

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