S1_Table

Population I. DSM only

Uniprot-ID	Protein Name	Gene Name	LFQ Intensity DRM	LFQ Intensity
A0A033UA13	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	V070_02751	1,000E+00	6,892E+08
A0A033ULA4	Heme ABC transporter, heme-binding protein isdE	V070_02180	1,000E+00	3,365E+08
A0A033UTI3	Uncharacterized protein	V070_01525	1,000E+00	4,922E+07
A0A033UVP1	Uncharacterized protein	V070_01199	1,000E+00	1,639E+09
A0A033V047	Ribonuclease R	rnr	1,000E+00	3,923E+08
A0A033V433	DNA topoisomerase 4 subunit A	parC	1,000E+00	4,115E+08
A0A069G604	Probable GTP-binding protein EngB	engB	1,000E+00	3,293E+08
A0A069G848	Serine--tRNA ligase	serS	1,000E+00	9,651E+07
A0A069G9N6	Exonuclease DnaQ family/helicase DinG family	CO98_1927	1,000E+00	2,001E+08
A0A069GCH7	ABC transporter, ATP-binding protein	CO98_2450	1,000E+00	3,091E+08
A0A069GEH3	Catabolite control protein A	ccpA	1,000E+00	1,138E+07
A0A077U6B2	PaaD-like protein involved in Fe-S cluster assembly;DNA methyltransferase;Uncharacterized protein	paaD;ACH32_11700;NWMN_08	1,000E+00	8,277E+07
A0A0D1FUI0	Uncharacterized protein;Putative uncharcterised protein;Putative membrane protein	ACR58_14070;ERS179246_01967;BN1326_90089	1,000E+00	4,583E+07
A0A0D1GJW4	Arsenate reductase;Putative oxidoreductase with thioredoxin domain	ACH32_03055;yusI	1,000E+00	1,207E+10
A0A0D1GV70	6-carboxy-5,6,7,8-tetrahydropterin synthase;6-pyruvoyl tetrahydropterin synthase;6-carboxy-5,6,7,8-tetrahydropterin synthase O	queD;ST398NM01_0788	1,000E+00	5,694E+07
A0A0D1GVC8	GntR family transcriptional regulator;GntR family regulatory protein;Transcriptional regulator, GntR family protein	ACR58_12515;NWMN_1870	1,000E+00	2,977E+08
A0A0D1H5K7	Putative DUF2187-containing protein	ACH32_11995	1,000E+00	3,390E+07
A0A0D1I1R5	HTH-type transcriptional regulator rot	ACH32_01675;HMPREF0776_2797	1,000E+00	5,619E+08
A0A0D1I4Y4	RNA-binding protein;S4 domain protein YaaA	ACH32_07050;yaaA	1,000E+00	2,391E+08
A0A0D1I792	ArsR family transcriptional regulator	czrA	1,000E+00	5,241E+08
A0A0D1ID37	Heat shock protein 15;Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit	ACH32_09740;SAZ172_0508	1,000E+00	1,565E+09
A0A0D1IFV2	Acetyltransferase;O-acetyl transferase	ACR58_06610;SAKOR_00136;ST398NM01_0170	1,000E+00	4,848E+07
A0A0D1IGG4	DNA-binding protein;Uncharacterized protein	ACR58_02295;ST398NM01_1314;SAKOR	1,000E+00	2,972E+08
A0A0D1IJ80	Purine nucleoside phosphorylase DeoD-type	deoD;de	1,000E+00	1,120E+09
A0A0D1IWZ6	Uncharacterized protein	ACH32_12430	1,000E+00	1,008E+08
A0A0D1JL45	XRE family transcriptional regulator	ACR58_00595	1,000E+00	3,021E+09
A0A0D1JPP9	Peptidoglycan-binding protein LysM	QU38_13840	1,000E+00	1,476E+07
A0A0D1JT97	Cro/CI family transcriptional regulator;HTH domain protein%2C binds to mecA promoter region	ACH32_02150;BN1326_90082	1,000E+00	1,058E+09
A0A0D1JZR1	HAD family hydrolase;Hydrolase (HAD superfamily)	ACR58_01155;SAKOR_01540	1,000E+00	7,562E+07
A0A0D1K2T0	Putative cytosolic protein	ACH32_02455	1,000E+00	7,212E+07
A0A0D1K3I9	Cold shock protein	cspC	1,000E+00	4,787E+08
A0A0D3Q6G5	Cell division protein ZapA	zapA;QU38_12010	1,000E+00	1,433E+08
A0A0D3QB11	Uncharacterized protein	AFO87_06250;ERS179246_01401;HMPREF0776_0566	1,000E+00	4,166E+08
A0A0D6G8V3	N-acetylglucosamine-6-phosphate deacetylase	nagA;SAOUHSC_00710	1,000E+00	1,406E+08
A0A0D6GHT2	IolE protein-like protein;Sugar phosphate isomerase/epimerase;Uncharacterized protein	AFO87_08680;iolE;NWMN_0156	1,000E+00	1,269E+08
A0A0D6GSH2	Precorrin-2 dehydrogenase;SA2412 protein	sirC_2;SA2412;SAKOR_02615	1,000E+00	7,870E+07
A0A0D6GY03	Nickel transport ATP-binding protein;Peptide ABC transporter ATP-binding protein;NikE	cysA;QU38_08110;ST398NM01_2513	1,000E+00	5,250E+07
A0A0D6GYC2	Endoglucanase M;M42 glutamyl aminopeptidase;Peptidase M28	ysdC_1;HMPREF0776_0515;ysdC_2	1,000E+00	1,309E+09
A0A0D6GZA8	Epimerase;MW2366 protein;SA2231 protein;NAD dependent epimerase/dehydratase family protein	AFO87_00160;MW2366;SA2231	1,000E+00	6,853E+07
A0A0D6WDP8	Acetyl-CoA carboxylase;Acetyl-CoA carboxylase subunit (Biotin carboxyl carrier subunit);	accB_1;accB	1,000E+00	1,134E+09
A0A0E0VN88	Glyoxalase family protein;3-demethylubiquinone-9 3-methyltransferase	ST398NM01_1204;ACH32_12975	1,000E+00	2,939E+08
A0A0E0VQC1	Uncharacterized protein	ST398NM01_1688;ACH32_00965;S	1,000E+00	2,288E+07
A0A0E1AFQ2	Uncharacterized protein;Protein of uncharacterised function (DUF1806)	SAZ172_0570;yojF;NWMN_0	1,000E+00	8,616E+07
A0A0E1AHI2	Cell division protein SepF	sepF	1,000E+00	1,112E+08
A0A0E1AIJ6	Putative Dihydrolipoamide dehydrogenase;Uncharacterized protein;Dihydrolipoamide dehydrogenase	SAZ172_0597;SAOUHSC_00581	1,000E+00	6,977E+07
A0A0E1AJH9	Uncharacterized protein;UPF0435 protein SAOUHSC_02093;UPF0435 protein SA1696	SAZ172_1891;SAOUHSC_02093	1,000E+00	1,209E+08
A0A0E1VJ74	Uncharacterized protein;ComA operon protein 2	HMPREF0776_1933;SAZ172_0885;ydiI	1,000E+00	4,498E+07
A0A0E1VLN5	Uncharacterized protein;Uncharacterised protein	HMPREF0776_1574;AFO87_11205;BN1321_150022	1,000E+00	3,185E+08
A0A0E1VPK7	Uncharacterized protein;Putative EsaC protein analog (Listeria type 3)	HMPREF0776_0647;esaC_2;BN1321	1,000E+00	5,670E+07
A0A0E1VQD7	LytTr DNA-binding domain protein;Uncharacterized HTH-type transcriptional regulator SAOUHSC_02645;LytTR	HMPREF0776_0417;SAOUHSC_02645	1,000E+00	5,069E+08
A0A0E1XD35	Serine-rich adhesin for platelets;Adhesin;Serine-threonine rich protein	sraP;CH51_14150;RU53_2717	1,000E+00	1,293E+08
A0A0E7DX57	Peptidase%2C M16 family;Zinc protease;SA1122 protein	AFO87_05515;SAKOR_01207;SA1122	1,000E+00	3,266E+07
A0A0E7NTZ3	Aminopeptidase;M42 glutamyl aminopeptidase	ysdC_1;ysdC_2;HMPREF0776_2384	1,000E+00	3,764E+09
A0A0E7R738	3-ketoacyl-CoA thiolase;Putative acyl-CoA acetyltransferase FadA;Acetyl-CoA acetyltransferase, putative	thlA;fadA	1,000E+00	3,342E+08
A0A0E8HDY3	Phage capsid protein;Major capsid protein;Phage major capsid protein	AFO87_05745;ST398NM01_2929;SAZ172_1975	1,000E+00	1,510E+08
A0A0G2LR37	Uncharacterized protein;UPF0298 protein MW1004;UPF0298 protein SAZ172_1060	CH51_05440;MW1004;SAZ172_1060	1,000E+00	4,208E+07
A0A0G2LV93	Acetyltransferase;Acetyltransferase, GNAT family	CH51_13490;HMPREF0776_0579;AFO87_06175	1,000E+00	6,500E+07
A0A0G2LWI9	Acetyltransferase;SA2490 protein;Uncharacterized protein	CH51_14365;nhoA;SA2490	1,000E+00	1,256E+08
A0A0H2WYG3	Uncharacterized protein;Alanine racemase domain-containing protein	SACOL0929;AFO87_02380;BN1321_190049	1,000E+00	3,456E+07
A0A0H2WZ03	Acetyl-CoA carboxylase, biotin carboxyl carrier protein, putative;Acetyl-CoA carboxylase;MW1557 protein	SACOL1662;accB_1;MW155	1,000E+00	1,958E+08
A0A0H3JMN2	Uncharacterized protein;Addiction module toxin, Txe/YoeB family;Addiction module antitoxin RelB	SA2195;HMPREF0769_10737	1,000E+00	3,475E+08
A0A0H3JQ54	Uncharacterized protein	SA1340	1,000E+00	1,505E+08
A0A0H3JWG6	Uncharacterized protein;PadR family transcriptional regulator;Transcriptional regulator, PadR family	SA2484;AFO87_13960	1,000E+00	6,480E+07
A0A0H3JWX4	Uncharacterized protein;Osmotically inducible protein C	MW1664;AFO87_07105;SAKOR_01663	1,000E+00	1,815E+08
A0A0H3K279	MW0612 protein;Dihydroxyacetone kinase;PTS-dependent dihydroxyacetone kinase subunit I O	MW0612;dhaK	1,000E+00	5,945E+07
A0A0H3K8X5	Uncharacterized protein;Beta-lactamase	NWMN_1708;AFO87_00050	1,000E+00	2,575E+08
A0A0H3KIV1	Transcriptional regulator MarR family protein;MarR family transcriptional regulator	NWMN_2411;yvnA	1,000E+00	4,274E+07
A0A0M1TXD0	Ribosomal-protein-serine N-acetyltransferase;Acetyltransferase, GNAT family;50S ribosomal protein L7	RU53_317;HMPREF0776_1087	1,000E+00	1,964E+08
A0A0M1U3G4	Phospholipase/carboxylesterase;Carboxylesterase	RU53_2581;SAZ172_2616;AFO87_06190	1,000E+00	2,495E+07
A0A0M1U3N2	LPXTG cell wall surface anchor family protein;Uncharacterized protein;Adhesin	sasF;NWMN_2545;CH51_14110	1,000E+00	2,135E+07
A0A0S2J9G7	Phnb;3-demethylubiquinone-9 3-methyltransferase;PhnB protein;Uncharacterized protein OS	ASU36_11230;AFO87_06745;SAZ172_2712	1,000E+00	2,173E+08
A0A0T7M9R1	Uncharacterised protein;Uncharacterized protein;Unchara	ERS093009_02685;AFO87_09045;HMPREF0769_11886	1,000E+00	1,121E+08
A0A0U0TVG1	NADH-dependent dehydrogenase;Uncharacterized protein;Oxidoreductase, NAD-	ycjS_2;NWMN_0155	1,000E+00	1,178E+08
A0A0U1MDM9	Putative L-serine dehydratase, beta chain;L-serine dehydratase subunit beta;Serine dehydratase	BN1326_150037;sdhB_2;QU38_16485	1,000E+00	8,890E+07
A0A0U1MEZ0	Polysaccharide biosynthesis family protein;Polysaccharide biosynthesis protein	BN1321_120025;HMPREF0769_12807	1,000E+00	4,694E+07
A0A0U1MGU0	Acetyltransferase family protein;Uncharacterized protein;Acetyltransferase, GNAT family	BN1321_180034;MW0763;HMPREF0769_1	1,000E+00	1,361E+09
A0A0U1MIA1	Putative acetyltransferase;Acetyltransferase, GNAT family;Acetyltransferase GNAT family	BN1326_50159;BN1321_150097;ERS093009_00152	1,000E+00	5,348E+08
A0A0U1MIZ1	Ribulose-phosphate 3-epimerase	rpe	1,000E+00	6,906E+07
A0A0U1MJG3	Uncharacterized protein;Uncharacterized protein O	BN1321_240140;MW1174;CH51_06640	1,000E+00	1,375E+08
A0A0U1MKV3	50S ribosomal protein L7;Ribosomal protein L7Ae	rplGA;ACR58_02520	1,000E+00	4,040E+08
A0A0U1ML44	Endonuclease III	nth	1,000E+00	2,633E+08
A0A0U1MME7	Sucrose operon repressor	scrR	1,000E+00	8,436E+07
A0A0U1MN33	Integrase;Phage integrase;Bact	int;Int-Tn;ACR61_03850	1,000E+00	6,138E+07
A0A0U1MNE3	Aminotransferase class V;Soluble hydrogenase subunit;MW1665 protein OS	AUC48_08825;ERS092844_02144;ERS179246_02457	1,000E+00	1,160E+08
A0A0U1MTU7	DNA gyrase subunit B	gyrB	1,000E+00	1,684E+08
A0A0U1MVG7	CHAP domain protein;CHAP domain-containing protein	AUC48_12985;HMPREF0769_10606;ACR58_13710	1,000E+00	5,339E+08
A0A0U1MZS8	Glycerophosphoryl diester phosphodiesterase	glpQA	1,000E+00	4,157E+07
A0A0V1TIE0	MarR family transcriptional regulator;Uncharacterized protein	ACR61_14550;BN1321_410017	1,000E+00	9,296E+08
A6QGF9	Ribosome-recycling factor	frr	1,000E+00	8,170E+08
A6QHC8	30S ribosomal protein S20	rpsT	1,000E+00	6,763E+09
A6QJD1	Urease accessory protein UreE	ureE	1,000E+00	2,254E+08
D2J692	Uncharacterised protein	ERS092844_02683	1,000E+00	1,266E+07
D2J695	Hypothetical cytosolic protein;SAP031 protein;Uncharacterized protein	ERS092844_02686;SAP031;HMPREF0769_11640	1,000E+00	3,417E+09
D2J696	Putative transcriptional regulator;DNA-binding helix-turn-helix protein	ERS092844_02687;CO98_2119	1,000E+00	3,250E+08
G5ELA4	CsoR-like sulfur transferase-regulated gene B;Uncharacterized protein;Zn-dependent hydrolase	pksB_2;SAOUHSC_00036;QU38_	1,000E+00	5,695E+07
H6UH62	Sugar isomerase;Uncharacterized protein;Transcriptional regulator, RpiR family	BN1321_80036;NWMN_0259;ST398NM01_0330	1,000E+00	3,550E+08
P0A0J3	Superoxide dismutase [Mn] 1	sodA	1,000E+00	4,849E+09
P64147	Dihydroneopterin aldolase;7,8-dihydroneopterin aldolase;7,8-dihydr	folB	1,000E+00	7,942E+07
P65201	Adenylate kinase	adk;ST398NM01_2282	1,000E+00	6,847E+08
P66689	Ribonuclease P protein component	rnpA;	1,000E+00	6,170E+07
P66715	Probable DNA-directed RNA polymerase subunit delta;DNA-directed RNA polymerase subunit delta	rpoE	1,000E+00	3,358E+09
P66830	Superoxide dismutase [Mn/Fe] 2;Superoxide dismutase	sodM;sodA	1,000E+00	2,611E+08
P66863	SsrA-binding protein	smpB	1,000E+00	4,891E+08
P67249	UPF0122 protein SA1079;UPF0122 protein HMPREF0769_12542;UPF0122 protein ylxM	SA1079;HMPREF0769_12542;ylxM	1,000E+00	9,041E+07
P67403	Urease subunit alpha	ureC	1,000E+00	3,370E+08
P67620	Transcription factor FapR	fapR	1,000E+00	2,117E+08

P99068	Nucleoside diphosphate kinase	ndk	1,000E+00	6,077E+08
Q0WXP5	Domain of uncharacterised function (DUF1413)	AL493_01525	1,000E+00	3,784E+07
Q2FF55	Alanine racemase;Alanine racemase 1;Alanine racemase OS	alr;alr1	1,000E+00	1,195E+08
Q2FHG8	Ribosome-binding factor A	rbfA	1,000E+00	2,761E+08
Q2FHM8	DNA-directed RNA polymerase subunit omega	rpoZ	1,000E+00	8,024E+09
Q2FIL9	Triosephosphate isomerase	tpiA	1,000E+00	2,364E+09
Q2FJ70	3-hexulose-6-phosphate synthase;D-arabino-3-hexulose 6-phosphate formaldehyde lyase	SAUSA300_0555;SACOL0617	1,000E+00	1,152E+09
Q2FV40	Uncharacterized protein;5-carboxyvanillic acid decarboxylase	SAOUHSC_02899;ERS179246_01666;MW250	1,000E+00	3,169E+08
Q2FV63	Copper chaperone CopZ;Copper chaperone copZ	copZ;QU38_16345	1,000E+00	3,074E+08
Q2FVJ6	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase;Adenosylmethionine-8	bioA	1,000E+00	5,653E+06
Q2FWN3	10 kDa chaperonin	groS;groES	1,000E+00	2,531E+08
Q2FXW2	UPF0473 protein SAOUHSC_01719;UPF0473 protein V070_00674	SAOUHSC_01719;V070_00674	1,000E+00	4,116E+08
Q2FXW7	Transcription elongation factor GreA	greA	1,000E+00	9,739E+08
Q2FY47	Exodeoxyribonuclease 7 small subunit	xseB	1,000E+00	1,569E+08
Q2FYN6	Uncharacterized hydrolase SAOUHSC_01399;Putative zinc peptidase;Amidohydrolase	SAOUHSC_01399;RU53_1426	1,000E+00	5,145E+07
Q2FZD9	Phenylalanine--tRNA ligase alpha subunit	pheS	1,000E+00	1,239E+09
Q2G0I3	Uncharacterized protein;DNA-binding protein;Transcriptional regulator, BadM/Rrf2 family;DN	SAOUHSC_00582;ywnA;BN1321_150036	1,000E+00	2,031E+08
Q2G1R3	tRNA-dihydrouridine synthase;Probable tRNA-dihydrouridine synthase	SAOUHSC_00039;dus	1,000E+00	1,795E+08
Q2G2J7	Uncharacterized protein	SAOUHSC_01414	1,000E+00	3,320E+07
Q2G2M4	Mini-ribonuclease 3	mrnC	1,000E+00	7,981E+07
Q2TF02	CadX;Cadmium efflux system accessory protein;ArsR family transcriptional regulator;ArsR family transcriptional regulator	cadX;cadC;CH51_14500	1,000E+00	5,565E+08
Q5HD29	D-lactate dehydrogenase	ldhD	1,000E+00	1,215E+08
Q5HDM3	Formimidoylglutamase	hutG	1,000E+00	1,726E+08
Q5HDV8	50S ribosomal protein L3	rplC	1,000E+00	1,887E+08
Q5HE19	Zinc-type alcohol dehydrogenase-like protein SACOL2177;Uncharacterized protein	SACOL2177;SAKOR_02154	1,000E+00	5,320E+07
Q5HEM1	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C	gatC	1,000E+00	9,924E+08
Q5HF65	Alanine dehydrogenase 2;Alanine dehydrogenase	ald2;ald;SAKOR_01650	1,000E+00	3,841E+08
Q5HFH9	Protein GrpE	grpE	1,000E+00	5,202E+08
Q5HG56	Probable tautomerase SACOL1399;Tautomerase	SACOL1399;graC	1,000E+00	1,406E+09
Q5HGQ3	Transcriptional regulator MraZ	mraZ	1,000E+00	4,542E+09
Q5HGZ3	Peptide deformylase	def	1,000E+00	1,158E+09
Q5HH02	Phosphocarrier protein HPr	ptsH;ST398NM01_1080	1,000E+00	2,936E+08
Q5HH40	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase	menD	1,000E+00	1,585E+08
Q5HH86	Adapter protein MecA;Adapter protein MecA	mecA	1,000E+00	1,128E+08
Q5HJ88	Protein EsaB	esaB;SAOUHSC_00260	1,000E+00	5,012E+08
Q7A0X3	Cold shock protein CspA	cspA;V070_00472	1,000E+00	5,754E+09
Q7A1Y8	Heme oxygenase (staphylobilin-producing) 2;Heme oxygenase (staphylobilin-producing)	isdI;ACH32_08100	1,000E+00	2,581E+08
Q7A2N3	Endoribonuclease MazF;mRNA interferase;mRNA interfer	mazF;HMPREF0769_11093;ndoA	1,000E+00	1,985E+09
Q7DI47	IraB;Uncharacterized protein	iraB;BN1326_140282;QU38_16720;BN1321_41005	1,000E+00	4,173E+08
Q7DJC4	Glycerophophory diester phosphodiesterase homolog	ugpQ	1,000E+00	5,747E+07
Q8NUR1	Putative acetyltransferase MW2476;Maltose O-acetyltransferase;Bacterial transferase hexapeptide repeat protein	MW2476;RU53_2619	1,000E+00	8,106E+07
Q8NV90	Urease subunit beta	ureB	1,000E+00	8,297E+07
Q8NVT4	Uncharacterized RNA methyltransferase MW1838;Uncharacterized RNA methyltransferase SA1713	MW1838;SA1713	1,000E+00	6,182E+08
Q8NW56	UPF0173 metal-dependent hydrolase MW1650;UPF0173 metal-dependent hydrolase BN1321_260339	MW1650;BN1321_260339	1,000E+00	8,475E+08
Q8NX50	Fibrinogen-binding protein	fib	1,000E+00	3,371E+08
Q93CC9	Cro/CI family transcriptional regulator	stl	1,000E+00	6,055E+08
Q93SM4	Long-chain fatty acid--CoA ligase;Long-chain-fatty-acid--CoA ligase;SA0226 protein	fadE;fadD;SA0226	1,000E+00	2,594E+07
Q99S93	UPF0457 protein SA1975.1;Uncharacterized protein	SA1975.1;RU53_2241	1,000E+00	4,199E+09
Q99T00	Low molecular weight protein-tyrosine-phosphatase PtpA	ptpA	1,000E+00	5,091E+07
Q99T18	Peroxide-responsive repressor PerR;Transcriptional regulator (Fur family)	perR	1,000E+00	1,118E+08
Q99T33	UPF0342 protein SAV1845;UPF0342 protein HMPREF0769_11833;UPF0342 protein yheA	SAV1845;HMPREF0769_11833;yhe	1,000E+00	3,767E+09
Q99VH8	Organic hydroperoxide resistance protein-like;Peroxiredoxin, Ohr subfamily;Peroxiredoxin	SAV0828;HMPREF0776_1818	1,000E+00	6,588E+07
Q99WJ6	NADPH-dependent oxidoreductase	nfrA	1,000E+00	4,713E+07
Q9EUT0	Chromosome replication initiation protein dnaD;DnaD domain protein	dnaD;HMPREF0776_2477	1,000E+00	1,276E+08
Q9EZ11	4-hydroxy-tetrahydrodipicolinate reductase	dapB	1,000E+00	4,575E+07
Q9F4G3	HTH-type transcriptional regulator TcaR;Uncharacterized protein	tcaR;tcaR_1;SAOU	1,000E+00	3,158E+08
T1Y6J8	Histidine ammonia-lyase	hutH	1,000E+00	1,762E+08
T1Y8T9	PBS lyase HEAT-like repeat protein;Scaffolding protein	SAKOR_01367;cvfC_1;ACH32_14140	1,000E+00	3,696E+08
T1YCD3	Transcriptional regulator, TetR family protein;HTH-type transcriptional regulator MW2498	SAKOR_02572;MW2498	1,000E+00	5,402E+07
U5NYY0	Lysophospholipase	ytpA_1	1,000E+00	6,446E+08
W8TPW5	Uncharacterised protein;Uncharacterized protein	AFO87_11930;QU38_14935;BN1326_30033	1,000E+00	9,778E+07
W8TRW2	GntR family transcriptional regulator;Transcriptional regulator of pyridoxine metabolism	gabR;gabR_1;BN1321_130001	1,000E+00	6,660E+08
W8TV80	Cystine ABC transporter (ATP-binding protein);ArtP;GlnQ protein	glnQ;ST398NM01_1923	1,000E+00	9,670E+08
W8TVN3	DNA mismatch repair protein MutT;Uncharacterized protein	AFO87_12065;QU38_08565;BN1321_260308	1,000E+00	1,876E+08
W8U0B2	Glycerophosphodiester phosphodiesterase;Glycerophosphoryl diester phosphodiesterase	glpQ	1,000E+00	7,238E+07
W8U6A7	Uncharacterised protein	AFO87_10460	1,000E+00	9,774E+08
W8U862	Molecular chaperone GroEL;Uncharacterized protein	AFO87_12710;SA2238;ERS179246_00936	1,000E+00	3,036E+09
W8URR1	N5-carboxyaminoimidazole ribonucleotide mutase	purE	1,000E+00	9,677E+07
X5DWV7	Glycerophosphodiester phosphodiesterase;Glycerophosphodiester phosphodiesterase family protein;MW1663 protein	ugpQ_2;HMPREF0776_2752	1,000E+00	8,465E+08
X5E039	Riboflavin synthase alpha chain;Riboflavin synthase, alpha subunit	ribB;r	1,000E+00	2,126E+08
X5E1D9	Formate dehydrogenase;4-phosphoerythronate dehydrogenase	fdh;RU53_160;pdxB	1,000E+00	2,460E+08
X5E3N2	DNA-binding protein;Putative dNA-binding protein;Uncharacterized protein	AFO87_08250;BN1321_240015;AL078_05710	1,000E+00	5,534E+08
X5EKM1	Cro/CI family transcriptional regulator;Uncharacterized HTH-type transcriptional regulator YgzD;Putative transcriptional regulator	AFO87_05025;ygzD	1,000E+00	5,270E+08

Population II. DSM enriched

Uniprot-ID	Protein Name	Gene Name	LFQ Intensity DRM	LFQ Intensity
A0A033UTU4	Beta-lactam-inducible penicillin-binding protein	V070_01423	9,268E+08	1,817E+09
A0A033UZD3	Chaperone protein DnaK	dnaK	7,229E+07	1,909E+08
A0A033V2K7	Threonine--tRNA ligase	thrS	3,043E+08	4,514E+08
A0A062W679	CI-like repressor%2C phage associated	lexA_2	9,073E+08	8,369E+09
A0A069FM85	Export membrane protein	CO98_1599	5,442E+08	1,239E+09
A0A069FR69	Phosphoglycerate kinase	pgk	1,653E+08	2,359E+08
A0A069FSS7	DNA-directed RNA polymerase subunit beta	rpoB	2,594E+08	1,315E+09
A0A069FXY2	Ferritin	CO98_2184;V070_02700	2,733E+08	1,154E+09
A0A069G712	Pyruvate dehydrogenase E1 component subunit beta	pdhB	2,807E+09	1,851E+10
A0A069G7V5	Pyruvate kinase	pyk	2,381E+09	3,008E+09
A0A0B6XLW5	3-dehydroquinate dehydratase	aroC_1;aroD	4,240E+07	1,039E+08
A0A0B6XMY5	Alanine racemase;Pyridoxal-5-phosphate family protein	yggS;ACR58_02940;SAKOR_01114	5,415E+08	1,439E+09
A0A0B6XQ62	Aminopeptidase;Thermophilic metalloprotease (M29);Aminopeptidase T;Aminopeptidase	pepS;HMPREF0776_0019;CH51_10245	4,693E+08	8,646E+08
A0A0D1EZR2	Thioredoxin	ACH32_01585	4,293E+07	3,628E+08
A0A0D1F4Q8	Cell shape-determining protein MreC	ACH32_01090;SAKOR_01597	2,182E+09	5,106E+09
A0A0D1FER1	Uncharacterized protein;Putative cytosolic protein	ACR58_11475;NWMN_0576;ST398	7,092E+08	1,998E+09
A0A0D1FFQ5	Competence protein ComK;ComK family protein;Competence transcription factor	ACH32_11980;BN1326_60138;ST398NM01_1023	3,357E+09	1,080E+10
A0A0D1FGD6	Uncharacterized protein	ACH32_13395;BN1326_60402	5,868E+08	3,019E+09
A0A0D1FJV3	Glucose-6-phosphate 1-dehydrogenase	zwf	5,720E+08	6,702E+08
A0A0D1FLC7	Amino acid ABC transporter ATP-binding protein;MW2334 protein;Amino acid ABC transporter, ATP-binding protein	tcyC;MW2334	5,201E+09	1,947E+10
A0A0D1FY59	MarR family transcriptional regulator;MW2549 protein;Transcriptional regulator, MarR family	ACR58_09835;MW2549	4,569E+07	2,293E+09
A0A0D1G023	Uncharacterized protein	ACH32_05000;HMPREF0776_0373	1,615E+08	2,488E+08
A0A0D1GE69	Thioredoxin;Putative thiol-disulfide oxidoreductase with thioredoxin domain;Uncharacterized protein	ACR58_04520;yusE;HMP	3,383E+07	6,618E+07
A0A0D1GNT7	Bacillithiol system protein YtxJ;Putative cytosolic protein;YtxJ like protein	ACH32_11050;ST398NM01_0817;ERS093009_002	6,759E+07	1,581E+08
A0A0D1GX94	4-hydroxybenzoyl-CoA thioesterase;Thioesterase;4-hydroxybenzoyl-CoA thioesterase family active site protein	ACH32_13730;ST398NM01_1353	1,188E+08	4,092E+08
A0A0D1GYV5	ADP-dependent (S)-NAD(P)H-hydrate dehydratase	nnrD	1,367E+08	6,058E+08
A0A0D1H1G7	Cell division protein FtsA	ftsA	8,290E+09	1,240E+10
A0A0D1H3M2	Acetyltransferase;Acetyltransferase, GNAT family	ACR58_14475;SAKOR_01356;HMPREF0769_	1,248E+07	3,332E+08
A0A0D1H4D9	Putative universal stress protein;Universal stress family protein	ACH32_01360;HMPREF0776_2738	5,016E+09	6,537E+10
A0A0D1H5H3	Antibiotic ABC transporter ATP-binding protein;ABC transporter, ATP-binding protein;SA1745 protein	ACH32_02755;HMPREF0776_0093	1,487E+10	6,371E+10
A0A0D1H739	Peroxiredoxin Q/BCP;Bacterioferritin comigratory protein;Antioxidant, AhpC/TSA family	bcp;NWMN_1755;HMPR	1,934E+08	3,147E+09
A0A0D1HCR3	RNA-binding protein S1;Putative RNA degradation protein polyribonucleotide nucleotidyltransferase or phosphorylase	ACH32_09750;yugI_2	4,896E+07	4,907E+09
A0A0D1HV16	DNA-binding protein;Putative RNA binding protein putative new fold	ACH32_13295;ylxR	1,949E+08	1,584E+09
A0A0D1HYM2	DNA repair exonuclease;Calcineurin-like phosphoesterase family protein;Phosphoesterase	ACH32_02130;BN1321_290014;ST398	5,892E+09	1,316E+10
A0A0D1I3Y7	Uncharacterized protein;Uncharacterised protein	ACH32_09130;ERS179246_01599	2,224E+08	5,869E+08
A0A0D1I8F1	Thioredoxin;Uncharacterized protein;Uncharac	ACH32_02745;ERS179246_01904;HMPREF0776_0091	1,217E+10	2,975E+10
A0A0D1IKI9	Cell-cycle regulation protein HIT;Adenosine 5-monophosphoramidase	ACH32_02100;SAKOR_01791	3,652E+08	1,380E+09

A0A0D1IKS3	Ktr system potassium uptake protein C;Trk system potassium uptake protein trkA;Potassium uptake protein	ktrC;trkA	3,231E+09	5,700E+09
A0A0D1IP51	Aldo/keto reductase family oxidoreductase;Oxidoreductase of aldo/keto reductase family%2C subgroup 1;SA0658 protein	ACR58_05120;ERS179246_00200	3,112E+08	3,984E+08
A0A0D1IR83	RpiR family HTH-type transcriptional regulator;RpiR family regulatory protein	ACR58_07940;BN1326_140111	8,561E+08	1,985E+09
A0A0D1J251	HTH-type transcriptional regulator;Uncharacterized protein	ACH32_00975;SAOUHSC_01732	6,838E+08	3,665E+09
A0A0D1J5Y0	NifU domain-containing protein;NifU domain protein;NifU-like protein	ACH32_11510;SACOL0939;ST398NM01_0919	1,862E+08	2,336E+08
A0A0D1JF17	Nitrogen regulatory-like protein;Protein from nitrogen regulatory protein P-II (GLNB) family	ACH32_09610;yaaQ	8,069E+07	1,814E+09
A0A0D1JL07	2-oxoglutarate dehydrogenase	QU38_09355	1,190E+09	1,322E+09
A0A0D1JSZ8	DNA mismatch repair protein MutT;Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase);Mutator mutT protein	ACR58_08900;SAZ172_2586	4,262E+07	1,147E+08
A0A0D1JTT5	2,5-diketo-D-gluconic acid reductase;Morphine 6-dehydrogenase;Oxidoreductase, aldo/keto reductase family protein	ACR58_07330;ST398NM01_2260	1,346E+09	2,500E+09
A0A0D1JY50	HAD family hydrolase;Hydrolase (HAD superfamily);HAD hydrolase, IA, variant 1 family protein	ACR58_11515;ST398NM01_0692	6,669E+08	9,086E+08
A0A0D3Q434	Putative cytosolic protein;Uncharacterized protein	AFO87_05325;ERS195423_01542;ST398NM01_0310	5,820E+08	6,749E+08
A0A0D3Q6N2	Signal recognition particle receptor FtsY	ftsY	3,375E+09	4,113E+09
A0A0D3QA93	Zinc ABC transporter substrate-binding protein;Uncharacterized protein;MW2328 protein	zinT;BN1321_400054;MW2328	1,232E+09	2,216E+09
A0A0D3QAJ7	Uncharacterised protein;Uncharacterized protein;Uncharacterized protein OS	AFO87_00970;AUC48_11675;MW2214	5,613E+08	8,070E+08
A0A0D6FS79	Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin) (Nitric oxide dioxygenase);Oxidoreductase, FAD-binding protein	hmp;HMPREF0776_0968	9,589E+08	1,400E+09
A0A0D6G869	Glycosyl transferase family 1;Poly (Glycerol-phosphate) alpha-glucosyltransferase;SA0522 protein	tagE_2;RU53_552	2,247E+08	2,426E+09
A0A0D6G8D7	HAD family hydrolase;Cof-like hydrolase;Uncharacterized protein	ywpJ_1;BN1321_130047;MW0514	2,302E+09	2,390E+09
A0A0D6GAF3	Restriction endonuclease subunit M;Type I restriction-modification system, M subunit	hsdM;SAOUHSC_00397	7,807E+08	5,832E+09
A0A0D6GB57	Restriction endonuclease subunit S;Sau1hsdS1;Type I restriction modification DNA specificity domain protein	hsdS_1;sau1hsdS1;HMPREF076	1,399E+08	9,651E+08
A0A0D6GDE2	ABC transporter ATP-binding protein;ABC transporter family protein	AFO87_05015;BN1321_80070;SAKOR_	9,480E+08	4,607E+09
A0A0D6GH02	Oligoendopeptidase F	pepF1_1;ACH32_11840;ST398NM01_0996	5,894E+08	5,183E+09
A0A0D6GHM0	SepS16B protein;Uncharacterized protein	sepS16B;QU38_14805;s	3,191E+08	1,493E+09
A0A0D6GJ33	Pyruvate decarboxylase;MW0162 protein;Thiamine pyrophosphate enzyme, N-terminal TPP binding domain protein	ipdC;MW0162	5,662E+07	3,584E+08
A0A0D6H7B9	Alpha-acetolactate decarboxylase	aldC_2;aldB;budA1	2,187E+08	3,001E+08
A0A0D6HBX1	Radical SAM/CxCxxxC motif protein YfkAB;Thioredoxin-like oxidoreductase;Uncharacterized protein	AFO87_08785;SAKOR_01833	3,121E+08	2,092E+09
A0A0D6HDZ6	Aldo/keto reductase family protein;Oxidoreductase of aldo/keto reductase family, subgroup 1;2,5-diketo-D-gluconic acid reductase	yvgN;SAZ172_1799	9,027E+07	2,364E+08
A0A0D6HHA6	Malate dehydrogenase;NADP-dependent malic enzyme	maeB;SAZ172_1715;ACH32_01340	5,685E+08	1,081E+09
A0A0D6HHM0	Formamidopyrimidine-DNA glycosylase	mutM;fpg	1,050E+08	4,809E+08
A0A0D6HHM2	Free methionine-(R)-sulfoxide reductase;GAF domain protein;Uncharacterized protein	msrC;MW1661	1,162E+08	2,679E+08
A0A0D6HHY4	Oxidoreductase;NAD dependent epimerase/dehydratase family protein;Oxidoreductase ylbE	ylbE;HMPREF0776_1400	3,194E+08	1,761E+09
A0A0D6HJ55	Fic family protein;Adenosine monophosphate-protein transferase SoFic	AFO87_10960;RU53_1700	3,174E+08	4,931E+08
A0A0D6HL17	Tripeptidase T;Peptidase T, putative;MW1465 protein;Peptidase T-like protein	pepT_1;SAOUHSC_01606;MW1465	4,052E+08	4,161E+08
A0A0D6HLL6	ATP-dependent DNA helicase;DEAD/DEAH box helicase	recQ_2;BN1321_260120;recQ	3,822E+07	4,183E+07
A0A0D6HQE4	2-oxoacid ferredoxin oxidoreductase subunit alpha;2-oxoacid:acceptor oxidoreductase, alpha subunit	porA;HMPREF0769_12489	8,800E+07	4,048E+08
A0A0D6HTX7	LSU m5C1962 methyltransferase RlmI;Putative SAM-dependent methyltransferases;Uncharacterized protein	rlmI;RU53_1078	2,138E+09	1,053E+10
A0A0D6HWT3	NADH-dependent flavin oxidoreductase	AFO87_02530;CH51_04615;QU38	5,955E+08	1,597E+09
A0A0D6HWV3	Kinase;Kinase-associated protein B	kapB;ST398NM01_0936;ACH32_11595	1,238E+08	5,235E+08
A0A0D6HYA6	Ribonuclease R	rnr;CH51_04080	5,064E+08	9,280E+09
A0A0E0VLS3	Branched-chain-amino-acid aminotransferase	ST398NM01_0629;ilvE	2,498E+09	4,510E+09
A0A0E0VN64	DNA Polymerase X family;DNA polymerase;PHP domain protein	ST398NM01_1139;polX;HMPREF0769_12639	7,422E+07	3,488E+08
A0A0E0VP52	Phosphoribosylformylglycinamidine synthase subunit PurS	purS	3,481E+08	9,742E+08
A0A0E0VSL8	ParB;Chromosome partitioning protein ParB;DNA-binding protein Spo0J-like	ST398NM01_2754;ACH32_07010;noc	4,694E+08	4,515E+09
A0A0E0VSM0	ATP synthase subunit beta	atpD	7,269E+10	1,045E+11
A0A0E1AE12	Putative hydrolase;3-oxoadipate enol-lactonase	SAZ172_0626;dehH1	8,998E+08	6,612E+09
A0A0E1AFA2	2,3-cyclic-nucleotide 2-phosphodiesterase;2%2C3-cyclic-nucleotide 2-phosphodiesterase;2, 3-cyclic nucleotide 2-phosphodiesterase	SAZ172_0965;yfkN_3	1,042E+08	1,273E+08
A0A0E1AH29	Ribosomal RNA small subunit methyltransferase E;Ribosomal RNA small subunit methyltransferase E	SAZ172_1590;rsmE	1,465E+08	3,893E+08
A0A0E1AJ76	Putative esterase;Uncharacterized protein;MW2271 protein	SAZ172_2453;SAOUHSC_02627;MW2271	1,052E+09	3,362E+09
A0A0E1AKN8	Putative oxidoreductase YncB;Alcohol dehydrogenase;Oxidoreductase, zinc-binding dehydrogenase family protein	SAZ172_2291;curA	1,305E+09	1,694E+09
A0A0E1VI94	Ribosomal RNA small subunit methyltransferase H	mraW;rsmH	2,154E+09	2,999E+09
A0A0E1VIX6	Arginine repressor (Fragment);Arginine repressor	argR;ahrC	1,068E+09	2,188E+09
A0A0E1VJA5	Ornithine aminotransferase;Ornithine aminotransferase 2	rocD;rocD2;roc	4,479E+08	4,491E+09
A0A0E1VLD0	Thermonuclease	nuc	4,119E+07	3,985E+08
A0A0E1VLD1	S1 RNA binding domain protein;General stress protein	HMPREF0776_1944;yugI_1;QU38_11390	1,538E+08	3,114E+08
A0A0E1VMI0	Fructose-1,6-bisphosphate aldolase, class II;Fructose-bisphosphate aldolase	fba	1,258E+09	6,252E+09
A0A0E1VMK6	Cof-like hydrolase;HAD family hydrolase;Putative cytosolic protein	HMPREF0776_1393;ywpJ_2;SAKOR_02119	9,512E+07	1,851E+08
A0A0E1VMN2	Sensor protein SrrB;Osmosensitive K+ channel histidine kinase SrrB	srrB	1,477E+09	7,115E+09
A0A0E1VR62	Pseudouridine synthase	HMPREF0776_2518;rluB	9,786E+08	7,520E+09
A0A0E1VS63	50S ribosomal protein L19 (Fragment);50S ribosomal protein L19	rplS	7,019E+09	1,287E+10
A0A0E1VSM9	Coenzyme A disulfide reductase	cdr	6,207E+08	2,330E+09
A0A0E1VYN8	Uncharacterized protein;Leucine carboxyl methyltransferase	HMPREF0776_0175;AL493_12285;AF	5,871E+07	8,729E+07
A0A0E1VZ65	Uncharacterized protein;Putative membrane associated protein;Membrane associated protein	HMPREF0776_0022;ACH32_02485	4,072E+08	3,057E+09
A0A0E1X703	Uncharacterized protein;Uncharacterised protein	HMPREF0769_12194;AFO87_01630;MW1439	3,558E+08	2,065E+09
A0A0E1X7D7	Diaminopimelate decarboxylase	lysA	2,321E+08	2,919E+08
A0A0E1X7E5	Dehydrogenase E1 component;Branched-chain alpha-keto acid dehydrogenase E1	HMPREF0769_12161;bfmBAA	1,164E+09	1,407E+09
A0A0E1X7T8	Uncharacterized protein	HMPREF0769_11617;HMPREF0776_1686	9,216E+07	5,167E+08
A0A0E1XGT1	DivIVA domain protein;Cell division initiation protein;Cell division initiation protein DivIVA	HMPREF0769_12587;divIVA;Q	5,146E+08	1,163E+09
A0A0E7MG06	Pyridine nucleotide-disulfide oxidoreductase;Uncharacterized protein	AFO87_10185;SAZ172_1785	2,988E+07	5,742E+07
A0A0E7NNB9	Nitroreductase;Nitroreductase family protein;Uncharacterized protein	AFO87_10670;SAKOR_00809;MW0783	2,479E+08	2,106E+09
A0A0E7R271	Bacillithiol biosynthesis deacetylase BshB2	mshB;bshB2	1,794E+08	3,273E+08
A0A0E7RYR7	DNA-binding protein;Uncharacterized protein	AFO87_07720;SAOUHSC_02393	1,738E+09	2,600E+09
A0A0E8G694	Pseudouridine synthase	rluD	2,525E+09	4,322E+09
A0A0E8G771	Radical activating enzyme protein;Uncharacterized protein	AFO87_04435;BN1321_230004;HMPREF0776_2074	2,213E+09	2,425E+09
A0A0E8G8A7	Pyruvate carboxylase	cfiB_1;SAZ172_1053	1,313E+09	1,189E+10
A0A0E8GAU0	UvrABC system protein A	uvrA	2,665E+09	2,825E+09
A0A0E8GBF4	Aldo/keto reductase family protein;Uncharacterized protein;Aldo/keto reductase;Oxidoreductase	ydhF;ST398NM01_0766	1,473E+08	8,617E+08
A0A0E8GCM1	Fibronectin-binding protein;Uncharacterized protein;SA1051 protein	AFO87_09195;NWMN_1119;SA1051	6,262E+08	1,343E+09
A0A0E8GDK3	Dihydrolipoyl dehydrogenase;Dihydrolipoyl dehydrogen	pdhD;CH51_05315	2,207E+10	4,831E+11
A0A0E8GFB0	Putative cytosolic protein;Uncharacterized protein	ywqG	3,191E+08	3,207E+08
A0A0E8GNP9	Transaldolase	tal;ACH32_01770;BN1326_90019;S	4,008E+08	1,871E+09
A0A0E8GPH7	Smooth muscle caldesmon;Uncharacterized protein;Sm	AFO87_07005;NWMN_1631;SAUSA300_1684	2,412E+10	2,612E+10
A0A0E8GPJ7	NAD(FAD)-utilizing dehydrogenase;Uncharacterized protein;NAD	AL493_10735;ERS179246_01525;SA1576	2,994E+08	8,344E+08
A0A0E8HBP5	ABC transporter ATP-binding protein;ABC-type nitrate/sulfonate/bicarbonate transporter, TauB	ssuB_1;tauB	1,909E+09	5,287E+09
A0A0E8HLR7	Integrase;Uncharacterized protein	AL493_04605;SAZ172_2691;ER12_002930;CH51_	2,731E+08	4,084E+09
A0A0E8IKQ5	PhiSLT ORF78-like protein;Conserved hypothetical phage protein;Uncharacterized protein	AFO87_05895;SAUSA300_1965;CH51_08075	2,390E+08	3,265E+09
A0A0E8J2Q8	Single-stranded DNA-binding protein	ssb_2;MW2021;	3,895E+08	2,369E+09
A0A0E8JDK7	Methionine--tRNA ligase;Methionine--tR	metS;metG	9,735E+08	3,150E+09
A0A0G2LQP6	Nitrogen fixation protein NifU;Iscu;Iron-sulfur cluster assembly scaffold protein NifU	CH51_04420;ST398NM01_0900;nifU	4,483E+07	1,014E+08
A0A0G2LVP9	RpiR family transcriptional regulator	CH51_12515;ybbH_2;QU38_0	6,269E+08	1,051E+09
A0A0H2AL62	DNA topoisomerase 4 subunit A	parC	6,516E+08	9,686E+09
A0A0H2B964	Uncharacterized conserved protein;Uncharacterized protein	AFO87_00900;SAZ172_2408;HMPREF076	8,861E+08	2,767E+09
A0A0H2WYK8	Uncharacterized protein;Phi77 ORF017-like protein;Toxin-antitoxin system, toxin component, MazF family	SACOL0319;AFO87_03400;BN1326_100140	4,354E+08	7,180E+08
A0A0H2XHQ4	Alkyl hydroperoxide reductase, subunit F;Alkyl hydroperoxide reductase subunit F;Alkyl hydroperoxide reductase, F subunit	ahpF	5,447E+09	8,497E+09
A0A0H2XI89	Ribosomal RNA small subunit methyltransferase B	sun;rsmB	1,250E+09	2,005E+09
A0A0H3JK71	SA0653 protein;DeoR C terminal sensor domain protein;Transcriptional regulator, DeoR family	SA0653;ACH32_10815	4,555E+07	2,595E+08
A0A0H3JN52	SA1675 protein;Amino acid ABC transporter periplasmic protein;Extracellular glutamine-binding protein	SA1675;artQ	6,472E+08	1,641E+09
A0A0H3JNF9	2-dehydropantoate 2-reductase	SA2232;panE_1;QU38_08000	5,054E+08	6,689E+08
A0A0H3JP54	Tagatose-6-phosphate kinase;Tagatose-6-phosphate kinase O	fruB	9,921E+07	1,106E+08
A0A0H3JPQ1	SA1000 protein;Extracellular fibrinogen binding protein	SA1000;ecb	1,215E+09	2,463E+09
A0A0H3JSM8	SA0224 protein;3-hydroxyacyl-CoA dehydrogenase, NAD binding domain protein;3-hydroxyacyl-CoA dehydrogenase	SA0224;HMPREF0776_0960	4,486E+08	2,815E+09
A0A0H3JTK4	Uncharacterized protein;Disulfide oxidoreductase	SA0798;ACR58_04270;NWMN_0808	1,007E+08	1,793E+08
A0A0H3JTX5	Aldehyde-alcohol dehydrogenase	adhE;ACR58_06650	2,220E+07	3,526E+07
A0A0H3JUR8	SA1666 protein;Uncharacterized protein;LuxR family transcriptional regulator	SA1666;ST398NM01_1914;ACR58	8,381E+07	6,923E+08
A0A0H3JUX8	Aldehyde dehydrogenase	aldH;ST398NM01_2015	3,872E+09	3,880E+10
A0A0H3JWJ1	Uncharacterized protein;Putative tRNA-m1A22 methylase	MW1512;SACOL1617;trmK	4,766E+07	7,174E+07
A0A0H3JXF0	Uncharacterized protein;Choloylglycine hydrolase	MW1866;SAZ172_1938;QU38_06900	2,494E+08	9,986E+08
A0A0H3JY52	Cmp-binding-factor 1;3-5 exonuclease	cbf1;ACH32_02120;yhaM	8,049E+08	4,375E+09
A0A0H3JZ81	Probable methylated DNA-protein cysteine methyltransferase	adaB	4,694E+08	1,725E+09
A0A0H3JZU4	Primosomal protein N	priA	1,768E+08	6,784E+08
A0A0H3K1I2	IMMUNOGLOBULIN G BINDING PROTEIN A;Peptigoglycan-binding protein LysM;Immunoglobulin G binding protein	spa;CH51_00450	2,613E+08	1,950E+09
A0A0H3K1V2	MW0336 protein;SA0348 protein;Site-specific DNA-binding protein;ParB-like protein	MW0336;SA0348;parB	3,578E+08	6,049E+08
A0A0H3K5L3	Uncharacterized protein;Transcriptional regulator, GntR family;Cell wall surface anchor family protein	NWMN_0079;ST398NM01_0149	7,638E+07	9,987E+08
A0A0H3K763	UvrB/UvrC motif domain protein;DNA binding protein, UvrB/UvrC family protein;Protein-arginine kinase activator protein	NWMN_0485;SAKOR_00508	5,302E+07	7,054E+07
A0A0H3K908	FtsK/SpoIIIE (DNA translocase stage III) family protein;Cell division protein FtsK	NWMN_1634;sftA	2,108E+09	4,212E+09
A0A0H3KCP9	Uncharacterized protein;TelA-like protein SAOUHSC_01408;Tellurite resistance protein	NWMN_1317;SAOUHSC_01408;ERS17924	1,940E+09	2,187E+09
A0A0H3KED7	50S ribosomal protein L29	rpmC	9,949E+08	1,964E+10
A0A0K7CIC9	Invertase;Invertase O	scrB;QU38_06710	4,535E+08	7,142E+08
A0A0K7UDI1	Putative glutathione transporter%2C ATP-binding component;ABC transporter ATP-binding protein	oppF_3;oppF_1	1,012E+09	1,077E+09
A0A0M1TX48	Putative bifunctional signaling protein/50S ribosomal protein L9;Phosphoesterase%2C DHH family protein	RU53_16;nrnA_2	5,441E+09	1,954E+10

A0A0M1U096	Cysteine-rich secretory protein family protein;Uncharacterized protein;SCP family extracellular protein	RU53_1343;MW1225	1,940E+08	2,047E+08
A0A0M1U0I5	Ferric uptake regulation protein Fur;Ferric uptake regulation protein;Ferric uptake regulation protein FUR	fur	3,549E+08	6,723E+08
A0A0M1U0W4	Dihydrolipoyl dehydrogenase	lpdA;AFO	6,819E+07	9,024E+08
A0A0M1U105	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	bfmB	1,577E+08	2,168E+08
A0A0M1U3S0	Phage infection protein;Putative membrane spanning protein;SA2436 protein	RU53_2706;SAKOR_02644	4,647E+09	5,602E+09
A0A0T7M2Z6	Fibrinogen-binding protein;Clumping factor A	clfA	1,502E+09	6,247E+09
A0A0T7M3E5	Putative glycosyl transferases;Glycosyl transferase family 1;Glycosyl transferase, group 1 family protein	tagE_3;NWMN_0906	6,578E+08	9,746E+09
A0A0T7M481	2-oxoglutarate oxidoreductase%2C beta subunit;2-oxoglutarate ferredoxin oxidoreductase subunit beta	porB;HMPREF0776_2291	1,713E+08	2,617E+08
A0A0T7M4M7	5-nucleotidase;LPXTG-motif cell wall anchor domain protein;MW0023 protein	yfkN_2;BN1321_430113	3,686E+07	2,866E+08
A0A0T7M6B9	DNA/RNA helicase of DEAD/DEAH box family	srmB;	5,020E+08	5,485E+09
A0A0T7M7H9	Glycosyl transferase family protein;Glycosyl transferase;Glycosyl transferase group 2 family protein	ERS093009_01950;AFO87_07610;NWMN_01	3,915E+09	1,755E+10
A0A0T7M883	SdrH protein;Serine-aspartate repeat family protein;SA1839 protein	ERS093009_02099;ST398NM01_2069;SA1839	4,598E+07	4,726E+07
A0A0T7MUQ9	Two component system histidine kinase ArlS	arlS	2,244E+09	4,090E+09
A0A0T7MUR4	Acyl-CoA dehydrogenase;MW2203 protein;Putative acyl-CoA dehydrogenase YdbM	hsaA;MW2203	2,374E+08	3,329E+08
A0A0U0TR45	LysR family regulatory protein;MW2253 protein	cynR;NWMN_2233;MW2253	2,875E+08	6,509E+08
A0A0U1MI56	Uncharacterized protein;Membrane protein	BN1321_230026;ERS093009_00534;RU53_1101	2,862E+08	4,440E+08
A0A0U1MJX5	Catalase	katA;ST398NM01_1	3,234E+09	1,888E+10
A0A0U1MK69	Pyruvate dehydrogenase (E1 beta subunit)	pdhB	1,733E+10	8,803E+10
A0A0U1MLN5	ADP-ribose pyrophosphatase;ADP-ribose pyrophosphatase, NudF	nudF	3,121E+08	6,418E+08
A0A0U1MLZ6	HTH-type transcriptional regulator MalR;Maltose operon transcriptional repressor MalR%2C LacI family	malR;mal	1,081E+08	5,881E+08
A0A0U1MMC9	tRNA threonylcarbamoyladenosine dehydratase (T(6)A37 dehydratase);ThiF/MoeB family protein	tcdA;ST398NM01_1692	8,439E+08	1,174E+09
A0A0U1MMN4	Beta-ketoacyl-acyl carrier protein reductase;3-ketoacyl-ACP reductase;3-oxoacyl-[acyl-carrier-protein] reductase FabG	fabG;ACH32_13095	3,448E+09	5,368E+09
A0A0U1MNK9	Transcriptional regulator (Fur family);Ferric uptake regulation protein	zur;fur	1,069E+08	1,504E+08
A0A0U1MP91	Cell shape-determining protein MreC	BN1326_80190	4,374E+08	6,767E+08
A0A0U1MQQ6	Acetolactate synthase	ilvB	7,660E+06	2,211E+07
A0A0U1MQU9	YwpF protein;Uncharacterized protein	ywpF;ACR58_10765;NWMN_2002	4,999E+08	5,943E+08
A0A0U1MRD1	Regulatory protein RecX;Regulatory protein Rec	recX	5,595E+07	1,089E+09
A0A0U1MSV9	Nitrate reductase (Beta subunit);Nitrate reductase beta chain narH;NarH protein;Nitrate reductase O	narH	3,321E+07	1,157E+08
A0A0U1MTM3	Transcriptional regulator, TetR family;TetR family transcriptional regulator;Uncharacterized protein	BN1321_420075;ACH32_06275	8,180E+07	2,610E+08
A0A0U1MTZ5	Mannose-6-phosphate isomerase	pmi	3,442E+07	8,975E+07
A0A0U1MTZ8	Isochorismatase family protein;Isochorismatase	BN1321_430024;ACR58_09925;HMPREF	6,935E+07	2,073E+08
A0A0U1MWF6	Multiple sugar-binding transporter ATP-binding protein;Multiple sugar-binding transport ATP-binding protein	msmX	2,798E+08	5,916E+08
A0A0U1MWH3	Glycosyl transferase 2 family protein	BN1321_60071	1,093E+08	2,631E+08
A0A0U1MX95	Putative sporulation transcription regulator WhiA	whiA	3,381E+08	3,445E+08
A0A0U1MXR4	Histidine transporter;Na+/H+ antiporter family protein;Na+/H+ antiporter NhaC-like protein	hisP;SACOL0946;ACH32_11545	2,755E+08	3,585E+08
A6QD96	HTH-type transcriptional regulator SarS	sarS	2,350E+08	7,731E+09
A6QED3	Nucleoid-associated protein NWMN_0443	NWMN_0443	9,228E+07	5,375E+08
A6QEF5	Peptidyl-tRNA hydrolase	pth	4,585E+08	7,881E+08
A6QEH1	Pyridoxal 5-phosphate synthase subunit PdxS	pdxS	2,489E+09	4,446E+09
A6QEJ7	30S ribosomal protein S12	rpsL	1,821E+09	1,095E+10
A6QEN4	Uracil-DNA glycosylase	ung	7,933E+07	4,525E+08
A6QF37	NADPH-dependent 7-cyano-7-deazaguanine reductase	queF	1,114E+08	2,438E+08
A6QFE5	D-alanine--poly(phosphoribitol) ligase subunit 2	dltC	5,487E+08	8,636E+08
A6QFH3	Glucose-6-phosphate isomerase	pgi	1,098E+08	9,934E+09
A6QFL7	NAD kinase	nadK;ppnKA	3,905E+08	3,464E+09
A6QG41	Ribonuclease HIII	rnhC	8,731E+07	1,106E+08
A6QGD8	30S ribosomal protein S16	rpsP	7,932E+08	2,491E+10
A6QGE5	Succinyl-CoA ligase [ADP-forming] subunit beta	sucC	1,756E+09	4,755E+09
A6QGG8	Translation initiation factor IF-2	infB	3,348E+10	4,333E+10
A6QGH0	tRNA pseudouridine synthase B	truB	3,756E+08	8,292E+08
A6QH73	Elongation factor P;Translation elongation factor P%3B Translation initiation factor 5A	efp	3,912E+08	2,484E+09
A6QHF7	Putative pre-16S rRNA nuclease	NWMN_1517;yrrK	3,322E+08	8,317E+08
A6QHN4	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	accA	2,021E+09	2,238E+09
A6QHU1	Leucine--tRNA ligase	leuS	7,482E+08	1,563E+09
A6QIG2	65 kDa membrane protein;77 kDa membrane protein;Protein map	NWMN_1872;SACOL2002;CH51_10545	9,219E+10	2,018E+11
A6QJ81	50S ribosomal protein L24	rplX	4,669E+07	5,333E+09
A6QJ90	50S ribosomal protein L23	rplW	2,726E+09	1,988E+10
A6QJ91	50S ribosomal protein L4	rplD	2,441E+09	1,569E+10
A6QK89	L-lactate dehydrogenase 2;L-lactate dehydrogenase	ldh2;ldhB;ldh	1,357E+09	3,681E+09
A8IK61	Uncharacterised protein	AL493_00390	2,558E+09	1,290E+10
A8IK64	Rep protein;Replication protein Rep;Replication protein	ERS092844_02738;ERS365775_02652;SAKOR_02719	2,435E+08	2,868E+09
D2J6B7	DNA integration/recombination/inversion protein;BinL protein;Resolvase, N-terminal domain protein	bin;binL;HMPREF0769_11633	1,419E+08	2,181E+09
E9KNS1	Ornithine carbamoyltransferase	arcB;arcB_2;argF	7,308E+07	1,576E+08
I7H3R7	Abortive infection bacteriophage resistance protein;Abi-like protein	AFO87_10805;HMPREF0769_10093	4,817E+08	1,450E+09
P0A037	Glyceraldehyde-3-phosphate dehydrogenase 1;Glyceraldehyde-3-phosphate dehydrogenase	gapA1;gapA	3,820E+09	7,225E+09
P0A081	Peptide methionine sulfoxide reductase MsrA 1;Peptide methionine sulfoxide reductase MsrA	msrA1;msrA	6,998E+08	1,071E+09
P0A0A1	Pyruvate dehydrogenase E1 component subunit beta	pdhB	2,365E+10	6,193E+11
P0A0K0	Uncharacterized protein SAV1875;General stress protein;Intracellular protease, PfpI family	SAV1875;QU38_07190	1,108E+08	1,274E+09
P0A0M6	Putative acetyltransferase SAV1054;Uncharacterized protein;Acetyltransferase, GNAT family	SAV1054;BN1321_220017	2,025E+08	2,955E+08
P0A0N9	Tyrosine recombinase XerD	xerD;xerD_2	1,488E+08	5,194E+08
P0C048	Protein EssC;Type VII secretion protein EssC;Protein essC	essC	6,302E+09	9,332E+09
P0C1S3	Transcription termination/antitermination protein NusG	nusG	5,059E+09	6,561E+09
P60070	Anti-sigma-B factor antagonist	rsbV	1,726E+08	1,516E+09
P60090	Pyruvate dehydrogenase E1 component subunit alpha;Pyruvate dehydrogenase E1 component alpha subunit	pdhA;ST398NM01_1090	1,210E+10	3,995E+11
P60380	Regulatory protein Spx;Regulatory protein Spx OS	spxA	7,193E+07	1,504E+09
P60430	50S ribosomal protein L2	rplB	8,257E+09	6,052E+10
P60448	50S ribosomal protein L3	rplC	1,841E+09	2,020E+10
P63844	GTP-sensing transcriptional pleiotropic repressor CodY	codY	2,708E+10	3,440E+10
P63871	Cysteine synthase	cysK;SAKOR_00498	2,360E+10	6,655E+10
P64108	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	fabZ	7,905E+07	5,497E+09
P64213	Glycine cleavage system H protein	gcvH	2,545E+08	1,231E+09
P64290	Glutathione peroxidase homolog BsaA;Glutathione peroxidase	bsaA;HMPREF0776_2306	6,380E+08	1,857E+09
P64333	Delta-aminolevulinic acid dehydratase	hemB;QU38_08615	1,438E+08	9,458E+08
P65139	Translation initiation factor IF-3	infC	8,907E+08	1,532E+10
P65330	S-ribosylhomocysteine lyase	luxS	2,267E+08	3,876E+08
P65645	Probable transglycosylase IsaA;Putative transglycosylase IsaA	isaA	1,298E+08	3,022E+08
P65806	Peptidase T	pepT;pepT_1	6,448E+07	2,276E+08
P65862	Phosphate acetyltransferase	pta;p	4,732E+08	2,096E+09
P65907	Dihydroorotase	pyrC	7,337E+08	1,007E+09
P65924	CTP synthase	pyrG	7,901E+08	1,497E+09
P66061	50S ribosomal protein L7/L12	rplL	4,211E+08	8,954E+09
P66133	50S ribosomal protein L27	rpmA	3,692E+08	5,771E+09
P66196	50S ribosomal protein L31 type B	rpmE2	3,145E+08	4,353E+09
P66232	50S ribosomal protein L33 2;50S ribosomal protein L33 3;50S ribosomal protein L33	rpmG2;rpmG3;rpmG_2	2,257E+08	2,586E+08
P66317	50S ribosomal protein L9	rplI	4,427E+08	5,798E+09
P66388	30S ribosomal protein S13	rpsM	2,252E+09	2,941E+10
P66545	30S ribosomal protein S2	rpsB	2,072E+10	2,541E+10
P66562	30S ribosomal protein S4	rpsD	9,214E+09	5,369E+10
P66646	30S ribosomal protein S9	rpsI	2,875E+09	3,409E+10
P66775	Diacetyl reductase [(S)-acetoin forming];Diacetyl reductase ((S)-acetoin forming);(R,R)-butanediol dehydrogenase	butA	6,984E+09	9,285E+09
P66866	Succinyl-CoA ligase [ADP-forming] subunit alpha;Succinyl-CoA ligase	sucD;SAZ172_1250	7,040E+08	3,408E+09
P66962	Transketolase	tkt;tk	2,326E+09	7,851E+09
P67021	Glutamate--tRNA ligase	gltX	5,189E+07	3,040E+09
P67765	Serine acetyltransferase#	cysE	1,449E+09	2,844E+09
P68819	Phosphoglycerate kinase	pgk	4,004E+09	4,889E+09
P95844	RNA polymerase sigma factor;RNA polymerase	sigB	6,717E+07	6,891E+08
P99065	Peptide methionine sulfoxide reductase MsrB	msrB	1,926E+08	3,774E+08
P99110	Chaperone protein DnaK;Ch	dnaK	8,429E+09	2,578E+10
P99148	Aconitate hydratase A;Aconitate hydratase;Aconitate hy	acnA;citB;QU38_13120	4,922E+09	1,016E+10
P99157	Alkaline shock protein 23	asp23	8,241E+09	4,725E+10
P99175	Catabolite control protein A;Transcriptional regulator (LacI family)	ccpA;QU38_08240	7,523E+09	2,445E+10
Q1XG25	Uncharacterised protein	SAP003	2,000E+09	2,463E+09
Q2FDH4	UPF0312 protein SAUSA300_2620;Uncharacterized protein;YceI-like domain protein	SAUSA300_2620;QU38_15655;ERS179246_00851	3,042E+08	5,259E+08
Q2FDQ4	Fructose-bisphosphate aldolase class 1	fda	6,548E+09	1,371E+10
Q2FDS6	Uncharacterized hydrolase SAUSA300_2518;Uncharacterized hydrolase MW2501;Uncharacterized hydrolase SAOUHSC_02900	SAUSA300_2518;MW2501	4,245E+09	5,365E+09
Q2FDY9	Fructose-1,6-bisphosphatase class 3	fbp	4,791E+07	7,084E+08
Q2FE21	Uncharacterized oxidoreductase SAUSA300_2422;Oxidoreductase, short-chain dehydrogenase/reductase family;Short-chain alc	SAUSA300_2422;SAZ172_2580	1,647E+09	2,343E+09
Q2FEQ3	30S ribosomal protein S8	rpsH	2,077E+09	1,325E+10

Q2FER5	DNA-directed RNA polymerase subunit alpha	rpoA	3,034E+09	3,140E+10
Q2FES1	50S ribosomal protein L13	rplM	4,258E+09	3,777E+10
Q2FEX1	Phosphoglucosamine mutase;Phosphoglucosamine	glmM	1,613E+09	1,988E+09
Q2FF10	Peptide chain release factor 1	prfA	7,177E+08	1,592E+09
Q2FF15	Serine hydroxymethyltransferase	glyA;CH	2,430E+09	1,419E+10
Q2FF21	ATP synthase subunit delta	atpH	1,972E+09	1,935E+10
Q2FF25	ATP synthase epsilon chain	atpC	1,392E+09	6,780E+09
Q2FFK2	Bacterial non-heme ferritin#	ftnA;HMPREF0769_11279;ST398NM01_1986	4,222E+10	5,718E+10
Q2FG06	Formate--tetrahydrofolate ligase	fhs	2,727E+09	1,424E+10
Q2FG30	Uncharacterized peptidase SAUSA300_1654;Uncharacterized peptidase SAV1708;Uncharacterized peptidase MW1651	SAUSA300_1654;SAV1708	1,021E+08	3,460E+08
Q2FG58	50S ribosomal protein L20	rplT	2,414E+09	2,185E+10
Q2FG80	50S ribosomal protein L21	rplU	8,674E+09	5,457E+10
Q2FG84	UPF0735 ACT domain-containing protein SAUSA300_1599;UPF0735 ACT domain-containing protein MW1593	SAUSA300_1599;MW1593	7,223E+07	7,224E+07
Q2FGE8	30S ribosomal protein S21	rpsU	3,302E+08	4,530E+09
Q2FGG6	Probable endonuclease 4	nfo	6,321E+07	2,207E+09
Q2FGK9	N utilization substance protein B homolog	nusB	4,487E+08	4,832E+08
Q2FH94	LexA repressor	lexA	4,815E+07	2,238E+09
Q2FH96	GMP reductase	guaC	1,066E+08	2,787E+09
Q2FHG5	30S ribosomal protein S15;30S ribosomal	rpsO	1,490E+09	1,519E+10
Q2FHH3	Ribosome maturation factor RimP	rimP	1,567E+08	2,057E+09
Q2FHI5	ATP-dependent protease subunit HslV	hslV;clpQ	2,379E+08	2,874E+08
Q2FHI8	DNA topoisomerase 1	topA	5,463E+07	6,119E+09
Q2FHT5	UvrABC system protein C	uvrC	3,203E+08	7,063E+08
Q2FHT6	Thioredoxin	trxA;ST398NM01_1141	1,538E+09	1,073E+10
Q2FHV3	50S ribosomal protein L32	rpmF	2,738E+08	6,996E+09
Q2FHX4	UPF0637 protein SAUSA300_1006;UPF0637 protein MW0989;UPF0637 protein QU38_05785	SAUSA300_1006;MW0989;QU38_057	2,566E+09	2,352E+10
Q2FI12	Phosphoribosylaminoimidazole-succinocarboxamide synthase	purC	1,624E+09	1,903E+09
Q2FI15	Bifunctional protein FolD	folD	5,934E+09	1,048E+10
Q2FIA8	ATP-dependent helicase/nuclease subunit A	addA	4,397E+08	2,087E+09
Q2FIL7	Enolase	eno	7,703E+09	1,472E+11
Q2FIM5	ATP-dependent Clp protease proteolytic subunit	clpP	8,349E+08	6,003E+09
Q2FIX0	Probable transcriptional regulatory protein SAUSA300_0655;Probable transcriptional regulatory protein yeeI	SAUSA300_0655;yeeI	7,040E+08	1,718E+09
Q2FJ94	30S ribosomal protein S7	rpsG	8,964E+09	4,886E+10
Q2FJ97	DNA-directed RNA polymerase subunit beta	rpoC	2,371E+10	7,843E+10
Q2FJ98	DNA-directed RNA polymerase subunit beta	rpoB	1,418E+10	5,992E+10
Q2FJE2	Bifunctional protein GlmU	glmU	4,254E+08	8,918E+08
Q2FJE4	Putative septation protein SpoVG	spoVG	1,842E+08	3,630E+10
Q2FKQ0	DNA gyrase subunit A;DNA gyrase subunit A	gyrA	4,696E+09	2,055E+10
Q2FUQ3	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	mnmG	3,013E+08	1,263E+09
Q2FUU5	Lipase 1;Lipase;Triacylglycerol lipase	lipA;lipA_2;SAKOR_02673	3,079E+09	1,018E+10
Q2FVK8	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	gpmA	4,338E+08	4,186E+09
Q2FVV9	Putative formate dehydrogenase SAOUHSC_02582;Formate dehydrogenase%2C alpha subunit;Putative formate dehydrogenase SA2	SAOUHSC_02582;CH51_12440	3,691E+09	1,152E+10
Q2FVW4	Putative 2-hydroxyacid dehydrogenase SAOUHSC_02577;Putative 2-hydroxyacid dehydrogenase SAV2305	SAOUHSC_02577;SAV2305	9,242E+08	4,234E+09
Q2FW28	Translation initiation factor IF-1	infA	2,011E+08	2,677E+09
Q2FW31	30S ribosomal protein S11	rpsK	3,290E+09	1,147E+10
Q2FW96	Mannitol-1-phosphate 5-dehydrogenase	mtlD	1,569E+08	3,577E+08
Q2FWE6	Uracil phosphoribosyltransferase	upp	1,141E+10	1,442E+10
Q2FWE9	ATP synthase gamma chain	atpG	9,367E+09	1,734E+10
Q2FXD1	Type I restriction-modification enzyme, S subunit, EcoA family, putative;Probable specificity determinant HsdS	SAOUHSC_01932;hsdS	2,472E+08	1,898E+09
Q2FXG2	6,7-dimethyl-8-ribityllumazine synthase	ribH	1,471E+08	7,363E+09
Q2FXI2	tRNA (guanine-N(7)-)-methyltransferase	trmB	1,307E+08	2,047E+08
Q2FXP1	Dephospho-CoA kinase	coaE	1,202E+08	7,456E+08
Q2FXQ0	50S ribosomal protein L35	rpmI	6,515E+07	5,885E+08
Q2FXQ6	Trigger factor	tig	5,886E+08	1,731E+10
Q2FXQ8	Probable GTP-binding protein EngB	engB	5,069E+08	2,468E+09
Q2FY15	DEAD-box ATP-dependent RNA helicase CshB	cshB	3,557E+09	6,936E+09
Q2FY68	Pyrroline-5-carboxylate reductase	proC	6,688E+08	9,570E+08
Q2FY77	Segregation and condensation protein B	scpB	1,750E+08	1,855E+08
Q2FYH2	Uncharacterized protein;Putative TPR-repeat-containing protein, component of Menaquinone-cytochrome C reductase	SAOUHSC_01480;AFO87_08460	2,392E+08	6,222E+08
Q2FYN7	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	dapH	3,432E+08	4,936E+08
Q2FYP3	Conserved virulence factor B	cvfB	8,372E+08	1,044E+10
Q2FZ23	Elongation factor Ts;Elongation factor	tsf	1,215E+10	4,948E+10
Q2FZ44	Ribosome maturation factor RimM	rimM	1,091E+08	1,377E+09
Q2FZ71	Orotidine 5-phosphate decarboxylase	pyrF	7,792E+07	1,198E+08
Q2FZ82	Isoleucine--tRNA ligase	ileS	1,606E+09	5,420E+09
Q2FZ91	Cell division protein DivIB	divIB;ftsQ	1,884E+09	2,920E+09
Q2FZF6	Uncharacterized protein;Site-specific DNA-methyltransferase (Adenine-specific)	SAOUHSC_01074;RU53_1119	2,051E+08	2,911E+08
Q2FZG8	UPF0356 protein SAOUHSC_01036;UPF0356 protein QU38_05700	SAOUHSC_01036;QU38_05700	1,959E+08	7,567E+09
Q2FZX0	Acid sugar phosphatase;HAD family hydrolase	nagD;ACH32_11470	6,113E+08	1,245E+09
Q2G045	HPr kinase/phosphorylase	hprK	6,768E+08	1,446E+09
Q2G0F8	Arginine--tRNA ligase	argS	1,634E+09	2,789E+09
Q2G0F9	Uncharacterized protein	SAOUHSC_00610;MW0570;ACH32_10350	4,284E+07	6,295E+07
Q2G0P0	50S ribosomal protein L1	rplA	1,903E+10	6,504E+10
Q2G0P5	ATP-dependent Clp protease ATP-binding subunit ClpC;Clp protease ATP binding subunit;Clp protease ClpX	clpC;RU53_511	3,001E+10	5,155E+10
Q2G1C0	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	ispD	8,937E+08	1,844E+09
Q2G1D8	Formate acetyltransferase;Formate C-acetyltransferase;Pyruvate formate lyase I	pflB	1,185E+09	2,128E+09
Q2G1J0	Putative aldehyde dehydrogenase AldA;Aldehyde dehydrogenase B	aldA	1,837E+08	5,205E+09
Q2G1W2	Phosphoenolpyruvate carboxykinase [ATP]	pckA	3,074E+08	3,574E+09
Q2G1Y0	DNA ligase	ligA;lig	4,999E+08	4,446E+09
Q2G227	Phosphopentomutase	deoB;drm	7,442E+08	1,925E+09
Q2G235	Nicotinate phosphoribosyltransferase	SAOUHSC_02133;ERS092844_01372	1,957E+08	2,233E+09
Q2G236	NH(3)-dependent NAD(+) synthetase	nadE	6,752E+08	8,709E+08
Q2G260	Uncharacterized protein SAOUHSC_00094;Putative cell-wall-anchored protein SasD (LPXAG motif)	SAOUHSC_00094;sasD	2,696E+07	4,999E+08
Q2G2F3	Signal transduction protein TRAP	traP	7,479E+08	7,992E+09
Q53725	Cell division protein FtsI (Peptidoglycan synthetase);Penicillin-binding protein 1	pbpA	1,088E+10	1,388E+10
Q53753	Methyltransferase;Ribosomal RNA methyltransferase	ORF202;ybxB;QU38_09720	1,582E+08	1,328E+09
Q53757	DNA integration/recombination/inversion protein;Transposon DNA-invertase	sin;ACR62_14520;B	2,164E+08	2,485E+09
Q5HCQ9	Immunodominant staphylococcal antigen B	isaB	2,679E+09	1,493E+10
Q5HCV3	3-methyl-2-oxobutanoate hydroxymethyltransferase	panB	3,945E+07	3,238E+09
Q5HDL2	Putative 3-methyladenine DNA glycosylase	SACOL2339;ERS179246_01328	6,196E+07	7,677E+07
Q5HDT4	Molybdopterin molybdenumtransferase	moeA	3,358E+08	7,010E+08
Q5HDV7	30S ribosomal protein S10	rpsJ	3,634E+09	5,644E+09
Q5HDW2	30S ribosomal protein S19	rpsS;rps	2,595E+09	4,312E+10
Q5HDW8	50S ribosomal protein L14	rplN	7,838E+09	1,787E+10
Q5HDX4	50S ribosomal protein L18	rplR	5,851E+08	8,997E+09
Q5HDX6	50S ribosomal protein L30	rpmD	2,806E+08	1,870E+09
Q5HDX7	50S ribosomal protein L15	rplO	6,544E+09	7,739E+10
Q5HDY1	50S ribosomal protein L36	rpmJ	7,128E+08	4,587E+09
Q5HDY5	50S ribosomal protein L17	rplQ	5,467E+08	1,975E+10
Q5HDY9	tRNA pseudouridine synthase A	truA	5,374E+07	6,656E+07
Q5HE08	Lactose phosphotransferase system repressor	lacR	9,693E+07	1,755E+08
Q5HE95	ATP synthase subunit alpha	atpA	2,360E+10	1,626E+11
Q5HEF5	Redox-sensing transcriptional repressor Rex	rex	1,222E+09	2,141E+09
Q5HEH2	60 kDa chaperonin	groL;groEL	5,263E+09	1,041E+10
Q5HEN6	Methionine aminopeptidase	map;mapB	5,723E+08	2,115E+09
Q5HF61	Probable thiol peroxidase	tpx	5,926E+08	2,585E+09
Q5HFA8	Valine--tRNA ligase	valS	1,048E+09	1,646E+09
Q5HFC1	Holliday junction ATP-dependent DNA helicase RuvA	ruvA	2,426E+08	9,445E+08
Q5HFE4	Alanine--tRNA ligase;Alanine--	alaS	2,906E+09	3,165E+09
Q5HFE5	UPF0297 protein SACOL1672;UPF0297 protein ST398NM01_1681	SACOL1672;ST398NM01_1681	3,021E+08	3,286E+08
Q5HFI2	Ribosomal protein L11 methyltransferase	prmA	4,968E+08	5,847E+08
Q5HFK1	GTP cyclohydrolase 1 type 2 homolog	SACOL1616;MW1511	7,556E+07	1,874E+08
Q5HFM2	Aminomethyltransferase	gcvT	6,910E+08	1,402E+09
Q5HFM3	Probable glycine dehydrogenase (decarboxylating) subunit 1	gcvPA	7,276E+08	2,052E+09
Q5HFR2	6-phosphogluconate dehydrogenase, decarboxylating	gnd;gndA	2,597E+08	3,222E+09
Q5HFV7	Chorismate synthase	aroC;aroC_1;aroC_2	6,826E+08	6,913E+08
Q5HFZ9	Glucose-specific phosphotransferase enzyme IIA component;PTS system, glucose subfamily, IIA component	crr;ptbA	3,052E+08	2,268E+09
Q5HG04	Response regulator ArlR;Two-component response regulator (YkoH)	arlR;ykoG	4,578E+08	5,884E+08

Q5HGC3	Glutamine synthetase;Glutamine synthetase OS	glnA	2,155E+10	4,175E+10
Q5HGC9	tRNA dimethylallyltransferase	miaA	1,540E+08	3,047E+08
Q5HGF6	Ribonuclease J 2;Ribonuclease J	rnj2;ERS179246_02419;HMPREF0769_12503	5,443E+09	3,318E+10
Q5HGP5	Cell division protein FtsZ	ftsZ	3,974E+10	7,374E+10
Q5HGT2	Non-canonical purine NTP pyrophosphatase	SACOL1162;QU38_12065	1,238E+08	2,122E+08
Q5HGU5	Phenylalanine--tRNA ligase beta subunit	pheT	4,951E+08	6,069E+09
Q5HGV4	Iron-regulated surface determinant protein A;Iron (Fe2+)-regulated surface determinant protein IsdA	isdA	2,001E+08	6,214E+08
Q5HH01	Phosphoenolpyruvate-protein phosphotransferase;Phosphoenolpyruvate-protein phosphotransferase OS	ptsI	3,641E+09	5,490E+09
Q5HH16	Phosphoribosylformylglycinamidine synthase subunit PurQ	purQ	9,267E+07	1,397E+08
Q5HH71	Putative phosphoesterase SACOL1020;Putative phosphoesterase SAV1015	SACOL1020;SAV1015	1,250E+10	5,042E+10
Q5HH88	Tryptophan--tRNA ligase;Tryptophan--tRNA ligase	trpS	4,767E+08	7,717E+08
Q5HHA1	3-oxoacyl-[acyl-carrier-protein] synthase 2	fabF	7,181E+08	1,038E+09
Q5HHA2	3-oxoacyl-[acyl-carrier-protein] synthase 3	fabH	1,362E+08	2,429E+08
Q5HHB8	ATP-dependent helicase/deoxyribonuclease subunit B	addB	1,103E+08	1,239E+09
Q5HHK4	Methionine import ATP-binding protein MetN 2;Methionine import ATP-binding protein MetN	metN2;metN	9,211E+09	1,192E+10
Q5HHQ4	Thioredoxin reductase	trxB;ST398NM01_0840	7,353E+08	2,652E+09
Q5HI51	Transcriptional regulator SarA;Staphylococcal accessory regulator A (SarA)	sarA	1,371E+09	7,727E+10
Q5HIC5	Putative pyridoxal phosphate-dependent acyltransferase	SACOL0596	5,880E+08	1,091E+09
Q5HID8	50S ribosomal protein L11;50S ribosomal protein	rplK	1,326E+09	6,536E+09
Q5HIR0	UPF0355 protein SACOL0457;Transcriptional regulator;UPF0355 protein SA0372	SACOL0457;ERS179246_01611;SA0372	5,361E+08	4,262E+09
Q5HIR5	Alkyl hydroperoxide reductase subunit C;Alkyl hydroperoxide reductase (Small subunit)	ahpC	2,010E+10	6,100E+10
Q5HIS7	30S ribosomal protein S18	rpsR	4,615E+08	3,837E+09
Q5HIS8	Single-stranded DNA-binding protein 1;Single-stranded DNA-binding protein	ssb	1,335E+08	2,745E+09
Q5HIS9	30S ribosomal protein S6	rpsF	4,179E+08	4,636E+10
Q5HJH8	Type-1 restriction enzyme R protein;Type I restriction-modification system restriction subunit	hsdR;SAKOR_00175	1,689E+09	3,271E+09
Q5HJZ1	DNA gyrase subunit B	gyrB	5,137E+09	7,580E+09
Q6PST7	CidC;Putative thiamine pyrophosphate-containing protein YdaP;Putative pyruvate oxidase	cidC;ydaP;HMPREF0769_10612	1,128E+10	1,279E+10
Q7A0V6	Cell cycle protein GpsB	gpsB	2,107E+08	1,047E+10
Q7A0W1	Conserved virulence factor C	cvfC	1,472E+08	1,798E+08
Q7A0Y9	Uncharacterized protein MW1239;Uncharacterized protein;HesB-like protein	MW1239;BN1321_250043;HMPREF0769_12396	4,014E+08	5,827E+09
Q7A154	UPF0348 protein MW1008;UPF0348 protein ERS093009_00554;UPF0348 protein SAZ172_1064	MW1008;ERS093009_00554;SAZ172_1064	1,056E+08	1,802E+08
Q7A1C0	Putative peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase	MW0836;BN1321_190076	6,206E+08	5,308E+09
Q7A1G5	Uncharacterized protein MW0714;Uncharacterized protein SACOL0815;Ribosomal subunit interface protein	MW0714;SACOL0815;hpf	1,563E+10	5,530E+10
Q7A2R1	Putative dipeptidase SAV1751;Dipeptidase PepV;Aminoacyl-histidine dipeptidase	SAV1751;QU38_04625	6,097E+09	7,635E+09
Q7A2R6	Transcriptional regulatory protein SrrA;Two-component response regulator	srrA;resD	1,334E+09	2,156E+09
Q7A455	DNA topoisomerase 3;Putative DNA topoisomerase;DNA topoisomerase	topB;HMPREF07	1,539E+08	1,297E+09
Q7A460	50S ribosomal protein L22	rplV	3,734E+09	5,273E+10
Q7A466	50S ribosomal protein L6	rplF	5,495E+09	5,364E+10
Q7A4P4	Uncharacterized protein SA1737;Uncharacterized protein SAUSA300_1902;Uncharacterized protein	SA1737;SAUSA300_1902;BN1321_3	2,247E+08	7,728E+08
Q7A4R9	Response regulator protein VraR;LuxR family two component transcriptional regulator	vraR	1,787E+09	3,565E+09
Q7A4T3	Putative multidrug export ATP-binding/permease protein SA1683	SA1683;ST398N	4,148E+08	2,103E+09
Q7A5M6	UPF0403 protein SA1261;Uncharacterized protein	SA1261;CH51_07495;QU38_13560	1,191E+08	2,360E+08
Q7A5V7	Aerobic glycerol-3-phosphate dehydrogenase;Glycerol-3-phosphate dehydrogenase	glpD;HMPREF0776_2302	8,336E+09	2,378E+10
Q7A5Z3	Malonyl CoA-acyl carrier protein transacylase	fabD	2,219E+08	6,461E+08
Q7A6R4	Peptide chain release factor 2	prfB	1,951E+08	6,405E+08
Q7A6X2	HTH-type transcriptional regulator MgrA	mgrA	4,596E+09	3,226E+10
Q7A7B3	50S ribosomal protein L25	rplY	5,159E+09	2,410E+10
Q7A7S4	Virulence factor EsxA;WXG100 family type VII secretion target;ESAT-6-like protein	esxA;HMPREF0776_1016	5,275E+08	2,863E+09
Q7BWD1	Beta-lactamase regulator BlaI;CopY family transcriptional regulator	blaI;ACR61_14565;A	1,895E+08	2,099E+08
Q8NUR2	1-pyrroline-5-carboxylate dehydrogenase	rocA	1,495E+09	1,783E+10
Q8NUR7	ATP-dependent Clp protease ATP-binding subunit ClpL	clpL	8,712E+09	1,839E+10
Q8NVA9	Lipid II:glycine glycyltransferase	femX	2,561E+09	1,366E+10
Q8NVB4	30S ribosomal protein S17	rpsQ;rps	5,253E+08	3,006E+09
Q8NVF5	Deoxyribose-phosphate aldolase 2;Deoxyribose-phosphate aldolase	deoC2;dra_2	2,616E+09	9,170E+09
Q8NW84	tRNA-specific 2-thiouridylase MnmA	mnmA	1,528E+09	1,701E+09
Q8NWD0	Probable glycine dehydrogenase (decarboxylating) subunit 2;Glycine dehydrogenase	gcvPB;CH51_08350	1,058E+09	2,516E+09
Q8NWM8	30S ribosomal protein S1;SSU ribosomal protein S1P	rpsA;QU38_13800;SAKOR_01419	1,782E+10	7,704E+10
Q8NWQ9	Dihydrofolate reductase	folA;dfrA	1,734E+08	4,300E+08
Q8NWR6	2-oxoglutarate dehydrogenase E1 component	odhA	1,002E+09	1,739E+11
Q8NWR7	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	odhB	1,753E+09	8,090E+10
Q8NX76	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	pdhC	1,247E+10	6,021E+11
Q8NXL5	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	gpmI	3,909E+08	1,258E+09
Q8NXY2	Molecular chaperone Hsp31 and glyoxalase 3	hchA	1,031E+09	5,426E+09
Q8NY70	Inosine-5-monophosphate dehydrogenase	guaB	5,765E+10	6,591E+10
Q8NY94	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	metE	4,569E+08	1,404E+09
Q8NY95	Probable acetyl-CoA acyltransferase	MW0330;SACOL0426	2,103E+08	2,967E+08
Q8NYY2	Serine--tRNA ligase	serS	3,280E+08	1,405E+09
Q931G1	Urocanate hydratase;Urocanate hydratase	hutU;CH51_12550	3,478E+08	9,935E+08
Q931T1	Ribonuclease 3	rnc;	1,720E+09	3,867E+09
Q99RP3	HTH-type transcriptional regulator SarZ	sarZ	1,226E+09	1,625E+09
Q99S28	50S ribosomal protein L16	rplP	1,601E+09	3,158E+09
Q99S39	Protein translocase subunit SecY	secY	4,962E+09	5,241E+09
Q99TF3	Putative universal stress protein SAV1710	SAV1710	3,249E+10	3,406E+10
Q99TQ0	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase	mtnN	6,853E+07	1,563E+08
Q99TT5	RNA polymerase sigma factor SigA	sigA	4,046E+08	7,533E+09
Q99U17	DNA-binding protein HU;Non-specific DNA-binding protein HBsu signal recognition particle-like (SRP) component	hup;hbs	4,203E+09	5,930E+11
Q99U34	Probable ATP-dependent helicase DinG homolog;ATP-dependent helicase	dinG	7,378E+08	2,951E+09
Q99U83	Acylphosphatase	acyP;SAKOR_01341;ST398NM01_1406	1,952E+09	3,638E+09
Q99UJ8	Polyribonucleotide nucleotidyltransferase;Polyribonucleotide nucleotidyltransferase	pnp;pnpA	2,215E+09	1,670E+10
Q99UT4	Uncharacterized N-acetyltransferase SA1019;Uncharacterized N-acetyltransferase SAV1176;Uncharacterized N-acetyltransferase	SA1019;SAV1176	1,749E+09	7,040E+09
Q99UZ0	UPF0358 protein SAV1112;Uncharacterized protein;UPF0358 protein ST398NM01_1109	SAV1112;ACH32_12440	8,594E+07	9,903E+07
Q99V03	Spermidine/putrescine import ATP-binding protein PotA	potA	6,055E+08	7,813E+08
Q99V09	Ribonuclease J 1	rnj1;ST398NM01_1086;SAKOR_01011	1,417E+10	4,872E+10
Q99X11	FMN-dependent NADH-azoreductase	azoR;azo	1,849E+09	2,497E+09
Q9AGT0	Putative TrmH family tRNA/rRNA methyltransferase;23S rRNA Gm2251 methyltransferase	NWMN_0494;SAKOR_00517	7,706E+08	5,459E+09
Q9EZ12	4-hydroxy-tetrahydrodipicolinate synthase	dapA	6,854E+07	1,781E+08
Q9EZ13	Aspartate-semialdehyde dehydrogenase	asd	2,797E+09	4,013E+09
Q9F0R1	HTH-type transcriptional regulator SarR	sarR	1,561E+09	3,348E+10
Q9FDP3	Replication initiator A domain-containing protein;Rep protein	rep;ERS093009_02656	7,705E+08	5,544E+09
Q9KWZ8	Putative staphylococcal protein;Uncharacterized protein;Uncharacterised protein	ORF141;HMPREF0776_2786;ERS179246_01528	9,501E+08	9,267E+09
Q9L4P8	Betaine aldehyde dehydrogenase;Betaine-aldehyde dehydrogenase	gbsA;QU38_16060	2,779E+06	6,077E+06
Q9R744	PBP2;Penicillin binding transpeptidase domain protein;Uncharacterized protein	pbp2;BN1321_260090	1,158E+10	1,969E+10
Q9RL93	DNA-3-methyladenine glycosidase;DNA-3-methyladenine glycosylase;DNA-3-methyladenine glycosylase I	tag;SACOL1711;	2,223E+08	4,127E+09
T1Y6B2	Acid phosphatase;5-nucleotidase	SAKOR_00299;hel;SAZ172_0307	2,870E+09	9,761E+09
T1Y6D6	33 kDa chaperonin	hslO	5,408E+08	1,011E+09
T1Y6P6	Putative heme-dependent peroxidase SAKOR_00577;Putative heme-dependent peroxidase SAV0587	SAKOR_00577;SAV0587	3,218E+08	1,875E+09
T1Y6T0	Glyoxylate reductase (NADP+);2-ketogluconate reductase;Glyoxylate reductase / Glyoxylate reductase / Hydroxypyruvate reductase	SAKOR_00841;ghrB_1	2,851E+08	3,865E+08
T1Y735	GTP cyclohydrolase FolE2	folE2	3,338E+08	7,352E+08
T1Y7K1	GTP pyrophosphokinase	SAKOR_00922;ACH32_11865;SA	9,920E+07	2,656E+08
T1Y8S5	Staphopain;Staphopain B	SAKOR_00968;sspB	6,143E+08	1,592E+09
T1Y8Z3	Cytidylate kinase	cmk;CH51_07730	1,028E+09	1,130E+09
T1Y913	D-alanine--poly(phosphoribitol) ligase subunit 1	dltA	3,329E+08	6,726E+08
T1Y918	23S rRNA methyltransferase;SpoU rRNA methylase family protein;RNA methyltransferase, TrmH family	SAKOR_01058;spoU	3,880E+08	2,196E+09
T1Y925	Queuine tRNA-ribosyltransferase	tgt	4,298E+08	2,237E+09
T1Y9B4	Methionyl-tRNA formyltransferase	fmt	4,130E+08	1,484E+09
T1YA47	Fumarate hydratase class II	fumC	8,961E+08	2,217E+09
T1YA57	DNA polymerase	SAKOR_01630;polA	2,409E+09	1,323E+10
T1YAB2	Pseudouridine synthase	SAKOR_01695;ORF231;HMPREF0776_2787	7,082E+07	3,966E+08
T1YAM2	Single-stranded-DNA-specific exonuclease recJ;Single-stranded-DNA exonuclease;MW1586 protein	SAKOR_01583;recJ;MW1586	2,669E+08	4,025E+08
T1YBG9	Salicylate hydroxylase;FAD binding domain protein	SAKOR_02272;HMPREF0776_0355;nagX	2,268E+09	2,489E+09
T1YBI2	Glyoxalase family protein;Glyoxalase;Glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	SAKOR_02511;catE_1	8,705E+07	1,680E+08
T1YBW1	Sulfite reductase [NADPH] flavoprotein alpha-component	SAKOR_02616;SAOUHSC_02947	3,204E+08	3,406E+08
T1YBW9	Transcription accessory protein (S1 RNA binding domain);RNA-binding transcriptional accessory protein	SAKOR_02028;AFO87_07805	1,451E+09	6,772E+09
T1YCC7	Carboxylic ester hydrolase	SAKOR_02435;pnbA;NWMN_2350	5,732E+08	6,091E+08
W8TPA6	Uncharacterised protein;Uncharacterized protein	AFO87_12365;MW0362;ST398NM01_0463	6,287E+08	8,901E+08
W8TRI2	Protein of uncharacterised function (DUF402);Uncharacterized protein	AFO87_03035;BN1321_170001;NWMN_0640	2,834E+08	1,461E+09
W8TRN2	Exported protein;Uncharacterized protein	AFO87_03325;RU53_676;HMPREF0776_	1,227E+09	2,790E+09
W8TU69	DNA-binding transcriptional regulator;DeoR-like helix-turn-helix domain protein;DeoR faimly transcriptional regulator	AFO87_00880;BN1321_380150	3,333E+08	1,466E+09

W8TVI2	Glutamyl aminopeptidase;MW1688 protein;Peptidase M28;M42 family glutamyl aminopeptidase OS	pepA_2;MW1688;QU38_08185	1,092E+09	4,591E+09
W8TZV9	DNA-binding protein;Putative cytosolic protein;Uncharacterized protein	ylbN;SAKOR_01048;BN1326_60243	6,900E+07	1,398E+08
W8U115	Uncharacterised protein;Uncharacterized protein	AFO87_02995;ST398NM01_0756	8,094E+09	1,498E+10
W8U1I5	Signal peptidase;PSP1 C-terminal domain protein;Signal peptidase II	yaaT;HMPREF0769_12828;QU38_03060	1,550E+09	3,610E+09
W8U2C9	Alpha-helical coiled-coil protein;Uncharacterized protein	srpF;AL077_00800;BN1326_30034	2,953E+08	1,223E+09
W8U3A1	Alkyl hydroperoxide reductase AhpD	AFO87_06430;ST398NM01_2524;	8,849E+08	3,946E+09
W8U4T0	Uncharacterised protein;Uncharacterized protein	AFO87_13550;ERS093009_00540;HMPREF0776_2104	1,384E+09	2,527E+09
W8U4V4	Glucosamine-6-phosphate deaminase;Glucosamine-6-phosphate isomerase;Glucosamine-6-phosphate isomerase family protein	AFO87_07265;QU38_03975	1,665E+10	5,758E+10
W8U565	tRNA-binding domain-containing protein;Putative tRNA binding protein;tRNA-binding protein	pheT_2;ytpR;QU38_08200	5,179E+08	1,448E+09
W8U635	Oligoendopeptidase F;MW1272 protein	pepF1_1;MW1272;QU38_13330	3,511E+07	1,677E+09
W8U665	6-phospho 3-hexuloisomerase;6-phospho-3-hexuloisomerase (PHI);SIS domain protein	hxlB	6,970E+07	1,948E+08
W8U6C2	ATP-dependent zinc metalloprotease FtsH	ftsH	4,239E+10	4,643E+10
W8U8R7	Glyoxalase-like domain protein;Putative cytosolic protein;Uncharacterized protein	AFO87_01145;SAKOR_02227;NWMN_2164	5,187E+08	1,025E+09
W8URL3	Uncharacterised protein;Uncharacterized protein	AFO87_13610;HMPREF0776_2115;QU38_05870	9,295E+07	1,069E+08
W8UVT0	Uncharacterised protein;Uncharacterized protein;Uncharacterized protein OS	AFO87_08135;NWMN_2088;QU38_03705	7,032E+10	9,201E+10
W8UWM8	Pseudouridine synthase;Ribosomal large subunit pseudouridine synthase D-like protein;Pseudouridine synthase, RluA family	yhcT;SAZ172_1861	1,578E+09	1,173E+10
W8UXT9	Glyoxalase;Glyoxalase family protein	AFO87_05460;HMPREF0776_2430;SAKOR_01348	9,304E+09	1,570E+10
X5DRN2	Ribosome biogenesis GTPase A	rbgA;MW1126;SA1086	1,127E+09	1,325E+09
X5DRS2	Lipoprotein;Uncharacterized protein	AFO87_12765;SA0943;SAZ172_1031	5,732E+09	6,544E+09
X5DRY1	ABC transporter;Uncharacterized protein;Protein co-occurring with transport systems	yigZ;CH51_03905;SAZ172_0758	1,302E+08	1,406E+08
X5DSI3	Metal dependent hydrolase;Uncharacterized protein;Phosphohydrolase	yedJ;MW2012;SA1892	1,224E+08	2,186E+08
X5DXG8	Mechanosensitive ion channel protein MscS	kefA	2,920E+09	4,161E+09
X5DYJ1	Transcription termination/antitermination protein NusA	nusA	6,758E+09	1,538E+10
X5DZ51	Ribosomal silencing factor RsfS	ybeB;rsfS	1,025E+08	1,298E+09
X5DZG3	Glutathione S-transferase;Uncharacterized protein;Glutathione S-transferase-related transmembrane protein	AFO87_00395;SA2193;ERS179246_017	1,667E+08	3,132E+08
X5E0J0	Ribonuclease H;SA1266 protein;MW1323 protein	rnhA;SA1266;MW1323	1,339E+08	1,721E+08
X5E0N6	Uncharacterised protein;Uncharacterized protein	AFO87_10535;AL077_10410;BN1326_60450	6,117E+08	2,022E+09
X5E151	Toxin	map-w	4,428E+07	1,065E+08
X5E164	Thioredoxin;Putative thioredoxin or thiol-disulfide isomerase;MW0784 protein	trxA_3;ydbP;MW0784	3,763E+08	3,929E+09
X5E1N1	DNA-binding protein;Uncharacterized protein	AFO87_12370;HMPREF0769_10071;ERS179246_01609	1,948E+07	6,274E+09
X5E2F5	N6-adenine-specific DNA methylase;Methyltransferase;Site-specific DNA-methyltransferase (Adenine-specific)	rlmL;SAKOR_01386	1,953E+08	1,673E+09
X5EG20	Glycine betaine ABC transport system%2C ATP-binding protein OpuAA;Glycine betaine transport ATP-binding protein	proV_1;SAKOR_00720	5,665E+09	8,456E+09
X5EGR8	General stress protein;Pyridoxamine 5-phosphate oxidase family protein	ydaG;HMPREF0769_10765;QU3	5,476E+09	1,022E+10
X5EH11	Leucine aminopeptidase 3, chloroplastic	pepA_2;pepA_1	1,366E+09	1,459E+09
X5EJM2	Aldo/keto reductase family protein;Oxidoreductase ion channel;Oxidoreductase, aldo/keto reductase family protein	iolS;HMPREF0769_	5,072E+08	1,003E+09
X5EJX1	Heptaprenyl diphosphate synthase (HEPPP synthase) subunit 1 family protein;Heptaprenyl diphosphate synthase component I	AFO87_08500;SAKOR_01414	3,353E+08	3,792E+08
X5EKN6	Threonine synthase	thrC;ST398NM01_1331	2,947E+08	3,763E+08
X5EKP1	RNA binding protein;RNA-binding protein, YhbY family;RNA-binding protein	yhbY;HMPREF0769_12085;ACH32_00820	1,460E+09	8,516E+09
X5EL59	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase	ybaK;HMPREF0769_11602	1,352E+08	3,771E+08
X5ELM4	Glycosyl transferase family 1;Poly(Glycerol-phosphate) alpha-glucosyltransferase;MW0520 protein	tagE_1;SAKOR_00553;MW0520	7,288E+08	6,469E+09
X5EMW4	HAD family hydrolase;Haloacid dehalogenase-like hydrolase	AFO87_10530;RU53_1336	2,893E+09	3,700E+09
X5ENI9	Acyl-CoA thioester hydrolase;Uncharacterized protein	AFO87_05945;RU53_2601;QU38_16	1,189E+08	2,098E+08

Population III. DRM enriched

Uniprot-ID	Protein Name	Gene Name	LFQ Intensity DRM	LFQ Intensity
A0A033V1Y1	Asparagine--tRNA ligase	asnS	2,053E+09	9,933E+08
A0A068DYF6	ATP-dependent helicase;DNA polymerase III alpha subunit	dnaQ;ST398NM01_2958	1,910E+09	1,031E+09
A0A069G068	ATP synthase subunit b	atpF	1,172E+10	1,683E+09
A0A069G2W6	DEAD-box ATP-dependent RNA helicase CshA	cshA	7,171E+08	6,466E+08
A0A069G852	DNA gyrase subunit B	gyrB	6,130E+08	5,085E+08
A0A069G9I2	Citrate synthase	citZ	4,711E+08	4,423E+08
A0A069GED4	Tyrosine--tRNA ligase	tyrS	1,472E+08	1,099E+08
A0A0B6XMR5	Signal recognition particle protein;Signal recognition particle	ffh;CH51_06360	3,350E+09	2,450E+09
A0A0D1FGD2	Cro/CI family transcriptional regulator;Helix-turn-helix family protein	ACR58_02450;BN1321_240130	5,031E+09	1,581E+08
A0A0D1G477	Alkaline stress response protein;Uncharacterized protein	ACH32_00470;yqhY	4,651E+09	1,620E+09
A0A0D1GMN8	Hydrolase;Cof-like hydrolase;Hydrolase (HAD superfamily)	ACH32_11695;HMPREF0769_11409;yidA	1,089E+09	3,504E+08
A0A0D1GNJ9	Putative pit accessory protein;TIGR00153 family protein	ACH32_10630;CO98_0830	1,858E+09	1,553E+09
A0A0D1GPL9	RipR family HTH-type transcriptional regulator;RpiR family transcriptional regulator	ACH32_08240;ybbH_3	1,485E+09	9,300E+08
A0A0D1GQ49	Antibiotic ABC transporter ATP-binding protein;ATP-binding cassette transporter A	bmrA;MW0605	6,767E+10	1,463E+10
A0A0D1GTH3	Uncharacterized protein	ACR58_08110;HMPREF0776_0401	6,686E+08	5,532E+08
A0A0D1GXI2	Uncharacterized protein	ACH32_03885;BN1326_110071	3,746E+09	3,756E+08
A0A0D1H0H5	Membrane protein;Uncharacterized protein;Uncharacterized protein (Fragment)	ACH32_13775;yhhT_2;BN1326_60478	1,307E+10	5,717E+08
A0A0D1H1I6	Calcineurin-like phosphoesterase family protein;Putative metallophosphoesterase	ACH32_13400;HMPREF0769_12490	1,548E+09	6,014E+08
A0A0D1H5S7	Preprotein translocase subunit YajC	yajC	2,270E+10	1,686E+09
A0A0D1H7B3	Octopine dehydrogenase;Opine dehydrogenase;NAD/NADP octopine/nopaline dehydrogenase, alpha-helical domain protein	ACR58_07860;SAKOR_02267	4,734E+09	1,677E+09
A0A0D1H7N5	Uncharacterized protein	ACH32_02105	2,566E+10	2,794E+09
A0A0D1H8Q7	Allophanate hydrolase;Allophanate hydrolase subunit 2 family protein;Regulator of kinase autophosphorylation inhibitor	ACH32_10920;ERS179246_00185	9,699E+08	2,257E+08
A0A0D1HAI9	Manganese ABC transporter substrate-binding protein;ABC transporter, substrate-binding protein, putative	mntA;SAOUHSC_00634	4,886E+11	2,390E+10
A0A0D1HE14	Exported protein;Putative N-acetyltransferase YedL	ACH32_02720;CO98_1537	3,531E+10	2,273E+09
A0A0D1HEG6	Ribonucleoside-diphosphate reductase beta chain	nrdF;ST398NM01_0809	1,591E+10	6,774E+09
A0A0D1HFY3	Bacitracin ABC transporter ATP-binding protein;ABC transporter, ATP-binding protein	ACR58_11760;HMPREF0776_1664	1,013E+09	4,416E+08
A0A0D1HHD7	Alpha-hemolysin;Alpha-Hemolysin	QU38_12130;hly	3,904E+09	2,235E+09
A0A0D1HHR3	Aspartokinase	ACH32_13600;lysC2;thrA	6,653E+08	1,857E+08
A0A0D1HLR6	Iron transporter;Uncharacterized protein	ACR58_01050;BN1321_260210;AL078_01305	1,198E+10	9,481E+08
A0A0D1HPR5	Uncharacterized protein;CBS domain protein	ACH32_11455;yutD;NWMN_0797	1,083E+09	2,864E+08
A0A0D1HRD3	GTP pyrophosphokinase;GTP pyrophosphokinase (RelA/SpoT)	ACR58_01360;relA;rsh	8,185E+09	5,970E+09
A0A0D1HT39	NADH dehydrogenase;MW0820 protein;Pyridine nucleotide-disulfide oxidoreductase	ACH32_11520;MW0820	7,792E+09	4,372E+09
A0A0D1HVY3	Nitroreductase;Nitroreductase family protein	ACR58_11995;HMPREF0769_11129	3,294E+08	7,232E+07
A0A0D1HW65	GTP-binding protein YqeH;GTP-binding protein YqeH, required for biogenesis of 30S ribosome subunit;GTP-binding protein	ACR58_01175;SAZ172_1609	8,785E+08	4,535E+08
A0A0D1HWL9	Acetyltransferase;Acetyltransferase family protein	ACR61_11680;BN1321_340069;RU53_2191	6,362E+08	5,191E+08
A0A0D1HYP5	HTH-type transcriptional regulator;Uncharacterized protein	ACH32_03840;NWMN_2027;BN1326_110062	1,743E+08	7,126E+07
A0A0D1HZ15	Cell division protein DivIC;Putative cell division protein	divIC;BN1326_40028	1,549E+09	1,439E+09
A0A0D1I198	Ferrichrome transport ATP-binding protein fhuC;Ferrichrome transport ATP-binding protein fhuA	fhuC;fhuA	6,409E+08	5,042E+08
A0A0D1I4G6	SAM-dependent methyltransferase	QU38_14455;ubiE_1	6,072E+07	1,922E+07
A0A0D1IB15	Phosphoserine phosphatase rsbU;RsbU;Putative sigma factor sigB regulation protein	rsbU;ST398NM01_2108	4,179E+09	1,432E+09
A0A0D1ICI0	Pur operon repressor;PurR: transcription regulator associated with purine metabolism	ACH32_09685;purR	8,779E+09	4,096E+09
A0A0D1IGF8	Replicative DNA helicase	ACH32_07115;dnaC;SAKOR_000	8,769E+08	6,117E+08
A0A0D1IIB4	Riboflavin biosynthesis protein	ribC;ribF	1,250E+09	4,214E+08
A0A0D1IMW5	Cytoplasmic protein;Uncharacterized protein	ACR58_07015;HMPREF0776_0816;	6,041E+07	4,544E+07
A0A0D1IQC2	DoxX family protein;Uncharacterized protein	ACH32_10865;AUC48_03600;BN1326_50209	3,048E+10	5,420E+08
A0A0D1IUZ1	Citrate synthase;Uncharacterized protein	citZ;HMPREF0769_11994	3,762E+09	2,676E+09
A0A0D1JJX2	Mevalonate kinase	mvk;mvaK1;ST398NM01_0664	2,294E+08	1,381E+08
A0A0D1JP24	Alkaline shock protein;General stress protein%2C Gls24 family;Uncharacterized protein	ACH32_13065;ERS179246_01154;yloU	8,853E+09	2,620E+09
A0A0D1JPY7	Zinc metallopeptidase;Neutral zinc metallopeptidase family;Putative neutral zinc metallopeptidase	ACH32_00135;yugP	3,036E+10	1,092E+09
A0A0D1JZA3	1-acyl-sn-glycerol-3-phosphate acyltransferase	ACH32_01480;plsC	3,076E+09	1,039E+09
A0A0D1K1L5	ABC transporter permease;ABC transporter%2C permease protein YbbP clustered with maltose/maltodextrin transporter / Tlr1762 p	ACH32_04135;cdaA	4,177E+09	1,890E+08
A0A0D1K376	Ribosomal RNA small subunit methyltransferase A	rsmA	1,442E+09	6,097E+08
A0A0D1K843	ComE operon protein 2	comEB;HMPREF0769_12091;HMP	4,911E+08	2,329E+08
A0A0D3Q3Y1	Outer surface protein;Uncharacterized protein	AFO87_12035;SAOUHSC_00156;MW0164	1,213E+09	4,345E+08
A0A0D3Q467	Putative secretion accessory protein EsaA/YueB	esaA;e	1,619E+10	5,095E+09
A0A0D3Q4J1	Putative cytosolic protein	AL493_02900	2,407E+08	8,838E+07
A0A0D3Q4K0	ABC transporter permease protein;ABC transporter permease;ABC superfamily ATP binding cassette transporter, membrane protein	AFO87_05235;AL077_01500	5,539E+09	2,882E+08
A0A0D3Q778	ABC transporter ATP-binding protein;ABC efflux transporter (ATP-binding protein)	yheS_1;ykpA;CH51_07295	6,513E+09	3,986E+09
A0A0D3Q7N8	DNA repair protein RecN	recN;SAOUHSC_01615	1,708E+09	6,613E+08
A0A0D3Q886	Acetoin utilization protein;Protein acetyltransferase	acuA;QU38_08250	1,093E+09	4,769E+08
A0A0D3Q8P4	Lantibiotic ABC transporter ATP-binding protein;Lantibiotic immunity protein F;Lantibiotic transport ATP-binding protein SrtF	bsaF;	4,364E+09	2,367E+09
A0A0D3Q904	ABC transporter ATP-binding protein;Multidrug ABC transporter ATP-binding protein	ecsA_3;ACH32_02095;ST398NM01_19	8,139E+08	4,856E+08
A0A0D3Q935	Exported protein;Uncharacterized protein	AFO87_15140;HMPREF0776_2820;QU38_04795	9,830E+10	1,301E+10
A0A0D3Q9P6	ATPase;ATPase AAA	clpB_1;CH51_11960	9,721E+08	1,983E+08
A0A0D3QA12	Multidrug effluc protein;Multidrug resistance protein (Function not yet clear)	AFO87_00670;yhbJ;ERS092844_01653	3,305E+09	4,477E+08
A0A0D3QA76	ABC-type transport system%2C ATPase component;ABC transporter, ATP-binding protein	ecsA_2	7,293E+09	7,136E+09
A0A0D3QAA6	Amino acid permease;Uncharacterized protein	AFO87_00175;AL078_02870;HMPREF0769_10705	7,640E+09	1,590E+09
A0A0D3QAD8	Membrane protein;Putative membrane protein;Uncharacterized protein	AFO87_00935;BN1321_380138;ERS179246_01286	2,819E+09	8,167E+08

A0A0D3QBD9	Activator of the mannose operon (Transcriptional antiterminator)%2C BglG family;Transcription antiterminator, BglG family;SA2433	licR_1;RU53_2703	3,304E+08	1,101E+08
A0A0D3QBK7	Threonylcarbamoyl-AMP synthase	rimN_2;SACOL2108;SAOUHSC_02	8,025E+08	6,878E+08
A0A0D6G5Y4	Alpha/beta fold family hydrolase;Hydrolase, alpha/beta domain protein;Lysophospholipase	pip;HMPREF0776_1620;QU	3,513E+08	1,573E+08
A0A0D6G8E8	PTS system trehalose-specific transporter subunit IIBC;Trehalose permease IIC protein	treB;QU38_03485	8,574E+09	2,470E+08
A0A0D6GCD0	Lipoprotein;Peptidase;Putative secreted protease inhibitor	AFO87_12435;CH51_01905;ACH32_09125	4,202E+10	8,575E+09
A0A0D6GEC2	Acetyl esterase;Uncharacterized protein;Uncharacterized protein	AFO87_05170;MW0298;SAKOR_00315	2,996E+08	1,621E+08
A0A0D6GFF2	Uncharacterized conserved protein	AFO87_05290	8,808E+08	5,855E+08
A0A0D6GFY0	CDP-glycerol glycerophosphotransferase;Uncharacterized protein;MW0230 protein	tagF_2;NWMN_0188;MW0230	8,747E+08	3,712E+08
A0A0D6GG32	Ribokinase;Probable ribokinase	rbsK	3,185E+08	2,960E+08
A0A0D6GG59	Glycerophosphodiester phosphodiesterase;Glycerophosphoryl diester phosphodiesterase	ugpQ_1;NWMN_0164	1,708E+09	4,591E+08
A0A0D6GHM9	ABC-type nitrate/sulfonate/bicarbonate transporter%2C TauA;SA0167 protein	tauA	9,986E+09	4,055E+08
A0A0D6GM89	LysR family transcriptional regulator;Transcriptional regulator, LysR family	gltR;QU38_15300	4,476E+08	3,721E+08
A0A0D6GS23	Tributyrin esterase;MW2550 protein;Putative esterase	AFO87_06510;MW2550;SAZ172_2748	3,195E+08	1,232E+08
A0A0D6GTK5	3-hydroxy-3-methylglutaryl coenzyme A reductase	mvaA;CH51_13615	1,756E+09	9,572E+08
A0A0D6GUP8	Esterase;Alpha/beta hydrolase fold-3 domain-containing protein	mlhB_1;ST398NM01_2585;aes	1,310E+10	6,052E+09
A0A0D6GV05	3-hydroxy-3-methylglutaryl CoA synthase;Hydroxymethylglutaryl-CoA synthase	mvaS;SAKOR_02536;BN1321_	9,762E+08	5,698E+08
A0A0D6GXG5	Methionine ABC transporter ATP-binding protein;ABC transporter, ATP-binding protein	ybbL_2;HMPREF0776_0514	6,472E+08	6,284E+08
A0A0D6GZM2	Nitrate reductase;Nitrate reductase (Alpha subunit);Respiratory nitrate reductase subunit alpha	narG	9,286E+07	8,696E+07
A0A0D6H1J5	PTS maltose transporter subunit IIBC;Phosphotransferase system (PTS) trehalose-specific enzyme IIBC component	scrA;treP	4,860E+09	9,974E+07
A0A0D6H9G0	Lytic regulatory protein;Putative membrane protein;Uncharacterized protein	AFO87_07705;BN1321_350011;HMPREF0769_11010	2,957E+09	8,989E+08
A0A0D6HAQ4	Histidine kinase;Sensor protein kdpD;KdpD	kdpD;QU38_06480;SAKOR_02044	1,241E+09	8,386E+08
A0A0D6HB15	Cell wall surface anchor family protein;Uncharacterized protein;Plasmin and fibronectin-binding protein A	pfbA;SAKOR_01880	9,302E+08	5,871E+08
A0A0D6HBZ8	Lipoprotein;Lipoprotein (Pheromone)	AFO87_10325;QU38_07020;camS	1,395E+10	1,378E+09
A0A0D6HC09	Inactive protein of metal-dependent protease family%2C putative molecular chaperone	ydiC;NWMN_1958	7,692E+08	2,722E+08
A0A0D6HD63	DNA repair protein Rad50;Uncharacterized protein	AFO87_07330;NWMN_1735;MW1784	6,179E+10	1,801E+10
A0A0D6HDA2	UDP-N-acetylmuramate--alanine ligase;UDP-N-acetylmuramyl tripeptide synthetase, putative	AFO87_14830;ERS179246_02392	1,611E+09	6,722E+08
A0A0D6HDD9	Protoporphyrinogen IX oxidase%2C aerobic;Protoporphyrinogen oxidase	hemY	1,886E+09	5,771E+08
A0A0D6HDQ3	Sugar ABC transporter ATPase;Teichoic acid ABC transporter ATP-binding protein;ABC transporter, ATP-binding protein	tagH_2;QU38_07210	8,909E+09	1,299E+09
A0A0D6HFK0	Adenine methyltransferase;Adenine-specific DNA methylase-like protein	AFO87_07160;QU38_08375	1,057E+09	6,411E+08
A0A0D6HHK7	Luciferase family monooxygenase;Uncharacterized protein	limB_2;CH51_08785	2,169E+09	9,172E+08
A0A0D6HHV2	Uncharacterised protein;Uncharacterized protein	AFO87_12060;QU38_08570;HMPREF0776_2710	6,298E+08	2,913E+08
A0A0D6HHY3	Bifunctional oligoribonuclease and PAP phosphatase nrnA;DHHA1 domain protein;Exopolyphosphatase-like protein	nrnA;HMPREF0776_2736	6,134E+08	4,040E+08
A0A0D6HIY4	DNA repair protein RecO	recO	9,895E+07	3,083E+07
A0A0D6HM65	Aldo/keto reductase;Uncharacterized protein;Similar to oxidoreductase;Aldo/keto reductase family protein	yhdN;SA1331	3,213E+09	1,042E+09
A0A0D6HT57	Glycerophosphodiester phosphodiesterase;Glycerophosphoryl diester phosphodiesterase	ugpQ_3;ST398NM01_1117	4,036E+09	1,518E+09
A0A0D6W9J7	Oligopeptide ABC transporter permease OppC;ABC transporter, permease protein;OppC	oppC_1;HMPREF0776_1976	6,706E+09	6,660E+07
A0A0D6WD10	Acetyltransferase	paiA	5,317E+07	4,598E+07
A0A0D6WGH1	Lipoprotein;Uncharacterized protein;Putative lipoprotein	AM595_02130;ACR58_05445;MW0354	8,008E+09	3,532E+09
A0A0E0VMZ2	L-threonine 3-dehydrogenase;Uncharacterized epimerase/dehydratase SAOUHSC_00535	ST398NM01_0628;SAOUHSC_00535	1,135E+09	3,233E+08
A0A0E0VN55	Uncharacterized protein;Nucleoside permease	ST398NM01_0596;ACH32_09900	2,328E+10	5,199E+08
A0A0E0VNH8	Threonine/Serine Exporter;Integral membrane protein;Putative membrane protein	ST398NM01_0821;ACH32_11070;yjjP	5,423E+08	1,322E+08
A0A0E0VPM3	Uncharacterized protein;Chitinase	ST398NM01_1100;ACR58_03410;HMPRE	7,145E+09	5,275E+09
A0A0E0VPZ2	Large-conductance mechanosensitive channel	mscL	7,609E+10	1,106E+10
A0A0E0VQW3	KdpE;DNA-binding response regulator KdpE;PhoB family transcriptional regulator;Response regulator	ST398NM01_2121;kdpE	1,955E+09	1,329E+09
A0A0E0VR77	Uncharacterized protein;Membrane protein	ST398NM01_2049;ACR58_12545;BN1321_320021	9,492E+09	3,081E+09
A0A0E0VRI2	Sodium/proline symporter	ST398NM01_1996;putP	4,133E+09	4,828E+07
A0A0E0VRI6	Molybdopterin-guanine dinucleotide biosynthesis protein B;Putative molybdopterin-guanine dinucleotide biosynthesis protein B	ST398NM01_2323;mob	7,978E+07	4,834E+07
A0A0E0VRM0	Uncharacterized protein;Exported protein	ST398NM01_2438;ACH32_05335;ERS179246_01371	3,832E+09	1,323E+09
A0A0E0VRN4	UPF0354 protein ST398NM01_1796	ST398NM01_1796	1,232E+09	1,062E+09
A0A0E0VTG0	Uncharacterized protein;ATPase 1-like protein	ST398NM01_2376;ACH32_05015;MW2246	7,684E+08	6,636E+08
A0A0E1ADE1	Tandem lipoprotein within Pathogenicity island;Uncharacterized lipoprotein SACOL0486	SAZ172_0446;SACOL0486	1,579E+10	1,045E+09
A0A0E1ADP9	N-acetyl-L,L-diaminopimelate deacetylase;Putative N-acyl-L-amino acid amidohydrolase	SAZ172_0551;yxeP_1	1,023E+09	3,602E+08
A0A0E1ADX5	Pili retraction protein pilT;Uncharacterized protein;Membrane protein	SAZ172_0529;SAOUHSC_00508;pilT	1,013E+10	9,920E+08
A0A0E1AFC3	;Putative 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	SAZ172_0985;menH	1,238E+08	1,118E+08
A0A0E1AGA5	Lysophospholipase;Hydrolase;Hydrolase, alpha/beta domain protein	SAZ172_1305;CH51_06690;HMPREF0776_2303	2,610E+09	1,199E+09
A0A0E1AGR4	Uncharacterized protein;CBS domain protein	SAZ172_1577;ccpN	6,303E+08	2,591E+08
A0A0E1AGR7	Oligopeptide transport system permease protein OppB;Oligopeptide transport system permease protein oppB	oppB;SAKOR_00903	6,889E+09	9,760E+07
A0A0E1AIA2	Magnesium and cobalt efflux protein CorC;Hemolysin-like protein containing CBS domains;Putative transporter or sensor	SAZ172_0713;ytfL	4,277E+09	6,684E+08
A0A0E1AIR4	Cell surface hydrolase (Putative);Alpha/beta hydrolase	SAZ172_2292;AFO87_08115;QU38_03685	3,854E+09	1,573E+08
A0A0E1AJB4	Uncharacterized protein;NTPase	SAZ172_1821;AL493_11020;NWMN_1698	4,226E+08	7,172E+07
A0A0E1AJK7	Phosphoglucosamine mutase / Phosphomannomutase;Phosphoglucomutase	SAZ172_2588;pgcA	9,486E+08	4,955E+08
A0A0E1AK20	Two-component system histidine kinase;Histidine kinase	SAZ172_2743;graS;nsaS	1,303E+09	1,241E+08
A0A0E1AKG4	Chromosome partition protein Smc	smc	3,063E+09	1,325E+09
A0A0E1AL79	Uncharacterized protein;Putative cytosolic protein;Lipoprotein	SAZ172_1503;ST398NM01_1556;AFO87_01655	9,234E+09	9,836E+08
A0A0E1ALA4	L-Cystine ABC transporter, permease protein TcyB;Amino acid ABC transporter permease	SAZ172_2517;QU38_07805	1,004E+10	5,928E+09
A0A0E1ALV6	Phosphate regulon sensor protein PhoR (SphS);Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase domain protein	phoR;SAOUHSC_01799	9,516E+08	6,246E+08
A0A0E1ANC6	Uncharacterized protein;Integral membrane protein	SAZ172_2445;yhaI;MW2263	2,000E+09	2,242E+08
A0A0E1AND1	Magnesium transport protein CorA	corA;corA_2	1,793E+09	1,111E+08
A0A0E1APE5	Transport ATP-binding protein CydD;ABC transporter ATPase/permease;MW2352 protein	SAZ172_2534;irtA;MW2352	3,181E+08	5,390E+07
A0A0E1APK1	Uncharacterized protein;Uncharacterized lipoprotein SAUSA300_2430;Tandem lipoprotein	SAZ172_2584;SAUSA300_2430	1,239E+09	5,474E+07
A0A0E1VHL5	SWIM zinc finger domain protein;SWIM zinc finger domain-containing protein	HMPREF0776_2395;AFO87_04285	3,307E+08	1,897E+08
A0A0E1VHW9	Peptidase M16 inactive domain protein;Non-proteolytic protein, peptidase family M16	HMPREF0776_2279;SAKOR_01206	5,041E+08	3,138E+08
A0A0E1VIN0	Magnesium transporter MgtE	mgtE;MW0890;	4,642E+09	4,485E+08
A0A0E1VJG8	Ribonucleoside-diphosphate reductase	HMPREF0776_1739;nrdE	3,897E+10	2,669E+10
A0A0E1VK03	ACT domain protein;ACT domain-containing protein;Protein with ACT domain	HMPREF0776_2282;ACH32_13365;BN1326_60	9,191E+08	5,329E+08
A0A0E1VK25	GTPase HflX	hflX	4,069E+08	7,673E+07
A0A0E1VK72	Glyoxalase family protein (Fragment);Uncharacterized protein	HMPREF0776_1493;MW1077	1,364E+08	6,966E+07
A0A0E1VKC4	Cardiolipin synthase	HMPREF0776_1457;cls;QU38_06435	8,928E+09	2,253E+09
A0A0E1VKT7	Periplasmic binding protein	HMPREF0776_2026	2,269E+09	1,721E+08
A0A0E1VKX0	Amidophosphoribosyltransferase	purF	4,728E+08	2,857E+08
A0A0E1VLN4	HD domain protein;Uncharacterized protein;HD domain-containing protein	HMPREF0776_1767;BN1321_170090;ACR58_048	2,818E+09	1,528E+09
A0A0E1VM10	CobW/P47K family protein;Cobalamin biosynthesis protein CobW;MW0649 protein	HMPREF0776_1691;yjiA_1;MW0649	3,565E+08	1,289E+08
A0A0E1VM29	Response regulator SaeR	saeR	3,163E+09	3,012E+09
A0A0E1VMU0	Ribosomal RNA small subunit methyltransferase I	rsmI	2,094E+08	6,422E+07
A0A0E1VN29	ABC transporter, substrate-binding protein, QAT family;Glycine/betaine ABC transporter substrate-binding protein	HMPREF0776_0506;opuCC_2	1,208E+10	1,240E+09
A0A0E1VNG3	Luciferase-like monooxygenase;Luciferase	HMPREF0776_1083;luxA;RU53_	6,171E+08	3,382E+08
A0A0E1VP82	Uncharacterized protein;Exported protein	HMPREF0776_0088;SAZ172_1939;AFO87_13215	2,660E+09	1,015E+08
A0A0E1VQD5	Hydrolase, alpha/beta domain protein;Alpha/beta hydrolase domain-containing protein;Uncharacterized protein OS	HMPREF0776_2798;ACH32_01680	3,056E+09	2,991E+09
A0A0E1VQF1	Uncharacterized protein;Membrane protein	HMPREF0776_2813;AFO87_10145;QU38_04760	4,077E+09	9,059E+08
A0A0E1VSQ2	Putative phage head-tail adaptor;Oligopeptide ABC transporter%2C periplasmic oligopeptide-binding protein oppA	HMPREF0776_1979;oppA_1	9,855E+09	7,592E+08
A0A0E1VW39	Sensor protein LytS;Autolysis histidine kinase LytS	lytS	2,132E+09	4,933E+08
A0A0E1VWL4	Transporter, lactate permease (LctP) family;L-lactate permease	HMPREF0776_0843;lctP_1;lctP	2,911E+10	9,731E+08
A0A0E1VXG7	Uncharacterized protein;Membrane protein;ABC transporter ATP-binding protein	HMPREF0776_0572;AFO87_06210;QU38_	2,166E+08	1,872E+07
A0A0E1X4S8	TIGR00370 family protein;Uncharacterized protein;Allophanate hydrolase	HMPREF0769_12070;SAOUHSC_01712;kipI_2	2,001E+08	1,090E+08
A0A0E1X4Z9	KH domain protein;Phosphate starvation-inducible protein PhoH, predicted ATPase;Phosphate starvation protein PhoH	HMPREF0769_12108;SAZ172_1584	3,592E+09	1,923E+09
A0A0E1X623	MIP family channel protein;Aquaporin;Glycerol permease	HMPREF0769_12480;glpF	7,359E+09	3,805E+08
A0A0E1X6Q9	Phosphoribosylglycinamide formyltransferase	purN	2,451E+08	1,848E+07
A0A0E1X849	Uncharacterized protein;Threonine serine exporter;Putative membrane protein	HMPREF0769_11747;ACH32_10230;BN1326_50069	1,217E+09	5,925E+07
A0A0E1X887	DNA repair protein radA	radA;AFO87_13065;ACH32_09930	1,587E+09	5,382E+08
A0A0E1XBY7	HAD hydrolase, family IA, variant 3;HAD family hydrolase;HAD hydrolase, IA, variant 1 family protein	HMPREF0769_10834;ACR58_07965	9,031E+08	8,713E+08
A0A0E1XHC1	Adenylate cyclase	HMPREF0769_12782;HMPREF0776_1992;ACR58	1,545E+09	5,010E+08
A0A0E1XM44	Inositol monophosphatase family protein;Inositol monophosphatase	HMPREF0769_10843;suhB_1	3,322E+08	1,954E+08
A0A0E7MS50	Putative DUF86-containing protein;Uncharacterized protein	yutE;SAOUHSC_00864;QU38_11250	1,475E+09	1,065E+09
A0A0E7X8W5	D-3-phosphoglycerate dehydrogenase	serA	6,903E+09	1,996E+09
A0A0E7XUD2	3-beta hydroxysteroid dehydrogenase;Uncharacterized protein;SA0317 protein	AFO87_05130;SAOUHSC_00309;SA0317	3,275E+09	9,215E+08
A0A0E7YL28	Amidohydrolase;HmrA protein	hmrA;HMPREF0769_11024	6,640E+08	4,508E+08
A0A0E8G7K7	Isochorismate synthase	entC;QU38_05455	6,492E+08	2,298E+08
A0A0E8G8K9	D-alanyl-lipoteichoic acid biosynthesis protein;D-alanyl-lipoteichoic acid biosynthesis protein DltD;Poly D-alanine transfer protein	dltD	2,089E+10	4,142E+09
A0A0E8G9T5	Di/tripeptide permease YjdL;Di-/tripeptide transporter;Di-tripeptide transporter	yjdL;ST398NM01_0804;OO23_0206745	5,915E+09	4,553E+08
A0A0E8GA15	Autolysin;Bifunctional autolysin	atl_1;atl	1,185E+11	9,140E+10
A0A0E8GDF5	Phosphomevalonate	mvaK2;ACH32_10260	3,639E+08	1,321E+08
A0A0E8GDN8	ABC transporter;ABC transporter, ATP-binding protein;ABC transporter ATP-binding protein uup	yjjK;SAUSA300_0704	3,276E+09	1,036E+09
A0A0E8GE10	PepSY-associated TM helix family protein;Uncharacterized protein	AL498_04090;NWMN_1352;SA1275	4,751E+08	3,853E+07
A0A0E8GF34	Pahtogenicity island protein	AFO87_10795;ERS179246_01627	1,568E+09	1,310E+09
A0A0E8HH43	Small heat shock protein;Crystallin;Small heat shock protein Hsp20;Heat shock protein	ERS092844_01933;CH51_12820;NWMN_2287	1,538E+08	1,056E+08
A0A0E8HHC4	Nitrite reductase	nasD	6,751E+07	2,432E+07
A0A0E8HIR1	Drug resistance transporter;Putative transport protein;MW2273 protein	emrB_1;emrB_2	9,087E+08	1,204E+08
A0A0E8I3P7	Fructose phosphotransferase system enzyme fruA homolog;PTS system, fructose-specific IIABC component, putative	manP;SAOUHSC_02975	1,324E+10	2,239E+09

A0A0E8IS76	Succinyl-diaminopimelate desuccinylase;Uncharacterized protein	dapE;NWMN_1929	8,343E+08	2,304E+08
A0A0E8J639	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase;UDP-N-acetylmuramoyl-tripeptide--D-a	murF	1,107E+09	6,111E+08
A0A0E8J986	ATPase;Superfamily I DNA/RNA helicase protein;MW0068 protein;SA0089 protein	AFO87_03745;ERS093009_00884;MW0068	1,691E+08	1,274E+08
A0A0G2LPA2	Membrane protein;Lipase family protein;Putative cytosolic protein	CH51_02265;AFO87_01950;ERS093009_02540	1,287E+09	2,245E+08
A0A0G2LQC9	Central glycolytic genes regulator;Central glycolytic gene regulator;Putative sugar-binding domain protein	CH51_04035;ACH32_11220	7,121E+08	4,522E+08
A0A0G2LTJ0	Octanoyltransferase;Octanoyltransferase LipM	CH51_08340;lipM	4,112E+09	1,382E+09
A0A0H2BKJ8	Ribosome-binding ATPase YchF	ychF;engD	1,670E+10	6,697E+09
A0A0H2CCY2	Glycine betaine transport ATP-binding protein;Glycine betaine/carnitine/choline ABC transporter	proV_2;opuCA	3,159E+09	3,080E+09
A0A0H2GUK8	LysR family regulatory protein;Transcriptional regulator, LysR family	AL077_11715;HMPREF0776_1964	1,631E+08	7,098E+07
A0A0H2IDV7	Conserved cytoplasmic protein;Uncharacterized protein	AFO87_10570;SA0738	7,958E+07	5,300E+07
A0A0H2JAS5	ATPase;Phage membrane protein;Phi PVL ORF 30-like protein	AFO87_01640;AL077_01570;BN1326_80029	2,266E+10	2,976E+08
A0A0H2WWQ7	Uncharacterized protein;Uncharacterised protein	SACOL2204;AFO87_12745;SAOUHSC_02474	1,191E+09	6,193E+08
A0A0H2WXL1	Aminotransferase, putative;Aspartate aminotransferase	SACOL2000;CH51_10535;aspC	2,389E+09	1,016E+09
A0A0H2X055	Uncharacterized protein;Uncharacterised protein	SACOL0267;AFO87_12600;ST398NM01_0295	2,580E+10	7,266E+09
A0A0H2XHM0	Capsular polysaccharide biosynthesis protein Cap5I;Glycosyltransferase;Uncharacterized protein	cap5I;SAKOR_00137	2,969E+08	1,722E+08
A0A0H2XIZ6	Antibiotic transport-associated protein-like protein;Membrane protein;Uncharacterized protein	SAUSA300_2489;mmpL8;SAO	1,484E+09	7,605E+07
A0A0H2XKA3	Accessory gene regulator protein C;Histidine kinase	agrC;SAOUHSC_02264	5,702E+09	5,225E+08
A0A0H3JKG5	Branched-chain amino acid transport system carrier protein	SA0180;SAKOR_00166	2,896E+09	3,925E+07
A0A0H3JKT9	Uncharacterized protein;Orf2	SA0078;NWMN_0024;AL493_01725	1,108E+09	4,807E+08
A0A0H3JLP7	Uncharacterized protein;Thiamine diphosphokinase	SA1066;HMPREF0776_2222	2,070E+08	2,053E+08
A0A0H3JMT9	Uncharacterized protein;tRNA methylthiotransferase YqeV;30S ribosomal protein S12 methylthiotransferase	SA1405;yqeV	6,310E+08	4,560E+08
A0A0H3JNF8	RGD-containing lipoprotein;Putative lipoprotein;Uncharacterized protein	rlp;SAUSA300_0203;HMPR	3,340E+09	6,616E+07
A0A0H3JP15	Uncharacterized protein;Efflux transporter	SA0601;yxkD	1,190E+09	1,238E+08
A0A0H3JSJ5	Uncharacterized protein;Putative cytosolic protein	SA0170;AFO87_11960;SAZ172_0185	4,382E+08	4,305E+08
A0A0H3JV05	Fructose specific permease;PTS fructose transporter subunit IIC	fruA	3,442E+10	2,279E+09
A0A0H3JV29	Transcription activator of glutamate synthase operon	gltC	5,350E+08	1,128E+08
A0A0H3JVF9	MW0891 protein;TrkA C-terminal domain protein;Monovalent cation:H+ antiporter-2	MW0891;HMPREF0769_12776;ACR	3,424E+09	4,821E+07
A0A0H3JVM5	Uncharacterized protein;Fe-S cluster assembly protein SufD	MW0796;SA0775;ACH32_11395	3,484E+09	3,159E+09
A0A0H3JW61	Uncharacterized protein;Acetyltransferase%2C GNAT family;GNAT family acetyltransferase	SA2355;AFO87_06865;QU38_16295	5,787E+08	4,086E+08
A0A0H3JWI6	5-formyltetrahydrofolate cyclo-ligase	MW1502;SAZ172_1563	2,245E+08	2,022E+08
A0A0H3JWW2	MW0990 protein;Inositol monophosphatase;SA0958 protein	MW0990;suhB_1;SA0958	1,748E+09	4,558E+08
A0A0H3JX27	MW1823 protein;Ribonuclease BN;Similar to transporter	MW1823;yihY;SAV1883	2,065E+10	1,333E+09
A0A0H3JXA7	Uncharacterized protein	MW1298;SA1240;HMPREF0776_	4,278E+08	2,008E+08
A0A0H3JY62	MW1802 protein;SA1679 protein;D-isomer specific 2-hydroxyacid dehydrogenase family protein	MW1802;SA1679;SACOL19	1,018E+08	9,902E+07
A0A0H3JYG8	MW2545 protein;Response regulator receiver domain protein;Two-component response regulator YvcP	MW2545;HMPREF0769_10522	1,216E+08	9,347E+07
A0A0H3JYP5	Acetate-CoA ligase;Acyl--CoA ligase;AMP-dependent synthetase and ligase	MW2528;ACR58_09690;acsA2	2,981E+09	1,908E+09
A0A0H3JYT9	Cystathionine gamma-synthase	metB	2,635E+08	5,451E+07
A0A0H3JYY8	MW0527 protein;HAD family hydrolase;Uncharacterized protein	MW0527;gph;NWMN_0535	2,649E+08	1,011E+08
A0A0H3JZN6	MW0933 protein;Aminotransferase, class I/II;Aminotransferase, class I	MW0933;HMPREF0769_12733;patA	1,446E+09	5,712E+08
A0A0H3K0H4	Chromosome replication initiation/membrane attachment protein	dnaB;HMPREF077	1,211E+09	7,832E+08
A0A0H3K3C3	MW1508 protein;ABC transporter ATP-binding protein;Zinc ABC transporter	MW1508;mreA;znuC	1,262E+09	8,608E+08
A0A0H3K4A0	MW2249 protein;NAD(P)-dependent oxidoreductase;Oxidoreductase	MW2249;yghA;RU53_2388	1,377E+09	7,075E+08
A0A0H3K687	Uncharacterized protein;Non-ribosomal peptide synthetase;Aureusimine non-ribosomal peptide synthetase	NWMN_0123;grsB	1,930E+09	3,902E+08
A0A0H3K8T7	Propeptide, PepSY amd peptidase M4;Uncharacterized protein;Putative secreted propeptide peptidase	NWMN_1639;MW1689	8,647E+09	6,855E+08
A0A0H3K9Q7	Uncharacterized protein;Membrane protein;Uncharacterized protein OS	NWMN_1977;MW1996;ORF4	6,708E+08	3,866E+08
A0A0H3KA27	Uncharacterized protein;MW0149 protein;SA0169 protein	NWMN_0119;MW0149;SA0169	9,511E+09	4,724E+09
A0A0H3KAC4	Uncharacterized protein;Uncharacterised protein	NWMN_0226;HMPREF0776_1024;AFO87_0534	1,343E+08	8,384E+07
A0A0H3KAJ7	Uncharacterized protein;Integral membrane protein	NWMN_2407;HMPREF0776_0567	1,042E+09	5,615E+07
A0A0H3KBU5	Oligopeptide ABC transporter, ATP-binding protein;Oligopeptide transport ATP-binding protein oppF;ABC transporter, ATP-binding p	oppF;oppF_3	5,462E+09	4,757E+09
A0A0H3KDB3	Aminotransferase, class V;Uncharacterized protein;Aminotransferase	NWMN_1610;SAOUHSC_01825;iscS_1	2,265E+08	7,630E+07
A0A0J7T0R5	Flavin reductase;FAD-dependent oxidoreductase;Putative flavin reductase	AL493_01015;SAKOR_02656;AFO87_04150	4,522E+08	2,527E+08
A0A0J7WVX5	Dynamin family protein;GTPases (Dynamin-related);Dynamin family protein	AL493_08785;ERS411017_01529;ERS093009_01170	4,563E+09	2,186E+09
A0A0K6TZ04	Oligopeptide transport ATP-binding protein oppD;Oligopeptide transport ATP-binding protein OppD	oppD_2;oppD	4,603E+09	4,326E+09
A0A0K6Z0X1	LysR family regulatory protein CidR;LysR family regulatory protein;Transcriptional regulator, LysR family, putative	cidR	2,541E+08	9,054E+07
A0A0K7F311	Integral membrane protein;Membrane protein;Bacterial membrane protein YfhO OS	ERS365775_00155;CH51_06385;AFO87_09375	1,091E+09	3,263E+08
A0A0K7KAG9	Putative polyribitolphosphotransferase;TagB protein, putative	tagF_1;tagF_3;SAOUHSC_00222	2,710E+09	1,294E+09
A0A0K7VUK1	Alpha-acetolactate decarboxylase	aldC_2;aldB	2,021E+08	8,033E+07
A0A0K8EWW4	Alpha/beta hydrolase;Uncharacterized protein	ydeN;ACH32_02060;NWMN_1722	5,835E+09	1,388E+09
A0A0M1TWI2	Uncharacterized protein;Membrane protein	RU53_110;AFO87_03905;SA0121	2,699E+09	5,641E+08
A0A0M1TWW5	Iron (Fe3+) ABC superfamily ATP binding cassette transporter, binding protein;Iron ABC transporter substrate-binding protein	sirA;ACR58_06845	9,139E+09	1,774E+08
A0A0M1TXC0	Lipoprotein	RU53_427;MW0418;metQ_2;met	6,213E+10	2,091E+09
A0A0M1TXC5	Putative antitoxin YezG;QueA protein;Uncharacterized protein	yezG_2;AL493_02910;SAOUHSC_00275	2,751E+08	1,613E+08
A0A0M1TXR4	Nucleoside triphosphate pyrophosphohydrolase	mazG_1;mazG	1,209E+09	6,030E+08
A0A0M1TY42	Putative permease;ABC transporter permease;Bacitracin ABC transporter permease	RU53_724;vraG	1,214E+09	3,900E+08
A0A0M1TY86	Uncharacterized protein;Putative lipoprotein;Un	RU53_873;SACOL0851;AFO87_10560	4,836E+10	2,303E+09
A0A0M1TYC5	Putative Mg2+ and Co2+ transporter, CorB;CBS domain protein;CorC	RU53_915;SACOL0921;ST398NM0	5,539E+08	2,161E+08
A0A0M1TYD0	ABC superfamily ATP binding cassette transporter, ABC protein;Manganese transport system ATP-binding protein	mntA;ACR58_11615	2,050E+10	1,513E+10
A0A0M1TZ07	Teichoic acid biosynthesis protein B;Teichoic acid biosynthesis protein	tagB	3,051E+08	1,882E+08
A0A0M1TZ20	Alpha/beta hydrolase;Lipase;Lipase LipA;Similar to lipase LipA	RU53_717;lipA_1;QU38_10295	3,699E+09	1,100E+08
A0A0M1U010	ABC superfamily ATP binding cassette transporter, ABC protein;ABC transporter, ATP-binding protein	ykoD;HMPREF0776_2068	4,621E+08	1,639E+08
A0A0M1U044	Putative competence-damage inducible protein	cinA	1,253E+09	5,411E+08
A0A0M1U069	Exonuclease;5-3 exonuclease;DNA polymerase I	RU53_1467;ST398NM01_1439;ypcP	1,580E+09	2,784E+08
A0A0M1U097	Putative succinate dehydrogenase flavoprotein subunit;SdhA protein;Succinate dehydrogenase flavoprotein subunit	sdhA	8,521E+10	4,240E+10
A0A0M1U0K9	Alpha/beta hydrolase fold-3 domain-containing protein;Probable L-asparaginase;L-asparaginase	ansA	1,113E+09	6,595E+08
A0A0M1U0L1	Putative geranyltranstransferase;Polyprenyl synthetase;Geranyl transferase	ispA;HMPREF0776_2557;i	3,870E+08	2,288E+08
A0A0M1U118	Uncharacterized protein;Lipoprotein	RU53_1630;ST398NM01_1596;ACH32_	8,428E+09	4,926E+08
A0A0M1U143	Uroporphyrinogen decarboxylase	hemE	4,329E+08	2,292E+08
A0A0M1U1F3	ABC superfamily ATP binding cassette transporter, ABC protein;ABC transporter ATP-binding protein;ABC transporter, ATP-binding p	RU53_2071;drrA	2,141E+09	4,090E+08
A0A0M1U2H4	Formate/nitrite transporter family protein;SA2191 protein;Formate/nitrite transporter	RU53_2463;SA2191;nirC	8,767E+08	2,242E+08
A0A0M1U2N6	Putative lipoprotein YehR;Uncharacterized protein;Lipoprotein	yehR;HMPREF0776_0518;	2,683E+10	1,653E+09
A0A0M1U330	Glycerophosphotransferase, TarF;Uncharacterized protein	tarF_2;SAKOR_02344	5,115E+08	2,453E+08
A0A0M1U376	Aminobenzoyl-glutamate transport protein	RU53_2538;abgT	2,094E+09	5,468E+07
A0A0M1U3F4	MerR family transcriptional regulator;Transcriptional regulator, MerR family	RU53_2570;zntR	8,553E+08	1,329E+08
A0A0M1U3J5	Molybdenum (Mo2+) ABC superfamily ATP binding cassette transporter, binding protein;Probable molybdate-binding protein	modA	2,632E+10	7,283E+08
A0A0S2JAW7	Trehalose operon repressor;GntR family transcriptional regulator;GntR	treR;treR_2	4,688E+07	4,313E+07
A0A0T7M338	D-alanyl transfer protein DltB;Activated D-alanine transport protein;Putative D-alanine esterase for lipoteichoic acid and wall teichoi	dltB	4,181E+08	1,768E+08
A0A0T7M3C5	Enoyl-[acyl-carrier-protein] reductase [NADPH];Enoyl-[acyl-carrier-protein] reductase [NADPH] FabI	fabI	7,148E+09	2,178E+09
A0A0T7M7V7	Cation efflux family protein;MW0143 protein;SA0163 protein	czcD_1;MW0143;SA0163	6,368E+08	9,142E+07
A0A0T7M903	Putative tRNA (cytidine(34)-2-O)-methyltransferase	trmL	3,088E+08	2,347E+08
A0A0T7M913	Trehalose-6-phosphate hydrolase;Glucohydrolase	treA;SAZ172_0476	1,430E+08	1,359E+08
A0A0T7M9C7	Acetyl-coenzyme A synthetase;Acetyl-CoA synthetase;AMP-binding	acsA	7,710E+09	2,357E+09
A0A0T7M9K4	Telomeric repeat-binding factor 2 family protein;Uncharacterized protein	ERS093009_02688;HMPREF0769_11889	6,569E+09	3,650E+08
A0A0T7MRS9	Iron-sulfur cluster assembly ATPase SufC;ATP-dependent transporter sufC;FeS assembly ATPase SufC	yurY;ACH32_11390;sufC	7,714E+09	4,224E+09
A0A0T7MTX1	Thioredoxin reductase;Putative FAD-dependent disulfide oxidoreductase	trxB_2;ypdA	1,711E+08	1,277E+08
A0A0T7MUK3	Na+/H+ antiporter;Na+/H+ antiporter, putative;Putative Na+/H+ antiporter	nhaK_2;SACOL2442;HMPREF0769_10706	6,238E+09	1,022E+09
A0A0T7MV30	LytR family transcriptional regulator	lytR_1;ACH32_04930	1,728E+10	4,132E+09
A0A0T7MW09	Putative polyribitolphosphotransferase;CDP-ribitol ribitolphosphotransferase	tagF_1;ACR58_06110;tag	1,036E+10	6,148E+09
A0A0U0TSZ8	Allophanate hydrolase subunit 2;Allophanate hydrolase;Uncharacterized protein	ERS195423_00878;AFO87_10985;SAOUHSC_01711	2,816E+08	7,492E+07
A0A0U1MF40	Putative membrane protein;Membrane protein;Uncharacterized protein	BN1321_150055;CH51_03255;ACR58_11530	2,154E+09	3,579E+08
A0A0U1MF84	Iron dependent repressor, N-terminal DNA binding domain protein;DtxR family transcriptional regulator	BN1321_150074;ACH32_10480	2,316E+09	2,263E+09
A0A0U1MFR0	Putative beta-lactamase;Penicillin binding protein 4	BN1321_150082;pbp4	3,939E+09	2,896E+08
A0A0U1MFY6	DNA polymerase III (Gamma and tau subunits);DNA polymerase III gamma and tau subunits	dnaX	2,816E+09	1,108E+09
A0A0U1MH00	Bacterial regulatory helix-turn-helix , lysR family protein;LysR substrate binding domain protein	BN1321_170002;HMPREF0769_11660	7,708E+08	2,384E+08
A0A0U1MHE2	Glycerate kinase family protein;SA0697 protein;Glycerate kinase	BN1321_170076;SA0697;glxK_1	6,231E+08	5,139E+08
A0A0U1MHP2	1,4-dihydroxy-2-naphthoate octaprenyltransferase	menA	2,222E+09	1,363E+08
A0A0U1MIE4	Putative ribonuclease with PIN and NYN domains;Uncharacterized protein;Putative cytosolic protein	yacP;HMPREF0769_11801;	5,771E+08	3,439E+08
A0A0U1MJ68	Putative membrane protein;Uncharacterized protein	BN1321_230002;SAUSA300_0980;HMPREF0769_127	2,437E+09	7,612E+08
A0A0U1MKY9	Putative integral membrane protein;Putative membrane protein;Membrane protein	ypdP;HMPREF0769_12315;ACR58_14545	5,465E+08	7,011E+07
A0A0U1ML47	Malate glycosyltransferase for bacillithiol synthesis;N-acetyl-alpha-D-glucosaminyl L-malate synthase;Glycosyltransferase	bshA;QU38_13715;	2,315E+08	9,391E+07
A0A0U1MLC2	tRNA N6-adenosine threonylcarbamoyltransferase	tsaD	9,217E+08	4,485E+08
A0A0U1MM24	Succinate dehydrogenase (Iron-sulfur protein);Succinate dehydrogenase iron-sulfur subunit	sdhB	5,462E+10	2,272E+10
A0A0U1MM50	Putative 5-bromo-4-chloroindolyl phosphate hydrolysis protein;5-bromo-4-chloroindolyl phosphate hydrolase;Uncharacterized prot	BN1326_60523;ACR58_01750	6,244E+08	2,583E+08
A0A0U1MM97	Anaphase-promoting complex, cyclosome, subunit 3 family protein;Tetratricopeptide repeat protein	BN1321_260257;HMPREF0776_2657	7,769E+07	7,370E+07
A0A0U1MMF3	ATP-dependent RecD-like DNA helicase	recD;recD_2	1,051E+09	6,279E+08
A0A0U1MMT8	ATP synthase epsilon chain	atpC	6,097E+08	2,547E+08
A0A0U1MMU7	Acetate kinase	ackA	4,769E+10	4,504E+10
A0A0U1MP49	Alpha-acetolactate synthase;Acetolactate synthase, catabolic;Acetolactate synthase	alsS	1,674E+09	6,720E+08
A0A0U1MP68	Bacterial ABC transporter protein EcsB;EcsB	BN1321_290006;AFO87_07365;HMPREF0769_11843	2,669E+09	4,165E+08

A0A0U1MQC8	Autolysin;Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase	AUC48_09100;ACR58_09010;HMPREF0776	1,795E+10	1,198E+09
A0A0U1MR46	Uncharacterized protein	BN1321_340076;MW2059;SACOL2127	2,960E+09	9,417E+08
A0A0U1MR56	Uncharacterized protein;EVE domain protein	BN1321_350004;ERS093009_02338;AFO87_07675	3,702E+09	2,132E+09
A0A0U1MRF8	Putative exported protein	BN1326_90074	5,664E+09	8,477E+08
A0A0U1MRQ5	CAAX protease self-immunity family protein;CAAX amino terminal protease family protein;Uncharacterized protein	BN1321_380152;HMPREF0769_10841	1,557E+09	1,018E+08
A0A0U1MRS4	Phosphotransferase system (PTS) maltose-specific enzyme IICB component;PTS system%2C arbutin-like IIBC component	malP;glvC	1,139E+09	8,928E+07
A0A0U1MRW1	ABC-2 transporter family protein;ABC superfamily ATP binding cassette transporter, membrane protein;Uncharacterized protein	BN1321_390008;RU53_2400	7,518E+09	1,816E+08
A0A0U1MS08	L-lactate permease;MW2287 protein;SA2156 protein	lctP;MW2287;SA2156;	1,374E+09	1,495E+08
A0A0U1MT23	Ribosomal RNA methyltransferase FmrO domain protein;Uncharacterized protein	BN1321_410046;SA2257	3,041E+08	2,085E+08
A0A0U1MV17	Homoserine O-acetyltransferase	BN1321_430102;metX	6,642E+08	1,330E+08
A0A0U1MVJ1	D-lactate dehydrogenase;MW2480 protein;SA2346 protein;D-specific D-2-hydroxyacid dehydrogenase-l	ldhD;MW2480;SA2346	1,505E+08	1,270E+08
A0A0U1MVR0	ABC transporter, solute-binding protein	BN1321_60021;HMPREF0769_10274	1,537E+09	1,470E+08
A0A0U1MWK7	Uncharacterized protein;Membrane protein;Isoprenylcysteine carboxyl methyltransferase family protein	BN1326_30078;ACH32_08335	1,126E+09	1,336E+08
A0A0U1MWT4	Putative ribitol-5-phosphate dehydrogenase;SA0246 protein	tarJ;SA0246	8,116E+09	2,884E+09
A0A0U1MWX3	Putative hemin import ATP-binding protein HrtA;Peptide ABC transporter ATP-binding protein;ABC transporter ATP-binding protein	hrtA;ACR58_05805	4,690E+08	3,789E+08
A0A0U1MXC0	Putative phosphoglycerate mutase family protein;MW0351 protein;Phosphoglycerate mutase	BN1321_80100;MW0351;gpmA	1,308E+08	4,085E+07
A0A0U1MXZ3	Putative membrane protein;Uncharacterized protein;Membrane protein	BN1326_60124;BN1321_210016;ACR58_03900	1,007E+10	2,100E+08
A0A0U1MZF1	Glycine betaine transporter;Glycine betaine transporter 1;Transporter, betaine/carnitine/choline family	opuD;NWMN_1261	9,106E+09	1,676E+08
A0A0U1MZP0	Putative sulfur transferase;Putative rhodanese domain-containing sulfurtransferase	yqhL;ACH32_00510	1,297E+10	2,260E+09
A0A0U1N079	NADPH-dependent aldo-keto reductase	yqkF	1,127E+09	5,198E+08
A0A0U1N151	Putative membrane protein;Uncharacterized protein;Membrane protein	BN1326_60502;RU53_1388;ACH32_13890	6,499E+09	4,861E+08
A0A0V1SBS2	NADPH:quinone reductase;Putative quinone oxidoreductase YhfP	ACR61_14545;yhfP	2,428E+09	1,093E+09
A0A0V1TBG6	Beta-lactamase	ACR61_14555	2,466E+11	1,233E+11
A6QDH3	PTS system glucose-specific EIICBA component;Phosphotransferase system (PTS) glucose-specific enzyme IICBA component	ptsG	3,380E+10	3,930E+09
A6QDN3	Iron-sulfur cluster repair protein ScdA	scdA	7,922E+07	3,856E+07
A6QEJ1	50S ribosomal protein L10	rplJ	8,666E+09	3,136E+09
A6QGA1	Aspartate carbamoyltransferase	pyrB	1,792E+09	9,519E+08
A6QGC9	Phosphate acyltransferase	plsX	2,328E+09	1,250E+09
A6QGJ5	DNA mismatch repair protein MutL	mutL	2,036E+09	1,177E+09
A6QGP7	Nuclease SbcCD subunit D;Exonuclease;DNA repair exonuclease	sbcD;CH51_07065	1,116E+08	4,257E+07
A6QH23	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	gpsA	1,764E+09	7,261E+08
A6QH29	Elastin-binding protein EbpS;Cell surface elastin binding protein	ebpS;ebp	4,032E+10	2,620E+10
A6QHB3	Endoribonuclease YbeY	ybeY;rnrY	7,514E+08	2,318E+08
A6QHC2	Chaperone protein DnaJ	dnaJ	2,940E+09	2,016E+09
A6QHH3	Histidine--tRNA ligase	hisS	1,449E+09	1,032E+09
A6QHH7	Adenine phosphoribosyltransferase;Adenine phos	apt	8,093E+07	4,908E+07
A6QI49	UPF0374 protein NWMN_1759;UPF0374 protein ygaC;UPF0374 protein ST398NM01_1960	NWMN_1759;ygaC;ST398NM01_1960	4,781E+08	3,388E+08
A6QK99	Oxygen-dependent choline dehydrogenase	betA	8,742E+08	6,011E+08
A6QKD8	Protein translocase subunit SecA 2;Protein translocase subunit SecA	secA2	5,732E+08	3,301E+08
B1Q017	Gamma-hemolysin subunit A;Panton-Valentine leukocidin chain S	lukS-PV	1,117E+09	4,419E+08
B6V384	Lipoprotein;Uncharacterized protein	AL493_04610;QU38_07495;HMPREF0769_12466	1,273E+10	2,785E+08
D2J7P6	Cadmium resistance protein;Cadmium transporter	cadD;ACR61_14535;SAKOR_02717	1,372E+09	2,735E+07
D2J801	Beta-lactamase;Penicillin-binding protein, transpeptidase domain protein	blaR1;ACR61_14560;HMPR	1,209E+09	4,265E+08
H6UH58	Glucokinase;Glucose kinase	glcK	4,373E+08	3,022E+08
O05154	Putative glycosyltransferase TagX;Glycosyl transferase;Teichoic acid biosynthesis protein X	tagX;SAKOR_00634	1,227E+09	9,843E+08
O86491	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L-lysine ligase	murE	3,652E+09	2,174E+09
P0A022	DNA polymerase III subunit beta	dnaN;ST398NM01_0002	1,334E+10	7,478E+09
P0A092	Nitric oxide synthase oxygenase	nos;SA	1,131E+08	2,169E+07
P0A0H6	Serine-protein kinase RsbW;Serine/threonine protein kinase	rsbW	4,528E+09	2,156E+09
P0A0Q1	Uncharacterized protein SAV1055;LytR family transcriptional regulator;Transcriptional regulator, LytR family protein	SAV1055;AL077_04510	2,641E+08	1,666E+08
P31337	UPF0758 protein SAOUHSC_01763;UPF0758 protein MW1604;Uncharacterized protein	SAOUHSC_01763;MW1604;QU38_086	2,658E+08	1,856E+08
P52078	Uncharacterized protein SAOUHSC_00997;Transcriptional regulator, LytR family protein;Uncharacterized protein	SAOUHSC_00997;SAKOR_00977	8,496E+09	5,237E+08
P60087	Arginase	arg;QU38_06060;argl	1,904E+09	5,679E+08
P60610	Sensory transduction protein LytR;Two-component response regulator (LytS)	lytR;lytT	2,540E+08	1,262E+08
P63757	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase;CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransfer	pgsA	4,981E+09	4,504E+08
P63790	ATP-dependent Clp protease ATP-binding subunit ClpX;ATP-dependent protease	clpX	6,662E+09	4,312E+09
P64124	Ferrochelatase;Ferrochelatase O	hemH	3,463E+08	2,320E+08
P64235	Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase TrmFO	trmFO	1,048E+09	4,657E+08
P65181	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	ispE	6,111E+08	2,036E+08
P65228	Homoserine kinase;Homoserine	thrB	4,513E+08	9,188E+07
P65445	Peptide methionine sulfoxide reductase MsrA 2;Peptide methionine sulfoxide	msrA2	2,478E+08	1,996E+08
P65475	UDP-N-acetylmuramate--L-alanine ligase	murC	3,846E+09	1,855E+09
P65694	ATP-dependent 6-phosphofructokinase	pfkA	4,184E+09	2,302E+09
P65937	Uridylate kinase;Uridylate kinase OS	pyrH	5,519E+09	2,131E+09
P65943	Bifunctional protein PyrR	pyrR	2,530E+09	1,556E+09
P66695	Ribose-5-phosphate isomerase A	rpiA	2,774E+08	2,581E+08
P66758	Holliday junction ATP-dependent DNA helicase RuvB	ruvB	3,134E+08	9,404E+07
P67062	Demethylmenaquinone methyltransferase;Menaquinone biosynthesis methyltransferase, putative	menG;ubiF	3,843E+09	2,035E+09
P67108	Nucleotide-binding protein SAV0765;Nucleotide-binding protein HMPREF0769_11525;Nucleotide-binding protein SAZ	SAV0765;HMPREF0769_11525	4,033E+09	1,119E+09
P67277	Ribonuclease Y	rny	3,323E+10	6,827E+09
P67291	UPF0154 protein SA1178;UPF0154 protein yneF;UPF0154 protein V070_00396;UPF0154 protein CO98_0281 OS	SA1178;yneF;V070_00396	2,446E+10	1,097E+09
P67410	Uridine kinase	udk	6,150E+08	2,679E+08
P68811	Protein NrdI	nrdI	2,051E+08	8,627E+07
P95695	Capsular polysaccharide type 5 biosynthesis protein cap5A;Capsular polysaccharide type 8 biosynthesis protein cap8A	cap5A;cap8A	9,518E+08	1,206E+08
P95696	Cap5B;Capsular polysaccharide synthesis enzyme;Capsular polysaccharide synthesis enzyme Cap5B	cap5b;capB	7,962E+07	4,169E+07
P95706	Cap5M;Cap8M;Galactosyl transferase;Capsular biosynthesis protein	cap5M;cap8M;SAZ172_0171	2,305E+08	6,148E+07
P99151	Alanine dehydrogenase 1;Alanine dehydrogenase	ald1	1,390E+07	9,611E+06
Q0H0G8	Deoxyadenosine kinase;Deoxyguanosine kinase;SA0515 protein	dgk;QU38_09800	2,239E+08	5,715E+07
Q0H0H0	Deoxyadenosine kinase;Deoxynucleoside kinase	dak;RU53_544;dck	9,492E+08	3,860E+08
Q2FC27	Beta-lactamase	blaZ;ACR62_14540	1,873E+09	9,638E+08
Q2FDV0	Copper-exporting P-type ATPase A;Copper-translocating P-type ATPase	copA	8,515E+09	2,407E+09
Q2FEA6	Oxygen regulatory protein NreC;Two-component response regulator;LuxR family transcriptional regulator	nreC	2,894E+08	1,372E+08
Q2FEC8	Uncharacterized lipoprotein SAUSA300_2315;Uncharacterized protein	SAUSA300_2315;HMPREF0776_0422	4,226E+10	4,447E+09
Q2FED4	Heme sensor protein HssS	hssS	1,097E+09	9,959E+08
Q2FEG6	Imidazolonepropionase	hutI	1,128E+09	3,506E+08
Q2FEK0	Urease accessory protein UreG	ureG;ure	3,270E+08	2,773E+08
Q2FEQ6	30S ribosomal protein S5	rpsE	1,172E+10	8,082E+09
Q2FER7	Energy-coupling factor transporter ATP-binding protein EcfA1	ecfA1	1,367E+09	9,009E+08
Q2FER8	Energy-coupling factor transporter ATP-binding protein EcfA2;Energy-coupling factor transporter ATP-binding protein EcfA	ecfA2;ecfA1_1	6,771E+08	1,890E+08
Q2FES9	Uncharacterized hydrolase SAUSA300_2163;Uncharacterized hydrolase SA2005	SAUSA300_2163;SA2005;ERS179246_00655	4,421E+08	3,455E+08
Q2FF06	Putative aldehyde dehydrogenase SAUSA300_2076;Aldehyde dehydrogenase	SAUSA300_2076;ERS179246_00402	5,451E+09	2,532E+09
Q2FF13	Low molecular weight protein-tyrosine-phosphatase PtpB;Low molecular weight protein tyrosine phosphatase	ptpB	3,955E+08	1,770E+08
Q2FF20	ATP synthase subunit b	atpF	3,823E+10	3,129E+09
Q2FFI4	UPF0316 protein SAUSA300_1892;UPF0316 protein SA1727;UPF0316 protein ST398NM01_2006	SAUSA300_1892;SA1727	1,015E+10	2,658E+09
Q2FFQ5	Foldase protein PrsA	prsA	3,504E+10	3,511E+09
Q2FFU9	2-succinylbenzoate--CoA ligase	menE	2,096E+08	1,116E+08
Q2FFZ9	UPF0478 protein SAUSA300_1685	SAUSA300_1685	2,830E+11	2,214E+10
Q2FG51	Transcriptional repressor NrdR	nrdR	5,018E+08	2,518E+08
Q2FG69	Glutamate-1-semialdehyde 2,1-aminomutase 1	hemL1	6,533E+08	5,538E+08
Q2FG97	Aspartate--tRNA ligase	aspS	2,733E+09	1,092E+09
Q2FGE1	Heat-inducible transcription repressor HrcA;Heat-inducible transcription repressor	hrcA	5,394E+08	9,991E+07
Q2FGG0	Putative pyruvate, phosphate dikinase regulatory protein	SAUSA300_1523;SAV1563	3,269E+09	1,741E+09
Q2FGW7	GTPase Der	der	6,192E+09	2,538E+09
Q2FGX6	3-phosphoshikimate 1-carboxyvinyltransferase	aroA	5,121E+08	2,194E+08
Q2FGY6	Asparagine--tRNA ligase;Asparagine--tRNA ligase O	asnS	2,953E+10	9,092E+09
Q2FH20	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	murG	6,677E+09	2,479E+09
Q2FH58	Putative oligopeptide transport ATP-binding protein oppF2	oppF2;opp-2F	8,266E+07	4,265E+07
Q2FH78	Protein GlcT;Transcriptional regulator	glcT;CH51_07120;QU38_13160	3,462E+08	2,711E+08
Q2FH88	Nuclease SbcCD subunit C	sbcC	1,300E+09	5,051E+08
Q2FHM9	Guanylate kinase	gmk	9,609E+08	8,026E+08
Q2FHQ4	UDP-N-acetylmuramoylalanine--D-glutamate ligase	murD	1,359E+09	7,313E+08
Q2FHT1	Glutamate racemase	murI	6,084E+09	2,284E+09
Q2FHU8	High-affinity heme uptake system protein IsdE;Heme transporter IsdDEF, lipoprotein IsdE	isdE	2,031E+09	4,048E+07
Q2FI05	Bifunctional purine biosynthesis protein PurH	purH	1,555E+09	6,268E+08
Q2FI17	Probable quinol oxidase subunit 2;Quinol oxidase subunit 2;Cytochrome aa3-600 quinol oxidase (Subunit II)	qoxA;QU38_05550;	9,226E+10	1,350E+10
Q2FI55	Serine protease HtrA-like;Serine protease, DegP/HtrA, do-like protein	SAUSA300_0923;SACOL1028	7,147E+09	3,027E+09
Q2FIM4	Epimerase family protein SAUSA300_0753;Cell division inhibitor	SAUSA300_0753;SAKOR_00773;CH51_	9,333E+09	2,906E+09
Q2FJ31	Alcohol dehydrogenase;Zinc-binding alcohol dehydrogenase	adh;adh1;RU53_668	5,110E+08	5,006E+08

Q2FJ92	Elongation factor Tu	tuf;tufA	4,920E+11	3,642E+11
Q2FJ93	Elongation factor G	fusA;fus	6,358E+10	5,740E+10
Q2FJC0	Pyridoxal 5-phosphate synthase subunit PdxT	pdxT	4,814E+08	3,956E+08
Q2FJH7	N-acetylmuramoyl-L-alanine amidase sle1;Autolysin;N-acetylmuramoyl-L-alanine amidase	sle1;SAZ172_0466;amiD	8,721E+08	7,037E+08
Q2FJI9	UPF0753 protein SAUSA300_0426;UPF0753 protein SAOUHSC_00413;UPF0753 protein QU38_03380	SAUSA300_0426;SAOUHSC_00413	2,766E+09	2,081E+09
Q2FK59	Uncharacterized protein SAUSA300_0205;Uncharacterized protein SA0203;Uncharacterized protein SAV0210	SAUSA300_0205;SA0203	1,022E+09	8,767E+07
Q2FKI2	Probable copper-transporting P-type ATPase B;ATPase;Copper-exporting ATPase	copB;CO98_2152	8,813E+10	2,854E+09
Q2FKJ8	Carbamate kinase 3	arcC3	2,487E+08	6,588E+07
Q2FKQ5	Chromosomal replication initiator protein DnaA	dnaA	6,981E+09	5,136E+09
Q2FUQ4	Ribosomal RNA small subunit methyltransferase G	rsmG	5,940E+08	5,871E+08
Q2FUW3	Accessory Sec system protein Asp1;Uncharacterized protein	asp1;SAV2652	1,729E+08	8,079E+07
Q2FUW4	Accessory Sec system protein Asp2;Accessory secretory protein Asp2;Uncharacterized protein	asp2;NWMN_2550	1,487E+08	1,107E+08
Q2FVA2	Uncharacterized protein;HAD family hydrolase;Cof-like hydrolase	SAOUHSC_02831;supH;HMPREF0776_0583	6,813E+07	4,622E+07
Q2FVE6	Uncharacterized protein	SAOUHSC_02768;SAUSA300_2412;N	1,287E+09	3,825E+08
Q2FVE7	Peptide ABC transporter, peptide-binding protein, putative;Peptide ABC transporter, peptide-binding proteiin	SAOUHSC_02767;SACOL2476	5,812E+09	8,699E+07
Q2FVI3	Uncharacterized protein;Putative lipoprotein	SAOUHSC_02727;AFO87_00200;ST398NM01_2488	8,229E+08	2,424E+08
Q2FVR9	Isopentenyl-diphosphate delta-isomerase	fni	1,306E+09	4,204E+08
Q2FVT7	Uncharacterized protein;N-acetyl-L%2CL-diaminopimelate deacetylase;Amino acid amidohydrolase	SAOUHSC_02605;yxeP_3	1,258E+08	9,938E+07
Q2FW81	Probable uridylyltransferase SAOUHSC_02423;Probable uridylyltransferase SA1974;Uridylyltransferase	SAOUHSC_02423;SA1974	1,125E+09	9,567E+08
Q2FWH3	D-alanine--D-alanine ligase	ddl	7,767E+09	6,630E+09
Q2FWK9	Uncharacterized protein	SAOUHSC_02280;MW1976;SA1857	4,673E+08	2,447E+08
Q2FWL5	ABC transporter, ATP-binding protein, putative;ABC transporter ATP-binding protein;Putative ABC transporter ATP-binding protein	SAOUHSC_02274;yheS_1	1,947E+09	5,187E+08
Q2FWL7	Uncharacterized protein;Putative transport system permease protein;Putative membrane spanning protein	SAOUHSC_02272;yeeE	3,837E+08	1,045E+08
Q2FWY9	Glutamyl-tRNA(Gln) amidotransferase subunit A;Glutamyl-tRNA(Gln) amidotransferase subunit A	gatA	6,003E+09	3,032E+09
Q2FWZ0	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	gatB	6,714E+09	3,819E+09
Q2FX99	UPF0754 membrane protein SAOUHSC_01978;Uncharacterized protein;UPF0754 membrane protein MW1787	SAOUHSC_01978;RU53_1946	4,408E+09	6,024E+08
Q2FXJ8	Uncharacterized protein;PTS glucose transporter subunit IIBC	SAOUHSC_01836;ptaA	3,649E+09	6,536E+07
Q2FXP7	Threonine--tRNA ligase	thrS	1,013E+10	4,864E+09
Q2FXT8	Protein-export membrane protein SecDF;Bifunctional preprotein translocase subunit SecD/SecF	SAOUHSC_01746;secD	3,416E+10	9,749E+09
Q2FXU8	Uncharacterized protein;Putative ATPase (AAA family);DNA-dependent ATPase;Uncharacterized protein O	SAOUHSC_01734;rarA	2,515E+09	6,845E+08
Q2FXZ8	Uncharacterized protein;Serine protease;Membrane-bound serine protease	SAOUHSC_01677;QU38_09060;BN1321_260212	6,306E+09	1,278E+09
Q2FY32	Shikimate kinase	aroK	2,090E+08	7,950E+07
Q2FY82	Conserved hypothetical phage protein;Lipoprotein;Uncharacterized protein	SAOUHSC_01583;AFO87_01650;SAZ172_1502	7,650E+08	1,309E+08
Q2FYG6	Heptaprenyl diphosphate syntase component II, putative;Farnesyl pyrophosphate synthetase	SAOUHSC_01486;hepT	7,554E+08	1,526E+08
Q2FYQ7	Putative oligopeptide transport ATP-binding protein oppD2;Putative oligopeptid	oppD2	1,611E+08	2,958E+07
Q2FYZ5	Glycerol kinase	glpK	2,616E+09	9,596E+08
Q2FYZ9	DNA mismatch repair protein MutS	mutS	2,701E+09	1,362E+09
Q2FZ09	Protein RecA	recA	1,223E+10	6,276E+09
Q2FZ18	Uncharacterized protein;DNA translocase FtsK	SAOUHSC_01253;ftsK	2,761E+09	2,390E+09
Q2FZ28	ATP-dependent protease ATPase subunit HslU;ATP-dependent protease ATPase subunit	hslU	2,206E+09	1,307E+09
Q2FZ63	Uncharacterized protein;Ribosome small subunit-dependent GTPase A	SAOUHSC_01188;rsgA	3,650E+08	1,360E+08
Q2FZ95	Cell division protein FtsL	ftsL	3,907E+08	1,058E+08
Q2FZJ0	Phosphoribosylformylglycinamidine synthase subunit PurL	purL	2,140E+09	1,169E+09
Q2FZT4	Uncharacterized protein SAOUHSC_00906;Fumarylacetoacetate hydrolase family protein	SAOUHSC_00906;AL077_06395	1,406E+10	1,097E+10
Q2FZX4	Lipoyl synthase	lipA	8,932E+08	4,960E+08
Q2G042	Uncharacterized protein;TPR repeat family protein;TPR domain protein	SAOUHSC_00784;BN1321_180006;NWMN_0731	5,658E+08	1,616E+08
Q2G044	Prolipoprotein diacylglyceryl transferase	lgt;CH51_03970	4,261E+09	3,409E+08
Q2G093	Lipoteichoic acid synthase;Glycerol phosphate lipoteichoic acid synthase	ltaS;CH51_03760	6,125E+08	3,096E+08
Q2G0A6	Deoxyribodipyrimidine photolyase, putative;Deoxyribodipyrimidine photolyase;MW0653 protein	SAOUHSC_00699;phrB;MW0653	1,064E+08	7,613E+07
Q2G0F6	Iron compound ABC transporter, substrate-binding protein, putative;Periplasmic binding protein	SAOUHSC_00613;HMPREF0776_1614	1,959E+10	6,297E+08
Q2G0I1	Uncharacterized protein;Hypothetical fig|282458.1.peg.573 homolog	SAOUHSC_00584;AFO87_11280;MW05	9,353E+08	4,522E+08
Q2G0P6	Protein-arginine kinase	mcsB	1,453E+09	6,310E+08
Q2G0P8	Transcriptional regulator CtsR;CtsR	ctsR	1,461E+09	2,824E+08
Q2G0V2	Methionine import ATP-binding protein MetN 1;Methionine import ATP-binding protein MetN	metN1;metN	6,897E+09	4,005E+09
Q2G179	Uncharacterized protein;Putative cytosolic protein;ADP-ribosylating toxin	SAOUHSC_00268;ERS365775_01057;CH51_01365	5,595E+08	4,538E+08
Q2G1G5	PTS system EIIBC component SAOUHSC_00158;PTS system%2C IIB component / PTS system%2C IIC component	SAOUHSC_00158;ERS179246_01482	9,292E+10	8,505E+09
Q2G1P4	Uncharacterized protein;Putative Na+/Pi-cotransporter protein;Na/Pi cotransporter	SAOUHSC_00060;BN1321_40030;BN1326_150313	3,064E+09	3,388E+08
Q2G1X6	7-cyano-7-deazaguanine synthase	queC	2,067E+08	1,478E+08
Q2G1Z4	Proline--tRNA ligase	proS	7,170E+09	2,633E+09
Q2G218	L-lactate dehydrogenase 1;L-lactate dehydrogenase	ldh1;ldhA;ldh	4,097E+08	4,091E+08
Q2G252	Ribosomal RNA large subunit methyltransferase H	rlmH	9,375E+08	4,821E+08
Q2G275	DNA replication and repair protein RecF	recF	3,389E+08	1,175E+08
Q2G2E0	Uncharacterized protein;Na+/H+ antiporter;Sodium/hydrogen exchanger family protein;Na+/H	SAOUHSC_00633;nhaK_1;BN1321_150070	7,604E+09	3,167E+08
Q2G2N1	Uncharacterized protein;Putative membrane protein;Membrane protein	SAOUHSC_02001;BN1326_100006;ACR58_12900	3,526E+09	5,626E+08
Q2G2P5	Uncharacterized protein;ABC superfamily ATP binding cassette transporter%2C binding protein	SAOUHSC_00201;gsiB	3,806E+09	1,185E+09
Q2G2S0	Adenylosuccinate lyase	purB	1,306E+09	1,273E+09
Q2G2U3	Uncharacterized protein;Lipoprotein	SAOUHSC_00022;yycH;ACH32_07145	6,754E+09	6,447E+07
Q2G2W2	Uncharacterized protein;Membrane protein	SAOUHSC_02628;AFO87_00680;ERS179246_01335	1,184E+10	4,604E+08
Q33C61	AraC family regulatory protein;MW1460 protein;AraC family transcriptional regulator	graE;MW1460;ACR58_00715	2,619E+08	1,230E+08
Q53635	o-succinylbenzoate synthase	menc;menC	2,873E+08	1,615E+08
Q53700	NAD-dependent protein deacetylase	cobB	2,907E+08	1,148E+08
Q53727	ATP-dependent DNA helicase PcrA;DNA helicase	pcrA;	3,496E+09	1,016E+09
Q5FBD2	LukF-PV	lukF-PV	2,437E+09	5,204E+08
Q5HCI3	tRNA modification GTPase MnmE	mnmE	1,414E+09	5,518E+08
Q5HCU5	Probable malate:quinone oxidoreductase 2;Probable malate:quinone oxidoreductase	mqo2;mqo	4,411E+10	2,471E+10
Q5HDB2	Protein flp;Beta-lactamase family protein;Beta-lactamase	flp;fmtA_2	1,637E+09	3,959E+08
Q5HDJ0	Probable malate:quinone oxidoreductase 1;Probable malate:quinone oxidoreductase	mqo1;mqo	6,614E+09	2,307E+09
Q5HDJ9	Membrane-associated protein TcaA;Membrane-associated protein	tcaA	4,246E+09	9,756E+07
Q5HDT3	Cyclic pyranopterin monophosphate synthase accessory protein	moaC	1,148E+08	1,032E+08
Q5HDW4	30S ribosomal protein S3	rpsC	5,169E+10	4,101E+10
Q5HE76	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2;UDP-N-acetylglucosamine 1-carboxyvinyltransferase	murA2;murA	4,682E+08	2,626E+08
Q5HE81	Thymidine kinase	tdk	3,811E+08	1,843E+08
Q5HE91	ATP synthase subunit a	atpB;atpA_1	2,514E+09	1,580E+09
Q5HEA0	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1;UDP-N-acetylglucosamine 1-carboxyvinyltransferase	murA1;murA	4,214E+09	1,683E+09
Q5HEA9	Membrane protein insertase YidC	yidC	1,272E+10	4,576E+08
Q5HEB9	DEAD-box ATP-dependent RNA helicase CshA	cshA	6,525E+09	5,347E+09
Q5HEE5	Ketol-acid reductoisomerase	ilvC	2,573E+09	1,005E+09
Q5HEK1	Probable manganese-dependent inorganic pyrophosphatase	ppaC	1,300E+10	1,119E+10
Q5HEL3	Staphopain A	sspP;s	9,411E+08	4,777E+08
Q5HEQ0	Monofunctional glycosyltransferase	mgt;sgtB	1,156E+09	1,044E+09
Q5HEY9	S-adenosylmethionine synthase	metK	1,004E+10	6,153E+09
Q5HF24	D-alanine aminotransferase;D-alanine	dat	1,729E+09	1,656E+09
Q5HF39	Acetoin utilization protein AcuC;Acetoin utilization acuC protein	acuC	5,528E+08	2,847E+08
Q5HF56	Septation ring formation regulator EzrA	ezrA;ezrA_1	1,535E+11	1,749E+10
Q5HF59	Probable tRNA sulfurtransferase	thiI	5,925E+08	3,429E+08
Q5HF76	Pyruvate kinase	pyk;pykA;QU38_08455	6,307E+10	4,724E+10
Q5HF86	Glyceraldehyde-3-phosphate dehydrogenase 2;Glyceraldehyde-3-phosphate dehydrogenase	gapA2;gap2	2,859E+09	1,532E+09
Q5HFB9	GTPase Obg	obg	6,435E+09	3,790E+09
Q5HFC3	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	queA	7,579E+08	4,569E+08
Q5HFD1	Probable cell wall amidase LytH;Probable cell wall amidase lytH	lytH	4,386E+09	2,010E+09
Q5HFH6	Elongation factor 4	lepA	5,485E+09	2,817E+09
Q5HFJ5	Glycine--tRNA ligase	glyQS	1,029E+10	9,638E+09
Q5HFJ8	DNA primase	dnaG	8,488E+08	2,800E+08
Q5HFP8	Exodeoxyribonuclease 7 large subunit	xseA	5,439E+08	3,937E+08
Q5HFR8	Ribonuclease Z	rnz;rn	7,842E+07	7,330E+07
Q5HFZ6	Thymidylate synthase	thyA	2,330E+08	1,951E+08
Q5HG01	Probable CtpA-like serine protease;Carboxy-terminal processing proteinase ctpA;Serine protease	SACOL1455;ctpA;CH51_07455	1,237E+10	9,157E+09
Q5HG45	Aminoacyltransferase FemA;Methicillin resistance protein FemA;FemAB family protein	femA;HM	2,509E+09	2,194E+09
Q5HG59	Phosphatidylglycerol lysyltransferase;FmtC (MprF) protein involved in methicillin resistance / L-lysine modification of phosphatidylgl	mprF	4,369E+09	1,019E+09
Q5HG65	DNA topoisomerase 4 subunit B	parE;gyrB	2,557E+09	2,148E+09
Q5HGA3	Cardiolipin synthase 1;Cardiolipin synthase	cls1;NWMN_1230	7,529E+09	2,689E+09
Q5HGG7	DNA polymerase III PolC-type	polC	3,299E+09	1,270E+09
Q5HGG9	Putative zinc metalloprotease SACOL1281;Zinc metalloprotease;Putative zinc metalloprotease MW1145	SACOL1281;ERS179246_01117;MW	1,305E+10	4,427E+08
Q5HGM7	Orotate phosphoribosyltransferase	pyrE	6,174E+08	5,284E+08
Q5HGN0	Carbamoyl-phosphate synthase small chain	carA	3,978E+09	2,293E+09
Q5HGV3	Iron-regulated surface determinant protein C	isdC	6,772E+08	6,322E+07
Q5HH13	Phosphoribosylformylglycinamidine cyclo-ligase;Phosphoribosylformylglycinamidine c	purM	1,675E+09	3,543E+08
Q5HH38	1,4-dihydroxy-2-naphthoyl-CoA synthase	menB	1,456E+10	8,007E+09

Q5HHB0	Chaperone protein ClpB	clpB	8,516E+09	7,195E+09
Q5HHB9	Signal peptidase IB;Signal peptidase I	spsB;SAOUHSC_00903	2,993E+10	8,997E+08
Q5HHG8	UPF0051 protein SACOL0918;Uncharacterized protein;FeS cluster formation protein	SACOL0918;ST398NM01_0901;sufB	1,635E+09	1,491E+09
Q5HHH0	Probable cysteine desulfurase;Cysteine desulfurase;Selenocysteine lyase	csd	7,456E+08	5,256E+08
Q5HHR7	Protein translocase subunit SecA 1;Protein translocase subunit SecA	secA1;secA	2,357E+10	2,206E+10
Q5HHT2	UDP-N-acetylenolpyruvoylglucosamine reductase	murB	3,078E+08	2,185E+08
Q5HHY5	Undecaprenyl-diphosphatase;U	uppP	5,898E+09	1,677E+08
Q5HI09	Response regulator protein GraR	graR	4,293E+08	3,216E+08
Q5HI96	Putative pyridoxine kinase;Phosphomethylpyrimidine kinase	pdxK;thiD	4,279E+09	2,231E+09
Q5HIG5	Hypoxanthine-guanine phosphoribosyltransferase;Hypoxanthine phosphoribosyltransferase	hpt	9,188E+08	2,717E+08
Q5HIH5	Ribose-phosphate pyrophosphokinase	prs	1,763E+10	5,733E+09
Q5HIJ5	Thymidylate kinase	tmk	1,558E+09	1,044E+09
Q5HIQ9	Xanthine phosphoribosyltransferase	xpt;xprT	9,816E+09	6,241E+09
Q5HJ87	Protein EssB;Type VII secretion protein EssB;Putative secretion system component EssB/YukC	essB	6,100E+09	9,976E+08
Q5HJR8	Uncharacterized HTH-type transcriptional regulator SACOL0084;Uncharacterized protein;Transcriptional regulator, AraC family	SACOL0084;NWMN_0046	1,055E+08	9,548E+07
Q5HJX6	Sensor protein kinase WalK	walK	7,741E+09	3,055E+09
Q6WS49	Domain of uncharacterised function (DUF3578);Uncharacterized protein	ORF;SACOL0026;SAKOR_0002	3,717E+08	1,935E+08
Q70MI7	Gamma-aminobutyrate permease;Lysine-specific permease	lysP	1,359E+09	1,308E+08
Q79C39	35-aminoglycoside phosphotransferase	aphA-3	2,316E+10	1,401E+10
Q7A0T9	UPF0403 protein MW1467;Uncharacterized protein	MW1467;HMPREF0776_2549	5,136E+08	4,267E+08
Q7A2T0	Protein FmtA;Methicillin resistance protein FmtA	fmtA;QU38_05530	5,736E+09	2,321E+09
Q7A2V2	Uncharacterized membrane protein SAV0746;Uncharacterized membrane protein in llm 5region;Uncharacterized membrane proteir	SAV0746;BN1321_170080	2,973E+09	1,627E+08
Q7A3E1	Dehydrosqualene synthase;Squalene/phytoene synthase	crtM;RU53_2626	1,980E+08	9,605E+07
Q7A3H8	Putative NAD(P)H nitroreductase SA2311;Putative NAD(P)H nitroreductase SACOL2534;Nitroreductase family protein	SA2311;SACOL2534	9,287E+08	6,537E+08
Q7A3W1	Ferredoxin--NADP reductase	SA2162;SAV2372	1,180E+09	5,492E+08
Q7A4B3	PTS system mannitol-specific EIICB component;PTS mannitol transferase subunit IIB	mtlA	1,983E+09	1,381E+08
Q7A537	Tyrosine--tRNA ligase	tyrS	8,276E+08	4,406E+08
Q7A5N7	Uncharacterized protein SA1241;Uncharacterized protein SAUSA300_1302;Putative nitric-oxide reductase	SA1241;SAUSA300_1302;	4,981E+08	3,667E+08
Q7A5W3	tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase	miaB	7,356E+08	2,542E+08
Q7A5Z4	Uncharacterized protein SA1069;Putative dihydroxyacetone/glyceraldehyde kinase;Dihydroxyacetone kinase family protein	SA1069;yloV;ERS09300	6,635E+09	4,478E+09
Q7A6H8	NAD-specific glutamate dehydrogenase;Glutamate dehydrogenase	gluD;gudB	8,891E+09	7,366E+09
Q7A6J4	NADH dehydrogenase-like protein SA0802;Pyridine nucleotide-disulfide oxidoreductase;NADH dehydrogenase family	SA0802;RU53_936	1,564E+10	1,517E+10
Q7A6T6	Putative lipid kinase SA0681;Putative lipid kinase NWMN_0695;Putative lipid kinase MW0688	SA0681;NWMN_0695;MW	1,776E+09	1,443E+09
Q7A782	FMN-dependent NADPH-azoreductase;FMN-dependent NADH-azoreductase	azo1;azo	8,382E+09	6,362E+09
Q7A7B2	Transcription-repair-coupling factor	mfd	2,879E+09	1,406E+09
Q7A8E1	Transcriptional regulatory protein WalR;Two-component response regulator WalR;Transcriptional regulatory protein YycF	walR;yycF	6,766E+09	6,656E+09
Q7BGA5	Ferric hydroxamate receptor 2;Iron (Fe+3) ABC superfamily ATP binding cassette transporter, binding protein	fhud2;fhuD	2,797E+10	6,657E+08
Q7BHL7	Regulatory protein MsrR;LytR family transcriptional regulator;Peptide methionine sulfoxide reductase regulator MsrR	msrR;ACH32_13790	6,138E+08	6,123E+08
Q7DHH4	MecA;Penicillin-binding protein MecA;PBP2a;Beta-lactam-inducible penicillin-binding protein	mecA;SAKOR_00039	4,744E+10	4,420E+10
Q83TG5	Lipoprotein;Electron transfer DM13 family protein;Uncharacterized protein	AFO87_02840;BN1321_170041;MW0670	1,866E+11	1,364E+10
Q840P7	Histidine protein kinase SaeS	saeS	1,027E+11	3,604E+10
Q8NUN2	Pantothenate synthetase	panC	1,178E+09	5,970E+08
Q8NUQ6	Dehydrosqualene desaturase	crtN	9,552E+08	5,559E+08
Q8NUS2	PTS system glucoside-specific EIICBA component;PTS system glucose-specific transporter subunit IICBA	glcB;QU38_16450	2,235E+09	6,077E+08
Q8NVE6	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]	glmS	9,012E+09	3,762E+09
Q8NVH5	Thiamine-phosphate synthase	thiE	4,099E+08	1,224E+08
Q8NVJ5	tRNA N6-adenosine threonylcarbamoyltransferase;tRNA N6-adenosine threonylcarbamoyltransferase	tsaD	8,733E+08	3,867E+08
Q8NVK5	Accessory gene regulator protein B	agrB	3,893E+09	1,099E+09
Q8NVS5	Sodium-dependent dicarboxylate transporter SdcS;Sodium-dependent dicarboxylate transporter SdcS	sdcS	8,185E+08	1,286E+08
Q8NVU6	Glutamate-1-semialdehyde 2,1-aminomutase 2;Glutamate-1-semialdehyde 2,1-aminomutase	hemL2	1,583E+09	8,674E+08
Q8NW59	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	accD	2,271E+09	1,265E+09
Q8NW61	Isocitrate dehydrogenase [NADP]	icd	3,473E+10	2,038E+10
Q8NW74	Porphobilinogen deaminase	hemC	9,448E+08	8,801E+08
Q8NW95	UPF0271 protein MW1555;UPF0271 protein SACOL1660;UPF0271 protein SA1433;UPF027	MW1555;SACOL1660;SA1433	4,020E+08	1,636E+08
Q8NWQ4	L-threonine dehydratase catabolic TdcB;Threonine dehydratase	tdcB;ilvA;S	6,027E+08	2,830E+08
Q8NWR0	DegV domain-containing protein MW1315;Uncharacterized protein;DegV domain-containing protein SA1258	MW1315;SAZ172_1438	5,414E+09	3,939E+09
Q8NWU0	Aminoacyltransferase FemB;FemB%2C factor involved in methicillin resistance / Glycine interpeptide bridge formation OS	femB	4,566E+09	2,835E+09
Q8NWZ5	Isoprenyl transferase	uppS	4,485E+08	1,951E+08
Q8NX11	ATP-dependent DNA helicase RecG	recG	5,912E+08	4,655E+08
Q8NX16	Probable dual-specificity RNA methyltransferase RlmN	rlmN	7,850E+08	4,626E+08
Q8NX38	Putative cysteine ligase BshC	bshC	7,490E+07	4,096E+07
Q8NX56	Endonuclease MutS2	mutS2;mutSB	1,066E+09	3,399E+08
Q8NXF2	Argininosuccinate synthase	argG	2,168E+08	4,754E+07
Q8NXM4	DegV domain-containing protein MW0711;EDD domain protein, DegV family	MW0711;HMPREF0776_1759	1,669E+09	1,407E+09
Q8NXR5	Sensor histidine kinase GraS;Histidine kinase	graS;QU38_10325	1,332E+09	2,547E+08
Q8NXS6	Teichoic acids export ATP-binding protein TagH	tagH	3,686E+09	2,300E+09
Q8NXZ0	Lysine--tRNA ligase	lysS	1,730E+10	9,843E+09
Q8NXZ2	Dihydropteroate synthase;Dihydr	folP	1,256E+09	8,211E+08
Q8NY69	GMP synthase [glutamine-hydrolyzing]	guaA	1,789E+10	1,236E+10
Q8NYC2	Lipase 2;Glycerol ester hydrolase%3B Lipase;Truncated triacylglycerol lipase	lip2;geh	1,550E+10	1,126E+10
Q8VUV7	ACP synthase;Uncharacterized protein	AL493_01530;SAUSA300_0041	3,154E+08	1,104E+08
Q8VUV8	AAA family ATPase;Putative transcriptional regulator	AL493_01535;ERS411017_01126	2,226E+09	8,581E+08
Q931H9	Accessory gene regulator A;Accessory protein regulator protein A	agrA	1,008E+10	7,393E+09
Q99R74	4,4-diaponeurosporenoate glycosyltransferase	crtQ	1,368E+08	5,517E+07
Q99RD4	UTP--glucose-1-phosphate uridylyltransferase	gtaB	3,280E+08	1,419E+08
Q99RL2	Immunoglobulin-binding protein sbi	sbi	3,445E+09	3,140E+08
Q99S33	50S ribosomal protein L5	rplE	1,557E+10	1,326E+10
Q99SC3	Pyrimidine-nucleoside phosphorylase	pdp	1,152E+10	9,994E+09
Q99SN8	Uncharacterized leukocidin-like protein 1;Leukocidin F subunit LukF	SAV2004;SACOL2004	2,756E+09	4,787E+08
Q99UZ7	Divalent metal cation transporter MntH	mntH	4,134E+09	1,051E+08
Q99V32	N5-carboxyaminoimidazole ribonucleotide synthase	purK	3,453E+08	1,219E+08
Q99V37	Probable quinol oxidase subunit 1;Cytochrome aa3-600 quinol oxidase (Subunit I)	qoxB	2,292E+10	3,295E+09
Q99V72	Peptide chain release factor 3	prfC	3,300E+09	1,096E+09
Q99V86	UPF0738 protein SAV1005;UPF0738 protein SACOL1009;UPF0738 protein SAKOR_00921	SAV1005;SACOL1009	1,648E+08	9,944E+07
Q99VJ2	Extracellular matrix protein-binding protein emp	emp	7,324E+07	3,827E+07
Q99W36	Putative proline/betaine transporter	proP	6,167E+08	4,849E+07
Q99W73	Cysteine--tRNA ligase	cysS	1,929E+09	1,812E+09
Q99X00	Uncharacterized response regulatory protein SAV0223;Uncharacterized response regulatory protein SAUSA300_0217	SAV0223;SAUSA300_0217	5,475E+08	1,605E+08
Q9EYL5	Disulfide bond protein A;Thiol:disulfide interchange protein dsbA;Lipoprotein	dsbA;SAKOR_02387;BN1321_400055	7,233E+09	1,968E+08
Q9F1K0	DNA polymerase III subunit alpha	dnaE	5,124E+08	3,128E+08
Q9KWK9	Putative uncharacterized protein yvqF;Transporter;Putative membrane protein	yvqF;QU38_07135;BN1326_100027	2,387E+09	1,881E+08
Q9RDT1	Uncharacterized protein;YycH family protein	yycI	2,571E+09	5,026E+07
Q9REV4	UDP-GlcNAc 2-epimerase;UDP-N-acetylglucosamine 2-epimerase	mnaA	1,160E+09	4,319E+08
Q9RL81	Phosphorylated protein phosphatase;Protein phosphatase;Protein phosphatase 2C	prpC;QU38_12430;SAKOR_01146	5,741E+08	2,309E+08
Q9RQG6	Multidrug transporter;SA2056 protein;RND transporter, HAE1/HME family, permease protein	swrC;SA2056;HMPREF0776	2,804E+10	6,872E+09
Q9RQQ0	Biofilm operon icaADBC HTH-type negative transcriptional regulator IcaR;Transcriptional regulator	icaR;QU38_15745	6,544E+08	3,076E+08
Q9S446	LPXTG specific sortase A;Sortase	srtA;ST398NM01_2578	1,224E+10	5,765E+08
Q9ZAH8	Membrane protein;Membrane-flanked domain-containing protein;Uncharacterized protein	ORF3;RU53_2135;NWMN_1978	3,441E+09	5,734E+08
Q9ZAH9	Bacterial membrane flanked domain protein;Uncharacterized protein	ORF2;RU53_2136	1,229E+09	1,853E+08
T1Y6D9	Ribosomal-protein-alanine acetyltransferase;Acetyltransferase, GNAT family	SAKOR_00676;BN1321_170010	1,025E+08	3,989E+07
T1Y6E4	Transport ATP-binding protein cydD;ABC superfamily ATP binding cassette transporter, ABC protein	SAKOR_00681;RU53_747	2,427E+09	3,002E+08
T1Y6N4	Two-component sensor kinase yesM;Uncharacterized sensor-like histidine kinase MW0199;Uncharacterized sensor-like histidine kin	SAKOR_00197;MW0199	5,926E+08	5,581E+08
T1Y720	Histidinol-phosphate aminotransferase	hisC	1,569E+08	1,019E+08
T1Y7D4	N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-beta-D-mannosaminyltransferase;Putative N-acetylmannosaminyltransferase	SAKOR_00630;tagA	1,043E+09	5,399E+08
T1Y893	Serine/threonine protein kinase;Serine/threonine-protein kinase PrkC;Non-specific serine/threonine protein kinase	SAKOR_01147;prkC	5,615E+09	2,064E+09
T1Y8P5	Kinase autophosphorylation inhibitor kipI;Allophanate hydrolase	SAKOR_00714;kipI_1;QU38_10625	1,181E+09	8,785E+08
T1Y9P2	Integral membrane protein;UPF0421 protein MW1829	SAKOR_01846;MW1829;ERS093009_02228	1,118E+09	4,461E+08
T1Y9Y4	Carbamoyl-phosphate synthase (glutamine-hydrolyzing);Carbamoyl-phosphate synthase large chain	SAKOR_01129;carB	1,277E+10	5,230E+09
T1YAA1	Diacylglycerol kinase family protein;Diacylglycerol kinase	SAKOR_01857;dagK	2,195E+09	9,158E+08
T1YAM7	Leukocidin S subunit LukS;Leukocidin/lemolysin toxin family protein;Uncharacterized leukocidin-like protein 2	SAKOR_01987;lukS	8,610E+09	1,849E+09
T1YAQ5	DNA mismatch repair protein mutS;DNA mismatch repair ATPase;MW1972 protein	SAKOR_02012;RU53_2105	1,149E+10	1,893E+08
T1YAY1	Penicillin binding protein transpeptidase	SAKOR_01499	1,946E+10	1,355E+09
T1YAZ7	GTPase Era	era	6,324E+09	3,326E+09
T1YBL4	Putative membrane protein insertion efficiency factor	SAKOR_01739;SACOL1842	2,415E+08	2,320E+08
T1YBN3	Staphyloxanthin biosynthesis protein CrtP;Diapolycopene oxygenase	SAKOR_02556;crtP	5,165E+08	1,054E+08
T1YBW8	Uncharacterized protein	SAKOR_02417;ST398NM01_2485;MW	1,154E+10	1,072E+09
T1YC07	Uncharacterized protein;Lysostaphin resistance protein A	SAKOR_02305;lyrA	1,157E+10	1,070E+09
T1YCI5	Rod shape-determining protein rodA;Cell shape determining protein RodA;Rod shape-determining protein RodA	SAKOR_02049;rodA	3,063E+09	1,923E+08

T1YCQ6	Acyltransferase family protein;O-acetyltransferase OatA;O-acetyltransferase	SAKOR_02560;oatA	3,351E+09	1,481E+09
T1YCS8	Putative membrane associated protein;Putative uncharacterized protein orf2;Uncharacterized protein	SAKOR_02129;orf2;QU38	2,570E+10	9,442E+08
T1YCU2	Siderophore synthase;Sialic acid synthase;Uncharacterized protein	SAKOR_02149;iucC_2;SAOUHSC_02436	1,615E+09	1,030E+09
T1YCZ2	ABC transporter permease protein;ABC superfamily ATP binding cassette transporter, membrane protein	SAKOR_02620;RU53_2684	1,894E+08	9,036E+07
T1YD14	N-acetylmuramidase;N-acetylmuramoyl-L-alanine amidase domain-containing protein SAOUHSC_02979	SAKOR_02645;SAOUHSC_02979	1,314E+09	3,686E+08
T1YD26	Nickel transport ATP-binding protein nikD;Nickel import ATP-binding protein NikD	SAKOR_02448;opp-1D	4,518E+07	4,086E+07
T1YDP5	Glycosyltransferase stabilizing protein Gtf2	gtf2	6,172E+07	4,007E+07
U5NVV0	Diamine N-acetyltransferase	speG	2,438E+08	2,251E+08
U5NZ28	Universal stress protein	AL493_01650	7,673E+09	3,832E+09
U5NZ39	Lipoprotein;Uncharacterized protein;PF07563 family protein	ydhK;CO98_2151	3,087E+10	1,048E+09
W8TQF1	Allergen V5/Tpx-1 like protein;SCP-like protein	AFO87_13590;HMPREF0776_2111;ERS179246_00546	9,228E+09	4,205E+08
W8TR17	AraC family regulatory protein;Transcriptional regulator, AraC family	melR_2;HMPREF077	1,758E+09	1,204E+09
W8TRE7	Glycine/betaine ABC transporter periplasmic protein;ABC transporter, quaternary amine uptake transporter family, substrate-bindin	opuCC_1;BN1321_170056	1,665E+10	2,818E+09
W8TRJ9	Iron-sulfur cluster carrier protein	apbC;SAZ172_2267	9,300E+09	3,812E+09
W8TRM3	Putative thiol-disulfide oxidoreductase%2C DCC family;Uncharacterized protein	AFO87_07670;SAKOR_02108	1,054E+09	3,091E+08
W8TRQ9	Amino acid permease;Putative amino acid permease;MW0539 protein	lysP_1;BN1326_50067;MW0539	1,754E+09	5,256E+07
W8TSS5	Cytosolic protein containing multiple CBS domains;CBS domain containing protein;Uncharacterized protein	ytoI;ST398NM01_1758	2,298E+08	1,650E+08
W8TSU2	DnaI;Primosomal protein;Primosomal protein DnaI	dnaI;HMPREF0776_2717	2,131E+09	2,028E+09
W8TSW2	Bifunctional folylpolyglutamate synthase/dihydrofolate synthase;Folylpolyglutamate synthase;Bifunctional protein FolC	folC;QU38_08645	6,289E+08	2,618E+08
W8TTH4	TetR family regulatory protein;Transcriptional regulator, TetR family;Uncharacterized protein	AFO87_06025;BN1321_420056;NWMN_2452	2,989E+08	2,646E+08
W8TTZ1	Glycerol uptake operon antiterminator regulatory protein;Glycerol uptake operon antiterminator	glpP	2,885E+08	8,721E+07
W8TUK8	DNA starvation/stationary phase protection protein;General stress protein	dps;ACH32_04035	7,223E+09	1,689E+09
W8TV14	ABC-2 transporter family protein;Uncharacterized protein	AFO87_13195;ST398NM01_2051;ERS179246_01903	8,457E+09	3,526E+08
W8TVJ6	Multimodular transpeptidase-transglycosylase;Membrane carboxypeptidase;Transglycosylase domain protein	sgtA;mrcB	1,172E+09	1,603E+08
W8TVM3	Alkaline phosphatase synthesis transcriptional regulatory protein;PhoP;PhoP family transcriptional regulator	phoP;ST398NM01_1747	2,726E+09	2,720E+09
W8TW18	Acetyl-CoA carboxylase biotin carboxylase subunit;Biotin carboxylase of acetyl-CoA carboxylase	cfiB_2;accC	2,023E+09	1,015E+09
W8TWI0	Amino acid carrier protein;Sodium:alanine symporter	alsT;QU38_13155	1,537E+10	3,121E+08
W8TWY8	Bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	coaBC;SAKOR_01138	1,762E+09	9,194E+08
W8TZX4	GTP-binding protein TypA;GTP-binding protein TypA/BipA	typA;QU38_05800;ST398NM01_1106	7,794E+09	6,052E+09
W8U0W4	Lipoprotein;Uncharacterized protein	AFO87_04860;HMPREF0776_1750;QU38_10750	2,142E+09	3,755E+08
W8U1K0	Membrane spanning protein;Uncharacterized protein;YibE/F-like protein	AL077_09845;BN1321_100034;AFO87_01830	3,446E+09	2,203E+08
W8U224	Uncharacterised protein;Uncharacterized protein	AL493_02735;BN1326_30130;OO23_0212065	3,798E+08	2,699E+08
W8U2B2	N-acetylmuramic acid 6-phosphate etherase	murQ	2,947E+08	1,607E+08
W8U2Z7	NAD dependent epimerase/dehydratase family protein;NmrA family protein	azoB;HMPREF0776_0637	6,042E+08	3,143E+08
W8U368	GTP pyrophosphokinase;RelA/SpoT domain protein	ywaC;HMPREF0776_0565	2,602E+09	1,162E+09
W8U3T6	Inosine-uridine preferring nucleoside hydrolase	rihB;BN1321_380119	1,938E+08	9,051E+07
W8U3Y4	Energy-coupling factor transporter transmembrane protein EcfT	ecfT	3,093E+08	1,017E+08
W8U414	Cobalamin Fe3+-siderophores ABC transporter periplasmic protein;Iron(III) dicitrate-binding protein	yhfQ_1;SAKOR_02144	4,000E+10	3,922E+09
W8U458	Transcription termination factor Rho	rho	3,304E+09	1,395E+09
W8U4T8	Membrane spanning protein;Uncharacterized protein	AFO87_08830;ERS195423_02627;RU53_2001	1,290E+09	2,298E+08
W8U570	Bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase	aroA_2;aroX	1,181E+10	4,825E+09
W8U5G4	Acetyltransferase;Lactococcal prophage ps3 protein 05	AFO87_10655;QU38_11085;ERS179246_00099	3,265E+08	2,319E+08
W8U5S1	Cobalamin Fe3+-siderophores ABC transporter periplasmic protein;Periplasmic binding protein	yclQ;HMPREF0776_1746	7,661E+09	2,864E+08
W8U5T5	ATP-dependent DNA helicase RecQ;Putative ATP-dependent DNA helicase RecQ	recQ_1;QU38_10650;recQ	5,795E+08	1,544E+08
W8U6M5	Lipoprotein;Uncharacterized protein;Putative lipoprotein	AL078_05920;HMPREF0776_2212;ERS179246_01166	8,713E+09	4,197E+08
W8U6S6	Succinate dehydrogenase;Succinate dehydrogenase (Cytochrome b558 subunit)	sdhC	2,545E+09	7,615E+08
W8U7R7	ABC transporter ATP-binding protein;Bacteriocin ABC transporter ATP-binding protein	lolD_2;lolD_3;QU38	2,691E+08	1,884E+08
W8U818	Gluconate permease;Transporter, gluconate:H+ symporter family	gntP;CH51_13400	3,967E+08	2,526E+08
W8U876	Bicyclomycin resistance protein TcaB;Drug resistance transporter, Bcr/CflA subfamily	tcaB;HMPREF0769_10711	1,077E+09	2,219E+08
W8U8D2	Exported protein;Putative exported protein;Uncharacterized protein	AFO87_00505;BN1326_140180;BN1321_400032	3,543E+10	3,611E+09
W8U8F4	CorA-like Mg2+ transporter protein;Magnesium transporter CorA	corA_2;QU38_07630;BN1326_140175	2,207E+08	9,396E+07
W8U8Y3	Membrane protein;Small integral membrane protein	AFO87_08140;QU38_03710;AL077_04070	4,996E+10	1,397E+09
W8U9K9	CobB/CobQ-like glutamine amidotransferase domain-containing protein;Adenosylcobyric acid synthase;Uncharacterized protein	AFO87_14825;RU53_2023	4,982E+08	2,455E+08
W8UA21	Serine protease;Putative protease	degP;QU38_08290;BN1326_80259	1,061E+11	2,815E+10
W8UB09	Gamma-aminobutyrate permease;Amino acid permease	lysP_3;CH51_07000;HMPREF0776_2348	9,035E+09	4,049E+08
W8UB14	Homoserine dehydrogenase;Homoserine	hom;dhoM;ST398NM01_1330	2,158E+09	1,324E+09
W8USJ1	Gluconeogenesis factor	AFO87_13450;mgfK;QU38_10895	1,598E+09	5,604E+08
W8UT87	Acetyltransferase;Acetyltransferase, GNAT family	AFO87_01785;HMPREF0769_10006;QU38_03505	1,064E+08	7,570E+07
W8UVH2	Amino acid permease;MW2237 protein	yifK;MW2237;HMPREF0776_0367	3,629E+09	5,536E+07
W8UVI1	Autolysin;Peptidoglycan endo-beta-N-acetylglucosaminidase	atl_1;ST398NM01_2357;QU38_05315	2,591E+08	1,809E+08
W8UVT5	Siderophore biosynthesis protein;Uncharacterized protein;Siderophore biosynthesis protein, lucA/lucC family	iucA;MW2105;H	9,843E+08	3,030E+08
W8UW64	Abortive infection protein;CAAX amino terminal protease family;CAAX protease	AFO87_12330;ST398NM01_2068;QU38_06765	4,683E+09	4,441E+08
W8UXA3	Acetyl-CoA carboxylase biotin carboxylase subunit;Uncharacterized protein;MW1556 protein	accC;SAKOR_01553;MW1556	1,936E+09	6,394E+08
W8UYI1	5-nucleotidase;Putative HAD-hydrolase YfnB;Uncharacterized protein	yfnB;QU38_12210	2,484E+08	1,027E+08
X5DRT5	GntR family transcriptional regulator;Transcriptional regulator;UbiC transcription regulator-associated domain protein	phnF;QU38_12745	9,469E+08	4,880E+08
X5DU21	DNA polymerase III delta prime subunit;DNA polymerase III subunit delta;Probable DNA polymerase III, delta prime subunit	holB	3,999E+08	2,073E+08
X5DUZ9	Carboxylesterase	est_1;QU38_03400;est_2	8,695E+08	3,412E+08
X5DVD1	Iron ABC transporter substrate-binding protein;ABC transporter, solute-binding protein	AFO87_08705;HMPREF0776_0951	1,302E+09	2,410E+08
X5DW62	Methyltransferase;Caffeoyl-CoA O-methyltransferase	AFO87_11015;QU38_08860;RU53_1711	1,828E+08	9,088E+07
X5DXD1	HAD family hydrolase;HAD hydrolase, family IA, variant 1	ppaX;HMPREF0769_11778;QU38_09790	7,822E+08	7,090E+08
X5DXF1	ABC transporter ATP-binding protein;ABC transporter, ATP-binding protein	ybhF_1;HMPREF0776_1008	9,714E+08	8,294E+08
X5DXF6	UvrABC system protein B	uvrB_2;uvrB	5,845E+09	2,669E+09
X5DXL6	Flavin reductase domain-containing protein FMN-binding;FAD-dependent oxidoreductase;Uncharacterized protein	AFO87_04130;SAKOR_02661	3,000E+08	8,821E+07
X5DYK0	Membrane protein;Rhomboid family protein;Putative membrane peptidase%2C contains TPR repeat domain	gluP;BN1321_260187	3,512E+09	1,176E+09
X5DZQ4	Cysteine ABC transporter ATP-binding protein;Transport ATP-binding protein cydC;SA0640 protein	cydC;SAKOR_00682;SA0640	1,234E+09	5,751E+08
X5E0C0	Lipoprotein	metQ_2;HMPREF0776_1830;QU38_11155	4,966E+10	1,179E+09
X5E0Z1	Lantibiotic ABC transporter ATP-binding protein;MW2433 protein;ABC transporter, ATP-binding protein	ecsA_2;MW2433	1,385E+10	1,116E+10
X5E203	ABC transporter%2C periplasmic spermidine putrescine-binding protein potD;ABC transporter, solute-binding protein;PotD protein	potD;HMPREF0776_2095	3,158E+09	2,021E+07
X5E2G5	Sodium:dicarboxylate symporter;Sodium:dicarboxylate symporter family protein;MW0359 protein	tcyP;MW0359	2,956E+10	1,411E+09
X5E353	Glutaryl-CoA dehydrogenase;Acyl-CoA dehydrogenase, N-terminal domain protein;Acyl-CoA dehydrogenase FadD homolog	AFO87_07470;BN1321_60039	1,102E+09	3,882E+08
X5E3A4	M24B family Xaa-Pro dipeptidase;Met-Xaa and Xaa-Pro aminopeptidase;Xaa-Pro dipeptidase;Xaa-Pro dipeptidase OS	AFO87_09715;yqhT;ERS093009_01324	1,555E+09	1,502E+09
X5E3G6	Alcohol dehydrogenase;Quinone oxidoreductase, YhdH/YhfP family;Putative zinc-binding dehydrogenase	yhfP;HMPREF0776_0424	1,646E+09	5,291E+08
X5E405	Deoxyguanosinetriphosphate triphosphohydrolase;DNTP triphosphohydrolase, putative;Putative metal-dependent phosphohydrolas	AFO87_11365;SAZ172_0617	2,268E+09	1,255E+09
X5E4F8	Cysteine desulfurase;Cysteine desulfurase involved in tRNA thiolation;Cysteine desulfurase, NifS	iscS_1;iscSA;nifS	2,279E+08	1,032E+08
X5E4M7	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase;Hydroxymethylpyrimidine/phosphomethylpyrimidine	thiD	3,844E+08	1,148E+08
X5E5Y5	Dihydroorotate dehydrogenase (quinone)	pyrD	2,851E+09	4,910E+08
X5EEX2	Conserved protein YbcLA;Uncharacterized protein;Putative cytosolic protein	ybcI;QU38_03385	2,700E+08	2,521E+08
X5EEY9	Integral membrane protein;Uncharacterized protein	AFO87_09795;BN1321_260151;ACH32_00410	3,956E+08	2,890E+07
X5EG65	Protein of uncharacterised function (DUF2529);Uncharacterized protein	AFO87_13840;BN1321_340065;RU53_	1,183E+09	3,255E+08
X5EGU1	FMN reductase;NADPH-dependent FMN reductase family protein;SA0328 protein	ssuE;BN1321_80059;SA0328	6,186E+07	2,806E+07
X5EHG2	Cytokinin riboside 5-monophosphate phosphoribohydrolase	yvdD	6,821E+08	4,815E+08
X5EHQ5	Uncharacterised protein;Uncharacterized protein	AFO87_10500;HMPREF0776_2339;QU38_12985	3,912E+10	7,222E+09
X5EIN0	Acetyltransferase;GNAT family acetyltransferase;Acetyltransferase (GNAT) family protein	AFO87_01190;QU38_05050;ERS179246_00699	2,805E+08	1,470E+08
X5EIP1	HAD superfamily hydrolase;Uncharacterized protein	yqeG;SA1426;QU38_08945	1,242E+09	1,770E+08
X5EIQ4	Dihydroxyacetone kinase;Dihydroxyacetone kinase, L subunit	dhaL;QU38_10275	1,442E+08	1,185E+08
X5EIX3	PTS glucose transporter subunit IIB;PTS system maltose/glucose-specific IICB component;SA0233 protein	ptsG_2;RU53_218	1,012E+09	4,611E+07
X5EIY4	Inosine-uridine preferring nucleoside hydrolase;Pyrimidine-specific ribonucleoside hydrolase RihA;Inosine/uridine-preferring nucleo	rihA	9,746E+07	7,198E+07
X5EJB2	DNA polymerase III delta subunit;DNA polymerase III, delta subunit;DNA polymerase III subunit delta	holA;BN1321_260225;CH51_08610	3,943E+08	3,316E+08
X5EJN4	Amino acid ABC transporter substrate-binding protein;SA2202 protein	AFO87_00345;SA2202	1,545E+11	3,595E+09
X5EKK9	Proline dehydrogenase;SA1585 protein	fadM;QU38_04695;SA1585	1,815E+10	8,774E+09
X5EKR3	Lipoate--protein ligase;Lipoate--protein ligase 1;Lipoate--protein l	lplJ_2;SAV1028	3,433E+09	2,597E+09
X5ELX0	2-oxoisovalerate dehydrogenase;2-oxoisovalerate dehydrogenase beta subunit;Branched-chain alpha-keto acid dehydrogenase E1 s	bfmBAB;ST398NM01_1582	1,207E+09	5,272E+08
X5EMG1	Ferredoxin-dependent glutamate synthase;Glutamate synthase-ferredoxin large subunit;MW2383 protein	gltB_2;gltB2;	3,186E+09	1,943E+09
X5EMJ0	Molybdenum ABC transporter ATP-binding protein;Molybdenum transport ATP-binding protein ModC	modC;ACH32_04755	2,545E+08	1,023E+08
X5EML3	TetR family regulatory protein of MDR cluster;SA2144 protein;TetR family transcriptional regulator	AFO87_00665;SA2144;ACH32_	1,111E+08	4,557E+07
X5EN63	Peptidase U32;Peptidase U32 family protein	yhbU_2;QU38_08865;RU53_1710	1,636E+08	8,700E+07

Population IV. DRM only

Uniprot-ID	Protein Name	Gene Name	LFQ Intensity DRM	LFQ Intensity
A0A033UAK4	Copper-translocating P-type ATPase;Copper-exporting ATPase	V070_02647;HMPREF0769_11632	5,619E+08	1,000E+00
A0A033UHR6	DNA-directed RNA polymerase subunit beta	rpoC	5,790E+08	1,000E+00
A0A033UJ34	Copper-exporting P-type ATPase A	V070_02321	3,246E+08	1,000E+00
A0A033UK35	Pyridoxal 5-phosphate synthase subunit PdxS	pdxS	3,269E+08	1,000E+00

A0A033UNE9	Uncharacterized protein	V070_01857	3,654E+07	1,000E+00
A0A033UV54	Uncharacterized protein	V070_01283	4,537E+07	1,000E+00
A0A033UVX6	Tryptophan--tRNA ligase;Tryptophanyl-tRNA synthetase (Fragment)	trpS;V070_01096	5,102E+07	1,000E+00
A0A033V3I1	GTPase Der	der	7,054E+08	1,000E+00
A0A069FUU8	Phosphoribosylformylglycinamidine synthase subunit PurL	purL	3,318E+07	1,000E+00
A0A069FZR1	Cobalt transport protein	CO98_1968	1,339E+08	1,000E+00
A0A069G4D8	AntA/AntB antirepressor	CO98_0206	1,785E+07	1,000E+00
A0A069G4W6	Preprotein translocase, YajC subunit	CO98_1375	5,367E+08	1,000E+00
A0A069GC35	Succinate dehydrogenase flavoprotein subunit	sdhA	4,463E+09	1,000E+00
A0A069GEF2	PF06103 family protein	CO98_1067	2,514E+08	1,000E+00
A0A077UBG8	General stress protein-like protein	ytxG	1,615E+08	1,000E+00
A0A077UG21	Component of the preprotein translocase	yajC	3,075E+09	1,000E+00
A0A0B6XKR3	UDP-D-quinovosamine 4-dehydrogenase;Capsular polysaccharide biosynthesis protein Cap5D, putative	capD_1;ERS092844_01182	9,129E+07	1,000E+00
A0A0B6XLP0	Azaleucine resistance protein AzlC;AzlC family protein;Uncharacterized protein	ygaZ;BN1321_430100;NWMN_0009	2,319E+08	1,000E+00
A0A0D1FYV9	Glycerol-3-phosphate cytidylyltransferase	tagD	1,444E+08	1,000E+00
A0A0D1GCF8	Beta-lactamase domain-containing protein;Metallo-beta-lactamase;Hydroxyacylglutathione hydrolase	ACR58_00915;BN1321_260183;ERS179246_01030	5,690E+07	1,000E+00
A0A0D1H6D2	Transport permease protein	tagG;AL077_08370;HMPREF0776_1	3,114E+09	1,000E+00
A0A0D1HE99	Putative rRNA methylase;SAM-dependent methyltransferase%2C MraW methylase family;Putative RNA methylase	ACR58_09085;ERS179246_01518;ytqB	7,843E+07	1,000E+00
A0A0D1I100	Guanine permease;Uncharacterized protein;Hypoxanthine/guanine permease	pbuG;SAOUHSC_02516	1,674E+09	1,000E+00
A0A0D1I4H7	Putative ribitol-5-phosphate dehydrogenase;SA0242 protein	OO23_0205575;tarJ;SA024	1,400E+08	1,000E+00
A0A0D1IFH5	Peptidase family U32;MW1562 protein;Peptidase, U32 family	ACH32_00905;MW1562;SACOL1667	1,679E+08	1,000E+00
A0A0D1J6Y7	Glucarate transporter;Putative transporter protein;MFS family major facilitator transporter, glucarate:cation symporter	ACH32_05960;BN1326_150015	6,968E+07	1,000E+00
A0A0D1JI26	Uncharacterized protein	ACR58_03075;SAOUHSC_01123;BN1326_60280	1,995E+08	1,000E+00
A0A0D1JL38	Lipoprotein;Putative cytosolic protein;Uncharacterized protein	QU38_09485;ST398NM01_1487;BN1326_70047	3,190E+07	1,000E+00
A0A0D1JR08	Membrane protein;Tellurite resistance protein terC;TerC	ACH32_11950;SAKOR_00939;ST398NM01_1017	9,708E+08	1,000E+00
A0A0D1JWB0	Uncharacterized protein	QU38_16700	6,489E+07	1,000E+00
A0A0D1K059	Phage infection protein;ABC-2 transporter family protein;ABC-2 family transporter protein	QU38_07620;BN1321_400025	8,824E+08	1,000E+00
A0A0D1K2Q2	Cytosolic protein containing cobalamin binding site	ACH32_02625	1,029E+08	1,000E+00
A0A0D1K4U9	Uncharacterized protein	ACH32_10575;BN1326_50155	8,002E+07	1,000E+00
A0A0D3Q479	ABC transporter permease;Uncharacterized protein;Putative membrane protein	AFO87_05020;BN1321_80069;BN1326_30218	1,274E+08	1,000E+00
A0A0D3Q4R0	Deacetylase SIR2;SIR2 family protein	AFO87_05140;ERS179246_01076;ST398NM01_0406	5,953E+07	1,000E+00
A0A0D3Q617	Uncharacterised protein;Uncharacterized protein	AFO87_04680;MW0918;HMPREF0769_12748	1,650E+08	1,000E+00
A0A0D3QA44	Conserved domain protein%2C putative;Uncharacterized protein	AFO87_12755;CH51_11955;NWMN_2113	2,791E+08	1,000E+00
A0A0D3QBB6	Na+/H+ antiporter NhaC;Putative Na+/H+ antiporter;Sodium:proton antiporter OS	nhaC	1,090E+08	1,000E+00
A0A0D6G261	Glycosyltransferase;MW0666 protein;SA0659 protein;Glycosyltransferase, group 2 family protein OS	yfdH;MW0666;SA0659	3,354E+08	1,000E+00
A0A0D6GGT6	ATP synthase subunit c	ktrB_1;QU38_11725;ktrD	3,688E+08	1,000E+00
A0A0D6GHQ4	Membrane protein;Uncharacterized protein;Membrane protein, putative	AFO87_07485;NWMN_0172;SAOUHSC_00200	1,917E+09	1,000E+00
A0A0D6GJI1	Capsular polysaccharide synthesis enzyme Cap8N;UDP-N-acetyl-D-quinovosamine 4-epimerase;Cap8N	capN;SAKOR_00142;cap8N	1,350E+08	1,000E+00
A0A0D6H0U4	3-hydroxyacyl-CoA dehydrogenase;Uncharacterized protein	AFO87_00695;SA2138;ACH32_05125	5,215E+07	1,000E+00
A0A0D6HBS7	Aliphatic amidase amiE;Hydrolase, carbon-nitrogen family;Beta-ureidopropionase	amiE;HMPREF0769_11128;ST398NM01_207	7,023E+07	1,000E+00
A0A0D6HVU1	Phosphoribosylamine--glycine ligase	purD	4,156E+07	1,000E+00
A0A0D6HZA6	Carboxylesterase;MW0741 protein	est_2;SAKOR_00783;est	1,833E+08	1,000E+00
A0A0E0VL70	SgaT;PTS system, L-ascorbate specific IIC component ulaA;Putative membrane protein	ST398NM01_0410;SAKOR_00324;BN13	1,437E+08	1,000E+00
A0A0E0VN96	Antibacterial protein 3	ST398NM01_1170;psm	1,973E+09	1,000E+00
A0A0E0VQS2	Multidrug resistance protein;Multidrug MFS transporter;Transporter, major facilitator family protein	ST398NM01_1812;yttB	9,749E+07	1,000E+00
A0A0E0VTN7	Anaerobic ribonucleoside-triphosphate reductase;Anaerobic ribonucleosid	ST398NM01_2664;ACH32_06515	3,993E+07	1,000E+00
A0A0E1AG73	Putative hydrolase;Uncharacterized protein;Hydrolase	SAZ172_1387;MW1265;ERS179246_01232	1,815E+08	1,000E+00
A0A0E1AGR6	Uncharacterized protein;ABC transporter permease protein;Binding-protein-dependent transport system inner membrane protein	SAZ172_0183;ssuC	1,669E+09	1,000E+00
A0A0E1AJI7	Oligopeptide transporter putative membrane permease domain protein;NikC;Peptide ABC transporter permease	opp-1C;ST398NM01_2515	1,528E+08	1,000E+00
A0A0E1AJK2	Uncharacterized protein;Uncharacterized protein SAOUHSC_02783;Tandem lipoprotein	SAZ172_2583;SAOUHSC_02783	1,694E+08	1,000E+00
A0A0E1AKC0	Uncharacterized protein;YlmH protein;RNA binding protein	SAZ172_1193;ylmH;ERS179246_02049	7,011E+07	1,000E+00
A0A0E1AKG7	Release factor glutamine methyltransferase	prmC	5,811E+07	1,000E+00
A0A0E1AKM3	Heme ABC type transporter HtsABC, permease protein HtsC;Cobalamin Fe3+-siderophores ABC transporter permease	SAZ172_2276;fecD	9,374E+07	1,000E+00
A0A0E1AM31	Glycosyltransferase Gtf1;Glycosyltrans	gtf1;gftA	4,669E+07	1,000E+00
A0A0E1APM1	Fibronectin binding protein FnbA;Fibronectin-binding protein A	fnbA	9,698E+07	1,000E+00
A0A0E1VHB5	3-dehydroquinate synthase	aroB	3,188E+08	1,000E+00
A0A0E1VJC0	Oxidoreductase, short chain dehydrogenase/reductase family protein;Short chain dehydrogenase	HMPREF0776_2527;SAZ172_1515	1,745E+08	1,000E+00
A0A0E1VMF5	Uncharacterized protein;ATP-grasp domain protein	HMPREF0776_1412;AFO87_12885;HMPRE	4,133E+07	1,000E+00
A0A0E1VQD3	Uncharacterized protein;Integral membrane protein	HMPREF0776_0412;AFO87_00635;BN1321_400004	1,558E+09	1,000E+00
A0A0E1XC35	Molybdenum cofactor biosynthesis protein A;Cyclic pyranopterin monophosphate synthase	moaA	2,984E+07	1,000E+00
A0A0E7DYF4	Staphylococcus aureus paralogous family;Uncharacterized protein	AFO87_11285;SAOUHSC_00585;MW0552	1,622E+09	1,000E+00
A0A0E7Y8C1	ACT domain protein;Prephenate dehydratase;Prephenate dehydratase	pheA;BN1321_320008;HMPREF0769_11255	8,776E+07	1,000E+00
A0A0E8G8W5	Enterotoxin I;Staphylococcal enterotoxin Q;Staphylococcal enterotoxin type I	entQ;CH51_04275;seq	1,114E+08	1,000E+00
A0A0E8GAK5	Ferrichrome transport system permease protein fhuG	fhuG	2,137E+08	1,000E+00
A0A0E8GLL3	Uncharacterised protein	ERS092844_00944	6,570E+07	1,000E+00
A0A0E8H1H6	Lipoate--protein ligase	lplJ_1;HMPREF0776_1072	4,112E+07	1,000E+00
A0A0E8HMR4	Molybdenum cofactor biosynthesis protein B	moaB	7,437E+07	1,000E+00
A0A0G2LRX1	Histidine kinase;Two-component sensor histidine kinase	CH51_06940;desK	3,508E+08	1,000E+00
A0A0H2AM14	Uncharacterised protein;Uncharacterized protein	AFO87_05335;NWMN_0227;MW0267	1,937E+08	1,000E+00
A0A0H2DL58	Uncharacterised protein	AL493_15205	3,009E+08	1,000E+00
A0A0H2F9P7	Membrane protein;Uncharacterized protein	AFO87_06755;SAZ172_2710;QU38_16180	5,030E+08	1,000E+00
A0A0H2WXU5	Peptide ABC transporter, permease protein;Membrane protein	SACOL0185;gsiC;QU38_14790	7,319E+08	1,000E+00
A0A0H2XDV0	Uncharacterised protein;Putative cytosolic protein	SAUSA300_0294;AFO87_05300;HMPREF0	5,745E+07	1,000E+00
A0A0H2XFJ7	Transporter gate domain protein;Membrane protein;Putative membrane spanning protein	SAUSA300_2133;AFO87_12560;SAKOR_02	5,624E+08	1,000E+00
A0A0H2XGP6	PTS system, mannitol specific IIA component;Mannitol-specific phosphotransferase enzyme IIA component	mtlA;mtlF	1,379E+08	1,000E+00
A0A0H2XH23	Putative lipoprotein;Lipoprotein;Uncharacterized protein	SAUSA300_2355;AFO87_00365;SAOUHSC_02695	3,898E+08	1,000E+00
A0A0H2XI08	Alcohol dehydrogenase, zinc-containing;Alcohol dehydrogenase	SAUSA300_0055;flhA	2,612E+08	1,000E+00
A0A0H3JL25	Uncharacterized protein;Branched-chain amino acid transport protein	SA0609;HMPREF0776_1657	2,997E+09	1,000E+00
A0A0H3JL37	SA0628 protein;Sugar efflux transpoter;Sugar efflux transporter	SA0628;SAZ172_0685;ST398NM01_0751	2,402E+08	1,000E+00
A0A0H3JLG2	Uncharacterized protein;Uncharacterised protein	SA0377;ST398NM01_0484;AFO87_08885	1,915E+08	1,000E+00
A0A0H3JPF1	Uncharacterized protein;Membrane protein;Putative membrane protein	SA2483;AFO87_13965;BN1321_430068	1,357E+09	1,000E+00
A0A0H3JPI5	SA0871 protein;Uncharacterized protein;Sodium/proton-dependent alanine transporter	SA0871;SAOUHSC_00949;yrbD	1,038E+08	1,000E+00
A0A0H3JPP1	NPQTN specific sortase B;Sortase, SrtB family	srtB	1,060E+08	1,000E+00
A0A0H3JQ67	Glycerol-3-phosphate transporter;Glycerol-3-phosphate ABC transporter	glpT	1,760E+09	1,000E+00
A0A0H3JTB1	Uncharacterized protein;Transporter, DASS family;DASS family divalent anion:sodium (Na+) symporter	SA0645;HMPREF0776_1694	2,705E+08	1,000E+00
A0A0H3JUT0	Uncharacterized protein;Uncharacterized conserved protein	MW0277;ERS195423_01553;AFO87_05280	4,744E+07	1,000E+00
A0A0H3JV25	Uncharacterized protein;Membrane protein	MW0420;ACH32_09500;SA0424	1,544E+08	1,000E+00
A0A0H3JV73	Octanoyl-[GcvH]:protein N-octanoyltransferase;Octanoyl-[GcvH]:protein N-octanoyltransferase	lipL	1,008E+08	1,000E+00
A0A0H3JVB3	MW0257 protein;SA0270 protein;Staphyloxanthin biosynthesis protein	MW0257;SA0270;QU38_14380	6,810E+07	1,000E+00
A0A0H3JYD3	Uncharacterized protein;Fructosamine kinase;Ribulosamine/erythrulosamine 3-kinase potentially involved in protein deglycation	MW2508;AFO87_06765	1,329E+08	1,000E+00
A0A0H3JYJ9	MW2093 protein;Multidrug MFS transporter;Multidrug resistance protein B	MW2093;emrB_1;emrB_3	5,309E+07	1,000E+00
A0A0H3JYW6	Uncharacterized protein;Acetyltransferase;GNAT family acetyltransferase	MW2324;ytmI	4,319E+07	1,000E+00
A0A0H3JZ35	MW2432 protein;SA2301 protein;Alkaline phosphatase	MW2432;SA2301;ACH32_05965	5,307E+08	1,000E+00
A0A0H3JZ54	Uncharacterized protein	MW2455;SAZ172_2631;SAOUHSC_02	4,461E+08	1,000E+00
A0A0H3JZ55	Uncharacterized protein;3-beta hydroxysteroid dehydrogenase	MW0620;AFO87_03105;RU53_720	5,592E+08	1,000E+00
A0A0H3K0K9	Riboflavin biosynthesis protein RibD	ribD;CH51_09495	1,325E+08	1,000E+00
A0A0H3K193	Uncharacterized protein;Transporter, major facilitator family protein;Multidrug MFS transporter	MW2184;HMPREF0776_0313	1,932E+08	1,000E+00
A0A0H3K1Q0	MW0188 protein;M23/M37 peptidase domain protein;Peptidase M23;Peptidase family M23 O	MW0188;SAZ172_0212;lytM_2	2,222E+08	1,000E+00
A0A0H3K4A6	MW2266 protein;Sodium/glutamate symporter;Sodium:glutamate symporter	MW2266;gltS;ACH32_05110	1,032E+09	1,000E+00
A0A0H3K7E4	Ferrichrome transport permease fhuB;Ferrichrome ABC transporter (Permease);Iron (Fe3+) ABC superfamily ATP binding cassette tr	fhuB;feuB	9,241E+07	1,000E+00
A0A0H3K8M8	Uncharacterized protein	NWMN_1353;MW1332;ACR58_00050	2,953E+08	1,000E+00
A0A0H3K9T0	ABC transporter, ATP-binding protein;ABC transporter ATP-binding protein;ABC superfamily ATP binding cassette transporter, ABC p	NWMN_2055;metN_2	4,953E+07	1,000E+00
A0A0H3KDG3	Capsular polysaccharide biosynthesis protein CapP;UDP-N-acetylglucosamine 2-epimerase	capP;HMPREF0776_0900	1,025E+08	1,000E+00
A0A0K6ZPG0	Zn-dependent hydrolase (Beta-lactamase superfamily);Metallohydrolase;Uncharacterized protein	ERS365775_01675;AFO87_14245;ST398NM01_0	6,945E+07	1,000E+00
A0A0M1TWJ4	Uncharacterized protein	RU53_15;MW0013;SAZ172	1,352E+08	1,000E+00
A0A0M1TWM0	ABC-2 family transporter protein;Uncharacterized protein	RU53_256;MW0255;S	7,640E+08	1,000E+00
A0A0M1TXD5	Putative sodium/glucose cotransporter;MW0291 protein;SA0303 protein	RU53_289;MW0291;SA0303	1,378E+08	1,000E+00
A0A0M1TXN4	Sa tandem lipoprotein;Lipoprotein;Uncharacterized lipoprotein SAUSA300_0410	lpl1_1;lpl9_4;SAUSA300_0410	1,043E+08	1,000E+00
A0A0M1TY95	Uncharacterized protein	RU53_654;BN1326_50091;SAOUHSC_0059	7,827E+07	1,000E+00
A0A0M1TYL8	Uncharacterized protein;Membrane protein	RU53_738;AFO87_03010;ACH32_10700	4,178E+08	1,000E+00
A0A0M1TZ82	Anthranilate synthase;Aminobenzoate synthetase;Para-aminobenzoate synthetase component I	pabB	7,213E+07	1,000E+00
A0A0M1U1R9	Toxin regulatory protein;SA1676 protein;PTS system, IIC component	RU53_1960;SA1676;AL077_07310	1,782E+09	1,000E+00
A0A0M1U1V5	Uncharacterized protein;Uncharacterised protein	RU53_2022;CH51_10300;ERS179246_02390	4,670E+07	1,000E+00
A0A0M1U279	Iron compound ABC transporter permease;Cobalamin Fe3+-siderophores ABC transporter permease;Uncharacterized protein	RU53_2244;htsB	6,103E+08	1,000E+00
A0A0M1U338	ABC superfamily ATP binding cassette transporter, ABC/membrane protein;SA2216 protein	RU53_2490;SA2216	2,485E+08	1,000E+00
A0A0M1U353	MFS family major facilitator transporter;Integral membrane efflux protein;MW2368 protein	RU53_2508;NWMN_2343	1,846E+09	1,000E+00
A0A0S3DYH0	Uncharacterized protein	BN1321_170073;MW0701;HMPREF0769_11554	3,906E+07	1,000E+00
A0A0T7M2E8	Acetyltransferase;Putative acetyltransferase	ERS093009_00097;ACR58_11465;BN1326_50102	1,239E+08	1,000E+00

A0A0T7M7L5	Membrane protein;Uncharacterized protein;Putative membrane protein	ERS093009_01925;BN1321_80002;BN1326_30139	9,933E+07	1,000E+00
A0A0T7M7R2	Oligopeptide transport system permease protein;MW0183 protein;SA0200 protein	gsiD_2;MW0183;SA0200	2,824E+08	1,000E+00
A0A0T7M7U6	2-isopropylmalate synthase	leuA_2;leuA	6,163E+06	1,000E+00
A0A0T7M9H7	Putative deoxyribonuclease YcfH;Hydrolase, TatD family;DNase, TatD family	ycfH;HMPREF0776_1340;ACH32_09660	1,668E+08	1,000E+00
A0A0T7MUK5	ABC transporter permease;Uncharacterized protein;ABC-2 transporter family protein	ERS179246_01102;SAOUHSC_00334;ASU36_13395	1,333E+09	1,000E+00
A0A0T7MW40	Uncharacterised protein;Uncharacterized protein;Un	ERS179246_01728;SA0090;SAZ172_0111	9,070E+08	1,000E+00
A0A0T7MXQ6	Phage membrane protein;Uncharacterized protein	ERS179246_02309;CH51_10715;ERS365775_02601	2,114E+08	1,000E+00
A0A0T7MY12	Citrate transporter;CitMHS family citrate-magnesium (Mg2+):proton (H+) citrate-calcium (Ca2+):proton (H+) symporter;MW2538 prc	citN;citM	1,572E+09	1,000E+00
A0A0U0TXD8	Lipoprotein;Uncharacterized protein	ERS195423_01708;AFO87_04020;SAKOR_02684	1,655E+08	1,000E+00
A0A0U0U0N7	Membrane lipoprotein;Uncharacterized lipoprotein SAUSA300_0417;Lipoprotein	lpl9_4;SAUSA300_0417;lpl9_1	6,795E+08	1,000E+00
A0A0U0U2M9	Staphylococcal tandem lipoprotein;Uncharacterized lipoprotein SACOL0481;Uncharacterized lipoprotein SAUSA300_0414	lpl9_2;SACOL0481	1,001E+08	1,000E+00
A0A0U0USQ1	UDP-sugar hydrolase%3B 5-nucleotidase;Bifunctional 5-nucleotidase/2,3-cyclic phosphodiesterase;5-nucleotidase	yhcR;RU53_919;	8,268E+07	1,000E+00
A0A0U0V0S8	Acetyltransferase;N-acetyltransferase GCN5;Acetyltransferase, GNAT family	bltD;RU53_431;HMPREF0769_10016	6,265E+07	1,000E+00
A0A0U1MD67	Putative Oligopeptide transporter membrane permease;Oligopeptide transporter putative membrane permease domain protein	BN1326_140266;opp-1B	3,045E+07	1,000E+00
A0A0U1MDU5	N-acetylmuramoyl-L-alanine amidase domain-containing protein SAOUHSC_02979	BN1326_150163	7,616E+07	1,000E+00
A0A0U1MEU0	Transcriptional regulator (GntR family);GntR family transcriptional regulator;Gluconate operon transcriptional repressor	gntR;AUC48_12780;ydfH	1,603E+08	1,000E+00
A0A0U1MF79	Uncharacterized protein;Membrane protein	BN1321_150075;MW0597;ACR58_11625	2,853E+08	1,000E+00
A0A0U1MFQ7	ABC transporter permease protein;Uncharacterized protein	BN1326_150208;MW2602;SA2475	5,516E+07	1,000E+00
A0A0U1MG12	Putative PTS multidomain regulator;Transcription antiterminator, BglG family;Bacterial regulatory s, luxR family protein	BN1326_30200;SAKOR_00327	7,132E+06	1,000E+00
A0A0U1MGK2	PTS-dependent dihydroxyacetone kinase, phosphotransferase subunit dhaM;PTS mannnose transporter subunit IIA	dhaM;ACR58_11710	2,486E+08	1,000E+00
A0A0U1MHE1	ABC transporter, substrate-binding protein, family 5;Oligopeptide ABC transporter substrate-binding protein+	BN1321_200025;RU53_986	2,260E+08	1,000E+00
A0A0U1MHH0	Uncharacterized protein;Membrane protein	BN1321_200019;ERS092844_00420;ST398NM01_0981	5,047E+08	1,000E+00
A0A0U1MHR5	Acyltransferase family protein;Putative acetyltransferase;Uncharacterized protein	BN1321_220013;RU53_1047	2,471E+08	1,000E+00
A0A0U1MI94	Uncharacterized protein;Protein of hypothetical function DUF72	yunF;yecE;HMPREF0776_1910	1,229E+08	1,000E+00
A0A0U1MIL4	Putative membrane protein;Transporter, drug/metabolite exporter family protein;Triose-phosphate Transporter family protein	BN1326_50233;SAKOR_00729	3,676E+08	1,000E+00
A0A0U1MJW8	Putative cytochrome bd menaquinol oxidase subunit I;Cytochrome d ubiquinol oxidase subunit I;Cytochrome ubiquinol oxidase	ythA;cydA	4,929E+08	1,000E+00
A0A0U1MKY3	KR domain protein;Putative 3-oxoacyl-acyl carrier protein reductase;Acetoacetyl-CoA reductase	BN1321_240128;RU53_1279	7,824E+07	1,000E+00
A0A0U1ML00	Serine/threonine exchanger SteT;Amino acid permease;Serine/threonine	steT;SACOL1476;ACR58_00015	1,341E+08	1,000E+00
A0A0U1ML69	DNA polymerase III PolC-type	polC	1,048E+08	1,000E+00
A0A0U1MLF1	Segregation and condensation protein A	scpA	7,561E+07	1,000E+00
A0A0U1MLK1	Thermonuclease;Micrococcal nuclease;Nuclease-like protein	nucl;nuc;HMPREF0769_12423	1,605E+09	1,000E+00
A0A0U1MLS4	Putative ABC transport system permease protein;Spermidine/putrescine ABC transporter, permease	BN1326_60216;BN1321_230022	1,027E+09	1,000E+00
A0A0U1MM79	Putative membrane protein	BN1326_110014	9,082E+07	1,000E+00
A0A0U1MQ49	Glycine betaine transporter;Choline transport protein BetT;MW2111 protein	opuD;betT;MW2111	1,936E+09	1,000E+00
A0A0U1MRA3	Putative permease of an ABC transporter;ABC superfamily ATP binding cassette transporter, membrane protein;Conserved hypotehtybbM;RU53_2517		2,097E+08	1,000E+00
A0A0U1MRL7	Molybdopterin biosynthesis adenylyltransferase;Molybdopterin biosynthesis MoeB protein;Thiamine/molybdopterin biosynthesis TH	moeB;moeB_2	1,185E+08	1,000E+00
A0A0U1MRN8	Potassium/proton-divalent cation antiporter;Cation diffusion facilitator family transporter;Cation transporter	czcD;czrB	1,114E+08	1,000E+00
A0A0U1MSJ3	Aminoacyltransferase FemA;FemAB family peptidoglycan biosynthesis protein;FmhA protein	femA;fmhA	2,500E+07	1,000E+00
A0A0U1MSP2	Glycine betaine/carnitine/choline/choline sulfate ABC transporter (Permease);ABC transporter, permease protein;Glycine/betaine A	opuCB;HMPREF0769_10698	6,860E+08	1,000E+00
A0A0U1MSP9	Staphylococcal secretory antigen ssaA2	ssaA;ssaA2	1,849E+09	1,000E+00
A0A0U1MTV5	2-dehydropantoate 2-reductase	BN1321_420101;MW2519;SA2393	1,840E+08	1,000E+00
A0A0U1MU98	HTH-type transcriptional regulator NorG;Bacterial regulatory s%2C gntR family protein;Uncharacterized protein	norG;SAKOR_00082	3,403E+07	1,000E+00
A0A0U1MUD9	Uncharacterized protein;Adenine nucleotide alpha hydrolases superfamily protein	BN1321_420094;AFO87_06750;BN1326_150097	8,880E+07	1,000E+00
A0A0U1MUE8	Proton/sodium-glutamate symport protein;Proton/sodium-glutamate symporter;Glutamate-aspartate carrier protein	gltT;NWMN_2284	4,445E+09	1,000E+00
A0A0U1MUG2	Amino acid permease family protein;Amino acid permease	BN1321_420104;BN1326_150108;HMPREF0769_10549	1,553E+08	1,000E+00
A0A0U1MUH8	Arabinogalactan oligomer permease;Maltose/maltodextrin ABC transporter%2C permease protein MalF	ganP;malF	1,012E+08	1,000E+00
A0A0U1MVW6	Putative membrane protein;Low temperature requirement protein A	BN1326_30221;CH51_01695;AFO87_05005	1,014E+08	1,000E+00
A0A0U1MXG7	Methionine ABC transporter, permease component;ABC transporter permease protein;Uncharacterized protein	metP;metI;SA0770	1,075E+09	1,000E+00
A0A0U1MXU3	UDP-N-acetylglucosamine:undecaprenyl-P N-acetylglucosaminyl-1-P transferase;Undecaprenyl-phosphate N-acetylglucosaminyl 1-p	tagO;llm	5,256E+08	1,000E+00
A0A0U1MY64	ABC-2 transporter family protein;Uncharacterized protein	BN1321_70020;MW0254;SA0267	5,954E+08	1,000E+00
A0A0U1N0H6	Putative lantibiotic ABC transporter protein;Lantibiotic ABC transporter permease	BN1326_90051;AFO87_00060	1,676E+09	1,000E+00
A6QFG0	Na(+)/H(+) antiporter subunit C1;ShaC;Na(+) H(+) antiporter subunit C	mnhC1;ST398NM01_0933;mnhC	1,494E+09	1,000E+00
B6V385	Putative exported protein;Uncharacterized protein;Transposon-related protein	AFO87_14660;CH51_06835;AN169_05145	1,080E+09	1,000E+00
C4B834	Coagulase;Staphylocoagulase repeat protein	coa;HMPREF0776_	3,453E+07	1,000E+00
D2J6A6	Bacitracin ABC ATP binding cassette transporter%2C membrane protein	AL078_10275	1,788E+08	1,000E+00
D7URR6	Membrane protein;Uncharacterized protein	AFO87_12985;AL078_01705;QU38_08675	7,968E+08	1,000E+00
O34091	Uroporphyrinogen III synthase;Uroporphyrinogen III synthase O	hemD;CH51_08970	7,990E+07	1,000E+00
P0A071	Gamma-hemolysin component A;Gamma-hemolysin subunit A	hlgA;QU38_07850;hlgA_1	3,636E+07	1,000E+00
P0A0M2	Delta-hemolysin;Delta hemolysin	hld	5,156E+10	1,000E+00
P0A0N0	DegV domain-containing protein SAV0749;DegV family protein	SAV0749;SAKOR_00751	4,150E+07	1,000E+00
P0C7Y5	Phenol-soluble modulin alpha 1 peptide;Phenol-soluble modulin alpha 2 peptide	psmA1;psmA2	5,499E+09	1,000E+00
P63820	Phosphopantetheine adenylyltransferase	coaD	7,264E+07	1,000E+00
P65267	Lipoprotein signal peptidase;Signal peptidase II	lspA	8,431E+08	1,000E+00
Q2FH64	Tryptophan synthase beta chain	trpB	1,546E+07	1,000E+00
Q2FHI6	Tyrosine recombinase XerC	xerC	5,356E+07	1,000E+00
Q2FI19	Probable quinol oxidase subunit 3;Cytochrome aa3-600 quinol oxidase (Subunit III)	qoxC	2,068E+07	1,000E+00
Q2FIC9	Na(+)/H(+) antiporter subunit G1;ShaG	mnhG1;mnhG;ST398NM01_0929	2,107E+09	1,000E+00
Q2FK78	N-acetyl-gamma-glutamyl-phosphate reductase	argC	3,762E+07	1,000E+00
Q2FKF9	Uncharacterized lipoprotein SAUSA300_0102;Staphylococcus tandem lipoproteins;Uncharacterized lipoprotein SACOL0081/SACOL0(	SAUSA300_0102;AFO87_03770	8,675E+08	1,000E+00
Q2FUR5	Permease, putative;VraE protein;ABC transporter permease	SAOUHSC_03037;vraE;AL493_01245	1,152E+08	1,000E+00
Q2FUW5	Accessory Sec system protein Asp3;Accessory secretory protein Asp3	asp3;NWMN_2549;as	6,632E+07	1,000E+00
Q2FVB0	Uncharacterized protein;Putative membrane protein	SAOUHSC_02823;AUC48_12850;BN1326_150022	3,407E+08	1,000E+00
Q2FVL1	Uncharacterized protein;Drug resistance transporter EmrB/QacA subfamily protein	SAOUHSC_02700;NWMN_2314	5,359E+08	1,000E+00
Q2FVU1	Na+/H+ antiporter, putative;Na+/H+ antiporter family protein;NhaC family sodium:proton (Na+:H) antiporter	SAOUHSC_02601;BN1321_380165	1,259E+09	1,000E+00
Q2FVX3	Sulfurtransferase FdhD	fdhD	1,160E+08	1,000E+00
Q2FVY4	Probable molybdenum cofactor guanylyltransferase;Molybdopterin-guanine dinucleotide biosynthesis protein A	mobA;CH51_12245	7,284E+07	1,000E+00
Q2FXD3	Uncharacterized protein;Exported protein	SAOUHSC_01930;AFO87_09085;SAKOR_01753	1,193E+08	1,000E+00
Q2FXI1	Uncharacterized protein;Choline kinase;Phosphotransferase enzyme family	SAOUHSC_01866;AFO87_06950;HMPREF0	5,180E+07	1,000E+00
Q2FZA8	Uncharacterized protein;Arginine/ornithine antiporter;ArcD-like protein	SAOUHSC_01130;SAKOR_01092;arcD-like	3,003E+08	1,000E+00
Q2FZX9	Probable nitronate monooxygenase;Enoyl-(Acyl-carrier-protein) reductase (FMN);2-nitropropane dioxygenase	SAOUHSC_00855;SAZ172_0862	9,813E+07	1,000E+00
Q2G129	Uncharacterized protein;Putative high-affinity Fe2+/Pb2+ permease-like protein;High-affinity iron permease	SAOUHSC_00327;RU53_320	4,450E+07	1,000E+00
Q2G165	Uncharacterized protein;Regulatory protein;Perfringolysin O regulator protein	SAOUHSC_00290;pfoR_1;pfoR	2,641E+08	1,000E+00
Q2G1P5	Uncharacterized protein;SA0099 protein;Antibiotic resistance-related transmembrane efflux protein	SAOUHSC_00058;SA0099;	4,442E+08	1,000E+00
Q2G1T1	Uncharacterized protein;Phosphoglycerate mutase family protein	SAOUHSC_00827;gpmA1	5,659E+07	1,000E+00
Q2G256	CCA-adding enzyme	SAOUHSC_01474;cca;papS	5,913E+07	1,000E+00
Q2G2I3	Uncharacterized protein;Drug resistance transporter, Bcr/CflA family protein;Bicyclomycin transporter TcaB	SAOUHSC_02633;SAKOR_02330	2,550E+08	1,000E+00
Q53645	Fructokinase;Kinase, PfkB family	iolC;HMPREF0776_0189;SAZ172_2040	1,780E+07	1,000E+00
Q5HDD3	Gamma-hemolysin component B	hlgB	2,686E+08	1,000E+00
Q5HDT6	Molybdopterin synthase catalytic subunit;Molybdopterin synthase (Large subunit);Molybdenum cofactor biosynthesis protein E	moaE	6,088E+07	1,000E+00
Q5HHC0	Inactive signal peptidase IA;Signal peptidase I	spsA;lepB	3,051E+08	1,000E+00
Q5HHD6	Na(+)/H(+) antiporter subunit D1	mnhD1	1,106E+09	1,000E+00
Q5HHD7	Na(+)/H(+) antiporter subunit E1;Non essential component of Na+/H+ antiporter;Na(+) H(+) antiporter subunit E	mnhE1;mrpE;mnhE	1,384E+09	1,000E+00
Q5HHN9	Probable protein-export membrane protein SecG;Protein translocase subunit SecG	secG;SAOUHSC_00801	2,161E+09	1,000E+00
Q5HHU8	Putative 5(3)-deoxyribonucleotidase;5(3)-deoxyribonucleotidase	SACOL0785;AL493_05230	2,448E+08	1,000E+00
Q5HHX4	Quinolone resistance protein NorA;Multidrug MFS transporter	norA;QU38_105	4,858E+08	1,000E+00
Q5HIC3	Ribulokinase	araB	4,324E+07	1,000E+00
Q5HIN4	Uncharacterized lipoprotein SACOL0483;Tandem lipoprotein	SACOL0483;lpl8	1,650E+08	1,000E+00
Q5HIN5	Uncharacterized lipoprotein SACOL0482	SACOL0482	5,471E+07	1,000E+00
Q5HJX8	Adenylosuccinate synthetase	purA	5,881E+07	1,000E+00
Q6X7U0	Diaminopimelate decarboxylase	sbnH;QU38_15175;ST398NM01_01	1,731E+07	1,000E+00
Q6X7U6	2,3-diaminopropionate biosynthesis protein SbnB;Ornithine cyclodeaminase, putative;Ornithine cyclodeaminase family protein	sbnB;SACOL0101	6,829E+07	1,000E+00
Q7A039	Heme response regulator HssR;Heme transporter CcmC;Two-component response regulator	hssR;QU38_07450;SAKOR_0	1,296E+08	1,000E+00
Q7A2Q0	Sensor protein VraS	vraS;liaS	2,913E+09	1,000E+00
Q7A3U8	Probable nitrate transporter NarT;Nitrate transporter NarT	narT;QU38_	3,538E+08	1,000E+00
Q7A4E6	ATP synthase subunit c	atpE;V070_02071	7,430E+06	1,000E+00
Q7A5C5	UPF0365 protein SA1402;UPF0365 protein SAOUHSC_01676	SA1402;SAOUHSC_01676	6,309E+10	1,000E+00
Q7A5Q7	Putative oligopeptide transport system permease protein oppC2	oppC2	9,770E+07	1,000E+00
Q7A6D2	Processive diacylglycerol beta-glucosyltransferase	ugtP	4,139E+07	1,000E+00
Q7A7M5	UPF0324 membrane protein SA0329;UPF0324 membrane protein SACOL0411;Membrane protein	SA0329;SACOL0411;CH51_01630	4,175E+08	1,000E+00
Q8NUH8	Putative ABC transporter ATP-binding protein MW2603;Putative ABC transporter ATP-binding protein SACOL2708	MW2603;SACOL2708	2,210E+08	1,000E+00
Q8NX68	Protoheme IX farnesyltransferase	ctaB	5,746E+06	1,000E+00
Q8NYB7	Protein-ADP-ribose hydrolase;Macro domain protein	MW0302;SACOL0396;RU5	1,904E+08	1,000E+00
Q8NYU1	Uncharacterized lipoprotein MW0072;Uncharacterized lipoprotein SAOUHSC_00053;Tandem lipoprotein within Pathogenicity island	MW0072;SAOUHSC_00053	1,530E+08	1,000E+00
Q931V3	UPF0413 protein SAV1001;UPF0413 protein SACOL1006;Uncharacterized protein	SAV1001;SACOL1006;H	6,657E+07	1,000E+00
Q93PN3	Ferric hydroxamate receptor 1	fhuD1;BN1321_330035;fhuD	2,429E+09	1,000E+00
Q99R72	Glycosyl-4,4-diaponeurosporenoate acyltransferase	crtO	6,132E+07	1,000E+00
Q99RN7	Oxygen sensor histidine kinase NreB;Sensor histidine kinase	nreB	2,584E+08	1,000E+00
Q99S77	PTS system lactose-specific EIICB component;PTS system, lactose-specific IIB component / PTS system	lacE	1,690E+08	1,000E+00

Q99S97	Multidrug efflux pump SdrM;Multidrug resistance protein B;MW2095 protein	sdrM;bmr3;MW2095	1,200E+09	1,000E+00
Q99SC8	Type II pantothenate kinase	coaW	1,724E+08	1,000E+00
Q99U80	Putative branched-chain amino acid carrier protein SAV1407;Branched-chain amino acid transport system carrier protein	SAV1407;BN1321_260047	2,288E+08	1,000E+00
Q99W51	tRNA-specific adenosine deaminase	tadA	9,715E+07	1,000E+00
Q99WT7	Virulence factor EsxB	esxB	1,461E+08	1,000E+00
Q99WT8	Protein EsaC;Uncharacterized protein	esaC	2,483E+08	1,000E+00
Q9FDP4	Membrane protein	ERS092844_02688	1,308E+09	1,000E+00
Q9X668	Na+ dependent nucleoside transporter domain-containing protein;Purine nucleoside transport protein NupG;MW0607 protein	nupG;MW0607	4,047E+09	1,000E+00
Q9ZGN7	Antibiotic resistance protein;MW2386 protein;Transporter, putative	AFO87_06460;MW2386;SACOL2471	3,074E+07	1,000E+00
Q9ZHA1	Cell division protein;Factor involved in shape determination and osmotic tolerance;YGGT family protein	ylmG;HMPREF0776_	7,646E+08	1,000E+00
T1Y4U6	Capsular polysaccharide synthesis glycosyltransferase CapL;Glycosyltransferase, group 1 family protein	SAKOR_00140;BN1321_50024	3,058E+07	1,000E+00
T1Y5C0	Na+ driven multidrug efflux pump;Multidrug export protein MepA	SAKOR_00330;mepA	1,487E+08	1,000E+00
T1Y5P6	ABC transporter permease protein;Methionine ABC transporter, permease component;Binding-protein-dependent transport system	SAKOR_00446;metP	3,809E+09	1,000E+00
T1Y6U1	Type VII secretion protein EssA;Protein EssA	SAKOR_00267;essA	9,639E+07	1,000E+00
T1Y878	Phosphate-binding protein;Phosphate-binding protein PstS;Phosphate ABC transporter periplasmic protein	SAKOR_01326;pstS	1,298E+08	1,000E+00
T1Y890	Peptide deformylase;Peptide deformylase-like	def;MW1098;SAV1215	4,605E+07	1,000E+00
T1Y931	Sodium/proton antiporter protein shaA;Na(+)/H(+) antiporter subunit A1	SAKOR_00864;mnhA1	2,391E+09	1,000E+00
T1Y9Y1	Multidrug resistance protein B;Quinolone resistance protein NorB	SAKOR_01378;norB	1,764E+08	1,000E+00
T1YA34	Phosphatidate cytidylyltransferase	SAKOR_01189;cdsA	7,362E+08	1,000E+00
T1YC30	2-oxoglutarate/malate translocator;2-oxoglutarate translocator;Sodium:sulfate symporter family protein	SAKOR_02696;2486	3,905E+09	1,000E+00
T1YDK8	Integral membrane protein;Putative membrane protein;Membrane protein	SAKOR_02444;BN1321_410038;ERS195423_01356	8,225E+07	1,000E+00
U5NW20	Nickel (Ni2+)/peptide ABC superfamily ATP binding cassette transporter, binding protein	nikA;CO98_1215	9,056E+08	1,000E+00
W8TPT7	Antiporter;Hexose phosphate transporter;Hexose phosphate transport protein	uhpT;QU38_14720	1,002E+09	1,000E+00
W8TQV7	Glycerate kinase;Uncharacterized protein	glxK_2;glxK;MW2356	7,704E+07	1,000E+00
W8TR97	Membrane protein;Uncharacterized protein	AFO87_10600;QU38_10965;HMPREF0769_11511	3,444E+09	1,000E+00
W8TSC7	Lipoprotein;Uncharacterized protein	AFO87_05265;QU38_14280;ERS179246_01053	9,520E+08	1,000E+00
W8TTE9	Short chain dehydrogenase/reductase oxidoreductase;Short-chain dehydrogenase/reductase family oxidoreductase;Short chain deh	cpnA;BN1321_420082	2,417E+08	1,000E+00
W8TTV5	MerR family transcriptional regulator;MW2312 protein	mta;MW2312	4,434E+09	1,000E+00
W8TWM6	Uncharacterised protein;Uncharacterized protein	AFO87_10370;HMPREF0769_12452;ST398NM01_131	5,943E+07	1,000E+00
W8U174	NAD(P)H-dependent oxidoreductase;Putative NAD(P)H-dependent FMN-containing oxidoreductase YwqN	ywqN_2;QU38_10030	1,006E+08	1,000E+00
W8U1Z5	Formate nitrite transporter;Formate/nitrite transporter;Formate/nitrite transporter family protein	focA;QU38_14270;NWMN_02	4,353E+08	1,000E+00
W8U3F9	Cation diffusion facilitator family transporter;Uncharacterized transporter YdbO;Cobalt-zinc-cadmium resistance protein	fieF;ydbO	3,624E+08	1,000E+00
W8U4M8	Membrane protein;Uncharacterized protein	AFO87_13210;SAKOR_01901;SAOUHSC_02148	1,047E+09	1,000E+00
W8U4P5	Putative cysteine protease inhibitor (Staphostatin A);Staphostatin A;Uncharacterized protein	sspA_2;HMPREF0769_11261	9,862E+07	1,000E+00
W8U5G5	Iron transporter;Membrane spanning protein;Mn2 and Fe2 transporter	AFO87_10965;ERS092844_01089;ERS365775_01407	3,300E+08	1,000E+00
W8U5U5	7-carboxy-7-deazaguanine synthase	queE	1,173E+08	1,000E+00
W8U5Y5	Inorganic phosphate transporter;Low-affinity inorganic phosphate transporter	pitA;SAV0664	3,401E+08	1,000E+00
W8U6S2	Phosphoesterase	AFO87_08370;BN1321_230075;NWMN_1065	1,912E+08	1,000E+00
W8UA48	D-serine/D-alanine/glycine transporter;Gamma-aminobutyrate permease	aapA;QU38_08460;ydgF	2,293E+09	1,000E+00
W8UBG3	Uracil permease;Putative permease	pyrP;ACH32_12935;HMPREF0769_12580	1,492E+09	1,000E+00
W8UT95	DNA mismatch repair protein MutT;MutT domain containing protein	AL078_09265;AFO87_01845;NWMN_0431	7,887E+07	1,000E+00
W8UTD9	Xanthine permease	pbuX;SAKOR_00387	1,013E+07	1,000E+00
W8UWY3	Polysaccharide biosynthesis protein;Putative polysaccharide biosynthesis protein	ytgP_2;BN1326_80287;BN1321_260388	6,941E+08	1,000E+00
X5DTA3	Damage-inducible protein DinB;Uncharacterized protein	AFO87_13955;SA2485;SAKOR_02695	1,180E+08	1,000E+00
X5DU72	Phosphate/phosphite/phosphonate ABC transporter, periplasmic binding family protein;MW0117 protein;SA0138 protein	phnD;MW0117	6,504E+08	1,000E+00
X5DYC0	Glucokinase;SA0305 protein	bglK;SA0305;SAKOR_00310	1,012E+08	1,000E+00
X5DZB1	Urea transporter;MW2205 protein;SA2081 protein	AFO87_01020;MW2205;SA2081	1,169E+08	1,000E+00
X5DZU0	3-beta hydroxysteroid dehydrogenase;Putative nucleoside-diphosphate-sugar epimerase;NmrA family protein	qorB;BN1321_90012;HM	1,670E+08	1,000E+00
X5E034	Acetyltransferase;Acetyltransferase, GNAT family protein	AFO87_01045;ERS093009_01698;NWMN_2181	5,114E+07	1,000E+00
X5E195	Membrane protein;Uncharacterized protein;Uncharacterized protein	AFO87_08905;MW0380;SA0380	8,660E+08	1,000E+00
X5E273	GCN5-related N-acetyltransferase (GNAT);Acetyltransferase, GNAT family;Acetyltransferase, GNAT family protein	AFO87_03445;BN1326_100148;	2,787E+07	1,000E+00
X5EH84	2-amino-4-hydroxy-6-hydroxymethyldihydropteridin e pyrophosphokinase;2-amino-4-hydroxy-6-hydroxymethyldihydropteridine py	folK	8,183E+07	1,000E+00
X5EIW2	Membrane protein;Putative membrane spanning protein;Putative membrane protein	AFO87_03740;ST398NM01_0108;BN1326_150294	3,792E+08	1,000E+00
X5EK76	Orf1;Uncharacterized protein	AFO87_04135;ASU36_11630;MW2578	7,334E+08	1,000E+00
X5ELZ2	Histidine kinase;MW1790 protein;Two-component sensor protein yhcY;YhcY	vraS_1;MW1790;SAKOR_01805	5,600E+07	1,000E+00