

												Water		Theanine		Water	Theanine		Glutamate(20170411)			
G/3	T/3	Gene length	168			Function	Product	Name	Chromosome	Region	RPKM	Unique gene reads	RPKM	Unique gene reads	RPKM+0.01	RPKM+0.01	T/3	RPKM(+0.01)	Unique gene reads	G/T	G/3	
	1.365325	3.737461	2418	nasD	ResD regulon, SigA regulon, TnrA regulon, NsrR regulon, Fur regulon	nitrite reductase large subunit	assimilatory nitrite reductase (subunit)	B4U62_R5C	Bacillus sub	compleme	48.44	1384	181.07	5519	48.45	181.08	3.74	66.15	2801	0.365308	1.365325	
	1.313253	29.39036	1206	nasA	TnrA regulon	NarK family nitrate/nitrite MFS transporter	nitrate uptake	nitrate transporter	B4U62_R5C	Bacillus sub	362980..36	4.14	59	121.96	1854	4.15	121.97	29.39	5.45	115	0.044683	1.313253
	2.977497	8.064118	642	lipC	KipR regulon, TnrA regulon	germination protein	spore germination	spore coat phospholipase B	B4U62_R5C	Bacillus sub	462472..46	32.43	246	261.59	2117	32.44	261.6	8.06	96.59	1086	0.369228	2.977497
	2.450207	3.530299	489	purE	SigA regulon, PurR regulon, G-box	5-(carboxyamino)imidazole ribonucleotide mutase	purine biosynthesis	phosphoribosylaminoimidazole carboxylase (ATP-dependent)	B4U62_R5C	Bacillus sub	698654..69	113.36	655	400.22	2467	113.37	400.23	3.53	277.78	2379	0.694051	2.450207
	2.801554	3.750869	1143	purK	SigA regulon, PurR regulon, G-box	5-(carboxyamino)imidazole ribonucleotide synthase	purine biosynthesis	phosphoribosylaminoimidazole carboxylase (ATP-dependent)	B4U62_R5C	Bacillus sub	699135..70	184.07	2486	690.45	9948	184.08	690.46	3.75	515.71	10324	0.746908	2.801554
	2.788377	3.845962	726	purC	SigA regulon, PurR regulon, G-box	phosphoribosylaminoimidazole succinocarboxamide synthase	purine biosynthesis	phosphoribosylaminoimidazole succinocarboxamide synthase	B4U62_R5C	Bacillus sub	701643..70	300.76	2580	1,156.74	10586	300.77	1156.75	3.85	838.66	10664	0.725014	2.788377
	2.504637	3.517327	255	purS	SigA regulon, PurR regulon, G-box	phosphoribosylformylglycinamide synthase subunit PurS	purine biosynthesis	phosphoribosylformylglycinamide synthase	B4U62_R5C	Bacillus sub	702361..70	225.36	679	792.69	2548	225.37	792.7	3.52	564.47	2521	0.712085	2.504637
	2.897992	3.678806	684	purQ	SigA regulon, PurR regulon, G-box	phosphoribosylformylglycinamide synthase subunit PurQ	purine biosynthesis	phosphoribosylformylglycinamide synthase	B4U62_R5C	Bacillus sub	702612..70	342.12	2765	1,258.62	10852	342.13	1258.63	3.68	991.49	11878	0.787753	2.897992
	2.894217	3.100162	1431	purF	SigA regulon, PurR regulon, G-box	amidophosphoribosyltransferase	purine biosynthesis	glutamine phosphoribosylidiphosphate amidotransferase	B4U62_R5C	Bacillus sub	705483..70	519.45	8783	1,610.40	29049	519.46	1610.41	3.10	1503.43	37681	0.93357	2.894217
	2.703589	3.290668	1041	purM	SigA regulon, PurR regulon, G-box	phosphoribosylformylglycinamide cyclo-ligase	purine biosynthesis	phosphoribosylaminoimidazole synthetase	B4U62_R5C	Bacillus sub	707015..70	362.19	4455	1,191.87	15640	362.2	1191.88	3.29	979.24	17854	0.821593	2.703589
	2.730591	3.365446	588	purN	SigA regulon, PurR regulon, G-box	phosphoribosylglycinamide formyltransferase	purine biosynthesis	phosphoribosylglycinamide formyltransferase	B4U62_R5C	Bacillus sub	708052..70	365.16	2537	1,228.95	9109	365.17	1228.96	3.37	997.13	10269	0.811361	2.730591
	2.315337	3.211814	1539	purH	SigA regulon, PurR regulon, G-box	bifunctional phosphoribosylaminoimidazole carboxamide formyltransferase/inosine monophosphate cyclohydrolase	purine biosynthesis	phosphoribosylaminoimidazole carboxamide formyltransferaseand inosine-monophosphate cyclohydrolase	B4U62_R5C	Bacillus sub	708636..71	513.79	9343	1,650.22	32014	513.8	1650.23	3.21	1189.62	32066	0.720881	2.315337
	0.621643	3.393797	333	tnrA	GlnR regulon, TnrA regulon, TnrA regulon	MerR family transcriptional regulator	regulation of nitrogen assimilation	transcription activator/ repressor (MerR family)	B4U62_R5C	Bacillus sub	compleme	74.47	293	252.76	1061	74.48	252.77	3.39	46.3	270	0.18317	0.621643
	2.695166	3.012384	498	ykvM	preQ1 riboswitch	NADPH-dependent 7-cyano-7-deazaguanine reductase QueF	tRNA modification	nitrile reductase	B4U62_R5C	Bacillus sub	1441323..1	41.98	247	126.48	794	41.99	126.49	3.01	113.17	987	0.894695	2.695166
	0.353354	3.356363	408	glnR	SigA regulon, GlnR regulon, TnrA regulon, GlnR regulon	MerR family transcriptional regulator	regulation of glutamine synthesis	transcription repressor (MerR family)	B4U62_R5C	Bacillus sub	1877991..1	837.62	4038	2,811.38	14459	837.63	2811.39	3.36	295.98	2115	0.105279	0.353354
	0.429204	3.17704	1335	glnA	SigA regulon, GlnR regulon, TnrA regulon	glutamine synthetase	glutamine biosynthesis, control of TnrA and GlnR activity	trigger enzyme	B4U62_R5C	Bacillus sub	1878457..1	4,615.95	72812	14,665.08	246788	4615.96	14665.09	3.18	1981.19	46324	0.135096	0.429204
	1.262869	5.053323	546	iseA	WalR regulon	hypothetical protein	protection against cell envelope stress	inhibitor of autolysins	B4U62_R5C	Bacillus sub	2002669..2	184.15	1188	930.61	6405	184.16	930.62	5.05	232.57	2224	0.249909	1.262869
	1.069705	16.04424	1455	yrbD	TnrA regulon	sodium:alanine symporter	uptake of alanine	sodium/proton-dependent alanine transporter	B4U62_R5C	Bacillus sub	2841629..2	7.45	128	119.68	2195	7.46	119.69	16.04	7.98	203	0.066672	1.069705
	2.448927	3.02191	1761	sdhA	SigA regulon, FsrA regulon	succinate dehydrogenase flavoprotein subunit	TCA cycle	succinate dehydrogenase (flavoprotein subunit)	B4U62_R5C	Bacillus sub	compleme	198.53	4131	599.96	13318	198.54	599.97	3.02	486.21	14996	0.810391	2.448927
	2.574081	3.431759	1008	bioB	BirA regulon	biotin synthase	biosynthesis of biotin	biotin synthase	B4U62_R5C	Bacillus sub	compleme	296.22	3528	1,016.58	12917	296.23	1016.59	3.43	762.52	13462	0.750076	2.574081
	0.94879	10.82555	1596	pucR	sigA regulon, TnrA regulon, PucR regulon	purine catabolism regulatory protein	regulation of purine utilization	transcriptional regulator of puc genes (PucR family)	B4U62_R5C	Bacillus sub	3328777..3	17.76	335	192.36	3870	17.77	192.37	10.83	16.86	471	0.087644	0.94879
	0.318587	3.490015	1350	pucJ	sigA regulon, TnrA regulon, PucR regulon	Uric acid permease PucJ	purine utilization	uric acid permease	B4U62_R5C	Bacillus sub	3330517..3	32.54	519	113.59	1933	32.55	113.6	3.49	10.37	245	0.091285	0.318587
	0.280026	3.516645	1293	pucK	sigA regulon, TnrA regulon, PucR regulon	uric acid permease PucK	purine utilization	uric acid permease	B4U62_R5C	Bacillus sub	3331872..3	30.63	468	107.74	1756	30.64	107.75	3.52	8.58	194	0.079629	0.280026
	0.2105	3.690873	1485	pucL	sigA regulon, TnrA regulon, PucR regulon	bifunctional 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazole decarboxylase/factor independent urate hydroxylase	purine utilization	uricase	B4U62_R5C	Bacillus sub	3333177..3	40.75	715	150.43	2816	40.76	150.44	3.69	8.58	223	0.057033	0.2105
	0.183408	3.021983	345	pucM	sigA regulon, TnrA regulon, PucR regulon	5-hydroxyisourate hydrolase	purine utilization	uricase	B4U62_R5C	Bacillus sub	3334661..3	62.31	254	188.32	819	62.32	188.33	3.02	11.43	69	0.060691	0.183408
	0.595935	37.73999	1215	amtB	SigA regulon, TnrA regulon	ammonium transporter NrgA	ammonium uptake	ammonium transporter	B4U62_R5C	Bacillus sub	3756828..3	16.72	240	631.38	9670	16.73	631.39	37.74	9.97	212	0.015791	0.595935
	0.449876	15.91619	351	glnK		nitrogen regulatory PII-like protein	regulation of the glnA-glnT operon	two-component sensor kinase	B4U62_R5C	Bacillus sub	3758054..3	68.72	285	1,093.91	4840	68.73	1093.92	15.92	30.92	190	0.028265	0.449876
	0.687436	3.270165	1710	ureC	SigA regulon, GlnR regulon, TnrA regulon, CodY regulon, SigH regulon	urease subunit alpha	utilization of urea as alternative nitrogen source	urease (alpha subunit)	B4U62_R5C	Bacillus sub	compleme	166.74	3369	545.29	11754	166.75	545.3	3.27	114.63	3433	0.210215	0.687436
	0.829933	3.437628	375	ureB	SigA regulon, PucR regulon, GlnR regulon, TnrA regulon, CodY regulon, SigH regulon	urease subunit beta	utilization of urea as alternative nitrogen source	urease (beta subunit)	B4U62_R5C	Bacillus sub	compleme	68.61	304	235.88	1115	68.62	235.89	3.44	56.95	374	0.241426	0.829933
	0.552802	3.22131	318	ureA	SigA regulon, PucR regulon, GlnR regulon, TnrA regulon, CodY regulon, SigH regulon	urease subunit gamma	utilization of urea as alternative nitrogen source	urease (gamma subunit)	B4U62_R5C	Bacillus sub	compleme	63.34	238	204.06	818	63.35	204.07	3.22	35.02	195	0.171608	0.552802
	0.10069	5.581149	183	#N/A		hypothetical protein			B4U62_R5C	Bacillus sub	compleme	21.74	47	121.38	280	21.75	121.39	5.58	2.19	7	0.018041	0.10069