Table S5. Prediction of the transmembrane domains for FraC, FraD, SjcF1 and SepJ. The program used and the position of the individual TM domains are given. Predictions with low significance are written in *italics*. **For Sep J:** (*) Additional helix with low probability at amino acid residues (aa) 469-488. (**) Only primary helices were considered. For TM5 only four out of ten programs identified a TM region with certainty, while all other programs predict no TM helix or a helix of low certainty. Thus, the polypeptide stretch from aa 565 to 595 was analyzed individually; Minnou did not identify a transmembrane region in this peptide, whereas TM-Finder, TMHMM and SPLIT showed a low significance TM when the section was analyzed individually. Because of experimental evidences (results from a GFP-mut2 fusion (19) and BACTH analysis (Fig 6) localize the C-terminus in the cytoplasm, and interaction with FtsQ (39) and with the SH3 domain of SjcF1 (Supplementary Fig 6) place the N-terminal part in the periplasm) and low reliability for prediction of TM5, we omitted this TM from our assignment. **For FraD and FraC:** A study with a GFP-mut2 fusion has suggested that the C terminus of FraC and the N terminus of FraD is cytoplasmic (21).

	PROGRAM	TM1	TM2	TM3	TM4	TM5	TM6	TM7	TM8	TM9	TM10
SepJ	DAS	415-430	458-481	518-534	540-556	*575-584*	600-616	628-646	664-681	697-713	721-734
	PHDtm	415-432	458-477	*515-532*	537-554	*570-587*	601-618	628-646	665-682	695-712	717-734
	TMHMM*	412-434	*446-465*	512-534	539-561	566-588	592-614	626-648	663-685	692-714	719-738
	TM-Finder	414-435	443-480	515-534	541-559	571-587	600-619	628-644	664-682	699-718	719-735
	SOSUI**	413-435	455-477	512-534	540-562		598-620	627-648	658-680	690-712	719-741
	Minnou	423-440	459-482	508-535	540-560	568-584	596-620	627-646	659-688	693-712	720-737
	TopCon	*414-434*	*463-483*	514-534	541-561	*570-590*	595-615	628-648	661-681	694-714	717-737
	TMPred	412-430	461-484	512-532	537-559		596-615	631-648	661-682	696-713	722-738
	MEMSAT		461-484	515-534	541-561	*571-587*	597-615	626-646	664-686	695-713	722-738
	SPLIT	413-435	458-477	514-534	538-560	568-590	596-619	624-649	659-684	692-714	719-738
	CONSENSUS	**415-435**	**458-482**	**512-534**	**540-560**	**----------**	**596-616**	**628-648**	**661-682**	**695-713**	**720-737**
FraD	DAS	37-51	57-71	87-102	114-128	152-170					
	PHDtm	31-51	56-76	85-105	111-131	152-172					
	TMHMM*	31-53	58-75	85-104	*114-128*	152-171					
	TM-Finder	33-50	51-77	89-105	110-129						
	SOSUI**	27-49	54-75	82-104	111-133	154-176					
	Minnou	33-50	51-77		110-125	149-174					
	TopCon	31-51	56-76	85-105	111-131	152-172					
	TMPred	37-50	51-73	86-104	*114-133*	152-172					
	MEMSAT	25-47	58-74	85-103	115-132	152-170					
	SPLIT	37-50	51-73	86-104		152-172					
	CONSENSUS	**33-51**	**54-75**	**85-104**	**111-131**	**152-172**					
FraC	DAS	14-28	55-70	97-121	*168-174*						
	PHDtm	13-33	46-66	99-119	157-175						
	TMHMM*	10-32	45-67	98-120	154-176						
	TM-Finder	14-30	45-68	97-124	159-174						
	SOSUI**	11-33	49-71	100-122							
	Minnou	12-38	44-69	94-123							
	TopCon	13-33	46-66	99-119	*155-175*						
	TMPred	10-29	46-67	95-116	*156-176*						
	MEMSAT	10-34	46-67	95-115	*155-173*						
	SPLIT	10-34	46-75	95-121	*155-179*						
	CONSENSUS	**11-33**	**46-68**	**97-119**	----------						
SjCF1	DAS	aa42-56									
	PHDtm	aa40-60									
	TMHMM*	*aa38-55*									
	TM-Finder	aa39-58									
	SOSUI**	aa42-65									
	Minnou										
	TopCon	aa37-57									
	TMPred	aa37-56									
	MEMSAT	aa41-57									
	SPLIT	aa37-56									
	CONSENSUS	**aa37-58**									