

Table S4. Unique genes of LMO referenced to *L.vanovii* 1638

| ORF_id | Sequence_id | Group_id | start | end | strand | COG_id | COG_annotation | VFDB_annotation | UniProt_annotation |
|----------|-------------|------------|----------|----------|--------|---------|---|--|---|
| orf_22 | CP034771.1 | group_1724 | 23762 | 24055 | - | COG0360 | J.Ribosomal protein S6;RpsJ-Ribosome 30S subunit | - | 30S ribosomal protein S6;OS-Listeria welshimeri serovar 6b (strain ATCC 35897 / DSM 20650 / CIP 8149 / NCTC 11857 / SLCC 5334 / V8) OX=386043 GN=rpS6 PE=3 SV=1 |
| orf_24 | CP034771.1 | group_1801 | 25646 | 26305 | - | COG0586 | M.Membrane integrity protein DedA, putative transporter, DedA/T | - | Protein DedA OX=Escherichia coli (strain K12) OX=83333 GN=dedA PE=1 SV=1 |
| orf_25 | CP034771.1 | group_2402 | 26407 | 27186 | - | COG1737 | K.DNA-binding transcriptional regulator, Murf/Rpf family, contain | - | Uncharacterized HTH-type transcriptional regulator H_0143 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=Hh_0143 PE=5 SV=2 |
| orf_26 | CP034771.1 | group_149 | 27200 | 28113 | - | COG0957 | I.Agmatine (peptidylarginine) deiminase;AgaJ; | - | Putative agmatine deiminase 2 OS=Listeria monocytogenes serotype 4b (strain F2365) OX=265669 GN=agaJ2 PE=3 SV=1 |
| orf_27 | CP034771.1 | group_2391 | 28417 | 29361 | - | COG0549 | E.Carbamate kinase;ArcC; | - | Carbamate kinase OS=Lactilactobacillus sakei OX=1599 GN=arc- PE=3 SV=1 |
| orf_28 | CP034771.1 | group_143 | 29371 | 30465 | - | COG0257 | E.Agmatine (peptidylarginine) deiminase;AgaJ; | - | Putative agmatine deiminase 1 OS=Listeria monocytogenes serotype 4b (strain F2365) OX=265669 GN=agaJ1 PE=3 SV=1 |
| orf_29 | CP034771.1 | group_2397 | 30462 | 31835 | - | COG0531 | E.Serine transporter YbeC, amino acid/H ⁺ symporter family;POT; | - | Probable agmatine/putrescine antiporter AgaJ OS=Lactococcus lactis subsp. lactis (strain IL1403) OX=272623 GN=agaJ OS=agud PE=3 SV=1 |
| orf_70 | CP034771.1 | group_2663 | 75494 | 81312 | - | - | - | - | Internalin I OS=Listeria monocytogenes serotype 4b (strain F2365) OX=265669 GN=iniI PE=3 SV=1 |
| orf_85 | CP034771.1 | group_2071 | 98192 | 98545 | - | - | - | - | - |
| orf_86 | CP034771.1 | group_2231 | 98648 | 99070 | - | COG1846 | K.DNA-binding transcriptional regulator, MarR family;MarK; | - | HTH-type transcriptional regulator MhpR OS=Basillus subtilis (strain 168) OX=224308 GN=mhpR PE=2 SV=1 |
| orf_93 | CP034771.1 | group_2663 | 107155 | 109816 | - | - | - | - | Picidatal crystal protein Cya22A OS=Basillus thuringiensis OX=1428 GN=cya22A PE=2 SV=1 |
| orf_116 | CP034771.1 | group_1897 | 129433 | 129636 | - | COG4481 | S.Uncharacterized conserved protein, DUF951 family | - | Uncharacterized protein Y0M OS=Basillus subtilis (strain 168) OX=224308 GN=y0M PE=1 SV=1 |
| orf_131 | CP034771.1 | group_2113 | 143822 | 144634 | - | COG1455 | G.Phosphotransferase system cellobiose-specific component IIC-Ce- | - | PTS system N,N'-diacetylchitobiose-specific EIIc component OS=Escherichia coli (strain K12) OX=83333 GN=chcC PE=1 SV=2 |
| orf_134 | CP034771.1 | group_2441 | 146703 | 146813 | - | - | - | - | - |
| orf_157 | CP034771.1 | group_312 | 174795 | 175751 | - | COG1609 | K.DNA-binding transcriptional regulator, LacI/PurR family;PurK; | - | Catabolite control protein B OS=Basillus subtilis (strain 168) OX=224308 GN=ccpB PE=1 SV=1 |
| orf_184 | CP034771.1 | group_3706 | 198731 | 199204 | - | - | - | - | - |
| orf_185 | CP034771.1 | group_2058 | 199355 | 199519 | - | - | - | - | - |
| orf_197 | CP034771.1 | group_284 | 208364 | 210631 | - | - | - | - | - |
| orf_202 | CP034771.1 | group_2683 | 214067 | 214507 | - | COG0494 | V.8-oxo-dGTP pyrophosphatase MutT and related house-keeping T | - | Alpha-xylosidase OS=Emmericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=agdD PE=1 SV=1 |
| orf_241 | CP034771.1 | group_1876 | 255606 | 256709 | - | COG0772 | D.Peptidoglycan polymerase FtsW/RodA/SpoVE/FtsW; | - | Peptidoglycan glycosyltransferase RodA OS=Basillus subtilis (strain 168) OX=224308 GN=rodA PE=1 SV=1 |
| orf_257 | CP034771.1 | group_2384 | 271553 | 271921 | - | - | - | - | - |
| orf_301 | CP034771.1 | group_1642 | 316258 | 317337 | - | COG1477 | HO;FAD;protein FMN transferase ApbE;ApbE; | - | FAD;protein FMN transferase OS=Klebsiella pneumoniae (strain 342) OX=507522 GN=apbE2 PE=3 SV=1 |
| orf_344 | CP034771.1 | group_3446 | 344006 | 344671 | - | - | - | - | - |
| orf_345 | CP034771.1 | group_2131 | 345077 | 346603 | - | COG1705 | MN;Flagellum-specific peptidoglycan hydrolase FliG;FliG; | - | Protein Ami OS=Listeria monocytogenes serotype 1/2a (strain EGD / Mackson) OX=1334565 GN=ami PE=3 SV=1 |
| orf_346 | CP034771.1 | group_2140 | 347011 | 348039 | - | COG0489 | D;Fe-S cluster carrier ATPase, Mrp/AbpC/NBP35 family;Mrp; | - | Iron-sulfur cluster carrier protein OS=Basillus subtilis (strain 168) OX=224308 GN=saA PE=1 SV=1 |
| orf_347 | CP034771.1 | group_2370 | 348480 | 349781 | - | COG4886 | K.Leucine-rich repeat (LRR) protein;LRR; | - | Internalin I OS=Listeria monocytogenes serotype 1/2a (strain EGD / Mackson) OX=1334565 GN=iniC PE=1 SV=1 |
| orf_348 | CP034771.1 | group_2370 | 350212 | 351102 | - | COG4886 | K.Leucine-rich repeat (LRR) protein;LRR; | [iniC] Internalin C [iniC] (VF0438) - Immune modulation [VF0258] [Listeria monocytogenes serotype 1/2a (strain EGD / Mackson) OX=1334565 GN=iniC PE=1 SV=1 | |
| orf_349 | CP034771.1 | group_3529 | 351503 | 351775 | - | - | - | - | - |
| orf_356 | CP034771.1 | group_3606 | 360032 | 360385 | - | - | - | - | - |
| orf_362 | CP034771.1 | group_1593 | 364892 | 365158 | - | - | - | - | - |
| orf_388 | CP034771.1 | group_2117 | 389953 | 390387 | - | COG1937 | R.Cupin domain protein related to quercetin diogenase;QdoI; | - | Uncharacterized HTH-type transcriptional regulator YdfY OS=Basillus subtilis (strain 168) OX=224308 GN=ydfY PE=4 SV=1 |
| orf_389 | CP034771.1 | group_3532 | 390384 | 390707 | - | COG0599 | R.Uncharacterized conserved protein YurZ, alkylglycerol phosphat | - | 4-carboxymuconolactone decarboxylase OS=Acinetobacter baylii (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=pcpA PE=4 SV=2 |
| orf_390 | CP034771.1 | group_3482 | 390734 | 391903 | - | - | - | - | - |
| orf_475 | CP034771.1 | group_2240 | 479464 | 479799 | - | - | - | - | - |
| orf_495 | CP034771.1 | group_62 | 501116 | 504391 | - | COG1501 | G.Alpha-glucosidase/xylosidase, GH31 family;YliC; | - | 1,3-alpha-D-glucanase OS=Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399) OX=479435 GN=Kfla_1895 PE=1 SV=1 |
| orf_496 | CP034771.1 | group_2313 | 504500 | 505394 | - | - | - | - | - |
| orf_497 | CP034771.1 | group_305 | 505407 | 507026 | - | COG1501 | G.Alpha-glucosidase/xylosidase, GH31 family;YliC; | - | Internalin C OS=Listeria monocytogenes serotype 1/2a (strain EGD / Mackson) OX=1334565 GN=iniC PE=1 SV=1 |
| orf_498 | CP034771.1 | group_305 | 507036 | 509333 | - | COG1501 | G.Alpha-glucosidase/xylosidase, GH31 family;YliC; | - | Alpha-xylosidase OS=Saccharobolus sulfataricus (strain ATCC 50592 / DSM 1617 / JCM 11322 / P2) OX=273057 GN=xyIS PE=1 SV=1 |
| orf_509 | CP034771.1 | group_2164 | 517802 | 517966 | - | - | - | - | - |
| orf_534 | CP034771.1 | group_1805 | 539718 | 540083 | - | COG4272 | S.Uncharacterized membrane protein | - | - |
| orf_544 | CP034771.1 | group_1693 | 547103 | 547336 | - | COG4844 | S.Uncharacterized conserved protein YuzB, UPF0349 family;YuzB | - | UPF0349 protein lwe2340 OS=Listeria welshimeri serovar 6b (strain ATCC 35897 / DSM 20650 / CIP 8149 / NCTC 11857 / SLCC 5334 / V8) OX=386043 GN=lwe2340 PE=3 SV=1 |
| orf_545 | CP034771.1 | group_2586 | 551841 | 552470 | - | - | - | - | - |
| orf_582 | CP034771.1 | group_2035 | 587994 | 589598 | - | COG1574 | R.Predicted amidohydrolase YliC;YliC; | - | Putative amidohydrolase YliC OS=Basillus subtilis (strain 168) OX=224308 GN=yliC PE=3 SV=1 |
| orf_599 | CP034771.1 | group_1812 | 610541 | 611443 | - | COG1284 | S.Uncharacterized membrane-anchored protein YitT, contains DUF | - | UPF0750 membrane protein YitT OS=Basillus subtilis (strain 168) OX=224308 GN=yitT PE=3 SV=2 |
| orf_603 | CP034771.1 | group_1845 | 613688 | 614563 | - | COG2133 | R.Predicted N-acetyltransferase, GNAT family;ElaA; | - | Uncharacterized protein AF_1281 OS=Archaeoglobus fulgidus (strain ATCC 49558 / DSM 4204 / JCM 9628 / NBRC 100126 / VC-16) OX=224325 GN=AF_1281 PE=3 SV=1 |
| orf_604 | CP034771.1 | group_1809 | 615744 | 616265 | - | COG0693 | V.Protein/nucleotide deglycase, Pflg/YagJ/Di-1 family; related to | - | Putative phosphatase YhmC OS=Basillus subtilis (strain 168) OX=224308 GN=yhmC PE=3 SV=1 |
| orf_609 | CP034771.1 | group_2145 | 618149 | 618778 | - | COG0637 | G.Beta-phosphoglucomutase, HAD superfamily;YglJ; | - | Bifunctional transcriptional activator/DNA repair enzyme AdaA OS=Basillus subtilis (strain 168) OX=224308 GN=adaA PE=1 SV=1 |
| orf_622 | CP034771.1 | group_2185 | 629307 | 629861 | - | COG2169 | L.Methylphosphotriester-DNA- superfamily;Methylphosphatransferase | - | - |
| orf_664 | CP034771.1 | group_1694 | 672963 | 673958 | - | COG0180 | L.Tryptophanyl-tRNA synthetase;TrpS;Aminoacyl-tRNA synthetases | - | Tryptophan--tRNA ligase OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) OX=272626 GN=trpS PE=3 SV=1 |
| orf_692 | CP034771.1 | group_2242 | 715119 | 715777 | - | - | - | - | - |
| orf_712 | CP034771.1 | group_1797 | 730285 | 730926 | - | COG4330 | S.Uncharacterized membrane protein, DUF1361 domain | - | - |
| orf_724 | CP034771.1 | group_2146 | 741693 | 742547 | - | COG0091 | G.Fructose/tagatose biphosphate aldolase;FbaGlycolysis | - | D-tagatose-1,6-bisphosphate aldolase subunit GatY OS=Escherichia coli (strain K12) OX=83333 GN=gatY PE=1 SV=1 |
| orf_754 | CP034771.1 | group_2513 | 776707 | 777282 | - | COG1136 | M.ABC-type lipoprotein export system, ATPase component;LolD; | - | Uncharacterized ABC transporter ATP-binding protein YvtD OS=Basillus subtilis (strain 168) OX=224308 GN=yvtD PE=3 SV=2 |
| orf_768 | CP034771.1 | group_2586 | 792882 | 791449 | - | COG1762 | G.Phycoerythrin-specific EIIa component OS=Escherichia coli (strain K12) OX=83333 GN=peiA PE=1 SV=1 | - | Phycoerythrin-specific EIIa component OS=Escherichia coli (strain K12) OX=83333 GN=peiA PE=1 SV=1 |
| orf_771 | CP034771.1 | group_2079 | 793125 | 794057 | - | COG1105 | G1-phosphoglucoylkinase or 6-phosphofructokinase II;FruK; | - | Tagatose-6-phosphate kinase OS=Staphylococcus epidermidis (strain ATCC 35984 / RP624) OX=176279 GN=hacC PE=3 SV=1 |
| orf_778 | CP034771.1 | group_3562 | 800654 | 801178 | - | COG3177 | K.Fc-fatty protein;Glc | - | - |
| orf_811 | CP034771.1 | group_2349 | 831493 | 833637 | - | COG2015 | Q.Akyl sulfate BGS1 and related hydrolases, metallo-beta-lactan | - | - |
| orf_812 | CP034771.1 | group_2586 | 833801 | 834106 | - | - | - | - | - |
| orf_901 | CP034771.1 | group_3491 | 931669 | 933315 | - | - | - | - | - |
| orf_906 | CP034771.1 | group_1760 | 937523 | 938410 | - | COG1131 | V.ABC-type multidrug transport system, ATPase component;CcmA; | - | Linear primary alkylsulfatase OS=Pseudomonas sp. OX=306 GN=sdap PE=1 SV=1 |
| orf_978 | CP034771.1 | group_1009 | 10093705 | 10093847 | - | COG4912 | L3-methyladenine DNA glycosylase AbdA;AbdA; | - | Arylsulfate sulfotransferase Axt OS=Escherichia coli O6:H1 (strain CT073) / ATCC 700298 / UPEC OX=199310 GN=astT PE=1 SV=1 |
| orf_981 | CP034771.1 | group_1684 | 1011422 | 1011910 | - | - | - | - | Multidrug efflux system ATP-binding protein Ynf218C OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=ynf218C PE=1 SV=1 |
| orf_982 | CP034771.1 | group_2438 | 1012002 | 1012739 | - | COG0778 | C.Nitroreductase;NfnB;Pyrimidine degradation | - | CR(VI) reductase OS=Pseudomonas sp. (strain G-1) OX=79677 GN=nfnB PE=3 SV=1 |
| orf_983 | CP034771.1 | group_2437 | 1012959 | 1013822 | - | COG0583 | K.DNA-binding transcriptional regulator, LysR family;LysR; | - | HTH-type transcriptional regulator CtrR OS=Basillus subtilis (strain 168) OX=224308 GN=ctrR PE=3 SV=2 |
| orf_984 | CP034771.1 | group_2437 | 1017310 | 1017765 | - | - | - | - | Uncharacterized protein YgdI OS=Basillus subtilis (strain 168) OX=224308 GN=ygdI PE=1 SV=1 |
| orf_1005 | CP034771.1 | group_2447 | 1036313 | 1037674 | - | - | - | - | Glutaryl endopeptidase OS=Escherichia coli (strain ATCC 14580 / DSM 13 / JCM 2505 / CCUG 7422 / NBRC 12200 / NCIMB 9375 / NCTC 10341 / NRRL N5-1264 / Gisslon 46) OX=279010 GN=hdsA PE=1 SV=2 |
| orf_1102 | CP034771.1 | group_1641 | 1128849 | 1129973 | - | COG0026 | F.Phosphoribosylaminimidazole carboxylase (NCAR) synthetase;F- | - | N5-carboxymuconimide ribonucleotide synthase OS=Basillus subtilis (strain 168) OX=224308 GN=pcrK PE=3 SV=2 |
| orf_1115 | CP034771.1 | group_2158 | 1141850 | 1143205 | - | COG2733 | R.NA-dependent transporter, SNA family;YocK; | - | Uncharacterized ABC transporter ATP-binding protein YvtD OS=Basillus subtilis (strain 168) OX=224308 GN=yvtD PE=3 SV=2 |
| orf_1116 | CP034771.1 | group_1640 | 1143411 | 1144088 | - | COG1646 | I.Glycyl-L-phosphatidylserine synthase;PsdB; | - | Sensor protein BcsB OS=Alkalihalobacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) OX=272558 GN=bcsB PE=3 SV=1 |
| orf_1138 | CP034771.1 | group_1661 | 1146371 | 1148387 | - | COG0772 | L.DNA-dependent DNA ligase;Lig | - | Glutamine transporter ATP-binding protein GlnC OS=Escherichia coli (strain K12) OX=83333 GN=glnC PE=1 SV=1 |
| orf_1122 | CP034771.1 | group_1811 | 1151405 | 1152835 | - | COG0064 | J.Asp-tRNAAsn-Glu-tRNAArg amidotransferase B subunit;GatAmi | - | DNA ligase OS=Listeria monocytogenes serotype 4a (strain HC23) OX=552536 GN=hga PE=3 SV=1 |
| orf_1124 | CP034771.1 | group_1883 | 1153954 | 1154814 | - | - | - | - | Aspartyl/glutamyl-tRNA(Gln) amidotransferase subunit B OS=Listeria welshimeri serovar 6b (strain ATCC 35897 / DSM 20650 / CIP 8149 / NCTC 11857 / SLCC 5334 / V8) OX=386043 GN=gatB PE=3 SV=1 |
| orf_1126 | CP034771.1 | group_2052 | 1156549 | 1157103 | - | COG4884 | S.Uncharacterized conserved protein Yfc5, contains WGR domain;1 | - | - |
| orf_1127 | CP034771.1 | group_1639 | 1157131 | 1157661 | - | COG0703 | E.Shikimate kinase;AroK;Aromatic amino acid biosynthesis | - | Shikimate kinase OS=Enterococcus faecalis (strain ATCC 700802 / V583) OX=226185 GN=aroK PE=3 SV=1 |
| orf_1128 | CP034771.1 | group_1633 | 1157840 | 1158343 | - | - | - | - | - |
| orf_1129 | CP034771.1 | group_2022 | 1158387 | 1159254 | - | COG0388 | C.Omega-oxidase YnfN/12, hydrolyses alpha-ketoglutarate;Nac | - | N-carbamoylputrescine amidase OS=Arabisopsis thaliana (strain OX=3702 GN=CPA PE=1 SV=2 |
| orf_1130 | CP034771.1 | group_2058 | 1159408 | 1160175 | - | COG1136 | M.ABC-type lipoprotein export system, ATPase component;LolD; | - | Bactracin export ATP-binding protein BceA OS=Basillus subtilis (strain 168) OX=224308 GN=bceA PE=1 SV=1 |
| orf_1132 | CP034771.1 | group_1728 | 1162206 | 1162883 | - | COG0745 | T.KDNA-binding response regulator, OmpR family, contains Rec A | - | Sensory transduction protein BceR OS=Alkalihalobacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) OX=272558 GN=bceR PE=3 SV=1 |
| orf_1136 | CP034771.1 | group_1668 | 1166086 | 1167126 | - | COG0642 | T.Signal transduction histidine kinase;BaeS; | - | Sensor protein BceS OS=Alkalihalobacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) OX=272558 GN=bceS PE=3 SV=1 |
| orf_1137 | CP034771.1 | group_2591 | 1166256 | 1168403 | - | COG0765 | E.ABC-type amino acid transport system, permease component;Hic | - | Probable ABC transporter permease protein YnfC OS=Basillus subtilis (strain 168) OX=224308 GN=ynfC PE=3 SV=1 |
| orf_1138 | CP034771.1 | group_299 | 1168173 | 1168820 | - | COG1126 | E.ABC-type polar amino acid transport system, ATPase component | - | Glutamine transporter ATP-binding protein GlnC OS=Escherichia coli (strain K12) OX=83333 GN=glnC PE=1 SV=1 |
| orf_1139 | CP034771.1 | group_1777 | 1168821 | 1169636 | - | COG0834 | ET-ABC-type amino acid transport/signal transduction system, per | - | L-cystine-binding protein TcyJ OS=Escherichia coli (strain K12) OX=83333 GN=tcyJ PE=1 SV=1 |
| orf_1141 | CP034771.1 | group_2127 | 1170837 | 1171355 | - | COG1033 | R.Predicted N-acetyltransferase YhmB;YhmB; | - | Uncharacterized N-acetyltransferase YhmQ OS=Escherichia coli (strain K12) OX=83333 GN=yhmQ PE=3 SV=1 |
| orf_1146 | CP034771.1 | group_2586 | 1171897 | 1180020 | - | COG1175 | G.ABC-type sugar transport system, permease component;LigA; | - | Probable ABC transporter permease protein YnfC OS=Basillus subtilis (strain 168) OX=224308 GN=ynfC PE=3 SV=1 |
| orf_1153 | CP034771.1 | group_2455 | 1190002 | 1190682 | - | COG1131 | V.ABC-type multidrug transport system, ATPase component;CcmA; | - | Uncharacterized ABC transporter ATP-binding protein YhmC OS=Basillus subtilis (strain 168) OX=224308 GN=yhmC PE=3 SV=1 |
| orf_1154 | CP034771.1 | group_2454 | 1190675 | 1191448 | - | - | - | - | - |
| orf_1162 | CP034771.1 | group_3496 | 1201253 | 1202593 | - | COG4886 | K.Leucine-rich repeat (LRR) protein;LRR; | - | Internalin C OS=Listeria monocytogenes serotype 1/2a (strain EGD / Mackson) OX=1334565 GN=iniC PE=1 SV=1 |
| orf_1164 | CP034771.1 | group_2230 | 1202593 | 1203928 | - | COG1104 | E.Dipeptidyl tripeptide permease;PTI2; | - | NaGL1, UGL1, NcYJmC1 antiporter OS=Pyrococcus maritimus OX |

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|----------|------------|------------|---------|---------|---|---------|--|---|---|
| orf_2492 | CP034771.1 | group_177 | 2554919 | 2555203 | - | - | - | - | - |
| orf_2507 | CP034771.1 | group_2878 | 2574558 | 2578127 | - | COG4886 | K,Leucine-rich repeat (LRR) protein,LRR; | - | - |
| orf_2510 | CP034771.1 | group_3722 | 2584590 | 2586137 | - | - | - | - | - |
| orf_2512 | CP034771.1 | group_3645 | 2587057 | 2587779 | - | COG1028 | i,NAD(P)-dependent dehydrogenase, short-chain alcohol dehydrog- | - | - |
| orf_2528 | CP034771.1 | group_2557 | 2600643 | 2600786 | - | - | - | - | - |
| orf_2534 | CP034771.1 | group_178 | 2605417 | 2605518 | - | - | - | - | - |
| orf_2535 | CP034771.1 | group_178 | 2605557 | 2605658 | - | - | - | - | - |
| orf_2539 | CP034771.1 | group_3397 | 2608282 | 2608794 | + | - | - | - | - |
| orf_2540 | CP034771.1 | group_3417 | 2608791 | 2610098 | + | COG1215 | N,Glycosyltransferase, catalytic subunit of cellulose synthase and p- | - | Poly-beta-1,6-N-acetyl-D-glucosamine synthase OS=Escherichia coli (strain K12) OX=83333 GN=pguC PE=1 SV=1 |
| orf_2542 | CP034771.1 | group_2409 | 2611062 | 2611565 | + | COG1595 | K,DNA-directed RNA polymerase specialized sigma subunit, sigma2 | - | RNA polymerase sigma factor sigV OS=Bacillus subtilis (strain 168) OX=224308 GN=sigV PE=1 SV=1 |
| orf_2543 | CP034771.1 | group_3650 | 2611555 | 2612406 | + | - | - | - | Anti-sigma-V factor RsiV OS=Bacillus subtilis (strain 168) OX=224308 GN=rsvV PE=1 SV=1 |
| orf_2544 | CP034771.1 | group_3568 | 2612420 | 2613262 | + | - | - | - | Putative polysaccharide deacetylase YheN OS=Bacillus subtilis (strain 168) OX=224308 GN=yheN PE=3 SV=1 |
| orf_2552 | CP034771.1 | group_3731 | 2618392 | 2619507 | + | COG4292 | S,Low temperature requirement protein LtrA (function unknown)1 | - | Uncharacterized protein RA0937 OS=Rhizobium meliloti (strain 1021) OX=266834 GN=RA0937 PE=4 SV=2 |
| orf_2557 | CP034771.1 | group_141 | 2625040 | 2625243 | + | COG1476 | K,DNA-binding transcriptional regulator, XRE-family HTH domain,XI [cyIR2] cytolysin regulator R2 [Cytolysin (VF0356) - Exotoxin (VFC0235)] | - | Uncharacterized HTH-type transcriptional regulator M10272 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=M10272 PE=4 SV=2 |
| orf_2579 | CP034771.1 | group_3668 | 2644996 | 2645181 | - | - | - | - | - |
| orf_2593 | CP034771.1 | group_3604 | 2652326 | 2652451 | - | - | - | - | - |
| orf_2632 | CP034771.1 | group_2468 | 2699165 | 2700607 | - | COG3866 | G,Glycosidase/amyase (phosphorylase)AmyA; | - | Sucrose phosphorylase OS=Streptococcus mutans serotype c (strain ATCC 700610 / UA159) OX=210007 GN=pgfA PE=1 SV=4 |
| orf_2634 | CP034771.1 | group_2469 | 2702320 | 2703150 | - | COG3833 | G,ABC-type maltose transport system, permease component MalG- | - | Galactooligosaccharides transport system permease protein GanQ OS=Bacillus subtilis (strain 168) OX=224308 GN=ganQ PE=1 SV=1 |
| orf_2635 | CP034771.1 | group_2467 | 2703152 | 2704489 | - | COG1175 | G,ABC-type sugar transport system, permease componentUggA; | - | Galactooligosaccharides transport system permease protein GanP OS=Bacillus subtilis (strain 168) OX=224308 GN=ganP PE=1 SV=1 |
| orf_2636 | CP034771.1 | group_2462 | 2704507 | 2705733 | - | COG2182 | G,Maltose-binding periplasmic protein MalE,MalE; | - | Galactooligosaccharide-binding protein OS=Bacillus subtilis (strain 168) OX=224308 GN=ganS PE=1 SV=1 |
| orf_2637 | CP034771.1 | group_2466 | 2705871 | 2706866 | - | COG1609 | K,DNA-binding transcriptional regulator, LacI/PurR family,PurR; | - | NTD biosynthesis operon regulator NtrR OS=Bacillus subtilis (strain 168) OX=224308 GN=ntrR PE=4 SV=1 |
| orf_2689 | CP034771.1 | group_2042 | 2766242 | 2766916 | + | - | - | - | Uncharacterized protein Lin0241 OS=Listeria innocua serovar 6a (strain ATCC BAA-630 / CUP 11352) OX=272626 GN=lin0241 PE=4 SV=1 |
| orf_2691 | CP034771.1 | group_3438 | 2767360 | 2768154 | - | - | - | - | Uncharacterized protein M10912 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=M10912 PE=4 SV=1 |
| orf_2694 | CP034771.1 | group_3603 | 2769642 | 2772566 | - | - | - | - | - |
| orf_2705 | CP034771.1 | group_1679 | 2784659 | 2785336 | - | COG0845 | MV-Multidrug efflux pump subunit AcrA (membrane fusion protein) | - | - |
| orf_2706 | CP034771.1 | group_3554 | 2785495 | 2786313 | - | COG0503 | F,Adenine/guanine phosphoribosyltransferase or related PRPP-bin- | - | Pur operon repressor OS=Bacillus subtilis (strain 168) OX=224308 GN=purR PE=1 SV=1 |
| orf_2707 | CP034771.1 | group_846 | 2786481 | 2787218 | - | COG3394 | G,Chitoooligosaccharide deacetylase ChbG, YdJ/CelG family,ChbG; | - | Carbohydrate deacetylase OS=Listeria welshimeri serovar 6b (strain ATCC 35897 / DSM 20650 / CIP 8149 / NCTC 11857 / SLCC 5334 / V8) OX=386043 GN=hw0160 PE=3 SV=1 |
| orf_2715 | CP034771.1 | group_284 | 2794229 | 2796520 | - | COG1501 | G,Alpha-glucosidase/xylosidase, GH31 family,YiCi; | - | Alpha-glucosidase 2 OS=Bacillus thermoamyloqueliciens OX=1425 PE=3 SV=1 |
| orf_2716 | CP034771.1 | group_62 | 2796523 | 2799825 | - | COG1501 | G,Alpha-glucosidase/xylosidase, GH31 family,YiCi; | - | 1,3-alpha-isomaltosidase OS=Klebsiella fauvis (strain DSM 17836 / JCM 10339 / NBRC 14399) OX=479435 GN=kfta_1895 PE=1 SV=1 |
| orf_2717 | CP034771.1 | group_1980 | 2799920 | 2801176 | - | COG1653 | G,ABC-type glycerol-3-phosphate transport system, periplasmic coi- | - | Putative binding protein BRA0748/BS1330_10741 OS=Brucella suis biovar 1 (strain 1330) OX=204722 GN=BRA0748 PE=3 SV=1 |
| orf_2719 | CP034771.1 | group_147 | 2802052 | 2802930 | - | COG1175 | G,ABC-type sugar transport system, permease componentUggA; | - | Probable ABC transporter permease protein YeeP OS=Bacillus subtilis (strain 168) OX=224308 GN=yeeP PE=3 SV=1 |
| orf_2720 | CP034771.1 | group_227 | 2802967 | 2804181 | - | COG1940 | GK,Sugar kinase of the NBD/HSP70 family, may contain an N-termi- | - | Xylose repressor OS=Caldicellulosiruptor bescii (strain ATCC BAA-1888 / DSM 6725 / Z-1320) OX=521460 GN=xyIR PE=3 SV=1 |
| orf_2726 | CP034771.1 | group_3118 | 2818085 | 2819703 | - | COG2362 | E,D-aminopeptidase,DppA; | - | D-aminopeptidase OS=Bacillus subtilis (strain 168) OX=224308 GN=dppA PE=1 SV=3 |
| orf_2738 | CP034771.1 | group_3105 | 2821381 | 2822160 | - | COG2367 | V,Beta-lactamase class A,PenP; | - | - |
| orf_2748 | CP034771.1 | group_156 | 2833038 | 2833637 | - | - | - | - | - |
| orf_2773 | CP034771.1 | group_2375 | 2858082 | 2858369 | + | COG0640 | K,DNA-binding transcriptional regulator, ArsR family,ArsR; | - | Uncharacterized HTH-type transcriptional regulator YcgG OS=Bacillus subtilis (strain 168) OX=224308 GN=ycgG PE=4 SV=1 |
| orf_2775 | CP034771.1 | group_3712 | 2859861 | 2861261 | - | COG2190 | G,Phosphatransferase system IIA component,NagE; | - | PTS system beta-glucoside-specific EIIBCA component OS=Bacillus subtilis (strain 168) OX=224308 GN=hgBP PE=3 SV=2 |
| orf_2776 | CP034771.1 | group_2329 | 2861401 | 2862393 | + | - | - | - | Regulatory protein Pocr OS=Salmonella typhimurium (strain LT2 / SGGSC1412 / ATCC 700720) OX=99287 GN=pocr PE=1 SV=2 |
| orf_2788 | CP034771.1 | group_3566 | 2872695 | 2873387 | - | COG0235 | EG,S-methylthioribulose/5-deoxyribulose/Fuculose 1-phosphate al- | - | L-fuculose phosphate aldolase OS=Methanococcus maripaludis (strain C7 / ATCC BAA-1331) OX=426368 GN=fucA PE=3 SV=1 |
| orf_2796 | CP034771.1 | group_2370 | 2882991 | 2883893 | - | COG4886 | K,Leucine-rich repeat (LRR) protein,LRR; | - | Internalin C OS=Listeria monocytogenes serotype 1/2a (strain EGD / Mackness) OX=1334565 GN=iniC PE=1 SV=1 |
| orf_2799 | CP034771.1 | group_3280 | 2886378 | 2886899 | - | - | - | - | - |
| orf_2803 | CP034771.1 | group_2179 | 2890010 | 2890783 | - | COG2513 | G,2-Methylisocitrate lyase and related enzymes, PEP mutase family,- | - | Uncharacterized protein Rv1998c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv1998c PE=1 SV=1 |