

Table of contents - Appendix

Appendix Figure S1. Imaging-based whole blood phagocytosis.

Appendix Figure S2. DDA peptide spectra

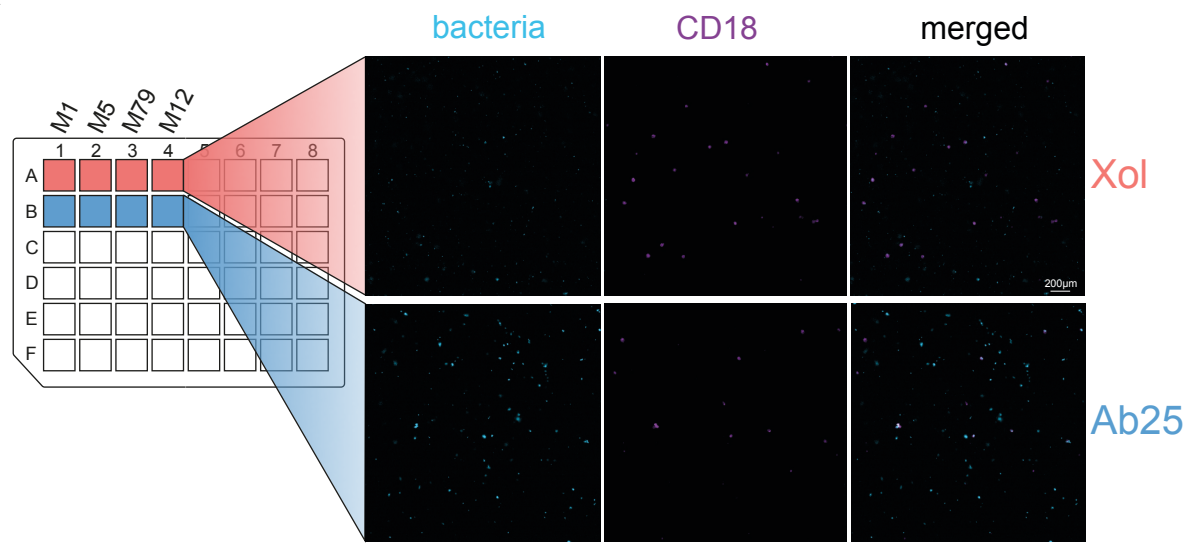
Appendix Figure S3. SDS-PAGE analysis of the antibodies used for the binding assays.

Appendix Table S1. Statistical test p values.

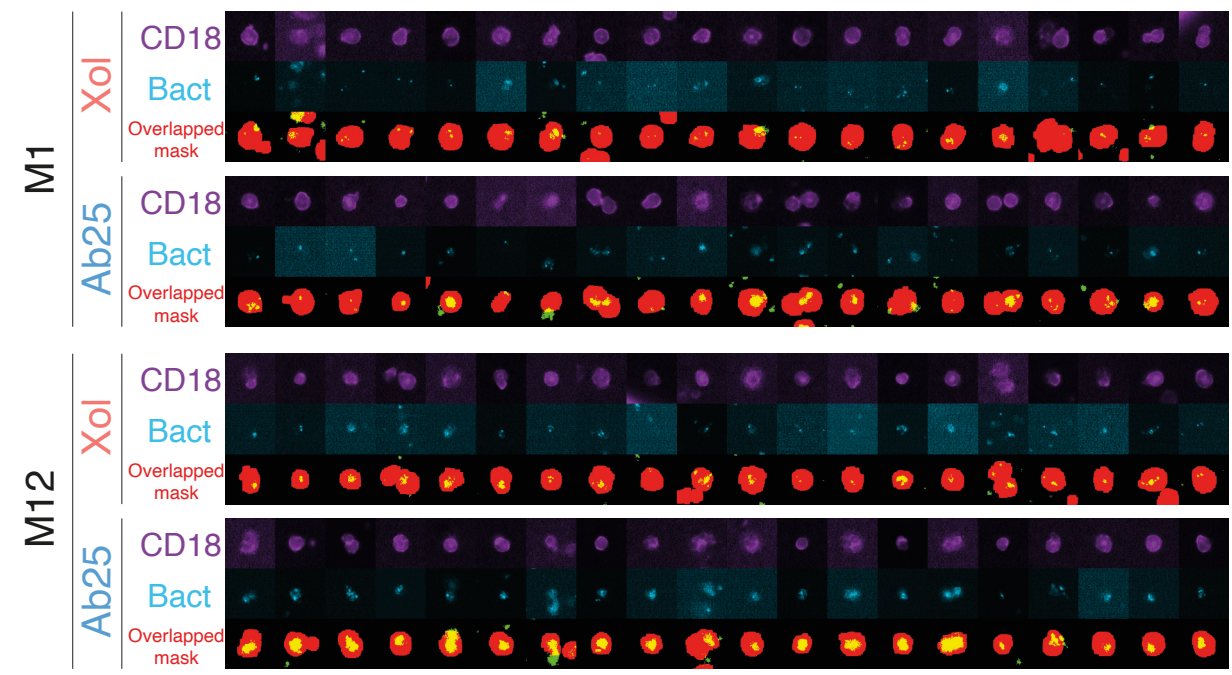
Appendix Data 1. M protein amino acid sequences.

Appendix Data 2. M protein alignments.

A

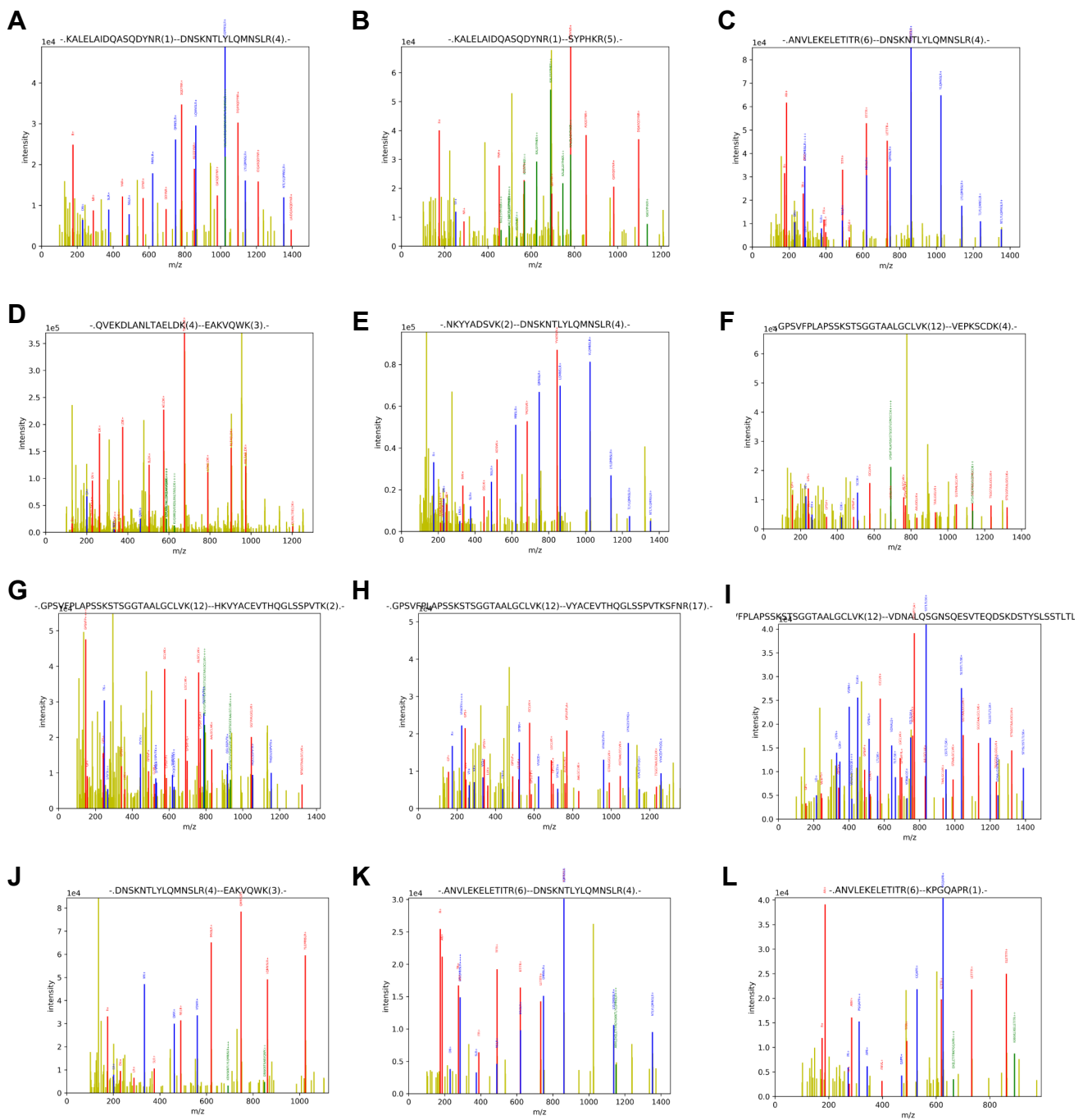


B



Appendix Figure S1. Imaging-based whole blood phagocytosis.

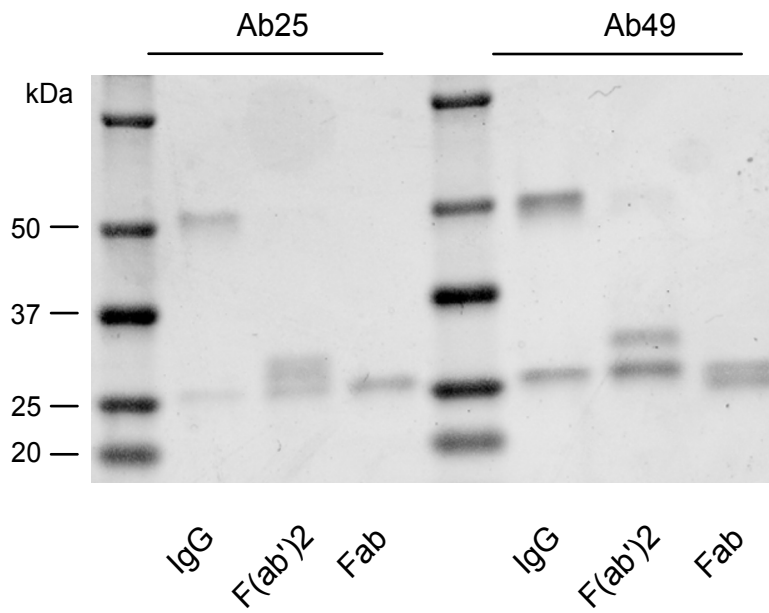
Imaging-based whole blood phagocytosis. A) Whole blood was diluted and infected with 4 different strains of GAS expressing GFP (FITC). After 30 minutes, the infection was fixed with PFA and the cells were stained with anti-CD18 (BV421, shown in magenta). The blood was immobilized onto glass-bottom 96-well plates which were precoated with anti-CD29. Images were acquired on a widefield epifluorescence microscope using a 20X objective (NA = 0.75). The acquisition of images was automated using Nikon JOBs by scanning through a 96 well plate acquiring 25 images/sample. GFP (bacteria) and BV421 (CD18 positive leukocytes) were segmented based on a signal above 5 and 4 std of the background respectively. The overlapping mask for both channels was generated and the area of overlap was measured. Contrast adjustment is set to the same for all shown images. More than 560 cells were analyzed for this experiment B) Magnified images of cells representative cells were randomly selected and compared side-by-side to highlight the GFP area change with and without pre-opsonization. The presented images are chosen from a dataset representing the median of each population. The differences seen across the two groups, therefore, are fully representative of the data shown in Fig 3F.



Appendix Figure S2. DDA peptide spectra

Example DDA peptide spectra of cross-linked interactions identified (see also Table EV 1 for more details). One spectrum is shown for each cross-linked peptide pair. The red and the blue peptides represent parent peptides, respectively, whereas the green signal arises from the aforementioned peptides containing an additional DSS cross-linker arm.

Antibody fragment generation



Appendix Figure S3. SDS-PAGE analysis of the antibodies used for the binding analysis

Appendix Table S1 - p values

Comparison	p value
Fig 2	
B	
Ab25 vs. Xolair	0.0412
Ab49 vs. Xolair	0.0126
E	
M1+xol vs. M1+Ab mix	0.0001
M1+xol vs. M1+Ab25	0.0421
Fig 3	
B	
Xolair vs. IVIG	0.0556
Xolair vs. Ab25	0.0032
D	
Xolair vs. IVIG	0.0292
Xolair vs. Ab25	0.0014
F	
M1 Xol P1 vs. M1 Ab25 P1	<0,0001
M1 Xol P1 vs. M1 Ab25 P2	<0,0001
M1 Xol P1 vs. M1 Ab25 P3	0.9995
M5 Xol P1 vs. M5 Ab25 P1	0.8371
M5 Xol P2 vs. M5 Ab25 P2	>0,9999
M5 Xol P3 vs. M5 Ab25 P3	>0,9999
M12 Xol P1 vs. M12 Ab25 P1	<0,0001
M12 Xol P2 vs. M12 Ab25 P2	<0,0001
M12 Xol P3 vs. M12 Ab25 P3	<0,0001
M79 Xol P1 vs. M79 Ab25 P1	<0,0001
M79 Xol P2 vs. M79 Ab25 P2	0.9988
M79 Xol P3 vs. M79 Ab25 P3	0.0322
E	
Ab25 vs Xolair	<0,0001
Fig 4	
Liver	
IVIG vs Untreated	0.0011
Ab25 vs untreated	0.0027
Kidney	
IVIG vs Untreated	0.0329
Ab25 vs untreated	0.0024
Spleen	
IVIG vs Untreated	0.0329
Ab25 vs untreated	0.0043
Fig 6	
A	
Untreated vs. Ab25	0.0005
Untreated vs. Ab32	0.9607
Untreated vs. Ab49	0.4265
Untreated vs. IVIG 10ug/ml	0.6491
Untreated vs. IVIG 100ug/ml	0.8049
B	
Xolair vs. Ab25	<0,0001
Xolair vs. Ab25 fabs	0.0784
C	
Ab25 vs. Ab25 Ides	>0,9999
Ab25 vs. Ab25 fabs	<0,0001
Ab25 Ides vs. Ab25 fabs	<0,0001
Ab49 Ides vs. Ab49 fabs	<0,0001
Ab49 vs. Ab49 Ides	0.3676
Ab49 vs. Ab49 fabs	<0,0001
D	
Plasma vs. Plasma fabs	<0,0001
Plasma Ides vs. Plasma fabs	<0,0001
F	
M1	
Ab25 IgG vs. Ab25 Fabs	<0,0001
Ab25 F(ab') ₂ vs. Ab25 Fabs	0.0001
M5	
Ab25 IgG vs. Ab25 Fabs	0.0031
Ab25 F(ab') ₂ vs. Ab25 Fabs	0.0071
M12	
Ab25 IgG vs. Ab25 Fabs	0.005
Ab25 F(ab') ₂ vs. Ab25 Fabs	0.2286
M79	
Ab25 IgG vs. Ab25 Fabs	<0,0001
Ab25 F(ab') ₂ vs. Ab25 Fabs	<0,0001
Fig EV 2	
Xolair vs. Ab25	0.0001
Xolair vs. Ab32	0.0002
Xolair vs. Ab49	0.0002
Xolair vs. Plasma	<0,0001

Data EV1. M protein sequences

M1-90-226-CTG	<p>>gene_1147 GeneMark.hmm 306_aa + 113293 114210 >NODE_5_length_114211_cov_48.735082 MAKNNNTNRHYSRLRKLKTGTASVAVALTVLGAGFANQTEVKANGDGNPREVIEDLAANNPA IQNIRLRHENKDLKARLENAMEVAGRDFKRAEELEKAKQALEDQRKDLETKLKELQQDYD LAKESTSWDRQRLEKELEEKKEALELAIDQASRDYHRATALEKELEEKKKALELAIDQAS QDYNRANVLEKELETITREQEINRNLLGNAKLELDQLSSEKEQLTIEKAKLEEEKQISDA SRQSLRRDLASREAKKQVEKDLANLTAELDKVKEEKQISDASRQGLRRDLASREAKKQ VEKDLA</p>
M4-BS4-CTG	<p>>gene_436 GeneMark.hmm 222_aa + 185954 186619 >NODE_2_length_186620_cov_148.285713 MARKDTNKQYSLRKLKTGTASVAVAVAVLGAGFANQTEVKAAEIKKPQADSAWNWPKEYN ALLKENEELKVEREKYLSYADDKEKDPQYRALMGENQDLRREGQYQDKIEELEKERKEK QERQEQLERQYQIEADKHYQEQQKKHQEQEQQLAEKQKLAQKQISDASRQGLSRDLEA SREAKKKVEADLAALTAEHQKLKEDKQISDASRQGLSRDLEA</p>
M5-Manfredo-CTG	<p>>gene_1398 GeneMark.hmm 194_aa + 61232 61813 >NODE_10_length_61815_cov_235.110363 MARENTNKHYSRLRKLKGTASVAVALSVLGAGLVVNTNEVSAAVTRGTINDPQRAKEALD KYELNHDLKTKNEGLKTENEGKLTENEGKLTENEGKTEKKEHEAENDKQQRDTLST QKETLREVVQNTQYNNETLKIKNGLTKELNKTROELANKQEQSKENEKALNELLEKTVK DKIAKEQENKETIG</p>
M8-BB3-CTG	<p>>gene_1160 GeneMark.hmm 238_aa - 2 715 >NODE_7_length_101418_cov_178.048943 MARKDTNKQYSLRKLKTGTASVAVAVAVLGAGFANQTEVKAESPESHISISNEQLINELN DLIEENNDLKDKLARNLDLLDNTREKDPQYRALMGENQDLREKEGKYQDKIKKLEEKEN LEKKSSEDVERHYLKKLDQEHKEQERQKNLEELERQSREIDKRYQEQLQKQQQLETEKQ ISEASRKSLSRDLEASRAAKKDLEAEHQKLKEEKQISDASRQGLSRDLEASREAKKKV</p>
M12-BS3-CTG	<p>>gene_1710 GeneMark.hmm 575_aa + 13619 15346 >NODE_21_length_15967_cov_54.040096 MAKNTTNRHYSRLRKLKTGTASVAVALTVVGAGLVAGQTVRADHSDLVAEKQRLEDLGQKF ERLKQRSELYLQQYYDNKSNQYKGDWVYVQQLKMLNRDLEQAYNELSGEAHKDALGKLGID NADLKAKITELEKSVEEKNDVLSQIKKELEEAEKDIQFGREVHAADLLRHKQEI AEKENV ISKLNQELQPLKQVDETRNLQEQEKQKVLSEQLAVTKENAKKDFELAALGHQLADKE YNAKIAELESKLADAKKDFELAALGHQHAHNEYQAKLAEKDQKQLEEQQKILDASRKG TARDLEAVRQAKKATEAELNLLKAEALAKVTEQKQILDASRKG TARDLEAVRKAQAQVEAA LKQLEEQNKISEASRKLRRDLASREAKKQVEKDLANLTAELDKVKEEKQISDASRQGL RRDLDASREAKKQVEKALEANSKLALEKLNKELEESKLTKEKAELQAKLAEAKAL KEQLAKQAEELAKLRAGKASDSQTPDAKPGNKAVPGKGQAPQAGTKPNQNKAPMKETKRQ LPSTGEAANPFFTAALVMATAGVAAVVKKREEN</p>
M28-BB5-CTG	<p>>gene_950 GeneMark.hmm 358_aa - 4735 5811 >NODE_5_length_210162_cov_207.134746 MARKDTNKQYSLRKLKTGTASVAVAVAVLGAGFANQTEVKAESPSTETSANGADKLAD AYNTLLTEHEKLRDEYTLIDAKKEEPRYKALRGENQDLREKEGKYQDKIKKLEEKENL EKKSEDVERHYLKKLDQEHKEQEERQKNLEELERQSREIDKRYQEQLQKQQQLETEKQI SEASRKSLSRDLEASRAAKKDLEAEHQKLKEEKQISDASRQGLSRDLEASREAKKKVEAD LAEANSKLQALEKLNKELEEGKLLSEKEKAELQARLEAEAKALKEQLAKQAEELAKLGN QTPNAKVAPQANRSRSAMTQQKRTL PSTGEAANPFFTAATAATVMVSAGMLALKRKEEN</p>
M75-BS7-CTG	<p>>gene_561 GeneMark.hmm 387_aa - 31358 32521 >NODE_3_length_208685_cov_62.045909 MARKDTNKQYSLRKLKTGTASVAVAVAVLGAGFANQTEVKAEEERTFTELPYEARYKAWK SENDELRENYRRTLDKFNTEQGGKTRLEEQNKKLHSELASVTETLTSVTEADDKIKDLT DRDKISSNLLGNAKDQINKLTTEKDTLAEKAKKLEEDKQISDASRKSLSRDLEASRAAKK ELEANHQKLETEHKKLKEEKQISDASRQGLSRDLEASREAKKKVEADLAALTAEHQKLKE EKQISDASRQGLSRDLEASREAKKKVEADLAEANSKLQALEKLNKELEEGKLLSEKEKAE LQARLEAEAKALKEQLAKQAEELAKLGNQTPNAKVAPQANRSRSAMTQQKRTL PSTGEA ANPFFTAATAATVMVSAGMLALKRKEEN</p>

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M81-BB6-CTG	<p>>gene_94 GeneMark.hmm 396_aa - 101371 102561 >NODE_1_length_190029_cov_107.359270 MVRKDTNKQYSLRKLKTGTASVAVAVAVLGAGFANQTEVKAAGSEENVPKQQYNALWEEN EDLRGRERKYIAKLEKEEIQNGELNEKNRLEADIADLQDVIEDNDQEIKRKDRMYEAF KQSKDQVKDLTAEKDTLAEKAKKLEEDKQISDASRKSLSRDLEGSRAAKKELEAKHQKLE TEHQKLEKEDKQISDASRQGLSRDLEASREAKKKVEADLAALTAEHQKLEEKQISDASRQ GLSRDLEASREAKKKVEADLAEANSKLQALEKLNKELEEGKKLSEKEKAELQARLEAEAK ALKEQLAKQAEELAKLRAGKASDSQTPDAKPGNKVVPKGQAPQAGTKPNQNKAPMKETK RQLPSTGEAANPFFATAAATVMVSAGMLALKRKEEN</p>
M85-SP5-CTG	<p>>gene_158 GeneMark.hmm 402_aa - 835 2043 >NODE_2_length_119743_cov_614.138920 MVRKDTNKQYSLRKLKTGTASVAVAVAVLGAGFANQTEVKAEEQRAPOAKGTSVSADLYN SLWDENKTLREKQGEYITKIQNEETKNKELDKNKELDSRVTDLIDVIEHDDQELERKER MYEAFKQSKDQVNNLTAEKDTLAEKAKKLEEDKQISDASRKSLSRDLEGSRAAKKELEA KHQKLETEHQKLEKEDKQISDASRQGLSRDLEASREAKKKVEADLAALTAEHQKLEEKQI SDASRQGLSRDLEASREAKKKVEADLAEANSKLQALEKLNKELEEGKKLSEKEKAELQAR LEAEAKALKEQLAKQAEELAKLRAGKASDSQTPDAKPGNKVVPKGQAPQAGTKPNQNK PMKETKRQLPSTGEAANPFFATAAATVMVSAGMLALKRKEEN</p>
M87-BB10-CTG	<p>>gene_1714 GeneMark.hmm 238_aa - 3 716 >NODE_26_length_15865_cov_62.755661 MARKDTNKQYSLRKLKTGTASVAVAVAVLGAGFANQTEVKAESPREVTNELAASVWKKKV EEAKEKASKLEKQLEEAQKDYSEIEGKLEQFWHDYDKLEKENKEYASQLGKNQEEREKLE LEYLRKSDEEYKEHQYRQEQEERQKNLEELERQNKREIDKRYQEQLKQKQQLLETEKQIS EASRKSLSRDLEASRAAKKELEAEHQKLEEKQISDASRKSLSRDLEASREAKKKVEA</p>
M89-BSA4-CTG	<p>>gene_1171 GeneMark.hmm 244_aa - 2 733 >NODE_8_length_78604_cov_108.090657 MARKDTNKQYSLRKLKTGTASVAVAVAVLGAGFANQTTVKADSDNINRSVSKDNEKELH NKIADLEEERGEHLKIDELKEELKAKEKSENVERHYLRKLDQYKEQKERQKNLEELE RQSQRVEVKRYQEQLKQKQQLLETEKQISEASRKSLSRDLEASRAAKKDLEAEHQKLEEK QISDASRQGLSRDLEASREAKKKVEADLAALTAEHQKLEEKQISDASRQGLSRDLEASR EAKK</p>
M118-SP1-CTG	<p>>gene_1703 GeneMark.hmm 332_aa - 4820 5818 >NODE_14_length_20826_cov_45.853546 MARKDTNKQYSLRKLKTGTASVAVAVAVLGAGFANQTEVKAEEKVEVADSNASSVAKLY NQIADLTDKNGEYLERIEELEERQKNLEKLERQSQVAADKHQYEQVKKHQEYKQEQEERQ KNLEELERQNKREIDKRYQEQLKQKQQLLETEKQISEASRKSLSRDLEASRAAKKDLEAEH QKLEEKQISDASRQGLSRDLEASREAKKKVEADLAEANSKLQALEKLNKELEEGKKLSE KEKAELQAKLEAEAKALKEQLAKQAEELAKLGNQTPNAKVAPQANRSRSAMTQQKRTLP STGETANPFFATAAATVMVSAGMLALKRKEEN</p>
M179-BB12-CTG	<p>>gene_92 GeneMark.hmm 433_aa - 100604 101905 >NODE_1_length_264627_cov_344.813212 MVRKDTNRHYSRLRKLKTGTASVAVALSVLGAGLAVNQTEVSAKSVTRSTAQDPDKSRQAI TEYEVENHKLQEKNALNTRNQELTDENGELKTANEALRQRGDTLNFQRVKLEKQVQEKE HNNKTLKIENGELKTENGDLTKKLEDETRQELANKQQESKENEKTLNELLEKTVKDIAKE QENKETIGTLKLLDETVKDIAKEQKSKQDFGALKQELAKKEEQNKISDASRQGLRRDL NASREAKKQVEKDLANLTAELDKVKEEKQVSDASRQGLRRDLASREAKKQVEKALEEAN SKLAALEKLNKELEESKKLTEKEKAELQAKLEAEAKALKEKLAKQAEELAKLRAGKASDS QTPDAKPGNKAVPGKGQAPQAGTKPNQNKAPMKETKRQLPSTGEAANPFFATAAALTMAT AGVAAVVKRKKEN</p>


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# -sprotein1
# -sprotein2
# Align_format: pair
# Report_file: stdout
#####

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# 2: M89_sequence
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# Extend_penalty: 0.5
#
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# Identity:      148/487 (30.4%)
# Similarity:    191/487 (39.2%)
# Gaps:          246/487 (50.5%)
# Score: 574.0
=====

Reference_M1_      1 MAKNNNTRHYSLRKLTGTASVAVALTVLGAGFANQTEVKANGDGNPREV      50
                   ||:..|:|.|||||:|||||:|.|||||:|.||:|.|||.||
M89_sequence       1 MARKDTNKQYSLRKLKGTASVAVAVAVLGAGFANQTTVKADSDNINRSV      50

Reference_M1_     51 IEDLAANNPAIQNIRLRYENKDLKARLENAMVAGRDFKRAEELEKAKQA      100
                   :
M89_sequence       51 -----S                                                    51

Reference_M1_     101 LEDQRKDLETKLKELOQDYDLAKESTSWDRQRLEK--ELEEKKEALELAI      148
                   :|.||:|.||:|.||:|.||:|.||:|.||:|.||:|.||:|.||:|.||:|.||
M89_sequence       52 VKDNEKELHNKIADLEEERG-----EHLDKIDELKEELKAKEKSS      91

Reference_M1_     149 DQASRDYHRATALE-KELEEKKKALELAIDQASQDYNRANVLEKELETIT      197
                   :...|.||:|.|||.||:|.||:|.||:|.||:|.||:|.||:|.||:|.||
M89_sequence       92 ENVERHYLRKLDQEYKEQERQKNLE-ELERQSQ-----REVEKRY      131

Reference_M1_     198 REQEINRNLLGNAKLELDQLSSEKEQLTIEKAKLEEEKQISDASRQSLRR      247
                   :|| .:|:| :||.||||:|:|:|.||
M89_sequence       132 QEQ-----LQKQQ-----QLETEKQISEASRKSLSR      157

Reference_M1_     248 DLDASREAKKQVEKDLANLTAELDKVKEDKQISDASRQGLRRDLASREA      297
                   ||:|:|.|||.||:|.||:|.||:|.||:|.||:|.||:|.||:|.||
M89_sequence       158 DLEASRAAKKDL-----AEHQKLEEKQISDASRQGLSRDLEASREA      200

Reference_M1_     298 KKQVEKDLANLTAELDKVKEEKQISDASRQGLRRDLASREAKKQVEKAL      347
                   ||:|:|.|||.|||.||:|.||:|.||:|.||:|.||:|.||:|.||
M89_sequence       201 KKKVEADLAALTAEHQKLEEKQISDASRQGLSRDLEASREAKK-----      244

Reference_M1_     348 EEANSKLALEKLNKELEESKLLTEKEKAEQAKLEAEAKALKEQLAKQA      397
M89_sequence       245 -----      244

Reference_M1_     398 EELAKLRAGKASDSQTPDTKPGNKAVPGKGQAPQAGTKPNQNKAPMKETK      447
M89_sequence       245 -----      244

Reference_M1_     448 RQLPSTGETANPFFTAALTVMATAGVAAVVKRKEEN      484
M89_sequence       245 -----      244

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#-----

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#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

=====
# Aligned_sequences: 2
# 1: Reference_M1_sequence
# 2: M179_sequence
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 498
# Identity:      294/498 (59.0%)
# Similarity:   332/498 (66.7%)
# Gaps:         79/498 (15.9%)
# Score: 1218.5
=====

Reference_M1_      1 MAKNNNTNRHYSLRKLTGTASVAVALTVLGAGFA-NQTEVKANGDGNPRE      49
M179_sequence     1 MVRKDTNRHYSLRKLTGTASVAVALSVLGAGLAVNQTEVSAK--SVTRS      48
Reference_M1_     50 VIEDLAANNPAIQNIRLRYENKDLKARLE-NAMEVAGRDFKRAEELEKAK      98
M179_sequence     49 TAQDPDKSRQAI----TEYEVENHKLQEKNA-----LTNRN          81
Reference_M1_     99 QALEDQRKDLETKLKELQDYDLAKESTSWDRQRLEKELEEEK----- 141
M179_sequence     82 QELTDENGELKTANEALRQRGDTLFDN---QVRKLEKQVQEKHNKTLK    127
Reference_M1_    142 -EALELAIDQASRDYHRATALEKELEKKALELAIDQASQDYNRA---N    187
M179_sequence    128 IENGELKTENGD-----LTKKLDETRQ--ELANKQQESKENEKTLNE    167
Reference_M1_    188 VLEKEL-ETITREQEINRNLLGNAKLELDQLSSEKEQLTIEKAKLEEEKQ   236
M179_sequence    168 LLEKTVKDKIAKEQE-NKETIGTLKLLDETVKDK-----IAKEQKSKQ   210
Reference_M1_    237 ISDASRQLRRDLASREAKKQVEKDLANLTAELDKVKEDKQISDASRQG   286
M179_sequence    211 -----DFGALKQELAKKEEQNKISDASRQG   235
Reference_M1_    287 LRRDLASREAKKQVEKDLANLTAELDKVKEEKQISDASRQGLRRDLAS   336
M179_sequence    236 LRRDLNASREAKKQVEKDLANLTAELDKVKEEKQVSDASRQGLRRDLAS   285
Reference_M1_    337 REAKKQVEKALEEANSKLAALEKLNKELEESKKLTEKEKAELQAKLEAEA   386
M179_sequence    286 REAKKQVEKALEEANSKLAALEKLNKELEESKKLTEKEKAELQAKLEAEA   335
Reference_M1_    387 KALKEQLAKQAEELAKLRAGKASDSQTPDTKPGNKAVPGKGQAPQAGTKP   436
M179_sequence    336 KALKEQLAKQAEELAKLRAGKASDSQTPDAKPGNKAVPGKGQAPQAGTKP   385
Reference_M1_    437 NQNKAPMKETKRQLPSTGETANPFFTAALTVMATAGVAAVVKKREEN     484
M179_sequence    386 NQNKAPMKETKRQLPSTGEAANPFFTAALTVMATAGVAAVVKKKEN     433

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#-----

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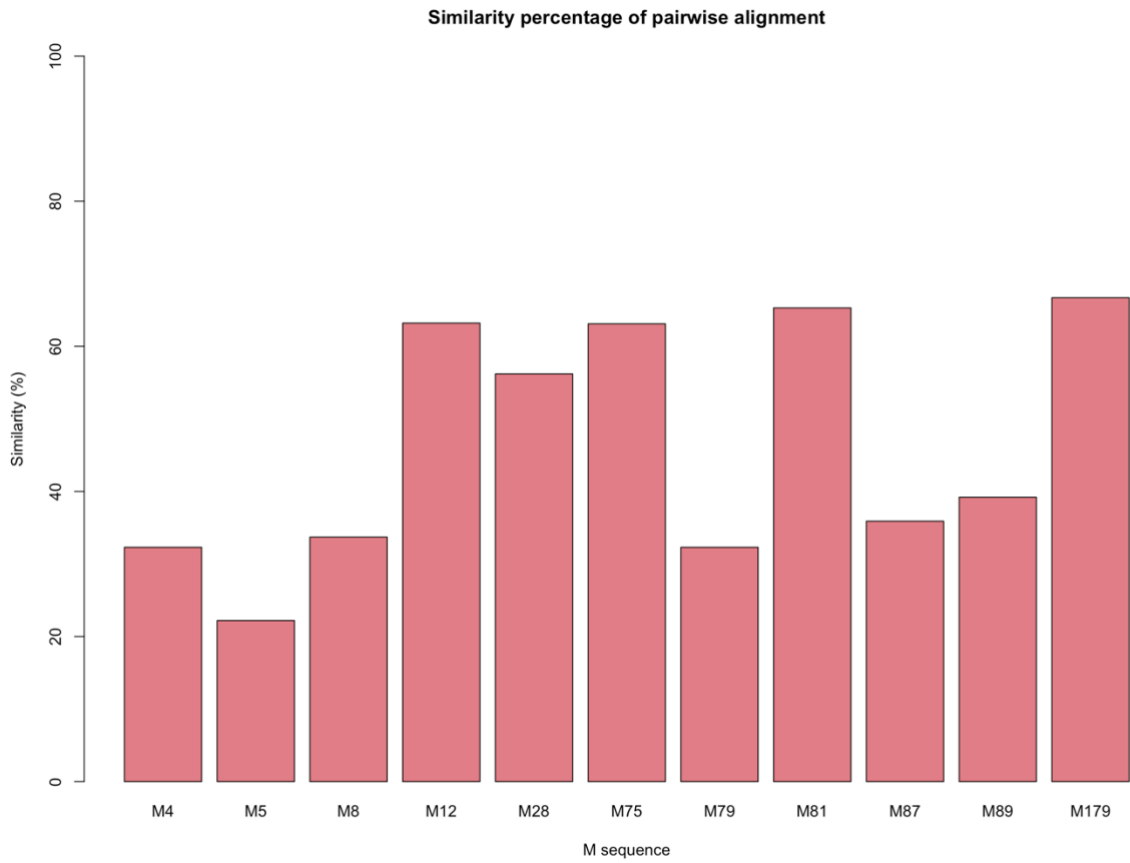


Figure S1. Similarity percentage for each M sequence aligned to M1 reference sequence

Binding peptides similarity in each sequence

Here, only the two peptides of M1 protein in the binding interface with ab25 *i.e.*, “KALELAIDQASQDYNRANVLEKE”, and “REAKKQVEKDLANLTAELDKVKE” were searched in each target M sequence to detect the similar patterns. Below, we report the result of the alignment and the similarity percentage with each of the detected peptides.

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# Commandline: needle
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#   -stdout
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#   -bsequence emboss_needle-I20210917-134146-0008-34466034-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#=====
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# 2: M4_similar_p1
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# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 26
# Identity:      10/26 (38.5%)
# Similarity:    12/26 (46.2%)
# Gaps:          3/26 (11.5%)
# Score: 29.0
#
#
#=====

Binding_pep1      1 KALELAIDQASQDYN---RANVLEKE      23
                   ||.:...||...:|  ..|.|.||
M4_similar_p1    1 KAAEIKKPQADSAWNWPKEYNALLKE      26

#-----
#-----
```

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# Commandline: needle
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#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M4_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      17/23 (73.9%)
# Similarity:   19/23 (82.6%)
# Gaps:         0/23 ( 0.0%)
# Score: 76.0
#
#
#=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   |||||:|.|||.||||..|:|
M4_similar_p2    1 REAKKKVEADLAALTAEHQKLKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-135430-0963-60062530-p2m.asequence
#   -bsequence emboss_needle-I20210917-135430-0963-60062530-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M5_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      6/23 (26.1%)
# Similarity:    10/23 (43.5%)
# Gaps:          0/23 ( 0.0%)
# Score: 17.0
#
#
#=====
```

```
Binding_pep1      1 KALELAIDQASQDYNRANVLEKE      23
                   |||...:~::~|.....||
M5_similar_p1    1 KALNELLEKTVKDKIAKEQENKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-135546-0415-63161967-p2m.asequence
#   -bsequence emboss_needle-I20210917-135546-0415-63161967-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M5_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      3/23 (13.0%)
# Similarity:    8/23 (34.8%)
# Gaps:          10/23 (43.5%)
# Score: 18.0
#
#
#=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   ...|:.:|:..:|
M5_similar_p2    1 STQKETLEREVQN-----      13
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-135644-0668-46832847-p2m.asequence
#   -bsequence emboss_needle-I20210917-135644-0668-46832847-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M8_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 25
# Identity:      6/25 (24.0%)
# Similarity:    13/25 (52.0%)
# Gaps:          2/25 ( 8.0%)
# Score: 17.5
#
#
=====
```

```
Binding_pep1      1 KALELAIDQASQDYNR--ANVLEKE      23
                   :..|...:::..|:|..|  ...|::|
M8_similar_p1    1 EEKEKNLEKKSEDVERHYLKKLDQE      25
```

```
#-----
#-----
```



```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-135804-0655-27464049-p2m.asequence
#   -bsequence emboss_needle-I20210917-135804-0655-27464049-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M8_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      10/23 (43.5%)
# Similarity:    13/23 (56.5%)
# Gaps:          3/23 (13.0%)
# Score: 34.0
#
#
=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   .||.:...:||  |.||..|:||
M8_similar_p2    1 LEASRAAKKD---LEAEHQKLKE      20
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-135919-0762-92494436-p2m.asequence
#   -bsequence emboss_needle-I20210917-135919-0762-92494436-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M12_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      7/23 (30.4%)
# Similarity:    12/23 (52.2%)
# Gaps:          0/23 ( 0.0%)
# Score: 29.0
#
#
=====
```

```
Binding_pep1      1 KALELAIDQASQDYNRANVLEKE      23
                   |.:|.|:..|:.....|.||
M12_similar_p     1 KQVEKALEEANSKLAALEKLNKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140032-0915-10411681-p2m.asequence
#   -bsequence emboss_needle-I20210917-140032-0915-10411681-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M12_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      23/23 (100.0%)
# Similarity:    23/23 (100.0%)
# Gaps:          0/23 ( 0.0%)
# Score: 110.0
#
#
=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   |||
M12_similar_p     1 REAKKQVEKDLANLTAELDKVKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140131-0771-94163540-p2m.asequence
#   -bsequence emboss_needle-I20210917-140131-0771-94163540-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M28_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      6/23 (26.1%)
# Similarity:    10/23 (43.5%)
# Gaps:          0/23 ( 0.0%)
# Score: 22.0
#
#
=====
```

```
Binding_pep1      1 KALELAIDQASQDYNRANVLEKE      23
                   |.:|...:|:.....|.||
M28_similar_p     1 KKVEADLAEANSKQLQALEKLNKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140229-0375-95050436-p2m.asequence
#   -bsequence emboss_needle-I20210917-140229-0375-95050436-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M28_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      11/23 (47.8%)
# Similarity:    17/23 (73.9%)
# Gaps:          0/23 ( 0.0%)
# Score: 54.0
#
#
#=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   |||||:|.|||. . . . :|. . . . :
M28_similar_p     1 REAKKKVEADLAEANSKLALEK      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140324-0121-43219167-p2m.asequence
#   -bsequence emboss_needle-I20210917-140324-0121-43219167-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M75_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      6/23 (26.1%)
# Similarity:    10/23 (43.5%)
# Gaps:          0/23 ( 0.0%)
# Score: 22.0
#
#
=====
```

```
Binding_pep1      1 KALELAIDQASQDYNRANVLEKE      23
                   |.:|...:|:.....|.||
M75_similar_p     1 KKVEADLAEANSKQLQALEKLNKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140421-0869-93139689-p2m.asequence
#   -bsequence emboss_needle-I20210917-140421-0869-93139689-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M75_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      17/23 (73.9%)
# Similarity:    19/23 (82.6%)
# Gaps:          0/23 ( 0.0%)
# Score: 76.0
#
#
=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   |||||:|.|||.||||..|:|
M75_similar_p    1 REAKKKVEADLAALTAEHQKLKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140533-0491-60880675-plm.asequence
#   -bsequence emboss_needle-I20210917-140533-0491-60880675-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M79_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 26
# Identity:      10/26 (38.5%)
# Similarity:    12/26 (46.2%)
# Gaps:          3/26 (11.5%)
# Score: 29.0
#
#
#=====
```

```
Binding_pep1      1 KALELAIDQASQDYN---RANVLEKE      23
                   ||.:...||...:|  ..|.|.||
M79_similar_p     1 KAAEIKKPQADSAWNPKEYNALLKE      26
```

```
#-----
#-----
```



```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140643-0717-60803203-p2m.asequence
#   -bsequence emboss_needle-I20210917-140643-0717-60803203-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M79_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      17/23 (73.9%)
# Similarity:    19/23 (82.6%)
# Gaps:          0/23 ( 0.0%)
# Score: 76.0
#
#
=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   |||||:|.|||.||||..|:|
M79_similar_p    1 REAKKKVEADLAALTAEHQKLKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140742-0256-53359928-p2m.asequence
#   -bsequence emboss_needle-I20210917-140742-0256-53359928-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M81_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      6/23 (26.1%)
# Similarity:    10/23 (43.5%)
# Gaps:          0/23 ( 0.0%)
# Score: 22.0
#
#
=====
```

```
Binding_pep1      1 KALELAIDQASQDYNRANVLEKE      23
                   |.:|...:|:.....|.||
M81_similar_p     1 KKVEADLAEANSKQLQALEKLNKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140900-0106-40553270-p2m.asequence
#   -bsequence emboss_needle-I20210917-140900-0106-40553270-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M81_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      17/23 (73.9%)
# Similarity:    19/23 (82.6%)
# Gaps:          0/23 ( 0.0%)
# Score: 76.0
#
#
=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   |||||:|.|||.||||..|:|
M81_similar_p     1 REAKKKVEADLAALTAEHQKLKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-140947-0333-77671278-plm.asequence
#   -bsequence emboss_needle-I20210917-140947-0333-77671278-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M87_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 34
# Identity:      9/34 (26.5%)
# Similarity:   15/34 (44.1%)
# Gaps:         11/34 (32.4%)
# Score: 32.0
#
#
=====
```

```
Binding_pep1      1 KALELAIDQASQDYNRA-----NVLEKE      23
                   ..||..:::|.::|:..           :.||||
M87_similar_p     1 SKLEKQLEEAQKDYSEIEGKLEQFWHDYDKLEKE  34
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-141049-0262-1155708-p2m.asequence
#   -bsequence emboss_needle-I20210917-141049-0262-1155708-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M87_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      10/23 (43.5%)
# Similarity:    13/23 (56.5%)
# Gaps:          7/23 (30.4%)
# Score: 35.0
#
#
=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   |.|||:|          ||..:|
M87_similar_p     1 RAAKKELE-----AEHQKLKE      16
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-141135-0412-59042471-p2m.asequence
#   -bsequence emboss_needle-I20210917-141135-0412-59042471-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M89_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      7/23 (30.4%)
# Similarity:   12/23 (52.2%)
# Gaps:         2/23 ( 8.7%)
# Score: 20.5
#
#
=====
```

```
Binding_pep1      1 KALELAIDQASQDYNRANVLEKE      23
                   ||.|.:...:..|.|. |::|
M89_similar_p     1 KAKEKSENVERHYLRK--LDQE      21
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-141215-0123-81889031-plm.asequence
#   -bsequence emboss_needle-I20210917-141215-0123-81889031-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M89_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      17/23 (73.9%)
# Similarity:   19/23 (82.6%)
# Gaps:         0/23 ( 0.0%)
# Score: 76.0
#
#
#=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   |||||:|.|||.||||..|:|
M89_similar_p    1 REAKKKVEADLAALTAEHQKLKE      23
```

```
#-----
#-----
```

```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-141302-0615-69440915-plm.asequence
#   -bsequence emboss_needle-I20210917-141302-0615-69440915-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep1
# 2: M179_similar_p1
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      7/23 (30.4%)
# Similarity:   12/23 (52.2%)
# Gaps:         0/23 ( 0.0%)
# Score: 29.0
#
#
=====
```

```
Binding_pep1      1 KALELAIDQASQDYNRANVLEKE      23
                   |.:|.|:..|:.....|.||
M179_similar_    1 KQVEKALEEANSKLAALEKLNKE      23
```

```
#-----
#-----
```



```
#####
# Program: needle
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20210917-141404-0386-78941509-plm.asequence
#   -bsequence emboss_needle-I20210917-141404-0386-78941509-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Binding_pep2
# 2: M179_similar_p2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 23
# Identity:      23/23 (100.0%)
# Similarity:    23/23 (100.0%)
# Gaps:          0/23 ( 0.0%)
# Score: 110.0
#
#
=====
```

```
Binding_pep2      1 REAKKQVEKDLANLTAELDKVKE      23
                   |||
M179_similar_    1 REAKKQVEKDLANLTAELDKVKE      23
```

```
#-----
#-----
```

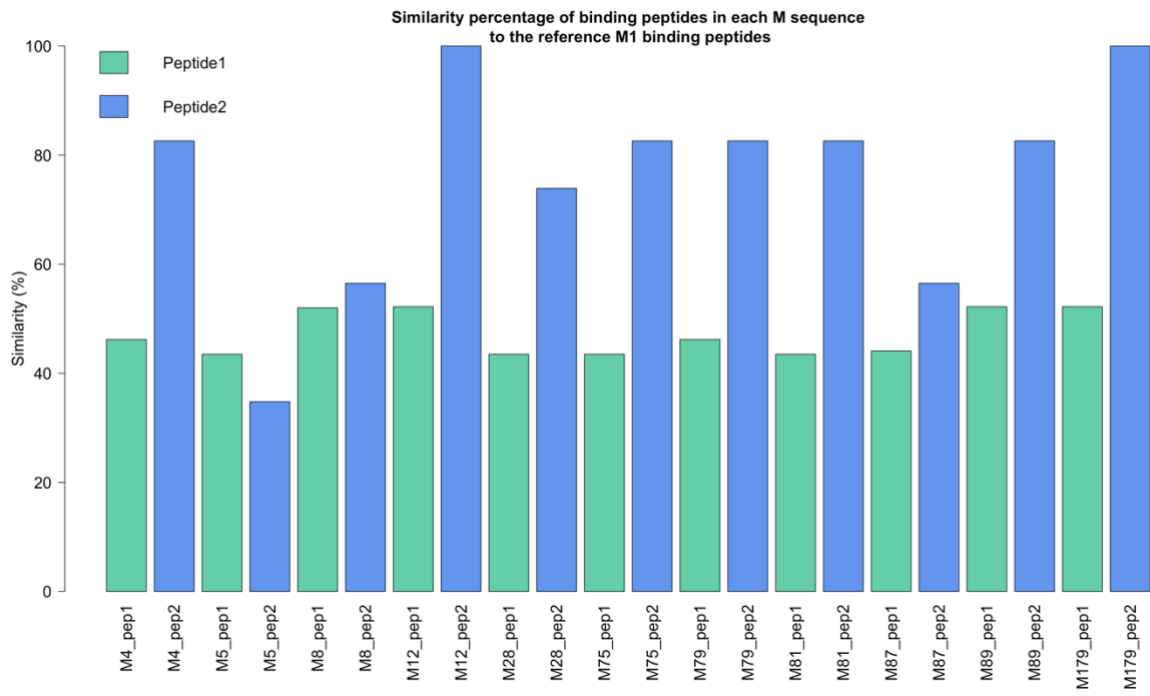


Figure S2. Similarity percentage for binding peptides of M1 against most similar peptide in each M sequence


```

#####
# Program: needle
# Rundate: Wed 6 Oct 2021 09:51:02
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20211006-095058-0469-54470083-p2m.asequence
#   -bsequence emboss_needle-I20211006-095058-0469-54470083-p2m.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#=====
#
# Aligned_sequences: 2
# 1: Ref_M79_sequence
# 2: M4_sequence
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 222
# Identity:      222/222 (100.0%)
# Similarity:    222/222 (100.0%)
# Gaps:          0/222 ( 0.0%)
# Score: 1113.0
#
#
#=====

Ref_M79_seque      1  MARKDNTNKQYSLRKLKTGTASVAVAVAVLGGAGFANQTEVKAAEIKKPQAD      50
  |||
M4_sequence        1  MARKDNTNKQYSLRKLKTGTASVAVAVAVLGGAGFANQTEVKAAEIKKPQAD      50

Ref_M79_seque     51  SAWNWPKEYNALLKENEELKVEREKYLSYADDKEKDPQYRALMGENQDLR      100
  |||
M4_sequence       51  SAWNWPKEYNALLKENEELKVEREKYLSYADDKEKDPQYRALMGENQDLR      100

Ref_M79_seque    101  KREGQYQDKIEELEKERKEKQERQEQLEQYQIEADKHYQEQQKKHQEQ      150
  |||
M4_sequence      101  KREGQYQDKIEELEKERKEKQERQEQLEQYQIEADKHYQEQQKKHQEQ      150

Ref_M79_seque    151  QQLEAEKQKLAKDKQISDASRQGLSRDLEASREAKKKVEADLAALTAEHQ      200
  |||
M4_sequence      151  QQLEAEKQKLAKDKQISDASRQGLSRDLEASREAKKKVEADLAALTAEHQ      200

Ref_M79_seque    201  KLKEDKQISDASRQGLSRDLEA      222
  |||
M4_sequence      201  KLKEDKQISDASRQGLSRDLEA      222

#-----
#-----

```



```
#####
# Program: needle
# Rundate: Wed 6 Oct 2021 10:07:10
# Commandline: needle
# -auto
# -stdout
# -asequence emboss_needle-I20211006-100706-0795-49043706-p2m.asequence
# -bsequence emboss_needle-I20211006-100706-0795-49043706-p2m.bsequence
# -datafile EBLOSUM62
# -gapopen 10.0
# -gapextend 0.5
# -endopen 10.0
# -endextend 0.5
# -aformat3 pair
# -sprotein1
# -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Ref_M79_sequence
# 2: M81_sequence
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 223
# Identity: 124/223 (55.6%)
# Similarity: 148/223 (66.4%)
# Gaps: 18/223 ( 8.1%)
# Score: 509.5
#
#
=====
```

Ref_M79_seque	1	MARKDTNKQYSLRKLKTGTASVAVAVAVL	GAGFANQTEVKAAEIKKPQAD	50
		.		.
M81_sequence	1	MVRKDTNKQYSLRKLKTGTASVAVAVAVL	GAGFANQTEVKA-----AG	43
Ref_M79_seque	51	SAWNWPK-EYNALLKENEELKVEREKYLSY	ADDKEKDPQYRALMGENQDL	99
		.	:	:
M81_sequence	44	SEENVPKQQYNALWEENEDLRGRERKYIAK	LEKEE--IQNGELNEKNRKL	91
Ref_M79_seque	100	RKREGQYQDKIEELEKERKEKQERQQLER	QYQIEADKHYQEQQKHKHQQE	149
		:
M81_sequence	92	EADIADLQDVIEDNDQEIKRK-----	DRMYEAFI-KQSKDQVKDLTAE	133
Ref_M79_seque	150	QQQLEAEKQKLAKDKQISDASRQGLSRD	LEASREAKKVEADLAALTAEH	199
		:..	:
M81_sequence	134	KDTLAEKAKKLEEDKQISDASRKSLSRD	LEGSRAAKKELEAKHQKLETEH	183
Ref_M79_seque	200	QKLKEDKQISDASRQGLSRDLEA	222	
M81_sequence	184	QKLKEDKQISDASRQGLSRDLEA	206	

```
#-----
#-----
```



```
#####
# Program: needle
# Rundate: Wed 6 Oct 2021 10:13:16
# Commandline: needle
# -auto
# -stdout
# -asequence emboss_needle-I20211006-101315-0196-46816129-p2m.asequence
# -bsequence emboss_needle-I20211006-101315-0196-46816129-p2m.bsequence
# -datafile EBLOSUM62
# -gapopen 10.0
# -gapextend 0.5
# -endopen 10.0
# -endextend 0.5
# -aformat3 pair
# -sprotein1
# -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
=====
#
# Aligned_sequences: 2
# 1: Ref_M79_sequence
# 2: M179_sequence
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 289
# Identity: 118/289 (40.8%)
# Similarity: 154/289 (53.3%)
# Gaps: 72/289 (24.9%)
# Score: 447.0
#
#
=====
```

Ref_M79_seque	1	MARKDNTNKQYSLRKLKLTGTASVAVAVAVL	GAGFA-NQTEVKA AEI-----	44
M179_sequence	1	MVRKDTNRHYSLRKLKLTGTASVAVALSVL	GAGLAVNQTEVSAKSVTRSTA	50
Ref_M79_seque	45	----KKPQADSAW-----NWPKEYNALL	KENEEL-----	69
M179_sequence	51	QDPDKSRQAI TEYEVENHKLTQEKNAL	TNRNQELTDENGELKTANEALRQ	100
Ref_M79_seque	70	-----KVEREKYLSYADDKEKDPQY	RALMGENQDLRKREGQYQDKIE	111
M179_sequence	101	RGDTLNFNRVKLEKQV----QEKEHNNK	TLKIENGELKTENGDLTKKLD	145
Ref_M79_seque	112	ELEKERKEKQERQEQLERQY----QIE	ADKHYQEQQK-----	144
M179_sequence	146	ETRQELANKQQESKENEKTLNELLEK	TVKDKIAKEQENKETIGTLKKLLD	195
Ref_M79_seque	145	-----KHQQEQQLEAEKQKLA	KDKQ---ISDASRQGLSRDLEASRE	183
M179_sequence	196	ETVKDKIAKEQKSKQDFGALKQELAK	KKEEQNKISDASRQGLRRDLNASRE	245
Ref_M79_seque	184	AKKKVEADLAALTAEHQKLEKEDKQI	SDASRQGLSRDLEA	222
M179_sequence	246	AKKQVEKDLANLTAELDKVKEEKQV	SDASRQGLRRDLDA	284

```
-----
#-----
```

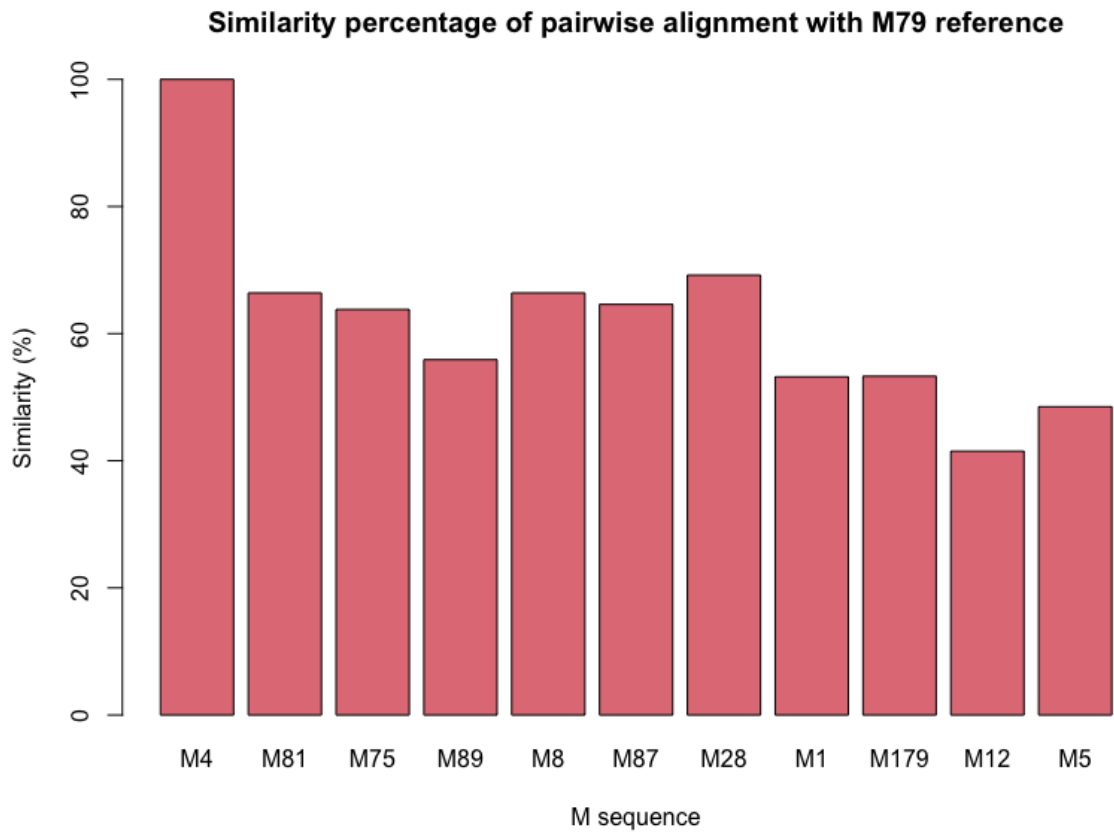


Figure S3. Similarity percentage for truncated M sequences against M79 partial reference sequence