

# Supplementary Material: Scavenger Receptor C1 Mediates Toxicity of Binary Toxin from *Lysinibacillus sphaericus* to Ag55 Cells

## SCR-C1 sequence

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1 - ATGCTGTTATCAAGAAGCTCGAAGGGAGCAACCCCTGCTTGGGGGGTGTGTTGGATCGTTTCTTCGCCAATTGGTTCGCTGGCCAATTAACCCCTTACGGCTCGAGAGCGCCCTCCATG - 120
1 - M L L S R S S K G A T L L G G L L W I V F F A N L Y A G Q L T L Y G S R A P S M - 40

121 - CGTCGTCGCTCACTAGACAGTTGGTGGGCAATGCCCTGCGCGTACTTCCCGAACGGGGAGGCGAAAAATTCGAAACCGTGGCCGAATGATGCGCTTCGACTGTGCGTACGGGTTTAAG - 240
41 - R R P L T R Q L V G Q C P A P Y F P N G E A K I R N R B G R M M R F D C A Y G F K - 80

241 - CTGGTCGGCAATCGGTACTCCAAGTCCGAGAACGGTGGTGGGACACATCGATCCGGTTGTGTGAAATCCGGATGCGAGCTGCTCGCCCCAATAGAGTCCGGCCACGTGCTGTACGAG - 360
81 - L V G N R Y S N C Q N G R W D T S I P V C V K S G C S L L A P I E S G H V L Y E - 120

361 - ATGAACAAGCGTCCGCTTCTGTCTGCTTTGAGGGGACCGAGCTGGCGGGCTCGAGAACCGCTACTGCAACGGGACGCACTGGGATCGACCGCTCGGTATCTGCCGCGTACGGGA - 480
121 - M N K A S A F L S C F E G T E L A G S R N A Y C N G T H W D R P L G I C R R T G - 160

481 - CAGGCGACACCGACGGCTGCGACTTCGAGACCGAGTCGCTGTGCGGGTGGTCCACGATGCGCTGCACGATTTGACTGGAAGCGCAGCGACGGTACGCTGAACCCGCGCGCACTCCGA - 600
161 - Q A T P T A C D F E T E S L C G W S N D A L H D F D W K R S D G T L N P R A L R - 200

601 - ACCGGGCCAAGTACGACCAACACGATGCGAGCGAAGGCGGGCCACTTCATGATAGTGATTCCGGCGAGCAGCTAACGAACGATACGGCCCGCTTCATATCGCCGCTGTTGAGCGG - 720
201 - T G P K Y D H T T M Q P K A G H F M I V D S G E Q L T N D T A R F I S P L F E P - 240

721 - GAGCTGAGCGTGGTGGTGTCTCCAGTTTACTATCACATGTACGGGGAGTGGTGGGCGACGCTGAAGGTGTTTGTGAAGCCGATGAGCGCCGACCTGTACGATCTGCAGCCGGTGT - 840
241 - L S V G A Y S N C Q N G R W D T S I P V C V K S G C S L L A P I E S G H V L Y E - 280

841 - GTGCAGCGGGCAATCAGAAGAAGTTTGGCACAGGGTCACGTTGAGTGGGCGAGCAAGCGGAGCGCTTTCAGTGGTGATCGAGCGAGCGCTGGGCGATCGCTACAGAGCGACATT - 960
281 - V Q R G N Q K N V W H E G H V E V G Q Q A E R F Q V V I E A S L G M R Y K S D I - 320

961 - GCGATCGACGATGTGAGCTTGTCTGCAGGGCGACAGTTGCCGGGTGGCGGTGAGGATGCGAGGAGCCACCACCGCCGAGGTGGAGAAGCTGCCGGTGAAGATAGAGTCTGCGCAAAAC - 1080
321 - A I D D V S L L Q G D S C R V V E D G E E P P P A E V E N V P V K I E S C E N - 360

1081 - CGGTGCGGAAGCAGTATGCGCGCGTGCTGAACGCGAAGCAGATACGATTGTGCACTGCGACTGCGCACGAGGACTGTGTGACGAGTGAGACCTGCTGTCCGATTACCGGGAACGGTGC - 1200
361 - R C G S S M A A V L N A N D T I V H C D C H E D C V T S E T C C P D Y R E R C V - 400

1201 - TTTTCAGGTAGCGGTTGGAGGGAGTAACGTAAGTACGACCAACCCGCTTCTGTACCGTGCAGCTGTACCAACGGTTAGGACAACCTACGCAAAAGCTGCTGCCACTACGCTACGCGGCGG - 1320
401 - F G V A V G S N V S T T T P V P V S T T V R T T T A K A A A T T S T R P - 440

1321 - GTGACAACGACTTCCACAACGGTCAGTACGACTTACCACCACCTACCACCACCAACCAACCACTGCAAGGCAACAAACGTCAGGCTACTACGACAGGAGTACCACTACAAAA - 1440
441 - V T T T S T T V S S T T T T T T T T T T T T A K P T T S S A T T T R S T T T K - 480

1441 - CCATCCACGACGTCCTACTGTCTCCACGACACCAAGAGTACAATCTACGCCAAGGCTAGTCTCGTTCCGCTTACCAATCGACACAGCTGCCACCAACCAACCAACGAGCTGCA - 1560
481 - P S T T S T V S T T T T K K Y N L R P R P S L V P L T N R P Q L P P T T T P A A - 520

1561 - ACGACTCGCAAAACAACTACGCCAAGCAGCAGCCACCTCCACAGCGGTGACAACGACCATCCCAACCACTCAATCCGACCTGGTGGCGGTTGAACAGTCCGTGCGCATCAACAAAC - 1680
521 - T T R K T T T P T T T A T S T A V T T T I P T T T Q S D L V A V E Q S V P S T R - 560

1681 - GAGGAGGTGATAATGCCCGCTGGCCATGGCCCCACTGCAACCGGTAGAAAACTCCACTCCACTCCGAGTCTGATGAAGTTCTTCGTGTACGCCATATCGACCGTAGTGTGTTTTCG - 1800
561 - E E V I M P G L A M A P L Q P V E K L H S T P S L M K F F V Y A I S T V V L F A - 600

1801 - TGCATTTTAAGCGCTGCGTACCTTTACGACGAGGTCGCGTTCAGCGTGGCAAGGTTGAAGGAAAAATCGCAAAAGAGTGGCTTCGAGGACATCCGGTTTCTGGCTGCGCATGAA - 1920
601 - C I L S A A Y L Y A R R S R S S V L A R L K E K S Q K S G F E D I R F L A G D E - 640

1921 - GACTTAGACTTTAATATTACGACGGGCGGATGTGAGGAGGAGGAGGTGCTGGAAAAGGAGGCAAGGGGAGGCAAAAGCAAAACAGGAAACCAAGCAAGAGGACGCA - 2040
641 - D L D F N I T H G R D V E E G E E V L E K E G K G E A K A K Q E T K P S K K D A - 680

2041 - AAAGCGGACATC - 2052
681 - K A D I - 720

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**Figure S1.** Sequence of scavenger receptor C1 (SCR1): signal leading peptide (bold) and transmembrane domain were underlined with red; CCP (complement control protein) domain (aa 49-103) was underlined with blue and MAM domain (aa 162-335) underlined with orange. Black underline denotes region expressed for preparing antisera.

**SCR-BQ2 sequence**

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1 - tggcgtaggcaagtggtggaatcattgtgtagcgggtgaaaataaagcacactggatgagctgataagagggacacagctgogcgtgacgacaccaaactaccgccacaaggacagc - 120
121 - ggccataaaaataccaaagcaatatagaggcgttataacgcaatccaccaaaacaaaattatgcctcagctgcaaactacaATGTGTTCCACCATGTACAGACTTTCAGAAAAAGTTTAT - 240
1 - M C S P C T D F Q K K F I - 13
241 - ATCACTAGGATGTTCTGTCCTTTCTAATCTTGCTAGCGATTACACTAGGCGTGCTTTGGCCATCCCTGTCCGACCAGGTGCTGCACAATAAAGTGGTTATTAATAATGGATCGTCGAACTA - 360
14 - S L G C S S F L I L L A I T L G V L W P S L S D Q V L H N K L V I K N G S S N Y - 53
361 - TGACAACTGGATTCGGACACCTATACCCATGTATCTGGAGGTATATTTCTTTAACTGGACTAATCCGGATGACGTAAAGACGAAGAACGGTACAAAGCCACACTTTGTGGAGATGGGACC - 480
54 - D N W I R T P I P M Y L E V Y F F N W T N P D D V K T K N G T K P H F V E M G P - 93
481 - GTACACGTTTTCCGAGGTTTCACGAACGTGTCAACCTAGTCTGGAACGCTAACAGTACGGTAACATATGAGCAGCGCAGGACGTGGCATTTTGTACCGGAGCTATCGAAAGGCACACTGGGA - 600
94 - Y T F S E V H E R V N L V W N A N S T V T Y E Q R R T W H F V P E L S K G T L D - 133
601 - TGATCAAGTTACAAATTGAACGTTATCACCTTGAATGCTGCACATTTTACGCAATACATATCCCCTGCTTAGACCACCTAATAAATATATTCCTTAAACCGGATGGTTTCGTGTGCTGTG - 720
134 - D Q V T N L N V I T L N A A H F L R N T Y P L L R P L I N I F L K T D G S L L W - 173
721 - GAAAAACAAACAGTGCAGGAGCTGCTGTTGGAAGGCGTTAAAGATCCACTGCTAGATCTGCTGAAGACTATCAATAGCACATCACTGAACATACCGTTTGATAAGTTTGGCTGGTTTGT - 840
174 - K N K P V R E L L F E G V K D P L L D L L K T I N S T S L N I P F D K F G W F V - 213
841 - TGGGCGTAATCTGAGCGACACGTTTGACGGCACCTTCACGATGAGAACGGGTGCGGATGGGCTGGAAAGCATGGGCTTCCTAACGCAGTGGAAACGGTTACCCACACCGGCATGTACCG - 960
214 - G R N L S D T F D G T F T M R T G A D G L E S M G F L T Q W N G S P N T G M Y R - 253
961 - GGGAAAGTGGCGGAAGTGACGGTACGTCGGCGAGCTTTGGCCAGCCTTAGCAATGTTCCGGCAAACATTACACTCTTCCCATCGGACATTTGCCGTTCCATTACGCTGCAAGGCAG - 1080
254 - G K C G E V Y G T S G E L W P A S S N V P A N I T L F P S D I C R S I T L Q G R - 293
1081 - GGAACAAGTTTCGCTGTACAAACATACAGGCGACGAAGTACGTTGGCGACGATCGTGTTCGACAACGGTGTAAATACCCCGAGGCTAGCTGCTGGTGCAACTCCCAATCCCAACCAATG - 1200
294 - E Q V S L Y N I Q G T K Y V G D D R V F D N G V K Y P E A S C W C N S N P T Q C - 333
1201 - CCCTGACCTTAAGCCGGGTGTGTTAATGCTTCCGCCGTGCAATATGGATCGCCAACGTTCTGATCGTTTCCGCACCTTTTATCTGGCCGATGAAAGCTACCAAACTGCTGTAACGGGACT - 1320
334 - P G L K P G V F N A S A C K Y G S P T F V S F P H F Y L A D E S Y Q T A V T G L - 373
1321 - GCGGCCAATCAACCGGAGCACGAGTTTACATGGCAATCGAGCCATCGACTGGCATTCGTTGGACGTTCTGTGCCAGCTGCAGATCAATGAGCACTTGACGCGGATAAAAGGGTTTAG - 1440
374 - R P N Q T E H E F Y M A I E P S T G I P L D V R A Q L Q I N E H L Q P I K G F S - 413
1441 - TTTCTACGAGCATGTACCGGACGTAATGGTACCGATGATCTGGTTCCGACAACGTGCAACCTGACGCAAGAGCTGGCAGAACAGGCGAAGCTTGCACTGGCACTACCGTCGCTCGGCAT - 1560
414 - F Y E H V P D V M V P M I W F R Q R A T L T Q E L A E Q A K L A L A L P S L G I - 453
1561 - CTACGTGGCGGTCTTCTTTGGCTCTATCGGTATTATCATGACGTCCGTATTCCTATCTGCAGTATCAAAAAATGGTCCCAAGCGCAGAGGTAGTTCCGTACGAAGAGCTACAAAAATTA - 1680
454 - Y V A V F F G S I G I I M T S V F L F C S I K K W S Q S A E V V P Y E E L Q N * - 492
1681 - Acgtgttaaaagcatcgacgcaacaaaaaataatataca

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**Figure S2.** Sequence of scavenger receptor BQ2: signal leading peptide (bold) and transmembrane domain were underlined with red. The region of SCR BQ2 expressed for preparing antisera is underlined in black.

**Figure S3.** CLUSTAL O (1.2.4) multiple sequence alignment of Ag55 SCRC1 (GH) and SCRC1 homologues from *A. arabiensis* (XP\_040167338.1), *A. coluzzii* (XP\_040235850.2), and *A. gambiae* XP\_061518211.1

SCRC1_GH	-----MLLSRSSKGATLLGGLLWIVFFANLVAGQLTLYGSRAPSMRRPLTRQLV	49
arabiensis	-----MLLSRSSKGATLLGGLLWIVFFANLVAGQLTLYGSRAPSMRRPLTRQLV	49
coluzzii	MCAYCSRI LPPMLLSRSSKGATLLGGLLWIVFFANLVAGQLTLYGSRAPSMRRPLTRQLV	60
gambiae	-----MVLSRSLKGATLLGGLLWIVFFANLVAGQLTLYGSRAPSMRRPLTRQLV	49
	*:**** *****	
SCRC1_GH	GQCPAPYFPNGEAKIRNRGRMMRFDCAYGFKLVGNRYSNCQNGRWDTSIPVCVKSGCSLL	109
arabiensis	GQCPAPYFPNGEAKIRNRGRMMRFDCAYGFKLVGNRYSNCQNGRWDTSIPVCVKSGCSLL	109
coluzzii	GQCPAPYFPNGEAKIRNRGRMMRFDCAYGFKLVGNRYSNCQNGRWDTSIPVCVKSGCSLL	120
gambiae	GQCPAPYFPNGEAKIRNRGRMMRFDCAYGFKLVGNRYSNCQNGRWDTSIPVCVKSGCSLL	109
	*****	
SCRC1_GH	APIESGHVLYEMNKASAF LSCFEGTELAGSRNAYCNGTHWDRPLGICRRTGQATPTACDF	169
arabiensis	APIESGHVLYEMNKASAF LSCFEGTELAGSRNAYCNGTHWDRPLGICRRTGQATPTACDF	169
coluzzii	APIESGHVLYEMNKASAF LSCFEGTELAGSRNAYCNGTHWDRPLGVCRRTGQATPTACDF	180
gambiae	APIESGHVLYEMNKASAF LSCFEGTELAGSRNAYCNGTHWDRPLGVCRRTGQATPTACDF	169
	*****:*****	
SCRC1_GH	ETESLCGWSNDALHDFDWKRS DGT LNPRLRTGPKYDHTTMQPKAGHFMIVDSGEQLTND	229
arabiensis	ETESLCGWSNDALHDFDWKRS DGT LNPRLRTGPKYDHTTMQPKAGHFMIVDSGEQLTND	229
coluzzii	ETESLCGWSNDALHDFDWKRS DGT LNPRLRTGPKYDHTTMQPKAGHFMIVDSGEQLTND	240
gambiae	ETESLCGWSNDALHDFDWKRS DGT LNPRLRTGPKYDHTTMQPKAGHFMIVDSGEQLTND	229
	*****	
SCRC1_GH	TARFISPLFEPELSVGACFQFYHYMYGESVGT LKVFVKPMSADLYDLQPVFVQRGNQKNV	289
arabiensis	TARFISPLFEPELSVGACFQFYHYMYGESVGT LKVFVKPMSADLYDLQPVFVQRGNQKNV	289
coluzzii	TARFISPLFEPELSVGACFQFYHYMYGESVGT LKVFVKPMSADLYDLQPVFVQRGNQKNV	300
gambiae	TARFISPLFEPELSVGACFQFYHYMYGESVGT LKVFVKPMSADLYDLQPVFVQRGNQKNV	289
	*****	
SCRC1_GH	WHEGHVEVGQQAERFQV VIEASLG MRYKSDIAIDDV SLLQG DSCRVAVEDGE EPPPAEVE	349
arabiensis	WHEGHVEVGQQAERFQV VIEASLG MRYKSDIAIDDV SLLQG DSCRVAVEDGE EPPPAEVE	349
coluzzii	WHEGHVEVGQQAERFQV VIEASLG MRYKSDIAIDDV SLLQG DSCRVAVEDGE EPPPAEVE	360
gambiae	WHEGHVEVGQQAERFQV VIEASLG MRYKSDIAIDDV SLLQG DSCRVAVEDGE EPPPAEVE	349
	*****	
SCRC1_GH	NVPVKIESCENRCGSSMAAVLNANDTIVHCDCHEDCVTSETCCPDYRERCVFQVAVGGSN	409
arabiensis	NVPVKIESCENRCGSSMAAVLNANDTIVHCDCHEDCVTSETCCPDYRERCVFQVAVGGSN	409
coluzzii	NVPVKIESCENRCGSSMAAVLSANDTIVHCDCHEDCVTSETCCPDYRERCVFQVAVGGSN	420

gambiae	NVPVKIESCENRCGSSMAAVLNANDTIVHCDCHEDCVTSETCCPDYRERCVFQVAVGGSN	409
*****.*****		
SCRC1_GH	VSTTTPVPVPSTSTTVRTTAKAAATTSTRPVTTTSTTVSSTTTTTT-TTTTTTTAKPTT	468
arabiensis	VSTTTPVPVPSTSTTVRTTAKAAATTSTRPVTTTSTTVSSTTTTTT-TTTTTTTAKPTT	468
coluzzii	VSTTTPVPVPSTSTTVRTTAKAAATTSTRPVTTTSTTVSSTTTTTTTTTTTTTTAKPTT	480
gambiae	VSTTTPVPVPSTSTTVRTTAKAAATTSTRPVTTTSTTVSSTTTT---TTTTTTAKPTT	465
*****		
SCRC1_GH	SSATTTSTTTKPSTTSTVSTTTTKYNLRPRPSLVPLTNRQLPPTTTTAAATTRKTTTP	528
arabiensis	SSATTTSTTTKPSTTSTVSTTTTKYNLRPRPSLVPLTNRQLPPTTTTAAATTRKTTTP	528
coluzzii	SSATTTSTTTKPSTTSTVSTTTTKYNLRPRPSLVPLTNRQLPPTTTTAAATTRKTTTP	540
gambiae	SSATTTSTTTKPSTTSTVSTTTTKYNLRPRPSLVPLTNRQLPPTTTTAAATTRKTTTP	525
*****.*****		
SCRC1_GH	TTTATSTAVTTTIPTTTQSDLVAVEQSVPTSTEEVIMPGLAMAPLQPVEKLHSTPSLMKF	588
arabiensis	TTTATSTTVTTTIPTTTQSDLVAVEQSVPTSTEEVIMPGLAMAPLQPVEKLHSTPSLMKF	588
coluzzii	TTTATSTTVTTTIPTTTQSDLVAVEQSVPTSTEEVIMPGLAMAPLQPVEKLHSAPSLMKF	600
gambiae	TTTATSTTVTTTIPTTTQSDLVAVEQSVPTSTEEVIMPGLAMAPLQPVEKLHSAPSLMKF	585
*****.*****.*****		
SCRC1_GH	FVYAISTVVLFACILSAAYLYARRSRSSVLARLKEKSQKSGFEDIRFLAGDEDLDFNITH	648
arabiensis	FVYAISTVVLFACILSAAYLYARRSRSSVLARLKEKSQKSGFEDIRFLAGDEDLDFNITH	648
coluzzii	FVYAISTVVLFACILSAAYLYARRSRSSVLARLKEKSQKSGFEDIRFLAGDEDLDFNISH	660
gambiae	FVYAISTVVLFACILTAAYLYARRSRSSVLARLKEKSQKSGFEDIRFLAGDEDLDFNISH	645
*****.*****.*****		
SCRC1_GH	GRDVEEGEEVLEKEGKEAKAKQETKPSKKDAKADIVRMAKQEDKKNLATHGRGEEDSNT	684
arabiensis	GRDVEEGEEVLEKEGKEAKAKQETKPSKKDAKADIVRMAKQEDKKNLATHGRGEEDSNT	708
coluzzii	GRDVEEGEEVLEKKNGEAKAKQETKSSKKDAKADIVRMAKQEDKKNLATHGRGEEDSNT	720
gambiae	GRDVEEGEEVLEKKNGEAKAKQETKPSKKDAKADIVRMAKQEDKKNLATHGRGEEDSNT	705
*****.*.*****		
SCRC1_GH	DSDASTDDGAGGGGAKRTHGKPNKKAYQKYVKHHDEDMASSLL	752
arabiensis	DSDASTDDGAGGGGAKRTHGKPNKKAYQKYVKHHDEDMASSLL	752
coluzzii	DSDASTDDGAGGGGAKRTHGKPNKKAYQKYVKHHDEDMASSLL	764
gambiae	DSDASTDDGAGGGGAKRTHGKPNKKAYQKYVKHHDEDMASSLL	749
*****		

**Figure S4.** CLUSTAL O (1.2.4) multiple sequence alignment of Ag55 SCRBQ2 (GH) and SCRBQ2 homologues from *A. arabiensis* (XP\_040167338.1), *A. coluzzii* (XP\_040234709.2), and *A. gambiae* (XP\_061510019.1)

BQ2-GH	MCSPCTDFQKKFISLGCSFLILLAITLGVLWPSLSEQLHNKLVIKNGSSNYDNWIRTP	60
<i>gambiae</i>	MCSPCTDFQKKFISLGCSFLILLAITLGVLWPSLSEQLHNKLVIKNGSSNYDNWIRTP	60
<i>arabiensis</i>	MCSPCTDFQKKFISLGCSFLILLAITLGVLWPSLSEQLHNKLVIKNGSSNYDNWIRTP	60
<i>coluzzii</i>	MCSPCTDFQKKFISLGCSFLILLAITLGVLWPSLSEQLHNKLVIKNGSSNYDNWIRTP	60
*****		
BQ2-GH	IPMYLEVYFFNWTNPDDVKTKNGTKPHFVEMGPYTFSEVHERVNLVWVANSTVTYEQRR	120
<i>gambiae</i>	IPMYLEVYFFNWTNPDDVKTKNGTKPHFVEMGPYTFSEVHERVNLVWVANSTVTYEQRR	120
<i>arabiensis</i>	IPMYLEVYFFNWTNPDDVKTKNGTKPHFVEMGPYTFSEVHERVNLVWVANSTVTYEQRR	120
<i>coluzzii</i>	IPMYLEVYFFNWTNPDEVKTKNGTKPHFVEMGPYTFSEVHERVNLVWVANSTVTYEQRR	120
*****		
BQ2-GH	WHFVPELSKGTLDQVTNLNVITLNAAHFLRNTYPLLRPLINIFLKTGSLWKNKPVR-	180
<i>gambiae</i>	WHFVPELSKGTLDQVTNLNVITLNAAHFLRNTYPLLRPLINIFLKTGSLWKNKPVRE	180
<i>arabiensis</i>	WHFVPELSKGTLDQVTNLNVITLNAAHFLRNTYPLLRPLINIFLKTGSLWKNKPVRE	180
<i>coluzzii</i>	WHFVPELSKGTLDQVTNLNVITLNAAHFLRNTYPLLRPLINIFLKTGSLWKNKPVRE	180
*****		
BQ2-GH	LLFEGVKDPLDLLKTKINSTSLNIPFDKFGWFVGRNLSDTFDGFTMRTGADGLESMGFL	240
<i>gambiae</i>	LLFEGVKDPLDLLKTKINSTSLNIPFDKFGWFVGRNLSDTFDGFTMRTGADGLESMGFL	240
<i>arabiensis</i>	LLFEGVKDPLDLLKTKINSTSLNIPFDKFGWFVGRNLSDTFDGFTMRTGADGLESMGFL	240
<i>coluzzii</i>	LLFEGVKDPLDLLKTKINSTSLNIPFDKFGWFVGRNLSDTFDGFTMRTGADGLESMGFL	240
*****		
BQ2-GH	TQWNGSPNTGMYRGKCEVYGTSGELWPASSNPANITLFPSDICRSITLQGREQVSLYN	300
<i>gambiae</i>	TQWNGSPNTGMYRGKCEVYGTSGELWPASSNPANITLFPSDICRSITLQGREQVSLYN	300
<i>arabiensis</i>	TQWNGSPNTGMYRGKCEVYGTSGELWPASSNPANITLFPSDICRSITLQGREQVSLYN	300
<i>coluzzii</i>	TQWNGSPNTGMYRGKCEVYGTSGELWPASSNPANITLFPSDICRSITLQGREQVSLYN	300
*****		
BQ2-GH	IQGTKYVGDDRVFDNGVKYPEASCWCNSNPTQCPGLKPGVFNASACKYGSPTFVSFPHFY	360
<i>gambiae</i>	IQGTKYVGDDRVFDNGVKYPEASCWCNSNPTQCPDLKPGVFNASACKYGSPTFVSFPHFY	360
<i>arabiensis</i>	IQGTKYVGDDRVFDNGVKYPEASCWCNSNPTQCPDLKPGVFNASACKYGSPTFVSFPHFY	360
<i>coluzzii</i>	IQGTKYVGDDRVFDNGVKYPEASCWCNSNPTQCPDLKPGVFNASACKYGSPTFVSFPHFY	360
*****		
BQ2-GH	LADESQYQAVTGLRPNQTEHEFYMAIEPSTGIPLDVRAQLQINEHLQPIKGFsfYEHPD	420
<i>gambiae</i>	LADESQYQAVTGLRPNQTEHEFYMAIEPSTGIPLDVRAQLQINEHLQPIKGFsfYEHPD	420
<i>arabiensis</i>	LADESQYQAVTGLRPNQTEHEFYMAIEPSTGIPLDVRAQLQINEHLQPIKGFsfYEHPD	420

coluzzii	LADESQYQAVTGLRPNQTEHEFYMAIEPSTGIPLDVRAQLQINEHLQPIKGFsfYEHVPD	420
*****		
BQ2-GH	VMVPMIwFRQRATLTQELAEQAKLALALPSLGIYVAVFFGSIGIIMTSVFLFCSIkkWSQ	480
gambiae	VMVPMIwFRQRATLTQELAEQAKLALALPSLGIYVAVFFGSIGIIMTSVFLFCSIkkWSQ	480
arabiensis	VMVPMIwFRQRATLTQELAEQAKLALALPSLGIYVAVFFGSIGIIMTSVFLFCSIkkWSQ	480
coluzzii	VMVPMIwFRQRATLTQELAEQAKLALALPSLGIYVAVFFGSIGIIMTSVFLFCSIkkWSQ	480
*****		
BQ2-GH	SAEVVPYEELQN	492
gambiae	SAEVVPYEELQN	492
arabiensis	SAEVVPYEELQN	492
coluzzii	SAEVVPYEELQN	492
*****		

**Figure S5.** CLUSTAL 2.1 multiple sequence alignment of Ag55 SCRC1 (GH) with *Aedes aegypti* homologues. A BLAST search with Ag55 SCRC1 protein identified XP\_021710624. A second scavenger receptor called AeSC-C (AAEL006361) in *A. aegypti* is reported by Xiao et al. (2014. Plos Pathogens, 10: e1004027) in their study of flavivirus and the role of inducing antimicrobial peptides and control of flavivirus infections.

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AgSCRC1 (GH)      --MLLSRSSKGATLLGGLLWIVFFANLVAGQLTLYGSRAPSMRRPLTRQLVGQCPAPYFP
XP_021710624     MFAHLSEVSILAVALLALEISSTTGLVQYRLTPLRTGGRPMKQPQLKSGP-ECPTPYFP
AeSC-C           ----MNIDRLSQTFIFVVLALVVDISAYDGRYSPVLRNSYSN-----ICPKPEFQ
                  :.      . :   * :   .   : :   . .      ** * *

AgSCRC1          NGEAKIRNRGRMMRFDCAYGFKLVGNRYSNQNGRWDTSIPVCVKSGCSLLAPIESGHVL
XP_021710624     NGVAKPRQRNKMIRFTCASGFTLVGNMYSMCEKGRWDTPIPICIRSGCPDLELVANGQIS
AeSC-C           NGFIRMRLRGKYLRFEFYADFTLVGLPLLLCKNGRWNSQVPICVKPGCSDLSDVNGFIFF
                  **   : * *. : : ** *   .*.***      *::***:: :*:*:*.**.*   : . * :

AgSCRC1          YEMNKASAFLLSCFEGTELAGSRNAYCNGTHWDRPLGICRRTGQATPTACDFETESLCGWS
XP_021710624     YEYGQAAAMLFCSSGYQVAGASKAYCNGTHWDRPLGNCRETGIGVETSCDFEAPDLCGWM
AeSC-C           YNNMKAATLFCDSGYKLAGSMYSYCNGTAWDRSLGSCRRTNWTVAACDFEVSDLCGWE
                  *:   :*: * * * . * :*: : :***** ***.** **.*.   . .:*****. .*****

AgSCRC1          NDALHDFDWKRS DGT LNPRALRTGPKYDHTTMQPKAGHFMI VDSGEQLTNDTARFISPLF
XP_021710624     NEATHDFDWKRS DGIVHPKALKTGPKFDHTTGSALAGHFMMVDSVEQFTNETARLLSPMY
AeSC-C           SEATHRLDWERS SSGDASRRARKTGPTHDHTTGEPLNGHFMMVDSSQANMNETARFISPIY
                  .: * * :*:*:*. *   : * :***.***** ..   ****:*** :   *::*:*:*:*:

AgSCRC1          EPELSVGACFQFYHYMYGESVGT LKVFVKPMSADLYDLQP---VFVQRGNQKNVWHEGHV
XP_021710624     PANYSTNACFSFYHYMYGDGVGTLSVYVRPASQQLD SYSSKDAIFSLKGNQRNVWNEGYF
AeSC-C           STNYSKNACFRLFYHMF GD-AGTLAIYVKPLSVNLREMAKQSAPFSVSGNQGNWIEGCL
                  .: * .*** :*:*:*: :.*** :*: * * : * .      *   *** *. * ** .

AgSCRC1          EVGQQAERFQV VIEASLG MRYKSDIAIDDVSL LQGDSCRVAVEDGEE-----PPPAEV
XP_021710624     DLKQFSEEFQIVIEASLG MKA KSDIAIDDVSL LYGEDCRPMAESEDEEITPEVLPPDVPS
AeSC-C           DLEQQNESFQIVIQASLG MRYKSDVAIDDVQLFGGCNCNSNGTSEEP-----VTES
                  : : *   * **:*:*:*:*: : ***:***. *: * *.   . :   .

AgSCRC1          ENVPVKIESCENRCGSSMAAVLNANDT---IVHCDCHEDCVTSETCCPDYRERCVFQVAV
XP_021710624     DDNIFKLGSCENRCGVNVSSVVTIPDTSVNFVQCDCFE GCVDSKTCCPDYAERCVFNETA
AeSC-C           DDDMFQIDSCVGRCGQDVSDSSDV GERS--MIHCGCNND CNEDNTCCPDYVELCVPDE--
                  : :   . : : ** .*** . : :   :   :*: * . : * .:***** * ** :

AgSCRC1          GGSNVSTTTVPVPSTSTTVRTTTAKAAATTSTRPVTTTSTTVSSTTTTTTTTTTTT--TT
XP_021710624     FAASTISTSTKILPSTTETTRPTTTPTTSTTTTIRT TQPTTKPTTPTKPTTSTRPTT

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AeSC-C -----

AgSCRC1 AKPTTSSATTTRSTTTKPSTTSTVSTTTTKKYNLRPRPSLVPLTNRQLPPTTTPAATTR  
XP\_021710624 PRSTSTTAVQTSSSTTIKTTLKPKVPTTTTTKSYNLRPRNITTSSTTTKPMLLPMVRTR  
AeSC-C ----STAADGYEDQFKFPVTPKPIGSNSCKAMEFMG-----  
          :::\*      .  .      \*  ..  ..:  .  .

AgSCRC1 KTTTPTTTATSTTVTTTIPTTTQSDLVAVEQSVPTTEEVIMPLAMAPLQPVEKLHSTP  
XP\_021710624 RPTTSTTTTTST-----PTTEEVVLKLVARFGDVSSEFPAS-----VLEYGDNKP  
AeSC-C -----

AgSCRC1 SLMKFFVYAISTVVLFACILSAAAYLYARR-SRSSVLARLKEKSQKS-----GFEDIRFL  
XP\_021710624 NLARVFLFSGIGVVSFGCVILLIVLHIRRNSGENVLNRLKQKSMKSKLGSNEGFEVDVRL  
AeSC-C ----IFLIILSIIMAMICFSQTSRSQISSMFRKIRPNRVDDAFGMA-----EDVQYL  
          .\*:          :::  \*  .                  .      \*:::      :          \*\*:::\*

AgSCRC1 AGDEDLDFNITHGRDVEEGEEVLEKEGKGEAKAKQETKPSKKDAKADIVRMAKQEDKKNL  
XP\_021710624 AADEHLDFSLPD-----DEVEEAVEGGDGNNDAEQKPSKKGKK-----  
AeSC-C AVN-----DTISNFGDNGSVASMRLP-----  
\*  :                  :.  .      ....      \*

AgSCRC1 ATHGRGEEDSNTDSDASTDDDGAGGGGAKRTHGKPNKKAYQKYVKHHDEDMASLL  
XP\_021710624 -----  
AeSC-C -----