**Figure S1.** Amino Acid sequence alignment of lipoic acid biosynthesis and salvage enzymes.
*Bs – B. subtilis; Lm – L. monocytogenes; Sa – S. aureus*

```
Bs LipA   1     MAKKDEH-LRKPEWLKIKLNTNENYTGLKKLMRENNLHTVCEEAKCPNIHECWAVRRTAT   59
                MA K+E  LRKP+WLKIKLNTNENYTGLKK+MRE NL+TVCEEAKCPNIHECW  RRTAT
Sa LipA   1     MATKNEEILRKPDWLKIKLNTNENYTGLKKMMREKNLNTVCEEAKCPNIHECWGARRTAT   60

Bs LipA   60    FMILGSVCTRACRFCAVKTGLPTELDLQEPERVADSVALMNLKHAVITAVARDDQKDGGA   119
                FMILG+VCTRACRFCAVKTGLP ELDL EPERVA+SV LMNLKH VITAVARDD +D G+
Sa LipA   61    FMILGAVCTRACRFCAVKTGLPNELDLNEPERVAESVELMNLKHVVITAVARDDLRDAGS   120

Bs LipA   120   GIFAETVRAIRRKSPFTTIEVLPSDMGGNYDNLKTLMDTRPDILNHNIETVRRLTPRVRA   179
                 ++AETVR +R ++PFTTIE+LPSDMGG+YD L+TLM +RPDILNHNIETVRRLTPRVRA
Sa LipA   121   NVYAETVRKVRERNPFTTIEILPSDMGGDYDALETLMASRPDILNHNIETVRRLTPRVRA   180

Bs LipA   180   RATYDRSLEFLRRAKEMQPDIPTKSSIMIGLGETKEEIIEVMDDLLANNVDIMAIGQYLQ   239
                RATYDR+LEFLRR+KE+QPDIPTKSSIM+GLGET EEI E MDDL AN+VDI+ IGQYLQ
Sa LipA   181   RATYDRTLEFLRRSKELQPDIPTKSSIMVGLGETIEEIYETMDDLRANDVDILTIGQYLQ   240

Bs LipA   240   PTKKHLKVQKYYHPDEFAELKEIAMQKGFSHCEAGPLVRSSYHADEQVNEASKKRQAQA    298
                P++KHLKVQKYY P EF +L+++AM KGF HC+AGPLVRSSYHADEQVNEA+K++Q Q
Sa LipA   241   PSRKHLKVQKYYTPLEFGKLRKVAMDKGFKHCQAGPLVRSSYHADEQVNEAAKEKQRQG    299

                                                            79% Identity
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Bs LipM   4     ETWRFIDSGNASPAFNMALDEALLYWHSEKKIPPVIRFYGWNPATLSVGYFQNIKKEINF   63
                ETW FI++G+  P +NMA+DEALL + S  +I PVIRFY WNPATLS+GYFQ ++KEI+
Sa LipM   3     ETWNFINTGSKDPYYNMAMDEALLNFVSRGEIDPVIRFYTWNPATLSIGYFQRLQKEIDI   62

Bs LipM   64    EAVHKYNLGFVRRPTGGRGVLHDQELTYSVIVSEEHPEMPATVTEAYRVISEGILQGFRN   123
                + V +   G VRR TGGRGVLHD+ELTYSVIV E HP MP+TVTEAYRVIS+G+L+GF+N
Sa LipM   63    DKVKEKGFGLVRRQTGGRGVLHDKELTYSVIVPESHPNMPSTVTEAYRVISQGLLEGFKN   122

Bs LipM   124   LGLDAYFAIPRTEKEKESLKNPRSSVCFDAPSWYELVVEGRKVAGSAQTRQKGVILQHGS   183
                LG D YFA+P+T +E++ LK PRSSVCFDAPSWYELVVEGRK+AGSAQTRQKGVILQHGS
Sa LipM   123   LGFDTYFAVPKTPEERQKLKQPRSSVCFDAPSWYELVVEGRKIAGSAQTRQKGVILQHGS   182

Bs LipM   184   ILLDLDEDKLFDLFLYPSERVRERMQRNFKNKAVAINELIEKRVTMDEARKAFKEGFETG   243
                IL D+D D+LFD+F+Y +ER++ +M+  F  KAVAIN++ ++ +T+ +  +AF++GF+ G
Sa LipM   183   ILQDIDIDELFDMFIYKNERLKLKMKEAFVEKAVAINDISDEHITISQMEEAFEKGFKKG   242

Bs LipM   244   LNIHLEPYELSQEELDFVHHLAETKYASDEWNYKR  278
                LNI  +P EL++ +L  V  L E KY SDEW +++           62% Identity
Sa LipM   243   LNIEFKPLELTEAQLAEVEELTE-KYRSDEWMFRK  276
```

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Bs LipL   30    QSFAMDDTLCMSVGKGVSPATARSWVHHDTIVLGIQDTRLPFLQDGISLLESE-GYRVIV   88
                QSFA DDT C SVGK +S    R+W+H  T++LGI D+RLPFL+DGI  L +E GY  IV
Sa LipL   2     QSFAFDDTFCESVGKDISDNVVRTWIHQHTVILGIHDSRLPFLKDGIDYLTNEIGYNAIV   61

Bs LipL   89    RNSGGLAVVLDDGVLNISLIFEDEKKGIDIDKGYEAMVELMRRMLRPYNAKIEAYEIEGS   148
                RNSGGL VVLD GVLNISL+F+ + +   ID+ +  M  L+ +M    N  I+  EIE S
Sa LipL   62    RNSGGLGVVLDQGVLNISLMFKGQTE-TTIDEAFTVMYLLISKMFENENVDIDTMEIEHS   120

Bs LipL   149   YCPGSYDLSINGKKFAGISQRRVRGGVAVQIYLCADKSGSERADLIRRFYQAALKDKQND   208
                YCPG +DLSI+GKKFAGISQRRVRGG+AVQIYLC + SGSERA +++ FY+ ALK +
Sa LipL   121   YCPGKFDLSIDGKKFAGISQRRVRGGIAVQIYLCVEGSGSERALMMQTFYEHALKGEVTK   180

Bs LipL   209   KKGVYPEIRPETMASLSELLQKDISVQDLMFALLTELKALSTHLYSAGLSIDEEMEFEKN   268
                 K  YPEI P  MASL  LL K I+VQD+MF LL  +K L   L    ++ +E   ++
Sa LipL   181   FK--YPEIEPSCMASLETLLNKTITVQDVMFLLLYAIKDLGGVLNMTPITQEEWQRYDTY   238

Bs LipL   269   LVRMAERNAKV  279
                  +M ERN K+        54% Identity
Sa LipL   239   FDKMIERNKKM  249
```

**Figure S1.** Amino Acid sequence alignment of lipoic acid biosynthesis and salvage enzymes.
*Bs – B. subtilis; Lm – L. monocytogenes; Sa – S. aureus*

```
Bs LplJ  1    MLFIDNQNINDPRINLAIEEYCVKHLDPEQQYLLFYVNQPSIIIGKNQNTIEEINTKYVE  60
              M FI N NI DP +NLA+EEY +K+L  E+ Y LFY+N+PSII+GKNQNTIEE+N  Y++
Sa LplA1 1    MKFISNNNITDPTLNLAMEEYVLKNLPAEESYFLFYINRPSIIVGKNQNTIEEVNQTYID  60

Bs LplJ  61   ENGIIVVRRLSGGGAVYHDLGNLNFSFITKDDGDSFHNFKKFTEPVIQALHQLGVEAELS  120
               + I VVRR+SGGGAVYHD GNLNFSFIT DDG+SFHNF+KFTEP++QAL  LGV AEL+
Sa LplA1 61   AHNIDVVRRISGGGAVYHDTGNLNFSFITDDDGNSFHNFQKFTEPIVQALQSLGVNAELT  120

Bs LplJ  121  GRNDIVVDGRKISGNAQFATKGRIFSHGTLMFDSAIDHVVSALKVKKDKIESKGIKSIRS  180
              GRNDI V   KISGNA    K R+FSHGTLM +S +D V +ALKV   KI+SKGIKS+R
Sa LplA1 121  GRNDIQVGQAKISGNAMVKVKNRMFSHGTLMLNSDLDEVQNALKVNPAKIKSKGIKSVRK  180

Bs LplJ  181  RVANISEFLDDKMTTEEFRSHLLRHIFNTNDVGNVPEYKLTEKDWETIHQISKERYQNWD  240
              RVANI EFL+D +   EEF+  +L+ IF   +   V EYKLT++DWE I ++S ++Y+ W+
Sa LplA1 181  RVANIQEFLNDPLEIEEFKKIILKTIFGETE---VEEYKLTDEDWENIEKLSNDKYRTWE  237

Bs LplJ  241  WNYGRSPKFNLNHSKRYPVGSIDLHLEVKKGKIEDCKIFGDFFGVGDVSEIENLLVGKQY  300
              WNYGR+PK+N    +++  G + +  +VK+GKIE  KIFGDFFGVGDV+++EN LVG  +
Sa LplA1 238  WNYGRNPKYNFEREEKFEKGFVQIKFDVKRGKIEHAKIFGDFFGVGDVTDLENALVGCLH  297

Bs LplJ  301  ERSVIADVLEGVNLKHYFGNITKEDFLDLI  330
              +   I + L   +L HYFG+I + + + L+         57% Identity
Sa LplA1 298  DFEHIEEALSEYDLYHYFGDIDRHELIRLM  327



Bs LplJ  9    INDPRINLAIEEYCVKHLDPEQQYLLFYVNQPSIIIGKNQNTIEEINTKYVEENGIIVVR  68
              I D  I LA++ Y  +H+  ++  L  Y   P + IG+ QNT  E+N  Y++++ I VVR
Sa LplA2 13   ITDGAIALAMQVYVNQHIFLDEDILFPYYCDPKVEIGRFQNTAIEVNQDYIDKHSIQVVR  72

Bs LplJ  69   RLSGGGAVYHDLGNLNFSFITKDDGDSFHNFKKFTEPVIQALHQLGV-EAELSGRNDIVV  127
              R +GGGAVY D G +N   I + D   + +F++F +P I+ALH LG  +   SGRND+ +
Sa LplA2 73   RDTGGGAVYVDKGAVNMCCILEQDTSIYGDFQRFYQPAIKALHTLGATDVVQSGRNDLTL  132

Bs LplJ  128  DGRKISGNAQFATKGRIFSHGTLMFDSAIDHVVSALKVKKDKIESKGIKSIRSRVANISE  187
              +G+K+SG A      RI+   +L+ D   + +   LK  + KI SKGIKS+R+RV ++ E
Sa LplA2 133  NGKKVSGAAMTLMNNRIYGGYSLLLDVNYEAMDKVLKPNRKKIASKGIKSVRARVGHLRE  192

Bs LplJ  188  FLDDK---MTTEEFRSHLLRHIFNTNDVGNVPEYKLTEKDWETIHQISKERYQNWDWNYG  244
               LD+K   +T EEF++ ++  I   +D+     Y+LT+ DWE I +++ ++Y+NWDWNYG
Sa LplA2 193  ALDEKYRDITIEEFKNLMVTQILGIDDIKEAKRYELTDADWEAIDELADKKYKNWDWNYG  252

Bs LplJ  245  RSPKFNLNHSKRYPVGSIDLHLEVKKGKIEDCKIFGDFFGVGDVSEIENLLVGKQYERSV  304
              +SPK+  N S+R   G++D+ + V++ +I DC+I+GDFFG GD+ ++E  L G +  R
Sa LplA2 253  KSPKYEYNRSERLSSGTVDITISVEQNRIADCRIYGDFFGQGDIKDVEEALQGTKMTRED  312

Bs LplJ  305  IADVLEGVNLKHYFGNITKEDFLDLI  330
              +   L+ +++ +YF N+T E  +D+I             39% Identity
Sa LplA2 313  LTHQLKQLDIVYYFSNVTVEALVDMI  338
```

**Figure S1.** Amino Acid sequence alignment of lipoic acid biosynthesis and salvage enzymes.
*Bs – B. subtilis; Lm – L. monocytogenes; Sa – S. aureus*

```
Lm LplA1   1     MYFIDNNNEKDPRINLAVEEFILTELNLDEPVLLFYINKPSIIIGRNQNTVEEIDTEYVE  60
                 M FI NNN  DP +NLA+EE++L  L  +E   LFYIN+PSII+G+NQNT+EE++  Y++
Sa LplA1   1     MKFISNNNITDPTLNLAMEEYVLKNLPAEESYFLFYINRPSIIVGKNQNTIEEVNQTYID  60

Lm LplA1   61    KNDVIVVRRLSGGGAVYHDEGNLNFSFITEDDGESFHNFAKFTQPIVEALKRLGVNAELK  120
                  +++ VVRR+SGGGAVYHD GNLNFSFIT+DDG SFHNF KFT+PIV+AL+ LGVNAEL
Sa LplA1   61    AHNIDVVRRISGGGAVYHDTGNLNFSFITDDDGNSFHNFQKFTEPIVQALQSLGVNAELT  120

Lm LplA1   121   GRNDLLIDGFKVSGNAQFATKGKMFSHGTLMYDLNLDNVAASLKPRKDKIESKGIKSVRS  180
                 GRND+ +   K+SGNA    K +MFSHGTLM + +LD V  +LK    KI+SKGIKSVR
Sa LplA1   121   GRNDIQVGQAKISGNAMVKVKNRMFSHGTLMLNSDLDEVQNALKVNPAKIKSKGIKSVRK  180

Lm LplA1   181   RVANISDFMDQEMTTEEFRDLLLLYIFGVEKVEDVKEYKLTAADWEKIHEISAKRYGNWD  240
                 RVANI +F++  +  EEF+ ++L  IFG  +VE   EYKLT  DWE I ++S  +Y  W+
Sa LplA1   181   RVANIQEFLNDPLEIEEFKKIILKTIFGETEVE---EYKLTDEDWENIEKLSNDKYRTWE  237

Lm LplA1   241   WNYGKSPKFDLTRTKRFPVGAVDVRLNVQKGVITDIKIFGDFFGVKNVADIEEKLVNTTY  300
                 WNYG++PK++  R ++F  G V ++ +V++G I   KIFGDFFGV +V D+E  LV   +
Sa LplA1   238   WNYGRNPKYNFEREEKFEKGFVQIKFDVKRGKIEHAKIFGDFFGVGDVTDLENALVGCLH  297

Lm LplA1   301   KREVLAEALVDIDVKEYFGNITKDEFLDLL  330
                   E + EAL + D+  YFG+I + E + L+           53% Identity
Sa LplA1   298   DFEHIEEALSEYDLYHYFGDIDRHELIRLM  327
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```
Lm LplA1   1     MYFID--NNNE--KDPRINLAVEEFILTELNLDEPVLLFYINKPSIIIGRNQNTVEEIDT  56
                 MY I+   N E   D  I LA++ ++   + LDE +L  Y   P + IGR QNT  E++
Sa LplA2   1     MYLIEPIRNGEYITDGAIALAMQVYVNQHIFLDEDILFPYYCDPKVEIGRFQNTAIEVNQ  60

Lm LplA1   57    EYVEKNDVIVVRRLSGGGAVYHDEGNLNFSFITEDDGESFHNFAKFTQPIVEALKRLGVN  116
                 +Y++K+ + VVRR +GGGAVY D+G +N   I E D   + +F +F QP ++AL  LG
Sa LplA2   61    DYIDKHSIQVVRRDTGGGAVYVDKGAVNMCCILEQDTSIYGDFQRFYQPAIKALHTLGAT  120

Lm LplA1   117   AELK-GRNDLLIDGFKVSGNAQFATKGKMFSHGTLMYDLNLDNVAASLKPRKDKIESKGI  175
                   ++ GRNDL ++G KVSG A      +++   +L+ D+N + +   LKP + KI SKGI
Sa LplA2   121   DVVQSGRNDLTLNGKKVSGAAMTLMNNRIYGGYSLLLDVNYEAMDKVLKPNRKKIASKGI  180

Lm LplA1   176   KSVRSRVANISDFMDQ---EMTTEEFRDLLLLYIFGVEKVEDVKEYKLTAADWEKIHEIS  232
                 KSVR+RV ++ + +D+   ++T EEF++L++  I G++ +++ K Y+LT ADWE I E++
Sa LplA2   181   KSVRARVGHLREALDEKYRDITIEEFKNLMVTQILGIDDIKEAKRYELTDADWEAIDELA  240

Lm LplA1   233   AKRYGNWDWNYGKSPKFDLTRTKRFPVGAVDVRLNVQKGVITDIKIFGDFFGVKNVADIE  292
                  K+Y NWDWNYGKSPK++  R++R   G VD+ ++V++  I D +I+GDFFG  ++ D+E
Sa LplA2   241   DKKYKNWDWNYGKSPKYEYNRSERLSSGTVDITISVEQNRIADCRIYGDFFGQGDIKDVE  300

Lm LplA1   293   EKLVNTTYKREVLAEALVDIDVKEYFGNITKDEFLDLL  330
                 E L  T   RE L   L  +D+  YF N+T +  +D++       41% Identity
Sa LplA2   301   EALQGTKMTREDLTHQLKQLDIVYYFSNVTVEALVDMI  338
```

**Figure S1.** Amino Acid sequence alignment of lipoic acid biosynthesis and salvage enzymes.
*Bs – B. subtilis; Lm – L. monocytogenes; Sa – S. aureus*

```
Lm LplA2  1    MIYLDNEDVLDQAYNFAMEEYALRSLDENETYFMFYRMKPTIIVGKNQNTLEEINHPFVK  60
               M ++ N ++ D   N AMEEY L++L   E+YF+FY  +P+IIVGKNQNT+EE+N  ++
Sa LplA1  1    MKFISNNNITDPTLNLAMEEYVLKNLPAEESYFLFYINRPSIIVGKNQNTIEEVNQTYID  60

Lm LplA2  61   DHHIDVLRRLSGGGAVYNDEGNISFSMITKDDGNSFQNFAKFTEPVIRALRKLGVNAELS  120
                H+IDV+RR+SGGGAVY+D GN++FS IT DDGNSF NF KFTEP+++AL+ LGVNAEL+
Sa LplA1  61   AHNIDVVRRISGGGAVYHDTGNLNFSFITDDDGNSFHNFQKFTEPIVQALQSLGVNAELT  120

Lm LplA2  121  GRNDIEVNGKKISGNAQFATKGRLYSHGTLLFDVDLSMLEKALQVDPEKYLSKGVKSVRS  180
               GRNDI+V   KISGNA    K R++SHGTL+ + DL  ++ AL+V+P K  SKG+KSVR
Sa LplA1  121  GRNDIQVGQAKISGNAMVKVKNRMFSHGTLMLNSDLDEVQNALKVNPAKIKSKGIKSVRK  180

Lm LplA2  181  RVTTIREHLAEDIDILTFKQILLESIFETKDIPRYTFTEADKQGIEKLRTERYRNWDWTY  240
               RV  I+E L + ++I  FK+I+L++IF   ++  Y  T+ D + IEKL  ++YR W+W Y
Sa LplA1  181  RVANIQEFLNDPLEIEEFKKIILKTIFGETEVEEYKLTDEDWENIEKLSNDKYRTWEWNY  240

Lp LplA2  241  GKSPKATIKRKKRFPAGTIEFQVSLEKGQVKEATIYGDFFGTEDVAELAEKIIGCRFERK  300
               G++PK   +R+++F  G ++ +  +++G+++ A I+GDFFG  DV +L   ++GC  + +
Sa LplA1  241  GRNPKYNFEREEKFEKGFVQIKFDVKRGKIEHAKIFGDFFGVGDVTDLENALVGCLHDFE  300

Lm LplA2  301  SIQNAWQEINAKDYFGGIEKEAILDML  327
                I+ A  E +   YFG I++  ++ ++           47% Identity
Sa LplA1  301  HIEEALSEYDLYHYFGDIDRHELIRLM  327
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Lm LplA2  5    DNEDVLDQAYNFAMEEYALRSLDENETYFMFYRMKPTIIVGKNQNTLEEINHPFVKDHHI  64
               + E + D A   AM+ Y  + +  +E     Y   P + +G+ QNT  E+N  ++  H I
Sa LplA2  9    NGEYITDGAIALAMQVYVNQHIFLDEDILFPYYCDPKVEIGRFQNTAIEVNQDYIDKHSI  68

Lm LplA2  65   DVLRRLSGGGAVYNDEGNISFSMITKDDGNSFQNFAKFTEPVIRALRKLGVNAEL-SGRN  123
                V+RR +GGGAVY D+G ++   I + D + + +F +F +P I+AL  LG    + SGRN
Sa LplA2  69   QVVRRDTGGGAVYVDKGAVNMCCILEQDTSIYGDFQRFYQPAIKALHTLGATDVVQSGRN  128

Lm LplA2  124  DIEVNGKKISGNAQFATKGRLYSHGTLLFDVDLSMLEKALQVDPEKYLSKGVKSVRSRVT  183
               D+ +NGKK+SG A      R+Y   +LL DV+   ++K L+ + +K  SKG+KSVR+RV
Sa LplA2  129  DLTLNGKKVSGAAMTLMNNRIYGGYSLLLDVNYEAMDKVLKPNRKKIASKGIKSVRARVG  188

Lm LplA2  184  TIREHLAE---DIDILTFKQILLESIFETKDIP---RYTFTEADKQGIEKLRTERYRNWD  237
                +RE L E   DI I  FK +++  I    DI    RY  T+AD + I++L  ++Y+NWD
Sa LplA2  189  HLREALDEKYRDITIEEFKNLMVTQILGIDDIKEAKRYELTDADWEAIDELADKKYKNWD  248

Lm LplA2  238  WTYGKSPKATIKRKKRFPAGTIEFQVSLEKGQVKEATIYGDFFGTEDVAELAEKIIGCRF  297
               W YGKSPK    R +R  +GT++  +S+E+ ++ +  IYGDFFG  D+ ++ E + G +
Sa LplA2  249  WNYGKSPKYEYNRSERLSSGTVDITISVEQNRIADCRIYGDFFGQGDIKDVEEALQGTKM  308

Lm LplA2  298  ERKSIQNAWQEINAKDYFGGIEKEAILDMLF  328
                R+ + +  ++++   YF  +  EA++DM+            37% Identity
Sa LplA2  309  TREDLTHQLKQLDIVYYFSNVTVEALVDMIL  339
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