

Supplementary material

Table S1. Quantification of cDNA libraries using Nanodrop (absorbance values). Treatments: *Xf*: *X. fastidiosa* 9a5c; *Xf+Mm*: *X. fastidiosa* 9a5c + *M. mesophilicum* SR1.6/6; *Mm*: *M. mesophilicum* SR1.6/6.

		Replicate 1		Replicate 2		Replicate 3			
Treatment	ng/μl	A260/A280 (nm)	A260/A230 (nm)	ng/μl	A260/A280 (nm)	A260/A230 (nm)	ng/μl	A260/A280 (nm)	A260/A230 (nm)
<i>Xf</i>	64.7	1.89	2.23	79.1	1.88	2.29	71.4	1.86	2.19
<i>Xf+Mm</i>	35.1	1.89	2.20	46.5	1.87	2.20	50.9	1.87	2.11
<i>Mm</i>	22.6	1.90	1.98	42.7	1.85	1.96	29.6	1.89	2.13

Table S2. Amount of reads per run and per treatment. Treatments: *Xf*: *X. fastidiosa* 9a5c; *Xf+Mm*: *X. fastidiosa* 9a5c + *M. mesophilicum* SR1.6/6; *Mm*: *M. mesophilicum* SR1.6/6.

Treatment (replicate)	Index	Runs	Reads percentage	Number of reads per treatment	Total reads of the run (PF-pass filter)	Total reads >Q30* (%)
<i>Xf</i> (1)	AGTTCC	1	14.96	3,469,612	24,782,942	64.85
<i>Xf+Mm</i> (1)	CCGTCC		14.97	3,708,938		
<i>Mm</i> (1)	GTCCGC		13.57	3,345,697		
<i>Xf</i> (2)	CTTGTA	2	17.38	5,387,824	31,143,494	78.69
<i>Xf+Mm</i> (2)	ATGTCA		16.00	4,982,959		
<i>Mm</i> (2)	GTGAAA		14.67	4,546,950		
<i>Xf</i> (3)	AGTCAA	3	15.12	4,080,772	26,989,232	80.97
<i>Xf+Mm</i> (3)	ATGTCA		16.80	4,534,191		
<i>Mm</i> (3)	GTCCGC		14.86	4,010,600		

*Q30 score means an error probability of 1-1000 of a nucleotide assignment.

Table S3. Number of mapped reads in *Xf* and *Mm* using CLC Genomics Workbench software. *Xf*: *X. fastidiosa*; *Mm*: *M. mesophilicum*.

Treatment	Biological replicate	Number of reads	Mapped reads in pairs	% mapped reads	Unique fragments
<i>X. fastidiosa</i> monoculture					

<i>Xf</i>	1	3,706,786	2,898,062	78.18	1,449,031
<i>Xf</i> pXF51			59,234	1.60	29,617
<i>Xf</i>	2	5,413,426	4,259,328	78.68	2,129,664
<i>Xf</i> pXF51			94,616	1.75	47,308
<i>Xf</i>	3	4,082,770	3,414,068	83.62	1,700,027
<i>Xf</i> pXF51			110,856	2.44	55,330
Average		4,400,994	3,523,819	80.16	1,759,574
Co-culture mapped in <i>Xf</i> genome					
<u><i>Xf+Mm</i></u> in <i>Xf</i>	1	3,708,938	1,514,052	40.82	757,026
<u><i>Xf+Mm</i></u> in <i>Xf</i> pXF51			56,182	1.51	28,091
<u><i>Xf+Mm</i></u> in <i>Xf</i>	2	4,987,168	2,695,846	54.06	1,347,923
<u><i>Xf+Mm</i></u> in <i>Xf</i> pXF51			103,718	2.08	51,859
<u><i>Xf+Mm</i></u> in <i>Xf</i>	3	4,536,488	2,644,388	58.29	1 317,944
<u><i>Xf+Mm</i></u> in <i>Xf</i> pXF51			89,750	2.20	29,417
Average		4,410,865	2,284,762	51.05	1,140,964
Co-culture mapped in <i>Mm</i> genome					
<u><i>Xf+Mm</i></u> in <i>Mm</i>	1	3,708,938	1,053,066	28.39	526,533
<u><i>Xf+Mm</i></u> in <i>Mm</i>	2	4,987,168	1,287,294	25.81	643,647
<u><i>Xf+Mm</i></u> in <i>Mm</i>	3	4,536,488	1,135,146	25.02	564,667
Average		4,410,865	1,158,502	26.41	578,282
<i>M. mesophilicum</i> monoculture					
<i>Mm</i>	1	3,362,754	1,853,878	55.13	926,939
<i>Mm</i>	2	4,568,912	3,575,600	78.26	1,787,800
<i>Mm</i>	3	4,011,524	3,248,148	80.97	1,617,962
Average		3,981,063	2,892,542	71.45	1,444,234

Table S4. Differentially expressed genes in the endophyte *Xf* only and during co-culture.

Class	Genic Category		SeqName	Gene product name	log2FoldChange	Description	Length	#Hits	#GO	GO Names list	Enzyme Codes list	InterPro IDs
Macromolecule metabolism	RNA metabolism	ribosomal protein	XF9a_01063	ribosomal protein L2, bacterial/organellar	-0.429978502	RL2_XYLFA ame: Full=50S ribosomal L2	275	5	5	F:structural constituent of ribosome; C:large ribosomal subunit; F:transferase activity; F:rRNA binding; P:translation		IPR022669 (SMART); IPR002171 (SMART); IPR022669 (PFAM); IPR005880 (TIGRFAM); IPR014726 (G3DSA:4.10.950.GENE3D); IPR022666 (PFAM); IPR002171 (PIRSF); G3DSA:2.40.50.140 (GENE3D); IPR014722 (G3DSA:2.30.30.GENE3D); PTHR13691:SF5 (PANTHER); IPR002171 (PANTHER); IPR005880 (HAMAP); IPR012340 (SUPERFAMILY); IPR008991 (SUPERFAMILY)
	RNA metabolism	ribosomal protein	XF9a_02489	Ribosomal protein L10	-0.572760956	RL10_XYLFA ame: Full=50S ribosomal L10	175	5	5	F:structural constituent of ribosome; P:ribosome biogenesis; C:ribosome; F:large ribosomal subunit rRNA binding; P:translation		G3DSA:3.30.70.1730 (GENE3D); IPR001790 (PFAM); PTHR11560 (PANTHER); PTHR11560:SF8 (PANTHER); IPR022973 (HAMAP); SSF160369 (SUPERFAMILY)
	RNA metabolism	ribosomal protein	XF9a_02485	ribosomal protein S12, bacterial/organelle	-0.650397594	RS12_XYLFT ame: Full=30S ribosomal S12	132	5	5	F:structural constituent of ribosome; C:small ribosomal subunit; F:tRNA binding; F:rRNA binding; P:translation		IPR006032 (PRINTS); IPR006032 (PIRSF); IPR005679 (TIGRFAM); IPR006032 (PFAM); G3DSA:2.40.50.140 (GENE3D); PTHR11652:SF1 (PANTHER); IPR006032 (PANTHER); IPR005679 (HAMAP); IPR012340 (SUPERFAMILY)
	RNA metabolism	ribosomal protein	XF9a_02441	ribosomal protein S2, bacterial type	-0.55705189	RS2_XYLFT ame: Full=30S ribosomal S2	266	5	3	F:structural constituent of ribosome; C:small ribosomal subunit; P:translation		IPR001865 (PRINTS); G3DSA:3.40.50.10490 (GENE3D); IPR005706 (TIGRFAM); G3DSA:1.10.287.610 (GENE3D); IPR001865 (PFAM); IPR005706 (PANTHER); PTHR12534:SFO (PANTHER); IPR005706 (HAMAP); IPR023591 (SUPERFAMILY)
	RNA metabolism	ribosomal protein	XF9a_01083	ribosomal protein S4, bacterial/organelle type	-0.588341505	RS4_XYLFA ame: Full=30S ribosomal S4	208	5	5	P:positive regulation of translational fidelity; F:structural constituent of ribosome; C:small ribosomal subunit; F:rRNA binding; P:translation		IPR002942 (SMART); IPR001912 (SMART); G3DSA:1.10.1050.10 (GENE3D); IPR002942 (PFAM); IPR036986 (G3DSA:3.10.290.GENE3D); IPR005709 (TIGRFAM); IPR001912 (PFAM); IPR022801 (PANTHER); IPR005709 (PTHR11831:PANTHER); IPR005709 (HAMAP); IPR002942 (PROSITE_PROFILES); SSF55174 (SUPERFAMILY)
	RNA metabolism	Elongation factor	XF9a_02440	translation elongation factor Ts	-0.518813753	EFTS_XYLFA ame: Full=Elongation factor Ts Short=EF-Ts	292	5	3	F:translation elongation factor activity; C:cytoplasm; P:translational elongation		IPR036402 (G3DSA:3.30.479.GENE3D); G3DSA:1.10.286.20 (GENE3D); IPR014039 (PFAM); G3DSA:1.10.8.10 (GENE3D);

											IPR001816 (TIGRFAM); IPR036402 (G3DSA:3.30.479.GENE3D); IPR001816 (PANTHER); IPR001816 (HAMAP); IPR009060 (SUPERFAMILY); IPR036402 (SUPERFAMILY); IPR036402 (SUPERFAMILY)
	RNA metabolism	Elongation factor	XF9a_02483	translation elongation factor EF-G	-0.398759307	EFG_XYLFA ame: Full=Elongation factor G Short=EF-G	705	5	5	F:GTP binding; F:translation elongation factor activity; C:cytoplasm; F:GTPase activity; P:translational elongation	IPR000795 (PRINTS); IPR000640 (SMART); IPR005517 (SMART); IPR005517 (PFAM); G3DSA:2.40.30.10 (GENE3D); G3DSA:3.30.70.240 (GENE3D); IPR005225 (TIGRFAM); IPR004161 (PFAM); IPR014721 (G3DSA:3.30.230.GENE3D); G3DSA:3.40.50.300 (GENE3D); PF14492 (PFAM); IPR000795 (PFAM); IPR000640 (PFAM); IPR004540 (TIGRFAM); G3DSA:3.30.70.870 (GENE3D); PTHR43261:SF1 (PANTHER); PTHR43261 (PANTHER); IPR000795 (PROSITE_PROFILES); IPR004540 (HAMAP); IPR027417 (SUPERFAMILY); IPR035647 (SUPERFAMILY); IPR035647 (SUPERFAMILY); IPR009000 (SUPERFAMILY); IPR020568 (SUPERFAMILY)
	RNA metabolism	Elongation factor	XF9a_02333	translation elongation factor P	-0.577403731	EF_P_XYLFT ame: Full=Elongation factor P Short=EF-P	188	5	3	F:translation elongation factor activity; C:cytoplasm; P:translational elongation	IPR015365 (SMART); IPR001059 (SMART); IPR020599 (PIRSF); IPR013185 (PFAM); IPR011768 (TIGRFAM); IPR001059 (PFAM); G3DSA:2.40.50.140 (GENE3D); IPR014722 (G3DSA:2.30.30.GENE3D); IPR015365 (PFAM); G3DSA:2.40.50.140 (GENE3D); IPR020599 (PANTHER); IPR011768 (HAMAP); IPR008991 (SUPERFAMILY); IPR012340 (SUPERFAMILY); IPR012340 (SUPERFAMILY)
	RNA metabolism	Elongation factor	XF9a_02099	elongation factor P- like protein YeiP	0.854980632	EFPL_XYLFA ame: Full=Elongation factor P	188	5	3	F:translation elongation factor activity; C:cytoplasm; P:translational elongation	IPR015365 (SMART); IPR001059 (SMART); G3DSA:2.40.50.140 (GENE3D); IPR015365 (PFAM); IPR013185 (PFAM); IPR014722 (G3DSA:2.30.30.GENE3D); IPR020599 (PIRSF); IPR011897 (TIGRFAM); IPR001059 (PFAM); G3DSA:2.40.50.140 (GENE3D); PTHR30053:SF5 (PANTHER); IPR020599 (PANTHER); IPR011897 (HAMAP); IPR008991 (SUPERFAMILY); IPR012340 (SUPERFAMILY); IPR012340 (SUPERFAMILY)

	RNA metabolism		XF9a_02511	Predicted N6-adenine-specific DNA methylase (EC:2.1.1.173)	0.526446529	RLMKL_XYLFA ame: Full=Ribosomal RNA large subunit methyltransferase K L Includes: ame: Full=23S rRNA m2G2445 methyltransferase ame: Full=rRNA (guanine-N(2)-)-methyltransferase Includes: ame: Full=23S rRNA m7G2069 methyltransferase ame: Full=rRNA (guanine-N(7)-)-methyltransferase	748	5	5	F:RNA binding; C:cytoplasm; F:rRNA (guanine-N7)-methyltransferase activity; F:23S rRNA (guanine(2445)-N(2))-methyltransferase activity; P:rRNA (guanine-N7)-methylation	EC:2.1.1.173	IPR004114 (SMART); IPR017244 (PIRSF); G3DSA:3.30.750.80 (GENE3D); G3DSA:3.30.2130.30 (GENE3D); IPR004114 (PFAM); G3DSA:3.40.50.150 (GENE3D); G3DSA:3.40.50.150 (GENE3D); IPR000241 (PFAM); IPR019614 (PFAM); PTHR18895 (PANTHER); PTHR18895:SF62 (PANTHER); IPR004114 (PROSITE_PROFILES); IPR017244 (HAMAP); IPR029063 (SUPERFAMILY); IPR029063 (SUPERFAMILY)
	RNA metabolism	transcription factor binding	XF9a_02233	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	0.633263148	Y2439_ANADF ame: Full=Response regulator receiver Anaef109_2439	236	5	3	P:regulation of cellular process; F:binding; P:cellular process		IPR001789 (SMART); IPR008207 (PFAM); IPR036641 (G3DSA:1.20.120.GENE3D); G3DSA:3.40.50.2300 (GENE3D); IPR001789 (PFAM); PTHR26402 (PANTHER); IPR001789 (PROSITE_PROFILES); IPR008207 (PROSITE_PROFILES); IPR011006 (SUPERFAMILY); IPR036641 (SUPERFAMILY)
	RNA metabolism		XF9a_02299	integration host factor, beta subunit	-0.625635812	IHFB_XYLFA ame: Full=integration host factor subunit beta Short=IHf-beta	104	5	7	P:regulation of translation; F:DNA binding; P:transcription, DNA-templated; P:DNA recombination; C:cytosol; P:regulation of transcription, DNA-templated; C:chromosome		IPR000119 (PRINTS); IPR000119 (SMART); IPR000119 (PFAM); IPR010992 (G3DSA:4.10.520.GENE3D); IPR005685 (TIGRFAM); IPR000119 (PANTHER); PTHR33175:SF5 (PANTHER); IPR005685 (HAMAP); IPR010992 (SUPERFAMILY)
	RNA metabolism		XF9a_01462	Predicted nucleic acid-binding protein, contains PIN domain	-0.629265663	Y4JK_RHISN ame: Full=ribonuclease Y4JK Short=RNase Y4JK ame: Full= plasmid stability Y4JK ame: Full=Toxin Y4JK	142	5	5	P:nucleic acid phosphodiester bond hydrolysis; F:protein binding; F:metal ion binding; P:migration in host; F:nuclease activity		IPR002716 (PFAM); G3DSA:3.40.50.1010 (GENE3D); PTHR33653:SF1 (PANTHER); PTHR33653 (PANTHER); IPR022907 (HAMAP); IPR029060 (SUPERFAMILY)
	RNA metabolism	post transcriptional regulation	XF9a_01626	hypothetical protein	-0.605930558	TDRD7_MOUSE ame: Full=Tudor domain-containing 7 ame: Full=PCTAIRE2-binding ame: Full=Tudor repeat associator with PCTAIRE-2 Short=Trap	208	2	17	P:germ cell development; C:ribonucleoprotein granule; C:chromatoid body; P:lens morphogenesis in camera-type eye; P:posttranscriptional regulation of gene expression; F:protein binding; C:intracellular ribonucleoprotein complex; C:cytoplasm; C:mitochondrial matrix; F:protein N-terminus binding; C:P granule; P:cell differentiation; F:mRNA binding; P:lens fiber cell differentiation		no IPS match
	RNA metabolism	miscRNA	XF9a_01899	6S / SsrS RNA (miscRNA) (XF9a_gi57014152.1: 2679305bp)	1.0111716		186					no IPS match
	RNA metabolism	miscRNA	XF9a_00950	Bacterial signal recognition particle RNA (miscRNA) (XF9a_gi57014152.1: 2679305bp)	0.809822873		100					no IPS match

	RNA metabolism	miscRNA	XF9a_00973	Bacterial RNase P class A (miscRNA) (XF9a_gi57014152.1: 2679305bp)	2.329311093		350					no IPS match
	Protein metabolism	tRNA	XF9a_00214	tRNA_Met_CAT (tRNA) (XF9a_gi57014152.1: 2679305bp)	-0.755430102		77					no IPS match
	Protein metabolism	tRNA	XF9a_02429	asparaginyl-tRNA synthetase (EC:6.1.1.22)	-0.481090758	SYN_XYLFA ame: Full=Asparagine--tRNA ligase ame: Full=Asparaginyl-tRNA synthetase Short=	466	5	5	F:nucleic acid binding; F:ATP binding; C:cytoplasm; F:asparagine-tRNA ligase activity; P:asparaginyl-tRNA aminoacylation	EC:6.1.1.22	IPR002312 (PRINTS); G3DSA:3.30.930.10 (GENE3D); G3DSA:2.40.50.140 (GENE3D); IPR004364 (PFAM); IPR004522 (TIGRFAM); IPR004365 (PFAM); PTHR22594 (PANTHER); PTHR22594:SF44 (PANTHER); IPR006195 (PROSITE_PROFILES); IPR004522 (HAMAP); SSF55681 (SUPERFAMILY); IPR012340 (SUPERFAMILY)
	Protein metabolism	tRNA	XF9a_00387	tryptophanyl-tRNA synthetase (EC:6.1.1.2)	0.677162266	SYW_XYLFA ame: Full=Tryptophan--tRNA ligase ame: Full=Tryptophanyl-tRNA synthetase Short=	430	5	4	F:ATP binding; C:cytoplasm; P:tryptophanyl-tRNA aminoacylation; F:tryptophan-tRNA ligase activity	EC:6.1.1.2	IPR002306 (PRINTS); G3DSA:1.10.240.10 (GENE3D); IPR014729 (G3DSA:3.40.50.GENE3D); IPR002306 (TIGRFAM); IPR002305 (PFAM); PTHR43766 (PANTHER); IPR024109 (HAMAP); IPR036913 (SUPERFAMILY); SSF52374 (SUPERFAMILY)
	Protein metabolism	tRNA	XF9a_02509	glutamyl-tRNA reductase (EC:1.2.1.70)	0.528218218	HEM1_XYLFA ame: Full=Glutamyl-tRNA reductase Short=	418	5	4	F:NADP binding; F:glutamyl-tRNA reductase activity; P:oxidation-reduction process; P:protoporphyrinogen IX biosynthetic process	EC:1.2.1.70	IPR015895 (PFAM); IPR000343 (TIGRFAM); IPR006151 (PFAM); IPR000343 (PIRSF); G3DSA:3.40.50.720 (GENE3D); IPR015896 (PFAM); IPR036343 (G3DSA:3.30.460.GENE3D); PTHR43013 (PANTHER); IPR000343 (HAMAP); IPR036453 (SUPERFAMILY); IPR036343 (SUPERFAMILY); IPR036291 (SUPERFAMILY)
				presente no biofilme - trabalho de proteoma								
Intermediary metabolism	Energy Production	electron transport	XF9a_01056	ATP synthase, F0 subunit c (EC:3.6.3.14)	-0.476177408	ATPL_VEREI ame: Full=ATP synthase subunit c ame: Full=ATP synthase F(0) sector subunit c ame: Full=F-type ATPase subunit c Short=F-ATPase subunit c ame: Full=Lipid-binding	101	5	6	P:ATP hydrolysis coupled proton transport; C:plasma membrane proton-transporting ATP synthase complex, coupling factor F(o); C:integral component of membrane; F:lipid binding; P:ATP synthesis coupled proton transport; F:proton-transporting ATP synthase activity, rotational mechanism		IPR000454 (PRINTS); IPR005953 (TIGRFAM); IPR038662 (G3DSA:1.20.20.GENE3D); IPR002379 (PFAM); IPR000454 (PANTHER); PTHR10031:SF0 (PANTHER); IPR000454 (HAMAP); IPR035921 (SUPERFAMILY)
		Sulfur Metabolism / ATP byssintesis	XF9a_01373	sulfate adenyltransferase, small subunit (EC:2.7.7.4) 60:60	-0.906128907	CYSD_XYLFA ame: Full=Sulfate adenyltransferase subunit 2 ame: Full=ATP-sulfurylase	304	5	5		EC:2.7.7.4	IPR011784 (PIRSF); IPR014729 (G3DSA:3.40.50.GENE3D); IPR002500 (PFAM); IPR011784 (TIGRFAM); PTHR43196 (PANTHER); IPR011784

						small subunit ame: Full=Sulfate adenylate transferase Short=SAT						(HAMAP); SSF52402 (SUPERFAMILY)
		Sulfur Metabolism	XF9a_01374	sulfate adenyltransferase, large subunit (EC:2.7.1.25,EC:2.7.7.4)	-0.444791682	CYSNC_XYLFA ame: Full=Bifunctional enzyme Includes: ame: Full=Sulfate adenyltransferase subunit 1 ame: Full=ATP-sulfurylase large subunit ame: Full=Sulfate adenylate transferase Short=SAT Includes: ame: Full=Adenyl-sulfate kinase ame: Full=APS kinase ame: Full=ATP adenosine-5 - phosphosulfate 3 - phosphotransferase	660	5	8	F:GTP binding; F:ATP binding; P:hydrogen sulfide biosynthetic process; F:GTPase activity; F:adenylsulfate kinase activity; F:sulfate adenyltransferase (ATP) activity; P:phosphorylation; P:sulfate assimilation	EC:2.7.7.4; EC:2.7.1.25	IPR000795 (PRINTS); G3DSA:3.40.50.300 (GENE3D); IPR011779 (TIGRFAM); PFO1583 (PFAM); G3DSA:2.40.30.10 (GENE3D); IPR002891 (TIGRFAM); IPR000795 (PFAM); G3DSA:2.40.30.10 (GENE3D); G3DSA:3.40.50.300 (GENE3D); PTHR11055:SF27 (PANTHER); PTHR11055 (PANTHER); IPR011779 (HAMAP); IPR002891 (HAMAP); IPR000795 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); IPR009001 (SUPERFAMILY); IPR009000 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
		Faz NADPH	XF9a_01709	ketol-acid reductoisomerase (EC:1.1.1.86)	-0.483212318	ILVC_XYLFA ame: Full=Ketol-acid reductoisomerase (NADP(+)) Short=KARI ame: Full=Acetohydroxy-acid isomeroeductase Short=AHIR ame: Full=Alpha-keto-beta- hydroxylacyl reductoisomerase ame: Full=Ketol-acid reductoisomerase type 1 ame: Full=Ketol-acid reductoisomerase type I	335	5	4	P:isoleucine biosynthetic process; P:valine biosynthetic process; P:oxidation-reduction process; F:ketol-acid reductoisomerase activity	EC:1.1.1.86	IPR013116 (PFAM); IPR014359 (PIRSF); G3DSA:1.10.3730.40 (GENE3D); G3DSA:3.40.50.720 (GENE3D); IPR000506 (PFAM); IPR013023 (TIGRFAM); PTHR21371:SF1 (PANTHER); IPR013023 (PANTHER); IPR000506 (PROSITE_PROFILES); IPR013116 (PROSITE_PROFILES); IPR013023 (HAMAP); IPR036291 (SUPERFAMILY); IPR008927 (SUPERFAMILY)
		Faz NADPH	XF9a_02062	nicotinate (nicotinamide) nucleotide adenyltransferase (EC:2.7.7.18)	0.608755034	NADD_XYLFA ame: Full=Probable nicotinate-nucleotide adenyltransferase ame: Full=Deamido- NAD(+) diphosphorylase ame: Full=Deamido-NAD(+) pyrophosphorylase ame: Full=Nicotinate mononucleotide adenyltransferase Short= adenyltransferase	222	5	3	F:ATP binding; F:nicotinate- nucleotide adenyltransferase activity; P:NAD biosynthetic process	EC:2.7.7.18	IPR004821 (TIGRFAM); IPR004821 (PFAM); IPR005248 (TIGRFAM); IPR014729 (G3DSA:3.40.50.GENE3D); PTHR21342 (PANTHER); IPR005248 (HAMAP); SSF52374 (SUPERFAMILY)
		electron transport	XF9a_00841	ubiquinol-cytochrome c reductase, iron-sulfur subunit (EC:1.10.2.2)	1.012664941	UCRI_ALLVD ame: Full=Ubiquinol- cytochrome c reductase iron-sulfur subunit ame: Full=Rieske iron-sulfur Short=RISP	210	5	7	F:oxidoreductase activity; C:intracellular membrane- bounded organelle; P:metabolic process; C:cytoplasmic part; C:membrane part; F:binding; P:single-organism process		IPR005805 (PRINTS); IPR036922 (G3DSA:2.102.10.GENE3D); IPR006317 (TIGRFAM); IPR019470 (PFAM); IPR017941 (PFAM); PTHR10134:SF1 (PANTHER); IPR014349 (PANTHER); IPR017941 (PROSITE_PROFILES); IPR036922 (SUPERFAMILY)

		citric acid cycle	XF9a_01739	hydro-lyases, Fe-S type, tartrate/fumarate subfamily, alpha region/hydro-lyases, Fe-S type, tartrate/fumarate subfamily, beta region (EC:4.2.1.2)	0.48574495	FUMB_ECOLI ame: Full=Fumarate hydratase class anaerobic ame: Full=D-tartrate dehydratase ame: Full=Fumarase B	530	5	3	F:hydro-lyase activity; F:binding; P:cellular process	IPR011167 (PIRSF); IPR004646 (TIGRFAM); IPR004647 (PFAM); IPR004646 (PFAM); IPR036660 (G3DSA:3.20.130.GENE3D); IPR004647 (TIGRFAM); PTHR30389 (PANTHER); IPR036660 (SUPERFAMILY)
Cell division			XF9a_02226	Predicted integral membrane proteins containing uncharacterized repeats	0.558717254	---NA---	732				IPR005546 (SMART); G3DSA:2.40.128.130 (GENE3D); IPR005546 (PROSITE_PROFILES); IPR036709 (SUPERFAMILY)
			XF9a_00732	Cell division septal protein	1.009145116	FTSQ_XANCP ame: Full=Cell division	278	5	4	P:cell division; C:integral component of membrane; C:plasma membrane; P:cell cycle	G3DSA:3.10.20.310 (GENE3D); IPR013685 (PFAM); IPR005548 (PFAM); G3DSA:3.40.50.11690 (GENE3D); IPR026579 (PANTHER); IPR026579 (HAMAP); IPR034746 (PROSITE_PROFILES)
			XF9a_01036	MAF protein	0.763840866	Y1124_XYLFA ame: Full=Maf XF_1124	199	5	1	C:cytoplasm	IPR003697 (TIGRFAM); IPR029001 (G3DSA:3.90.950.GENE3D); IPR003697 (PFAM); IPR003697 (PIRSF); IPR003697 (PANTHER); PTHR43213:SF7 (PANTHER); IPR003697 (HAMAP); IPR029001 (SUPERFAMILY)
Transport	The accumulation of this protein is enhanced under phosphate starvation	import nutrientes (phosphate starvation)	XF9a_02027	phosphate ABC transporter, phosphate-binding protein	-0.50833056	PSTS_XYLFA ame: Full=Phosphate-binding Short=PBP Flags: Precursor	364	5	6	C:periplasmic space; F:phosphate ion binding; P:cellular response to phosphate starvation; F:ATPase-coupled phosphate ion transmembrane transporter activity; C:ATP-binding cassette (ABC) transporter complex; P:phosphate ion transmembrane transport	IPR005673 (PIRSF); G3DSA:3.40.190.10 (GENE3D); IPR005673 (TIGRFAM); IPR024370 (PFAM); G3DSA:3.40.190.10 (GENE3D); PTHR42996 (PANTHER); PTHR42996:SF2 (PANTHER); PS51257 (PROSITE_PROFILES); SSF53850 (SUPERFAMILY)
		transport ions	XF9a_00833	Mg2+ and Co2+ transporters	0.662012976	CORA_THEMA ame: Full=Cobalt magnesium transport	337	5	8	F:magnesium ion binding; P:cobalt ion transport; C:integral component of plasma membrane; F:cobalt ion transmembrane transporter activity; P:protein homooligomerization; F:magnesium ion transmembrane transporter activity; P:magnesium ion transmembrane transport; F:cobalt ion binding	G3DSA:1.20.58.340 (GENE3D); G3DSA:1.20.58.340 (GENE3D); G3DSA:3.30.460.20 (GENE3D); IPR002523 (PFAM); PTHR21535 (PANTHER); PTHR21535:SF33 (PANTHER); SSF143865 (SUPERFAMILY); SSF144083 (SUPERFAMILY)
		transport sulphate, thiosulphate,	XF9a_01231	sulfate ABC transporter, permease protein CysW	0.480031167	CYSW_SYNE7 ame: Full=Sulfate transport system permease	319	5	5	P:sulfate transport; P:sulfate assimilation; C:plasma membrane;	IPR000515 (PFAM); IPR011866 (TIGRFAM); IPR035906 (G3DSA:1.10.3720.GENE3D);

		selenate, and selenite.								C:plastid; F:sulfate transmembrane transporter activity		IPR005667 (TIGRFAM); IPR011866 (PTHR30406:PANTHER); IPR005667 (PANTHER); IPR000515 (PROSITE_PROFILES); IPR035906 (SUPERFAMILY)
			XF9a_00121	Predicted permeases	0.588757018	LPTF_HAEIN ame: Full=Lipopolysaccharide export system permease	361	4	17	P:transmembrane transport; P:deoxyribonucleoside monophosphate biosynthetic process; P:transport; F:thymidine kinase activity; C:plasma membrane; F:nucleotide binding; F:ATP binding; F:metal ion binding; C:membrane; C:integral component of membrane; P:DNA biosynthetic process; P:phosphorylation; F:transferase activity; F:kinase activity; F:lipopolysaccharide-transporting ATPase activity; C:ATP-binding cassette (ABC) transporter complex; P:lipopolysaccharide transport		IPR030922 (TIGRFAM); IPR005495 (PFAM); IPR005495 (PANTHER); PTHR33529:SF6 (PANTHER)
		small peptides, secondary amino acids bound to metals, and glutathione	XF9a_02149	putative oligopeptide transporter, OPT family	0.466887786	Y561_HAEIN ame: Full= oligopeptide transporter HI_0561	653	4	1	P:transport		IPR004814 (TIGRFAM); IPR004813 (PFAM); IPR004813 (TIGRFAM); PTHR31645 (PANTHER); PTHR31645:SF0 (PANTHER)
		transport sugars, amino acids, organo cations	XF9a_02141	transporter, SSS family	0.601176148	ACTP_PECPP ame: Full=Cation acetate symporter ame: Full=Acetate permease ame: Full=Acetate transporter	577	5	6	F:tellurite uptake transmembrane transporter activity; F:glycolate transmembrane transporter activity; C:integral component of plasma membrane; P:plasma membrane acetate transport; F:acetate transmembrane transporter activity; P:tellurite transport		IPR001734 (TIGRFAM); IPR038377 (G3DSA:1.20.1730.GENE3D); IPR001734 (PFAM); PTHR43291 (PANTHER); PTHR43291:SF2 (PANTHER); IPR001734 (PROSITE_PROFILES)
Response to stress		ascorbate metabolism	XF9a_02311	Uncharacterized protein conserved in bacteria	0.461290917	DLGD_HAEIG ame: Full=2,3-diketo-L-gulonate reductase Short=2,3-DKG reductase ame: Full=3-dehydro-L-gulonate 2-dehydrogenase	533	2	7	F:oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; C:cytoplasm; F:oxidoreductase activity; P:metabolic process; P:oxidation-reduction process; F:NAD+ binding; F:3-dehydro-L-gulonate 2-dehydrogenase activity		IPR016883 (PIRSF); G3DSA:1.50.10.140 (GENE3D); IPR019282 (PFAM); PS51257 (PROSITE_PROFILES)
			XF9a_02312	Stress-induced morphogen (activity unknown)	0.814400062	SUFE1_ARATH ame: Full= chloroplastic mitochondrial ame: Full=Chloroplastic Short= uFE ame: Full= EMBRYO DEFECTIVE 1374 ame: Full= SULFUR E Short= ame: Full= SULFUR E 1 Short= 1 Flags: Precursor	96	5	7	F:protein binding; P:transcription, DNA-templated; C:mitochondrion; C:cytosol; F:enzyme activator activity; P:iron-sulfur cluster assembly		G3DSA:3.30.300.90 (GENE3D); IPR002634 (PIRSF); IPR002634 (PFAM); IPR002634 (PANTHER); PTHR12735:SF23 (PANTHER); IPR036065 (SUPERFAMILY)
	virulence factor		XF9a_01278	lactoylglutathione lyase (EC:4.4.1.5)	0.733008607	LGUL_PSEPU ame: Full=Lactoylglutathione lyase ame: Full=Aldoketomutase ame: Full=Glyoxalase I	163	5	9	P:osteoclast differentiation; P:carbohydrate metabolic process; F:zinc ion binding; C:extracellular exosome; P:glutathione metabolic	EC:4.4.1.5	IPR029068 (G3DSA:3.10.180.GENE3D); IPR004361 (TIGRFAM); IPR004360 (PFAM); PTHR10374:SF16 (PANTHER);

						Short=Glx I ame: Full=Ketone-aldehyde mutase ame: Full=Methylglyoxalase ame: Full=S-D-lactoylglutathione methylglyoxal lyase				process; P:methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione; P:negative regulation of apoptotic process; F:lactoylglutathione lyase activity; P:regulation of transcription from RNA polymerase II promoter		PTHR10374 (PANTHER); IPR037523 (PROSITE_PROFILES); IPR029068 (SUPERFAMILY)
	chaperone		XF9a_00903	Molecular chaperone, HSP90 family	-0.438068132	HTPG_XYLFA ame: Full=Chaperone ame: Full=Heat shock ame: Full=High temperature G	637	5	5	F:ATP binding; C:cytoplasm; F:unfolded protein binding; P:protein folding; P:response to stress		IPR020575 (PRINTS); IPR003594 (SMART); G3DSA:3.40.50.11260 (GENE3D); G3DSA:3.30.230.80 (GENE3D); IPR003594 (PFAM); IPR037196 (G3DSA:1.20.120.GENE3D); IPR001404 (PIRSF); IPR001404 (PFAM); IPR036890 (G3DSA:3.30.565.GENE3D); IPR001404 (PANTHER); PTHR11528:SF54 (PANTHER); IPR001404 (HAMAP); IPR037196 (SUPERFAMILY); IPR036890 (SUPERFAMILY); IPR020568 (SUPERFAMILY)
	chaperone		XF9a_00557	chaperonin GroL	-0.783203974	CH60_XYLFT ame: Full=60 kDa chaperonin ame: Full= ame: Full=Cpn60	547	5	4	F:ATP binding; C:cytoplasm; F:unfolded protein binding; P:protein refolding		IPR001844 (PRINTS); IPR027413 (G3DSA:1.10.560.GENE3D); IPR002423 (PFAM); IPR027409 (G3DSA:3.50.7.GENE3D); IPR027410 (G3DSA:3.30.260.GENE3D); IPR001844 (TIGRFAM); PTHR11353:SF169 (PANTHER); PTHR11353 (PANTHER); IPR001844 (HAMAP); IPR027413 (SUPERFAMILY); IPR027409 (SUPERFAMILY); IPR027410 (SUPERFAMILY)
	chaperone		XF9a_00558	Co-chaperonin GroES (HSP10)	-0.679042378	CH10_XYLFT ame: Full=10 kDa chaperonin ame: Full= ame: Full=Cpn10	95	5	7	F:ATP binding; F:metal ion binding; F:chaperone binding; P:chaperone mediated protein folding requiring cofactor; F:unfolded protein binding; P:response to unfolded protein; C:GroEL-GroES complex		IPR020818 (PRINTS); IPR020818 (SMART); IPR037124 (G3DSA:2.30.33.GENE3D); IPR020818 (PFAM); PTHR10772:SF24 (PANTHER); IPR020818 (PANTHER); IPR020818 (HAMAP); IPR011032 (SUPERFAMILY)
	chaperone		XF9a_02217	chaperone protein DnaK	-0.691999608	DNAK_XYLFA ame: Full=Chaperone ame: Full=HSP70 ame: Full=Heat shock 70 kDa ame: Full=Heat shock 70	638	5	3	F:ATP binding; F:unfolded protein binding; P:protein folding		IPR013126 (PRINTS); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.90.640.10 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); IPR013126 (PFAM); IPR012725 (TIGRFAM); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PANTHER); PTHR19375:SF333 (PANTHER); IPR012725 (HAMAP); SSF53067 (SUPERFAMILY); IPR029047

[illegible]

		lysozyme activity	XF9a_00840	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	0.582319236	YIBJ_BACSU ame: Full=murein lytic transglycosylase	297	5	6	P:entry into host via enzymatic degradation of host anatomical structure; P:catabolism by organism of cell wall peptidoglycan in other organism; F:lyase activity; C:virion membrane; P:cellular process; F:lysozyme activity	EC:3.2.1.17	G3DSA:1.10.530.10 (GENE3D); IPR008258 (PFAM); PTHR45529 (PANTHER); IPR023346 (SUPERFAMILY)
	bacterial pathogeneis	lipase activity	XF9a_00323	Esterase/lipase	-0.530879896	LIPA_PSEAS ame: Full=Lipase A Short=Flags: Precursor	422	1	5	P:lipid catabolic process; P:lipid metabolic process; F:triglyceride lipase activity; C:extracellular region; F:hydrolase activity		IPR029058 (G3DSA:3.40.50.GENE3D); IPR005152 (PIRSF); IPR005152 (PFAM); IPR029058 (SUPERFAMILY)
		protease	XF9a_00171	Membrane protease subunits, stomatin/prohibitin homologs	-0.509672157	QMCA_ECOLI ame: Full=	318	5	21	P:positive regulation of cardiolipin metabolic process; P:positive regulation of mitochondrial DNA replication; C:T cell receptor complex; F:receptor binding; F:cardiolipin binding; C:mitochondrial inner membrane; P:mitochondrial calcium ion transport; P:mitochondrion organization; P:mitochondrial ATP synthesis coupled proton transport; C:immunological synapse; P:cellular calcium ion homeostasis; C:mitochondrial intermembrane space; P:positive regulation of mitochondrial membrane potential; F:GTPase binding; C:membrane raft; C:actin cytoskeleton; C:integral component of membrane; C:COP9 signalosome; C:extrinsic component of plasma membrane; P:T cell receptor signaling pathway; P:protein oligomerization		IPR001972 (PRINTS); IPR001107 (SMART); G3DSA:3.30.479.30 (GENE3D); IPR001107 (PFAM); IPR032435 (PFAM); PTHR43327 (PANTHER); PTHR43327:SF15 (PANTHER); IPR036013 (SUPERFAMILY)
		Peptidase	XF9a_01835	Zn-dependent oligopeptidases (EC:3.4.15.5)	-0.61550075	DCP_ECOLI ame: Full=Dipeptidyl carboxypeptidase ame: Full=Peptidyl-dipeptidase Dcp	723	5	9	F:carboxypeptidase activity; P:cellular macromolecule metabolic process; P:peptide metabolic process; P:proteolysis; C:cytosol; C:outer membrane-bounded periplasmic space; C:intracellular organelle part; F:metalloendopeptidase activity	EC:3.4.24	IPR001567 (PFAM); G3DSA:1.10.1370.40 (GENE3D); IPR024077 (G3DSA:1.10.1370.GENE3D); PTHR43660 (PANTHER); SSF55486 (SUPERFAMILY)
	Nutrient assimilation	Iron storage proteins	XF9a_00357	bacterioferritin	0.564105152	BFR_ECOL6 ame: Full=Bacterioferritin Short=BFR ame: Full=Cytochrome b-1 ame: Full=Cytochrome b-557	154	5	7	F:identical protein binding; F:iron ion binding; C:cytosol; P:intracellular sequestering of iron ion; F:ferritinase activity; C:plasma membrane; F:heme binding	EC:1.16.3.1	IPR002024 (PRINTS); IPR002024 (TIGRFAM); IPR002024 (PIRSF); IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); PTHR30295:SF0 (PANTHER); PTHR30295 (PANTHER); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY)
		Copper biding	XF9a_00870	uncharacterized protein, YfiH family	0.64463894	POLOX_XYLFA ame: Full=Polyphenol oxidase ame: Full=Multicopper oxidase XF_0940	260	5	2	F:copper ion binding; C:cytosol		IPR003730 (PFAM); IPR038371 (G3DSA:3.60.140.GENE3D); IPR003730 (TIGRFAM); PTHR30616:SF2 (PANTHER); IPR003730 (PANTHER); IPR011324 (SUPERFAMILY)

			XF9a_00872	Uncharacterized protein conserved in bacteria	0.914102568	Y1259_ARATH ame: Full=DCC family chloroplastic Flags: Precursor	150	2	1	C:plastoglobule		IPR007263 (PFAM); PTHR33639:SF2 (PANTHER); PTHR33639 (PANTHER)
			XF9a_00125	Predicted acyltransferases	0.641265353	---NA---	380					IPR002656 (PFAM); PTHR23028:SF53 (PANTHER); PTHR23028 (PANTHER)
			XF9a_01725	Uncharacterized conserved protein	-0.621647161	Y473_VIBC3 ame: Full=UPF0312 VC0395_0473 VC395_A0785 Flags: Precursor	237	5	4	P:biological_process; C:periplasmic space; C:cellular_component; F:molecular_function		IPR007372 (SMART); IPR007372 (PFAM); IPR036761 (G3DSA:2.40.128.GENE3D); PTHR34406 (PANTHER); IPR036761 (SUPERFAMILY)
			XF9a_01038	TIGR02099 family protein	0.486464537	YHDP_ECOLIRecName: Full=Uncharacterized protein YhdP; Flags: Precursor	1291	1				IPR032712 (PFAM); IPR011836 (TIGRFAM); IPR025263 (PFAM); IPR011836 (PANTHER)
			XF9a_01165	hypothetical protein	-0.451038693	---NA---	293					SSF82171 (SUPERFAMILY)
			XF9a_01240	hypothetical protein	0.760319939	---NA---	159					no IPS match
			XF9a_01241	Uncharacterized protein required for cytochrome oxidase assembly	0.653412489	---NA---	387					IPR003780 (PFAM); PTHR35457 (PANTHER)
			XF9a_01460	hypothetical protein	-0.997445841	---NA---	82					no IPS match
			XF9a_01903	hypothetical protein	0.642951999	---NA---	182					no IPS match
			XF9a_01997	hypothetical protein	0.662464265	---NA---	80					no IPS match
			XF9a_01998	hypothetical protein	0.833060274	---NA---	83					no IPS match
			XF9a_02098	hypothetical protein	0.579292064	---NA---	149					no IPS match
			XF9a_02150	hypothetical protein	0.743111509	---NA---	61					no IPS match
Total: 69			XF9a_00562	hypothetical protein	0.708776861	---NA---	96					no IPS match

Class	Genic Category	SeqName	Ncbi Locus tag	Gene product name	Description Blast2go	log2FoldChange	Length	#Hits	e-Value	sim mean	#GO	GO Names list	Enzy me Codes list	InterPro IDs
Macromolecule metabolism	DNA metabolism	DNA replication	MMSR116 RS14125	IS1182 family transposase	RFC5_PIC1O ame: Full=Replication factor C small subunit Short=RFC small subunit ame: Full=Clamp loader small subunit	1.952894924	478	1	8.65E-3	56%	6	F:nucleotide binding; F:DNA binding; F:ATP binding; F:DNA clamp loader activity; P:DNA replication; C:DNA replication factor C complex		no IPS match
	DNA metabolism	DNA replication	MMSR116 RS04575	DNA methylase family protein	MTB1_BRUME ame: Full=Modification methylase Short= ame: Full=Adenine-specific methyltransferase ame:	-1.460170741	444	5	9.78E-16	49%	10	F:nucleic acid binding; F:DNA binding; P:DNA methylation; F:N-methyltransferase activity; P:DNA replication; F:methyltransferase activity; F:transferase activity; P:DNA		IPR002187 (PRINTS); IPR002187 (SMART);

					Full=DNA methyltransferase ame: Full= ortholog							methylation on adenine; F:site-specific DNA- methyltransferase (adenine-specific) activity; P:methylation	IPR015867 (G3DSA:3.30.70. GENE3D); IPR002187 (PIRSF); IPR002187 (PFAM); PTHR301115:SF1 7 (PANTHER); IPR002187 (PANTHER); IPR002187 (PROSITE_PROFI LES); IPR011322 (SUPERFAMILY)
	DNA metabolism	DNA replication	MMSR116_RS06775	ribonucleoside-diphosphate reductase, adenosylcobalamin- dependent	NRDJ_BRADU ame: Full=Vitamin B12-dependent ribonucleotide reductase ame: Full=Ribonucleoside- diphosphate reductase	-0.93963467	1243	5	0.00E+00	72.8%	9	F:nucleotide binding; F:ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor; F:cobalamin binding; P:DNA replication; P:deoxyribonucleotide biosynthetic process; P:DNA biosynthetic process; P:oxidation-reduction process; C:ribonucleoside-diphosphate reductase complex; F:cobalt ion binding	IPR003846 (PFAM); PTHR32057 (PANTHER); IPR003846 (HAMAP)
	DNA metabolism	DNA replication	MMSR116_RS05125	DUF4112 domain-containing protein	DPB2_KLULA ame: Full=DNA polymerase epsilon subunit B ame: Full=DNA polymerase II subunit 2	1.573558555	167	1	9.46E-2	48%	15	F:nucleotidyltransferase activity; P:DNA replication; P:DNA- dependent DNA replication; F:double-stranded DNA binding; P:DNA-dependent DNA replication maintenance of fidelity; P:mitotic DNA replication initiation; P:error-prone translesion synthesis; C:epsilon DNA polymerase complex; F:DNA binding; C:nucleus; F:DNA-directed DNA polymerase activity; C:nuclear chromatin; C:cytoplasm; C:cytosol; F:transferase activity	IPR010707 (PIRSF); G3DSA:3.10.540 .10 (GENE3D); IPR023361 (G3DSA:2.30.27 0.GENE3D); IPR010707 (PFAM)
	DNA metabolism	DNA replication	MMSR116_RS14985	nucleoid-associated protein, YbaB/Ebfc family	Y275_METS8 ame: Full=Nucleoid-associated MsiI_Q275	1.159032008	107	5	1.27E-32	77%	3	F:DNA binding; C:bacterial nucleoid; C:cytoplasm	IPR027275 (PFAM); G3DSA:2.30.30. 240 (GENE3D); PTHR36505 (PANTHER); IPR011033 (SUPERFAMILY)
	DNA metabolism	nucleic acid metabolism	MMSR116_RS06070	HD domain-containing protein	SPOT_HAEIN ame: Full=Guanosine-3',5'- bis(diphosphate) 3'- pyrophosphohydrolase ame: Full=Penta-phosphate guanosine-3'- pyrophosphohydrolase Short=(ppGpp)ase	1.453764245	164	5	5.57E-4	44.4%	16	P:guanosine tetraphosphate biosynthetic process; P:metabolic process; P:response to starvation; F:guanosine- 3',5'-bis(diphosphate) 3'-diphosphatase activity; C:plasma membrane; F:GTP diphosphokinase activity; F:nucleotide binding; F:GTP binding; F:ATP binding; C:cell wall; P:guanosine tetraphosphate metabolic process; P:phosphorylation; F:amino acid binding; F:transferase activity; F:kinase activity; F:hydrolase activity	IPR018648 (PFAM)
	DNA metabolism	DNA repair	MMSR116_RS22200	DNA repair protein MmcB- related protein	---NA---	1.144702594	170					EC:4.2 .1.1	IPR001765 (SMART); IPR036874 (G3DSA:3.40.10 50.GENE3D); IPR001765 (PFAM); PTHR11002 (PANTHER); PTHR11002:SF1 3 (PANTHER); IPR036874 (SUPERFAMILY)
	DNA metabolism	Plasmid partition protein A	MMSR116_RS02080	ParA family protein	VIRC1_AGRRH ame: Full= virC1	-1.609143843	215	5	2.22E-6	47.6%	13	F:ATPase activity; P:nucleic acid phosphodiester bond hydrolysis; F:nucleotide binding; F:DNA binding; F:ATP binding; F:protein binding; P:anion transmembrane transport; P:response to arsenic-containing substance; F:endonuclease activity; P:cation transmembrane transport; P:detoxification of arsenic-containing substance; F:hydrolase activity; F:ATPase-coupled arsenite transmembrane transporter activity	IPR008807 (PFAM); G3DSA:1.10.10. 1550 (GENE3D)
	RNA metabolism	ribosomal silencing factors	MMSR116_RS22505	Uma2 family endonuclease	Y925_SYNY3RecName: Full=Uncharacterized protein slI0925	1.31493907	187	3	6.95E-4	51.67%			IPR031811 (PFAM)
	RNA metabolism		MMSR116_RS30410	ribonuclease P protein component	RNPA_RUEPO ame: Full=Ribonuclease P component Short=RNase P Short=R ame: Full= C5	-1.324393197	204	4	1.55E-4	61%	11	P:RNA phosphodiester bond hydrolysis, endonucleolytic; P:nucleic acid phosphodiester bond hydrolysis; F:ribonuclease P activity; P:RNA phosphodiester bond hydrolysis; F:RNA binding; P:tRNA processing;	IPR00572 (PFAM); IPR036374 (G3DSA:3.90.42

												F:endonuclease activity; F:nuclease activity; F:tRNA binding; P:tRNA 5'-leader removal; F:hydrolase activity	0.GENE3D); PTHR43032:SF3 (PANTHER); PTHR43032 (PANTHER); IPR022867 (HAMAP); IPR006311 (PROSITE_PROFILES); IPR036374 (SUPERFAMILY)
	RNA metabolism	Regulation of gene expression (stress)	MMSR116_RS00525	ECF subfamily RNA polymerase sigma-24 factor	SIGK_MYCSS ame: Full=RNA polymerase sigma factor ame: Full=Sigma-K factor	-1.454061703	185	5	4.17E-29	54.6%	5	P:regulation of gene expression; F:binding; P:regulation of primary metabolic process; P:regulation of cellular metabolic process; C:cell periphery	PRO0173 (PRINTS); IPR001991 (PFAM); IPR036458 (G3DSA:1.10.38.60.GENE3D); PTHR42865:SF1 (PANTHER); PTHR42865 (PANTHER); IPR023954 (HAMAP); IPR036458 (SUPERFAMILY)
	RNA metabolism		MMSR116_RS05315	transcription termination factor Rho	RHO_RHOS4 ame: Full=Transcription termination factor Rho ame: Full=ATP-dependent helicase Rho	-1.37334379	428	5	0.00E+00	87%	6	F:ATP binding; F:RNA binding; F:RNA-dependent ATPase activity; P:regulation of transcription, DNA-templated; F:helicase activity; P:DNA-templated transcription, termination	IPR011129 (SMART); IPR003593 (SMART); IPR011112 (SMART); G3DSA:3.40.50.300 (GENE3D); IPR011112 (PFAM); IPR004665 (TIGRFAM); IPR000194 (PFAM); IPR011113 (PFAM); G3DSA:1.10.720.10 (GENE3D); G3DSA:2.40.50.140 (GENE3D); PTHR15184 (PANTHER); IPR004665 (PTHR15184:PANTHER); IPR004665 (HAMAP); IPR027417 (SUPERFAMILY); IPR036269 (SUPERFAMILY); IPR012340 (SUPERFAMILY)
	RNA metabolism	Transcription	MMSR116_RS11170	RNA polymerase sigma factor RpoH	RPOH_RHIRD ame: Full=RNA polymerase sigma factor ame: Full=RNA polymerase sigma-32 factor	1.44455512	297	5	6.21E-152	74.8%	9	P:transcription initiation from bacterial-type RNA polymerase promoter; F:DNA binding; F:sigma factor activity; F:transcription factor activity, sequence-specific DNA binding; F:zinc ion binding; P:response to heat; C:cytoplasm; P:regulation of transcription, DNA-templated; P:sporulation resulting in formation of a cellular spore	IPR002433 (PRINTS); IPR000183 (PRINTS); IPR022643 (PFAM); IPR029066 (G3DSA:3.20.20.GENE3D); IPR009006 (G3DSA:2.40.37.GENE3D); IPR022644 (PFAM); PTHR11482 (PANTHER); PTHR11482:SF6

																(PANTHER); IPR029066 (SUPERFAMILY); IPR009006 (SUPERFAMILY)
	RNA metabolism	Transcription	MMSR116_RS04830	DNA-binding response regulator	ACTR_SINMW ame: Full=Acid tolerance regulatory	2.094536867	199	5	5.61E-84	82.4%	6	P:transcription, DNA-templated; P:phosphorelay signal transduction system; P:regulation of transcription, DNA-templated; F:sequence- specific DNA binding; C:intracellular; F:phosphorelay response regulator activity				no IPS match
	RNA metabolism	transcriptional regulator	MMSR116_RS05115	MucR family transcriptional regulator	MUCR_RHIME ame: Full=Transcriptional regulatory	1.216525504	180	5	3.24E-33	65.6%	1	F:binding				G3DSA:3.40.174 0.10 (GENE3D); IPR003774 (PFAM); IPR003774 (PANTHER); IPR003774 (HAMAP); SSF143456 (SUPERFAMILY)
	RNA metabolism	transcriptional regulator	MMSR116_RS26055	MucR family transcriptional regulator	MUCR_RHIME ame: Full=Transcriptional regulatory	1.191641256	153	5	4.79E-38	64.2%	1	F:binding			EC:3.4 .18	IPR038063 (G3DSA:2.40.44 0.GENE3D); IPR005490 (PFAM); PTHR30582:SF2 4 (PANTHER); PTHR30582 (PANTHER); PSS1257 (PROSITE_PROFI LES); IPR038063 (SUPERFAMILY)
	RNA metabolism	transcriptional regulator	MMSR116_RS18630	MucR family transcriptional regulator	MUCR_RHIME ame: Full=Transcriptional regulatory	1.267343676	153	5	6.5E-30	64.4%	1	F:binding				IPR001789 (SMART); IPR001789 (PFAM); IPR002197 (PFAM); G3DSA:1.10.10. 60 (GENE3D); G3DSA:3.40.50. 2300 (GENE3D); PTHR32071:SF5 1 (PANTHER); PTHR32071 (PANTHER); IPR001789 (PROSITE_PROFI LES); IPR011006 (SUPERFAMILY)
	RNA metabolism	transcriptional regulator	MMSR116_RS07440	MucR family transcriptional regulator	ROS_RHIRD ame: Full=Transcriptional regulatory ros	1.99224614	164	5	9.62E-27	64%	1	F:binding			EC:1.1 .99.14	IPR004113 (PFAM); IPR016171 (G3DSA:1.10.45. GENE3D); G3DSA:3.30.465 .40 (GENE3D); G3DSA:3.30.70. 2740 (GENE3D); IPR006094 (PFAM); PTHR42934:SF1 (PANTHER); PTHR42934 (PANTHER); IPR016166 (PROSITE_PROFI LES); IPR036318 (SUPERFAMILY); IPR016164 (SUPERFAMILY)
	RNA metabolism	transcriptional regulator - metal sensing regulator	MMSR116_RS14485	MerR family DNA-binding transcriptional regulator	ZNTR_ECO57 ame: Full=HTH- type transcriptional regulator ame: Full=Zn(II)-responsive regulator of zntA	1.183609797	140	5	1.45E-24	58.2%	3	F:transcription factor activity, sequence-specific DNA binding; P:positive regulation of transcription, DNA-templated; F:binding				IPR021273 (PFAM)

	RNA metabolism	transcriptional regulator - stress response	MMSR116_RS00375	Crp/Fnr family transcriptional regulator	FNRL_RHOS4 ame: Full=Transcriptional activator	1.364127111	246	5	1.96E-13	44.8%	6	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated; P:nitrogen fixation; C:intracellular	EC:1.8 .4.11	IPR036509 (G3DSA:3.30.10.60.GENE3D); IPR002569 (PFAM); IPR002569 (TIGRFAM); PTHR42799 (PANTHER); PTHR42799:SF6 (PANTHER); IPR002569 (HAMAP); IPR036509 (SUPERFAMILY)
	RNA metabolism	transcriptional regulator - stress response	MMSR116_RS30165	bifunctional DNA-binding transcriptional regulator/O6-methylguanine-DNA methyltransferase Ada	ADA_ECOLI ame: Full=Bifunctional transcriptional activator DNA repair enzyme Ada ame: Full=Regulatory of adaptive response Includes: ame: Full=Methylphosphotriester-DNA--cysteine S-methyltransferase ame: Full=Methylphosphotriester-DNA methyltransferase Includes: ame: Full=Methylated-DNA--cysteine methyltransferase ame: Full=O6-methylguanine-DNA alkyltransferase	1.631496098	369	5	7.49E-115	64.8%	8	P:DNA dealkylation involved in DNA repair; F:zinc ion binding; F:protein binding; P:DNA demethylation; P:response to nitrosative stress; F:methylated-DNA-[protein]-cysteine S-methyltransferase activity; F:damaged DNA binding; C:plasma membrane	EC:3.6 .1.3	IPR002586 (PFAM); IPR010223 (TIGRFAM); G3DSA:3.40.50.300 (GENE3D); IPR025501 (PIRSF); PTHR43384 (PANTHER); PTHR43384:SF1 (PANTHER); IPR027417 (SUPERFAMILY)
	RNA metabolism	transcription	MMSR116_RS23260	methyltransferase domain-containing protein	ARSR_ECOLI ame: Full=Arsenical resistance operon repressor	1.569178409	336	5	2.47E-12	62.2%	4	F:DNA binding; P:transcription, DNA-templated; P:response to arsenic-containing substance; P:regulation of transcription, DNA-templated		no IPS match
	RNA metabolism	transcriptional regulator	MMSR116_RS08620	transcriptional regulator	YDEP_BACSU ame: Full=Uncharacterized HTH-type transcriptional regulator	1.71309569	121	5	3.58E-22	61%	3	F:DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated		no IPS match
	RNA metabolism	transcriptional regulator	MMSR116_RS06015	DNA-binding response regulator	OMPR_ECOLI ame: Full=Transcriptional regulatory	1.417934447	239	5	3.89E-55	59.8%	7	F:transcription factor activity, sequence-specific DNA binding; F:identical protein binding; P:negative regulation of transcription, DNA-templated; P:positive regulation of transcription, DNA-templated; P:phosphorelay signal transduction system; C:cytosol; F:phosphorelay response regulator activity		IPR008258 (PFAM); G3DSA:1.10.530.10 (GENE3D); IPR023346 (SUPERFAMILY)
	RNA metabolism	Transcription	MMSR116_RS28615	nitrogen regulatory protein P-II	GLNB_RHILO ame: Full=Nitrogen regulatory P-II	1.048806401	112	5	9.09E-66	91.8%	7	F:nucleotide binding; P:transcription, DNA-templated; P:regulation of catalytic activity; P:regulation of transcription, DNA-templated; P:regulation of nitrogen utilization; P:nitrogen fixation; F:enzyme regulator activity		IPR002563 (PFAM); IPR012349 (G3DSA:2.30.11.0.GENE3D); PTHR43567:SF1 (PANTHER); PTHR43567 (PANTHER); SSF50475 (SUPERFAMILY)
	Protein metabolism	Translation	MMSR116_03410	peptide chain release factor 2	RF2_MAGSA ame: Full=Peptide chain release factor 2 Short=RF-2	-1.263522363	375	5	4.33E-176	76%	3	P:translational termination; C:cytoplasm; F:translation release factor activity, codon specific		no IPS match
	Protein metabolism	Translation	MMSR116_RS20855	50S ribosomal protein L28	RL28_METRJ ame: Full=50S ribosomal L28	-1.750003006	100	5	8.81E-66	92.6%	3	F:structural constituent of ribosome; C:ribosome; P:translation		IPR003684 (PFAM)
	Protein metabolism	Translation	MMSR116_RS10555	30S ribosomal protein S20	RS20_METRJ ame: Full=30S ribosomal S20	-1.264945184	88	5	2.18E-48	94.2%	4	F:structural constituent of ribosome; C:ribosome; F:rRNA binding; P:translation	EC:1.3 .99.7	G3DSA:2.40.110.10 (GENE3D); IPR009075 (PFAM); IPR013786 (PFAM); IPR006091 (PFAM); G3DSA:1.20.140.10 (GENE3D); IPR037069 (G3DSA:1.10.54

																0.GENE3D); PTHR42807 (PANTHER); IPR009100 (SUPERFAMILY); IPR036250 (SUPERFAMILY)
	Protein metabolism	translation	MMSR116_RS03090	30S ribosomal protein S21	RS21_METNO ame: Full=30S ribosomal S21	-1.164760906	111	5	2.07E-28	90.8%	3	C:ribosomal subunit; F:structural constituent of ribosome; P:translation			EC:1.2 .4.2	IPR005475 (SMART); IPR032106 (PFAM); IPR001017 (PFAM); G3DSA:3.40.50. 11610 (GENE3D); IPR011603 (TIGRFAM); G3DSA:1.10.287 .1150 (GENE3D); G3DSA:3.40.50. 12470 (GENE3D); IPR031717 (PFAM); IPR005475 (PFAM); IPR011603 (PIRSF); G3DSA:3.40.50. 970 (GENE3D); IPR011603 (PANTHER); IPR029061 (SUPERFAMILY); IPR029061 (SUPERFAMILY)
	Protein metabolism	translation	MMSR116_RS25435	RNA helicase	RHLE_ECOLI ame: Full=ATP- dependent RNA helicase	-1.643055132	511	5	1.61E- 119	63.6%	9	F:nucleotide binding; P:response to heat; F:RNA strand- exchange activity; F:RNA strand annealing activity; F:ATP- dependent 5'-3' RNA helicase activity; P:RNA secondary structure unwinding; C:cytosol; P:ribosome assembly; F:ATP- dependent 3'-5' RNA helicase activity				IPR010105 (TIGRFAM); IPR036942 (G3DSA:2.40.17 0.GENE3D); IPR037066 (G3DSA:2.170.1 30.GENE3D); IPR000531 (PFAM); IPR012910 (PFAM); PTHR32552:SF6 5 (PANTHER); PTHR32552 (PANTHER); SSF56935 (SUPERFAMILY)
	Protein metabolism	translation	MMSR116_RS25130	quinoprotein dehydrogenase- associated SoxYZ-like	SYP_HALOH ame: Full=Proline-- tRNA ligase ame: Full=Prolyl- tRNA synthetase Short=	1.795242569	279	1	7.26E-2	38%	11	F:nucleotide binding; P:tRNA aminoacylation for protein translation; F:ATP binding; F:aminoacyl-tRNA ligase activity; C:cytoplasm; P:regulation of translational fidelity; F:proline- tRNA ligase activity; F:aminoacyl-tRNA editing activity; P:prolyl-tRNA aminoacylation; F:ligase activity; P:translation				IPR029032 (G3DSA:1.20.12 90.GENE3D); PTHR34846 (PANTHER); PTHR34846:SF2 (PANTHER); IPR029032 (SUPERFAMILY)
	Protein metabolism	nucleotide biding	MMSR116_RS12120	ATP-dependent helicase	DEAD_BUCBP ame: Full=ATP- dependent RNA helicase ame: Full=Cold-shock DEAD box A	-1.280011433	584	5	5.67E-69	48.2%	3	F:nucleic acid binding; F:helicase activity; P:cellular process				IPR030395 (PFAM); IPR017946 (G3DSA:3.20.20. GENE3D); PTHR43620:SF7 (PANTHER); PTHR43620 (PANTHER); IPR030395 (PROSITE PROFI

																		LES); IPR017946 (SUPERFAMILY)
	Protein metabolism	Protein folding	MMSR116_RS20870	molecular chaperone DnaJ	YCB2_PSEDE ame: Full=Uncharacterized kDa in cobS 5 region ame: Full=ORF2	1.080068559	206	5	3.42E-43	65.8%	1	F:ion binding						IPR000100 (PFAM); IPR000100 (TIGRFAM); IPR014721 (G3DSA:3.30.23.0.GENE3D); IPR000100 (PANTHER); IPR000100 (HAMAP); IPR020568 (SUPERFAMILY)
	Protein metabolism	Protein biding	MMSR116_RS22230	tetratricopeptide repeat-containing protein	Y940_METJA ame: Full=TPR repeat-containing MJ0940	-1.21586595	290	5	1.21E-17	47.6%	19	P:positive regulation of cellular protein metabolic process; F:UDP-glycosyltransferase activity; P:response to organic substance; P:carbohydrate derivative metabolic process; P:regulation of biosynthetic process; P:response to oxygen-containing compound; P:regulation of carbohydrate metabolic process; C:nucleus; F:protein binding; P:cellular glucose homeostasis; P:rhythmic process; C:cytoplasm; P:regulation of protein phosphorylation; P:histone modification; P:regulation of gene expression; P:cellular response to stimulus; F:N-acetyltransferase activity; P:negative regulation of protein modification process; P:peptidyl-lysine modification					IPR032807 (PFAM); PTHR32309 (PANTHER); PTHR32309:SF13 (PANTHER)	
	Protein metabolism	Post translation modification	MMSR116_RS02310	isoprenylcysteine carboxylmethyltransferase	NRM_XENLA ame: Full=Nurim ame: Full=Nuclear envelope membrane ame: Full=Nuclear rim	1.828852014	244	5	1.21E-10	48.6%	2	C:nucleus; C:membrane						IPR018661 (PFAM)
	Protein metabolism	novel chaperonins	MMSR116_RS13530	ABC-1 domain protein	COQ8_YEAST ame: Full=Atypical kinase mitochondrial ame: Full=Activity of bc1 complex 1 ame: Full=Coenzyme Q 8 ame: Full=Ubiquinone biosynthesis COQ8 Flags: Precursor	1.153805314	453	5	1.13E-31	47.8%	6	C:mitochondrial part; C:membrane; P:phosphorylation; F:binding; F:kinase activity; P:organic substance metabolic process						IPR027405 (G3DSA:1.10.10.0.GENE3D); IPR009282 (PFAM); IPR027405 (SUPERFAMILY)
	Protein metabolism	chaperone	MMSR116_RS29890	cytochrome c maturation protein CcmE	CCME_METRJ ame: Full=Cytochrome c-type biogenesis ame: Full=Cytochrome c maturation E ame: Full=Heme chaperone	1.120750101	170	5	1.78E-102	90.4%	5	F:metal ion binding; C:integral component of membrane; P:protein-heme linkage; P:cytochrome complex assembly; C:plasma membrane						IPR013785 (G3DSA:3.20.20.0.GENE3D); IPR008567 (PFAM); IPR008567 (PANTHER); PTHR37418:SF2 (PANTHER)
Intermediary metabolism	Energy Production	electron transfer activity	MMSR116_RS19245	ATP synthase F0 subunit C	ATPL_JANSC ame: Full=ATP synthase subunit c ame: Full=ATP synthase F(0) sector subunit c ame: Full=F-type ATPase subunit c Short=F-type ATPase subunit c ame: Full=Lipid-binding	-1.808372095	75	5	3.18E-6	73.4%	13	P:proton transport; P:ATP hydrolysis coupled proton transport; C:proton-transporting two-sector ATPase complex, proton-transporting domain; F:hydrogen ion transmembrane transporter activity; F:lipid binding; P:ATP biosynthetic process; P:transport; C:plasma membrane; P:ion transport; C:proton-transporting ATP synthase complex, coupling factor F(0); C:membrane; C:integral component of membrane; P:ATP synthesis coupled proton transport						IPR009531 (PFAM)
	Energy Production	electron transfer activity	MMSR116_RS22760	(2Fe-2S)-binding protein	IORA_BREDI ame: Full=Isouquinoline 1-oxidoreductase subunit alpha	1.677697423	151	5	3.00E-51	57.8%	6	P:aromatic compound catabolic process; F:oxidoreductase activity, acting on CH or CH2 groups; C:cytoplasm; F:oxidoreductase activity, acting on the aldehyde or oxo group of donors; P:oxidation-reduction process; F:2 iron, 2 sulfur cluster binding						IPR009593 (PIRSF); IPR009593 (PFAM)
	Energy Production	unknown fuction iron sufler cluster	MMSR116_RS28290	YdiU family protein	Y5402_METPB ame: Full=UPF0061 Mpop_5402	1.178340739	489	5	0.00E+00	80%								IPR012910 (PFAM); IPR010105 (TIGRFAM); IPR037066 (G3DSA:2.170.130.GENE3D); IPR000531 (PFAM); IPR036942 (G3DSA:2.40.17.0.GENE3D); PTHR32552

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	Energy Production	electron-transfer proteins	MMSR116_RS23965	cytochrome c family protein	CYC2_BLA VI ame: Full=Cytochrome c2 Flags: Precursor	-1.062926614	123	5	4.58E-27	67.2%	6	F:metal ion binding; F:electron carrier activity; P:oxidation-reduction process; P:photosynthesis; C:periplasmic space; F:heme binding		no IPS match
	Energy Production	<u>NAD(+)</u> <u>biosynthesis</u>	MMSR116_RS22325	alkene reductase	NEMA_ECOLI ame: Full=N-ethylmaleimide reductase ame: Full=N-ethylmaleimide reducing enzyme	1.10349884	364	5	3.63E-90	57.6%	9	P:monocarboxylic acid biosynthetic process; F:N-ethylmaleimide reductase activity; F:FMN binding; P:nitroglycerin metabolic process; P:2,4,6-trinitrotoluene catabolic process; F:chromate reductase activity; C:cytosol; F:oxidoreductase activity, acting on other nitrogenous compounds as donors, with NAD or NADP as acceptor; P:fatty acid metabolic process		IPRO04147 (PFAM); PTHR43851.SF3 (PANTHER); IPRO34646 (PANTHER); IPRO11009 (SUPERFAMILY)
	Energy Production	<u>NAD(+)</u> <u>biosynthesis</u>	MMSR116_RS13000	aldo/keto reductase	Y2408_MYCS2 ame: Full=Uncharacterized oxidoreductase MSMEG_2408 MSMEI_2347	1.256531541	276	5	9.93E-99	67.6%	2	F:oxidoreductase activity; P:oxidation-reduction process		IPRO36909 (G3DSA:1.10.76.0.GENE3D); IPRO09056 (PFAM); IPRO30991 (TIGRFAM); PTHR37823 (PANTHER); PTHR37823.SF1 (PANTHER); IPRO09056 (PROSITE_PROFI LES); IPRO36909 (SUPERFAMILY)
	Energy Production	<u>NAD(+)</u> <u>biosynthesis</u>	MMSR116_RS20305	KR domain-containing protein	YXNA_BACSU ame: Full=Uncharacterized oxidoreductase	1.241503923	337	5	5.69E-26	45.4%	7	P:cellular ketone metabolic process; F:oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; C:intracellular membrane-bounded organelle; C:membrane; C:cytoplasmic part; P:ammonium ion metabolic process; P:sphingolipid metabolic process		no IPS match
	Energy Production	<u>NAD(+)</u> <u>biosynthesis</u>	MMSR116_RS30315	KR domain-containing protein	YVAG_BACSU ame: Full=Uncharacterized oxidoreductase	1.015049458	265	5	7.04E-81	54.6%	2	F:oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; P:single-organism metabolic process		G3DSA:3.40.630.10 (GENE3D); IPRO17439 (TIGRFAM); IPRO11650 (PFAM); IPRO17439 (PIRSF); G3DSA:3.30.70.360 (GENE3D); IPRO02933 (PFAM); PTHR11014.SF1 41 (PANTHER); PTHR11014 (PANTHER); IPRO36264 (SUPERFAMILY); SSF53187 (SUPERFAMILY)
	Energy Production	<u>NAD(+)</u> <u>biosynthesis</u>	MMSR116_RS27740	flavin reductase family protein	YDFE_BACSURecName: Full=Uncharacterized protein Ydfe	1.58749893	249	2	4.76E-45	53.5%	4	F:oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor; F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction process		PRO1036 (PRINTS); IPRO11701 (PFAM); G3DSA:1.20.172.0.10 (GENE3D); G3DSA:1.20.125.0.20 (GENE3D); PTHR23501 (PANTHER); PTHR23501.SF1 06 (PANTHER); IPRO20846 (PROSITE_PROFI LES); IPRO36259 (SUPERFAMILY)
	Energy Production	<u>NAD(+)</u> <u>biosynthesis</u>	MMSR116_RS08300	flavin reductase family protein	P152_METTH ame: Full=MTH_152	1.119533127	230	5	1.26E-46	46.6%	4	F:oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor; F:FMN binding; F:oxidoreductase activity; P:oxidation-reduction process	EC:3.3.2.10	IPRO00639 (PRINTS); IPRO00073 (PRINTS); IPRO00073 (PFAM); IPRO29058 (G3DSA:3.40.50.GENE3D);

	Energy Production	FAD	MMSR116_RS05110	FAD-binding oxidoreductase	GLCD_ECOL6 ame: Full=Glycolate oxidase subunit	1.399373638	477	5	1.24E-124	53.6%	5	P:glycolate catabolic process; C:membrane; F:glycolate dehydrogenase activity; C:cytoplasmic part; P:cellular response to DNA damage stimulus		no IPS match
	Energy Production	NADP	MMSR116_RS08270	aldo/keto reductase	YRPG_BACSU ame: Full=Uncharacterized oxidoreductase	-2.345369915	329	5	1.12E-128	54.4%	4	C:cytoplasm; C:membrane; P:single-organism metabolic process; P:organic substance metabolic process		IPR003593 (SMART); G3DSA:3.40.50.300 (GENE3D); IPR003439 (PFAM); PTHR42794 (PANTHER); IPR003439 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
	Energy Production	NADP/FAD	MMSR116_RS02450	dehydrogenase	FDHA_DESGI ame: Full=Formate dehydrogenase subunit alpha Short=FDH subunit alpha ame: Full=Formate dehydrogenase large subunit Flags: Precursor	1.302504318	197	5	2.99E-33	57.8%	15	F:formate dehydrogenase (quinone) activity; P:anaerobic respiration; F:selenium binding; F:electron carrier activity; F:molybdenum ion binding; P:cellular response to DNA damage stimulus; C:formate dehydrogenase complex; P:molybdenum incorporation into iron-sulfur cluster; F:protein binding; C:membrane; F:formate dehydrogenase (cytochrome-c-553) activity; C:cytosol; C:outer membrane-bounded periplasmic space; F:4 iron, 4 sulfur cluster binding; P:formate oxidation		IPR018677 (PFAM)
	Energy Production	<u>NAD(+)</u> biosynthesis	MMSR116_RS12995	quinolinate synthase NadA	NADA2_RHILO ame: Full=Quinolinate synthase A 2	2.077021219	338	5	6.78E-172	84.6%	7	P:quinolinate biosynthetic process; C:cytoplasm; F:metal ion binding; P:NAD biosynthetic process; F:4 iron, 4 sulfur cluster binding; F:quinolinate synthetase A activity; F:transferase activity, transferring alkyl or aryl (other than methyl) groups		IPR001296 (PFAM); G3DSA:3.40.50.2000 (GENE3D); G3DSA:3.40.50.2000 (GENE3D); IPR028098 (PFAM); PTHR12526 (PANTHER); PTHR12526:SF554 (PANTHER); SSF53756 (SUPERFAMILY)
	Energy Production	<u>NAD(+)</u> biosynthesis	MMSR116_RS19090	NADH dehydrogenase	NUON_DESAP ame: Full=NADH-quinone oxidoreductase subunit N ame: Full=NADH dehydrogenase I subunit N ame: Full=NDH-1 subunit N	-1.187346084	584	5	1.35E-22	49.4%	1	P:transport		IPR036526 (G3DSA:3.60.11.0.GENE3D); IPR003010 (PFAM); PTHR23088 (PANTHER); PTHR23088:SF27 (PANTHER); IPR003010 (PROSITE_PROFILES); IPR036526 (SUPERFAMILY)
	Energy Production	Luciferase	MMSR116_RS22605	LLM class flavin-dependent oxidoreductase	YHBW_ECOL6 ame: Full=Luciferase-like monooxygenase	1.827202051	342	5	4.16E-79	55.8%	1	C:cytosol		G3DSA:3.40.50.1980 (GENE3D); G3DSA:3.40.50.1980 (GENE3D); IPR002491 (PFAM); PTHR30535 (PANTHER); IPR002491 (PROSITE_PROFILES); SSF53807 (SUPERFAMILY)
	Energy Production	Regulation of macromolecule metabolic process - Luciferase	MMSR116_RS04130	SMP-30/gluconolactonase/LRE family protein	GALAB_RHIME ame: Full= sugar lactone lactonase	2.244206328	296	5	5.18E-88	48.8%	8	P:positive regulation of hydrolase activity; P:regulation of macromolecule metabolic process; F:metal ion binding; C:intracellular part; P:single-organism process; P:positive regulation of biological process; P:regulation of primary metabolic process; P:negative regulation of cellular metabolic process		IPR025668 (PFAM); IPR008490 (PFAM); PTHR33408:SF2 (PANTHER); PTHR33408 (PANTHER)
	Energy Production		MMSR116_RS06605	GNAT family N-acetyltransferase	---NA---	1.515096631	197							IPR001155 (PFAM); IPR013785

															(PANTHER); IPRO06311 (PROSITE_PROFI LES); SSF53850 (SUPERFAMILY)
	Energy Production	Glycerophospholipid metabolism	MMSR116_R528550	glycerophosphoryl diester phosphodiesterase	A4177_ARTBC ame: Full=Extracellular ARB_04177	1.251883106	408	5	5.02E-87	46.4%	14	P:glycerol metabolic process; C:cell outer membrane; C:periplasmic space; C:extracellular region; F:glycerophosphodiester phosphodiesterase activity; C:vacuole; C:plasma membrane; F:metal ion binding; F:calcium ion binding; C:cell wall; P:lipid metabolic process; C:membrane; F:phosphoric diester hydrolase activity; F:hydrolase activity			IPRO10827 (PFAM); G3DSA:3.10.20. 310 (GENE3D); IPRO23707 (PIRSF); G3DSA:2.40.160. .50 (GENE3D); G3DSA:2.40.160. .50 (GENE3D); G3DSA:3.10.20. 310 (GENE3D); IPRO23707 (TIGRFAM); G3DSA:3.10.20. 310 (GENE3D); IPRO00184 (PFAM); G3DSA:3.10.20. 310 (GENE3D); G3DSA:3.10.20. 310 (GENE3D); IPRO23707 (PTHR12815:PAN THER); PTHR12815 (PANTHER); IPRO23707 (HAMAP); IPRO34746 (PROSITE_PROFI LES)
	Energy Production	fatty acid biosynthesis	MMSR116_R506645	beta-ketoacyl-[acyl-carrier- protein] synthase I	FABP_PSEAB ame: Full=3-oxoacyl-[acyl-carrier-] synthase 1 ame: Full=3-oxoacyl-	0.9220399	408	5	2.78E-165	71.6%	3	F:3-oxoacyl-[acyl-carrier- protein] synthase activity; C:cytosol; P:fatty acid biosynthetic process		EC:6.2 .1.5; EC:6.2 .1.4	PRO1798 (PRINTS); IPRO03781 (SMART); IPRO05811 (PFAM); G3DSA:3.40.50. 720 (GENE3D); IPRO16102 (G3DSA:3.40.50. GENE3D); IPRO05810 (PIRSF); IPRO03781 (PFAM); IPRO05810 (TIGRFAM); PTHR11117:SF2 (PANTHER); PTHR11117 (PANTHER); IPRO05810 (HAMAP); IPRO16102 (SUPERFAMILY); IPRO36291 (SUPERFAMILY)
	Energy Production	fatty acid	MMSR116_R503285	acyl-CoA dehydrogenase	GCDH_CAEEL ame: Full=Probable glutaryl-mitochondrial Short=GCD Flags: Precursor	0.958418912	409	5	2.53E-179	78%	12	P:fatty-acyl-CoA biosynthetic process; P:fatty acid beta-oxidation using acyl-CoA dehydrogenase; C:mitochondrial matrix; F:fatty-acyl-CoA binding; F:flavin adenine dinucleotide binding; F:electron carrier activity; F:oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor; P:lipid homeostasis; F:glutaryl-CoA dehydrogenase activity; P:tryptophan metabolic process; C:mitochondrial inner membrane; P:lysine catabolic process			IPRO01650 (SMART); IPRO14001 (SMART); G3DSA:3.40.50. 300 (GENE3D); G3DSA:3.40.50. 300 (GENE3D); IPRO01650 (PFAM); IPRO05580 (PFAM);

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																	(PROSITE_PROFI LES); IPRO36282 (SUPERFAMILY); IPRO36249 (SUPERFAMILY)
	Energy Production	amino acid	MMSR116_RS07215	aspartate-semialdehyde dehydrogenase	DHAS_AQUAE ame: Full=Aspartate-semialdehyde dehydrogenase Short=ASA dehydrogenase ame: Full=Aspartate-beta- semialdehyde dehydrogenase	0.950720408	345	5	2.68E- 133	68.2%	6	F:nucleotide binding; P:methionine biosynthetic process; P:lysine biosynthetic process; F:coenzyme binding; P:diaminopimelate metabolic process; F:oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor					no IPS match
	Energy Production	amino acid	MMSR116_RS01745	D-amino acid dehydrogenase	DADA3_RHILO ame: Full=D- amino acid dehydrogenase 3	1.202565188	420	5	0.00E+00	58%	2	F:oxidoreductase activity; P:D-amino acid catabolic process				IPRO14440 (PIRSF); G3DSA:3.40.30. 10 (GENE3D); IPRO01853 (PFAM); PTHR42943:SF2 (PANTHER); PTHR42943 (PANTHER); IPRO36249 (SUPERFAMILY)	
	Energy Production	amino acid degradation	MMSR116_RS25555	methylmalonate-semialdehyde dehydrogenase (CoA acylating)	BAUC_PSEAE ame: Full= 3- oxopropanoate dehydrogenase	0.910031492	498	5	0.00E+00	67%	12	F:aldehyde dehydrogenase (NAD) activity; P:response to oxidative stress; P:brown fat cell differentiation; C:extracellular exosome; F:copper ion binding; P:beta- alanine biosynthetic process; C:mitochondrial matrix; F:methylmalonate-semialdehyde dehydrogenase (acylating) activity; P:valine catabolic process; P:thymine catabolic process; F:malonate-semialdehyde dehydrogenase (acetylating) activity; C:nucleoplasm					PF13515 (PFAM); IPRO32692 (PFAM)
	Energy Production	amino acid - serine	MMSR116_RS11755	D-serine ammonia-lyase	SDHD_PSEP1 ame: Full=Probable D-serine dehydratase ame: Full=D-serine deaminase Short=DSD	1.132621646	429	5	1.37E-91	60%	3	F:lyase activity; P:serine family amino acid metabolic process; P:D- amino acid metabolic process				IPRO02347 (PRINTS); IPRO02347 (PRINTS); PF13561 (PFAM); G3DSA:3.40.50. 720 (GENE3D); PTHR42898:SF8 (PANTHER); PTHR42898 (PANTHER); IPRO36291 (SUPERFAMILY)	
	Energy Production	protease	MMSR116_RS01620	serine protease	DEGPL_CHLTR ame: Full=Probable periplasmic serine endoprotease -like ame: Full=59 kDa immunogenic ame: Full=Protease Do ame: Full=SK59 Flags: Precursor	1.156233945	324	5	1.71E-10	47.6%	10	P:proteolysis; C:membrane; C:integral component of membrane; F:serine-type endopeptidase activity; F:serine- type peptidase activity; C:outer membrane-bounded periplasmic space; C:cell outer membrane; F:peptidase activity; C:periplasmic space; F:hydrolase activity					IPRO04046 (PFAM); G3DSA:1.20.105 0.10 (GENE3D); G3DSA:3.40.30. 10 (GENE3D); IPRO04045 (PFAM); PTHR44051 (PANTHER); PTHR44051:SF1 (PANTHER); IPRO10987 (PROSITE_PROFI LES); IPRO04045 (PROSITE_PROFI LES); IPRO36249 (SUPERFAMILY); IPRO36282 (SUPERFAMILY)
	Energy Production	amino acid - serine	MMSR116_RS25615	serine O-acetyltransferase	CYSE_SALTY ame: Full=Serine acetyltransferase Short=SAT ame: Full=Serine transacetylase	1.032283522	283	5	6.05E-97	69.2%	5	F:serine O-acetyltransferase activity; C:cytosol; C:cysteine synthase complex; P:sulfate assimilation; P:cysteine biosynthetic process from serine					IPRO18077 (SMART); IPRO02053 (PFAM); G3DSA:3.20.20. 80 (GENE3D); PTHR34135:SF2 (PANTHER); PTHR34135 (PANTHER);

																	IPR017853 (SUPERFAMILY)
	Energy Production	amino acid - serine	MMSR116_RS24210	PrkA family serine protein kinase	PRKA_BACSU ame: Full=	1.685977014	650	3	0.00E+00	62%	2	F:protein kinase activity; P:protein phosphorylation					IPR020013 (TIGRFAM); IPR010930 (PFAM); IPR001444 (PFAM); PTHR30435:SF1 (PANTHER); PTHR30435 (PANTHER); IPR037925 (SUPERFAMILY)
	Energy Production	amino acid	MMSR116_RS21385	hypothetical protein	PKN1_CHLPN ame: Full=Serine threonine- kinase pkn1	2.033602624	595	5	7.45E-15	42.4%	14	F:protein homodimerization activity; C:endoplasmic reticulum; F:protein kinase activity; F:protein serine/threonine kinase activity; P:protein phosphorylation; F:nucleotide binding; C:endoplasmic reticulum lumen; F:ATP binding; F:oxidoreductase activity; F:metal ion binding; P:oxidation-reduction process; P:phosphorylation; F:transferase activity; F:kinase activity				G3DSA:3.40.162 0.10 (GENE3D); TIGR01552 (TIGRFAM); IPR006442 (PFAM); IPR036165 (SUPERFAMILY)	
		purine metabolism,	MMSR116_RS22755	xanthine dehydrogenase family protein	IORB_BREDI ame: Full=Isoquinoline 1- oxidoreductase subunit beta	1.348806998	731	5	6.59E-88	42.8%	4	P:regulation of cellular process; F:oxidoreductase activity; F:binding; P:negative regulation of biological process			EC:2.7 .1.69	IPR036662 (G3DSA:3.40.50. GENE3D); IPR004701 (PFAM); PTHR33799 (PANTHER); PTHR33799:SF1 (PANTHER); IPR004701 (PROSITE_PROFI LES); IPR036662 (SUPERFAMILY)	
		pyrimidine metabolism,	MMSR116_RS29495	hypothetical protein	CODA_ECOLI ame: Full=Cytosine deaminase Short=CD Short=CDA Short=CDase ame: Full=Cytosine aminohydrolase ame: Full=Isoguanine deaminase	1.199115381	410	5	2.08E-53	45.2%	9	P:cellular nitrogen compound catabolic process; P:aromatic compound catabolic process; F:transition metal ion binding; P:organic cyclic compound catabolic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines; C:cytoplasm; P:organonitrogen compound catabolic process; P:heterocycle catabolic process; F:deaminase activity				no IPS match	
		pyrimidine metabolism,	MMSR116_RS09635	NUDIX domain-containing protein	ADPP_METJA ame: Full=ADP- ribose pyrophosphatase ame: Full=ADP-ribose diphosphatase ame: Full=ADP-ribose phosphohydrolase ame: Full=Adenosine diphosphoribose pyrophosphatase Short=ADPR- PPase	1.888358904	243	1	8.32E-6	51%	3	F:ADP-ribose diphosphatase activity; F:metal ion binding; F:hydrolase activity				no IPS match	
		biosynthesis of the pyrimidine	MMSR116_RS15475	NMT1/THIS-like domain- containing protein	SSUA_ECOLI ame: Full= aliphatic sulfonates-binding Flags: Precursor	2.096549284	316	5	8.65E-7	47.8%	10	C:ATP-binding cassette (ABC) transporter complex, substrate-binding subunit-containing; P:sulfur compound metabolic process; F:alkanesulfonate transporter activity; C:membrane; P:alkanesulfonate transport; C:periplasmic space; P:transport; P:thiamine diphosphate biosynthetic process; C:plasma membrane; P:thiamine biosynthetic process				G3DSA:3.40.630 .30 (GENE3D); IPR007434 (PFAM); PTHR31384:SF4 2 (PANTHER); PTHR31384 (PANTHER); IPR016181 (SUPERFAMILY)	
		stress reponse	MMSR116_RS14700	polyphosphate kinase 2	PK21C_RHIME ame: Full=Polyphosphate:ADP phosphotransferase 3 ame: Full=Polyphosphate kinase PPK2 3	1.887535652	280	5	4.34E- 108	72.2%	2	P:phosphorylation; F:polyphosphate kinase activity				no IPS match	
Cell division			MMSR116_RS28465	hypothetical protein	SLMA_SHEBS ame: Full=Nucleoid occlusion factor	1.651132292	242	5	3.3E-2	48.4%	9	C:nucleoid; P:cell division; P:regulation of cell division; F:DNA binding; C:bacterial nucleoid; C:cytoplasm; P:negative regulation of barrier septum assembly; F:sequence-specific DNA binding; P:cell cycle				IPR001789 (SMART); IPR001789 (PFAM); G3DSA:3.40.50. 2300 (GENE3D); PTHR43228 (PANTHER); IPR001789	

																(PROSITE_PROFI LES); IPRO11006 (SUPERFAMILY)
			MMSR116_RS07170	tetratricopeptide repeat protein	Y3534_RHIEC ame: Full=TPR repeat-containing Flags: Precursor	1.09925917	203	5	9.03E-20	51%	29	P:cell proliferation; C:nucleoplasm; F:protein complex scaffold; P:negative regulation of transcription, DNA- templated; C:intracellular membrane-bounded organelle; C:cytosol; P:metaphase/anaphase transition of mitotic cell cycle; P:protein K11-linked ubiquitination; F:protein phosphatase binding; C:anaphase-promoting complex; C:endoplasmic reticulum; P:defense response to bacterium; P:protein ubiquitination involved in ubiquitin-dependent protein catabolic process; P:defense response to bacterium, incompatible interaction; C:spindle microtubule; C:nucleus; P:proteasome-mediated ubiquitin-dependent protein catabolic process; C:centrosome; C:perinuclear region of cytoplasm; F:protein binding; C:cytoplasm; C:integral component of membrane; C:spindle; P:anaphase-promoting complex-dependent catabolic process; P:regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle; P:positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition; P:negative regulation of defense response; P:protein ubiquitination; P:negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle			no IPS match	
			MMSR116_RS12015	cell division topological specificity factor	MINE_METRJ ame: Full=Cell division topological specificity factor	-1.478018814	112	5	2.19E-48	84.2%	3	P:cell division; P:regulation of barrier septum assembly; P:cell cycle			IPRO01867 (SMART); IPRO01789 (SMART); IPRO01867 (PFAM); IPRO36388 (G3DSA:1.10.10. GENE3D); G3DSA:3.40.50. 2300 (GENE3D); IPRO01789 (PFAM); PTHR26402:SF7 19 (PANTHER); PTHR26402 (PANTHER); IPRO01867 (PROSITE_PROFI LES); IPRO01789 (PROSITE_PROFI LES); IPRO11006 (SUPERFAMILY); IPRO16032 (SUPERFAMILY)	
			MMSR116_RS19700	cell division protein FtsA	FTSA_AGRFC ame: Full=Cell division	-1.208080745	440	5	1.23E- 146	59.6%	4	P:cell division; F:protein binding; C:plasma membrane; P:cell cycle			G3DSA:1.10.321 0.10 (GENE3D); IPRO03607 (PFAM); PTHR21262:SF2 7 (PANTHER); PTHR21262 (PANTHER); SSF109604 (SUPERFAMILY)	
			MMSR116_RS30440	hypothetical protein	NUF2_RAT ame: Full=Kinetochore Nuf2 ame: Full=Cell division cycle- associated 1	-1.473068699	163	2	3.53E-5	54%	8	P:cell division; C:nucleus; C:Ndc80 complex; C:membrane; P:mitotic nuclear division; C:condensed chromosome kinetochore; P:transport; P:protein secretion				IPRO00182 (PFAM); G3DSA:3.40.630 .30 (GENE3D); IPRO00182 (PROSITE_PROFI LES); IPRO16181 (SUPERFAMILY)
			MMSR116_RS30380	UDP-N-acetylglucosamine 1- carboxyvinyltransferase	MURA_METRJ ame: Full=UDP- N-acetylglucosamine 1- carboxyvinyltransferase ame: Full=Enoylpyruvate transferase ame: Full=UDP-N- acetylglucosamine enolpyruvyl transferase Short=EPT	-1.678445869	429	5	0.00E+00	94.6%	8	P:regulation of cell shape; P:cell division; F:UDP- N-acetylglucosamine 1-carboxyvinyltransferase activity; C:cytoplasm; P:peptidoglycan biosynthetic process; P:UDP-N- acetylglucosamine biosynthetic process; P:cell wall organization; P:cell cycle				no IPS match

Transport		K+ channels	MMSR116_RS24965	mechanosensitive ion channel family protein	---NA---	1.174333667	374									no IPS match
		Anion transporter	MMSR116_RS02620	oxalate/formate MFS antiporter	OXLT_OXAFO ame: Full=Oxalate:formate antiporter Short=OFA ame: Full=Oxalate:formate antiport ame: Full=Oxalate:formate exchange	1.004986847	425	5	4.22E-61	45%	3	C:membrane; C:cell part; P:transport				no IPS match
		anion transporters	MMSR116_RS21710	STAS/SEC14 domain-containing protein	---NA---	1.11312872	120									no IPS match
		ion transport	MMSR116_RS16110	citrate transporter	MEMP_CUPNH ame: Full=Membrane	2.649028173	432	1	3.51E-10	46%	6	P:sodium ion transport; P:transmembrane transport; C:membrane; C:integral component of membrane; F:transporter activity; C:plasma membrane				no IPS match
		inorganic anion uptake transporters	MMSR116_RS01695	SulP family inorganic anion transporter	YVDB_BACSU ame: Full= sulfate transporter	1.285344313	516	2	1.12E-3	59.5%	17	P:sulfate transport; P:L-aspartate transmembrane transport; P:fumarate transport; F:secondary active sulfate transmembrane transporter activity; P:transmembrane transport; F:succinate transmembrane transporter activity; P:sulfate transmembrane transport; F:L-aspartate transmembrane transporter activity; P:transport; C:plasma membrane; C:integral component of plasma membrane; C:membrane; C:integral component of membrane; P:succinate transmembrane transport; P:aspartate transport; F:fumarate transmembrane transporter activity; F:sulfate transmembrane transporter activity			IPR006698 (PFAM); IPR006698 (PANTHER); IPR006698 (HAMAP)	
		sulfate exporter	MMSR116_RS08495	putative sulfate exporter family transporter	Y3189_BRADU ame: Full=UPF0324 membrane blr3189	1.44770817	362	5	8.49E-96	73.4%	1	C:membrane				IPR019284 (PFAM)
		sugars, drugs, metabolites, oligosaccharides, amino acids	MMSR116_RS22290	MFS transporter	MMLH_CUPPJ ame: Full=Probable 4- methylmuconolactone transporter	1.0875658	434	5	2.72E-82	51.2%	2	P:transport; F:transporter activity				IPR014025 (PRINTS); IPR011900 (TIGRFAM); IPR002109 (PFAM); G3DSA:3.40.30. 10 (GENE3D); PTHR10168:SF1 80 (PANTHER); PTHR10168 (PANTHER); IPR002109 (PROSITE_PROFI LES); IPR036249 (SUPERFAMILY)
			MMSR116_RS27205	MFS transporter	YUSP_BACSU ame: Full=Uncharacterized MFS-type transporter	1.368803508	490	5	1.78E-60	49.8%	7	P:transmembrane transport; C:membrane; C:integral component of membrane; P:response to antibiotic; P:transport; C:plasma membrane; F:transporter activity				IPR008258 (PFAM); G3DSA:1.10.530 .10 (GENE3D); IPR023346 (SUPERFAMILY)
			MMSR116_RS21120	MFS transporter	YQJV_BACSU ame: Full=Uncharacterized MFS-type transporter	1.63659724	398	3	1.36E-3	47.33%	8	P:transmembrane transport; C:membrane; C:integral component of membrane; P:aldonate transport; P:transport; F:organic anion transmembrane transporter activity; C:plasma membrane; F:transporter activity				no IPS match
			MMSR116_RS07435	MFS transporter	YDHP_ECOLI ame: Full=inner membrane transport	1.284195567	391	5	2.51E-52	58.4%	1	C:plasma membrane				IPR007833 (PFAM)
		carbohydrate transport uptake	MMSR116_RS15270	PTS fructose transporter subunit IIA	PTNAB_ECOLI ame: Full=PTS system mannose-specific EIIB component ame: Full=EIIAB- Man ame: Full=EIII-Man Includes: ame: Full=Mannose- specific phosphotransferase enzyme IIA component ame: Full=PTS system mannose- specific EIIB component Includes: ame: Full=Mannose- specific phosphotransferase enzyme IIB component ame: Full=PTS system mannose- specific EIIB component	1.275389799	133	5	6.94E-11	51.4%	4	C:cytoplasm; C:integral component of membrane; F:protein-N(P)-phosphohistidine- sugar phosphotransferase activity; P:hexose transport			EC:1.8 .4.11	IPR002569 (PFAM); IPR002569 (TIGRFAM); IPR036509 (G3DSA:3.30.10 60.GENE3D); PTHR42799:SF2 (PANTHER); PTHR42799 (PANTHER); IPR002569 (HAMAP); IPR036509 (SUPERFAMILY)

		facilitates protein transport	MMSR116_RS16730	nuclear transport factor 2 family protein	---NA---	1.449285575	143									no IPS match
		amino acid	MMSR116_RS20220	dicarboxylate/amino acid:cation symporter	DCTA_GEOBB ame: Full=C4-dicarboxylate transport	1.272086242	425	5	1.54E-76	61%	2	P:dicarboxylic acid transport; C:membrane				IPR011780 (TIGRFAM); G3DSA:3.40.50.1100 (GENE3D); G3DSA:3.40.50.1100 (GENE3D); IPR001926 (PFAM); PTHR43419 (PANTHER); IPR011780 (PTHR43419:PA NTH); IPR011780 (HAMAP); IPR036052 (SUPERFAMILY)
		amino acid	MMSR116_RS15440	dicarboxylate/amino acid:cation symporter	DCTA_OCHA4 ame: Full=C4-dicarboxylate transport	-1.609513405	447	5	0.00E+00	85.2%	5	P:dicarboxylic acid transport; P:transmembrane transport; C:integral component of membrane; F:symporter activity; C:plasma membrane				IPR036707 (G3DSA:3.30.10.70.GENE3D); IPR005527 (TIGRFAM); IPR005527 (PFAM); IPR005527 (PANTHER); PTHR33404:SF2 (PANTHER); IPR005527 (HAMAP); IPR036707 (SUPERFAMILY)
		amino acid - leucine	MMSR116_RS29515	ABC transporter substrate-binding protein	LIVK_ECOLI ame: Full=Leucine-specific-binding Short=L-BP Short=LS-BP Flags: Precursor	1.549732529	393	5	1.38E-14	43.2%	1	P:amino acid transport				IPR017102 (PIRSF); IPR014710 (G3DSA:2.60.12.0.GENE3D); IPR013096 (PFAM); IPR011051 (SUPERFAMILY)
		amino acid - glutamine	MMSR116_RS29475	ABC transporter substrate-binding protein	GLNH_BACSU ame: Full=ABC transporter glutamine-binding Flags: Precursor	1.119526118	279	5	1.02E-19	47.6%	9	C:membrane; C:periplasmic space; P:ionotropic glutamate receptor signaling pathway; F:ionotropic glutamate receptor activity; P:transport; P:amino acid transport; C:plasma membrane; F:transporter activity; C:cell surface				IPR021252 (PFAM)
		cobalamin - vit B (Co+N)	MMSR116_RS08125	ABC transporter substrate-binding protein	BTUFA_HALSA ame: Full=Cobalamin-binding ame: Full=Vitamin B12-binding Flags: Precursor	-0.98222713	277	5	2.97E-10	42.6%	8	F:cobalamin binding; C:membrane; F:small molecule binding; C:outer membrane-bounded periplasmic space; C:periplasmic space; P:cobalamin transport; P:transport; C:plasma membrane				IPR036388 (G3DSA:1.10.10.10.GENE3D); G3DSA:3.90.79.10 (GENE3D); IPR000086 (PFAM); PTHR22769 (PANTHER); PTHR22769:SF5 9 (PANTHER); IPR036390 (SUPERFAMILY); IPR015797 (SUPERFAMILY)
		sulfate importer	MMSR116_RS22370	sulfate ABC transporter substrate-binding protein	SUBI_ECOLI ame: Full=Sulfate-binding ame: Full=Sulfate starvation-induced 2 Short=SSI2 Flags: Precursor	-1.344937858	345	5	1.4E-115	65%	4	P:sulfur compound metabolic process; F:sulfate binding; C:outer membrane-bounded periplasmic space; P:transport				IPR007390 (PFAM); IPR007390 (PANTHER)
		heme (Fe)	MMSR116_RS08115	ABC transporter ATP-binding protein	HMOV_PSEPK ame: Full=Hemin import ATP-binding	-1.165754767	271	5	1.21E-45	58%	3	F:ATPase activity, coupled to transmembrane movement of substances; P:transport; C:plasma membrane			EC:3.4 .24; EC:3.6 .1.3	IPR003593 (SMART); IPR000642 (PFAM); G3DSA:2.40.50.920 (GENE3D);

															G3DSA:1.10.8.6 O (GENE3D); G3DSA:3.40.50. 300 (GENE3D); IPR005936 (TIGRFAM); G3DSA:1.20.58. 760 (GENE3D); IPR011546 (PFAM); IPR003959 (PFAM); PTHR23076:SF9 3 (PANTHER); PTHR23076 (PANTHER); IPR005936 (HAMAP); IPR027417 (SUPERFAMILY); IPR037219 (SUPERFAMILY)
		iron importer	MMSR116_RS08120	iron ABC transporter permease	YVRB_BACSU ame: Full=Uncharacterized ABC transporter permease	-1.125429077	348	5	9.46E-9	60.2%	9	P:iron ion homeostasis; F:cobalamin transporter activity; P:ion transport; C:membrane; C:integral component of membrane; P:cobalamin transport; P:transport; C:plasma membrane; F:transporter activity			IPR020471 (PRINTS); IPR023210 (PFAM); IPR036812 (G3DSA:3.20.20. GENE3D); IPR020471 (PIRSF); PTHR43827:SF3 (PANTHER); PTHR43827 (PANTHER); IPR036812 (SUPERFAMILY)
			MMSR116_RS28065	TonB-dependent siderophore receptor	FCT_DICD3 ame: Full=Ferrichrysobactin receptor Flags: Precursor	1.83532312	780	5	1.28E- 100	50.6%	2	C:membrane; F:binding			G3DSA:1.10.10. 1550 (GENE3D); IPR008807 (PFAM)
			MMSR116_RS13925	TonB-dependent receptor	YNCD_ECOLI ame: Full=Probable -dependent receptor Flags: Precursor	-1.748519161	856	5	2.04E-9	48.2%	12	F:cobalamin transporter activity; P:ion transport; P:transmembrane transport; F:porin activity; F:metal ion binding; C:membrane; C:integral component of membrane; C:pore complex; C:cell outer membrane; P:cobalamin transport; F:receptor activity; P:transport			IPR001107 (PFAM)
			MMSR116_RS23315	TonB-dependent siderophore receptor	FCT_DICD3 ame: Full=Ferrichrysobactin receptor Flags: Precursor	-1.047502856	639	5	2.65E-52	43.6%	1	F:binding			IPR002295 (PRINTS); IPR003115 (SMART); IPR015840 (PIRSF); G3DSA:3.90.153 0.30 (GENE3D); G3DSA:3.40.50. 150 (GENE3D); IPR002941 (PFAM); IPR003115 (PFAM); PTHR13370 (PANTHER); PTHR13370:SF8 (PANTHER); IPR029063 (SUPERFAMILY); IPR036086 (SUPERFAMILY)
			MMSR116_RS21805	TonB-dependent siderophore receptor	FOXA_SALTS ame: Full=Ferrioxamine B receptor Flags: Precursor	-1.511467015	727	5	1.81E-21	39%	1	F:binding			IPR009656 (PFAM); IPR010915 (PIRSF); IPR010915 (TIGRFAM);

[illegible]

																(G3DSA:1.20.58-GENE3D); IPR002583 (PFAM); PTHR33398:SF1 (PANTHER); IPR002583 (PANTHER); IPR002583 (PRODOM); IPR002583 (HAMAP); IPR036510 (SUPERFAMILY)
			MMSR116_RS24035	lipopolysaccharide biosynthesis protein	WZXC_ECOLI ame: Full=Lipopolysaccharide biosynthesis	-1.279064241	477	4	1.67E-29	44.5%	1	C:membrane				IPR006685 (PFAM); PTHR30566 (PANTHER); PTHR30566:SF5 (PANTHER); IPR010920 (SUPERFAMILY)
			MMSR116_RS20520	capsule polysaccharide biosynthesis protein	KPSS5_ECOLX ame: Full=Capsule polysaccharide export	-1.254505444	435	4	2.95E-60	48%	7	P:polysaccharide transport; P:polysaccharide biosynthetic process; C:membrane; P:carbohydrate transport; P:nitrogen fixation; P:transport; C:plasma membrane				IPR038740 (PFAM); IPR016181 (SUPERFAMILY)
			MMSR116_RS14895	group 1 glycosyl transferase	MSHA_JONDD ame: Full=D-inositol 3-phosphate glycosyltransferase ame: Full=N-acetylglucosamine-inositol-phosphate N-acetylglucosaminyltransferase Short= c-ins-P N-acetylglucosaminyltransferase	-1.339501171	408	5	3.49E-11	42.8%	6	F:magnesium ion binding; F:transferase activity, transferring glycosyl groups; F:acetylglucosaminyltransferase activity; F:metal ion binding; F:transferase activity; P:mycothiol biosynthetic process				no IPS match
Biofilm and cell adhesion		Biofilm and cell adhesion	MMSR116_RS19060	hypothetical protein	CSGA_SALTY ame: Full=Major curlin subunit ame: Full=Fimbrin SEF17 Flags: Precursor	-1.247862243	695	3	1.22E-5	57%	4	P:single-species biofilm formation; P:cell adhesion; C:pilus; P:amyloid fibril formation				no IPS match
		BIOFILM	MMSR116_RS21670	hypothetical protein	ALGJ_PSEFL ame: Full=Probable alginate O-acetylase ame: Full=Alginate biosynthesis Flags: Precursor	1.264019029	320	4	7.39E-9	45.5%	7	F:transferase activity, transferring acyl groups; C:membrane; P:alginic acid biosynthetic process; C:periplasmic space; P:alginic acid acetylation; F:transferase activity; C:plasma membrane				G3DSA:1.20.125.0.20 (GENE3D); IPR011701 (PFAM); PTHR43124:SF3 (PANTHER); PTHR43124 (PANTHER); IPR020846 (PROSITE_PROFILE); IPR036259 (SUPERFAMILY)
		cell adhesion	MMSR116_RS30445	Flp family type IVb pilin	cell adhesion	-1.125668136	54									IPR009915 (PFAM); G3DSA:1.20.120.1630 (GENE3D); IPR033580 (PANTHER)
		cell adhesion	MMSR116_RS12315	outer membrane protein assembly factor BamA	BAMA_NEIMB ame: Full=Outer membrane assembly factor ame: Full=Outer membrane Omp85 Flags: Precursor	-1.194987442	856	5	2.67E-73	43.2%	7	P:membrane assembly; P:Gram-negative-bacterium-type cell outer membrane assembly; C:membrane; C:integral component of membrane; C:outer membrane; C:outer membrane; P:protein insertion into membrane				IPR010275 (PFAM); IPR009045 (G3DSA:3.30.13.80.GENE3D); IPR009045 (SUPERFAMILY)
		cell adhesion	MMSR116_RS22310	outer membrane protein assembly factor BamE	BAME_VIBCH ame: Full=Outer membrane assembly factor Flags: Precursor	-1.147066215	165	5	6.07E-5	52.6%	5	P:Gram-negative-bacterium-type cell outer membrane assembly; C:membrane; C:cell outer membrane; C:outer membrane; P:protein insertion into membrane				G3DSA:2.40.160.20 (GENE3D); PTHR34001 (PANTHER); IPR011250 (SUPERFAMILY)
Pigments		Photosynthesis - light-independent protochlorophyllide reductase	MMSR116_RS21975	ferredoxin:protochlorophyllide reductase	BCHL_METRJ ame: Full=Light-independent protochlorophyllide reductase iron-sulfur ATP-binding	1.830028914	297	5	0.00E+00	96.2%	8	F:ATP binding; F:oxidoreductase activity, acting on the CH-group of donors, iron-sulfur protein as acceptor; F:metal ion binding; P:photosynthesis, dark reaction; P:light-independent bacteriochlorophyll biosynthetic process; P:oxidation-reduction process; F:4 iron, 4 sulfur cluster				no IPS match

					Short=DPOR subunit L Short=LI-POR subunit L								binding; F:oxidoreductase activity, acting on iron-sulfur proteins as donors	
		Photosynthesis	MMSR116_RS09450	photosystem reaction center subunit H	---NA---	1.440146213	113							IPR038696 (G3DSA:2.60.40. GENE3D); IPR010642 (PFAM)
		bacteriochlorophyll	MMSR116_RS21940	bacteriochlorophyll/chlorophyll synthetase	BCHG_RHOS4 ame: Full=Bacteriochlorophyll synthase 33 kDa chain ame: Full=Geranylgeranyl bacteriochlorophyll synthase	1.317214714	294	5	1.08E-108	61.6%	4	F:prenyltransferase activity; C:membrane; C:chloroplast thylakoid; P:bacteriochlorophyll biosynthetic process	EC:1.1 .99.8; EC:1.1 .2.8	IPR018391 (SMART); G3DSA:2.140.10 .10 (GENE3D); IPR017512 (TIGRFAM); IPR002372 (PFAM); IPR002372 (PFAM); PTHR32303 (PANTHER); PTHR32303:SF1 6 (PANTHER); IPR011047 (SUPERFAMILY)
		carotenoid biosynthetic process	MMSR116_RS09475	cytochrome P450	LUT5_ARATH ame: Full= LUTEIN DEFICIENT chloroplastic ame: Full=Cytochrome P450 97A3 Flags: Precursor	1.110792955	462	5	1.92E-52	49.4%	6	P:carotenoid biosynthetic process; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; C:membrane; C:chloroplast envelope; F:binding; F:monooxygenase activity	EC:2.7 .7.65; EC:3.1 .4.52	IPR000160 (SMART); IPR003660 (SMART); IPR000014 (SMART); IPR001633 (SMART); G3DSA:3.30.70. 270 (GENE3D); IPR035919 (G3DSA:3.20.20. GENE3D); PF12860 (PFAM); IPR001633 (PFAM); IPR000014 (PFAM); IPR003660 (PFAM); IPR024478 (PFAM); G3DSA:1.20.148 0.50 (GENE3D); G3DSA:3.30.450 .20 (GENE3D); IPR000160 (TIGRFAM); IPR000160 (PFAM); PTHR44757 (PANTHER); PTHR44757:SF2 (PANTHER); IPR003660 (PROSITE_PROFI LES); IPR000160 (PROSITE_PROFI LES); IPR001633 (PROSITE_PROFI LES); IPR035965 (SUPERFAMILY); IPR029787 (SUPERFAMILY); SSF158472 (SUPERFAMILY); IPR035965 (SUPERFAMILY); IPR035919 (SUPERFAMILY)

		pigment precursor	MMSR116_RS21930	geranylgeranyl diphosphate reductase	BCHP_RHOCB ame: Full=Geranylgeranyl diphosphate reductase ame: Full=Geranylgeranyl reductase	1.325018272	408	5	1.04E-121	54%	8	P:chlorophyll biosynthetic process; F:oxidoreductase activity; C:membrane; C:chloroplast thylakoid; C:chloroplast envelope; F:binding; P:phospholipid metabolic process; P:terpenoid metabolic process		no IPS match
		chemotaxis	MMSR116_RS22055	HAMP domain-containing protein	MCP4_THEMA ame: Full=Methyl-accepting chemotaxis 4	-1.290457648	579	5	5.11E-54	50%	6	P:chemotaxis; P:signal transduction; C:membrane; C:integral component of membrane; F:signal transducer activity; C:plasma membrane		IPR010432 (PFAM)
		chemotaxis	MMSR116_RS26365	chemotaxis phosphatase CheZ	CHEZ_SHELP ame: Full=phosphatase ame: Full=Chemotaxis	-1.02637435	177	2	3.61E-5	38%	9	P:chemotaxis; F:phosphoprotein phosphatase activity; C:bacterial-type flagellum; P:archaeal or bacterial-type flagellum-dependent cell motility; C:cytoplasm; F:catalytic activity; P:protein dephosphorylation; P:regulation of chemotaxis; F:hydrolase activity		IPR000943 (PRINTS); G3DSA:1.20.140.160 (GENE3D); IPR009042 (PFAM); IPR007630 (PFAM); IPR012759 (TIGRFAM); IPR014284 (TIGRFAM); IPR007627 (PFAM); IPR000943 (PIRSF); G3DSA:1.20.120.1810 (GENE3D); PTHR30376:SF4 (PANTHER); PTHR30376 (PANTHER); IPR012759 (HAMAP); IPR013325 (SUPERFAMILY); IPR013324 (SUPERFAMILY)
		chemotaxis	MMSR116_RS26370	response regulator	CHEY_ENTCL ame: Full=Chemotaxis	-1.14629955	127	5	6.09E-43	71.2%	8	F:magnesium ion binding; P:chemotaxis; F:protein binding; F:acetyltransferase activity; P:internal peptidyl-lysine acetylation; P:phosphorelay signal transduction system; C:cytosol; P:bacterial-type flagellum-dependent cell motility		IPR004329 (PFAM); G3DSA:2.40.50.140 (GENE3D); IPR004329 (PANTHER); IPR004329 (HAMAP); IPR036127 (SUPERFAMILY)
		signal transduction	MMSR116_RS00370	histidine kinase	LOVHK_BRUA1 ame: Full=Blue-light-activated histidine kinase	1.13915372	239	5	7.3E-19	51.2%	1	P:cellular process		no IPS match
		Signalling	MMSR116_RS25880	GGDEF domain-containing protein	VDCA_VIBCH ame: Full=Diguanylate cyclase Short=DGC	-1.171911306	352	5	1.5E-46	55.6%	6	F:diguanylate cyclase activity; F:protein binding; P:negative regulation of cellular component movement; P:single-species submerged biofilm formation; P:single-organism process; C:plasma membrane		IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (PFAM); IPR036396 (G3DSA:1.10.63.0.GENE3D); PTHR24291 (PANTHER); PTHR24291:SF109 (PANTHER); IPR036396 (SUPERFAMILY)
		signal transduction,	MMSR116_RS21395	calcium-binding protein	FRP3_NEIMB ame: Full=Iron-regulated	1.072778802	174	5	6.81E-22	64.6%	2	C:membrane; P:multi-organism process		no IPS match
		signal transduction AMPc	MMSR116_RS05500	cyclic nucleotide-binding protein	YCCS_ECOLI ame: Full=Inner membrane	1.323197794	721	5	1.57E-5	44.4%	3	C:membrane; C:integral component of membrane; C:plasma membrane		PTHR34001 (PANTHER); IPR011250 (SUPERFAMILY)
		regulatory role bind AMP or ATP	MMSR116_RS09735	CBS domain-containing protein	CBSX3_ARATH ame: Full=CBS domain-containing mitochondrial Flags: Precursor	0.983207739	143	5	2.35E-17	56%	2	F:metal ion binding; P:single-organism cellular process		IPR013108 (PFAM); IPR011059

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															(PFAM); PTHR30483 (PANTHER); IPR028082 (SUPERFAMILY)
		Anti oxidant system	MMSR116_RS16640	protein-methionine-sulfoxide reductase catalytic subunit MsrP	MSRP_PCCP ame: Full= - methionine-sulfoxide reductase catalytic subunit Flags: Precursor	1.276085261	316	5	2.53E-87	65.4%	2	F:oxidoreductase activity; P:metabolic process			no IPS match
			MMSR116_RS25875	iron-sulfur cluster assembly accessory protein	ISAM1_ARATH ame: Full=Iron- sulfur assembly -like mitochondrial Flags: Precursor	1.574298856	125	5	4.02E-36	70.4%	3	P:response to magnetism; C:mitochondrion; F:binding			G3DSA:3.40.190 .10 (GENE3D); IPR015168 (PFAM); G3DSA:3.40.190 .10 (GENE3D); PTHR30024 (PANTHER); PTHR30024:SF3 0 (PANTHER); SF53850 (SUPERFAMILY)
			MMSR116_RS13660	iron-sulfur cluster assembly accessory protein	ERPA_RUTMC ame: Full=Iron- sulfur cluster insertion	1.544263394	108	5	3.13E-30	64.2%	1	F:binding			no IPS match
			MMSR116_RS09760	iron-sulfur cluster assembly scaffold protein	ISCU_THEMA ame: Full=Iron- sulfur cluster assembly scaffold ame: Full=Sulfur acceptor	1.234439956	147	5	1.91E-8	47%	1	F:binding			G3DSA:3.40.109 0.10 (GENE3D); IPR002641 (PFAM); PTHR14226 (PANTHER); PTHR14226:SF2 9 (PANTHER); IPR002641 (PROSITE_PROFI LES); IPR016035 (SUPERFAMILY)
		iron-sulfur (Fe-S) cluster assembly factor that facilitates [2Fe-2S] cluster	MMSR116_RS10375	glutaredoxin 3	GLRX_PSEAE ame: Full=Glutaredoxin	1.122817368	89	5	2.81E-31	68%	5	F:protein disulfide oxidoreductase activity; F:glutathione binding; C:cytosol; P:single- organism cellular process; P:single-organism metabolic process			IPR010292 (PIRSF); IPR010292 (PFAM); IPR010292 (PANTHER); PTHR37952:SF2 (PANTHER)
			MMSR116_RS19155	Fe-S cluster assembly protein SufB	Y074_SYNY3 ame: Full=UPF0051 slr0074	1.173724852	489	5	0.00E+00	79.4%	3	C:chloroplast; C:cyanelle; P:iron-sulfur cluster assembly			IPR000595 (SMART); IPR012318 (SMART); IPR000595 (PFAM); IPR036388 (G3DSA:1.10.10. GENE3D); IPR012318 (PFAM); IPR014710 (G3DSA:2.60.12 0.GENE3D); PTHR24567 (PANTHER); IPR012318 (PROSITE_PROFI LES); IPR018490 (SUPERFAMILY); IPR036390 (SUPERFAMILY)
		iron detoxification and storage	MMSR116_RS22705	ferritin-like domain-containing protein	YCIE_ECOLI ame: Full=	1.511943	169	2	6.53E-20	50%	1	P:cellular response to DNA damage stimulus			no IPS match
		iron detoxification and storage	MMSR116_RS18390	ferritin-like domain-containing protein	---NA---	1.414686519	164								no IPS match
Host defence		host defence	MMSR116_RS07060	cupin domain-containing protein	---NA---	1.165978966	146								G3DSA:1.20.58. 660 (GENE3D); IPR007420 (PFAM)

		Antitoxin	MMSR116_RS02995	type II toxin-antitoxin system Phd/YefM family	When bound to their toxin partners, they can bind DNA via the N terminus and repress the expression of operons containing genes encoding the toxin and the antitoxin	2.029313361	84								IPR004090 (PRINTS); IPR003660 (SMART); IPR004089 (SMART); IPR033480 (SMART); IPR033480 (PFAM); IPR004089 (PFAM); G3DSA:3.30.450.20 (GENE3D); G3DSA:1.10.287.950 (GENE3D); IPR003660 (PFAM); G3DSA:1.10.8.500 (GENE3D); PTHR32089 (PANTHER); PTHR32089:SF92 (PANTHER); IPR004089 (PROSITE_PROFILES); IPR003660 (PROSITE_PROFILES); IPR000727 (PROSITE_PROFILES); SSF58104 (SUPERFAMILY)
		Antitoxin	MMSR116_RS12905	antitoxin	VPB22_MYCTU ame: Full=Antitoxin 22	1.118844273	80	1	7.49E-2	55%	2	P:positive regulation of translation; P:growth			G3DSA:2.160.20.100 (GENE3D); IPR001646 (PFAM); G3DSA:2.160.20.80 (GENE3D); SSF141571 (SUPERFAMILY)
		virulence - stress	MMSR116_RS01175	invasion-associated locus B family protein	---NA---	-1.346599581	259								IPR014027 (SMART); IPR014026 (PFAM); G3DSA:3.40.50.720 (GENE3D); IPR001732 (PFAM); G3DSA:3.40.50.720 (GENE3D); IPR028357 (PIRSF); IPR017476 (PIRSF); G3DSA:1.20.5.100 (GENE3D); IPR014027 (PFAM); IPR017476 (TIGRFAM); PTHR43750:SF3 (PANTHER); PTHR43750 (PANTHER); PSS1257 (PROSITE_PROFILES); IPR008927 (SUPERFAMILY); IPR036220 (SUPERFAMILY); IPR036291 (SUPERFAMILY)
	Cleavage of Xf cell wall		MMSR116_RS27065	amidohydrolase	HIPO_CAMJE ame: Full=Hippurate hydrolase ame: Full=Benzoylelglycine	1.200078563	385	5	5.6E-84	56.4%	5	C:intracellular membrane-bounded organelle; P:metabolic process; C:endomembrane system; C:cytoplasmic part; F:hydrolase activity			IPR012349 (G3DSA:2.30.110.GENE3D); IPR002563

					amidohydrolase ame: Full=Hippuricase												(PFAM); PTHR43567 (PANTHER); PTHR43567:SF1 (PANTHER); SSF50475 (SUPERFAMILY)
	Cleavage of Xf cell wall		MMSR116_RS27230	alpha/beta hydrolase	YN93_YEAST ame: Full=Uncharacterized hydrolase YNR064C	1.056267904	322	5	4.98E-70	46.4%	1	F:epoxide hydrolase activity					IPR018762 (PFAM); G3DSA:1.10.287 .130 (GENE3D); IPR036890 (G3DSA:3.30.56 5.GENE3D)
	Cleavage of Xf cell wall		MMSR116_RS27470	alpha/beta hydrolase	YFHM_BACSU ame: Full=AB hydrolase superfamily	1.506332266	285	5	6.99E-80	55.6%	8	P:biological_process; F:catalytic activity; C:membrane; C:integral component of membrane; C:extracellular region; C:cellular_component; F:molecular_function; F:hydrolase activity					IPR000788 (PRINTS); IPR013344 (TIGRFAM); IPR013678 (PFAM); G3DSA:3.20.70. 20 (GENE3D); IPR000788 (PFAM); PTHR43371 (PANTHER); IPR029072 (SUPERFAMILY); SSF51998 (SUPERFAMILY)
	Cleavage of Xf cell wall		MMSR116_RS01255	cell wall hydrolase SleB	SLEB_OCEIH ame: Full=Spore cortex-lytic enzyme Short=SCLF Flags: Precursor	-1.325453939	201	3	1.67E-4	50.33%	6	P:spore germination; F:catalytic activity; P:cell wall organization; C:intracellular immature spore; P:sporulation resulting in formation of a cellular spore; F:hydrolase activity					IPR013153 (SMART); IPR013153 (PFAM); IPR010650 (PFAM); IPR016230 (PIRSF); PTHR30267 (PANTHER); IPR027417 (SUPERFAMILY)
	Cleavage of Xf cell wall		MMSR116_RS03180	glycoside hydrolase	LYSM1_STRGL ame: Full=Lysozyme M1 ame: Full=1,4-beta-N- acetylmuramidase M1 Flags: Precursor	-1.104893825	294	5	2.64E-32	50.2%	12	P:cell wall macromolecule catabolic process; P:carbohydrate metabolic process; P:cytolysis; C:extracellular space; F:catalytic activity; P:peptidoglycan catabolic process; P:metabolic process; C:extracellular region; P:defense response to bacterium; F:lysozyme activity; F:hydrolase activity; F:hydrolase activity, acting on glycosyl bonds					IPR029039 (G3DSA:3.40.50. GENE3D); IPR005025 (PFAM); PTHR30543:SF1 (PANTHER); PTHR30543 (PANTHER); IPR029039 (SUPERFAMILY)
	Cleavage of Xf cell wall		MMSR116_RS14565	hypothetical protein	MLTB_ECOLI ame: Full=Membrane-bound lytic murein transglycosylase B ame: Full=35 kDa soluble lytic transglycosylase ame: Full=Murein hydrolase B ame: Full=SR35 Flags: Precursor	-1.049543614	264	1	3.44E-15	49%	2	P:peptidoglycan biosynthetic process; F:lytic transglycosylase activity					IPR012910 (PFAM); IPR000531 (PFAM); IPR037066 (G3DSA:2.170.1 30.GENE3D); PTHR32552:SF4 1 (PANTHER); PTHR32552 (PANTHER); SSF56935 (SUPERFAMILY)
			MMSR116_RS03845	lytic transglycosylase domain- containing protein	EXLYS_BPDPK ame: Full=Peptidoglycan hydrolase gp181 ame: Full=Gene product 181 Short=Gp181	-1.172796613	427	1	1.7E-22	52%	1	P:entry into host					PR00421 (PRINTS); IPR005746 (PIRSF); IPR005746 (TIGRFAM); G3DSA:3.40.30. 10 (GENE3D); IPR013766 (PFAM);

														IPR036188 (G3DSA:3.50.50.50.GENE3D); IPR023753 (PFAM); PTHR43256 (PANTHER); PTHR43256:SF1 (PANTHER); IPR016156 (SUPERFAMILY); IPR036188 (SUPERFAMILY)
Unknown fuction			MMSR116_RS27330	DUF2934 domain-containing protein	ATPF2_RHOFT ame: Full=ATP synthase subunit b 2 ame: Full=ATP synthase F(0) sector subunit b 2 ame: Full=ATPase subunit I 2 ame: Full=F-type ATPase subunit b 2 Short=F- ATPase subunit b 2	-1.387436964	132	1	7.49E-2	75%	12	P:ion transport; P:proton transport; F:hydrogen ion transmembrane transporter activity; C:proton-transporting ATP synthase complex, coupling factor F(o); C:membrane; C:integral component of membrane; P:ATP biosynthetic process; P:transport; C:plasma membrane; P:ATP synthesis coupled proton transport; P:plasma membrane ATP synthesis coupled proton transport; F:proton-transporting ATP synthase activity, rotational mechanism		IPR032807 (PFAM); IPR003856 (PFAM); PTHR32309 (PANTHER); PTHR32309:SF1 3 (PANTHER)
			MMSR116_RS14885	DUF1150 domain-containing protein	--NA--	1.126227657	94						IPR000531 (PFAM); IPR036942 (G3DSA:2.40.170.0.GENE3D); IPR012910 (PFAM); IPR010105 (TIGRFAM); IPR037066 (G3DSA:2.170.130.GENE3D); PTHR32552 (PANTHER); PTHR32552:SF70 (PANTHER); SSF56935 (SUPERFAMILY)	
			MMSR116_RS12650	DUF1465 domain-containing protein	--NA--	1.645032759	176						G3DSA:2.170.150.20 (GENE3D); IPR002579 (TIGRFAM); IPR002579 (PFAM); PTHR43234 (PANTHER); IPR002579 (PROSITE_PROFILES); IPR011057 (SUPERFAMILY)	
			MMSR116_RS12470	DUF2076 domain-containing protein	Y170_BUCBRecName: Full=Uncharacterized protein bbp_170; AltName: Full=yba2	1.633019249	255	3	3.61E-8	60.67%			IPR000674 (SMART); G3DSA:3.30.365.10 (GENE3D); IPR012368 (PIRSF); G3DSA:3.30.365.10 (GENE3D); G3DSA:3.30.365.10 (GENE3D); G3DSA:3.30.365.10 (GENE3D); G3DSA:3.90.1170.50 (GENE3D); IPR008274 (PFAM); PTHR11908:SF2 (PANTHER); PTHR11908 (PANTHER); IPR006311 (PROSITE_PROFILES); IPR037165 (SUPERFAMILY);	

																	IPR037165 (SUPERFAMILY)
			MMSR116_RS07015	DUF1203 domain-containing protein	---NA---	2.395699669	159										IPR036444 (G3DSA:1.20.90. GENE3D); P551257 (PROSITE_PROFI LES); IPR036444 (SUPERFAMILY)
			MMSR116_RS07710	DUF2852 domain-containing protein	---NA---	1.602143222	154										IPR019734 (SMART); IPR011990 (G3DSA:1.25.40. GENE3D); PF13414 (PFAM); IPR011990 (G3DSA:1.25.40. GENE3D); IPR011990 (G3DSA:1.25.40. GENE3D); IPR001440 (PFAM); PTHR44858 (PANTHER); IPR013026 (PROSITE_PROFI LES); IPR019734 (PROSITE_PROFI LES); IPR011990 (SUPERFAMILY)
			MMSR116_RS28610	DUF2735 domain-containing protein	GSTL_RHILE ame: Full=Glutamine synthetase translation inhibitor	2.147338058	59	1	1.75E-3	45%							no IPS match
			MMSR116_RS08695	DUF2157 domain-containing protein	---NA---	1.359178063	445										no IPS match
			MMSR116_RS27575	DUF1285 domain-containing protein	---NA---	1.208819124	194										IPR000537 (PFAM); G3DSA:1.20.120 .1780 (GENE3D); IPR006372 (TIGRFAM); G3DSA:1.10.357 .140 (GENE3D); PTHR42723 (PANTHER)
			MMSR116_RS09950	DUF179 domain-containing protein	Y6268_METS4 ame: Full=UPF0301 M446_6268	1.09269248	195	5	3.43E- 108	80%							IPR001623 (SMART); IPR036869 (G3DSA:1.10.28 7.GENE3D); IPR001623 (PFAM); IPR007791 (PFAM); IPR029024 (G3DSA:1.10.36 80.GENE3D); IPR001623 (PROSITE_PROFI LES); IPR029024 (SUPERFAMILY); IPR036869 (SUPERFAMILY)
			MMSR116_RS20455	DUF3597 domain-containing protein	---NA---	1.116917454	137										IPR000825 (PFAM); IPR010231 (TIGRFAM); PTHR30508 (PANTHER); PTHR30508:SF1 (PANTHER);

																IPR037284 (SUPERFAMILY)
			MMSR116_RS26380	DUF2093 domain-containing protein	---NA---	1.921268462	72									IPR003918 (PRINTS); IPR001750 (PFAM); PTHR42703 (PANTHER)
			MMSR116_RS26135	DUF937 domain-containing protein	YIDB_ECOLIRecName: Full=Uncharacterized protein YidB	1.103027937	235	1	9.4E-9	60%						no IPS match
			MMSR116_RS25990	DUF2794 domain-containing protein	---NA---	1.082722343	124									IPR001623 (PRINTS); IPR001623 (SMART); IPR036869 (G3DSA:1.10.28 7.GENE3D); IPR001623 (PFAM); IPR001623 (PROSITE_PROFI LES); IPR036869 (SUPERFAMILY)
			MMSR116_RS20055	DUF4926 domain-containing protein	---NA---	1.47341565	83									IPR036444 (G3DSA:1.20.90. GENE3D); IPR036444 (SUPERFAMILY)
			MMSR116_RS22250	DUF465 domain-containing protein	---NA---	1.881405117	60									no IPS match
			MMSR116_RS25415	DUF1508 domain-containing protein	Y1088_NEIMB ame: Full=UPF0339 NMB1088	1.091554947	61	5	4.34E-15	69%						IPR000182 (PFAM); G3DSA:3.40.630 .30 (GENE3D); PTHR43441\$F1 (PANTHER); PTHR43441 (PANTHER); IPR000182 (PROSITE_PROFI LES); IPR016181 (SUPERFAMILY)
			MMSR116_RS13505	DUF882 domain-containing protein	YCBK_ECOS7RecName: Full=Uncharacterized protein YcbK; Flags: Precursor	-1.44148514	481	3	4.63E-28	58.33%	2	C:membrane; C:integral component of membrane			EC:2.7 .7.65	IPR000160 (SMART); IPR000160 (TIGRFAM); G3DSA:3.30.70. 270 (GENE3D); IPR000160 (PFAM); PTHR45138 (PANTHER); IPR000160 (PROSITE_PROFI LES); IPR029787 (SUPERFAMILY)
			MMSR116_RS14240	pentapeptide repeat- containing protein	PIP82_SALTY ame: Full=Secreted effector 2 ame: Full=Type III effector 2	1.419673342	266	5	2.06E-19	50.8%	4	C:membrane; C:extracellular region; P:pathogenesis; C:host cell membrane				G3DSA:3.75.10. 10 (GENE3D); IPR033195 (PANTHER); SF55909 (SUPERFAMILY)
			MMSR116_RS09630	band 7 protein	---NA---	2.353796332	325									no IPS match
Hypothetical protein			MMSR116_RS03055	hypothetical protein	FLGE_BRUAB ame: Full=Flagellar hook	-1.352325453	424	5	1.1E-30	48%	1	C:cell part			EC:1.8 .4.11	IPR002569 (PFAM); IPR036509 (G3DSA:3.30.10 60.GENE3D); IPR002569 (TIGRFAM); PTHR42799

															(PANTHER); PTHR42799:SF2 (PANTHER); IPR002569 (HAMAP); IPR036509 (SUPERFAMILY)
			MMSR116_RS24385	hypothetical protein	--NA--	1.248287421	118								IPR003494 (SMART); IPR020823 (TIGRFAM); G3DSA:3.30.149 0.110 (GENE3D); IPR020823 (PIRSF); G3DSA:3.30.420 .40 (GENE3D); IPR003494 (PFAM); G3DSA:3.90.640 .10 (GENE3D); G3DSA:3.30.420 .40 (GENE3D); PF14450 (PFAM); PTHR32432 (PANTHER); PTHR32432:SF4 (PANTHER); IPR020823 (HAMAP); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
			MMSR116_RS24380	hypothetical protein	--NA--	-1.329257911	376								IPR001270 (PRINTS); IPR003593 (SMART); IPR019489 (SMART); IPR019489 (PFAM); IPR013461 (TIGRFAM); G3DSA:1.10.8.6 0 (GENE3D); IPR004176 (PFAM); G3DSA:3.40.50. 300 (GENE3D); IPR003959 (PFAM); IPR036628 (G3DSA:1.10.17 80.GENE3D); G3DSA:3.40.50. 300 (GENE3D); G3DSA:1.10.8.6 0 (GENE3D); IPR003959 (PFAM); PTHR11638:SF1 11 (PANTHER); PTHR11638 (PANTHER); IPR027417 (SUPERFAMILY); IPR036628 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
			MMSR116_RS24360	hypothetical protein	--NA--	3.055545399	96							EC:3.3 .1.1	IPR015878 (SMART); IPR000043

														(SMART); G3DSA:3.40.50.1480 (GENE3D); G3DSA:3.40.50.720 (GENE3D); IPR015878 (PFAM); IPR000043 (PFAM); IPR000043 (PIRSF); IPR000043 (TIGRFAM); PTHR23420:SF0 (PANTHER); IPR000043 (PANTHER); IPR034373 (HAMAP); SSF52283 (SUPERFAMILY); IPR036291 (SUPERFAMILY)
			MMSR116_RS24215	hypothetical protein	Y6755_BRADU ame: Full=UPF0229 bil6755	0.885553514	433	5	4.96E-167	66.8%				IPR000454 (PRINTS); IPR002379 (PFAM); IPR005953 (TIGRFAM); IPR038662 (G3DSA:1.20.20. GENE3D); IPR000454 (PANTHER); IPR000454 (HAMAP); IPR035921 (SUPERFAMILY)
			MMSR116_RS24205	hypothetical protein	---NA---	0.99370564	147							IPR002327 (PRINTS); IPR009056 (PFAM); IPR036909 (G3DSA:1.10.76 0.GENE3D); PTHR11961:SF2 2 (PANTHER); IPR002327 (PANTHER); IPR009056 (PROSITE_PROFILES); IPR036909 (SUPERFAMILY)
			MMSR116_RS24150	hypothetical protein	---NA---	1.879551619	84							no IPS match
			MMSR116_RS15245	hypothetical protein	---NA---	1.152258942	66							no IPS match
			MMSR116_RS13960	hypothetical protein	---NA---	-1.303916069	117							IPR001845 (PRINTS); IPR001845 (SMART); IPR036388 (G3DSA:1.10.10. GENE3D); IPR013216 (PFAM); G3DSA:3.40.50.150 (GENE3D); IPR001845 (PFAM); PTHR43464:SF1 7 (PANTHER); PTHR43464 (PANTHER);

															IPR001845 (PROSITE_PROFI LES); IPR036390 (SUPERFAMILY); IPR029063 (SUPERFAMILY)
			MMSR116_RS12625	hypothetical protein	---NA---	1.233121186	129								IPR001041 (PFAM); G3DSA:1.10.150 .120 (GENE3D); IPR012675 (G3DSA:3.10.20. GENE3D); IPR002888 (PFAM); PTHR44379 (PANTHER); IPR001041 (PROSITE_PROFI LES); IPR036010 (SUPERFAMILY); IPR036884 (SUPERFAMILY)
			MMSR116_RS12455	hypothetical protein	---NA---	1.246085478	63								IPR010287 (PFAM); IPR012347 (G3DSA:1.20.12 60.GENE3D); PTHR30565 (PANTHER); PTHR30565:SF1 (PANTHER); IPR009078 (SUPERFAMILY)
			MMSR116_RS11690	hypothetical protein	---NA---	1.4822949	224								IPR019949 (TIGRFAM); IPR036661 (G3DSA:3.20.20. GENE3D); IPR011251 (PFAM); PTHR30137:SF6 (PANTHER); PTHR30137 (PANTHER); IPR036661 (SUPERFAMILY)
			MMSR116_RS05605	hypothetical protein	---NA---	1.452271212	148								G3DSA:3.40.190 .10 (GENE3D); G3DSA:3.40.190 .10 (GENE3D); PF13531 (PFAM); IPR005669 (TIGRFAM); IPR005669 (PANTHER); SSF53850 (SUPERFAMILY)
			MMSR116_RS05655	hypothetical protein	---NA---	1.058976227	157							EC:1.9 7.1	IPR013785 (G3DSA:3.20.20. GENE3D); IPR001155 (PFAM); PTHR22893 (PANTHER); PTHR22893:SF1 4 (PANTHER); SSF51395 (SUPERFAMILY)
			MMSR116_RS31300	hypothetical protein	---NA---	1.883643499	91								IPR037873 (G3DSA:3.30.14 50.GENE3D); IPR007450 (PFAM); IPR026592

																(PANTHER); PSS1257 (PROSITE_PROFI LES)
			MMSR116_RS05660	hypothetical protein	---NA---	1.286525316	71									G3DSA:1.20.125 0.20 (GENE3D); IPR011701 (PFAM); PTHR23508 (PANTHER); PTHR23508:SF2 O (PANTHER); IPR020846 (PROSITE_PROFI LES); IPR036259 (SUPERFAMILY)
			MMSR116_RS05705	hypothetical protein	---NA---	1.562666018	105									no IPS match
			MMSR116_RS03700	hypothetical protein	---NA---	1.234141878	121									IPR009394 (PFAM); IPR011856 (G3DSA:3.40.13 50.GENE3D); IPR009394 (PIRSF)
			MMSR116_RS27000	hypothetical protein	---NA---	2.647016966	69									PR00091 (PRINTS); IPR005971 (TIGRFAM); IPR000392 (PFAM); IPR000392 (PIRSF); G3DSA:3.40.50. 300 (GENE3D); IPR000392 (PANTHER); IPR005971 (PTHR42864:PA NTH); IPR005971 (HAMAP); IPR000392 (PROSITE_PROFI LES); IPR027417 (SUPERFAMILY)
			MMSR116_RS27595	hypothetical protein	---NA---	1.186874323	209									PR00420 (PRINTS); IPR011777 (TIGRFAM); IPR023753 (PFAM); IPR010253 (TIGRFAM); IPR002938 (PFAM); IPR036188 (G3DSA:3.50.50. GENE3D); PTHR42685 (PANTHER); IPR036188 (SUPERFAMILY)
			MMSR116_RS28235	hypothetical protein	---NA---	1.439558942	87									no IPS match
			MMSR116_RS28525	hypothetical protein	---NA---	1.162851911	112									G3DSA:3.30.9.1 O (GENE3D); IPR036188 (G3DSA:3.50.50. GENE3D); IPR006076 (PFAM); PTHR13847 (PANTHER);

															PTHR13847:SF250 (PANTHER); IPR036188 (SUPERFAMILY); SSF54373 (SUPERFAMILY)
			MMSR116_RS28545	hypothetical protein	---NA---	2.196266531	79								no IPS match
			MMSR116_RS29570	hypothetical protein	---NA---	1.633520361	60								IPR009009 (PFAM); IPR012997 (TIGRFAM); IPR036908 (G3DSA:2.40.40.GENE3D); PTHR34183 (PANTHER); PTHR34183:SF1 (PANTHER); IPR034718 (HAMAP); IPR036908 (SUPERFAMILY)
			MMSR116_RS08700	hypothetical protein	---NA---	1.494512997	223								no IPS match
			MMSR116_RS08860	hypothetical protein	CHPT_BRUA2 ame: Full=phosphotransferase ame: Full=Histidine phosphotransferase	-1.269531231	241	1	1.54E-29	62%					IPR006680 (PFAM); G3DSA:3.20.20.140 (GENE3D); IPR011059 (G3DSA:2.30.40.GENE3D); PTHR11271:SF37 (PANTHER); PTHR11271 (PANTHER); IPR032466 (SUPERFAMILY); IPR011059 (SUPERFAMILY)
			MMSR116_RS08915	hypothetical protein	---NA---	2.019291405	87								IPR011105 (PFAM); G3DSA:1.10.10.2520 (GENE3D); PSS1257 (PROSITE_PROFILES)
			MMSR116_RS09420	hypothetical protein	---NA---	2.256621725	89								no IPS match
			MMSR116_RS09830	hypothetical protein	---NA---	-1.19589816	74								IPR001650 (SMART); IPR014001 (SMART); IPR011545 (PFAM); G3DSA:3.40.50.300 (GENE3D); G3DSA:3.40.50.300 (GENE3D); IPR001650 (PFAM); PTHR24031:SF349 (PANTHER); PTHR24031 (PANTHER); IPR001650 (PROSITE_PROFILES); IPR014014 (PROSITE_PROFILES); IPR014001 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)

			MMSR116_RS05495	hypothetical protein	---NA---	2.272628587	75									IPR038162 (G3DSA:2.60.40. GENE3D); IPR013783 (G3DSA:2.60.40. GENE3D); IPR014880 (PFAM); IPR030831 (TIGRFAM); IPR032711 (PFAM); IPR014756 (SUPERFAMILY)
			MMSR116_RS05550	hypothetical protein	---NA---	1.252647944	77									G3DSA:3.40.50. 10610 (GENE3D); IPR005586 (PFAM); PTHR36698 (PANTHER); PTHR36698.SF3 (PANTHER); PSS1257 (PROSITE_PROFI LES); SSF159594 (SUPERFAMILY)
			MMSR116_RS26110	hypothetical protein	---NA---	1.250887845	82									IPR026569 (PFAM); IPR037147 (G3DSA:2.30.17 O.GENE3D); IPR001383 (TIGRFAM); IPR026569 (PANTHER); IPR001383 (HAMAP); IPR034704 (SUPERFAMILY)
			MMSR116_RS24515	hypothetical protein	---NA---	1.926636403	92									IPR001453 (SMART); IPR001453 (TIGRFAM); IPR012245 (PIRSF); IPR001453 (PFAM); IPR036425 (G3DSA:3.40.98 O.GENE3D); IPR013484 (TIGRFAM); IPR012245 (PANTHER); PTHR43232.SF3 (PANTHER); IPR036425 (SUPERFAMILY)
			MMSR116_RS24580	hypothetical protein	---NA---	1.166874756	152									G3DSA:1.20.125 0.20 (GENE3D); IPR011701 (PFAM); PTHR23501 (PANTHER); PTHR23501.SF9 8 (PANTHER); IPR020846 (PROSITE_PROFI LES); IPR036259 (SUPERFAMILY)
			MMSR116_RS24620	hypothetical protein	---NA---	1.610033884	122									IPR005511 (PRINTS); IPR011042 (G3DSA:2.120.1 O.GENE3D);

															IPR013658 (PFAM); PTHR10907:SF7 6 (PANTHER); PTHR10907 (PANTHER); SSF63829 (SUPERFAMILY)
			MMSR116_RS00460	hypothetical protein	---NA---	1.090119398	183								IPR005814 (PFAM); IPR015422 (G3DSA:3.90.11 50.GENE3D); IPR015421 (G3DSA:3.40.64 0.GENE3D); IPR005814 (PIRSF); PTHR42684 (PANTHER); PTHR42684:SF4 (PANTHER); IPR015424 (SUPERFAMILY)
			MMSR116_RS23765	hypothetical protein	---NA---	1.783529633	85								IPR021866 (PFAM); IPR038396 (G3DSA:3.40.50. GENE3D); IPR036513 (SUPERFAMILY)
			MMSR116_RS23515	hypothetical protein	---NA---	1.922385956	69								no IPS match
			MMSR116_RS22285	hypothetical protein	---NA---	1.463654622	164								PR00313 (PRINTS); IPR011049 (G3DSA:2.150.1 0.GENE3D); IPR011049 (G3DSA:2.150.1 0.GENE3D); IPR001343 (PFAM); IPR011049 (SUPERFAMILY)
			MMSR116_RS22270	hypothetical protein	---NA---	1.0386519	156								IPR018044 (PRINTS); G3DSA:3.40.710 .10 (GENE3D); IPR001967 (PFAM); PTHR21581 (PANTHER); PTHR21581:SF2 0 (PANTHER); IPR012338 (SUPERFAMILY)
			MMSR116_RS21810	hypothetical protein	---NA---	-1.755563283	488								IPR011547 (PFAM); IPR001902 (PANTHER); PTHR11814:SF1 84 (PANTHER)
			MMSR116_RS01880	hypothetical protein	---NA---	1.084167517	107								IPR025737 (PFAM)
			MMSR116_RS17280	hypothetical protein	---NA---	-0.986908344	66							EC:1.1 .1.244	G3DSA:3.40.50. 1970 (GENE3D); IPR001670 (PFAM); G3DSA:1.20.109 0.10 (GENE3D); PTHR11496:SF9 3 (PANTHER); PTHR11496

															(PANTHER); SSF56796 (SUPERFAMILY)
			MMSR116_RS16960	hypothetical protein	---NA---	1.63936624	81							EC:1.2 .1.27; EC:1.2 .1.3; EC:1.2 .1.18	IPR016163 (G3DSA:3.40.30 9.GENE3D); IPR010061 (TIGRFAM); IPR016162 (G3DSA:3.40.60 5.GENE3D); IPR015590 (PFAM); PTHR43866:SF4 (PANTHER); IPR010061 (PANTHER); IPR016161 (SUPERFAMILY)
			MMSR116_RS01210	hypothetical protein	---NA---	1.55011465	107							EC:2.3 .1.30	IPR010493 (SMART); G3DSA:2.160.10 .10 (GENE3D); IPR001451 (PFAM); IPR010493 (PFAM); IPR005881 (TIGRFAM); G3DSA:1.10.313 0.10 (GENE3D); PTHR42811 (PANTHER); PTHR42811:SF4 (PANTHER); IPR011004 (SUPERFAMILY)
			MMSR116_RS01035	hypothetical protein	---NA---	1.268237081	85								IPR032568 (PFAM)
			MMSR116_RS30720	hypothetical protein	---NA---	1.023119833	177								PR00173 (PRINTS); IPR001991 (PFAM); IPR036458 (G3DSA:1.10.38 60.GENE3D); PTHR42865 (PANTHER); IPR033380 (PTHR42865:PA NTH); PS51257 (PROSITE_PROFI LES); IPR036458 (SUPERFAMILY)
			MMSR116_RS04135	hypothetical protein	---NA---	2.258050102	83								IPR002347 (PRINTS); SM00822 (SMART); IPR002347 (PFAM); G3DSA:3.40.50. 720 (GENE3D); PTHR43391:SF2 7 (PANTHER); PTHR43391 (PANTHER); IPR036291 (SUPERFAMILY)
			MMSR116_RS21675	hypothetical protein	---NA---	1.913339653	74								IPR010287 (PFAM); IPR012347 (G3DSA:1.20.12 60.GENE3D); PTHR30565:SF9

															(PANTHER); PTHR30565 (PANTHER); IPR009078 (SUPERFAMILY)
			MMSR116_RS01705	hypothetical protein	---NA---	1.846789278	112								G3DSA:1.10.10.1550 (GENE3D); IPR008807 (PFAM)
			MMSR116_RS20310	hypothetical protein	---NA---	1.168804326	83								no IPS match
			MMSR116_RS16365	hypothetical protein	---NA---	1.81994079	191								IPR019626 (PFAM)
			MMSR116_RS17490	hypothetical protein	---NA---	1.495317871	69								no IPS match
			MMSR116_RS02920	hypothetical protein	CREA_ECO57 ame: Full= ame: Full=Catabolite regulation A Flags: Precursor	1.076792398	174	1	3.21E-44	73%	1	C:cytosol			IPR036812 (G3DSA:3.20.20. GENE3D); IPR023210 (PFAM); PTHR43364:SF5 (PANTHER); PTHR43364 (PANTHER); IPR036812 (SUPERFAMILY)
Total : 273			MMSR116_RS25090	hypothetical protein	Y6063_BRADURecName: Full=Uncharacterized protein bli6063	1.02680165	193	1	6.4E-12	52%	2	C:membrane; C:integral component of membrane			IPR035903 (G3DSA:2.60.30 0.GENE3D); IPR016092 (TIGRFAM); IPR000361 (PFAM); PTHR10072 (PANTHER); PTHR10072:SF4 1 (PANTHER); IPR035903 (SUPERFAMILY)

Table S6. Trends in genes detected in transcriptome and secretome of *Mm*.

locustag	Mm co PPT	Mm PPT	Mm co TPM	Mm TPM	Proteome ratio	Transcriptome ratio
MMSR116_RS00865	0.77	0.57	728.51	963.17	1.34	0.76
MMSR116_RS07030	15.95	7.50	1089.62	798.16	2.13	1.37
MMSR116_RS09540	4.37	4.28	498.57	365.07	1.02	1.37
MMSR116_RS09940	3.24	3.42	2579.86	2656.27	0.95	0.97
MMSR116_RS11970	29.55	7.01	1366.25	924.46	4.22	1.48
MMSR116_RS12040	36.86	44.59	2830.85	5132.78	0.83	0.55
MMSR116_RS12140	52.76	40.74	438.22	287.88	1.30	1.52
MMSR116_RS14980	2.14	0.86	1204.83	770.74	2.50	1.56
MMSR116_RS16505	61.05	63.26	3970.14	1868.01	0.97	2.13
MMSR116_RS16515	39.97	80.68	851.35	325.67	0.50	2.61
MMSR116_RS20185	18.62	9.75	1020.18	511.39	1.91	1.99
MMSR116_RS20190	500.33	4.73	750.15	364.23	105.85	2.06
MMSR116_RS20370	1.72	1.32	1195.88	1176.25	1.30	1.02
MMSR116_RS20480	0.68	0.40	986.09	556.53	1.70	1.77
MMSR116_RS23965	177.41	155.80	4759.12	1408.80	1.14	3.38
MMSR116_RS25265	0.91	8.87	7347.90	6676.29	0.10	1.10
MMSR116_RS27490	7.80	8.40	1630.13	651.58	0.93	2.50
MMSR116_RS29630	1.04	0.78	685.73	440.28	1.34	1.56

Table S7. Trends in genes detected in transcriptome and secretome of *Xf*.

Name	Xfp co PPT	Xfp PPT	Xfp co TPM	Xfp TPM	Proteome ratio	Transcriptome ratio
XF_0082	51.32	412.41	532.21	211.85	0.12	2.51
XF_0239	10.53	85.24	2093.05	820.72	0.12	2.55
XF_0343	9348.55	8742.67	9529.04	3071.42	1.07	3.10
XF_0357	12.81	418.63	122.54	37.11	0.03	3.30
XF_0363	1417.21	8918.05	2884.86	1283.20	0.16	2.25
XF_0550	6.44	48.98	243.94	98.69	0.13	2.47

XF_0565	71.36	984.90	418.32	171.10	0.07	2.44
XF_0615	61.55	363.02	4395.44	949.56	0.17	4.63
XF_0644	68.80	1381.47	1074.85	343.43	0.05	3.13
XF_0668	1677.88	1028.33	185.32	90.44	1.63	2.05
XF_0820	1.79	58.67	207.96	100.37	0.03	2.07
XF_0898	506.33	7945.16	244.59	80.36	0.06	3.04
XF_0964	322.86	3283.51	968.03	373.94	0.10	2.59
XF_0975	305.53	3196.04	288.67	93.58	0.10	3.08
XF_1011	626.44	424.26	57.71	25.68	1.48	2.25
XF_1026	3049.67	1983.71	411.67	185.12	1.54	2.22
XF_1219	31781.85	11249.77	4035.89	1526.69	2.83	2.64
XF_1547	28782.96	24207.11	1588.22	712.88	1.19	2.23
XF_1649	35.39	298.43	13.21	11.48	0.12	1.15
XF_1803	18342.24	18835.12	24109.20	6849.07	0.97	3.52
XF_1840	57.67	654.97	1408.53	389.58	0.09	3.62
XF_1851	46.44	453.28	582.00	286.41	0.10	2.03
XF_1887	23.62	248.56	425.54	204.34	0.10	2.08
XF_1897	20.51	388.34	266.98	100.61	0.05	2.65
XF_1981	1140.33	1261.49	644.08	298.78	0.90	2.16
XF_2237	846.58	832.74	328.55	116.71	1.02	2.82
XF_2340	15.16	139.73	943.47	251.21	0.11	3.76
XF_2349	1305.60	1257.60	349.46	238.69	1.04	1.46
XF_2407	20.56	123.74	94.64	45.78	0.17	2.07
XF_2586	12.86	499.25	262.23	91.39	0.03	2.87
XF_2713	28.79	271.38	153.78	75.45	0.11	2.04
XF_2775	0.38	3.42	8.57	5.76	0.11	1.49
