

A	SEED Rank3	S1	SE	S2	SE	S3	SE	S4	SE	S5	SE	S6	SE
	[Protein-PII]uridylyltransferase(EC2.7.7.59)	3636	623	3053	564	2588	399	3277	971	3611	996	6280	2086
	6-phosphofructokinase(EC2.7.1.11)	4876	1119	4862	1088	5694	1300	7261	1464	6925	1921	14208	5049
	Alkalinephosphatase(EC3.1.3.1)	95697	72056	79460	57722	71543	50535	24971	15054	25721	16437	43130	28640
	Allantoicase(EC3.5.3.4)	52248	NA	52235	NA	27552	NA	3106	NA	4062	NA	8887	NA
	Ammoniumtransporter	9848	2433	8442	1857	9378	1950	31695	10466	25613	8555	29516	9577
	Arginase(EC3.5.3.1)	4730	2820	1866	511	2805	584	3550	362	4265	609	5777	2578
	Argininosuccinatelyase(EC4.3.2.1)	19029	15509	24333	21334	19557	15681	17460	14575	22728	19752	32344	28503
	Argininosuccinatesynthase(EC6.3.4.5)	4386	580	3559	625	5316	827	4992	809	4399	738	5793	1071
	ATPSynthasebetachain(EC3.6.3.14)	24846	5753	20179	4044	19641	2820	16724	2448	15535	2434	19767	2814
	Branched-chainaminoacidtransport LivM(TC3.A.1.4.1)	72096	62137	46386	37046	53340	42430	10085	4771	7207	3531	23592	17021
	Chitinase(EC3.2.1.14)	4976	1303	3964	2269	4175	2124	8608	6850	8801	6479	7665	4888
	D-xylosetransportATP-bindingproteinXylG	17416	16126	9328	7462	10019	6011	887	0	1625	NA	2222	444
	GlutaminesynthetasetypeI(EC6.3.1.2)	15385	10018	8395	4816	12096	7823	15716	6683	19620	10865	16833	7605
	HistidineABCtransporter;permeaseprotein HisQ(TC3.A.1.3.1)	10966	8386	3420	2487	4008	1475	25736	NA	35747	NA	26218	25329
	Manganesesuperoxidedismutase(EC1.15.1.1)	9375	3902	6668	2191	9121	4492	5446	1399	3906	954	8999	3123
	Myo-inositol2-dehydrogenase1(EC1.1.1.18)	2580	NA	933	NA	1002	NA	2219	444	3250	1196	7999	2434
	NAD-specificglutamatedehydrogenase(EC1.4.1.2)	10023	4564	7462	3133	11203	6552	13213	8451	11455	6762	17686	8225
	NitricoxidereductaseactivationproteinNorQ	47733	41928	33813	25884	28053	23044	3772	666	5687	0	10221	1333
	OligopeptidetransportATP- bindingproteinOppD(TC3.A.1.5.1)	13062	9506	9094	6042	7765	4383	19561	13883	21123	15529	19641	13921
	OligopeptidetransportATP- bindingproteinOppF(TC3.A.1.5.1)	7095	5805	24252	NA	21040	NA	26845	17971	29654	22342	23552	16442
	Ornithinecarbamoyltransferase(EC2.1.3.3)	4039	694	3604	789	3822	720	4369	1455	4718	1592	6344	1381
	PhosphateABCtransporter;periplasmic PstS(TC3.A.1.7.1)	9995	1909	9823	2143	6981	1209	10684	2650	4875	827	5608	1110
	Phosphatetransportsystemregulatoryprotein PhoU	7257	2166	6107	1641	4774	1518	7575	3770	8818	5333	12169	6689
	Phospholipid-lipopolysaccharideABCtransporter	1613	323	2705	519	2505	808	887	0	812	NA	889	0
	PhosphonateABCtransporterphosphate- binding(TC3.A.1.9.1)	10660	3916	9690	3876	8369	3553	18613	8733	12806	6090	19997	9672
	PredictederythritolABCtransporter1	1290	NA	2798	NA	3006	NA	72327	NA	63370	NA	128868	NA
	Sucrose-6-phosphatehydrolase(EC3.2.1.B3)	6020	860	3381	658	3945	1832	7543	3596	4062	1544	8621	5729
	Sucrosephosphorylase(EC2.4.1.7)	3969	574	2798	384	6155	1928	2041	398	1990	455	7110	2974
	Trehalase(EC3.2.1.28)	74825	NA	59697	NA	71135	NA	5325	NA	4062	NA	16886	NA
	Ubiquinol-cytochromeCreductaseFe- Ssubunit(EC1.10.2.2)	26342	20556	24330	19469	27767	22114	26528	20758	30948	25290	43373	37269
	UreaABCtransporter;ureabindingprotein	8601	4789	6840	4516	4342	2338	9873	7319	9749	8937	13553	10303
	XyloseABCtransporter, XylF	37025	22007	17523	9728	15386	8519	6268	1458	6053	2027	11998	3738

B	SEED Rank 3	S1	S1SE	S2	S2SE	S3	S3SE	S4	S4SE	S5	S5SE	S6	S6SE
	Fructose-1,6- biphosphatase,GlpXtype(EC3.1.3.11)	168033	1119	32913	1088	24964	1300	7163	1464	3192	1921	2555	5049
	Fructose- biphosphatealdolaseclassI(EC4.1.2.13)	122975	8909	87237	7243	73787	9604	36211	2510	51692	2127	66481	2648
	Fructose- biphosphatealdolaseclassII(EC4.1.2.13)	97626	81075	62523	88396	45409	49481	29342	37449	25047	47950	30150	117887
	Phosphoglyceratekinase(EC2.7.2.3)	318204	165453	242534	31981	111712	22769	55543	3778	19671	1080	14259	488
	MalatesynthaseG(EC2.3.3.9)	81223	115502	57954	81586	55812	65362	14544	31653	12956	47916	13189	60668
	Malatedehydrogenase(EC1.1.1.37)	117940	78488	68335	51050	150913	28073	142374	18159	9389	14528	15479	16895
	Succinatedehydrogenaseflavoproteinsub (EC1.3.99.1)	229626	2255	134734	1875	151665	2031	22564	3868	21965	2744	33923	3534
	Aconitatehydratase(EC4.2.1.3)	22029	761	16819	1166	19550	1829	10546	3907	9436	3412	12523	7746
	6-phosphofructokinase(EC2.7.1.11)	4876	110032	4862	62439	5694	142959	7261	136088	6925	3858	14208	5958
	Ribose- phosphatepyrophosphokinase(EC2.7.6.1)	8839	78071	7258	55543	9857	52322	9924	10153	8147	10205	11418	9969
	Aldehydedehydrogenase(EC1.2.1.3)	89541	308341	94161	235389	53808	102679	41788	46604	51295	11806	122631	4289
	Pyruvatekinase(EC2.7.1.40)	18772	4557	16315	3602	16289	6001	43762	3655	47226	3278	38906	3925

L-lactatedehydrogenase(EC1.1.2.3)	6966	3588	5342	3494	8416	2562	11023	6303	9614	4648	11634	5507
Lactoylglutathionelyase(EC4.4.1.5)	4193	12213	4431	9967	6011	8164	7395	37295	6616	41352	10887	30948
PyruvatedehydrogenaseE1compalphasub (EC1.2.4.1)	15072	1246	13021	1050	16225	1631	14813	1609	13526	1434	16134	2163
PyruvatedehydrogenaseE1compbetasub (EC1.2.4.1)	10552	187928	10594	107999	8471	127364	14209	11242	11841	13070	15208	22281

Table 6

Bacterial absolute counts of transcripts (grouped by SEED Rank3 category) per volume (mL) represent the mean of absolute counts per transcript normalized to one mRNA standard at a time: pTZ19R (546nt), pFN19R (970nt), to account for transcript length (Satinsky et al. 2013; Beier et al. 2018). SE – standard error of absolute counts per category. A) Carbon, Nitrogen and Phosphorous uptake and utilization, B) Carbon-cycling.