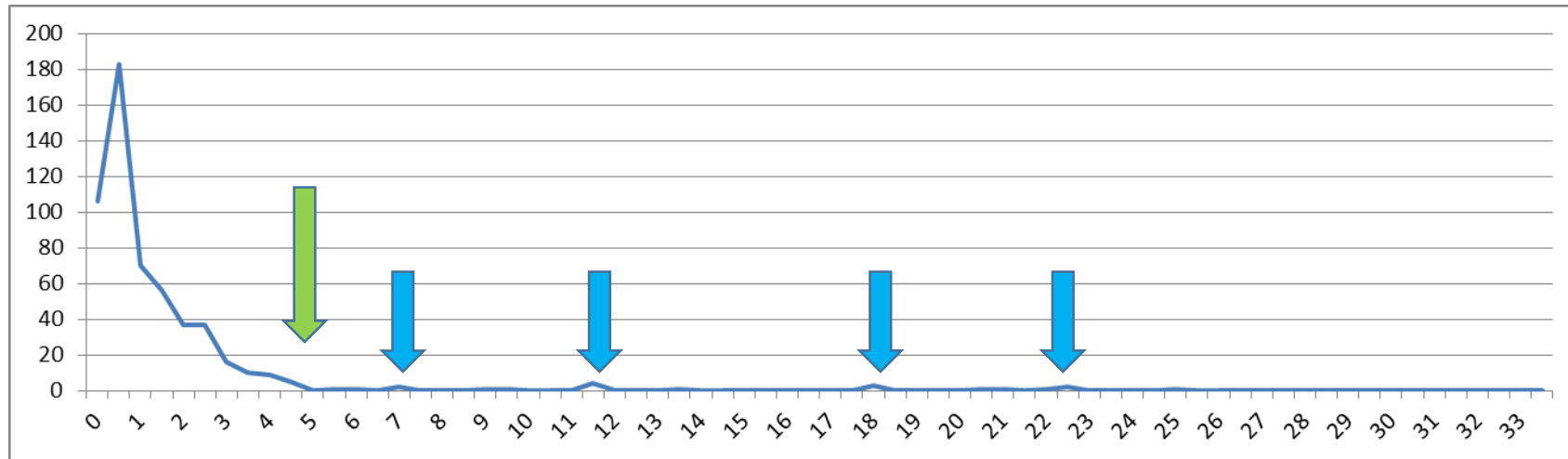


Fig. S1 distribution of supernatant-pellet ratios for Mmc-95010 MS/MS results



**Legend:** The fold-change value between supernatant and pellet was first calculated for each of the proteins that were detected by tandem mass spectrometry (relative frequency in supernatant/relative frequency in pellet). All values were then analysed by a frequency distribution for values ranging from 0 to 33 and 0,5 intervalls (X axis). Values over 33 were not included. A modified value of 1 was substituted to 0 when no spectral counts were detected in the pellet. The Y axis shows the number of proteins within the 0,5 intervalls.

The curve shows a negative exponential shape for values above 1 (proteins detected more frequently in the supernatant). The green arrow represents the limit for outliers, here 5. Blue arrows pinpoint outlier proteins.

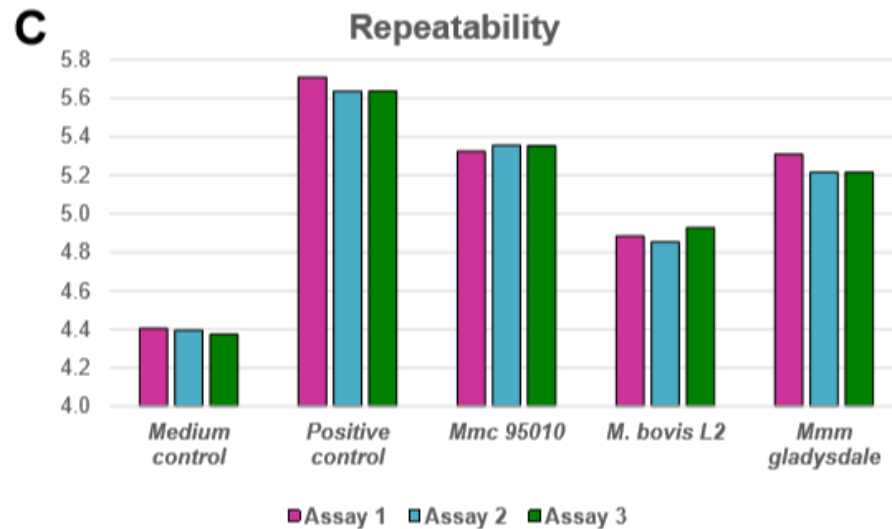
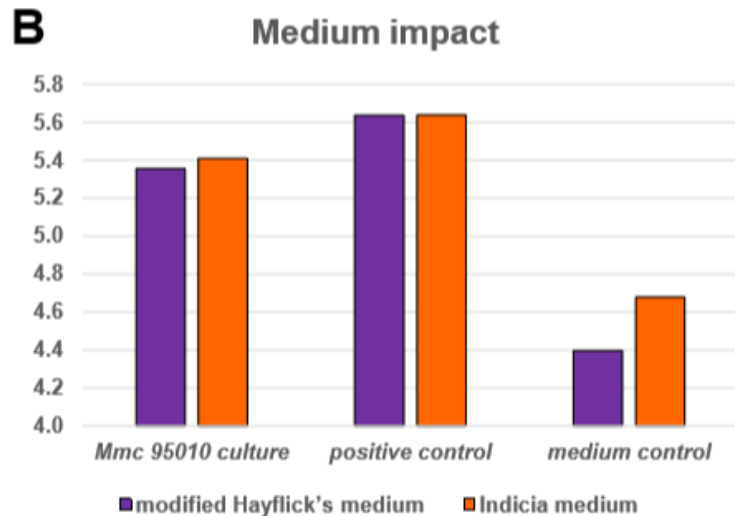
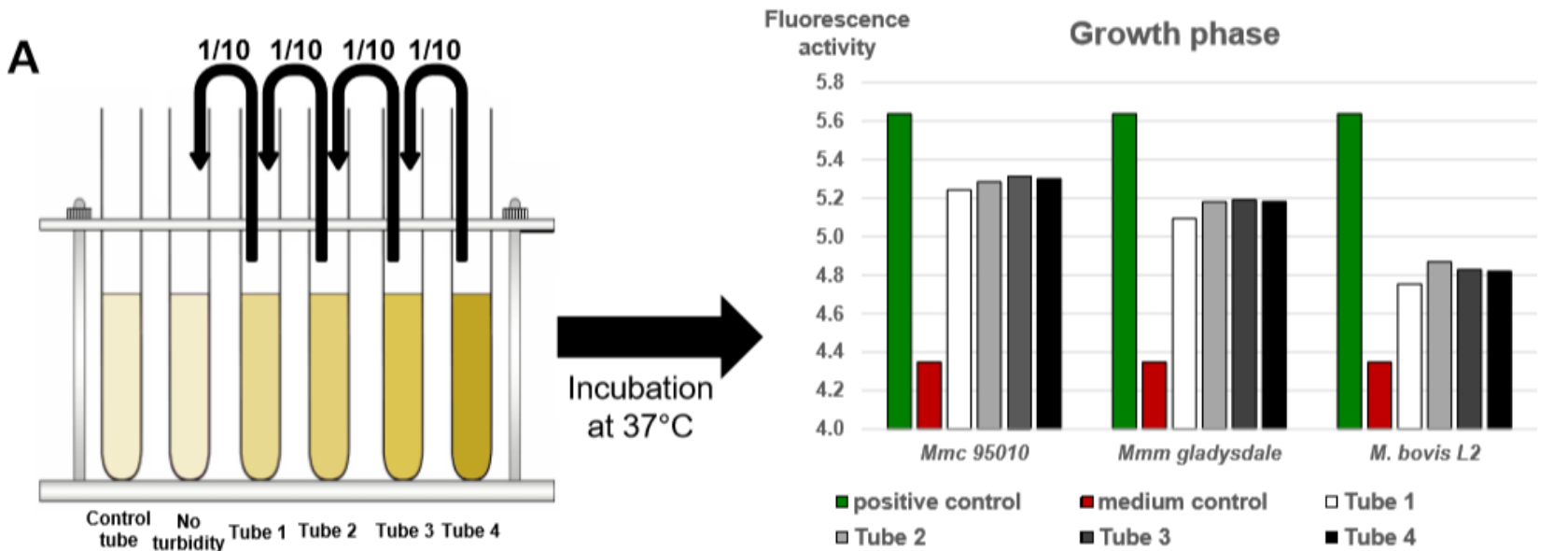


Fig. S2

**Title:** caseinolytic activity measurement robustness evaluation

**Legend:** Caseinolytic activity was assessed on whole cultures of *Mmc* (strain 95010), *Mmm* (strain Gladysdale) and *M. bovis* (strain L2) in modified Hayflick's medium. Each strain was seeded in tenfold dilutions series and incubated until observation of four dilutions showing growth, as evidenced by turbidity of the medium. Tube 1 was the first of the series showing a faint turbidity. The caseinolytic activity of the four cultures were measured and compared with the positive control of the kit and the negative control consisting of a non-seeded medium. Results showed that the caseinolytic activity was stable whatever the length of incubation (A). The possible impact of medium composition was evaluated by comparing the caseinolytic activity of strain *Mmc*-95010 in two media, the modified Hayflick medium and the Indicia medium (B). There was no significant difference of activity between the two media although modified Hayflick medium yielded a lower background value. Finally, the robustness of the method was evaluated by repeating the measurements on three strains having various caseinolytic activities on three different occasions (C). Results showed that the values obtained were very consistent from one day to another.

**Table S1. :** Predicted protease coding genes, expression and foldchange within supernatant and pellet fractions.

**A:** comparisons within *M. capricolum* (Ck, Ck-mut and Mccp-Abomsa); **B:** comparisons within *M. mycoides* (Mmc 95010, Mmm-Rita and Mmm Rita-mut); **C:** *M. bovirhinis* MV5

The proteins for which a significant number of specific peptides were detected, either in the pellet or supernatant (ratio X 10000>10) have their mnemonics highlighted blue. Foldchanges that are significant are highlighted green. Values in a sample that differ significantly (>3 or <1/3) from the closest related sample are highlighted orange. For example, the S41 protease ABC01466.1 is detected almost exclusively in the supernatant of Mcc-Ck strain while it is no more detected in Ck-mut.

**A**

Protein	Ck			Mnemonic	gene name	Annotation (MEROPS and MAGE)	Ck-mut			Mccp-Abomsa			Mnemonic		
	Pellet ratio x10000 (30719)	Supernatant ratio x10000 (8005)	foldchange				Pellet ratio x10000 (31885)	Supernatant ratio x10000 (7323)	foldchange	Protein	Pellet ratio x10000 (28163)	Supernatant ratio x10000 (9607)		foldchange	
ABC01758.1	80.0	20.0	0.25	MCAP_0017	ftsH	FtsH-2 peptidase	83.4	42.3	0.5						
ABC01080.1	4.6	12.5	2.74	MCAP_0093		serotaxin ErbB	2.8	2.7	0.9		CDZ17807.1	55	40.6	0.7	MCCP01_0017
ABC01332.1	2.6	0	0	MCAP_0127		family S9 unassigned peptidase	0.9	0	0		CDZ17906.1	13	26	2	MCCP01_0116
ABC01602.1	44.9	72.5	1.6	MCAP_0133	pyrG	GTP synthetase	46.7	39	2.1		CDZ17944.1	3.5	0	0	MCCP01_0154
ABC01463.1	105.8	252.3	2.4	MCAP_0157	pepA1	family M17 unassigned peptidase	75.2	221.2	2.9		CDZ17950.1	56.8	89.5	1.6	MCCP01_0160
ABC01673.1	61.2	107.4	1.76	MCAP_0193	pepF	aliquipeptidase F	53.3	111.9	2.1		CDZ17976.1	164	199	1.2	MCCP01_0186
ABC01289.1	177.1	334.8	2.23	MCAP_0195	pepA2	family M17 unassigned peptidase	118.8	331	2.8		CDZ18015.1	54.6	72.8	1.3	MCCP01_0225
ABC01466.1	0.32	117.4	360.7	MCAP_0240		subfamily S41A non-peptidase hamalaquer	1.5	0	0		CDZ18017.1	85.5	125.9	1.5	MCCP01_0227
ABC01790.1	0.32	0	0	MCAP_0328		subfamily S41A non-peptidase hamalaquer	0.31	0	0		CDZ18087.1	5.6	8.3	1.5	MCCP01_0237
ABC01488.1	3.26	13.7	4.22	MCAP_0329		subfamily S41A non-peptidase hamalaquer	3.1	17.7	5.7		CDZ18190.1	0	0	0	MCCP01_0400
ABC01430.1	68.0	184.9	2.71	MCAP_0341		subfamily M24B unassigned peptidase	47.3	135.2	2.9		CDZ18191.1	5.3	10.4	1.9	MCCP01_0401
ABC01110.1	1.3	0	0	MCAP_0392		Predicted hydrolase	0.6	2.7	4.3		CDZ18202.1	134	303	2.3	MCCP01_0413
ABC01667.1	0	0	0	MCAP_0394	lzpA	family A8 non-peptidase hamalaquer	0	0	0		CDZ18263.1	2.1	2.1	1	MCCP01_0476
ABC01761.1	29.3	86.2	2.9	MCAP_0420	pepY	peptidase Y	32.3	107.8	3.3		CDZ18265.1	0	0	0	MCCP01_0478
ABC01505.1	12.0	1.3	0.1	MCAP_0434	nagA	family M38 non-peptidase hamalaquer	8.5	0	0		CDZ18290.1	27.3	70.8	2.6	MCCP01_0503
ABC01615.1	11.7	29.9	2.6	MCAP_0445		family S33 unassigned peptidase, lipase	4.7	12.3	2.6		CDZ18310.1	18.4	5.2	0.3	MCCP01_0523
ABC01873.1	2.9	1.2	0.4	MCAP_0446		family S33 unassigned peptidase, lipase	0.9	0	0		CDZ18314.1	8.5	9.4	1	MCCP01_0527
ABC01314.1	29.3	16.2	0.6	MCAP_0466	pepO	family M13 unassigned peptidase	35.7	12.3	0.3		CDZ18315.1	14.9	48.9	3.3	MCCP01_0528
ABC01696.1	0	0	0	MCAP_0509		family C39 unassigned peptidase	0	0	0						
ABC01186.1	12.4	24.9	2	MCAP_0510		family C56 non-peptidase hamalaquer	10.6	15	1.4		CDZ18378.1	0	0	0	MCCP01_0531
ABC01709.1	41.7	32.5	0.8	MCAP_0516	lon	Lon-A peptidase	67.4	90.1	1.3		CDZ18379.1	17.4	17.7	1	MCCP01_0532
ABC01533.1	0	0	0	MCAP_0606		family S33 unassigned peptidase	0	0	0		CDZ18387.1	46.1	33.3	0.7	MCCP01_0600
ABC01133.1	0	0	0	MCAP_0638		subfamily C1A unassigned peptidase	0	0	0		CDZ18464.1	0	0	0	MCCP01_0677
ABC01688.1	0	0	0	MCAP_0675	map	subfamily M24A unassigned peptidase	3.4	8.2	2.4						
ABC01575.1	0	0	0	MCAP_0715		family M79 unassigned peptidase	0	0	0		CDZ18558.1	10.3	26	2.5	MCCP01_0771
ABC01578.1	0.3	0	0	MCAP_0739		family S9 unassigned peptidase	1.2	0	0		CDZ18598.1	1	0	0	MCCP01_0811
ABC01238.1	2.3	0	0	MCAP_0822		family S9 unassigned peptidase	0.9	0	0						
ABC01232.1	10.4	0	0	MCAP_0841	pldB	family S33 unassigned peptidase	13.1	1.3	0.1		CDZ18722.1	7.4	2.1	0.3	MCCP01_0935
ABC01631.1	0	0	0	MCAP_0046	pepQ	Praline dipeptidase	0	0	0		CDZ18750.1	0	0	0	MCCP01_0968
ABC01450.1	0.3	0	0	MCAP_0072		Putative peptidase DUF31	1.5	0	0		CDZ17841.1	0	0	0	MCCP01_0051
ABC01290.1	5.5	0	0	MCAP_0231		Putative peptidase DUF31	8.5	0	0						
ABC01572.1	0.3	1.2	3.8	MCAP_0267		metalloendopeptidase	1.5	1.4	0.9		CDZ18723.1	0	0	0	MCCP01_0090
ABC01081.1	7.8	6.2	0.8	MCAP_0346		Putative peptidase DUF31; Mycoplasma lqG protease	16.3	5.4	0.3		CDZ18538.1	1	0	0	MCCP01_0811
ABC01493.1	30.6	20	0.6	MCAP_0350		Putative peptidase DUF31; Mycoplasma lqG protease	27.3	8.2	0.3						
ABC01767.1	29.6	12.5	0.4	MCAP_0352		Putative peptidase DUF31; Mycoplasma lqG protease	50.2	3.6	0.2		CDZ18166.1	1.4	0	0	MCCP01_0376
ABC01738.1	37.7	23.7	0.6	MCAP_0366		ATP-dependent Clp protease, ATP-binding subunit ClpB	43.3	34.1	0.8		CDZ18223.1	46.5	26	0.6	MCCP01_0434
ABC01856.1	0	0	0	MCAP_0413		family C108 unassigned peptidase	0	0	0						
ABC01813.1	0.3	0	0	MCAP_0508		Metalloprotease catalytic domain superfamily, predicted	0.9	0	0		CDZ18239.1	58.9	53	0.9	MCCP01_0450
ABC01224.1	6.5	12.5	1.9	MCAP_0513		Papain-like cysteine peptidase superfamily	7.2	15	2		CDZ18281.1	0	0	0	MCCP01_0494
ABC01698.1	20.8	46.2	2.2	MCAP_0514		Papain-like cysteine peptidase superfamily	16.9	30	1.8		CDZ18377.1	1.8	2	1.2	MCCP01_0530
ABC01102.1	0.3	1.2	3.8	MCAP_0758		Papain-like cysteine peptidase superfamily	0.3	0	0						
ABC01766.1	0.9	0	0	MCAP_0804		zinc metalloprotease	0.3	0	0		CDZ18385.1	8.9	8.3	0.9	MCCP01_0538
ABC01727.1	2.9	0	0	MCAP_0821		Oxialaql caprotoxin endopeptidase	1.6	0	0						
ABC01562.1	1.3	0	0	MCAP_0846		Putative peptidase DUF31	6.6	0	0		CDZ18698.1	0	0	0	MCCP01_0911
											CDZ18722.1	7.4	2.1	0.3	MCCP01_0935
											CDZ18743.1	13.1	3.1	0.2	MCCP01_0966

B

Protein	Mmc 35010	Mmc 35010	Mmc 35010	Macromoi	Gene	Annotation (MEROPS and MAGE)	Protein	Rita	Rita	Rita	Macromoi	Macromoi	Rita-mut	Rita-mut	Rita-mut
	ratio	Supernat	foldcha					Pellet	Supernat	foldcha			Pellet	Supernat	foldcha
	x10000	at ratio	age					ratio	ratio	ratio			x10000	x10000	age
	(26893)	(11964)						(29391)					(29866)	(7838)	
CBW53764.1	50	2	0,0	MLC_0360	ftsH	FtsH-2 peptidase	ADK69293.1	73	46	0,6	MMS_A0039	MSC_0039	70	63	0,9
CBW53797.1	0	0		MLC_0630		family S9 unassigned peptidases	ADK69778.1	0	0	0,0	MMS_A0086	MSC_0082	0	0	0,0
CBW53831.1	1	1		MLC_1030		subfamily S41A non-peptidase homologues	ADK69367.1	2	0	0,0	MMS_A0112	MSC_0107	9	8	0,8
CBW53842.1	1	0		MLC_1140		family S9 unassigned peptidases	ADK69533.1	2	0	0,0	MMS_A0132	MSC_0116	3	0	0,0
CBW53849.1	42	14	0,3	MLC_1210	pyrG	CTP synthetase	ADK70097.1	53	46	0,9	MMS_A0155	MSC_0134	58	69	1,2
CBW53854.1	4	0	0,0	MLC_1260		subfamily S8A unassigned peptidases									
CBW53874.1	141	317	2,2	MLC_1460	pepA	family M17 unassigned peptidases	ADK69755.1	124	268	2,1	MMS_A0189	MSC_0163	127	259	2,0
CBW53913.1	56	37	0,6	MLC_1850	pepF	oligopeptidase F	ADK69955.1	42	45	1,0	MMS_A0268	MSC_0237	43	52	1,2
CBW53915.1	84	195	2,3	MLC_1870	pepA	family M17 unassigned peptidases					MSC_0235				
CBW53985.1	0	397	397,0	MLC_2570		subfamily S41A non-peptidase homologues	ADK69439.1	0	0	0,0	MMS_A0313	MSC_0281	0	0	0,0
CBW54055.1	0	38	38,4	MLC_3270		subfamily S41A non-peptidase homologues					MSC_0343				
CBW54056.1	3	53	13,2	MLC_3280		subfamily S41A non-peptidase homologues					MSC_0345				
CBW54067.1	45	165	3,6	MLC_3390	pepQ	subfamily M24B unassigned peptidases	ADK69979.1	47	136	2,8	MMS_A0393	MSC_0357	40	85	2,1
CBW54074.1	0	0		MLC_3460		subfamily C1A unassigned peptidases									
CBW54082.1	0	2		MLC_3540	lip1	family S33 unassigned peptidases	ADK69331.1	0	0	0,0	MMS_A0406	MSC_0368	0	0	0,0
CBW54162.1	49	16	0,3	MLC_4340	lon	Lon-A peptidase	ADK69133.1	38	13	0,3	MMS_A0504	MSC_0454	42	26	0,6
CBW54168.1	5	16	2,7	MLC_4400		family C56 non-peptidase homologues	ADK69820.1	2	0	0,0	MMS_A0508	MSC_0458	4	1	0,3
CBW54169.1	0	0		MLC_4410	abc	family C39 unassigned peptidases					MSC_0459				
CBW54212.1	40	18	0,5	MLC_4840	pepD	family M13 unassigned peptidases					MSC_0504				
CBW54233.1	50	29	0,6	MLC_5050	lip2	family S33 unassigned peptidases	ADK69239.1	26	13	0,5	MMS_A0582	MSC_0530	25	20	0,8
CBW54234.1	15	0	0,0	MLC_5060	lip2	family S33 unassigned peptidases									
CBW54235.1	14	16	1,1	MLC_5070	lip3	family S33 unassigned peptidases	ADK69648.1	1	0	0,0	MMS_A0583	MSC_0531	1	0	0,0
CBW54242.1	12	3	0,2	MLC_5140	nagA	family M38 non-peptidase homologues	ADK70009.1	13	0	0,0	MMS_A0585	MSC_0533	13	4	0,3
CBW54257.1	0	0		MLC_5230		subfamily C1A unassigned peptidases	ADK69950.1	0	0	0,0	MMS_A0602	MSC_0550	0	0	0,0
CBW54260.1	35	66	1,8	MLC_5320	pepV	peptidase V	ADK69226.1	37	69	1,8	MMS_A0606	MSC_0554	32	74	2,3
CBW54267.1	0	0		MLC_5390		family C108 unassigned peptidases	ADK69253.1	0	0	0,0	MMS_A0613	MSC_0561	0	0	0,0
CBW54280.1	0	0		MLC_5520	ispA	family A8 non-peptidase homologues	ADK69628.1	0	0	0,0	MMS_A0642	MSC_0584	0	0	0,0
CBW54282.1	1	0		MLC_5540	pepD	subfamily S9C unassigned peptidases	ADK69713.1	0	0	0,0	MMS_A0644	MSC_0586	0	0	0,0
CBW54326.1	2	0		MLC_5980		subfamily S8A unassigned peptidases									
CBW54404.1	6	21	2,9	MLC_6750	map	subfamily M24A unassigned peptidases	ADK69880.1	8	13	1,5	MMS_A0795	MSC_0724	9	18	1,7
CBW54445.1	0	0		MLC_7150		family M79 unassigned peptidases	ADK70111.1	0	0	0,0	MMS_A0841	MSC_0767	0	0	0,0
CBW54490.1	7	0	0,0	MLC_7600	pidB	family S33 unassigned peptidases	ADK69837.1	21	0	0,0	MMS_A0919	MSC_0837	19	1	0,1
CBW54520.1	6	14	1,9	MLC_7900		esterase EstB					MSC_0861				
CBW54631.1	0	0		MLC_9010		subfamily M23B non-peptidase homologues									
CBW54632.1	0	1		MLC_9020		subfamily M23B non-peptidase homologues									
CBW54642.1	3	0	0,0	MLC_9120		subfamily S8A unassigned peptidases	ADK70002.1	15	0	0,0	MMS_A1133	MSC_1061	20	11	0,6
CBW53777.1	22	29	1,3	MLC_0490		Putative peptidase DUF31	ADK69751.1	0	0	0,0	MMS_A0054	MSC_0052	0	0	0,0
CBW53798.1	3	0	0,0	MLC_0700		Oriallycaprotein endopeptidase	ADK69037.1	4	0	0,0	MMS_A0087	MSC_0083	4	1	0,2
CBW53816.1	0	0		MLC_0880	pepQ	Proline dipeptidase	ADK69817.1	0	0	0,0	MMS_A0094	MSC_0090	0	0	0,0
CBW53878.1	0	0		MLC_1500		Papain-like cysteine peptidases superfamily					MSC_0170				
CBW53944.1	2	1		MLC_2160		Peptidase_M78									
CBW53958.1	3	3	0,8	MLC_2300		Inactive homolog of metal-dependent proteases	ADK70014.1	2	0	0,0	MMS_A0343	MSC_0312	1	1	0,6
CBW53994.1	1	10	5,8	MLC_2660		Putative peptidase DUF31	ADK69165.1	1	0	0,0	MMS_A0304	MSC_0271	14	24	1,6
CBW54029.1	0	0		MLC_3010		Peptidase_M78									
CBW54081.1	1	8	4,8	MLC_3530		Papain-like cysteine peptidases superfamily									
CBW54164.1	1	1		MLC_4360		Papain-like cysteine peptidases superfamily									
CBW54165.1	12	12	0,9	MLC_4370		Papain-like cysteine peptidases superfamily									
CBW54170.1	1	0		MLC_4420		Metalloprotease catalytic domain superfamily, predicted	ADK69668.1	1	0	0,0	MMS_A0511	MSC_0461	0	0	0,0
CBW54304.1	30	10	0,3	MLC_5760	clpB	ATP dependent Clp protease ATP binding subunit	ADK69129.1	44	24	0,5	MMS_A0674	MSC_0613	44	37	0,8
CBW54318.1	13	11	0,8	MLC_5900		Putative peptidase DUF31; Mycoplasma IgG protease	ADK69475.1	59	56	0,9	MMS_A0686	MSC_0625	71	110	1,5
CBW54320.1	18	44	2,4	MLC_5920		Putative peptidase DUF31; Mycoplasma IgG protease	ADK69746.1	44	45	1,0	MMS_A0688	MSC_0627	52	66	1,2
CBW54322.1	4	0	0,0	MLC_5940		Putative peptidase DUF31; Mycoplasma IgG protease	ADK69723.1	19	28	1,4	MMS_A0696	MSC_0635	30	57	1,8
CBW54324.1	7	14	1,8	MLC_5960		Putative peptidase DUF31; Mycoplasma IgG protease									
CBW54539.1	1	1		MLC_8090		Putative peptidase DUF31	ADK69542.1	0	0		MMS_A0983	MSC_0897	2	0	0,0
CBW54606.1	0	0		MLC_8760		zinc metalloprotease	ADK69190.1	0	0		MMS_A1002	MSC_0915	0	0	0,0

C

**Predicted protease coding genes and tandem mass spectrometry detection of proteases for *M. borviridis* (strain MV5)**

Protein	ratio		foldchange	Mnemonic	gene name	Annotation
	supernatant x10000	pellet x10000				
BBA22062.1	33	0	0	MBVR14_L_0	pepF	PepF Oligoendopeptidase F
BBA22075.1	71	60	1	MBVR14_L_0	pepO	PepO Predicted metalloendopeptidase
BBA22077.1	0	0		MBVR14_L_0	lepB	LepB Signal peptidase I
BBA22091.1	0	0		MBVR14_L_0	lspA	LspA lipoprotein signal peptidase
BBA22105.1	0	0		MBVR14_L_0	map	Map Methionine aminopeptidase
				MBVR14_L_0180		Peptidase_S8 Subtilase family
BBA22164.1	104	246	2	MBVR14_L_0	pepB (pepB)	PepB Leucyl aminopeptidase
				MBVR14_L_0214		Peptidase S8 family domain
BBA22185.1	94	326	10	MBVR14_L_0224		DUF31 Putative peptidase
BBA22211.1	34	299	9	MBVR14_L_0284		DUF31 Putative peptidase
				MBVR14_L_0377		DUF31 Putative peptidase
BBA22270.1	24	155	6	MBVR14_L_0378		DUF31 Putative peptidase
BBA22288.1	3	0	0	MBVR14_L_0403		proline iminopeptidase
BBA22289.1	42	30	1	MBVR14_L_0404		peptidase M24 family protein
				MBVR14_L_0407		DUF31 Putative peptidase
BBA22293.1	1	6	3	MBVR14_L_0414		proline dipeptidase
BBA22294.1	30	26	1	MBVR14_L_0	pepB (pepB)	PepB Leucyl aminopeptidase
BBA22400.1	22	45	2	MBVR14_L_0605		FrvX Putative aminopeptidase
BBA22412.1	0	0		MBVR14_L_0625		N-terminal double-glycine peptidase domain
				MBVR14_L_0683		Peptidase S8 family domain
				MBVR14_L_0723		Putative aminopeptidase FrvX
BBA22489.1	31	448	5	MBVR14_L_0756		DUF31 Putative peptidase
BBA22490.1				MBVR14_L_0760		DUF31 Putative peptidase
BBA22491.1	3	123	33	MBVR14_L_0761		DUF31 Putative peptidase
BBA22507.1	5	0	0	MBVR14_L_0794		FrvX Putative aminopeptidase
BBA22542.1	2	118	38	MBVR14_L_0853		DUF31 Putative peptidase
BBA22552.1	76	4	0	MBVR14_L_0	lon	ATP-dependent Lon protease
BBA22557.1	0	4	4	MBVR14_L_0875		Peptidase S8 family domain
BBA22600.1	0	0		MBVR14_L_0	clp	ATP-dependent protease ClpP
BBA22067.1	0	0		MBVR14_L_0020		AprE Serine protease
BBA22069.1	1	0		MBVR14_L_0022		AprE Serine protease
				MBVR14_L_0090		AprE Serine protease
BBA22231.1	7	0	0	MBVR14_L_0314		ThiJ Putative intracellular protease/amidase
BBA22246.1	63	2	0	MBVR14_L_0	ftsH	HflB ATP-dependent Zn proteases
BBA22300.1	0	0		MBVR14_L_0432		serine protease
BBA22308.1	1	2		MBVR14_L_0445		AprE Serine protease
				MBVR14_L_0687		AprE Serine protease
BBA22467.1	14	4	0	MBVR14_L_0707		AprE Serine protease
BBA22541.1	57	317	5	MBVR14_L_0	ftsN* (pape)	FtsN Cell division protein

The mnemonics highlighted in blue correspond to proteins which are detected by mass spectrometry (>4 spectral counts)

The proteins highlighted in green are those which proportion is significantly higher in the supernatant than in the cell pellet.

Protease coding genes were data-mined from the MV5 genome annotation.

An estimation of the protein ratio in the sample, pellet or supernatant, was calculated by dividing the number of specific spectral counts for this protein by the total number of spectral counts for the sample. These proportions were compared by calculating a foldchange value (supernatant/pellet). Proteins which are consistently detected (ratio X 10000>10) have their mnemonic highlighted blue. Proteins which are significantly more detected in the supernatant are highlighted in green. For strain MV5, four DUF31 putative peptidases were the only proteases that were significantly overrepresented in the supernatant.

## Supl. Material

This Material shows the BLASTP results obtained either with the full MLC\_2570 peptidic sequence through the MAGE interface against various mycoplasma genomes or the BLASTP results obtained when using the conserved peptidase S41 superfamily domain and interrogating the nr NCBI database excluding mycoplasma sequences.

For each sequence an alignment is shown, followed by the protein full sequence with the main characteristics highlighted (N-terminal signal sequence, C-terminal transmembrane sequence, active site of the serine protease and eventually LPXTG sortase domain, for *Ruminococcus* sequences) as well as the TMHMM results.

The N-terminal signal sequence is highlighted in blue when ending with a C and potentially a predicted lipoprotein.

### Query

```
>MLC_2570|ID:18101481| transmembrane protein and tail
specific protease [Mycoplasma mycoides subsp. capri LC
95010]
MKLVKKIGFLSLSAISILGPLAMINNLTTDNNLLITKRFLSSSNSNVGLKSYDYINLINN
KYIPAKINLHDHNGIAYIGVKEFLNSLDGLISFSKIKVRPYQANFYKEKEISYNYKDNK
VVLNSISKYSNNKTTNYQLEIDSKNKTITVSDNDFFTDIFTFYRGEEDLNIDFLNTEI
VNKNKHIVFDLNKYGIEILNDQNDLYLPLVLINQLFLNQSNVQLYFNGQSVNLFAYSKTL
GKVELLKQLKHSYLNQNHIPAGLKDFQYKYLGFDFDHFYGIKLDKNASYKDLFKKYEKY
IKADNTTHYLTSRYLIEQLDDLHSSYLLTGYYNKDLETINKAVLKTTTPRSDFKDIARR
LSAYYDKELNYKNVYTPDRITSVISFKNFEANSAPFKIEESLQAQRDGIKNIVLDVSFNS
GGYLGTAFEIMGFLTDKPFKSYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFSFSAGN
IFPQLVKDNNVAKVIGFKTAGGASAISQAILFTGDIQLSSNNVLTNKSHQSLEYGVNPD
ITLGFDPFKQTEKFFASAYIQQAINKDTNTLNSIPATHSSVIEPNYVHELVEQPQPLQLS
RKTDETEIKNLNNLFSSIKETERKDAYFVLGALGVVISLAISFVIIKLLK*
```

In red, the peptides detected by tandem massspectrometry from the supernatant sample

**S** : active site of the serine protease

Grey: N-terminal transmembrane segment with a Signal Peptidase I domain

Yellow: C-terminal transmembrane segment

Green: peptidase S41 superfamily

*M. agalactiae*

**Q** - 1 - **MAG\_5760** [Mycoplasma agalactiae PG2 chromosome NC\_009497]  
hypothetical protein | automatic/finished

Length=643

Score = 212 bits (539), Expect = 1e-66  
Identities = 102/154 (66%), Positives = 127/154 (82%), Gaps = 0/154 (0%)

```

Query 1 TSVISFKNFANSFAFKIEESLKQAQRDGIKNIIVLDVFSNNGYLGTAFEMGFLTDKPFK 60
      TSVISFK FE NSA IE+SL +A+ GIKNI+ +V+ N GGY+G A+EIMGFL+DKPF
Sbjct 357 TSVISFKAFEENSAVSIKSLNEAKEKGIKNIIFNVTHNGGGYIGAAAYEIMGFLSDKPFN 416

Query 61 SYSYNPLTKQKQVETIKSRFKKYDFNYVLTSPFSFAGNIFPQLVKDNNVAKVIGFKTA 120
      +++NPLT E K+ETIKS+ KYDFNY+VLT+PFSSAGNIFPQLV+DNN+ K+IG+ T
Sbjct 417 VVWTHNPLTGENKIETIKSKKTKYDFNYFVLTAPFSFAGNIFPQLVRDNNLTKIIGYDTF 476

Query 121 GGASAIQAILPTGDIIQLSSNNVLTNKSHQSLE 154
      GG+SAI ILPTGDIIQLSSN V T+K+ ++ E
Sbjct 477 GGSSAIGYYILPTGDIIQLSSNTVFTDKNFKTTE 510

```

```

>MAG_5760|ID:18180474| hypothetical protein [Mycoplasma agalactiae PG2]
MKLKKLKHIFLASCVTAPFIGLSAIVNNSNDEISSKLNEFDLIPLAKELNRQPKNKKVK
MYMHNVPYIGIKEFLDAVSKI VKNENIEYSFDVKKVLTLYKTDEGKNSLKIVIDYDKQ
KITVSDYSFFISILRNHERGEEKLDIEFLKSENKNTKEFEYDLRKYDIFILKDKSDLYL
PQILLNQIFL NESNIQTYFNGEVNLNFRFVESLSGSGYFYLRQSIKNNETSIPSGLKEFQ
AKYFSLLDHYGKIFNEDETMNESYKGFIEYTKNRITHTNSDIHYLTTREIIRDLDSDH
TAYILDGYYSKNNEVLKHPKSNKRI TDRFNLGKGLKLYFKSNIEYQNVFTPDGKTSVI
SFKAFEENSAVSIKSLNEAKEKGIKNIIFNVTHNGGGYIGAAAYEIMGFLSDKPFNVWTH
NPLTGENKIETIKSKKTKYDFNYFVLTAPFSFAGNIFPQLVRDNNLTKIIGYDTFGSS
AIGYYILPTGDIIQLSSNTVFTDKNFKTTEFGISPDPFKENIETGAKNLYDLQKQFV
NDINKEKKEPNKPINKPDPTEPLPKPAEPSVPI SRPHNNPEFNSDNGNIMI IIPDSGFTP
NNIEKSGKGRKAGI IAGISVGIASGVAALSMSYFLVKKFRK*

```

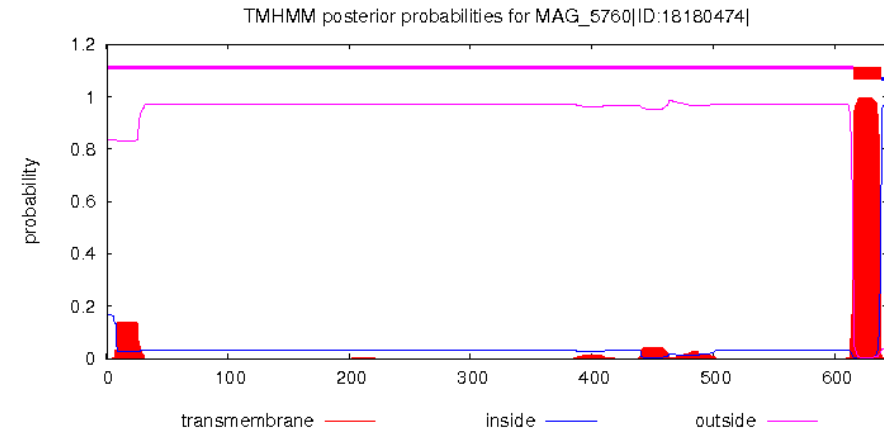
### TMHMM result

[HELP](#) with output formats

```

# MAG_5760|ID:18180474| Length: 643
# MAG_5760|ID:18180474| Number of predicted TMHs: 1
# MAG_5760|ID:18180474| Exp number of AAs in TMHs: 27.26879
# MAG_5760|ID:18180474| Exp number, first 60 AAs: 2.75652
# MAG_5760|ID:18180474| Total prob of N-in: 0.16586
MAG_5760|ID:18180474| TMHMM2.0 outside 1 615
MAG_5760|ID:18180474| TMHMM2.0 THelix 616 638
MAG_5760|ID:18180474| TMHMM2.0 inside 639 643

```





M. alkalescens

1 - AMWK\_v1\_90025 [Mycoplasma alkalescens 14918 WGS NZ\_AMWK] conserved exported protein of unknown function | automatic/finished

Length=665

Score = 225 bits (573), Expect = 2e-71
Identities = 108/154 (70%), Positives = 133/154 (86%), Gaps = 0/154 (0%)

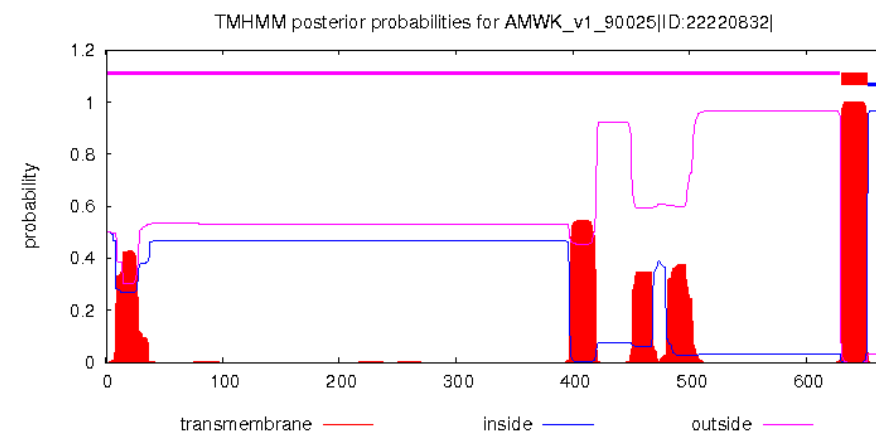
Query 1 TSVISFKNFANSFAKIEESLQQRDGIKNIVLDVSNFSGGYLGTAFEIMGFITDKPFFK 60
Sbjct 367 TSVISFK FE +SA IE+SLK+A+ G+KNIV +++ N GG++G AFEIMGF+TDKPFK 426
Query 61 SYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFSFAGNIFPQLVKDNNVAKVIGFKTA 120
Sbjct 427 SY+YNPL+ E+K+E I+S++ KYDFNYVLTSP++FSAGNIFPQ+VKDNNV KVIG+KT 486
Query 121 GGASAISQAILPTGDIIQLSSNNVLTNKSHQSLE 154
Sbjct 487 GGASAISYAILPTGDIIQLSSNTVFTDKHFRTE 520

>AMWK\_v1\_90025|ID:22220832| conserved exported protein of unknown function [Mycoplasma alkalescens 14918]

MKISKLKNLIVISSTFILPFAVISAACATKADPPFAVISAACATKADFDESALKEFLIPLA
KELNSQNNRNKIKMYMHNVDVAYVGIKEFLRSISTIIKHDKLTFSFNNDKVKLVKTDLD
EKNNPSLIVDYKSKKIIVSNYKFFTEILKKYERGEKELKISFLKRENQNLNQEFEFDLKK
YNIDILKGGDDLYLPQILLNQVILNESNIQTYFNEDVFNIFRFAESLTGFGSITLKMSPK
NNVKNIPDGLKNFQLKYYPFLLFDYGGIKLDKNKSYKEFFNNYKTDILSNDSDTHYLSLK
KIISDLDLHTAYKLDGYDKSRLSSQIANKTRTNGQIEIGNHLQKYYFKNNTEYQNV
YTSDNKTSVISFKAFEEDSASHIEKSLKEAKEKGVKNIVFNLTNLGGGFIGAFAEIMGFM
TDKPFKSYTYNPLSGEKKIELIQSKYPKYDFNYVLTSPYAFAGNIFPQMVKDNVGVK
IGYKTFGGASAISYAILPTGDIIQLSSNTVFTDKHFRTEFGIEPNFKYDLSKNPEKL
YDLTNIQNIWNISQGFDDVIEVKESDPETKSEHKTSKNNPHMTSNLI PRDSSKHHFSL
NSNSSTIENKSGNISKLAKPVNMSNNVKTAILSTVVIAILAIAISVYFVIRKQKRKLN
LKNEI\*

HELP with output formats

# AMWK\_v1\_90025|ID:22220832| Length: 665
# AMWK\_v1\_90025|ID:22220832| Number of predicted TMs: 1
# AMWK\_v1\_90025|ID:22220832| Exp number of AAs in TMs: 58.41398
# AMWK\_v1\_90025|ID:22220832| Exp number, first 60 AAs: 8.60435
# AMWK\_v1\_90025|ID:22220832| Total prob of N-in: 0.50019
AMWK\_v1\_90025|ID:22220832| TMHMM2.0 outside 1 629
AMWK\_v1\_90025|ID:22220832| TMHMM2.0 TMhelix 630 652
AMWK\_v1\_90025|ID:22220832| TMHMM2.0 inside 653 665





M. auris



- 1 - AORI\_v1\_120043 [Mycoplasma auris 15026 WGS NZ\_AORI]  
conserved exported protein of unknown function | automatic/finished

Length=731

Score = 209 bits (531), Expect = 3e-65  
Identities = 99/154 (64%), Positives = 132/154 (86%), Gaps = 0/154 (0%)

```

Query 1  TSVISFKNFEANSFAKIEESLKQQRDGIKNIVLDVSNSSGGYLGTAFEIMGFLLDKPFFK 60
          T +ISF+ F+ +A IE+SL+ A+ +GIKNIV +++ NSGGY+G+AFEIMGF+T+KPF
Sbjct 393  TGIISFRAFDMKTASGIEKSLEIAKNEGIKNIVFNITVNSGGYVGSFAFEIMGFMTNKPFY 452

Query 61  SYSYNPLTKEQKQVETIKSRFKKYDFNYVLTSPFSFSAAGNIFPQLVKDNNVAKVIGFKTA 120
          SY+YNPL++E+ VE IKS++KKYDFNY++LTSPFSFSA NI Q+VKDN VAKVIG+KT
Sbjct 453  SYTYNPLSQEKSVEEIKSKYKDYDFNYFILTSPPFSF[AANILAQMVKDNKVAKVIKGYKTH 512

Query 121  GGASAIQAILPTGDIIQLSSNNVLTNKSQSLE 154
          GGASAI+ AILPTGDIIQ+SSN+V ++K+ ++E
Sbjct 513  GGASAINYAILPTGDIIQISSNHVFSKDNFNIE 546

```

>AORI\_v1\_120043|ID:2222831| conserved exported protein of unknown function [Mycoplasma auris 15026]

```

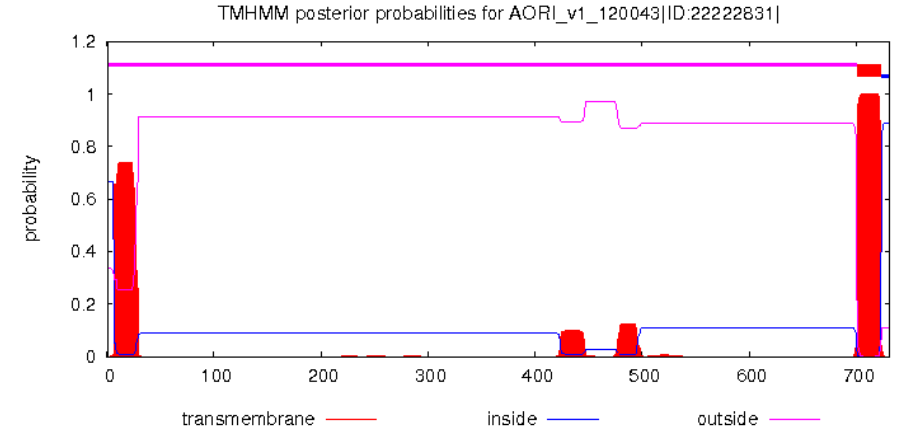
MRLGKKTFFIFSLLVNAILPMSLLSFSVQNKNTNKRLLNKNKLLKNNSSSTFKLKEYEFS
LTKNNSNELKKIELGLYNDVAYIGIKEFLKATKTVTNFNDYSFSWIKLNNKLYKKQKYLE
HNFKDNKVTNLVINKLVNDSDDDDQIQNKYSIEIDFQTKKINVSNYKFFTEILKDYKRGE
EELQIEFLSKKNLNEKTHFSYDLSKYDIEILKDKKDYLPVLLNQILLNESNYQTYFNG
EYFNLFNYFETLGSYGPALLKQSNVNNENIPLGLKEFYKYFPFLFDYIYGIKNKNNQS
YKNFFATYEDDILAENDNHYLATKDIINDLGLDLSHSTSIDGYNHNDNDAIKNIEKEFRKI
RRIRKRAEIEENELGKRDFGKIEYSITYTPDRKTGIISFRAFDMKTASGIEKSLEIAKNEG
IKNIVFNITVNSGGYVGSFAFEIMGFMTNKPFYSYTYNPLSQEKSVEEIKSKYKDYDFNYF
ILTSPPFSF[AANILAQMVKDNKVAKVIKGYKTHGGASAINYAILPTGDIIQISSNHVFSK
NFNIEFGVVKPDIFFEEDIYKNQDQLYDLNLIQQIVNKETNEEAKQDISFLIKNPNLGLL
KSSDFVSLYEALKNKNPNFNIAFDLLEFQSINKIPNEKNEYEVSLKIKDNNNTNYFGTIKL
IFSLEENAKFPNPNNGNTEDRNEKDKNNADKNRPKNKTLR[ILGIFGSLLLVISLILVIVF
LVLKLKKTQK*

```

```

# AORI_v1_120043|ID:2222831| Length: 731
# AORI_v1_120043|ID:2222831| Number of predicted TMHs: 1
# AORI_v1_120043|ID:2222831| Exp number of AAs in TMHs: 43.1445
# AORI_v1_120043|ID:2222831| Exp number, first 60 AAs: 15.49605
# AORI_v1_120043|ID:2222831| Total prob of N-in: 0.66538
# AORI_v1_120043|ID:2222831| POSSIBLE N-term signal sequence
AORI_v1_120043|ID:2222831| TMHMM2.0 outside 1 700
AORI_v1_120043|ID:2222831| TMHMM2.0 TMhelix 701 723
AORI_v1_120043|ID:2222831| TMHMM2.0 inside 724 731

```



# plot in postscript, script for making the plot in gnuplot, data for plot

*M. bovis*



- 1 - [MBOVPG45\\_0421](#) [Mycoplasma bovis PG45 chromosome NC 014760]  
S41B peptidase family lipoprotein | automatic/finished

Length=652

Score = 223 bits (569), Expect = 6e-71  
Identities = 107/154 (69%), Positives = 132/154 (86%), Gaps = 0/154 (0%)

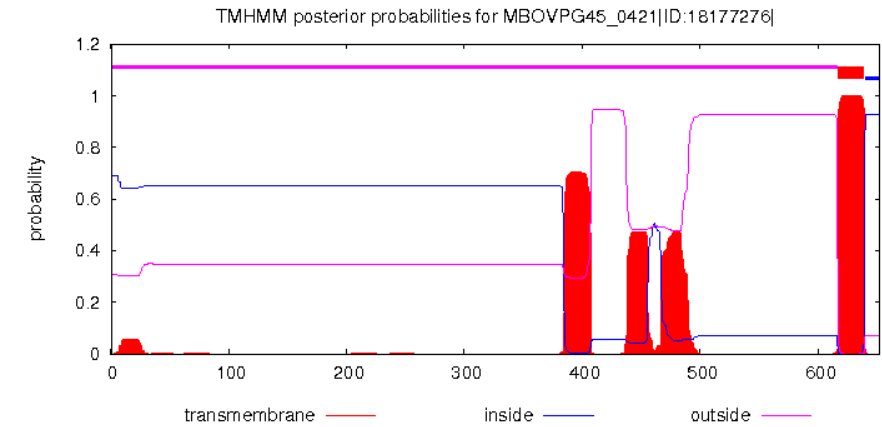
```
Query 1 TSVISFKNF EANS AFKIEESLQAQRDGIKNIVLDVSNSSGGYLGTA FEIMGFLTDKPFK 60
      TSVISFK FE +SA IE+SLK+A+ +KNIV +++ N GG++G AFEIMGF+TDKPFK
Sbjct 354 TSVISFKTFEEDSASHIEKSLKEAKEKSVKNIVFNLTNLGGGFIGA AFEIMGFMTDKPFK 413

Query 61 SYSYNPLTKEQKVETIKSRFKKYDFNYYVLTSPFSFSAGNIFPQLVKDNNVAKVIGFKTA 120
      SY+YNPL+ E+K+E I+S++ KYDFNYYVLTSP++FSAGNIFPQ+VKDNNV KVIG+KT
Sbjct 414 SYTYNPLS GEEKKIELIQSKYPKYDFNYYVLTSPYAFSAGNIFPQMVKDNNVGVIGYKTF 473

Query 121 GGAS AISQA ILPTGDI IQLSSNNVLTNKSHQSLE 154
      GGAS AIS AILPTGDI IQLSSN V T+K ++ E
Sbjct 474 GGAS AISYAILPTGDI IQLSSNTVFTDKHFRTTE 507
```

```
>MBOVPG45_0421|ID:18177276| S41B peptidase family lipoprotein [Mycoplasma bovis PG45]
MKISKIRNLVISSAFILPFTVISATCETKADFDESALKEFLIIPLAKELNGRIDRKNNKI
KMYMHNDAVAYVGIKEFLRSISTIKHDKLTFNFNDKVKLVKTDLDEKNNPSLTVDYKL
KKIIVSNYKFFTEILKKYERGEKLIKISFLKRENQNLNEEFEDLKKYNIDILKGDLDLY
LPQILLNQVILNESNIQTYFNDDVFNIFRFAESLTGFGSISLKMSPKNNVKNIPDGLKNF
QLKYYPFLFDYGYGKLDKNKSYKEFFNNYKTDILSNDSDTHYLSTKKIISDLDDPHTAY
KLDGYDYSRDLSSRQIANKKRTNGQIELGNHLQKQYFKNNEYQNVYTPDNKTSVISFK
TFEEDSASHIEKSLKEAKEKSVKNIVFNLTNLGGGFIGA AFEIMGFMTDKPFKSYTYNPL
SGEEKKIELIQSKYPKYDFNYYVLTSPYAF SAGNIFPQMVKDNNVGVIGYKTFGGAS AIS
YAILPTGDI IQLSSNTVFTDKHFRTTEFGIEPNFKFYDLSKNPEKLYDLTNIQNI VNNI
SQGKFDVIEVKESEPETKSEHKT SKNNPHMNSNLMPRNSSKEHFSLNSNSSTIENKSDN
ISKLSAKSVNMSNNVKIAIILSTVVIAILAIAISVYFVIKKQKRKLNKNEI
```

```
# MBOVPG45_0421|ID:18177276| Length: 652
# MBOVPG45_0421|ID:18177276| Number of predicted TMHs: 1
# MBOVPG45_0421|ID:18177276| Exp number of AAs in TMHs: 58.92705
# MBOVPG45_0421|ID:18177276| Exp number, first 60 AAs: 1.08566
# MBOVPG45_0421|ID:18177276| Total prob of N-in: 0.69144
MBOVPG45_0421|ID:18177276| TMHMM12.0 outside 1 616
MBOVPG45_0421|ID:18177276| TMHMM12.0 TMhelix 617 639
MBOVPG45_0421|ID:18177276| TMHMM12.0 inside 640 652
```



# [plot](#) in postscript, [script](#) for making the plot in gnuplot, [data](#) for plot

2 - **MCAP\_0328** [Mycoplasma capricolum subsp. capricolum ATCC 27343 chromosome NC\_007633]  
 hypothetical protein | automatic/finished

Length=682

Score = 226 bits (575), Expect = 1e-71  
 Identities = 107/154 (69%), Positives = 132/154 (86%), Gaps = 0/154 (0%)

```

Query 1  TSVISFKNFANSFAFKIEESLKAQRDGIKNIVLDVSNFSGGYLGTAFAEIMGFLLTDKPFK 60
          TSVISFK FE ++A +IE+SLK+AQ GIKNI+ +V+ N GG++G A+E+MGFLLTDKPF
Sbjct 348 TSVISFKQFEIDTAKQIEKSLKEAQNKGIKNIIFNVTQNGGGFIGAAYELMGFLLTDKPFN 407

Query 61  SYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFSFAGNIFPQLVKDNNVAKVIGFKTA 120
          Y+YNPL+KEQKVETIKS++ KY+FNYY+LTSP+SFSAGNIFPQ+ KDN VAK+IG+KT
Sbjct 408 VYNYNPLSKEQKVETIKSKYNKYNFNYYILTSFYFAGNIFPQITKDNKVAKLIIGYKTF 467

Query 121 GGASAIQAILPTGDIIQLSSNNVLTNKSQSLE 154
          GGAS+I ILPTGDIIQLS+NNV TN +SLE
Sbjct 468 GGASSIGYFILPTGDIIQLSTNNVFTNKKFRSLE 501
  
```

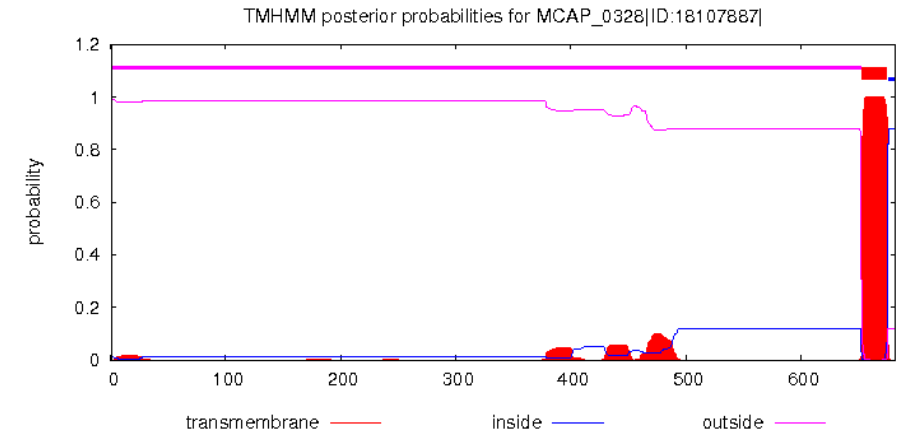
>MCAP\_0328|ID:18107887| hypothetical protein [Mycoplasma capricolum subsp. capricolum ATCC 27343]

```

MKLLLSLFLFSNTITPVLTSVNIIVSTNNTLSLKEYKLNLSLTKSVEIKNKKKINLHLHK
DVGYSIKIEFLDSIEPIIKFNDIKHEFKNNKAIITLNSKI PNLKIEFDYKTQDIIVSNNN
IFTEILKYKERGEEKLNLEFQNLKNEPNTQFKYHLKDYDIEMLDKQKDIYLPVLLNQI
FLNESNIQVYFNDDEVNIFRFADSLKDISGIVNLKMSKANMSNSIPKSLKEFQYKYFAFL
FDHYYGIKLPNNKSYIDYFKKYEQKIINFNSDLHYLTTTRQIVADLDDPHSAYILDGFYFK
EKDINKVQITGNTKEHRYDWNINIQSLLAQHDPSKIEYQNRFLSDNKTSVLSFKQFEIDT
AKQIEKSLKEAQNKGIKNIIFNVTQNGGGFIGAAYELMGFLLTDKPFNVYNYNPLSKEQKV
ETIKSKYNKYNFNYYILTSFYFAGNIFPQITKDNKVAKLIIGYKTFGGASSIGYFILPT
GDIIQLSTNNVFTNKKFRSLEFGVVKPDVMLNGSVETNAKDLYDDNKLELNLKADKISFT
NDDSTIKPIDTIPLKPKPNKNEIKPKLSLSKLIKNNKIKISKNDPITLLKELFENNDP
INFDQEIRISLQPNKAEIYLENNPNDKIVNFVSKDISEQNQNVKNNKTKLIIIISSS
LLVVIVSLLLTFLIIKKLKNKK*
  
```


```

# MCAP_0328|ID:18107887| Length: 682
# MCAP_0328|ID:18107887| Number of predicted TMHs: 1
# MCAP_0328|ID:18107887| Exp number of AAs in TMHs: 27.42851
# MCAP_0328|ID:18107887| Exp number, first 60 AAs: 0.33329
# MCAP_0328|ID:18107887| Total prob of N-in: 0.01047
MCAP_0328|ID:18107887| TMHMM2.0 outside 1 652
MCAP_0328|ID:18107887| TMHMM2.0 TMhelix 653 675
MCAP_0328|ID:18107887| TMHMM2.0 inside 676 682
  
```



# [plot](#) in postscript, [script](#) for making the plot in gnuplot, [data](#) for plot

*M. capricolum* subsp. *capripneumoniae*

 - 1 - [MCCP01v2\\_0297](#) [*Mycoplasma capricolum* subsp *capripneumoniae* Abomsa chromosome AbomsaV06]

putative conserved membrane protein | validated/finished

Length=656

Score = 276 bits (706), Expect = 6e-91  
Identities = 138/154 (90%), Positives = 149/154 (97%), Gaps = 0/154 (0%)

```
Query 1 TSVISFKNFEANSAFKIEESLQQRDGIKNIIVLDVSFNSSGGYLGTAFEIMGFLLTKPFK 60
Sbjct 384 TS+ISFKNFE +SA KIE+SL +A+++ +KNIVLDVSFNSSGG LGTA+EIMGFLLTKPFK 443

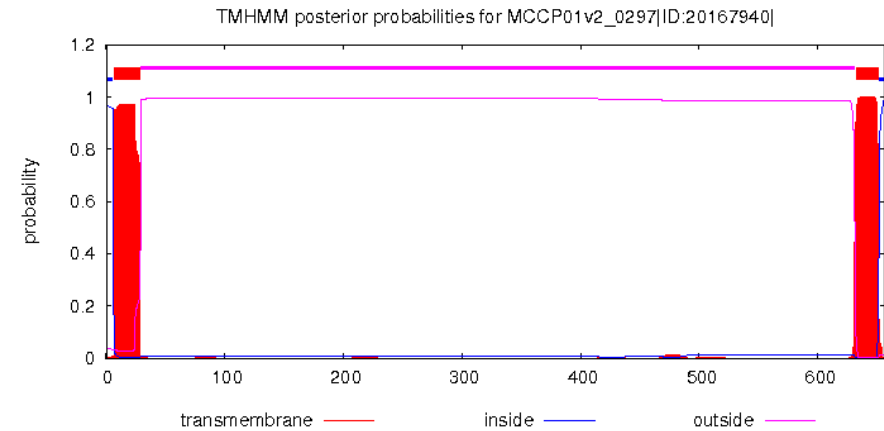
Query 61 SYSYNPLTKEQKVETIKSRFKKYDFNYYVLTSPFSFSAGNIFPQLVKDNNVAKVIGFKTA 120
Sbjct 444 SYSYNPLTKEQKVETIKSRFKKYDFNYYVLTSPFSFSAGNIFPQLVKDNNVAKVIGFKTA 503

Query 121 GGASAIQAILPTGDIQLSSNNVLTNKSHQSLE 154
Sbjct 504 GGASAIQAILPTGDIVQLSSNHVLTNKSHQSLE 537
```


>MCCP01v2\_0297|ID:20167940| putative conserved membrane protein [*Mycoplasma capricolum* subsp *capripneumoniae* Abomsa]

```
MKLVTKLSAISLGAFSIFAPIAVINLLTTKNNLLITKRFLSSNSNSNFEKAYDYVNLIDNKYLDKINLHNNHGIAYIGVKEFLKALDGLISFSKIRVKPTHNSTFFKEKEITYKFNKDKVTLNSVTKYSNNSQNNNTNYQLEIDSKNNTITVSDNDFFTDIFAFYRRGEEDLNIDFLDTKILNKNKHIVFDLKKYDIDVLDNKKDLYLPLVLINQLFLNQSNVQLYFNGERINLFAYSKTLRRVDFLKQLKQSYFNNVNTISLGLKDFQHKYLGFLFDHYGKLDKNASYKDLFKKYEKYIKADNTTHYLTSRYLIEQLDDLHSSYLLTGYYNKNLDTINRAVLNTSTPRSDKYKDIARRLSFYNKELNYKNVYTPDKKTSIISFKNFEIDSACKIEQSLIEAKNNVKNIVLDVSFNSSGGLLGTAYEIMGFLLTKPFKSYSYNPLTKEQKVETIKSRFKKYDFNYYVLTSPFSFAGNIFPQLVKDNNVAKVIGFKTAGGASAIQAILPTGDIVQLSSNHVLTNKSHQSLEYGVSFDIKFNFPNETKKLFDSSFIQDVVNKDTSKLKNPNFSQTSFVEPNLVHELLKKPTSLQLNKDQKQENDIKNNNSLFSLSKSELRTKEALFVLGVIGLLASITTFIIKKIKK
```

```
# MCCP01v2_0297|ID:20167940| Length: 656
# MCCP01v2_0297|ID:20167940| Number of predicted TMHs: 2
# MCCP01v2_0297|ID:20167940| Exp number of AAs in TMHs: 42.23023
# MCCP01v2_0297|ID:20167940| Exp number, first 60 AAs: 21.40802
# MCCP01v2_0297|ID:20167940| Total prob of N-in: 0.96572
# MCCP01v2_0297|ID:20167940| POSSIBLE N-term signal sequence
MCCP01v2_0297|ID:20167940| TMHMM2.0 inside 1 6
MCCP01v2_0297|ID:20167940| TMHMM2.0 TMhelix 7 29
MCCP01v2_0297|ID:20167940| TMHMM2.0 outside 30 631
MCCP01v2_0297|ID:20167940| TMHMM2.0 TMhelix 632 651
MCCP01v2_0297|ID:20167940| TMHMM2.0 inside 652 656
```



# [plot](#) in postscript, [script](#) for making the plot in gnuplot, [data](#) for plot

 - 2 - [MCCP01v2\\_0400](#) [Mycoplasma capricolum susbp capripneumoniae Abomsa chromosome AbomsaV06]

Peptidase, S41 family | validated/finished

Length=683

Score = 228 bits (580), Expect = 3e-72  
Identities = 108/154 (70%), Positives = 133/154 (86%), Gaps = 0/154 (0%)

```
Query 1 TSVISFKNFANSFAFKIEESLKQQRDGIKNIVLDVSNFSGGVLGTAFEIMGFLTDKPFK 60
      TSVISFK FE ++A +IE+SLK+AQ GIKNI+ +V+ N GG++G A+E+MGFLTDKPFK
Sbjct 349 TSVISFKQFEIDTAKQIEKSLKEAQNKGIKNIIFNVNQNGGGFIGAAYELMGFLTDKPFK 408

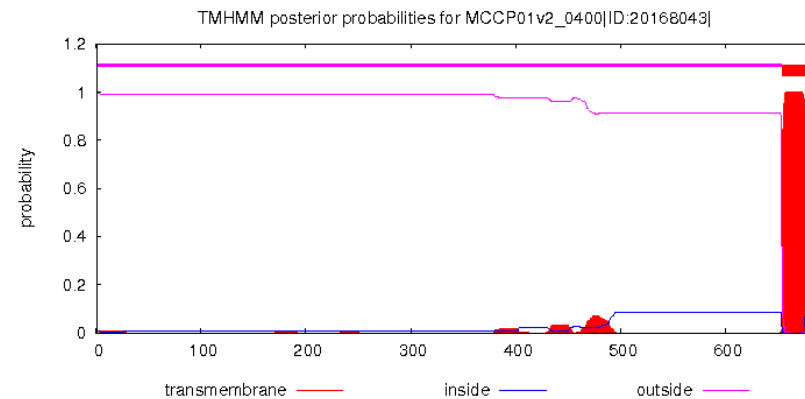
Query 61 SYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFSFSGAGNIFPQLVKDNNVAKVIGFKTA 120
      Y+YNPL+KEQKVETIKS++ KY+FNYY+LTSP+SFSAGNIFPQ+ KDN VAK+IG+KT
Sbjct 409 VYNYNPLSKEQKVETIKSKYKNYFNYYILTSPYFSAGNIFPQITKDNKVAKIIGYKTF 468

Query 121 GGASAIQAILPTGDIIQLSSNNVLTNKSQSLE 154
      GGAS+I ILPTGDIIQLS+NNV TN +SLE
Sbjct 469 GGASSIGYFILPTGDIIQLSTNNVFTNNKFKSLE 502
```

>MCCP01v2\_0400|ID:20168043| Peptidase, S41 family [Mycoplasma capricolum susbp capripneumoniae Abomsa]


MKLLLTSLFLFSNTITPVLTN SINIVENTSNTISLKEYKLNLSLTKDIKTMKKKINLHLH  
NNVGYSVKEFLDSIEPIIKFNDIKHEFKNNKTIITLTSKIPNLKIEFDYKTQDITVSNN  
NIFTEILKDKERGEKLNLEFQNLKNNENPNTQFKYHLKDYDIEMLDKQKDIYLPVLLNQ  
IFLNEISNIQVYFNDDEVNIFRFAETLSNFINIVNLKGLKSSQKTTIPKNLKEFQYNYLGF  
LFDHYYGIKLKDKNFYRNYFQSYKNWII SDSNNKHYLATKQLIADLDDPHSAFIMDGYFN  
KGEEYNKTKIESKSEVKRYKWDLHLLAQHDPKIEYQNRFLSDNKT SVISFKQFEID  
TAKQIEKSLKEAQNKGIKNIIFNVNQNGGGFIGAAYELMGFLTDKPFKVYNYNPLSKEQK  
VETIKSKYKNYFNYYILTSPYFSAGNIFPQITKDNKVAKIIGYKTFGGASSIGYFILP  
TGDIQLSTNNVFTNNKFKSLEFGVKPDVMLNGSVETNAKDLYDDNKLLELINKADKISF  
GNDDSTIKPIDTIPKPKDPNTNGIKPKISLSKLIKNNKIKISKNDPITLLKELFENN  
DINFQEIIRISLKQPNKAEIYLENNPNDKITVNFSLVKDISEQNQNIKNNKTKLIIISS  
SLLVVIVSLLLTFLIKKLNKK\*

```
# MCCP01v2_0400|ID:20168043| Length: 683
# MCCP01v2_0400|ID:20168043| Number of predicted TMHs: 1
# MCCP01v2_0400|ID:20168043| Exp number of AAs in TMHs: 25.45824
# MCCP01v2_0400|ID:20168043| Exp number, first 60 AAs: 0.1782
# MCCP01v2_0400|ID:20168043| Total prob of N-in: 0.00576
MCCP01v2_0400|ID:20168043| TMHMM2.0 outside 1 653
MCCP01v2_0400|ID:20168043| TMHMM2.0 TMhelix 654 676
MCCP01v2_0400|ID:20168043| TMHMM2.0 inside 677 683
```



# [plot](#) in postscript, [script](#) for making the plot in gnuplot, [data](#) for plot

*M. leachii*

 - 2 - [MSB\\_A0342](#) [Mycoplasma leachii PG50 chromosome NC\_014751]  
peptidase, S41 family | automatic/finished

Length=683

Score = 226 bits (576), Expect = 1e-71  
Identities = 108/154 (70%), Positives = 132/154 (86%), Gaps = 0/154 (0%)

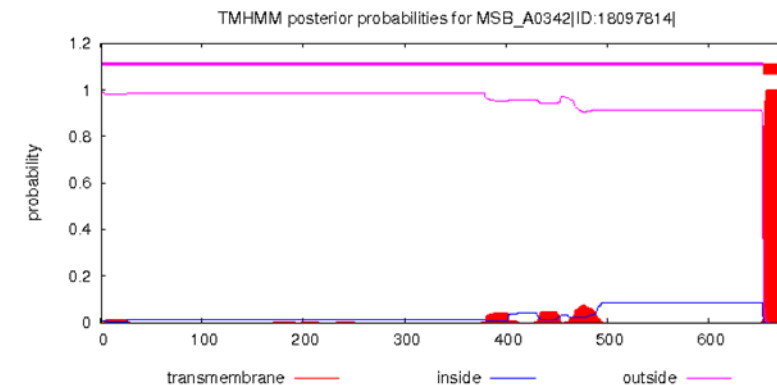
```
Query 1 TSVISFKNF EANS AFKIEESLKQAQRDGIKNI VLDVSN SGGYLGTA FEIMGFLTDKPFK 60
TSVISFK FE ++A +IE+SLK+AQ GIKNI+ +V+ N GG++G A+EIMGFLTDKPF
Sbjct 349 TSVISFKKFEIDTAKQIEKSLKEAQN RGIKNI IFNVTQNGGGFIGAAYEIMGFLTDKPFN 408

Query 61 SYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFS SAGNIFPQLVKDNNVAKVIGFKTA 120
Y+YNPL+KEQKVETIKS++ KY+FNYY+LTSP+SFSAGNIFPQ+ KDN VAK+IG+KT
Sbjct 409 VYNYNPLSKEQKVETIKSKYKNYFNYYILTSPYS SAGNIFPQITKDNKVAKIIGYKTF 468

Query 121 GGASAI SQAILPTGDIIQLSNNVLTNKSHQSLE 154
GGAS+I ILPTGDIIQLS+NNV TN +SLE
Sbjct 469 GGASSIGYFILPTGDIIQLSTNNVFTNNKFRSLE 502
```

```
>MSB_A0342|ID:18097814| peptidase, S41 family [Mycoplasma leachii PG50]
MKLLLTSLFLLSNTIAPVLTNSVNI IENTTNTLSLKEYKLN SLTKDVKTMKKKNISLHLH
KDVGYVSIKEFLDSIEPIIKFNDIKHEFKNNKTIVTLTSKIPNLKIEFDYKTQDIIVSNN
NIFTEILKNKERGEEKLNLEFQNLKNEPNTQPKYHLKDYDIEMLKDQKDIYLPVLLNQ
IFLNESNIQVYFNDDEVSI FRFAETLSNF INIVNLKGLKSSQKTTIPKTLKEFQYKYFAF
LFDHYYGIKLKNRFRYKNYFQNYKSQITSDSNDKHYLATKQLIEDLDDPHSAFTMDGYFN
KGEENKTKIESKSKVKRYKKWNTDLHLLAQHDP SKIEYQNRFLSDNKTSVISFKKFEID
TAKQIEKSLKEAQN RGIKNI IFNVTQNGGGFIGAAYEIMGFLTDKPFNVYNYNPLSKEQK
VETIKSKYKNYFNYYILTSPYSF SAGNIFPQITKDNKVAKIIGYKTFGGASSIGYFILP
TGDI IQLSTNNVFTNNKFRSLEFGV KPDVMLNGSVETNAKDLYDDNKLELILINKADKISF
KNDDSTIKPIDTIP LKPDKPNKNEIKPKISLSKLIKNKNIKISKNDPITLLKELFKNNP
DINF DQEIRISLQPNKAEIYLENNPNDKIIINF SIVKDISEQNQLKNNKTKL I I I I S S
SLLVVIVSLLLTFLIIKKLKNKK*
```

```
# MSB_A0342|ID:18097814| Length: 683
# MSB_A0342|ID:18097814| Number of predicted TMs: 1
# MSB_A0342|ID:18097814| Exp number of AAs in TMs: 26.54633
# MSB_A0342|ID:18097814| Exp number, first 60 AAs: 0.31539
# MSB_A0342|ID:18097814| Total prob of N-in: 0.00794
MSB_A0342|ID:18097814| TMHMM12.0 outside 1 653
MSB_A0342|ID:18097814| TMHMM12.0 TMhelix 654 676
MSB_A0342|ID:18097814| TMHMM12.0 inside 677 683
```



# [plot](#) in postscript, [script](#) for making the plot in gnuplot, [data](#) for plot

Mmm



- 1 - [MMS\\_A0313](#) [Mycoplasma mycoides subsp. mycoides SC Gladysdale chromosome NC\_021025]  
peptidase, S41 family | automatic/finished

Length=636

Score = 291 bits (744), Expect = 1e-96  
Identities = 149/154 (97%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

```

Query 1  TSVISFKNFANSFAKIEESLKQAQRDGIKNIVLDVSNFSGGGLGTAFEMGFLTDKPFK 60
          TSVISFKNFE NSAFKIEESLKQAQRDGIKNIVLDVSNFSGG LGTA+EIMGFLTDKPFK
Sbjct 380 TSVISFKNFEPNSAFKIEESLKQAQRDGIKNIVLDVSNFSGGLLTAYEIMGFLTDKPFK 439

Query 61 SYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFSSAGNIFPQLVKDNNVAKVIGFKTA 120
          SYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFSSAGNIF QLVKDNNVAKVIGFKTA
Sbjct 440 SYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFSSAGNIFSQLVKDNNVAKVIGFKTA 499

Query 121 GGASAISQAILPTGDIIQLSSNNVLTNKSHQSLE 154
           GGASAISQAILPTGDIIQLSSN VLTNKSHQSLE
Sbjct 500 GGASAISQAILPTGDIIQLSSNYVLTNKSHQSLE 533

```

>MMS\_A0313|ID:18111339| peptidase, S41 family [Mycoplasma mycoides subsp. mycoides SC Gladysdale]

```

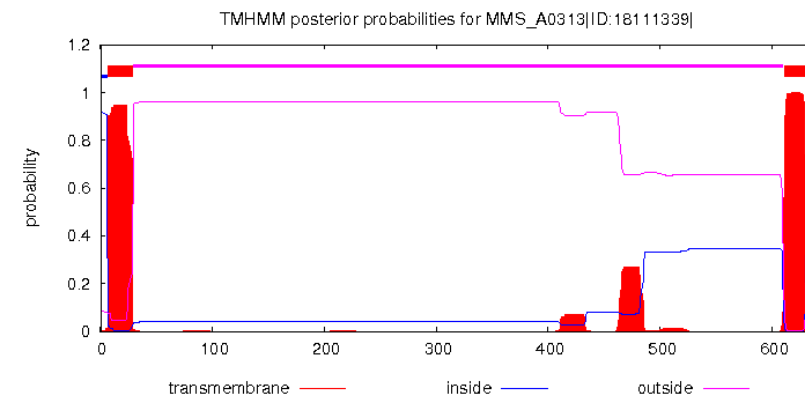
MKLVTKLSAISLGAFSIFAPIAVINNLTTENLLISKRFLLSSNSDFELKAYDYVNLIDN
KYINTKINLHNHNGVAYIGVKEFLKALDGLISFSKIIVKPTHNSTFFKEKEITYKFNKDK
VTLNSVTKYSNNNKTTNYQLEIDSKNKTITVSDNDFDTIDFTFYRRGEEDLNIDFLDTKI
LNKNKHIVFDLNKYGIEILNDQNDLYLPLVLINQLFLNQSNIQLYFNGERINLFAYSKTL
RRVDFLKQLKHSYLNQNHIPVGLKDFQHKYLGFLDFHFGYIKLDKNASYKDLFKKYEKY
IKADNTTHYLTSRYLIGQLDDLHSSYLLTGYYNKDLETINKAVLKTTPRSDRFKDIARR
LSAYYGLNKNVYTPDRKTSVISFKNFEPNSAFKIEESLKQAQRDGIKNIVLDVSNFSG
GLLTAYEIMGFLTDKPFKSYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFSSAGNI
FSQLVKDNNVAKVIGFKTAGGASAISQAILPTGDIIQLSSNYVLTNKSHQSLEYGVNPD
TLGFDPFKQTEKFFDSAYIQQAINKDTNTLNSIPATHSSVIEPNYVHELVEKQPQLQSR
KTDQTERKDAYFVLGALGVVISLAIPFVILKLLKK*

```

```


# MMS_A0313|ID:18111339| Length: 636
# MMS_A0313|ID:18111339| Number of predicted TMHs: 2
# MMS_A0313|ID:18111339| Exp number of AAs in TMHs: 48.63485
# MMS_A0313|ID:18111339| Exp number, first 60 AAs: 28.85361
# MMS_A0313|ID:18111339| Total prob of N-in: 0.91733
# MMS_A0313|ID:18111339| POSSIBLE N-term signal sequence
MMS_A0313|ID:18111339| TMHMM2.0      inside 1 6
MMS_A0313|ID:18111339| TMHMM2.0      TMhelix 7 29
MMS_A0313|ID:18111339| TMHMM2.0      outside 30 610
MMS_A0313|ID:18111339| TMHMM2.0      TMhelix 611 630
MMS_A0313|ID:18111339| TMHMM2.0      inside 631 636

```



# plot in postscript, [script](#) for making the plot in gnuplot, [data](#) for plot



 - 2 - **MMS\_A0112** [*Mycoplasma mycoides* subsp. *mycoides* SC Gladysdale chromosome NC\_021025]  
peptidase, S41 family | automatic/finished

Length=711

Score = 211 bits (538), Expect = 4e-66  
Identities = 102/154 (66%), Positives = 127/154 (82%), Gaps = 0/154 (0%)

```

Query 1   TSVISFKNFEANSAFKIEESLQKQARDGIKNIIVLDVSNFSGGYLGTAFEIMGFLTDPKPFK 60
          TSVISF F+ S I +SLKQA+ + IKNI+ +++ N GGY+G AFEI+GFLT+KPF
Sbjct 343 TSVISFSKFDEKSTDYILKSLKQAKENNIKNIIFNLTQNGGGYIGVAFEILGFLTNPFPN 402

Query 61  SYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFSFSAAGNIFPQLVKDNNVAKVIGFKTA 120
          YSYNPL+KE+KVETIKS+++ +DF YY+LTSP+SFSAGNIFPQ+ +DN VAK+IG+KT
Sbjct 403 VYSYNPLSKEKKVETIKSKYENFDFKYYILTSFYSAAGNIFPQVARDNKVAKLIGYKTF 462

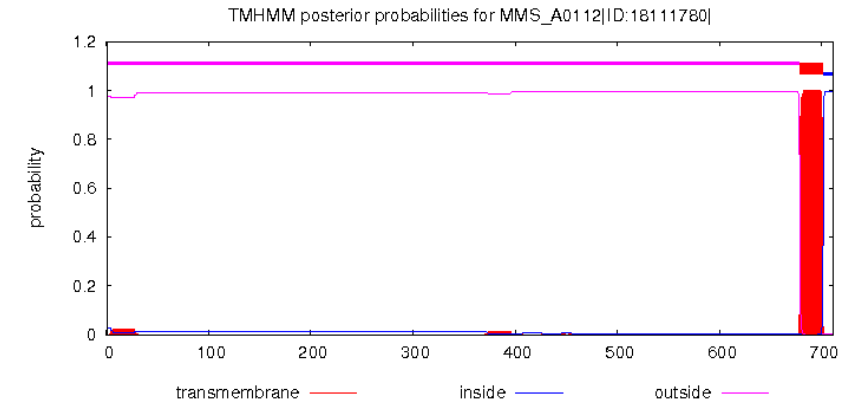
Query 121 GGASAIQAAILPTGDIIQLSSNNVLTNKSQSLE 154
          GGASAI+ ILPTGDIIQLSSNNV TN +SLE
Sbjct 463 GGASAINYYILPTGDIIQLSSNNVFTNDKFESLE 496
  
```

>MMS\_A0112|ID:18111780| peptidase, S41 family [*Mycoplasma mycoides* subsp. *mycoides* SC Gladysdale]


MKITTILSSLSLSSLSSTPVLNLSFINTTTNKIQTKFNLDNLTIKNNRTSKKIQAFLH  
NDVFYTSINEFLKNIDSVINYSNLEHSFKDNKTTIKLKNDSNFFVEFDYLLKKIIVSNNK  
IFTKILKNYKRAEEDLKIEFIKEQNLNNTNQFEIDLKYNIDILKQNDLYLPSILLNQV  
FLSKSNIQTYFNGDDFKIFRFYEGLSLPGTFYLYKQSDKNNQNKIPIGLRRFQYEYLSFLF  
DNYYAIIKLDNKSFKYFKYETQILSESSNEHYLATKKIINDLDDPHSAYVLDGYYDKD  
RNFHKTLEFENKQVRKNSDKILDLLARNDPNKIDVNSFINDDTSVISFSKDFDEKSTDYIL  
KSLKQAKENNIKNIIFNLTQNGGGYIGVAFEILGFLTNPFPNVYSYNPLSKEKKVETIKS  
KYENFDFKYYILTSFYSAAGNIFPQVARDNKVAKLIGYKTFGGASAINYYILPTGDIIQ  
LSSNNVFTNDKFESLEFGVTPDVELDQVYKNSAIYQKETLLDLIKKADSIIKTKKEIR  
TEKLTKILDISKKIENNKTELTKKPKDVKVLLKKEEIIYKKPDSINHNAENDEIKNELIK  
EKTNIESLNINKNLNLGKLDKIDENQILIALKKNLELDINNLEVKNITNNSAEILQKNTD  
QKFIVHFLKTPVKTSNKNTI**WIVLIIIGLTLGLINFIIR**KLKTKKLNK\*

```

# MMS_A0112|ID:18111780| Length: 711
# MMS_A0112|ID:18111780| Number of predicted TMHs: 1
# MMS_A0112|ID:18111780| Exp number of AAs in TMHs: 23.79443
# MMS_A0112|ID:18111780| Exp number, first 60 AAs: 0.53607
# MMS_A0112|ID:18111780| Total prob of N-in: 0.02528
MMS_A0112|ID:18111780| TMHMM2.0 outside 1 678
MMS_A0112|ID:18111780| TMHMM2.0 TMhelix 679 701
MMS_A0112|ID:18111780| TMHMM2.0 inside 702 711
  
```



*M. putrefaciens*

 - 1 - [MPUT\\_0240](#) [Mycoplasma putrefaciens KS1 chromosome NC\_015946]  
automatic/finished

Length=487

Score = 211 bits (536), Expect = 2e-67  
Identities = 100/154 (65%), Positives = 132/154 (86%), Gaps = 0/154 (0%)

```
Query 1 TSVISFKNFANSFAFKIEESLKQAQRDGIKNIVLDFVNSGGYLGTAFEIMGFLLTKPFK 60
      T +I F+ F+ ++A +E SLKQA++ +KNIVLD+S N GG++G+A+EI+GFLTD+ FK
Sbjct 185 TGIIGFQGFHDSTAKHLENSLKQAKQLNLKNIVLDFSRNGGGFFIGSAYEILGFLLDQAFK 244

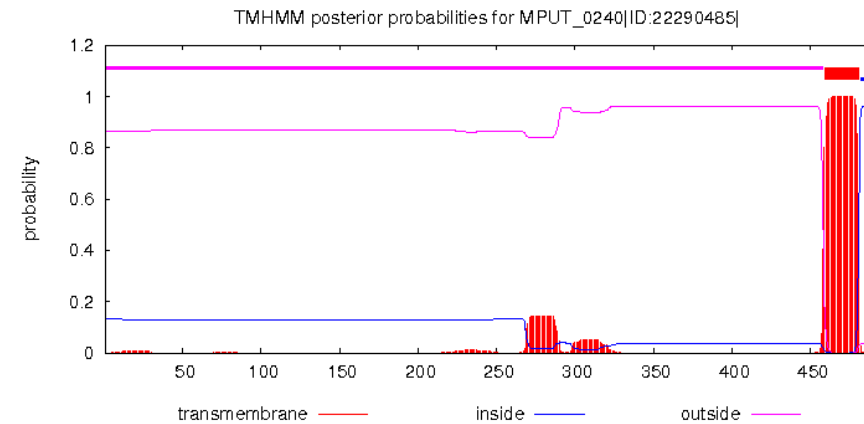
Query 61 SYSYNPLTKEQKVETIKSRFKKYDFNYVLTSPFVSAGNIFPQLVKDNNVAKVIGFKTA 120
      YSYNPL+K+QK+ETIKS+++KYDFNYVLT SP+SFS NIF Q+ KDNN+AKVIG+++
Sbjct 245 IYSYNPLSKDQKIETIKSKYQKYDFNYVLTISPYSFSAANIFAQITKDNNLAKVIGYQSF 304

Query 121 GGASAISQAILPTGDIIQLSSNNVLTNKSHQSLE 154
      GGASAIS A+LPTGDIIQLSSN+V T+K +SLE
Sbjct 305 GGASAISYAVLPTGDIIQLSSNDVFTDKHFKSLE 338
```

**Annotated as pseudo-gene with a frameshift at the N-terminal part.**

```
>MPUT_0240|ID:22290485| [Mycoplasma putrefaciens KS1]
MLKDQTDIYLPFVLLNQLFLNQSNIQLYFNDSEVNFRRFAESLSDLIATVHLKRSVPVQQ
NKIPNGLKQFYRYLAFLLDHYAIAKPKNTTSYKDLLKYYHDQILATNSTDHYLATRKLII
KELDDPHSAYILDGYDKAKDFNKLTLTNNNSNPRTEFKNQLFNLLASYDKPKFEYQLLTT
ADQQTGIIGFQGFHDSTAKHLENSLKQAKQLNLKNIVLDFSRNGGGFFIGSAYEILGFLLD
QAFKIYSYNPLSKDQKIETIKSKYQKYDFNYVLTISPYSFSAANIFAQITKDNNLAKVIG
YQSFGGASAISYAVLPTGDIIQLSSNDVFTDKHFKSLEFGVSPDLKLPNDINDFKNLYN
YYLLQDLINKDNPSTDLANKTSLLALIKNTNLKVAKNDPKTLVQALIQSNAEVDLANKEL
IVILKAANRAEIIYLADDDPNKITVTFQVVGSNHFNQSSTTILAILAPIIVILLVSVIVFF
NKNKLLK*
```

```
# MPUT_0240|ID:22290485| Length: 487
# MPUT_0240|ID:22290485| Number of predicted TMHs: 1
# MPUT_0240|ID:22290485| Exp number of AAs in TMHs: 26.78106
# MPUT_0240|ID:22290485| Exp number, first 60 AAs: 0.1212
# MPUT_0240|ID:22290485| Total prob of N-in: 0.13490
MPUT_0240|ID:22290485| TMHMM2.0 outside 1 458
MPUT_0240|ID:22290485| TMHMM2.0 TMhelix 459 481
MPUT_0240|ID:22290485| TMHMM2.0 inside 482 487
```



```

# VEU54887.1 Length: 683
# VEU54887.1 Number of predicted TMHs: 1
# VEU54887.1 Exp number of AAs in TMHs: 26.54633
# VEU54887.1 Exp number, first 60 AAs: 0.31539
# VEU54887.1 Total prob of N-in: 0.00794
VEU54887.1 TMHMM2.0 outside 1 653
VEU54887.1 TMHMM2.0 TMhelix 654 676
VEU54887.1 TMHMM2.0 inside 677 683

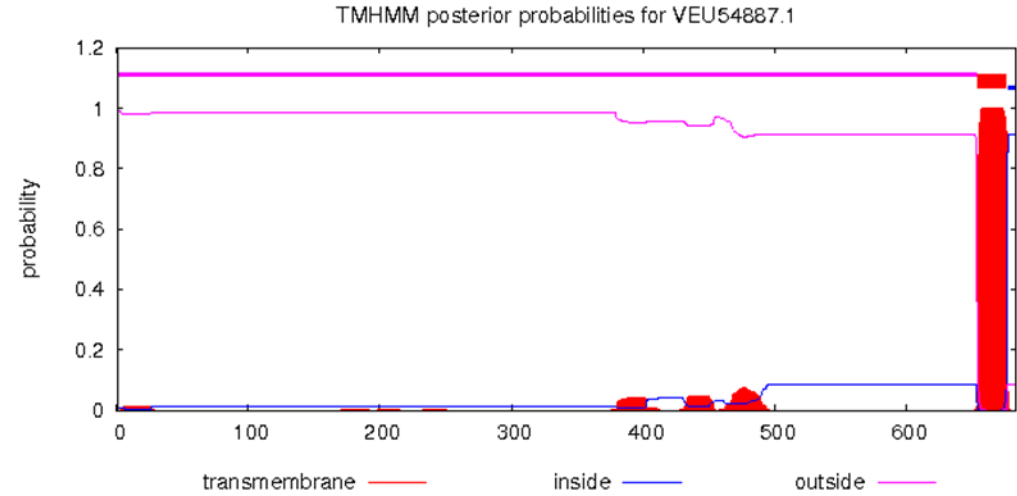
```

**M. salivarium**

```

>VEU54887.1 Probable CtpA-like serine protease [Mycoplasma salivarium]
MKLLLSLFLLSNTIAPVLTNSVNIIENTTNTLSLKEYKLNLSLTKDVKTMKKKNISLHLHKDVGYSIKE
FLDSIEPIIKFNNDIKHEFKNNKTIVTLTSKIPNLKIEFDYKTQDIIVSNNNIFTEILKNKERGEEKLNLE
FQNLKNENPNTQFKYHLKDYDIEMLDKQKDIYLPVLLNQIFL NESNIQVYFNDDEVSIFRFAETLSNFI
NIVNLKGLKSSQKTTIPKTLKEFQYKYFAFLFDHYYGIKLDNRFYKNYFQNYKSQITSDSNDKHYLQTK
QLIEDLDDPHSAFTMDGYFNKGEEYNTKIESKSKVKRYKKWNTLHLLAQHDPSKIEYQNRFLSDNKTS
VISFKKFEIDTAKQIEKSLKEAQNRIKNIIFNVTQNGGGFIGAAEIMGFLTDKPFVNYNPLSKEQK
VETIKSKYKNYFNYYILTSYSPYSFAGNIFPQITKDNKVAKIIGYKTFGGASSIGYFILPTGDIQLSTN
NVFTNNKFRSLFEGVDPVMLNGSVETNAKDLDDNKLEL INKADKISFKNDDSTIKPIDTIPKPKDK
PNKNEIKPKISLSKLIKKNKIKSKNDPITLLKELFKNNPDINFDQEIRISLQPNKAEIYLENNPNDKI
IINFSIVKDISEQNQLKNNKTKLIIISSLLVVIVSLLTFLIKKLNKK

```



**VEU54887.1**

Prediction: Signal peptide (Sec/SPI)

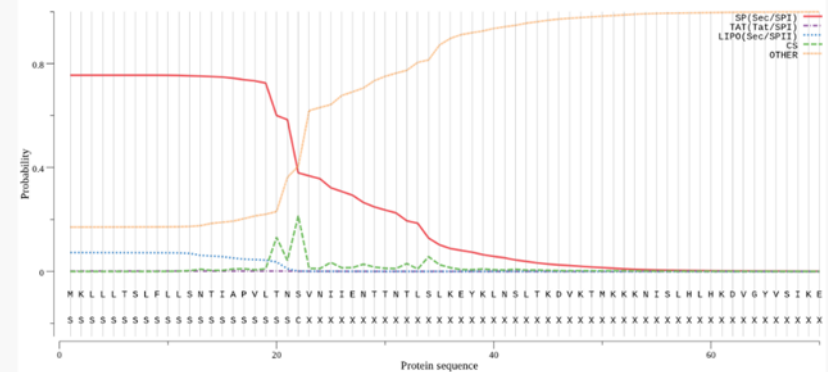
Cleavage site between pos. 22 and 23: TNS-VN

Probability: 0.2142

Protein type	Signal peptide (Sec/SPI)	TAT signal peptide (Tat/SPI)	Lipoprotein signal peptide (Sec/SPII)
Likelihood	0.7542	0.0016	0.0723

Download: [PNG](#) / [EPS](#) / [Tabular](#)

SignalP-5.0 prediction (Gram-positive): VEU54887.1



**Ruminococcus flavefaciens**

lipoprotein [Ruminococcus flavefaciens]

Sequence ID: [WP\\_009982655.1](#) Length: 810 Number of Matches: 1

Range 1: 434 to 575 [GenPeptGraphics](#) [Next Match](#) [Previous Match](#)

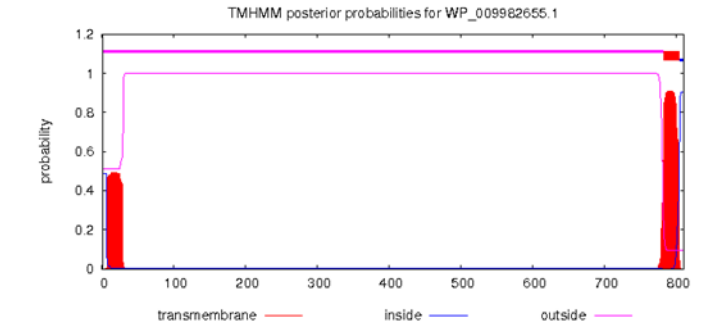
Alignment statistics for match #1

Score	Expect	Method	Identities	Positives
70.9 bits (172) adjust. 47/149 (32%)	3e-11	Compositional matrix	71/149 (47%)	30/149 (20%)

Query	29	IKNIVLDVSNSSGGYLGTAFEIM-----GFLTDPFKSYSYN	65
		IK +V DV+ N+GG + TA +M	G +TD +++
Sbjct	434	IKKLVFDVATNTGGNMMTAMYMMNLIKGLNSVSLKNTSVMAGDSEGLITDDFKTDRNFD	493
Query	66	PLTKEQKVETIKSRFKKYDFNYVLTSPFSFSAGNIFPQLVKDNNVAKVIGFKTAGGASA	125
		+ E K K+D Y V+TS SFS GN FP L KDNN+ VIG ++ GG+ A	
Sbjct	494	KVIDE-----KDDAIKFDLQYGVITSKMSFSCGNWFPSLCKDNNIV-VIGERSGGGSCA	546
Query	126	ISQAILPTGDIIQLSSNNVLTNKSHQSLE	154
		+ ++LP G I S+ L + +S++	
Sbjct	547	VDLSVLPDGMIIYSYSTGITLVDSKGESID	575

>WP\_009982655.1 lipoprotein [Ruminococcus flavefaciens]  
 MNFKKTIAGISALSMLLSTSAVSAVNFAADDETTNYTDKTIINAYLYSNDNVDTMTARFYNDKPNIPYLR  
 ISEFYKKWLDQDLEITNKNDGTYDVKVPFGTVGTDFDVEKDTIHSDDVGKFFIPEDDANSTSAASDLFIRE  
 EEAEKAVDVTDFDGAYNIDFLGDENDIWLPAPTLCLDFAGTDKQSLYLDGSMYFCGYLLSDYSRSLIPQ  
 TQEHITNLIEDFKDGRPADLIKYNIDEFCFLMDSGYGYPGRIPFNDIMKEKGFDMLEEGNETTKKIKEL  
 LNSTDLYEYCAGLELLNGYFFDGGHTSFLPIPYTYDANFEILDGEFAAKVDAVIEGLGELKDNVDLKLEE  
 KNLEASIIIGVENARKAMAETADYTEELSSSVYIEKGDVAVLMFDTFVIDLDSWDGYYHNGAELPEDEVTD  
 FYKAVQKADSNPAIKKLVFDVATNTGGNMMTAMYMMNLIKGLNSVSLKNTSVMAGDSEGLITDDFKTDR  
 NFDKVIDEKDDAIKFDLQYGVITSKMSFSCGNWFPSLCKDNNIVVIGERSGGGSCAVDLSVLPDGMIIYSY  
 STGITLVDSKGESIDLGIQPDYENVKIAEDGSKDFSETFNFDNISKIFDEFYGNTTTTTAAETTTTTTTT  
 TSATTSTTTSSSTNTSTDTTTTTTTTTAAKSTKSEETTTAAATTKAEDKT  
 IGTNDEITKMVEKDYFVKTKGNAASSETNVNKDGLTVELKDENGVIDKYTVDPETGKGTADAGNEVDL  
 PQTGINSLGTAGAAVGAVMLMLAGAAVHGSGLVLRKKEND

```
# WP_009982655.1 Length: 810
# WP_009982655.1 Number of predicted TMs: 1
# WP_009982655.1 Exp number of AAs in TMs: 31.41054
# WP_009982655.1 Exp number, first 60 AAs: 10.98539
# WP_009982655.1 Total prob of N-in: 0.48931
# WP_009982655.1 POSSIBLE N-term signal sequence
WP_009982655.1 TM#12.0 outside 1 781
WP_009982655.1 TM#12.0 TMhelix 782 804
WP_009982655.1 TM#12.0 inside 805 810
```

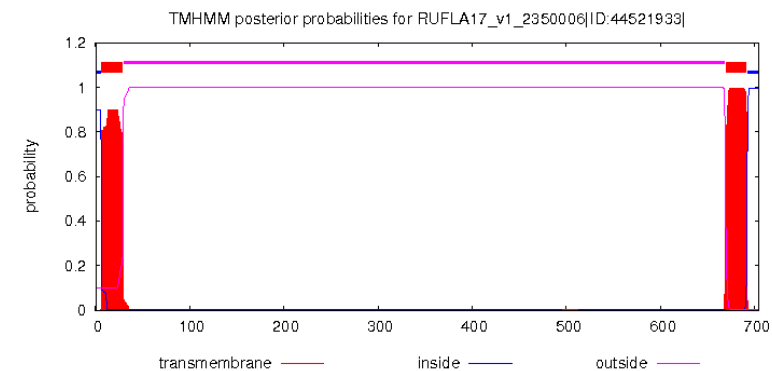


>RUFLA17\_v1\_2350006|ID:44521933| exported protein of unknown function [Ruminococcus flavefaciens 17] WP 028518726.1

MNIKKTLAGISALSWLISSGAFAMNAFAADAAEYRTGQITAHLYSEDNLRDIECRYND  
 MPNVPIKLSDYSCWTSQELQITNKNGTYEVTVPIGATGIIDVKNKDTVSSDDIGGFCY  
 PQYVIESNTSNLYTYVKSISKPNKESYTTDFSDYKIDLRGDDNDIWWPVATLCDFYDFN  
 LNQGALIDDNLYFFNSILDIKYSRTAIGNSAAHKEAFIEKYQNGRPKDMVEYNYNELCFN  
 FDRTYGFPGRFIYNDLLAETNFDTMLSTASDSTKKIKELLLSEDAHEYCAGYELLNRYFW  
 DGGHTFFYGTMISEESDFTAKVAEVFASISGLKDAMNYRAINANSEYSGNSAYTALIKMC  
 ETADTYEEFNNSIYAVKGD TAVFSFLMFNDESDKWSSYYYENGEMPQDLITEFYNCVTKA  
 NADPAIKNFVIDLGNFNGGSAAVLEYMMGIIISDLNITIIILGNGDKSVTEQYLVDKNLDK  
 SYDEKDKAMKLDLNFGIITSNYSF CANLMPALAKDAGIMLVGEKSGGGTCATNRYVTPD  
 GLVYALSTGQKQFVDKAGTPIIDNGIQPDYDVKINDDGTKDYSEVYNFSMLSSLFSDFYGK  
 KAETDPSVTTTTTTTTTTTTTTTTTTTTSSSSTTTSETTTVSSTSSSSASTSGNTTTTNANGT  
 LPKTGNNSAGTAAAAACAAVIT IAGGALIFISRRTRNKEDNGIS\*

LPKTG sorting signal

```
# RUFLA17_v1_2350006|ID:44521933| Length: 704
# RUFLA17_v1_2350006|ID:44521933| Number of predicted TMs: 2
# RUFLA17_v1_2350006|ID:44521933| Exp number of AAs in TMs: 42.64751
# RUFLA17_v1_2350006|ID:44521933| Exp number, first 60 AAs: 20.07843
# RUFLA17_v1_2350006|ID:44521933| Total prob of N-in: 0.90010
# RUFLA17_v1_2350006|ID:44521933| POSSIBLE N-term signal sequence
RUFLA17_v1_2350006|ID:44521933| TMHMM2.0      inside  1  6
RUFLA17_v1_2350006|ID:44521933| TMHMM2.0      T$helix  7  29
RUFLA17_v1_2350006|ID:44521933| TMHMM2.0      outside 30 668
RUFLA17_v1_2350006|ID:44521933| TMHMM2.0      T$helix 669 691
RUFLA17_v1_2350006|ID:44521933| TMHMM2.0      inside  692 704
```



```

>WP_082325677.1 LPXTG cell wall anchor domain-containing protein
[Ruminococcus flavefaciens]
MGFRITYKRNKRFFQQRKMLCFLYLDPDKLSRRII//MNIKKTLAGISALSWLISSGAFTAMNFAADAAEYR
TGQITAHLYSEDNLRDIECRYNDMPNVPYIKLSDYYSWCWTSQELQITNKNGTYEVTVPIGATGIIDVN
KDTVSSDDIGGFCYPQYVIESNTSNLYTYVKSISKPNKESYTTDFSDYKIDLRGDDNDIWWPVATLCDF
YDFNLNQGALIDDNLYFFNSILDIKYSRTAIGNSAAHKEAFIEKYQNGRPKDMVEYNYNELCFNFDRTYG
FPGRFIYNDLLAETNFDTMLSTASDSTKKIKELLSEDAHEYCAGYELLNNYFWDGGHTFFYGTMISEES
DFTAKVAEVFASISGLKDAMNYRAINANSEYSGNSAYTALIKMCETADTYEEFNNSIYAVKGD TAVFSFL
MFNDESDKWSSYYYENGEMPQDLITEFYNCVTKANADPAIKNFVIDLGANFGGSAAVLEYMMGIISDLN
ITIIILGNGDKSVTEQYLVDKNLDKSYDEKDKAMKLDLNFGLIITSNYSFSCANLMPALAKDAGIMLVGEKS
GGGTCATNRYVTPDGLVYALSTGQKFVDKAGTPIDNGIQPDYDIVKINDDGT KDYSEVYNF SMLSSLFSD
FYGKKAETDPSVTTTTSTTTTTSTTTTTTTTTSSSSTTTSETTTVSSTSSSSASTSGNTTTTNANGTLPKLTGN
NSAGTAAAAACA AVIT IAGGALIFISRRTRNKEDNGIS

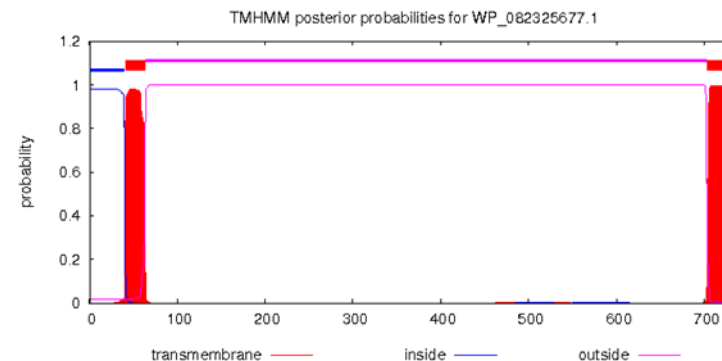
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/// : alternative start (this study)

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# WP_082325677.1 Length: 738
# WP_082325677.1 Number of predicted TMMs: 2
# WP_082325677.1 Exp number of AAs in TMMs: 44.57823
# WP_082325677.1 Exp number, first 60 AAs: 19.47697
# WP_082325677.1 Total prob of N-in: 0.98122
# WP_082325677.1 POSSIBLE N-term signal sequence
WP_082325677.1 TMM#12.0 inside 1 40
WP_082325677.1 TMM#12.0 THelix 41 63
WP_082325677.1 TMM#12.0 outside 64 702
WP_082325677.1 TMM#12.0 THelix 703 725
WP_082325677.1 TMM#12.0 inside 726 738

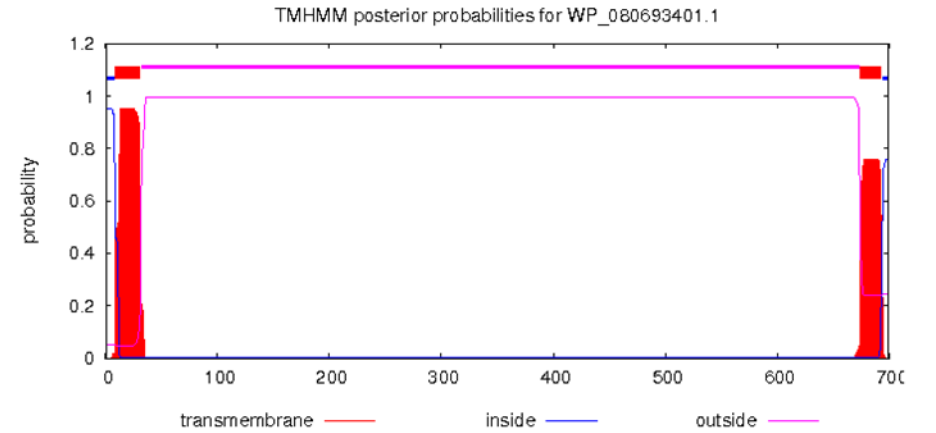
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>WP\_080693401.1 LPXTG cell wall anchor domain-containing protein [Ruminococcus flavefaciens]

MIMNSKKT IAGLSALSVL I SSGAFTAMTAF AADTA EYTTGKMTAHLYSDEKLKEIECRYYNDMPNVPYIK  
LSDYYSCWLCQYPDQELAITNKNDGT YEVKMPIGATGIIDTNKDTVSTDDAAGFLYPQYIILESENGENIFT  
YVKGDS SAEDEDEKVS YTDQDFSVYDIDIRGDEKDIWWPATTLCDFYEYSLNQGAVIDDDLYFFPQILST  
YSRTALAGTPEHTAAFIEKYKNGRPKDMIEYNYNELCFCFDRNYGFPGRFKYNELLEENGFDKMLSTASD  
GTTKIKELLLSEDL YDYCAGYEMLNDYLWDGGHTVFTDFMLQNSKDLASAVSAKFQTIAMPEDAFDHYAV  
LNNSNNSGYTALKTREEMYKTADTYEKGNGSEYSVKGD TAFFAFNFFEDNAAGWYNYFFNNGELPQDVVS  
EFYNSIKKADADPAVKNFVIDLSTNGGGSLSIVQYMMGLINDLDNVTVMNGKTENAKFVIDKNL DKAYD  
DKDKAFKTDLRFGIITSNYSFSCANLMP SLAKDAGIMLIGERSGGGTCATNRYFTPDGLLYALSTGLKFV  
DKDGNTIDDGIVPDYDIVKKNADGTKDYSDVYNYSKLSALFDEFYGKKT DSSQSTSTTTTTTTTTTTTSAT  
TTTSATTTAASSTSTSSAASSTSGSTTTTTNVSTLPQTGNKSA A A A C A A V L V M A G G A F M L M S R K K E N

```
# WP_080693401.1 Length: 699
# WP_080693401.1 Number of predicted TMs: 2
# WP_080693401.1 Exp number of AAs in TMs: 36.02416
# WP_080693401.1 Exp number, first 60 AAs: 21.05507
# WP_080693401.1 Total prob of N-in: 0.94982
# WP_080693401.1 POSSIBLE N-term signal sequence
WP_080693401.1 TMHMM2.0      inside      1      8
WP_080693401.1 TMHMM2.0      TMhelix     9     31
WP_080693401.1 TMHMM2.0      outside     32    673
WP_080693401.1 TMHMM2.0      TMhelix    674    693
WP_080693401.1 TMHMM2.0      inside     694    699
```





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>WP_082320460.1 hypothetical protein [Ruminococcus flavefaciens]
MTSYQLYFEPQAVKLLSRRIT///MKIKKTIAGIAALSVIISGAFALTASAAETS DYTTSKMTAHVYSDEN
LIDIECRYYS DMPHVPIKLSDYSCWTGQELEINAKNDGIYEVKVPYGATGIIDINKEYMSSE DIEHFI
CPAYVFDSNDQSYETYTKENTESEEPQFGDIDLSEYKIDIRGDENEVWVPAATLCDIFEYPLNEGMCVEE
ELYFCGHVNSEYNRKDNALNPAHAAEYLEKYKDGRPKDMAEFNYNELCFEIDNIYGFPGRITYNDLLAEK
GFDGMLSEASDGTRKVKEMLLSEDPYEYCAGLELLNYYFWDGGHTFFNNLAAIGSKEQVEKVG EYLVSPD
ELEGAFIWADNAQASASGYLAQEARIAMFETADTYEAPPHPDDTLPYEYAVKGD TAFFSFSGFNANTP
AWLNYYYNNGELPKDLISDFYSCITRADKDP AIKNFVIDLGTNRGGS LDVLMYMMGLINDLDHINLASGS
NDEPQKSEFLVDKNLDKAFDEKDDAFKTDLNFGIITSNYSFSCANLMPSLAKDSGIMLIGERSGGGACST
DYHATADGMIYAMSYGIK FADKDGKSIDEGIEPDYALVKLNEDGSKDYS DVYNFANLSSLFADFYKKDAP
QEPSEPETETTTTTTTTTVTTTTTTTTT VSTTSDKDTTSSATSSASGSSSETTTTTT D ASDLPKKTGNNSMGT
AAAAACAFIMT LSGGAAMMAAYRLRRKDENGSL

```

/// : alternative start (this study)

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# WP_082320460.1 Length: 733
# WP_082320460.1 Number of predicted TMHs: 2
# WP_082320460.1 Exp number of AAs in TMHs: 43.04645
# WP_082320460.1 Exp number, first 60 AAs: 21.65657
# WP_082320460.1 Total prob of N-in: 0.96450
# WP_082320460.1 POSSIBLE N-term signal sequence
WP_082320460.1 TMHMM2.0 inside 1 27
WP_082320460.1 TMHMM2.0 TMhelix 28 50
WP_082320460.1 TMHMM2.0 outside 51 699
WP_082320460.1 TMHMM2.0 TMhelix 700 722
WP_082320460.1 TMHMM2.0 inside 723 733

```

