

	Fjoh_4750	Fjoh_2273	Fjoh_1985	Fjoh_4538	Fjoh_1645	Fjoh_3952	Fjoh_3478	Fjoh_3971	SprB	Fjoh_1720	Fjoh_4934	Fjoh_1123
Fjoh_4750	100.00											
Fjoh_2273	25.00	100.00										
Fjoh_1985	23.60	29.47	100.00									
Fjoh_4538	26.51	37.50	48.35	100.00								
Fjoh_1645	23.33	32.98	37.50	62.37	100.00							
Fjoh_3952	26.67	30.85	38.54	58.06	68.00	100.00						
Fjoh_3478	29.35	38.14	38.30	41.86	34.41	32.26	100.00					
Fjoh_3971	32.61	43.01	46.67	53.09	43.18	43.18	57.45	100.00				
SprB	28.42	33.33	27.59	30.86	26.14	26.14	34.83	37.08	100.00			
Fjoh_1720	23.16	34.07	29.21	27.50	26.44	22.99	32.61	25.00	36.56	100.00		
Fjoh_4934	27.37	36.26	28.41	30.38	23.26	22.09	34.78	26.04	40.86	44.44	100.00	
Fjoh_1123	23.40	31.11	30.68	29.11	22.09	23.26	31.87	27.08	41.94	45.45	56.57	100.00

Table 1. Percentage identity matrix of the alignment of the last 100 amino acids of the 12 Type B CTDs found in *F. johnsoniae*. Alignments were realized using ClustalOmega (Madeira et al., 2024)