

S2 Table

Protein description	Gene identification	UniProt ID	Number peptides <sup>a</sup>	<i>C. difficile</i>
<b>Germination</b>				
Peptidase M20/M25/M40 family protein	H477_0435	T0E6L8	8/7	-
Peptidase M20/M25/M40 family protein	H477_0436	T0CTM7	3/2	-
Putative peptidoglycan binding domain protein	H477_0372	T0D2M7	3/7	-
<b>Pathogenicity</b>				
Translation elongation factor Tu	H477_0026 ( <i>tuf</i> )	T0D4X3	15/23	CD0071 ( <i>tuf1</i> )
TCP-1/cpn60 chaperonin family protein	H477_0241	T0D415	4/4	CD0194 ( <i>groL</i> )
Hsp70 family protein	H477_2996	T0CNF5	7/5	CD2461 ( <i>dnaK</i> )
Phosphopyruvate hydratase	H477_4609 ( <i>eno</i> )	T2REI3	1/4	CD3170 ( <i>eno</i> )
<b>Spore assembly</b>				
Glycosyl hydrolases 18 family protein	H477_2042	T0E6S9	10/10	CD1433 ( <i>cotE</i> )
Manganese containing catalase family protein	H477_3485	T0DWI1	4/2	CD2401 ( <i>cotD</i> )
Manganese containing catalase family protein	H477_3486	T0DR76	3/4	-
Uncharacterized protein	H477_3144	T0DXD7	52/21	CD1067 ( <i>cdeC</i> )
<b>Spore resistance</b>				
Reverse rubrerythrin-1	H477_0313	T0D302	4/4	-
Reverse rubrerythrin-1	H477_0314	T0EAX3	4/4	-
Uncharacterized protein	H477_2973	T0DRL7	7/12	CD1511 ( <i>cotB</i> )
Small, acid-soluble spore protein beta	H477_4660	T2RDK8	7/16	-
<b>Unknown putative role</b>				
Putative amidase domain protein	H477_1207	T0E528	1/1	-
Uncharacterized protein	H477_1422	T0E0I6	16/7	-
Uncharacterized protein	H477_1423	T0CMC7	12/5	-
Coat F domain protein	H477_1527	T0E0R1	1/1	-
Uncharacterized protein	H477_1731	T0E5Y2	1/3	-
Cupin domain protein	H477_1872	T0E1S4	1/1	-
Uncharacterized protein	H477_1876	T0E6D8	2/3	-
Uncharacterized protein	H477_2974	T0CDB2	1/5	-
Uncharacterized protein	H477_3325	T0CLP4	6/5	-
Uncharacterized protein	H477_3327	T0DW21	9/5	-
Uncharacterized protein	H477_3692	T2RFS0	1/4	-
Uncharacterized protein	H477_3966	T2RGS3	3/2	-
Uncharacterized protein	H477_4099	T2RG98	23/29	-
Uncharacterized protein	H477_4384	T2RFG7	3/8	-
Fascin domain protein	H477_5266	T0EB21	2/3	-
Uncharacterized protein	H477_5615	T0D6Z2	1/1	-

Cytosolic proteins					
50S ribosomal protein L7/L12	H477_0034 ( <i>rplL</i> )	T0CV21	4/3	NA	
Small GTP-binding domain protein	H477_0047	T0ECN6	1/2	NA	
30S ribosomal protein S8	H477_0067 ( <i>rpsH</i> )	T0D495	1/3	NA	
S4 domain protein	H477_0085	T0E826	2/1	NA	
50S ribosomal protein L17	H477_0088 ( <i>rplQ</i> )	T0D4U1	2/2	NA	
Peptidyl-prolyl cis-trans isomerase	H477_0324	T0EAY0	2/2	NA	
Acyl-CoA dehydrogenase, N-terminal domain protein	H477_0355	T0E6E7	4/2	NA	
CO dehydrogenase/acetyl-CoA synthase complex beta subunit	H477_0479	T0EB97	3/1	NA	
Pyruvate formate lyase family protein	H477_0509	T0D3J0	3/2	NA	
Branched-chain-amino-acid aminotransferase	H477_0714 ( <i>ilvE</i> )	T0CZT3	2/1	NA	
Glycine/sarcosine/betaine reductase complex component C subunit beta domain protein	H477_0807	T0E3Z3	1/1	NA	
Acetate kinase (Acetokinase)	H477_1003 ( <i>ackA</i> )	T0CRP9	1/1	NA	
Propanediol utilization PduL family protein	H477_1156	T0E9N3	1/1	NA	
Pyruvate formate lyase family protein	H477_1816	T0E668	2/2	NA	
Peroxiredoxin	H477_2044	T0CP16	9/8	NA	
Putative membrane protein	H477_2616	T0CFK2	2/3	NA	
Elongation factor Ts	H477_2726 ( <i>tsf</i> )	T0CFX2	1/2	NA	
30S ribosomal protein S2	H477_2728 ( <i>rpsB</i> )	T0CQV5	3/2	NA	
M42 glutamyl aminopeptidase family protein	H477_2794	T0DZF4	1/1	NA	
Tryptophanase 2	H477_3251 ( <i>tnaA2</i> )	T0CM84	3/2	NA	
ATP synthase subunit beta, sodium ion specific	H477_4865 ( <i>atpD</i> )	T2RDU1	3/6	NA	
ATP synthase F1, alpha subunit	H477_4869	T2RCL9	1/2	NA	
M42 glutamyl aminopeptidase family protein	H477_4964	T2RCT6	2/4	NA	

<sup>a</sup> Number of unique peptides in replicate 1/ number of unique peptides in replicate 2.

## S2 Table. Proteins identified by LC MS/MS in the exosporial extracts of *C. sordellii* strain

**ATCC9714.** *C. difficile* exosporial proteins [1] that showed homology to *C. sordellii* proteins are recorded here as gene identifications. Only proteins that were identified with at least one unique peptide in both biological replicates have been included in this table.

## Reference

1. Díaz-González F, Milano M, Olguin-Araneda V, Pizarro-Cerda J, Castro-Córdova P, Tzeng SC, et al. Protein composition of the outermost exosporium-like layer of *Clostridium difficile* 630 spores. Journal of Proteomics. 2015;123:1-13. doi: 10.1016/j.jprot.2015.03.035.