

Unique CDSs in paralogous families/Analyses	PSORTb												
	Subcellular localization				Features				SignalP		LipoP		
	Unknown	Cytoplasmic Membrane	Cytoplasmic	Extracellular	1 internal helix	2 internal helices	3 internal helices	Signal peptide	YES	NO	SpI	SpII	TMH
<i>M. parvum</i> strain Indiana													
Family 1 (12 CDSs)	5	0	7	0	1	0	0	0	0	12	3	1	0
Family 2 (9 CDSs)	3	0	6	0	0	0	0	0	9	0	0	0	0
Family 4 (6 CDSs)	4	0	2	0	4	0	0	0	6	3	0	2	0
Family 7 (5 CDSs)	3	0	2	0	0	0	0	0	5	0	0	0	0
Family 8 (5 CDSs)	5	0	0	0	4	0	0	0	5	1	0	0	0
Family 11 (4 CDSs)	3	0	1	0	4	0	0	0	4	0	0	0	0
Family 12 (4 CDSs)	3	0	1	0	0	0	0	0	4	0	0	0	0
Family 19 (3 CDSs)	0	0	3	0	1	0	0	0	3	0	0	0	0
Family 22 (3 CDSs)	1	0	1	1	1	0	0	0	3	0	0	0	0
Family 24 (3 CDSs)	3	0	0	0	2	0	0	0	3	0	0	0	0
Family 28 (2 CDSs)	2	0	0	0	0	0	0	0	2	0	0	0	0
Family 30 (2 CDSs)	1	1	0	0	2	0	0	0	2	1	0	1	0
Family 31 (2 CDSs)	1	1	0	0	1	0	0	0	2	0	0	0	0
Family 32 (2 CDSs)	2	0	0	0	0	0	1	0	2	1	0	0	0
Family 35 (2 CDSs)	1	1	0	0	0	0	0	0	2	0	0	0	0
Total (64)	37	3	23	1	20	0	0	1	0	64	9	1	3
<i>M. suis</i> strain Illinois													
Family 1 (37 CDSs)	24	4	9	0	35	0	0	6	1	36	8	0	8
Family 7 (11 CDSs)	5	0	5	1	6	0	0	0	11	2	0	0	0
Family 10 (9 CDSs)	7	0	2	0	5	0	0	3	9	5	1	2	0
Family 11 (9 CDSs)	5	1	3	0	9	0	0	1	9	2	0	0	0
Family 14 (8 CDSs)	8	0	0	0	0	0	0	0	8	0	0	0	0
Family 16 (7 CDSs)	3	0	3	1	6	0	0	0	7	2	0	1	0
Family 17 (6 CDSs)	3	0	3	0	6	0	0	0	6	3	0	0	0
Family 18 (6 CDSs)	6	0	0	0	3	0	0	1	3	3	0	0	0
Family 19 (6 CDSs)	4	2	0	0	5	0	0	0	5	4	0	0	0
Family 22 (5 CDSs)	3	0	2	0	4	0	0	0	5	5	0	3	0
Family 23 (5 CDSs)	3	0	2	0	3	0	0	1	5	1	0	0	0
Family 24 (5 CDSs)	3	0	0	2	5	0	0	2	5	3	0	3	0
Family 27 (4 CDSs)	3	0	0	1	4	0	0	0	4	2	0	0	0
Family 28 (4 CDSs)	4	0	0	0	4	0	0	2	4	0	0	0	0
Family 30 (4 CDSs)	3	1	0	0	2	0	0	1	3	2	0	1	0
Family 32 (4 CDSs)	3	1	0	0	4	0	0	0	4	0	0	0	0
Family 33 (4 CDSs)	3	0	0	1	4	0	0	3	4	2	0	1	0
Family 36 (3 CDSs)	1	1	1	0	3	0	0	0	3	0	0	0	0
Family 37 (3 CDSs)	1	0	2	0	2	0	0	1	2	2	0	1	0
Family 38 (3 CDSs)	0	0	3	0	3	0	0	0	3	1	0	1	0
Family 39 (3 CDSs)	3	0	0	0	3	0	0	0	3	0	0	0	0
Family 40 (3 CDSs)	1	0	2	0	1	0	0	0	3	0	0	0	0

Family 41 (3 CDSs)	2	0	0	1	3	0	0	2	0	3	2	0	2
Family 42 (3 CDSs)	1	1	1	0	3	0	0	0	0	3	1	0	0
Family 43 (3 CDSs)	3	0	0	0	3	0	0	0	0	3	2	0	0
Family 46 (2 CDSs)	1	0	0	1	2	0	0	0	0	2	2	0	1
Family 48 (2 CDSs)	1	0	1	0	2	0	0	0	0	2	0	0	0
Family 50 (2 CDSs)	2	0	0	0	2	0	0	0	0	2	0	0	0
Family 53 (2 CDSs)	2	0	0	0	2	0	0	0	0	2	1	0	1
Family 54 (2 CDSs)	1	0	1	0	0	0	0	0	0	2	0	0	0
Family 56 (2 CDSs)	2	0	0	0	2	0	0	2	0	2	1	0	0
Family 57 (2 CDSs)	1	0	1	0	2	0	0	1	0	2	1	0	1
Family 58 (2 CDSs)	2	0	0	0	2	0	0	0	0	2	0	0	0
Family 59 (2 CDSs)	2	0	0	0	1	0	0	0	0	2	1	0	0
Family 60 (2 CDSs)	2	0	0	0	2	0	0	2	0	2	2	0	0
Family 61 (2 CDSs)	2	0	0	0	1	0	0	1	0	2	1	0	0
Family 62 (2 CDSs)	1	0	1	0	2	0	0	0	0	2	2	0	2
Family 63 (2 CDSs)	1	1	0	0	2	0	0	0	0	2	0	0	0
Family 65 (2 CDSs)	2	0	0	0	2	0	0	1	0	2	2	0	1
Family 66 (2 CDSs)	2	0	0	0	2	0	0	1	0	2	0	0	0
Total (188)	125	12	43	8	153	0	0	31	8	100	65	1	29

PSORTb: results were obtained using the output for Gram-negative bacteria without outer membrane.

SignalP: YES: signal peptide present, NO: signal peptide absent.

LipoP: SpI: signal peptide (signal peptidase I), SpII: lipoprotein signal peptide (signal peptidase II), TMH: n-terminal transmembrane helix. **Note from the software: TMH is generally not a very reliable prediction and should be tested. This part of the model is mainly there to avoid transmembrane helices being falsely predicted as signal peptides.**