-cereus                     GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACAACAAC 388
Streptococcus-equinus               GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Bacillus-cereus-B1T                 GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACAACAAC 388
Streptococcus-equinus-KLDS3.06      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Enterococcus-faecalis               GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Lactococcus-lactis                  GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Enterococcus-faecium                GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Enterococcus-faecalis-KLDS4.03      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Lactococcus-lactis-LCT              GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Enterococcus-faecium-IB1T           GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Pediococcus-acidilactici            GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Proteus-mirabilis                   GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 390
Lactobacillus-plantarum             GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Morganella-morganii                 GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 390
Bacillus-subtilis                   GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Hafnia-alvei                        GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 390
Chryseobacterium-vietnamense        GCTCGTTGCAGGACTTAACCTAACACCTCACGGCACGAGCTGACGACAAC 389
Streptococcus-anginosus             GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Bacillus-subtilis-N11T              GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Hafnia-alvei-E117T                  GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 390
Staphylococcus-aureus               GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Escherichia-fergusonii              GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Enterobacter-mori-R3-3T             GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Staphylococcus-aureus-NBRC1271      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Escherichia-fergusonii-G7T          GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Enterobacter-ludwigii-NRCG12T       GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Staphylococcus-epidermidis-BBN      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Enterobacter-cloacae-478T           GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Staphylococcus-warneri              GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Klebsiella-variicola                GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Citrobacter-freundii                GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Staphylococcus-warneri-FUA2075      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Klebsiella-variicola-7T             GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Enterobacter-mori                   GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Staphylococcus-epidermidis          GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Enterobacter-cloacae                GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Serratia-marcescens-A4T             GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Staphylococcus-pasteuri             GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Acinetobacter-baumannii             GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGC 389
Staphylococcus-pasteuri-C1PO1T      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Acinetobacter-baumannii-DSM300      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGC 389
Klebsiella-pneumoniae               GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Staphylococcus-hominis-S9-624T      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Klebsiella-pneumoniae-SDM45T        GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Serratia-marcescens                 GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
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Staphylococcus-hominis              GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Citrobacter-freundii-MRB070408      GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Proteus-penneri                     GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 390
Morganella-morganii-MFS05T          GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 391
Enterobacter-ludwigii               GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 389
Lactobacillus-plantarum-KLDS1.      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Proteus-penneri-Z2T                 GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 390
Chryseobacterium-vietnamense-G      GCTCGTTGCAGGACTTAACCTAACACCTCACGGCACGAGCTGACGACAAC 389
Streptococcus-anginosus-CO2T        GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Pediococcus-acidilactici-L169T      GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC 388
Proteus-mirabilis-ALK419T           GCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGC 390
                                    ********* ********** ****  ****  *********** *** *

Bacillus-cereus                     CATGCACCACCTGTCACTCTGCTCCC--GAAGGA-AAAGC--CCTATCTC 433
Streptococcus-equinus               CATGCACCACCTGTCACCGATGTTCC--GAAG-A-AACTT--CCTATCTC 432
Bacillus-cereus-B1T                 CATGCACCACCTGTCACTCTGCTCCC--GAAGGA-AAAGC--CCTATCTC 433
Streptococcus-equinus-KLDS3.06      CATGCACCACCTGTCACCGATGTTCC--GAAG-A-AACTT--CCTATCTC 432
Enterococcus-faecalis               CATGCACCACCTGTCACTTTGTCCCC--GAAGGG-AAAGC--TCTATCTC 433
Lactococcus-lactis                  CATGCACCACCTGT-ATCCCGTGTCC--CGAAGG-AACTT--CCTATCTC 432
Enterococcus-faecium                CATGCACCACCTGTCACTTTGTCCCC--GAAGGG-AAAGC--TCTATCTC 433
Enterococcus-faecalis-KLDS4.03      CATGCACCACCTGTCACTTTGTCCCC--GAAGGG-AAAGC--TCTATCTC 433
Lactococcus-lactis-LCT              CATGCACCACCTGT-ATCCCGTGTCC--CGAAGG-AACTT--CCTATCTC 432
Enterococcus-faecium-IB1T           CATGCACCACCTGTCACTTTGTCCCC--GAAGGG-AAAGC--TCTATCTC 433
Pediococcus-acidilactici            CATGCACCACCTGTCATTCTGTCCCC--GAAGGG-AACGC--CTAATCTC 433
Proteus-mirabilis                   CATGCAGCACCTGTCTCAGCGTTCCC--GAAGGC-ACTCC--TCTATCTC 435
Lactobacillus-plantarum             CATGCACCACCTGTATCCATGTCCCC--GAAGGG-AACGT--CTAATCTC 433
Morganella-morganii                 CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--AGCATCTC 435
Bacillus-subtilis                   CATGCACCACCTGTCACTCTGCCCCC--GAAGGG-GACGT--CCTATCTC 433
Hafnia-alvei                        CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACTAA--GCTATCTC 435
Chryseobacterium-vietnamense        CATGCAGCACCT-TGAAAAATGT-CC--GAAGA--AAAGT--C-TATTTC 430
Streptococcus-anginosus             CATGCACCACCTGTCACCGATGTTCC--GAAGA--AACTT--CCTATCTC 432
Bacillus-subtilis-N11T              CATGCACCACCTGTCACTCTGCCCCC--GAAGGG-GACGT--CCTATCTC 433
Hafnia-alvei-E117T                  CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACTAA--GCTATCTC 435
Staphylococcus-aureus               CATGCACCACCTGTCACTTTGTCCCCC-GAAGGG-GAAGGC-TCTATCTC 435
Escherichia-fergusonii              CATGCAGCACCTGTCTCACGGTTCCC--GAAGGC-ACATTC-TC-ATCTC 434
Enterobacter-mori-R3-3T             CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-AC-CAA-TCCATCTC 434
Staphylococcus-aureus-NBRC1271      CATGCACCACCTGTCACTTTGTCCCCC-GAAGGG-GAAGGC-TCTATCTC 435
Escherichia-fergusonii-G7T          CATGCAGCACCTGTCTCACGGTTCCC--GAAGGC-ACATTC-TC-ATCTC 434
Enterobacter-ludwigii-NRCG12T       CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAAA-GC-ATCTC 434
Staphylococcus-epidermidis-BBN      CATGCACCACCTGTCACTCTGTCCCCC-GAAGGG-GAAAAC-TCTATCTC 435
Enterobacter-cloacae-478T           CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--TCCATCTC 434
Staphylococcus-warneri              CATGCACCACCTGTCACTTTGTCCCCCGAAGGGG-AAGAC--TCTATCTC 435
Klebsiella-variicola                CATGCAGCACCTGTCTCACAGTTCCC--GAAGGC-ACCAA--TCCATCTC 434
Citrobacter-freundii                CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--AGCATCTC 434
Staphylococcus-warneri-FUA2075      CATGCACCACCTGTCACTTTGTCCCCCGAAGGGG-AAGAC--TCTATCTC 435
Klebsiella-variicola-7T             CATGCAGCACCTGTCTCACAGTTCCC--GAAGGC-ACCAA--TCCATCTC 434
Enterobacter-mori                   CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--TCCATCTC 434
Staphylococcus-epidermidis          CATGCACCACCTGTCACTCTGTCCCCC-GAAGGG-GAAAAC-TCTATCTC 435
Enterobacter-cloacae                CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--TCCATCTC 434
Serratia-marcescens-A4T             CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--TCCATCTC 434
Staphylococcus-pasteuri             CATGCACCACCTGTCACTTTGTCCCCC-GAAGGGGAAGAC--TCTATCTC 435
Acinetobacter-baumannii             CATGCAGCACCTGT-ATCTAGATTCCC-GAAGGC-ACCAA--TCCATCTC 434
Staphylococcus-pasteuri-C1P01T      CATGCACCACCTGTCACTTTGTCCCCC-GAAGGGGAAGAC--TCTATCTC 435
Acinetobacter-baumannii-DSM300      CATGCAGCACCTGT-ATCTAGATTCCC-GAAGGC-ACCAA--TCCATCTC 434
Klebsiella-pneumoniae               CATGCAGCACCTGTCTCACAGTTCCC--GAAGGC-ACCAA--TCCATCTC 434
Staphylococcus-hominis-S9-624T      CATGCACCACCTGTCACTTTGTCCCC--CGAAGG-GGAAACTTCTATCTC 435
Klebsiella-pneumoniae-SDM45T        CATGCAGCACCTGTCTCACAGTTCCC--GAAGGC-ACCAA--TCCATCTC 434
Serratia-marcescens                 CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--TCCATCTC 434
Staphylococcus-hominis              CATGCACCACCTGTCACTTTGTCCCC--CGAAGG-GGAAACTTCTATCTC 435
Citrobacter-freundii-MRB070408      CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--AGCATCTC 434
Proteus-penneri                     CATGCAGCACCTGTCTCAGCGTTCCC--GAAGGC-ACTCC--TCTATCTC 435
Morganella-morganii-MFS05T          CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--AGCATCTC 436
Enterobacter-ludwigii               CATGCAGCACCTGTCTCAGAGTTCCC--GAAGGC-ACCAA--AGCATCTC 434
Lactobacillus-plantarum-KLDS1.      CATGCACCACCTGTATCCATGTCCCC--GAAGGG-AACGT--CTAATCTC 433
Proteus-penneri-Z2T                 CATGCAGCACCTGTCTCAGCGTTCCC--GAAGGC-ACTCC--TCTATCTC 435
Chryseobacterium-vietnamense-G      CATGCAGCACCT-TGAAAAATGT-CC--GAAGA--AAAGT--C-TATTTC 430
Streptococcus-anginosus-CO2T        CATGCACCACCTGTCACCGATGTTCC--GAAGA--AACTT--CCTATCTC 432
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Pediococcus-acidilactici-L169T      CATGCACCACCTGTCATTCTGTCCCC--GAAGGG-AACGC--CTAATCTC 433
Proteus-mirabilis-ALK419T           CATGCAGCACCTGTCTCAGCGTTCCC--GAAGGC-ACTCC--TCTATCTC 435
                                    ****** ***** *         **                  ** **

Bacillus-cereus                     T-AGGGTTGTCAA-AG--GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Streptococcus-equinus               T-AGGAATAGCATCGG--GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Bacillus-cereus-B1T                 T-AGGGTTGTCAA-AG--GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Streptococcus-equinus-KLDS3.06      T-AGGAATAGCATCGG--GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Enterococcus-faecalis               T-AG-AGTGGTCAAAG--GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Lactococcus-lactis                  T-AGGAATAGCACGAG--TATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Enterococcus-faecium                T-AG-AGTGGTCAAAG--GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Enterococcus-faecalis-KLDS4.03      T-AG-AGTGGTCAAAG--GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Lactococcus-lactis-LCT              T-AGGAATAGCACGAG--TATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Enterococcus-faecium-IB1T           T-AG-AGTGGTCAAAG--GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Pediococcus-acidilactici            TTAGG--TTGGCAGAA--GATGTCAAGACCTGGTAAGGTTCTTCGCGTAG 479
Proteus-mirabilis                   TAAAGGATTCGCTG----GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 481
Lactobacillus-plantarum             T--TAGATTTGCATAG--TATGTCAAGACCTGGTAAGGTTCTTCGCGTAG 479
Morganella-morganii                 TGCTAAGTTCTC-TGG---ATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 481
Bacillus-subtilis                   TAG--GATTGTC-AGAG-GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Hafnia-alvei                        TAGCAAATTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 481
Chryseobacterium-vietnamense        TAA--ACCTGTC-ATTTCCCATTTAAGCCTTGGTAAGGTTCCTCGCGTAT 477
Streptococcus-anginosus             TAG--AAATAGC-ATCGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Bacillus-subtilis-N11T              TAG--GATTGTC-AGAG-GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Hafnia-alvei-E117T                  TAGCAAATTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 481
Staphylococcus-aureus               TAGAGTTGTCAA-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Escherichia-fergusonii              TGAAAACTTCCG-TG---GATGTCAAGACCAGGTAAGGTTCTTCGCGTTG 480
Enterobacter-mori-R3-3T             TGGAAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Staphylococcus-aureus-NBRC1271      TAGAGTTGTCAA-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Escherichia-fergusonii-G7T          TGAAAACTTCCG-TG---GATGTCAAGACCAGGTAAGGTTCTTCGCGTTG 480
Enterobacter-ludwigii-NRCG12T       TGCTAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Staphylococcus-epidermidis-BBN      TAGAGGGGTCAG-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Enterobacter-cloacae-478T           TGGAAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Staphylococcus-warneri              TAGAGCGGTCAA-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Klebsiella-variicola                TGGAAAGTTCTG-TG---GATGTCAAGACCAGGTAAGGTTCTTCGCGTTG 480
Citrobacter-freundii                TGCTAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Staphylococcus-warneri-FUA2075      TAGAGCGGTCAA-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Klebsiella-variicola-7T             TGGAAAGTTCTG-TG---GATGTCAAGACCAGGTAAGGTTCTTCGCGTTG 480
Enterobacter-mori                   TGGAAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Staphylococcus-epidermidis          TAGAGGGGTCAG-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Enterobacter-cloacae                TGGAAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Serratia-marcescens-A4T             TGGAAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Staphylococcus-pasteuri             TAGAGCGGTCAA-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Acinetobacter-baumannii             TGGAAAGTTTCT-AG---TATGTCAAGGCCAGGTAAGGTTCTTCGCGTTG 480
Staphylococcus-pasteuri-C1P01T      TAGAGCGGTCAA-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Acinetobacter-baumannii-DSM300      TGGAAAGTTTCT-AG---TATGTCAAGGCCAGGTAAGGTTCTTCGCGTTG 480
Klebsiella-pneumoniae               TGGAAAGTTCTG-TG---GATGTCAAGACCAGGTAAGGTTCTTCGCGTTG 480
Staphylococcus-hominis-S9-624T      TAGAAGGGTCAA-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Klebsiella-pneumoniae-SDM45T        TGGAAAGTTCTG-TG---GATGTCAAGACCAGGTAAGGTTCTTCGCGTTG 480
Serratia-marcescens                 TGGAAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Staphylococcus-hominis              TAGAAGGGTCAA-AG---GATGTCAAGATTTGGTAAGGTTCTTCGCGTTG 481
Citrobacter-freundii-MRB070408      TGCTAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Proteus-penneri                     TAAAGGATTCGC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 481
Morganella-morganii-MFS05T          TGCTAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 482
Enterobacter-ludwigii               TGCTAAGTTCTC-TG---GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 480
Lactobacillus-plantarum-KLDS1.      TTA--GATTTGCATAGT--ATGTCAAGACCTGGTAAGGTTCTTCGCGTAG 479
Proteus-penneri-Z2T                 TAAAGGATTCGC-TGG---ATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 481
Chryseobacterium-vietnamense-G      TAAACCTGTCATTTC---CCATTTAAGCCTTGGTAAGGTTCCTCGCGTAT 477
Streptococcus-anginosus-C02T        TAGAAATAGCATCGG---GATGTCAAGACCTGGTAAGGTTCTTCGCGTTG 479
Pediococcus-acidilactici-L169T      TTAGG--TTGGCAGAA--GATGTCAAGACCTGGTAAGGTTCTTCGCGTAG 479
Proteus-mirabilis-ALK419T           TAAAGGATTCGCTG----GATGTCAAGAGTAGGTAAGGTTCTTCGCGTTG 481
                                    *                   * ***    ********** ******

Bacillus-cereus                     CTTCAAATTAAACCACATGCTCCACCGCTGGTGCGGGCCCCCGTCAATTC 529
Streptococcus-equinus               CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Bacillus-cereus-B1T                 CTTCAAATTAAACCACATGCTCCACCGCTGGTGCGGGCCCCCGTCAATTC 529
Streptococcus-equinus-KLDS3.06      CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Enterococcus-faecalis               CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
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Lactococcus-lactis                CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Enterococcus-faecium              CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Enterococcus-faecalis-KLDS4.03    CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Lactococcus-lactis-LCT            CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Enterococcus-faecium-IB1T         CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Pediococcus-acidilactici          CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Proteus-mirabilis                 CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 531
Lactobacillus-plantarum           CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Morganella-morganii               CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 531
Bacillus-subtilis                 CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Hafnia-alvei                      CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 531
Chryseobacterium-vietnamense      CATCGAATTAAACCACATAATCCACCGCTTGTGCGGGCCCCCGTCAATTC 527
Streptococcus-anginosus           CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Bacillus-subtilis-N11T            CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Hafnia-alvei-E117T                CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 531
Staphylococcus-aureus             CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Escherichia-fergusonii            CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Enterobacter-mori-R3-3T           CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Staphylococcus-aureus-NBRC1271    CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Escherichia-fergusonii-G7T        CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Enterobacter-ludwigii-NRCG12T     CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Staphylococcus-epidermidis-BBN    CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Enterobacter-cloacae-478T         CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Staphylococcus-warneri            CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Klebsiella-variicola              CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Citrobacter-freundii              CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Staphylococcus-warneri-FUA2075    CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Klebsiella-variicola-7T           CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Enterobacter-mori                 CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Staphylococcus-epidermidis        CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Enterobacter-cloacae              CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Serratia-marcescens-A4T           CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Staphylococcus-pasteuri           CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Acinetobacter-baumannii           CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Staphylococcus-pasteuri-C1PO1T    CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Acinetobacter-baumannii-DSM300    CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Klebsiella-pneumoniae             CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Staphylococcus-hominis-S9-624T    CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Klebsiella-pneumoniae-SDM45T      CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Serratia-marcescens               CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Staphylococcus-hominis            CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTC 531
Citrobacter-freundii-MRB070408    CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Proteus-penneri                   CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 531
Morganella-morganii-MFS05T        CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 532
Enterobacter-ludwigii             CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 530
Lactobacillus-plantarum-KLDS1.    CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Proteus-penneri-Z2T               CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 531
Chryseobacterium-vietnamense-G    CATCGAATTAAACCACATAATCCACCGCTTGTGCGGGCCCCCGTCAATTC 527
Streptococcus-anginosus-CO2T      CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Pediococcus-acidilactici-L169T    CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 529
Proteus-mirabilis-ALK419T         CATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC 531
                                  * ** *************  ********* ******* ************

Bacillus-cereus                   CTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Streptococcus-equinus             CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Bacillus-cereus-B1T               CTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Streptococcus-equinus-KLDS3.06    CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Enterococcus-faecalis             CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Lactococcus-lactis                CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTATTGC 579
Enterococcus-faecium              CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Enterococcus-faecalis-KLDS4.03    CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Lactococcus-lactis-LCT            CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTATTGC 579
Enterococcus-faecium-IB1T         CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Pediococcus-acidilactici          TTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGATTACTTAATGC 579
Proteus-mirabilis                 ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 581
Lactobacillus-plantarum           CTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAGGCGGAATGCTTAATGC 579
Morganella-morganii               ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 581
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Bacillus-subtilis                CTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Hafnia-alvei                     ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 581
Chryseobacterium-vietnamense     CTTTGAGTTTCAAACTTGCGTTCGTACTCCCCAGGTGGCTAACTTATCAC 577
Streptococcus-anginosus          CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Bacillus-subtilis-N11T           CTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Hafnia-alvei-E117T               ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 581
Staphylococcus-aureus            CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Escherichia-fergusonii           ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Enterobacter-mori-R3-3T          ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Staphylococcus-aureus-NBRC1271   CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Escherichia-fergusonii-G7T       ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Enterobacter-ludwigii-NRCG12T    ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Staphylococcus-epidermidis-BBN   CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Enterobacter-cloacae-478T        ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Staphylococcus-warneri           CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Klebsiella-variicola             ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 580
Citrobacter-freundii             ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Staphylococcus-warneri-FUA2075   CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Klebsiella-variicola-7T          ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 580
Enterobacter-mori                ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Staphylococcus-epidermidis       CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Enterobacter-cloacae             ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Serratia-marcescens-A4T          ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 580
Staphylococcus-pasteuri          CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Acinetobacter-baumannii          ATTTGAGTTTTAGTCTTGCGACCGTACTCCCCAGGCGGTCTACTTATCGC 580
Staphylococcus-pasteuri-C1P01T   CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Acinetobacter-baumannii-DSM300   ATTTGAGTTTTAGTCTTGCGACCGTACTCCCCAGGCGGTCTACTTATCGC 580
Klebsiella-pneumoniae            ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 580
Staphylococcus-hominis-S9-624T   CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Klebsiella-pneumoniae-SDM45T     ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 580
Serratia-marcescens              ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 580
Staphylococcus-hominis           CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 581
Citrobacter-freundii-MRB070408   ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Proteus-penneri                  ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 581
Morganella-morganii-MFS05T       ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 582
Enterobacter-ludwigii            ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAACGC 580
Lactobacillus-plantarum-KLDS1.   CTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAGGCGGAATGCTTAATGC 579
Proteus-penneri-Z2T              ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 581
Chryseobacterium-vietnamense-G   CTTTGAGTTTCAAACTTGCGTTCGTACTCCCCAGGTGGCTAACTTATCAC 577
Streptococcus-anginosus-CO2T     CTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGC 579
Pediococcus-acidilactici-L169T   TTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGATTACTTAATGC 579
Proteus-mirabilis-ALK419T        ATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGATTTAACGC 581
                                  ********* *  ******  ************ **     ***   *

Bacillus-cereus                  GTTAACTTCAGCA-------CTAAAGGGCGGAAACCCTCTAACACTTAG- 621
Streptococcus-equinus            GTTAGCTGCGGCA-------CTAAGCCCCGGAAAGGGCCTAACACCTAG- 621
Bacillus-cereus-B1T              GTTAACTTCAGCA-------CTAAAGGGCGGAAACCCTCTAACACTTAG- 621
Streptococcus-equinus-KLDS3.06   GTTAGCTGCGGCA-------CTAAGCCCCGGAAAGGGCCTAACACCTAG- 621
Enterococcus-faecalis            GTTTGCTGCAGCA-------CTGAAGGGCGGAAACCCTCCAACACTTAG- 621
Lactococcus-lactis               GTTAGCTGCGATA-------C-AGAGAACTTATAGCTCCCTACATCTAG- 620
Enterococcus-faecium             GTTTGCTGCAGCA-------CTGAAGGGCGGAAACCCTCCAACACTTAG- 621
Enterococcus-faecalis-KLDS4.03   GTTTGCTGCAGCA-------CTGAAGGGCGGAAACCCTCCAACACTTAG- 621
Lactococcus-lactis-LCT           GTTAGCTGCGATA-------C-AGAGAACTTATAGCTCCCTACATCTAG- 620
Enterococcus-faecium-IB1T        GTTTGCTGCAGCA-------CTGAAGGGCGGAAACCCTCCAACACTTAG- 621
Pediococcus-acidilactici         GTTAGCTGCAGCA-------CTGAAGGGCGGAAACCCTCCAACACTTAG- 621
Proteus-mirabilis                GTTAGCTCCAGAA-------GCCACGGTTCAAGACCA-CAACCTCTAAA- 622
Lactobacillus-plantarum          GTTAGCTGCAGCA-------CTGAAGGGCGGAAACCCTCCAACACTTAG- 621
Morganella-morganii              GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------G- 622
Bacillus-subtilis                GTTAGCTGCAGCA-------CTAAGGGGCGGAAACCCCCTAACACTTAG- 621
Hafnia-alvei                     GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------G- 622
Chryseobacterium-vietnamense     TTTCGCTTAGTCT-------CTGAATCC--GAAA--ACCCAAAAACGAG- 615
Streptococcus-anginosus          GTTAGCTGCGGCA-------CTAAGTCCCGGAAAGGACCTAACACCTAG- 621
Bacillus-subtilis-N11T           GTTAGCTGCAGCA-------CTAAGGGGCGGAAACCCCCTAACACTTAG- 621
Hafnia-alvei-E117T               GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------G- 622
Staphylococcus-aureus            GTTAGCTGCAGCA-------CTAAGGGGCGGAAACCCCCTAACACTTAG- 623
Escherichia-fergusonii           GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------G- 621
Enterobacter-mori-R3-3T          GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------G- 621
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Staphylococcus-aureus-NBRC1271      GTTAGCTGCAGCA-------CTAAGGGGCGGAAACCCCCTAACACTTAG- 623
Escherichia-fergusonii-G7T          GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------G- 621
Enterobacter-ludwigii-NRCG12T       GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------G- 621
Staphylococcus-epidermidis-BBN      GTTAGCTGCAGCA-------CTAAGGGGCGGAAACCCCCTAACACTTAG- 623
Enterobacter-cloacae-478T           GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------G- 621
Staphylococcus-warneri              GTTAGCTGCAGCA-------CTAAGGGGCGGAAA-CCCCCTAAC---AC- 619
Klebsiella-variicola                GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAA------- 621
Citrobacter-freundii                GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAG------- 621
Staphylococcus-warneri-FUA2075      GTTAGCTGCAGCA-------CTAAGGGGCGGAAA-CCCCCTAAC---AC- 619
Klebsiella-variicola-7T             GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAA------- 621
Enterobacter-mori                   GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAG------- 621
Staphylococcus-epidermidis          GTTAGCTGCAGCA-------CTAAGGGGCGGAAACCCCCTAACACTTAG- 623
Enterobacter-cloacae                GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------G- 621
Serratia-marcescens-A4T             GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAA------A- 621
Staphylococcus-pasteuri             GTTAGCTGCAGCA-------CTAAGGGGCGGAAACCCCCTAACACTTAG- 623
Acinetobacter-baumannii             GTTAGCTGCGCCA-------CTAAAGC-CTCAAAGGCCCCAACGGCTAG- 621
Staphylococcus-pasteuri-C1P01T      GTTAGCTGCAGCA-------CTAAGGGGCGGAAACCCCCTAACACTTAG- 623
Acinetobacter-baumannii-DSM300      GTTAGCTGCGCCA-------CTAAAGC-CTCAAAGGCCCCAACGGCTAG- 621
Klebsiella-pneumoniae               GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAA------- 621
Staphylococcus-hominis-S9-624T      GTTAGCTGCAGCA-------CTAAGGGGCGGAAA-CCCCCTAAC---AC- 619
Klebsiella-pneumoniae-SDM45T        GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAA------- 621
Serratia-marcescens                 GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAA------- 621
Staphylococcus-hominis              GTTAGCTGCAGCA-------CTAAGGGGCGGAAA-CCCCCTAAC---AC- 619
Citrobacter-freundii-MRB070408      GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAG------- 621
Proteus-penneri                     GTTAGCTCCAGAAGCCACGGTTCAAGACCACAA--CCTCTAAA------- 622
Morganella-morganii-MFS05T          GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAG------- 623
Enterobacter-ludwigii               GTTAGCTCCGGAAGCCACGCCTCAAGGGCACAA--CCTCCAAG------- 621
Lactobacillus-plantarum-KLDS1.      GTTAGCTGCAGCA-------CTGAAGGGCGGAAACCCTCCAACACTTAGC 622
Proteus-penneri-Z2T                 GTTAGCTCCAGAA-------GCCACGGTTCAAGACCA--CAACCTCTAA- 621
Chryseobacterium-vietnamense-G      TTTCGCTTAGTCT-------CTGAATCC--GAAA--ATCCAAAAACGAG- 615
Streptococcus-anginosus-CO2T        GTTAGCTGCGGCA-------CTAAGTCCCGGAAAGGACCTAACACCTAG- 621
Pediococcus-acidilactici-L169T      GTTAGCTGCAGCA-------CTGAAGGGCGGAAACCCTCCAACACTTAG- 621
Proteus-mirabilis-ALK419T           GTTAGCTCCAGAA-------GCCACGGTTCAAGACCA-CAACCTCTAAA- 622
                                     **  **                  *

Bacillus-cereus                     -CACTCA----TCGTTTACGGCGTGAACTACCAGGGTATCTAATCCTGTT 666
Streptococcus-equinus               -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Bacillus-cereus-B1T                 -CACTCA----TCGTTTACGGCGTGAACTACCAGGGTATCTAATCCTGTT 666
Streptococcus-equinus-KLDS3.06      -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Enterococcus-faecalis               -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Lactococcus-lactis                  -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 665
Enterococcus-faecium                -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Enterococcus-faecalis-KLDS4.03      -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Lactococcus-lactis-LCT              -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 665
Enterococcus-faecium-IB1T           -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Pediococcus-acidilactici            -TAATCA----TCGTTTACGGCATGGACTACCAGGGTATCTAATCCTGTT 666
Proteus-mirabilis                   -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 667
Lactobacillus-plantarum             -CATTCA----TCGTTTACGGTATGGACTACCAGGGTATCTAATCCTGTT 666
Morganella-morganii                 -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 667
Bacillus-subtilis                   -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Hafnia-alvei                        -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 667
Chryseobacterium-vietnamense        -TTAGCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 660
Streptococcus-anginosus             -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Bacillus-subtilis-N11T              -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Hafnia-alvei-E117T                  -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 667
Staphylococcus-aureus               -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Escherichia-fergusonii              -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Enterobacter-mori-R3-3T             -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Staphylococcus-aureus-NBRC1271      -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Escherichia-fergusonii-G7T          -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Enterobacter-ludwigii-NRCG12T       -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Staphylococcus-epidermidis-BBN      -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Enterobacter-cloacae-478T           -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Staphylococcus-warneri              -TTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Klebsiella-variicola                -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Citrobacter-freundii                -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Staphylococcus-warneri-FUA2075      -TTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
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Klebsiella-variicola-7T             -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Enterobacter-mori                   -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Staphylococcus-epidermidis          -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Enterobacter-cloacae                -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Serratia-marcescens-A4T             -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Staphylococcus-pasteuri             -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Acinetobacter-baumannii             -TAGACA----TCGTTTACGGCATGGACTACCAGGGTATCTAATCCTGTT 666
Staphylococcus-pasteuri-C1PO1T      -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Acinetobacter-baumannii-DSM300      -TAGACA----TCGTTTACGGCATGGACTACCAGGGTATCTAATCCTGTT 666
Klebsiella-pneumoniae               -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Staphylococcus-hominis-S9-624T      -TTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Klebsiella-pneumoniae-SDM45T        -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Serratia-marcescens                 -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Staphylococcus-hominis              -TTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Citrobacter-freundii-MRB070408      -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Proteus-penneri                     -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 667
Morganella-morganii-MFS05T          -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 668
Enterobacter-ludwigii               -TCGACA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Lactobacillus-plantarum-KLDS1.      ATT--CA----TCGTTTACGGTATGGACTACCAGGGTATCTAATCCTGTT 666
Proteus-penneri-Z2T                 ATCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 667
Chryseobacterium-vietnamense-G      -TTAGCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 660
Streptococcus-anginosus-CO2T        -CACTCA----TCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTT 666
Pediococcus-acidilactici-L169T      -TAATCA----TCGTTTACGGCATGGACTACCAGGGTATCTAATCCTGTT 666
Proteus-mirabilis-ALK419T           -TCGACA----TCGTTTACAGCGTGGACTACCAGGGTATCTAATCCTGTT 667
                                         **    ******** *  ** ************************

Bacillus-cereus                     TGCTCCCCACG-CTTTCGCGCCTCAGTGTCAGTTACAGACCAGAAAAGTC 715
Streptococcus-equinus               TGCTCCCCACG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGA-GCC 714
Bacillus-cereus-B1T                 TGCTCCCCACG-CTTTCGCGCCTCAGTGTCAGTTACAGACCAGAAAAGTC 715
Streptococcus-equinus-KLDS3.06      TGCTCCCCACG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGA-GCC 714
Enterococcus-faecalis               TGCTCCCCACG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGA-GCC 714
Lactococcus-lactis                  TGCTCCCCACG-CTTTCGAGCCTCAGTGTCAGTTACAGGCCAGAGA-GCC 713
Enterococcus-faecium                TGCTCCCCACG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGA-GCC 714
Enterococcus-faecalis-KLDS4.03      TGCTCCCCACG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGA-GCC 714
Lactococcus-lactis-LCT              TGCTCCCCACG-CTTTCGAGCCTCAGTGTCAGTTACAGGCCAGAGA-GCC 713
Enterococcus-faecium-IB1T           TGCTCCCCACG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGA-GCC 714
Pediococcus-acidilactici            CGCTACCCATG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGACA-GCC 714
Proteus-mirabilis                   TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 715
Lactobacillus-plantarum             TGCTACCCATA-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGACA-GCC 714
Morganella-morganii                 TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 715
Bacillus-subtilis                   CGCTCCCCACG-CTTTCGCTCCTCAGCGTCAGTTACAGACCAGAGA-GTC 714
Hafnia-alvei                        TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 715
Chryseobacterium-vietnamense        CGCTCCCCACG-CTTTCGTCCATCAGCGTCAGTTGTTGCTTAGTAA-CCT 708
Streptococcus-anginosus             CGCTCCCCACG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGA-GCC 714
Bacillus-subtilis-N11T              CGCTCCCCACG-CTTTCGCTCCTCAGCGTCAGTTACAGACCAGAGA-GTC 714
Hafnia-alvei-E117T                  TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 715
Staphylococcus-aureus               TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Escherichia-fergusonii              TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTCGTCCAGGGG-GCC 714
Enterobacter-mori-R3-3T             TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Staphylococcus-aureus-NBRC1271      TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Escherichia-fergusonii-G7T          TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTCGTCCAGGGG-GCC 714
Enterobacter-ludwigii-NRCG12T       TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Staphylococcus-epidermidis-BBN      TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Enterobacter-cloacae-478T           TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Staphylococcus-warneri              TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Klebsiella-variicola                TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Citrobacter-freundii                TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Staphylococcus-warneri-FUA2075      TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Klebsiella-variicola-7T             TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Enterobacter-mori                   TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Staphylococcus-epidermidis          TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Enterobacter-cloacae                TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Serratia-marcescens-A4T             TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTCGTCCAGGGG-GCC 714
Staphylococcus-pasteuri             TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Acinetobacter-baumannii             TGCTCCCCATG-CTTTCGTACCTCAGCGTCAGTATTAGGCCAGATG-GCT 714
Staphylococcus-pasteuri-C1PO1T      TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Acinetobacter-baumannii-DSM300      TGCTCCCCATG-CTTTCGTACCTCAGCGTCAGTATTAGGCCAGATG-GCT 714
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Klebsiella-pneumoniae                TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Staphylococcus-hominis-S9-624T       TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Klebsiella-pneumoniae-SDM45T         TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Serratia-marcescens                  TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTCGTCCAGGGG-GCC 714
Staphylococcus-hominis               TGATCCCCACG-CTTTCGCACATCAGCGTCAGTTACAGACCAGAAA-GTC 716
Citrobacter-freundii-MRB070408       TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Proteus-penneri                      TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 715
Morganella-morganii-MFS05T           TGCTCCCCACGTCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 717
Enterobacter-ludwigii                TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 714
Lactobacillus-plantarum-KLDS1.       TGCTACCCATA-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGACA-GCC 714
Proteus-penneri-Z2T                  TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 715
Chryseobacterium-vietnamense-G       CGCTCCCCACG-CTTTCGTCCATCAGCGTCAGTTGTTGCTTAGTAA-CCT 708
Streptococcus-anginosus-CO2T         CGCTCCCCACG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGAGA-GCC 714
Pediococcus-acidilactici-L169T       CGCTACCCATG-CTTTCGAGCCTCAGCGTCAGTTACAGACCAGACA-GCC 714
Proteus-mirabilis-ALK419T            TGCTCCCCACG-CTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGG-GCC 715
                                      * * ****   ******  * * ** ******    *   **

Bacillus-cereus                      GCCTTCGCCACTGGTGTTCCTCCATATATCTCTACGCATTTCACCGCTACAC 765
Streptococcus-equinus                GCTTTCGCCACCGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 764
Bacillus-cereus-B1T                  GCCTTCGCCACTGGTGTTCCTCCATATATCTCTACGCATTTCACCGCTACAC 765
Streptococcus-equinus-KLDS3.06       GCTTTCGCCACCGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 764
Enterococcus-faecalis                GCCTTCGCCACTGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 764
Lactococcus-lactis                   GCTTTCGCCACCGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 763
Enterococcus-faecium                 GCCTTCGCCACTGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 764
Enterococcus-faecalis-KLDS4.03       GCCTTCGCCACTGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 764
Lactococcus-lactis-LCT               GCTTTCGCCACCGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 763
Enterococcus-faecium-IB1T            GCCTTCGCCACTGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 764
Pediococcus-acidilactici             GCCTTCGCCACTGGTGTTCTTCCATATATCTACGCATTTCACCGCTACAC 764
Proteus-mirabilis                    GCCTTCGCCACCGGTATTCCTCCACATCTCTACGCATTTCACCGCTACAC 765
Lactobacillus-plantarum              GCCTTCGCCACTGGTGTTCTTCCATATATCTACGCATTTCACCGCTACAC 764
Morganella-morganii                  GCCTTCGCCACCGGTATTCCTCCACATCTCTACGCATTTCACCGCTACAC 765
Bacillus-subtilis                    GCCTTCGCCACTGGTGTTCCTCCACATCTCTACGCATTTCACCGCTACAC 764
Hafnia-alvei                         GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 765
Chryseobacterium-vietnamense         GCCTTCGCAATTGGTGTTCTAAGTAATATCTATGCATTTCACCGCTACAC 758
Streptococcus-anginosus              GCTTTCGCCACCGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 764
Bacillus-subtilis-N11T               GCCTTCGCCACTGGTGTTCCTCCACATCTCTACGCATTTCACCGCTACAC 764
Hafnia-alvei-E117T                   GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 765
Staphylococcus-aureus                GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Escherichia-fergusonii               GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Enterobacter-mori-R3-3T              GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Staphylococcus-aureus-NBRC1271       GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Escherichia-fergusonii-G7T           GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Enterobacter-ludwigii-NRCG12T        GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Staphylococcus-epidermidis-BBN       GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Enterobacter-cloacae-478T            GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Staphylococcus-warneri               GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Klebsiella-variicola                 GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Citrobacter-freundii                 GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Staphylococcus-warneri-FUA2075       GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Klebsiella-variicola-7T              GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Enterobacter-mori                    GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Staphylococcus-epidermidis           GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Enterobacter-cloacae                 GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Serratia-marcescens-A4T              GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Staphylococcus-pasteuri              GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Acinetobacter-baumannii              GCCTTCGCCATCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Staphylococcus-pasteuri-C1P01T       GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Acinetobacter-baumannii-DSM300       GCCTTCGCCATCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Klebsiella-pneumoniae                GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Staphylococcus-hominis-S9-624T       GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Klebsiella-pneumoniae-SDM45T         GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Serratia-marcescens                  GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Staphylococcus-hominis               GCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCATTTCACCGCTACAC 766
Citrobacter-freundii-MRB070408       GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
Proteus-penneri                      GCCTTCGCCACCGGTATTCCTCCACATCTCTACGCATTTCACCGCTACAC 765
Morganella-morganii-MFS05T           GCCTTCGCCACCGGTATTCCTCCACATCTCTACGCATTTCACCGCTACAC 767
Enterobacter-ludwigii                GCCTTCGCCACCGGTATTCCTCCAGATCTCTACGCATTTCACCGCTACAC 764
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Lactobacillus-plantarum-KLDS1.      GCCTTCGCCACTGGTGTTCTTCCATATATCTACGCATTTCACCGCTACAC 764
Proteus-penneri-Z2T                 GCCTTCGCCACCGGTATTCCTCCACATCTCTACGCATTTCACCGCTACAC 765
Chryseobacterium-vietnamense-G      GCCTTCGCAATTGGTGTTCTAAGTAATATCTATGCATTTCACCGCTACAC 758
Streptococcus-anginosus-CO2T        GCTTTCGCCACCGGTGTTCCTCCATATATCTACGCATTTCACCGCTACAC 764
Pediococcus-acidilactici-L169T      GCCTTCGCCACTGGTGTTCTTCCATATATCTACGCATTTCACCGCTACAC 764
Proteus-mirabilis-ALK419T           GCCTTCGCCACCGGTATTCCTCCACATCTCTACGCATTTCACCGCTACAC 765
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Bacillus-cereus                     ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTCTCCCAGTTTCCAATG 814
Streptococcus-equinus               ATGGAATTCCACTCTCC-CCTTCTGCACTCAAGTCTAACAGTTTCCAA-A 812
Bacillus-cereus-B1T                 ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTCTCCCAGTTTCCAATG 814
Streptococcus-equinus-KLDS3.06      ATGGAATTCCACTCTCC-CCTTCTGCACTCAAGTCTAACAGTTTCCAA-A 812
Enterococcus-faecalis               ATGGAATTCCACTCTCC-TCTTCTGCACTCAAGTCTCCCAGTTTCCAATG 813
Lactococcus-lactis                  ATGGAATTCCACTCTCC-TCTCCTGCACTCAAGTCTACCAGTTTCCAATG 812
Enterococcus-faecium                ATGGAATTCCACTCTCC-TCTTCTGCACTCAAGTCTCCCAGTTTCCAATG 813
Enterococcus-faecalis-KLDS4.03      ATGGAATTCCACTCTCC-TCTTCTGCACTCAAGTCTCCCAGTTTCCAATG 813
Lactococcus-lactis-LCT              ATGGAATTCCACTCTCC-TCTCCTGCACTCAAGTCTACCAGTTTCCAATG 812
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Proteus-mirabilis                   ATGGAATTCTACCCCCC-TCTACAAGACTCTAGCCAACCAGTTTCAGATG 814
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Bacillus-subtilis                   GTGGAATTCCACTCTCC-TCTTCTGCACTCAAGTTCCCCAGTTTCCAATG 813
Hafnia-alvei                        CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCTTGCCAGTTTCAAATG 814
Chryseobacterium-vietnamense        TACTTATTCCAGCTACT-TCAACAACACTCAAGACTTGCAGTATCAATGG 807
Streptococcus-anginosus             ATGGAATTCCACTCTCC-CCTTCTGCACTCAAGTTAAACAGTTTCCAAAG 813
Bacillus-subtilis-N11T              GTGGAATTCCACTCTCC-TCTTCTGCACTCAAGTTCCCCAGTTTCCAATG 813
Hafnia-alvei-E117T                  CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCTTGCCAGTTTCAAATG 814
Staphylococcus-aureus               ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Escherichia-fergusonii              CTGGAATTCTACCCCCC-TCTACGAGACTCAAGCTTGCCAGTATCAGATG 813
Enterobacter-mori-R3-3T             CTGGAATTCTACCCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGAATG 814
Staphylococcus-aureus-NBRC1271      ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Escherichia-fergusonii-G7T          CTGGAATTCTACCCCCC-TCTACGAGACTCAAGCTTGCCAGTATCAGATG 813
Enterobacter-ludwigii-NRCG12T       CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGAATG 813
Staphylococcus-epidermidis-BBN      ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Enterobacter-cloacae-478T           CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGAATG 813
Staphylococcus-warneri              ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Klebsiella-variicola                CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGAATG 813
Citrobacter-freundii                CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGGATG 813
Staphylococcus-warneri-FUA2075      ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Klebsiella-variicola-7T             CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGAATG 813
Enterobacter-mori                   CTGGAATTCTACCCCCCCTCTACAAGACTCTAGCCTGCCAGTTTCGAATG 814
Staphylococcus-epidermidis          ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Enterobacter-cloacae                CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGAATG 813
Serratia-marcescens-A4T             CTGGAATTCTACCCCCC-TCTACGAGACTCTAGCTTGCCAGTTTCAAATG 813
Staphylococcus-pasteuri             ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Acinetobacter-baumannii             CTGGAATTCTACCATCC-TCTCCCATACTCTAGCTCACCAGTATCGAATG 813
Staphylococcus-pasteuri-C1PO1T      ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Acinetobacter-baumannii-DSM300      CTGGAATTCTACCATCC-TCTCCCATACTCTAGCTCACCAGTATCGAATG 813
Klebsiella-pneumoniae               CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGAATG 813
Staphylococcus-hominis-S9-624T      ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Klebsiella-pneumoniae-SDM45T        CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGAATG 813
Serratia-marcescens                 CTGGAATTCTACCCCCC-TCTACGAGACTCTAGCTTGCCAGTTTCAAATG 813
Staphylococcus-hominis              ATGGAATTCCACTTTCC-TCTTCTGCACTCAAGTTTTCCAGTTTCCAATG 815
Citrobacter-freundii-MRB070408      CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGGATG 813
Proteus-penneri                     ATGGAATTCTACCCCCC-TCTACAAGACTCTAGCCAACCAGTTTCAGATG 814
Morganella-morganii-MFS05T          ATGGAATTCTACCCCCC-TCTACAAGACTCTAGCTGACCAGTATCAGATG 816
Enterobacter-ludwigii               CTGGAATTCTACCCCCC-TCTACAAGACTCTAGCCTGCCAGTTTCGAATG 813
Lactobacillus-plantarum-KLDS1.      ATGGAGTTCCACTGTCC-TCTTCTGCACTCAAGTTTCCCAGTTTCCGATG 813
Proteus-penneri-Z2T                 ATGGAATTCTACCCCCC-TCTACAAGACTCTAGCCAACCAGTTTCAGATG 814
Chryseobacterium-vietnamense-G      TACTTATTCCAGCTACT-TCAACAACACTCAAGACTTGCAGTATCAATGG 807
Streptococcus-anginosus-CO2T        ATGGAATTCCACTCTCC-CCTTCTGCACTCAAGTTAAACAGTTTCCAAAG 813
Pediococcus-acidilactici-L169T      ATGGAGTTCCACTGTCC-TCTTCTGCACTCAAGTCTCCCAGTTTCCAATG 813
Proteus-mirabilis-ALK419T           ATGGAATTCTACCCCCC-TCTACAAGACTCTAGCCAACCAGTTTCAGATG 814
                                          *** *    *   *  *   **** **     **** **

Bacillus-cereus                     ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAACCACC 864
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Bacillus-cereus-B1T                ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAACCACC 864
Streptococcus-equinus-KLDS3.06     GCGAACAATGGTTAAGCCACTGCCTTTAACTTCAGACTTATTAAACCGCC 862
Enterococcus-faecalis              ACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCC 863
Lactococcus-lactis                 -CATACAATGGTTGAGCCACTGCCTTTTACACCAGACTTAATAAACCACC 861
Enterococcus-faecium               ACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCC 863
Enterococcus-faecalis-KLDS4.03     ACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCC 863
Lactococcus-lactis-LCT             -CATACAATGGTTGAGCCACTGCCTTTTACACCAGACTTAATAAACCACC 861
Enterococcus-faecium-IB1T          ACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCC 863
Pediococcus-acidilactici           CACTTCTTCGGTTGAGCCGAAGGCTTTCACATTAGACTTAAAAGACCGCC 863
Proteus-mirabilis                  CAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCC 864
Lactobacillus-plantarum            CACTTCTTCGGTTGAGCCGAAGGCTTTCACATCAGACTTAAAAAACCGCC 863
Morganella-morganii                CAATTCCCGGGTTAAGCCCGGGGATTTCACATCTGACTCAATCAACCGCC 864
Bacillus-subtilis                  ACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCC 863
Hafnia-alvei                       CAGTTCCCAAGTTAAGCTCGGGGATTTCACATCTGACTTAACAAACCGCC 864
Chryseobacterium-vietnamense       CAGTTTCACAGTTAAGCTGTGAGATTTCACCACTGACTTACAAATCAGCC 857
Streptococcus-anginosus            CC-TACAATGGTTGAGCCACTGCCTTTCACTTCAGACTTTTCTAACCGCC 862
Bacillus-subtilis-N11T             ACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCC 863
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Staphylococcus-aureus              ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCC 865
Escherichia-fergusonii             CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCTGACTTAACAAACCGCC 863
Enterobacter-mori-R3-3T            CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC 864
Staphylococcus-aureus-NBRC1271     ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCC 865
Escherichia-fergusonii-G7T         CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCTGACTTAACAAACCGCC 863
Enterobacter-ludwigii-NRCG12T      CAGTTCCCAGGTTGAGCCC-GGGATTTCACATCCGACTTGACAGACCGCC 862
Staphylococcus-epidermidis-BBN     ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCC 865
Enterobacter-cloacae-478T          CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC 863
Staphylococcus-warneri             ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCC 865
Klebsiella-variicola               CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC 863
Citrobacter-freundii               CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC 863
Staphylococcus-warneri-FUA2075     ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCC 865
Klebsiella-variicola-7T            CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC 863
Enterobacter-mori                  CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC 864
Staphylococcus-epidermidis         ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCC 865
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Serratia-marcescens-A4T            CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCTGACTTAACAAACCGCC 863
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Acinetobacter-baumannii            CAATTCCCAAGTTAAGCTCGGGGATTTCACATCCGACTTAATAAGCCGCC 863
Staphylococcus-pasteuri-C1P01T     ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCC 865
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Klebsiella-pneumoniae              CAGTTCCCAGGTTGAGCCCGGGGATTTCACATCCGACTTGACAGACCGCC 863
Staphylococcus-hominis-S9-624T     ACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCC 865
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Morganella-morganii-MFS05T         CAATTCCCGGGTTAAGCCCGGGGATTTCACATCTGACTCAATCAACCGCC 866
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Lactobacillus-plantarum-KLDS1.     CACTTCTTCGGTTGAGCCGAAGGCTTTCACATCAGACTTAAAAAACCGCC 863
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Streptococcus-anginosus-CO2T       CC-TACAATGGTTGAGCCACTGCCTTTCACTTCAGACTTTTCTAACCGCC 862
Pediococcus-acidilactici-L169T     CACTTCTTCGGTTGAGCCGAAGGCTTTCACATTAGACTTAAAAGACCGCC 863
Proteus-mirabilis-ALK419T          CAATTCCCAAGTTAAGCTCGGGGCTTTCACATCTGACTTAATTGACCGCC 864
                                             *** ***       *** **    ****       *  **

Bacillus-cereus                    TGCGCGCGCTTTACGCCC-AATAATTCCGGATA 896
Streptococcus-equinus              TGCGCTCGCTTTACGCCC-AATAAATCCGGACA 894
Bacillus-cereus-B1T                TGCGCGCGCTTTACGCCC-AATAATTCCGGATA 896
Streptococcus-equinus-KLDS3.06     TGCGCTCGCTTTACGCCC-AATAAATCCGGACA 894
Enterococcus-faecalis              TGCGCTCGCTTTACGCCC-AATAAATCCGGACA 895
Lactococcus-lactis                 TGCGCTCGCTTTACGCCC-AATAAATCCGGACA 893
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Enterococcus-faecium-IB1T          TGCGCTCGCTTTACGCCC-AATAAATCCGGACA 895
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Pediococcus-acidilactici            TGCGCTCGCTTTACGCCC-AATAAATCCGGATA 895
Proteus-mirabilis                   TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 896
Lactobacillus-plantarum             TGCGCTCGCTTTACGCCC-AATAAATCCGGACA 895
Morganella-morganii                 TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 896
Bacillus-subtilis                   TGCGAGCCCTTTACGCCC-AATAATTCCGGACA 895
Hafnia-alvei                        TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 896
Chryseobacterium-vietnamense        TACGGACCCTTTAAACCC-AATAAATCCGGATA 889
Streptococcus-anginosus             TGCGCTCGCTTTACGCCC-AATAAATCCGGACA 894
Bacillus-subtilis-N11T              TGCGAGCCCTTTACGCCC-AATAATTCCGGACA 895
Hafnia-alvei-E117T                  TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 896
Staphylococcus-aureus               TACGCGCGCTTTACGCCC-AATAATTCCGGATA 897
Escherichia-fergusonii              TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 895
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Staphylococcus-aureus-NBRC1271      TACGCGCGCTTTACGCCC-AATAATTCCGGATA 897
Escherichia-fergusonii-G7T          TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 895
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Staphylococcus-epidermidis-BBN      TACGCGCGCTTTACGCCC-AATAATTCCGGATA 897
Enterobacter-cloacae-478T           TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 895
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Klebsiella-variicola                TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 895
Citrobacter-freundii                TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 895
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Staphylococcus-epidermidis          TACGCGCGCTTTACGCCC-AATAATTCCGGATA 897
Enterobacter-cloacae                TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 895
Serratia-marcescens-A4T             TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 895
Staphylococcus-pasteuri             TACGCGCGCTTTACGCCC-AATAATTCCGGATA 897
Acinetobacter-baumannii             TACGCACGCTTTACGCCC-AGTAAATCCGATTA 895
Staphylococcus-pasteuri-C1P01T      TACGCGCGCTTTACGCCC-AATAATTCCGGATA 897
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Staphylococcus-hominis-S9-624T      TACGCGCGCTTTACGCCC-AATAATTCCGGATA 897
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Serratia-marcescens                 TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 895
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Proteus-penneri                     TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 896
Morganella-morganii-MFS05T          TGCGTGCGCTTTACGCCCCAGTAATTCCGATTA 899
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Lactobacillus-plantarum-KLDS1.      TGCGCTCGCTTTACGCCC-AATAAATCCGGACA 895
Proteus-penneri-Z2T                 TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 896
Chryseobacterium-vietnamense-G      TACGGACCCTTTAAACCC-AATAAATCCGGATA 889
Streptococcus-anginosus-CO2T        TGCGCTCGCTTTACGCCC-AATAAATCCGGACA 894
Pediococcus-acidilactici-L169T      TGCGCTCGCTTTACGCCC-AATAAATCCGGATA 895
Proteus-mirabilis-ALK419T           TGCGTGCGCTTTACGCCC-AGTAATTCCGATTA 896
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❖ Appendix-2

A-1- Enterobacter ludwigii partial *16S rDNA* gene, strain IRQBAS1.(GeneBank).

NCBI

Enterobacter ludwigii partial *16S rDNA* gene, strain IRQBAS1.

Gen Bank: HG003646.1

FASTAGraphics

Go to:

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LOCUS       HG003646 1443 bp    DNA     linear   BCT 27-JUN-2013
DEFINITION  Enterobacter ludwigii partial 16S rRNA gene, strain
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ACCESSION   HG003646
VERSION     HG003646.1  GI:511630606
KEYWORDS    .
SOURCE      Enterobacter ludwigii
  ORGANISM  Enterobacter ludwigii
            Bacteria; Proteobacteria; Gammaproteobacteria;
            Enterobacteriales;Enterobacteriaceae; Enterobacter.
REFERENCE   1
  AUTHORS   Abd Al-Abbas,M.J. and Husseen,K.A.
  TITLE     Genetic study of bacteria from denture and orthopedic tools
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1443)
  AUTHORS   Abd Al-Abbas,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-2013) Biology, University of Basrah,
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     rRNA            <1..>1443
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
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       61 cgagtggcgg acgggtgagt aatgtctggg aaactgcctg atggaggggg ataactactg
      121 gaaacggtag ctaataccgc ataacgtcgc aagaccaaag aggggacct tcgggcctct
      181 tgccatcaga tgtgcccaga tgggattagc tagtaggtgg ggtaacggct cacctaggcg
      241 acgatcccta gctggtctga gaggatgacc agccacactg gaactgagac acggtccaga
      301 ctcctacggg aggcagcagt ggggaatatt gcacaatggg cgcaagcctg atgcagccat
      361 gccgcgtgta tgaagaaggc cttcgggttg taaagtactt tcagcgggga ggaaggcgat
      421 aaggttaata accttgtcga ttgacgttac ccgcagaaga agcaccggct aactccgtgc
      481 cagcagccgc ggtaatacgg agggtgcaag cgttaatcgg aattactggg cgtaaagcgc
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B-1- Enterobacter cloacae partial *16SrDNA* gene, strain IRQBAS2. (GeneBank)

NCBI

Enterobacter cloacae partial *16SrDNA* gene, strain IRQBAS2.

GenBank: HG003647.1

FASTAGraphics

Go to:

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LOCUS       HG003647  1430 bp    DNA     linear   BCT 27-JUN-2013
DEFINITION  Enterobacter cloacae partial 16S rRNA gene, strain  IRQBAS2.
ACCESSION   HG003647
VERSION     HG003647.1  GI:511630607
KEYWORDS    .
SOURCE      Enterobacter cloacae
  ORGANISM  Enterobacter cloacae
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            Enterobacteriales;Enterobacteriaceae; Enterobacter; Enterobacter
            cloacae complex.
REFERENCE   1
  AUTHORS   Abd Al-Abbas,M.J. and Husseen,K.A.
  TITLE     Genetic study of bacteria from denture and orthopedic tools
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1430)
  AUTHORS   Abd Al-Abbas,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-2013) Biology, University of Basrah,
            Iraq/Basrah/University of Basrah/Biology Departmet, 61004, IRAQ
FEATURES             Location/Qualifiers
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C-1- Chryseobacterium vietnamense partial *16SrDNA* gene, strain IRQBAS3 . (GeneBank).

NCBI

Chryseobacterium vietnamense partial *16S rDNA* gene, strain IRQBAS3.

GenBank: HG003648.1

FASTAGraphics

Go to:

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VERSION     HG003648.1  GI:511630629
KEYWORDS    .
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  ORGANISM  Chryseobacterium vietnamense
            Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
            Flavobacteriaceae; Chryseobacterium.
REFERENCE   1
  AUTHORS   Abd Al-Abbas,M.J. and Husseen,K.A.
  TITLE     Genetic study of bacteria from denture and orthopedic   tools
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1356)
  AUTHORS   Abd Al-Abbas,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-2013) Biology, University of Basrah,
            Iraq/Basrah/University of Basrah/Biology Departmet, 61004, IRAQ
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      421 aatacggagg gtgcaagcgt tatccggatt tattgggttt aaagggtccg taggctgatt
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D-1- Morganella morganii partial *16S rDNA* gene, strain IRQBAS4 (GeneBank).

NCBI

Morganella morganii partial *16S rDNA* gene, strain IRQBAS4

GenBank: HG003649.1

FASTAGraphics

Go to:

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VERSION     HG003649.1  GI:511630630
KEYWORDS    .
SOURCE      Morganella morganii
  ORGANISM  Morganella morganii
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Morganella.
REFERENCE   1
  AUTHORS   Abd Al-Abbas,M.J. and Husseen,K.A.
  TITLE     Genetic study of bacteria from denture and orthopedic tools
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1451)
  AUTHORS   Abd Al-Abbas,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-2013) Biology, University of Basrah,
            Iraq/Basrah/University of Basrah/Biology Departmet, 61004, IRAQ
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