

**Table S1.** ESI-LC-MS/MS analysis of the wall proteomes of pH 7- and pH 4-grown biomats

AA, amino acid. The data correspond to the data presented in Table 1 of the main paper and are from duplicate runs.

Protein	AA no.	Sequence of identified peptides	Position	Presence*	
				pH 7	pH 4
Als1	1260	YTTSQTSVDLTADGVK	77-92	+	
		STVDPSGYLYASR	176-188	+	
Als3	1155	FTTSQTSVDLTAHGVK	77-92	+	
		CFTAGTNTVTFNDGGKK	150-166	+	
		ISINVDFER	167-175	+	
		TCSSNGIFITYK	255-266	+	
		TLSYANEYTCAGGYWQR	289-305	+	
Als4	2100	FITDQTSIDL VADGR	77-91	+	+
Cht2	583	SNQVALYWGQNGAGGQER	22-39	+	
		TVLLSLGGGVGDYGFSDVASATK	99-21	+	
		FADTLWNK	122-129	+	+
		NYFLSAAPQCPYPDASLGDLLSK	178-200	+	
		VPLDFAFIQFYNNYCSINGQFNYDTWSK	201-228	+	
		LFVGV PATSNIAGYVDTSK	240-258	+	+
		LSSAIEEIK	259-267	+	
		CDSHFAGVSLWDASGAWLNTDEKGENFVVQVK	268-299	+	
Crh11	453	SSDCSPVPALGSSFLEK	29-45	+	
		RFDNPSFK	77-84		
		SNFYIMFGR	85-93	+	
		DYHTYVIDWTK	159-169	+	+
		DAVTWSVDG SVIR	170-182	+	
		SVLVADYSSGK	236-246		+

		QYSYSDQSGSWESIK	247-261		+
		YDQAQDDIK	271-279	+	
Ecm33	423	TGLTAGITSAESVVISDTGLSSLTGINVFK	139-168		+
		VELAELTSIGNSLTINKNDDLTELDFPK	246-273		+
		TIGGALQISDNSELK	276-290	+	+
		VSGGFILK	322-329		
		LSCSAFNK	334-341	+	+
Hyr1	919	EWTNNGLIVAYQNQK	143-157	+	
		HQDFVPATK	181-189	+	
		GTGCVTADEDTWIK	192-205	+	
Ihd1	392	QQSCGGTDDVSSQSATLK	35-52	+	+
Mp65	378	GITYSPYSDNGGCK	128-141	+	+
		SESQIASEIAQLSGFDVIR	142-160		+
		LYGVDCDQVSAVLK	161-174	+	
		SNQQAASSIK	334-344		+
		ADGPYNAEKYWGIYSN (C-terminal peptide)	363-378		+
Pga4	451	GVDYQPGGSSELEDPLADTNVCER	42-65		+
		YFQELGINTIR	69-79	+	+
		AGIYVILDVNTPHSSITR	99-116		+
		SAASVDEYRLPSGLYFNCGDDDMAR	190-214		
		LPSGLYFNCGDDDMAR	199-214		+
		GDSVTTNDDFDNLK	302-315	+	+
		GDSVTTNDDFDNLKSQFEK	302-320		+
		TKNPSGDGGYLK	321-332	+	+
		GLAEPTGHGFDAYVQGNCNAK	365-385		+
Phr1	548	GIAYQQDAAGSVSSGYDADPNR	49-70	+	
		STFETSGYKDR	245-255	+	

		LFQEIGTLYSDK	280-291	+	
		GEYGVASFCSKDR	424-437	+	
		LSYVLNQYYLDQDKK	438-452	+	
Phr2	544	DDPSWDLDLFER	126-137		+
		KSNTDASAFVK	164-174		+
		SIPVGYSANDDSAIR	191-205		+
		ASGYESATNDYK	239-250		+
		DKLSFVMNLYYEQNKESK	424-441		+
Pir1	346	ACSSANNLEMTLHDSVLK	249-266		+
		ACSSANNLEMTLHDSVLKDOTHER	249-271		+
		NLEMTLHDSVLK	255-261		
		WGAIIVANHQFQFDGPIQAGTIYSAGWSIK	271-301	+	+
Rbt1	721	IVTDFESNCPEFDAIK	172-187	+	
Rbt5	241	QSTSSTPCPYWDTGCLCVMPQFAGAVGNCVAK	61-92		+
		VMPQFAGAVGNCVAK	78-92		
Rhd3	204	SDDSKVDGLGLYSK	26- 39	+	+
		SDDSKVDGLGLYSKHEGAAIDYLFLGK	26-52		
		QSFTLGGDVYELGATDNFIPVTINK	79-103		+
		DGTLSTGDDKVYASK	104-119	+	+
		YSESEYAVSNK	127-137	+	+
		YSESEYAVSNKK	127-138		+
		KTDDSAPIVAK	138-150	+	+
Sod4	232	GDSPISTDSK	16-25	+	
		TPAALELGDLGR	105-117		+
Sod5	228	GDAPISTDSK	16-25	+	
		GSPSLIAK	26-33	+	
		SNIEGTIK	40-47	+	

		AATPAAHEVGDLAGK	103-117	+	
		TPAAHEVGDLAGK	105-117		
		PAAHEVGDLAGK	106-117		
		HGNIMGESYKTEYDDSYISLNEK	118-140	+	
		TEYDDSYISLNEK	128-140	+	
Ssr1	234	PACLLACVAK	25-34		
		CSGLNDLSCICTTK	41-54	+	+
		EICPNGDADTAISAFK	64-79	+	+
Tos1	468	TLQYGEATCSCWK	358-370	+	
Utr2	470	HCPEDKPPCCSQFGICGTGAYCLGGCDIR	34-61	+	
		YDYPQTPSR	245-253		+
		IQFSLWPGGDSSNAK	254-268	+	+
		GTIEWAGGLINWDEDIKK	269-287		+
Ywp1	533	VITVVACDEHK	329-339	+	+

\*Probabilistic Mascot scoring was used to evaluate the identified peptides and an individual peptide score of at least 30 ( $P < 0.05$ ) was considered significant for peptide identification.