

PC1 negative loadings - no modern humans

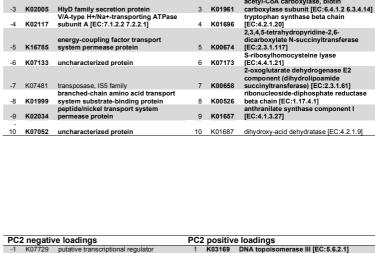
-1 **K03205**

K16926

K02005

type IV secretion system protein VirD4 [EC:7.4.2.8]

energy-coupling factor transport system substrate-specific compone



1 K01903

3 K01961

K01902

PC1 positive loadings - no modern humans

succinyl-CoA synthetase beta subunit [EC:6.2.1.5]

succinyl-CoA synthetase alpha subunit [EC:6.2.1.5] acetyl-CoA carboxylase, biotin

PC2	PC2 negative loadings			positiv	e 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]
		5-(carboxyamino)imidazole			· /-
-8	K01589	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-			type IV secretion system protein VirD4
10	K01990	binding protein	10	K03205	[EC:7.4.2.8]

PC2 negative loadings - no modern humans			PC2 positive loadings - no modern humans		
-1	K03169	DNA topoisomerase III [EC:5.6.2.1]	1	K03574	8-oxo-dGTP diphosphatase [EC:3.6.1.5
		carbamoyl-phosphate synthase large			probable phosphoglycerate mutase
-2	K01955	subunit [EC:6.3.5.5]	2	K15634	[EC:5.4.2.12]
		rod shape-determining protein MreB			multiple sugar transport system
-3	K03569	and related proteins	3	K02027	substrate-binding protein
		malate dehydrogenase (oxaloacetate-			protein-tyrosine phosphatase
4	K00027	decarboxylating) [EC:1.1.1.38]	4	K01104	[EC:3.1.3.48]
		DNA-directed RNA polymerase subunit			
5	K03043	beta [EC:2.7.7.6] (rpoB)	5	K07052	uncharacterized protein
		iron(III) transport system substrate-			transcriptional regulator of arginine
6	K02012	binding protein	6	K03402	metabolism
		DNA-directed RNA polymerase subunit			multiple sugar transport system permease
-7	K03046	beta' [EC:2.7.7.6] (rpoC)	7	K02026	protein
		phosphoenolpyruvate carboxykinase			
-8	K01610	(ATP) [EC:4.1.1.49]	8	K02440	glycerol uptake facilitator protein
					phosphoribosyl-AMP cyclohydrolase
-9	K01759	lactoylglutathione lyase [EC:4.4.1.5]	9	K01496	[EC:3.5.4.19]
-					ABC-2 type transport system ATP-
0	K00615	transketolase [EC:2.2.1.1]	10	K01990	binding protein