



STRUCTURAL
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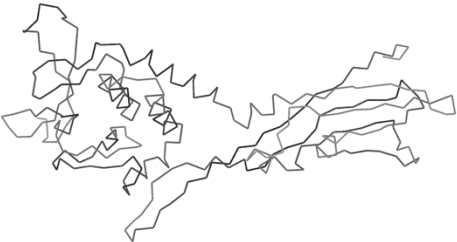
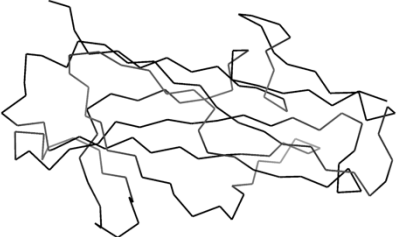
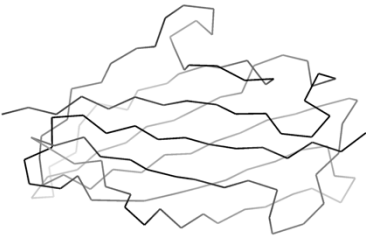
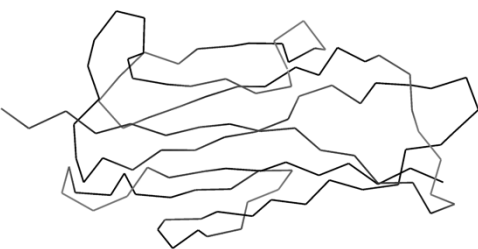
Supporting information for article:


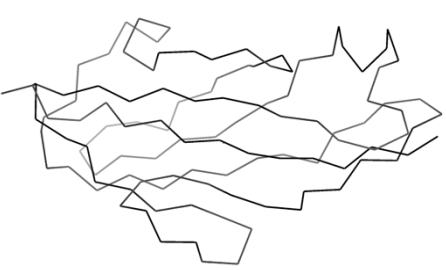

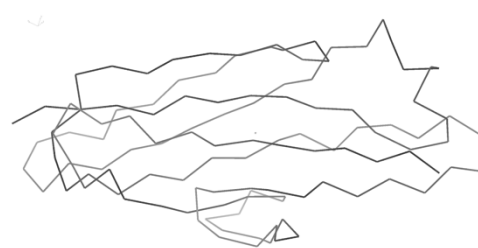

**Domain structure and cross-linking in a giant adhesin from the
Mobiluncus mulieris bacterium**

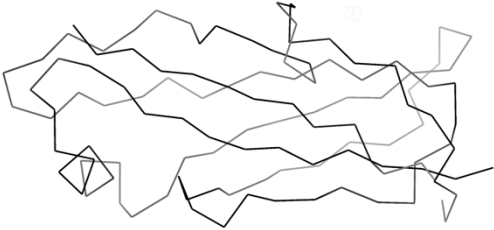
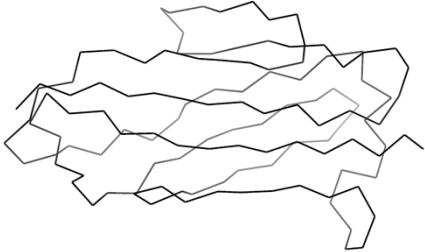
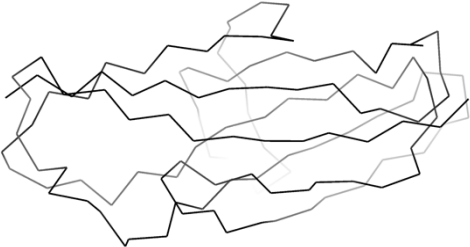
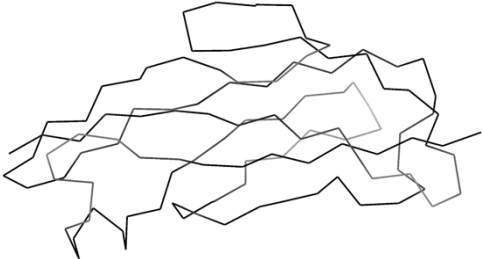
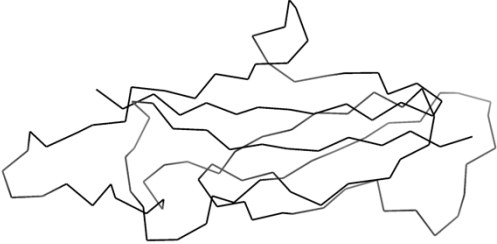
**Paul G. Young, Jacob M. Paynter, Julia K. Wardega, Martin J. Middleditch, Leo
S. Payne, Edward N. Baker and Christopher J. Squire**

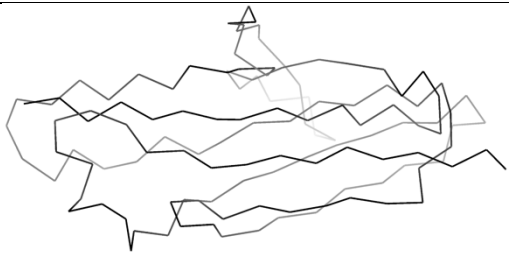
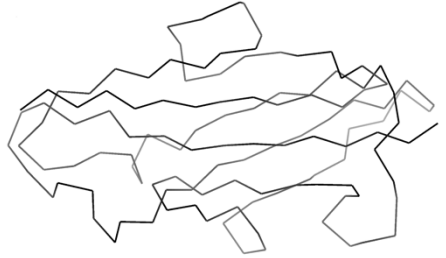
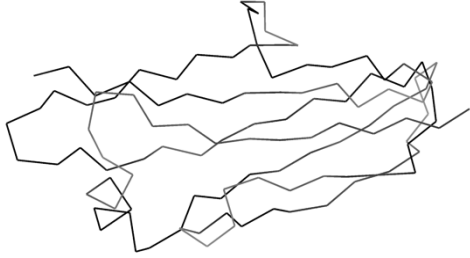
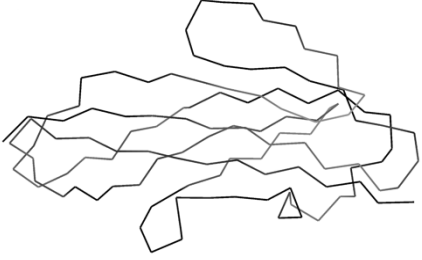
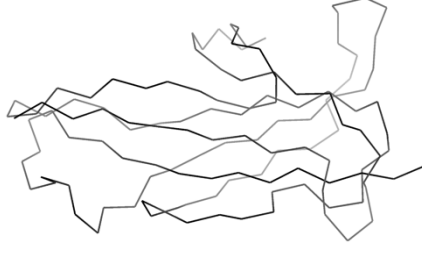
Table S1 *M. mulieris* adhesin AlphaFold2 structure predictions for individual domains.


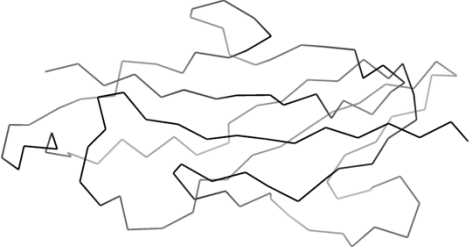

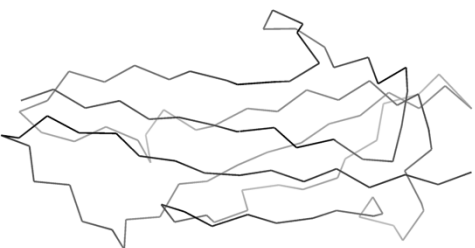
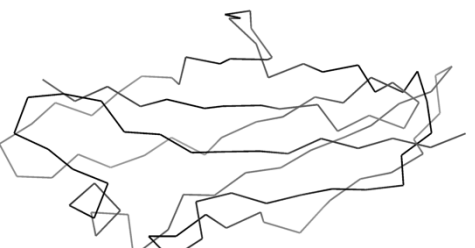
For RMSD calculation, putative isopeptide bond-containing domains were aligned to the major pilin Spy0128 from *Streptococcus pyogenes* (PDB ID 3B2M), and putative ester bond-containing domains were aligned to a repeat domain from *Clostridium perfringens* adhesin Cpe0147 (PDB ID 4NI6). The putative adhesin domain was aligned to the thioester domain of *Enterococcus faecium*, TIE86 (PDB ID 6FWY).

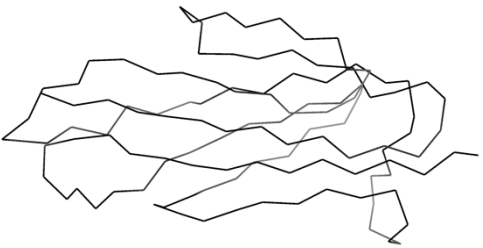
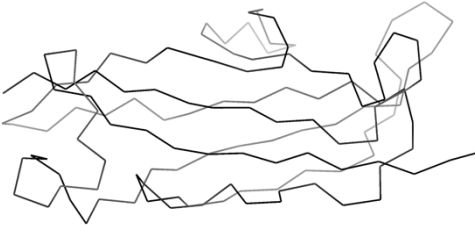
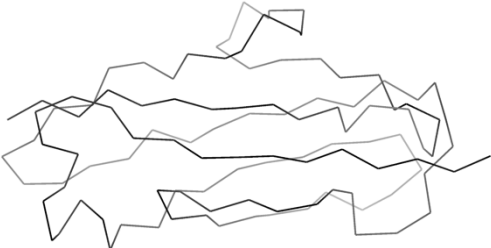
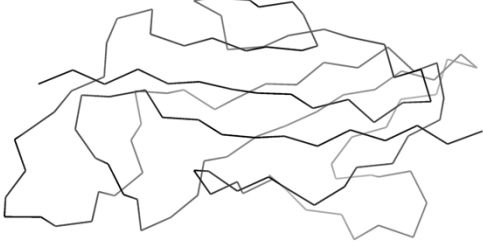
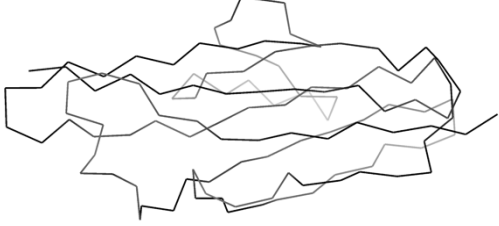
Domain Identifier	Amino acid range	RMSD (Å)	No. C α aligned	Sequence identity (%)	Predicted structure
n/a	Met1 - Pro472	n/a	n/a	n/a	no structure predicted
A	Ile473 - Ser765	5.33	53/293	9.43	 thioester domain†
1	Ser764 - Gly919	2.92	121/156	16.53	 ester
2	Ser920 - Ala1061	3.11	86/142	9.30	 isopeptide
3	Asp1062 - Glu1181	3.08	95/120	16.84	 isopeptide

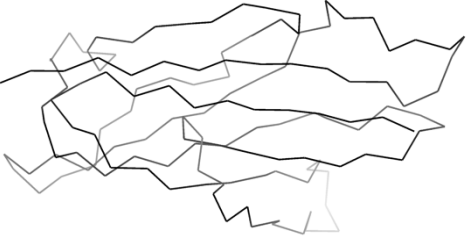
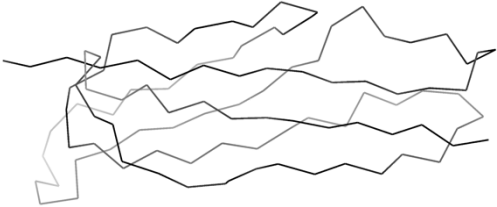

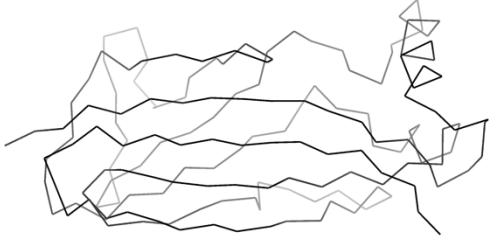

4	Leu1182 - Val1330	3.26	91/149	12.09	✓		isopeptide
5	Pro1331 - Lys1447	2.09	81/117	16.05			isopeptide
6	Asp1448 - Pro1574	3.16	90/127	23.33			isopeptide
7	Lys1575 - Asp1694	3.13	84/120	11.90	↓		isopeptide
8	Ile1695 - Arg1821	3.68	97/127	6.19			isopeptide

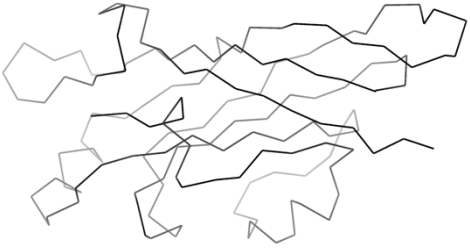
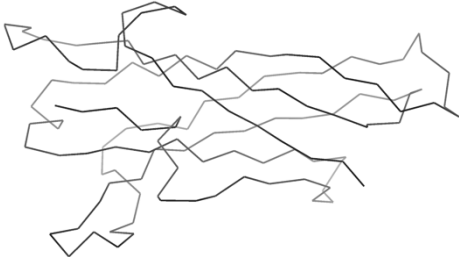

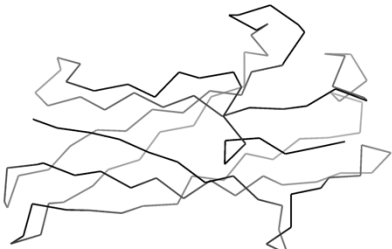
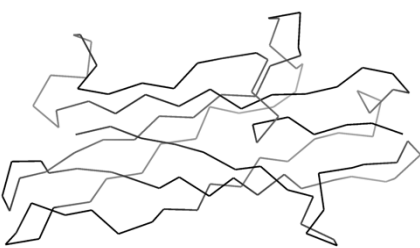
9	Lys1822 - Thr1940	2.70	85/119	8.24	
					isopeptide
10	Pro1941 - Arg2062	2.12	88/122	14.77	
					isopeptide
11	Gln2063 - Val2191	2.39	87/129	14.94	
					isopeptide
12	Gln2192 - Tyr2308	2.34	87/117	19.54	
					isopeptide
13	Asn2309 - Val2430	3.14	91/122	10.99	
					isopeptide

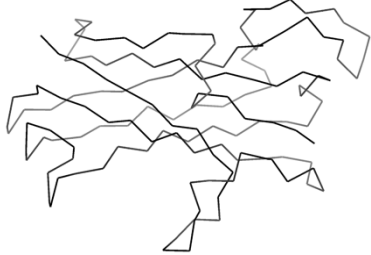
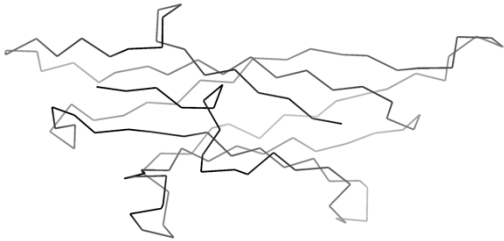
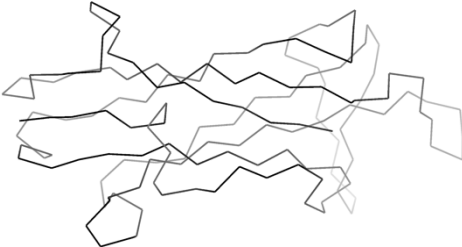
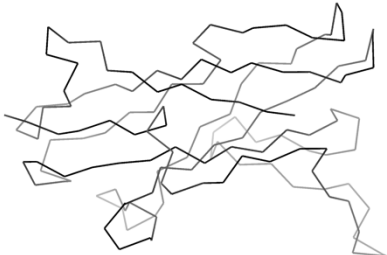
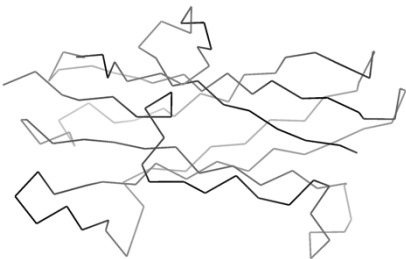
14	Ser2431 - Ile2556	3.10	86/126	4.65	 <p>A ribbon diagram of a protein structure, showing a complex fold with multiple alpha-helices and beta-strands. The structure is rendered in a light gray color.</p>
					isopeptide
15	Pro2557 - Arg2682	3.59	92/126	9.78	 <p>A ribbon diagram of a protein structure, showing a complex fold with multiple alpha-helices and beta-strands. The structure is rendered in a light gray color.</p>
					isopeptide
16	Lys2683 - Pro2797	3.15	87/115	5.75	 <p>A ribbon diagram of a protein structure, showing a complex fold with multiple alpha-helices and beta-strands. The structure is rendered in a light gray color.</p>
					isopeptide
17	Tyr2798 - His2919	2.52	90/122	10.00	 <p>A ribbon diagram of a protein structure, showing a complex fold with multiple alpha-helices and beta-strands. The structure is rendered in a light gray color.</p>
					isopeptide
18	Gln2920 - Val3048	2.67	92/129	11.96	 <p>A ribbon diagram of a protein structure, showing a complex fold with multiple alpha-helices and beta-strands. The structure is rendered in a light gray color.</p>
					isopeptide

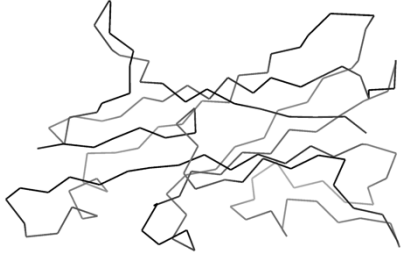
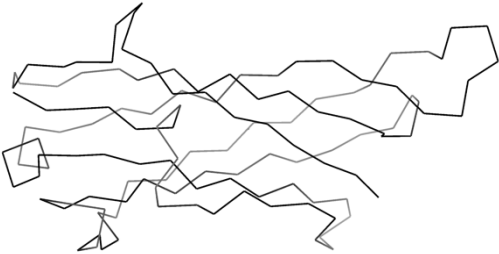
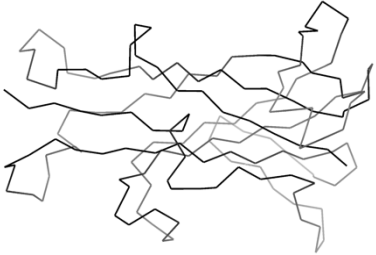
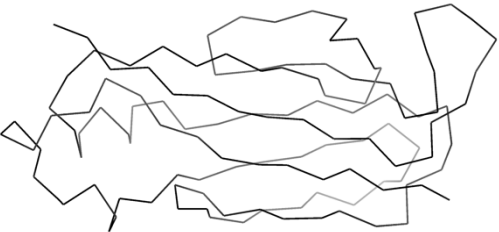
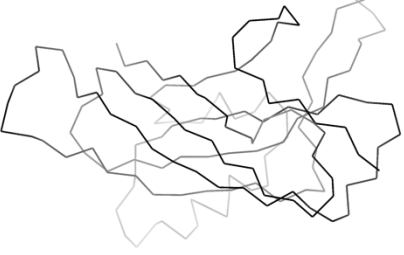
19	His3049 - Thr3164	2.56	88/116	20.45	 <p>isopeptide</p>
20	Tyr3165 - Pro3294	3.25	97/130	27.84	 <p>isopeptide</p>
21	Gln3295 - Val3422	3.06	90/128	13.33	 <p>isopeptide</p>
22	Ser3423 - Arg3543	3.60	89/121	11.24	 <p>isopeptide</p>
23	Glu3544 - Thr3662	2.34	97/119	12.37	 <p>isopeptide</p>

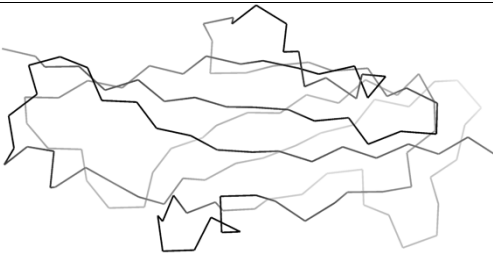
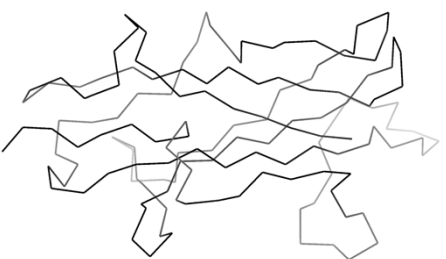

24	Pro3663 - Asp3782	2.00	96/120	22.92	 <p>isopeptide</p>
25	Arg3783 - Val3918	4.73	73/136	6.85	 <p>isopeptide</p>
26	Gln3919 - Tyr4032	2.32	86/114	12.79	 <p>isopeptide</p>
27	Asp4033 - Glu4166	2.78	101/134	27.72	 <p>isopeptide</p>
28	Lys4167 - Ile4293	2.91	87/127	9.20	 <p>isopeptide</p>

29	Pro4294 - Thr4427	3.62	96/134	10.42	
					isopeptide
30	Arg4428 - Asp4533	3.91	47/106	4.26	
					isopeptide
31	Ser4534 - Gln4676	2.49	86/143	11.63	
					isopeptide
32	Thr4677 - Ser4839	3.34	97/163	5.15	
					isopeptide
33	Phe4838 - Pro5000	2.42	109/163	13.76	
					ester

34	Ile5001 - Phe5147	3.84	59/147	16.95	 <p>ester</p>
35	Thr5148 - Ser5279	1.51	106/132	31.13	 <p>ester</p>
36	Pro5280 - Thr5428	1.58	116/149	31.90	 <p>ester</p>
37	Val5429 - Asn5553	1.59	105/125	25.71	 <p>ester</p>
38	Gly5554 - Gln5680	1.70	108/127	27.78	 <p>ester</p>

39	Glu5681 - Pro5826	2.11	112/146	25.00	 <p>ester</p>
40	Ser5827 - Val5956	1.93	109/130	28.44	 <p>ester</p>
41	Gly5857 - Pro6101	1.56	105/145	28.57	 <p>ester</p>
42	Ser6102 - Thr6248	3.28	81/147	25.93	 <p>ester</p>
43	Ser6249 - His6384	5.63	44/136	9.09	 <p>ester</p>


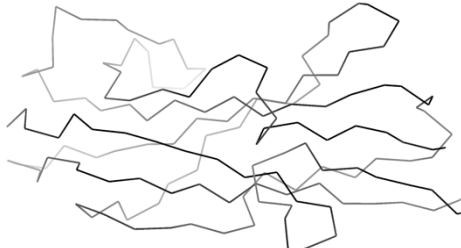
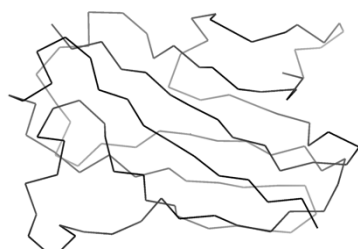
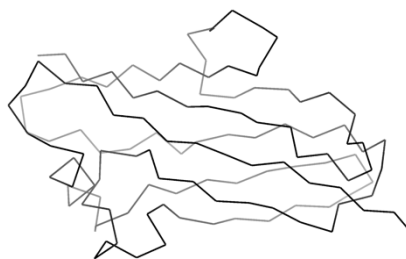
44	Asn6385 - Lys6541	2.00	111/157	22.52	 <p>ester</p>
45	Ala6542 - Lys6668	1.88	109/127	30.28	 <p>ester</p>
46	Lys6669 - Gln6834	1.73	106/166	20.75	 <p>46E ester domain – X-ray crystal structure also determined</p>
47	Phe6835 - Tyr6959	2.75	82/125	10.98	 <p>47I isopeptide domain – X-ray crystal structure also determined</p>
48	Asp6960 - Ser7119	2.39	102/160	23.53	 <p>ester</p>

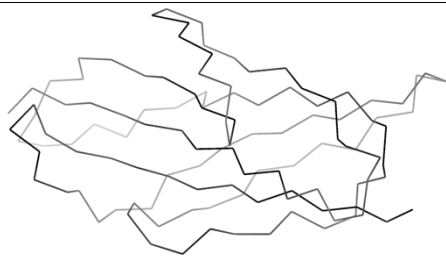
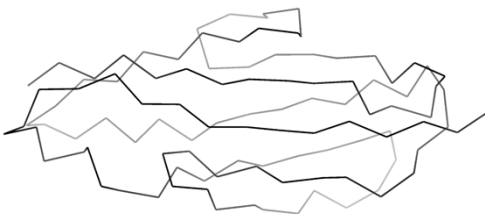
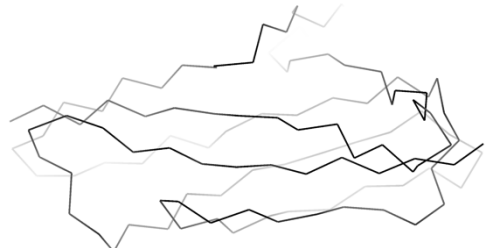
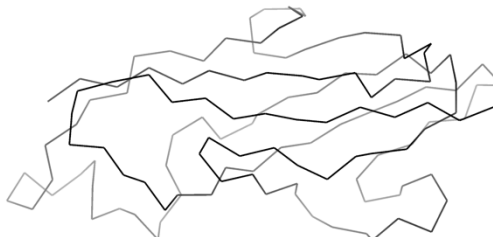

49	Ser7120 - Tyr7263	2.91	93/144	12.90	
					isopeptide
50	Pro7264 - Lys7410	1.44	112/147	35.89	
					ester
51	Leu7411 - Thr7544	1.49	105/134	32.38	
					ester

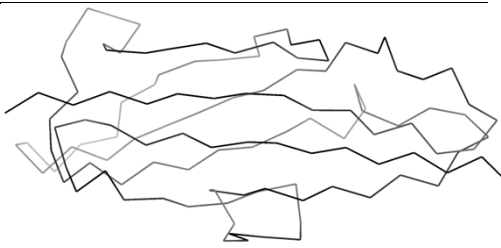
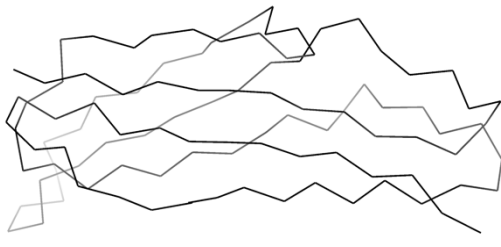
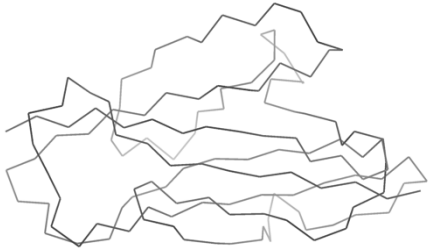
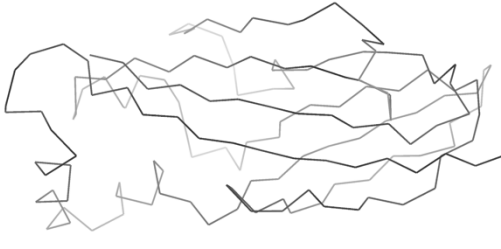

† AlphaFold2 has accurately predicted the expected secondary structure elements of a thioester (TIE) adhesin domain (e.g. PDB ID 6FWY), but has not produced the correct 3D fold.


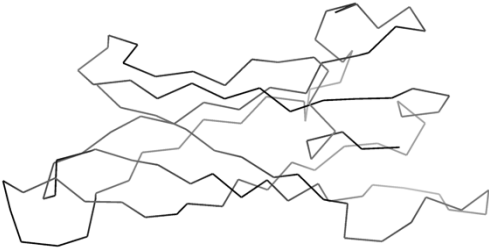
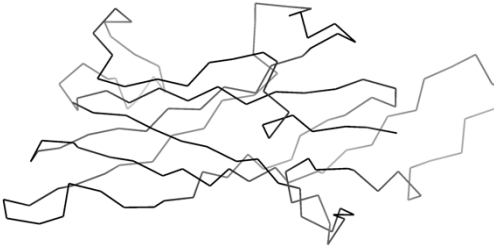


Table S2 *M. curtisii* adhesin AlphaFold2 structure predictions for individual domains.

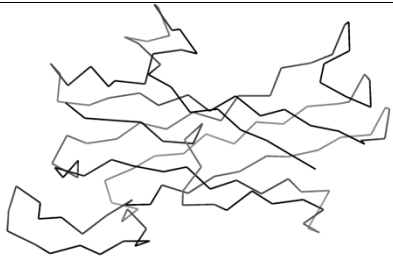
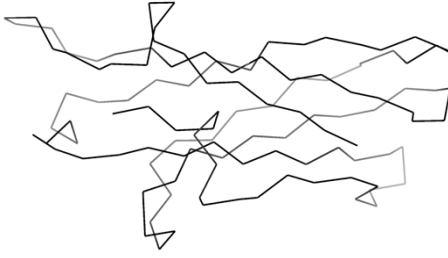
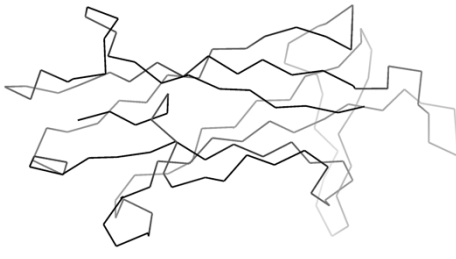
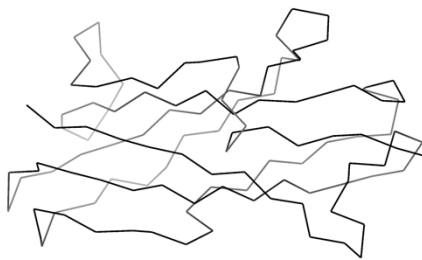
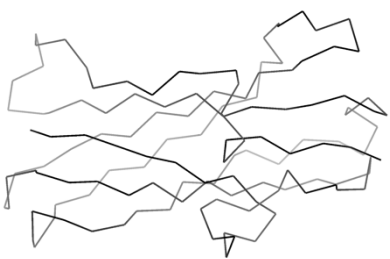
For RMSD calculation, putative isopeptide bond-containing domains were aligned to the major pilin Spy0128 from *Streptococcus pyogenes* (PDB ID 3B2M), and putative ester bond-containing domains were aligned to a repeat domain from *Clostridium perfringens* adhesin Cpe0147 (PDB ID 4NI6). The putative adhesin domain was aligned to the thioester domain of *Enterococcus faecium*, TIE86 (PDB ID 6FWY).


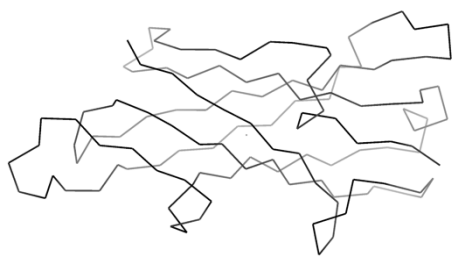

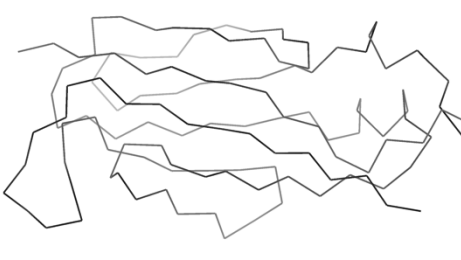

Domain Identifier	Amino acid range	RMS D (Å)	No. C α aligned	Sequence identity (%)	Predicted structure
n/a	Met1 - Val421	n/a	n/a	n/a	no structure predicted
A	Pro422 - Gln724	6.31	48/303	10.42	 thioester domain†
1	Ile22 - Asn175	2.10	119/154	16.81	 ester
2	Lys176 - Arg304	3.09	78/129	6.41	 isopeptide
3	Glu305 - Pro340	2.14	93/126	22.58	 isopeptide

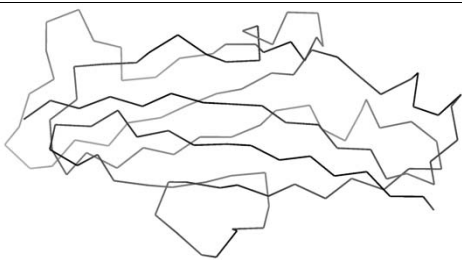
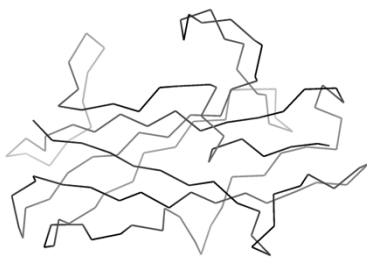
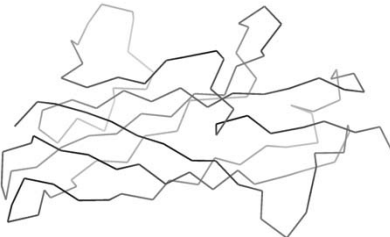
4	Ala341 - Gln548	3.15	85/118	8.24	 <p>isopeptide</p>
5	Lys549 - Ala655	2.99	85/107	20	 <p>isopeptide</p>
6	Asn656 - Tyr771	2.47	81/116	17.28	 <p>isopeptide</p>
7	Asp772 - Glu905	3.57	70/133	4.29	 <p>isopeptide</p>
8	Lys905 - Val1034	2.93	86/130	4.65	 <p>isopeptide</p>

9	Pro1035 - Glu1158	3.52	98/124	9.18	
					isopeptide
10	Leu1159 - Lys1264	4.51	59/106	6.78	
					isopeptide
11	Ala1265 - Tyr1406	2.86	88/142	9.09	
					isopeptide
12	Glu1407 - Cys1566	5.02	87/160	5.75	
					isopeptide
13	Phe1567 - Gln1731	1.99	105/16 5	15.24	
					ester

14	Trp1732 - Tyr1877	1.64	102/14 6	22.55	 <p>ester</p>
15	Thr1878 - Tyr2003	3.70	58/126	12.07	 <p>ester</p>
16	Asn2004 - Pro2161	1.82	115/15 8	33.91	 <p>ester</p>
17	Gly2161 - His2296	1.47	103/13 5	29.13	 <p>ester</p>
18	Ser2297 - Asn2433	1.93	108/13 7	25.00	 <p>ester</p>

19	Ser2434 - Pro2578	2.09	111/14 5	24.32	 <p>ester</p>
20	Ser2579 - Arg2695	1.56	103/11 7	26.21	 <p>ester</p>
21	Val2696 - Trp2840	1.58	104/14 5	27.88	 <p>ester</p>
22	Ser2841 - Val2966	1.85	103/12 6	25.24	 <p>ester</p>
23	Lys2967 - Asp3096	1.67	114/13 0	25.44	 <p>ester</p>

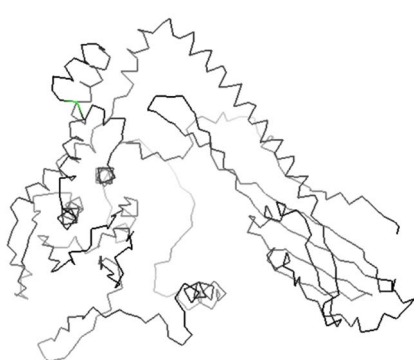
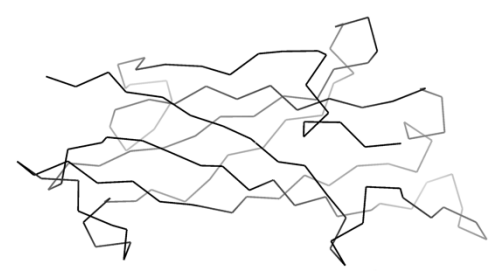
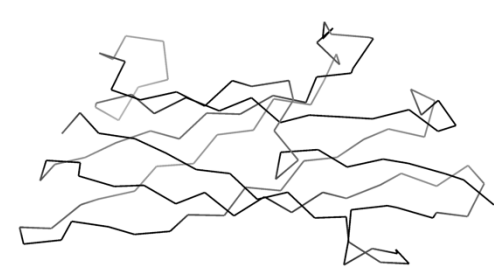

24	Tyr3097 - Asp3244	1.43	107/14 8	22.43	 <p>ester</p>
25	Val3245 - Lys3378	2.03	112/13 4	25.89	 <p>ester</p>
26	His3379 - Pro3548	1.77	106/17 0	21.70	 <p>ester</p>
27	Glu3549Asn36 74	2.88	84/126 74	13.10	 <p>isopeptide</p>
28	Glu3765 - Thr3824	2.29	103/15 0	25.24	 <p>ester</p>

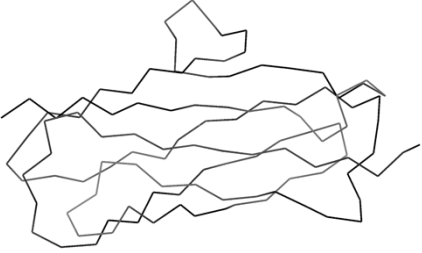
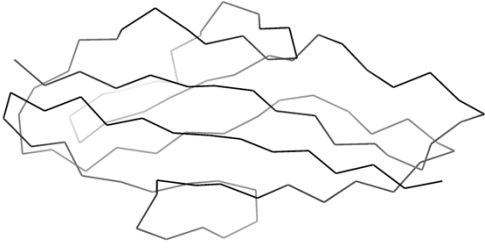
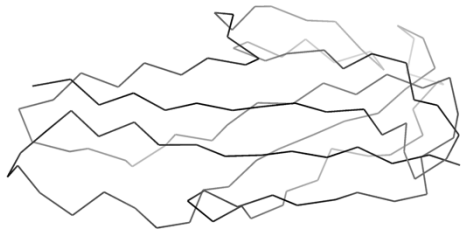
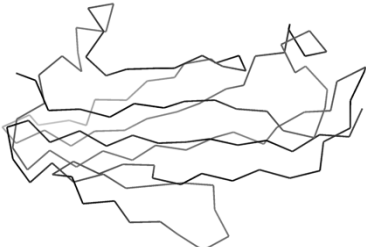

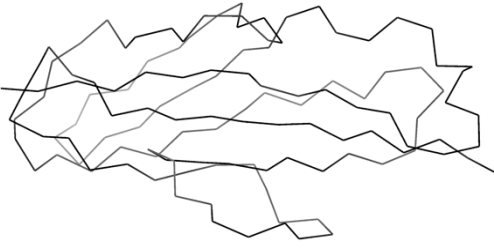
29	His3825 - Val3959	3.24	95/135	11.58	
					isopeptide
30	Lys3960 - Arg4102	1.93	111/14 3	25.23	
					ester
31	Pro4103 - Pro4239	1.26	99/138	36.36	
					ester

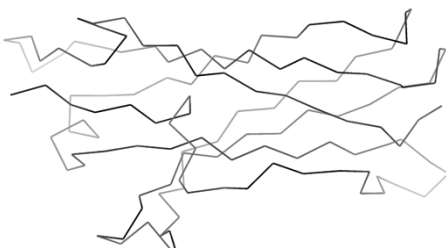
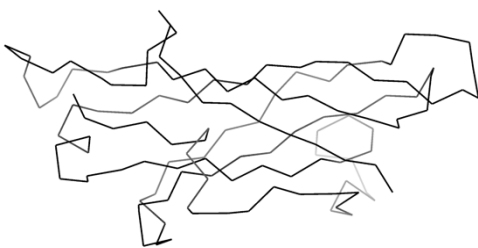
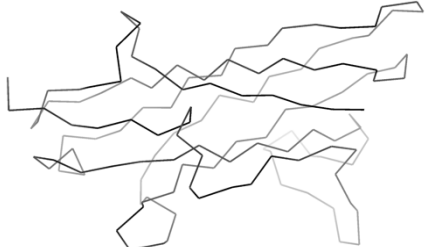
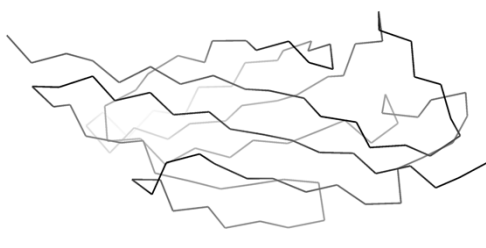
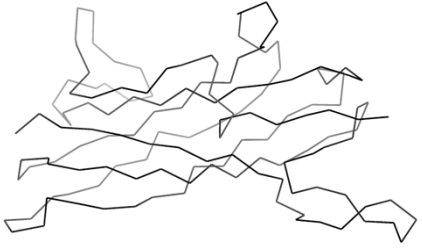
† AlphaFold2 has accurately predicted the expected secondary structure elements of a thioester (TIE) adhesin domain (e.g. PDB ID 6FWY), but has not produced the correct 3D fold.

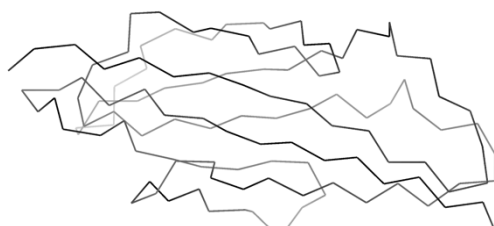

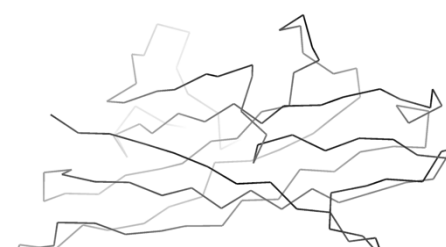
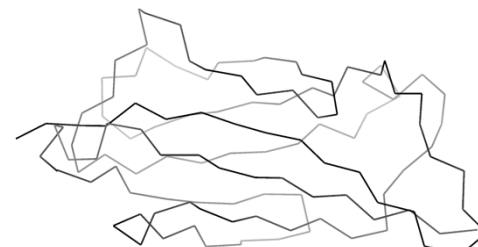

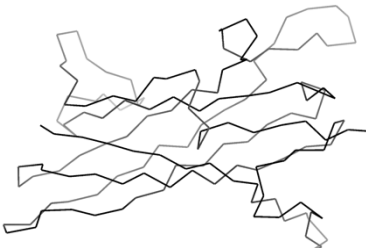
Table S3 *V. cambrienseu* adhesin AlphaFold2 structure predictions for individual domains.

For RMSD calculation, putative isopeptide bond-containing domains were aligned to the major pilin Spy0128 from *Streptococcus pyogenes* (PDB ID 3B2M), and putative ester bond-containing domains were aligned to a repeat domain from *Clostridium perfringens* adhesin Cpe0147 (PDB ID 4NI6). The putative adhesin domain was aligned to the thioester domain of *Enterococcus faecium*, TIE86 (PDB ID 6FWY).

Domain Identifier	Amino acid range	RMSD (Å)	No. C α aligned	Sequence identity (%)	Predicted structure
1	Leu19 - Thr513	4.57	49/511	8.16	
					thioester†
2	Ala515 - Thr652	2.12	111/138	21.62	
					ester
3	Glu653 - Lys788	1.55	107/136	30.84	
					ester
4	Lys791 - Pro921	1.59	105/131	27.62	
					ester

5	Pro924 - Pro1037	2.15	87/114	11.49	
					isopeptide
6	Gln1039 - Glu1146	3.14	86/108	6.98	
					isopeptide
7	Thr1148 - Asn1274	2.95	91/127	14.29	
					isopeptide
8	Lys1276 - Gln1407	1.84	97/132	23.71	
					isopeptide
9	Leu1409 - Ile1545	3.35	77/137	7.79	
					isopeptide
10	Lys1548 - Asp1671	2.89	100/124	17.00	

11	Pro1670 - Pro1802	1.20 1.62	108/133	25.93	isopeptide 
12	Asn1801 - Gly1935	1.94	110/135	28.18	ester 
13	Pro1936 - 2069	1.53 2.06	108/134	27.77	ester 
14	Ser2072 - Pro2196	3.25	87/125	10.34	ester 
15	Glu2197 - Thr2340	3.40 2.02	106/144	25.47	isopeptide  ester

16	Pro2344 - Met2469	3.28	97/126	11.34	
					isopeptide
17	Gly2470 - Glu2606	2.05	111/137	34.23	
					ester
18	Ala2607 - Glu2742	2.72 2.22	104/136	27.88	
					ester
19	Lys2745 - Lys2873	2.849	90/129	14.44	
					isopeptide
20	Asp2874 - Ala3013	3.62 1.67	108/140	25.00	
					ester
21	Thr3019 - Pro3174	2.16 6.46	49/156	6.12	

ester

† AlphaFold2 has accurately predicted the expected secondary structure elements of a thioester (TIE) adhesin domain (e.g. PDB ID 6FWY), but has not produced the correct 3D fold.

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MView

Reference sequence (1): WP_004013458.1
Identities normalised by aligned length.
Colored by: identity

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2 WP_013188882.1	62.4%	35.2%	
consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			
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2 WP_013188882.1	62.4%	35.2%	
consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			
	cov	pid	161	240
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2 WP_013188882.1	62.4%	35.2%	
consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			
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1 WP_004013458.1	100.0%	100.0%	KQTAESPVENPKESLASKEGGETQAQKDVPPNGSESSNSSESAPELAKPTPAETSTAEETEPKETKPKSETKPSQFVEEKG	
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consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			
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consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			
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consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			
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consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			
	cov	pid	561	640
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consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			
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consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			
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consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			

6/17/2018

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			consensus/80%			
			consensus/70%			
				881			960
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			consensus/100%			
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			consensus/80%			
			consensus/70%			
				961			1040
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			consensus/90%			
			consensus/80%			
			consensus/70%			
				1041			1120
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			consensus/70%			
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			consensus/100%			
			consensus/90%			
			consensus/80%			
			consensus/70%			
				1201			1280
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			consensus/90%			
			consensus/80%			
			consensus/70%			
				1281			1360
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			consensus/70%			
				1361			1440
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			consensus/100%			
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			consensus/80%			
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				1601			1680
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			consensus/100%			

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consensus/90%				
consensus/80%				
consensus/70%				
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consensus/80%				
consensus/70%				
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consensus/80%				
consensus/70%				
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consensus/100%				
consensus/90%				
consensus/80%				
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consensus/90%				
consensus/80%				
consensus/70%				
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consensus/90%				
consensus/80%				
consensus/70%				
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consensus/100%				
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consensus/70%				
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consensus/90%				
consensus/80%				
consensus/70%				
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consensus/90%				
consensus/80%				
consensus/70%				
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consensus/100%				
consensus/90%				
consensus/80%				
consensus/70%				
	cov	pid	2481	5	2560

6/17/2018

MView

```
1 WP_004013458.1 100.0% 100.0% IGENKVKLPVGTICALWEDSFKLEDEAKPETKMLGSSSEIKTEKVKDAQGNTHDGVNFEIKSEKDFTSVTAQNKFDIP
2 WP_013188882.1 62.4% 35.2% -----PKECITKANRFDTMGD-MKGTPTRWGDYDA-L--EQV-----
consensus/100% .....sPcChhhtspFcphTD.hK(sps+W.thsu.1..EpV-----
consensus/90% .....sPcChhhtspFcphTD.hK(sps+W.thsu.1..EpV-----
consensus/80% .....sPcChhhtspFcphTD.hK(sps+W.thsu.1..EpV-----
consensus/70% .....sPcChhhtspFcphTD.hK(sps+W.thsu.1..EpV-----

cov pid 2561 6 2640
1 WP_004013458.1 100.0% 100.0% STELKVKKLVKADKASKVAAGKQFTVVIVTQCVPTDGGQTYTIADEKDGKVFKNQKFTKTDKSGKPIPVGAICITVTELV
2 WP_013188882.1 62.4% 35.2% -----APDRG-----KIAQKPLGQNAPMIGFG-----
consensus/100% .....hPscG.....KhppshutpsPhshG.....
consensus/90% .....hPscG.....KhppshutpsPhshG.....
consensus/80% .....hPscG.....KhppshutpsPhshG.....
consensus/70% .....hPscG.....KhppshutpsPhshG.....

cov pid 2641 7 2720
1 WP_004013458.1 100.0% 100.0% ASADVPGHNSVQIADGTSVVKHTH-----TRVVPKAGKTVITNDYERKVGSKLKFVAGVDVNTALAAND
2 WP_013188882.1 62.4% 35.2% -----AVIIFPGSSSATLFPNPSGSASRAATSDRSAAEPEEEDADTLTSLLEPIE-----GEATET--GATQ
consensus/100% .....sWsl..usUsSsl.hps.....ppst.PcttcsstLT.shE.h.....G.sspT..uAsp
consensus/90% .....sWsl..usUsSsl.hps.....ppst.PcttcsstLT.shE.h.....G.sspT..uAsp
consensus/80% .....sWsl..usUsSsl.hps.....ppst.PcttcsstLT.shE.h.....G.sspT..uAsp
consensus/70% .....sWsl..usUsSsl.hps.....ppst.PcttcsstLT.shE.h.....G.sspT..uAsp

cov pid 2721 8 2800
1 WP_004013458.1 100.0% 100.0% AKFEFKYNCLDGLPVKDGITISLSATQMSTEITGIPAGA/CVVFSEPKVAPHGAVPTLSNKKLDGAQAADGATITIGNT
2 WP_013188882.1 62.4% 35.2% AR-IFGKT---ADPSGDSGTSSTEPS-GAGNAPQLPANPEEPSSAP-----ELSPESA-PAAVGEDRA-NPT
consensus/100% A+.Fths.....ucPstDushShpsO.hushpstlPASscpsSTP.....PLS.c.su..AAsGpsphs.ssT
consensus/90% A+.Fths.....ucPstDushShpsO.hushpstlPASscpsSTP.....PLS.c.su..AAsGpsphs.ssT
consensus/80% A+.Fths.....ucPstDushShpsO.hushpstlPASscpsSTP.....PLS.c.su..AAsGpsphs.ssT
consensus/70% A+.Fths.....ucPstDushShpsO.hushpstlPASscpsSTP.....PLS.c.su..AAsGpsphs.ssT

cov pid 2801 9 2880
1 WP_004013458.1 100.0% 100.0% STLDATNTYTPYQVKFDLK--KLV---KANDQAKLDGDFTFQVSCAQTSDV-----V
2 WP_013188882.1 62.4% 35.2% PTKTILSGAVPFYKFEPTMKEIKLKFDPSVDKDTAIANFNKQVDEAQAQVDMNQLEQFMNGKPFARDTKKAMVDNLNLQF
consensus/100% sThshhshsPathKF-.p.c.lh.....usDpsph.usFshQVspAQssV.....h
consensus/90% sThshhshsPathKF-.p.c.lh.....usDpsph.usFshQVspAQssV.....h
consensus/80% sThshhshsPathKF-.p.c.lh.....usDpsph.usFshQVspAQssV.....h
consensus/70% sThshhshsPathKF-.p.c.lh.....usDpsph.usFshQVspAQssV.....h

cov pid 2881 9 2960
1 WP_004013458.1 100.0% 100.0% TLNQANDYSNDSSKFAKPILSGE----TC---TIVETGADIANYNHKSVEYTVSGSIVTKGNKAPAIQVGSFTLPKIG
2 WP_013188882.1 62.4% 35.2% DNLKQGLANFEEQYSKHPASAKFPGKACEDNGPIVPGSIFLV-----K-----NMTAATIG
consensus/100% s..ptpsuH.pppaut+P.hst.....sC...sIV.sGoh.ls.....K.....saHsppG
consensus/90% s..ptpsuH.pppaut+P.hst.....sC...sIV.sGoh.ls.....K.....saHsppG
consensus/80% s..ptpsuH.pppaut+P.hst.....sC...sIV.sGoh.ls.....K.....saHsppG
consensus/70% s..ptpsuH.pppaut+P.hst.....sC...sIV.sGoh.ls.....K.....saHsppG

cov pid 2961 0 3040
1 WP_004013458.1 100.0% 100.0% DASVSV-----TATNTYDHQLGSLQLTAVSVKDNAAIPMDNKSYGFTVDCYQPGEGEGVGEKLSIAVSLAAGETKIV
2 WP_013188882.1 62.4% 35.2% EPNVWQMARKHRNEGQAYHAAIDFLALYPS----DTKNF--KVDGQASFCVPEFYGYIGNHKYYTD-----
consensus/100% -ssV.....stspYcttIs.LtLh.u.....sstNsa..Ks.G.ss.ChpPh.G.QlGp+hsHps.....
consensus/90% -ssV.....stspYcttIs.LtLh.u.....sstNsa..Ks.G.ss.ChpPh.G.QlGp+hsHps.....
consensus/80% -ssV.....stspYcttIs.LtLh.u.....sstNsa..Ks.G.ss.ChpPh.G.QlGp+hsHps.....
consensus/70% -ssV.....stspYcttIs.LtLh.u.....sstNsa..Ks.G.ss.ChpPh.G.QlGp+hsHps.....

cov pid 3041 1 3120
1 WP_004013458.1 100.0% 100.0% VEKAIVGIVCFVKETVADTPD-----VTNQLTWENAGTTVTSPPDGV
2 WP_013188882.1 62.4% 35.2% ---PSKSTIYWAKD-NPEKAETVKALAWHYAKYRNGANNHGYQNAIMWIFGITDNGRAMNLDSMSGDTGVTDVKDL-I
consensus/100% ...sphuIhasK-.ss-ps-.....shsQhOmtssGsTssps..l
consensus/90% ...sphuIhasK-.ss-ps-.....shsQhOmtssGsTssps..l
consensus/80% ...sphuIhasK-.ss-ps-.....shsQhOmtssGsTssps..l
consensus/70% ...sphuIhasK-.ss-ps-.....shsQhOmtssGsTssps..l

cov pid 3121 2 3200
1 WP_004013458.1 100.0% 100.0% ANARRVWIAEDQGTTPAMSVIATNRLEVHYGTFTLQKLTGFAAEDVTKTPVNFVKKCGDLSEQVTVIPGGAPVDYA
2 WP_013188882.1 62.4% 35.2% QQ---ALTAYQHRDGNVVKAL--ETMHLDQVSLQPADNGSSL-----LTVQL-----NDYNS
consensus/100% tp....sIst.Qt+psu.sVpAh...phHshphoLQ.s.sGpuh.....hpVph.....sDYS
consensus/90% tp....sIst.Qt+psu.sVpAh...phHshphoLQ.s.sGpuh.....hpVph.....sDYS
consensus/80% tp....sIst.Qt+psu.sVpAh...phHshphoLQ.s.sGpuh.....hpVph.....sDYS
consensus/70% tp....sIst.Qt+psu.sVpAh...phHshphoLQ.s.sGpuh.....hpVph.....sDYS

cov pid 3201 3 3280
1 WP_004013458.1 100.0% 100.0% TATGQKVIIVGTACTVHEVPAKIVTGVSELTWQG---SGTAAADNGVSEIPAVGAPNVAIKAVNNVTY---NKAAFKIK
2 WP_013188882.1 62.4% 35.2% PNST-----EGRIIGDQVYLVTVGATYADGKIPNNRISLL-----EALNGVTLKIANQNAFKIS
consensus/100% ssoS.....u+lHgsps.LthQG...sGpPhssNt1S1.....cAInsvTh...NpsAFKIp
consensus/90% ssoS.....u+lHgsps.LthQG...sGpPhssNt1S1.....cAInsvTh...NpsAFKIp
consensus/80% ssoS.....u+lHgsps.LthQG...sGpPhssNt1S1.....cAInsvTh...NpsAFKIp
consensus/70% ssoS.....u+lHgsps.LthQG...sGpPhssNt1S1.....cAInsvTh...NpsAFKIp

cov pid 3281 3 3360
1 WP_004013458.1 100.0% 100.0% KTVDPVATKFLGDFQFTYRCVAPNGKVVYQATPFNNOASQYVSVAAGEESAIEIIVPTDSKCTVTEADPQTTIPAVDNKGA
2 WP_013188882.1 62.4% 35.2% FAG-----SVKNVEDPYFIDNPNPTQAQVVLRLKDL----DLSGSL-----EVKW---TYIPQPKPAIS---
consensus/100% hss.....ltshp.sYhssPNG.s.sQssshppph.....sLuuu.....sKh...ph.PQspPAIS...
consensus/90% hss.....ltshp.sYhssPNG.s.sQssshppph.....sLuuu.....sKh...ph.PQspPAIS...
consensus/80% hss.....ltshp.sYhssPNG.s.sQssshppph.....sLuuu.....sKh...ph.PQspPAIS...
consensus/70% hss.....ltshp.sYhssPNG.s.sQssshppph.....sLuuu.....sKh...ph.PQspPAIS...
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https://www.ebi.ac.uk/Tools/services/rest/mview/result/mview-I20180617-113615-0661-42718863-p1m/aln.html

4/10

6/17/2018

MView

Accession	Species	cov	pid	Sequence	Accession
1 WP_004013458.1	100.0%	100.0%	3361	hss.....ltshp.sYhhsPNG.s.Qssshpph.....sluuu.....skh...ph.PQspPAIs...	3440
2 WP_013188882.1	62.4%	35.2%		NPV(KYSGTQFTGGKGLTSAFVTKGTVEVATA--KNLYVPTTGFQFSKAVSNNVANHPGKFNFGYTC(LP)NGKQT TTAKVNGAESVPGGAETA--TFSS--RADEVITLDDVKYENIPADTGMN-----RKYLGISLTKVSEGIAG sssKhsGsp.sPGGtths..oFo..+usEVLThTs..K...lPtsTGhp.....tKa.hg.hsklspg.tp consensus/100% sssKhsGsp.sPGGtths..oFo..+usEVLThTs..K...lPtsTGhp.....tKa.hg.hsklspg.tp consensus/90% sssKhsGsp.sPGGtths..oFo..+usEVLThTs..K...lPtsTGhp.....tKa.hg.hsklspg.tp consensus/80% sssKhsGsp.sPGGtths..oFo..+usEVLThTs..K...lPtsTGhp.....tKa.hg.hsklspg.tp consensus/70% sssKhsGsp.sPGGtths..oFo..+usEVLThTs..K...lPtsTGhp.....tKa.hg.hsklspg.tp	
1 WP_004013458.1	100.0%	100.0%	3441	AVKTEQLGAN--D-----PAVNITDLPVGECEVLWEESVEKTPQSEK-ISTTWTVGAAKPVVGSQKADHGGI PHDN	3520
2 WP_013188882.1	62.4%	35.2%		KVLTVQADADISDQGTVTGLFPYEVKASEVKKGD-RFYEEILVTSDPKYAGGETAFITKGYGNLNV---IAKHTGENPDQ tVhTp.hsAs..D.....tVpso-l.hGs.phhaEE.l.poppPp.t.hpTsathGhup.sV...AchpGps.Dp consensus/100% tVhTp.hsAs..D.....tVpso-l.hGs.phhaEE.l.poppPp.t.hpTsathGhup.sV...AchpGps.Dp consensus/90% tVhTp.hsAs..D.....tVpso-l.hGs.phhaEE.l.poppPp.t.hpTsathGhup.sV...AchpGps.Dp consensus/80% tVhTp.hsAs..D.....tVpso-l.hGs.phhaEE.l.poppPp.t.hpTsathGhup.sV...AchpGps.Dp consensus/70% tVhTp.hsAs..D.....tVpso-l.hGs.phhaEE.l.poppPp.t.hpTsathGhup.sV...AchpGps.Dp	
1 WP_004013458.1	100.0%	100.0%	3521	AVKFKVDEKNEFAVSTIAENTFVSGTELVKKIVTKDNNSETADSKSFKVSTIKCVPTDK----AEHTATNFP(L)NGQ	3600
2 WP_013188882.1	62.4%	35.2%		TVLIANKIK-----AELTLSKEAIGA-ADKADGNVTFR--VSCDDGTAATLYAPARGGVANTPNAWAG- sVhthtsK.....sELTlpKpshts.sschssshoF+.lpCs.stst....ActslAsspPhnsG. consensus/100% sVhthtsK.....sELTlpKpshts.sschssshoF+.lpCs.stst....ActslAsspPhnsG. consensus/90% sVhthtsK.....sELTlpKpshts.sschssshoF+.lpCs.stst....ActslAsspPhnsG. consensus/80% sVhthtsK.....sELTlpKpshts.sschssshoF+.lpCs.stst....ActslAsspPhnsG. consensus/70% sVhthtsK.....sELTlpKpshts.sschssshoF+.lpCs.stst....ActslAsspPhnsG.	
1 WP_004013458.1	100.0%	100.0%	3601	SKTFKTDGTGAIIPVGAICTVTEDETSKVA--GHTWKL---EVKDPNQVSTKGL-----SAEKDKAKNTVELVD	3680
2 WP_013188882.1	62.4%	35.2%		----YQASSIEVTPGAICTVEETYSAPVLDLATAPRIVGNGAEMVSDPTPVNNGKTIQSKAKFKMGDAGDINLAVTNT ...hpsouhtlssGAhCTVpes.osA.Vs...u.pilh..VpDps.VsspGh.....t.tDtc.sltlSns consensus/100% ...hpsouhtlssGAhCTVpes.osA.Vs...u.pilh..VpDps.VsspGh.....t.tDtc.sltlSns consensus/90% ...hpsouhtlssGAhCTVpes.osA.Vs...u.pilh..VpDps.VsspGh.....t.tDtc.sltlSns consensus/80% ...hpsouhtlssGAhCTVpes.osA.Vs...u.pilh..VpDps.VsspGh.....t.tDtc.sltlSns consensus/70% ...hpsouhtlssGAhCTVpes.osA.Vs...u.pilh..VpDps.VsspGh.....t.tDtc.sltlSns	
1 WP_004013458.1	100.0%	100.0%	3681	YKREVGFKLTKAVAGIK-IDFAKAAANNGKFEFTYDVLDDG--KTVKNGKRLDLTKDQQTVEKIPIDATCTLKET	3760
2 WP_013188882.1	62.4%	35.2%		YREPTGGFKVFKVNSDGKFDAYTAANNGKFNFYRCDDKIAGSFPALPEPSTADGDPWSVEKDLPIGARCSVTM Y+c.sGGFKLkhVsucg.hDhhpAAsANSgKfPhYcCshsh..phshstcspHstD..ohEVKDIphsApColpEh consensus/100% Y+c.sGGFKLkhVsucg.hDhhpAAsANSgKfPhYcCshsh..phshstcspHstD..ohEVKDIphsApColpEh consensus/90% Y+c.sGGFKLkhVsucg.hDhhpAAsANSgKfPhYcCshsh..phshstcspHstD..ohEVKDIphsApColpEh consensus/80% Y+c.sGGFKLkhVsucg.hDhhpAAsANSgKfPhYcCshsh..phshstcspHstD..ohEVKDIphsApColpEh consensus/70% Y+c.sGGFKLkhVsucg.hDhhpAAsANSgKfPhYcCshsh..phshstcspHstD..ohEVKDIphsApColpEh	
1 WP_004013458.1	100.0%	100.0%	3761	APTAPGF AAPATMKGIST--TSDSGMVIKEGQTAEVVATNTYTPYQVKFTLKKVIAK--DKTLDDGFQFVKCGDK	3840
2 WP_013188882.1	62.4%	35.2%		KPTAPSGYDVTISAADALVKPVQSNTVSRPDIRADFANQVFMNQYLPADASFRLRRIARFTDGLINDNFALHYS CSR tPTAPoGasshuss.tlsp.s.osssuhhsI+ts.sspVshhNpYhPhpspFoL+Klh+..sphlssFthphoCud+ consensus/100% tPTAPoGasshuss.tlsp.s.osssuhhsI+ts.sspVshhNpYhPhpspFoL+Klh+..sphlssFthphoCud+ consensus/90% tPTAPoGasshuss.tlsp.s.osssuhhsI+ts.sspVshhNpYhPhpspFoL+Klh+..sphlssFthphoCud+ consensus/80% tPTAPoGasshuss.tlsp.s.osssuhhsI+ts.sspVshhNpYhPhpspFoL+Klh+..sphlssFthphoCud+ consensus/70% tPTAPoGasshuss.tlsp.s.osssuhhsI+ts.sspVshhNpYhPhpspFoL+Klh+..sphlssFthphoCud+	
1 WP_004013458.1	100.0%	100.0%	3841	QTSVTLNKDNKYTMESSELKTPQILSGVICHILEETSEQAFKSHTWKSLDYQVDGQVDSVDKDAKRVTFLTPA'GDAIV	3920
2 WP_013188882.1	62.4%	35.2%		SGKTV-SGDVTVAGNGEAVSVKGVKAGMTCTITEPRKPAIAKANFKDLSFDLSGTQYNSV---NSERLEFDVPRNPAAV otpss.stDspshpuptlps.tlhuGhpCpIpEspc.AhtptsaksLSaplsGpthssS...sucRlPfsIPtssASV consensus/100% otpss.stDspshpuptlps.tlhuGhpCpIpEspc.AhtptsaksLSaplsGpthssS...sucRlPfsIPtssASV consensus/90% otpss.stDspshpuptlps.tlhuGhpCpIpEspc.AhtptsaksLSaplsGpthssS...sucRlPfsIPtssASV consensus/80% otpss.stDspshpuptlps.tlhuGhpCpIpEspc.AhtptsaksLSaplsGpthssS...sucRlPfsIPtssASV consensus/70% otpss.stDspshpuptlps.tlhuGhpCpIpEspc.AhtptsaksLSaplsGpthssS...sucRlPfsIPtssASV	
1 WP_004013458.1	100.0%	100.0%	3921	TIATNTYDRNKALQIQKVAKLNQDQVSKDAKANPLNHHQYQFVTCVDPADNGLGAKTQAV'VPLQAGAPPTVIKDA	4000
2 WP_013188882.1	62.4%	35.2%		LVTATNVYEQKAGSFTLQKTVK----AGESNPLKGTAFTRISCGEEDPF-----TVSLKAG--QTWTSKSY hITATNSY-pptGuhpLQKssK.....sucUNPL.sptapFcloCh..ss.....TVsLpAG...phs.Ksh consensus/100% hITATNSY-pptGuhpLQKssK.....sucUNPL.sptapFcloCh..ss.....TVsLpAG...phs.Ksh consensus/90% hITATNSY-pptGuhpLQKssK.....sucUNPL.sptapFcloCh..ss.....TVsLpAG...phs.Ksh consensus/80% hITATNSY-pptGuhpLQKssK.....sucUNPL.sptapFcloCh..ss.....TVsLpAG...phs.Ksh consensus/70% hITATNSY-pptGuhpLQKssK.....sucUNPL.sptapFcloCh..ss.....TVsLpAG...phs.Ksh	
1 WP_004013458.1	100.0%	100.0%	4001	PVGSVCFIKETPVKTEAVIGTLSWEGDGTNAVGGPDAANVRKVVWIGGEGDVQQVNV(AV)NDLTVQYGFSLHKEITGIA	4080
2 WP_013188882.1	62.4%	35.2%		PVGTECLIEHYDPSTQAAITSVSYQGAMP--GTTDA-----VLT-VKEGKAARKVEAVNTVKANYGKFLTKKVEGDA PVGo.ChI+EhsspTpAshuTlSapGshs...GssSA.....Vls..KtshtTVpVCAVns1pspYhFuLpKClpGDA consensus/100% PVGo.ChI+EhsspTpAshuTlSapGshs...GssSA.....Vls..KtshtTVpVCAVns1pspYhFuLpKClpGDA consensus/90% PVGo.ChI+EhsspTpAshuTlSapGshs...GssSA.....Vls..KtshtTVpVCAVns1pspYhFuLpKClpGDA consensus/80% PVGo.ChI+EhsspTpAshuTlSapGshs...GssSA.....Vls..KtshtTVpVCAVns1pspYhFuLpKClpGDA consensus/70% PVGo.ChI+EhsspTpAshuTlSapGshs...GssSA.....Vls..KtshtTVpVCAVns1pspYhFuLpKClpGDA	
1 WP_004013458.1	100.0%	100.0%	4081	QNKDVKSKDFFFTVKCPGLDD--QKVTLKGGETKTLPFGKMKVGTCKSVHEVPA'VAGVTFDPVSMQNAARTDGG--	4160
2 WP_013188882.1	62.4%	35.2%		KAA---ATTFAFDYKCNDAANTNGTLVRRGGTKTVG-DNILLVGTTCYIKKPVQIDGVITP-SWVTNLPNGTGAYAS pss....upsFtFshlCsshsc..tpIp1+GGPTKTLs.sphhVGTpC.l+EhPsp1sGVThSP.SWSpshsStTsu... consensus/100% pss....upsFtFshlCsshsc..tpIp1+GGPTKTLs.sphhVGTpC.l+EhPsp1sGVThSP.SWSpshsStTsu... consensus/90% pss....upsFtFshlCsshsc..tpIp1+GGPTKTLs.sphhVGTpC.l+EhPsp1sGVThSP.SWSpshsStTsu... consensus/80% pss....upsFtFshlCsshsc..tpIp1+GGPTKTLs.sphhVGTpC.l+EhPsp1sGVThSP.SWSpshsStTsu... consensus/70% pss....upsFtFshlCsshsc..tpIp1+GGPTKTLs.sphhVGTpC.l+EhPsp1sGVThSP.SWSpshsStTsu...	
1 WP_004013458.1	100.0%	100.0%	4161	GIDVTI--PATG-VKDLSTATNAKAVYDKATFQIQKVISSTENLAFEDGFKFTYTCAP'IGKTFQKAPFGAQTGVDITN	4240
2 WP_013188882.1	62.4%	35.2%		YKQFTIPQPNQKAQLVLEAKNTLEYDKASFYIKKVIQGGAVFDPDA'FKFTYSCKAPDGKTYQATP'FGSQAKAKFIE	

6/17/2018

MView

consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4241			3	4320
1	WP_004013458.1	100.0%	100.0%	VKAGP	PSGII	VPOGSKC	TVSEANPKD
2	WP_013188882.1	62.4%	35.2%	VVAGQ	ESAIVV	PGSKCSV	SEPAQLYVTNQ
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4321				4 4400
1	WP_004013458.1	100.0%	100.0%	VIA	TNTY	VEKIT	IGQFQK
2	WP_013188882.1	62.4%	35.2%	FAA	TNVT	TEKMT	GFKFYK
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4401				4480
1	WP_004013458.1	100.0%	100.0%	PKNA	EKVST	TWTID	GKPV
2	WP_013188882.1	62.4%	35.2%	AQAN	EKVT	TKVTG	TAEPV
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4481				4560
1	WP_004013458.1	100.0%	100.0%	ADK	GKFD	VITC	YPTD
2	WP_013188882.1	62.4%	35.2%	GNI	SKVLS	ATCKY	PTDNA
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4561				4640
1	WP_004013458.1	100.0%	100.0%	VET	KQAD	QTKSE	PEPYTA
2	WP_013188882.1	62.4%	35.2%	DKA	-----	TATVTL	NAEKGR
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4641				4720
1	WP_004013458.1	100.0%	100.0%	INV	GEA-	AVSSQQ	IPVGYK
2	WP_013188882.1	62.4%	35.2%	GVT	DKGYK	IVDGI	PLGYK
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4721				8 4800
1	WP_004013458.1	100.0%	100.0%	K	LALPL	NATYN	FEMWCGP
2	WP_013188882.1	62.4%	35.2%	T	-A	IADGT	YEFYV
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4801				4880
1	WP_004013458.1	100.0%	100.0%	T	TGAT	SVKAP	VLVDS
2	WP_013188882.1	62.4%	35.2%	T	MQ	GVEPT	-YQAV
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4881				4960
1	WP_004013458.1	100.0%	100.0%	W	NSYYQ	AIGG	FVTRNF
2	WP_013188882.1	62.4%	35.2%	M	KQ	-YGA	YRYMNR
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							
	cov	pid	4961				5040
1	WP_004013458.1	100.0%	100.0%	H	SVDMS	AKSLD	GI--
2	WP_013188882.1	62.4%	35.2%	H	KAVIT	ATDAS	GKALAS
consensus/100%							
consensus/90%							
consensus/80%							
consensus/70%							

			MView			
					1	5120
6/17/2018						
	cov	pid				
	5041					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5121					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5201					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5281					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5361					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5441					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5441					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5521					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5601					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5681					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5761					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5841					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					
	consensus/90%					
	consensus/80%					
	consensus/70%					
	cov	pid				
	5841					
1	WP_004013458.1	100.0%	100.0%			
2	WP_013188882.1	62.4%	35.2%			
	consensus/100%					

6/17/2018

MView

				consensus/80%		consensus/70%			
				cov	pid				
					5921			0 6000	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6001			6080	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6081			6160	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6161			6240	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6241			6320	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6321			6400	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6401			6480	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6481			6560	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6561			6640	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6641			6720	
1	WP_004013458.1	100.0%	100.0%						
2	WP_013188882.1	62.4%	35.2%						
				consensus/100%					
				consensus/90%					
				consensus/80%					
				consensus/70%					
				cov	pid				
					6721			6800	
1	WP_004013458.1	100.0%	100.0%						

				MView				
6/17/2018								
2	WP_013188882.1	62.4%	35.2%	LKLVA ^{YEYL} RASLVTGD--D--ATIKASVTDASKWDATHAQNDRQTVVVDVPRIGIKLYAQGGKVWEHGDNV				
	consensus/100%			hKLV ^{AYEYL} LshS ^{S.sshs}th.tshupsuppwsATHApsNDstqTVVvcsP+IGlpLpYuQu.KsVw.udpvcL				
	consensus/90%			hKLV ^{AYEYL} LshS ^{S.sshs}th.tshupsuppwsATHApsNDstqTVVvcsP+IGlpLpYuQu.KsVw.udpvcL				
	consensus/80%			hKLV ^{AYEYL} LshS ^{S.sshs}th.tshupsuppwsATHApsNDstqTVVvcsP+IGlpLpYuQu.KsVw.udpvcL				
	consensus/70%			hKLV ^{AYEYL} LshS ^{S.sshs}th.tshupsuppwsATHApsNDstqTVVvcsP+IGlpLpYuQu.KsVw.udpvcL				
		cov	pid	6801	:	:	6880	
1	WP_004013458.1	100.0%	100.0%	TDTVEYFNLPKTKYTL ^{SL} GLMGGS ^{AE} LS ^{DT} GV ^K ATTEFTTAAANGAQTVSGT-----AVVKFVTPREVLNEIKL				
2	WP_013188882.1	62.4%	35.2%	TDFVEYFNLLPATEYTLNGKLMGIATDGKVS ^{DT} GVVGTAKFTTPKATNGATRVSGTIADKTA ^K AVEFVPLSVLKA ND KL				
	consensus/100%			TdhVEYanL.PtTCYT ^{Ls} GpLMGhsostpIS ^{DT} GVhu ^{tsc} FTTP ^{TA} SNGAppV ^{SG} T.....AhVcFTVPhpVLctN-KL				
	consensus/90%			TdhVEYanL.PtTCYT ^{Ls} GpLMGhsostpIS ^{DT} GVhu ^{tsc} FTTP ^{TA} SNGAppV ^{SG} T.....AhVcFTVPhpVLctN-KL				
	consensus/80%			TdhVEYanL.PtTCYT ^{Ls} GpLMGhsostpIS ^{DT} GVhu ^{tsc} FTTP ^{TA} SNGAppV ^{SG} T.....AhVcFTVPhpVLctN-KL				
	consensus/70%			TdhVEYanL.PtTCYT ^{Ls} GpLMGhsostpIS ^{DT} GVhu ^{tsc} FTTP ^{TA} SNGAppV ^{SG} T.....AhVcFTVPhpVLctN-KL				
		cov	pid	6881	:	9	6960	
1	WP_004013458.1	100.0%	100.0%	VAYEYLTIDG ^{NPVASHED} PKDENQTVTSKIKPGVGY ^{AV} VDKLF ^{AFD} VDG-----KKDAFTIKDTRVLRVNWEEGKTY ^A				
2	WP_013188882.1	62.4%	35.2%	VAYEALLKGPVADHEDPNDENQTVKVKHPGVGTIAHVGD ^D NLEWEGVNOEGK ^K APET ^Y VHDVIRVNWVEEGKTY ^A				
	consensus/100%			VAYEHlHlcGpPVAshEDPpDENQTVpsk+PGVgThApVsc.psh-Vh-G.....t.-saTl+DsIRhhnVVEEGKTY ^A				
	consensus/90%			VAYEHlHlcGpPVAshEDPpDENQTVpsk+PGVgThApVsc.psh-Vh-G.....t.-saTl+DsIRhhnVVEEGKTY ^A				
	consensus/80%			VAYEHlHlcGpPVAshEDPpDENQTVpsk+PGVgThApVsc.psh-Vh-G.....t.-saTl+DsIRhhnVVEEGKTY ^A				
	consensus/70%			VAYEHlHlcGpPVAshEDPpDENQTVpsk+PGVgThApVsc.psh-Vh-G.....t.-saTl+DsIRhhnVVEEGKTY ^A				
		cov	pid	6961	:	0	7040	
1	WP_004013458.1	100.0%	100.0%	IAGQ ^{LYEQ} S ^{VAGD} --EG:ALAKAATTVK ^{IV} ASMAKPAT ^{EV} E ^K KYGE ^D V ^K VYETE ^{MD} LTVKRE ^D LTKNQV ^{KDD} I ^{AL} V ^Y				
2	WP_013188882.1	62.4%	35.2%	LGGQ ^V YSK ^N AY ^D AN ^{AQ} TALAA ^{NA} KT ^V KV ^{AD} M ^{AK} PA ^T DAE ^K AQ ^G AD ^V K ^V YET ^S MD ^{IP} V ^K AA ^I KT----HGDKLV ^F				
	consensus/100%			luGQlYppshss...pssALAtsApTVKIV ^{ASMAKPAT} -SEKspY ^{ED} V ^K YETpMDIsV ^K ctDlpp....cs.tlVva				
	consensus/90%			luGQlYppshss...pssALAtsApTVKIV ^{ASMAKPAT} -SEKspY ^{ED} V ^K YETpMDIsV ^K ctDlpp....cs.tlVva				
	consensus/80%			luGQlYppshss...pssALAtsApTVKIV ^{ASMAKPAT} -SEKspY ^{ED} V ^K YETpMDIsV ^K ctDlpp....cs.tlVva				
	consensus/70%			luGQlYppshss...pssALAtsApTVKIV ^{ASMAKPAT} -SEKspY ^{ED} V ^K YETpMDIsV ^K ctDlpp....cs.tlVva				
		cov	pid	7041	:	1	7120	
1	WP_004013458.1	100.0%	100.0%	EQLNAE ^{GT} Y ^{EK} VD ^{NT} VT ^{PK} GK ^{SE} PVA ^{HND} PQ ^{SS} IS ^{IT} -AEPQ ^{FG} SLK ^L K ^T V ^{GN} EDA ^{FA} VAR ^{PE} SY ^K FT ^V CK ^Q				
2	WP_013188882.1	62.4%	35.2%	EQLNAE ^{GT} Y ^{ES} AD ^{GG} K ^{VT} PKGN ^{HK} PVA ^A HE ^{INT} ADS ^Q SIN ^{VNR} PE ^{FG} SL ^L T ^K AV ^T GI ^D ENT ^{AV} E ^{RA} KA ^{VT} Y ^F VI ^{CA} Q				
	consensus/100%			EQLNAE ^{GT} Y ^E ps ^{sss} c ^V PKgppcPVA tH N-.pusSQS ^I s.scPpFGS ^L pL ^T K ^S V ^{IG} N--shApV ^{TR} CS ^{Ao} Y ^H FT ^V CS ^Q				
	consensus/90%			EQLNAE ^{GT} Y ^E ps ^{sss} c ^V PKgppcPVA tH N-.pusSQS ^I s.scPpFGS ^L pL ^T K ^S V ^{IG} N--shApV ^{TR} CS ^{Ao} Y ^H FT ^V CS ^Q				
	consensus/80%			EQLNAE ^{GT} Y ^E ps ^{sss} c ^V PKgppcPVA tH N-.pusSQS ^I s.scPpFGS ^L pL ^T K ^S V ^{IG} N--shApV ^{TR} CS ^{Ao} Y ^H FT ^V CS ^Q				
	consensus/70%			EQLNAE ^{GT} Y ^E ps ^{sss} c ^V PKgppcPVA tH N-.pusSQS ^I s.scPpFGS ^L pL ^T K ^S V ^{IG} N--shApV ^{TR} CS ^{Ao} Y ^H FT ^V CS ^Q				
		cov	pid	7121	:	:	2	7200
1	WP_004013458.1	100.0%	100.0%	HGSVDE ^{FT} LKEGE ^E KTVEGIP ^{LG} DC ^{TI} ES ^{ED} VQ ^{AV} NQ ^{AG} LK ^{DT} V ^K FA ^V GV ^T V ^S QV ^{NG} AV ^V K ^{IGG} A ^{NG} SD ^V IA ^V				
2	WP_013188882.1	62.4%	35.2%	HGSVD ^{TI} LHEGGS ^{HT} IDGIPV ^{GK} CT ^{IT} ED ^{VQ} HA ^E LQ ^{AG} LK ^{DT} V ^K FA ^V GV ^T V ^S QV ^{NG} AV ^V K ^{IGG} A ^{NG} SD ^V IA ^V				
	consensus/100%			HGSVdphl+Egtp+Tl-GIPIgDpCTIoEDVQTA..QAGLKDTVKFTst ^{sh} GVTV-S.hnGfusVhIGGtunGopPvsIV				
	consensus/90%			HGSVdphl+Egtp+Tl-GIPIgDpCTIoEDVQTA..QAGLKDTVKFTst ^{sh} GVTV-S.hnGfusVhIGGtunGopPvsIV				
	consensus/80%			HGSVdphl+Egtp+Tl-GIPIgDpCTIoEDVQTA..QAGLKDTVKFTst ^{sh} GVTV-S.hnGfusVhIGGtunGopPvsIV				
	consensus/70%			HGSVdphl+Egtp+Tl-GIPIgDpCTIoEDVQTA..QAGLKDTVKFTst ^{sh} GVTV-S.hnGfusVhIGGtunGopPvsIV				
		cov	pid	7201	:	:	7280	
1	WP_004013458.1	100.0%	100.0%	EVTAE ^{NS} F ^{SD} VP ^{IT} TTNTI ^{SQ} G ^{KL} ENG ^{GL} TD ^{TV} TY ^K MPAG ^{NY} VL ^{HT} Y ^{FM} V ^K DE ^{AT} G ^T VA ^K ID ^V VP ^{SV} FE ^{QT}				
2	WP_013188882.1	62.4%	35.2%	TVVAD ^N K ^{FT} NE ^{VT} IG ^{NT} TG ^{FG} G ^K S ^{NG} G ^K IT ^D V ^K Y ^Q NL ^Q AG ^K Y ^L L ^H TY ^F VE ^Y D ^K AG----QAH ^I DI ^Y V ^P SE ^{VE} R ^{VT}				
	consensus/100%			pVsA-NpFo.-ssISTNT ^{hu} Q ^{FG} K ^h .pNGGH ^{LD} hV ^p ypph.AgpY ^{IL} H ^{TY} FV ^h sK stA+KID ^Y V ^P S.VpE.T				
	consensus/90%			pVsA-NpFo.-ssISTNT ^{hu} Q ^{FG} K ^h .pNGGH ^{LD} hV ^p ypph.AgpY ^{IL} H ^{TY} FV ^h sK stA+KID ^Y V ^P S.VpE.T				
	consensus/80%			pVsA-NpFo.-ssISTNT ^{hu} Q ^{FG} K ^h .pNGGH ^{LD} hV ^p ypph.AgpY ^{IL} H ^{TY} FV ^h sK stA+KID ^Y V ^P S.VpE.T				
	consensus/70%			pVsA-NpFo.-ssISTNT ^{hu} Q ^{FG} K ^h .pNGGH ^{LD} hV ^p ypph.AgpY ^{IL} H ^{TY} FV ^h sK stA+KID ^Y V ^P S.VpE.T				
		cov	pid	7281	:	3	7360	
1	WP_004013458.1	100.0%	100.0%	VKADATTPENGYNGTWTVSD ^{IP} DL ^{HE} VG ^{KK} VV ^{NQ} DPV ^{AP} Q ^{TA} DM ^T FK ^{FG} L ^{NK} LS ^{AG} ET ^S KA ^V LVV ^{SH} HE ^T SE ^Q				
2	WP_013188882.1	62.4%	35.2%	VEGG--YYPGGHS ^{GT} MS ^{VD} MT ^{PE} L ^{TE} L ^{QA} HK ^{TV} VW ^{ED} Y ^K L ^P Q ND --FTT ^{EL} SK ^L PT ^{GR} --GAGL ^L SHH ^{ED} NL ^{GA}				
	consensus/100%			Vcus..hs.sGasGT ^{Mo} Vshs ^I PpLp st K ^{PVV} V ^W pD ^I Yh ^p Q ^{SS} D..pfpstL ^S K ^L SS ^G Ct...sAtL ^L SHH ^{ES} .tt				
	consensus/90%			Vcus..hs.sGasGT ^{Mo} Vshs ^I PpLp st K ^{PVV} V ^W pD ^I Yh ^p Q ^{SS} D..pfpstL ^S K ^L SS ^G Ct...sAtL ^L SHH ^{ES} .tt				
	consensus/80%			Vcus..hs.sGasGT ^{Mo} Vshs ^I PpLp st K ^{PVV} V ^W pD ^I Yh ^p Q ^{SS} D..pfpstL ^S K ^L SS ^G Ct...sAtL ^L SHH ^{ES} .tt				
	consensus/70%			Vcus..hs.sGasGT ^{Mo} Vshs ^I PpLp st K ^{PVV} V ^W pD ^I Yh ^p Q ^{SS} D..pfpstL ^S K ^L SS ^G Ct...sAtL ^L SHH ^{ES} .tt				
		cov	pid	7361	:	4	7440	
1	WP_004013458.1	100.0%	100.0%	GdG ^Y Q ^{FK} V ^S SN ^Y GS ^{FQ} VEK ^{TV} EN ^G AG ^L SEN ^{VS} R ^L PK ^{TF} K ^F E ^Y E ^A K ^L PAG ^{ALL} K ^{PG} T ^Q PK ^{GF} EL ^T V ^D SS ^N PAL ^A K ^{SP} V				
2	WP_013188882.1	62.4%	35.2%	GAGT ^Q N ^{LE} V ^S TH ^{FG} G ^F Q ^V N ^K V ^K P ^{AP} D ^L PA ^D V ^I SK ^{IP} T ^{WN} F ^Y VA ^K L ^{PD} G ^K K ^A KE ^G TA ^{LE} GN ^L TV ^{DP} K ^D PS ^{KA} V ^S Q ^K				
	consensus/100%			GsGhQ ^h CvS ^{opa} Gu ^F Q ^V p ^K S ^V cuss ^L st ^S v.pp ^{IP} T ^{ap} F ^{Py} .AK ^{LP} s ^G th ^h K.G ^{Tt} .cG ^F SL ^T V ^D SP ^s pu ^h A ^h .h				
	consensus/90%			GsGhQ ^h CvS ^{opa} Gu ^F Q ^V p ^K S ^V cuss ^L st ^S v.pp ^{IP} T ^{ap} F ^{Py} .AK ^{LP} s ^G th ^h K.G ^{Tt} .cG ^F SL ^T V ^D SP ^s pu ^h A ^h .h				
	consensus/80%			GsGhQ ^h CvS ^{opa} Gu ^F Q ^V p ^K S ^V cuss ^L st ^S v.pp ^{IP} T ^{ap} F ^{Py} .AK ^{LP} s ^G th ^h K.G ^{Tt} .cG ^F SL ^T V ^D SP ^s pu ^h A ^h .h				
	consensus/70%			GsGhQ ^h CvS ^{opa} Gu ^F Q ^V p ^K S ^V cuss ^L st ^S v.pp ^{IP} T ^{ap} F ^{Py} .AK ^{LP} s ^G th ^h K.G ^{Tt} .cG ^F SL ^T V ^D SP ^s pu ^h A ^h .h				
		cov	pid	7441	:	5	7520	
1	WP_004013458.1	100.0%	100.0%	FEFG ^P VG ^E VA ^{IT} ETG ^V EM ^{PT} GAT ^M ST ^T WA ^T AD ^G AK ^T KA ^{MS} DR ^K SD ^I V ^T I ^Q PR ^{GL} LQ ^V K ^{AT} NH ^F EST ^Y PK ^L AT ^L				
2	WP_013188882.1	62.4%	35.2%	FDG ^{FP} MG ^E IT ^{ET} T ^{ED} AK ^A Q ^{IP} T ^Q AK ^L K ^V MS ^K S-----EGMT ^{DAA} EG ^{PT} K ^T FT ^{IT} PA ^{AT} SV ^{AL} NE ^F SL ^V PK ^{PL} TA ^V				
	consensus/100%			F-G ^F PH ^G E ^L SI ^T ET ^{ss} cuph ^P T ^A phsoli ^{to}cu ^{Mo} ssst ^{cus} ph ^T hp ^P tuh ^{Ip} Vp ^A h ^N C ^f .sh ^P PL ^{AT} I				
	consensus/90%			F-G ^F PH ^G E ^L SI ^T ET ^{ss} cuph ^P T ^A phsoli ^{to}cu ^{Mo} ssst ^{cus} ph ^T hp ^P tuh ^{Ip} Vp ^A h ^N C ^f .sh ^P PL ^{AT} I				
	consensus/80%			F-G ^F PH ^G E ^L SI ^T ET ^{ss} cuph ^P T ^A phsoli ^{to}cu ^{Mo} ssst ^{cus} ph ^T hp ^P tuh ^{Ip} Vp ^A h ^N C ^f .sh ^P PL ^{AT} I				
	consensus/70%			F-G ^F PH ^G E ^L SI ^T ET ^{ss} cuph ^P T ^A phsoli ^{to}cu ^{Mo} ssst ^{cus} ph ^T hp ^P tuh ^{Ip} Vp ^A h ^N C ^f .sh ^P PL ^{AT} I				
		cov	pid	7521	:	6	7600	
1	WP_004013458.1	100.0%	100.0%	ATT ^V OG ^A ML ^K P ^{SE} AT ^P V ^{LD} TV ^Y OS ^{GL} VAD ^{REY} ML ^L TQ ^{LV} YD-----DST ^P VL ^{GA} DG ^Q PLAR ^W K ^V S ^{AG} K ^D GO ^{GT} W ^V				
2	WP_013188882.1	62.4%	35.2%	ART ^{AD} DG ^K ML ^K P ^{SE} ED ^{TAV} VD ^{TV} Y ^T NL ^{VQ} RD ^Y ML ^K TE ^{LV} YD ^{GT} PD ^{PN} D ^{NQ} PV ^{LG} AD ^{GN} PL ^V K ^W K ^T V ^{AE} GD-NSE ^{IV} W				
	consensus/100%			Ap ^T S ^D su ^K ML ^K P ^{SE} ST ^S V ^{ID} TV ^Y OS ^{LV} TS ^R -Y ^W L ^H T ^p LV ^Y S ^DDsp ^{PV} LG ^{AD} Gp ^{PL} S-W ^T K ^V o ^{At} D ^D .pu ^p W ^V				
	consensus/90%			Ap ^T S ^D su ^K ML ^K P ^{SE} ST ^S V ^{ID} TV ^Y OS ^{LV} TS ^R -Y ^W L ^H T ^p LV ^Y S ^DDsp ^{PV} LG ^{AD} Gp ^{PL} S-W ^T K ^V o ^{At} D ^D .pu ^p W ^V				
	consensus/80%			Ap ^T S ^D su ^K ML ^K P ^{SE} ST ^S V ^{ID} TV ^Y OS ^{LV} TS ^R -Y ^W L ^H T ^p LV ^Y S ^DDsp ^{PV} LG ^{AD} Gp ^{PL} S-W ^T K ^V o ^{At} D ^D .pu ^p W ^V				
	consensus/70%			Ap ^T S ^D su ^K ML ^K P ^{SE} ST ^S V ^{ID} TV ^Y OS ^{LV} TS ^R -Y ^W L ^H T ^p LV ^Y S ^DDsp ^{PV} LG ^{AD} Gp ^{PL} S-W ^T K ^V o ^{At} D ^D .pu ^p W ^V				

6/17/2018

MView

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cov pid 7601
1 WP_004013458.1 100.0% 100.0% DRENPLVPETTDSQRDLVFFESLFEVNPtPGDAGTKPPDPTDPSNPPIVEHKDPKQVVS5RPKLEMQVA IGAIV 7680
2 WP_013188882.1 62.4% 35.2% DKDNPMVVPANANPNADVFFESLYEMTKDGGQP-----KVGDKPIVEHRDNADPKQIITRRPALSLQTTAELS-GV
consensus/100% D+-NPhVVPtssssptDlVFFESLaEhspssGps.....csus.PIVEH+DstdPKQllopRPTLphQtsAplu.sV
consensus/90% D+-NPhVVPtssssptDlVFFESLaEhspssGps.....csus.PIVEH+DstdPKQllopRPTLphQtsAplu.sV
consensus/80% D+-NPhVVPtssssptDlVFFESLaEhspssGps.....csus.PIVEH+DstdPKQllopRPTLphQtsAplu.sV
consensus/70% D+-NPhVVPtssssptDlVFFESLaEhspssGps.....csus.PIVEH+DstdPKQllopRPTLphQtsAplu.sV

cov pid 7681
1 WP_004013458.1 100.0% 100.0% KTIKPGEAVRITDTVSYNGLKAGGVYTLVGLKLVKKTGDGEDVSTPVTKTGLVAASGS GKWTMDIPLTAETKKNLKGDEL 7
2 WP_013188882.1 62.4% 35.2% KSITAGEGATVNDKVTYSGLKAGAEYTLVGTLVKKS DGSIVGSPVTAAGLKA EADGS GWKMSIPLAKDTAGLTDGKEL
consensus/100% KoIpsGEusp1sDpVoYsGLKAGU.YTLVGP LV+KodGp.VuoPVttsGLhA-AsGS GpMpMsIPLTAcpttsLppG-cL
consensus/90% KoIpsGEusp1sDpVoYsGLKAGU.YTLVGP LV+KodGp.VuoPVttsGLhA-AsGS GpMpMsIPLTAcpttsLppG-cL
consensus/80% KoIpsGEusp1sDpVoYsGLKAGU.YTLVGP LV+KodGp.VuoPVttsGLhA-AsGS GpMpMsIPLTAcpttsLppG-cL
consensus/70% KoIpsGEusp1sDpVoYsGLKAGU.YTLVGP LV+KodGp.VuoPVttsGLhA-AsGS GpMpMsIPLTAcpttsLppG-cL

cov pid 7761
1 WP_004013458.1 100.0% 100.0% VVFEKAVLGMEDAAANP--NLKPILAHEDFKDAGQTVVVEETPDTPTTPTTTPPYTTPPVSPSTTTPPTTPPVVPPVSP
2 WP_013188882.1 62.4% 35.2% VVFEKAVAGKLP EAGTAPAGTYTTLAHFDLQDASQTVNWKPTPPPPYTPPVESKTTTPPP-----PPVKs
consensus/100% VVFEKAVhGkh.-AuoSP..shpPILAHEDhpdAuQTVsVvcssssPPhTPPps.hTTPPs.....PPVps
consensus/90% VVFEKAVhGkh.-AuoSP..shpPILAHEDhpdAuQTVsVvcssssPPhTPPps.hTTPPs.....PPVps
consensus/80% VVFEKAVhGkh.-AuoSP..shpPILAHEDhpdAuQTVsVvcssssPPhTPPps.hTTPPs.....PPVps
consensus/70% VVFEKAVhGkh.-AuoSP..shpPILAHEDhpdAuQTVsVvcssssPPhTPPps.hTTPPs.....PPVps

cov pid 7841
1 WP_004013458.1 100.0% 100.0% SITTPPTT-----PPPPAPPVAPATTIPPAQAMMPPTLARTGAQAAALVGMLSLAMIAGGAGLGLLAAARRKRETT- 9
2 WP_013188882.1 62.4% 35.2% ETTKPPSTPSSSTPPDTPSPVAPATTVPPMHPKVPPTLARTGAQAAIFGGLSILMIAAGAGLGLLAAARRKRESEVK
consensus/100% phTppPoT.....sPPu.PVAPATTlPphpskhPPTLARTGAQAAAlhGhLSlhMIAAGuu1GLLAAARRKREop..
consensus/90% phTppPoT.....sPPu.PVAPATTlPphpskhPPTLARTGAQAAAlhGhLSlhMIAAGuu1GLLAAARRKREop..
consensus/80% phTppPoT.....sPPu.PVAPATTlPphpskhPPTLARTGAQAAAlhGhLSlhMIAAGuu1GLLAAARRKREop..
consensus/70% phTppPoT.....sPPu.PVAPATTlPphpskhPPTLARTGAQAAAlhGhLSlhMIAAGuu1GLLAAARRKREop..

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[MView](#) 1.63, Copyright © 1997-2018 [Nigel P. Brown](#)

<https://www.ebi.ac.uk/Tools/services/rest/mview/result/mview-I20180617-113615-0661-42718863-p1m/aln.html>

10/10

Figure S1 Pairwise sequence alignment between *M. mulieris* and *M. curtisii* mega-adhesin. Sequences were aligned using Clustal Omega and visualised using MView.

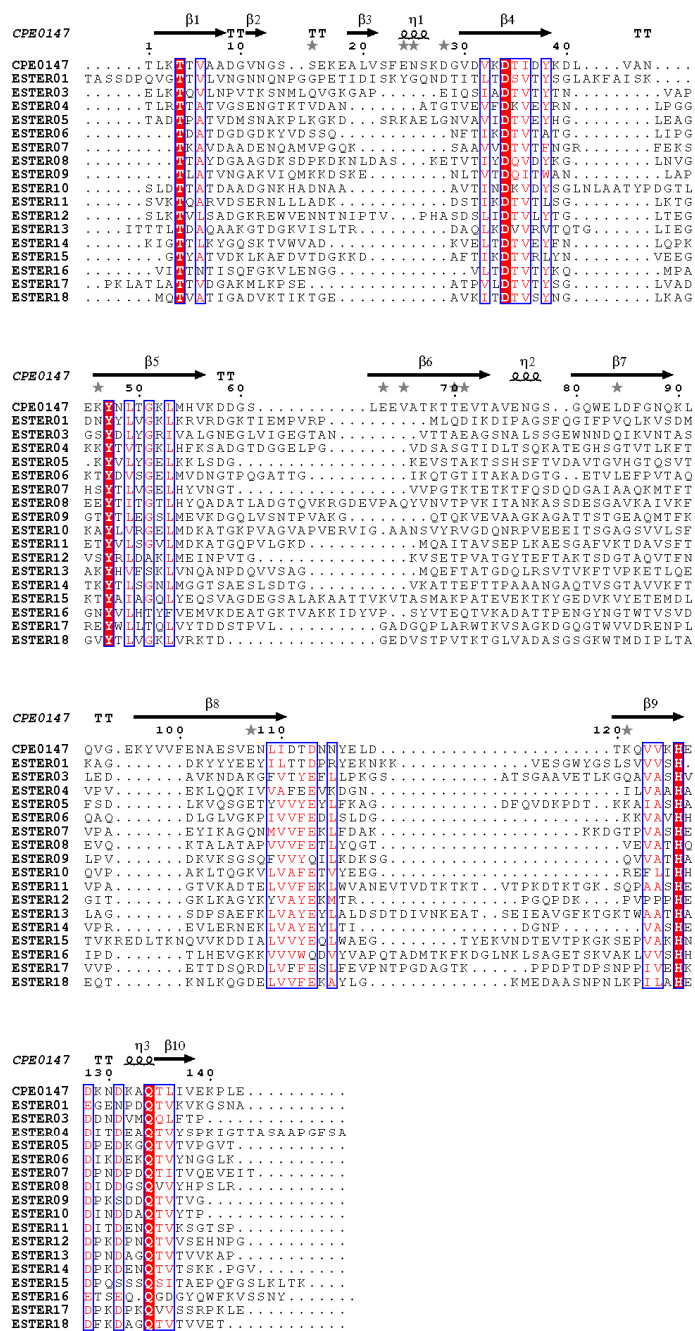


Figure S2 Multiple sequence alignment between ester bond domains within *M. mulieris* mega-adhesin. Sequences were aligned using Clustal Omega and visualised using MView.

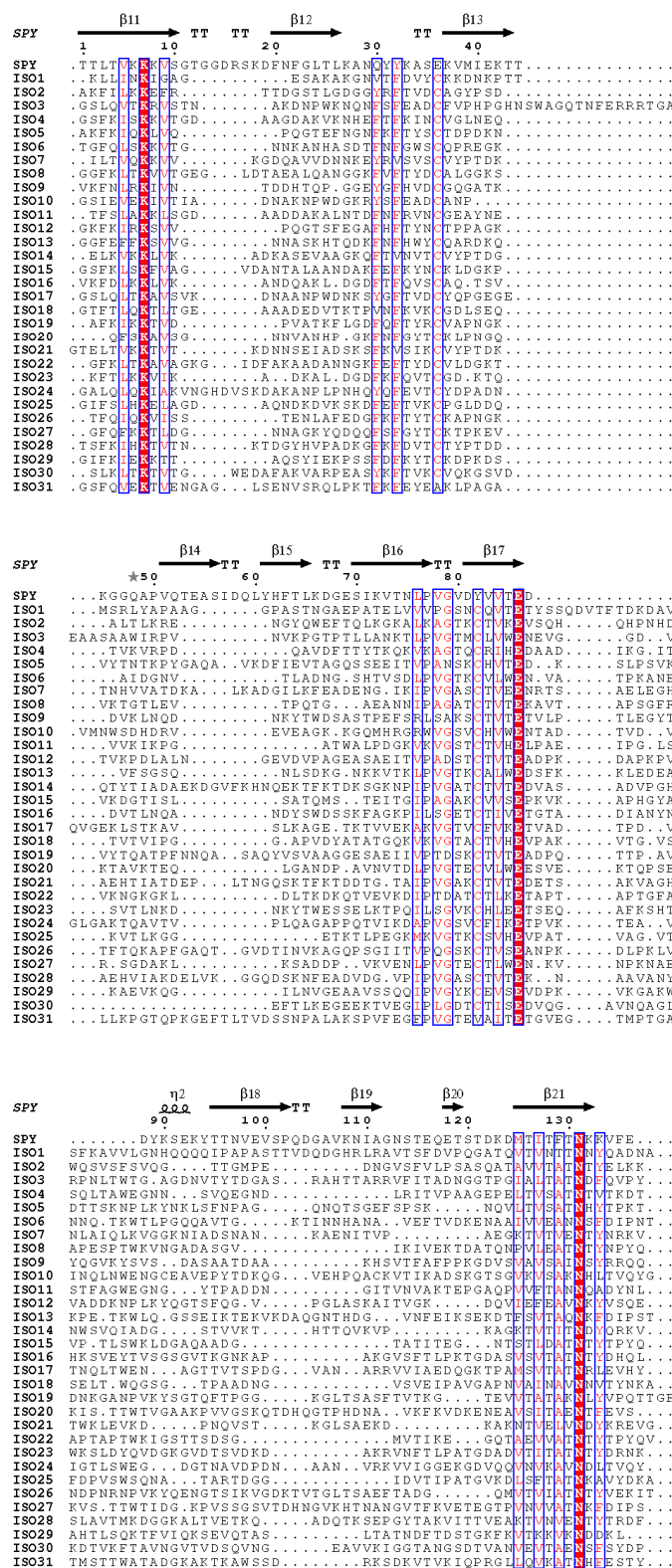


Figure S3 Multiple sequence alignment between isopeptide domains within *M. mulieris* mega-adhesin. Sequences were aligned using Clustal Omega and visualised using MView.

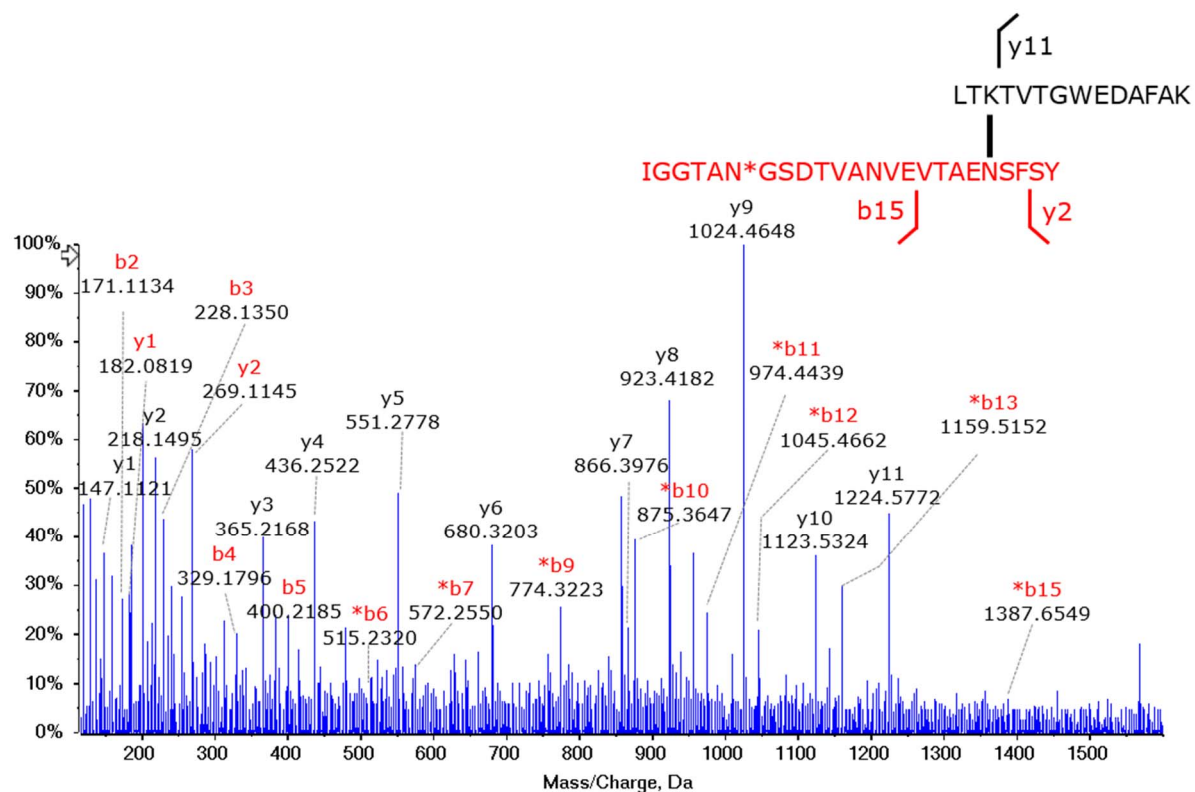


Figure S4 LC-MS/MS analysis of isopeptide bond formation in *M. mulieris* protein construct 46E-47I. The 4+ ion (m/z 988.97) representing an isopeptide cross-linked peptide from the tryptic digest was collisionally dissociated during LC-MS/MS. Fragment ions labelled in red are derived from the peptide IGGTANGSDTVANVEVTAENSFSY, while those in black are from the peptide LTKTVTGWEDAFK, with the largest of the respective b and y series ions shown on the schematic of the cross-linked peptide sequences. The asterisk in the red sequence, and in the red b ion series peak labels, indicates the presence of a deamidated asparagine residue at position 6.

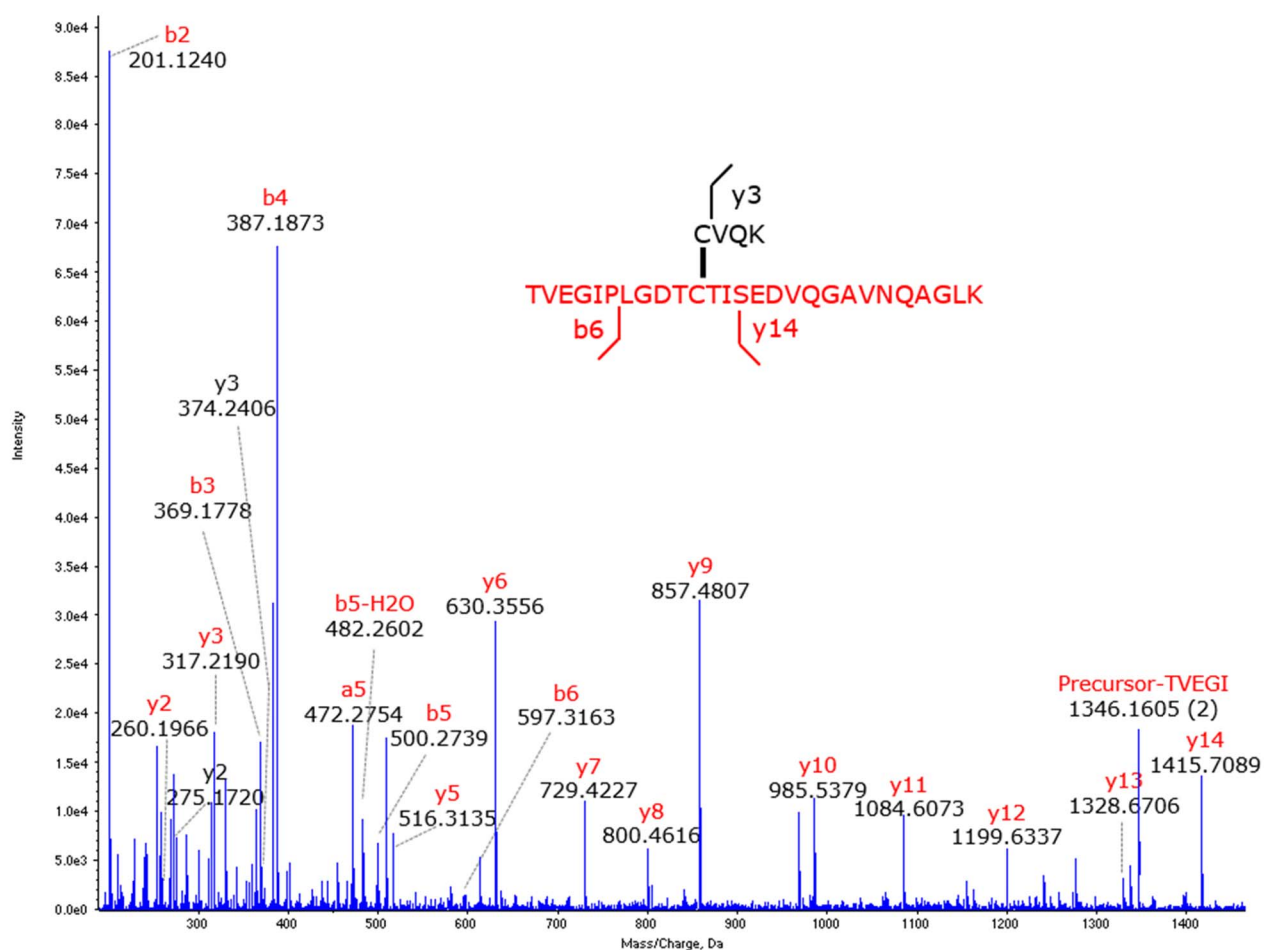


Figure S5 LC-MS/MS analysis of disulfide bond formation in *M. mulieris* protein construct 46E-47I. The 3+ ion (m/z 1063.87) representing a disulphide cross-linked peptide from the tryptic digest was collisionally dissociated during LC-MS/MS. Fragment ions labelled in red are derived from the peptide TVEGIPLGDTCTISEDVQGAVNQAGLK, while those in black are from the peptide CVQK, with the largest of the respective *b* and *y* series ions shown on the schematic of the cross-linked peptide sequences. Doubly-charged fragment ions indicated in parentheses.

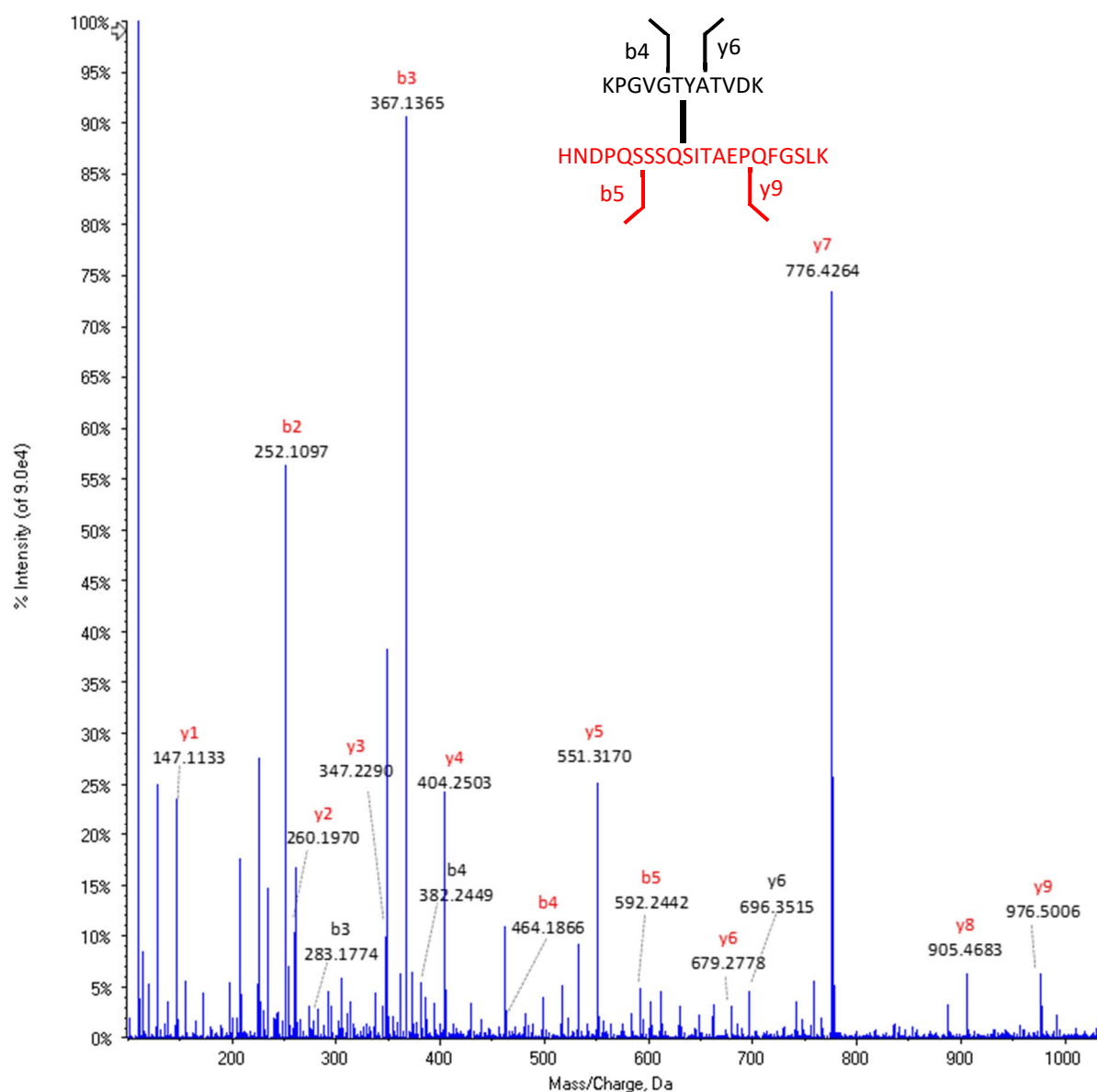


Figure S6 LC-MS/MS analysis of ester bond formation in *M. mulieris* protein construct 46E-47I.

The 3+ ion (m/z 1159.24) representing an ester cross-linked peptide from the tryptic digest was collisionally dissociated during LC-MS/MS. Fragment ions labelled in red are derived from the peptide HNDPQSSQSITAEPQFGSLK, while those in black are derived from the peptide KPGVGTATVDK, with the largest of the respective b and y series ions shown on the schematic of the cross-linked peptide.

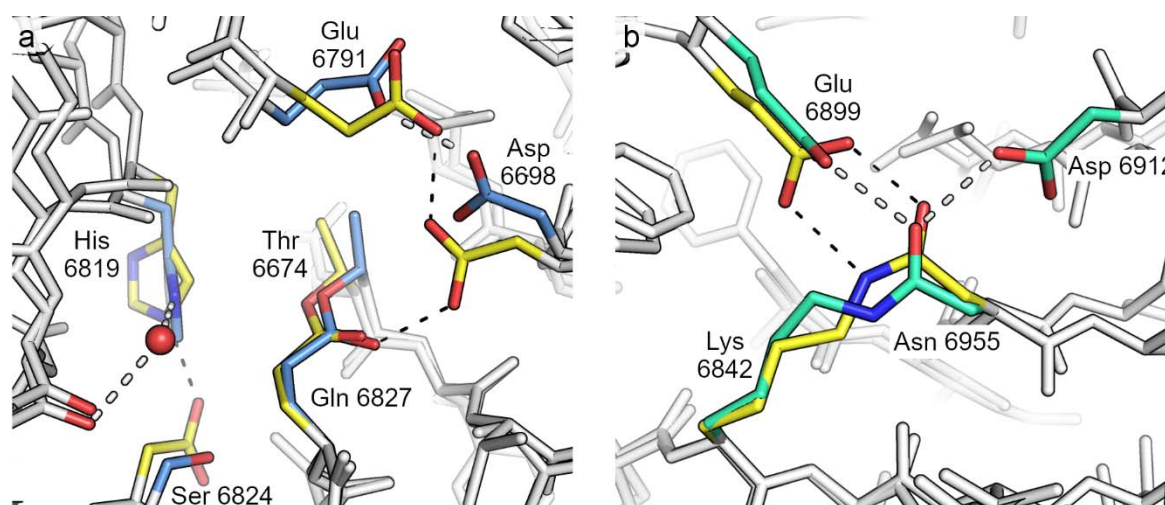


Figure S7 Comparison of *M. mulieris* domains 46E-47I crosslinks and exemplar crystal structures. **a)** Overlay of ester bond crosslinks in domain 46E (*M. mulieris*) and domain 1 of the Cpe0147 adhesin (PDB 4NI6). **b)** Overlay of isopeptide bond crosslinks in domain 47I (*M. mulieris*) and domain 2 of the Spy0128 pilin protein (PDB 3B2M). Hydrogen bonds are shown as dashed lines; sequences are numbered for the 46E-47I *M. mulieris* protein. An integral water molecule is highlighted as a red sphere.

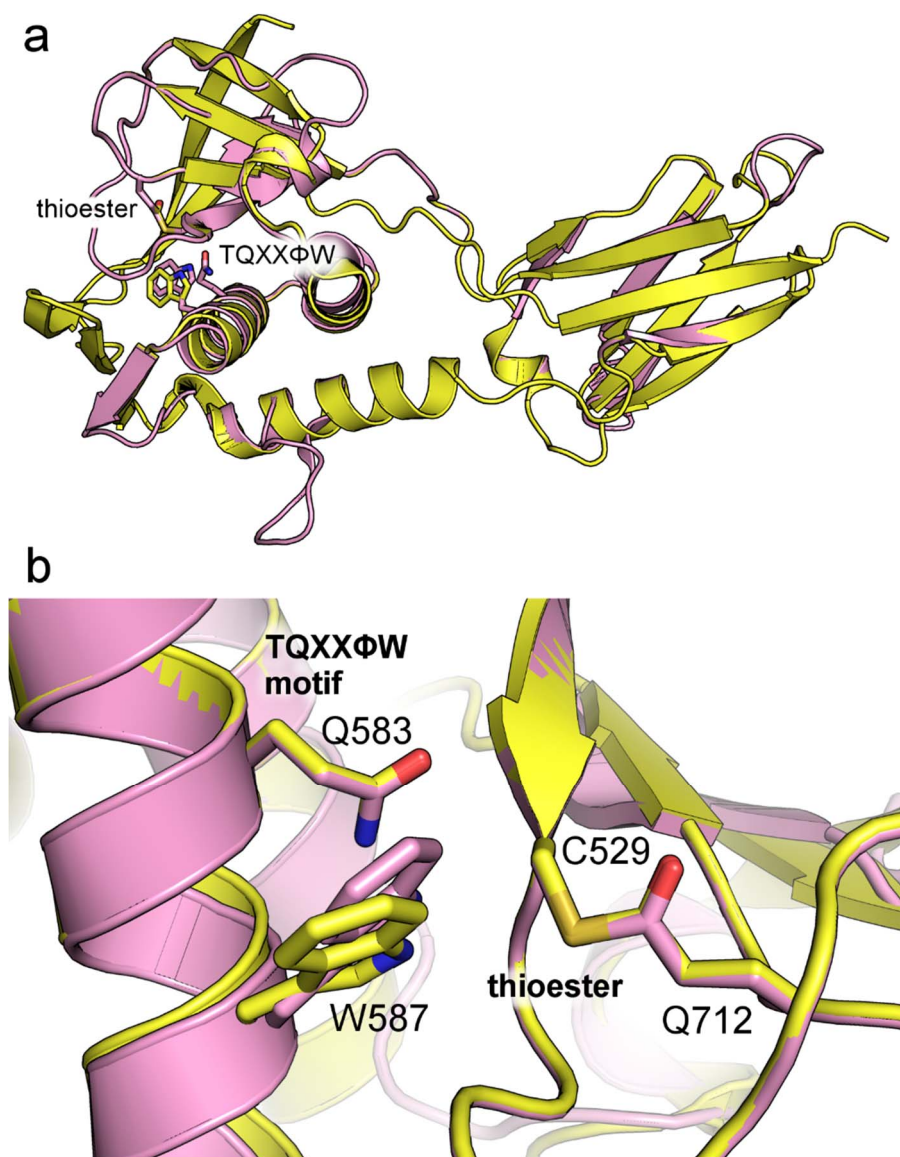


Figure S8 Structure prediction of the N-terminal thioester (TED) domain of *M. mulieris* adhesin. **a)** The predicted *M. mulieris* model (pink) overlaid with the X-ray crystal structure of the class II TED from vancomycin-resistant *Staphylococcus aureus*, SaTIE (yellow; PDB ID 6FX6). **b)** Zoomed view highlighting the predicted intramolecular thioester bond and the conserved TQXXφW motif. The structure was predicted using the AlphaFold2 server.

Reference sequence (1): WP_004013458.1
 Identities normalised by aligned length.
 Colored by: idenLily

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                                cov  pid  1 [ . . . . . : . . . . . 80
1 WP_004013458.1 100.0% 100.0% MGDKTRGTQGRMPVSGLIKVGKGRRRRTTRNNGAAFVAASVAVAWTVGGLVMPDMAEPAVIGKVHPEVNISGGGTAMVS
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% -----
consensus/90% -----
consensus/80% -----
consensus/70% -----

                                cov  pid  81 . . . . . 1 . . . . . : . . . . . 160
1 WP_004013458.1 100.0% 100.0% LAGQNTNLVYAAALSTNLFTTIDRVYAQKMYGKTEQLGDFTAQYLPRACFVRDDRTISNEPLGNFIRMDEGGPSYLGRRYV
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% -----
consensus/90% -----
consensus/80% -----
consensus/70% -----

                                cov  pid  161 . . . . . 2 . . . . . : . . . . . 240
1 WP_004013458.1 100.0% 100.0% AHWLYPNGSKSFSVDSKSRSDRSVDSPPVDDADDTEDTLKLTLDKLSFDDVVGDAAAAADKEFSDSQLPNEKTGKEQ
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% -----
consensus/90% -----
consensus/80% -----
consensus/70% -----

                                cov  pid  241 . . . . . 3 . . . . . : . . . . . 320
1 WP_004013458.1 100.0% 100.0% KQTAEVSPVNPKESLASKEGGETQAKDVPVNGSESSNSSESAPELAKPTPAETSTAETEPKETKPKSETKPSQFVEEKV
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% -----
consensus/90% -----
consensus/80% -----
consensus/70% -----

                                cov  pid  321 . . . . . : . . . . . 4 400
1 WP_004013458.1 100.0% 100.0% HKAGNLDKESKSLDRSAVSKQGKDSAENS NKADKNQGDRAVLFSAFQLKTKELKVKFDPQKSKDKAIEDVN
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% -----
consensus/90% -----
consensus/80% -----
consensus/70% -----

                                cov  pid  401 . . . . . : . . . . . 480
1 WP_004013458.1 100.0% 100.0% KQVDEIQKDALQQLDEFVTKNRVPQDIADKFRTKLNIQFENMRRQAVEFLEKKYAKGAI GADEWRNCQSGP IVPDGLV
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% -----
consensus/90% -----

```

```
consensus/80%
consensus/70%
cov pid 481 5 560
1 WP_004013458.1 100.0% 100.0% LVNEARLDNHNKKAWYLGVKQNDYITSRLLQYASEGSGNIKADGADSFVCEPLKGLQPGAHNIYTHPSTLEWAQNHPERA
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
cov pid 561 6 640
1 WP_004013458.1 100.0% 100.0% ELVKALAWHYKQFAQPKKEYAKYQNAIWSVVMGLPSMVGSDGMKRFWVSEPGSSAGLISAAESAYKTRPSVWQALKSMHL
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
cov pid 641 7 720
1 WP_004013458.1 100.0% 100.0% DQTSVDTAPDGSKSVIFLQLNDVYKSSERIRRAIGNSVYLVRTGATTPGKPVDRVSLFEAERGVHFLVKIQDQFSVAFAG
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
cov pid 721 8 800
1 WP_004013458.1 100.0% 100.0% TLNNAQDAVFLDKPSHDTQAQVTVLSKKITVSGSLKTQWGTASSDPQVGTTVLVNGNQNPGGPETVDISKYQNDTIT
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
cov pid 801 880
1 WP_004013458.1 100.0% 100.0% LQTSVTVSGLAKFAISKDNVYLVGKLRVRDGTIEMVPRPMLQDIKDI PAGESFQGI FVPVQLKVSMDKAGDKYVEEYIL
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
cov pid 881 9 960
1 WP_004013458.1 100.0% 100.0% TTDPRYEKHKVVEGSGWYGPLSVVVSHEGENPDQTVKVGSNAKLLINKIGAGESAKAKGNVTFDVKYKDNKPTTMSRLY
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
cov pid 961 0 1040
1 WP_004013458.1 100.0% 100.0% APAAGGPASTNGAEPATELVVPGSNQVETETYSQQDVTFTDKDAVSFKAVVLGNHQQQIPAPASTTVQDGHRLRAVT
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
cov pid 1041 1 1120
1 WP_004013458.1 100.0% 100.0% SFDVPPQATQVTVNTNMYQADNAAKFILKKEFRRTDGS TLGDGGYRFTVDCAGYPSDAL TLKRENGYQWFE TQLKGGKAL
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
cov pid 1121 2 1200
1 WP_004013458.1 100.0% 100.0% KAGTKCTVKEVSGHQHPNHDWQVSVFSVQGTGMPEDNGVSVLPSASQATAVVTATNTYELKKGSLQVTKRVSTNAKDN
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
cov pid 1201 1280
1 WP_004013458.1 100.0% 100.0% PMKNQNFSEADCFVPHPGHNSWAGQTNFERRRTGAEAAASAAWIRPVNVKPGTPTLLANKTL PVGMTCLVWENEVGGDVR
2 WP_101929469.1 37.0% 15.7%
consensus/100%
consensus/90%
consensus/80%
consensus/70%
```

```

cov pid 1281 . 3 . . . . . 1360
1 WP_004013458.1 100.0% 100.0% PNLTHTGAGDNVITYDGASRAHTTARRVFITADNGGTPGIALTATNDFQVPYGSFKISKKVTGDAAGDAKVKNHFTFKI
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 1361 . 4 . . . . . 1440
1 WP_004013458.1 100.0% 100.0% NCVGLNEQTVKVRPDQAVDFTTYTKQVKAGTQCRIHEDAADIKGITSQLTAWEGMNSVQEGNDLKITVPAAGEPELTVS
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 1441 : 5 . . . . . 1520
1 WP_004013458.1 100.0% 100.0% ATNTVTKDTAKFKIQKLVQPQGFENGNFKFTYSCDTPDKNVYTNTKPYGAQAVKDFIEVITAGQSEETVPANSKCHVT
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 1521 . . . . . 6 1600
1 WP_004013458.1 100.0% 100.0% EDKSLPSVKDTSKINPLKYKLSFNAGQNTSGEFSPSKNQVLTVSATNHVTPKTTGFQLSKKVTVGNKANKHASDTFNF
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 1601 . . . . . 1680
1 WP_004013458.1 100.0% 100.0% GWSQCPREGKAIDGNVTLADNGSHTVSDLPVGTCKVLWENVATPKANENQTKWTLPGQAVTGKTIINNHANAVEFTVDK
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 1681 . 7 . . . . . 1760
1 WP_004013458.1 100.0% 100.0% ENAAIVVEANNSFDIPNTSLTVQKVVKGQAVVDNNKEYRVSVCVPTDKTNHVVATDKALKADGILKFEADENGIKI
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 1761 . 8 . . . . . 1840
1 WP_004013458.1 100.0% 100.0% PVGASCTVEENRTSAELEGHNLAIQLKVGKKNIAADSNANKAENITVPAEGKTVVENTYNRKLGKFLTKVVTGEGLDTA
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 1841 : 9 . . . . . 1920
1 WP_004013458.1 100.0% 100.0% EALQANGGKVFVTDYCALGGKSVKGTLEVTPTQTGAENIPAGATCTLTEKAVTAPSGFRAPERPTWIKVNGADASGVIK
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 1921 . . . . . 0 2000
1 WP_004013458.1 100.0% 100.0% IVEKTDATQNPVLEATNTYTPYQVKFNLRKIVNTDDHTQPGGEYGFHVDCGQGATKDVKLNQDNKYTWDSASTPEFSRLS
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 2001 . . . . . 2080
1 WP_004013458.1 100.0% 100.0% AKSCTVTEVTLPTLEGYTYQGVKYSVSDASAAATDAAKRSVTFAPPPKGDVSVAVSATNSYRRQGGSIIEVKIVTIADNAK
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 2081 . 1 . . . . . 2160
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```

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2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2161 2 2240
1 WP_004013458.1 100.0% 100.0% VEHPQACKVTIKADSKGTSGVKVSANKHLTVQYGTFSLAKKLSGDAADDAKALNTDFNFRVNCGEAYNEVVKIKPGATWA
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2241 3 2320
1 WP_004013458.1 100.0% 100.0% LPDGGKVGSTCTVHELPAEIPGLSSTFAGWEGNGYTPADDNGITVNVAKTEPGAQPVVFTANNQADYNLGFKFKIRKSVV
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2321 4 2400
1 WP_004013458.1 100.0% 100.0% PQGTSFEGTFHTYTNCTPPAGKTVKPDALNNGEVDVPAGEASAEITVPADSTCTVTEADPKDAPKPVVADDKNPLKYQGT
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2401 5 2480
1 WP_004013458.1 100.0% 100.0% SFQGVPLGASKAITVGKDQVIEFFAVNKVYVQEGGFVFFKSVVGNNAASKHTQDKFNHFWYCQARDKQVFSGSQLSDKGN
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2481 6 2560
1 WP_004013458.1 100.0% 100.0% KKVTKLPVGTKCALWEDSFKKLEDEAKPETKKNLQGSSEIKTEKVKAQGNTHDGVNFEFKSEKDTFVSVAQNKFDPISPE
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2561 7 2640
1 WP_004013458.1 100.0% 100.0% LKVKKLVKADKASKVAAGKQFTVNVTCVYPTDGGTYTIADAEDAEGVFKHNQEKTFKTDKSGKNPIPVGAICTVTEVDASA
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2641 8 2720
1 WP_004013458.1 100.0% 100.0% DVPGHNSVQIADGTVVKTHTTRVKVPKAGKTVTITNDYERKVGSKLSKVFVAGVDVNTALAAANDAKFEFKYCNCKLDGK
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2721 9 2800
1 WP_004013458.1 100.0% 100.0% PVKDGITISLSATQMSITEITGIPAGAKCVVSEP---KVKAPHGYAVPTLSWKLDDGAQAADGTA-TITEGNTSLDATNTY
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2801 9 2880
1 WP_004013458.1 100.0% 100.0% TPYQVKFDLKKLVKANDQAKLDGDFTFQVSCAQTSDVTLNQANDYSKDSKSF-----AGKPILSGETCTIVETGTA
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%
      cov pid 2881 9 2960
1 WP_004013458.1 100.0% 100.0% DIANYNHKSVEYTVSGSGVTKGNKAPAKGVSTLPKTGDAS---VSVTANTYDHLGSLQLTKAVSVKDNAANPWIDNK
2 WP_101929469.1 37.0% 15.7%
  consensus/100%
  consensus/90%
  consensus/80%
  consensus/70%

```

consensus/100%			sIhsh.hKslphssst...T+hshsPtKulpaph.tstshS....uhhts.sYspphGs.pLschVshCdssh...c.tp	
consensus/90%			sIhsh.hKslphssst...T+hshsPtKulpaph.tstshS....uhhts.sYspphGs.pLschVshCdssh...c.tp	
consensus/80%			sIhsh.hKslphssst...T+hshsPtKulpaph.tstshS....uhhts.sYspphGs.pLschVshCdssh...c.tp	
consensus/70%			sIhsh.hKslphssst...T+hshsPtKulpaph.tstshS....uhhts.sYspphGs.pLschVshCdssh...c.tp	
cov pid 2961			0 3040	
1	WP_004013458.1	100.0%	100.0%	YGFVTDCYQPGEGEVG-EKLSTKAVSLKAGETKTVEKAVGTVCVFKETVADTPDVTNQLTIENAGTTVTS PDGVANA
2	WP_101929469.1	37.0%	15.7%	YPAIGDFYNMMLIEAQRDAVAKISLKNPQ-----KYQVLQGLAWAINR-----
consensus/100%			YshhsDhYpss.u...u.cchssKhhSLKssp.....p.pVhptLswt.st.....	
consensus/90%			YshhsDhYpss.u...u.cchssKhhSLKssp.....p.pVhptLswt.st.....	
consensus/80%			YshhsDhYpss.u...u.cchssKhhSLKssp.....p.pVhptLswt.st.....	
consensus/70%			YshhsDhYpss.u...u.cchssKhhSLKssp.....p.pVhptLswt.st.....	
cov pid 3041			1 3120	
1	WP_004013458.1	100.0%	100.0%	RRVVAIEDQGKTPAMSVTATNRLVHYGTFTLQKLTGEEAAEDVTKTPVNFVKCGDLSQETVTVIPGGAPVDYATAT
2	WP_101929469.1	37.0%	15.7%	-----GN
consensus/100%		us	
consensus/90%		us	
consensus/80%		us	
consensus/70%		us	
cov pid 3121			2 3200	
1	WP_004013458.1	100.0%	100.0%	GQKVKVGTACTVHEVPAKV-TGVSSELTWQSGTAPADNGVSEIPAVGAPNVAIKAVNNVTYNKAAFKIKKTVDPVATK
2	WP_101929469.1	37.0%	15.7%	TDLAIGDNCTYIDQYKTANCQNKELTQLA-----HDVYADLKVMASSEL--KMYEAYAKYKQFKNKR--DEYE-K
consensus/100%			sphltlGscTThh...tps.stVspELT.u.....psV.s-l.shuuspl..Khhpshsh.KttFK.K+..D.ht.K	
consensus/90%			sphltlGscTThh...tps.stVspELT.u.....psV.s-l.shuuspl..Khhpshsh.KttFK.K+..D.ht.K	
consensus/80%			sphltlGscTThh...tps.stVspELT.u.....psV.s-l.shuuspl..Khhpshsh.KttFK.K+..D.ht.K	
consensus/70%			sphltlGscTThh...tps.stVspELT.u.....psV.s-l.shuuspl..Khhpshsh.KttFK.K+..D.ht.K	
cov pid 3201			3 3280	
1	WP_004013458.1	100.0%	100.0%	FLGDFQ-FYRCVAPNGKVYQATPFNNQASAYVSVAA-G-----EESAEII-----VPTDS
2	WP_101929469.1	37.0%	15.7%	ALKKWQEETQRQVEANEKLYQTKNELSSII-KIYVDKTDGKLAIKLHGSEALALLQSKTINIDVNLVNGKTVPVNG
consensus/100%			hLtcAQ..T.RpVtsNtKlYppsp.h.sph.t.YVshss.G.....pEuhtll.....VPssu	
consensus/90%			hLtcAQ..T.RpVtsNtKlYppsp.h.sph.t.YVshss.G.....pEuhtll.....VPssu	
consensus/80%			hLtcAQ..T.RpVtsNtKlYppsp.h.sph.t.YVshss.G.....pEuhtll.....VPssu	
consensus/70%			hLtcAQ..T.RpVtsNtKlYppsp.h.sph.t.YVshss.G.....pEuhtll.....VPssu	
cov pid 3281			3 3360	
1	WP_004013458.1	100.0%	100.0%	KCTVTEADPQTTPAVDNKGAMPVKVSYGTQFPGGKGLTSASFVTV--KGTEVVTATAKNLYVPQTTFQFSKAVSGNMV
2	WP_101929469.1	37.0%	15.7%	VSVAAAASPEGIPV-----PVDSTGLGCDQKLAGVTASFSGEIEISGTYIFD--GRNKLRQVVLQYKVKAVSGN--
consensus/100%			hssstAsPshPs.....Pvc.oGhtsh.thtGhsoASFosp...pGT.lhs.u+Nhh..Qssh.paphAVSGN..	
consensus/90%			hssstAsPshPs.....Pvc.oGhtsh.thtGhsoASFosp...pGT.lhs.u+Nhh..Qssh.paphAVSGN..	
consensus/80%			hssstAsPshPs.....Pvc.oGhtsh.thtGhsoASFosp...pGT.lhs.u+Nhh..Qssh.paphAVSGN..	
consensus/70%			hssstAsPshPs.....Pvc.oGhtsh.thtGhsoASFosp...pGT.lhs.u+Nhh..Qssh.paphAVSGN..	
cov pid 3361			4 3440	
1	WP_004013458.1	100.0%	100.0%	ANHPGKFNFGYTCPLNGQKTAVKTEQLGANDPAV-----NVTDLVPGTECVLWEESEVKTQPSKEI
2	WP_101929469.1	37.0%	15.7%	--TSHDFSFAGTCVPAPERKIGITLLE--GSDGAKVIDTAGKRRKTEKVTLDVKVFNELKGGQNVVIGKELVDGNGN----
consensus/100%			..pstcFsfuhtC.lsstpKhusphE..GussstV.....phpsL.sGpphVlhtE.V-tsts...	
consensus/90%			..pstcFsfuhtC.lsstpKhusphE..GussstV.....phpsL.sGpphVlhtE.V-tsts...	
consensus/80%			..pstcFsfuhtC.lsstpKhusphE..GussstV.....phpsL.sGpphVlhtE.V-tsts...	
consensus/70%			..pstcFsfuhtC.lsstpKhusphE..GussstV.....phpsL.sGpphVlhtE.V-tsts...	
cov pid 3441			5 3520	
1	WP_004013458.1	100.0%	100.0%	STTWVGAAPVVGSKQADHGTPHDNAVKFKVDKENEAVSITAENTFVSGTELTVKKTVTKDNNEIASDKSFKVSIK
2	WP_101929469.1	37.0%	15.7%	-----GVGVTGSET--FDPKA--SGATDNGNGVSYGTINMTFQVPVQ-----TIRDNQ-----KLVAFE
consensus/100%		uhsVsGoppS...hsP+s...phtsDptNthhShThp.TFpVssp.....sh+DNP.....hhVuhc	
consensus/90%		uhsVsGoppS...hsP+s...phtsDptNthhShThp.TFpVssp.....sh+DNP.....hhVuhc	
consensus/80%		uhsVsGoppS...hsP+s...phtsDptNthhShThp.TFpVssp.....sh+DNP.....hhVuhc	
consensus/70%		uhsVsGoppS...hsP+s...phtsDptNthhShThp.TFpVssp.....sh+DNP.....hhVuhc	
cov pid 3521			6 3600	
1	WP_004013458.1	100.0%	100.0%	CVVPTDKAEHTIATNEPLT-----NGQS--KTFKTDGTGAIIPVGAKTCTVTEDETSAKVAGHTWKLKLVKDP
2	WP_101929469.1	37.0%	15.7%	TLYQGRPEPTGKVKTEHKDNDENQTVTEKPRIGTSAEAGGESDDGKVAVPEEGKDLI-----KDVTVTKMLK--P
consensus/100%			sLY.sD+sEpshtsE.hs.....GpS...ps.poDDstsAIP.tuKsslh.....hsshTwp.h..P	
consensus/90%			sLY.sD+sEpshtsE.hs.....GpS...ps.poDDstsAIP.tuKsslh.....hsshTwp.h..P	
consensus/80%			sLY.sD+sEpshtsE.hs.....GpS...ps.poDDstsAIP.tuKsslh.....hsshTwp.h..P	
consensus/70%			sLY.sD+sEpshtsE.hs.....GpS...ps.poDDstsAIP.tuKsslh.....hsshTwp.h..P	
cov pid 3601			7 3680	
1	WP_004013458.1	100.0%	100.0%	NQVSTKGLSAEKDKAKNTVELVNDYKREVGFKLTKAVAGKIDFAKAADA-----NNGKF EFTYDCVL
2	WP_101929469.1	37.0%	15.7%	GTY-----TLGQMLKKGQVQVAVAGTKAAKNFTVNTGQLEGTQELFTLPAKQIEAGASYVYVEKVF
consensus/100%			sph.....pLspphh+cVGs.hLshAssttuhsFshssst.....psGT..hsY-pVh	
consensus/90%			sph.....pLspphh+cVGs.hLshAssttuhsFshssst.....psGT..hsY-pVh	
consensus/80%			sph.....pLspphh+cVGs.hLshAssttuhsFshssst.....psGT..hsY-pVh	
consensus/70%			sph.....pLspphh+cVGs.hLshAssttuhsFshssst.....psGT..hsY-pVh	
cov pid 3681			7 3760	
1	WP_004013458.1	100.0%	100.0%	DGKTVKNGKGLDLTKDKQTEVVKIDPTDATCTLKETAPTPTGFAAP--TAPTWKIGSTSD-----SGMVTIKE--
2	WP_101929469.1	37.0%	15.7%	KGANNTAG--ILVAS-----HEDPNKGGQ---TVTVNPKQHKLPTIKTAVMVRDDGNSL.TSIVTEADGKDFKVKDKI
consensus/100%			cGtsspsG..hLsho.....+-.PsDtsp...TssssPptathP..pssWhhssssS.....ut.hp1K...	
consensus/90%			cGtsspsG..hLsho.....+-.PsDtsp...TssssPptathP..pssWhhssssS.....ut.hp1K...	

consensus /80%			cGtsspsG..hLsho.....+-..PsDtsp....TssssPptathP..pssswHhssssS.....ut.hp1K-..		
consensus /70%			cGtsspsG..hLsho.....+-..PsDtsp....TssssPptathP..pssswHhssssS.....ut.hp1K-..		
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	3761	8	3840
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			IYNDLKPGTYTAFATLVNKNPKIEIASGRQVFTNGAENGSTLVELAVAGSKVKADGKYVVFERIQGEQTSSEPSGEPYA		
consensus /90%				
consensus /80%				
consensus /70%				
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	3841	9	3920
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			----GQAEVVATNTYTPYQVQKFTL-KKVIKADKTLGDFKFQVTCGDKTQSVTLNKNKYTWESSSELKTPQILSGVKC		
consensus /90%			KHQETIGDKSQITIVAPKNVPFAEFKIVKKTVDGNANTDRVDFDVAACDGYTGTVSVVVRKGGTQGETKVSNSALSTSGMSC		
consensus /80%		GppupsLsssshsPh.scFpL.KKs1tsstshDtsFcFpVsCsshTtoVolshcpt.T.tpoclpsstlhSGhPc		
consensus /70%		GppupsLsssshsPh.scFpL.KKs1tsstshDtsFcFpVsCsshTtoVolshcpt.T.tpoclpsstlhSGhPc		
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	3921		0 4000
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			HLEETSEQAFKSHTWKSLDQVQDGVDTSVDKDAKRVTFTL PATGDADVTITATNTYDRNKALQLQKVAKLNQDQVSK		
consensus /90%			QV-----		
consensus /80%			pL.....		
consensus /70%			pL.....		
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	4001		4080
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			DAKANPLPNHQYQF EVTCYDPADNGLGAKTQAVTVPLQAGAPPQTVIKDAPVGSVCFIKETPVKTEAVIGTISWEGDGTN		
consensus /90%			-----SEQAVQDDQNTVKVQFSGTDTN		
consensus /80%		pEpsVps-tshsp1papGssTN		
consensus /70%		pEpsVps-tshsp1papGssTN		
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	4081	1	4160
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			AVGPDNAANVRKVIIGGEGDQVQVNVKAVNDLVTVQYGFSLHKELTGDAQNDKDVSKDFEFTVCKPGLDDQKV--TLK		
consensus /90%			SDGTVAKFNLT-----ENNAKTVVVTAATNTFTPKQAKFTVRKNVVEAAGV-THFSVPNSFDFSYCKDGDAYMKAIPTLK		
consensus /80%			usGsssthNlp.....cssppVpAsNshTsp.uhFol+Kp1pusu..s+.shspF-FohKCsG.s..Ks..TLK		
consensus /70%			usGsssthNlp.....cssppVpAsNshTsp.uhFol+Kp1pusu..s+.shspF-FohKCsG.s..Ks..TLK		
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	4161	2	4240
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			GGETKTLPEGKMKVGTCKSVHEVPATVAGVTFDPVSWSONATARTDGGIDVTIPATGVKDLFSFATNKAVYDKATFIQK		
consensus /90%			AGETS--AAIKVKPGVECVQKENSPTENLD-RTLEWLGAQSQ--AGGT-ATFRDANNTVALVATNTYTEKGTQLIEISK		
consensus /80%			uGETp..sthKhKsGscCpV+EssuTstsls.cslpw.tstot..sGGh.sTh.ssuspluhsATNphs.cpuphpIpK		
consensus /70%			uGETp..sthKhKsGscCpV+EssuTstsls.cslpw.tstot..sGGh.sTh.ssuspluhsATNphs.cpuphpIpK		
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	4241	3	4320
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			--VISSTENLAFEDGFKFTYTCKAPNGKFTTQKAPFGAQTGVDITNVKAGQPSGII TVPQGSCKTVEANPK-DLPKLVN		
consensus /90%			QVVDGTAGAGTIPGTFEMKYICATGQKAE-----SVTKLTSISVNGGSATITGIPVGSQCAVYEDTTGINVNTLN		
consensus /80%			..V.uostshsh.ssfChpYhCtsspttp.....uspptlsoIsVptGtsusIhs1P.GSpCsV.Essst.s1Pphs.		
consensus /70%			..V.uostshsh.ssfChpYhCtsspttp.....uspptlsoIsVptGtsusIhs1P.GSpCsV.Essst.s1Pphs.		
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	4321		4 4400
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			DP--NRNPVKYQENGTSIKVGDKTVTG--LTSAEFTADGQMVTVIATNTYVE-KITGFQFKKTL DGN--NAGKYDQDQF		
consensus /90%			TTTTFNGKAPQ-----QVTIGGQVLHNAALSNPIKAGESQKATINVENKYVQKAGGFVEKELVAGVTNPGTVLKDVAF		
consensus /80%			ss...s+sP.....p1p1Gsp1ps..Loss.hsu-uQhsTL.spNpYVp.KhsGFphcKh1sGs..sushhpD.tF		
consensus /70%			ss...s+sP.....p1p1Gsp1ps..Loss.hsu-uQhsTL.spNpYVp.KhsGFphcKh1sGs..sushhpD.tF		
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	4401		4480
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			SFGYCTKTPKEVRSGDAKL-----KSADDPVKVENL PVGTECTLWENKVPKNAEYVTTWTIDGKPVSSGVSVDH		
consensus /90%			DFGYSCEIPGNAHAVKGSFKLKHGETFTSADPANPQLNLPVNTVCKWEEETPKSSANADYV-----GSELRA---SAT		
consensus /80%			sFGYoCchPtps+uscuph.....pusssssplpNLPVsT.Cp1WEppspssstchs.....Gp.lpu...osp		
consensus /70%			sFGYoCchPtps+uscuph.....pusssssplpNLPVsT.Cp1WEppspssstchs.....Gp.lpu...osp		
	cov	pid			
1 WP_004013458.1	100.0%	100.0%	4481	5	4560
2 WP_101929469.1	37.0%	15.7%			
consensus /100%			NGVKHTNA---NGVTFKVE TEGTPVNVVATNKFDIPSTSFKIHKTVTNKTDGYHVPADKGFKDFVCTYPTDDAEHVIK		
consensus /90%			NGAEVGTGDGKLELTIKLNKAAAKALITATNQYSQQLGGFTLKKVEVQGSADQAL--DIQSYKFKL--TYMDGNTNTH/KE		
consensus /80%			NGschTss....t1ThKlpptus.spl1ATNpas...suFp1+KpVpspsDthh..s.puaKFcl..TY.sssspHVht.		
consensus /70%			NGschTss....t1ThKlpptus.spl1ATNpas...suFp1+KpVpspsDthh..s.puaKFcl..TY.sssspHVht.		

	cov	pid			
1	100.0%	100.0%	4561	6	4640
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
1	100.0%	100.0%	4641	7	4720
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
1	100.0%	100.0%	4721	8	4800
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
1	100.0%	100.0%	4801	9	4880
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
1	100.0%	100.0%	4881	9	4960
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
1	100.0%	100.0%	4961	0	5040
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
1	100.0%	100.0%	5041	1	5120
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
1	100.0%	100.0%	5121	2	5200
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
1	100.0%	100.0%	5201	3	5280
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
1	100.0%	100.0%	5281	3	5360
1	100.0%	100.0%			
2	37.0%	15.7%			
consensus/100%					
consensus/90%					
consensus/80%					
consensus/70%					
	cov	pid			
				4	5440

1	WP_004013458.1	100.0%	100.0%	LLPKGSATSGAAVETLKGQAVASHVDDNDVMQ-----QLFTPTLRRTATVGSENGTKTVDANATGTVEVDFKVEYR			
2	WP_101929469.1	37.0%	15.7%	IYRQGDVDENGNVKDGKK-PVVEHSDLNDKAQVTVTGEEQSPVPTTLTLQKVVKS-----EGL			
	consensus/100%			lh.pGsspsusVcshKt.sVspHsD.NDhHQ.....p.hTPTLphptsVtS.....Ehh			
	consensus/90%			lh.pGsspsusVcshKt.sVspHsD.NDhHQ.....p.hTPTLphptsVtS.....Ehh			
	consensus/80%			lh.pGsspsusVcshKt.sVspHsD.NDhHQ.....p.hTPTLphptsVtS.....Ehh			
	consensus/70%			lh.pGsspsusVcshKt.sVspHsD.NDhHQ.....p.hTPTLphptsVtS.....Ehh			
		cov	pid	5441	:	:	5
1	WP_004013458.1	100.0%	100.0%	NLPGGKKYVTGK-----LHFK-----SADGTDGGELPGVDSASGTIDLTSQKATEGHSGT			5520
2	WP_101929469.1	37.0%	15.7%	EVPSTKQFAFTLKCSSPIDGKSQQTQYTAGSKISLPVVKGANCTLTEDREGAKVAGIAPSQVTFSADEKIGL-ITSD			
	consensus/100%			pIPusKpashThK.....lph.....s-sp-GuclSgIssupsThshsSpKhs..hous			
	consensus/90%			pIPusKpashThK.....lph.....s-sp-GuclSgIssupsThshsSpKhs..hous			
	consensus/80%			pIPusKpashThK.....lph.....s-sp-GuclSgIssupsThshsSpKhs..hous			
	consensus/70%			pIPusKpashThK.....lph.....s-sp-GuclSgIssupsThshsSpKhs..hous			
		cov	pid	5521	:	:	6
1	WP_004013458.1	100.0%	100.0%	VTLKFTVPVEKLQQKIVVAFEVKGDNLLVAHADITDEAQTIVYSPKIGTTASAAPGFSATADTPATVDMsNAKPLKGGK			5600
2	WP_101929469.1	37.0%	15.7%	NSASFMPAAE-----TTEVNVLTATNTY---PAPEKPTVATSAK-----DANGTKMGYGS			
	consensus/100%			sohpFphPsEc.....sp-sNllsApssh.....ss.pPpluToAp.....DhsssKshGps			
	consensus/90%			sohpFphPsEc.....sp-sNllsApssh.....ss.pPpluToAp.....DhsssKshGps			
	consensus/80%			sohpFphPsEc.....sp-sNllsApssh.....ss.pPpluToAp.....DhsssKshGps			
	consensus/70%			sohpFphPsEc.....sp-sNllsApssh.....ss.pPpluToAp.....DhsssKshGps			
		cov	pid	5601	:	:	6
1	WP_004013458.1	100.0%	100.0%	SR---KAEI GNVAVIDTVEYHGLEAGKYVLYGELKCLSDGKEVSTAKTSSHSFTVDAVTVG-HGTQSVTFSDLKVQSGET			5680
2	WP_101929469.1	37.0%	15.7%	KQANQVYAGTSAKIVDEVSANLLPGDYVLIGKLMDEKTKGAVTSYTSPPAPFTVAKAGEKGLDNTFTVSGDLSKAGSH			
	consensus/100%			pp...hhtssstlIldVpatsl.sGcYVLLhGclhchpsGktVooohpoostsFTVcAspts.+hsphThSs.pIpuGpp			
	consensus/90%			pp...hhtssstlIldVpatsl.sGcYVLLhGclhchpsGktVooohpoostsFTVcAspts.+hsphThSs.pIpuGpp			
	consensus/80%			pp...hhtssstlIldVpatsl.sGcYVLLhGclhchpsGktVooohpoostsFTVcAspts.+hsphThSs.pIpuGpp			
	consensus/70%			pp...hhtssstlIldVpatsl.sGcYVLLhGclhchpsGktVooohpoostsFTVcAspts.+hsphThSs.pIpuGpp			
		cov	pid	5681	:	:	7
1	WP_004013458.1	100.0%	100.0%	YVVEYLFKAGDFQVDKPDTKKA-IASHADPEDKQTVTPGVTTDADTGDGKYVDSQNFITIKDTATGLIP--GKT			5760
2	WP_101929469.1	37.0%	15.7%	YVVEYIYRAGDVNGATPNNGAKPVVEHAVITDADQVTEAI--TPPTPP-----AAKVKIMKKVVASGMEVSNRA			
	consensus/100%			YVVEYIa+AGDhpspssttt.lspHAS.pDtsQTVps...Tsssss.....utphpIhcvVsAoGh.s.s+s			
	consensus/90%			YVVEYIa+AGDhpspssttt.lspHAS.pDtsQTVps...Tsssss.....utphpIhcvVsAoGh.s.s+s			
	consensus/80%			YVVEYIa+AGDhpspssttt.lspHAS.pDtsQTVps...Tsssss.....utphpIhcvVsAoGh.s.s+s			
	consensus/70%			YVVEYIa+AGDhpspssttt.lspHAS.pDtsQTVps...Tsssss.....utphpIhcvVsAoGh.s.s+s			
		cov	pid	5761	:	:	8
1	WP_004013458.1	100.0%	100.0%	YDVSGELMVDGTPQGATT-----GIKQT-----GTIT-----AKADGTGETVLE			5840
2	WP_101929469.1	37.0%	15.7%	YIFTLSCRDKDGNAAAGDKTLVLRPKATEVTLGRSGYVCSINEDLAAIEQQVTPSISLSTGTFNGFSVQDSTAGAAHFT			
	consensus/100%			Y.hohphhscDGsstGspT.....Gl+ps.....soIo.....tpssssGtshhp			
	consensus/90%			Y.hohphhscDGsstGspT.....Gl+ps.....soIo.....tpssssGtshhp			
	consensus/80%			Y.hohphhscDGsstGspT.....Gl+ps.....soIo.....tpssssGtshhp			
	consensus/70%			Y.hohphhscDGsstGspT.....Gl+ps.....soIo.....tpssssGtshhp			
		cov	pid	5841	:	:	9
1	WP_004013458.1	100.0%	100.0%	FPVTAQAQD-----LGLVGKPIVVFEDLSLDGKKAHVHHDIKDEKQTVYNGGLKTKAVDAADENQAMVPGQKSAAV			5920
2	WP_101929469.1	37.0%	15.7%	VPAATEQVPEVLVNVNTYNYKMGKPE-----LQTNVAVT--DNGSSSVQAGTATTV			
	consensus/100%			hPssspQs.....hshhGKP.....LpTAVs..Dpspu.V.utpussV			
	consensus/90%			hPssspQs.....hshhGKP.....LpTAVs..Dpspu.V.utpussV			
	consensus/80%			hPssspQs.....hshhGKP.....LpTAVs..Dpspu.V.utpussV			
	consensus/70%			hPssspQs.....hshhGKP.....LpTAVs..Dpspu.V.utpussV			
		cov	pid	5921	:	:	0
1	WP_004013458.1	100.0%	100.0%	VDTVTFNFRFEKSHSYTLVGLHYVNV--GTVVPGTKTETIKTFQSDQD-GAIAAQKMTFVPAEYIKAGQNMVFEKLF			6000
2	WP_101929469.1	37.0%	15.7%	TDKVTWKNL--PEGKYLLTGKLMHITDDNAAVAGVTEPVPVLEITKDNLASGTTMKFNPAGAISSQAGKYVVEYLIN			
	consensus/100%			sDpVTapsh...ptpYhLsGclhals...ussVsGspEseshp.spD.uhhuuppMpFsvPAtIptutphVvAEhLas			
	consensus/90%			sDpVTapsh...ptpYhLsGclhals...ussVsGspEseshp.spD.uhhuuppMpFsvPAtIptutphVvAEhLas			
	consensus/80%			sDpVTapsh...ptpYhLsGclhals...ussVsGspEseshp.spD.uhhuuppMpFsvPAtIptutphVvAEhLas			
	consensus/70%			sDpVTapsh...ptpYhLsGclhals...ussVsGspEseshp.spD.uhhuuppMpFsvPAtIptutphVvAEhLas			
		cov	pid	6001	:	:	0
1	WP_004013458.1	100.0%	100.0%	AKKDKGT-----PVASHEDPNPDQITVQVEIITTA--YDGAAGDKSDPKDKNLDAKSETVTIYDQVDYKGLNVGE			6080
2	WP_101929469.1	37.0%	15.7%	YEDTDGHKPKPNTSTVSHNDPDDAQTVMVTEAPSVSTTATTDGAN-----EKEIQKG-KAAVVDTVWKNL PAGN			
	consensus/100%			hccpDgP.....sVsShpDpsDssQTLsVpEs..soTs..hdGAs.....-KpIptu.csssIhdPvsaKsLssGp			
	consensus/90%			hccpDgP.....sVsShpDpsDssQTLsVpEs..soTs..hdGAs.....-KpIptu.csssIhdPvsaKsLssGp			
	consensus/80%			hccpDgP.....sVsShpDpsDssQTLsVpEs..soTs..hdGAs.....-KpIptu.csssIhdPvsaKsLssGp			
	consensus/70%			hccpDgP.....sVsShpDpsDssQTLsVpEs..soTs..hdGAs.....-KpIptu.csssIhdPvsaKsLssGp			
		cov	pid	6081	:	:	1
1	WP_004013458.1	100.0%	100.0%	EYITGTLHYQADATLADGTQVQRGDEVPAQYVNVVTPVKITANKASDESDEGAVKAIKVFQKTLALATAPVVVFETLYQG			6160
2	WP_101929469.1	37.0%	15.7%	YQALSELVDS-----KGNPVAGATTKAVPF---TVNNGEEAGSVKTKIQLPATATSTAGAKVVFERIYRA			
	consensus/100%			..slothlc.....+Gs.VsuthspssPh...shssu-EuGuVKshlph.sptTuhAsA.hVVFepLYpu			
	consensus/90%			..slothlc.....+Gs.VsuthspssPh...shssu-EuGuVKshlph.sptTuhAsA.hVVFepLYpu			
	consensus/80%			..slothlc.....+Gs.VsuthspssPh...shssu-EuGuVKshlph.sptTuhAsA.hVVFepLYpu			
	consensus/70%			..slothlc.....+Gs.VsuthspssPh...shssu-EuGuVKshlph.sptTuhAsA.hVVFepLYpu			
		cov	pid	6161	:	:	2
1	WP_004013458.1	100.0%	100.0%	TVEVATH-QDIDDGQVYVHPS-----LRTLATVNGAKVIQMKKSKENLTVTDQITWANLAPGTYTLEGLMEVKDG			6240
2	WP_101929469.1	37.0%	15.7%	SDVDSQTRPAQNAQPVVSELDLNAIQTVRVVEVSPKPPAITFTKVT-----KALDGG			

consensus/100%				os.supp.pshpsup.VV.c.s.....lRsl1tospGs.sIphpKsoc.....cshDG		
consensus/90%				os.supp.pshpsup.VV.c.s.....lRsl1tospGs.sIphpKsoc.....cshDG		
consensus/80%				os.supp.pshpsup.VV.c.s.....lRsl1tospGs.sIphpKsoc.....cshDG		
consensus/70%				os.supp.pshpsup.VV.c.s.....lRsl1tospGs.sIphpKsoc.....cshDG		
		cov	pid	6241	3	6320
1	WP_004013458.1	100.0%	100.0%	QLVSNTPVAKGQQTQKEVAAGKAGATTS	TGAEQMFKL	PVDKVKSGSQFVVYQILKDKSGQVVATHADPKSDDQTVTVGS
2	WP_101929469.1	37.0%	15.7%	QVPD-----	KDRKFQFTISCDKNFGGAYS--FEMP--	AGVSAALPA----DKQLQAGT
consensus/100%				t-tphpFp1ssDKshuGu...aph...uG.ssAh.A....Dpp1psGo		
consensus/90%				Q1ss.....t-tphpFp1ssDKshuGu...aph...uG.ssAh.A....Dpp1psGo		
consensus/80%				Q1ss.....t-tphpFp1ssDKshuGu...aph...uG.ssAh.A....Dpp1psGo		
consensus/70%				Q1ss.....t-tphpFp1ssDKshuGu...aph...uG.ssAh.A....Dpp1psGo		
		cov	pid	6321	4	6400
1	WP_004013458.1	100.0%	100.0%	LDTTADAADGNKHADNAAAVTINDKVDYSG	LNLAAATYPDGLTKAYLVRGELMDKATGKPVAGVAPVERVIGAAANSVYRV	
2	WP_101929469.1	37.0%	15.7%	VCT-----	TEMLTDEA----NADGLPDAISFSSSKAMAV	
consensus/100%				L.....pt.LhDcA...sssG1hPsthshuuuNpshtV		
consensus/90%				LsT.....L.....pt.LhDcA...sssG1hPsthshuuuNpshtV		
consensus/80%				LsT.....L.....pt.LhDcA...sssG1hPsthshuuuNpshtV		
consensus/70%				LsT.....L.....pt.LhDcA...sssG1hPsthshuuuNpshtV		
		cov	pid	6401	4	6480
1	WP_004013458.1	100.0%	100.0%	GQNRPVVEEITSAGSGLVLSFQVPAKLTQ--	GKVLVAFETVYEEGRFLIHHDINDDAQTVYTPSVKTAQARVDSERN--	
2	WP_101929469.1	37.0%	15.7%	SKI-----	NNQTAQFTVPDVTQKVPVETIQVTIKNIYSKD-----	FPELGTIARDNADQKV
consensus/100%				uc.....ss.shpFpVpsh.Tp..scl.Vshcs1Ypcs.....hPp1t.ARssu-ps..		
consensus/90%				uc.....ss.shpFpVpsh.Tp..scl.Vshcs1Ypcs.....hPp1t.ARssu-ps..		
consensus/80%				uc.....ss.shpFpVpsh.Tp..scl.Vshcs1Ypcs.....hPp1t.ARssu-ps..		
consensus/70%				uc.....ss.shpFpVpsh.Tp..scl.Vshcs1Ypcs.....hPp1t.ARssu-ps..		
		cov	pid	6481	5	6560
1	WP_004013458.1	100.0%	100.0%	LLL-ADKSTIKDVTLSGLKTGETYVLSGVL	MDKATGQPVLGKDMQAITAVSEPLKAESGAFVKTDVAVFTVPAGTVKA	
2	WP_101929469.1	37.0%	15.7%	LDLKKGENAQVQDVAWTKNLA-PGYTMMGT	LMDKLTGKPVVGGANTPAVDFQ----	VKKGEKGTIIVALFTVPGDKVST
consensus/100%				L.L.tscsup1pDssThpsLt.stpYsh.GsLMDKhtGpPVIgTsh.A1sh.....scpGthstT.hs.FTVpusVps		
consensus/90%				L.L.tscsup1pDssThpsLt.stpYsh.GsLMDKhtGpPVIgTsh.A1sh.....scpGthstT.hs.FTVpusVps		
consensus/80%				L.L.tscsup1pDssThpsLt.stpYsh.GsLMDKhtGpPVIgTsh.A1sh.....scpGthstT.hs.FTVpusVps		
consensus/70%				L.L.tscsup1pDssThpsLt.stpYsh.GsLMDKhtGpPVIgTsh.A1sh.....scpGthstT.hs.FTVpusVps		
		cov	pid	6561	6	6640
1	WP_004013458.1	100.0%	100.0%	DTELVVFEEKLWANEVTVDTKTKTVPKDTK	TGKSGQPAASHEDITDENQTVKSGTSPSLKTVLS----	ADGKREW--
2	WP_101929469.1	37.0%	15.7%	KASVWVFEKVKASDVKDGKVV-----	KATPVVDHNSLEDADQTVQVTPPPASQEQTREIATVAKNGTTFNDG	
consensus/100%				cspHVVFEK1ahAs-Vpssphsp.....KupPsssHps1pDtsQTVpssssPu.pp.ho.....Acstppas..		
consensus/90%				cspHVVFEK1ahAs-Vpssphsp.....KupPsssHps1pDtsQTVpssssPu.pp.ho.....Acstppas..		
consensus/80%				cspHVVFEK1ahAs-Vpssphsp.....KupPsssHps1pDtsQTVpssssPu.pp.ho.....Acstppas..		
consensus/70%				cspHVVFEK1ahAs-Vpssphsp.....KupPsssHps1pDtsQTVpssssPu.pp.ho.....Acstppas..		
		cov	pid	6641	7	6720
1	WP_004013458.1	100.0%	100.0%	--ENNTNIPTV-PHASDLSIDTVLYTGLTEG	VSRYLDAKLMEINPVT-----GKV-SETPVATGYTEFTAKTSDGTA	
2	WP_101929469.1	37.0%	15.7%	TKDPNLGKPVLTGQDAVIVDTVKKNLEPG-	EYITGSLMDKSTNAPLTYLKDGNQKDGATAERGSFAVKEGGTEGET	
consensus/100%				..sNshPsl.Pttsssl1DThapsLp.G.pYp1supLM-hssss.....Gp..stssstpG.hthpttpo-Gps		
consensus/90%				..sNshPsl.Pttsssl1DThapsLp.G.pYp1supLM-hssss.....Gp..stssstpG.hthpttpo-Gps		
consensus/80%				..sNshPsl.Pttsssl1DThapsLp.G.pYp1supLM-hssss.....Gp..stssstpG.hthpttpo-Gps		
consensus/70%				..sNshPsl.Pttsssl1DThapsLp.G.pYp1supLM-hssss.....Gp..stssstpG.hthpttpo-Gps		
		cov	pid	6721	8	6800
1	WP_004013458.1	100.0%	100.0%	QVTFNIGTKLKGKGYVAYEKMTRPGQPKPVP	-----	PPHEDKPNQTVVSEH
2	WP_101929469.1	37.0%	15.7%	KVYFTVKGEAIQANRQYVVFEDLYKTADIDE	HGQPTPGAEKVAQHHDINDAAQTLSGDKPKPGTTPPETPKTPNT-----	
consensus/100%				pVhFsshsttlpAshpYVsaEchh+sup.Dc.s.....sP.EsPKsPnP.....		
consensus/90%				pVhFsshsttlpAshpYVsaEchh+sup.Dc.s.....sP.EsPKsPnP.....		
consensus/80%				pVhFsshsttlpAshpYVsaEchh+sup.Dc.s.....sP.EsPKsPnP.....		
consensus/70%				pVhFsshsttlpAshpYVsaEchh+sup.Dc.s.....sP.EsPKsPnP.....		
		cov	pid	6801	9	6880
1	WP_004013458.1	100.0%	100.0%	NPGITTTLDAQAAGTGDGKVISLTRD-AQLKDV	VVRVT-QTGLIEGAKYHVFSKLVNQANPDQVVSAGMFEFATGDQLR	
2	WP_101929469.1	37.0%	15.7%	PGTTPPGPTPRTPSGFRGVVSTVLAKTGSTT	GIMAMTGVLAMVAGIQLVIRRYQRELEED-----	
consensus/100%				.PGhTsshsspspGhcGhV.o1htc.uphps1hthT..huhltGthhhhp+h.ppt..D.....		
consensus/90%				.PGhTsshsspspGhcGhV.o1htc.uphps1hthT..huhltGthhhhp+h.ppt..D.....		
consensus/80%				.PGhTsshsspspGhcGhV.o1htc.uphps1hthT..huhltGthhhhp+h.ppt..D.....		
consensus/70%				.PGhTsshsspspGhcGhV.o1htc.uphps1hthT..huhltGthhhhp+h.ppt..D.....		
		cov	pid	6881	9	6960
1	WP_004013458.1	100.0%	100.0%	SVTVKFTVPKETLQELAGSDPSAEFLVAYEY	LALDSDTDIVNKEATSIEAVGFKTGKTAATHADPNDAQTVVKA	
2	WP_101929469.1	37.0%	15.7%	-----	-----	-----
consensus/100%				-----		-----
consensus/90%				-----		-----
consensus/80%				-----		-----
consensus/70%				-----		-----
		cov	pid	6961	0	7040
1	WP_004013458.1	100.0%	100.0%	PKIGTTLKYGQSKTWWADKVELTDTVEYFN	LQPKTKYTLGSLMGGTSAESLSDTGKATTEFTTPAAANGAQTVSGTA	
2	WP_101929469.1	37.0%	15.7%	-----	-----	-----
consensus/100%				-----		-----
consensus/90%				-----		-----

```
consensus/80% .....
consensus/70% .....

cov pid 7041 : 1 7120
1 WP_004013458.1 100.0% 100.0% VVKFTVPREVLERNEKLVAYEYLIDGNQPVASHEDPKDENQTVTSKKPGVGYATVDKLFKAFDVTGKKAFTIKDVTRL
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 7121 : 2 7200
1 WP_004013458.1 100.0% 100.0% YNVEEGKTYAIAQQLYEQSVAGDEGSALAKAATTVKVTASMAKPATEVEKTKYGEDVKVYETEMDLTVKREDLTKNQVVK
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 7201 : 7280
1 WP_004013458.1 100.0% 100.0% DDTALVVEQLNAEGTYEKVNDTEVTPKGGSEPVAKHNDPQSSSQSITAEPQFGSLKLTKTVTGWEDAFKAVARPEASVK
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 7281 : 3 7360
1 WP_004013458.1 100.0% 100.0% FTVKCVQKGSVDFTLKEGEEKTEVGIPLDGTCITISEDVQGAVNQAGLKDTVKFTAANGVTVDSQVNGEAVVKIGGTANG
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 7361 : 4 7440
1 WP_004013458.1 100.0% 100.0% SDTVANVEVTAENSFSYDPVITNTNISQFGKLENGGVLTDVTYKQMPAGNYVLHTYFVEMVKDEATGKTVAKKIDYVP
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 7441 : 5 7520
1 WP_004013458.1 100.0% 100.0% SYVTEQTVKADATTPENGYNGTWTVSDIPDTLHEVGKVVVWQDVVYAPQTADMTKFKDGLNKL SAGETSKVAKLVVSH
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 7521 : 6 7600
1 WP_004013458.1 100.0% 100.0% HETSEQQGGYQWFKVSSNYGVSFQVEKTVENGAGLSENVSRQLPKTKFKFEYEA KLPAGALLKPGTQPKGEFTLTVDSNP
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 7601 : 7680
1 WP_004013458.1 100.0% 100.0% ALAKSPVFE GPPVGTEVAITETGVEGTMPTGATMSTTWTATADGKAKTKAMSSDRKSDKVTVKIQPRGLLQVKATNHFEST
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 7681 : 7 7760
1 WP_004013458.1 100.0% 100.0% YPKLATLATTVDGAKMLKPSSEATPVLDTVTYSGLVADREYWL LTQLVYTDSTPVLGADGQPLARWTKVSAKDGQGTWV
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

cov pid 7761 : 8 7840
1 WP_004013458.1 100.0% 100.0% VDRENPLVVPETDTSQRDLVFFESLFEVPNTPGDAGTKPPDPTDPSNPPIVEHKDPKPKQVSSRPKLEMOTVATIGAD
2 WP_101929469.1 37.0% 15.7% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....
```

```

      cov  pid 7841          :          9          . 7920
1 WP_004013458.1 100.0% 100.0% VKTIKPGEAVKI TDTVSYNGLKAGGVYTLVGKLVKRTDGEDVSTPVTKTGLVADASGSGKWTMDIPLTAEQTKNLKQGDE
2 WP_101929469.1  37.0%  15.7% -----
consensus/100% -----
consensus/90% -----
consensus/80% -----
consensus/70% -----

      cov  pid 7921          :          0 8000
1 WP_004013458.1 100.0% 100.0% LVVFEKAYLGMEDAASNPNLKPILAHEDFKDAGQTVTVVETPDTPPTTPPTTPPYTTTPPVSPSTTTPPTTPPNPPVSPS
2 WP_101929469.1  37.0%  15.7% -----
consensus/100% -----
consensus/90% -----
consensus/80% -----
consensus/70% -----

      cov  pid 8001          :          1 8069
1 WP_004013458.1 100.0% 100.0% ITTPPTPPPPAPPVAPATTIPPAQAKMPPTLARTGAQAALVGMLSLAMIAAGGAIGLLAARRKRETTE
2 WP_101929469.1  37.0%  15.7% -----
consensus/100% -----
consensus/90% -----
consensus/80% -----
consensus/70% -----
```

MView (<https://desmid.github.io/mview/>) 1.63, Copyright © 1997-2018 Nigel P. Brown (<mailto:bionview@gmail.com>).

Figure S9 Pairwise sequence alignment between *M. mulieris* and *V. cambriense* mega-adhesin. Sequences were aligned using Clustal Omega and visualised using MView.