

PC2 negative loadings			PC2 positive loadings		
-1	K07729	putative transcriptional regulator	1	K03169	DNA topoisomerase III [EC:5.6.2.1]
-2	K03574	8-oxo-dGTP diphosphatase [EC:3.6.1.55]	2	K03569	rod shape-determining protein MreB and related proteins
-3	K15634	probable phosphoglycerate mutase [EC:5.4.2.12]	3	K00027	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]
-4	K01104	protein-tyrosine phosphatase [EC:3.1.3.48]	4	K02012	iron(III) transport system substrate-binding protein
-5	K07052	uncharacterized protein	5	K03043	DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]
-6	K03402	transcriptional regulator of arginine metabolism	6	K00794	6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]
-7	K02027	multiple sugar transport system substrate-binding protein	7	K01610	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]
-8	K01589	5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]	8	K01507	inorganic pyrophosphatase [EC:3.6.1.1]
-9	K02440	glycerol uptake facilitator protein	9	K01759	lactoylglutathione lyase [EC:4.4.1.5]
-		ABC-2 type transport system ATP-binding protein			type IV secretion system protein VirD4
10	K01990		10	K03205	[EC:7.4.2.8]