COG ID	Function name	ME3880	TH2746	ME12612	ME12173	TE4605	ME6381	ME8366	TH2747	TH3004	TH0989	TH2519	TE1800	TH4590	ME2014	ME12657	TE1301	TH4093	ME30509	TH4820
Carbohydrate transport and metabolism																				
COG2814	Arabinose efflux permease	0	11	2	2	9	1	7	10	5	10	4	6	6	2	4	4	3	0	6
COG2271	Sugar phosphate permease	0	1	0	2	3	5	5	5	4	8	6	5	4	4	1	3	0	0	2
COG0738	Fucose permease	2	2	0	0	1	2	0	4	2	3	3	3	1	2	1	2	0	0	3
COG1762	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	2	1	1	1	1	0	1	2	1	4	1	1	3	0	0	1	4	3	2
COG2211	Na+/melibiose symporter and related transporters	1	2	0	0	0	0	1	5	5	3	0	1	0	0	0	0	7	0	0
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components	0	1	0	2	1	1	4	2	2	3	0	0	0	1	1	0	0	2	0
COG1879	ABC-type sugar transport system, periplasmic component	0	0	0	1	0	2	3	3	2	2	0	0	2	1	1	1	0	1	0
COG0580	Glycerol uptake facilitator and related permeases	1	1	2	0	2	1	1	1	0	2	1	1	0	2	1	2	1	0	0
COG1129	ABC-type sugar transport system, ATPase component	0	1	0	1	1	1	3	1	1	2	1	1	0	1	1	0	0	1	0
COG1925	Phosphotransferase system, HPr-related proteins	1	1	1	0	1	0	1	1	1	0	1	1	1	1	1	1	1	1	1
COG1653	ABC-type sugar transport system, periplasmic component	0	1	0	0	0	0	0	0	1	0	0	0	10	0	0	0	1	0	1
COG1682	ABC-type polysaccharide/polyol phosphate export systems, permease component	1	0	0	0	0	0	0	0	1	1	0	0	2	0	0	0	0	0	2
COG1134	ABC-type polysaccharide/polyol phosphate transport system, ATPase component	1	0	0	0	0	0	0	0	1	1	0	0	2	0	0	0	0	0	2
COG0395	ABC-type sugar transport system, permease component	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	1	0	0
COG3839	ABC-type sugar transport systems, ATPase components	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0	1	0	0
COG4213	ABC-type xylose transport system, periplasmic component	0	0	0	0	1	1	0	0	0	0	1	1	1	0	0	0	0	0	0
COG1869	ABC-type ribose transport system, auxiliary component	0	1	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0
COG1175	ABC-type sugar transport systems, permease components	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0
COG4214	ABC-type xylose transport system, permease component	0	0	0	0	1	0	0	0	0	0	1	1	1	0	0	0	0	0	0
COG2610	H+/gluconate symporter and related permeases	0	0	0	0	0	1	0	0	0	0	0	1	0	0	1	1	0	0	0
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
COG1445	Phosphotransferase system fructose-specific component IIB	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
COG1299	Phosphotransferase system, fructose-specific IIC component	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
COG4975	Putative glucose uptake permease	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Sum		**9**	**23**	**6**	**9**	**21**	**15**	**26**	**35**	**27**	**46**	**20**	**23**	**43**	**14**	**12**	**15**	**20**	**8**	**19**
Amino acid transport and metabolism																				
COG0591	Na+/proline symporter	2	0	2	1	1	2	2	2	4	5	3	3	4	0	1	1	6	0	0
COG0601	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	0	0	2	1	3	1	2	2	0	1	1	1	1	2	3	2	2	1	1
COG0531	Amino acid transporters	0	3	0	0	2	2	2	0	1	4	2	3	1	0	0	1	0	0	3
COG0444	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	1	1	1	1	2	2	1	1	0	1	1	1	2	1	1	1	1	1	0
COG4166	ABC-type oligopeptide transport system, periplasmic component	0	0	1	1	2	2	1	1	0	0	3	4	2	0	1	0	0	0	0
COG3104	Dipeptide/tripeptide permease	0	1	0	1	1	1	2	1	1	2	1	1	2	1	1	1	0	0	1
COG1173	ABC-type dipeptide/oligopeptide/nickel transport systems, permease components	0	0	1	1	2	1	1	2	0	1	1	1	1	1	1	1	1	0	1
COG3842	ABC-type spermidine/putrescine transport systems, ATPase components	0	1	2	0	2	1	1	1	0	2	1	1	1	1	1	1	0	1	0
COG0747	ABC-type dipeptide transport system, periplasmic component	0	1	1	1	1	2	1	1	0	1	0	0	0	1	1	1	2	1	0
COG1280	Putative threonine efflux protein	0	1	0	1	0	0	0	1	1	1	2	2	1	1	1	1	0	0	1
COG0410	ABC-type branched-chain amino acid transport systems, ATPase component	0	0	0	1	0	0	1	1	1	2	0	0	1	0	0	1	0	0	0
COG0683	ABC-type branched-chain amino acid transport systems, periplasmic component	0	0	0	0	0	0	1	1	1	2	0	0	2	0	0	0	1	0	0
COG0559	Branched-chain amino acid ABC-type transport system, permease components	0	0	0	1	0	0	1	1	1	2	0	0	1	0	0	1	0	0	0
COG4177	ABC-type branched-chain amino acid transport system, permease component	0	0	0	1	0	0	1	0	1	2	0	0	1	0	0	1	0	0	0
COG1177	ABC-type spermidine/putrescine transport system, permease component II	1	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0
COG0411	ABC-type branched-chain amino acid transport systems, ATPase component	0	0	0	0	0	0	1	1	1	1	0	0	1	0	0	0	0	0	0
COG1176	ABC-type spermidine/putrescine transport system, permease component I	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0
COG0687	Spermidine/putrescine-binding periplasmic protein	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
COG0687	Spermidine/putrescine-binding periplasmic protein	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
COG0765	ABC-type amino acid transport system, permease component	0	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
COG1126	ABC-type polar amino acid transport system, ATPase component	0	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
COG0834	ABC-type amino acid transport/signal transduction systems, periplasmic component	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
COG4608	ABC-type oligopeptide transport system, ATPase component	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0
COG4413	Urea transporter	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
COG1115	Na+/alanine symporter	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sum		**7**	**12**	**15**	**14**	**23**	**18**	**21**	**18**	**12**	**29**	**15**	**17**	**21**	**8**	**11**	**13**	**18**	**4**	**7**