

Supplementary Table 1 List of <i>M. succiniciproducens</i> MBEL55E genes. Gene names, locations, sizes and annotation results are shown.											
Gene name	Gene locations	Gene locations	Size(bp)	Highest similar gene from COG	E-value of BLAST	Organism (Col. E)	Functional categories of COG	COG number matched	Gene description (based on COG database)	Available short name of the gene (using COG DB)	Annotation results based on non-redundant database search for comparison (see footnote)
MS0001	3770	4132	363	none	none	No-des	none	No-des	No-des	none	none
MS0002	4489	4400	90	none	none	No-des	none	No-des	No-des	none	none
MS0003	4475	5164	690	PM1753	3.00E-55	Pmu	S	COG1285	Uncharacterized membrane protein	SapB (BS)	(NC_002663) unknown [Pasteurella multocida]
MS0004	6152	5205	948	PM1631	1.00E-111	Pmu	I	COG2267	Lysophospholipase	PldB	(NC_002663) PldB [Pasteurella multocida]
MS0005	6182	6307	126	none	none	No-des	none	No-des	No-des	none	none
MS0006	7427	6318	1110	HI0646	0	Hin	E	COG0136	Aspartate-semialdehyde dehydrogenase	Asd	(NC_000907) aspartate-semialdehyde dehydrogenas...
MS0007	8554	7577	978	PM1521	1.00E-132	Pmu	D	COG2177	Cell division protein	FtsX	(NC_002663) FtsX [Pasteurella multocida]
MS0008	9171	8524	648	PM1520	1.00E-104	Pmu	D	COG2884	Predicted ATPase involved in cell division	FtsE	(NC_002663) FtsE [Pasteurella multocida]
MS0009	9662	9312	351	none	none	No-des	none	No-des	No-des	none	none
MS0010	9875	9738	138	none	none	No-des	none	No-des	No-des	none	none
MS0011	10401	9853	549	NMB1796	6.00E-21	Nme	R	COG0431	Predicted flavoprotein		chromate reductase [Pseudomo...
MS0012	10949	10647	303	none	none	No-des	none	No-des	No-des	none	none
MS0013	12463	11012	1452	HI0553	0	Hin	G	COG0362	6-phosphogluconate dehydrogenase/family 1	Gnd	(NC_000907) 6-phosphogluconate dehydrogenase/d...
MS0014	13375	12620	756	PM1626	2.00E-79	Pmu	M	COG1794	Aspartate racemase	RacX (BS)	(NC_002663) unknown [Pasteurella multocida]
MS0015	14113	13418	696	PM1550	6.00E-95	Pmu	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase	NagB	6-PHOSPHOGLUCONOLACTONASE (6PGL)
MS0016	15686	14205	1482	PM1549	0	Pmu	G	COG0364	Glucose-6-phosphate 1-dehydrogenase	Zwf	(NC_002663) Zwf [Pasteurella multocida]
MS0017	16564	15764	801	PM1548	5.00E-74	Pmu	P	COG1218	3'-Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase	CysQ	CYSO PROTEIN HOMOLOG
MS0018	18722	16719	2004	NMA0207	0	NmA	S	COG1297	Uncharacterized membrane protein		(NC_003116) putative integral membrane protein ...
MS0019	19455	18907	549	PM1544	1.00E-66	Pmu	L/R	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	MutT	(NC_002663) unknown [Pasteurella multocida]
MS0020	20315	19641	675	PM0766	8.00E-99	Pmu	G	COG0269	3-hexulose-6-phosphate synthase and related proteins	SgbH	(NC_002663) unknown [Pasteurella multocida]
MS0021	20837	20373	465	PM0765	9.00E-59	Pmu	G/T	COG1762	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	PtsN	(NC_002663) unknown [Pasteurella multocida]
MS0022	22700	20889	1812	PM0764	0	Pmu	S	COG3037	Uncharacterized BCR	SgaT	(NC_002663) unknown [Pasteurella multocida]
MS0023	22987	24129	1143	PM0763	1.00E-177	Pmu	R	COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold		(NC_002663) unknown [Pasteurella multocida]
MS0024	24206	24970	765	PM0762	3.00E-82	Pmu	K/G	COG1349	Transcriptional regulators of sugar metabolism	GlpR	(NC_002663) unknown [Pasteurella multocida]
MS0025	25933	25088	846	HI0269	1.00E-140	Hin	K	COG0568	DNA-directed RNA polymerase sigma subunits (sigma70/sigma32)	RpoD	(NC_000907) RNA polymerase sigma-32 factor (rpo...
MS0026	27025	26072	954	PM1587	2.00E-80	Pmu	P	COG1275	Tellurite resistance protein and related permeases	TehA	(NC_002663) TehA [Pasteurella multocida]
MS0027	27339	27028	312	PM1588	2.00E-32	No-des	none	No-des	No-des	none	none
MS0028	28379	27357	1023	PM1589	1.00E-147	Pmu	M	COG0812	UDP-N-acetylmuramate dehydrogenase	MurB	(NC_002663) MurB [Pasteurella multocida]
MS0029	28425	28526	102	none	none	No-des	none	No-des	No-des	none	none
MS0030	29699	28494	1206	HI1530	1.00E-152	Hin	E	COG0786	Na ⁺ /glutamate symporter	GltS	(NC_000907) glutamate permease (gltS) [Haemophi...
MS0031	30324	29893	432	HI0670	3.00E-53	Hin	J	COG1490	D-Tyr-tRNA ^{Tyr} deacylase	Did	(NC_000907) conserved hypothetical protein [Hae...
MS0032	31184	30324	861	PM1616	3.00E-91	Pmu	J	COG1295	tRNA-processing ribonuclease BN	Rbn	(NC_002663) Rbn [Pasteurella multocida]
MS0033	31651	31169	483	HI0277	1.00E-52	Hin	S	COG3012	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS0034	31731	33278	1548	PM1435	0	Pmu	R	COG0433	Predicted ATPase		(NC_002663) unknown [Pasteurella multocida]
MS0035	33808	33359	450	PM1573	9.00E-77	Pmu	K	COG1522	Transcriptional regulators	Lrp	(NC_002663) AsnC [Pasteurella multocida]
MS0036	33987	34976	990	PM1574	1.00E-165	Pmu	E	COG2502	Asparagine synthetase A	AsnA	(NC_002663) AsnA [Pasteurella multocida]
MS0037	35055	35147	93	none	none	No-des	none	No-des	No-des	none	none
MS0038	36556	35240	1317	PM1423	1.00E-150	Pmu	C	COG1883	Na ⁺ -transporting methylmalonyl-CoA/oxaloacetate decarboxylase beta subunit	OadB	(NC_002663) unknown [Pasteurella multocida]
MS0039	38369	36564	1806	PM1422_1	0	Pmu	C	COG3632	Na ⁺ -transporting methylmalonyl-CoA/oxaloacetate decarboxylase alpha subunit	OadA	(NC_002663) unknown [Pasteurella multocida]
MS0040	38657	38394	264	PM1421	5.00E-23	Pmu	C	COG3630	Na ⁺ -transporting methylmalonyl-CoA/oxaloacetate decarboxylase gamma subunit	OadG	(NC_002663) unknown [Pasteurella multocida]
MS0041	39852	38824	1029	HI0985	2.00E-97	Hin	L/N	COG0758	Predicted Rossmann-fold nucleotide-binding protein involved in DNA uptake	Smf	(NC_000907) DNA processing chain A (dprA) [Haem...
MS0042	39983	39828	156	none	none	No-des	none	No-des	No-des	none	none
MS0043	40059	39970	90	none	none	No-des	none	No-des	No-des	none	none
MS0044	40957	40052	906	PM1283	1.00E-119	Pmu	K	COG0583	Transcriptional regulator	LysR	(NC_002663) IlvY [Pasteurella multocida]
MS0045	41152	42630	1479	HI0682	0	Hin	E/H	COG0059	Ketol-acid reductoisomerase	IlvC	(NC_000907) ketol-acid reductoisomerase (ilvC) ...
MS0046	43401	42712	690	PM1244	1.00E-96	Pmu	G	COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	AraD	(NC_002663) AraD [Pasteurella multocida]
MS0047	44255	43398	858	PM1245	1.00E-147	Pmu	G	COG3623	Putative L-xylulose-5-phosphate 3-epimerase	SgaU	(NC_002663) unknown [Pasteurella multocida]
MS0048	45761	44307	1455	PM1247	0	Pmu	G	COG1070	Sugar (pentulose and hexulose) kinases	XylB	(NC_002663) Lyx [Pasteurella multocida]
MS0049	46882	45896	987	PM1252	1.00E-149	Pmu	G	COG1638	Dicarboxylate-binding periplasmic protein	DctP	(NC_002663) unknown [Pasteurella multocida]
MS0050	47933	46950	984	HI1028	1.00E-151	Hin	G	COG1638	Dicarboxylate-binding periplasmic protein	DctP	(NC_000907) conserved hypothetical protein [Hae...
MS0051	49285	48011	1275	PM1253	1.00E-143	Pmu	S	COG1593	Integral membrane protein possible transporter		(NC_002663) unknown [Pasteurella multocida]
MS0052	49764	49285	480	PM1254	3.00E-59	Pmu	S	COG3090	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0053	50235	49777	459	PM1255	1.00E-48	Pmu	S	COG2731	Uncharacterized BCR	EbgC	(NC_002663) unknown [Pasteurella multocida]
MS0054	51454	50342	1113	HI1031	1.00E-172	Hin	C	COG2055	Malate/L-lactate dehydrogenases		(NC_000907) conserved hypothetical protein [Hae...
MS0055	51479	52297	819	HI1032	4.00E-87	Hin	K	COG1414	Transcriptional regulator	IclR	(NC_000907) transcriptional regulator putative...

MS0056	52337	53011	675	PM0766	8.00E-99	Pmu	G	COG0269	3-hexulose-6-phosphate synthase and related proteins	SgbH	(NC_002663) unknown [Pasteurella multocida]
MS0057	53202	55196	1995	HI1023	0	Hin	G	COG0021	Transketolase	TktA	(NC_000907) transketolase 1 (ktA) [Haemophilus...
MS0058	56821	55337	1485	ZaraA	1.00E-167	EcZ	G	COG2160	L-arabinose isomerase	AraA	(NC_003143) L-arabinose isomerase [Yersinia pes...
MS0059	58453	56852	1602	HI1113	4.00E-16	Hin	G	COG1070	Sugar (pentulose and hexulose) kinases	XylB	(NC_003030) Sugar kinase/possible xylulose kin...
MS0060	59501	58647	855	ZaraC	8.00E-66	EcZ	K	COG2207	AraC-type DNA-binding domain-containing proteins	AraC	ARABINOSE OPERON REGULATORY PROTEIN
MS0061	60487	59516	972	araH	1.00E-125	Eco	G	COG1172	Ribose/xylulose/arabinose/galactoside ABC-type transport systems/permease components	AraH	(NC_000913) ABC-type arabinose transport system...
MS0062	61992	60487	1506	araG	1.00E-169	Eco	G	COG1129	ABC-type sugar (aldose) transport system/ATPase component	MglA	(NC_003143) L-arabinose transport ATP-binding p...
MS0063	63063	62053	1011	ZaraF	1.00E-136	EcZ	G	COG1879	Periplasmic sugar-binding proteins	RbsB	(NC_002655) L-arabinose-binding periplasmic pro...
MS0064	65267	63300	1968	PM2014	0	Pmu	F	COG0737	5'-nucleotidase/2[3'-cyclic phosphodiesterase and related esterases	UshA	(NC_002663) CpdB [Pasteurella multocida]
MS0065	65517	66770	1254	BH0802	1.00E-22	Bha	S	COG3395	Uncharacterized BCR		(NC_003197) putative inner membrane protein [Sa...
MS0066	66788	67786	999	BH0804	3.00E-82	Bha	H	COG1995	Pyridoxal phosphate biosynthesis protein	PdxA	(NC_003197) pyridoxine phosphate biosynthetic p...
MS0067	67808	68683	876	VNG0444G	1.00E-45	Hbs	E J	COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	DapA	(NC_002607) dihydrodipicolinate synthase; DapA ...
MS0068	68693	69670	978	MTH970	9.00E-56	Mth	E	COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	SerA	(NC_000916) phosphoglycerate dehydrogenase [Met...
MS0069	69686	70837	1152	BS_gbsB	7.00E-61	Bsu	C	COG1454	Alcohol dehydrogenase IV	EutG	(AF052750) alcohol dehydrogenase [Pseudomonas put...
MS0070	70842	70937	96	none	none	No-des	none	No-des	No-des	none	none
MS0071	71026	71526	501	none	none	No-des	none	No-des	No-des	none	none
MS0072	71542	73032	1491	PM1681	1.00E-80	Pmu	S	COG3333	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0073	73056	74036	981	BH2007	1.00E-19	No-des	none	No-des	No-des	none	HYPOTHETICAL 35.6 KD PROTEIN IN GBD 5'REGIO...
MS0074	74118	74870	753	ygbI	2.00E-41	Eco	K G	COG1349	Transcriptional regulators of sugar metabolism	GlpR	(NC_003198) putative transcriptional regulator ...
MS0075	75873	75052	822	HI1523	1.00E-106	No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS0076	76019	75894	126	none	none	No-des	none	No-des	No-des	none	none
MS0077	76505	76023	483	NMA1822	1.00E-23	No-des	none	No-des	No-des	none	(NC_003116) hypothetical protein [Neisseria men...
MS0078	77256	76501	756	hfaE	2.00E-12	No-des	none	No-des	No-des	none	(AY027935) orf32 [Haemophilus influenzae phage HP2]
MS0079	78158	77271	888	stfE	3.00E-22	No-des	none	No-des	No-des	none	(NC_003198) bacteriophage tail fiber protein [S...
MS0080	78770	78180	591	none	none	No-des	none	No-des	No-des	none	(NC_003198) putative bacteriophage tail fiber p...
MS0081	79845	78751	1095	XF2488	6.00E-17	No-des	none	No-des	No-des	none	(NC_003198) putative bacteriophage baseplate as...
MS0082	80226	79858	369	none	none	No-des	none	No-des	No-des	none	(NC_003197) putative phage baseplate protein [S...
MS0083	80808	80275	534	XF2492	6.00E-08	No-des	none	No-des	No-des	none	(NC_003198) putative bacteriophage baseplate pr...
MS0084	81859	80798	1062	PA0628	4.00E-18	Pae	R	COG3500	Phage protein D		(NC_003198) putative bacteriophage regulatory p...
MS0085	82085	81855	231	none	none	No-des	none	No-des	No-des	none	(NC_003197) putative inner membrane protein [Sa...
MS0086	83007	82066	942	none	none	No-des	none	No-des	No-des	none	(NC_003198) hypothetical protein [Salmonella en...
MS0087	85652	83010	2643	XF0730	1.00E-61	No-des	none	No-des	No-des	none	(AF420275) phage-related tail protein [Wolbachia ...
MS0088	85663	86073	411	none	none	No-des	none	No-des	No-des	none	none
MS0089	86220	86092	129	none	none	No-des	none	No-des	No-des	none	none
MS0090	86621	86241	381	none	none	No-des	none	No-des	No-des	none	none
MS0091	87126	86611	516	none	none	No-des	none	No-des	No-des	none	(NC_003197) putative phage tail core protein [S...
MS0092	88534	87143	1392	XF2485	2.00E-23	Xfa	R	COG3497	Phage tail sheath protein FI		(AB045036) tail sheath protein [Pectobacterium c...
MS0093	89050	88565	486	none	none	No-des	none	No-des	No-des	none	(NC_003198) hypothetical protein [Salmonella en...
MS0094	89487	89056	432	HI1508	9.00E-09	No-des	none	No-des	No-des	none	(NC_003198) conserved bacteriophage hypothetica...
MS0095	89723	89490	234	none	none	No-des	none	No-des	No-des	none	none
MS0096	90757	89816	942	none	none	No-des	none	No-des	No-des	none	(NC_003198) hypothetical protein [Salmonella en...
MS0097	91930	90803	1128	none	none	No-des	none	No-des	No-des	none	(NC_003198) hypothetical protein [Salmonella en...
MS0098	92598	92140	459	HI1568	5.00E-08	No-des	none	No-des	No-des	none	(NC_000907) G protein (muG-2) [Haemophilus infl...
MS0099	92659	92889	231	none	none	No-des	none	No-des	No-des	none	none
MS0100	94434	93160	1275	NMA1850_2	1.00E-27	No-des	none	No-des	No-des	none	(NC_003116) hypothetical protein [Neisseria men...
MS0101	95875	94430	1446	NMB1095	4.00E-26	No-des	none	No-des	No-des	none	(NC_003198) hypothetical protein [Salmonella en...
MS0102	97520	95988	1533	HI1500	1.00E-103	No-des	none	No-des	No-des	none	(NC_003198) conserved hypothetical protein [Sal...
MS0103	98068	97520	549	none	none	No-des	none	No-des	No-des	none	(NC_003198) hypothetical protein [Salmonella en...
MS0104	98375	98076	300	none	none	No-des	none	No-des	No-des	none	(NC_003198) hypothetical protein [Salmonella en...
MS0105	98656	98378	279	none	none	No-des	none	No-des	No-des	none	(NC_003197) putative inner membrane protein [Sa...
MS0106	98859	98683	177	none	none	No-des	none	No-des	No-des	none	none
MS0107	99135	98875	261	none	none	No-des	none	No-des	No-des	none	none
MS0108	99678	99172	507	NMA1230	1.00E-61	No-des	none	No-des	No-des	none	(NC_003112) hypothetical protein [Neisseria men...
MS0109	100381	100121	261	none	none	No-des	none	No-des	No-des	none	none
MS0110	101444	100377	1068	none	none	No-des	none	No-des	No-des	none	none
MS0111	101872	101444	429	none	none	No-des	none	No-des	No-des	none	none
MS0112	102351	101875	477	NMB1007	2.00E-16	Nme	K	COG1396	Predicted transcriptional regulators	HipB	(NC_003112) transcriptional regulator [Neisseri...
MS0113	102388	102624	237	NMB1004	3.00E-08	No-des	none	No-des	No-des	none	(NC_003112) hypothetical protein [Neisseria men...
MS0114	103011	102733	279	none	none	No-des	none	No-des	No-des	none	none
MS0115	103126	103221	96	none	none	No-des	none	No-des	No-des	none	none

MS0116	103035	103301	267	NMB1005	1.00E-14	No-des	none	No-des	No-des	none	(NC_003112) hypothetical protein [Neisseria men...
MS0117	103421	103588	168	none	none	No-des	none	No-des	No-des	none	none
MS0118	103564	103887	324	NMA1223	4.00E-12	No-des	none	No-des	No-des	none	(NC_003116) hypothetical protein NMA1223 [Neiss...
MS0119	103946	104839	894	NMB1002	7.00E-44	No-des	none	No-des	No-des	none	(NC_003112) hypothetical protein [Neisseria men...
MS0120	104852	106666	1815	VC1799	3.00E-71	No-des	none	No-des	No-des	none	(NC_003198) hypothetical protein [Salmonella en...
MS0121	106673	107863	1191	VC1798	2.00E-57	Vch	N	COG3267	General secretion pathway protein A	ExeA	(AF091717) Eha [Salmonella typhi]
MS0122	107869	108390	522	HI1483	7.00E-45	No-des	none	No-des	No-des	none	(NC_000907) host-nuclease inhibitor protein (ga...
MS0123	108390	108599	210	none	none	No-des	none	No-des	No-des	none	none
MS0124	108604	108762	159	none	none	No-des	none	No-des	No-des	none	none
MS0125	108762	109172	411	none	none	No-des	none	No-des	No-des	none	none
MS0126	109222	109503	282	NMA1874	1.00E-11	No-des	none	No-des	No-des	none	(NC_003116) hypothetical protein [Neisseria men...
MS0127	109496	109876	381	HI1488	3.00E-11	No-des	none	No-des	No-des	none	(NC_003198) conserved hypothetical protein [Sal...
MS0128	109880	110251	372	VC1796	6.00E-06	No-des	none	No-des	No-des	none	(NC_003198) putative bacteriophage transcriptio...
MS0129	110257	110598	342	none	none	No-des	none	No-des	No-des	none	(NC_003198) hypothetical protein [Salmonella en...
MS0130	112399	110753	1647	PM1267	0	Pmu	S	COG1322	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0131	112537	113094	558	PM1269	1.00E-74	Pmu	L	COG0551	Zn-finger domain associated with topoisomerase type I	TopA	(NC_002663) unknown [Pasteurella multocida]
MS0132	113100	113648	549	PM1270	1.00E-73	Pmu	J	COG0009	Putative translation factor (SUA5)	SUA5	(NC_002663) unknown [Pasteurella multocida]
MS0133	113655	115013	1359	PM1271	1.00E-111	Pmu	E	COG0169	Shikimate 5-dehydrogenase	AroE	(NC_002663) AroE [Pasteurella multocida]
MS0134	115051	115872	822	Ta1445	1.00E-16	No-des	none	No-des	No-des	none	(NC_002758) hypothetical protein [Staphylococcu...
MS0135	115882	117138	1257	XFI738	4.00E-95	Xfa	C	COG3202	ATP/ADP translocase		(NC_002488) hypothetical protein [Xylella fasti...
MS0136	117311	118642	1332	PM0365	1.00E-138	Pmu	P	COG0025	NhaP-type Na+/H+ and K+/H+ antiporters	NhaP	(NC_002663) NhaP [Pasteurella multocida]
MS0137	120627	118702	1926	HI0658	0	Hin	R	COG0488	ATPase components of ABC transporters with duplicated ATPase domains	Uup	(NC_000907) ABC transporter(ATP-binding protei...
MS0138	120697	121311	615	PM1581	1.00E-75	Pmu	S	COG2095	Integral membrane proteins of the MarC family	MarC	(NC_002663) unknown [Pasteurella multocida]
MS0139	121984	121373	612	HI0767	4.00E-77	Hin	L	COG0742	N6-adenine-specific methylase		(NC_000907) conserved hypothetical protein [Hae...
MS0140	122119	123522	1404	PM1519	1.00E-158	Pmu	N	COG0552	Signal recognition particle GTPase	FtsY	(NC_002663) FtsY [Pasteurella multocida]
MS0141	124358	123579	780	CC2958	2.00E-57	Ccr	S	COG3384	Uncharacterized ACR		(NC_003143) conserved hypothetical protein [Yer...
MS0142	125278	124433	846	ZytG	4.00E-68	EcZ	M/G	COG0702	Predicted nucleoside-diphosphate-sugar epimerases		(NC_002655) putative oxidoreductase [Escherichi...
MS0143	125417	125797	381	ytH	9.00E-34	Eco	K	COG1733	Predicted transcriptional regulators		(NC_002695) hypothetical protein [Escherichia c...
MS0144	125797	126120	324	Z1870	3.00E-13	EcZ	P	COG2076	Membrane transporters of cations and cationic drugs	EmrE	(NC_003198) putative multidrug transporter [Sal...
MS0145	126163	127002	840	PM0638	1.00E-113	Pmu	R	COG1752	Predicted esterase of the alpha-beta hydrolase superfamily	RssA	(NC_002663) unknown [Pasteurella multocida]
MS0146	128019	127096	924	HI1114	1.00E-163	Hin	M/G	COG0451	Nucleoside-diphosphate-sugar epimerases	WcaG	(NC_000907) ADP-L-glycero-D-mannoheptose-6-epim...
MS0147	128165	128040	126	none	none	No-des	none	No-des	No-des	none	none
MS0148	129142	128123	1020	PA2320	1.00E-32	Pae	K	COG1609	Transcriptional regulators	PurR	(NC_003197) putative transcriptional regulator ...
MS0149	129277	129744	468	zcmbB	3.00E-26	EcZ	G/T	COG1762	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	PtsN	(AF286670) unknown [Escherichia coli]
MS0150	129769	130035	267	BH0222	4.00E-07	Bha	G	COG3414	Phosphotransferase system component IIB of unknown specificity	SgaB	(NC_003198) putative sugar phosphotransferase c...
MS0151	130049	131404	1356	SPy1949	7.00E-90	Spy	S	COG3037	Uncharacterized BCR	SgaT	(NC_003198) putative membrane protein [Salmonel...
MS0152	131605	132276	672	HI1116	7.00E-85	Hin	F	COG0274	Deoxyribose-phosphate aldolase	DeoC	(NC_000907) deoxyribose-phosphate aldolase (deo...
MS0153	133083	132430	654	PM1345	4.00E-80	Pmu	K	COG1309	Transcriptional regulator	AcrR	(NC_002663) unknown [Pasteurella multocida]
MS0154	133984	133079	906	HI0571	1.00E-135	Hin	K	COG0583	Transcriptional regulator	LysR	(NC_000907) hydrogen peroxide-inducible genes a...
MS0155	134106	134834	729	PM1347_1	2.00E-83	Pmu	O	COG0678	Peroxisomal protein	AHP1	(NC_000907) membrane protein [Haemophilus influ...
MS0156	135168	134917	252	PM1348	1.00E-25	Pmu	S	COG2900	Uncharacterized BCR	SlyX	(NC_002663) SlyX [Pasteurella multocida]
MS0157	135227	136060	834	PM1349	4.00E-60	Pmu	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases 1	FkpA	(NC_002663) SlyD [Pasteurella multocida]
MS0158	136085	136795	711	PM1350	4.00E-84	Pmu	S	COG2964	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0159	136798	137175	378	HI0576	1.00E-45	Hin	P	COG1553	Uncharacterized ACR involved in intracellular sulfur reduction	DsrE	(NC_000907) conserved hypothetical protein [Hae...
MS0160	137175	137531	357	HI0576.1	9.00E-40	Hin	P	COG2923	Uncharacterized protein involved in the oxidation of intracellular sulfur	DsrF	(NC_000907) conserved hypothetical protein [Hae...
MS0161	137536	137823	288	HI0577	5.00E-20	No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS0162	137962	138333	372	HI0581	2.00E-60	Hin	J	COG0048	Ribosomal protein S12	RpsL	(NC_000907) ribosomal protein S12 (rps12) [Haem...
MS0163	138428	138931	504	PM1355	2.00E-78	Pmu	J	COG0049	Ribosomal protein S7	RpsG	(NC_002663) RpS7 [Pasteurella multocida]
MS0164	139025	141124	2100	HI0579	0	Hin	J	COG0480	Translation elongation and release factors (GTPases)	FusA	(NC_000907) elongation factor G (fusA) [Haemoph...
MS0165	141198	142379	1182	HI0632	0	Hin	J/E	COG0050	GTPases - translation elongation factors	TufB	(NC_000907) elongation factor Tu (tufA) [Haemop...
MS0166	142615	143091	477	HI0766	1.00E-80	Hin	J	COG0219	Predicted rRNA methylase (SpoU class)	CspR (BS)	(NC_000907) rRNA methylase[putative [Haemophil...
MS0167	143168	143064	105	none	none	No-des	none	No-des	No-des	none	none
MS0168	143805	143113	693	PM1388	1.00E-109	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0169	145088	143832	1257	PM1387_3	1.00E-89	Pmu	H	COG3172	Nicotinamide mononucleotide-binding domain	NadR	(NC_002663) NadR [Pasteurella multocida]
MS0170	145087	145182	96	none	none	No-des	none	No-des	No-des	none	none
MS0171	145205	145327	123	none	none	No-des	none	No-des	No-des	none	none
MS0172	145527	146168	642	PM1385	1.00E-95	Pmu	H	COG0108	3/4-dihydroxy-2-butanone 4-phosphate synthase	RibB	(NC_002663) RibB [Pasteurella multocida]
MS0173	146478	146227	252	HI0721	8.00E-32	Hin	K	COG0425	Predicted transcriptional regulators	SirA	(NC_000907) conserved hypothetical protein [Hae...
MS0174	146552	147157	606	PM1497	5.00E-75	Pmu	S	COG1739	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS0175	147172	148632	1461	PM1498	1.00E-159	Pmu	P	COG0168	Trk-type K+ transport systems(membrane components	TrkG	(NC_002663) TrkH [Pasteurella multocida]

MS0176	148635	149147	513	PM1499	7.00E-55	Pmu	C	COG0716	Flavodoxins	FldA	(NC_002663) unknown [Pasteurella multocida]
MS0177	151115	151240	126	none	none	No-des	none	No-des	none	none	none
MS0178	154936	154841	96	none	none	No-des	none	No-des	none	none	none
MS0179	155347	154961	387	L35965	5.00E-19	Lla	K	COG0789	Predicted transcriptional regulators	SoxR	(NC_003212) similar to transcriptional regulato...
MS0180	155392	155808	417	L35675	2.00E-33	Lia	S	COG0599	Uncharacterized ACR/homolog of gamma-carboxymuconolactone decarboxylase subunit		(NC_002662) gamma-carboxymuconolactone decarbox...
MS0181	157173	155845	1329	HI0747	0	Hin	C	COG1252	NADH dehydrogenase/FAD-containing subunit	Ndh	(NC_000907) NADH dehydrogenase (ndh) [Haemophil...
MS0182	157369	158169	801	PM1735	1.00E-103	Pmu	L	COG2816	NTP pyrophosphohydrolases containing a Zn-finger/probably nucleic-acid-binding	NPY1	(NC_002663) unknown [Pasteurella multocida]
MS0183	158215	159276	1062	PM1734	0	Pmu	H	COG0407	Uroporphyrinogen-III decarboxylase	HemE	(NC_002663) UroD [Pasteurella multocida]
MS0184	159336	159923	588	PM1733	8.00E-83	Pmu	S	COG3068	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0185	160092	160364	273	HI0430	3.00E-39	Hin	L	COG0776	Bacterial nucleoid DNA-binding protein	HimA	(NC_000907) DNA-binding protein HU-alpha (hupA)...
MS0186	160398	160502	105	none	none	No-des	none	No-des	none	none	none
MS0187	160502	161275	774	VC0486	7.00E-87	Vch	K/G	COG1349	Transcriptional regulators of sugar metabolism	GlpR	(NC_002505) transcriptional regulator[DeoR fam...
MS0188	161342	161593	252	HI0429	7.00E-29	Hin	M	COG0449	Glucosamine 6-phosphate synthetase/contains amidotransferase and phosphosugar isomerase domains	GlmS	(NC_000907) glucosamine--fructose-6-phosphate a...
MS0189	161631	163172	1542	HI0429	0	Hin	M	COG0449	Glucosamine 6-phosphate synthetase/contains amidotransferase and phosphosugar isomerase domains	GlmS	(NC_000907) glucosamine--fructose-6-phosphate a...
MS0190	163189	163368	180	none	none	No-des	none	No-des	none	none	none
MS0191	163361	164569	1209	PM0835	1.00E-174	Pmu	G/E PIR	COG0477	Permeases of the major facilitator superfamily	ProP	(NC_002663) unknown [Pasteurella multocida]
MS0192	164699	165262	564	CJ0167c	6.00E-40	Cje	S	COG1971	Predicted membrane protein		(NC_002163) putative integral membrane protein ...
MS0193	166076	165354	723	PM1838	4.00E-56	Pmu	H	COG3201	Nicotinamide mononucleotide transporter	PnuC	(NC_002663) unknown [Pasteurella multocida]
MS0194	166508	166338	171	none	none	No-des	none	No-des	none	none	none
MS0195	166488	169388	2901	PM1837	0	Pmu	K/L	COG0553	Superfamily II DNA/RNA helicases/SNF2 family	HepA	(NC_002663) HepA [Pasteurella multocida]
MS0196	169634	171019	1386	HI0189	0	Hin	E	COG0334	glutamate dehydrogenase/leucine dehydrogenase	GdhA	(NC_000907) glutamate dehydrogenase (gdhA) [Hae...
MS0197	172053	171193	861	PA1950	6.00E-35	Pae	G	COG0524	Sugar kinases/ribo kinase family	RbsK	(NC_003143) ribokinase [Yersinia pestis]
MS0198	172924	172067	858	rpiR	1.00E-48	Eco	K	COG1737	Transcriptional regulators	RpiR	RPIR PROTEIN (ALS OPERON REPRESSOR)
MS0199	173862	172933	930	BS_rbsC	4.00E-56	Bsu	G	COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems/permease components	AraH	(NC_003143) putative sugar transport system/pe...
MS0200	175378	173852	1527	BS_rbsA	1.00E-114	Bsu	G	COG1129	ABC-type sugar (aldose) transport system/ATPase component	MglA	(NC_000964) ribose ABC transporter (ATP-binding...
MS0201	176443	175403	1041	alsB	5.00E-37	Eco	G	COG1879	Periplasmic sugar-binding proteins	RbsB	(NC_000913) putative LACI-type transcriptional ...
MS0202	177472	176492	981	TM1071	3.00E-17	No-des	none	No-des	none	none	Xylose isomerase
MS0203	178588	177863	726	PM1839	8.00E-77	Pmu	Q/R	COG0500	SAM-dependent methyltransferases	SmtA	(NC_002663) unknown [Pasteurella multocida]
MS0204	178775	179185	411	PM1745	6.00E-28	Pmu	N	COG0690	Preprotein translocase subunit SecE	SecE	(NC_002663) SecE [Pasteurella multocida]
MS0205	179190	179741	552	PM1744	3.00E-91	Pmu	K	COG0250	Transcription antiterminator	NusG	(NC_002663) NusG [Pasteurella multocida]
MS0206	179816	179950	135	none	none	No-des	none	No-des	none	none	none
MS0207	179966	180391	426	HI0517	2.00E-60	Hin	J	COG0080	Ribosomal protein L11	RplK	(NC_000907) ribosomal protein L11 (rplL1) [Haem...
MS0208	180399	181085	687	HI0516	1.00E-95	Hin	J	COG0081	Ribosomal protein L1	RplA	(NC_000907) ribosomal protein L1 (rplL1) [Haemop...
MS0209	181386	181874	489	PM1739	4.00E-80	Pmu	J	COG0244	Ribosomal protein L10	RplJ	(NC_002663) RplL10 [Pasteurella multocida]
MS0210	181926	182300	375	HI0641	3.00E-35	Hin	J	COG0222	Ribosomal protein L7/L12	RplL	(NC_000907) ribosomal protein L7/L12 (rplL7/L12)...
MS0211	182472	182612	141	none	none	No-des	none	No-des	none	none	none
MS0212	182813	186838	4026	PM1737	0	Pmu	K	COG0085	DNA-directed RNA polymerase beta subunit/140 kD subunit (split gene in Mjan Mthe Aful)	RpoB	(NC_002663) RpoB [Pasteurella multocida]
MS0213	186924	191237	4314	PM1736	0	Pmu	K	COG0086	DNA-directed RNA polymerase beta' subunit/160 kD subunit (split gene in archaea and Syn)	RpoC	(NC_002663) RpoC [Pasteurella multocida]
MS0214	191368	191964	597	ZycA	6.00E-25	EcZ	R	COG3318	Predicted metal-binding protein related to the C-terminal domain of SecA		(NC_003197) putative metal-binding protein rela...
MS0215	192008	192109	102	none	none	No-des	none	No-des	none	none	none
MS0216	192190	195633	3444	HI1258	0	Hin	L/K	COG1197	Transcription-repair coupling factor - superfamily II helicase	Mfd	(NC_000907) transcription-repair coupling facto...
MS0217	195777	195652	126	none	none	No-des	none	No-des	none	none	none
MS0218	195824	196303	480	HI1181	7.00E-84	Hin	G	COG0279	Phosphoheptose isomerase	GmhA	(NC_000907) phosphoheptose isomerase (gmhA) [Ha...
MS0219	196540	197268	729	HI1180	1.00E-104	Hin	E	COG1126	ABC-type polar amino acid transport system/ATPase component	GlnQ	(NC_000907) arginine ABC transporter(ATP-bindi...
MS0220	197210	198004	795	HI1179	1.00E-105	Hin	E	COG0834	ABC-type amino acid transport system/periplasmic component	ArlI	(NC_000907) arginine ABC transporter/periplasm...
MS0221	198014	198682	669	PM0125	1.00E-103	Pmu	E	COG0765	ABC-type amino acid transport system/permease component	ArtM	(NC_002663) ArtQ [Pasteurella multocida]
MS0222	198685	199365	681	HI1177	2.00E-94	Hin	E	COG0765	ABC-type amino acid transport system/permease component	ArtM	(NC_000907) arginine ABC transporter/permease ...
MS0223	199568	200968	1401	PM0939	0	Pmu	P	COG1858	Cytochrome c peroxidase	MauG	(AF200362) cytochrome c peroxidase [Hae...
MS0224	201447	201022	426	PM0770	1.00E-23	Pmu	S	COG2363	Uncharacterized small membrane protein		(NC_002663) unknown [Pasteurella multocida]
MS0225	201534	204428	2895	PM1065_2	0	Pmu	L	COG0749	DNA polymerase I - 3'-5' exonuclease and polymerase domains	PolA	(NC_002663) PolA [Pasteurella multocida]
MS0226	204566	204474	93	none	none	No-des	none	No-des	none	none	none
MS0227	204869	206926	2058	PM1791	0	Pmu	M	COG1292	Choline-glycine betaine transporter	BetT	(NC_002663) unknown [Pasteurella multocida]
MS0228	208387	207008	1380	PM1833	0	Pmu	H	COG0635	Coproporphyrinogen III oxidase and related FeS oxidoreductases	HemN	(NC_002663) HemN [Pasteurella multocida]
MS0229	208854	208402	453	PM1834	2.00E-28	No-des	none	No-des	none	none	(NC_002663) unknown [Pasteurella multocida]
MS0230	209451	208870	582	PM1835	2.00E-49	Pmu	S	COG3078	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0231	210262	209606	657	HI0617	1.00E-106	Hin	J	COG0564	Pseudouridylate synthases/23S RNA-specific	RluA	(NC_000907) conserved hypothetical protein [Hae...
MS0232	210366	210256	111	none	none	No-des	none	No-des	none	none	none
MS0233	211538	210399	1140	PM1117	1.00E-178	Pmu	E	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	ArgE	(NC_002663) ArgE [Pasteurella multocida]
MS0234	211647	211525	123	none	none	No-des	none	No-des	none	none	none
MS0235	211639	212646	1008	PM1118	1.00E-159	Pmu	E	COG0002	Acetylglutamate semialdehyde dehydrogenase	ArgC	(NC_002663) ArgC [Pasteurella multocida]

MS0236	212651	213421	771	PM1119	1.00E-115	Pmu	E		COG0548	Acetylglutamate kinase		ArgB	(NC_002663) ArgB [Pasteurella multocida]
MS0237	213513	214892	1380	PM1120	0	Pmu	E		COG0165	Argininosuccinate lyase		ArgH	(NC_002663) ArgH [Pasteurella multocida]
MS0238	215748	215020	729	HI0303	1.00E-113	Hin	S		COG1385	Uncharacterized BCR			(NC_000907) conserved hypothetical protein [Hae...
MS0239	216025	216708	684	HI0332	1.00E-103	Hin	L		COG1381	Recombinational DNA repair protein		RecO	(NC_000907) DNA repair protein (recO) [Haemophi...
MS0240	216718	218037	1320	HI0333	1.00E-165	Hin	J		COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase		TrmA	(NC_000907) RNA methyltransferase/putative [Ha...
MS0241	218053	220275	2223	PM1865	0	Pmu	TIK		COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases		SpoT	(NC_002663) RelA [Pasteurella multocida]
MS0242	220341	220694	354	PM1864	5.00E-32	Pmu	M		COG0818	Diacylglycerol kinase		DgkA	(NC_002663) DgkA [Pasteurella multocida]
MS0243	221925	220669	1257	HI0874	4.00E-86	Hin	M		COG3307	Lipid A core - O-antigen ligase and related enzymes		RfaL	(NC_000907) H. influenzae predicted coding regi...
MS0244	223086	222010	1077	PM1861	0	Pmu	G		COG0191	Fructose/tagatose bisphosphate aldolase		Fba	(NC_002663) Fba [Pasteurella multocida]
MS0245	224349	223183	1167	HI0525	0	Hin	G		COG0126	3-phosphoglycerate kinase		Pgk	(NC_000907) phosphoglycerate kinase (pgk) [Haem...
MS0246	225301	224576	726	PM1859	4.00E-71	No-des	none	No-des	No-des			none	(NC_002663) unknown [Pasteurella multocida]
MS0247	225415	225672	258	PM1858	2.00E-44	Pmu	C		COG1145	Ferredoxin 2		NapF	(NC_002663) unknown [Pasteurella multocida]
MS0248	226804	225698	1107	PM1857	1.00E-101	Pmu	J		COG0566	rRNA methylases		SpoU	(NC_002663) unknown [Pasteurella multocida]
MS0249	226830	226958	129	none	none	No-des	none	No-des	No-des			none	none
MS0250	226955	228313	1359	PM1856	0	Pmu	I		COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardioplin synthases and related enzymes		Cls	(NC_002663) PssA [Pasteurella multocida]
MS0251	229037	228396	642	HI0272	1.00E-100	Hin	F		COG0461	Orotate phosphoribosyltransferase		PyrE	(NC_000907) orotate phosphoribosyltransferase (...)
MS0252	229845	229126	720	HI0273	1.00E-118	Hin	J		COG0689	RNase PH		Rph	(NC_000907) ribonuclease PH (rph) [Haemophilus ...]
MS0253	230009	230869	861	HI0467	1.00E-139	Hin	S		COG1561	Uncharacterized stress-induced protein			(NC_000907) conserved hypothetical protein [Hae...
MS0254	230881	231711	831	HI0466	1.00E-89	Hin	R		COG0354	Predicted aminomethyltransferase related to GcvT			(NC_000907) conserved hypothetical protein [Hae...
MS0255	231961	233640	1680	HI1077	0	Hin	F		COG0504	CTP synthase (UTP-ammonia lyase)		PyrG	(NC_000907) CTP synthetase (pyrG) [Haemophilus ...]
MS0256	233749	235056	1308	HI0932	0	Hin	G		COG0148	Enolase		Eno	(NC_000907) enolase (eno) [Haemophilus influen...
MS0257	235800	235186	615	PM1100	1.00E-69	Pmu	O		COG0625	Glutathione-S-transferases		Gst	(U89957) UreX [Actinobacillus pleuropneumoniae]
MS0258	235876	236541	666	BH3089	1.00E-45	Bha	LJR		COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes		MutT	(AB004104) ORF10291-1 [Clostridium perfringens]
MS0259	236554	236955	402	HI0931	6.00E-43	No-des	none	No-des	No-des			none	(NC_000907) H. influenzae predicted coding regi...
MS0260	237078	237704	627	PM1869	2.00E-70	Pmu	K		COG1678	Putative transcriptional regulator			(NC_002663) unknown [Pasteurella multocida]
MS0261	237701	238120	420	HI0305	6.00E-64	Hin	L		COG0816	Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. subtilis)			(NC_000907) conserved hypothetical protein [Hae...
MS0262	239663	238239	1425	HI0865	0	Hin	E		COG0174	Glutamine synthase		GlnA	(NC_000907) glutamine synthetase (glnA) [Haemop...
MS0263	240050	242011	1962	HI0864	0	Hin	N		COG1217	Predicted membrane GTPase involved in stress response		TypA	(NC_000907) GTP-binding protein [Haemophilus in...]
MS0264	242544	242077	468	PM1052	3.00E-66	Pmu	O		COG1225	Peroxioredoxin		Bcp	(NC_002663) Bcp [Pasteurella multocida]
MS0265	242674	243567	894	PM1051	1.00E-135	Pmu	EJM		COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase		DapA	(NC_002663) DapA [Pasteurella multocida]
MS0266	243610	244074	465	L9876	4.00E-33	Lla	R		COG2153	Predicted acyltransferases		ElaA	(NC_002662) HYPOTHETICAL PROTEIN [Lactococcus l...
MS0267	244147	245154	1008	PM1050	7.00E-91	Pmu	M		COG3317	Uncharacterized lipoprotein		NlpB	(NC_002663) unknown [Pasteurella multocida]
MS0268	245275	245153	123	none	none	No-des	none	No-des	No-des			none	none
MS0269	245325	245696	372	none	none	No-des	none	No-des	No-des			none	none
MS0270	245789	245688	102	none	none	No-des	none	No-des	No-des			none	none
MS0271	245813	246331	519	ZhsIV	1.00E-61	EcZ	O		COG0638	Proteasome protease subunit		HslV	ATP-dependent protease hslV (Protein lapC) ...
MS0272	246434	247753	1320	PM1748	0	Pmu	O		COG1220	ATP-dependent protease/ATPase subunit		HslU	ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBU...
MS0273	249179	247869	1311	PM1815	1.00E-146	Pmu	H		COG3071	Uncharacterized enzyme of heme biosynthesis		HemY	(NC_002663) HemY [Pasteurella multocida]
MS0274	250462	249194	1269	PM1814	1.00E-113	Pmu	S		COG2959	Uncharacterized BCR		HemX	(NC_002663) unknown [Pasteurella multocida]
MS0275	251229	250483	747	PM1813	1.00E-79	Pmu	H		COG1587	Uroporphyrinogen-III synthase		HemD	(NC_002663) HemX [Pasteurella multocida]
MS0276	252165	251236	930	PM1812	1.00E-124	Pmu	H		COG0181	Porphobilinogen deaminase		HemC	(NC_002663) Pbg [Pasteurella multocida]
MS0277	252314	254815	2502	PM1811	0	Pmu	F		COG3072	Adenylyate cyclase		CyaA	(NC_002663) CyaA [Pasteurella multocida]
MS0278	254806	255483	678	PM1810	7.00E-90	Pmu	TIK		COG2197	Response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain		CitB	(NC_002663) NarP [Pasteurella multocida]
MS0279	255763	256710	948	VC1334	6.00E-27	Vch	S		COG3181	Uncharacterized BCR			HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD L...
MS0280	256755	257198	444	none	none	No-des	none	No-des	No-des			none	none
MS0281	257209	258717	1509	BH2009	2.00E-83	Bha	S		COG3333	Uncharacterized BCR			(NC_002570) BH2009--unknown conserved protein in...
MS0282	258707	259654	948	VC2157	5.00E-17	Vch	EJM		COG0329	Dihydrodipicolinate synthase/N-acetylneuraminate lyase		DapA	(NC_003064) AGR_pAT_576p [Agrobacterium tumefac...
MS0283	259689	260618	930	PM0152	1.00E-119	Pmu	G		COG0524	Sugar kinases/ribokinase family		RbsK	(NC_002663) RbsK [Pasteurella multocida]
MS0284	260673	261674	1002	PM0151	1.00E-117	Pmu	K		COG1609	Transcriptional regulators		PurR	(NC_002663) RbsR [Pasteurella multocida]
MS0285	261805	263577	1773	PM1809	0	Pmu	M		COG0729	Predicted outer membrane protein			(NC_002663) unknown [Pasteurella multocida]
MS0286	263606	267508	3903	HI0696	0	Hin	S		COG2911	Uncharacterized BCR			(NC_000907) conserved hypothetical protein [Hae...
MS0287	267526	269079	1554	PM1807	0	Pmu	FIP		COG0248	Exopolysphatase		GppA	(NC_002663) unknown [Pasteurella multocida]
MS0288	270045	269206	840	PM1071	1.00E-112	Pmu	R		COG2985	Predicted permease			(NC_002663) unknown [Pasteurella multocida]
MS0289	270859	269969	891	PM1071	2.00E-98	Pmu	R		COG2985	Predicted permease			(NC_002663) unknown [Pasteurella multocida]
MS0290	270990	272819	1830	PM1072	0	Pmu	I		COG1133	ABC-type long-chain fatty acid transport system/fused permease and ATPase components		SbmA	(NC_002663) unknown [Pasteurella multocida]
MS0291	273108	274766	1659	ZybyW	0	EcZ	C		COG1151	6Fe-6S prismane cluster-containing protein			(NC_003143) putative prismane protein homologue...
MS0292	274812	275879	1068	Z1106	6.00E-85	EcZ	C		COG1018	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1		Hmp	(NC_002655) putative enzyme [Escherichia coli O...
MS0293	276099	276500	402	NMB1622	6.00E-45	Nme	P		COG3256	Nitric oxide reductase large subunit		NorB	(NC_003112) nitric oxide reductase [Neisseria m...
MS0294	276466	278337	1872	NMA1886	0	NmA	P		COG3256	Nitric oxide reductase large subunit		NorB	(NC_003116) nitric oxide reductase [Neisseria m...
MS0295	279118	278558	561	yddH	9.00E-20	Eco	R		COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases/DIM6/NTAB family			HYPOTHETICAL 21.0 KDA PROTEIN IN TEHB-ANSP ...

MS0296	279814	279197	618	none	none	No-des	none	No-des	No-des		none	none
MS0297	281448	280084	1365	PM1851	0	Pmu	F	COG0015	Adenylosuccinate lyase		PurB	(NC_002663) PurB [Pasteurella multocida]
MS0298	282083	281472	612	PM1850	1.00E-75	Pmu	R	COG2915	Uncharacterized protein involved in purine metabolism			(NC_002663) unknown [Pasteurella multocida]
MS0299	282247	282155	93	none	none	No-des	none	No-des	No-des		none	none
MS0300	282677	282255	423	CJ0225	9.00E-25	Cje	R	COG0456	Acetyltransferases		RimI	(NC_002163) putative acetyltransferase [Campylo...
MS0301	283957	282758	1200	PM1336	1.00E-179	Pmu	J	COG0482	Predicted tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase[contains the PP-loop ATPase domain]		TrmU	(NC_002663) unknown [Pasteurella multocida]
MS0302	284296	284054	243	PM1335	2.00E-12	Pmu	S	COG2991	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS0303	285354	284302	1053	HI0172	1.00E-134	Hin	H	COG1477	Membrane-associated lipoprotein involved in thiamine biosynthesis		ApbE	(NC_000907) lipoprotein/putative [Haemophilus ...]
MS0304	286688	285462	1227	HI0171	0	Hin	C	COG2871	Na+-transporting NADHubiquinone oxidoreductase beta subunit		NqrF	(NC_000907) NqrF subunit of Na-translocating NA...
MS0305	287295	286702	594	PM1332	9.00E-99	Pmu	C	COG2209	Na+-transporting NADHubiquinone oxidoreductase subunit 5		NqrE	(NC_002663) NqrE [Pasteurella multocida]
MS0306	287922	287302	621	HI0168	3.00E-95	Hin	C	COG1347	Na+-transporting NADHubiquinone oxidoreductase subunit 4		NqrD	(NC_000907) NADHubiquinone oxidoreductase/Na ...
MS0307	288692	287925	768	NMA0750	5.00E-83	NmA	C	COG2869	Na+-transporting NADHubiquinone oxidoreductase gamma subunit		NqrC	(NC_003116) putative Na(+)-translocating NADH-u...
MS0308	289927	288695	1233	HI0166	0	Hin	C	COG1805	Na+-transporting NADHubiquinone oxidoreductase subunit 2		NqrB	(NC_000907) NADHubiquinone oxidoreductase/sub...
MS0309	291261	289933	1329	HI0164	0	Hin	C	COG1726	Na+-transporting NADHubiquinone oxidoreductase alpha subunit		NqrA	(NC_000907) NADHubiquinone oxidoreductase sub...
MS0310	291563	291465	99	none	none	No-des	none	No-des	No-des		none	none
MS0311	291938	291633	306	PM1324	8.00E-34	Pmu	T	COG0271	Stress-induced morphogen (activity unknown)		BolA	(NC_002663) unknown [Pasteurella multocida]
MS0312	292120	292716	597	HI0162	3.00E-42	Hin	M	COG3056	Uncharacterized lipoprotein			(NC_000907) lipoprotein/putative [Haemophilus ...]
MS0313	293251	292793	459	none	none	No-des	none	No-des	No-des		none	none
MS0314	293775	293650	126	none	none	No-des	none	No-des	No-des		none	none
MS0315	294879	293797	1083	HI0761	1.00E-148	Hin	M	COG0741	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)		MtE	(NC_000907) membrane-bound lytic murein transgl...
MS0316	295151	294879	273	HI0760	4.00E-44	Hin	S	COG2924	Uncharacterized BCR			(NC_000907) conserved hypothetical protein [Hae...
MS0317	296265	295132	1134	PM1319	1.00E-169	Pmu	L	COG1194	A/G-specific DNA glycosylase		MutY	(NC_002663) MutY [Pasteurella multocida]
MS0318	296388	297146	759	PM1317	1.00E-119	Pmu	R	COG0220	Predicted S-adenosylmethionine-dependent methyltransferase			(NC_002663) unknown [Pasteurella multocida]
MS0319	297180	297521	342	PM1316	9.00E-56	Pmu	S	COG3171	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS0320	297952	298899	948	PM1315	1.00E-149	Pmu	P	COG0598	Mg2+ and Co2+ transporters		CorA	(NC_002663) CorA [Pasteurella multocida]
MS0321	298953	299588	636	PM1314	2.00E-48	Pmu	S	COG0762	Predicted integral membrane protein			(NC_002663) unknown [Pasteurella multocida]
MS0322	299623	299907	285	PM1313	1.00E-35	Pmu	S	COG1872	Uncharacterized ACR			(NC_002663) unknown [Pasteurella multocida]
MS0323	300378	299947	432	PM1312	3.00E-57	Pmu	K/R	COG0454	Histone acetyltransferase HPA2 and related acetyltransferases		WecD	(NC_002663) unknown [Pasteurella multocida]
MS0324	300566	301330	765	HI0678	1.00E-122	Hin	G	COG0149	Triosephosphate isomerase		TpiA	(NC_000907) triosephosphate isomerase (tpiA) [H...
MS0325	301751	301449	303	HI0907	4.00E-20	No-des	none	No-des	No-des		none	(NC_000907) H. influenzae predicted coding regi...
MS0326	301841	302158	318	PM1220	1.00E-08	No-des	none	No-des	No-des		none	(NC_002663) unknown [Pasteurella multocida]
MS0327	302263	304950	2688	PM1219	0	Pmu	N	COG0653	Preprotein translocase subunit SecA (ATPase/RNA helicase)		SecA	(AF116183) SecA homolog [Actinobacillus...]
MS0328	305031	305432	402	HI0910	8.00E-59	Hin	L/R	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes		MutT	(NC_000907) mutator mutT protein (mutT) [Haemop...
MS0329	305928	305506	423	PM0474	2.00E-43	Pmu	T	COG0589	Universal stress protein UspA and related nucleotide-binding proteins		UspA	(NC_002663) unknown [Pasteurella multocida]
MS0330	308613	305980	2634	PM0473	0	Pmu	S	COG1593	Integral membrane protein/possible transporter			(NC_002663) unknown [Pasteurella multocida]
MS0331	309762	308722	1041	PM0472	1.00E-130	Pmu	R	COG2358	Predicted periplasmic binding protein			(NC_002663) unknown [Pasteurella multocida]
MS0332	310926	309892	1035	HI0923	1.00E-105	Hin	L	COG1466	DNA polymerase III delta subunit		HolA	(NC_000907) DNA polymerase IIIdelta subunit (...)
MS0333	311151	312575	1425	ml14272	1.00E-130	Mlo	E	COG0065	3-isopropylmalate dehydratase large subunit		LeuC	(NC_003197) putative 3-isopropylmalate isomeras...
MS0334	312581	313186	606	CCO195	8.00E-49	Ccr	E	COG0066	3-isopropylmalate dehydratase small subunit		LeuD	(NC_003197) putative 3-isopropylmalate isomeras...
MS0335	313205	314530	1326	PA1051	1.00E-46	Pae	G/E	COG2610	H+/gluconate symporter and related permeases		GntT	(NC_002516) probable transporter [Pseudomonas a...
MS0336	315496	314567	930	ygiP	4.00E-66	Eco	K	COG0583	Transcriptional regulator		LysR	(NC_003197) putative transcriptional regulator/...
MS0337	316008	315502	507	PM1215	3.00E-63	Pmu	M	COG2980	Rare lipoprotein B		RlpB	(NC_002663) unknown [Pasteurella multocida]
MS0338	318657	316078	2580	PM1214	0	Pmu	J	COG0495	Leucyl-tRNA synthetase		LeuS	(NC_002663) LeuS [Pasteurella multocida]
MS0339	318742	318840	99	none	none	No-des	none	No-des	No-des		none	none
MS0340	319980	318886	1095	ymdD	2.00E-11	No-des	none	No-des	No-des		none	(NC_003305) conserved hypothetical protein [Agr...
MS0341	320480	320211	270	PM1213	3.00E-16	Pmu	P	COG2608	Copper chaperone		CopZ	(NC_002663) MerP [Pasteurella multocida]
MS0342	320839	320480	360	HI1049	1.00E-30	No-des	none	No-des	No-des		none	(NC_000907) mercuric ion transport protein (mer...
MS0343	321917	320817	1101	HI1048	1.00E-169	Hin	E	COG1305	Transglutaminase-like enzymes/putative cysteine proteases			(NC_000907) H. influenzae predicted coding regi...
MS0344	322680	322066	615	HI0552	1.00E-87	No-des	none	No-des	No-des		none	(NC_000907) H. influenzae predicted coding regi...
MS0345	323648	322749	900	HI0812	1.00E-144	Hin	M	COG1210	UDP-glucose pyrophosphorylase		GalU	(NC_000907) glucosylphosphate uridylyltransferas...
MS0346	325086	323725	1362	ZmanB	0	EcZ	G	COG1109	Phosphomannomutase		CpsG	(AY012183) phosphomannomutase [Salmonella bongori]
MS0347	325293	325111	183	PM1288	6.00E-23	Pmu	T	COG1551	Carbon storage regulator (could also regulate swarming and quorum sensing)		CsrA	(NC_002663) CsrA [Pasteurella multocida]
MS0348	328083	325459	2625	HI0814	0	Hin	J	COG0013	Alanyl-tRNA synthetase		AlaS	(NC_000907) alanyl-tRNA synthetase (alaS) [Haem...
MS0349	328695	328270	426	HI0815	2.00E-66	Hin	T	COG0589	Universal stress protein UspA and related nucleotide-binding proteins		UspA	(NC_000907) universal stress protein A (uspA) [...]
MS0350	328735	328971	237	none	none	No-des	none	No-des	No-des		none	none
MS0351	328979	329680	702	PM1285	2.00E-84	Pmu	R	COG1694	Predicted pyrophosphatase		MazG	(NC_002663) MazG [Pasteurella multocida]
MS0352	330071	329754	318	HI0257	4.00E-47	Hin	J	COG1544	Ribosome-associated protein Y (PSrp-1)			(NC_000907) sigma(54) modulation protein/putat...
MS0353	331711	330323	1389	HI0883	0	Hin	E	COG1115	Na+/alanine symporter		AlaT (BS)	(NC_000907) amino acid carrier protein/putativ...
MS0354	331789	331902	114	none	none	No-des	none	No-des	No-des		none	none
MS0355	331951	331862	90	none	none	No-des	none	No-des	No-des		none	none

MS0356	332158	332021	138	none	none	No-des	none	No-des	No-des		none	none
MS0357	332393	332124	270	PM0090	6.00E-27	Pmu	R	COG2388	Predicted acetyltransferase			(NC_002663) unknown [Pasteurella multocida]
MS0358	332628	332413	216	PM0089	7.00E-23	Pmu	S	COG3024	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS0359	333250	332609	642	HI0890m	4.00E-73	Hin	H	COG0237	Dephospho-CoA kinase	CoaE		hypothetical protein HI0890 - Haemophilus influenzae...
MS0360	333993	333280	714	HI0296	2.00E-30	Hin	N	COG1989	Signal peptidase/cleaves prepin-like proteins	PppA		(AF268318) PilB [Actinobacillus actinom...
MS0361	335024	333993	1032	HI0297	5.00E-90	Hin	N	COG1459	General secretory pathway protein F	HofF		(NC_000907) protein transport protein [Haemophi...
MS0362	335214	335089	126	none	none	No-des	none	No-des	No-des	none		none
MS0363	336634	335207	1428	HI0298	1.00E-155	Hin	N	COG2804	Predicted ATPases involved in pili biogenesis/PilB homologs	GspE		(AF268318) PilB [Actinobacillus actinom...
MS0364	337700	336621	450	PM0084	6.00E-36	Pmu	N	COG2165	General secretory pathway proteins G and H and related periplasmic/secreted proteins	HofG		(NC_002663) unknown [Pasteurella multocida]
MS0365	337174	337743	570	HI0300	2.00E-77	Hin	M	COG3023	Negative regulator of beta-lactamase expression	AmpD		(NC_000907) ampD signalling protein (ampD) [Hae...
MS0366	337884	338351	468	HI0178	6.00E-31	No-des	none	No-des	No-des	none		(NC_000907) H. influenzae predicted coding regi...
MS0367	339382	338432	951	HI0013	1.00E-155	Hin	R	COG1159	GTPases	Era		(NC_000907) GTP-binding protein (era) [Haemophi...
MS0368	340053	339382	672	PM0061	2.00E-98	Pmu	K	COG0571	dsRNA-specific ribonuclease	Rnc		(NC_002663) Rnc [Pasteurella multocida]
MS0369	340783	340058	726	BU259	9.00E-30	Buc	N	COG0681	Signal peptidase I	LepB		(NC_003198) signal peptidase I [Salmonella ente...
MS0370	341845	340796	1050	PM0062	1.00E-155	Pmu	N	COG0681	Signal peptidase I	LepB		(NC_002663) LepB [Pasteurella multocida]
MS0371	343808	341829	1980	HI0016	0	Hin	N	COG0481	Membrane GTPase LepA	LepA		(NC_000907) GTP-binding membrane protein (lepA)...
MS0372	344245	343865	381	HI0017	7.00E-63	Hin	R	COG3445	Acid-induced glycol radical enzyme			(NC_000907) conserved hypothetical protein [Hae...
MS0373	344642	345313	672	PM0065	1.00E-104	Pmu	L	COG0692	Uracil DNA glycosylase	Ung		(NC_002663) Ung [Pasteurella multocida]
MS0374	345360	346133	774	PM0066	1.00E-122	Pmu	S	COG3022	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS0375	346140	346736	597	PM0067	5.00E-56	No-des	none	No-des	No-des	none		(NC_002663) unknown [Pasteurella multocida]
MS0376	346732	347622	891	PM0068	3.00E-95	Pmu	P	COG0053	Predicted Co/Zn/Cd cation transporters	MMT1		(NC_002663) unknown [Pasteurella multocida]
MS0377	347749	348711	963	HI0982	1.00E-161	Hin	G	COG0205	6-phosphofructokinase	PfkA		(NC_000907) 6-phosphofructokinase (pfkA) [Haemo...
MS0378	348846	348754	93	none	none	No-des	none	No-des	No-des	none		none
MS0379	349606	348827	780	PM1640_1	3.00E-94	Pmu	G	COG0149	Triosephosphate isomerase	TpiA		(NC_002663) TpiA [Pasteurella multocida]
MS0380	350388	349627	762	L0031	8.00E-24	Lia	K/G	COG1349	Transcriptional regulators of sugar metabolism	GlpR		(NC_002662) lactose transport regulator [Lactoc...
MS0381	350580	351584	1005	BH0804	9.00E-93	Bha	H	COG1995	Pyridoxal phosphate biosynthesis protein	PdxA		(NC_002570) pyridoxal phosphate biosynthetic pr...
MS0382	351603	352955	1353	BH0802	4.00E-37	Bha	S	COG3395	Uncharacterized BCR			(NC_002570) BH0802-unknown conserved protein in...
MS0383	352980	353429	450	PM1645	2.00E-58	Pmu	G	COG0698	Ribose 5-phosphate isomerase RpiB	RpiB		(NC_002663) RpiA [Pasteurella multocida]
MS0384	353464	354564	1101	BS_kdgT	3.00E-33	No-des	none	No-des	No-des	none		(NC_003198) 2-keto-3-deoxygluconate permease [S...
MS0385	354702	355166	465	PM2013	1.00E-23	Pmu	O	COG2020	Putative protein-S-isoprenylcysteine methyltransferase			(NC_002663) unknown [Pasteurella multocida]
MS0386	355278	355156	123	none	none	No-des	none	No-des	No-des	none		none
MS0387	355716	357338	1623	PM1042	0	Pmu	R	COG2194	Predicted membrane-associated/metal-dependent hydrolase			(NC_002663) unknown [Pasteurella multocida]
MS0388	357389	357499	111	none	none	No-des	none	No-des	No-des	none		none
MS0389	358141	357479	663	PM0001	1.00E-90	Pmu	P	COG0605	Superoxide dismutase	SodA		(NC_002663) SodA [Pasteurella multocida]
MS0390	360653	358383	2271	HI1245_1	0	Hin	C	COG0281	Malic enzyme	MaeB*		(NC_002663) Mdh [Pasteurella multocida]
MS0391	360892	361629	738	PM0003	1.00E-101	Pmu	J	COG1187	16S rRNA uridine-516 pseudouridylation synthase and related pseudouridylation synthases	RsuA		(NC_002663) RsuA [Pasteurella multocida]
MS0392	361648	362832	1185	HI1242	1.00E-156	Hin	G/E/PIR	COG0477	Permeases of the major facilitator superfamily	ProP		(NC_000907) bicyclomycin resistance protein (bc...
MS0393	362847	363074	228	PM0127	3.00E-19	No-des	none	No-des	No-des	none		(NC_002663) unknown [Pasteurella multocida]
MS0394	363214	365055	1842	HI1051	0	Hin	Q	COG1132	ABC-type multidrug/protein/lipid transport system/ATPase component	MdIB		(NC_000907) ABC transporter/ATP-binding protei...
MS0395	366314	365148	1167	HI0958	1.00E-154	Hin	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase	TrmA		(NC_000907) RNA methyltransferase/putative [Ha...
MS0396	367438	366398	1041	PM0071	1.00E-150	Pmu	G	COG1472	Beta-glucosidase-related glycosidases	BglX		(NC_002663) unknown [Pasteurella multocida]
MS0397	367815	367450	366	HI0960	2.00E-25	No-des	none	No-des	No-des	none		(NC_000907) H. influenzae predicted coding regi...
MS0398	368151	368294	144	none	none	No-des	none	No-des	No-des	none		none
MS0399	368305	367859	447	HI0961	2.00E-52	Hin	F/G/R	COG0537	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	Hit (BS)		(NC_000907) hit-related protein [Haemophilus in...
MS0400	368529	369377	849	PM0074	1.00E-127	Pmu	P	COG2116	Formate/nitrite family of transporters	FocA		(NC_002663) unknown [Pasteurella multocida]
MS0401	369464	371773	2310	HI0180	0	Hin	C	COG1882	Pyruvate-formate lyase	PfID		FORMATE ACETYLTRANSFERASE (PYRUVATE FORMAT...
MS0402	371793	371897	105	none	none	No-des	none	No-des	No-des	none		none
MS0403	371964	372701	738	PM0077	1.00E-111	Pmu	O	COG1180	Pyruvate-formate lyase-activating enzyme	PfIA		(NC_002663) Act [Pasteurella multocida]
MS0404	373281	372754	528	HI0906	2.00E-66	Hin	F/J	COG0590	Cytosine/adenosine deaminases			(NC_000907) conserved hypothetical protein [Hae...
MS0405	374295	373447	849	PM0079	1.00E-153	Pmu	F	COG0207	Thymidylate synthase	ThyA		(NC_002663) ThyA [Pasteurella multocida]
MS0406	375120	374317	804	PM0080	1.00E-123	Pmu	M	COG0682	Protoporphyrin diacylglyceroltransferase	Lgt		(NC_002663) Lgt [Pasteurella multocida]
MS0407	375938	375141	798	HI0902	6.00E-75	Hin	R	COG0730	Predicted permeases			(NC_000907) conserved hypothetical protein [Hae...
MS0408	376533	375943	591	PM0082	2.00E-73	Pmu	L/R	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	MutT		(NC_002663) unknown [Pasteurella multocida]
MS0409	377666	377151	516	PM1063	2.00E-64	No-des	none	No-des	No-des	none		(NC_002663) Mtl [Pasteurella multocida]
MS0410	378884	377739	1146	PM1062	1.00E-154	Pmu	G	COG0246	Mannitol-1-phosphate/altronate dehydrogenases	MtID		(NC_002663) MtID [Pasteurella multocida]
MS0411	380845	378977	1869	PM1061_1	0	Pmu	C	COG2213	Phosphotransferase system/mannitol-specific HBC component	MtIA		(NC_002663) PtmA [Pasteurella multocida]
MS0412	381119	381331	213	PM1060	5.00E-11	No-des	none	No-des	No-des	none		(NC_002663) unknown [Pasteurella multocida]
MS0413	381338	383350	2013	HI0649	0	Hin	L	COG0210	Superfamily I DNA and RNA helicases	UvrD		(NC_000907) ATP-dependent DNA helicase (rep) [H...
MS0414	384325	383894	432	none	none	No-des	none	No-des	No-des	none		none
MS0415	384806	384423	384	PM1058	6.00E-33	No-des	none	No-des	No-des	none		(NC_002663) unknown [Pasteurella multocida]

MS0416	384773	385513	741	HI0488	4.00E-56	Hin	R	COG0637	Predicted phosphatase/phosphohexomutase		(NC_000907) conserved hypothetical protein [Hae...
MS0417	385516	386115	600	PM1056	1.00E-62	Pmu	R	COG0110	Acetyltransferases (the isoleucine patch superfamily)	WbbJ	(NC_002663) unknown [Pasteurella multocida]
MS0418	386118	386600	483	PM1055	2.00E-32	Pmu	S	COG1238	Uncharacterized membrane protein		(NC_002663) unknown [Pasteurella multocida]
MS0419	386760	387263	504	HI0491	1.00E-74	Hin	T	COG1854	LuxS protein involved in autoinducer AI2 synthesis	LuxS	(NC_000907) conserved hypothetical protein [Hae...
MS0420	387295	388479	1185	PM1053	0	Pmu	F	COG0027	Formate-dependent phosphoribosylglycinamide formyltransferase (GAR transformylase)	PurT	(NC_002663) Pur [Pasteurella multocida]
MS0421	388589	388458	132	none	none	No-des	none	No-des	No-des	none	none
MS0422	388602	389792	1191	HI1060	1.00E-164	Hin	M	COG0763	Lipid A disaccharide synthetase	LpxB	(NC_000907) lipid-A-disaccharide synthetase (lp...
MS0423	389788	390381	594	HI1059	2.00E-78	Hin	L	COG0164	Ribonuclease HII	RnhB	(NC_000907) ribonuclease HII (rnhB) [Haemophilu...
MS0424	390431	392284	1854	PM1999	0	Pmu	P	COG0471	Di- and tricarboxylate transporters	CitT	(NC_002663) unknown [Pasteurella multocida]
MS0425	392316	392906	591	HI0336	1.00E-90	Hin	H	COG0521	Molybdopterin biosynthesis enzymes	MoaB	(NC_000907) molybdopterin biosynthesis protein...
MS0426	392951	393286	336	PM2004	2.00E-55	Pmu	E	COG0347	Nitrogen regulatory protein PII	GlnK	(NC_002663) GlnB [Pasteurella multocida]
MS0427	393359	393736	378	PM0670	8.00E-14	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0428	393749	394792	1044	HI0338	1.00E-112	Hin	R	COG0628	Predicted permease	PerM	(NC_000907) conserved hypothetical transmembran...
MS0429	395431	394898	534	PM0046	1.00E-52	Pmu	O	COG1495	Disulfide bond formation protein DsbB	DsbB	(NC_002663) DsbB [Pasteurella multocida]
MS0430	396992	395448	1545	PM0047	0	Pmu	P	COG3067	Na ⁺ /H ⁺ antiporter	NhaB	(NC_002663) NhaB [Pasteurella multocida]
MS0431	397126	397869	744	PM0048	2.00E-85	Pmu	K	COG2186	Transcriptional regulators	FadR	(NC_002663) FadR [Pasteurella multocida]
MS0432	398845	398009	837	HI0620	4.00E-99	Hin	M	COG1464	Lipoprotein[attached to the cytoplasmic membrane	NlpA	OUTER MEMBRANE LIPOPROTEIN I PRECURSOR (PLP...
MS0433	399595	398885	711	PM1729	2.00E-72	Pmu	R	COG2011	Permease component of an uncharacterized ABC transporter		(NC_002663) unknown [Pasteurella multocida]
MS0434	400598	399564	1035	HI0621	1.00E-155	Hin	R	COG1135	Uncharacterized ABC-type transport system ATPase component	Abc	(NC_000907) ABC transporter/ATP-binding protei...
MS0435	400763	401332	570	HI0621.1	6.00E-83	Hin	E	COG0241	Histidinol phosphatase and related phosphatases	HisB	(NC_000907) conserved hypothetical protein [Hae...
MS0436	401469	401570	102	none	none	No-des	none	No-des	No-des	none	none
MS0437	408377	407616	762	PM1190	2.00E-76	Pmu	O	COG0501	Zn-dependent protease with chaperone function	HipX	(NC_002663) unknown [Pasteurella multocida]
MS0438	408552	409310	759	HI0653	1.00E-115	Hin	M	COG0463	Glycosyltransferases involved in cell wall biogenesis	WcaA	(NC_000907) lipopolysaccharide biosynthesis pro...
MS0439	410386	409361	1026	HI0523	1.00E-125	Hin	M	COG0859	ADP-heptoseLPS heptosyltransferase	RfaF	(NC_000907) conserved hypothetical protein [Hae...
MS0440	410569	410814	246	PM1294a	1.00E-37	Pmu	J	COG0228	Ribosomal protein S16	RpsP	(NC_002663) ribosomal protein S16 [Pasteurella ...
MS0441	410845	411378	534	HI0203	1.00E-87	Hin	J	COG0806	RimM protein[required for 16S rRNA processing	RimM	(NC_000907) conserved hypothetical protein [Hae...
MS0442	411436	412200	765	HI0202	1.00E-126	Hin	J	COG0336	tRNA-(guanine-N1)-methyltransferase	TrmD	(NC_000907) tRNA (guanine-N1)-methyltransferase...
MS0443	412242	412589	348	HI0201	4.00E-58	Hin	J	COG0335	Ribosomal protein L19	RplS	50S RIBOSOMAL PROTEIN L19
MS0444	413541	412666	876	PA0429	1.00E-12	No-des	none	No-des	No-des	none	(NC_002516) hypothetical protein [Pseudomonas a...
MS0445	414554	413532	1023	PM1144	1.00E-113	Pmu	M	COG0859	ADP-heptoseLPS heptosyltransferase	RfaF	(NC_002663) unknown [Pasteurella multocida]
MS0446	415291	414572	720	PM1143	2.00E-73	Pmu	M	COG3306	Glycosyltransferase involved in LPS biosynthesis		(AF143905) putative LPS biosynthesis pr...
MS0447	416189	415263	927	HI0258	6.00E-52	Hin	M	COG1442	Lipopolysaccharide biosynthesis proteins[LPSglycosyltransferases	RfaJ	(NC_000907) glycosyl transferase/putative [Hae...
MS0448	416476	416252	225	HI0758	9.00E-34	Hin	J	COG0254	Ribosomal protein L31	RpmE	(NC_000907) ribosomal protein L31 (rpl31) [Haem...
MS0449	416699	418915	2217	PM1137	0	Pmu	L	COG1198	Primosomal protein N' (replication factor Y) - superfamily II helicase	PriA	(NC_002663) PriA [Pasteurella multocida]
MS0450	419009	419785	777	PM1136	2.00E-26	Pmu	D	COG3087	Cell division protein	FtsN	(NC_002663) unknown [Pasteurella multocida]
MS0451	419922	419818	105	none	none	No-des	none	No-des	No-des	none	none
MS0452	420052	419897	156	none	none	No-des	none	No-des	No-des	none	none
MS0453	420044	420607	564	HI0893	1.00E-62	Hin	K	COG1309	Transcriptional regulator	AcrR	(NC_000907) transcriptional repressor (Bm3R1) [...
MS0454	420640	421833	1194	HI0894	1.00E-142	Hin	Q	COG0845	Membrane-fusion protein	AcrA	hypothetical protein HI0894 - Haemophilus influenzae...
MS0455	422189	422094	96	none	none	No-des	none	No-des	No-des	none	none
MS0456	421858	424938	3081	HI0895	0	Hin	Q	COG0841	Cation/multidrug efflux pump	AcrB	(NC_000907) acriflavine resistance protein (acr...
MS0457	425090	425572	483	PM1105	7.00E-25	Pmu	R	COG3030	Protein affecting phage T7 exclusion by the F plasmid	FxsA	(NC_002663) unknown [Pasteurella multocida]
MS0458	425787	425954	168	PM1106	5.00E-24	Pmu	O	COG0234	Co-chaperonin GroES (HSP10)	GroS	(NC_002663) GroES [Pasteurella multocida]
MS0459	426055	427695	1641	HI0543	0	Hin	O	COG0459	Chaperonin GroEL (HSP60 family)	GroL	(NC_000907) heat shock protein (groEL) [Haemoph...
MS0460	427946	428395	450	HI1062	8.00E-70	Hin	I	COG0764	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases	FabA	(NC_000907) (3R)-hydroxymyristol (acyl carrier ...
MS0461	428430	429215	786	PM1996	1.00E-134	Pmu	M	COG1043	Acyl-acyl carrier protein--UDP-N-acetylglucosamine O-acyltransferase	LpxA	(NC_002663) LpxA [Pasteurella multocida]
MS0462	430107	429358	750	BH2078	4.00E-57	Bha	EiP	COG1124	ABC-type dipeptide/oligopeptide/nickel transport system/ATPase component	OppF	(NC_002570) oligopeptide ABC transporter (ATP-b...
MS0463	430943	430107	837	BH0570	2.00E-40	Bha	EiP	COG0444	ABC-type dipeptide/oligopeptide/nickel transport system/ATPase component	DppD	(NC_002758) oligopeptide transporter putative A...
MS0464	431784	430939	846	BH2076	3.00E-51	Bha	EiP	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems/permease components	DppC	(NC_002570) oligopeptide ABC transporter (perme...
MS0465	432718	431789	930	BH0568	4.00E-59	Bha	EiP	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems/permease components	DppB	(NC_002570) nickel transport system (permease) ...
MS0466	434287	432728	1560	nika	1.00E-117	Eco	EiP	COG0747	ABC-type dipeptide/oligopeptide/nickel transport systems/periplasmic components	OppA	(NC_000913) periplasmic binding protein for nic...
MS0467	435114	434347	768	BS_ycgJ	1.00E-10	Bsu	Q/R	COG0500	SAM-dependent methyltransferases	SmtA	(NC_003063) AGR_L_2861p [Agrobacterium tumefaci...
MS0468	435209	435616	408	HI1623	1.00E-40	Hin	K	COG0789	Predicted transcriptional regulators	SoxR	mercuric resistance operon regulatory protein homolo...
MS0469	435754	436128	375	PM1180	4.00E-67	Pmu	J	COG0360	Ribosomal protein S6	RpsF	(NC_002663) Rps6 [Pasteurella multocida]
MS0470	436097	436438	342	PM1179	4.00E-38	Pmu	L	COG2965	Primosomal replication protein N	PriB	(NC_002663) PriB [Pasteurella multocida]
MS0471	436459	436683	225	PM1178	1.00E-37	Pmu	J	COG0238	Ribosomal protein S18	RpsR	(NC_002663) Rps18 [Pasteurella multocida]
MS0472	436707	437153	447	PM1177	4.00E-50	Pmu	J	COG0359	Ribosomal protein L9	RplI	(NC_002663) Rpl9 [Pasteurella multocida]
MS0473	437326	439716	2391	PM1954	0	Pmu	K	COG0557	Exoribonucleases	VacB	(NC_002663) VacB [Pasteurella multocida]
MS0474	439719	440453	735	PM1953	1.00E-119	Pmu	J	COG0566	rRNA methylases	SpoU	(NC_002663) unknown [Pasteurella multocida]
MS0475	441136	441005	132	none	none	No-des	none	No-des	No-des	none	none

MS0476	440771	440502	270	HI0858	4.00E-39	Hin	H	COG0212	5-formyltetrahydrofolate cyclo-ligase		(NC_000907) conserved hypothetical protein [Hae...
MS0477	441744	441361	384	PM1722	1.00E-29	Pmu	S	COG3027	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0478	441762	442352	591	PM1723	1.00E-72	Pmu	S	COG3079	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0479	442365	443690	1326	PM1724	0	Pmu	E	COG0006	Xaa-Pro aminopeptidase	Pepp	(NC_002663) Pepp [Pasteurella multocida]
MS0480	445091	443730	1362	PM1166	0	Pmu	R	COG0486	Predicted GTPase	ThdF	(NC_002663) ThdF [Pasteurella multocida]
MS0481	446826	445207	1620	PM1165	0	Pmu	N	COG0706	Preprotein translocase subunit YidC	YidC (BS)	(NC_002663) YidC [Pasteurella multocida]
MS0482	447044	446829	216	PM1164	2.00E-34	Pmu	S	COG0759	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS0483	447409	447044	366	HI0999	8.00E-52	Hin	J	COG0594	RNase P protein component	RnpA	ribonuclease P (EC 3.1.26.5) protein component - Hae...
MS0484	447559	447428	132	PM1162	3.00E-18	Pmu	J	COG0230	Ribosomal protein L34	RpmH	(NC_002663) RpL34 [Pasteurella multocida]
MS0485	447961	449331	1371	PM1161	1.00E-180	Pmu	L	COG0593	ATPase involved in DNA replication initiation	DnaA	(NC_002663) DnaA [Pasteurella multocida]
MS0486	449336	450445	1110	PM1160	1.00E-178	Pmu	L	COG0592	DNA polymerase III beta subunit	DnaN	(NC_002663) DnaN [Pasteurella multocida]
MS0487	450485	451564	1080	PM1159	1.00E-166	Pmu	L	COG1195	Recombinational DNA repair ATPase	RecF	(NC_002663) RecF [Pasteurella multocida]
MS0488	452902	451598	1305	PM1873	1.00E-126	Pmu	E	COG1114	Branched-chain amino acid permeases	BrrQ	(NC_002663) BrrQ [Pasteurella multocida]
MS0489	453768	452980	789	PM1116	1.00E-118	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0490	454559	456025	1467	HI0274	0	Hin	J	COG0008	Glutamyl- and glutamyl-tRNA synthetases	GlnS	(NC_000907) glutamyl-tRNA synthetase (gltX) [Hae...
MS0491	456075	456284	210	none	none	No-des	none	No-des	No-des	none	none
MS0492	456291	456389	99	none	none	No-des	none	No-des	No-des	none	none
MS0493	456524	458635	2112	HI0229	0	Hin	J	COG1185	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)	Pnp	(NC_000907) polynucleotide phosphorylase (pnp) ...
MS0494	458818	459789	972	HI0230	1.00E-102	Hin	R	COG0457	TPR-repeat-containing proteins	NrfG	(NC_000907) conserved hypothetical protein [Hae...
MS0495	459877	461715	1839	HI0231	0	Hin	L K J	COG0513	Superfamily II DNA and RNA helicases	SrmB	(NC_000907) ATP-dependent RNA helicase (deaD) [...
MS0496	461756	461860	105	none	none	No-des	none	No-des	No-des	none	none
MS0497	463695	461881	1815	PM0948	0	Pmu	P	COG0659	Sulfate permease and related transporters (MFS superfamily)	SUL1	(NC_002663) unknown [Pasteurella multocida]
MS0498	464218	464916	699	PM1889	2.00E-97	Pmu	S	COG1738	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS0499	464945	466249	1305	PA4903	1.00E-92	Pae	G E P R	COG0477	Permeases of the major facilitator superfamily	ProP	(AF425229) vanillate transporter VanK [...
MS0500	466355	466579	225	PM1689	2.00E-19	Pmu	N	COG1826	Sec-independent protein secretion pathway components	TatA	(NC_002663) unknown [Pasteurella multocida]
MS0501	466586	467197	612	HI0187b	5.00E-31	Hin	N	COG1826	Sec-independent protein secretion pathway components	TatA	(NC_000907) Sec-independent protein secretion p...
MS0502	467219	467986	768	PM1691	1.00E-118	Pmu	N	COG0805	Sec-independent protein secretion pathway component TatC	TatC	(NC_002663) TatC [Pasteurella multocida]
MS0503	468064	469083	1020	PM1692	1.00E-161	Pmu	H	COG0113	Delta-aminolevulinic acid dehydratase	HemB	(NC_002663) HemB [Pasteurella multocida]
MS0504	469165	469257	93	none	none	No-des	none	No-des	No-des	none	none
MS0505	469704	469264	441	HI0331	3.00E-17	No-des	none	No-des	No-des	none	opacity associated protein B - Haemophilus influenza...
MS0506	471138	469720	1419	HI0330	2.00E-63	Hin	M	COG3061	Cell envelope opacity-associated protein A	OapA	(NC_000907) opacity associated protein (oapA) [...
MS0507	472219	471212	1008	PM0099	1.00E-147	Pmu	E	COG1509	Lysine 2/3-aminomutase	KamA	(NC_002663) unknown [Pasteurella multocida]
MS0508	472243	472818	576	PM0100	1.00E-103	Pmu	J	COG0231	Translation elongation factor P/translation initiation factor eIF-5A	Efp	(NC_002663) Efp [Pasteurella multocida]
MS0509	473591	472872	720	PM0102	2.00E-90	Pmu	S	COG2908	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0510	473714	474436	723	HI0734	1.00E-105	Hin	I	COG0204	1-acyl-sn-glycerol-3-phosphate acyltransferase	PlsC	(NC_000907) 1-acyl-glycerol-3-phosphate acyltra...
MS0511	474446	475846	1401	PM0104	1.00E-161	Pmu	Q	COG2132	Putative multicopper oxidases	SufI	(NC_002663) SufI [Pasteurella multocida]
MS0512	476644	475925	720	ZyqgA	5.00E-62	EcZ	R	COG1811	Uncharacterized membrane protein/possible Na+ channel or pump		(NC_002655) putative transport protein [Escheri...
MS0513	477509	476763	747	PM1188	1.00E-38	Pmu	M	COG0810	Periplasmic protein TonB/links inner and outer membranes	TonB	(NC_002663) TonB [Pasteurella multocida]
MS0514	477897	477514	384	PM1187	2.00E-56	Pmu	N	COG0848	Biopolymer transport protein	ExbD	(NC_002663) ExbD [Pasteurella multocida]
MS0515	478357	477902	456	PM1186	2.00E-52	Pmu	N	COG0811	Biopolymer transport proteins	TolQ	(NC_002663) ExbB [Pasteurella multocida]
MS0516	480531	478573	1959	ZchuA	8.00E-58	EcZ	P	COG1629	Outer membrane receptor proteins/mostly Fe transport	CirA	(NC_002655) outer membrane heme/hemoglobin rece...
MS0517	482289	481033	1257	PM1185	1.00E-176	Pmu	R	COG1253	Uncharacterized CBS domain-containing proteins		(NC_002663) unknown [Pasteurella multocida]
MS0518	483232	482408	825	PM1184	2.00E-75	Pmu	O	COG0755	ABC-type transport system involved in cytochrome c biogenesis/permease component	CcmC	(NC_002663) unknown [Pasteurella multocida]
MS0519	483382	484770	1389	HI0106	0	Hin	N	COG0541	Signal recognition particle GTPase	Ffh	(NC_000907) signal recognition particle protein...
MS0520	484820	484990	171	none	none	No-des	none	No-des	No-des	none	none
MS0521	485991	484993	999	NMA0046	1.00E-105	NmA	R	COG0385	Predicted Na+-dependent transporter		(NC_003116) putative transmembrane transport pr...
MS0522	487019	486306	714	PM1700	4.00E-77	Pmu	R	COG1011	Predicted hydrolases of the HAD superfamily		(NC_002663) unknown [Pasteurella multocida]
MS0523	487915	487031	885	HI0676	1.00E-135	Hin	L	COG0582	Integrase	XerC	(NC_000907) integrase/recombinase (xerC) [Haemo...
MS0524	488877	487942	936	ZyjiM	1.00E-64	EcZ	K	COG1802	Transcriptional regulators	GnrR (BS)	(NC_002655) yjiM gene product [Escherichia coli...
MS0525	488995	489999	1005	ZyjiN	1.00E-105	EcZ	E R	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	Tdh	(NC_002655) putative oxidoreductase [Escherichi...
MS0526	490151	491134	984	HI0146	5.00E-33	Hin	G	COG1638	Dicarboxylate-binding periplasmic protein	DctP	(NC_003078) putative C4-dicarboxylate transport...
MS0527	491194	491679	486	BH0702	2.00E-13	Bha	S	COG3090	Uncharacterized BCR		(NC_002570) C4-dicarboxylate transport system (...)
MS0528	491686	492975	1290	TM0324	3.00E-96	Tma	S	COG1593	Integral membrane protein/possible transporter		(NC_003078) putative large C4-dicarboxylate upt...
MS0529	493003	494457	1455	uxaB	0	Eco	G	COG0246	Mannitol-1-phosphate/altronate dehydrogenases	MitD	(NC_002695) altronate oxidoreductase [Escherich...
MS0530	494473	495957	1485	ZuxaA	0	EcZ	G	COG2721	Altronate dehydratase	UxaA	(NC_003143) altronate hydrolase [Yersinia pesti...
MS0531	496346	496050	297	PM1086	2.00E-49	Pmu	K L	COG2901	Factor for inversion stimulation Fis/transcriptional activator	Fis	(NC_002663) Fis [Pasteurella multocida]
MS0532	497378	496356	1023	PM1087	1.00E-154	Pmu	R	COG0042	Predicted TIM-barrel enzymes/possibly dehydrogenases/infr3 family		(NC_002663) unknown [Pasteurella multocida]
MS0533	498347	497469	879	PM1088	1.00E-134	Pmu	J	COG2264	Ribosomal protein L11 methylase	PrmA	(NC_002663) PrmA [Pasteurella multocida]
MS0534	498333	498428	96	none	none	No-des	none	No-des	No-des	none	none
MS0535	499294	498410	885	VCI1656	2.00E-47	Vch	G E R	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	RhaT	(NC_002505) conserved hypothetical protein [Vib...

MS0536	499373	499275	99	none	none	No-des	none	No-des	No-des		none	none
MS0537	500547	499366	1182	HI0055	0	Hin	G	COG1312	D-mannonate dehydratase		UxaA	(NC_000907) mannonate dehydratase (uxuA) [Haemo...
MS0538	501335	500583	753	HI0054	3.00E-86	Hin	K	COG2186	Transcriptional regulators		FadR	(NC_000907) uxu operon regulator (uxuR) [Haemop...
MS0539	503728	501341	2388	BH0704	0	Bha	G	COG1501	Alpha-glucosidases/family 31 of glycosyl hydrolases			(NC_003143) putative glucosidase [Yersinia pest...
MS0540	505049	503751	1299	BH0703	1.00E-118	Bha	S	COG1593	Integral membrane protein/possible transporter			(NC_003197) putative integral membrane protein...
MS0541	505552	505064	489	BH0702	3.00E-30	Bha	S	COG3090	Uncharacterized BCR			(NC_002570) C4-dicarboxylate transport system (...)
MS0542	505667	506776	1110	BH0701	7.00E-76	Bha	G	COG1638	Dicarboxylate-binding periplasmic protein		DctP	(NC_003197) putative dicarboxylate-binding peri...
MS0543	506797	507684	888	HI0048	1.00E-125	Hin	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)		FabG	(NC_000907) oxidoreductase [Haemophilus influen...
MS0544	507611	509101	1491	uxaC	0	Eco	G	COG1904	Glucuronate isomerase		UxaC	(NC_003197) putative uronate isomerase [Salmon...
MS0545	509115	510050	936	HI0049	1.00E-110	Hin	G	COG0524	Sugar kinases/ribokinase family		RbsK	(NC_000907) 2-dehydro-3-deoxyglucokinase (kdg...
MS0546	510102	510737	636	HI0047	1.00E-83	Hin	G	COG0800	2-keto-3-deoxy-6-phosphogluconate aldolase		Eda	(NC_000907) 4-hydroxy-2-oxoglutarate aldolase/2...
MS0547	510724	510831	108	none	none	No-des	none	No-des	No-des		none	none
MS0548	511044	511697	654	Z3933	4.00E-58	EcZ	T	COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases		ApaH	(NC_002655) unknown protein encoded by prophage...
MS0549	511965	513164	1200	proV	1.00E-122	Eco	E	COG1125	ABC-type proline/glycine betaine transport systems/ATPase components		ProV	(NC_003143) glycine betaine/L-proline transport...
MS0550	513164	514177	1014	ZproW	1.00E-108	EcZ	E	COG1174	ABC-type proline/glycine betaine transport systems/permease component		ProW	(NC_003143) glycine betaine/L-proline transport...
MS0551	514190	515170	981	proX	1.00E-109	Eco	E	COG2113	ABC-type proline/glycine betaine transport systems/periplasmic components		ProX	(NC_003143) glycine betaine-binding periplasmic...
MS0552	516677	515271	1407	PM0162	1.00E-175	Pmu	E	COG0531	Amino acid transporters		PotE	(NC_002663) ArcD [Pasteurella multocida]
MS0553	517599	516706	894	mlr1281	2.00E-31	Mlo	E	COG2040	Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)		MHT1	(NC_003062) AGR_C_4290p [Agrobacterium tumefaci...
MS0554	517741	517652	90	none	none	No-des	none	No-des	No-des		none	none
MS0555	518869	517781	1089	PM0163	0	Pmu	R	COG0012	Predicted GTPase			(NC_002663) unknown [Pasteurella multocida]
MS0556	519500	518919	582	PM0164	4.00E-85	Pmu	J	COG0193	Peptidyl-tRNA hydrolase		Phh	(NC_002663) Phh [Pasteurella multocida]
MS0557	520038	519625	414	PA5444	2.00E-24	Pae	S	COG2510	Predicted membrane protein			(NC_003305) conserved hypothetical protein [Agr...
MS0558	520183	520512	330	PM0166	1.00E-33	Pmu	S	COG2914	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS0559	520517	521713	1197	HI0396	1.00E-177	Hin	S	COG2850	Uncharacterized ACR			(NC_000907) conserved hypothetical protein [Hae...
MS0560	521732	523051	1320	HI0397	1.00E-176	Hin	L	COG1570	Exonuclease VII/large subunit		XseA	(NC_000907) exodeoxyribonuclease VII/large sub...
MS0561	523546	524574	1029	PM0389	1.00E-54	Pmu	M	COG3203	Outer membrane protein (porin)		OmpC	(NC_002663) OmpH [Pasteurella multocida]
MS0562	525512	524721	792	Z2874	9.00E-90	EcZ	K	COG1414	Transcriptional regulator		IclR	(NC_002695) putative regulator [Escherichia col...
MS0563	525706	526503	798	kduD	1.00E-99	Eco	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)		FabG	2-DEOXY-D-GLUCONATE 3-DEHYDROGENASE (2-KETO...
MS0564	526491	527183	693	SPy0637	3.00E-57	Spy	G	COG0698	Ribose 5-phosphate isomerase RpiB		RpiB	(NC_003143) putative sugar-phosphate isomerase ...
MS0565	527244	528185	942	HI0049	1.00E-112	Hin	G	COG0524	Sugar kinases/ribokinase family		RbsK	(NC_000907) 2-dehydro-3-deoxyglucokinase (kdg...
MS0566	528198	528833	636	HI0047	8.00E-90	Hin	G	COG0800	2-keto-3-deoxy-6-phosphogluconate aldolase		Eda	(NC_000907) 4-hydroxy-2-oxoglutarate aldolase/2...
MS0567	528446	529166	321	BH0496	1.00E-19	Bha	S	COG1917	Uncharacterized ACR/double-stranded beta-helix domain			(NC_003030) Possible pectin degradation protein...
MS0568	529374	530444	1071	HI0457	1.00E-118	Hin	R	COG1559	Predicted periplasmic solute-binding protein			(NC_000907) conserved hypothetical protein [Hae...
MS0569	530477	531118	642	HI0456	9.00E-92	Hin	F	COG0125	Thymidylate kinase		Tmk	dTMP kinase (EC 2.7.4.9) - Haemophilus influenzae (s...
MS0570	531097	532098	1002	PM1674	1.00E-120	Pmu	L	COG0470	ATPase involved in DNA replication		HolB	(NC_002663) HolB [Pasteurella multocida]
MS0571	532152	532931	780	HI0454	1.00E-107	Hin	L	COG0084	Mg-dependent DNase		TatD	(AF174390) HI0454 [Haemophilus influenzae]
MS0572	532956	533486	531	HI0453	2.00E-61	No-des	none	No-des	No-des		none	(NC_000907) conserved hypothetical protein [Hae...
MS0573	533576	534874	1299	PM1677	1.00E-168	Pmu	R	COG1253	Uncharacterized CBS domain-containing proteins			(NC_002663) unknown [Pasteurella multocida]
MS0574	534977	538453	3477	PM0034	0	Pmu	L	COG0587	DNA polymerase III alpha subunit		DnaE	(NC_002663) DnaE [Pasteurella multocida]
MS0575	539931	538627	1305	PA1507	8.00E-74	Pae	F	COG2233	Xanthine/uracil permeases		UraA	(NC_003030) Xanthine permease [Clostridium acet...
MS0576	539993	540121	129	none	none	No-des	none	No-des	No-des		none	none
MS0577	540162	541004	843	SPy1552	2.00E-30	Spy	S	COG2315	Uncharacterized BCR		MmcQ	(NC_002737) hypothetical protein [Streptococcus...
MS0578	541071	541964	894	BH3866	1.00E-52	Bha	R	COG2962	Predicted permeases		RarD	(NC_003295) HYPOTHETICAL TRANSMEMBRANE PROTE...
MS0579	542052	541885	168	none	none	No-des	none	No-des	No-des		none	none
MS0580	543149	542070	1080	PA0323	8.00E-08	Pae	E	COG0687	Spermidine/putrescine-binding periplasmic protein		PotD	(NC_003143) putative exported protein [Yersinia...
MS0581	544021	543176	846	mlr1739	9.00E-27	Mlo	E	COG1177	ABC-type spermidine/putrescine transport system/permease component II		PotC	(NC_003143) putative binding-protein-dependent ...
MS0582	544025	544123	99	none	none	No-des	none	No-des	No-des		none	none
MS0583	544887	544021	867	mlr7677	1.00E-19	Mlo	E	COG1176	ABC-type spermidine/putrescine transport system/permease component I		PotB	(NC_003143) putative binding-protein-dependent ...
MS0584	545972	544887	1086	ZafuC	9.00E-73	EcZ	G	COG1130	ABC-type sugar/spermidine/putrescine/iron/thiamine transport systems/ATPase component		MalK	(NC_002695) putative ABC transporter ATP-bindin...
MS0585	546673	546191	483	HI0250	5.00E-61	Hin	L	COG0629	Single-stranded DNA-binding protein		Ssb	(U04997) SSB [Haemophilus influenzae]
MS0586	546825	549653	2829	HI0249	0	Hin	L	COG0178	Excinuclease ATPase subunit		UvrA	(NC_000907) excinuclease ABC[subunit A (uvrA) ...
MS0587	549891	550988	1098	HI0644	1.00E-122	Hin	C	COG3005	Nitrate/TMAO reductases/membrane-bound tetraheme cytochrome c subunit		TorC	(NC_000907) cytochrome C-type protein (yecK) [H...
MS0588	551019	553490	2472	HI0643	0	Hin	C	COG0243	Anaerobic dehydrogenases/typically selenocysteine-containing		BisC	(NC_000907) biotin sulfoxide reductase (bisC) [...
MS0589	553562	553678	117	none	none	No-des	none	No-des	No-des		none	none
MS0590	553718	554767	1050	HI0037	1.00E-173	Hin	D	COG1077	HSP70 class molecular chaperones involved in cell morphogenesis		MreB	ROD SHAPE-DETERMINING PROTEIN MREB
MS0591	554873	554760	114	none	none	No-des	none	No-des	No-des		none	none
MS0592	554864	555922	1059	PM1956	1.00E-135	Pmu	M	COG1792	Rod shape-determining protein		MreC	(NC_002663) MreC [Pasteurella multocida]
MS0593	555925	556410	486	PM1957	2.00E-47	Pmu	M	COG2891	Rod shape-determining protein		MreD	(NC_002663) MreD [Pasteurella multocida]
MS0594	556444	557271	828	HI1386	3.00E-07	No-des	none	No-des	No-des		none	(NC_000852) A111R [Paramecium bursaria Chlorell...
MS0595	557954	557337	618	HI0989	1.00E-103	Hin	E	COG0066	3-isopropylmalate dehydratase small subunit		LeuD	(NC_000907) 3-isopropylmalate dehydratase small...

MS0596	559439	558033	1407	HI0988		0	Hin	E	COG0065	3-isopropylmalate dehydratase large subunit	LeuC	(NC_000907) 3-isopropylmalate dehydratase[alph...
MS0597	559912	559532	381	BS_yyaH	7.00E-32		Bsu	E	COG0346	Lactoylglutathione lyase and related lyases	GloA	(NC_000964) yyaH [Bacillus subtilis]
MS0598	561009	559936	1074	HI0987		0	Hin	E	COG0473	Isocitrate/isopropylmalate dehydrogenase	LeuB	(NC_000907) 3-isopropylmalate dehydrogenase (be...
MS0599	562663	561074	1590	PM1962		0	Pmu	E	COG0119	Isopropylmalate/homocitrate/citramalate synthases	LeuA	(NC_002663) LeuA [Pasteurella multocida]
MS0600	562806	562919	114	none	none		No-des	none	No-des	none	none	
MS0601	563326	563970	645	HI1089	2.00E-81		Hin	Q	COG1131	ABC-type multidrug transport system ATPase component	CcmA	(NC_000907) heme exporter ATP-binding protein A...
MS0602	564001	564663	663	PM0006	4.00E-59		Pmu	O	COG2386	ABC-type transport system involved in cytochrome c biogenesis permease component	CcmB	(NC_002663) CcmB [Pasteurella multocida]
MS0603	564681	565409	729	PM0007	1.00E-120		Pmu	O	COG0755	ABC-type transport system involved in cytochrome c biogenesis permease component	CcmC	(NC_002663) CcmC [Pasteurella multocida]
MS0604	565465	565665	201	PM0008	2.00E-13		Pmu	N	COG3114	Heme exporter protein D	CcmD	(NC_002663) CcmD [Pasteurella multocida]
MS0605	565665	566201	537	PM0009	3.00E-72		Pmu	O	COG2332	Cytochrome c-type biogenesis protein CcmE	CcmE	(NC_002663) CcmE [Pasteurella multocida]
MS0606	566201	568144	1944	HI1094		0	Hin	O	COG1138	Cytochrome c biogenesis factor	CcmF	(NC_000907) cytochrome C-type biogenesis protei...
MS0607	568195	568740	546	HI1095	3.00E-71		Hin	O/C	COG0526	Thiol-disulfide isomerase and thioredoxins	TrxA	(NC_000907) thioldisulfide interchange protein...
MS0608	568743	569234	492	PM0012	4.00E-50		Pmu	O	COG3088	Uncharacterized protein involved in biosynthesis of c-type cytochromes	CcmH	(NC_002663) CcmH [Pasteurella multocida]
MS0609	569241	570155	915	PM0013	1.00E-102		Pmu	R	COG0457	TPR-repeat-containing proteins	NrFG	(NC_002663) CcmH [Pasteurella multocida]
MS0610	570508	570413	96	PM0014	4.00E-09		Pmu	E	COG0346	Lactoylglutathione lyase and related lyases	GloA	(NC_002663) unknown [Pasteurella multocida]
MS0611	570265	570672	408	PM0014	3.00E-47		Pmu	E	COG0346	Lactoylglutathione lyase and related lyases	GloA	(NC_002663) unknown [Pasteurella multocida]
MS0612	570647	571219	573	PM0015	7.00E-26		No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0613	571244	571552	309	HI1099	5.00E-07		No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS0614	572827	571625	1203	PM0829	1.00E-161		Pmu	G	COG1482	Phosphomannose isomerase	ManA	(NC_002663) Pmi [Pasteurella multocida]
MS0615	573312	572830	483	PM0830	1.00E-36		No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0616	574219	573386	834	PM0832	1.00E-112		No-des	none	No-des	No-des	none	(NC_002663) PtnD [Pasteurella multocida]
MS0617	575033	574236	798	PM0833	1.00E-121		No-des	none	No-des	No-des	none	(NC_002663) PtnC [Pasteurella multocida]
MS0618	576027	575047	981	PM0834_2	3.00E-79		Pmu	G	COG3444	Phosphotransferase system mannose/fructose/N-acetylgalactosamine-specific component IIB		(NC_002663) unknown [Pasteurella multocida]
MS0619	576628	576296	333	PM0158	6.00E-50		Pmu	P	COG2824	Uncharacterized Zn-ribbon-containing protein involved in phosphate metabolism	PhnA	(NC_002663) PhnA [Pasteurella multocida]
MS0620	576799	576686	114	none	none		No-des	none	No-des	No-des	none	
MS0621	577608	576781	828	HI1037	1.00E-124		Hin	R	COG0121	Predicted glutamine amidotransferase		(NC_000907) conserved hypothetical protein [Hae...
MS0622	579321	577894	1428	HI0078		0	Hin	J	COG0215	CysteinyI-tRNA synthetase	CysS	(NC_000907) cysteinyI-tRNA synthetase (cysS) [H...
MS0623	579375	579923	549	HI0079	7.00E-83		Hin	O	COG0652	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	PpiB	(NC_000907) peptidyl-prolyl cis-trans isomerase...
MS0624	58037	580591	555	ZppB	1.00E-65		EcZ	O	COG0652	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family	PpiB	(NC_003198) peptidyl-prolyl cis-trans isomerase...
MS0625	580651	581442	792	HI0081	7.00E-98		Hin	L	COG0084	Mg-dependent DNase	TatD	(NC_000907) conserved hypothetical protein [Hae...
MS0626	581545	582579	1035	PM0021	1.00E-164		Pmu	F	COG0150	Phosphoribosylaminoimidazol (AIR) synthetase	PurM	(NC_002663) PurM [Pasteurella multocida]
MS0627	582649	583284	636	HI1428	5.00E-84		Hin	F	COG0299	Folate-dependent phosphoribosylglycinamide formyltransferase PurN	PurN	(NC_000907) phosphoribosylglycinamide formyltra...
MS0628	583373	583909	537	PM1207	2.00E-81		Pmu	F	COG2065	Pyrimidine operon attenuation protein uracil phosphoribosyltransferase	PyrR (BS)	(NC_002663) PyrR [Pasteurella multocida]
MS0629	583875	584933	1059	PM1208	1.00E-102		Pmu	O	COG0760	Parvulin-like peptidyl-prolyl isomerase	SurA	(NC_002663) SurA [Pasteurella multocida]
MS0630	585059	585922	864	HI0549	1.00E-146		Hin	J	COG0030	Dimethyladenosine transferase (rRNA methylation)	KsgA	(NC_000907) dimethyladenosine transferase (ksgA...
MS0631	585982	586809	828	PM1210	1.00E-129		Pmu	T	COG0639	Diadenosine tetraphosphatase and related serine/threonine protein phosphatases	ApaH	(NC_002663) AdaH [Pasteurella multocida]
MS0632	587356	586883	474	HI1155	9.00E-80		Hin	O	COG0602	Organic radical activating enzymes	NrdG	(NC_000907) anaerobic ribonucleoside-triphospha...
MS0633	589776	587644	2133	HI0075		0	Hin	F	COG1328	Oxygen-sensitive ribonucleoside-triphosphate reductase	NrdD	(NC_000907) anaerobic ribonucleoside-triphospha...
MS0634	590797	590078	720	PM1066	1.00E-87		Pmu	P	COG0861	Membrane protein TerC possibly involved in tellurium resistance	TerC	(NC_002663) unknown [Pasteurella multocida]
MS0635	591467	590874	594	PM1067	5.00E-85		Pmu	L	COG3066	DNA mismatch repair protein	MutH	(NC_002663) MutH [Pasteurella multocida]
MS0636	591609	591460	150	none	none		No-des	none	No-des	No-des	none	
MS0637	592171	591635	537	HI0402	2.00E-63		Hin	L	COG0350	Methylated DNA-protein cysteine methyltransferase	Ada	(NC_000907) methylated-DNA--protein-cysteine me...
MS0638	593638	592238	1401	HI0401	1.00E-131		Hin	I	COG2067	Long-chain fatty acid transport protein	FadL	(M73494) outer membrane protein [Haemophilus infl...
MS0639	594899	593910	990	PM1038	5.00E-96		Pmu	G	COG1879	Periplasmic sugar-binding proteins	RbsB	(NC_002663) MglB [Pasteurella multocida]
MS0640	595090	595203	114	none	none		No-des	none	No-des	none	none	
MS0641	596190	595186	1005	PM1040	1.00E-136		Pmu	G	COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems permease components	AraH	(NC_002663) MglC [Pasteurella multocida]
MS0642	597724	596207	1518	HI0823		0	Hin	G	COG1129	ABC-type sugar (aldose) transport system ATPase component	MglA	(NC_000907) galactoside ABC transporter ATP-bi...
MS0643	598781	597792	990	PM1038	1.00E-152		Pmu	G	COG1879	Periplasmic sugar-binding proteins	RbsB	(NC_002663) MglB [Pasteurella multocida]
MS0644	59950	598949	1002	PM1037	1.00E-139		Pmu	K	COG1609	Transcriptional regulators	PurR	(NC_002663) GalR [Pasteurella multocida]
MS0645	600191	600337	147	PM1036	2.00E-17		Pmu	C	COG1085	Galactose-1-phosphate uridylyltransferase	GalT	(NC_002663) GalT [Pasteurella multocida]
MS0646	600253	600516	264	HI0820	1.00E-36		Hin	C	COG1085	Galactose-1-phosphate uridylyltransferase	GalT	(NC_000907) galactose-1-phosphate uridylyltrans...
MS0647	600516	601238	723	PM1036	1.00E-119		Pmu	C	COG1085	Galactose-1-phosphate uridylyltransferase	GalT	(NC_002663) GalT [Pasteurella multocida]
MS0648	601345	602499	1155	PM1035	1.00E-145		Pmu	G	COG0153	Galactokinase	GalK	(NC_002663) GalK [Pasteurella multocida]
MS0649	602469	603524	1056	HI0818	1.00E-134		Hin	G	COG2017	Galactose mutarotase and related enzymes	GalM	(NC_000907) aldose 1-epimerase (galM) [Haemophi...
MS0650	603455	603625	171	none	none		No-des	none	No-des	No-des	none	
MS0651	603869	604876	1008	PM1033	1.00E-128		Pmu	R	COG1253	Uncharacterized CBS domain-containing proteins		(NC_002663) unknown [Pasteurella multocida]
MS0652	605169	606713	1545	HI0302		0	Hin	M	COG0815	Apolipoprotein N-acyltransferase	Lnt	(NC_000907) apolipoprotein N-acyltransferase (c...
MS0653	606729	606827	99	none	none		No-des	none	No-des	No-des	none	
MS0654	607152	606814	339	HI0548	8.00E-39		Hin	J	COG0361	Translation initiation factor IF-1	InfA	(NC_000907) translation initiation factor 1 (in...
MS0655	607141	608328	1188	HI0866	9.00E-40		No-des	none	No-des	No-des	none	(AB041266) Wzz homolog [Actinobacillus actinomyc...

MS0656	608334	609137	804	none	none	No-des	none	No-des	No-des	none	(AJ006986) an alternative ATG initiation codon i...
MS0657	609112	610401	1290	MTT367	2.00E-62	Mth	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid	RbX	(NC_000916) O-antigen transporter [Methanotherm...
MS0658	610386	610841	456	aq_1368	1.00E-50	Aae	MIJ	COG0615	Cytidyltransferase	TagD (BS)	(NC_000918) glycerol-3-phosphate cytidyltransfe...
MS0659	610844	611929	1086	L151480	3.00E-18	Lla	M	COG1887	Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsI/RodC	TagB (BS)	(NC_002758) hypothetical protein [Staphylococcu...
MS0660	611959	613305	1347	none	none	No-des	none	No-des	No-des	none	none
MS0661	613404	614504	1101	GJ1439c	1.00E-131	Cje	M	COG0562	UDP-galactopyranose mutase	Glf	(AJ006986) UDP-galactopyranose mutase [Streptoco...
MS0662	614483	615943	1461	HI0872	0	Hin	M	COG2148	Sugar transferases involved in lipopolysaccharide synthesis	WcaJ	(NC_000907) undecaprenyl-phosphate galactosepho...
MS0663	615930	616301	372	yfdG	3.00E-31	No-des	none	No-des	No-des	none	BACTOPRENOL-LINKED GLUCOSE TRANSLOCASE
MS0664	616308	617237	930	yfdH	1.00E-119	Eco	M	COG0463	Glycosyltransferases involved in cell wall biogenesis	WcaA	(NC_003197) putative glycosyltransferase [Salmo...
MS0665	617233	619353	2121	none	none	No-des	none	No-des	No-des	none	none
MS0666	619338	619631	294	none	none	No-des	none	No-des	No-des	none	none
MS0667	619916	621217	1302	PM1029	1.00E-172	Pmu	E	COG0260	Leucyl aminopeptidase	PepB	(NC_002663) PepB [Pasteurella multocida]
MS0668	621230	621652	423	HI0876	5.00E-55	Hin	F	COG0105	Nucleoside diphosphate kinase	Ndk	(NC_000907) nucleoside diphosphate kinase (ndk)...
MS0669	621946	623094	1149	PM1027	0	Pmu	H	COG0192	S-adenosylmethionine synthetase	MetK	(NC_002663) MetX [Pasteurella multocida]
MS0670	623787	623221	567	Zdps	4.00E-15	EcZ	L	COG0783	Starvation-inducible DNA-binding protein	Dps	FINE TANGLED PILI MAJOR SUBUNIT (24 KD SURF...
MS0671	624364	626250	1887	Zgsp_2	1.00E-140	EcZ	E	COG0754	glutathionylspermidine synthase	Gsp	(NC_002655) glutathionylspermidine synthetase/a...
MS0672	626263	626604	342	HI1013	6.00E-49	Hin	P	COG1393	Arsenate reductase and related proteins glutaredoxin family	ArsC	(NC_000907) conserved hypothetical protein [Hae...
MS0673	626646	627191	546	HI0217	1.00E-60	Hin	L	COG1943	Predicted transposase	none	(NC_000907) conserved hypothetical protein [Hae...
MS0674	628057	629187	1131	HI1012	0	Hin	E	COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	ArgE	(NC_000907) succinyl-diaminopimelate desuccinyl...
MS0675	629192	629869	678	PM1021	2.00E-82	Pmu	M	COG1876	D-alanyl-D-alanine carboxypeptidase	VanY	(NC_002663) unknown [Pasteurella multocida]
MS0676	630582	629923	660	PM1260	8.00E-64	Pmu	H	COG0352	Thiamine monophosphate synthase	ThiE	(NC_002663) ThiE [Pasteurella multocida]
MS0677	631378	630572	807	HI0416	2.00E-94	Hin	H	COG0351	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	ThiD	(NC_000907) phosphomethylpyrimidine kinase (thi...
MS0678	631364	631507	144	none	none	No-des	none	No-des	No-des	none	none
MS0679	631635	631769	135	none	none	No-des	none	No-des	No-des	none	none
MS0680	633120	631783	1338	VCA0151	4.00E-77	Vch	C	COG1018	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1	Hmp	(NC_002506) oxidoreductase putative [Vibrio ch...
MS0681	633996	633463	534	HI1151	1.00E-68	Hin	S	COG3028	Uncharacterized BCR	none	(NC_000907) conserved hypothetical protein [Hae...
MS0682	634135	635487	1353	PM0120	0	Pmu	R	COG0312	Predicted Zn-dependent proteases and their inactivated homologs	TldD	(NC_002663) PmbA [Pasteurella multocida]
MS0683	635741	636277	537	PM0121	6.00E-85	Pmu	F	COG0634	Hypoxanthine-guanine phosphoribosyltransferase	Hpt	(NC_002663) Hpt [Pasteurella multocida]
MS0684	637526	636402	1125	anl4328	5.00E-67	Mlo	G	COG3386	Gluconolactonase	none	(NC_003296) PUTATIVE GLUCONOLACTONASE PRECUR...
MS0685	637610	637756	147	none	none	No-des	none	No-des	No-des	none	none
MS0686	639173	637797	1377	PM1740	1.00E-165	Pmu	G/E	COG2610	H+/gluconate symporter and related permeases	GntT	(NC_002663) GntP [Pasteurella multocida]
MS0687	640132	639284	849	Z2821	3.00E-72	EcZ	R	COG0656	Aldo/keto reductases related to diketoglutarate reductase	ARA1	(NC_003197) putative aldehyde reductase [Salmon...
MS0688	641619	640237	1383	BH0805	2.00E-91	Bha	G/E	COG2610	H+/gluconate symporter and related permeases	GntT	(NC_002570) gluconate permease [Bacillus halodur...
MS0689	643061	641736	1326	ygcX	0	Eco	H	COG1441	O-succinylbenzoate synthase and related enzymes	DgoA	(NC_002695) putative glucarate dehydratase [Esc...
MS0690	643112	643216	105	none	none	No-des	none	No-des	No-des	none	none
MS0691	643538	644305	768	ZyhaF	7.00E-98	EcZ	G	COG0469	Pyruvate kinase	PykF	(NC_003198) 5-keto-4-deoxy-D-glucarate aldolase...
MS0692	644388	645272	885	ZyhaE	1.00E-125	EcZ	I	COG2084	β-hydroxyisobutyrate dehydrogenase and related proteins	MmsB	(NC_002655) putative dehydrogenase [Escherichia...
MS0693	645384	646538	1155	ZyhaD	1.00E-120	EcZ	G	COG1929	Glycerate kinase	none	(NC_003197) putative glycerate kinase 2 [Salmon...
MS0694	646553	647701	1149	ZyaeG	1.00E-139	EcZ	TIQ	COG2508	Regulator of polyketide synthase expression	SrmR	(NC_003197) putative inner membrane protein [Sa...
MS0695	649356	647791	1566	ZyhaG	0	EcZ	G	COG2721	Altronate dehydratase	UxaA	(NC_002695) putative hydrolase [Escherichia col...
MS0696	650877	649564	1314	BH0703	1.00E-113	Bha	S	COG1593	Integral membrane protein possible transporter	none	(NC_003197) putative integral membrane protein ...
MS0697	651428	650880	549	BH0702	3.00E-27	Bha	S	COG3090	Uncharacterized BCR	none	(AF186091) putative small integral C4-d...
MS0698	652492	651509	984	BH0701	3.00E-66	Bha	G	COG1638	Dicarboxylate-binding periplasmic protein	DctP	(NC_003197) putative dicarboxylate-binding peri...
MS0699	652787	653053	267	HI1468	7.00E-33	Hin	J	COG0184	Ribosomal protein S15P/S13E	RpsO	(NC_000907) ribosomal protein S15 (rpS15) [Haem...
MS0700	654012	653455	558	PM0990	4.00E-31	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0701	655422	654070	1353	PM0989	0	Pmu	R	COG2056	Predicted permease	none	(NC_002663) unknown [Pasteurella multocida]
MS0702	656181	655513	669	HI0324	1.00E-101	Hin	L	COG0847	DNA polymerase III epsilon subunit and related 3'-5' exonucleases	DnaQ	(NC_000907) ribonuclease T (mt) [Haemophilus l...
MS0703	656647	656240	408	HI0323	2.00E-62	Hin	E	COG0346	Lactoylglutathione lyase and related lyases	GloA	(NC_000907) lactoylglutathione lyase (gloA) [Ha...
MS0704	657434	656718	717	PM0124	2.00E-83	Pmu	E	COG0834	ABC-type amino acid transport system periplasmic component	ArtI	ARGININE-BINDING PERIPLASMIC PROTEIN PRECUR...
MS0705	657413	657547	135	none	none	No-des	none	No-des	No-des	none	none
MS0706	658268	657546	723	HI0319	1.00E-118	Hin	Q/R	COG0500	SAM-dependent methyltransferases	SmtA	(NC_000907) conserved hypothetical protein [Hae...
MS0707	658243	658332	90	none	none	No-des	none	No-des	No-des	none	none
MS0708	658380	660149	1770	HI0317	0	Hin	J	COG0173	Aspartyl-tRNA synthetase	AspS	(NC_000907) aspartyl-tRNA synthetase (aspS) [Ha...
MS0709	660216	660659	444	HI0316	7.00E-52	Hin	L/R	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	MutT	(NC_003143) putative dATP pyrophosphohydrolase ...
MS0710	660988	661728	741	HI0315	1.00E-127	Hin	S	COG0217	Uncharacterized ACR	none	(NC_000907) conserved hypothetical protein [Hae...
MS0711	661759	662355	597	HI0314	2.00E-78	Hin	L	COG0817	Holliday junction resolvosome endonuclease subunit	RuvC	(NC_000907) crossover junction endodeoxyribonuc...
MS0712	662389	663033	645	HI0313	4.00E-86	Hin	L	COG0632	Holliday junction resolvosome DNA-binding subunit	RuvA	(NC_000907) Holliday junction DNA helicase (ruv...
MS0713	663046	664050	1005	HI0312	1.00E-171	Hin	L	COG2255	Holliday junction resolvosome helicase subunit	RuvB	(NC_000907) Holliday junction DNA helicase (ruv...
MS0714	664454	664143	312	PM0975	5.00E-26	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0715	665027	666595	1569	PM0974	0	Pmu	C	COG1271	Cytochrome bd-type quinol oxidase subunit 1	CydA	(NC_002663) CydA [Pasteurella multocida]

MS0716	666601	667734	1134	PM0973	1.00E-178	Pmu	C	COG1294	Cytochrome bd-type quinol oxidase subunit 2	AppB	(NC_002663) CytB [Pasteurella multocida]
MS0717	667750	667845	96	none	none	none	none	No-des	No-des	none	none
MS0718	667845	668135	291	PM0972	1.00E-22	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0719	668478	668876	399	HI0386	1.00E-49	Hin	R	COG0824	Predicted thioesterase	FcbC	(NC_000907) conserved hypothetical protein [Hae...
MS0720	668902	669585	684	PM0970	1.00E-102	Pmu	N	COG0811	Biopolymer transport proteins	TolQ	(NC_002663) TolQ [Pasteurella multocida]
MS0721	669623	670078	456	PM0969	1.00E-54	Pmu	N	COG0848	Biopolymer transport protein	ExbD	(NC_002663) TolR [Pasteurella multocida]
MS0722	670099	671274	1176	HI0383	2.00E-43	Hin	M	COG3064	Membrane protein involved in colicin uptake	TolA	tolA protein - Haemophilus influenzae
MS0723	671316	672608	1293	HI0382	0	Hin	N	COG0823	Periplasmic component of the Tol biopolymer transport system	TolB	(NC_000907) colicin tolerance protein (tolB) [H...
MS0724	673742	674269	528	HI0938	7.00E-27	Hin	N	COG2165	General secretory pathway proteins G and H and related periplasmic/secreted proteins	HofG	(NC_000907) H. influenzae predicted coding regi...
MS0725	674269	674907	639	PM0964	1.00E-32	none	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0726	674897	675595	699	HI0940	2.00E-27	No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS0727	675573	675866	294	HI0941	5.00E-23	No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS0728	675884	679384	3501	PM0961	0	Pmu	L	COG1330	Exonuclease V gamma subunit	RecC	(NC_002663) RecC [Pasteurella multocida]
MS0729	679953	679615	339	HI0445	5.00E-31	Hin	N	COG1314	Preprotein translocase subunit	SecG	(NC_000907) protein-export membrane protein (se...
MS0730	682001	680070	1932	HI0444	0	Hin	L	COG0550	Topoisomerase IA	TopA	(NC_000907) DNA topoisomerase III (topB) [Haemo...
MS0731	682250	684085	1836	TM1640	4.00E-51	Tma	ElR	COG0493	NADPH-dependent glutamate synthase beta chain and related oxidoreductases	GltD	(U73807) formate dehydrogenase beta subunit [Moor...
MS0732	684085	686889	2805	MTH1552	0	Mth	R	COG3383	Uncharacterized anaerobic dehydrogenase		(AJ312125) FdhA-II protein [Eubacterium acidamin...
MS0733	687070	686975	96	none	none	none	none	No-des	No-des	none	none
MS0734	687145	688665	1521	HI0136	0	Hin	R	COG1160	Predicted GTPases		(NC_000907) GTP-binding protein [Haemophilus in...
MS0735	689118	688837	282	HI0828	2.00E-32	Hin	S	COG2350	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS0736	689583	689122	462	PM0328	1.00E-56	Pmu	I	COG1607	Acyl-CoA hydrolase		(NC_002663) unknown [Pasteurella multocida]
MS0737	690134	689595	540	PM0329	4.00E-77	Pmu	D	COG2917	Intracellular septation protein A		(NC_002663) unknown [Pasteurella multocida]
MS0738	690675	690139	537	PM0330	1.00E-22	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0739	690914	690678	237	PM0330	2.00E-06	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0740	691141	691755	615	PM0331	1.00E-79	Pmu	M	COG3047	Outer membrane protein W	OmpW	(NC_002663) OmpW [Pasteurella multocida]
MS0741	693582	691909	1674	HI0070	0	Hin	L	COG0497	DNA Pases involved in DNA repair	RecN	(NC_000907) DNA repair protein (recN) [Haemophi...
MS0742	694649	693660	990	PM0333	1.00E-123	Pmu	R	COG0061	Predicted kinase		(NC_002663) unknown [Pasteurella multocida]
MS0743	694729	695340	612	PM0334	4.00E-78	Pmu	O	COG0576	Molecular chaperone GrpE (heat shock protein)	GrpE	(NC_002663) GrpE [Pasteurella multocida]
MS0744	696127	695453	675	PM1181	1.00E-101	Pmu	KIT	COG1974	SOS-response transcriptional repressors (RecA-mediated autopeptidases)	LexA	(NC_002663) LexA [Pasteurella multocida]
MS0745	696267	698735	2469	PM1182	0	Pmu	I	COG2937	Glycerol-3-phosphate O-acyltransferase	PlsB	(NC_002663) PlsB [Pasteurella multocida]
MS0746	698738	699631	894	HI0309	1.00E-143	Hin	L	COG0582	Integrase	XerC	(NC_000907) integrase/recombinase (xerD) [Haemo...
MS0747	699879	702023	2145	PM0304_1	1.00E-169	Pmu	L	COG0116	Predicted N6-adenine-specific DNA methylases		(NC_002663) unknown [Pasteurella multocida]
MS0748	702591	718787	16197	PM0714	1.00E-108	No-des	none	No-des	No-des	none	(NC_003028) cell wall surface anchor family pro...
MS0749	719014	722052	3039	TM1193	1.00E-155	Tma	G	COG3250	Beta-galactosidase/beta-glucuronidase	LacZ	BETA-GALACTOSIDASE (LACTASE)
MS0750	722856	722158	699	PM1855	3.00E-72	Pmu	S	COG1556	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS0751	724268	722859	1410	PM1854	0	Pmu	C	COG1139	Uncharacterized conserved protein containing a ferredoxin-like domain		(NC_002663) unknown [Pasteurella multocida]
MS0752	725001	724273	729	PM1853	1.00E-105	Pmu	C	COG0247	Fe-S oxidoreductases	GlpC	(NC_002663) unknown [Pasteurella multocida]
MS0753	726684	725092	1593	HI1218	0	Hin	C	COG1620	L-lactate permease	LldP	(NC_000907) L-lactate permease (lctP) [Haemophi...
MS0754	728260	726944	1317	PM0828_1	1.00E-116	Pmu	E	COG0548	Acetylglutamate kinase	ArgB	(NC_002663) ArgA [Pasteurella multocida]
MS0755	729131	728871	261	PM0827	2.00E-41	Pmu	O	COG0695	Glutaredoxin and related proteins	GrxC	(NC_002663) Grx [Pasteurella multocida]
MS0756	729195	729974	780	ZmdaA	1.00E-66	EcZ	C	COG0778	Nitroreductase	NfnB	(NC_003197) oxygen-insensitive NADPH nitroreduc...
MS0757	729984	730880	897	PM0826	1.00E-109	Pmu	HJ	COG0189	Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase)	RimK	(NC_002663) RimK [Pasteurella multocida]
MS0758	730956	731492	537	PM0825	2.00E-73	Pmu	R	COG3150	Predicted esterase		(NC_002663) unknown [Pasteurella multocida]
MS0759	732141	731536	606	PM0824	5.00E-56	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0760	733643	732249	1395	PM0823	0	Pmu	C	COG0114	Fumarase	FumC	(NC_002663) FumC [Pasteurella multocida]
MS0761	733822	734949	1128	PM0909	1.00E-103	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0762	734977	736017	1041	PM0908	1.00E-126	Pmu	K	COG3283	Transcriptional regulator of aromatic amino acids metabolism	TyrR	(NC_002663) TyrR [Pasteurella multocida]
MS0763	736225	737148	924	PM0421	1.00E-156	Pmu	K	COG0583	Transcriptional regulator	LysR	(NC_002663) MetR [Pasteurella multocida]
MS0764	737167	737889	723	HI1738	2.00E-95	Hin	E	COG1296	Predicted branched-chain amino acid permease (azaleucine resistance)	AziC (BS)	(NC_000907) conserved hypothetical protein [Hae...
MS0765	737902	738231	330	PM0423	3.00E-43	Pmu	E	COG1687	Predicted branched-chain amino acid permeases (azaleucine resistance)	AziD (BS)	(NC_002663) unknown [Pasteurella multocida]
MS0766	738562	738458	105	none	none	No-des	none	No-des	No-des	none	none
MS0767	738553	740019	1467	HI0183	1.00E-176	Hin	E	COG1115	Na+/alanine symporter	AlaT (BS)	(NC_000907) amino acid carrier protein putativ...
MS0768	741109	740135	975	PM0292	1.00E-138	Pmu	I	COG0825	Acetyl-CoA carboxylase alpha subunit	AccA	(NC_002663) AccA [Pasteurella multocida]
MS0769	741159	741260	102	none	none	No-des	none	No-des	No-des	none	none
MS0770	742000	741362	639	HI1244	3.00E-75	No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS0771	742290	743948	1659	PM1074	0	Pmu	G	COG1109	Phosphomannomutase	CpsG	(NC_002663) YhxB [Pasteurella multocida]
MS0772	745766	744198	1569	PM0293_2	1.00E-176	Pmu	F	COG0519	GMP synthase - PP-ATPase domain	GuaA	(NC_002663) GuaA [Pasteurella multocida]
MS0773	746114	745791	324	none	none	No-des	none	No-des	No-des	none	none
MS0774	747689	746229	1461	PM0295_3	1.00E-118	Pmu	F	COG0516	IMP dehydrogenase/GMP reductase	GuaB	(NC_000907) inosine-5'-monophosphate dehydrogen...
MS0775	747704	748783	1080	PM0296_2	6.00E-80	Pmu	H	COG0340	Biotin-(acetyl-CoA carboxylase) ligase	BirA	(NC_002663) BirA [Pasteurella multocida]

MS0776	749789	748827	963	PM0340	1.00E-166	Pmu	Q/R	COG0500	SAM-dependent methyltransferases	SmtA	(NC_002663) unknown [Pasteurella multocida]
MS0777	751307	749796	1512	PM0341	0	Pmu	E/H/R	COG0591	Na ⁺ /proline/Na ⁺ /panthothenate symporters and related permeases	PutP	(NC_002663) PutP [Pasteurella multocida]
MS0778	751517	752989	1473	PM0342	0	Pmu	J	COG1530	Ribonucleases G and E	CafA	(NC_002663) CafA [Pasteurella multocida]
MS0779	753202	753110	93	none	none	No-des	none	No-des	none	none	none
MS0780	753220	754665	1446	PM0343	0	Pmu	R	COG0312	Predicted Zn-dependent proteases and their inactivated homologs	TldD	(NC_002663) TldD [Pasteurella multocida]
MS0781	754725	754633	93	none	none	No-des	none	No-des	none	none	none
MS0782	754802	755830	1029	PM0344	1.00E-155	Pmu	E	COG0160	PLP-dependent aminotransferases	ArgD	(NC_002663) ArgD [Pasteurella multocida]
MS0783	755889	756002	114	PM0344	3.00E-07	Pmu	E	COG0160	PLP-dependent aminotransferases	ArgD	(NC_002663) ArgD [Pasteurella multocida]
MS0784	756250	757725	1476	PM1846_2	1.00E-137	Pmu	G	COG1263	Phosphotransferase system IIC components glucose/maltose/N-acetylglucosamine-specific	PtsG	(NC_002663) PtsB [Pasteurella multocida]
MS0785	758950	757790	1161	mlr2687	6.00E-35	Mlo	G/E/P/R	COG0477	Permeases of the major facilitator superfamily	ProP	(AL356592) putative membrane efflux protein. [St...
MS0786	760636	759221	1416	HI0419	0	Hin	O	COG0826	Collagenase and related proteases		(NC_000907) protease putative [Haemophilus inf...
MS0787	760861	761739	879	PM0235	1.00E-151	Pmu	E	COG0685	5 10-methylenetetrahydrofolate reductase	MetF	(NC_002663) MetF [Pasteurella multocida]
MS0788	761712	761804	93	none	none	No-des	none	No-des	none	none	none
MS0789	762634	761852	783	PM0241	1.00E-99	Pmu	P	COG1108	ABC-type Mn2+/Zn2+ transport systems permease components	ZnuB	(NC_002663) unknown [Pasteurella multocida]
MS0790	763479	762649	831	PM0242	1.00E-104	Pmu	P	COG1121	ABC-type Mn/Zn transport systems ATPase component	ZnuC	(NC_002663) YebM [Pasteurella multocida]
MS0791	763688	765154	1467	HI0409	1.00E-174	Hin	M	COG0739	Membrane proteins related to metalloendopeptidases	NlpD	(NC_000907) conserved hypothetical protein [Hae...
MS0792	765274	766224	951	BH1025	2.00E-98	Bha	P/H	COG0609	ABC-type cobalamin/Fe3+-siderophores transport systems permease components	BtuC	(NC_002570) ferrichrome ABC transporter (permea...
MS0793	766169	767197	1029	BS_ycIO	1.00E-100	Bsu	P/H	COG0609	ABC-type cobalamin/Fe3+-siderophores transport systems permease components	BtuC	(NC_000964) similar to ferrichrome ABC transpor...
MS0794	767191	767952	762	BH1027	3.00E-88	Bha	P/H	COG1120	ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components	FepC	(NC_002570) ferrichrome ABC transporter (ATP-bi...
MS0795	767958	768884	927	BS_ycIQ	9.00E-66	Bsu	P	COG0614	ABC-type Fe3+-siderophores transport systems periplasmic components	FecB	(NC_000964) similar to ferrichrome ABC transpor...
MS0796	769618	768965	654	HI0349	1.00E-113	Hin	F	COG0563	Adenylate kinase and related kinases	Adk	adenylate kinase (EC 2.7.4.3) - Haemophilus influenz...
MS0797	770945	769686	1260	NMB0360	1.00E-145	Nme	G/E/P/R	COG0477	Permeases of the major facilitator superfamily	ProP	(NC_003112) AmpG-related protein [Neisseria men...
MS0798	772131	771118	1014	PM0286	1.00E-169	Pmu	M	COG1087	UDP-glucose 4-epimerase	GalE	(NC_002663) GalE [Pasteurella multocida]
MS0799	772201	772296	96	none	none	No-des	none	No-des	none	none	none
MS0800	772310	772651	342	ZybaH	2.00E-19	EcZ	S	COG3152	Uncharacterized membrane protein		(NC_003198) putative membrane protein [Salmonel...
MS0801	772882	773079	198	none	none	No-des	none	No-des	none	none	none
MS0802	773226	774536	1311	PM0287	0	Pmu	R	COG2252	Permeases		(NC_002663) unknown [Pasteurella multocida]
MS0803	774523	775131	609	none	none	No-des	none	No-des	none	none	(AF219259) HlpB [Haemophilus ducreyi]
MS0804	776504	775227	1278	HI0404	1.00E-133	Hin	D	COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	MesJ	(NC_000907) cell cycle protein (mesJ) [Haemophi...
MS0805	777456	776599	858	PM0290	1.00E-119	Pmu	H	COG2240	Pyridoxal/pyridoxine/pyridoxamine kinase	PdsK	(NC_002663) PdsY [Pasteurella multocida]
MS0806	780862	777839	3024	TM1193	1.00E-159	Tma	G	COG3250	Beta-galactosidase/beta-glucuronidase	LacZ	BETA-GALACTOSIDASE (LACTASE)
MS0807	782152	780878	1275	Zlacy	1.00E-137	EcZ	G/E/P/R	COG0477	Permeases of the major facilitator superfamily	ProP	(NC_002655) galactoside permease (M protein) [E...
MS0808	782392	783837	996	Z3626	7.00E-83	EcZ	K	COG1609	Transcriptional regulators	PurR	(NC_002655) sucrose specific transcriptional re...
MS0809	784665	783520	1146	HI1344	1.00E-172	Hin	E	COG0687	Spermidine/putrescine-binding periplasmic protein	PotD	(AF077856) PotD [Actinobacillus actinomycetemcomi...
MS0810	785529	784762	768	PM0262	1.00E-103	Pmu	E	COG1177	ABC-type spermidine/putrescine transport system permease component II	PotC	(NC_002663) PotC [Pasteurella multocida]
MS0811	786389	785532	858	PM0263	1.00E-136	Pmu	E	COG1176	ABC-type spermidine/putrescine transport system permease component I	PotB	(NC_002663) PotB [Pasteurella multocida]
MS0812	787491	786373	1119	PM0264	1.00E-175	Pmu	G	COG1130	ABC-type sugar/spermidine/putrescine/iron/thiamine transport systems ATPase component	MalK	(NC_002663) PotA [Pasteurella multocida]
MS0813	787590	787724	135	none	none	No-des	none	No-des	none	none	none
MS0814	787848	787964	117	none	none	No-des	none	No-des	none	none	none
MS0815	787957	789180	1224	PM0265	1.00E-171	Pmu	E	COG2195	Di- and tripeptidases	PepD	(NC_002663) PepT [Pasteurella multocida]
MS0816	789253	789155	99	none	none	No-des	none	No-des	none	none	none
MS0817	791996	789270	2727	PM0266	0	Pmu	R	COG3008	Paraquat-inducible protein B	PqiB	(NC_002663) unknown [Pasteurella multocida]
MS0818	792450	792581	132	PM0267	4.00E-09	Pmu	S	COG2995	Uncharacterized paraquat-inducible protein A	PqiA	(NC_002663) unknown [Pasteurella multocida]
MS0819	793260	791908	1353	PM0267	1.00E-154	Pmu	S	COG2995	Uncharacterized paraquat-inducible protein A	PqiA	(NC_002663) unknown [Pasteurella multocida]
MS0820	793325	794032	708	PM0268	6.00E-68	Pmu	T	COG3109	Activator of osmoprotectant transporter ProP	ProQ	(NC_002663) ProQ [Pasteurella multocida]
MS0821	794133	796286	2154	PM0269	0	Pmu	M	COG0793	Periplasmic protease	Prc	(NC_002663) Prc [Pasteurella multocida]
MS0822	796364	797821	1458	PM0270	1.00E-157	Pmu	S	COG2989	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0823	797947	798510	564	PM0271	2.00E-77	Pmu	S	COG3108	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0824	798633	799259	627	PM0272	2.00E-86	Pmu	R	COG0491	Zn-dependent hydrolases including glyoxylases	GloB	(NC_002663) unknown [Pasteurella multocida]
MS0825	799432	799647	216	none	none	No-des	none	No-des	none	none	none
MS0826	799647	799979	333	L0316	4.00E-12	Lla	L	COG1555	DNA uptake protein and related DNA-binding proteins	ComEA (BS)	(NC_003212) similar to integral membrane protei...
MS0827	801651	800089	1563	HI0946.1	0	Hin	E	COG0076	Glutamate decarboxylase and related PLP-dependent proteins	GadB	(NC_000907) L-2 4-diaminobutyrate decarboxylase...
MS0828	801656	801763	108	none	none	No-des	none	No-des	none	none	none
MS0829	803111	801750	1362	HI0949	0	Hin	E	COG0160	PLP-dependent aminotransferases	ArgD	(NC_000907) aminotransferase [Haemophilus influ...
MS0830	803259	803360	102	none	none	No-des	none	No-des	none	none	none
MS0831	803969	803508	462	PM0892	4.00E-50	No-des	none	No-des	none	none	(NC_002663) ImpA [Pasteurella multocida]
MS0832	804248	805486	1239	PM0891	1.00E-149	Pmu	E	COG3633	Na ⁺ /serine symporter	SstT	(NC_002663) unknown [Pasteurella multocida]
MS0833	805628	807094	1467	PM0890	0	Pmu	P	COG1119	ABC-type molybdenum transport system ATPase component photorepair protein PhrA	ModF	(NC_002663) ModF [Pasteurella multocida]
MS0834	807159	808076	918	PM0889	1.00E-129	Pmu	O	COG0330	Membrane protease subunits stomatin/prohibitin homologs	HflC	(NC_002663) unknown [Pasteurella multocida]
MS0835	808102	808551	450	PM0888	2.00E-32	Pmu	N/O	COG1585	Membrane protein implicated in regulation of membrane protease activity		(NC_002663) unknown [Pasteurella multocida]

MS0836	808557	809162	606	PM0887	2.00E-75	Pmu	R	COG2249	Putative NADPH-quinone reductase (modulator of drug activity B)	MdaB	(NC_002663) unknown [Pasteurella multocida]
MS0837	809165	809722	558	HI1543	2.00E-65	Hin	R	COG3381	Uncharacterized component of anaerobic dehydrogenases	TorD	(NC_000907) conserved hypothetical protein [Hae...
MS0838	810224	809772	453	PM0393	3.00E-57	Pmu	S	COG3304	Uncharacterized membrane protein		(NC_002663) unknown [Pasteurella multocida]
MS0839	810755	810252	504	PM0394	5.00E-58	Pmu	G	COG1803	Methylglyoxal synthase	MgsA	(NC_002663) MgsA [Pasteurella multocida]
MS0840	810929	812866	1938	HI1300	0	Hin	R	COG0488	ATPase components of ABC transporters with duplicated ATPase domains	Uup	(NC_000907) ABC transporter/ATP-binding protei...
MS0841	815021	815149	129	none	none	No-des	none	No-des	No-des	none	none
MS0842	819708	818899	810	PM1243	2.00E-93	Pmu	R	COG0561	Predicted hydrolases of the HAD superfamily	Cof	(NC_002663) unknown [Pasteurella multocida]
MS0843	820914	819931	984	HI0009	1.00E-116	Hin	O	COG3058	Uncharacterized protein involved in formate dehydrogenase formation	FdhE	(NC_000907) fdhE protein (fdhE) [Haemophilus in...
MS0844	821733	821077	657	PM0395	7.00E-63	Pmu	S	COG3110	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0845	821909	822190	282	PM0396	1.00E-23	Pmu	C	COG1254	Acylphosphatases	AcyP	(NC_002663) unknown [Pasteurella multocida]
MS0846	822698	822372	327	PM0401	4.00E-49	Pmu	P	COG2920	Sulfite reductase/gamma subunit	DsrC	(NC_002663) unknown [Pasteurella multocida]
MS0847	823454	822786	669	PM0402	6.00E-88	Pmu	R	COG0670	Integral membrane protein/interacts with FtsH		(NC_002663) unknown [Pasteurella multocida]
MS0848	823764	823886	123	none	none	No-des	none	No-des	No-des	none	none
MS0849	824536	824655	120	HI0364	2.00E-10	Hin	M	COG1686	D-alanyl-D-alanine carboxypeptidase	DacC	(NC_000907) penicillin-binding protein 7/putat...
MS0850	824675	823869	807	HI0364	4.00E-97	Hin	M	COG1686	D-alanyl-D-alanine carboxypeptidase	DacC	(NC_000907) penicillin-binding protein 7/putat...
MS0851	824823	824668	156	none	none	No-des	none	No-des	No-des	none	none
MS0852	825663	824851	813	PM0915	2.00E-86	Pmu	E/P	COG1124	ABC-type dipeptide/oligopeptide/nickel transport system/ATPase component	OppF	(NC_002663) SapF [Pasteurella multocida]
MS0853	826727	825678	1050	PM0914	1.00E-161	Pmu	E/P	COG0444	ABC-type dipeptide/oligopeptide/nickel transport system/ATPase component	DppD	(NC_002663) unknown [Pasteurella multocida]
MS0854	827622	826738	885	PM0913	1.00E-103	Pmu	E/P	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems/permease components	DppC	(NC_002663) SapC [Pasteurella multocida]
MS0855	828577	827615	963	PM0912	1.00E-107	Pmu	E/P	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems/permease components	DppB	(NC_002663) SapB [Pasteurella multocida]
MS0856	830280	828580	1701	PM0911	0	Pmu	E/P	COG0747	ABC-type dipeptide/oligopeptide/nickel transport systems/periplasmic components	OppA	(NC_002663) SapA [Pasteurella multocida]
MS0857	830360	831763	1404	PM0910	0	Pmu	R	COG3106	Predicted ATPase		(NC_002663) unknown [Pasteurella multocida]
MS0858	834628	831965	2664	HI1264	0	Hin	L	COG0188	DNA gyrase (topoisomerase II) A subunit	GyrA	(NC_000907) DNA gyrase/subunit A (gyrA) [Haemo...
MS0859	835183	834758	426	PM0352	2.00E-63	Pmu	P	COG0735	Fe2+/Zn2+ uptake regulation proteins	Fur	(NC_002663) Fur [Pasteurella multocida]
MS0860	835727	835206	522	PM0353	6.00E-90	Pmu	C	COG0716	Flavodoxins	FldA	(NC_002663) FldA [Pasteurella multocida]
MS0861	836062	835739	324	PM0354	1.00E-37	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0862	836918	836145	774	PM0355	2.00E-96	Pmu	R	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	MhpC	(NC_000907) esterase/lipase/putative [Haemophi...
MS0863	836996	837658	663	PM0356	7.00E-66	Pmu	L	COG3057	Negative regulator of replication initiationR	SeqA	(NC_002663) SeqA [Pasteurella multocida]
MS0864	837662	839068	1407	PM0357	1.00E-135	Pmu	I/Q	COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	CaiC	(NC_002663) MenE [Pasteurella multocida]
MS0865	839068	842421	3354	PM0358	0	Pmu	M	COG3264	Small-conductance mechanosensitive channel		(NC_002663) unknown [Pasteurella multocida]
MS0866	842437	843513	1077	PM0359	0	Pmu	E	COG0082	Chorismate synthase	AroC	(NC_002663) AroC [Pasteurella multocida]
MS0867	843619	844479	861	HI0197	1.00E-125	No-des	none	No-des	No-des	none	(NC_000907) penicillin-insensitive murein endop...
MS0868	844700	845261	792	PM0361	1.00E-113	Pmu	R	COG0730	Predicted permeases		(NC_002663) unknown [Pasteurella multocida]
MS0869	845242	846222	981	HI0199	1.00E-149	Hin	N	COG1560	Lauroyl/myristoyl acyltransferase involved in lipid A biosynthesis	HlrB	(NC_000907) Lipid A biosynthesis (kdo)2-(lauroy...
MS0870	846313	846876	564	HI1230	2.00E-81	Hin	F	COG0503	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	Apt	(NC_000907) adenine phosphoribosyltransferase (...)
MS0871	846934	849012	2079	HI1229	0	Hin	L	COG2812	DNA polymerase III/gamma/tau subunits	DnaX	(NC_000907) DNA polymerase III/subunits gamma ...
MS0872	849019	849882	864	ZyaID	1.00E-36	EcZ	S	COG3021	Uncharacterized BCR		(NC_003143) conserved hypothetical protein [Yer...
MS0873	849968	850681	714	HI1626	4.00E-80	No-des	none	No-des	No-des	none	(NC_000907) conserved hypothetical protein [Hae...
MS0874	850735	851415	681	PM0368	3.00E-47	Pmu	R	COG0790	TPR repeat proteins		(NC_002663) unknown [Pasteurella multocida]
MS0875	853724	851481	2244	HI1529	0	Hin	L	COG0188	DNA gyrase (topoisomerase II) A subunit	GyrA	(NC_000907) topoisomerase IV/subunit A (parC) ...
MS0876	854711	853776	936	NMB1623	6.00E-96	Nme	Q	COG2132	Putative multicopper oxidases	SufI	MAJOR OUTER MEMBRANE PROTEIN PAN 1 PRECURSO...
MS0877	854889	854800	90	none	none	No-des	none	No-des	No-des	none	none
MS0878	856838	854943	1896	PM0370	0	Pmu	L	COG0187	DNA gyrase (topoisomerase II) B subunit	GyrB	(NC_002663) ParE [Pasteurella multocida]
MS0879	857944	856964	981	NMA0909	6.00E-84	NmA	R	COG0385	Predicted Na+-dependent transporter		(NC_003116) putative transmembrane transport pr...
MS0880	857997	858116	120	none	none	No-des	none	No-des	No-des	none	none
MS0881	857990	858166	177	none	none	No-des	none	No-des	No-des	none	none
MS0882	858874	858134	741	slr1932	6.00E-11	Syn	R	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	MhpC	(NC_000911) unknown protein [Synechocystis sp. ...
MS0883	860364	859120	1245	TM0820	6.00E-79	Tma	C	COG1979	Uncharacterized oxidoreductases/Fe-dependent alcohol dehydrogenase family		(NC_000853) NADH-dependent butanol dehydrogenas...
MS0884	860411	861313	903	mlr7786	5.00E-21	Mlo	K	COG0583	Transcriptional regulator	LysR	(AF167577) transcriptional regulator Ap...
MS0885	862250	861369	882	PM0461	3.00E-99	Pmu	G/E/R	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	RhaT	(NC_002663) unknown [Pasteurella multocida]
MS0886	862639	862223	417	ybbI	4.00E-41	Eco	K	COG0789	Predicted transcriptional regulators	SoxR	(NC_003197) putative heavy metal transcriptiona...
MS0887	862742	863137	396	ZybaR	8.00E-11	EcZ	P	COG2217	Cation transport ATPases	ZntA	(NC_003143) putative cation-transporting ATPase...
MS0888	863199	865448	2250	ZybaR	0	EcZ	P	COG2217	Cation transport ATPases	ZntA	(NC_002655) putative ATPase [Escherichia coli O...
MS0889	866210	865533	678	HI0008	4.00E-96	Hin	C	COG2864	Cytochrome b subunit of formate dehydrogenase	FdnI	(NC_000907) formate dehydrogenase/gamma subuni...
MS0890	867148	866213	936	PM0407	1.00E-144	Pmu	C	COG0437	Fe-S-cluster-containing hydrogenase components 1	HybA	(NC_002663) FdhH [Pasteurella multocida]
MS0891	869574	867151	2424	PM0408	0	Pmu	C	COG0243	Anaerobic dehydrogenases/typically selenocysteine-containing	BisC	(NC_002663) FdsG [Pasteurella multocida]
MS0892	870210	869626	585	PM0409	2.00E-81	Pmu	C	COG0243	Anaerobic dehydrogenases/typically selenocysteine-containing	BisC	(NC_002663) FdsG [Pasteurella multocida]
MS0893	870491	871333	843	PM0410	1.00E-103	Pmu	C	COG1526	Uncharacterized protein required for formate dehydrogenase activity	FdhD	(NC_002663) FdhD [Pasteurella multocida]
MS0894	872487	871399	1089	PM0568	1.00E-156	Pmu	R	COG2933	Predicted SAM-dependent methyltransferase		(NC_002663) unknown [Pasteurella multocida]
MS0895	873391	872501	891	PM0567	1.00E-118	Pmu	K	COG0583	Transcriptional regulator	LysR	(NC_002663) GcvA [Pasteurella multocida]

MS0896	873863	874879	1017	PM0566	1.00E-161	Pmu	E/H	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	IivE	(NC_002663) IivE [Pasteurella multocida]
MS0897	876421	874955	1467	PM0735	3.00E-57	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0898	876723	878654	1932	PM0736	0	Pmu	O	COG0443	Molecular chaperone	DnaK	(NC_002663) DnaK [Pasteurella multocida]
MS0899	878790	879956	1167	PM0740	1.00E-169	Pmu	O	COG0484	Molecular chaperones (contain C-terminal Zn finger domain)	DnaJ	(NC_002663) DnaJ [Pasteurella multocida]
MS0900	880885	880106	780	PA3475	4.00E-55	Pae	E	COG0834	ABC-type amino acid transport system/periplasmic component	ArtI	(NC_002516) cyclohexadienyl dehydratase precurs...
MS0901	882064	880958	1107	PM0513	1.00E-117	Pmu	M	COG2951	Membrane-bound lytic murein transglycosylase B	MltB	(AB002668) lytic transglycosylase [Actinobacill...
MS0902	882888	882082	807	PM0512	2.00E-82	Pmu	M	COG0463	Glycosyltransferases involved in cell wall biogenesis	WcaA	(AB002668) unnamed protein product [Actinobacill...
MS0903	883772	882894	879	HI1696	1.00E-99	Hin	M	COG0463	Glycosyltransferases involved in cell wall biogenesis	WcaA	glycosyltransferase homolog - Actinobacillus actinom...
MS0904	884968	883775	1194	PM0510	1.00E-122	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0905	885753	884971	783	HI1697	5.00E-77	Hin	M	COG3306	Glycosyltransferase involved in LPS biosynthesis		hypothetical protein HI1697 (lsg locus) - Haemophilu...
MS0906	886939	885746	1194	none	none	No-des	none	No-des	No-des	none	none
MS0907	887918	886935	984	BS_yvIF	3.00E-60	No-des	none	No-des	No-des	none	(NC_000964) similar to hypothetical proteins fr...
MS0908	888132	888881	750	PM0506	5.00E-82	Pmu	S	COG1434	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS0909	890447	888942	1506	PM1848	1.00E-173	Pmu	G	COG1621	Beta-fructosidases (levanase/invertase)	SacC (BS)	(NC_002663) ScrB [Pasteurella multocida]
MS0910	891744	890464	1281	PM0462	0	Pmu	H	COG0001	Glutamate-1-semialdehyde aminotransferase	HemL	(NC_002663) HemL [Pasteurella multocida]
MS0911	891917	892984	1068	PM0463	1.00E-118	Pmu	M	COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N- acetylglucosamine-1-phosphate transferase	Rfe	(NC_002663) Rfe [Pasteurella multocida]
MS0912	893015	893794	780	PM0464	1.00E-38	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0913	893889	893683	207	none	none	No-des	none	No-des	No-des	none	none
MS0914	895364	893982	1383	PM0380	0	Pmu	R	COG0733	Na ⁺ -dependent transporters of the SNF family		(NC_002663) unknown [Pasteurella multocida]
MS0915	895390	895497	108	none	none	No-des	none	No-des	No-des	none	none
MS0916	896164	895532	633	PM0381	1.00E-97	Pmu	L	COG0177	Predicted EndoIII-related endonuclease	Nth	(NC_002663) Nth [Pasteurella multocida]
MS0917	896808	896164	645	PM0382	4.00E-93	Pmu	C	COG1347	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit 4	NqrD	Electron transport complex protein mIfE
MS0918	897438	896848	591	HI1687	4.00E-64	Hin	C	COG2869	Na ⁺ -transporting NADH:ubiquinone oxidoreductase gamma subunit	NqrC	(NC_000907) nitrogen fixation protein (nifG) [H...
MS0919	898502	897441	1062	PM0384	1.00E-132	Pmu	C	COG1805	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit 2	NqrB	(NC_002663) unknown [Pasteurella multocida]
MS0920	900690	898522	2169	PM0385_1	0	Pmu	C	COG1726	Na ⁺ -transporting NADH:ubiquinone oxidoreductase alpha subunit	NqrA	(NC_000907) conserved hypothetical protein [Hae...
MS0921	901284	900697	588	HI1684	3.00E-80	Hin	C	COG2878	Predicted alternative beta subunit of Na ⁺ -transporting NADH:ubiquinone oxidoreductase	nuoB	(NC_000907) iron-sulfur cluster binding protein...
MS0922	901928	901302	627	HI1683	2.00E-91	Hin	C	COG2209	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit 5	NqrE	(NC_000907) conserved hypothetical protein [Hae...
MS0923	902720	902010	711	PM0867	9.00E-80	Pmu	S	COG2949	Uncharacterized membrane protein	SanA	(NC_002663) SanA [Pasteurella multocida]
MS0924	902893	903981	1089	HI1263	1.00E-167	Hin	E	COG2021	Homoserine acetyltransferase	MET2	(NC_000907) homoserine acetyltransferase (met2)...
MS0925	904562	904080	483	PM0865	4.00E-54	Pmu	H	COG0801	7/8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	FolK	(NC_002663) FolK [Pasteurella multocida]
MS0926	905845	904571	1275	HI0063	0	Hin	J	COG0617	tRNA nucleotidyltransferase/poly(A) polymerase	PcnB	(NC_000907) poly(A) polymerase (pcnB) [Haemophi...
MS0927	906669	906223	447	PM0863	7.00E-71	Pmu	T	COG1734	DnaK suppressor protein	DksA	(NC_002663) DksA [Pasteurella multocida]
MS0928	906861	906727	135	none	none	No-des	none	No-des	No-des	none	none
MS0929	907051	906959	93	none	none	No-des	none	No-des	No-des	none	none
MS0930	907116	906979	138	none	none	No-des	none	No-des	No-des	none	none
MS0931	907200	909617	2418	PM0862_1	1.00E-122	Pmu	R	COG0658	Predicted multitransmembrane/metal-binding protein	ComEC (BS)	(NC_002663) Rec2 [Pasteurella multocida]
MS0932	909584	911440	1857	PM0861	0	Pmu	Q	COG1132	ABC-type multidrug/protein/lipid transport system/ATPase component	MdIB	(NC_002663) MdsA [Pasteurella multocida]
MS0933	911703	912686	984	PM0860	1.00E-130	Pmu	N	COG1663	Lipid A biosynthesis protein LpxK/tetraacyldisaccharide-1-P 4'-kinase	LpxK	(NC_002663) LpxK [Pasteurella multocida]
MS0934	912679	912861	183	PM0859	4.00E-13	Pmu	S	COG2835	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS0935	912861	913637	777	PM0858	1.00E-109	Pmu	M	COG1212	CMP-2-keto-3-deoxyoctulosonic acid synthetase	KdsB	(NC_002663) KdsB [Pasteurella multocida]
MS0936	913659	914300	642	PA3796	1.00E-13	No-des	none	No-des	No-des	none	(NC_002516) hypothetical protein [Pseudomonas a...
MS0937	914393	916216	1824	HI0057	0	Hin	L	COG0322	Nuclease subunit of the excinuclease complex	UvrC	(NC_000907) excinuclease ABC[subunit C (uvrC) ...
MS0938	916320	916219	102	none	none	No-des	none	No-des	No-des	none	none
MS0939	917045	916287	759	NMB2048	1.00E-77	Nme	L	COG1793	ATP-dependent DNA ligase	CDC9	DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHAS...
MS0940	917151	917026	126	none	none	No-des	none	No-des	No-des	none	none
MS0941	917370	918515	1146	L124252	1.00E-76	Lla	E	COG0620	Methionine synthase II (cobalamin-independent)	MetE	(NC_003212) similar to B. subtilis YxjH and Yxj...
MS0942	918627	918529	99	none	none	No-des	none	No-des	No-des	none	none
MS0943	919491	918631	861	yedI	6.00E-77	Eco	S	COG2354	Uncharacterized BCR		(NC_003197) putative inner membrane protein [Sa...
MS0944	921325	919568	1758	PM0687	0	Pmu	S	COG1944	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS0945	922102	921392	711	PM0686	3.00E-59	Pmu	Q/R	COG0500	SAM-dependent methyltransferases	SmtA	(NC_002663) unknown [Pasteurella multocida]
MS0946	922132	922839	708	HI1274	4.00E-86	Hin	R	COG0491	Zn-dependent hydrolases[including glyoxylases	GloB	(NC_000907) hydroxyacylglutathione hydrolase/p...
MS0947	922895	923779	885	PM0455	1.00E-122	Pmu	P	COG2837	Predicted iron-dependent peroxidase		(NC_002663) unknown [Pasteurella multocida]
MS0948	924737	923880	858	PM0570	1.00E-130	Pmu	I	COG1946	Acyl-CoA thioesterase	TesB	(NC_002663) TesB [Pasteurella multocida]
MS0949	926728	925001	1728	PM0571	0	Pmu	Q	COG1132	ABC-type multidrug/protein/lipid transport system/ATPase component	MdIB	(NC_002663) CycC [Pasteurella multocida]
MS0950	928532	926775	1758	PM0572	0	Pmu	Q	COG1132	ABC-type multidrug/protein/lipid transport system/ATPase component	MdIB	(NC_002663) CycD [Pasteurella multocida]
MS0951	929591	928638	954	PM0573	1.00E-148	Pmu	O	COG0492	Thioredoxin reductase	TrxB	(NC_002663) TrxB [Pasteurella multocida]
MS0952	930560	929661	900	HI1159m	1.00E-114	Hin	O	COG3118	Thioredoxin domain-containing protein		(NC_000907) Thioredoxin domain-containing prote...
MS0953	931311	930685	627	PM0793	2.00E-77	Pmu	G/E	COG2610	H ⁺ /gluconate symporter and related permeases	GntT	(NC_002663) GntP [Pasteurella multocida]
MS0954	932032	931268	765	PM0793	1.00E-101	Pmu	G/E	COG2610	H ⁺ /gluconate symporter and related permeases	GntT	(NC_002663) GntP [Pasteurella multocida]
MS0955	932878	932063	816	IdnO	1.00E-100	Eco	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	FabG	(NC_003143) gluconate 5-dehydrogenase [Yersinia...

MS0956	933878	932838	1041	tdnD	1.00E-126	Eco	E/R	COG1063	Threonine dehydrogenase and related Zn-dependent dehydrogenases	Tdh	(NC_000913) L-idonate dehydrogenase [Escherichi...
MS0957	934096	934608	513	PM0792	2.00E-78	Pnu	P	COG3265	Gluconate kinase	GntK	(NC_002663) Gik [Pasteurella multocida]
MS0958	934764	934633	132	none	none	No-des	none	No-des	No-des	none	none
MS0959	935760	935200	561	PM0856	7.00E-74	Pmu	I	COG0558	Phosphatidylglycerophosphate synthase	PgsA	(NC_002663) PgsA [Pasteurella multocida]
MS0960	937353	935929	1425	HI1330	0	Hin	M	COG2027	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 4)	DacB	(NC_000907) D-alanyl-D-alanine carboxypeptidase...
MS0961	937529	938002	474	HI1331	2.00E-74	Hin	K	COG0782	Transcription elongation factor	GreA	(NC_000907) transcription elongation factor (gr...
MS0962	938471	938070	402	PM0713	1.00E-44	Pmu	J	COG1534	Predicted RNA-binding protein containing KH domain possibly ribosomal protein		(NC_002663) unknown [Pasteurella multocida]
MS0963	938488	939111	624	PM0437	1.00E-106	Pmu	J	COG0293	Methyltransferase involved in cell division	FtsJ	(NC_002663) FtsJ [Pasteurella multocida]
MS0964	939235	941136	1902	PM0438	0	Pmu	O	COG0465	ATP-dependent Zn proteases	HflB	(NC_002663) FtsH [Pasteurella multocida]
MS0965	941298	941164	135	none	none	No-des	none	No-des	No-des	none	none
MS0966	941315	942139	825	PM0439	1.00E-118	Pmu	H	COG0294	Dihydropteroate synthase	FolP	(NC_002663) FolP [Pasteurella multocida]
MS0967	942178	943509	1332	HI1463	0	Hin	G	COG1109	Phosphomannomutase	CpsG	(NC_000907) mrsA protein (mrsA) [Haemophilus in...
MS0968	943726	944853	1128	PM0719	0	Pmu	F	COG0208	Ribonucleotide reductase beta subunit	NrdF	(NC_002663) NrdB [Pasteurella multocida]
MS0969	944962	945222	261	HI1309	5.00E-23	Hin	C	COG0633	Ferredoxin	Fdx	(NC_000907) conserved hypothetical protein [Hae...
MS0970	946748	945291	1458	BS_yfjS	1.00E-124	Bsu	P	COG0471	Di- and tricarboxylate transporters	CitT	(NC_000964) similar to 2-oxoglutarate/malate tr...
MS0971	947933	947124	810	HI1308	1.00E-118	Hin	E	COG0289	Dihydrodipicolinate reductase	DapB	(NC_000907) dihydrodipicolinate reductase (dapB...
MS0972	948610	947984	627	HI1307	1.00E-75	Hin	E	COG1280	Putative threonine efflux protein	RhtB	(NC_000907) conserved hypothetical protein [Hae...
MS0973	949124	948624	501	PM0728	1.00E-58	Pmu	I	COG1267	Phosphatidylglycerophosphatase A	PgpA	(NC_002663) PgpA [Pasteurella multocida]
MS0974	950129	949137	993	PM0729	1.00E-100	Pmu	H	COG0611	Thiamine monophosphate kinase	ThiL	(NC_002663) ThiL [Pasteurella multocida]
MS0975	950584	950156	429	HI1304	4.00E-57	Hin	K	COG0781	Transcription termination factor	NusB	(NC_000907) N utilization substance protein B (...)
MS0976	951064	950597	468	PM0731	6.00E-63	Pmu	H	COG0054	Riboflavin synthase beta-chain	RibH	(NC_002663) RibH [Pasteurella multocida]
MS0977	951243	952490	1248	PM0732	1.00E-158	Pnu	E	COG0814	Amino acid permeases	SdaC	(NC_002663) TyrP [Pasteurella multocida]
MS0978	954437	953655	783	PA0978	1.00E-54	Pae	L	COG2801	Putative transposase	Tra5	(NC_002516) conserved hypothetical protein [Pse...
MS0979	954790	954479	312	PA0979	9.00E-27	Pae	L	COG2963	Transposase		(NC_002516) conserved hypothetical protein [Pse...
MS0980	957487	957197	291	SPy1561	1.00E-25	Spy	S	COG1343	Uncharacterized ACR		(NC_002737) conserved hypothetical protein [Str...
MS0981	958607	957597	1011	BH0341	2.00E-82	Bha	S	COG1518	Uncharacterized ACR		(NC_002570) BH0341-unknown conserved protein in...
MS0982	959577	958657	921	none	none	No-des	none	No-des	No-des	none	(NC_002630) hypothetical protein [Enterococcus ...]
MS0983	961054	960233	822	slr1870	2.00E-42	Syn	S	COG1432	Uncharacterized ACR		(NC_000911) unknown protein [Synechocystis sp. ...]
MS0984	962782	961334	1449	PM1539	1.00E-102	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS0985	963429	962827	603	SPy1563	3.00E-34	Spy	L	COG1468	RecB family exonuclease		(NC_002737) conserved hypothetical protein [Str...
MS0986	964451	963489	963	SPy1564	3.00E-27	Spy	S	COG3649	Uncharacterized BCR		(NC_002737) conserved hypothetical protein [Str...
MS0987	966138	964363	1776	SPy1565	1.00E-07	No-des	none	No-des	No-des	none	(NC_002737) conserved hypothetical protein [Str...
MS0988	966812	966138	675	BH0337	1.00E-13	No-des	none	No-des	No-des	none	(NC_002570) BH0337-unknown [Bacillus halodurans...
MS0989	967611	966808	804	none	none	No-des	none	No-des	No-des	none	none
MS0990	968223	967615	609	none	none	No-des	none	No-des	No-des	none	none
MS0991	970689	968410	2280	BH0336	3.00E-78	Bha	R	COG1203	Predicted helicases		(NC_002570) BH0336-unknown conserved protein in...
MS0992	973053	970759	2295	HI1659	0	Hin	F	COG0209	Ribonucleotide reductase alpha subunit	NrdA	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA...
MS0993	974815	973349	1467	HI1259	1.00E-171	Hin	O	COG0265	Trypsin-like serine proteases typically periplasmic contain C-terminal PDZ domain	DegQ	(AF018152) HtrA [Haemophilus influenzae]
MS0994	974847	975038	192	none	none	No-des	none	No-des	No-des	none	none
MS0995	975605	975045	561	HI1679	2.00E-76	Hin	R	COG1778	Uncharacterized proteins of HAD superfamily CMP-Neu5Ac homologs		(NC_000907) conserved hypothetical protein [Hae...
MS0996	976524	975592	933	PM0525_1	8.00E-94	Pmu	M	COG0794	Predicted sugar phosphate isomerase involved in capsule formation	GutQ	(NC_002663) KpsF [Pasteurella multocida]
MS0997	977198	977365	168	none	none	No-des	none	No-des	No-des	none	none
MS0998	979596	977461	2136	HI1203_2	1.00E-162	Hin	C	COG0280	Phosphotransacetylase	Pta	(NC_000907) phosphate acetyltransferase (pta) [...]
MS0999	980935	979667	1269	PM0704	0	Pmu	C	COG0282	Acetate kinase	ackA	(NC_002663) AckA [Pasteurella multocida]
MS1000	981281	981168	114	none	none	No-des	none	No-des	No-des	none	none
MS1001	981280	981645	366	PM0703	8.00E-33	Pmu	S	COG3092	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1002	981815	982303	489	PM0702	2.00E-66	Pmu	R	COG1286	Uncharacterized membrane protein required for colicin V production	CvpA	(NC_002663) CvpA [Pasteurella multocida]
MS1003	982320	983828	1509	PM0701	0	Pmu	F	COG0034	Glutamine phosphoribosylpyrophosphate amidotransferase	PurF	(AF237920) amidophosphoribosyltransferase...
MS1004	984656	983934	723	HI1449	1.00E-109	Hin	H	COG0476	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	ThiF	(NC_000907) molybdopterin biosynthesis protein ...
MS1005	985889	984663	1227	PM0694	0	Pmu	H	COG0303	Molybdopterin biosynthesis enzyme	MoeA	(NC_002663) MoeA [Pasteurella multocida]
MS1006	986027	986752	726	PM0641	1.00E-94	Pmu	H	COG0132	Dethiobiotin synthetase	BioD	(NC_002663) BioD1 [Pasteurella multocida]
MS1007	986863	986774	90	none	none	No-des	none	No-des	No-des	none	none
MS1008	987071	986958	114	none	none	No-des	none	No-des	No-des	none	none
MS1009	987052	990732	3681	VC0390_2	0	Vch	E	COG1410	Methionine synthase cobalamin-binding domain	MetH	(NC_002505) 5-methyltetrahydrofolate-homocyste...
MS1010	990751	991338	588	HI0217	3.00E-74	Hin	L	COG1943	Predicted transposase		(NC_000907) conserved hypothetical protein [Hae...
MS1011	991526	991984	459	none	none	No-des	none	No-des	No-des	none	none
MS1012	992742	992008	735	PM1080	2.00E-29	Pmu	P/H	COG1120	ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components	FepC	(NC_003143) putative siderophore ABC transporte...
MS1013	993854	992826	1029	DRB0015	1.00E-32	Dra	P/H	COG0609	ABC-type cobalamin/Fe3+-siderophores transport systems permease components	BtuC	(NC_000958) hemin ABC transporter/permease pro...
MS1014	994814	993999	816	none	none	No-des	none	No-des	No-des	none	none
MS1015	996874	994823	2052	CCI1750	3.00E-50	Ccr	P	COG1629	Outer membrane receptor proteins mostly Fe transport	CirA	(NC_002696) TonB-dependent receptor [Caulobacte...

MS1016	997235	996915	321	HI1450	1.00E-45	Hin	S	COG3099	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1017	1000044	997405	2640	PM0546	0	Pmu	C	COG2352	Phosphoenolpyruvate carboxylase	Ppc	(NC_002663) Ppc [Pasteurella multocida]
MS1018	1000377	1001696	1320	PM0514	0	Pmu	R	COG2252	Permeases		(NC_002663) unknown [Pasteurella multocida]
MS1019	1001715	1002068	354	PM0515	2.00E-33	Pmu	P	COG1553	Uncharacterized ACR involved in intracellular sulfur reduction	DsrE	(NC_002663) unknown [Pasteurella multocida]
MS1020	1003165	1002239	927	PM0626	1.00E-104	Pmu	S	COG0391	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS1021	1003515	1004525	1011	HI1676	1.00E-152	Hin	H	COG2896	Molybdenum cofactor biosynthesis enzyme	MoaA	(NC_000907) molybdenum cofactor biosynthesis pr...
MS1022	1004604	1005077	474	HI1675	3.00E-72	Hin	H	COG0315	Molybdenum cofactor biosynthesis enzyme	MoaC	(NC_000907) molybdenum cofactor biosynthesis pr...
MS1023	1005081	1005323	243	HI1674	2.00E-29	Hin	H	COG1977	Molybdopterin converting factor <small>small</small> subunit	MoaD	molybdopterin biosynthesis protein D chain [similari...
MS1024	1005295	1005777	483	HI1673	3.00E-69	Hin	H	COG0314	Molybdopterin converting factor <small>large</small> subunit	MoaE	(NC_000907) molybdopterin converting factor <small>su...</small>
MS1025	1005881	1005759	123	none	none	No-des	none	No-des	No-des	none	none
MS1026	1005995	1007941	1947	PM0698	1.00E-77	Pmu	L	COG2189	Adenine specific DNA methylase Mod		TYPE III RESTRICTION-MODIFICATION SYSTEM ECO...
MS1027	1007931	1010918	2988	NMA1466	0	NmA	L	COG3587	Restriction endonuclease		(NC_003116) putative type III restriction-modif...
MS1028	1011658	1010981	678	HI0008	5.00E-96	Hin	C	COG2864	Cytochrome b subunit of formate dehydrogenase	FdnI	(NC_000907) formate dehydrogenase[gamma subun...
MS1029	1012596	1011661	936	PM0407	1.00E-144	Pmu	C	COG0437	Fe-S-cluster-containing hydrogenase components I	HybA	(NC_002663) FdsH [Pasteurella multocida]
MS1030	1015682	1012599	3084	ZfdnG	0	EcZ	C	COG0243	Anaerobic dehydrogenases/typically selenocysteine-containing	BisC	FORMATE DEHYDROGENASE/INTRATE-INDUCIBLE[M...
MS1031	1017214	1015955	1260	HI1617	1.00E-171	Hin	E	COG1448	Aspartate/aromatic aminotransferase	TyrB	(NC_000907) aspartate aminotransferase (aspC) [...
MS1032	1018376	1017291	1086	HI1616	1.00E-169	Hin	F	COG0026	Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase)	PurK	(NC_000907) phosphoribosylaminoimidazole carbox...
MS1033	1018937	1018443	495	HI1615	5.00E-64	Hin	F	COG0041	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase	PurE	(NC_000907) phosphoribosylaminoimidazole carbox...
MS1034	1019241	1021847	2607	HI1614	0	Hin	E	COG0308	Aminopeptidase N	PepN	(NC_000907) aminopeptidase N (pepN) [Haemophila...
MS1035	1021947	1022966	1020	HI1401	1.00E-155	Hin	F	COG0167	Dihydroorotate dehydrogenase	PyrD	(NC_000907) dihydroorotate dehydrogenase (pyrD)...
MS1036	1023083	1023946	864	PM0616	1.00E-110	Pmu	R	COG0613	Predicted metal-dependent phosphoesterases (PHP family)		(NC_002663) unknown [Pasteurella multocida]
MS1037	1024061	1024681	621	HI1198	1.00E-105	Hin	J	COG0009	Putative translation factor (SUA5)	SUA5	(NC_000907) conserved hypothetical protein [Hae...
MS1038	1024752	1025957	1206	PM0661	1.00E-147	Pmu	J	COG1187	16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases	RsuA	(NC_002663) unknown [Pasteurella multocida]
MS1039	1026013	1026981	969	PM0660	1.00E-156	Pmu	K	COG0583	Transcriptional regulator	LysR	(NC_002663) CysB [Pasteurella multocida]
MS1040	1027031	1027480	450	none	none	No-des	none	No-des	No-des	none	none
MS1041	1027729	1027499	231	none	none	No-des	none	No-des	No-des	none	none
MS1042	1029367	1027967	1401	PM0643	0	Pmu	J	COG0017	Aspartyl/asparaginyl-tRNA synthetases	AsnS	(NC_002663) AsnS [Pasteurella multocida]
MS1043	1029573	1030226	654	PM0693	1.00E-106	Pmu	H	COG0302	GTP cyclohydrolase I	FoIE	(NC_002663) FoIE [Pasteurella multocida]
MS1044	1030270	1030719	450	PM0531	7.00E-39	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS1045	1030862	1031263	402	none	none	No-des	none	No-des	No-des	none	none
MS1046	1031417	1031328	90	none	none	No-des	none	No-des	No-des	none	none
MS1047	1031412	1031774	363	PM0444	3.00E-25	Pmu	S	COG3100	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1048	1031811	1032633	825	PM0691	1.00E-131	Pmu	L	COG0708	Exonuclease III	XthA	(NC_002663) unknown [Pasteurella multocida]
MS1049	1032654	1033424	771	PM0690	2.00E-68	No-des	none	No-des	No-des	none	(AB041266) orfI [Actinobacillus actinomycetemcom...
MS1050	1034181	1033519	663	yniC	6.00E-35	Eco	R	COG0637	Predicted phosphatase/phosphohexomutase		(NC_003143) conserved hypothetical protein [Yer...
MS1051	1035050	1034184	867	PM0587	1.00E-123	Pmu	S	COG3001	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1052	1035209	1035856	648	PM0518	5.00E-72	Pmu	O	COG2999	Glutaredoxin 2	GrxB	(AF006830) glutaredoxin 2 [Actinobacillus actinom...
MS1053	1036042	1037970	1929	PM0593	0	Pmu	J	COG0441	Threonyl-tRNA synthetase	ThrS	(NC_002663) ThrS [Pasteurella multocida]
MS1054	1038335	1038745	411	HI1318m	1.00E-53	Hin	J	COG0290	Translation initiation factor IF3	InfC	(NC_000907) Translation initiation factor IF3 [...
MS1055	1038960	1039190	231	PM0603	1.00E-16	Pmu	J	COG0291	Ribosomal protein L35	RpmI	(U32811) ribosomal protein L35 (rpl35) [Haemophil...
MS1056	1039287	1039637	351	HI1320	5.00E-51	Hin	J	COG0292	Ribosomal protein L20	RpIT	(NC_000907) ribosomal protein L20 (rpl20) [Haem...
MS1057	1040321	1039692	630	none	none	No-des	none	No-des	No-des	none	none
MS1058	1041361	1040327	1035	BS_yhfI	1.00E-100	Bsu	H	COG0095	Lipoate-protein ligase A	LplA	(NC_003212) similar to lipoate protein ligase A...
MS1059	1043417	1041567	1851	PM0532	0	Pmu	HI	COG1154	Deoxyxylulose-5-phosphate synthase	Dxs	(NC_002663) Dxs [Pasteurella multocida]
MS1060	1044344	1043445	900	PM0533	1.00E-114	Pmu	H	COG0142	Geranylgeranyl pyrophosphate synthase	IspA	(NC_002663) IspA [Pasteurella multocida]
MS1061	1044593	1044348	246	PM0534	6.00E-27	Pmu	L	COG1722	Exonuclease VII small subunit	XseB	(NC_002663) XseB [Pasteurella multocida]
MS1062	1044864	1046321	1458	PM0535_1	0	Pmu	H	COG0301	Thiamine biosynthesis ATP pyrophosphatase	ThiI	(NC_002663) ThiI [Pasteurella multocida]
MS1063	1047410	1046409	1002	PM0547	1.00E-144	Pmu	K	COG1609	Transcriptional regulators	PurR	(NC_002663) PurR [Pasteurella multocida]
MS1064	1047579	1047674	96	none	none	No-des	none	No-des	No-des	none	none
MS1065	1048452	1047751	702	PM0575	1.00E-118	Pmu	P	COG0288	Carbonic anhydrase	CynT	(NC_002663) unknown [Pasteurella multocida]
MS1066	1048498	1049472	975	PM0470	1.00E-138	Pmu	Q	COG1131	ABC-type multidrug transport system/ATPase component	CcmA	(NC_002663) YagD [Pasteurella multocida]
MS1067	1049477	1050241	765	PM0471	1.00E-117	Pmu	R	COG0842	ABC-type multidrug transport system/permease component		(NC_002663) unknown [Pasteurella multocida]
MS1068	1051787	1050333	1455	PM0475	0	Pmu	R	COG1611	Predicted Rossmann fold nucleotide-binding protein		(NC_002663) unknown [Pasteurella multocida]
MS1069	1052556	1051714	843	PM0476_2	3.00E-61	Pmu	R	COG0780	Enzyme related to GTP cyclohydrolase I		(NC_000907) conserved hypothetical protein [Hae...
MS1070	1053365	1052586	780	PM0477	3.00E-99	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS1071	1053439	1053756	318	HI1436	1.00E-25	Hin	S	COG3098	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1072	1053763	1054470	708	PM0479	1.00E-108	Pmu	J	COG0564	Pseudouridylate synthases/23S RNA-specific	RluA	(NC_002663) unknown [Pasteurella multocida]
MS1073	1055645	1054644	1002	HI0596	1.00E-165	Hin	E	COG0078	Ornithine carbamoyltransferase	ArgF	(NC_000907) ornithine carbamoyltransferase (arc...
MS1074	1055686	1055916	231	PM0480	2.00E-12	Pmu	S	COG3140	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1075	1055906	1055998	93	none	none	No-des	none	No-des	No-des	none	none

MS1076	1056910	1055957	954	PM0669	1.00E-131	Pmu	T	COG0589	Universal stress protein UspA and related nucleotide-binding proteins	UspA	(NC_002663) unknown [Pasteurella multocida]
MS1077	1057847	1057050	798	HI1425	1.00E-126	Hin	T	COG0664	cAMP-binding domains - Catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Crp	(D89096) putative hemolysin [Actinobacillus acti...
MS1078	1058117	1058019	99	none	none	No-des	none	No-des	No-des	none	none
MS1079	1058618	1058124	495	HI1385	8.00E-67	Hin	P	COG1528	Ferritin-like protein	Fin	(NC_000907) ferritin (rsgA) [Haemophilus influe...
MS1080	1059127	1058636	492	PM0666	2.00E-77	Pmu	P	COG1528	Ferritin-like protein	Fin	(NC_002663) RsgA [Pasteurella multocida]
MS1081	1061370	1059955	1416	HI1377	0	Hin	L	COG2925	Exonuclease I	SbcB	(NC_000907) exodeoxyribonuclease I (sbcB) [Haem...
MS1082	1062157	1061396	762	PM0610	2.00E-86	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS1083	1062326	1062186	141	none	none	No-des	none	No-des	No-des	none	none
MS1084	1066845	1062349	4497	HI1374	0	Hin	D	COG3096	Uncharacterized protein involved in chromosome partitioning	MukB	(AJ417690) MukB protein [Actinobacillus actinomy...
MS1085	1067570	1066848	723	PM0608	1.00E-107	Pmu	D	COG3095	Uncharacterized protein involved in chromosome partitioning	MukE	(NC_002663) KicA [Pasteurella multocida]
MS1086	1069009	1067675	1335	HI1372	0	Hin	D	COG3006	Uncharacterized protein involved in chromosome partitioning	MukF	(NC_000907) killing protein (kicB) [Haemophilus...
MS1087	1069219	1070154	936	HI1371.1	1.00E-151	Hin	D	COG0037	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	MesJ	(NC_000907) conserved hypothetical protein [Hae...
MS1088	1070682	1070206	477	PM0627	1.00E-60	Pmu	M	COG0791	Cell wall-associated hydrolases (invasion-associated proteins)	Spr	(NC_002663) unknown [Pasteurella multocida]
MS1089	1071060	1070767	294	PM0628	4.00E-43	Pmu	L	COG0776	Bacterial nucleoid DNA-binding protein	HimA	(NC_002663) HimA [Pasteurella multocida]
MS1090	1073452	1071068	2385	PM0629_2	0	Pmu	J	COG0072	Phenylalanyl-tRNA synthetase beta subunit	PhdT	(NC_002663) PhdT [Pasteurella multocida]
MS1091	1074461	1073475	987	HI1311	1.00E-168	Hin	J	COG0016	Phenylalanyl-tRNA synthetase alpha subunit	PhoS	(NC_000907) phenylalanyl-tRNA synthetase[alpha...
MS1092	1075076	1074738	339	PM0519	1.00E-46	Pmu	S	COG3422	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1093	1075353	1075634	282	none	none	No-des	none	No-des	No-des	none	(NC_003047) CONSERVED HYPOTHETICAL PROTEIN [Sin...
MS1094	1075750	1075959	210	CC2867	1.00E-07	Ccr	N	COG3093	Plasmid maintenance system antidote protein	VapI	VIRULENCE-ASSOCIATED PROTEIN I
MS1095	1076269	1076063	207	PM0481	3.00E-32	Pmu	K	COG1278	Cold shock proteins	CspC	(NC_002663) CspD [Pasteurella multocida]
MS1096	1079134	1076531	2604	HI1365_1	0	Hin	L	COG0550	Topoisomerase IA	TopA	(NC_000907) DNA topoisomerase I (topA) [Haemoph...
MS1097	1079413	1080303	891	HI1364	1.00E-101	Hin	K	COG0583	Transcriptional regulator	LysR	(U20964) ORF2 [Haemophilus influenzae]
MS1098	1082273	1080345	1929	PM0517	0	Pmu	L	COG0507	ATP-dependent exoDNAse (exonuclease V)alpha subunit - helicase superfamily I member	RecD	(NC_002663) RecD [Pasteurella multocida]
MS1099	1085902	1082288	3615	PM0516	0	Pmu	L	COG1074	ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)	RecB	(NC_002663) RecB [Pasteurella multocida]
MS1100	1086006	1085902	105	none	none	No-des	none	No-des	No-des	none	none
MS1101	1087307	1086237	1071	PM0486	3.00E-97	Pmu	E	COG0136	Aspartate-semialdehyde dehydrogenase	Asd	(NC_002663) Usg1 [Pasteurella multocida]
MS1102	1088474	1087347	1128	HI1290_2	1.00E-115	Hin	E	COG0287	Prephenate dehydrogenase	TyrA	(NC_000907) chorismate mutase / prephenate dehy...
MS1103	1088465	1088557	93	none	none	No-des	none	No-des	No-des	none	none
MS1104	1089654	1088602	1053	PM0665	1.00E-158	Pmu	E	COG0722	3-Deoxy-D-arabino-heptulosonate 7-phosphate (DAH) synthase	AroG	(NC_002663) AroF [Pasteurella multocida]
MS1105	1089866	1090942	1077	ZyeaU	7.00E-89	EcZ	E	COG0473	Isocitrate/isopropylmalate dehydrogenase	LeuB	(NC_002033) 3-isopropylmalate dehydrogenase [No...
MS1106	1090917	1091012	96	none	none	No-des	none	No-des	No-des	none	none
MS1107	1092843	1091020	1824	HI1541	0	Hin	N/O	COG0616	Periplasmic serine proteases (ClpP class)	SppA	(NC_000907) protease IV (sppA) [Haemophilus inf...
MS1108	1092976	1092866	111	none	none	No-des	none	No-des	No-des	none	none
MS1109	1093086	1093637	552	HI1542	8.00E-66	Hin	C	COG0778	Nitroreductase	NfnB	(NC_000907) conserved hypothetical protein [Hae...
MS1110	1093624	1093722	99	none	none	No-des	none	No-des	No-des	none	none
MS1111	1093885	1095390	1506	L126168	3.00E-22	Lla	G	COG3525	N-acetyl-beta-hexosaminidase	Chb	(NC_003098) Beta-N-acetyl-hexosaminidase precu...
MS1112	1097094	1095865	1230	ZycdQ	2.00E-96	EcZ	M	COG1215	Glycosyltransferases/probably involved in cell wall biogenesis		(NC_003296) PUTATIVE HEMIN STORAGE TRANSMEMBR...
MS1113	1098901	1097105	1797	ZycdR	1.00E-101	EcZ	G	COG0726	Predicted xylanase/chitin deacetylase	CDA1	(NC_002655) orf1/hypothetical protein [Escheric...
MS1114	1101318	1098916	2403	ZycdS	4.00E-13	No-des	none	No-des	No-des	none	(NC_003143) haemin storage system[HmsH protein...
MS1115	1101612	1101725	114	none	none	No-des	none	No-des	No-des	none	none
MS1116	1102121	1101837	285	HI1630	4.00E-46	Hin	J	COG1825	Ribosomal protein L25 (general stress protein Ctc)	RplY	(NC_000907) ribosomal protein L25 (rpl25) [Haem...
MS1117	1102393	1102274	120	none	none	No-des	none	No-des	No-des	none	none
MS1118	1102368	1102976	609	HI1629	1.00E-73	Hin	S	COG0586	Uncharacterized membrane-associated protein	DedA	(NC_000907) dedA protein/putative [Haemophilus...
MS1119	1105659	1103206	2454	PM0545	0	Pmu	G	COG0058	Glucan phosphorylase	GlgP	(NC_002663) GlgP [Pasteurella multocida]
MS1120	1107175	1105745	1431	PM0544	0	Pmu	G	COG0297	Glycogen synthase	GlgA	(NC_002663) GlgA [Pasteurella multocida]
MS1121	1108575	1107274	1302	PM0543	0	Pmu	G	COG0448	ADP-glucose pyrophosphorylase	GlgC	(NC_002663) GlgC [Pasteurella multocida]
MS1122	1110601	1108619	1983	HI1358	0	Hin	G	COG1523	Pullulanase and related glycosidases	GlgX	(NC_000907) glycogen operon protein (glgX) [Hae...
MS1123	1112850	1110664	2187	PM0541	0	Pmu	G	COG0296	1[4-alpha-glucan branching enzyme	GlgB	(NC_002663) GlgB [Pasteurella multocida]
MS1124	1114949	1112862	2088	HI1356	0	Hin	G	COG1640	4-alpha-glucanotransferase	MalQ	(NC_000907) 4-alpha-glucanotransferase (malQ) [...
MS1125	1115619	1115119	501	PM0539	6.00E-67	Pmu	S	COG2983	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS1126	1115798	1115658	141	HI1192	5.00E-09	No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS1127	1117462	1115801	1662	PM0528	0	Pmu	J	COG0008	Glutamyl- and glutaminyI-tRNA synthetases	GlnS	(NC_002663) GlnS [Pasteurella multocida]
MS1128	1117727	1118908	1182	NMA0728	4.00E-85	NmA	Q	COG0845	Membrane-fusion protein	AcrA	(NC_003116) putative periplasmic protein [Neiss...
MS1129	1118934	1120862	1929	NMA0729_2	1.00E-109	NmA	R	COG0577	ABC-type transport systemsinvolved in lipoprotein release/permease components		(NC_003112) ABC transporter/ATP-binding protei...
MS1130	1121015	1120923	93	none	none	No-des	none	No-des	No-des	none	none
MS1131	1121002	1122372	1371	HI1462	0	Hin	M/N	COG1538	Outer membrane protein	TolC	(NC_000907) conserved hypothetical protein [Hae...
MS1132	1122571	1122476	96	HI1563	1.00E-06	Hin	S	COG3101	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1133	1123071	1122598	474	HI1563	6.00E-61	Hin	S	COG3101	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1134	1124086	1123235	852	PM0468	1.00E-121	Pmu	O	COG0501	Zn-dependent protease with chaperone function	HtpX	(NC_002663) HtpX [Pasteurella multocida]
MS1135	1125305	1124241	1065	PM0467	1.00E-131	Pmu	L	COG0389	Nucleotidyltransferase/DNA polymerase involved in DNA repair	DinP	(NC_002663) DinP [Pasteurella multocida]

MS1136	1125300	1125428	129	none	none	No-des	none	No-des	No-des		none	none
MS1137	1127007	1125448	1560	PM0466	1.00E-165	Pmu	L	COG3593	Predicted ATP-dependent endonuclease of the OLD family			(NC_002663) unknown [Pasteurella multocida]
MS1138	1127099	1128001	903	PM0465	1.00E-110	Pmu	S	COG2431	Uncharacterized membrane protein			(NC_002663) unknown [Pasteurella multocida]
MS1139	1128047	1128238	192	none	none	No-des	none	No-des	No-des		none	none
MS1140	1130031	1128685	1347	ynjE	3.00E-65	Eco	P	COG2897	Rhodanese-related sulfurtransferases		SseA	PUTATIVE THIOSULFATE SULFURTRANSFERASE YNJE
MS1141	1131564	1130101	1464	ynjE	2.00E-59	Eco	P	COG2897	Rhodanese-related sulfurtransferases		SseA	PUTATIVE THIOSULFATE SULFURTRANSFERASE YNJE
MS1142	1132474	1132382	93	none	none	No-des	none	No-des	No-des		none	none
MS1143	1132493	1131480	1014	yeeE	5.00E-72	Eco	R	COG2391	Predicted transporter components			(NC_000913) putative transport system permease ...
MS1144	1133024	1132815	210	PM0655	2.00E-28	Pmu	K	COG1278	Cold shock proteins		CspC	(NC_002663) MsmB [Pasteurella multocida]
MS1145	1134229	1133414	816	PM0586_1	7.00E-61	Pmu	J	COG2913	Small protein A (tmRNA-binding)		SmpA	(NC_002663) Plp4 [Pasteurella multocida]
MS1146	1135457	1134399	1059	PM0585	1.00E-123	Pmu	N/O	COG0616	Periplasmic serine proteases (ClpP class)		SppA	(NC_002663) SohB [Pasteurella multocida]
MS1147	1135460	1135558	99	none	none	No-des	none	No-des	No-des		none	none
MS1148	1135914	1135810	105	none	none	No-des	none	No-des	No-des		none	none
MS1149	1135894	1137429	1536	HI1387	0	Hin	E/H	COG0147	Anthranilate/para-aminobenzoate synthases component I		TrpE	(NC_000907) anthranilate synthase component I (...)
MS1150	1137447	1138022	576	HI1388	2.00E-82	Hin	E/H	COG0512	Anthranilate/para-aminobenzoate synthases component II		PabA	(NC_000907) anthranilate synthase component II ...
MS1151	1138042	1139067	1026	PM0581	1.00E-129	Pmu	E	COG0547	Anthranilate phosphoribosyltransferase		TrpD	(NC_002663) TrpD [Pasteurella multocida]
MS1152	1139083	1140486	1404	HI1389_1_1	1.00E-102	Hin	E	COG0134	Indole-3-glycerol phosphate synthase		TrpC	(NC_000907) indole-3-glycerol phosphate synthas...
MS1153	1140635	1141828	1194	HI1431	0	Hin	E	COG0133	Tryptophan synthase beta chain		TrpB	(NC_000907) tryptophan synthase beta subunit (...)
MS1154	1141831	1142634	804	HI1432	1.00E-126	Hin	E	COG0159	Tryptophan synthase alpha chain		TrpA	(NC_000907) tryptophan synthase alpha subunit (...)
MS1155	1142993	1142862	132	none	none	No-des	none	No-des	No-des		none	none
MS1156	1143021	1142881	141	none	none	No-des	none	No-des	No-des		none	none
MS1157	1143843	1143968	126	XF0933	1.00E-11	Xfa	P	COG0370	Ferrous ion uptake system protein FeoB (predicted GTPase)		FeoB	(NC_003296) PROBABLE FERROUS IRON TRANSPORT B...
MS1158	1144894	1143026	1869	XF0933	1.00E-171	Xfa	P	COG0370	Ferrous ion uptake system protein FeoB (predicted GTPase)		FeoB	(NC_003296) PROBABLE FERROUS IRON TRANSPORT B...
MS1159	1145223	1144966	258	none	none	No-des	none	No-des	No-des		none	none
MS1160	1145312	1145440	129	none	none	No-des	none	No-des	No-des		none	none
MS1161	1145456	1146133	678	PM1025	2.00E-38	Pmu	M	COG3637	Opacity protein and related surface antigens			(NC_002663) Opa [Pasteurella multocida]
MS1162	1147944	1146667	1278	none	none	No-des	none	No-des	No-des		none	none
MS1163	1151004	1148878	2127	NMB1768	7.00E-41	Nme	M	COG3210	Putative hemagglutinin/hemolysin		FhaB	(NC_003112) hemagglutinin/hemolysin-related pro...
MS1164	1153467	1152010	1458	none	none	No-des	none	No-des	No-des		none	none
MS1165	1153896	1153474	423	none	none	No-des	none	No-des	No-des		none	none
MS1166	1154590	1154691	102	none	none	No-des	none	No-des	No-des		none	none
MS1167	1164440	1155063	9378	NMB1768	0	Nme	M	COG3210	Putative hemagglutinin/hemolysin		FhaB	(NC_003296) PROBABLE HEMAGGLUTININ-RELATED PR...
MS1168	1164994	1164491	504	NMB1210	4.00E-32	Nme	O	COG2994	ACPhemolysine acyltransferase (hemolysin-activating protein)		HlyC	(NC_003112) toxin-activating protein/putative ...
MS1169	1166763	1165000	1764	XF2550	1.00E-126	Xfa	N	COG28361	Hemolysin activation/secretion protein		FhaC	(NC_002663) PROBABLE ACTIVATION/SECRETION PROT...
MS1170	1168003	1167353	651	PM0633	2.00E-87	Pmu	J	COG0564	Pseudouridylate synthases/23S RNA-specific		RluA	(NC_002663) unknown [Pasteurella multocida]
MS1171	1167957	1169489	1533	cls	1.00E-137	Eco	I	COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardioli...in synthases and related enzymes		Cls	(NC_003143) cardiolipin synthetase [Yersinia pe...
MS1172	1169526	1170167	642	PM0634	8.00E-59	Pmu	G	COG0406	Phosphoglycerate mutase/fructose-2/6-bisphosphatase		GpmB	(NC_002663) GpmB [Pasteurella multocida]
MS1173	1171579	1170257	1323	PM0635	1.00E-175	Pmu	H	COG0285	Folylpolyglutamate synthase		FolC	(NC_002663) FolC [Pasteurella multocida]
MS1174	1172514	1171582	933	PM0636	1.00E-134	Pmu	I	COG0777	Acetyl-CoA carboxylase beta subunit		AccD	(NC_002663) AccD [Pasteurella multocida]
MS1175	1173385	1172576	810	HI1644	1.00E-125	Hin	J	COG0101	Pseudouridylate synthase (tRNA psi55)		TruA	(NC_000907) pseudouridylate synthase I (truA) [...]
MS1176	1173523	1173410	114	none	none	No-des	none	No-des	No-des		none	none
MS1177	1174546	1173722	825	HI1634	1.00E-144	Hin	E	COG2171	Tetrahydronicotinamide N-succinyltransferase		DapD	(NC_000907) 2/3/4/5-tetrahydropyridine-2-carbox...
MS1178	1174671	1175942	1272	ZyeiO	1.00E-115	EcZ	G/E P/R	COG0477	Permeases of the major facilitator superfamily		ProP	SUGAR EFFLUX TRANSPORTER
MS1179	1176054	1176164	111	none	none	No-des	none	No-des	No-des		none	none
MS1180	1176170	1176766	597	ZychE	3.00E-53	EcZ	S	COG2095	Integral membrane proteins of the MarC family		MarC	(NC_003143) putative membrane protein [Yersinia...
MS1181	1178541	1176895	1647	HI1576	0	Hin	G	COG0166	Glucose-6-phosphate isomerase		Pgi	Glucose-6-phosphate isomerase (GPI) (Phosph...
MS1182	1179717	1178647	1071	PM0413	1.00E-164	Pmu	M	COG0787	Alanine racemase		Alr	(NC_002663) Alr [Pasteurella multocida]
MS1183	1181209	1179755	1455	HI1574	0	Hin	L	COG0305	Replicative DNA helicase		DnaB	(NC_000907) replicative DNA helicase (dnaB) [Ha...
MS1184	1182539	1181388	1152	HI1547	1.00E-171	Hin	E	COG0722	3-Deoxy-D-arabino-heptulosonate 7-phosphate (DAH) synthase		AroG	(NC_000907) phospho-2-dehydro-3-deoxyheptonate ...
MS1185	1183883	1182645	1239	PM0562	1.00E-152	Pmu	R	COG0577	ABC-type transport systems/involved in lipoprotein release/permease components			(NC_002663) unknown [Pasteurella multocida]
MS1186	1184582	1183899	684	HI1549	1.00E-101	Hin	R	COG1136	ABC-type transport systems/involved in lipoprotein release/ATPase components		PhnL	(NC_000907) ABC transporter/ATP-binding protei...
MS1187	1185835	1184645	1191	HI1555	1.00E-137	Hin	R	COG0577	ABC-type transport systems/involved in lipoprotein release/permease components			(NC_000907) conserved hypothetical transmembran...
MS1188	1186988	1185957	1032	HI1556	1.00E-148	Hin	C/H/R	COG1052	Lactate dehydrogenase and related dehydrogenases		LdhA	(NC_000907) 2-hydroxyacid dehydrogenase [Haemop...
MS1189	1187852	1187001	852	HI1557	1.00E-148	Hin	M	COG2877	3-Deoxy-D-manno-octulosonic acid (KDO) 8-phosphate synthase		KdsA	2-DEHYDRO-3-DEOXYPHOSPHOCTONATE ALDOLASE
MS1190	1188671	1187880	792	PM0557	1.00E-84	Pmu	S	COG2912	Uncharacterized ACR			(NC_002663) unknown [Pasteurella multocida]
MS1191	1189690	1188671	1020	PM0556	9.00E-91	Pmu	J	COG2890	Predicted rRNA or tRNA methylase		HemK	(NC_002663) HemK [Pasteurella multocida]
MS1192	1190870	1189791	1080	HI1561	0	Hin	J	COG0216	Protein chain release factor A		PrfA	(NC_000907) peptide chain release factor 1 (prf...
MS1193	1191421	1190960	462	none	none	No-des	none	No-des	No-des		none	none
MS1194	1192150	1191620	531	PM0484	9.00E-91	Pmu	I	COG0764	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases		FabA	(NC_002663) FabA [Pasteurella multocida]
MS1195	1194078	1192309	1770	PM0483	0	Pmu	O	COG1067	Predicted ATP-dependent protease		LonB (BS)	(NC_002663) unknown [Pasteurella multocida]

MS1196	1194224	1194685	462	HI1323		4.00E-66	Hin	S		COG3120	Uncharacterized BCR			(NC_000907) conserved hypothetical protein [Hae...
MS1197	1196350	1194773	1578	PM0653		0	Pmu	G		COG0469	Pyruvate kinase		PykF**	(NC_002663) PykA [Pasteurella multocida]
MS1198	1196396	1196881	486	PM0441		4.00E-42	Pmu	T		COG2062	Phosphohistidine phosphatase SixA		SixA	(NC_002663) unknown [Pasteurella multocida]
MS1199	1199190	1197154	2037	HI0214		0	Hin	E		COG0339	Zn-dependent oligopeptidases		Dcp	(NC_000907) oligopeptidase A (prC) [Haemophilu...
MS1200	1199406	1199296	111	none	none	none	none	none	none	No-des	No-des	none	none	none
MS1201	1199398	1200159	762	HuuC		3.00E-73	Eco	PH		COG1120	ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components		FepC	(NC_003305) ABC transporter nucleotide binding...
MS1202	1200172	1201017	846	ZhuD		4.00E-23	EcZ	P		COG0614	ABC-type Fe3+-siderophores transport systems periplasmic components		FecB	(NC_003305) ABC transporter substrate binding ...
MS1203	1201014	1202921	1908	ZhuB		3.00E-87	EcZ	PH		COG0609	ABC-type cobalamin/Fe3+-siderophores transport systems permease components		BtuC	(AJ007906) FhuB [Rhizobium leguminosarum]
MS1204	1202940	1204616	1677	yojI		1.00E-135	Eco	Q		COG1132	ABC-type multidrug/protein/lipid transport system ATPase component		MdIB	(NC_003197) putative ABC-type multidrug/protein...
MS1205	1204616	1206709	2094	VC0200		8.00E-98	Vch	P		COG1629	Outer membrane receptor proteins mostly Fe transport		CirA	(NC_002505) iron(III) compound receptor [Vibrio...
MS1206	1206729	1206938	210	none	none	none	No-des	none	No-des	No-des	No-des	none	none	none
MS1207	1207540	1206863	678	PM1936		2.00E-74	No-des	none	No-des	No-des	No-des	none	none	(NC_002663) unknown [Pasteurella multocida]
MS1208	1208167	1207547	621	PM1937		8.00E-10	Pmu	L		COG1662	Insertion element IS1 protein InsB putative transposase		InsB	(NC_003143) putative exported protein [Yersinia...
MS1209	1209201	1208302	900	TM1009		2.00E-83	Tma	R		COG0656	Aldo/keto reductases related to diketogulonate reductase		ARA1	(NC_003210) similar to oxidoreductase aldo/ket...
MS1210	1209406	1210317	912	PA2220		5.00E-58	Pae	K		COG0583	Transcriptional regulator		LysR	(NC_003037) Putative LysR -type transcription f...
MS1211	1210373	1211743	1371	hlp1281_2		2.00E-45	jHp	G		COG0063	Predicted sugar kinase			(NC_000921) putative [Helicobacter pylori J99] ...
MS1212	1212185	1211856	330	HI1165		2.00E-51	Hin	O		COG0278	Glutaredoxin-related proteins			(NC_000907) conserved hypothetical protein [Hae...
MS1213	1212248	1212385	138	none	none	none	No-des	none	No-des	No-des	No-des	none	none	none
MS1214	1212378	1212256	123	none	none	none	No-des	none	No-des	No-des	No-des	none	none	none
MS1215	1213087	1212281	807	PM0783		1.00E-60	Pmu	R		COG1512	Beta-propeller domains of methanol dehydrogenase type			(NC_002663) unknown [Pasteurella multocida]
MS1216	1213610	1213083	528	PM0784		4.00E-50	No-des	none	No-des	No-des	No-des	none	none	(NC_002663) unknown [Pasteurella multocida]
MS1217	1214194	1213613	582	PM0785		2.00E-88	Pmu	S		COG1704	Uncharacterized ACR		LemA	(NC_002663) unknown [Pasteurella multocida]
MS1218	1215429	1214326	1104	HI1164		1.00E-115	Hin	M		COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins		OmpA	(AJ007317) outer membrane protein [Haemophilus sp.]
MS1219	1216249	1216001	249	PM0786		6.00E-21	Pmu	M		COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins		OmpA	(AF133259) outer membrane protein PomA ...
MS1220	1217051	1216233	819	HI1164		9.00E-77	Hin	M		COG2885	Outer membrane protein and related peptidoglycan-associated (lipo)proteins		OmpA	OUTER MEMBRANE PROTEIN P5 PRECURSOR (OMP P5...
MS1221	1217433	1220522	3090	PM0787_1		0	Pmu	C		COG0277	FAD/FMN-containing dehydrogenases		GlcD	(NC_000907) conserved hypothetical protein [Hae...
MS1222	1221217	1220624	594	PM0751		3.00E-74	Pmu	L		COG3663	GT/U mismatch-specific DNA glycosylase		Mug	(NC_002663) unknown [Pasteurella multocida]
MS1223	1222765	1221341	1425	PM0752		0	Pmu	C		COG1282	NAD/NADP transhydrogenase beta subunit		PntB	(NC_002663) PntB [Pasteurella multocida]
MS1224	1224309	1222780	1530	PM0753		0	Pmu	C		COG3288	NAD/NADP transhydrogenase alpha subunit		PntA	(NC_002663) PntA [Pasteurella multocida]
MS1225	1224509	1224402	108	none	none	none	No-des	none	No-des	No-des	No-des	none	none	none
MS1226	1224730	1224557	174	none	none	none	No-des	none	No-des	No-des	No-des	none	none	none
MS1227	1226849	1224714	2136	BH2223		3.00E-78	Bha	G		COG3345	Alpha-galactosidase		GalA	(NC_003143) alpha-galactosidase [Yersinia pesti...
MS1228	1228229	1226856	1374	ZmeIB		1.00E-169	EcZ	G		COG2211	Na+/melibiose symporter and related transporters		MelB	(NC_003197) GPH family melibiose permease II [...]
MS1229	1228378	1229457	1080	ZmeIR		2.00E-82	EcZ	K		COG2207	AraC-type DNA-binding domain-containing proteins		AraC	(NC_002695) regulator of melibiose operon [Esch...
MS1230	1229470	1230186	717	PM0754		1.00E-108	Pmu	G		COG1489	Sugar fermentation stimulation protein (uncharacterized)		SfsA	(NC_002663) SfsA [Pasteurella multocida]
MS1231	1230390	1230268	123	none	none	none	No-des	none	No-des	No-des	No-des	none	none	none
MS1232	1230528	1231712	1185	PM0755		0	Pmu	J		COG0162	Tyrosyl-tRNA synthetase		TyrS	(NC_002663) TyrS [Pasteurella multocida]
MS1233	1231772	1232701	930	PM1849		1.00E-113	Pmu	G		COG0524	Sugar kinases ribokinase family		RbsK	(NC_002663) unknown [Pasteurella multocida]
MS1234	1232813	1232926	114	none	none	none	No-des	none	No-des	No-des	No-des	none	none	none
MS1235	1233043	1233741	699	none	none	none	No-des	none	No-des	No-des	No-des	none	none	(AF338705) transposase [Corynebacterium...
MS1236	1235681	1234062	1620	IreC		0	Eco	G		COG0366	Glycosidases		AmyA	(NC_000913) trehalase 6-P hydrolase [Escherich...
MS1237	1237444	1236020	1425	VC0910_2		1.00E-152	Vch	G		COG1263	Phosphotransferase system IIC components glucose/maltose/N-acetylglucosamine-specific		PtsG	(NC_003143) PTS system trehalose-specific IIBC...
MS1238	1238491	1237556	936	IreR		1.00E-63	Eco	K		COG1609	Transcriptional regulators		PurR	(NC_003143) trehalose operon repressor [Yersini...
MS1239	1238677	1238564	114	none	none	none	No-des	none	No-des	No-des	No-des	none	none	none
MS1240	1239142	1240821	1680	PM0425		0	Pmu	R		COG0488	ATPase components of ABC transporters with duplicated ATPase domains		Uup	(NC_002663) unknown [Pasteurella multocida]
MS1241	1241873	1240896	978	HI0200m		1.00E-139	Hin	E		COG0709	Selenophosphate synthase		SelD	(NC_000907) Selenophosphate synthase [Haemophil...
MS1242	1242156	1243151	996	PM0791		1.00E-150	Pmu	K		COG1609	Transcriptional regulators		PurR	(NC_002663) unknown [Pasteurella multocida]
MS1243	1243355	1244023	669	HI1677		1.00E-85	Hin	D		COG2846	Regulator of cell morphogenesis and NO signaling			(NC_000907) conserved hypothetical protein [Hae...
MS1244	1245278	1244079	1200	PM0215		1.00E-127	Pmu	T		COG0642	Sensory transduction histidine kinases		BaeS	(NC_002663) YgiY [Pasteurella multocida]
MS1245	1245466	1245251	216	PM0215		5.00E-11	Pmu	T		COG0642	Sensory transduction histidine kinases		BaeS	(NC_002663) YgiY [Pasteurella multocida]
MS1246	1246143	1245466	678	PM0214		1.00E-105	Pmu	TK		COG0745	Response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain		OmpR	(NC_002663) YgiX [Pasteurella multocida]
MS1247	1246922	1246326	597	ZygW		4.00E-13	EcZ	S		COG3111	Uncharacterized ACR			(NC_002655) orf hypothetical protein [Escheric...
MS1248	1247020	1248132	1113	aaq_421		1.00E-124	Aae	E		COG0436	PLP-dependent aminotransferases		AvtA	(NC_000918) aminotransferase (AspC family) [Aque...
MS1249	1250001	1248238	1764	NMB1189		0	Nme	P		COG0155	Sulfite reductase hemoprotein beta-component		CysI	(AF378783) NADPH-sulfite reductase hemo...
MS1250	1251807	1250017	1791	NMA1363		0	NmA	P		COG0369	Sulfite reductase flavoprotein subunit		CysJ	(NC_003116) putative sulphite reductase alpha s...
MS1251	1253180	1251879	1302	NMB1191		1.00E-151	Nme	P		COG2895	GPases - Sulfate adenylyltransferase subunit 1		CysN	(NC_003112) sulfate adenylyltransferase subuni...
MS1252	1254297	1253374	924	NMB1192		1.00E-138	Nme	E H		COG0175	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes		CysH	(NC_003112) sulfate adenylyltransferase subuni...
MS1253	1255120	1254392	729	NMB1193		7.00E-86	Nme	E H		COG0175	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes		CysH	(NC_003112) 3'-phosphoadenosine phosphosulfate red...
MS1254	1256595	1255165	1431	NMA1367_2		1.00E-99	NmA	H		COG0007	Uroporphyrinogen-III methylase		CysG	(NC_003116) sirohaem synthase [Neisseria mening...
MS1255	1257524	1256595	930	NMA1243		3.00E-82	NmA	P		COG1613	ABC-type sulfate transport system periplasmic component		Sbp	(NC_003116) putative sulphate-binding protein [...]

MS1256	1257639	1257520	120	none	none	No-des	none	No-des	No-des	none	none
MS1257	1257809	1257907	99	none	none	No-des	none	No-des	No-des	none	none
MS1258	1257874	1257770	105	none	none	No-des	none	No-des	No-des	none	none
MS1259	1257897	1258703	807	NMA1100	2.00E-76	NmA	P	COG0555	ABC-type sulfate/molybdate transport systems/permease components	CysU	(NC_003116) putative sulphate permease inner me...
MS1260	1258708	1259523	816	NMB0880	3.00E-77	Nme	P	COG0555	ABC-type sulfate/molybdate transport systems/permease components	CysU	(NC_003112) sulfate ABC transporter/permease p...
MS1261	1259540	1260613	1074	BH3130	1.00E-104	Bha	P	COG1118	ABC-type sulfate/molybdate transport systems/ATPase component	CysA	(NC_002570) sulfate ABC transporter (ATP-bindin...
MS1262	1262150	1260723	1428	HI1526	0	Hin	M	COG2870	ADP-heptose synthase/bifunctional sugar kinase/adenylyltransferase	RfaE	(NC_000907) ADP-heptose synthase (rfaE) [Haemoph...
MS1263	1262294	1263229	936	PM0885	1.00E-115	Pmu	N	COG1560	Lauroyl/myristoyl acyltransferase involved in lipid A biosynthesis	HtrB	(NC_002663) unknown [Pasteurella multocida]
MS1264	1263878	1263375	504	PM0391	2.00E-72	Pmu	S	COG2840	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1265	1263910	1264941	1032	PM0390	1.00E-127	Pmu	J	COG2890	Predicted rRNA or tRNA methylase	HemK	(NC_002663) unknown [Pasteurella multocida]
MS1266	1265944	1265009	936	PM0550	1.00E-112	Pmu	C	COG0039	Malate/lactate dehydrogenases	Mdh	(NC_002663) Mdh [Pasteurella multocida]
MS1267	1266189	1266653	465	PM0549	3.00E-65	Pmu	E	COG1438	Arginine repressor	ArgR	ARGININE REPRESSOR
MS1268	1266659	1267552	894	PM0548	2.00E-84	Pmu	R	COG1090	Predicted nucleoside-diphosphate sugar epimerases (SutA family)		(NC_002663) unknown [Pasteurella multocida]
MS1269	1268975	1267623	1353	PM0878	0	Pmu	F	COG0232	dGTP triphosphohydrolase	Dgt	(NC_002663) unknown [Pasteurella multocida]
MS1270	1269666	1268986	681	HI1298	1.00E-62	Hin	M	COG1346	Putative effector of murein hydrolase	LrgB	(NC_000907) conserved hypothetical transmembran...
MS1271	1270097	1269666	432	HI1297	3.00E-32	Hin	R	COG1380	Putative effector of murein hydrolase LrgA		(NC_000907) conserved hypothetical protein [Hae...
MS1272	1270249	1270767	519	PM0881	5.00E-41	Pmu	L	COG1525	Micrococcal nuclease (thermonuclease) homologs		(NC_002663) unknown [Pasteurella multocida]
MS1273	1270770	1271966	1197	HI1295	1.00E-167	Hin	E	COG0520	Selenocysteine lyase	CsdB	(NC_000907) niS protein/putative [Haemophilus...
MS1274	1271970	1272353	384	PM0883	1.00E-47	Pmu	R	COG2166	SufE protein probably involved in Fe-S center assembly		(NC_002663) unknown [Pasteurella multocida]
MS1275	1273184	1272438	747	NMB0789	1.00E-115	Nme	E	COG1126	ABC-type polar amino acid transport system/ATPase component	GlnQ	(NC_003112) amino acid ABC transporter/ATP-bin...
MS1276	1273902	1273189	714	NMA0999	1.00E-101	NmA	E	COG0765	ABC-type amino acid transport system/permease component	ArtM	(NC_003116) putative amino acid permease integr...
MS1277	1274680	1273895	786	NMA0997	1.00E-103	NmA	E	COG0834	ABC-type amino acid transport system/periplasmic component	ArtI	(NC_003116) putative amino acid permease substr...
MS1278	1274927	1277869	2943	PM0375	0	Pmu	O/T	COG1391	Glutamine synthetase adenylyltransferase	GlnE	(NC_002663) GlnE [Pasteurella multocida]
MS1279	1278154	1277960	195	none	none	No-des	none	No-des	No-des	none	none
MS1280	1278455	1278129	327	HI1440	1.00E-44	Hin	R	COG2969	Stringent starvation protein B	SspB	(NC_000907) stringent starvation protein B (ssp...
MS1281	1279083	1278448	636	PM0522	1.00E-108	Pmu	O	COG0625	Glutathione-S-transferases	Gst	(NC_002663) SspA [Pasteurella multocida]
MS1282	1279729	1279337	393	PM0521	1.00E-64	Pmu	J	COG0103	Ribosomal protein S9	RpsI	(NC_002663) RpS9 [Pasteurella multocida]
MS1283	1280188	1279748	441	HI1443	1.00E-76	Hin	J	COG0102	Ribosomal protein L13	RplM	(NC_000907) ribosomal protein L13 (rplL3) [Haem...
MS1284	1280291	1280407	117	none	none	No-des	none	No-des	No-des	none	none
MS1285	1280431	1280333	99	none	none	No-des	none	No-des	No-des	none	none
MS1286	1280799	1281218	420	PM0688	3.00E-21	Pmu	S	COG3105	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1287	1282160	1281315	846	HI1654	1.00E-128	Hin	R	COG0313	Predicted methyltransferases		(NC_000907) conserved hypothetical protein [Hae...
MS1288	1282237	1283958	1722	PM0646	0	Pmu	R	COG3107	Putative lipoprotein	LppC	(NC_002663) LppC [Pasteurella multocida]
MS1289	1283963	1284319	357	PM0647	3.00E-50	Pmu	L	COG0792	Predicted endonuclease distantly related to archaeal Holliday junction resolvase		(NC_002663) unknown [Pasteurella multocida]
MS1290	1284291	1284908	618	PM0648	2.00E-71	Pmu	G	COG0279	Phosphoheptose isomerase	GmhA	(NC_002663) unknown [Pasteurella multocida]
MS1291	1284969	1285523	555	HI1658	5.00E-45	Hin	R	COG2823	Predicted periplasmic or secreted lipoprotein	OsmY	(NC_000907) hemolysin/putative [Haemophilus in...
MS1292	1286935	1285655	1281	PM0681	1.00E-156	No-des	none	No-des	No-des	none	none
MS1293	1289599	1288460	1140	MJ0449	2.00E-24	Mja	P	COG0053	Predicted Co/Zn/Cd cation transporters	MMT1	(NC_003030) C-terminal region cation efflux sys...
MS1294	1290016	1289792	225	BS_ysdA	1.00E-08	Bsu	S	COG3326	Predicted membrane protein		(NC_000964) ysdA [Bacillus subtilis]
MS1295	1291248	1289989	1260	HI0889	0	Hin	E	COG0112	Glycine hydroxymethyltransferase	GlyA	(NC_000907) serine hydroxymethyltransferase (se...
MS1296	1292836	1291550	1287	HI0888	0	Hin	F	COG0151	Phosphoribosylamine-glycine ligase	PurD	(NC_000907) phosphoribosylamine-glycine ligase...
MS1297	1294734	1293139	1596	HI0887	0	Hin	F	COG0138	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in AfuI)	PurH	(NC_000907) phosphoribosylaminoimidazolecarboxa...
MS1298	1295431	1294934	498	ZyeaK	2.00E-51	No-des	none	No-des	No-des	none	none
MS1299	1297738	1296029	1710	HI0885	1.00E-167	Hin	O/C	COG0526	Thiol-disulfide isomerase and thioredoxins	TrxA	(NC_000907) thioldisulfide interchange protein...
MS1300	1298394	1297849	546	BH0719	2.00E-08	Bha	K	COG1309	Transcriptional regulator	AcrR	(NC_003030) Transcriptional regulators/AcrR fa...
MS1301	1298540	1299517	978	PM1983	2.00E-67	Pmu	Q	COG0845	Membrane-fusion protein	AcrA	(NC_002663) unknown [Pasteurella multocida]
MS1302	1299523	1302255	2733	PM1982_1	0	Pmu	Q	COG1131	ABC-type multidrug transport system/ATPase component	CcmA	(NC_002663) unknown [Pasteurella multocida]
MS1303	1302259	1303386	1128	PM1981	1.00E-106	Pmu	R	COG0842	ABC-type multidrug transport system/permease component		(NC_002663) unknown [Pasteurella multocida]
MS1304	1303493	1304893	1401	PM1980	5.00E-87	Pmu	M/N	COG1538	Outer membrane protein	TolC	(NC_002663) tbeB [Pasteurella multocida]
MS1305	1307563	1304939	2625	PM0460	0	Pmu	O	COG2844	UTPGlnB (protein PIT) uridylyltransferase	GlnD	(NC_002663) GlnD [Pasteurella multocida]
MS1306	1308530	1307721	810	HI1722	1.00E-125	Hin	J	COG0024	Methionine aminopeptidase	Map	(NC_000907) methionine aminopeptidase (map) [Ha...
MS1307	1308708	1309046	339	HI1723	5.00E-54	Hin	S	COG0316	Uncharacterized ACR	IscA	(NC_000907) conserved hypothetical protein [Hae...
MS1308	1309019	1309417	399	PM0457	9.00E-39	Pmu	S	COG3112	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1309	1309489	1309394	96	none	none	No-des	none	No-des	No-des	none	none
MS1310	1309541	1309428	114	none	none	No-des	none	No-des	No-des	none	none
MS1311	1309661	1311022	1362	HI0288	0	Hin	E	COG1760	L-serine deaminase	SdaA	(NC_000907) L-serine deaminase (sdaA) [Haemophi...
MS1312	1311218	1313554	2337	PM0456	0	Pmu	M	COG0744	Membrane carboxypeptidase (penicillin-binding protein)	MrcA	(NC_002663) PonB [Pasteurella multocida]
MS1313	1314246	1313626	621	HI1613	2.00E-84	Hin	H	COG0307	Riboflavin synthase alpha chain	RibC	(NC_000907) riboflavin synthase/alpha chain (r...
MS1314	1314310	1315704	1395	PM0651	1.00E-161	Pmu	Q	COG0534	Na+-driven multidrug efflux pump	NorM	(NC_002663) unknown [Pasteurella multocida]
MS1315	1315893	1318037	2145	NMA1558	0	NmA	P	COG1629	Outer membrane receptor proteins/mostly Fe transport	CirA	(NC_003116) putative TonB-dependent receptor pr...

MS1316	1318101	1319873	1773	HI1467		0	Hin	I	COG1133	ABC-type long-chain fatty acid transport system/fused permease and ATPase components	SbmA	(NC_000907) ABC transporter(ATP-binding protei...
MS1317	1320917	1319928	990	PM0868	1.00E-106		Pmu	K	COG1609	Transcriptional regulators	PurR	(NC_002663) FnrR [Pasteurella multocida]
MS1318	1321622	1321134	489	PM0869	3.00E-77		Pmu	E	COG0440	Acetolactate synthase[small subunit	IlvH	(NC_002663) IlvH [Pasteurella multocida]
MS1319	1323348	1321627	1722	PM0870		0	Pmu	E/H	COG0028	Thiamine pyrophosphate-requiring enzymes acetolactate synthase pyruvate dehydrogenase (cytochrome) glyoxylate carboligase phosphonopyruvate	IlvB	(NC_002663) IlvI [Pasteurella multocida]
MS1320	1323537	1323644	108	none	none			none	No-des		none	none
MS1321	1325150	1323615	1536	HI1586		0	Hin	C	COG1757	Na ⁺ /H ⁺ antiporter	NhaC	(NC_000907) conserved hypothetical integral mem...
MS1322	1325696	1326097	402	PM0872	2.00E-26		Pmu	R	COG2916	DNA-binding protein H-NS	Hns	(NC_002663) Hns [Pasteurella multocida]
MS1323	1326130	1326966	837	HI1588	1.00E-143		Hin	F	COG0788	Formyltetrahydrofolate hydrolase	PurU	(NC_000907) formyltetrahydrofolate deformylase ...
MS1324	1328347	1327016	1332	PM0684	1.00E-167		Pmu	H	COG0373	Glutamyl-tRNA reductase	HemA	(NC_002663) Glx [Pasteurella multocida]
MS1325	1330172	1328547	1626	PM0678	1.00E-130		Pmu	E/P	COG0747	ABC-type dipeptide/oligopeptide/nickel transport systems/periplasmic components	OppA	(NC_002663) unknown [Pasteurella multocida]
MS1326	1330700	1330242	459	PM0554	3.00E-38		Pmu	M	COG3133	Outer membrane lipoprotein	SlyB	(NC_002663) Lpp [Pasteurella multocida]
MS1327	1331060	1330725	336	PM0553	5.00E-17		No-des	none	No-des		none	(NC_002663) unknown [Pasteurella multocida]
MS1328	1331647	1331060	588	PM0552	1.00E-64		Pmu	S	COG3102	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1329	1331624	1331716	93	none	none		No-des	none	No-des		none	none
MS1330	1331746	1333473	1728	HI1583		0	Hin	J	COG0018	Arginyl-tRNA synthetase	ArgS	(NC_000907) arginyl-tRNA synthetase (argS) [Hae...
MS1331	1333620	1334543	924	PM0982	6.00E-12		No-des	none	No-des		none	(NC_002663) unknown [Pasteurella multocida]
MS1332	1334515	1335567	1053	PM0982	8.00E-26		No-des	none	No-des		none	(NC_002663) unknown [Pasteurella multocida]
MS1333	1336204	1335647	558	HI1652	4.00E-44		Hin	M	COG0791	Cell wall-associated hydrolases (invasion-associated proteins)	Spr	(NC_000907) lipoprotein (spr) [Haemophilus infl...
MS1334	1337935	1336397	1539	HI1231		0	Hin	C	COG1249	Dihydrolipoamide dehydrogenase glutathione oxidoreductase and related enzymes	Lpd	(NC_000907) dihydrolipoamide dehydrogenase (lpd...
MS1335	1339861	1337957	1905	PM0894		0	Pmu	C	COG0508	Dihydrolipoamide acyltransferases	AceF	(NC_002663) AceF [Pasteurella multocida]
MS1336	1342611	1339963	2649	HI1233		0	Hin	C	COG2609	pyruvate dehydrogenase decarboxylase component	AceE	(NC_000907) pyruvate dehydrogenase E1 componen...
MS1337	1344238	1343144	1095	PM0831	2.00E-37		Pmu	M	COG3203	Outer membrane protein (porin)	OmpC	(NC_002663) OmpH [Pasteurella multocida]
MS1338	1344641	1345501	861	HI1275_2	4.00E-82		Hin	Q/R	COG0500	SAM-dependent methyltransferases	SmtA	(NC_000907) tellurite resistance protein (tehB)...
MS1339	1346605	1346204	402	HI1162	3.00E-22		Hin	S	COG2852	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1340	1347705	1346650	1056	PM0742	1.00E-124		Pmu	P	COG1118	ABC-type sulfate/molybdate transport systems ATPase component	CysA	(NC_002663) ModC [Pasteurella multocida]
MS1341	1348462	1347692	771	HI1692	4.00E-81		Hin	P	COG0555	ABC-type sulfate/molybdate transport systems/permease components	CysU	(NC_000907) molybdenum ABC transporter/permeas...
MS1342	1349248	1348490	759	PM0744	5.00E-77		Pmu	P	COG0725	ABC-type molybdate transport system/periplasmic component	ModA	(NC_002663) ModA [Pasteurella multocida]
MS1343	1349235	1349378	144	none	none		No-des	none	No-des		none	none
MS1344	1349374	1350144	771	PM0746	5.00E-92		Pmu	R	COG2005	N-terminal domain of molybdenum-binding protein	ModE	(NC_002663) ModE [Pasteurella multocida]
MS1345	1350163	1350588	426	HI1161	9.00E-51		Hin	Q	COG2050	Uncharacterized protein possibly involved in aromatic compounds catabolism	Paal	(NC_000907) conserved hypothetical protein [Hae...
MS1346	1350581	1351549	969	HI1160	1.00E-125		Hin	H	COG0276	Protoheme ferro-lyase (ferrochelatase)	HemH	(NC_000907) ferrochelatase (hemH) [Haemophilus ...
MS1347	1351608	1352603	996	PM0738	1.00E-130		Pmu	E	COG2873	O-acetylhomoserine sulphydrylase	none	(NC_002663) MetC [Pasteurella multocida]
MS1348	1352607	1352966	360	PM0738	1.00E-42		Pmu	E	COG2873	O-acetylhomoserine sulphydrylase	none	(NC_002663) MetC [Pasteurella multocida]
MS1349	1352947	1353639	693	HI1278	3.00E-77		Hin	C	COG0778	Nitroreductase	NfnB	(NC_000907) H-flavin oxidoreductase [Haem...
MS1350	1354263	1353703	561	HI0966	2.00E-55		No-des	none	No-des		none	(NC_000907) H. influenzae predicted coding regi...
MS1351	1355213	1354347	867	PM0281	1.00E-132		Pmu	C	COG0074	Succinyl-CoA synthetase alpha subunit	SucD	(NC_002663) SucD [Pasteurella multocida]
MS1352	1356381	1355218	1164	PM0280	1.00E-169		Pmu	C	COG0045	Succinyl-CoA synthetase beta subunit	SucC	(NC_002663) SucC [Pasteurella multocida]
MS1353	1356560	1356423	138	none	none		No-des	none	No-des		none	none
MS1354	1358066	1356861	1206	PM0278	1.00E-167		Pmu	C	COG0508	Dihydrolipoamide acyltransferases	AceF	(NC_002663) SucB [Pasteurella multocida]
MS1355	1360895	1358097	2799	PM0277		0	Pmu	C	COG0567	Pyruvate and 2-oxoglutarate dehydrogenases E1 component	SucA	(NC_002663) SucA [Pasteurella multocida]
MS1356	1361123	1361010	114	none	none		No-des	none	No-des		none	none
MS1357	1362269	1361130	1140	PM0706	1.00E-139		Pmu	J	COG0349	Ribonuclease D	Rnd	(NC_002663) Rnd [Pasteurella multocida]
MS1358	1364045	1362360	1686	PM0707		0	Pmu	I/Q	COG0318	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	CaiC	(NC_002663) FadD [Pasteurella multocida]
MS1359	1364651	1364070	582	PM0708	5.00E-42		Pmu	M	COG3065	Starvation-inducible outer membrane lipoprotein	Slp	(NC_002663) unknown [Pasteurella multocida]
MS1360	1365382	1364663	720	HI0388	3.00E-91		Hin	O	COG1214	Inactive homologs of metal-dependent proteases putative molecular chaperones		(NC_000907) conserved hypothetical protein [Hae...
MS1361	1367334	1365403	1932	PM0710		0	Pmu	L	COG1199	Rad3-related DNA helicases	DinG	(NC_002663) Dnt [Pasteurella multocida]
MS1362	1367245	1368216	972	PM0711	7.00E-85		Pmu	G	COG0676	Uncharacterized enzymes related to aldose 1-epimerase		(AF174389) HI1317 [Haemophilus influenzae]
MS1363	1369251	1368295	957	PM0712	3.00E-78		Pmu	R	COG0679	Predicted permeases		(NC_002663) unknown [Pasteurella multocida]
MS1364	1370403	1369423	981	PM0240	1.00E-149		Pmu	E/P	COG1124	ABC-type dipeptide/oligopeptide/nickel transport system ATPase component	OppF	(NC_002663) DppF [Pasteurella multocida]
MS1365	1371379	1370399	981	PM0239	1.00E-143		Pmu	E/P	COG0444	ABC-type dipeptide/oligopeptide/nickel transport system ATPase component	OppD	(NC_000907) dipeptide ABC transporter ATP-bind...
MS1366	1372277	1371393	885	PM0238	1.00E-126		Pmu	E/P	COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems/permease components	DppC	(NC_002663) DppC [Pasteurella multocida]
MS1367	1373291	1372290	1002	PM0237	1.00E-158		Pmu	E/P	COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems/permease components	DppB	(NC_002663) DppB [Pasteurella multocida]
MS1368	1375813	1373633	2181	PM0411		0	Pmu	L	COG0210	Superfamily I DNA and RNA helicases	UvrD	(NC_002663) UvrD [Pasteurella multocida]
MS1369	1376031	1376168	138	none	none		No-des	none	No-des		none	none
MS1370	1376197	1377126	930	PM0203	1.00E-104		Pmu	H	COG1840	ABC-type iron/thiamine transport systems/periplasmic component	TbpA	(NC_002663) unknown [Pasteurella multocida]
MS1371	1379242	1377209	2034	HI1247		0	Hin	L	COG0556	Helicase subunit of the DNA excision repair complex	UvrB	(NC_000907) excinuclease ABC[subunit B (uvrB) ...
MS1372	1379958	1380932	975	PM0428	1.00E-90		Pmu	P	COG0530	Ca ²⁺ /Na ⁺ antiporter	none	(NC_002663) unknown [Pasteurella multocida]
MS1373	1382049	1381006	1044	HI0945	1.00E-126		Hin	O	COG0265	Trypsin-like serine proteases typically periplasmic contain C-terminal PDZ domain	DegQ	(NC_000907) protease (degS) [Haemophilus influe...
MS1374	1383177	1382059	1119	HI0944_2	3.00E-78		Hin	H	COG1985	Pyrimidine reductase riboflavin biosynthesis	RibD	(NC_000907) riboflavin biosynthesis protein (ri...
MS1375	1383629	1383183	447	PM0750	4.00E-65		Pmu	K	COG1327	Predicted transcriptional regulator consists of a Zn-ribbon and ATP-cone domains		(NC_002663) unknown [Pasteurella multocida]

MS1376	1383877	1384371	495	PM1470	4.00E-77	Pmu	R	COG1881	Phospholipid-binding protein		(NC_002663) unknown [Pasteurella multocida]
MS1377	1384404	1384511	108	none	none	No-des	none	No-des	No-des	none	none
MS1378	1384549	1385937	1389	PM1167	1.00E-165	Pmu	P	COG0471	Di- and tricarboxylate transporters	CitT	(NC_002663) unknown [Pasteurella multocida]
MS1379	1386074	1386343	270	NMB1653	1.00E-36	Nme	R	COG2716	ACT domain-containing protein	GcvR	(NC_003112) conserved hypothetical protein [Nei...
MS1380	1386355	1387710	1356	NMB1652	0	Nme	S	COG2848	Uncharacterized ACR		(NC_003112) conserved hypothetical protein [Nei...
MS1381	1387948	1387817	132	none	none	No-des	none	No-des	No-des	none	none
MS1382	1388037	1387858	180	none	none	No-des	none	No-des	No-des	none	none
MS1383	1388290	1388087	204	none	none	No-des	none	No-des	No-des	none	none
MS1384	1388432	1388325	108	none	none	No-des	none	No-des	No-des	none	none
MS1385	1388901	1388428	474	NMA1517	1.00E-37	NmA	K	COG0789	Predicted transcriptional regulators	SoxR	(NC_003112) transcriptional regulator/MerR fam...
MS1386	1388986	1390104	1119	HI0185	1.00E-178	Hin	C	COG1062	Zn-dependent alcohol dehydrogenases/class III	AdhC	(NC_000907) alcohol dehydrogenase/class III (a...
MS1387	1390107	1390952	846	NMB1305	1.00E-101	Nme	R	COG0627	Predicted esterase		(NC_003112) esterase/putative [Neisseria menin...
MS1388	1392050	1391079	972	SPy0441	3.00E-74	Spy	R	COG0673	Predicted dehydrogenases and related proteins	MviM	(NC_002737) conserved hypothetical protein [Str...
MS1389	1392177	1392085	93	none	none	No-des	none	No-des	No-des	none	none
MS1390	1394016	1392187	1830	PM0466	2.00E-07	Pmu	L	COG3593	Predicted ATP-dependent endonuclease of the OLD family		(NC_002663) unknown [Pasteurella multocida]
MS1391	1394228	1394031	198	none	none	No-des	none	No-des	No-des	none	none
MS1392	1394532	1394431	102	none	none	No-des	none	No-des	No-des	none	none
MS1393	1394450	1394608	159	none	none	No-des	none	No-des	No-des	none	none
MS1394	1394682	1395716	1035	BS_yybT	9.00E-73	Bsu	C	COG2141	Coenzyme F420-dependent N5[N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases		(NC_002758) conserved hypothetical protein [Sta...
MS1395	1396751	1395858	894	XFI768	5.00E-68	Xfa	K	COG0583	Transcriptional regulator	LysR	(NC_003143) putative LysR-family transcriptiona...
MS1396	1396958	1397449	492	none	none	No-des	none	No-des	No-des	none	none
MS1397	1397463	1398560	1098	none	none	No-des	none	No-des	No-des	none	(NC_003143) putative exported protein [Yersinia...
MS1398	1400101	1398755	1347	PM0257	1.00E-107	Pmu	L	COG2256	Uncharacterized ATPase related to the helicase subunit of the Holliday junction resolvase		(NC_003030) ATPase related to the helicase subu...
MS1399	1400556	1400134	423	none	none	No-des	none	No-des	No-des	none	none
MS1400	1400645	1401484	840	CC2403	1.00E-12	Ccr	K	COG2207	AraC-type DNA-binding domain-containing proteins	AraC	probable transcription regulator - Streptomyces coel...
MS1401	1402710	1401721	990	NMB1750	9.00E-32	Nme	L	COG3547	Transposase		(AF282240) pilin inverting protein [Aci...
MS1402	1403586	1402975	612	none	none	No-des	none	No-des	No-des	none	none
MS1403	1404574	1403684	891	PA1223	2.00E-64	Pae	K	COG0583	Transcriptional regulator	LysR	(NC_003295) PROBABLE TRANSCRIPTION REGULATOR I
MS1404	1404712	1405236	525	jhp0584	3.00E-40	No-des	none	No-des	No-des	none	(NC_003295) PROBABLE TRANSPORT TRANSMEMBRANE
MS1405	1405486	1406064	579	Z2446	9.00E-39	EcZ	R	COG2910	Putative NADH-flavin reductase	nuoK	(NC_002655) Z2446 gene product [Escherichia col...
MS1406	1406045	1406899	855	TM0441	8.00E-15	Tma	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	FabG	(NC_003295) PUTATIVE OXIDOREDUCTASE PROTEIN [Ra...
MS1407	1407170	1408357	1188	PM1533	2.00E-46	Pmu	G/E PIR	COG0477	Permeases of the major facilitator superfamily	ProP	(NC_003295) PROBABLE TRANSPORT TRANSMEMBRANE
MS1408	1408871	1408422	450	VC0964	3.00E-22	Vch	G	COG2190	Phosphotransferase system IIA components	NagE	(NC_003030) PTS enzyme II ABC component [Clostr...
MS1409	1410236	1408884	1353	BS_ynaJ	6.00E-62	Bsu	G	COG2211	Na ⁺ /melibiose symporter and related transporters	MelB	PUTATIVE XYLOSE-PROTON SYMPORTER (XYLOSE TR...
MS1410	1410321	1410416	96	none	none	No-des	none	No-des	No-des	none	none
MS1411	1412049	1410454	1596	L52019	3.00E-07	Lla	G	COG1070	Sugar (pentulose and hexulose) kinases	XylB	(NC_003030) Sugar kinase/possible xylulose kin...
MS1412	1412919	1412143	777	Rv1928c	1.00E-60	Mtu	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	FabG	(NC_000962) hypothetical protein Rv1928c [Mycob...
MS1413	1413122	1414237	1116	BH0700	4.00E-28	Bha	K	COG1940	Transcriptional regulators	NagC	(NC_003030) XylR transcriptional regulator [Clo...
MS1414	1415430	1414459	972	SPy0441	3.00E-76	Spy	R	COG0673	Predicted dehydrogenases and related proteins	MviM	(NC_002737) conserved hypothetical protein [Str...
MS1415	1416471	1415566	906	mfr0648	3.00E-46	Mlo	K	COG0583	Transcriptional regulator	LysR	(NC_002678) transcriptional regulator [Mesorhiz...
MS1416	1416589	1416882	294	none	none	No-des	none	No-des	No-des	none	(NC_003143) conserved hypothetical protein [Yer...
MS1417	1416896	1417447	552	CC0205	6.00E-26	Ccr	R	COG2249	Putative NADPH-quinone reductase (modulator of drug activity B)	MdaB	(NC_002696) NADPH(H) oxidoreductase [Caulobacter...
MS1418	1417437	1418408	972	BS_jolS	1.00E-37	Bsu	C	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	Tas	(AY050325) AtIg06690/F4H5_17 [Arabidopsis thaliana]
MS1419	1418424	1419503	1080	DRB0033_1	4.00E-34	Dra	I	COG0657	Esterase/lipase	Aes	(NC_000958) arylesterase/monooxygenase [Deinococ...
MS1420	1419554	1419922	369	msl7859	1.00E-11	No-des	none	No-des	No-des	none	(NC_002678) unknown protein [Mesorhizobium loti...
MS1421	1419980	1420720	741	TM1724	1.00E-37	Tma	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	FabG	(NC_003064) AGR_pAT_564p [Agrobacterium tumefac...
MS1422	1420799	1421818	1020	Zyao	2.00E-83	EcZ	C	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	Tas	(NC_003210) similar to oxidoreductase [Listeria...
MS1423	1421954	1422637	684	XFI137	2.00E-72	Xfa	R	COG0693	Putative intracellular protease/amidase	ThiJ	(NC_002488) NonF-related protein [Xylella fasti...
MS1424	1422650	1423348	699	L178933	8.00E-12	Lla	S	COG0599	Uncharacterized ACR/homolog of gamma-carboxymuconolactone decarboxylase subunit		(NC_003037) 4-carboxymuconolactone decarboxylas...
MS1425	1423383	1423481	99	none	none	No-des	none	No-des	No-des	none	none
MS1426	1423503	1424207	705	slr0619	3.00E-16	Syn	R	COG2159	Predicted metal-dependent hydrolase of the TIM-barrel fold		(NC_002758) conserved hypothetical protein [Sta...
MS1427	1424224	1424553	330	slr0619	2.00E-18	Syn	R	COG2159	Predicted metal-dependent hydrolase of the TIM-barrel fold		(NC_002758) conserved hypothetical protein [Sta...
MS1428	1424582	1425712	1131	BH2089	2.00E-67	Bha	R	COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold		(NC_002570) BH2089-unknown conserved protein in...
MS1429	1425743	1426441	699	none	none	No-des	none	No-des	No-des	none	(NC_003037) conserved hypothetical protein [Sin...
MS1430	1426825	1426571	255	none	none	No-des	none	No-des	No-des	none	none
MS1431	1426984	1426841	144	none	none	No-des	none	No-des	No-des	none	none
MS1432	1427009	1427161	153	none	none	No-des	none	No-des	No-des	none	none
MS1433	1427609	1427220	390	PM1941	1.00E-24	Pmu	K	COG0789	Predicted transcriptional regulators	SoxR	(NC_002663) unknown [Pasteurella multocida]
MS1434	1427743	1428429	687	PM1337	8.00E-44	Pmu	P	COG1230	Co/Zn/Cd efflux system component	CzcD (BS)	(NC_002663) CzcD [Pasteurella multocida]
MS1435	1428434	1428541	108	none	none	No-des	none	No-des	No-des	none	none

MS1436	1428764	1429681	918	mlr4682	2.00E-30	Mlo	N/O	COG0616	Periplasmic serine proteases (ClpP class)		SppA	(NC_002678) hypothetical protein [Mesorhizobium...
MS1437	1433831	1429821	4011	HII070	0	Hin	L	COG1643	HrpA-like helicases		HrpA	(NC_000907) ATP-dependent helicase (hrpA) [Haem...
MS1438	1433939	1434754	816	PM1064	1.00E-105	Pmu	N	COG2503	Predicted secreted acid phosphatase			(NC_002663) unknown [Pasteurella multocida]
MS1439	1435256	1434810	447	PM0771	7.00E-47	Pmu	S	COG2707	Uncharacterized membrane protein			(NC_002663) unknown [Pasteurella multocida]
MS1440	1435395	1436321	927	BH2670	1.00E-08	Bha	R	COG0679	Predicted permeases			(NC_003030) Predicted permease [Clostridium ace...
MS1441	1437318	1436404	915	PM0756	1.00E-127	Pmu	J	COG0130	Pseudouridine synthase		TruB	(NC_002663) TruB [Pasteurella multocida]
MS1442	1437713	1437321	393	PM0757	4.00E-56	Pmu	J	COG0858	Ribosome-binding factor A		RbfA	(NC_002663) RbfA [Pasteurella multocida]
MS1443	1437742	1437837	96	none	none	none	No-des	none	No-des		none	none
MS1444	1440336	1437877	2460	PM0759	0	Pmu	J	COG0532	Translation initiation factor 2 (GTPase)		InfB	(NC_002663) InfB [Pasteurella multocida]
MS1445	1441856	1440354	1503	HII283	0	Hin	K	COG0195	Transcription terminator		NusA	transcription termination-antitermination factor nus...
MS1446	1442326	1441874	453	PM0761	1.00E-71	Pmu	S	COG0779	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS1447	1442812	1442693	120	none	none	No-des	none	No-des	No-des		none	none
MS1448	1443558	1442812	747	HII326	1.00E-62	No-des	none	No-des	No-des		none	(NC_000907) H. influenzae predicted coding regi...
MS1449	1443740	1444315	576	ZyceB	2.00E-19	No-des	none	No-des	No-des		none	(NC_003143) putative lipoprotein [Yersinia pest...
MS1450	1445697	1444408	1290	HII0110	0	Hin	J	COG0172	Seryl-tRNA synthetase		SerS	(NC_000907) seryl-tRNA synthetase (serS) [Haemo...
MS1451	1447136	1445799	1338	HII590	0	Hin	L	COG2256	Uncharacterized ATPase related to the helicase subunit of the Holliday junction resolvase			(NC_000907) conserved hypothetical protein [Hae...
MS1452	1447736	1447194	543	PM0256	4.00E-80	Pmu	M	COG2834	Outer membrane lipoprotein-sorting protein		LoIA	(NC_002663) LoIA [Pasteurella multocida]
MS1453	1447878	1447741	138	none	none	No-des	none	No-des	No-des		none	none
MS1454	1450726	1447850	2877	HII1595+4+2	0	No-des	none	No-des	No-des		none	(NC_000907) DNA segregation ATPase [Haemophilus...
MS1455	1451225	1450737	489	PM0254	6.00E-75	Pmu	K	COG1522	Transcriptional regulators		Lrp	(NC_002663) Lrp [Pasteurella multocida]
MS1456	1451434	1451766	333	PM0253	7.00E-35	No-des	none	No-des	No-des		none	(NC_002663) unknown [Pasteurella multocida]
MS1457	1452843	1451815	1029	HII0119	1.00E-105	Hin	P	COG0803	ABC-type Mn/Zn transport system/periplasmic Mn/Zn-binding (lipo)protein (surface adhesin A)		ZnuA	(NC_000907) conserved hypothetical protein [Hae...
MS1458	1453567	1452803	765	PM0927	1.00E-122	Pmu	H	COG1179	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 1			(NC_002663) unknown [Pasteurella multocida]
MS1459	1454767	1453646	1122	PM0928	1.00E-145	Pmu	M	COG2821	Membrane-bound lytic murein transglycosylase		MitA	(NC_002663) unknown [Pasteurella multocida]
MS1460	1454996	1455139	144	none	none	No-des	none	No-des	No-des		none	none
MS1461	1456173	1455163	1011	hypE	1.00E-122	Eco	O	COG0309	Hydrogenase maturation factor		HypE	(NC_000913) plays structural role in maturation...
MS1462	1457333	1456224	1110	hypD	1.00E-143	Eco	O	COG0409	Hydrogenase maturation factor		HypD	(NC_002695) hydrogenase isoenzyme HypD [Escheri...
MS1463	1458212	1457400	813	hypB	3.00E-87	Eco	O/K	COG0378	Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase		HypB	(NC_002695) hydrogenase isoenzyme HypB [Escheri...
MS1464	1458418	1459185	768	HII0105	1.00E-111	Hin	S	COG0327	Uncharacterized ACR			(NC_000907) conserved hypothetical protein [Hae...
MS1465	1459284	1459195	90	none	none	No-des	none	No-des	No-des		none	none
MS1466	1459398	1459300	99	none	none	No-des	none	No-des	No-des		none	none
MS1467	1459421	1460125	705	HII734	1.00E-121	Hin	I	COG0623	Enoyl-acyl-carrier-protein reductase (NADH)		FabI	ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NAD...
MS1468	1460226	1462202	1977	HII733	0	Hin	K	COG0557	Exoribonucleases		VacB	(NC_000907) exoribonuclease II (rnb) [Haemophil...
MS1469	1462301	1462648	348	HII253	1.00E-26	Hin	S	COG3094	Uncharacterized BCR			(NC_000907) conserved hypothetical protein [Hae...
MS1470	1462673	1462810	138	none	none	No-des	none	No-des	No-des		none	none
MS1471	1463108	1462797	312	PM0796	2.00E-35	Pmu	J	COG0023	Translation initiation factor (SUI1)		SUI1	(NC_002663) unknown [Pasteurella multocida]
MS1472	1463987	1463253	735	PM0797	1.00E-113	Pmu	F	COG0284	Orotidine-5'-phosphate decarboxylase		PyrF	(NC_002663) PyrF [Pasteurella multocida]
MS1473	1465167	1463974	1194	PM0798	1.00E-169	Pmu	G	COG2956	Predicted N-acetylglucosaminyl transferase			(NC_002663) unknown [Pasteurella multocida]
MS1474	1465463	1465170	294	PM0799	5.00E-20	No-des	none	No-des	No-des		none	(NC_002663) unknown [Pasteurella multocida]
MS1475	1465850	1465569	282	PM0800	2.00E-37	Pmu	L	COG0776	Bacterial nucleoid DNA-binding protein		HimA	(NC_002663) HimD [Pasteurella multocida]
MS1476	1467632	1465986	1647	PM0801	0	Pmu	J	COG0539	Ribosomal protein S1		RpsA	(NC_002663) RpS1 [Pasteurella multocida]
MS1477	1468412	1467738	675	PM0802	6.00E-81	Pmu	F	COG0283	Cytidylate kinase		Cmk	(NC_002663) CmkA [Pasteurella multocida]
MS1478	1468718	1469734	1017	BH3254	1.00E-78	Bha	R	COG3641	Predicted membrane protein[putative toxin regulator		Pf0R	(NC_002570) BH3254--unknown conserved protein in...
MS1479	1471195	1469864	1332	HII727	0	Hin	E	COG0137	Argininosuccinate synthase		ArgG	(NC_000907) argininosuccinate synthetase (argG)...
MS1480	1472134	1471316	819	PM0814	1.00E-114	Pmu	M/G	COG0451	Nucleoside-diphosphate-sugar epimerases		WcaG	(NC_002663) unknown [Pasteurella multocida]
MS1481	1473058	1472201	858	PM0815	1.00E-141	Pmu	F	COG0152	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase		PurC	(NC_002663) PurC [Pasteurella multocida]
MS1482	1473079	1473210	132	none	none	No-des	none	No-des	No-des		none	none
MS1483	1473244	1473104	141	none	none	No-des	none	No-des	No-des		none	none
MS1484	1474175	1473282	894	none	none	No-des	none	No-des	No-des		none	none
MS1485	1474381	1474473	93	none	none	No-des	none	No-des	No-des		none	none
MS1486	1476535	1474427	2109	PM1018_1	1.00E-122	Pmu	N	COG3206	Uncharacterized protein involved in exopolysaccharide biosynthesis		GumC	(NC_002663) Wzs [Pasteurella multocida]
MS1487	1477963	1476707	1257	PM1016	1.00E-142	Pmu	M	COG1596	Periplasmic protein involved in polysaccharide export		Wza	(NC_002663) Wza [Pasteurella multocida]
MS1488	1479815	1477893	1923	PM1015	0	Pmu	M/G	COG1086	Predicted nucleoside-diphosphate sugar epimerases			(NC_002663) Rfb [Pasteurella multocida]
MS1489	1481068	1479833	1236	PM1014	1.00E-170	Pmu	M	COG0399	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis		WecE	probable amino-transferase [imported] - Acinetobacte...
MS1490	1481706	1481038	669	MJ1437	6.00E-14	Mja	R	COG1011	Predicted hydrolases of the HAD superfamily			(AF320320) conserved hypothetical proteo...
MS1491	1482634	1481672	963	slr1616	4.00E-07	Syn	E/F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)		CarB	(AF320320) PgIB2 [Neisseria meningitidis]
MS1492	1483230	1482634	597	PM1011	3.00E-77	Pmu	M	COG2148	Sugar transferases involved in lipopolysaccharide synthesis		WcaJ	probable UDP-galactose phosphate transferase [import...
MS1493	1484513	1483230	1284	none	none	No-des	none	No-des	No-des		none	none
MS1494	1485696	1484518	1179	NMA0640	2.00E-60	NmA	M	COG0438	Predicted glycosyltransferases		RfaG	(NC_003116) hypothetical protein NMA0640 [Neiss...
MS1495	1486993	1485689	1305	PAB0783	3.00E-16	Pab	R	COG2244	Membrane protein involved in the export of O-antigen and teichoic acid		RfbX	(NC_000868) polysaccharide biosynthesis related...

MS1496	1488155	1487001	1155	NMA1057	1.00E-33	NmA	M		COG0438	Predicted glycosyltransferases	RfaG	(NC_003116) putative glycosyl transferase [Neis...
MS1497	1489258	1488158	1101	RP414	5.00E-13	Rpr	M		COG0438	Predicted glycosyltransferases	RfaG	(NC_003030) Glycosyltransferase [Clostridium ac...
MS1498	1490348	1489275	1074	PA3155	1.00E-156	Pae	M		COG0399	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	WecE	(NC_002516) probable aminotransferase WbpE [Pse...
MS1499	1490937	1490365	573	PA3156	5.00E-75	Pae	R		COG110	Acetyltransferases (the isoleucine patch superfamily)	WbbJ	(NC_002516) probable acetyltransferase WbpD [Ps...
MS1500	1492079	1491132	948	PA3158	3.00E-96	Pae	R		COG0673	Predicted dehydrogenases and related proteins	MviM	(NC_002516) probable oxidoreductase WpbB [Pseud...
MS1501	1493409	1492102	1308	PM1003	1.00E-148	Pnu	M		COG0677	UDP-N-acetyl-D-mannosaminuronate dehydrogenase	WecC	(AF035937) WbpO [Pseudomonas aeruginosa]
MS1502	1493787	1493921	135	none	none	No-des	none	No-des	No-des		none	none
MS1503	1493979	1495565	1587	PM0816	0	Pmu	J		COG0480	Translation elongation and release factors (GTPases)	FusA	(NC_002663) PrfC [Pasteurella multocida]
MS1504	1495817	1496524	708	PM0219	1.00E-116	Pmu	TK		COG0745	Response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain	OmpR	(NC_002663) ArcA [Pasteurella multocida]
MS1505	1497103	1496615	489	PM0217	2.00E-78	Pmu	O		COG0691	tmRNA-binding protein	SmpB	(NC_002663) SmpB [Pasteurella multocida]
MS1506	1497818	1497219	600	HI0443	2.00E-95	Hin	L		COG0353	Recombinational DNA repair protein	RecR	(NC_000907) recombination protein (recR) [Haemo...
MS1507	1498216	1497890	327	PM0205	1.00E-28	Pmu	S		COG0718	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1508	1498824	1498327	498	HI1711	1.00E-77	Hin	G		COG2190	Phosphotransferase system IIA components	NagE	(NC_000907) PTS system glucose-specific IIA co...
MS1509	1500611	1498887	1725	PM0897	0	Pmu	G		COG1080	Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)	PtsA	(NC_002663) PtsI [Pasteurella multocida]
MS1510	1500985	1500731	255	PM0898	3.00E-38	Pmu	G		COG1925	Phosphotransferase system HP-related proteins	FruB	(NC_002663) PtsH [Pasteurella multocida]
MS1511	1502325	1501270	1056	PM0899	1.00E-164	Pmu	R		COG1162	Predicted GTPases		(NC_002663) unknown [Pasteurella multocida]
MS1512	1502417	1502974	558	PM0900	2.00E-91	Pmu	F		COG1949	Oligoribonuclease (3'->5' exoribonuclease)	Orn	(NC_002663) unknown [Pasteurella multocida]
MS1513	1503095	1502955	141	none	none	No-des	none	No-des	No-des		none	none
MS1514	1503587	1504072	486	PM0902	6.00E-61	Pmu	R		COG0802	Predicted ATPase or kinase		(NC_002663) unknown [Pasteurella multocida]
MS1515	1504093	1505934	1842	HI066_1	1.00E-99	Hin	M		COG0860	N-acetylmuramoyl-L-alanine amidase	AmiC	(NC_002663) unknown [Pasteurella multocida]
MS1516	1505970	1507862	1893	PM0904	0	Pmu	L		COG0323	DNA mismatch repair enzyme (predicted ATPase)	MutL	(NC_002663) MutL [Pasteurella multocida]
MS1517	1507949	1508890	942	HI068	1.00E-141	Hin	J		COG0324	tRNA delta(2)-isopentenylpyrophosphate transferase	MiaA	(NC_000907) tRNA delta(2)-isopentenylpyrophosph...
MS1518	1508974	1509261	288	PM0906	3.00E-32	Pmu	R		COG1923	Uncharacterized ACR/host factor I protein	Hfq	(NC_002663) Hfq [Pasteurella multocida]
MS1519	1509267	1510610	1344	PM0907	1.00E-180	Pmu	R		COG2262	GTPases	HfiX	(NC_002663) HfiX [Pasteurella multocida]
MS1520	1511877	1510690	1188	HI0122	0	Hin	E		COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases	MetC	(NC_000907) cystathionine beta-lyase (metC) [Ha...
MS1521	1512041	1512640	600	PM0795	1.00E-102	Pmu	O		COG0450	Peroxiredoxin	AhpC	(NC_002663) TsaA [Pasteurella multocida]
MS1522	1513247	1512882	366	Rv3073c	6.00E-12	Mtu	S		COG3189	Uncharacterized BCR		(AL450289) hypothetical protein [Streptomyces co...
MS1523	1514279	1513272	1008	PM0379	1.00E-169	Pmu	H		COG0502	Biotin synthase and related enzymes	BioB	(NC_002663) BioB [Pasteurella multocida]
MS1524	1515013	1514369	645	PM0378	3.00E-79	Pmu	G		COG1130	ABC-type sugar/spermidine/putrescine/iron/thiamine transport systems ATPase component	MalK	(NC_002663) unknown [Pasteurella multocida]
MS1525	1516634	1515003	1632	PM0377	1.00E-143	Pmu	H		COG1178	ABC-type thiamine transport system/permease components	ThiP	(AF237938) putative thiamine ABC transpo...
MS1526	1517658	1516642	1017	PM0376	1.00E-110	Pmu	H		COG1840	ABC-type iron/thiamine transport systems periplasmic component	TbpA	(NC_002663) TbpA [Pasteurella multocida]
MS1527	1518994	1518035	960	PM0675	1.00E-136	Pmu	K		COG1940	Transcriptional regulators	NagC	(NC_002663) unknown [Pasteurella multocida]
MS1528	1520172	1519024	1149	CC1630	2.00E-35	Ccr	R		COG0673	Predicted dehydrogenases and related proteins	MviM	(NC_003047) PUTATIVE OXIDOREDUCTASE PROTEIN [S...
MS1529	1521239	1520187	1053	CC1631	1.00E-139	Ccr	G		COG1082	Sugar phosphate isomerases/epimerases	IolE	(NC_002696) conserved hypothetical protein [Cau...
MS1530	1522464	1521244	1221	ZyegT	1.00E-77	EcZ	GE PR		COG0477	Permeases of the major facilitator superfamily	ProP	(NC_002655) putative nucleoside permease protei...
MS1531	1523557	1522577	981	BH2313	2.00E-46	Bha	K		COG1609	Transcriptional regulators	PurR	(NC_002570) transcriptional regulator [Bacillus...
MS1532	1524368	1523595	774	PM0676	1.00E-72	Pmu	I		COG0671	Membrane-associated phospholipid phosphatase	PgpB	(NC_002663) PdpB [Pasteurella multocida]
MS1533	1524402	1525058	657	PM0677	1.00E-104	Pmu	H		COG0807	GTP cyclohydrolase II	RibA	GTP CYCLOHYDROLASE II
MS1534	1525272	1525901	630	HI1607	1.00E-60	Hin	M		COG3017	Outer membrane lipoprotein involved in outer membrane biogenesis	LoiB	OUTER-MEMBRANE LIPOPROTEIN LOIB PRECURSOR
MS1535	1525911	1526816	906	PM0245	1.00E-117	Pmu	I		COG1947	4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate synthase	IspE	(NC_002663) unknown [Pasteurella multocida]
MS1536	1526881	1527828	948	PM0244	1.00E-161	Pmu	F E		COG0462	Phosphoribosylpyrophosphate synthetase	PrsA	(NC_002663) PrsA [Pasteurella multocida]
MS1537	1528699	1528013	687	PM0194	9.00E-90	Pmu	F		COG0775	Nucleoside phosphorylase	Pfs	(NC_002663) Pfs [Pasteurella multocida]
MS1538	1529431	1528712	720	HI1215	2.00E-53	Hin	OC		COG0526	Thiol-disulfide isomerase and thioredoxins	TrxA	(NC_000907) thioldisulfide interchange protein...
MS1539	1531239	1529467	1773	PM0192	0	Pmu	L		COG0608	Single-stranded DNA-specific exonuclease	RecJ	(NC_002663) RecJ [Pasteurella multocida]
MS1540	1532010	1531324	687	HI1213	6.00E-86	Hin	O		COG1651	Protein-disulfide isomerase	DsbG	(NC_000907) thioldisulfide interchange protein...
MS1541	1532245	1532156	90	none	none	No-des	none	No-des	No-des		none	none
MS1542	1532314	1533288	975	HIN0621	1.00E-170	Hin	J		COG1186	Protein chain release factor B	PrfB	PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2)
MS1543	1533383	1534891	1509	HI1211	0	Hin	J		COG1190	Lyssyl-tRNA synthetase class II	LysU	(NC_000907) lyssyl-tRNA synthetase (lysU) [Haemo...
MS1544	1535009	1534902	108	none	none	No-des	none	No-des	No-des		none	none
MS1545	1534989	1535297	309	hybF	2.00E-23	Eco	R		COG0375	Zn finger protein HypA/HybF (possibly regulating hydrogenase expression)	HybF	PROBABLE HYDROGENASE NICKEL INCORPORATION P...
MS1546	1535467	1537776	2310	hypF	0	Eco	O		COG0068	Hydrogenase maturation factor	HypF	(NC_003198) hydrogenase maturation protein [Sal...
MS1547	1538008	1537871	138	none	none	No-des	none	No-des	No-des		none	none
MS1548	1539248	1538181	1068	PM0197	1.00E-154	Pmu	R		COG0795	Predicted permeases		(NC_002663) unknown [Pasteurella multocida]
MS1549	1540361	1539264	1098	PM0196	1.00E-97	Pmu	R		COG0795	Predicted permeases		(NC_002663) unknown [Pasteurella multocida]
MS1550	1540504	1541973	1470	PM0195	0	Pmu	E		COG0260	Leucyl aminopeptidase	PepB	(NC_002663) PepA [Pasteurella multocida]
MS1551	1543938	1542457	1482	VC0819	1.00E-120	Vch	C		COG1012	NAD-dependent aldehyde dehydrogenases	PutA	(NC_002758) aldehyde dehydrogenase homologue [S...
MS1552	1545435	1544170	1266	PM1300	0	Pmu	R		COG1473	Metal-dependent amidase/aminoacylase/carboxypeptidase	AbgB	(NC_002663) unknown [Pasteurella multocida]
MS1553	1546931	1545642	1290	PM1299	0	Pmu	C		COG3069	C4-dicarboxylate transporter	DcuC	(NC_002663) unknown [Pasteurella multocida]
MS1554	1547199	1547017	183	PM0454	4.00E-15	Pmu	E		COG3340	Peptidase E	PepE	(NC_002663) PepE [Pasteurella multocida]
MS1555	1547468	1548700	1233	PM0160	1.00E-180	Pmu	E		COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	ArgE	(NC_002663) unknown [Pasteurella multocida]

MS1556	1551637	1548776	2862	HI1391	0	Hin	J	COG0525	Valyl-tRNA synthetase	ValS	(NC_000907) valyl-tRNA synthetase (valS) [Haemo...
MS1557	1552206	1551766	441	PM0822	2.00E-45	Pmu	L	COG2927	DNA polymerase III chi subunit	HolC	(NC_002663) HolC [Pasteurella multocida]
MS1558	1552355	1553443	1089	PM0232	1.00E-168	Pmu	J	COG0809	S-adenosylmethionine:RNA-ribosyltransferase-isomerase (queuine synthetase)	QueA	(NC_002663) QueA [Pasteurella multocida]
MS1559	1553492	1554628	1137	HI0244	0	Hin	J	COG0343	Queuine/archaeosine tRNA-ribosyltransferase	Tgt	(NC_000907) tRNA-guanine transglycosylase (tgt)...
MS1560	1554660	1555241	582	HI0243	3.00E-50	No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS1561	1555262	1555477	216	HI0242	1.00E-07	Hin	K	COG0425	Predicted transcriptional regulators	SirA	(NC_000907) conserved hypothetical protein [Hae...
MS1562	1555595	1555891	297	PM0228	2.00E-40	Pmu	N	COG1862	Preprotein translocase subunit YajC	YajC	(NC_002663) YajC [Pasteurella multocida]
MS1563	1555928	1557775	1848	PM0227	0	Pmu	N	COG0342	Preprotein translocase subunit SecD	SecD	(NC_002663) SecD [Pasteurella multocida]
MS1564	1557788	1558753	966	HI0239	1.00E-109	Hin	N	COG0341	Preprotein translocase subunit SecF	SecF	(NC_000907) protein-export membrane protein (se...
MS1565	1558921	1561026	2106	PM0326	1.00E-170	Pmu	M	COG0741	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	MitE	(NC_002663) unknown [Pasteurella multocida]
MS1566	1561064	1561366	303	PM0325	2.00E-38	Pmu	K	COG2973	Trp operon repressor	TrpR	(NC_002663) TrpR [Pasteurella multocida]
MS1567	1561350	1562081	732	PM0324	3.00E-80	Pmu	M	COG0744	Membrane carboxypeptidase (penicillin-binding protein)	MrcA	MONOFUNCTIONAL BIOSYNTHETIC PEPTIDOGLYCAN
MS1568	1562150	1562893	744	PM0579	7.00E-84	Pmu	R	COG0300	Short-chain dehydrogenases of various substrate specificities	DltE (BS)	(NC_002663) YdG [Pasteurella multocida]
MS1569	1562937	1564913	1977	HI1246	0	Hin	M	COG1368	Phosphoglycerol transferase and related proteins/alkaline phosphatase superfamily	MdoB	(NC_000907) H. influenzae predicted coding regi...
MS1570	1566227	1565448	780	HI0137	1.00E-104	Hin	L	COG0847	DNA polymerase III epsilon subunit and related 3'-5' exonucleases	DnaQ	(NC_000907) DNA polymerase III epsilon subunit...
MS1571	1566286	1566759	474	PM0107	4.00E-77	Pmu	L	COG0328	Ribonuclease HI	RnhA	(NC_002663) Rnh [Pasteurella multocida]
MS1572	1567182	1566841	342	PM0836	4.00E-45	Pmu	S	COG2926	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1573	1567398	1568480	1083	PM0837	1.00E-158	Pmu	HIE	COG1932	Phosphoserine aminotransferase	SerC	(NC_002663) SerC [Pasteurella multocida]
MS1574	1568508	1569668	1161	HI1166	1.00E-166	Hin	E	COG0079	Histidinol-phosphate aminotransferase/Tyrosine aminotransferase	HisC	(NC_000907) histidinol-phosphate aminotransfera...
MS1575	1569727	1571025	1299	PM0839	0	Pmu	E	COG0128	5-enolpyruvylshikimate-3-phosphate synthase	AroA	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5...
MS1576	1571040	1571750	711	PM1509	3.00E-42	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS1577	1572931	1572149	783	PA0978	6.00E-54	Pae	L	COG2801	Putative transposase	Tra5	(NC_002516) conserved hypothetical protein [Pse...
MS1578	1573284	1572973	312	PA0979	9.00E-27	Pae	L	COG2963	Transposase		(NC_002516) conserved hypothetical protein [Pse...
MS1579	1574586	1573396	1191	PM0949	6.00E-97	Pmu	G	COG2814	Arabinose efflux permease	AraJ	(NC_002663) unknown [Pasteurella multocida]
MS1580	1575948	1574590	1359	HI0134	2.00E-38	No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS1581	1576540	1575959	582	HI0133	7.00E-92	Hin	F	COG0717	Deoxycytidine deaminase	Dcd	(NC_000907) deoxycytidine triphosphate deaminas...
MS1582	1577203	1576556	648	PM0952	5.00E-84	Pmu	F	COG0572	Uridine kinase	Udk	(NC_002663) Udk [Pasteurella multocida]
MS1583	1577425	1578462	1038	PM0953	1.00E-170	Pmu	H	COG1840	ABC-type iron/thiamine transport systems/periplasmic component	TbpA	(NC_002663) AfuA [Pasteurella multocida]
MS1584	1578435	1578533	99	none	none	No-des	none	No-des	none	none	
MS1585	1578548	1579582	1035	PM0955	1.00E-167	Pmu	H	COG1840	ABC-type iron/thiamine transport systems/periplasmic component	TbpA	(NC_002663) AfuA [Pasteurella multocida]
MS1586	1579627	1581720	2094	PM0956	0	Pmu	H	COG1178	ABC-type thiamine transport system/permease components	ThiP	FERRIC TRANSPORT SYSTEM PERMEASE PROTEIN AF...
MS1587	1581761	1582879	1119	PM0957	1.00E-169	Pmu	G	COG1130	ABC-type sugar/spermidine/putrescine/iron/thiamine transport systems/ATPase component	MalK	(NC_002663) AfuC [Pasteurella multocida]
MS1588	1583963	1582965	999	PM0958	1.00E-138	Pmu	J	COG2813	16S RNA G1207 methylase RsmC	RsmC	(NC_002663) unknown [Pasteurella multocida]
MS1589	1584447	1584554	408	PM0959	4.00E-31	No-des	none	No-des	No-des	none	(NC_002663) Hold [Pasteurella multocida]
MS1590	1584561	1585001	441	HI0010	7.00E-55	Hin	R	COG0456	Acetyltransferases	RimI	(NC_000907) ribosomal-protein-alanine acetyltra...
MS1591	1586283	1585066	1218	HI1533	0	Hin	IIQ	COG0304	3-oxoacyl-(acyl-carrier-protein) synthase	FabB	(NC_000907) beta-ketacyl-ACP synthase I (fabB)...
MS1592	1586501	1588516	2016	PM0338_2	1.00E-163	Pmu	E	COG0665	Glycine/D-amino acid oxidases (deaminating)	DadA	(NC_002663) unknown [Pasteurella multocida]
MS1593	1589631	1588570	1062	NMB0079	1.00E-149	Nme	M	COG1088	dTDP-D-glucose 4/6-dehydratase	RfbB	(AF213680) dTDP-D-glucose-4/6-dehydratase [Actino...
MS1594	1590900	1589731	1170	PM0351	1.00E-176	Pmu	R	COG0536	Predicted GTPase	Obg (BS)	(NC_002663) unknown [Pasteurella multocida]
MS1595	1591827	1590910	918	HI0878	2.00E-97	Hin	GIE/R	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	RhaT	(NC_000907) conserved hypothetical protein [Hae...
MS1596	1592521	1592646	126	none	none	No-des	none	No-des	none	none	
MS1597	1592753	1591830	924	PM0349	4.00E-91	Pmu	GIE/R	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	RhaT	(NC_002663) unknown [Pasteurella multocida]
MS1598	1593161	1592907	255	PM0348	1.00E-41	Pmu	J	COG0211	Ribosomal protein L27	RpmA	(NC_002663) RpL27 [Pasteurella multocida]
MS1599	1593544	1593185	360	PM0347	8.00E-44	Pmu	J	COG0261	Ribosomal protein L21	RplU	(NC_002663) RpL21 [Pasteurella multocida]
MS1600	1593644	1594717	1074	PM0346	1.00E-138	Pmu	H	COG0142	Geranylgeranyl pyrophosphate synthase	IspA	(NC_002663) IspB [Pasteurella multocida]
MS1601	1594781	1595518	738	HI0882	6.00E-99	Hin	S	COG1636	Uncharacterized BCR		(NC_000907) H. influenzae predicted coding regi...
MS1602	1596859	1596077	783	PA0978	6.00E-54	Pae	L	COG2801	Putative transposase	Tra5	(NC_002516) conserved hypothetical protein [Pse...
MS1603	1597212	1596901	312	PA0979	9.00E-27	Pae	L	COG2963	Transposase		(NC_002516) conserved hypothetical protein [Pse...
MS1604	1598600	1597344	1257	PM0936	1.00E-177	Pmu	E	COG0014	Gamma-glutamyl phosphate reductase	ProA	(NC_002663) ProA [Pasteurella multocida]
MS1605	1599292	1598612	681	PM0935	3.00E-79	Pmu	S	COG2860	Predicted membrane protein		(NC_002663) unknown [Pasteurella multocida]
MS1606	1599552	1600619	1068	Z1971	1.00E-152	EcZ	G	COG2376	Dihydroxyacetone kinase	DAK1	(NC_002655) putative dihydroxyacetone kinase (E...
MS1607	1600643	1601266	624	Z1970	2.00E-64	EcZ	G	COG2376	Dihydroxyacetone kinase	DAK1	(NC_002655) putative dihydroxyacetone kinase (E...
MS1608	1601278	1601685	408	ygcC_1	1.00E-38	Eco	S	COG3412	Uncharacterized BCR		(NC_000913) putative PTS system enzyme I [Esche...
MS1609	1603233	1601782	1452	PM1247	0	Pmu	G	COG1070	Sugar (pentulose and hexulose) kinases	XylB	(NC_002663) Lys [Pasteurella multocida]
MS1610	1604266	1603241	1026	PM1327	1.00E-130	Pmu	G	COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems/permease components	AraH	(NC_002663) RbsC [Pasteurella multocida]
MS1611	1605775	1604285	1491	PM1326	0	Pmu	G	COG1129	ABC-type sugar (aldose) transport system/ATPase component	MglA	(NC_002663) unknown [Pasteurella multocida]
MS1612	1605932	1606870	939	PM1325	1.00E-134	Pmu	G	COG1879	Periplasmic sugar-binding proteins	RbsB	(NC_002663) unknown [Pasteurella multocida]
MS1613	1608301	1606952	1350	PM0937	0	Pmu	E	COG0527	Aspartokinases	LysC	(NC_002663) unknown [Pasteurella multocida]
MS1614	1609788	1608430	1359	HI0121	0	Hin	M	COG0773	UDP-N-acetylmuramate-alanine ligase	MurC	(NC_000907) conserved hypothetical protein [Hae...
MS1615	1609950	1610954	1005	PM0930	1.00E-164	Pmu	G	COG0158	Fructose-1/6-biphosphatase	Fbp	(NC_002663) Fbp [Pasteurella multocida]

MS1616	1611872	1611048	825	PM0934		7.00E-58	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS1617	1612599	1611877	723	CC2843		1.00E-56	Ccr	O	COG0625	Glutathione-S-transferases	Gst	(NC_002696) glutathione S-transferase family pr...
MS1618	1612824	1612699	126	none	none		No-des	none	No-des	No-des	none	none
MS1619	1612829	1614058	1230	PM0117		1.00E-148	Pmu	O	COG0330	Membrane protease subunits/stomatin/prohibitin homologs	HflC	(NC_002663) HflC [Pasteurella multocida]
MS1620	1614061	1614945	885	PM0118		1.00E-141	Pmu	O	COG0330	Membrane protease subunits/stomatin/prohibitin homologs	HflC	(NC_002663) HflC [Pasteurella multocida]
MS1621	1615153	1616448	1296	HI1633		0	Hin	F	COG0104	Adenylosuccinate synthase	PurA	(NC_000907) adenylosuccinate synthetase (purA) ...
MS1622	1619501	1616622	2880	PM0991		0	Pmu	J	COG1530	Ribonucleases G and E	CafA	(NC_002663) Rne [Pasteurella multocida]
MS1623	1619800	1619702	99	none	none		No-des	none	No-des	No-des	none	none
MS1624	1620039	1621013	975	HI0412		1.00E-157	Hin	J	COG0564	Pseudouridylate synthases/23S RNA-specific	RluA	(NC_000907) conserved hypothetical protein [Hae...
MS1625	1621424	1621161	264	none	none		No-des	none	No-des	No-des	none	none
MS1626	1621801	1621481	321	PM0994		4.00E-44	Pmu	O/C	COG0526	Thiol-disulfide isomerase and thioredoxins	TrxA	(AB032759) thioredoxin [Actinobacillus actinomyc...
MS1627	1623109	1622003	1107	HI0086		0	Hin	E	COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases	MetC	(NC_000907) cystathionine gamma-synthase (metB)...
MS1628	1624016	1623858	159	none	none		No-des	none	No-des	No-des	none	none
MS1629	1624115	1624231	117	none	none		No-des	none	No-des	No-des	none	none
MS1630	1624254	1625231	978	aq_1054		3.00E-33	Aae	R	COG1408	Predicted phosphohydrolases		(NC_003030) Predicted phosphohydrolase [Clostri...
MS1631	1627374	1625317	2058	HI1276_1		0	Hin	J	COG0143	Methionyl-tRNA synthetase	MetG	(NC_000907) methionyl-tRNA synthetase (metG) [H...
MS1632	1627530	1628639	1110	PM0302		1.00E-161	Pmu	D	COG0489	ATPases involved in chromosome partitioning	Mrp	(NC_002663) Mrp [Pasteurella multocida]
MS1633	1629699	1628731	969	PM0202		1.00E-152	Pmu	J	COG2269	Truncated/possibly inactive Class II lysyl-tRNA synthetase		(NC_002663) LysU [Pasteurella multocida]
MS1634	1631482	1631210	273	none	none		No-des	none	No-des	No-des	none	none
MS1635	1632471	1631473	999	BH0341		9.00E-27	Bha	S	COG1518	Uncharacterized ACR		(NC_002570) BH0341--unknown conserved protein in...
MS1636	1632759	1632484	276	none	none		No-des	none	No-des	No-des	none	none
MS1637	1632844	1632734	111	none	none		No-des	none	No-des	No-des	none	none
MS1638	1634681	1633530	1152	none	none		No-des	none	No-des	No-des	none	none
MS1639	1635865	1634684	1182	VC1899		3.00E-25	No-des	none	No-des	No-des	none	(NC_002505) hypothetical protein [Vibrio cholerae]
MS1640	1636067	1635840	228	none	none		No-des	none	No-des	No-des	none	none
MS1641	1636257	1636090	168	none	none		No-des	none	No-des	No-des	none	none
MS1642	1637059	1636190	870	AF1859		4.00E-06	No-des	none	No-des	No-des	none	none
MS1643	1637069	1637200	132	none	none		No-des	none	No-des	No-des	none	none
MS1644	1637360	1637545	186	none	none		No-des	none	No-des	No-des	none	none
MS1645	1637589	1637888	300	none	none		No-des	none	No-des	No-des	none	none
MS1646	1637891	1639198	1308	BH1412		6.00E-27	Bha	L	COG3464	Transposase		(AF403298) transposase TnpA [Enterococcus faecalis]
MS1647	1640688	1639150	1539	none	none		No-des	none	No-des	No-des	none	none
MS1648	1641635	1640691	945	none	none		No-des	none	No-des	No-des	none	none
MS1649	1642339	1641647	693	TM1809		5.00E-22	Tma	S	COG1337	Uncharacterized ACR		(NC_000853) conserved hypothetical protein [The...
MS1650	1642734	1642354	381	none	none		No-des	none	No-des	No-des	none	none
MS1651	1644885	1642747	2139	PH0162		1.00E-39	Pho	R	COG1353	Predicted hydrolase of the HD superfamily (permuted catalytic motifs)		(NC_000961) hypothetical protein [Pyrococcus horikoshii]
MS1652	1645156	1646952	1797	HI0835		0	Hin	C	COG1053	Succinate dehydrogenase/fumarate reductase/flavoprotein subunits	SdhA	(NC_000907) fumarate reductase/flavoprotein su...
MS1653	1646888	1647715	828	PM0200		1.00E-143	Pmu	C	COG0479	Succinate dehydrogenase/fumarate reductase Fe-S protein	FrdB	(NC_002663) FrdB [Pasteurella multocida]
MS1654	1647727	1648113	387	PM0199		6.00E-22	Pmu	C	COG3029	Fumarate reductase subunit C	FrdC	(NC_002663) FrdC [Pasteurella multocida]
MS1655	1648129	1648470	342	HI0832		8.00E-36	Hin	C	COG3080	Fumarate reductase subunit D	FrdD	(NC_000907) fumarate reductase [13 kDa hydropho...
MS1656	1648574	1648473	102	none	none		No-des	none	No-des	No-des	none	none
MS1657	1649793	1648636	1158	PM0150_2		1.00E-133	Pmu	E	COG0077	Prephenate dehydratase	PheA	(NC_002663) PheA [Pasteurella multocida]
MS1658	1651533	1649884	1650	PM1193		0	Pmu	F	COG0737	5'-nucleotidase/2[3'-cyclic phosphodiesterase and related esterases	UshA	(NC_002663) unknown [Pasteurella multocida]
MS1659	1652767	1651853	915	PM0148		1.00E-138	Pmu	M	COG0774	UDP-3-O-acyl-N-acetylglucosamine deacetylase	LpxC	(NC_002663) LpxC [Pasteurella multocida]
MS1660	1652756	1652917	162	none	none		No-des	none	No-des	No-des	none	none
MS1661	1654035	1652824	1212	PM0147		1.00E-115	Pmu	D	COG0206	Cell division GTPase	FtsZ	(NC_002663) FtsZ [Pasteurella multocida]
MS1662	1655410	1654121	1290	HI1142		1.00E-166	Hin	D	COG0849	Predicted ATPases of the HSP70 class involved in cell division	FtsA	(NC_000907) cell division protein (ftsA) [Haemo...
MS1663	1656229	1655462	768	PM0145		3.00E-97	Pmu	M	COG1589	Cell division septal protein	FtsQ	(NC_002663) FtsQ [Pasteurella multocida]
MS1664	1657152	1656232	921	PM0144		1.00E-139	Pmu	M	COG1181	D-alanine-D-alanine ligase and related ATP-grasp enzymes	DdlA	(NC_002663) DdlB [Pasteurella multocida]
MS1665	1657178	1657267	90	none	none		No-des	none	No-des	No-des	none	none
MS1666	1658682	1657243	1440	PM0143		0	Pmu	M	COG0773	UDP-N-acetylmuramate-alanine ligase	MurC	(NC_002663) MurC [Pasteurella multocida]
MS1667	1659768	1658704	1065	PM0142		1.00E-148	Pmu	M	COG0707	UDP-N-acetylglucosamine-LPS N-acetylglucosamine transferase	MurG	(NC_002663) MurG [Pasteurella multocida]
MS1668	1660968	1659781	1188	PM0141		1.00E-159	Pmu	D	COG0772	Bacterial cell division membrane protein	FtsW	(NC_002663) FtsW [Pasteurella multocida]
MS1669	1662312	1660996	1317	PM0140		1.00E-178	Pmu	M	COG0771	UDP-N-acetylmuramoylalanine-D-glutamate ligase	MurD	(NC_002663) MurD [Pasteurella multocida]
MS1670	1663424	1662345	1080	PM0139		1.00E-180	Pmu	M	COG0472	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N- acetylglucosamine-1-phosphate transferase	Rfe	(NC_002663) MraY [Pasteurella multocida]
MS1671	1664803	1663421	1383	PM0138		1.00E-137	Pmu	M	COG0770	UDP-N-acetylmuramyl pentapeptide synthase	MurF	(NC_002663) MurF [Pasteurella multocida]
MS1672	1666330	1664867	1464	PM0137		1.00E-177	Pmu	M	COG0769	UDP-N-acetylmuramyl tripeptide synthase	MurE	(NC_002663) MurE [Pasteurella multocida]
MS1673	1668211	1666358	1854	PM0136		0	Pmu	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2	FtsI	(NC_002663) FtsI [Pasteurella multocida]
MS1674	1668541	1668224	318	PM0135		1.00E-28	Pmu	D	COG3116	Cell division protein	FtsL	(NC_002663) FtsL [Pasteurella multocida]
MS1675	1669509	1668544	966	PM0134		1.00E-141	Pmu	M	COG0275	Predicted S-adenosylmethionine-dependent methyltransferase involved in cell envelope biogenesis		(NC_002663) unknown [Pasteurella multocida]

MS1676	1670091	1669636	456	PM0133	7.00E-64	Pmu	S	COG2001	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1677	1671816	1670317	1500	PM0132	0	Pmu	T	COG1966	Carbon starvation protein predicted membrane protein	CstA	(NC_002663) unknown [Pasteurella multocida]
MS1678	1672132	1671938	195	none	none	No-des	none	No-des	No-des	none	HYPOTHETICAL PROTEIN HI1257
MS1679	1674018	1672228	1791	PM1043	1.00E-137	Pmu	R	COG1444	Predicted P-loop ATPase fused to an acetyltransferase		(NC_002663) unknown [Pasteurella multocida]
MS1680	1674488	1674021	468	HI0004	1.00E-65	Hin	R	COG0319	Predicted metal-dependent hydrolase		(NC_000907) conserved hypothetical protein [Hae...
MS1681	1675131	1674511	621	BH2932	1.00E-20	Bha	E	COG1280	Putative threonine efflux protein	RhtB	(NC_002695) threonine efflux protein [Escherich...
MS1682	1676275	1675175	1101	PM1046	1.00E-148	Pmu	T	COG1702	Phosphate starvation-inducible protein PhoH predicted ATPase	PhoH	(NC_002663) PhoH [Pasteurella multocida]
MS1683	1678934	1676640	2295	PM1048_1	0	Pmu	H	COG2918	Gamma-glutamylcysteine synthetase	GshA	(NC_002663) unknown [Pasteurella multocida]
MS1684	1679873	1679016	858	CJ0982c	3.00E-84	Cje	E	COG0834	ABC-type amino acid transport system periplasmic component	ArlI	(Y10872) cjaA [Campylobacter jejuni]
MS1685	1680631	1679897	735	CJ0469	4.00E-87	Cje	E	COG1126	ABC-type polar amino acid transport system ATPase component	GlnQ	(NC_002163) amino-acid ABC transporter ATP-bind...
MS1686	1681363	1680698	666	HP1170	9.00E-58	Hpy	E	COG0765	ABC-type amino acid transport system permease component	ArlM	(NC_003098) ABC transporter membrane-spanning p...
MS1687	1682038	1681370	669	HP1169	5.00E-50	Hpy	E	COG0765	ABC-type amino acid transport system permease component	ArlM	(NC_003098) ABC transporter membrane-spanning p...
MS1688	1682653	1682216	438	none	none	No-des	none	No-des	No-des	none	none
MS1689	1682796	1683692	897	mIrf0648	3.00E-50	Mlo	K	COG0583	Transcriptional regulator	LysR	(NC_002678) transcriptional regulator [Mesorhiz...
MS1690	1685197	1683776	1422	HI0019	0	Hin	J	COG0621	2-methylthioadenine synthetase	MiaB	(NC_000907) conserved hypothetical protein [Hae...
MS1691	1685661	1685371	291	none	none	No-des	none	No-des	No-des	none	(NC_003143) hypothetical protein [Yersinia pest...
MS1692	1685718	1686206	489	PA1234	8.00E-06	No-des	none	No-des	No-des	none	none
MS1693	1687115	1686285	831	PM1019	1.00E-120	Pmu	R	COG1409	Predicted phosphohydrolases	Icc	(NC_002663) Icc [Pasteurella multocida]
MS1694	1687988	1687266	723	PM1020	2.00E-76	Pmu	LjR	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes	MutT	(NC_002663) unknown [Pasteurella multocida]
MS1695	1688718	1688005	714	PM0116	5.00E-71	Pmu	Q	COG2091	Phosphopantetheinyl transferase	Slp (BS)	(NC_002663) unknown [Pasteurella multocida]
MS1696	1690646	1688769	1878	PM1024	0	Pmu	O	COG0326	Molecular chaperone HSP90 family	HtpG	Chaperone protein htpG (Heat shock protein ...
MS1697	1691383	1690853	531	PM1025	2.00E-35	Pmu	M	COG3637	Opacity protein and related surface antigens		(NC_002663) Opa [Pasteurella multocida]
MS1698	1691484	1691717	234	PM1026	4.00E-08	Pmu	S	COG3091	Uncharacterized BCR	SprT	(NC_002663) SprT [Pasteurella multocida]
MS1699	1692108	1691599	510	PM1026	8.00E-59	Pmu	S	COG3091	Uncharacterized BCR	SprT	(NC_002663) SprT [Pasteurella multocida]
MS1700	1692215	1692090	126	none	none	No-des	none	No-des	No-des	none	none
MS1701	1693512	1692238	1275	PM0115	0	Pmu	E	COG0498	Threonine synthase	ThrC	(NC_002663) ThrC [Pasteurella multocida]
MS1702	1694524	1693583	942	HI0088	1.00E-156	Hin	E	COG0083	Homoserine kinase	ThrB	(NC_000907) homoserine kinase (thrB) [Haemophil...
MS1703	1696986	1694539	2448	PM0113_1	0	Pmu	E	COG0527	Aspartokinases	LysC	(NC_002663) ThrA [Pasteurella multocida]
MS1704	1697937	1697314	624	PM1952	2.00E-68	Pmu	P	COG2032	Cu/Zn superoxide dismutase	SodC	(NC_002663) SodC [Pasteurella multocida]
MS1705	1698054	1698743	690	PM0112	2.00E-89	Pmu	R	COG0325	Predicted enzyme with a TIM-barrel fold		(NC_002663) unknown [Pasteurella multocida]
MS1706	1698762	1698911	150	none	none	No-des	none	No-des	No-des	none	none
MS1707	1700147	1698885	1263	PM0180	0	Pmu	M	COG0766	UDP-N-acetylglucosamine enolpyruvyl transferase	MurA	(NC_002663) MurZ [Pasteurella multocida]
MS1708	1700437	1700171	267	PM0179	5.00E-31	Pmu	T	COG0271	Stress-induced morphogen (activity unknown)	BolA	(NC_002663) unknown [Pasteurella multocida]
MS1709	1700820	1700461	360	PM0178	7.00E-32	Pmu	R	COG3113	STAS domain protein		(NC_002663) unknown [Pasteurella multocida]
MS1710	1701470	1700832	639	PM0177	8.00E-66	Pmu	S	COG2854	Uncharacterized periplasmic protein		(NC_002663) unknown [Pasteurella multocida]
MS1711	1702012	1701512	501	PM0176	1.00E-58	Pmu	R	COG1463	Permease component of an ABC-transporter		(NC_002663) unknown [Pasteurella multocida]
MS1712	1702848	1702069	780	HI1086	1.00E-111	Hin	R	COG0767	ABC-type toluene export system permease component		(NC_000907) conserved hypothetical protein [Hae...
MS1713	1703657	1702848	810	PM0174	1.00E-118	Pmu	R	COG1127	Uncharacterized ABC-type transport system ATPase component		(NC_002663) unknown [Pasteurella multocida]
MS1714	1703901	1704473	573	HI1150	4.00E-62	Hin	S	COG3117	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1715	1704457	1704969	513	HI1149m	6.00E-70	Hin	S	COG1934	Uncharacterized BCR		(NC_000907) Uncharacterized conserved protein [...
MS1716	1704982	1705704	723	PM0171	1.00E-116	Pmu	R	COG1137	ABC-type (unclassified) transport system ATPase component		(NC_002663) unknown [Pasteurella multocida]
MS1717	1705711	1706232	522	PM0170	2.00E-51	Pmu	G/T	COG1762	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	PtsN	(NC_002663) PtsN [Pasteurella multocida]
MS1718	1706251	1707129	879	PM0169	1.00E-122	Pmu	R	COG1660	Predicted P-loop-containing kinase		(NC_002663) unknown [Pasteurella multocida]
MS1719	1707428	1707237	192	ZyIHJ	5.00E-26	EcZ	S	COG2975	Uncharacterized BCR		(NC_002655) orf hypothetical protein [Escheric...
MS1720	1707769	1707431	339	HI0372	4.00E-51	Hin	C	COG0633	Ferredoxin	Fdx	(NC_000907) ferredoxin (fdx-1) [Haemophilus inf...
MS1721	1709644	1707797	1848	PM0322	0	Pmu	O	COG0443	Molecular chaperone	DnaK	(NC_002663) HscA [Pasteurella multocida]
MS1722	1710244	1709726	519	PM0321	6.00E-66	Pmu	O	COG1076	DnaJ-domain-containing proteins 1	DjIA	(NC_002663) HscB [Pasteurella multocida]
MS1723	1710622	1710251	372	PM0320	1.00E-45	Pmu	S	COG0316	Uncharacterized ACR	IscA	(NC_002663) unknown [Pasteurella multocida]
MS1724	1711059	1710679	381	HI0377	2.00E-63	Hin	C	COG0822	NifU homologs involved in Fe-S cluster formation	IscU	nifU protein homolog HI0377 - Haemophilus influenzae...
MS1725	1711382	1711092	291	none	none	No-des	none	No-des	No-des	none	none
MS1726	1712690	1711479	1212	PM0318	0	Pmu	E	COG1104	Cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes	NiFS (BS)	(NC_002663) NiFS [Pasteurella multocida]
MS1727	1713189	1712740	450	PM0317	1.00E-59	Pmu	K	COG1959	Predicted transcriptional regulator		(NC_002663) unknown [Pasteurella multocida]
MS1728	1713989	1713258	732	PM0316	2.00E-92	Pmu	J	COG0565	rRNA methylase	LasT	(NC_002663) unknown [Pasteurella multocida]
MS1729	1714163	1714975	813	PM0315	1.00E-131	Pmu	G	COG0483	Archaeal fructose-1/6-bisphosphatase and related enzymes of inositol monophosphatase family	SubB	(NC_002663) SubB [Pasteurella multocida]
MS1730	1716880	1715039	1842	PM0313_1	1.00E-115	Pmu	T	COG0642	Sensory transduction histidine kinases	BaeS	(NC_002663) ArcB [Pasteurella multocida]
MS1731	1717021	1717125	105	none	none	No-des	none	No-des	No-des	none	none
MS1732	1718656	1718561	96	none	none	No-des	none	No-des	No-des	none	none
MS1733	1720855	1720652	204	none	none	No-des	none	No-des	No-des	none	none
MS1734	1723927	1723115	813	PM0917	1.00E-103	Pmu	M	COG0796	Glutamate racemase	MurI	(NC_002663) MurI [Pasteurella multocida]
MS1735	1726060	1723982	2079	HI1740	0	Hin	L/K	COG1200	RecG-like helicases	RecG	(NC_000907) ATP-dependent DNA helicase (recG) [...

MS1736	1728189	1726069	2121	PM0920		0	Pmu	T/K	COG0317	Guanosine polyphosphate pyrophosphohydrolases/synthetases	SpoT	(NC_002663) SpoT [Pasteurella multocida]
MS1737	1728515	1728252	264	PM0921		1.00E-36	Pmu	K	COG1758	DNA-directed RNA polymerase subunit K/omega	RpoZ	(NC_002663) RpoZ [Pasteurella multocida]
MS1738	1729210	1728587	624	PM0922		3.00E-93	Pmu	F	COG0194	Guanylate kinase	Gmk	(NC_002663) Gmk [Pasteurella multocida]
MS1739	1729494	1730552	1059	HI0001		1.00E-172	Hin	G	COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase	GapA	(NC_000907) glyceraldehyde-3-phosphate dehydrog...
MS1740	1731857	1730682	1176	none	none	none	No-des	none	No-des	none	none	(AF135787) Ogl [Pectobacterium carotov...
MS1741	1733656	1731926	1731	slu1087		1.00E-20	Syn	E/H/R	COG0591	Na+/proline/Na+/panthothenate symporters and related permeases	PutP	(AL353815) putative sodium-coupled permease [Str...
MS1742	1736100	1733887	2214	BH0494		2.00E-67	No-des	none	No-des	No-des	none	(Y16797) exopolysaccharuronate lyase [Pectobacter...
MS1743	1737599	1736370	1230	HI0465		0	Hin	E	COG0111	Phosphoglycerate dehydrogenase and related dehydrogenases	SerA	(NC_000907) D-3-phosphoglycerate dehydrogenase ...
MS1744	1738281	1737625	657	HI0464		1.00E-103	Hin	G	COG0120	Ribose 5-phosphate isomerase	RpiA	(NC_000907) ribose 5-phosphate isomerase A (rpi...
MS1745	1738484	1738380	105	none	none	none	No-des	none	No-des	No-des	none	none
MS1746	1739695	1738541	1155	HI0463		0	Hin	H	COG0635	Coproporphyrinogen III oxidase and related FeS oxidoreductases	HemN	(NC_000907) oxygen-independent coproporphyrinog...
MS1747	1740306	1739710	597	HI0260		2.00E-78	Hin	F	COG0127	Xanthosine triphosphate pyrophosphatase		(NC_000907) conserved hypothetical protein [Hae...
MS1748	1740933	1740451	483	HI1008		1.00E-15	Hin	L	COG1555	DNA uptake protein and related DNA-binding proteins	ComEA (BS)	(NC_000907) conserved hypothetical protein [Hae...
MS1749	1741928	1740987	942	PM1664		1.00E-159	Pmu	I/M	COG0761	Penicillin tolerance protein	LytB	(NC_002663) LytB [Pasteurella multocida]
MS1750	1742422	1741928	495	HI1006		8.00E-64	Hin	N	COG0597	Lipoprotein signal peptidase	LspA	(NC_000907) lipoprotein signal peptidase (lspA)...
MS1751	1745325	1742512	2814	PM1662		0	Pmu	J	COG0060	Isolucyl-tRNA synthetase	IleS	(NC_002663) IleS [Pasteurella multocida]
MS1752	1746343	1745402	942	HI0963		1.00E-118	Hin	H	COG0196	FAD synthase	RibF	(NC_000907) riboflavin kinase / FMN adenylyltra...
MS1753	1747302	1746442	861	PM1475		7.00E-65	Pmu	G/E/R	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	RhaT	(NC_002663) unknown [Pasteurella multocida]
MS1754	1748191	1747313	879	PM1475		1.00E-57	Pmu	G/E/R	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	RhaT	(NC_002663) unknown [Pasteurella multocida]
MS1755	1749790	1748222	1569	PM1660		0	Pmu	R	COG0728	Uncharacterized membrane protein/putative virulence factor	MviN	(NC_002663) MviN [Pasteurella multocida]
MS1756	1750080	1750346	267	HI0965		2.00E-33	Hin	J	COG0268	Ribosomal protein S20	RpsT	(NC_000907) ribosomal protein S20 (rps20) [Haem...
MS1757	1751117	1750437	681	PM1658		9.00E-74	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS1758	1751212	1752180	969	PM1657		1.00E-107	Pmu	E	COG0560	Phosphoserine phosphatase	SerB	(NC_002663) SerB [Pasteurella multocida]
MS1759	1752198	1752686	489	HI1034		4.00E-80	Hin	S	COG1666	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1760	1754871	1752988	1884	PM1241		0	Pmu	K	COG0568	DNA-directed RNA polymerase sigma subunits (sigma70/sigma32)	RpoD	(NC_002663) RpoD [Pasteurella multocida]
MS1761	1756688	1754925	1764	PM1240		0	Pmu	L	COG0358	DNA primase (bacterial type)	DnaG	(NC_002663) DnaG [Pasteurella multocida]
MS1762	1757033	1756821	213	PM1239		1.00E-34	Pmu	J	COG0828	Ribosomal protein S21	RpsU	(NC_002663) RpsU [Pasteurella multocida]
MS1763	1757259	1758290	1032	HI0530		1.00E-170	Hin	O	COG0533	Metal-dependent proteases with possible chaperone activity	QR17	(NC_000907) O-sialoglycoprotein endopeptidase (...)
MS1764	1758363	1758947	585	HI0529		2.00E-90	Hin	F	COG1435	Thymidine kinase	Tdk	(NC_000907) thymidine kinase (tdk) [Haemophilus...
MS1765	1759051	1759185	135	none	none	none	No-des	none	No-des	No-des	none	none
MS1766	1761328	1759304	2025	HI1100		0	Hin	L	COG0272	NAD-dependent DNA ligase (contains BRCT domain type II)	Lig	(NC_000907) DNA ligase (lig) [Haemophilus influ...
MS1767	1761302	1761391	90	none	none	none	No-des	none	No-des	No-des	none	none
MS1768	1762480	1761404	1077	PM1695		2.00E-60	Pmu	D	COG3115	Cell division protein	ZipA	(NC_002663) ZipA [Pasteurella multocida]
MS1769	1762670	1763584	915	HI1102		9.00E-92	Hin	E	COG2981	Uncharacterized protein involved in cysteine biosynthesis	CysZ	(NC_000907) cysteine synthetase/putative (cysZ)...
MS1770	1763771	1764718	948	HI1103		1.00E-120	Hin	E	COG0031	Cysteine synthase	CysK	(NC_000907) cysteine synthetase (cysK) [Haemoph...
MS1771	1766770	1765148	1623	PM0843		2.00E-89	No-des	none	No-des	No-des	none	(NC_002663) TadG [Pasteurella multocida]
MS1772	1767395	1766796	600	PM0844		7.00E-40	No-des	none	No-des	No-des	none	(NC_002663) TadF [Pasteurella multocida]
MS1773	1767894	1767352	543	PM0845		1.00E-35	No-des	none	No-des	No-des	none	(NC_002663) TadE [Pasteurella multocida]
MS1774	1768689	1767925	765	PM0846		4.00E-78	Pmu	R	COG0457	TPR-repeat-containing proteins	NrfG	(AF237933) putative nonspecific tight a...
MS1775	1769560	1768685	876	PM0847		3.00E-76	Pmu	S	COG2064	Predicted membrane protein		(NC_002663) TadC [Pasteurella multocida]
MS1776	1770414	1769536	879	PM0848		1.00E-94	Pmu	I	COG2030	Predicted acyl dehydratase	MaoC	(AF152598) TadB [Actinobacillus actinom...
MS1777	1771691	1770414	1278	PM0849		0	Pmu	N	COG0630	Predicted ATPases involved in pili and flagella biosynthesis/VirB11 family	none	(NC_002663) TadA [Pasteurella multocida]
MS1778	1772828	1771710	1119	PM0850		1.00E-120	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS1779	1774223	1772850	1374	PM0852		1.00E-161	Pmu	N	COG1450	General secretory pathway protein D	GspD	(NC_002663) RcpA [Pasteurella multocida]
MS1780	1775036	1774263	774	PM0853		2.00E-46	No-des	none	No-des	No-des	none	(AF242856) RcpC [Actinobacillus actinom...
MS1781	1775573	1775076	498	PM0854		9.00E-31	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS1782	1775816	1775592	225	PM0855		6.00E-14	No-des	none	No-des	No-des	none	(AB071168) fimbrial protein Flp precursor [Actin...
MS1783	1779069	1776502	2568	PM1704		0	Pmu	O	COG0542	ATPases with chaperone activity/ATP-binding subunit	ClpA	(NC_002663) ClpB [Pasteurella multocida]
MS1784	1779305	1780126	822	PM1703		1.00E-133	Pmu	E	COG0253	Diaminopimelate epimerase	DapF	(NC_002663) DapF [Pasteurella multocida]
MS1785	1780198	1780908	711	PM1702		2.00E-71	Pmu	S	COG3159	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1786	1782387	1780957	1431	HI0975		0	Hin	E/H/R	COG0591	Na+/proline/Na+/panthothenate symporters and related permeases	PutP	(NC_000907) sodium/pantothenate symporter (panF...
MS1787	1782662	1782387	276	HI0974.1		3.00E-31	No-des	none	No-des	No-des	none	(NC_000907) conserved hypothetical protein [Hae...
MS1788	1784138	1782738	1401	HI0972		0	Hin	I	COG0439	Biotin carboxylase	AccC	(NC_000907) acetyl-CoA carboxylase/biotin carb...
MS1789	1784678	1784151	528	PM1092		2.00E-54	Pmu	I	COG0511	Biotin carboxyl carrier protein	AccB	(NC_002663) AccB [Pasteurella multocida]
MS1790	1785229	1784780	450	HI0970		2.00E-58	Hin	E	COG0757	3-dehydroquinate dehydratase II	AroQ	(NC_000907) 3-dehydroquinase (aroQ) [Haemophili...
MS1791	1786341	1785349	993	PM1094		1.00E-137	Pmu	H	COG1441	O-succinylbenzoate synthase and related enzymes	DgoA	(NC_002663) MenC [Pasteurella multocida]
MS1792	1787523	1786669	855	PM1096		1.00E-146	Pmu	H	COG0447	Dihydroxynaphthoic acid synthase	MenB	naphthoate synthase (EC 4.1.3.36) - Haemophilus para...
MS1793	1788373	1787612	762	HI0282		9.00E-87	Hin	R	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	MhpC	(NC_000907) conserved hypothetical protein [Hae...
MS1794	1790122	1788419	1704	PM0054		0	Pmu	H	COG1165	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	MenD	(NC_002663) MenD [Pasteurella multocida]
MS1795	1791441	1790116	1326	PM0053		1.00E-122	Pmu	H/Q	COG1169	Isochorismate synthase	MenF	(NC_002663) MenF [Pasteurella multocida]

MS1796	1791625	1791530	96	none	none	No-des	none	No-des	No-des	none	none
MS1797	1791667	1792878	1212	PM0052	0	Pmu	E	COG0436	PLP-dependent aminotransferases	AvtA	(NC_002663) unknown [Pasteurella multocida]
MS1798	1794178	1793036	1143	PM0094	1.00E-131	Pmu	G/E P/R	COG0477	Permeases of the major facilitator superfamily	ProP	(NC_002663) unknown [Pasteurella multocida]
MS1799	1794993	1794181	813	PM0095	7.00E-83	Pmu	E	COG0345	Pyroline-5-carboxylate reductase	ProC	(NC_002663) ProC [Pasteurella multocida]
MS1800	1795114	1796019	906	PM0096	1.00E-123	Pmu	L	COG2974	DNA recombination-dependent growth factor C	RdgC	(NC_002663) RdgC [Pasteurella multocida]
MS1801	1796241	1797446	1206	HI0225	1.00E-139	Hin	P	COG3004	Na ⁺ /H ⁺ antiporter	NhaA	(NC_000907) Na ⁺ /H ⁺ antiporter (nhaA) [Haemophil...
MS1802	1797700	1798869	1170	ZyiaY	1.00E-120	EcZ	C	COG1454	Alcohol dehydrogenase IV	EutG	(NC_002655) putative oxidoreductase [Escherichi...
MS1803	1799263	1799574	312	PA0979	9.00E-27	Pae	L	COG2963	Transposase		(NC_002516) conserved hypothetical protein [Pse...
MS1804	1799616	1800398	783	PA0978	6.00E-54	Pae	L	COG2801	Putative transposase	Tra5	(NC_002516) conserved hypothetical protein [Pse...
MS1805	1801067	1800396	672	PM1905	5.00E-58	Pmu	P	COG3338	Carbonic anhydrase	Cah	(NC_002663) unknown [Pasteurella multocida]
MS1806	1805250	1801360	3891	PM1085_1	0	Pmu	F	COG0046	Phosphoribosylformylglycinamide (FGAM) synthase/synthetase domain	PurL	(NC_002663) PurL [Pasteurella multocida]
MS1807	1805256	1805411	156	none	none	No-des	none	No-des	No-des	none	none
MS1808	1805490	1806992	1503	PM0045_1	1.00E-96	Pmu	E	COG0834	ABC-type amino acid transport system/periplasmic component	ArlI	(NC_002663) unknown [Pasteurella multocida]
MS1809	1806998	1807153	156	none	none	No-des	none	No-des	No-des	none	none
MS1810	1808433	1807228	1206	HI0933	1.00E-177	Hin	R	COG2081	Predicted flavoproteins		(NC_000907) conserved hypothetical transmembran...
MS1811	1809278	1808439	840	PM0030	3.00E-50	Pmu	R	COG0457	TPR-repeat-containing proteins	NrfG	(NC_002663) NrfF [Pasteurella multocida]
MS1812	1809745	1809278	468	HI0934_1	1.00E-37	Hin	O	COG3088	Uncharacterized protein involved in biosynthesis of c-type cytochromes	CcmH	CYTOCHROME C-TYPE BIOGENESIS PROTEIN NRFF P...
MS1813	1810276	1809749	528	HI0935	5.00E-55	Hin	O/C	COG0526	Thiol-disulfide isomerase and thioredoxins	TrxA	(NC_000907) thioldisulfide interchange protein...
MS1814	1810765	1810860	96	none	none	No-des	none	No-des	No-des	none	none
MS1815	1812215	1810284	1932	PM0027	0	Pmu	O	COG1138	Cytochrome c biogenesis factor	CcmF	(NC_002663) NrfE [Pasteurella multocida]
MS1816	1813269	1812301	969	HI1066	1.00E-145	Hin	P	COG3301	Formate-dependent nitrite reductase/membrane component	NrfD	(NC_000907) nitrite reductase/cytochrome pr...
MS1817	1813949	1813272	678	HI1067	1.00E-114	Hin	C	COG0437	Fe-S-cluster-containing hydrogenase components 1	HybA	(NC_000907) nitrite reductase/Fe-S protein (nr...
MS1818	1814593	1813949	645	HI1068	7.00E-71	No-des	none	No-des	No-des	none	(NC_000907) nitrite reductase/cytochrome C-typ...
MS1819	1816257	1814683	1575	HI1069	0	Hin	P	COG3303	Nitrite reductase/periplasmic cytochrome c subunit	NrfA	(NC_000907) nitrite reductase/cytochrome C552 ...
MS1820	1817634	1816744	891	PM1720	6.00E-93	Pmu	R	COG0457	TPR-repeat-containing proteins	NrfG	(NC_002663) unknown [Pasteurella multocida]
MS1821	1817753	1818733	981	HI0176	1.00E-162	Hin	J	COG0564	Pseudouridylyl synthases/23S RNA-specific	RluA	(NC_000907) sfhB protein (sfhB) [Haemophilus in...
MS1822	1818737	1819486	750	HI0175	2.00E-97	Hin	S	COG1496	Uncharacterized ACR		(NC_000907) conserved hypothetical protein [Hae...
MS1823	1820683	1819982	702	PM1696	6.00E-98	Pmu	S	COG0344	Predicted membrane protein		(NC_002663) unknown [Pasteurella multocida]
MS1824	1820720	1821073	354	PM1697	2.00E-52	Pmu	H	COG1539	Dihydroneopterin aldolase	FolB	(NC_002663) FolB [Pasteurella multocida]
MS1825	1821070	1821975	906	PM1698	1.00E-101	Pmu	G/E R	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	RhaT	(NC_002663) unknown [Pasteurella multocida]
MS1826	1823005	1822046	960	PM1930	1.00E-164	Pmu	H	COG0320	Lipote synthase	LipA	(NC_002663) LipA [Pasteurella multocida]
MS1827	1823723	1823013	711	PM1929	4.00E-94	Pmu	H	COG0321	Lipote-protein ligase B	LipB	(NC_002663) LipB [Pasteurella multocida]
MS1828	1824075	1823779	297	PM1928	4.00E-27	Pmu	S	COG2921	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS1829	1825440	1824259	1182	PM1927	0	Pmu	M	COG1686	D-alanyl-D-alanine carboxypeptidase	DacC	(NC_002663) DacA [Pasteurella multocida]
MS1830	1826171	1825587	585	HI0030	2.00E-53	Hin	M	COG0797	Lipoproteins	RlpA	(NC_000907) lipoprotein/putative [Haemophilus ...
MS1831	1827359	1826244	1116	HI0031	1.00E-154	Hin	D	COG0772	Bacterial cell division membrane protein	FtsW	(NC_000907) rod shape-determining protein (rodA...
MS1832	1829404	1827359	2046	PM1924	0	Pmu	M	COG0768	Cell division protein FtsI/penicillin-binding protein 2	FtsI	(NC_002663) Pbp2 [Pasteurella multocida]
MS1833	1829903	1829439	465	HI0033	2.00E-83	Hin	S	COG1576	Uncharacterized ACR		(NC_000907) conserved hypothetical protein [Hae...
MS1834	1830305	1830000	306	PM1922	8.00E-39	Pmu	S	COG0799	Uncharacterized ACR (homolog of plant lojap proteins)		(NC_002663) unknown [Pasteurella multocida]
MS1835	1831399	1830512	888	PM0259	2.00E-72	Pmu	F	COG0295	Cytidine deaminase	Cdd	(NC_002663) Cdd [Pasteurella multocida]
MS1836	1832825	1831575	1251	HI0892	1.00E-180	Hin	L K J	COG0513	Superfamily II DNA and RNA helicases	SrmB	(NC_000907) ATP-dependent RNA helicase (rhlB) [...
MS1837	1833030	1834385	1356	PM1920	0	Pmu	K	COG1158	Transcription termination factor	Rho	(NC_002663) Rho [Pasteurella multocida]
MS1838	1834419	1834529	111	none	none	No-des	none	No-des	No-des	none	none
MS1839	1835100	1834543	558	PM1168	2.00E-74	Pmu	H	COG0684	Demethylmenaquinone methyltransferase	MenG	(NC_002663) MenG [Pasteurella multocida]
MS1840	1836055	1835150	906	PM1169	5.00E-92	Pmu	H	COG1575	1[4-dihydroxy-2-naphthoate octaprenyltransferase	MenA	(AF101047) putative 1[4-dihydroxy-2-nap...
MS1841	1836061	1836873	813	PM1170	1.00E-101	Pmu	S	COG1720	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS1842	1837037	1836948	90	none	none	No-des	none	No-des	No-des	none	none
MS1843	1838967	1837102	1866	PM1979	0	Pmu	O	COG0760	Parvulin-like peptidyl-prolyl isomerase	SurA	(NC_002663) unknown [Pasteurella multocida]
MS1844	1841512	1839092	2421	PM1978	0	Pmu	O	COG0466	ATP-dependent Lon protease/bacterial type	Lon	(NC_002663) Lon [Pasteurella multocida]
MS1845	1841527	1841625	99	none	none	No-des	none	No-des	No-des	none	none
MS1846	1842880	1841645	1236	PM1977	0	Pmu	O	COG1219	ATP-dependent protease Clp/ATPase subunit	ClpX	(NC_002663) ClpX [Pasteurella multocida]
MS1847	1843476	1842898	579	PM1976	5.00E-86	Pmu	N/O	COG0740	Protease subunit of ATP-dependent Clp proteases	ClpP	(NC_002663) ClpP [Pasteurella multocida]
MS1848	1843644	1843528	117	none	none	No-des	none	No-des	No-des	none	none
MS1849	1845050	1843689	1362	PM1975	0	Pmu	O	COG0544	EKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)	Tig	(NC_002663) Tig [Pasteurella multocida]
MS1850	1845679	1845218	462	PM1974	2.00E-49	Pmu	S	COG1652	Uncharacterized BCR	XkdP (BS)	(NC_002663) unknown [Pasteurella multocida]
MS1851	1846153	1845791	363	PM1933	1.00E-49	Pmu	H	COG0190	5[10-methylene-tetrahydrofolate dehydrogenase	FolD	(NC_002663) FolD [Pasteurella multocida]
MS1852	1846639	1846190	450	PM1933	1.00E-67	Pmu	H	COG0190	5[10-methylene-tetrahydrofolate dehydrogenase	FolD	(NC_002663) FolD [Pasteurella multocida]
MS1853	1847053	1847151	99	none	none	No-des	none	No-des	No-des	none	none
MS1854	1848232	1847402	831	PM1973	1.00E-112	Pmu	R	COG2321	Predicted metalloprotease		(NC_002663) unknown [Pasteurella multocida]
MS1855	1848350	1849102	753	PM0186	1.00E-107	Pmu	R	COG0603	Predicted ATPase (PP-loop superfamily)/confers aluminum resistance		(NC_002663) unknown [Pasteurella multocida]

MS1856	1849119	1849544	426	HI1190	1.00E-62	Hin	H	COG0720	6-pyruvoyl-tetrahydropterin synthase			(NC_000907) 6-pyruvoyl tetrahydropterin synt...
MS1857	1849508	1850179	672	HI1189	2.00E-87	Hin	O	COG0602	Organic radical activating enzymes	NrdG		(NC_000907) conserved hypothetical protein [Hae...
MS1858	1850714	1850232	483	HI0899	5.00E-70	Hin	H	COG0262	Dihydrofolate reductase	FolA		(NC_000907) dihydrofolate reductase (folA) [Hae...
MS1859	1851212	1850751	462	PM1894	2.00E-56	Pmu	S	COG3610	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS1860	1852001	1851216	786	PM1895	1.00E-101	Pmu	S	COG2966	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS1861	1852132	1852236	105	none	none	No-des	none	No-des	No-des	none	none	
MS1862	1852239	1853321	1083	PM1896	1.00E-169	Pmu	E	COG0263	Glutamate 5-kinase	ProB		Glutamate 5-kinase (Gamma-glutamyl kinase) ...
MS1863	1854084	1853455	630	PM1898	3.00E-80	Pmu	O	COG0545	FKBP-type peptidyl-prolyl cis-trans isomerases I	FkpA		(NC_002663) unknown [Pasteurella multocida]
MS1864	1855084	1854182	903	PM1899	1.00E-130	Pmu	I	COG0688	Phosphatidylserine decarboxylase	Psd		(NC_002663) Psd [Pasteurella multocida]
MS1865	1855396	1855190	207	none	none	No-des	none	No-des	No-des	none	none	
MS1866	1855477	1855575	99	none	none	No-des	none	No-des	No-des	none	none	
MS1867	1855457	1855639	183	none	none	No-des	none	No-des	No-des	none	none	
MS1868	1855690	1856211	522	HI0159	2.00E-81	Hin	R	COG1399	Predicted metal-binding(possibly nucleic acid-binding protein			(NC_000907) conserved hypothetical protein [Hae...
MS1869	1856232	1856399	168	HI0158	6.00E-20	Hin	J	COG0333	Ribosomal protein L32	RpmF		(NC_000907) ribosomal protein L32 (rpl32) [Haem...
MS1870	1856430	1857443	1014	PM1913	1.00E-149	Pmu	I	COG0416	Fatty acid/phospholipid biosynthesis enzyme	PlsX		(NC_002663) PlsX [Pasteurella multocida]
MS1871	1857487	1858305	819	HI0157	1.00E-109	Hin	I	COG0332	3-oxoacyl-acyl-carrier-protein synthase III	FabH		(NC_000907) beta-ketoacyl-ACP synthase III (fab...
MS1872	1858262	1858435	174	HI0157	2.00E-25	Hin	I	COG0332	3-oxoacyl-acyl-carrier-protein synthase III	FabH		(NC_000907) beta-ketoacyl-ACP synthase III (fab...
MS1873	1858503	1859438	936	PM1915	1.00E-130	Pmu	I	COG0331	(acyl-carrier-protein) S-malonyltransferase	FabD		(NC_002663) FabD [Pasteurella multocida]
MS1874	1859531	1860256	726	HI0155	1.00E-118	Hin	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	FabG		(NC_000907) 3-ketoacyl-acyl carrier protein red...
MS1875	1860520	1860747	228	PM1917	4.00E-24	Pmu	I/Q	COG0236	Acyl carrier protein	AcpP		(NC_002663) AcpP [Pasteurella multocida]
MS1876	1860985	1860872	114	none	none	No-des	none	No-des	No-des	none	none	
MS1877	1860984	1862330	1347	HIN1287	0	Hin	R	COG2704	Anaerobic C4-dicarboxylate transporter	DcuB		(NC_000907) Anaerobic C4-dicarboxylate transpor...
MS1878	1863101	1862406	696	PM0017	3.00E-95	Pmu	L	COG0593	ATPase involved in DNA replication initiation	DnaA		(NC_002663) unknown [Pasteurella multocida]
MS1879	1864425	1863187	1239	PM0018	0	Pmu	F	COG2233	Xanthine/uracil permeases	UraA		(NC_002663) UraA [Pasteurella multocida]
MS1880	1865095	1864472	624	PM0019	1.00E-105	Pmu	F	COG0035	Uracil phosphoribosyltransferase	Upp		(NC_002663) Upp [Pasteurella multocida]
MS1881	1865881	1865243	639	PM1206_1	8.00E-45	Pmu	E	COG0139	Phosphoribosyl-AMP cyclohydrolase	HisI		(NC_000907) phosphoribosyl-AMP cyclohydrolase /...
MS1882	1866763	1865993	771	PM1204	1.00E-132	Pmu	E	COG0107	Imidazoleglycerol-phosphate synthase	HisF		(NC_002663) HisF [Pasteurella multocida]
MS1883	1867494	1866748	747	HI0473	1.00E-115	Hin	E	COG0106	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase	HisA		(NC_000907) phosphoribosylformimino-5-aminoimid...
MS1884	1868210	1867512	699	HI0279+8	2.00E-62	No-des	none	No-des	No-des	none	none	(NC_000907) Uncharacterized BCR [Haemophilus in...
MS1885	1868794	1868213	582	HI0472	7.00E-79	Hin	E	COG0118	Glutamine amidotransferase	HisH		(NC_000907) amidotransferase (hisH) [Haemophilu...
MS1886	1869742	1868816	927	VCA0458	3.00E-10	No-des	none	No-des	No-des	none	none	(NC_002506) hypothetical protein [Vibrio cholera...
MS1887	1870719	1870186	534	none	none	No-des	none	No-des	No-des	none	none	
MS1888	1871731	1870982	750	MPN562	2.00E-39	Mpn	H	COG0171	NAD synthase	NadE		hypothetical protein - Mycoplasma capricolum (SGC3) ...
MS1889	1873167	1871731	1437	BS_yueK	1.00E-111	Bsu	H	COG1488	Nicotinic acid phosphoribosyltransferase	PncB		(NC_003030) Nicotinic acid phosphoribosyltransf...
MS1890	1874467	1873373	1095	PM1200_2	3.00E-96	Pmu	E	COG0131	Imidazoleglycerol-phosphate dehydratase	HisB		(NC_002663) HisB [Pasteurella multocida]
MS1891	1875617	1874568	1050	PM1199	1.00E-145	Pmu	E	COG0079	Histidinol-phosphate aminotransferase/Tyrosine aminotransferase	HisC		(NC_002663) HisH [Pasteurella multocida]
MS1892	1876934	1875651	1284	PM1198	1.00E-174	Pmu	E	COG0141	Histidinol dehydrogenase	HisD		(NC_002663) HisD [Pasteurella multocida]
MS1893	1877909	1877013	897	PM1195	1.00E-135	Pmu	E	COG0040	ATP phosphoribosyltransferase (histidine biosynthesis)	HisG		(NC_002663) HisG [Pasteurella multocida]
MS1894	1878955	1878191	765	PM1194	1.00E-99	Pmu	Q/R	COG0500	SAM-dependent methyltransferases	SmtA		(NC_002663) unknown [Pasteurella multocida]
MS1895	1880343	1879030	1314	HI0287	1.00E-162	Hin	E	COG0814	Amino acid permeases	SdaC		(NC_000907) tryptophan-specific transport prote...
MS1896	1881120	1880467	654	PM1293	4.00E-47	Pmu	R	COG2364	Uncharacterized membrane protein			(NC_002663) unknown [Pasteurella multocida]
MS1897	1881345	1882607	1263	PM1292	0	Pmu	F	COG1972	Nucleoside permease	NupC		(NC_002663) unknown [Pasteurella multocida]
MS1898	1882747	1882616	132	none	none	No-des	none	No-des	No-des	none	none	
MS1899	1882762	1883475	714	PM1291	1.00E-121	Pmu	F	COG0813	Purine-nucleoside phosphorylase	DeoD		(NC_002663) DeoD [Pasteurella multocida]
MS1900	1883556	1883464	93	none	none	No-des	none	No-des	No-des	none	none	
MS1901	1883479	1883583	105	none	none	No-des	none	No-des	No-des	none	none	
MS1902	1883605	1884480	876	HI0271	1.00E-101	Hin	O	COG1076	DnaJ-domain-containing proteins I	DjIA		(NC_000907) conserved hypothetical protein [Hae...
MS1903	1884474	1885094	621	PM1879	4.00E-81	Pmu	S	COG3647	Predicted membrane protein			(NC_002663) unknown [Pasteurella multocida]
MS1904	1885097	1886029	933	HI0270	1.00E-135	Hin	R	COG0042	Predicted TIM-barrel enzymes(possibly dehydrogenases/nirR3 family			(NC_000907) conserved hypothetical protein [Hae...
MS1905	1886029	1886484	456	PM1881	4.00E-53	Pmu	R	COG1011	Predicted hydrolases of the HAD superfamily			(NC_002663) unknown [Pasteurella multocida]
MS1906	1886261	1886680	420	PM1881	4.00E-45	Pmu	R	COG1011	Predicted hydrolases of the HAD superfamily			(NC_002663) unknown [Pasteurella multocida]
MS1907	1887125	1886769	357	none	none	No-des	none	No-des	No-des	none	none	
MS1908	1888151	1887165	987	PM1882	0	Pmu	F/R	COG0402	Cytosine deaminase and related metal-dependent hydrolases	SsnA		(NC_002663) unknown [Pasteurella multocida]
MS1909	1890201	1888423	1779	PM1883	0	Pmu	R	COG3083	Predicted hydrolase of alkaline phosphatase superfamily			(NC_002663) unknown [Pasteurella multocida]
MS1910	1890457	1890230	228	PM1884	1.00E-24	Pmu	S	COG3082	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS1911	1890617	1891681	1065	HI0839	1.00E-137	Hin	R	COG3081	Nucleoid-associated protein			(NC_000907) conserved hypothetical protein [Hae...
MS1912	1891759	1892169	411	PM1886	4.00E-45	Pmu	J	COG2913	Small protein A (tmRNA-binding)	SmpA		(NC_002663) unknown [Pasteurella multocida]
MS1913	1892191	1892895	705	PM1887	2.00E-77	Pmu	T/K	COG0745	Response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain	OmpR		(NC_002663) CpxR [Pasteurella multocida]
MS1914	1892931	1894319	1389	PM1888	1.00E-114	Pmu	T	COG0642	Sensory transduction histidine kinases	BaeS		(NC_002663) CpxA [Pasteurella multocida]
MS1915	1895869	1894460	1410	PM1167	1.00E-165	Pmu	P	COG0471	Di- and tricarboxylate transporters	CitT		(NC_002663) unknown [Pasteurella multocida]

MS1916	1896233	1897345	1113	HI0365		0	Hin	R	COG0820	Predicted Fe-S-cluster redox enzyme		(NC_002663) unknown [Pasteurella multocida]
MS1917	1897388	1897951	564	PM2008	8.00E-46		Pnu	N	COG3063	Uncharacterized protein involved in fimbrial biogenesis	PilF	(NC_002663) unknown [Pasteurella multocida]
MS1918	1898107	1899078	972	PM2009	9.00E-77		Pmu	S	COG1426	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1919	1899094	1900197	1104	HI0368	0		Hin	M	COG0821	Essential bacterial protein[involved in density-dependent regulation of peptidoglycan biosynthesis]	GcpE	(NC_000907) gcpE protein (gcpE) [Haemophilus in...]
MS1920	1900257	1901537	1281	PM2011	0		Pmu	J	COG0124	Histidyl-tRNA synthetase	HisS	(NC_002663) HisS [Pasteurella multocida]
MS1921	1901544	1902155	612	PM2012	2.00E-44		Pnu	S	COG2976	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1922	1903405	1902383	1023	PM1994	1.00E-160		Pmu	M	COG1044	UDP-3-O-3-hydroxymyristoyl glucosamine N-acyltransferase	LpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltrans...
MS1923	1903947	1903408	540	HI0916	1.00E-47		Hin	M	COG2825	Outer membrane protein	HlpA	(AF109088) outer membrane protein 26 [H...
MS1924	1906427	1904061	2367	PM1992	0		Pmu	M	COG0729	Predicted outer membrane protein		(NC_002663) unknown [Pasteurella multocida]
MS1925	1907791	1906466	1326	PM1991	1.00E-174		Pnu	M	COG0750	Predicted membrane-associated Zn-dependent proteases 1		(U60831) ORF3 [Haemophilus influenzae]
MS1926	1908673	1907810	864	HI0919	3.00E-87		Hin	I	COG0575	CDP-diglyceride synthetase	CdsA	(U60831) CDP diglyceride synthetase [Haemophilus ...]
MS1927	1909410	1908697	714	PM1989	1.00E-105		Pmu	I	COG0020	Undecaprenyl pyrophosphate synthase	UppS	(NC_002663) unknown [Pasteurella multocida]
MS1928	1910729	1909497	1233	PM1988	0		Pmu	I	COG0743	1-deoxy-D-xylulose 5-phosphate reductoisomerase	Dxr	(NC_002663) Dxr [Pasteurella multocida]
MS1929	1911359	1910805	555	HI0808	1.00E-92		Hin	J	COG0233	Ribosome recycling factor	Fir	(NC_000907) ribosome releasing factor (rrf) [Ha...
MS1930	1912150	1911428	723	PM1986	1.00E-121		Pmu	F	COG0528	Uridylate kinase	PyrH	(NC_002663) PyrH [Pasteurella multocida]
MS1931	1912272	1913828	1557	HI1064	1.00E-130		Hin	R	COG2194	Predicted membrane-associated/metal-dependent hydrolase		(NC_000907) conserved hypothetical protein [Hae...
MS1932	1914795	1913953	843	HI0914	1.00E-129		Hin	J	COG0264	Translation elongation factor Ts	Tsf	(NC_000907) elongation factor Ts (tsf) [Haemoph...
MS1933	1915787	1915020	768	PM1984	1.00E-124		Pnu	J	COG0052	Ribosomal protein S2	RpsB	(NC_002663) RpsB [Pasteurella multocida]
MS1934	1916714	1916034	681	PM1157	4.00E-94		Pmu	T	COG0664	cAMP-binding domains - Catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	Crp	(L47539) cyclic AMP receptor protein [Haemophilus...]
MS1935	1916972	1916769	204	PM1156	7.00E-21		Pmu	S	COG3089	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1936	1917632	1916985	648	HI0955	1.00E-90		Hin	K	COG1309	Transcriptional regulator	AcrR	(NC_000907) transcriptional regulator (tkk) [Ha...
MS1937	1918091	1917639	453	HI0954	1.00E-77		Hin	F	COG0756	dUTPase	Dut	(NC_000907) deoxyuridinetriphosphatase (dut) [H...
MS1938	1919375	1918134	1242	PM1153	1.00E-163		Pmu	H	COG0452	Phosphopantothencysteine synthetase/decarboxylase	Dfp	(NC_002663) Dfp [Pasteurella multocida]
MS1939	1919773	1919339	435	HI0952	2.00E-19		Hin	L	COG2003	DNA repair proteins	RadC	(NC_000907) DNA repair protein (radC) [Haemophi...
MS1940	1919481	1919792	312	PM1152	3.00E-23		Pmu	L	COG2003	DNA repair proteins	RadC	(NC_002663) RadC [Pasteurella multocida]
MS1941	1919792	1920124	333	PM1152	3.00E-34		Pmu	L	COG2003	DNA repair proteins	RadC	(NC_002663) RadC [Pasteurella multocida]
MS1942	1920430	1920675	246	HI0951	4.00E-39		Hin	J	COG0227	Ribosomal protein L28	RpmB	(NC_000907) ribosomal protein L28 (rpl28) [Haem...
MS1943	1920690	1920857	168	HI0950	5.00E-26		Hin	J	COG0267	Ribosomal protein L33	RpmG	(NC_000907) ribosomal protein L33 (rpl33) [Haem...
MS1944	1920874	1921749	876	PM1145	1.00E-123		Pmu	L	COG0266	Formamidopyrimidine-DNA glycosylase	Nei	(NC_002663) Fpg [Pasteurella multocida]
MS1945	1921762	1921872	111	HI0753	1.00E-06		Hin	S	COG2377	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1946	1922912	1921788	1125	PM1831	1.00E-141		Pmu	S	COG2377	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1947	1923099	1923248	150	none	none	No-des	none	none	No-des		none	none
MS1948	1923086	1923412	327	none	none	No-des	none	none	No-des		none	none
MS1949	1923454	1924824	1371	HI0642	0		Hin	M	COG1207	N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)	GlmU	(NC_000907) UDP-N-acetylglucosamine pyrophospho...
MS1950	1924874	1926259	1386	PM1840	0		Pmu	L K J	COG0513	Superfamily II DNA and RNA helicases	SrmB	(NC_002663) SrmB [Pasteurella multocida]
MS1951	1926873	1926397	477	PM1304	2.00E-60		Pmu	H	COG0669	Phosphopantetheine adenylyltransferase	CoaD	(NC_002663) KdtB [Pasteurella multocida]
MS1952	1928150	1926873	1278	PM1305	1.00E-173		Pmu	M	COG1519	3-Deoxy-D-manno-octulosonic-acid transferase	KdtA	(NC_002663) KdtA [Pasteurella multocida]
MS1953	1928358	1929296	939	HI0927	1.00E-164		Hin	J	COG0752	Glycyl-tRNA synthetase/alpha subunit	GlyQ	(NC_000907) glycyl-tRNA synthetase/alpha chain...
MS1954	1929423	1929794	372	HI0925	5.00E-54		Hin	S	COG2852	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1955	1930074	1930679	606	PM1603	2.00E-46		No-des	none	No-des		none	(NC_002663) unknown [Pasteurella multocida]
MS1956	1930734	1932800	2067	PM1102	0		Pmu	J	COG0751	Glycyl-tRNA synthetase/beta subunit	GlyS	(NC_002663) GlyS [Pasteurella multocida]
MS1957	1933207	1932863	345	NMB1027_2	3.00E-10		Nme	S	COG3671	Predicted membrane protein		(NC_003112) dnaJ protein [Neisseria meningitidi...
MS1958	1934286	1933222	1065	PM1131	1.00E-118		Pmu	R	COG0628	Predicted permease	PerM	(NC_002663) PerM [Pasteurella multocida]
MS1959	1934457	1934804	348	HI0236	7.00E-37		Hin	P	COG1393	Arsenate reductase and related proteins glutaredoxin family	ArsC	(NC_000907) arsenate reductase putative [Haemo...
MS1960	1934844	1935146	303	PM1129	6.00E-23		Pmu	S	COG3036	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS1961	1935186	1935500	315	PM1128	1.00E-38		No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS1962	1936666	1935626	1041	PM1302	1.00E-156		Pmu	M	COG0859	ADP-heptoseLPS heptosyltransferase	RfaF	(NC_002663) OpxS [Pasteurella multocida]
MS1963	1936649	1936741	93	none	none	No-des	none	none	No-des		none	none
MS1964	1936741	1937472	732	PM1303	1.00E-91		Pmu	T	COG0515	Serine/threonine protein kinases	SPS1	(NC_002663) unknown [Pasteurella multocida]
MS1965	1938202	1937513	690	apqZ	2.00E-98		Eco	G	COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	GlpF	(NC_000913) transmembrane water channel; aquapo...
MS1966	1938374	1938745	372	PM1290	5.00E-54		Pmu	E K	COG3060	Transcriptional regulator of met regulon	MetJ	(NC_002663) MetJ [Pasteurella multocida]
MS1967	1939664	1938822	843	PM1222	1.00E-117		Pmu	L	COG0338	Site-specific DNA methylase	Dam	(AF263926) DNA-adenine methyltransferas...
MS1968	1940765	1939680	1086	PM1223	1.00E-173		Pmu	E	COG0337	3-dehydroquinate synthetase	AroB	(NC_002663) AroB [Pasteurella multocida]
MS1969	1941376	1940798	579	PM1224	7.00E-84		Pmu	E	COG0703	Shikimate kinase	AroK	(NC_002663) AroK [Pasteurella multocida]
MS1970	1942952	1941519	1434	HI0435	1.00E-147		Hin	N	COG1450	General secretory pathway protein D	GspD	(NC_000907) competence protein E (comE) [Haemop...
MS1971	1943326	1942919	408	PM1226	3.00E-09		No-des	none	No-des		none	(NC_002663) ComD [Pasteurella multocida]
MS1972	1943862	1943332	531	HI0437	2.00E-08		No-des	none	No-des	No-des	none	(NC_000907) competence protein C (comC) [Haemop...
MS1973	1944355	1943822	534	HI0438	3.00E-14		No-des	none	No-des	No-des	none	(NC_000907) competence protein B (comB) [Haemop...
MS1974	1945184	1944360	825	HI0439	3.00E-32		No-des	none	No-des	No-des	none	(NC_000907) competence protein A (comA) [Haemop...
MS1975	1945338	1947956	2619	HI0440	0		Hin	M	COG0744	Membrane carboxypeptidase (penicillin-binding protein)	MrcA	(NC_000907) penicillin-binding protein 1A (ponA...

MS1976	1948101	1948943	843	PM1234	1.00E-142	Pmu	S	COG2961	Uncharacterized BCR		(NC_002663) OrfJ [Pasteurella multocida]
MS1977	1950484	1949081	1404	ygbN	7.00E-87	Eco	GIE	COG2610	H ⁺ /gluconate symporter and related permeases	GntT	(AF242209) putative transport protein [...]
MS1978	1951337	1950543	795	HI1013	1.00E-115	Hin	G	COG3622	Hydroxypyruvate isomerase	Hfi	(NC_000907) conserved hypothetical protein [Hae...
MS1979	1951950	1951321	630	HI1012	1.00E-103	Hin	G	COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	AraD	(NC_000907) sugar isomerase/putative [Haemophi...
MS1980	1953191	1951950	1242	HI1011	0	Hin	S	COG3395	Uncharacterized BCR		(NC_000907) conserved hypothetical protein [Hae...
MS1981	1954137	1953196	942	HI1010	1.00E-128	Hin	I	COG2084	3-hydroxyisobutyrate dehydrogenase and related proteins	MmsB	(NC_000907) 3-hydroxyisobutyrate dehydrogenase/...
MS1982	1954117	1954242	126	none	none	No-des	none	No-des	No-des	none	none
MS1983	1954299	1955054	756	HI1009	2.00E-87	Hin	KIG	COG1349	Transcriptional regulators of sugar metabolism	GlpR	(NC_000907) glycerol-3-phosphate regulon repres...
MS1984	1956557	1955142	1416	HI0534	0	Hin	E	COG1027	Aspartate ammonia-lyase	AspA	(NC_000907) aspartate ammonia-lyase (aspA) [Hae...
MS1985	1956834	1958201	1368	PM1235	0	Pmu	C	COG1249	Dihydrolipoamide dehydrogenase/glutathione oxidoreductase and related enzymes	Lpd	(NC_002663) Gor [Pasteurella multocida]
MS1986	1958245	1958340	96	none	none	No-des	none	No-des	No-des	none	none
MS1987	1958348	1959259	912	HI0754	1.00E-115	Hin	R	COG2103	Predicted sugar phosphate isomerase		(NC_000907) conserved hypothetical protein [Hae...
MS1988	1960868	1959318	1551	HI0691	0	Hin	C	COG0554	Glycerol kinase	GlpK	(NC_000907) glycerol kinase (glpK) [Haemophilus...
MS1989	1960861	1960953	93	none	none	No-des	none	No-des	No-des	none	none
MS1990	1961030	1961920	891	TM1429	2.00E-64	Tma	G	COG0580	Glycerol uptake facilitator and related permeases (Major Intrinsic Protein Family)	GlpF	(NC_000853) glycerol uptake facilitator protein...
MS1991	1962244	1963698	1455	PM1443	0	Pmu	G	COG2271	Sugar phosphate permease	UhpC	(NC_002663) GlpT [Pasteurella multocida]
MS1992	1963831	1964934	1104	PM1444	1.00E-176	Pmu	C	COG0584	Glycerophosphoryl diester phosphodiesterase	UgpQ	(NC_002663) GlpQ [Pasteurella multocida]
MS1993	1965084	1966823	1740	HI0685	0	Hin	C	COG0578	Glycerol-3-phosphate dehydrogenase	GlpA	(NC_000907) anaerobic glycerol-3-phosphate dehy...
MS1994	1966816	1968108	1293	PM1441	1.00E-159	Pmu	E	COG3075	Anaerobic glycerol-3-phosphate dehydrogenase	GlpB	(NC_002663) GlpB [Pasteurella multocida]
MS1995	1968121	1969395	1275	HI0683	0	Hin	C	COG0247	Fe-S oxidoreductases	GlpC	(NC_000907) anaerobic glycerol-3-phosphate dehy...
MS1996	1969510	1969382	129	none	none	No-des	none	No-des	No-des	none	none
MS1997	1969602	1970216	615	HI1118	1.00E-99	Hin	R	COG0218	Predicted GTPases		(NC_000907) conserved hypothetical GTP-binding ...
MS1998	1970356	1971225	870	HI1117	1.00E-123	Hin	O	COG0606	Predicted ATPase with chaperone activity		(NC_000907) competence protein (comM) [Haemophi...
MS1999	1971320	1973128	1809	none	none	No-des	none	No-des	No-des	none	none
MS2000	1973140	1973694	555	none	none	No-des	none	No-des	No-des	none	none
MS2001	1973688	1973984	297	none	none	No-des	none	No-des	No-des	none	(NC_003062) AGR_C_3631p [Agrobacterium tumefaci...
MS2002	1974355	1974200	156	none	none	No-des	none	No-des	No-des	none	none
MS2003	1974734	1974351	384	none	none	No-des	none	No-des	No-des	none	none
MS2004	1975128	1974724	405	none	none	No-des	none	No-des	No-des	none	none
MS2005	1975508	1976143	636	none	none	No-des	none	No-des	No-des	none	(U21300) transposase [Corynebacterium striatum]
MS2006	1977172	1976342	831	PA1138	1.00E-22	Pae	K	COG0583	Transcriptional regulator	LysR	(NC_002147) Hypothetical gene [Agrobacterium tu...
MS2007	1977278	1977922	645	DR0659	5.00E-37	Dra	Q	COG2761	Predicted dithiol-disulfide isomerase involved in polyketide biosynthesis	FrnE	(NC_001263) frnE protein [Deinococcus radiodura...
MS2008	1978920	1977991	930	PA1138	7.00E-26	Pae	K	COG0583	Transcriptional regulator	LysR	(NC_003296) PROBABLE TRANSCRIPTIONAL REGULATO...
MS2009	1978971	1979384	414	BS_yusQ	3.00E-08	No-des	none	No-des	No-des	none	(NC_000964) similar to acylate catabolism [Bac...
MS2010	1979417	1980583	1167	L133858	1.00E-61	Lla	C	COG1902	NADHflavin oxidoreductases/Old Yellow Enzyme family	NemA	(NC_002662) NADH-dependent oxidoreductase [Lact...
MS2011	1980599	1981615	1017	mlr1349	3.00E-33	Mlo	R	COG0491	Zn-dependent hydrolases/including glyoxylases	GloB	(NC_003295) CONSERVED HYPOTHETICAL PROTEIN [Ra...
MS2012	1982105	1982947	843	BS_yqjM	8.00E-52	Bsu	C	COG1902	NADHflavin oxidoreductases/Old Yellow Enzyme family	NemA	(NC_003210) similar to NADH oxidase [Listeria m...
MS2013	1984526	1983069	1458	none	none	No-des	none	No-des	No-des	none	(AF277901) zinc finger protein HIT-10 [Rattus nor...
MS2014	1985605	1984490	1116	mlI9366	5.00E-07	No-des	none	No-des	No-des	none	(NC_002679) unknown protein [Mesorhizobium loti...
MS2015	1986450	1985566	885	mlr6274	7.00E-33	No-des	none	No-des	No-des	none	(Y17897) uiiB protein [Pseudomonas sp. ED23-33]
MS2016	1988405	1986453	1953	mlr6273	7.00E-73	Mlo	L	COG1425	Predicted transposase		(NC_003122) TniA protein [Plasmid pSB102]
MS2017	1989030	1988371	660	none	none	No-des	none	No-des	No-des	none	none
MS2018	1989165	1989863	699	PM1510	1.00E-105	Pmu	O	COG0606	Predicted ATPase with chaperone activity		(NC_002663) ComM [Pasteurella multocida]
MS2019	1990190	1992448	2259	PM0392	0	Pmu	S	COG1289	Uncharacterized membrane protein		(NC_002663) unknown [Pasteurella multocida]
MS2020	1992651	1992481	171	none	none	No-des	none	No-des	No-des	none	none
MS2021	1992695	1992600	96	none	none	No-des	none	No-des	No-des	none	none
MS2022	1993175	1992795	381	PM1389	4.00E-63	Pmu	J	COG0203	Ribosomal protein L17	RplQ	(NC_002663) Rpl17 [Pasteurella multocida]
MS2023	1994200	1993214	987	PM1390	0	Pmu	K	COG0202	DNA-directed RNA polymerase alpha subunit/40 kD subunit	RpoA	(NC_002663) RpoA [Pasteurella multocida]
MS2024	1994853	1994236	618	PM1391	1.00E-111	Pmu	J	COG0522	Ribosomal protein S4 and related proteins	RpsD	(NC_002663) Rps4 [Pasteurella multocida]
MS2025	1995272	1994886	387	PM1392	9.00E-55	Pmu	J	COG0100	Ribosomal protein S11	RpsK	(NC_002663) Rps11 [Pasteurella multocida]
MS2026	1995644	1995291	354	PM1393	7.00E-61	Pmu	J	COG0099	Ribosomal protein S13	RpsM	(NC_002663) Rps13 [Pasteurella multocida]
MS2027	1995897	1995787	111	PM1394	2.00E-15	Pmu	J	COG0257	Ribosomal protein L36	RpmJ	(NC_002663) Rpl36 [Pasteurella multocida]
MS2028	1997250	1995928	1323	PM1395	0	Pmu	N	COG0201	Preprotein translocase subunit SecY	SecY	(NC_002663) SecY [Pasteurella multocida]
MS2029	1997692	1997261	432	HI0797	3.00E-39	Hin	J	COG0200	Ribosomal protein L15	RplO	(NC_000907) ribosomal protein L15 (rpl15) [Haem...
MS2030	1997882	1997700	183	PM1397	2.00E-27	Pmu	J	COG1841	Ribosomal protein L30/L7E	RpmD	(NC_002663) Rpl30 [Pasteurella multocida]
MS2031	1998383	1997886	498	PM1398	1.00E-86	Pmu	J	COG0098	Ribosomal protein S5	RpsE	(NC_002663) Rps5 [Pasteurella multocida]
MS2032	1998752	1998402	351	PM1399	3.00E-52	Pmu	J	COG0256	Ribosomal protein L18	RplR	(NC_002663) Rpl18 [Pasteurella multocida]
MS2033	1999299	1998769	531	PM1400	7.00E-86	Pmu	J	COG0097	Ribosomal protein L6	RplF	(NC_002663) Rpl6 [Pasteurella multocida]
MS2034	1999707	1999318	390	HI0792	4.00E-66	Hin	J	COG0096	Ribosomal protein S8	RpsH	(NC_000907) ribosomal protein S8 (rps8) [Haemop...
MS2035	2000049	1999747	303	HI0791	2.00E-50	Hin	J	COG0199	Ribosomal protein S14	RpsN	(NC_000907) ribosomal protein S14 (rps14) [Haem...

MS2036	2000600	2000064	537	PM1403	6.00E-96	Pmu	J	COG0094	Ribosomal protein L5	RplE	(NC_002663) Rpl5 [Pasteurella multocida]
MS2037	2000929	2000621	309	PM1404	2.00E-51	Pmu	J	COG0198	Ribosomal protein L24	RplX	(NC_002663) Rpl24 [Pasteurella multocida]
MS2038	2001503	2001396	108	none	none	No-des	none	No-des	none	none	
MS2039	2001829	2001575	255	PM1406	1.00E-38	Pmu	J	COG0186	Ribosomal protein S17	RpsQ	(NC_002663) Rps17 [Pasteurella multocida]
MS2040	2002020	2001832	189	PM1407	9.00E-26	Pmu	J	COG0255	Ribosomal protein L29	RpmC	(NC_002663) Rpl29 [Pasteurella multocida]
MS2041	2002430	2002023	408	PM1408	1.00E-64	Pmu	J	COG0197	Ribosomal protein L16/L10E	RplP	(NC_002663) Rpl16 [Pasteurella multocida]
MS2042	2003184	2002447	738	PM1409	1.00E-116	Pmu	J	COG0092	Ribosomal protein S3	RpsC	(NC_002663) Rps3 [Pasteurella multocida]
MS2043	2003500	2003171	330	PM1410	9.00E-48	Pmu	J	COG0091	Ribosomal protein L22	RplV	(NC_002663) Rpl22 [Pasteurella multocida]
MS2044	2003786	2003514	273	PM1411	3.00E-48	Pmu	J	COG0185	Ribosomal protein S19	RpsS	(NC_002663) Rps19 [Pasteurella multocida]
MS2045	2004633	2003815	819	PM1412	1.00E-156	Pmu	J	COG0090	Ribosomal protein L2	RplB	(NC_002663) Rpl2 [Pasteurella multocida]
MS2046	2004959	2004657	303	PM1413	5.00E-35	Pmu	J	COG0089	Ribosomal protein L23	RplW	(NC_002663) Rpl23 [Pasteurella multocida]
MS2047	2005558	2004959	600	PM1414	1.00E-104	Pmu	J	COG0088	Ribosomal protein L4	RplD	50S RIBOSOMAL PROTEIN L4
MS2048	2006200	2005577	624	HI0777	1.00E-111	Hin	J	COG0087	Ribosomal protein L3	RplC	(NC_000907) ribosomal protein L3 (rpl3) [Haemophilus influenzae]
MS2049	2006585	2006220	366	HI0776	2.00E-59	Hin	J	COG0051	Ribosomal protein S10	RpsJ	(NC_000907) ribosomal protein S10 (rps10) [Haemophilus influenzae]
MS2050	2007927	2006863	1065	HI0745	1.00E-139	Hin	EJ	COG0252	L-asparaginase/archaeal Glu-tRNA ^{Gln} amidotransferase subunit D	AnsB	(NC_000907) L-asparaginase II (ansB) [Haemophilus influenzae]
MS2051	2008101	2009483	1383	PM1417	1.00E-168	Pmu	P	COG0038	Chloride channel protein EriC	EriC	(NC_002663) unknown [Pasteurella multocida]
MS2052	2009544	2010524	81	HI0634	1.00E-167	Hin	R	COG0042	Predicted TIM-barrel enzymes/possibly dehydrogenases/nirR3 family		(NC_000907) conserved hypothetical protein [Haemophilus influenzae]
MS2053	2012286	2010688	1599	PM0592	0	Pmu	EP	COG0747	ABC-type dipeptide/oligopeptide/nickel transport systems/periplasmic components	OppA	(NC_002663) HbpA [Pasteurella multocida]
MS2054	2013769	2012381	1389	PM1784	1.00E-145	Pmu	GE PR	COG0477	Permeases of the major facilitator superfamily	ProP	(NC_002663) unknown [Pasteurella multocida]
MS2055	2013878	2013786	93	none	none	No-des	none	No-des	none	none	
MS2056	2014359	2013799	561	PM1785	1.00E-63	Pmu	H	COG1763	Molybdopterin-guanine dinucleotide biosynthesis protein	MobB	(NC_002663) MobB [Pasteurella multocida]
MS2057	2014996	2014427	570	PM1799	3.00E-68	Pmu	H	COG0746	Molybdopterin-guanine dinucleotide biosynthesis protein A	MobA	(NC_002663) MobA [Pasteurella multocida]
MS2058	2015073	2015336	264	PM1800	3.00E-40	Pmu	S	COG3084	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS2059	2015323	2015979	657	HI0846	5.00E-74	Hin	OIC	COG0526	Thiol-disulfide isomerase and thioredoxins	TrxA	(NC_000907) periplasmic oxidoreductase (por) [Haemophilus influenzae]
MS2060	2016053	2016379	327	PM1802	2.00E-48	Pmu	S	COG3085	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS2061	2016479	2016369	111	none	none	No-des	none	No-des	none	none	
MS2062	2016744	2016460	285	BS_ycnE	7.00E-09	Bsu	S	COG1359	Uncharacterized ACR		(NC_000964) similar to hypothetical proteins [Bacillus subtilis]
MS2063	2018593	2016827	1767	HI0729	0	Hin	J	COG0442	Prolyl-tRNA synthetase	ProS	(NC_000907) prolyl-tRNA synthetase (proS) [Haemophilus influenzae]
MS2064	2019287	2018655	633	HI0863	3.00E-77	Hin	H	COG0259	Pyridoxamine phosphate oxidase	PdxH	(NC_000907) pyridoxamine phosphate oxidase (pdxH) [Haemophilus influenzae]
MS2065	2020291	2019440	852	ZmalM	9.00E-41	No-des	none	No-des	none	none	(NC_002655) periplasmic protein of mal regulon ...
MS2066	2021806	2020523	1284	ZlamB	1.00E-141	No-des	none	No-des	none	none	(NC_003143) maltoporin [Yersinia pestis]
MS2067	2023029	2021914	1116	ZmalK	1.00E-161	EcZ	G	COG1130	ABC-type sugar/spermidine/putrescine/iron/thiamine transport systems/ATPase component	MalK	(NC_003143) maltose/maltodextrin transport ATP-...
MS2068	2023391	2024578	1188	ZmalE	1.00E-162	EcZ	G	COG2182	Maltose-binding periplasmic proteins/domains	MalE	(NC_003143) maltose-binding periplasmic protein...
MS2069	2024663	2026195	1533	malF	1.00E-174	Eco	G	COG1175	ABC-type sugar transport systems/permease components	MalF	(NC_003143) maltose transport system permease p...
MS2070	2026254	2027141	888	ZmalG	1.00E-135	EcZ	G	COG0395	Sugar permeases	MalG	(NC_003143) maltose transport system permease p...
MS2071	2027352	2029406	2055	ZmalS	0	EcZ	G	COG0366	Glycosidases	AmyA	(NC_003143) alpha-amylase protein [Yersinia pes...
MS2072	2032200	2029477	2724	malT	0	Eco	K	COG2909	ATP-dependent transcriptional regulator	MalT	(NC_003143) maltose regulon positive regulatory...
MS2073	2032369	2034735	2367	ZmalP	0	EcZ	G	COG0058	Glucan phosphorylase	GlpP	(NC_002655) maltodextrin phosphorylase [Escheri...
MS2074	2034820	2036892	2073	malQ	0	Eco	G	COG1640	4-alpha-glucanotransferase	MalQ	(NC_003143) 4-alpha-glucanotransferase [Yersini...
MS2075	2037828	2037025	804	BS_ycsN	4.00E-68	Bsu	R	COG0656	Aldo/keto reductases/related to diketoglucuronate reductase	ARA1	(NC_000964) similar to aryl-alcohol dehydrogena...
MS2076	2037946	2037815	132	none	none	No-des	none	No-des	none	none	
MS2077	2038007	2037894	114	none	none	No-des	none	No-des	none	none	
MS2078	2038086	2037970	117	none	none	No-des	none	No-des	none	none	
MS2079	2039083	2038058	1026	NMB1685	1.00E-145	Nme	C H R	COG1052	Lactate dehydrogenase and related dehydrogenases	LdhA	(NC_003112) D-lactate dehydrogenase [Neisseria ...]
MS2080	2039077	2039223	147	none	none	No-des	none	No-des	none	none	
MS2081	2041171	2039261	1911	PM1427	0	Pmu	L	COG0514	Superfamily II DNA helicase	RecQ	(NC_002663) RecQ [Pasteurella multocida]
MS2082	2041479	2041174	306	HI0727.1	9.00E-46	Hin	P	COG1965	Protein implicated in iron transport/frataxin homolog	CyaY	(NC_000907) cyaY protein (cyaY) [Haemophilus in...]
MS2083	2041547	2041696	150	none	none	No-des	none	No-des	none	none	
MS2084	2041721	2042968	1248	HI0727	0	Hin	E	COG0019	Diaminopimelate decarboxylase	LysA	(NC_000907) diaminopimelate decarboxylase (lysA...
MS2085	2042985	2043599	615	HI0111	8.00E-61	Hin	O	COG0625	glutathione-S-transferases	Gst	(NC_000907) glutathione transferase (bphH) [Hae...
MS2086	2044155	2043778	378	mll3541	5.00E-09	No-des	none	No-des	none	none	(NC_002678) unknown protein [Mesorhizobium loti...
MS2087	2047213	2044151	3063	CC3197	0	Ccr	Q	COG0841	Cation/multidrug efflux pump	AcrB	(NC_003296) PROBABLE TRANSPORTER LIPOPROTEIN T...
MS2088	2047314	2047216	99	none	none	No-des	none	No-des	none	none	
MS2089	2048328	2047333	996	CC3196	3.00E-17	Ccr	Q	COG0845	Membrane-fusion protein	AcrA	(NC_003047) PUTATIVE TRANSPORT TRANSMEMBRANE
MS2090	2049188	2048337	852	PM0404	1.00E-94	No-des	none	No-des	none	none	(NC_002663) unknown [Pasteurella multocida]
MS2091	2049625	2049191	435	NMB1585	3.00E-13	Nme	K	COG1846	Transcriptional regulators	MarR	(NC_003112) transcriptional regulator/MarR fam...
MS2092	2050638	2049748	891	PA2877	1.00E-26	Pae	K	COG0583	Transcriptional regulator	LysR	(AF167577) transcriptional regulator Ap...
MS2093	2050746	2051708	963	TM1006	1.00E-89	Tma	C	COG0667	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	Tas	(NC_000853) oxidoreductase/aldo/keto reductase...
MS2094	2051727	2052239	513	BS_ylrL	4.00E-30	Bsu	R	COG2249	Putative NADPH-quinone reductase (modulator of drug activity B)	MdaB	(NC_000964) similar to NAD(P)H oxidoreductase [...]
MS2095	2052392	2052964	573	aq_928	1.00E-08	Aae	R	COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases/DIM6/NTAB family		flavoredoxin FLR [validated] - Desulfotoluidine gigas

MS2096	2052977	2053546	570	ydhH	4.00E-15	Eco	R	COG1853	Conserved protein/domain typically associated with flavoprotein oxygenases/DIM6/NTAB family		(NC_000913) orf1/hypothetical protein [Escheric...
MS2097	2054757	2053618	1140	BS_yqiG	2.00E-94	Bsu	C	COG1902	NADHflavin oxidoreductases/Old Yellow Enzyme family	NemA	(NC_000964) similar to NADH-dependent flavin ox...
MS2098	2054825	2054956	132	none	none	No-des	none	No-des	No-des	none	none
MS2099	2054803	2054967	165	none	none	No-des	none	No-des	No-des	none	none
MS2100	2055607	2054984	624	CC2843	6.00E-31	Ccr	O	COG0625	Glutathione-S-transferases	Gst	(NC_002696) glutathione S-transferase family pr...
MS2101	2056083	2055655	429	PA2850	2.00E-28	Pae	O	COG1764	Stress-induced protein	OsmC	(NC_003296) PROBABLE ORGANIC HYDROPEROXIDE RE
MS2102	2056564	2056127	438	yiiD	2.00E-11	Eco	K/R	COG0454	Histone acetyltransferase HPA2 and related acetyltransferases	WecD	(NC_003276) hypothetical protein [Nostoc sp. PC...
MS2103	2057379	2056591	789	yfaU	7.00E-60	Eco	G	COG0469	Pyruvate kinase	PykF	(NC_003198) putative 2/4-dihydroxyhept-2-ene-1]...
MS2104	2057860	2057402	459	VC0365	4.00E-14	Vch	P	COG2193	Bacterioferritin (cytochrome b1)	Bfr	(NC_002505) bacterioferritin [Vibrio cholerae] ...
MS2105	2057932	2058837	906	TM1005	6.00E-49	Tma	K	COG2207	AraC-type DNA-binding domain-containing proteins	AraC	(NC_000853) transcriptional regulator/putative...
MS2106	2058883	2058794	90	none	none	No-des	none	No-des	No-des	none	none
MS2107	2058854	2058946	93	none	none	No-des	none	No-des	No-des	none	none
MS2108	2058964	2059218	255	NMA1039	1.00E-06	No-des	none	No-des	No-des	none	(NC_003112) conserved hypothetical protein [Nei...
MS2109	2059226	2059339	114	none	none	No-des	none	No-des	No-des	none	none
MS2110	2060018	2059359	660	PA0573	7.00E-07	No-des	none	No-des	No-des	none	(NC_001496) pXO1-01 [Bacillus anthracis]
MS2111	2060350	2060240	111	none	none	No-des	none	No-des	No-des	none	none
MS2112	2060330	2060488	159	none	none	No-des	none	No-des	No-des	none	none
MS2113	2061943	2060729	1215	HI1038	4.00E-61	Hin	R	COG1373	Uncharacterized ATPases of the AAA superfamily		(NC_000907) conserved hypothetical protein [Hae...
MS2114	2062634	2062071	564	PM1890	7.00E-26	Pmu	S	COG3238	Uncharacterized BCR		(NC_002663) unknown [Pasteurella multocida]
MS2115	2063326	2062664	663	NMA1015	2.00E-97	NmA	C	COG0778	Nitroreductase	NfnB	(NC_003116) putative NAD(P)H-flavin oxidoreduct...
MS2116	2063431	2064345	915	slr1871	3.00E-38	Syn	K	COG0583	Transcriptional regulator	LysR	(NC_003047) HYPOTHETICAL TRANSCRIPTION REGULA
MS2117	2065117	2064662	456	PM1369	1.00E-76	Pmu	F	COG0503	Adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins	Apt	(NC_002663) Gpt [Pasteurella multocida]
MS2118	2065285	2066745	1461	PM1368	0	Pmu	E	COG2195	Di- and tripeptidases	PepD	(NC_002663) PepD [Pasteurella multocida]
MS2119	2066758	2066940	183	none	none	No-des	none	No-des	No-des	none	none
MS2120	2066933	2067985	1053	XF1739	5.00E-73	Xfa	R	COG2220	Predicted Zn-dependent hydrolases of the beta-lactamase fold		2.00E-84
MS2121	2067967	2068116	150	none	none	No-des	none	No-des	No-des	none	none
MS2122	2068165	2069340	1176	mlt2789	1.00E-80	No-des	none	No-des	No-des	none	(NC_002678) unknown protein [Mesorhizobium loti...
MS2123	2069426	2070175	750	mlt2788	5.00E-49	No-des	none	No-des	No-des	none	(NC_002678) unknown protein [Mesorhizobium loti...
MS2124	2071096	2070275	822	DR0779_2	7.00E-24	Dra	R	COG2819	Predicted hydrolase of the alpha/beta superfamily		(NC_003028) conserved hypothetical protein [Str...
MS2125	2071972	2071259	714	none	none	No-des	none	No-des	No-des	none	none
MS2126	2072203	2072307	105	none	none	No-des	none	No-des	No-des	none	none
MS2127	2072893	2072468	426	XF1751	7.00E-17	No-des	none	No-des	No-des	none	(NC_003295) CONSERVED HYPOTHETICAL PROTEIN [Ra
MS2128	2073489	2072896	594	mlr2192	1.00E-38	Mlo	R	COG0110	Acetyltransferases (the isoleucine patch superfamily)	WbbJ	(NC_003212) similar to acetyltransferase [Liste...
MS2129	2074674	2073538	1137	207347	1.00E-103	EcZ	R	COG1073	Hydrolases of the alpha/beta superfamily		(NC_002695) hypothetical protein [Escherichia c...
MS2130	2074805	2075701	897	mlr3418	3.00E-22	Mlo	K	COG0583	Transcriptional regulator	LysR	(AF167577) transcriptional regulator Ap...
MS2131	2076654	2075785	870	TM1005	3.00E-43	Tma	K	COG2207	AraC-type DNA-binding domain-containing proteins	AraC	(NC_000853) transcriptional regulator/putative...
MS2132	2078088	2076778	1311	BH0865	1.00E-108	Bha	C	COG1012	NAD-dependent aldehyde dehydrogenases	PutA	(NC_003272) aldehyde dehydrogenase [Nostoc sp. ...
MS2133	2078291	2078187	105	none	none	No-des	none	No-des	No-des	none	none
MS2134	2079150	2078266	885	PA2877	1.00E-34	Pae	K	COG0583	Transcriptional regulator	LysR	(NC_003037) putative LysR-family transcriptiona...
MS2135	2079253	2079939	687	yhhW	2.00E-75	Eco	R	COG1741	Pirin-related protein		(NC_000913) orf1/hypothetical protein [Escheric...
MS2136	2080034	2081842	1809	mlr0783_1	1.00E-89	Mlo	P	COG0475	Kef-type K+ transport systems/membrane components	KefB	(NC_003062) AGR_C_3111p [Agrobacterium tumefaci...
MS2137	2082320	2082201	120	NMA2196	3.00E-08	NmA	S	COG2259	Predicted membrane protein		(NC_003112) conserved hypothetical protein [Nei...
MS2138	2082048	2082449	402	NMA2196	7.00E-23	NmA	S	COG2259	Predicted membrane protein		(NC_003112) conserved hypothetical protein [Nei...
MS2139	2083075	2082527	549	CC0205	3.00E-27	Ccr	R	COG2249	Putative NADPH-quinone reductase (modulator of drug activity B)	MdaB	(NC_002696) NADP(H) oxidoreductase [Caulobacter...
MS2140	2083309	2083157	153	none	none	No-des	none	No-des	No-des	none	none
MS2141	2083440	2083309	132	none	none	No-des	none	No-des	No-des	none	none
MS2142	2083859	2083524	336	none	none	No-des	none	No-des	No-des	none	(NC_001988) Uncharacterized conserved protein]...
MS2143	2085029	2084067	963	PA2877	5.00E-38	Pae	K	COG0583	Transcriptional regulator	LysR	(NC_003295) PROBABLE TRANSCRIPTION REGULATOR I
MS2144	2085122	2085781	660	PA0117	8.00E-11	Pae	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	FabG	hypothetical protein 4 - Rhizobium leguminosarum bv....
MS2145	2085793	2086536	744	TM1724	2.00E-36	Tma	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	FabG	(NC_000853) 3-oxoacyl-(acyl carrier protein) re...
MS2146	2086730	2087164	435	NMB1585	3.00E-13	Nme	K	COG1846	Transcriptional regulators	MarR	(NC_003112) transcriptional regulator[MarR fam...
MS2147	2087167	2088018	852	PM0404	1.00E-94	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS2148	2087999	2088406	408	mlt13541	3.00E-09	No-des	none	No-des	No-des	none	(NC_002678) unknown protein [Mesorhizobium loti...
MS2149	2088501	2089190	690	CC0324	2.00E-23	Ccr	C	COG0778	Nitroreductase	NfnB	(NC_002696) NADH dehydrogenase [Caulobacter cre...
MS2150	2089357	2089187	171	none	none	No-des	none	No-des	No-des	none	none
MS2151	2090388	2089483	906	mlr0648	2.00E-40	Mlo	K	COG0583	Transcriptional regulator	LysR	(NC_002678) transcriptional regulator [Mesorhiz...
MS2152	2091283	2090420	864	mlr2579	4.00E-44	Mlo	K	COG0583	Transcriptional regulator	LysR	(AF426171) putative transcriptional reg...
MS2153	2091419	2092561	1143	BS_yqiG	3.00E-76	Bsu	C	COG1902	NADHflavin oxidoreductases/Old Yellow Enzyme family	NemA	(NC_000964) similar to NADH-dependent flavin ox...
MS2154	2092574	2093425	852	none	none	No-des	none	No-des	No-des	none	none
MS2155	2093782	2094678	897	BH2855	2.00E-06	No-des	none	No-des	No-des	none	(NC_002570) BH2855-unknown conserved protein in...

MS2156	2094916	2095860	945	BS_ydjP	9.00E-21	Bsu	R	COG0596	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	MhpC	(NC_003296) PUTATIVE HYDROLASE SIGNAL PEPTIDE P
MS2157	2096008	2096970	963	none	none	No-des	none	No-des	No-des	none	(NC_003030) Hypothetical protein [Clostridium a...
MS2158	2098250	2097168	1083	XF1766	2.00E-38	Xfa	S	COG0599	Uncharacterized ACR/homolog of gamma-carboxymuconolactone decarboxylase subunit	none	(NC_002488) hypothetical protein [Xylella fasti...
MS2159	2098799	2098269	531	none	none	No-des	none	No-des	No-des	none	(NC_003030) Multimeric flavodoxin WrbA family p...
MS2160	2099327	2098914	414	XF1736	2.00E-33	No-des	none	No-des	No-des	none	(NC_002488) hypothetical protein [Xylella fasti...
MS2161	2100413	2099370	1044	DRB0033_1	2.00E-38	Dra	I	COG0657	Esterase/lipase	Aes	(NC_000958) arylesterase/monooxygenase [Deinococ...
MS2162	2101151	2100471	681	BS_ywrO	2.00E-15	Bsu	R	COG2249	Putative NADPH-quinone reductase (modulator of drug activity B)	MdaB	(NC_000964) similar to NAD(P)H oxidoreductase [...]
MS2163	2101894	2101148	747	L179660	1.00E-92	Lla	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	FabG	(AF155139) unknown protein [Paenibacillus popilliae]
MS2164	2101880	2101993	114	none	none	No-des	none	No-des	No-des	none	none
MS2165	2102229	2104424	2196	CC0620	1.00E-135	Ccr	L	COG0286	Type I restriction-modification system methyltransferase subunit	HsdM	(NC_002696) type I restriction-modification sys...
MS2166	2104439	2105455	1017	none	none	No-des	none	No-des	No-des	none	none
MS2167	2105460	2105915	456	none	none	No-des	none	No-des	No-des	none	(NC_003270) ORF_IDalr9029-hypothetical protein...
MS2168	2105937	2106413	477	none	none	No-des	none	No-des	No-des	none	none
MS2169	2107580	2107485	96	none	none	No-des	none	No-des	No-des	none	none
MS2170	2106665	2108011	1347	CJ1051c_2	2.00E-29	Cje	L	COG0732	Restriction endonuclease S subunits	HsdS	(NC_003197) specificity determinant for hsdM an...
MS2171	2108030	2111089	3060	CC0623	1.00E-175	Ccr	L	COG0610	Restriction enzymes type I helicase subunits and related helicases	HsdR	(NC_002696) conserved hypothetical protein [Cau...
MS2172	2112241	2111162	1080	XF1750	1.00E-107	Xfa	R	COG1073	Hydrolases of the alpha/beta superfamily	none	(NC_002488) conserved hypothetical protein [Xyl...
MS2173	2112414	2113265	852	ybcM	4.00E-22	Eco	K	COG2207	AraC-type DNA-binding domain-containing proteins	AraC	(NC_003143) putative AraC-family transcriptiona...
MS2174	2114033	2113476	558	ybcL	2.00E-40	Eco	R	COG1881	Phospholipid-binding protein	none	(NC_003197) putative outer membrane protein [Sa...
MS2175	2115004	2114123	882	XF1741	5.00E-44	Xfa	Q/R	COG1028	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	FabG	(NC_002488) daunorubicin C-13 ketoreductase [Xy...
MS2176	2115063	2116046	984	mlr7786	4.00E-25	Mlo	K	COG0583	Transcriptional regulator	LysR	(AF167577) transcriptional regulator Ap...
MS2177	2116784	2116155	630	PM0946	8.00E-37	Pnu	S	COG2979	Uncharacterized BCR	none	(NC_002663) unknown [Pasteurella multocida]
MS2178	2118607	2116916	1692	HI0446_3	1.00E-127	Hin	G	COG1299	Phosphotransferase system/fructose-specific IIC component	FruA	(NC_000907) PTS system/fructose-specific IIBC ...
MS2179	2119538	2118600	939	HI0447	1.00E-132	Hin	G	COG1105	Fructose-1-phosphate kinase and related fructose-6-phosphate kinase (PfkB)	FruK	(NC_000907) 1-phosphofructokinase (fruK) [Haemo...
MS2180	2121050	2119545	1506	HI0448_1	1.00E-105	Hin	G/T	COG1762	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	PtsN	(NC_000907) PTS system/fructose-specific IIA/F...
MS2181	2121799	2121257	543	HI0449	3.00E-53	No-des	none	No-des	No-des	none	(NC_000907) H. influenzae predicted coding regi...
MS2182	2121935	2121777	159	none	none	No-des	none	No-des	No-des	none	none
MS2183	2121962	2122276	315	HI0679	4.00E-39	Hin	P	COG0607	Rhodanese-related sulfurtransferases	PspE	(NC_000907) glpE protein (glpE) [Haemophilus in...
MS2184	2122638	2122303	336	PM1437	6.00E-26	No-des	none	No-des	No-des	none	(NC_002663) unknown [Pasteurella multocida]
MS2185	2122689	2123561	873	PM1438	5.00E-70	Pnu	R	COG0705	Uncharacterized membrane protein (homolog of Drosophila rhomboid)	GlpG	(NC_002663) GlpG [Pasteurella multocida]
MS2186	2123605	2124360	756	PM1439	1.00E-103	Pnu	K/G	COG1349	Transcriptional regulators of sugar metabolism	GlpR	(NC_002663) GlpR [Pasteurella multocida]
MS2187	2125719	2124538	1182	HI0632	0	Hin	J/E	COG0050	GTases - translation elongation factors	TufB	(NC_000907) elongation factor Tu (tufA) [Haemop...
MS2188	2126449	2127399	951	HI0631	1.00E-125	Hin	H	COG1072	Panthothenate kinase	CoaA	(NC_000907) pantothenate kinase (coaA) [Haemoph...
MS2189	2127918	2127511	408	HI0719	7.00E-63	Hin	J	COG0251	Putative translation initiation inhibitor	TdcF	(NC_000907) conserved hypothetical protein [Hae...
MS2190	2130647	2128020	2628	PM1453_2	0	Pnu	C	COG1454	Alcohol dehydrogenase IV	EutG	(NC_002663) Adh2 [Pasteurella multocida]
MS2191	2131028	2132377	1350	none	none	No-des	none	No-des	No-des	none	none
MS2192	2132986	2132375	612	HI1169	2.00E-55	Hin	E/H	COG0115	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	IivE	(NC_000907) H. influenzae predicted coding regi...
MS2193	2133957	2132977	981	HI1170	1.00E-115	Hin	E/H	COG0147	Anthrnilate/para-aminobenzoate synthases component I	TrpE	(NC_000907) H. influenzae predicted coding regi...
MS2194	2134063	2134629	567	PM1463	8.00E-77	Pnu	E/H	COG0512	Anthrnilate/para-aminobenzoate synthases component II	PabA	(NC_002663) TrpG [Pasteurella multocida]
MS2195	2134689	2136062	1374	PM1563	0	Pnu	P	COG0569	K+ transport systems/NAD-binding component	TrkA	(NC_002663) TrkA [Pasteurella multocida]
MS2196	2136135	2136548	414	HI0626	6.00E-44	Hin	M	COG1970	Large-conductance mechanosensitive channel	MscL	(NC_000907) large conductance mechanosensitive ...
MS2197	2136631	2137062	432	HI0700	3.00E-54	Hin	S	COG3076	Uncharacterized BCR	none	(NC_000907) conserved hypothetical protein [Hae...
MS2198	2137117	2137818	702	PM1566	1.00E-38	Pnu	S	COG3471	Predicted periplasmic/secreted protein	none	(NC_002663) unknown [Pasteurella multocida]
MS2199	2137946	2138620	675	PM1567	1.00E-72	Pnu	O	COG1047	FKBP-type peptidyl-prolyl cis-trans isomerases 2	SlpA	(NC_002663) FkpA [Pasteurella multocida]
MS2200	2138636	2138782	147	none	none	No-des	none	No-des	No-des	none	none
MS2201	2138862	2139374	513	PM1559	2.00E-72	Pnu	J	COG0242	N-formylmethionyl-tRNA deformylase	Def	(NC_002663) Def [Pasteurella multocida]
MS2202	2139446	2140399	954	HI0623	1.00E-137	Hin	J	COG0223	Methionyl-tRNA formyltransferase	Fmt	(NC_000907) methionyl-tRNA formyltransferase (f...
MS2203	2140402	2141811	1410	HI0624	1.00E-179	Hin	J	COG0144	tRNA and rRNA cytosine-C5-methylases	Sun	(NC_002663) Sun [Pasteurella multocida]
MS2204	2143006	2141867	1140	PM0874	1.00E-169	Pnu	G	COG1820	N-acetylglucosamine-6-phosphate deacetylase	NagA	(NC_002663) NagA [Pasteurella multocida]
MS2205	2143862	2143062	801	PM0875	1.00E-130	Pnu	G	COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase	NagB	(NC_002663) NagB [Pasteurella multocida]
MS2206	2144469	2144005	465	PM1713	2.00E-42	Pnu	S	COG2731	Uncharacterized BCR	EbgC	(NC_002663) unknown [Pasteurella multocida]
MS2207	2146874	2144562	2313	PM1448	0	Pnu	R	COG2183	Predicted RNA binding protein/contains S1 domain	none	(NC_002663) unknown [Pasteurella multocida]
MS2208	2146998	2147471	474	PM1450	2.00E-80	Pnu	K	COG0782	Transcription elongation factor	GreA	(NC_002663) GreB [Pasteurella multocida]
MS2209	2147924	2147562	363	none	none	No-des	none	No-des	No-des	none	none
MS2210	2148172	2147966	207	none	none	No-des	none	No-des	No-des	none	none
MS2211	2148308	2148817	510	L103086	1.00E-11	Lla	K	COG1309	Transcriptional regulator	AcrR	(NC_003030) Transcriptional regulator/AcrR fam...
MS2212	2150215	2149421	795	HI0606	1.00E-126	Hin	E	COG1045	Serine acetyltransferase	CysE	(NC_000907) serine acetyltransferase (cysE) [Ha...
MS2213	2151244	2150240	1005	PM1431	1.00E-152	Pnu	C	COG0240	Glycerol 3-phosphate dehydrogenase	GpsA	(NC_002663) GpsA [Pasteurella multocida]
MS2214	2151849	2151343	507	HI0743	4.00E-75	Hin	N	COG1952	Preprotein translocase subunit SecB	SecB	(NC_000907) protein-export protein (secB) [Haem...
MS2215	2152298	2151864	435	PM1433	1.00E-44	Pnu	P	COG0607	Rhodanese-related sulfurtransferases	PspE	(NC_002663) unknown [Pasteurella multocida]

MS2216	2152549	2153868	1320	PM1434	1.00E-161	Pmu	R	COG2704	Anaerobic C4-dicarboxylate transporter		DcuB	(NC_002663) DcuB [Pasteurella multocida]
MS2217	2153840	2153983	144	none	none	none	none	No-des	No-des		none	none
MS2218	2155555	2154020	1536	PM1624	0	Pmu	E	COG1171	Threonine dehydratase		IlvA	(NC_002663) IlvA [Pasteurella multocida]
MS2219	2157487	2155643	1845	PM1625	0	Pmu	E G	COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase		IlvD	(NC_002663) IlvD [Pasteurella multocida]
MS2220	2157501	2157665	165	none	none	none	none	No-des	No-des		none	none
MS2221	2158279	2157752	528	HI0124	6.00E-90	Hin	C	COG0221	Inorganic pyrophosphatase		Pps	(NC_000907) inorganic pyrophosphatase (ppa) [Ha...
MS2222	2158640	2158377	264	PM1627	1.00E-09	Pmu	E	COG0440	Acetolactate synthase[small subunit]		IlvH	(NC_002663) IlvH [Pasteurella multocida]
MS2223	2160326	2158677	1650	PM1628	0	Pmu	E H	COG0028	Thiamine pyrophosphate-requiring enzymes acetolactate synthase pyruvate dehydrogenase (cytochrome) glyoxylate carboligase phosphonopyruvate		IlvB	(NC_002663) IlvG [Pasteurella multocida]
MS2224	2160497	2160390	108	none	none	none	none	No-des	No-des		none	none
MS2225	2160604	2161419	816	PM1629	1.00E-102	Pmu	R	COG0561	Predicted hydrolases of the HAD superfamily		Cof	(NC_002663) unknown [Pasteurella multocida]
MS2226	2161425	2161805	381	PM1630	6.00E-39	Pmu	D	COG0239	Integral membrane protein possibly involved in chromosome condensation		CrcB	(NC_002663) CrcB [Pasteurella multocida]
MS2227	2161869	2162138	270	PM1790	7.00E-28	Pmu	S	COG2938	Uncharacterized ACR			(NC_002663) unknown [Pasteurella multocida]
MS2228	2162234	2162827	594	PM1789	2.00E-96	Pmu	K	COG1595	DNA-directed RNA polymerase specialized sigma subunits sigma24 homologs		RpoE	(NC_002663) RpoE [Pasteurella multocida]
MS2229	2162847	2163419	573	PM1788	8.00E-56	Pmu	T	COG3073	Negative regulator of sigma E activity		RseA	(NC_002663) MclA [Pasteurella multocida]
MS2230	2163458	2164435	978	PM1787	9.00E-98	Pmu	T	COG3026	Negative regulator of sigma E activity		RseB	(NC_002663) RseB [Pasteurella multocida]
MS2231	2164448	2164879	432	PM1786	3.00E-53	Pmu	T	COG3086	Positive regulator of sigma E activity		RseC	(NC_002663) unknown [Pasteurella multocida]
MS2232	2165494	2164913	582	HI0433_2	7.00E-47	Hin	O	COG0694	Thioredoxin-like proteins and domains			(NC_002663) OrfG [Pasteurella multocida]
MS2233	2165606	2165475	132	none	none	none	none	No-des	No-des		none	none
MS2234	2166271	2165588	684	HI0434	1.00E-83	Hin	R	COG1040	Predicted amidophosphoribosyltransferases		ComFC (BS)	(NC_000907) competence protein F (comF) [Haemop...
MS2235	2166413	2167225	813	PM1555	1.00E-86	Pmu	R	COG0561	Predicted hydrolases of the HAD superfamily		Cof	(NC_002663) unknown [Pasteurella multocida]
MS2236	2170622	2167323	3300	PM1505	0	Pmu	E F	COG0458	Carbamoylphosphate synthase large subunit (split gene in MJ)		CarB	(NC_002663) CarB [Pasteurella multocida]
MS2237	2172061	2170937	1125	PM1502	0	Pmu	E F	COG0505	Carbamoylphosphate synthase small subunit		CarA	(NC_002663) CarA [Pasteurella multocida]
MS2238	2172189	2172302	114	none	none	none	none	No-des	No-des		none	none
MS2239	2172443	2173186	744	PM1501	1.00E-84	Pmu	M	COG2853	Surface lipoprotein		VacJ	(NC_002663) VacJ [Pasteurella multocida]
MS2240	2173235	2173726	492	PM1500	2.00E-74	Pmu	S	COG3013	Uncharacterized ACR			(NC_002663) unknown [Pasteurella multocida]
MS2241	2173797	2175425	1629	none	none	none	none	No-des	No-des		none	(NC_003064) AGR_pAT_374p [Agrobacterium tumefac...
MS2242	2175994	2175536	459	HI0599	6.00E-42	Hin	R	COG2137	Uncharacterized BCR		OraA	(NC_000907) regulatory protein (recX) [Haemophi...
MS2243	2177179	2176127	1053	HI0600	1.00E-168	Hin	L	COG0468	RecA/RadA recombinase		RecA	(NC_000907) recA protein (recA) [Haemophilus in...
MS2244	2177385	2179967	2583	PM1830	0	Pmu	L	COG0249	MutS-like ATPases involved in mismatch repair family 2		MutS	(NC_002663) MutS [Pasteurella multocida]
MS2245	2180042	2180455	414	PA2880	5.00E-23	No-des	none	No-des	No-des		none	(NC_002516) hypothetical protein [Pseudomonas a...
MS2246	2182461	2180569	1893	CC0119_2	5.00E-07	No-des	none	No-des	No-des		none	(AF180945) HmwC [Haemophilus influenzae]
MS2247	2183869	2182526	1344	PM1571	0	Pmu	J	COG0621	2-methylthioadenine synthetase		MiaB	(NC_002663) unknown [Pasteurella multocida]
MS2248	2184636	2184073	564	ZygaP	1.00E-44	EcZ	P	COG0607	Rhodanese-related sulfurtransferases		PspE	(NC_002655) orf1 hypothetical protein [Escheric...
MS2249	2184839	2187271	2433	PM1476	0	Pmu	L	COG0187	DNA gyrase (topoisomerase II) B subunit		GyrB	(NC_002663) GyrB [Pasteurella multocida]
MS2250	2187340	2187774	435	PM1484	1.00E-44	Pmu	C	COG0716	Flavodoxins		FldA	(NC_002663) MioC [Pasteurella multocida]
MS2251	2187780	2187890	111	none	none	none	none	No-des	No-des		none	none
MS2252	2187866	2188489	624	PM1618	3.00E-60	Pmu	R	COG1279	Lysine efflux permease			(NC_002663) unknown [Pasteurella multocida]
MS2253	2188772	2188557	216	PM1483	6.00E-20	Pmu	S	COG3074	Uncharacterized BCR			(NC_002663) unknown [Pasteurella multocida]
MS2254	2188969	2189979	1011	PM1482	1.00E-145	Pmu	G	COG1494	Fructose-1[6-bisphosphatase/sedoheptulose 1[7-bisphosphatase and related proteins		GlpX	(NC_002663) GlpX [Pasteurella multocida]
MS2255	2190244	2190993	750	aq_1571	9.00E-07	No-des	none	No-des	No-des		none	(NC_003030) Alpha/beta superfamily hydrolase [C...
MS2256	2191241	2191360	120	none	none	none	none	No-des	No-des		none	none
MS2257	2191360	2192328	969	PM1252	5.00E-64	Pmu	G	COG1638	Dicarboxylate-binding periplasmic protein		DctP	(NC_002663) unknown [Pasteurella multocida]
MS2258	2192542	2192384	159	none	none	none	none	No-des	No-des		none	none
MS2259	2193578	2192616	963	PM1843	1.00E-115	Pmu	M	COG0859	ADP-heptoseLPS heptosyltransferase		RfaF	(NC_002663) unknown [Pasteurella multocida]
MS2260	2194718	2193681	1038	PM1844	1.00E-155	Pmu	M	COG0859	ADP-heptoseLPS heptosyltransferase		RfaF	(NC_002663) RfaF [Pasteurella multocida]
MS2261	2194872	2195162	291	HI0636	9.00E-25	Hin	S	COG3691	Uncharacterized BCR			(NC_000907) conserved hypothetical protein [Hae...
MS2262	2196109	2195225	885	HI0810	1.00E-130	Hin	O	COG1281	Disulfide bond chaperones of the HSP33 family			(NC_000907) conserved hypothetical protein [Hae...
MS2263	2196095	2196229	135	none	none	none	none	No-des	No-des		none	none
MS2264	2196639	2196232	408	PM1546	2.00E-56	Pmu	J	COG1188	Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)			(NC_002663) unknown [Pasteurella multocida]
MS2265	2198537	2196762	1776	HI0002	0	Hin	I	COG1022	Long-chain acyl-CoA synthetases (AMP-forming)		FAA1	(NC_000907) long chain fatty acid coA ligase p...
MS2266	2199511	2198813	699	none	none	none	none	No-des	No-des		none	(AF338705) transposase [Corynebacterium...
MS2267	2199741	2199628	114	none	none	none	none	No-des	No-des		none	none
MS2268	2200723	2199914	810	HI0706	8.00E-67	Hin	M	COG0739	Membrane proteins related to metalloendopeptidases		NlpD	(NC_000907) lipoprotein [Haemophilus influenzae...
MS2269	2200860	2201327	468	PM1614	2.00E-20	Pmu	M	COG0739	Membrane proteins related to metalloendopeptidases		NlpD	(NC_002663) unknown [Pasteurella multocida]
MS2270	2201420	2201229	192	HI0704	2.00E-08	No-des	none	No-des	No-des		none	(NC_000907) H. influenzae predicted coding regi...
MS2271	2202005	2201433	573	HI0703	4.00E-85	Hin	S	COG1238	Uncharacterized membrane protein			(NC_000907) lipoprotein B (lppB) [Haemophilus i...
MS2272	2202863	2202048	816	PM1612	1.00E-117	Pmu	R	COG0496	Survival protein predicted acid phosphatase		SurE	(NC_002663) SurE [Pasteurella multocida]
MS2273	2203919	2202909	1011	PM1610	1.00E-139	Pmu	S	COG0585	Uncharacterized ACR			(NC_002663) unknown [Pasteurella multocida]
MS2274	2204392	2203916	477	HI0671	2.00E-69	Hin	I	COG0245	2C-methyl-D-erythritol 2-4-cyclodiphosphate synthase		IspF	(NC_000907) conserved hypothetical protein [Hae...
MS2275	2205135	2204452	684	PM1608	1.00E-83	Pmu	I	COG1211	4-diphosphocytidyl-2-methyl-D-erithritol synthase		IspD	(NC_002663) unknown [Pasteurella multocida]

MS2276	2205422	2205138	285	PM1607		1.00E-29	Pmu	O	COG2919	Septum formation initiator		(NC_002663) unknown [Pasteurella multocida]
MS2277	2206150	2205542	609	PM1598		3.00E-79	Pmu	C	COG3005	Nitrate/TMAO reductases/membrane-bound tetraheme cytochrome c subunit	TorC	(NC_002663) NapC [Pasteurella multocida]
MS2278	2206590	2206165	426	PM1597		6.00E-39	Pmu	C	COG3043	Nitrate reductase cytochrome c-type subunit	NapB	(NC_002663) NapB [Pasteurella multocida]
MS2279	2207547	2206657	891	PM1596		1.00E-113	Pmu	C	COG0348	Polyferredoxin	NapH	(NC_002663) NapH [Pasteurella multocida]
MS2280	2208452	2207550	903	HI0345		1.00E-106	Hin	C	COG1145	Ferredoxin 2	NapF	(NC_000907) ferredoxin-type protein (napF) [Hae...
MS2281	2211110	2208609	2502	PM1594		0	Pmu	C	COG0243	Anaerobic dehydrogenases/typically selenocysteine-containing	BisC	(NC_002663) NapA [Pasteurella multocida]
MS2282	2211431	2211171	261	PM1593		8.00E-13	Pmu	P	COG3062	Uncharacterized protein involved in formation of periplasmic nitrate reductase	NapD	(NC_002663) NapD [Pasteurella multocida]
MS2283	2212014	2211487	528	PM1592		2.00E-64	Pmu	C	COG1145	Ferredoxin 2	NapF	(NC_002663) NapF [Pasteurella multocida]
MS2284	2212416	2213792	1377	PM1341		0	Pmu	G	COG2271	Sugar phosphate permease	UhpC	(NC_002663) UhpT [Pasteurella multocida]
MS2285	2213825	2214499	675	PM1340		2.00E-80	Pmu	T/K	COG2197	Response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain	CitB	(NC_002663) UhpA [Pasteurella multocida]
MS2286	2214513	2216021	1509	PM1339		1.00E-136	Pmu	T	COG0642	Sensory transduction histidine kinases	BaeS	(NC_002663) UhpB [Pasteurella multocida]
MS2287	2216027	2217298	1272	PM1338		0	Pmu	G	COG2271	Sugar phosphate permease	UhpC	(NC_002663) UhpC [Pasteurella multocida]
MS2288	2217301	2219055	1755	PM1591		0	Pmu	T	COG0642	Sensory transduction histidine kinases	BaeS	(NC_002663) NarQ [Pasteurella multocida]
MS2289	2219067	2219594	528	BS_ywnH		8.00E-28	Bsu	M	COG1247	Sortase and related acyltransferases		(NC_000964) similar to phosphothricin acetyl...
MS2290	2220992	2219700	1293	HI0499		0	Hin	E	COG0665	Glycine/D-amino acid oxidases (deaminating)	DadA	(NC_000907) oxidoreductase/putative [Haemophil...
MS2291	2221346	2221257	90	none	none	0	none	none	No-des	none	none	none
MS2292	2221350	2222366	1017	HI0498		1.00E-135	Hin	E	COG0687	Spermidine/putrescine-binding periplasmic protein	PotD	SPERMIDINE/PUTRESCINE-BINDING PERIPLASMIC P...
MS2293	2224263	2222650	1614	PM1542		0	Pmu	C	COG1866	Phosphoenolpyruvate carboxykinase (ATP)	PckA	(NC_002663) PckA [Pasteurella multocida]
MS2294	2224443	2224348	96	none	none	0	none	none	No-des	none	none	none
MS2295	2224491	2225105	615	mlr0535		2.00E-29	Mlo	K	COG1309	Transcriptional regulator	AcrR	(NC_002678) probable transcriptional regulator ...
MS2296	2225123	2226262	1140	BS_yqjG		7.00E-93	Bsu	C	COG1902	NADH/flavin oxidoreductases/Old Yellow Enzyme family	NemA	(NC_000964) similar to NADH-dependent flavin ox...
MS2297	2226492	2226605	114	none	none	0	none	none	No-des	none	none	none
MS2298	2226853	2227164	312	PA0979		2.00E-20	Pae	L	COG2963	Transposase		(NC_002516) conserved hypothetical protein [Pse...
MS2299	2227206	2227988	783	PA0978		6.00E-54	Pae	L	COG2801	Putative transposase	Tra5	(NC_002516) conserved hypothetical protein [Pse...
MS2300	2228036	2228641	606	none	none	0	none	none	No-des	none	none	(AF338705) transposase [Corynebacterium...
MS2301	2229453	2228803	651	PM1558		6.00E-46	Pmu	N	COG3070	Regulator of competence-specific genes	TfoX	(NC_002663) TfoX [Pasteurella multocida]
MS2302	2230039	2230155	117	none	none	0	none	none	No-des	none	none	none
MS2303	2231549	2231454	96	none	none	0	none	none	No-des	none	none	none
MS2304	2233896	2233771	126	none	none	0	none	none	No-des	none	none	none
MS2305	2235835	2236659	825	PM0297		7.00E-99	No-des	none	No-des	none	none	(NC_002663) unknown [Pasteurella multocida]
MS2306	2238095	2236710	1386	HI1597		0	Hin	O	COG1066	Predicted ATP-dependent serine protease	Sms	DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR...
MS2307	2239297	2238104	1194	PM0251		2.00E-89	Pmu	S	COG3025	Uncharacterized ACR		(NC_002663) unknown [Pasteurella multocida]
MS2308	2239274	2239405	132	PM0250		3.00E-08	Pmu	P	COG1392	Phosphate transport regulator (distant homolog of PhoU)		(NC_002663) unknown [Pasteurella multocida]
MS2309	2239551	2239997	447	HI1603		1.00E-63	Hin	P	COG1392	Phosphate transport regulator (distant homolog of PhoU)		(NC_000907) conserved hypothetical protein [Hae...
MS2310	2240029	2241288	1260	PM0249		1.00E-161	Pmu	P	COG0306	Phosphate/sulphate permeases	PitA	(NC_002663) unknown [Pasteurella multocida]
MS2311	2241459	2242073	615	PM0248		3.00E-75	Pmu	T	COG3103	SH3 domain protein		(NC_002663) unknown [Pasteurella multocida]
MS2312	2242129	2243385	1257	PM0247		1.00E-176	Pmu	J	COG0617	tRNA nucleotidyltransferase/poly(A) polymerase	PcnB	(NC_002663) Cca [Pasteurella multocida]
MS2313	2243518	2243610	93	none	none	0	none	none	No-des	none	none	none
MS2314	2243669	2244394	726	none	none	0	none	none	No-des	none	none	none
MS2315	2244418	2245233	816	PM1429		1.00E-107	Pmu	E	COG0169	Shikimate 5-dehydrogenase	AroE	(NC_002663) unknown [Pasteurella multocida]
MS2316	2246052	2245279	774	srIR		3.00E-80	Eco	K/G	COG1349	Transcriptional regulators of sugar metabolism	GlpR	(NC_000913) regulator for gut (srI)glucitol o...
MS2317	2246687	2246184	504	PM0101		5.00E-56	No-des	none	No-des	none	none	(NC_002663) unknown [Pasteurella multocida]
MS2318	2247548	2246790	759	HI0280		1.00E-115	Hin	F	COG2820	Uridine phosphorylase	Udp	(NC_000907) uridine phosphorylase (udp) [Haemop...
MS2319	2248491	2247649	843	PM1508		1.00E-100	Pmu	S	COG2861	Uncharacterized BCR		hypothetical protein HI0755 - Haemophilus influenzae...
MS2320	2249711	2248491	1221	PM1507		1.00E-106	Pmu	M	COG0739	Membrane proteins related to metalloendopeptidases	NlpD	(NC_002663) unknown [Pasteurella multocida]
MS2321	2249865	2250545	681	PM1506		1.00E-105	Pmu	G	COG0588	Phosphoglycerate mutase 1	GpmA	(NC_002663) GpmA [Pasteurella multocida]
MS2322	2250790	2251593	804	ZrhaS		1.00E-52	EcZ	K	COG2207	AraC-type DNA-binding domain-containing proteins	AraC	(NC_003143) L-rhamnose operon regulatory protei...
MS2323	2251598	2252425	828	rhaR		6.00E-41	Eco	K	COG2207	AraC-type DNA-binding domain-containing proteins	AraC	(NC_003143) L-rhamnose operon transcriptional a...
MS2324	2252826	2252470	357	yiiL		4.00E-40	Eco	S	COG3254	Uncharacterized ACR		(NC_003143) conserved hypothetical protein [Yer...
MS2325	2253943	2252795	1149	ZrhaO		1.00E-152	EcZ	C	COG1454	Alcohol dehydrogenase IV	EutG	(NC_002655) L-12-propanediol oxidoreductase [E...
MS2326	2255008	2253977	1032	rhaT		1.00E-129	Eco	G/E/R	COG0697	Permeases of the drug/metabolite transporter (DMT) superfamily	RhaT	(NC_003143) L-rhamnose-proton symport protein [...
MS2327	2255918	2255103	816	rhaD		1.00E-111	Eco	G	COG0235	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	AraD	(NC_000913) rhamnulose-phosphate aldolase [Esch...
MS2328	2257181	2255931	1251	ZrhaA		0	No-des	none	No-des	none	none	(NC_003197) L-rhamnose isomerase [Salmonella ty...
MS2329	2258655	2257210	1446	ZrhaB		1.00E-149	EcZ	G	COG1070	Sugar (pentulose and hexulose) kinases	XylB	(NC_002695) rhamnulokinase [Escherichia coli O1...
MS2330	2258901	2259572	672	PM1619		1.00E-105	Pmu	G	COG0036	Pentose-5-phosphate-3-epimerase	Rpe	(NC_002663) Dod [Pasteurella multocida]
MS2331	2259587	2260258	672	HI0565		1.00E-107	Hin	R	COG0546	Predicted phosphatases	Gph	(NC_000907) phosphoglycolate phosphatase (gph) ...
MS2332	2260311	2261315	1005	PM1621		1.00E-155	Pmu	J	COG0180	Tryptophanyl-tRNA synthetase	TrpS	(NC_002663) TrpS [Pasteurella multocida]
MS2333	2262437	2261517	921	VC0480		3.00E-45	Vch	M	COG0668	Small-conductance mechanosensitive channel	MscS	(NC_002505) conserved hypothetical protein [Vib...
MS2334	2263085	2262561	525	HI1043		5.00E-41	Hin	C	COG1145	Ferredoxin 2	NapF	(NC_000907) ferredoxin-type protein (napF) [Hae...
MS2335	2263756	2263085	672	HI1044		2.00E-51	Hin	R	COG3381	Uncharacterized component of anaerobic dehydrogenases	TorD	(NC_000907) conserved hypothetical protein [Hae...

MS2336	2264026	2263772	255	HI1045	5.00E-18	Hin	R	COG3302	DMSO reductase anchor subunit		DmsC	(U26665) dimethyl sulphoxide reductase subunit C ...
MS2337	2264223	2264089	135	Z2576	3.00E-12	EcZ	C	COG0243	Anaerobic dehydrogenases/typically selenocysteine-containing		BisC	(NC_003198) putative dimethyl sulphoxide reduct...
MS2338	2264598	2265992	1395	HI0708	1.00E-175	Hin	E	COG1921	Selenocysteine synthase seryl-tRNA ^{Ser} selenium transferase		SeLa	(NC_000907) L-seryl-tRNA selenium transferase (...)
MS2339	2265997	2267853	1857	PM1766	0	Pmu	J	COG3276	Selenocysteine-specific translation elongation factor		SeIB	(NC_002663) SeIB [Pasteurella multocida]
MS2340	2268024	2268656	633	ZyagU	9.00E-73	EcZ	S	COG3477	Predicted periplasmic/secreted protein			(NC_002655) orf10/hypothetical protein [Escheric...
MS2341	2269185	2268730	456	PM1604	1.00E-56	Pmu	LJR	COG0494	NTP pyrophosphohydrolases including oxidative damage repair enzymes		MutT	(NC_002663) unknown [Pasteurella multocida]
MS2342	2269931	2269191	741	HI0694	6.00E-85	Hin	J	COG1187	16S rRNA uridine-516 pseudouridylyate synthase and related pseudouridylyate synthases		RsuA	(NC_000907) conserved hypothetical protein [Hae...
MS2343	2270769	2270011	759	none	none	none	none	No-des	No-des		none	none
MS2344	2271535	2270753	783	HI0003	6.00E-65	Hin	R	COG0561	Predicted hydrolases of the HAD superfamily		Cof	(NC_000907) conserved hypothetical protein [Hae...
MS2345	2272049	2271624	426	PM1495	5.00E-59	Pmu	C	COG0355	F0F1-type ATP synthase epsilon subunit (mitochondrial delta subunit)		AtpC	(NC_002663) AtpC [Pasteurella multocida]
MS2346	2273463	2272090	1374	HI0479	0	Hin	C	COG0055	F0F1-type ATP synthase beta subunit		atpD	(NC_000907) ATP synthase F1 subunit beta (atpD...
MS2347	2274348	2273482	867	HI0480	1.00E-135	Hin	C	COG0234	F0F1-type ATP synthase gamma subunit		atpG	(NC_000907) ATP synthase F1 subunit gamma (atp...
MS2348	2275907	2274369	1539	HI0481	0	Hin	C	COG0056	F0F1-type ATP synthase alpha subunit		AtpA	(NC_000907) ATP synthase F1 subunit alpha (atp...
MS2349	2276495	2275926	570	HI0482	9.00E-74	Hin	C	COG0712	F0F1-type ATP synthase delta subunit (mitochondrial oligomycin sensitivity protein)		atpH	(NC_000907) ATP synthase F1 subunit delta (atp...
MS2350	2276952	2276485	468	HI0483	5.00E-60	Hin	C	COG0711	F0F1-type ATP synthase b subunit		atpF	(NC_000907) ATP synthase F0 subunit b (atpF) [...
MS2351	2277286	2277023	264	HI0484	9.00E-38	Hin	C	COG0636	F0F1-type ATP synthase c subunit/Archaeal/vacuolar-type H ⁺ -ATPase subunit K		atpE	(NC_000907) ATP synthase F0 subunit c (atpE) [...
MS2352	2278116	2277331	786	HI0485	1.00E-138	Hin	C	COG0356	F0F1-type ATP synthase a subunit		AtpB	(NC_000907) ATP synthase F0 subunit a (atpB) [...
MS2353	2279255	2278617	639	PM1486	1.00E-74	Pmu	M	COG0357	Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division		GidB	(NC_002663) GidB [Pasteurella multocida]
MS2354	2281134	2279248	1887	PM1485	0	Pmu	D	COG0445	NAD/FAD-utilizing enzyme apparently involved in cell division		GidA	(NC_002663) GidA [Pasteurella multocida]
MS2355	2282552	2281602	951	HI1125	1.00E-157	Hin	G	COG0176	Transaldolase		MipB	(NC_000907) transaldolase B (talB) [Haemophilus ...]
MS2356	2282734	2283288	555	HI0654	2.00E-74	Hin	L	COG2818	3-Methyladenine DNA glycosylase		Tag	(NC_000907) DNA-3-methyladenine glycosidase I (...)
MS2357	2283378	2285726	2349	PM1600	0	Pmu	M	COG1452	Organic solvent tolerance protein Osta		Imp	(NC_002663) unknown [Pasteurella multocida]
MS2358	2286113	2285841	273	HIN0796	4.00E-33	Hin	O	COG0298	Hydrogenase maturation factor		hycC	(NC_000907) Hydrogenase maturation factor [Haem...
MS2359	2286657	2286148	510	hybE	7.00E-32	No-des	none	No-des	No-des		none	(NC_003198) hydrogenase-2 component protein [Sa...
MS2360	2287144	2286668	477	hybD	2.00E-42	Eco	C	COG0680	NiFe-hydrogenase maturation factor		HyaD	(NC_003198) hydrogenase-2 component protein [Sa...
MS2361	2288853	2287147	1707	ZhybC	0	EcZ	C	COG0374	NiFe-hydrogenase I large subunit		HyaB	(NC_003197) hydrogenase-2 large subunit [Salmo...
MS2362	2289909	2288869	1041	ZhybB	1.00E-127	No-des	none	No-des	No-des		none	(NC_003197) putative cytochrome Ni/Fe component...
MS2363	2289974	2290150	177	ZhybB	2.00E-06	No-des	none	No-des	No-des		none	(NC_002655) probable cytochrome Ni/Fe component...
MS2364	2291071	2290082	990	hybA	1.00E-133	Eco	C	COG0437	Fe-S-cluster-containing hydrogenase components I		HybA	(NC_002695) hydrogenase-2 small subunit [Escher...
MS2365	2292252	2291077	1176	Z4351	1.00E-144	EcZ	C	COG1740	NiFe-hydrogenase I small subunit		HyaA	(NC_002655) putative hydrogenase subunit [Esche...
MS2366	2292269	2292358	90	none	none	none	none	No-des	No-des		none	none
MS2367	2292505	2293596	1092	HI0848	1.00E-175	Hin	J	COG2265	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase		TrmA	(NC_000907) tRNA (uracil-5-)-methyltransferase ...
MS2368	2293601	2294356	756	PM1804	1.00E-100	Pmu	Q/R	COG0500	SAM-dependent methyltransferases		SmtA	(NC_002663) unknown [Pasteurella multocida]
MS2369	2297116	2294513	2604	PM0204	0	Pmu	C	COG1049	Aconitase B		AcnB	(NC_002663) AcnB [Pasteurella multocida]
MS2370	2298393	2297149	1245	PM1606	0	Pmu	C	COG0538	Isocitrate dehydrogenases		Icd	(NC_002663) Idp [Pasteurella multocida]
MS2371	2298673	2299953	1281	PM0276	0	Pmu	C	COG0372	Citrate synthase		GltA	(NC_002663) GltA [Pasteurella multocida]
MS2372	2301466	2300024	1443	xyiB	1.00E-158	Eco	G	COG1070	Sugar (pentulose and hexulose) kinases		XylB	(NC_003143) xylofucose kinase [Yersinia pestis]
MS2373	2302870	2301560	1311	HI1112	0	Hin	G	COG2115	Xylose isomerase		XylA	(NC_000907) xylose isomerase (xylA) [Haemophilu...
MS2374	2303109	2304551	1443	ZxylE	1.00E-153	EcZ	G/E P/R	COG0477	Permeases of the major facilitator superfamily		ProP	(NC_002655) xylose-proton symport [Escherichia ...]
MS2375	2304683	2305846	1164	HI1106_1	1.00E-105	Hin	K	COG1609	Transcriptional regulators		PurR	(NC_000907) xylose operon regulatory protein (x...
MS2376	2306275	2305895	381	none	none	No-des	none	No-des	No-des		none	none
MS2377	2307221	2306391	831	ZmanZ	3.00E-82	No-des	none	No-des	No-des		none	(NC_003143) PTS system mannose-specific IID co...
MS2378	2308036	2307239	798	PM0833	2.00E-73	No-des	none	No-des	No-des		none	(NC_003143) PTS system mannose-specific IIC co...
MS2379	2309018	2308056	963	manX_2	5.00E-36	Eco	G	COG3444	Phosphotransferase system mannotose/fructose/N-acetylgalactosamine-specific component IIB			(NC_003198) PTS system mannotose-specific IiAB c...
MS2380	2309202	2309300	99	none	none	No-des	none	No-des	No-des		none	none
MS2381	2309850	2309296	555	BS_ydeN	3.00E-32	Bsu	R	COG3545	Predicted esterase of the alpha beta hydrolase fold			(NC_000964) ydeN [Bacillus subtilis]
MS2382	2310152	2311657	1506	HI0736	0	Hin	R	COG0733	Na ⁺ -dependent transporters of the SNF family			(NC_000907) sodium-dependent transporter putat...
MS2383	2311662	2311751	90	none	none	No-des	none	No-des	No-des		none	none
MS2384	2311939	2312040	102	none	none	No-des	none	No-des	No-des		none	none

[illegible]