**Table 1.** Protein spots identification of 2-DE gels and MALDI-TOF sequencing results from *vanA E. durans* SG 2 isolate.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ***Spot*** | ***Protein Description*** | ***Species*** | ***Protein Name*** | ***Accession Number*** | ***Protein MW*** | ***Protein PI*** | ***Peptide Count*** | ***Protein Score*** | ***Protein Score C.I. %*** | ***Information*** | ***References*** |
| 1 | 50S ribosomal protein L28 | *Prochlorococcus marinus* | rpmB | Q7V7P3 | 8922.919922 | 11.81 | 7 | 77 | 99.318759 | Unknown function | ([Rocap et al., 2003](#_ENREF_26)) |
| 2 | 6-phosphofructokinase | *Enterococcus faecalis* | pfkA | Q836R3 | 34390.69922 | 5.55 | 9 | 101 | 99.997468 | Involved in the carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose: step 3/4. | ([Paulsen et al., 2003](#_ENREF_25)) |
| 2 | 6-phosphofructokinase | *Listeria monocytogenes* serotype 4b | pfkA | C1KVL8 | 34398.94922 | 5.46 | 6 | 69 | 96.169101 | ([HAMAP, 2008a](#_ENREF_16)) |
| 3 | Chaperone protein dnaK | *Enterococcus faecalis* | dnaK | Q835R7 | 65543.63281 | 4.59 | 9 | 117 | 100 | Acts as a chaperone | ([Paulsen et al., 2003](#_ENREF_25)) |
| 3 | Chaperone protein dnaK | *Streptococcus agalactiae* serotype III | dnaK | P0A3J2 | 64940.33984 | 4.63 | 9 | 119 | 100 | ([Glaser et al., 2002](#_ENREF_13)) |
| 3 | Chaperone protein dnaK | *Streptococcus thermophilus* | dnaK | Q5M6D1 | 64738.33984 | 4.62 | 9 | 119 | 100 | ([Bolotin et al., 2004](#_ENREF_8)) |
| 3 | Chaperone protein dnaK | *Streptococcus pyogenes* serotype M12 | dnaK | Q1JKD6 | 64965.30859 | 4.63 | 7 | 103 | 99.998403 | ([Beres et al., 2006](#_ENREF_4)) |
| 3 | Chaperone protein dnaK | *Streptococcus mutans* | dnaK | O06942 | 65246.42969 | 4.58 | 7 | 100 | 99.996663 | ([Ajdic et al., 2002](#_ENREF_1)) |
| 4 | 60 kDa chaperonin | *Enterococcus faecalis* | groL | Q93EU6 | 57074.92969 | 4.64 | 8 | 92 | 99.979426 | Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions | ([Paulsen et al., 2003](#_ENREF_25); [Teng et al., 2002](#_ENREF_27)) |
| 4 | 60 kDa chaperonin | *Streptococcus anginosus* | groL | Q8KJ20 | 56868.64063 | 4.63 | 8 | 90 | 99.969570 | ([Teng et al., 2002](#_ENREF_27)) |
| 4 | 60 kDa chaperonin | *Streptococcus constellatus* | groL | Q8KJ18 | 56851.71094 | 4.63 | 7 | 83 | 99.824894 | ([Teng et al., 2002](#_ENREF_27)) |
| 4 | 60 kDa chaperonin | *Streptococcus gordonii* | groL | Q8VT58 | 56734.67188 | 4.65 | 7 | 82 | 99.784572 | ([Teng et al., 2002](#_ENREF_27)) |
| 4 | 60 kDa chaperonin | *Streptococcus agalactiae* serotype III | groL | Q8CX22 | 57223.92969 | 4.71 | 7 | 79 | 99.625630 | ([Glaser et al., 2002](#_ENREF_13)) |
| 5 | Enolase | *Enterococcus hirae* | eno | Q8GR70 | 46382.42969 | 4.58 | 14 | 209 | 100 | Catalyzes the reversible conversion of 2-phosphoglycerate into phosphoenolpyruvate. It is essential for the degradation of carbohydrates via glycolysis | ([Hosaka et al., 2003](#_ENREF_18)) |
| 5 | Enolase | *Streptococcus equi* subsp. zooepidemicus | eno | B4U2B8 | 47211.89063 | 4.77 | 10 | 155 | 100 | ([Beres et al., 2008](#_ENREF_5)) |
| 5 | Enolase | *Streptococcus mutans* | eno | Q8DTS9 | 46828.60938 | 4.67 | 12 | 179 | 100 | Catalyzes the reversible conversion of 2-phosphoglycerate into phosphoenolpyruvate. It is essential for the degradation of carbohydrates via glycolysis By similarity. Binds plasminogen and human salivary mucin MG2 when expressed on the bacterial cell surface, potentially allowing the bacterium to acquire surface-associated proteolytic activity that may help the dissemination through oral tissues and entrance into the blood stream | ([Ajdic et al., 2002](#_ENREF_1)) |
| 5 | Enolase | *Streptococcus pneumoniae* serotype 19F | eno | B5E4P1 | 47073.78906 | 4.7 | 10 | 154 | 100 | Catalyzes the reversible conversion of 2-phosphoglycerate into phosphoenolpyruvate. It is essential for the degradation of carbohydrates via glycolysis | ([Dopazo et al., 2001](#_ENREF_10)) |
| 5 | Enolase | *Streptococcus* uberis | eno | B9DRR9 | 47277.71094 | 4.64 | 10 | 155 | 100 | ([Ward et al., 2009](#_ENREF_28)) |
| 6 | L-lactate dehydrogenase 1 | *Enterococcus faecalis* | ldh1 | Q839C1 | 35465.23828 | 4.77 | 5 | 146 | 100 | Involved in the fermentation; pyruvate fermentation to lactate; (S)-lactate from pyruvate: step 1/1. | ([Paulsen et al., 2003](#_ENREF_25)) |
| 6 | L-lactate dehydrogenase | *Streptococcus equi* subsp. zooepidemicus | ldh | B4U309 | 35250.21094 | 5.14 | 3 | 130 | 100 | ([Beres et al., 2008](#_ENREF_5)) |
| 6 | L-lactate dehydrogenase | *Streptococcus mutans* | ldh | P26283 | 35223.28906 | 5.01 | 2 | 124 | 100 | ([Ajdic et al., 2002](#_ENREF_1)) |
| 6 | L-lactate dehydrogenase | *Streptococcus uberis* | ldh | B9DS53 | 35460.28906 | 5.02 | 3 | 129 | 100 | ([Teng et al., 2002](#_ENREF_27)) |
| 6 | 50S ribosomal protein L19 | *Thermoanaerobacter* sp*.* | rplS | B0K1U6 | 13262.38965 | 10.55 | 9 | 82 | 99.816641 | This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site | ([HAMAP, 2008b](#_ENREF_17)) |
| 7 | L-lactate dehydrogenase 1 | *Enterococcus faecalis* | ldh1 | Q839C1 | 35465.23828 | 4.77 | 5 | 147 | 100 | Invoved in the fermentation; pyruvate fermentation to lactate; (S)-lactate from pyruvate: step 1/1. | ([Paulsen et al., 2003](#_ENREF_25)) |
| 7 | L-lactate dehydrogenase | *Streptococcus equi* subsp. zooepidemicus | ldh | B4U309 | 35250.21094 | 5.14 | 3 | 129 | 100 | ([Beres et al., 2008](#_ENREF_5)) |
| 7 | L-lactate dehydrogenase | *Streptococcus mutans* | ldh | P26283 | 35223.28906 | 5.01 | 2 | 122 | 100 | ([Ajdic et al., 2002](#_ENREF_1)) |
| 7 | L-lactate dehydrogenase | *Streptococcus uberis* | ldh | B9DS53 | 35460.28906 | 5.02 | 4 | 139 | 100 | ([Teng et al., 2002](#_ENREF_27)) |
| 8 | Uridylate kinase | *Enterococcus faecalis* | pyrH | Q831V1 | 26094.5 | 5.24 | 3 | 71 | 97.287931 | Catalyzes the reversible phosphorylation of UMP to UDP | ([Paulsen et al., 2003](#_ENREF_25)) |
| 9 | RNA polymerase sigma factor rpoD | *Listeria monocytogenes* | rpoD | P52331 | 42392.94141 | 4.78 | 8 | 71 | 97.526565 | Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released. This is the primary sigma factor of this bacterium. | ([Metzger et al., 1994](#_ENREF_23)) |
| 9 | RNA polymerase sigma factor rpoD | *Staphylococcus aureus* | rpoD | Q5HFJ9 | 42144.92188 | 4.99 | 8 | 70 | 96.424800 | Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released | ([Gill et al., 2005](#_ENREF_12)) |
| 10 | Enolase | *Enterococcus hirae* | eno | Q8GR70 | 46382.42969 | 4.58 | 11 | 154 | 100 | Catalyzes the reversible conversion of 2-phosphoglycerate into phosphoenolpyruvate. It is essential for the degradation of carbohydrates via glycolysis | ([Hosaka et al., 2003](#_ENREF_18)) |
| 10 | Enolase | *Streptococcus agalactiae* serotype III | eno | P64080 | 47101.62891 | 4.63 | 13 | 176 | 100 | ([Glaser et al., 2002](#_ENREF_13)) |
| 10 | Enolase | *Streptococcus equi* subsp. zooepidemicus | eno | B4U2B8 | 47211.89063 | 4.77 | 12 | 165 | 100 | ([Beres et al., 2008](#_ENREF_5)) |
| 10 | Enolase | *Streptococcus thermophilus* | eno | Q5M561 | 47006.69922 | 4.67 | 12 | 164 | 100 | ([Bolotin et al., 2004](#_ENREF_8)) |
| 10 | Enolase | *Streptococcus uberis* | eno | B9DRR9 | 47277.71094 | 4.64 | 13 | 176 | 100 | ([Ward et al., 2009](#_ENREF_28)) |
| 11 | Arginine deiminase | *Lactobacillus hilgardii* | arcA | Q8G999 | 47142.66016 | 5.4 | 3 | 83 | 99.836581 | Amino-acid degradation; L-arginine degradation via ADI pathway; carbamoyl phosphate from L-arginine: step 1/2 | ([Arena et al., 2002](#_ENREF_2)) |
| 11 | Arginine deiminase | *Lactobacillus brevis* | arcA | Q03NY8 | 45846.03125 | 4.96 | 3 | 83 | 99.828880 | ([Makarova et al., 2006](#_ENREF_22)) |
| 12 | Vancomycin/teicoplanin A-type resistance protein vanA | *Enterococcus faecium* | vanA | P25051 | 37419.10938 | 5.79 | 12 | 211 | 100 | Required for high-level resistance to glycopeptide antibiotics. D-Ala--D-Ala ligase of altered specificity which catalyzes ester bond formation between D-Ala and various D-hydroxy acids; produces a peptidoglycan which does not terminate in D-alanine but in D-lactate, thus preventing vancomycin or teicoplanin binding. | ([Dutka-Malen et al., 1990](#_ENREF_11)) |
| 13 | Inosine-5'-monophosphate dehydrogenase | *Streptococcus pyogenes* serotype M3 | guaB | Q8K5G1 | 52773.26172 | 5.72 | 6 | 107 | 100 | Involved in the purine metabolism; XMP biosynthesis via de novo pathway; XMP from IMP: step 1/1. | ([Beres et al., 2002](#_ENREF_6)) |
| 14 | Vancomycin/teicoplanin A-type resistance protein vanA | *Enterococcus faecium* | vanA | P25051 | 37419.10938 | 5.79 | 3 | 301 | 100 | Required for high-level resistance to glycopeptide antibiotics. D-Ala--D-Ala ligase of altered specificity which catalyzes ester bond formation between D-Ala and various D-hydroxy acids; produces a peptidoglycan which does not terminate in D-alanine but in D-lactate, thus preventing vancomycin or teicoplanin binding | ([Arthur et al., 1993](#_ENREF_3)) |
| 15 | 50S ribosomal protein L6 | *Enterococcus faecalis* | rplF | Q839E9 | 19397.24023 | 9.63 | 1 | 73.5 | 99.833586 | This protein binds to the 23S rRNA, and is important in its secondary structure. It is located near the subunit interface in the base of the L7/L12 stalk, and near the tRNA binding site of the peptidyltransferase center | ([Paulsen et al., 2003](#_ENREF_25)) |
| 16 | S-adenosylmethionine synthase | *Bacillus clausii* | metK | Q5WDZ8 | 43734.55859 | 5.21 | 6 | 180 | 100 | Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme | ([Kapatral et al., 2002](#_ENREF_19)) |
| 16 | S-adenosylmethionine synthase | *Staphylococcus aureus* | metK | A6U2Q1 | 43763.19922 | 4.86 | 4 | 154 | 100 | Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme. | ([HAMAP, 2007b](#_ENREF_15)) |
| 16 | S-adenosylmethionine synthase | *Bacillus amyloliquefaciens* | metK | A7Z7Y9 | 43873.39844 | 5.14 | 4 | 153 | 100 | Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme | ([Chen et al., 2007](#_ENREF_9)) |
| 16 | S-adenosylmethionine synthase | *Staphylococcus saprophyticus subsp.* saprophyticus | metK | Q49YL6 | 43883.42188 | 4.95 | 4 | 152 | 100 | Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme. | ([Kuroda et al., 2005](#_ENREF_21)) |
| 16 | S-adenosylmethionine synthase | *Staphylococcus epidermidis* | metK | Q8CNT5 | 43965.48828 | 4.95 | 4 | 150 | 100 | Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme. | ([Zhang et al., 2003](#_ENREF_29)) |
| 16 | S-adenosylmethionine synthase | *Alkaliphilus oremlandii* | metK | A8MJT0 | 42674 | 5.22 | 3 | 144 | 100 | Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme. | ([HAMAP, 2007a](#_ENREF_14)) |
| 16 | S-adenosylmethionine synthase | *Prochlorococcus marinus* | metK | Q46H57 | 44075.64063 | 5.16 | 3 | 142 | 100 | Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme | ([Kettler et al., 2007](#_ENREF_20)) |
| 16 | S-adenosylmethionine synthase | *Sulfurovum sp.* | metK | A6QBY6 | 41492.10156 | 5.2 | 2 | 134 | 100 | Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme. | ([Nakagawa et al., 2007](#_ENREF_24)) |
| 16 | S-adenosylmethionine synthase | *Synechococcus sp.* | metK | Q2JV74 | 44679.10156 | 5.47 | 2 | 134 | 100 | Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic reaction is composed of two sequential steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme. | ([Bhaya et al., 2007](#_ENREF_7)) |

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