

Supplementary Information

Supplementary Table 1: List of 180 enzymes with valid EC numbers identified from the unique pathways of *Listeria monocytogenes* EGD-e

S.No.	ID	Enzyme Name and Definition
1	lmo:lmo1984	K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6] (RefSeq) ilvB; acetolactate synth
2	lmo:lmo1985	K01653 acetolactate synthase I/III small subunit [EC:2.2.1.6] (RefSeq) ilvH; acetolactate synthase
3	lmo:lmo1988	K00052 3-isopropylmalate dehydrogenase [EC:1.1.1.85] (RefSeq) leuB; 3-isopropylmalate dehydrogenas
4	lmo:lmo1989	K01703 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35] (RefS
5	lmo:lmo1990	K01704 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35] (RefS
6	lmo:lmo1992	K01575 acetolactate decarboxylase [EC:4.1.1.5] (RefSeq) alpha-acetolactate decarboxylase
7	lmo:lmo2006	K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6] (RefSeq) alsS; acetolactate synth
8	lmo:lmo0359	K01624 fructose-bisphosphate aldolase, class II [EC:4.1.2.13] (RefSeq) D-fructose-1,6-biphosphate
9	lmo:lmo0411	K01007 pyruvate, water dikinase [EC:2.7.9.2] (RefSeq) phosphoenolpyruvate synthase
10	lmo:lmo0830	K04041 fructose-1,6-bisphosphatase III [EC:3.1.3.11] (RefSeq) fbp; fructose-1,6-bisphosphatase
11	lmo:lmo1168	K00925 acetate kinase [EC:2.7.2.1] (RefSeq) AckA2; acetate kinase
12	lmo:lmo1571	K00850 6-phosphofructokinase 1 [EC:2.7.1.11] (RefSeq) pfkA; 6-phosphofructokinase
13	lmo:lmo1581	K00925 acetate kinase [EC:2.7.2.1] (RefSeq) ackA; acetate kinase
14	lmo:lmo2103	K00625 phosphate acetyltransferase [EC:2.3.1.8] (RefSeq) eutD; phosphotransacetylase
15	lmo:lmo2133	K01624 fructose-bisphosphate aldolase, class II [EC:4.1.2.13] (RefSeq) fructose-1,6-biphosphate al
16	lmo:lmo2134	K01624 fructose-bisphosphate aldolase, class II [EC:4.1.2.13] (RefSeq) fructose-1,6-biphosphate al
17	lmo:lmo2205	K01834 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11] (RefSeq) phosphogly
18	lmo:lmo2455	K01689 enolase [EC:4.2.1.11] (RefSeq) eno; phosphopyruvate hydratase
19	lmo:lmo2456	K15633 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12] (RefSeq) pgm; pho
20	lmo:lmo2539	K00600 glycine hydroxymethyltransferase [EC:2.1.2.1] (RefSeq) glyA; serine hydroxymethyltransferas
21	lmo:lmo2586	K00123 formate dehydrogenase major subunit [EC:1.17.1.9] (RefSeq) formate dehydrogenase subunit al
22	lmo:lmo2720	K01895 acetyl-CoA synthetase [EC:6.2.1.1] (RefSeq) acetate-CoA ligase
23	lmo:lmo2824	K00058 D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase [EC:1.1.1.95 1.1.1.399] (RefS

24	lmo:lmo28 25	K00831 phosphoserine aminotransferase [EC:2.6.1.52] (RefSeq) serC; phosphoserine aminotransferase
25	lmo:lmo04 46	K01442 choloylglycine hydrolase [EC:3.5.1.24] (RefSeq) penicillin acylase
26	lmo:lmo20 67	K01442 choloylglycine hydrolase [EC:3.5.1.24] (RefSeq) bile acid hydrolase
27	lmo:lmo02 65	K01439 succinyl-diaminopimelate desuccinylase [EC:3.5.1.18] (RefSeq) succinyl-diaminopimelate desu
28	lmo:lmo08 56	K01929 UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase [EC:6.3.2.10] (RefSeq) murF; UDP
29	lmo:lmo10 06	K00841 aminotransferase [EC:2.6.1.-] (RefSeq) aminotransferase
30	lmo:lmo10 11	K05822 tetrahydrodipicolinate N-acetyltransferase [EC:2.3.1.89] (RefSeq) tetrahydrodipicolinate su
31	lmo:lmo10 12	K05823 N-acetyldiaminopimelate deacetylase [EC:3.5.1.47] (RefSeq) N-acyl-L-amino acid amidohydrola
32	lmo:lmo12 35	K00928 aspartate kinase [EC:2.7.2.4] (RefSeq) aspartate kinase
33	lmo:lmo14 35	K01714 4-hydroxy-tetrahydrodipicolinate synthase [EC:4.3.3.7] (RefSeq) dapA; dihydrodipicolinate s
34	lmo:lmo14 36	K00928 aspartate kinase [EC:2.7.2.4] (RefSeq) aspartate kinase
35	lmo:lmo14 37	K00133 aspartate-semialdehyde dehydrogenase [EC:1.2.1.11] (RefSeq) aspartate-semialdehyde dehydrog
36	lmo:lmo15 88	K00821 acetylmuramoyl-N-succinyl-diaminopimelate aminotransferase [EC:2.6.1.11 2.6.1.17] (RefSeq)
37	lmo:lmo16 20	K01439 succinyl-diaminopimelate desuccinylase [EC:3.5.1.18] (RefSeq) dipeptidase PepV
38	lmo:lmo19 07	K00215 4-hydroxy-tetrahydrodipicolinate reductase [EC:1.17.1.8] (RefSeq) dapB; dihydrodipicolinate
39	lmo:lmo19 52	K01586 diaminopimelate decarboxylase [EC:4.1.1.20] (RefSeq) lysA; diaminopimelate decarboxylase
40	lmo:lmo20 18	K01778 diaminopimelate epimerase [EC:5.1.1.7] (RefSeq) dapF; diaminopimelate epimerase
41	lmo:lmo20 38	K01928 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase [EC:6.3.2.13] (RefSeq)
42	lmo:lmo23 74	K00928 aspartate kinase [EC:2.7.2.4] (RefSeq) aspartate kinase
43	lmo:lmo25 47	K00003 homoserine dehydrogenase [EC:1.1.1.3] (RefSeq) hom; homoserine dehydrogenase
44	lmo:lmo03 72	K05350 beta-glucosidase [EC:3.2.1.21] (RefSeq) beta-glucosidase
45	lmo:lmo17 29	K05349 beta-glucosidase [EC:3.2.1.21] (RefSeq) beta-glucosidase
46	lmo:lmo19 40	K01424 L-asparaginase [EC:3.5.1.1] (RefSeq) asparaginase
47	lmo:lmo27 81	K05349 beta-glucosidase [EC:3.2.1.21] (RefSeq) beta-glucosidase
48	lmo:lmo08 55	K01921 D-alanine-D-alanine ligase [EC:6.3.2.4] (RefSeq) ddl; D-alanyl-alanine synthetase A
49	lmo:lmo08 86	K01775 alanine racemase [EC:5.1.1.1] (RefSeq) dal; alanine racemase
50	lmo:lmo09 72	K14188 D-alanine--poly(phosphoribitol) ligase subunit 2 [EC:6.1.1.13] (RefSeq) dltC; D-alanine--po

51	lmo:lmo09 74	K03367 D-alanine--poly(phosphoribitol) ligase subunit 1 [EC:6.1.1.13] (RefSeq) dltA; D-alanine--po
52	lmo:lmo16 19	K00824 D-alanine transaminase [EC:2.6.1.21] (RefSeq) daaA; D-amino acid aminotransferase
53	lmo:lmo14 20	K00075 UDP-N-acetylmuramate dehydrogenase [EC:1.3.1.98] (RefSeq) murB; UDP-N-acetylenolpyruvoylglu
54	lmo:lmo14 64	K00887 undecaprenol kinase [EC:2.7.1.66] (RefSeq) diacylglycerol kinase
55	lmo:lmo16 05	K01924 UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8] (RefSeq) murC; UDP-N-acetylmuramate--L-al
56	lmo:lmo16 23	K19302 undecaprenyl-diphosphatase [EC:3.6.1.27] (RefSeq) hypothetical protein
57	lmo:lmo18 55	K07260 zinc D-Ala-D-Ala carboxypeptidase [EC:3.4.17.14] (RefSeq) D-alanyl-D-alanine carboxypeptida
58	lmo:lmo18 92	K05366 penicillin-binding protein 1A [EC:2.4.1.129 3.4.16.4] (RefSeq) pbpA; penicillin-binding pro
59	lmo:lmo20 17	K19302 undecaprenyl-diphosphatase [EC:3.6.1.27] (RefSeq) hypothetical protein
60	lmo:lmo20 36	K01925 UDP-N-acetylmuramoylalanine--D-glutamate ligase [EC:6.3.2.9] (RefSeq) murD; UDP-N-acetylmur
61	lmo:lmo20 37	K01000 phospho-N-acetylmuramoyl-pentapeptide-transferase [EC:2.7.8.13] (RefSeq) mraY; phospho-N-ac
62	lmo:lmo22 29	K12555 penicillin-binding protein 2A [EC:2.4.1.129 3.4.16.4] (RefSeq) penicillin-binding protein
63	lmo:lmo25 26	K00790 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7] (RefSeq) murA; UDP-N-acetylgl
64	lmo:lmo25 52	K00790 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7] (RefSeq) murZ; UDP-N-acetylgl
65	lmo:lmo27 54	K07258 serine-type D-Ala-D-Ala carboxypeptidase (penicillin-binding protein 5/6) [EC:3.4.16.4] (Re
66	lmo:lmo10 81	K00973 glucose-1-phosphate thymidyltransferase [EC:2.7.7.24] (RefSeq) glucose-1-phosphate thymid
67	lmo:lmo10 82	K01790 dTDP-4-dehydrorhamnose 3,5-epimerase [EC:5.1.3.13] (RefSeq) dTDP-sugar epimerase
68	lmo:lmo10 83	K01710 dTDP-glucose 4,6-dehydratase [EC:4.2.1.46] (RefSeq) dTDP-D-glucose 4,6-dehydratase
69	lmo:lmo10 84	K00067 dTDP-4-dehydrorhamnose reductase [EC:1.1.1.133] (RefSeq) DTDP-L-rhamnose synthetase
70	lmo:lmo12 59	K00147 glutamate-5-semialdehyde dehydrogenase [EC:1.2.1.41] (RefSeq) proA; gamma-glutamyl phosphat
71	lmo:lmo12 60	K00931 glutamate 5-kinase [EC:2.7.2.11] (RefSeq) proB; gamma-glutamyl kinase
72	lmo:lmo10 66	K01092 myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25] (RefSeq) myo-inositol-1(or 4)-monophosph
73	lmo:lmo13 39	K00845 glucokinase [EC:2.7.1.2] (RefSeq) glucose kinase
74	lmo:lmo24 75	K01835 phosphoglucomutase [EC:5.4.2.2] (RefSeq) phosphoglucomutase
75	lmo:lmo18 97	K00812 aspartate aminotransferase [EC:2.6.1.1] (RefSeq) aspB; aspartate aminotransferase
76	lmo:lmo19 24	K04517 prephenate dehydrogenase [EC:1.3.1.12] (RefSeq) tyrA; prephenate dehydrogenase
77	lmo:lmo19 25	K00817 histidinol-phosphate aminotransferase [EC:2.6.1.9] (RefSeq) hisC; histidinol-phosphate amin

78	lmo:lmo06 46	K07104 catechol 2,3-dioxygenase [EC:1.13.11.2] (RefSeq) hypothetical protein
79	lmo:lmo14 14	K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9] (RefSeq) acetyl-CoA:acetyltransferase
80	lmo:lmo25 64	K01821 4-oxalocrotonate tautomerase [EC:5.3.2.6] (RefSeq) 4-oxalocrotonate isomerase
81	lmo:lmo08 49	K01426 amidase [EC:3.5.1.4] (RefSeq) amidase
82	lmo:lmo13 81	K01512 acylphosphatase [EC:3.6.1.7] (RefSeq) acylphosphatase
83	lmo:lmo24 01	K01101 4-nitrophenyl phosphatase [EC:3.1.3.41] (RefSeq) hypothetical protein
84	lmo:lmo16 34	K04072 acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1] (RefSeq) bifunctio
85	lmo:lmo21 72	K01026 propionate CoA-transferase [EC:2.8.3.1] (RefSeq) propionate CoA-transferase
86	lmo:lmo00 21	K02793 PTS system, mannose-specific IIA component [EC:2.7.1.191] (RefSeq) PTS fructose transporter
87	lmo:lmo00 22	K02794 PTS system, mannose-specific IIB component [EC:2.7.1.191] (RefSeq) PTS fructose transporter
88	lmo:lmo00 27	K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucos
89	lmo:lmo00 96	K02793 PTS system, mannose-specific IIA component [EC:2.7.1.191] K02794 PTS system, mannose-specific
90	lmo:lmo02 99	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-gl
91	lmo:lmo03 01	K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-gl
92	lmo:lmo03 57	K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS sugar transporter s
93	lmo:lmo03 58	K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] K02770 PTS system, fructose-specif
94	lmo:lmo03 74	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-gl
95	lmo:lmo03 98	K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS sugar transporter s
96	lmo:lmo03 99	K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] (RefSeq) PTS fructose transporte
97	lmo:lmo04 26	K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS fructose transporte
98	lmo:lmo04 27	K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] (RefSeq) PTS fructose transporte
99	lmo:lmo05 03	K02773 PTS system, galactitol-specific IIA component [EC:2.7.1.200] (RefSeq) PTS fructose transpor
100	lmo:lmo05 07	K02774 PTS system, galactitol-specific IIB component [EC:2.7.1.200] (RefSeq) PTS galactitol transp
101	lmo:lmo05 42	K02781 PTS system, glucitol/sorbitol-specific IIA component [EC:2.7.1.198] (RefSeq) PTS sorbitol t
102	lmo:lmo05 43	K02782 PTS system, glucitol/sorbitol-specific IIB component [EC:2.7.1.198] K02783 PTS system, glucit
103	lmo:lmo06 31	K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS fructose transporte
104	lmo:lmo07 38	K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucos

105	lmo:lmo07 83	K02794 PTS system, mannose-specific IIB component [EC:2.7.1.191] (RefSeq) PTS mannose transporter
106	lmo:lmo07 84	K02793 PTS system, mannose-specific IIA component [EC:2.7.1.191] (RefSeq) PTS mannose transporter
107	lmo:lmo08 74	K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS sugar t
108	lmo:lmo08 75	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-gl
109	lmo:lmo09 14	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS sugar t
110	lmo:lmo09 16	K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS sugar t
111	lmo:lmo10 03	K08483 phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9] (RefSeq) phosphotransferase system e
112	lmo:lmo10 17	K02777 PTS system, sugar-specific IIA component [EC:2.7.1.-] (RefSeq) PTS glucose transporter subu
113	lmo:lmo10 35	K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucos
114	lmo:lmo10 95	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbio
115	lmo:lmo12 55	K02818 PTS system, trehalose-specific IIB component [EC:2.7.1.201] K02819 PTS system, trehalose-spec
116	lmo:lmo17 19	K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS lichena
117	lmo:lmo17 20	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS lichena
118	lmo:lmo19 72	K02822 PTS system, ascorbate-specific IIB component [EC:2.7.1.194] (RefSeq) PTS pentitol transport
119	lmo:lmo19 73	K02821 PTS system, ascorbate-specific IIA component [EC:2.7.1.194] (RefSeq) PTS sugar transporter
120	lmo:lmo19 97	K02793 PTS system, mannose-specific IIA component [EC:2.7.1.191] (RefSeq) PTS mannose transporter
121	lmo:lmo20 02	K19507 PTS system, fructoselysine/glucoselysine-specific IIB component [EC:2.7.1.-] (RefSeq) PTS m
122	lmo:lmo20 97	K02774 PTS system, galactitol-specific IIB component [EC:2.7.1.200] (RefSeq) PTS galacticol transp
123	lmo:lmo20 98	K02773 PTS system, galactitol-specific IIA component [EC:2.7.1.200] (RefSeq) PTS galacticol transp
124	lmo:lmo21 36	K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] (RefSeq) PTS fructose transporte
125	lmo:lmo21 37	K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS fructose transporte
126	lmo:lmo22 59	K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-gl
127	lmo:lmo23 35	K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] K02769 PTS system, fructose-specif
128	lmo:lmo23 73	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-gl
129	lmo:lmo26 50	K02822 PTS system, ascorbate-specific IIB component [EC:2.7.1.194] (RefSeq) MFS transporter
130	lmo:lmo26 51	K02798 PTS system, mannitol-specific IIA component [EC:2.7.1.197] (RefSeq) PTS mannitol transporte
131	lmo:lmo26 66	K02774 PTS system, galactitol-specific IIB component [EC:2.7.1.200] (RefSeq) PTS galacticol transp

132	lmo:lmo26 67	K02773 PTS system, galactitol-specific IIA component [EC:2.7.1.200] (RefSeq) PTS galacticol transp
133	lmo:lmo26 83	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbio
134	lmo:lmo26 85	K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbio
135	lmo:lmo27 33	K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] K02769 PTS system, fructose-specif
136	lmo:lmo27 62	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbio
137	lmo:lmo27 65	K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbio
138	lmo:lmo27 72	K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucos
139	lmo:lmo27 80	K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbio
140	lmo:lmo27 82	K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbio
141	lmo:lmo27 87	K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucos
142	lmo:lmo27 97	K02798 PTS system, mannitol-specific IIA component [EC:2.7.1.197] (RefSeq) PTS mannitol transporte
143	lmo:lmo27 99	K02799 PTS system, mannitol-specific IIB component [EC:2.7.1.197] K02800 PTS system, mannitol-specif
144	lmo:lmo05 83	K03070 preprotein translocase subunit SecA [EC:7.4.2.8] (RefSeq) azi, div; preprotein translocase
145	lmo:lmo18 01	K03106 signal recognition particle subunit SRP54 [EC:3.6.5.4] (RefSeq) ffh; signal recognition par
146	lmo:lmo25 10	K03070 preprotein translocase subunit SecA [EC:7.4.2.8] (RefSeq) secA; preprotein translocase subu
147	lmo:lmo00 50	K07706 two-component system, LytTR family, sensor histidine kinase AgrC [EC:2.7.13.3] (RefSeq) his
148	lmo:lmo02 88	K07652 two-component system, OmpR family, sensor histidine kinase VicK [EC:2.7.13.3] (RefSeq) two-
149	lmo:lmo02 92	K04771 serine protease Do [EC:3.4.21.107] (RefSeq) heat-shock protein htrA serine protease
150	lmo:lmo03 55	K00244 fumarate reductase flavoprotein subunit [EC:1.3.5.4] (RefSeq) fumarate reductase subunit A
151	lmo:lmo06 83	K00575 chemotaxis protein methyltransferase CheR [EC:2.1.1.80] (RefSeq) chemotaxis protein CheR
152	lmo:lmo06 92	K03407 two-component system, chemotaxis family, sensor kinase CheA [EC:2.7.13.3] (RefSeq) cheA; tw
153	lmo:lmo09 38	K01104 protein-tyrosine phosphatase [EC:3.1.3.48] (RefSeq) protein-tyrosine-phosphatase
154	lmo:lmo10 21	K11617 two-component system, NarL family, sensor histidine kinase LiaS [EC:2.7.13.3] (RefSeq) two-
155	lmo:lmo10 61	K18345 two-component system, OmpR family, sensor histidine kinase VanS [EC:2.7.13.3] (RefSeq) two-
156	lmo:lmo12 99	K01915 glutamine synthetase [EC:6.3.1.2] (RefSeq) glnA; glutamine synthetase
157	lmo:lmo16 95	K14205 phosphatidylglycerol lysyltransferase [EC:2.3.2.3] (RefSeq) hypothetical protein
158	lmo:lmo18 00	K01104 protein-tyrosine phosphatase [EC:3.1.3.48] (RefSeq) protein-tyrosine phosphatase

159	lmo:lmo19 15	K00027 malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38] (RefSeq) malate dehydroge
160	lmo:lmo19 35	K01104 protein-tyrosine phosphatase [EC:3.1.3.48] (RefSeq) protein-tyrosine/serine phosphatase
161	lmo:lmo19 47	K07651 two-component system, OmpR family, sensor histidine kinase ResE [EC:2.7.13.3] (RefSeq) resE
162	lmo:lmo20 11	K07718 two-component system, sensor histidine kinase YesM [EC:2.7.13.3] (RefSeq) two-component sen
163	lmo:lmo25 00	K07636 two-component system, OmpR family, phosphate regulon sensor histidine kinase PhoR [EC:2.7.13.3]
164	lmo:lmo25 37	K01791 UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing) [EC:5.1.3.14] (RefSeq) UDP-N-acetylgl
165	lmo:lmo26 79	K07646 two-component system, OmpR family, sensor histidine kinase KdpD [EC:2.7.13.3] (RefSeq) hist
166	lmo:lmo26 81	K01547 potassium-transporting ATPase ATP-binding subunit [EC:7.2.2.6] (RefSeq) kdpB; potassium-tra
167	lmo:lmo27 17	K00426 cytochrome bd ubiquinol oxidase subunit II [EC:7.1.1.7] (RefSeq) cydB; cytochrome D ubiquin
168	lmo:lmo27 18	K00425 cytochrome bd ubiquinol oxidase subunit I [EC:7.1.1.7] (RefSeq) cydA; cytochrome D ubiquino
169	lmo:lmo02 05	K01114 phospholipase C [EC:3.1.4.3] (RefSeq) plcB; phospholipase C
170	lmo:lmo04 47	K01580 glutamate decarboxylase [EC:4.1.1.15] (RefSeq) glutamate decarboxylase
171	lmo:lmo05 39	K01635 tagatose 1,6-diphosphate aldolase [EC:4.1.2.40] (RefSeq) tagatose 1,6-diphosphate aldolase
172	lmo:lmo12 88	K07173 S-ribosylhomocysteine lyase [EC:4.4.1.21] (RefSeq) S-ribosylhomocysteinase
173	lmo:lmo16 32	K01658 anthranilate synthase component II [EC:4.1.3.27] (RefSeq) trpG; anthranilate synthase subun
174	lmo:lmo16 33	K01657 anthranilate synthase component I [EC:4.1.3.27] (RefSeq) trpE; anthranilate synthase subuni
175	lmo:lmo23 63	K01580 glutamate decarboxylase [EC:4.1.1.15] (RefSeq) glutamate decarboxylase
176	lmo:lmo24 34	K01580 glutamate decarboxylase [EC:4.1.1.15] (RefSeq) glutamate decarboxylase
177	lmo:lmo07 16	K02412 flagellum-specific ATP synthase [EC:7.4.2.8] (RefSeq) fliI; flagellum-specific ATP synthase
178	lmo:lmo27 45	K18104 ATP-binding cassette, subfamily B, bacterial AbcA/BmrA [EC:7.6.2.2] (RefSeq) ABC transporte
179	lmo:lmo01 29	K01448 N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28] (RefSeq) N-acetylmuramoyl-L-alanine amidas
180	lmo:lmo15 21	K01448 N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28] (RefSeq) N-acetylmuramoyl-L-alanine amidas

Supplementary Table 2: List of pathogen-host non-homologous proteins/enzymes
120 enzyme sequences revealed $\leq 35\%$ identity with human proteome, and 52 enzyme sequences did not show any hit against the human proteome

NOTE: Highlighted IDs denote the enzymes/proteins with no hits against *Homo sapiens*

S. No.	qseqid	sseqid	qstart	qend	qlen	sstart	send	slen	length	eval	bitscore	score	percent
1	lmo:lmo1985	XP_016879227.1	52	135	163	30	104	385	85	5.9	29.3	64	27.06
2	lmo:lmo1988	NP_004647.1	87	143	350	566	621	729	61	2.5	32.3	72	42.62
3	lmo:lmo1990	NP_001307870.1	70	145	193	592	667	713	77	1.2	32	71	25.97
4	lmo:lmo2006	XP_011536566.1	393	540	565	122	276	2249	163	3.2	33.1	74	26.99
5	lmo:lmo0411	XP_005267356.1	413	465	530	544	550	5695	58	9.2	31.2	69	32.76
6	lmo:lmo1168	XP_016869984.1	4	153	397	207	222	269	158	2.5	32.7	73	24.05
7	lmo:lmo1571	NP_057506.2	205	263	319	13	77	230	65	2.3	32.3	72	32.31
8	lmo:lmo2133	XP_011539873.1	245	299	299	492	550	626	59	0.26	35.4	80	33.9
9	lmo:lmo2134	XP_005260342.2	182	251	284	243	315	602	73	9.9	30	66	23.29
10	lmo:lmo2205	XP_011536319.1	150	205	229	228	234	4477	62	0.63	33.5	75	32.26
11	lmo:lmo2455	XP_005269872.1	4	94	430	68	161	423	95	0.63	34.7	78	26.32
12	lmo:lmo2456	NP_937793.1	408	508	510	288	382	536	105	0.49	35.4	80	27.62
13	lmo:lmo2586	XP_005270619.2	131	202	995	864	925	953	72	4.8	33.5	75	26.39
14	lmo:lmo2720	XP_016871813.1	164	191	525	304	331	715	28	3.3	32.7	73	50
15	lmo:lmo2825	XP_011514441.1	148	201	363	206	259	379	54	2.8	32.3	72	29.63
16	lmo:lmo0265	NP_001155052.1	33	96	379	264	327	359	64	7.2	31.2	69	28.12
17	lmo:lmo0856	NP_005129.2	74	138	457	155	212	266	65	3	32.7	73	30.77
18	lmo:lmo1006	NP_001893.2	100	202	381	92	190	405	106	0.65	34.7	78	26.42
19	lmo:lmo1011	XP_011511568.1	124	192	236	71	129	442	69	0.95	33.1	74	31.88
20	lmo:lmo1012	XP_011511763.1	50	124	371	466	540	584	76	9.3	30.8	68	30.26
21	lmo:lmo1435	XP_011514727.1	145	228	293	24	104	336	87	2.8	32	71	22.99
22	lmo:lmo1437	NP_001243728.1	37	190	347	14	166	293	163	1.2	33.5	75	24.54
23	lmo:lmo1588	XP_016884166.1	148	304	386	176	336	419	169	9.9	30.8	68	26.04

24	lmo:lmo 1620	XP_011535 858.1	38	103	47 0	412	481	81 9	70	9.1	31.2	69	27.1 4
25	lmo:lmo 1907	XP_006712 097.1	59	152	26 3	149 8	158 9	20 70	99	6	30.4	67	25.2 5
26	lmo:lmo 1952	NP_872198 .1	3	149	43 6	49	188	54 9	151	3.2	32.3	72	28.4 8
27	lmo:lmo 2018	NP_001243 728.1	46	193	32 9	69	213	29 3	155	0.94	33.9	76	26.4 5
28	lmo:lmo 2038	XP_016860 602.1	101	140	49 1	126	165	16 5	40	1.9	33.5	75	45
29	lmo:lmo 0372	XP_011516 104.1	63	171	48 0	73	177	51 7	118	9.1	31.2	69	27.1 2
30	lmo:lmo 1729	XP_006717 260.1	306	357	72 3	42	91	92 4	52	1.1	35	79	34.6 2
31	lmo:lmo 1940	NP_001307 279.1	104	138	32 0	127 2	130 2	15 53	35	2.2	32.3	72	40
32	lmo:lmo 0855	NP_942131 .1	124	321	37 0	264	476	23 83	231	9.9	30.4	67	19.4 8
33	lmo:lmo 0886	NP_085125 .1	275	321	36 8	364	412	50 4	49	2.3	32.7	73	32.6 5
34	lmo:lmo 0972	XP_016869 827.1	5	68	78 78	121	188	74 4	68	9.9	27.3	59	27.9 4
35	lmo:lmo 0974	XP_016882 823.1	154	173	51 0	227	246	61 0	20	5.2	32	71	65
36	lmo:lmo 1619	XP_016870 516.1	110	161	28 9	164	215	27 3	52	4.6	31.2	69	30.7 7
37	lmo:lmo 1605	NP_002891 .1	48	100	44 7	593	642	12 47	53	5.2	32	71	33.9 6
38	lmo:lmo 1623	NP_808211 .1	117	189	21 7	178	253	30 9	81	8.3	29.6	65	33.3 3
39	lmo:lmo 1855	XP_011528 468.1	59	128	27 4	18	87	19 5	70	9.5	30	66	22.8 6
40	lmo:lmo 1892	NP_001138 409.1	748	819	82 7	203	279	73 3	78	9.2	32	71	33.3 3
41	lmo:lmo 2017	NP_997182 .1	124	199	23 1	188	266	32 5	80	6.5	30	66	28.7 5
42	lmo:lmo 2036	XP_016859 830.1	258	328	45 5	101	168	44 69	71	1.5	33.9	76	26.7 6
43	lmo:lmo 2037	XP_016872 784.1	167	287	32 4	9	136	23 6	128	0.09 4	37	84	25
44	lmo:lmo 2754	XP_011537 127.1	169	208	44 5	508	547	10 73	40	9.3	31.2	69	42.5
45	lmo:lmo 1081	XP_011517 219.1	84	124	28 8	636	675	74 3	41	8.7	30.4	67	34.1 5
46	lmo:lmo 1082	NP_653213 .6	68	182	18 6	41	146	22 11	117	6.2	29.6	65	26.5
47	lmo:lmo 1083	XP_011544 263.1	4	161	32 8	13	170	36 9	172	0.04 1	38.1	87	27.9 1
48	lmo:lmo 1084	XP_011544 263.1	56	155	27 6	84	197	36 9	116	1.7	32.3	72	27.5 9
49	lmo:lmo 1259	XP_016879 847.1	113	333	41 5	101	354	42 4	264	1.4	33.5	75	21.9 7
50	lmo:lmo 1260	XP_006724 581.1	107	161	27 6	136	190	60 4	55	2.9	31.6	70	29.0 9

51	lmo:lmo 1066	NP_001290 542.1	112	147	25 7	66	100	11 3	36	3.7	31.2	69	38.8 9
52	lmo:lmo 1339	NP_001177 312.1	6	31	32 2	410	435	64 8	26	7.9	30.4	67	46.1 5
53	lmo:lmo 2475	NP_001186 847.1	305	548	57 6	195	426	44 1	253	8.2	31.6	70	24.5 1
54	lmo:lmo 1897	XP_011529 539.1	80	128	39 3	750	799	14 00	50	6.4	31.2	69	28
55	lmo:lmo 1924	NP_055204 .3	205	264	36 7	191	251	11 80	61	3.5	32	71	32.7 9
56	lmo:lmo 1925	NP_694574 .3	16	107	36 0	122	218	89 6	99	4.9	31.6	70	28.2 8
57	lmo:lmo 0646	NP_115990 .3	171	201	27 9	48	78	17 6	31	2.4	32	71	41.9 4
58	lmo:lmo 1414	XP_016879 152.1	127	177	38 9	838	887	12 47	51	9	30.8	68	35.2 9
59	lmo:lmo 0849	NP_001432 .2	195	367	61 6	100	266	57 9	175	2.1	33.9	76	28
60	lmo:lmo 1381	NP_001289 545.1	10	45	93 14	49	99	36 6	28.1	61	41.6 7		
61	lmo:lmo 2401	XP_011533 938.1	89	186	25 5	226 4	236 3	52 42	106	1.4	32.7	73	28.3
62	lmo:lmo 1634	NP_958831 .1	240	346	86 6	486	588	10 13	108	4.6	33.1	74	29.6 3
63	lmo:lmo 0021	NP_705838 .3	46	87	13 3	640	681	40 69	42	8.7	27.7	60	33.3 3
64	lmo:lmo 0022	XP_005266 118.1	107	145	16 2	267	305	49 8	39	3.8	30	66	35.9
65	lmo:lmo 0096	XP_016883 830.1	252	321	32 1	229	297	70 0	70	3.2	32	71	30
66	lmo:lmo 0301	NP_001181 988.1	44	105	11 3	357	419	44 0	63	9.9	27.3	59	30.1 6
67	lmo:lmo 0357	NP_015563 .2	106	142	14 8	581	617	13 66	37	3.3	29.6	65	40.5 4
68	lmo:lmo 0398	XP_016883 585.1	78	143	15 2	198	263	85 6	69	2.6	30	66	26.0 9
69	lmo:lmo 0426	XP_016867 690.1	9	137	15 4	130 7	142 1	18 10	136	2.9	30	66	26.4 7
70	lmo:lmo 0503	XP_005264 612.1	37	103	15 5	455	522	22 42	70	1.9	30.8	68	31.4 3
71	lmo:lmo 0507	XP_016883 551.1	4	78	97 406	474	59 9	77	5.4	28.5	62	29.8 7	
72	lmo:lmo 0542	NP_056485 .2	10	75	11 6	329	400	57 4	72	8.5	27.7	60	25
73	lmo:lmo 0631	XP_016859 677.1	11	62	15 0	6	60	47 4	55	8.8	28.5	62	27.2 7
74	lmo:lmo 0874	XP_005251 910.1	10	98	10 9	409	492	18 39	89	9.8	27.3	59	28.0 9
75	lmo:lmo 0875	XP_011539 161.1	3	42	11 1	19	58	10 44	40	9.8	27.3	59	32.5
76	lmo:lmo 0916	NP_001280 744.1	37	116	11 6	249	324	40 5	80	5.4	28.5	62	26.2 5
77	lmo:lmo 1003	XP_011531 514.1	318	371	57 2	549	602	19 34	54	7.4	32	71	24.0 7

78	lmo:lmo 1095	XP_011509 486.1	7	43	13 4	326 8	330 2	38 92	37	4.8	28.9	63	40.5 4
79	lmo:lmo 1719	XP_011518 725.1	25	84	10 0	676	735	80 9	60	4.4	28.5	62	31.6 7
80	lmo:lmo 1972	NP_001014 451.1	45	91	93	235	280	44 8	47	1.8	30	66	36.1 7
81	lmo:lmo 1973	NP_001099 050.1	50	122	14 7	17	103	46 7	87	2.3	30	66	25.2 9
82	lmo:lmo 2002	XP_011532 356.1	18	73	15 5	442	519	63 1	78	6.1	28.9	63	26.9 2
83	lmo:lmo 2097	XP_016857 214.1	16	87	91	431	499	53 0	78	4	28.9	63	33.3 3
84	lmo:lmo 2098	XP_016864 027.1	32	117	15 5	865	961	98 3	98	1.4	31.2	69	21.4 3
85	lmo:lmo 2136	NP_003095 .2	4	101	10 3	160	240	35 7	102	3.8	28.9	63	26.4 7
86	lmo:lmo 2259	NP_001265 430.1	59	107	11 6	45	86	12 6	49	5.3	28.5	62	32.6 5
87	lmo:lmo 2335	XP_016870 629.1	149	220	63 2	380	447	62 5	72	4.3	32.7	73	26.3 9
88	lmo:lmo 2667	XP_005260 522.1	47	137	15 4	59	158	14 95	102	3.5	29.6	65	26.4 7
89	lmo:lmo 2685	XP_016866 342.1	35	100	10 0	182 2	187 0	19 16	66	7.7	27.7	60	30.3
90	lmo:lmo 2765	NP_001230 075.1	30	97	10 2	3	68	66 7	68	9.5	27.7	60	27.9 4
91	lmo:lmo 2787	NP_872353 .2	32	105	64 0	99	172	22 7	74	5.7	32.3	72	27.0 3
92	lmo:lmo 0583	NP_055644 .2	77	208	77 6	398	535	10 31	142	3	33.5	75	26.0 6
93	lmo:lmo 1801	XP_011521 490.1	123	283	45 0	327	490	56 3	170	6	31.6	70	22.3 5
94	lmo:lmo 2510	XP_016879 601.1	407	543	83 7	314	443	77 5	139	9.8	32	71	28.0 6
95	lmo:lmo 0288	XP_016880 076.1	232	294	61 0	284	346	84 8	63	9.3	31.6	70	25.4
96	lmo:lmo 0292	XP_011515 122.1	422	455	50 0	524	557	66 4	34	9.7	31.2	69	44.1 2
97	lmo:lmo 0355	XP_011521 492.1	44	130	50 6	29	111	67 9	88	6.6	31.6	70	28.4 1
98	lmo:lmo 0692	NP_079478 .1	292	353	61 8	64	129	23 9	66	4	32.7	73	28.7 9
99	lmo:lmo 0938	NP_065846 .1	8	88	15 2	270	351	83 5	91	7.6	28.5	62	24.1 8
100	lmo:lmo 1021	NP_001073 867.1	162	235	35 2	833	913	20 17	84	3.2	32	71	36.9
101	lmo:lmo 1061	XP_016863 503.1	199	320	48 1	776	876	14 79	122	9.8	31.2	69	21.3 1
102	lmo:lmo 1299	NP_001137 412.1	18	97	44 4	85	173	20 8	92	0.02 7	39.3	90	25
103	lmo:lmo 1695	XP_006720 831.1	240	303	86 5	516	578	98 5	65	8.8	32.3	72	29.2 3
104	lmo:lmo 1800	NP_004081 .1	114	196	29 8	49	131	18 5	88	1.2	33.1	74	35.2 3

Supplementary Table 3: List of essential pathogen-host non-homologous proteins
 98 enzymes were found to be essential out of the 172 pathogen-host non-homologous enzymes of *Listeria monocytogenes*

NOTE: Filtering criteria $evalue < 1e-10$, $bitscore \geq 100$ and percentage identity > 30

S. No.	qseqid	sseqid	qstart	qend	qlen	sstart	send	slen	length	evalue	bitscore	score	percent
1	lmo:lmo0830	DEG10390097	5	653	653	15	664	665	650	0	692	1785	51.85
2	lmo:lmo2455	DEG10010237	1	430	430	1	430	430	430	0	723	1867	81.4
3	lmo:lmo2456	DEG10010238	1	510	510	1	511	511	511	0	730	1885	68.1
4	lmo:lmo2586	DEG10470294	5	972	999	6	973	979	970	0	1350	3495	64.95
5	lmo:lmo2526	DEG10010252	1	418	430	1	419	436	419	0	632	1631	72.55
6	lmo:lmo1634	DEG10110101	7	865	866	2	864	892	872	0	803	2073	48.62
7	lmo:lmo1003	DEG10020092	1	569	572	1	570	572	570	0	835	2157	69.65
8	lmo:lmo0583	DEG10010243	8	751	776	13	761	841	754	0	643	1659	45.89
9	lmo:lmo1801	DEG10010123	1	450	450	1	445	446	450	0	706	1823	81.56
10	lmo:lmo2510	DEG10470461	1	834	837	1	832	835	835	0	1201	3107	69.34
11	lmo:lmo1299	DEG10170172	4	444	444	6	446	446	441	0	716	1847	75.51
12	lmo:lmo2681	DEG10470071	2	675	681	29	692	696	675	0	761	1966	57.78
13	lmo:lmo0288	DEG10010262	1	610	610	1	609	611	613	1.00E-178	622	1603	50.24
14	lmo:lmo2475	DEG10370134	1	570	576	1	567	572	570	2.00E-178	621	1601	52.98
15	lmo:lmo2335	DEG10470314	1	629	632	1	616	618	634	3.00E-174	607	1566	52.21
16	lmo:lmo1581	DEG10020202	5	393	397	6	396	400	391	2.00E-168	587	1512	71.61
17	lmo:lmo1605	DEG10010217	1	431	447	1	431	432	431	6.00E-167	582	1501	61.72
18	lmo:lmo2038	DEG10010102	18	485	491	19	486	494	469	3.00E-164	573	1478	60.13
19	lmo:lmo0974	DEG10470127	5	509	510	3	503	504	507	2.00E-154	541	1393	50.69
20	lmo:lmo2537	DEG10470464	3	368	379	4	369	371	366	7.00E-150	525	1353	67.49
21	lmo:lmo2036	DEG10210060	1	449	455	1	448	450	450	4.00E-147	517	1331	56.67
22	lmo:lmo1437	DEG10470330	3	347	347	5	348	348	345	3.00E-142	499	1286	68.7
23	lmo:lmo1695	DEG10470134	8	842	865	2	857	873	865	1.00E-136	483	1242	34.57

24	lmo:lmo 1897	DEG1047 0142	3	393	39 3	1	390	39 5	391	1.00E- 131	465	119 6	58.3 1
25	lmo:lmo 1081	DEG1042 0194	1	288	28 8	1	288	28 9	288	7.00E- 131	462	118 8	76.3 9
26	lmo:lmo 1012	DEG1001 0094	2	364	37 1	3	365	37 4	363	5.00E- 129	456	117 3	60.6 1
27	lmo:lmo 1235	DEG1047 0164	1	400	40 4	1	398	40 9	400	2.00E- 128	454	116 9	
28	lmo:lmo 1571	DEG1001 0211	1	319	31 9	1	319	31 9	319	4.00E- 127	449	115 6	68.6 5
29	lmo:lmo 2552	DEG1007 0059	4	413	42 3	3	414	41 9	412	4.00E- 126	447	114 9	58.0 1
30	lmo:lmo 2799	DEG1007 0132	1	457	46 8	5	465	58 9	465	1.00E- 124	442	113 7	50.1 1
31	lmo:lmo 1168	DEG1002 0202	4	388	39 7	5	393	40 0	389	3.00E- 124	440	113 2	54.7 6
32	lmo:lmo 1892	DEG1017 0188	12	672	82 7	12	695	72 7	698	9.00E- 123	437	112 3	37.8 2
33	lmo:lmo 2103	DEG1017 0051	1	324	32 5	1	328	32 8	328	4.00E- 119	423	108 7	63.1 1
34	lmo:lmo 1259	DEG1013 0093	8	415	41 5	13	421	42 1	409	5.00E- 115	410	105 3	48.1 7
35	lmo:lmo 0855	DEG1001 0069	8	366	37 0	1	352	35 4	369	2.00E- 112	401	103 0	56.3 7
36	lmo:lmo 1414	DEG1017 0015	1	388	38 9	1	391	39 3	392	4.00E- 112	400	102 7	51.5 3
37	lmo:lmo 2825	DEG1043 0311	3	353	36 3	2	355	35 9	354	2.00E- 106	381	979	54.2 4
38	lmo:lmo 2718	DEG1025 0337	1	451	46 8	1	468	48 5	468	2.00E- 106	381	979	41.4 5
39	lmo:lmo 0856	DEG1001 0070	1	455	45 7	2	452	45 7	455	5.00E- 104	374	959	45.0 5
40	lmo:lmo 1083	DEG1023 0103	4	316	32 8	5	359	37 8	355	2.00E- 103	371	952	52.3 9
41	lmo:lmo 1952	DEG1040 0059	8	433	43 6	35	456	46 4	427	4.00E- 102	367	942	45.2
42	lmo:lmo 2037	DEG1001 0103	9	321	32 4	9	320	32 4	313	1.00E- 100	362	928	59.1 1
43	lmo:lmo 1011	DEG1001 0093	1	236	23 6	1	236	23 6	236	2.00E- 100	360	925	74.1 5
44	lmo:lmo 1988	DEG1005 0347	2	334	35 0	3	343	35 8	341	2.00E- 95	344	883	51.3 2
45	lmo:lmo 0358	DEG1047 0314	3	451	46 4	169	614	61 8	462	2.00E- 95	345	884	43.7 2
46	lmo:lmo 0886	DEG1001 0072	5	367	36 8	6	370	38 9	366	8.00E- 93	336	861	45.3 6
47	lmo:lmo 0292	DEG1047 0300	122	493	50 0	27	404	41 3	387	2.00E- 91	332	850	49.6 1
48	lmo:lmo 1006	DEG1047 0435	15	380	38 1	16	384	39 6	370	9.00E- 90	326	835	45.4 1
49	lmo:lmo 1435	DEG1001 0140	1	291	29 3	1	290	29 0	292	2.00E- 89	324	830	54.1 1
50	lmo:lmo 2720	DEG1002 0206	24	520	52 5	59	557	56 8	506	3.00E- 89	325	832	35.7 7

51	lmo:lmo 2745	DEG1040 0017	24	575	57 5	35	581	58 2	556	2.00E- 88	322	825	33.8 1
52	lmo:lmo 1907	DEG1007 0080	1	262	26 3	3	255	25 5	262	2.00E- 87	317	812	60.3 1
53	lmo:lmo 1588	DEG1041 0547	3	369	38 6	9	383	40 3	378	5.00E- 85	310	794	43.1 2
54	lmo:lmo 2205	DEG1021 0065	1	229	22 9	2	230	23 0	229	9.00E- 84	305	780	62.8 8
55	lmo:lmo 2547	DEG1040 0530	5	421	42 8	16	439	44 5	426	3.00E- 83	304	779	38.2 6
56	lmo:lmo 1633	DEG1040 0262	9	451	45 4	27	502	51 7	482	6.00E- 81	296	759	40.4 6
57	lmo:lmo 2229	DEG1041 0234	63	619	71 4	87	639	75 7	575	7.00E- 79	291	744	33.2 2
58	lmo:lmo 1084	DEG1042 0235	3	276	27 6	2	279	28 4	278	4.00E- 73	270	690	50.7 2
59	lmo:lmo 2733	DEG1047 0314	1	628	65 2	1	602	61 8	638	9.00E- 72	267	682	31.8 2
60	lmo:lmo 1947	DEG1001 0262	135	596	59 6	141	601	61 1	471	3.00E- 67	252	643	35.2 4
61	lmo:lmo 1619	DEG1047 0472	3	274	28 9	7	278	29 0	275	6.00E- 66	246	628	47.6 4
62	lmo:lmo 2500	DEG1017 0010	1	588	59 1	7	597	60 8	607	3.00E- 64	242	617	30.9 7
63	lmo:lmo 0692	DEG1030 0014	287	615	61 8	197 7	231 4	24 72	341	3.00E- 60	228	582	35.4 8
64	lmo:lmo 1260	DEG1040 0544	8	268	27 6	2	259	36 7	265	4.00E- 59	223	568	46.0 4
65	lmo:lmo 2717	DEG1027 0312	1	333	33 7	1	334	34 6	344	1.00E- 58	222	566	38.9 5
66	lmo:lmo 1436	DEG1047 0164	1	403	40 3	1	403	40 9	414	6.00E- 57	217	552	35.9 9
67	lmo:lmo 0738	DEG1047 0078	4	454	61 7	5	454	45 4	469	6.00E- 55	211	537	30.2 8
68	lmo:lmo 0359	DEG1001 0257	2	283	28 6	3	285	28 5	289	2.00E- 52	201	511	39.1
69	lmo:lmo 1021	DEG1002 0213	9	343	35 2	7	339	34 7	340	1.00E- 50	196	497	38.5 3
70	lmo:lmo 1035	DEG1047 0078	2	456	61 8	3	452	45 4	472	4.00E- 50	195	495	32.2
71	lmo:lmo 1082	DEG1041 0034	1	181	18 6	2	184	18 5	183	1.00E- 49	191	485	46.4 5
72	lmo:lmo 1990	DEG1044 0023	1	193	19 3	1	206	21 5	206	1.00E- 47	184	468	49.0 3
73	lmo:lmo 2133	DEG1017 0299	2	277	29 9	3	279	28 6	282	1.00E- 47	186	471	37.9 4
74	lmo:lmo 1632	DEG1040 0105	1	184	20 1	1	192	20 0	193	1.00E- 47	184	468	47.1 5
75	lmo:lmo 1925	DEG1028 0338	30	360	36 0	29	364	36 8	337	4.00E- 47	184	466	33.2 3
76	lmo:lmo 0411	DEG1043 0260	34	315	53 0	9	307	76 4	299	6.00E- 43	171	432	35.1 2
77	lmo:lmo 2134	DEG1017 0299	3	269	28 4	4	274	28 6	277	2.00E- 41	164	416	38.6 3

78	lmo:lmo 1521	DEG1017 0229	174	426	42 7	46	290	29 1	259	8.00E- 41	163	413	38.2 2
79	lmo:lmo 0716	DEG1029 0395	73	414	43 3	62	405	46 3	349	7.00E- 37	150	379	31.2 3
80	lmo:lmo 1985	DEG1013 0394	1	160	16 3	1	159	16 3	160	8.00E- 35	141	356	41.8 8
81	lmo:lmo 2754	DEG1028 0071	39	389	44 5	31	358	39 2	357	4.00E- 33	138	347	32.4 9
82	lmo:lmo 1066	DEG1048 0169	34	254	25 7	33	256	26 7	227	2.00E- 31	132	331	33.9 2
83	lmo:lmo 1017	DEG1033 0065	14	139	16 3	23	148	16 9	126	2.00E- 30	127	319	48.4 1
84	lmo:lmo 0938	DEG1015 0128	2	152	15 2	1	153	15 4	153	3.00E- 29	122	307	39.2 2
85	lmo:lmo 2017	DEG1008 0146	4	217	23 1	11	227	22 7	218	5.00E- 29	123	308	36.2 4
86	lmo:lmo 2683	DEG1047 0465	3	99	10 1	2	98	10 0	97	1.00E- 27	117	292	57.7 3
87	lmo:lmo 1940	DEG1018 0443	80	316	32 0	103	340	34 8	243	6.00E- 27	117	292	31.2 8
88	lmo:lmo 0426	DEG1002 0060	1	148	15 4	1	147	65 2	148	2.00E- 26	113	283	38.5 1
89	lmo:lmo 0849	DEG1036 0244	167	442	61 6	7	292	48 4	294	6.00E- 25	111	278	32.9 9
90	lmo:lmo 2018	DEG1034 0314	4	279	32 9	8	256	27 2	281	1.00E- 24	109	272	32.3 8
91	lmo:lmo 1464	DEG1038 0058	8	131	13 1	11	134	13 5	125	2.00E- 24	106	265	46.4
92	lmo:lmo 0027	DEG1002 0290	488	632	63 4	544	687	68 8	145	6.00E- 24	108	269	38.6 2
93	lmo:lmo 0427	DEG1002 0060	5	100	10 6	181	275	65 2	96	2.00E- 23	102	255	57.2 9
94	lmo:lmo 2787	DEG1002 0290	462	583	64 0	519	646	68 8	128	2.00E- 23	107	266	43.7 5
95	lmo:lmo 2797	DEG1018 0603	11	141	14 8	8	138	14 3	131	4.00E- 23	102	255	33.5 9
96	lmo:lmo 1623	DEG1008 0146	11	191	21 7	18	208	22 7	192	6.00E- 23	102	255	33.8 5
97	lmo:lmo 2373	DEG1047 0465	3	98	10 4	2	98	10 0	97	9.00E- 23	100	249	57.7 3
98	lmo:lmo 2772	DEG1033 0065	459	590	61 7	14	146	16 9	133	2.00E- 22	103	256	42.1 1

Supplementary Table 4: Sub-cellular localization of the of pathogen-host non-homologous proteins/enzymes of <i>Listeria monocytogenes</i> EDG-e using CELLO.											
Seq NO.	Comp. Result	Di-pep.Result	part-Comp. Result	chemo-type.Result	Neighbor	extra	wall	memb	cyto	#Most-likely-Location	#SeqName
1	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	0.20113095	0.065628786	1.26360705	3.4696336	Cytoplasmic	lmo:lmo1985 K01653 acetolactate synthase I/III small subunit [EC:2.2.1.6] (RefSeq) ilvH; acetolactate synthase small subunit (A)
2	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	Membrane	0.047842023	0.033609624	1.48886484	3.429683	Cytoplasmic	lmo:lmo1988 K00052 3-isopropylmalate dehydrogenase [EC:1.1.1.85] (RefSeq) leuB; 3-isopropylmalate dehydrogenase (A)
3	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.155657873	0.02106122	0.5748933	4.248389	Cytoplasmic	lmo:lmo1990 K01704 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35] (RefSeq) leuD; isopropylmalate isomerase small subunit (A)
4	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	0.09150978	0.031208015	0.75730302	4.119979	Cytoplasmic	lmo:lmo1992 K01575 acetolactate decarboxylase [EC:4.1.1.5] (RefSeq) alpha-acetolactate decarboxylase (A)
5	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.038252694	0.020631039	0.8668721	4.074244	Cytoplasmic	lmo:lmo2006 K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6] (RefSeq) alsS; acetolactate synthase (A)
6	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.05514751	0.034965612	0.30927973	4.600608	Cytoplasmic	lmo:lmo0359 K01624 fructose-bisphosphate aldolase, class II [EC:4.1.2.13] (RefSeq) D-fructose-1,6-bisphosphate aldolase (A)
7	Membrane	Membrane	Membrane	Cytoplasmic	Membrane	0.13656489	0.02796812	3.3595257	1.4759407	Membrane	lmo:lmo0411 K01007 pyruvate, water dikinase [EC:2.7.9.2] (RefSeq) phosphoenolpyruvate synthase (A)
8	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.05378066	0.013549854	0.6343945	4.298276	Cytoplasmic	lmo:lmo0830 K04041 fructose-1,6-bisphosphatase III [EC:3.1.3.11] (RefSeq) fbp; fructose-1,6-bisphosphatase (A)
9	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.028693	0.009426309	1.1697591	3.792121	Cytoplasmic	lmo:lmo1168 K00925 acetate kinase [EC:2.7.2.1] (RefSeq) AckA2; acetate kinase (A)
10	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.034106557	0.006311203	0.3914213	4.568159	Cytoplasmic	lmo:lmo1571 K00850 6-phosphofructokinase 1 [EC:2.7.1.11] (RefSeq) pfkA; 6-phosphofructokinase (A)
11	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.017969069	0.005682128	0.9576836	4.018665	Cytoplasmic	lmo:lmo1581 K00925 acetate kinase [EC:2.7.2.1] (RefSeq) ackA; acetate kinase (A)
12	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.06058212	0.024837992	0.8061943	4.108387	Cytoplasmic	lmo:lmo2103 K00625 phosphate acetyltransferase [EC:2.3.1.8] (RefSeq) eutD; phosphotransacetylase (A)

13	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.0420232	0.012497712	0.6037	4.341778	Cytoplasmic	lmo:lmo2133 K01624 fructose-bisphosphate aldolase, class II [EC:4.1.2.13] (RefSeq) fructose-1,6-bisphosphate aldolase type II (A)
14	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.11960621	0.017390352	0.5170056	4.345997	Cytoplasmic	lmo:lmo2134 K01624 fructose-bisphosphate aldolase, class II [EC:4.1.2.13] (RefSeq) fructose-1,6-bisphosphate aldolase type II (A)
15	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.015055661	0.00156969	0.06314261	4.920232	Cytoplasmic	lmo:lmo2205 K01834 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11] (RefSeq) phosphoglyceromutase (A)
16	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.017321196	0.009994386	0.018562139	4.954122	Cytoplasmic	lmo:lmo2455 K01689 enolase [EC:4.2.1.11] (RefSeq) eno; phosphopyruvate hydratase (A)
17	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.08378701	0.016398131	0.30679926	4.593016	Cytoplasmic	lmo:lmo2456 K15633 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12] (RefSeq) pgm; phosphoglyceromutase (A)
18	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	0.5563631	0.09458557	1.1755102	3.173539	Cytoplasmic	lmo:lmo2586 K00123 formate dehydrogenase major subunit [EC:1.17.1.9] (RefSeq) formate dehydrogenase subunit alpha (A)
19	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.0601285	0.011623974	0.6610684	4.267179	Cytoplasmic	lmo:lmo2720 K01895 acetyl-CoA synthetase [EC:6.2.1.1] (RefSeq) acetate-CoA ligase (A)
20	Membrane	Cytoplasmic	Membrane	Cytoplasmic	Membrane	0.39445666	0.054305529	1.8342272	2.717012	Cytoplasmic	lmo:lmo2825 K00831 phosphoserine aminotransferase [EC:2.6.1.52] (RefSeq) serC; phosphoserine aminotransferase (A)
21	Membrane	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	0.8112818	0.098064553	1.3109332	2.779721	Cytoplasmic	lmo:lmo0446 K01442 choloylglycine hydrolase [EC:3.5.1.24] (RefSeq) penicillin acylase (A)
22	Extracellular	Extracellular	Extracellular	Cytoplasmic	Extracellular	2.469455	0.04258563	0.8608563	1.627102	Extracellular	lmo:lmo2067 K01442 choloylglycine hydrolase [EC:3.5.1.24] (RefSeq) bile acid hydrolase (A)
23	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.06859936	0.02183234	0.47703862	4.432528	Cytoplasmic	lmo:lmo0265 K01439 succinyl-diaminopimelate desuccinylase [EC:3.5.1.18] (RefSeq) succinyl-diaminopimelate desuccinylase (A)
24	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.080948346	0.019031296	1.3002723	3.599748	Cytoplasmic	lmo:lmo0856 K01929 UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase [EC:6.3.2.10] (RefSeq) murF; UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diamino pimelate-D-alanyl-D-alanyl ligase (A)
25	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.04599623	0.042392383	2.0846691	2.8269404	Cytoplasmic	lmo:lmo1006 K00841 aminotransferase [EC:2.6.1.-] (RefSeq) aminotransferase (A)

26	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	0.0816075	0.02920766	1.202852	3.686334	Cytoplasmic	lmo:lmo1011 K05822 tetrahydrodipicolinate N-acetyltransferase [EC:2.3.1.89] (RefSeq) tetrahydrodipicolinate succinylase (A)
27	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.014175736	0.010000229	0.8943335	4.08149	Cytoplasmic	lmo:lmo1012 K05823 N-acetyldiaminopimelate deacetylase [EC:3.5.1.47] (RefSeq) N-acyl-L-amino acid amidohydrolyase (A)
28	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	0.021884237	0.012420134	1.678669	3.287027	Cytoplasmic	lmo:lmo1235 K00928 aspartate kinase [EC:2.7.2.4] (RefSeq) aspartate kinase (A)
29	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.13016182	0.0104861	1.10759	3.751762	Cytoplasmic	lmo:lmo1435 K01714 4-hydroxy-tetrahydrodipicolinate synthase [EC:4.3.3.7] (RefSeq) dapA; dihydrodipicolinate synthase (A)
30	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	0.05065811	0.02851474	1.4400234	3.480804	Cytoplasmic	lmo:lmo1436 K00928 aspartate kinase [EC:2.7.2.4] (RefSeq) aspartate kinase (A)
31	Membrane	Membrane	Membrane	Cytoplasmic	Membrane	0.08738899	0.043664477	2.8203535	2.0485929	Membrane	lmo:lmo1437 K00133 aspartate-semialdehyde dehydrogenase [EC:1.2.1.11] (RefSeq) aspartate-semialdehyde dehydrogenase (A)
32	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.024796777	0.004374092	0.5505927	4.420236	Cytoplasmic	lmo:lmo1588 K00821 acetylmuramoyl-N-succinyldiaminopimelate aminotransferase [EC:2.6.1.11 2.6.1.17] (RefSeq) argD; acetylmuramoyl-N-succinyldiaminopimelate aminotransferase (A)
33	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.0241413	0.006956895	0.06604926	4.902852	Cytoplasmic	lmo:lmo1620 K01439 succinyl-diaminopimelate desuccinylase [EC:3.5.1.18] (RefSeq) dipeptidase PepV (A)
34	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.003944444	0.001935979	0.11714902	4.87697	Cytoplasmic	lmo:lmo1907 K00215 4-hydroxy-tetrahydrodipicolinate reductase [EC:1.17.1.8] (RefSeq) dapB; dihydrodipicolinate reductase (A)
35	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.095022801	0.005365714	0.09161641	4.807995	Cytoplasmic	lmo:lmo1952 K01586 diaminopimelate decarboxylase [EC:4.1.1.20] (RefSeq) lysA; diaminopimelate decarboxylase (A)
36	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.23586202	0.064500356	0.3545124	4.345125	Cytoplasmic	lmo:lmo2018 K01778 diaminopimelate epimerase [EC:5.1.1.7] (RefSeq) dapF; diaminopimelate epimerase (A)
37	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.033577816	0.009443909	0.4752136	4.481764	Cytoplasmic	lmo:lmo2038 K01928 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase [EC:6.3.2.13] (RefSeq) murE; UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase (A)

38	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.047848127	0.004439698	0.50908739	4.438625	Cytoplasmic	lmo:lmo2374 K00928 aspartate kinase [EC:2.7.2.4] (RefSeq) aspartate kinase (A)
39	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.236484825	0.03720161	0.43166443	4.294649	Cytoplasmic	lmo:lmo2547 K00003 homoserine dehydrogenase [EC:1.1.1.3] (RefSeq) hom; homoserine dehydrogenase (A)
40	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.25971066	0.008935327	0.23590173	4.495452	Cytoplasmic	lmo:lmo0372 K05350 beta-glucosidase [EC:3.2.1.21] (RefSeq) beta-glucosidase (A)
41	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.20481739	0.063877378	0.39360896	4.337695	Cytoplasmic	lmo:lmo1729 K05349 beta-glucosidase [EC:3.2.1.21] (RefSeq) beta-glucosidase (A)
42	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	Membrane	0.04760887	0.013672303	2.0379464	2.9007712	Cytoplasmic	lmo:lmo1940 K01424 L-asparaginase [EC:3.5.1.1] (RefSeq) asparaginase (A)
43	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.147232967	0.049957535	0.74519578	4.057614	Cytoplasmic	lmo:lmo2781 K05349 beta-glucosidase [EC:3.2.1.21] (RefSeq) beta-glucosidase (A)
44	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.122772325	0.009522612	1.5222826	3.345422	Cytoplasmic	lmo:lmo0855 K01921 D-alanine-D-alanine ligase [EC:6.3.2.4] (RefSeq) ddl; D-alanyl-alanine synthetase A (A)
45	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.09320096	0.010488832	0.37756611	4.518744	Cytoplasmic	lmo:lmo0886 K01775 alanine racemase [EC:5.1.1.1] (RefSeq) dal; alanine racemase (A)
46	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.3883317	0.03651562	0.8507111	3.724442	Cytoplasmic	lmo:lmo0972 K14188 D-alanine--poly(phosphoribitol) ligase subunit 2 [EC:6.1.1.13] (RefSeq) dltC; D-alanine--poly(phosphoribitol) ligase subunit 2 (A)
47	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.12755675	0.025723704	1.0699133	3.776807	Cytoplasmic	lmo:lmo0974 K03367 D-alanine--poly(phosphoribitol) ligase subunit 1 [EC:6.1.1.13] (RefSeq) dltA; D-alanine--poly(phosphoribitol) ligase subunit 1 (A)
48	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.031310006	0.004864763	0.03692408	4.926901	Cytoplasmic	lmo:lmo1619 K00824 D-alanine transaminase [EC:2.6.1.21] (RefSeq) daaA; D-amino acid aminotransferase (A)
49	Membrane	Membrane	Membrane	Membrane	Membrane	0.4034763	0.08030644	3.708047	0.8081702	Membrane	lmo:lmo1464 K00887 undecaprenol kinase [EC:2.7.1.66] (RefSeq) diacylglycerol kinase (A)
50	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.159970513	0.019340104	0.6864099	4.134279	Cytoplasmic	lmo:lmo1605 K01924 UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8] (RefSeq) murC; UDP-N-acetylmuramate--L-alanine ligase (A)
51	Membrane	Membrane	Membrane	Membrane	Membrane	0.16794495	0.04684386	4.736948	0.04826354	Membrane	lmo:lmo1623 K19302 undecaprenyl-diphosphatase [EC:3.6.1.27] (RefSeq) hypothetical protein (A)
52	Extracellular	Cytoplasmic	Extracellular	Cytoplasmic	Cytoplasmic	1.922144	0.10216961	0.7204508	2.255237	Cytoplasmic	lmo:lmo1855 K07260 zinc D-Ala-D-Ala carboxypeptidase [EC:3.4.17.14]

											(RefSeq) D-alanyl-D-alanine carboxypeptidase (A)
53	Extracellular	Membrane	Membrane	Extracellular	Extracellular	2.683052	0.2366708	1.9878865	0.0923915	Extracellular	lmo:lmo1892 K05366 penicillin-binding protein 1A [EC:2.4.1.129 3.4.16.4] (RefSeq) pbpA; penicillin-binding protein 2A (A)
54	Membrane	Membrane	Membrane	Membrane	Membrane	0.03118951	0.05952397	4.888301	0.02098547	Membrane	lmo:lmo2017 K19302 undecaprenyl-diphosphatase [EC:3.6.1.27] (RefSeq) hypothetical protein (A)
55	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.066917088	0.018195627	0.820203	4.094686	Cytoplasmic	lmo:lmo2036 K01925 UDP-N-acetylmuramoylalanine--D-glutamate ligase [EC:6.3.2.9] (RefSeq) murD; UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase (A)
56	Membrane	Membrane	Membrane	Membrane	Membrane	0.01927783	0.015209866	4.956897	0.008614481	Membrane	lmo:lmo2037 K01000 phospho-N-acetylmuramoyl-pentapeptide-transferase [EC:2.7.8.13] (RefSeq) mraY; phospho-N-acetylmuramoyl-pentapeptide-transferase (A)
57	Membrane	Membrane	Membrane	Extracellular	Membrane	1.7434963	0.22266828	2.907837	0.1259989	Membrane	lmo:lmo2229 K12555 penicillin-binding protein 2A [EC:2.4.1.129 3.4.16.4] (RefSeq) penicillin-binding protein (A)
58	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.064519507	0.02116614	1.6105208	3.303793	Cytoplasmic	lmo:lmo2526 K00790 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7] (RefSeq) murA; UDP-N-acetylglucosamine 1-carboxyvinyltransferase (A)
59	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.225273455	0.047320979	0.74599762	3.981408	Cytoplasmic	lmo:lmo2552 K00790 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7] (RefSeq) murZ; UDP-N-acetylglucosamine 1-carboxyvinyltransferase (A)
60	Extracellular	Membrane	Membrane	Membrane	Cytoplasmic	1.1671357	0.174201	2.878523	0.7801406	Membrane	lmo:lmo2754 K07258 serine-type D-Ala-D-Ala carboxypeptidase (penicillin-binding protein 5/6) [EC:3.4.16.4] (RefSeq) D-alanyl-D-alanine carboxypeptidase (A)
61	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.052402006	0.008451583	0.8414548	4.097692	Cytoplasmic	lmo:lmo1081 K00973 glucose-1-phosphate thymidyltransferase [EC:2.7.7.24] (RefSeq) glucose-1-phosphate thymidyl transferase (A)
62	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.466998902	0.031106285	0.502642631	3.999252	Cytoplasmic	lmo:lmo1082 K01790 dTDP-4-dehydrorhamnose 3,5-epimerase [EC:5.1.3.13] (RefSeq) dTDP-sugar epimerase (A)
63	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.60821978	0.031121056	0.1215295	4.23913	Cytoplasmic	lmo:lmo1083 K01710 dTDP-glucose 4,6-dehydratase [EC:4.2.1.46]

											(RefSeq) dTDP-D-glucose 4,6-dehydratase (A)
64	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.73536718	0.2497507	0.8405878	3.174297	Cytoplasmic	lmo:lmo1084 K00067 dTDP-4-dehydrorhamnose reductase [EC:1.1.1.133] (RefSeq) DTDP-L-rhamnose synthetase (A)
65	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.050433954	0.00749754	0.9149299	4.02714	Cytoplasmic	lmo:lmo1259 K00147 glutamate-5-semialdehyde dehydrogenase [EC:1.2.1.41] (RefSeq) proA; gamma-glutamyl phosphate reductase (A)
66	Membrane	Cytoplasmic	Membrane	Cytoplasmic	Membrane	0.13531632	0.009347815	2.9741885	1.881146	Membrane	lmo:lmo1260 K00931 glutamate 5-kinase [EC:2.7.2.11] (RefSeq) proB; gamma-glutamyl kinase (A)
67	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.019276364	0.003982364	0.19943821	4.777303	Cytoplasmic	lmo:lmo1066 K01092 myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25] (RefSeq) myo-inositol-1(or 4)-monophosphatase (A)
68	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.10092962	0.014964325	0.16427399	4.719833	Cytoplasmic	lmo:lmo1339 K00845 glucokinase [EC:2.7.1.2] (RefSeq) glucose kinase (A)
69	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.047846144	0.008157358	0.280842	4.663153	Cytoplasmic	lmo:lmo2475 K01835 phosphoglucomutase [EC:5.4.2.2] (RefSeq) phosphoglucomutase (A)
70	Membrane	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.2035708	0.08770007	2.0384171	2.670311	Cytoplasmic	lmo:lmo1897 K00812 aspartate aminotransferase [EC:2.6.1.1] (RefSeq) aspB; aspartate aminotransferase (A)
71	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.06445279	0.03113572	1.641406	3.263006	Cytoplasmic	lmo:lmo1924 K04517 prephenate dehydrogenase [EC:1.3.1.12] (RefSeq) tyrA; prephenate dehydrogenase (A)
72	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.05138449	0.034583582	0.7036909	4.210341	Cytoplasmic	lmo:lmo1925 K00817 histidinol-phosphate aminotransferase [EC:2.6.1.9] (RefSeq) hisC; histidinol-phosphate aminotransferase (A)
73	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.00799296	0.001979037	0.07079047	4.919237	Cytoplasmic	lmo:lmo0646 K07104 catechol 2,3-dioxygenase [EC:1.13.11.2] (RefSeq) hypothetical protein (A)
74	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.290502648	0.019040237	1.3846293	3.305828	Cytoplasmic	lmo:lmo1414 K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9] (RefSeq) acetyl-CoA:acetyltransferase (A)
75	Cytoplasmic	Extracellular	Cytoplasmic	Membrane	Cytoplasmic	1.3889631	0.07532941	0.9973829	2.538325	Cytoplasmic	lmo:lmo2564 K01821 4-oxalocrotonate tautomerase [EC:5.3.2.6] (RefSeq) 4-oxalocrotonate isomerase (A)
76	Membrane	Membrane	Membrane	Extracellular	Membrane	1.3427671	0.15825085	3.352656	0.14632566	Membrane	lmo:lmo0849 K01426 amidase [EC:3.5.1.4] (RefSeq) amidase (A)
77	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.4578426	0.04957157	0.5766405	3.915946	Cytoplasmic	lmo:lmo1381 K01512 acylphosphatase [EC:3.6.1.7] (RefSeq) acylphosphatase (A)

78	Cytoplasmic	Membrane	Membrane	Membrane	Cytoplasmic	0.10593341	0.06235936	2.3290154	2.50269	Cytoplasmic	lmo:lmo2401 K01101 4-nitrophenyl phosphatase [EC:3.1.3.41] (RefSeq) hypothetical protein (A)
79	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.21527889	0.1803103	0.6277335	3.976677	Cytoplasmic	lmo:lmo1634 K04072 acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1] (RefSeq) bifunctional acetaldehyde-CoA/alcohol dehydrogenase (A)
80	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	Membrane	0.12244545	0.022753513	1.9041484	2.950653	Cytoplasmic	lmo:lmo0021 K02793 PTS system, mannose-specific IIA component [EC:2.7.1.191] (RefSeq) PTS fructose transporter subunit IIA (A)
81	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.27168389	0.0710148	0.93883193	3.718469	Cytoplasmic	lmo:lmo0022 K02794 PTS system, mannose-specific IIB component [EC:2.7.1.191] (RefSeq) PTS fructose transporter subunit IIB (A)
82	Membrane	Membrane	Membrane	Membrane	Membrane	0.077580514	0.07061273	4.676398	0.17540994	Membrane	lmo:lmo0027 K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucoside-specific IIB component [EC:2.7.1.-] K02757 PTS system, beta-glucoside-specific IIC component (RefSeq) PTS beta-glucoside transporter subunit IABC (A)
83	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.016523313	0.02061823	1.4223822	3.540475	Cytoplasmic	lmo:lmo0096 K02793 PTS system, mannose-specific IIA component [EC:2.7.1.191] K02794 PTS system, mannose-specific IIB component [EC:2.7.1.191] (RefSeq) PTS mannose transporter subunit IIAB (A)
84	Cytoplasmic	Extracellular	Cytoplasmic	Cytoplasmic	Membrane	1.4658428	0.02773886	1.2113888	2.295029	Cytoplasmic	lmo:lmo0299 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-glucoside transporter subunit IIB (A)
85	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.15979643	0.009975941	0.5624678	4.26776	Cytoplasmic	lmo:lmo0301 K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-glucoside transporter subunit IIA (A)
86	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.42174655	0.02016474	0.9632697	3.594819	Cytoplasmic	lmo:lmo0357 K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS sugar transporter subunit IIA (A)
87	Membrane	Membrane	Membrane	Membrane	Membrane	0.16725224	0.02425233	4.6424	0.166096059	Membrane	lmo:lmo0358 K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] K02770 PTS system, fructose-specific IIC component (RefSeq) PTS fructose transporter subunit IIBC (A)

88	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	0.6297857	0.024341	1.2056368	3.140237	Cytoplasmic	lmo:lmo0374 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-glucoside transporter subunit IIB (A)
89	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.105860076	0.022554725	1.3562443	3.515341	Cytoplasmic	lmo:lmo0398 K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS sugar transporter subunit IIA (A)
90	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.3805929	0.02975598	0.5689696	4.020682	Cytoplasmic	lmo:lmo0399 K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] (RefSeq) PTS fructose transporter subunit IIB (A)
91	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.015579709	0.02351028	0.1966189	4.764291	Cytoplasmic	lmo:lmo0426 K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS fructose transporter subunit IIA (A)
92	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	1.128015	0.14035574	0.9039976	2.82763	Cytoplasmic	lmo:lmo0427 K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] (RefSeq) PTS fructose transporter subunit IIB (A)
93	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.019185299	0.008336584	0.37657486	4.595903	Cytoplasmic	lmo:lmo0503 K02773 PTS system, galactitol-specific IIA component [EC:2.7.1.200] (RefSeq) PTS fructose transporter subunit IIA (A)
94	Cytoplasmic	Membrane	Membrane	Membrane	Membrane	0.9206987	0.10208298	2.4448051	1.5324145	Membrane	lmo:lmo0507 K02774 PTS system, galactitol-specific IIB component [EC:2.7.1.200] (RefSeq) PTS galactitol transporter subunit IIB (A)
95	Membrane	Membrane	Membrane	Cytoplasmic	Cytoplasmic	0.2070705	0.06296509	2.486834	2.243131	Membrane	lmo:lmo0542 K02781 PTS system, glucitol/sorbitol-specific IIA component [EC:2.7.1.198] (RefSeq) PTS sorbitol transporter subunit IIA (A)
96	Membrane	Membrane	Cytoplasmic	Membrane	Membrane	0.10537415	0.050577986	3.54665	1.29739792	Membrane	lmo:lmo0543 K02782 PTS system, glucitol/sorbitol-specific IIB component [EC:2.7.1.198] K02783 PTS system, glucitol/sorbitol-specific IIC component (RefSeq) PTS sorbitol transporter subunit IIBC (A)
97	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.06449026	0.017978498	0.8765362	4.040993	Cytoplasmic	lmo:lmo0631 K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS fructose transporter subunit IIA (A)
98	Membrane	Membrane	Membrane	Membrane	Membrane	0.069213005	0.03197276	4.831632	0.067182123	Membrane	lmo:lmo0738 K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucoside-specific IIB component [EC:2.7.1.-] K02757 PTS system, beta-glucoside-specific IIC component

											(RefSeq) PTS beta-glucoside transporter subunit IABC (A)
99	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.1377122	0.09000507	0.3234774	4.448805	Cytoplasmic	lmo:lmo0783 K02794 PTS system, mannose-specific IIB component [EC:2.7.1.191] (RefSeq) PTS mannose transporter subunit IIB (A)
100	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.177585	0.01948319	0.8625939	3.940336	Cytoplasmic	lmo:lmo0784 K02793 PTS system, mannose-specific IIA component [EC:2.7.1.191] (RefSeq) PTS mannose transporter subunit IIB (A)
101	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	0.140564	0.02155607	1.9901158	2.847763	Cytoplasmic	lmo:lmo0874 K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS sugar transporter subunit IIA (A)
102	Cytoplasmic	Cytoplasmic	Cytoplasmic	Extracellular	Cytoplasmic	0.60196115	0.01811843	0.8438167	3.536105	Cytoplasmic	lmo:lmo0875 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-glucoside transporter subunit IIB (A)
103	Cytoplasmic	Membrane	Membrane	Membrane	Cytoplasmic	0.71705974	0.027816736	1.7966093	2.4585146	Cytoplasmic	lmo:lmo0914 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS sugar transporter subunit IIB (A)
104	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.1730283	0.01747862	0.5696493	4.239843	Cytoplasmic	lmo:lmo0916 K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS sugar transporter subunit IIA (A)
105	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.006710221	0.001957289	0.05427569	4.937057	Cytoplasmic	lmo:lmo1003 K08483 phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9] (RefSeq) phosphotransferase system enzyme I (A)
106	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.14234296	0.029856771	0.5183305	4.309468	Cytoplasmic	lmo:lmo1017 K02777 PTS system, sugar-specific IIA component [EC:2.7.1.-] (RefSeq) PTS glucose transporter subunit IIA (A)
107	Membrane	Membrane	Membrane	Membrane	Membrane	0.048877194	0.019755217	4.886646	0.04472181	Membrane	lmo:lmo1035 K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucoside-specific IIB component [EC:2.7.1.-] K02757 PTS system, beta-glucoside-specific IIC component (RefSeq) PTS beta-glucoside transporter subunit IABC (A)
108	Extracellular	Cytoplasmic	Extracellular	Membrane	Cytoplasmic	1.4862444	0.08223955	1.757847	1.6736694	Membrane	lmo:lmo1095 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellobiose transporter subunit IIB (A)
109	Membrane	Membrane	Membrane	Membrane	Membrane	0.040536157	0.014541994	4.892216	0.052705299	Membrane	lmo:lmo1255 K02818 PTS system, trehalose-specific IIB component [EC:2.7.1.201] K02819 PTS system,

											trehalose-specific IIC component (RefSeq) PTS trehalose transporter subunit IIBC (A)
110	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.1663467	0.02013357	0.4092514	4.40427	Cytoplasmic	lmo:lmo1719 K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS lichenan transporter subunit IIA (A)
111	Membrane	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	0.5106631	0.05131116	2.430852	2.007174	Membrane	lmo:lmo1720 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS lichenan transporter subunit IIB (A)
112	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.15613295	0.01754699	2.048281	2.77804	Cytoplasmic	lmo:lmo1972 K02822 PTS system, ascorbate-specific IIB component [EC:2.7.1.194] (RefSeq) PTS pentitol transporter subunit IIB (A)
113	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.053689192	0.005816453	0.2713044	4.669191	Cytoplasmic	lmo:lmo1973 K02821 PTS system, ascorbate-specific IIA component [EC:2.7.1.194] (RefSeq) PTS sugar transporter subunit IIA (A)
114	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.049171742	0.010654871	0.5020931	4.438081	Cytoplasmic	lmo:lmo1997 K02793 PTS system, mannose-specific IIA component [EC:2.7.1.191] (RefSeq) PTS mannose transporter subunit IIA (A)
115	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.2116255	0.03226985	0.9200419	3.836063	Cytoplasmic	lmo:lmo2002 K19507 PTS system, fructoselysine/glucoselysine-specific IIB component [EC:2.7.1.-] (RefSeq) PTS mannose transporter subunit IIB (A)
116	Cytoplasmic	Extracellular	Membrane	Extracellular	Cytoplasmic	1.5072035	0.08524169	1.6923085	1.715245	Cytoplasmic	lmo:lmo2097 K02774 PTS system, galactitol-specific IIB component [EC:2.7.1.200] (RefSeq) PTS galactitol transporter subunit IIB (A)
117	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.10991207	0.14249504	0.533119	4.214475	Cytoplasmic	lmo:lmo2098 K02773 PTS system, galactitol-specific IIA component [EC:2.7.1.200] (RefSeq) PTS galactitol transporter subunit IIA (A)
118	Cytoplasmic	Cytoplasmic	Cytoplasmic	Extracellular	Cytoplasmic	0.9413383	0.04128688	1.101513	2.915861	Cytoplasmic	lmo:lmo2136 K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] (RefSeq) PTS fructose transporter subunit IIB (A)
119	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.10454347	0.07174196	0.6769363	4.146778	Cytoplasmic	lmo:lmo2137 K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] (RefSeq) PTS fructose transporter subunit IIA (A)
120	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.45323231	0.07412662	0.5836226	3.889018	Cytoplasmic	lmo:lmo2259 K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-glucoside transporter subunit IIA (A)
121	Membrane	Membrane	Membrane	Membrane	Membrane	0.15195836	0.035199709	4.502359	0.31048166	Membrane	lmo:lmo2335 K02768 PTS system, fructose-specific IIA component

											[EC:2.7.1.202] K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] K02770 PTS system, fructose-specific IIC component (RefSeq) fruA; PTS fructose transporter subunit IIABC (A)
122	Cytoplasmic	Cytoplasmic	Membrane	Extracellular	Cytoplasmic	1.32955283	0.03359253	1.0980795	2.5387744	Cytoplasmic	lmo:lmo2373 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS beta-glucoside transporter subunit IIB (A)
123	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	0.8616968	0.05255471	1.484646	2.601104	Cytoplasmic	lmo:lmo2650 K02822 PTS system, ascorbate-specific IIB component [EC:2.7.1.194] (RefSeq) MFS transporter (A)
124	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.2655021	0.009523146	0.16827357	4.556703	Cytoplasmic	lmo:lmo2651 K02798 PTS system, mannitol-specific IIA component [EC:2.7.1.197] (RefSeq) PTS mannitol transporter subunit IIA (A)
125	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	0.3585706	0.04616536	1.9983141	2.59695	Cytoplasmic	lmo:lmo2666 K02774 PTS system, galactitol-specific IIB component [EC:2.7.1.200] (RefSeq) PTS galacticol transporter subunit IIB (A)
126	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.118299315	0.012375871	0.54828863	4.321036	Cytoplasmic	lmo:lmo2667 K02773 PTS system, galactitol-specific IIA component [EC:2.7.1.200] (RefSeq) PTS galacticol transporter subunit IIA (A)
127	Membrane	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	0.6363087	0.05372955	2.496688	1.813273	Membrane	lmo:lmo2683 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbiose transporter subunit IIB (A)
128	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	0.3468477	0.02377672	0.9603677	3.669009	Cytoplasmic	lmo:lmo2685 K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbiose transporter subunit IIA (A)
129	Membrane	Membrane	Membrane	Membrane	Membrane	0.211100906	0.062404995	4.330281	0.39621287	Membrane	lmo:lmo2733 K02768 PTS system, fructose-specific IIA component [EC:2.7.1.202] K02769 PTS system, fructose-specific IIB component [EC:2.7.1.202] K02770 PTS system, fructose-specific IIC component (RefSeq) PTS fructose transporter subunit IIABC (A)
130	Membrane	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	0.6738777	0.03910463	2.078168	2.208852	Cytoplasmic	lmo:lmo2762 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbiose transporter subunit IIB (A)
131	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.4678374	0.02284708	0.9928224	3.516494	Cytoplasmic	lmo:lmo2765 K02759 PTS system, cellobiose-specific IIA component

											[EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbiose transporter subunit IIA (A)
132	Membrane	Membrane	Membrane	Membrane	Membrane	0.10995099	0.04538109	4.76439	0.08027799	Membrane	lmo:lmo2772 K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucoside-specific IIB component [EC:2.7.1.-] K02757 PTS system, beta-glucoside-specific IIC component (RefSeq) PTS beta-glucoside transporter subunit IIA (A)
133	Membrane	Extracellular	Cytoplasmic	Cytoplasmic	Membrane	1.02998495	0.01570543	1.4460925	2.508218	Cytoplasmic	lmo:lmo2780 K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbiose transporter subunit IIA (A)
134	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	0.52167607	0.03902263	1.681538	2.757763	Cytoplasmic	lmo:lmo2782 K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205] (RefSeq) PTS cellbiose transporter subunit IIB (A)
135	Membrane	Membrane	Membrane	Membrane	Membrane	0.098419072	0.05508877	4.76121	0.08528366	Membrane	lmo:lmo2787 K02755 PTS system, beta-glucoside-specific IIA component [EC:2.7.1.-] K02756 PTS system, beta-glucoside-specific IIB component [EC:2.7.1.-] K02757 PTS system, beta-glucoside-specific IIC component (RefSeq) bvrB; beta-glucoside-specific phosphotransferase enzyme II ABC component (A)
136	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.011490056	0.002731611	0.16305297	4.822726	Cytoplasmic	lmo:lmo2797 K02798 PTS system, mannitol-specific IIA component [EC:2.7.1.197] (RefSeq) PTS mannitol transporter subunit IIA (A)
137	Membrane	Membrane	Membrane	Membrane	Membrane	0.019583983	0.0159945	4.930373	0.03404904	Membrane	lmo:lmo2799 K02799 PTS system, mannitol-specific IIB component [EC:2.7.1.197] K02800 PTS system, mannitol-specific IIC component (RefSeq) PTS mannitol transporter subunit IIBC (A)
138	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.034621917	0.015713656	0.27761656	4.672048	Cytoplasmic	lmo:lmo0583 K03070 preprotein translocase subunit SecA [EC:7.4.2.8] (RefSeq) azi, div; preprotein translocase subunit SecA (A)
139	Membrane	Cytoplasmic	Membrane	Membrane	Membrane	0.05057891	0.01434848	3.212088	1.7229859	Membrane	lmo:lmo1801 K03106 signal recognition particle subunit SRP54 [EC:3.6.5.4] (RefSeq) ffh; signal recognition particle protein Ffh (A)
140	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.040272988	0.018913095	0.49240654	4.448408	Cytoplasmic	lmo:lmo2510 K03070 preprotein translocase subunit SecA [EC:7.4.2.8] (RefSeq) secA; preprotein translocase subunit SecA (A)

141	Membrane	Membrane	Membrane	Membrane	Membrane	0.127684751	0.06326914	4.789467	0.019579263	Membrane	lmo:lmo0050 K07706 two-component system, LytTR family, sensor histidine kinase AgrC [EC:2.7.13.3] (RefSeq) histidine kinase (A)
142	Cytoplasmic	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	0.05072394	0.019819203	1.875154	3.054304	Cytoplasmic	lmo:lmo0288 K07652 two-component system, OmpR family, sensor histidine kinase VicK [EC:2.7.13.3] (RefSeq) two-component sensor histidine kinase (A)
143	Extracellular	Extracellular	Extracellular	Extracellular	Extracellular	2.778111	0.6245558	0.9258028	0.6715313	Extracellular	lmo:lmo0292 K04771 serine protease Do [EC:3.4.21.107] (RefSeq) heat-shock protein htrA serine protease (A)
144	Membrane	Membrane	Cytoplasmic	Extracellular	Membrane	1.3238064	0.4292709	2.37468	0.8722411	Membrane	lmo:lmo0355 K00244 fumarate reductase flavoprotein subunit [EC:1.3.5.4] (RefSeq) fumarate reductase subunit A (A)
145	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.14181557	0.02200432	1.7363372	3.0998441	Cytoplasmic	lmo:lmo0683 K00575 chemotaxis protein methyltransferase CheR [EC:2.1.1.80] (RefSeq) chemotaxis protein CheR (A)
146	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.029426842	0.006583137	0.716105	4.247885	Cytoplasmic	lmo:lmo0692 K03407 two-component system, chemotaxis family, sensor kinase CheA [EC:2.7.13.3] (RefSeq) cheA; two-component sensor histidine kinase CheA (A)
147	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Membrane	0.11328063	0.010193543	1.2616313	3.614896	Cytoplasmic	lmo:lmo0938 K01104 protein-tyrosine phosphatase [EC:3.1.3.48] (RefSeq) protein-tyrosine-phosphatase (A)
148	Membrane	Membrane	Membrane	Membrane	Membrane	0.213423035	0.016526099	3.846323	0.9237277	Membrane	lmo:lmo1021 K11617 two-component system, NarL family, sensor histidine kinase LiaS [EC:2.7.13.3] (RefSeq) two-component sensor histidine kinase (A)
149	Membrane	Membrane	Membrane	Membrane	Membrane	0.2962564	0.11403947	3.859289	0.7304161	Membrane	lmo:lmo1061 K18345 two-component system, OmpR family, sensor histidine kinase VanS [EC:2.7.13.3] (RefSeq) two-component sensor histidine kinase (A)
150	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.001598697	0.003057301	0.04278047	4.952564	Cytoplasmic	lmo:lmo1299 K01915 glutamine synthetase [EC:6.3.1.2] (RefSeq) glnA; glutamine synthetase (A)
151	Membrane	Membrane	Membrane	Membrane	Membrane	0.21270636	0.08271379	4.59593	0.108648169	Membrane	lmo:lmo1695 K14205 phosphatidylglycerol lysyltransferase [EC:2.3.2.3] (RefSeq) hypothetical protein (A)
152	Extracellular	Extracellular	Extracellular	Cytoplasmic	Extracellular	2.09763573	0.20774488	1.0271152	1.667506	Extracellular	lmo:lmo1800 K01104 protein-tyrosine phosphatase [EC:3.1.3.48] (RefSeq) protein-tyrosine phosphatase (A)

153	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.06709902	0.033231679	0.3952294	4.50444	Cytoplasmic	lmo:lmo1935 K01104 protein-tyrosine phosphatase [EC:3.1.3.48] (RefSeq) protein-tyrosine/serine phosphatase (A)
154	Membrane	Membrane	Membrane	Membrane	Membrane	0.05726479	0.015427186	4.06933	0.85797822	Membrane	lmo:lmo1947 K07651 two-component system, OmpR family, sensor histidine kinase ResE [EC:2.7.13.3] (RefSeq) resE; two-component sensor histidine kinase (A)
155	Cytoplasmic	Membrane	Cytoplasmic	Membrane	Membrane	0.6347976	0.08269691	1.905755	2.37675	Cytoplasmic	lmo:lmo2011 K07718 two-component system, sensor histidine kinase YesM [EC:2.7.13.3] (RefSeq) two-component sensor histidine kinase (A)
156	Membrane	Membrane	Cytoplasmic	Cytoplasmic	Membrane	0.038437977	0.01706986	3.174982	1.7695106	Membrane	lmo:lmo2500 K07636 two-component system, OmpR family, phosphate regulon sensor histidine kinase PhoR [EC:2.7.13.3] (RefSeq) phoR; two-component sensor histidine kinase (A)
157	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.001329339	0.001494261	0.13186012	4.865316	Cytoplasmic	lmo:lmo2537 K01791 UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing) [EC:5.1.3.14] (RefSeq) UDP-N-acetylglucosamine 2-epimerase (A)
158	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	Membrane	0.190046393	0.067172323	2.741618	2.0011623	Membrane	lmo:lmo2679 K07646 two-component system, OmpR family, sensor histidine kinase KdpD [EC:2.7.13.3] (RefSeq) histidine kinase (A)
159	Membrane	Membrane	Membrane	Membrane	Membrane	0.07111583	0.02213825	4.815837	0.09090895	Membrane	lmo:lmo2681 K01547 potassium-transporting ATPase ATP-binding subunit [EC:7.2.2.6] (RefSeq) kdpB; potassium-transporting ATPase subunit B (A)
160	Membrane	Membrane	Membrane	Membrane	Membrane	0.101527556	0.03608365	4.82786	0.034528013	Membrane	lmo:lmo2717 K00426 cytochrome bd ubiquinol oxidase subunit II [EC:7.1.1.7] (RefSeq) cydB; cytochrome D ubiquinol oxidase subunit II (A)
161	Membrane	Membrane	Membrane	Membrane	Membrane	0.02139997	0.012461755	4.947146	0.018993272	Membrane	lmo:lmo2718 K00425 cytochrome bd ubiquinol oxidase subunit I [EC:7.1.1.7] (RefSeq) cydA; cytochrome D ubiquinol oxidase subunit I (A)
162	Extracellular	Extracellular	Extracellular	Extracellular	Extracellular	4.156287	0.0752697	0.2010513	0.56739221	Extracellular	lmo:lmo0205 K01114 phospholipase C [EC:3.1.4.3] (RefSeq) plcB; phospholipase C (A)
163	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.1669681	0.004704628	0.1769843	4.651344	Cytoplasmic	lmo:lmo0447 K01580 glutamate decarboxylase [EC:4.1.1.15] (RefSeq) glutamate decarboxylase (A)
164	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.0938075	0.017372904	0.10293159	4.785888	Cytoplasmic	lmo:lmo0539 K01635 tagatose 1,6-diphosphate aldolase [EC:4.1.2.40] (RefSeq) tagatose 1,6-diphosphate aldolase (A)

165	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.09680991	0.008504456	0.37670059	4.517984	Cytoplasmic	lmo:lmo1288 K07173 S-ribosylhomocysteine lyase [EC:4.4.1.21] (RefSeq) S-ribosylhomocysteinase (A)
166	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.01405005	0.009357264	0.9755273	4.001066	Cytoplasmic	lmo:lmo1632 K01658 anthranilate synthase component II [EC:4.1.3.27] (RefSeq) trpG; anthranilate synthase subunit beta (A)
167	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.005348115	0.002649102	0.05507041	4.936932	Cytoplasmic	lmo:lmo1633 K01657 anthranilate synthase component I [EC:4.1.3.27] (RefSeq) trpE; anthranilate synthase subunit alpha (A)
168	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.03360073	0.003941984	0.14991811	4.812538	Cytoplasmic	lmo:lmo2434 K01580 glutamate decarboxylase [EC:4.1.1.15] (RefSeq) glutamate decarboxylase (A)
169	Cytoplasmic	Membrane	Cytoplasmic	Cytoplasmic	Cytoplasmic	0.010115799	0.015706549	1.5412171	3.432961	Cytoplasmic	lmo:lmo0716 K02412 flagellum-specific ATP synthase [EC:7.4.2.8] (RefSeq) fliI; flagellum-specific ATP synthase (A)
170	Membrane	Membrane	Membrane	Membrane	Membrane	0.02969228	0.02547583	4.92448	0.020351892	Membrane	lmo:lmo2745 K18104 ATP-binding cassette, subfamily B, bacterial AbcA/BmrA [EC:7.6.2.2] (RefSeq) ABC transporter ATP-binding protein (A)
171	Extracellular	Cytoplasmic	Membrane	Extracellular	Cytoplasmic	1.5599287	0.27002547	1.4793245	1.6907216	Cytoplasmic	lmo:lmo0129 K01448 N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28] (RefSeq) N-acetylmuramoyl-L-alanine amidase (A)
172	Membrane	Membrane	Extracellular	Extracellular	Extracellular	2.740831	0.2574619	1.858459	0.14324733	Extracellular	lmo:lmo1521 K01448 N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28] (RefSeq) N-acetylmuramoyl-L-alanine amidase (A)

Supplementary Table 5: Structural Classification of the unique identified target enzymes/proteins from RCSB Protein Data Bank (PDB)

												Ligands		
	Predicted Enzyme name from <i>Listeria monocytogenes</i>	PDB Structure available	PDB ID	Classification	Organism(s)	Expression System	Mutation(s)	Seq Length	Chain	Experiment type	Gene Names	Name / Formula	ID	Chain
1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	2.23 Angstrom resolution crystal structure of UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA) from <i>Listeria monocytogenes</i> EGD-e	3R38	TRANSFERASE	<i>Listeria monocytogenes</i> EGD-e	<i>Escherichia coli</i> BL21	No	454	A	X-RAY DIFFRACTION	lmo2526, murA, murA1	SULFATE ION O4 S	S O4	A
												CHLORIDE ION Cl	CL	A
2	Phosphate acetyltransferase	The crystal structure of a possible phosphate acetyl/butaryl transferase	3U9E	TRANSFERASE	<i>Listeria monocytogenes</i> EGD-e	<i>Escherichia coli</i> BL21(DE3)	No	291	A, B	X-RAY DIFFRACTION	lmo1369	COENZYME A C21 H36 N7 O16 P3 S	CO A	A, B
												ARGININE C6 H15 N4 O2	ARG	B

		e (from <i>Listeria monocytogenes</i> EGD-e) in complex with CoA.										GLYCEROL C ₃ H ₈ O ₃	G O L	A, B
												CHLORIDE ION Cl	C L	A
3	Acetate kinase	Crystal structure of <i>Salmonella typhimurium</i> acetate kinase (AckA) with citrate bound at the dimeric interface	3S K3	TRANSFERASE	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhimurium</i>	<i>Escherichia coli</i>	No	41 5	A, B	X-RAY DIFFRACTION	ackA	Citric acid C ₆ H ₈ O ₇	CI T	A
												1,2-Ethanediol [Ethylene glycol] C ₂ H ₆ O ₂	E D O	A, B
4	Aspartate kinase	Mechanistic insight into the regulation of <i>Pseudomonas aeruginosa</i> aspartate kinase	5Y EI	TRANSFERASE	<i>Pseudomonas aeruginosa</i> PAO1	<i>Escherichia coli</i> BL21(DE3)	No	41 2	D, B, F, H, C, B, A, E	X-RAY DIFFRACTION	lysC, PA0904	Threonine C ₄ H ₉ NO ₃	T H R	D, F, G, A
												Lysine C ₆ H ₁₅ N ₂ O ₂	L Y S	C
												Glycerol [Glycerin; propane-1,2,3-Triol] C ₃ H ₈ O ₃	G O L	G, E

5	Penicillin-binding protein 2A	Crystal Structure of Penicillin Binding Protein 4 from <i>Listeria monocytogenes</i> in the Ampicillin bound form	3ZG8	PENICILLIN-BINDING PROTEIN	<i>Listeria monocytogenes</i>	<i>Escherichia coli</i> BL21(DE3)	No	47	A, B	X-RAY DIFFRACTION	N/A	(2r,4s)-2-[(1r)-1-[[[(2r)-2-Amino-2-Phenylacetyl]amino]-2-Oxoethyl]-5,5-Dimethyl-1,3-Thiazolidine-4-Carboxylic acid C16H21N3O4S	AI X	B
		Glycerol [Glycerin; propane-1,2,3-Triol] C3H8O3										G O L	B	
		Crystal Structure of Penicillin-Binding Protein D2 from <i>Listeria monocytogenes</i> in the apo form	5ZQA	ANTIBIOTIC	<i>Listeria monocytogenes</i> EGD-e	<i>Escherichia coli</i>	No	276	A	X-RAY DIFFRACTION	lmo2812	Di(hydroxyethyl)ether C4H10O3	P E G	A
6	Homoserine Dehydrogenase	Homoserine Dehydrogenase Complex	1EBU	OXIDOREDUCTASE	<i>Saccharomyces cerevisiae</i>	<i>Escherichia coli</i>	No	358	A, B, C, D	X-RAY DIFFRACTION	HOM6P	3-Aminomethyl-Pyridinium-Adenine-	N D A	D

		with NAD analogue and L-Homoserine									Dinucleotide C ₂₁ H ₂₉ N ₇ O ₁₃ P ₂			
											L-Homoserine C ₄ H ₉ NO ₃	H S E	D	
7	Cytochrome BD ubiquinol oxidase subunit I	The Structure of BD Oxidase from <i>Escherichia coli</i>	6RX4	OXIDOREDUCTASE	<i>Escherichia coli</i> K-12	<i>Escherichia coli</i> K-12	No	522	A, B	ELECTRON MICROSCOPY	cydA, cyd-1, b0733, JW0722	Heme b/c [Hybrid between b and c type hemes (protoporphyrin X)] C ₃₄ H ₃₄ FeN ₄ O ₄	H E B	A
											Cis-Heme d hydroxychlorin gamma-Spirolactone [Heme] C ₃₄ H ₃₂ FeN ₄ O ₅	H D D	A	
											1,2-Dioleoyl-Sn-Glycero-3-Phosphoethanolamine [Dope] C ₄₁ H ₈₃ NO ₈ P	P E E	B	

												Ubiquinone-8 [2,3-Dimethoxy-5-Methyl-6-[(6e,10e,14e,18e,22e,26e)-3,7,11,15,19,23,27,31-Octamethyl-dotriacont-2,6,10,14,18,22,26,30-Octaen-1-Yl]cyclohexa-2,5-Diene-1,4-Dione] C49H74O4	U Q 8	B
8	Fructose-bisphosphate aldolase, class II	The crystal structure of fructose 1,6-bisphosphate aldolase from <i>Bacillus anthracis</i> str. 'Ames Ancestor'	3Q94	LYASE	<i>Bacillus anthracis</i> str. 'Ames Ancestor'	<i>Escherichia coli</i>	No	288	A, B	X-RAY DIFFRACTION	fba2, BAS5184, BA_5580, GBAA5580, GBAA_5580	1,3-Dihydroxyacetonephosphate C3H7O6P	13 P	A
												Acetate ion C2H3O2	A C T	A
9	Undecaprenol kinase	N/A												

10	PTS system, fructose-specific IIB component	Crystal structure of the fructose specific IIB subunit of PTS system from <i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	2R48	TRANSFERASE, TRANSPORT PROTEIN	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	<i>Escherichia coli</i> BL21(DE3)	No	106	A	X-RAY DIFFRACTION	manP, BSU12010, yjdD EC: 2.7.1.191	N/A		
11	PTS system, mannitol-specific IIB component	Structure of IIB Domain of the Mannitol-Specific Permease Enzyme II	1VKR	TRANSFERASE	<i>Escherichia coli</i> O157:H7	<i>Escherichia coli</i>	No	125	A	SOLUTION NMR	N/A	N/A		
12	PTS system, cellobiose-specific IIB component	1.85 Angstrom Resolution Crystal Structure of PTS System Cellobiose-specific Transporter Subunit IIB from	4MGE	TRANSFERASE	<i>Bacillus anthracis</i> str. 'Ames Ancestor	<i>Escherichia coli</i> BL21(DE3)	No	116	A, B	X-RAY DIFFRACTION	celA2, BA_5444, BAS5059, GBAA_5444	1,2-Ethanediol [Ethylene glycol] C2H6O2	ED O	A

		<i>Bacillus anthracis.</i>												
1 3	PTS system, sugar-specific IIA component	Structure of the full-length Enzyme I of the PTS system from <i>Staphylococcus carnosus</i>	2H R O	TRANSFERASE	<i>Staphylococcus carnosus</i>	<i>Escherichia coli</i>	No	57 3	A	X-RAY DIFFRACTION	Pts1	Sulfate ion O4S2	S O 4	A
1 4	PTS system, beta-glucoside-specific IIA component	Three-Dimensional Structure of the <i>Escherichia coli</i> Phosphocarrier Protein III GLC	1F 3G	PHOSPHOTRANSFERASE	<i>Escherichia coli</i>	<i>Escherichia coli</i>	No	16 1	A	X-RAY DIFFRACTION	N/A	N/A		