Supplementary Data 3 - Protein accession numbers, oligonucleotide primers, DNA and amino-acid sequences of serum albumin-antibody fusion proteins (SA-scFv)

Fusion protein (code name)	Construct for expression
^{N}SA-CK138^{C} (SA138)	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK138-(Gly_4Ser)-His_6
^{N}SA-CK157^{C} (SA157)	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK157-(Gly_4Ser)-His_6
^{N}SA-CK129^{C} (SA129)	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK129-(Gly_4Ser)-His_6
^{N}SA-CK138-ds1^{C} (SA138-ds1)	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK138-ds1 ($V_L100^{Q>C}$ / $V_H44^{G>C}$)-(Gly_4Ser)-His_6
^{N}SA-CK138-ds2^{C} (SA138-ds2)	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK138-ds2 ($V_L43^{A>C}$ / $V_H105^{Q>C}$)-(Gly_4Ser)-His_6
^{N}SA-CK157-ds1^{C} (SA157-ds1)	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK157-ds1 ($V_L100^{Q>C}$ / $V_H44^{E>C}$)-(Gly_4Ser)-His_6
^{N}SA-CK157-ds2^{C} (SA157-ds2)	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK157-ds2 ($V_L43^{A>C}$ / $V_H105^{Q>C}$)-(Gly_4Ser)-His_6
^{N}SA-CK157-VL^{C} (SA157-VL)	gWiz-LS-mouse SA-(Gly_4Ser)-V_L CK157-His_6
^{N}SA-CK157-VH^{C} (SA157-VH)	gWiz-LS-mouse SA-(Gly_4Ser)-V_H CK157-His_6
^{N}SA-CK129-ds1^{C} (SA129-ds1)	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK129-ds1 ($V_L100^{Q>C}$ / $V_H44^{G>C}$)-(Gly_4Ser)-His_6
^{N}SA-CK129-ds2^{C} (SA129-ds2)	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK129-ds2 ($V_L43^{A>C}$ / $V_H105^{Q>C}$)-(Gly_4Ser)-His_6
^{N}SA-sm3e-ds^{C} (SA^{CTR})	gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_H-V_L) sm3E-ds ($V_H44^{R>C}$ / $V_L100^{G>C}$)-(Gly_4Ser)-His_6

Primer name	Primer sequence (5' to 3')
Forward-linker-His_6-gWiz	5′-GGAGGGGGCGGTTCCC-3′
Reverse-LS-SA-linker-gWiz	5′-CGACCCTCCGCCTCCGC-3′
Forward-SA138 (scFv)	5′-GGAGGCGGAGGGTCGGCTAGCGCTATCCAGATGACCC-3′
Reverse-SA138 (scFv)	5′-GGAACCGCCCCCTCCCGAGGAGACGGTGACCAGG-3′
Forward-SA157 (scFv)	5′-GGAGGCGGAGGGTCGGCCAGCGATATCCAGATGACCCAGTC-3′
Reverse-SA157 (scFv)	5′-GGAACCGCCCCCTCCCGAGGAGACGGTGACCAGGG-3′
Forward-SA129 (scFv)	5′-GGAGGCGGAGGGTCGGCTAGCGATATCCAGATGACCCAG-3′
Reverse-SA129 (scFv)	5′-GGAACCGCCCCCTCCCGAGGAGACGGTGACCAGG-3′
Forward-Mut-SA138-ds1 (V_L100)	5′-CTGATCACGTTCGGATGCGGTACCAAGGTGGAGATCAAAGGTACTACTGC-3′
Reverse-Mut-SA138-ds1 (V_L100)	5′-TCCGAACGTGATCAGAGAATAAGAAGATTGCTGAC-3′
Forward-Mut-SA138-ds1 (V_H44)	5′-CAGGCCCCGGGTAAGTGCCTGGAATGGGTTGCATACATTGCTTCTTAC-3′
Reverse-Mut-SA138-ds1 (V_H44)	5′-CTTACCCGGGGCCTGACG-3′
Forward-Mut-SA138-ds2 (V_L43)	5′-CAGAAACCAGGAAAATGCCCGAAGCTTCTGATTTACGGTGCATCC-3′
Reverse-Mut-SA138-ds2 (V_L43)	5′-TTTTCCTGGTTTCTGTTGATACCAGGCTGC-3′
Forward-Mut-SA138-ds2 (V_H105)	5′-ATGAACTACTGGGGTTGCGGAGCCCTGGTCACCGTC-3′
Reverse-Mut-SA138-ds2 (V_H105)	5′-ACCCCAGTAGTTCATACCAGCAGAGAAC-3′
Forward-Mut-SA157-ds1 (V_L100)	5′-CTGATCACGTTCGGATGCGGTACCGAGGTGGAGATCAAAGGTACTACTGC -3′

Reverse-Mut-SA157-ds1 (V_L100)	5′-TCCGAACGTGATCAGATGAGACGGTTGC-3′
Forward-Mut-SA157-ds1 (V_H44)	5′-CAGGCCCCGGGTGAGTGCCTGGAATGGGTTGCATCTATTGGTTCTTACCCTG-3′
Reverse-Mut-SA157-ds1 (V_H44)	5′-CTCACCCGGGGCCTGAC-3′
Forward-Mut-SA157-ds2 (V_L43)	5′-CAGAAACCAGGAAAATGCCCGAAGCTTCTGATTTACTCTGCATCC-3′
Reverse-Mut-SA157-ds2 (V_L43)	5′-TTTTCCTGGTTTCTGTTGATACCAGGCTAC-3′
Forward-Mut-SA157-ds2 (V_H105)	5′-ACTGACTACTGGGGTTGCGGAACCCTGGTCACCGTCTCC-3′
Reverse-Mut-SA157-ds2 (V_H105)	5′-ACCCCAGTAGTCAGTAGCATCGTACC-3′
Forward-SA157 (V_L)	5′-GGAGGCGGAGGGTCGGCCAGCGATATCCAGATGACCCAGTC-3′
Reverse-SA157 (V_L)	5′-GGAACCGCCCCCTCCTTTGATCTCCACCTCGGTACCCTGTC-3′
Forward-SA157 (V_H)	5′-GGAGGCGGAGGGTCGGCCGAGGTTCAGCTGGTGG-3′
Reverse-SA157 (V_H)	5′-GGAACCGCCCCCTCCCGAGGAGACGGTGACCAGGG-3′
Forward-Mut-SA129-ds1 (V_L100)	5′-CTGATCACGTTCGGATGCGGTACCAAGGTGGAGATCGAAGGTACTACTG-3′
Reverse-Mut-SA129-ds1 (V_L100)	5′-TCCGAACGTGATCAGAGCATGACCTC-3′
Forward-Mut-SA129-ds1 (V_H44)	5′-CAGGCCCCGGGTAAGTGCCTGGAATGGGTTGCATCTATTTACCC-3′
Reverse-Mut-SA129-ds1 (V_H44)	5′-CTTACCCGGGGCCTGACG-3′
Forward-Mut-SA129-ds2 (V_L43)	5′-CAGAAACCAGGAAAATGCCCGAAGCTTCTGATTTACGGTGCATCC-3′
Reverse-Mut-SA129-ds2 (V_L43)	5′-TTTTCCTGGTTTCTGTTGATACCAGGCTAC-3′
Forward-Mut-SA129-ds2 (V_H105)	5′-TTGGACTACTGGGGTTGCGGAACCCTGGTCACCGTCTCC-3′

Reverse-Mut-SA129-ds2 (V_H105)	5′-ACCCCAGTAGTCCAAAGCGAAGTAAGAG-3′
Forward-SA^{CTR} (scFv)	5′-GGAGGCGGAGGGTCGGCTAGCCAAGTTAAACTGGAACAGTCCGGTGC-3′
Reverse-SA^{CTR} (scFv)	5′-GGAACCGCCCCCTCCCTTGATTTCCAACTTCGTTCCACACCC-3′

Sequences of genes coding for antibody single-chain variable fragments (scFv) fused to the C-terminus of mouse serum albumin (SA): ^{N}SA-scFv^{C}

DNA sequences of genes are provided. Start and stop codons are shown in black bold. The sequences include the secretory leader peptide (LS, in grey underlined), the mouse serum albumin (SA, in grey), a long flexible $(Gly_4Ser)_3$ linker (in black italic and underlined), the antibody single-chain variable fragment (scFv, in blue bold), a short flexible (Gly_4Ser) linker (in black italic and underlined) and the hexa-histidine tag (His_6, in red bold). Cysteine residues introduced to form stabilizing intermolecular disulfide bridges (ds1 and ds2) are shown in in orange italic bold.

gWiz-LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK138-(Gly_4Ser)-His_6

ATGGACATGAGAGTGCCTGCTCAGCTGCTGGGCCTGCTGCTGCTGTGGCTGCCTGGTGCTAGATGCGAAGCACACAAGAGTGAGATCGCCCATCGGTATAA
TGATTTGGGAGAACAACATTTCAAAGGCCTAGTCCTGATTGCCTTTTCCCAGTATCTCCAGAAATGCTCATACGATGAGCATGCCAAATTAGTGCAGGAAG
TAACAGACTTTGCAAAGACGTGTGTTGCCGATGAGTCTGCCGCCAACTGTGACAAATCCCTTCACACTCTTTTTGGAGATAAGTTGTGTGCCATTCCAAAC
CTCCGTGAAAACTATGGTGAACTGGCTGACTGCTGTACAAAACAAGAGCCCGAAAGAAACGAATGTTTCCTGCAACACAAAGATGACAACCCCAGCCTACC
ACCATTTGAAAGGCCAGAGGCTGAGGCCATGTGCACCTCCTTTAAGGAAAACCCAACCACCTTTATGGGACACTATTTGCATGAAGTTGCCAGAAGACATC
CTTATTTCTATGCCCCAGAACTTCTTTACTATGCTGAGCAGTACAATGAGATTCTGACCCAGTGTTGTGCAGAGGCTGACAAGGAAAGCTGCCTGACCCCG
AAGCTTGATGGTGTGAAGGAGAAAGCATTGGTCTCATCTGTCCGTCAGAGAATGAAGTGCTCCAGTATGCAGAAGTTTGGAGAGAGAGCTTTTAAAGCATG
GGCAGTAGCTCGTCTGAGCCAGACATTCCCCAATGCTGACTTTGCAGAAATCACCAAATTGGCAACAGACCTGACCAAAGTCAACAAGGAGTGCTGCCATG
GTGACCTGCTGGAATGCGCAGATGACAGGGCGGAACTTGCCAAGTACATGTGTGAAAACCAGGCGACTATCTCCAGCAAACTGCAGACTTGCTGCGATAAA
CCACTGTTGAAGAAAGCCCACTGTCTTAGTGAGGTGGAGCATGACACCATGCCTGCTGATCTGCCTGCCATTGCTGCTGATTTTGTTGAGGACCAGGAAGT
GTGCAAGAACTATGCTGAGGCCAAGGATGTCTTCCTGGGCACGTTCTTGTATGAATATTCAAGAAGACACCCTGATTACTCTGTATCCCTGTTGCTGAGAC
TTGCTAAGAAATATGAAGCCACTCTGGAAAAGTGCTGCGCTGAAGCCAATCCTCCCGCATGCTACGGCACAGTGCTTGCTGAATTTCAGCCTCTTGTAGAA
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TCAGGTGTCAACCCCAACTCTCGTGGAGGCTGCAAGAAACCTAGGAAGAGTGGGCACCAAGTGTTGTACACTTCCTGAAGATCAGAGACTGCCTTGTGTGG
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AGGCGGCCATGCTTCTCTGCTCTGACAGTTGATGAAACATATGTCCCCAAAGAGTTTAAAGCTGAGACCTTCACCTTCCACTCTGATATCTGCACACTTCC
AGAGAAGGAGAAGCAGATTAAGAAACAAACGGCTCTTGCTGAGCTGGTGAAGCACAAGCCCAAGGCTACAGCGGAGCAACTGAAGACTGTCATGGATGACT
TTGCACAGTTCCTGGATACATGTTGCAAGGCTGCTGACAAGGACACCTGCTTCTCGACTGAGGGTCCAAACCTTGTCACTAGATGCAAAGACGCCTTAGCC
*GGTGGAGGAGGCTCTGGTGGAGGCGGTAGCGGAGGCGGAGGGTCG*GCTATCCAGATGACCCGGTCCCCGAGCTCCCTGTCCGCCTCTGTGGGCGATAGGGT
CACCATCACCTGCCGTGCCAGTCAGTACCACGACGGTTCTGCAGCCTGGTATCAACAGAAACCAGGAAAAGCTCCGAAGCTTCTGATTTACGGTGCATCCT

ACCTCTACTCTGGAGTCCCTTCCCGCTTCTCTGGTAGCCGTTCCGGGACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCGGAAGACTTCGCAACTTAT
TACTGTCAGCAATCTTCTTATTCTCTGATCACGTTCGGACAGGGTACCAAGGTGGAGATCAAAGGTACTACTGCCGCTAGTGGTAGTAGTGGTGGCAGTAG
CAGTGGTGCCGAGGTTCAGCTGGTGGAGTCTGACGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTTCAACCTCTCTT
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CTCTGGTTACAGTTACTCTCCGTATTATTCTTGGTTCTCTGCTGGTATGAACTACTGGGGTCAAGGAGCCCTGGTCACCGTCTCCTCG*GGAGGGGGCGGTT*
*CC***CACCATCACCACCATCAC****TGATAG**

gWiz-LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V_L-V_H) CK157-(Gly$_4$Ser)-His$_6$

ATGGACATGAGAGTGCCTGCTCAGCTGCTGGGCCTGCTGCTGCTGTGGCTGCCTGGTGCTAGATGCGAAGCACACAAGAGTGAGATCGCCCATCGGTATAA
TGATTTGGGAGAACAACATTTCAAAGGCCTAGTCCTGATTGCCTTTTCCCAGTATCTCCAGAAATGCTCATACGATGAGCATGCCAAATTAGTGCAGGAAG
TAACAGACTTTGCAAAGACGTGTGTTGCCGATGAGTCTGCCGCCAACTGTGACAAATCCCTTCACACTCTTTTTGGAGATAAGTTGTGTGCCATTCCAAAC
CTCCGTGAAAACTATGGTGAACTGGCTGACTGCTGTACAAAACAAGAGCCCGAAAGAAACGAATGTTTCCTGCAACACAAAGATGACAACCCCAGCCTACC
ACCATTTGAAAGGCCAGAGGCTGAGGCCATGTGCACCTCCTTTAAGGAAAACCCAACCACCTTTATGGGACACTATTTGCATGAAGTTGCCAGAAGACATC
CTTATTTCTATGCCCCAGAACTTCTTTACTATGCTGAGCAGTACAATGAGATTCTGACCCAGTGTTGTGCAGAGGCTGACAAGGAAAGCTGCCTGACCCCG
AAGCTTGATGGTGTGAAGGAGAAAGCATTGGTCTCATCTGTCCGTCAGAGAATGAAGTGCTCCAGTATGCAGAAGTTTGGAGAGAGAGCTTTTAAAGCATG
GGCAGTAGCTCGTCTGAGCCAGACATTCCCCAATGCTGACTTTGCAGAAATCACCAAATTGGCAACAGACCTGACCAAAGTCAACAAGGAGTGCTGCCATG
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AGAGAAGGAGAAGCAGATTAAGAAACAAACGGCTCTTGCTGAGCTGGTGAAGCACAAGCCCAAGGCTACAGCGGAGCAACTGAAGACTGTCATGGATGACT
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*GGTGGAGGAGGCTCTGGTGGAGGCGGTAGCGGAGGCGGAGGGTCG***GATATCCAGATGACCCAGTCCCCGAGCTCCCTGTCCGCCTCTGTGGGCGATAGGGT**
CACCATCACCTGCCGTGCCAGTCAGTCTTACGGTGGTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCCCCGAAGCTTCTGATTTACTCTGCATCCTACC
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TGTCAGCAACCATCTCATCTGATCACGTTCGGACAGGGTACCGAGGTGGAGATCAAAGGTACTACTGCCGCTAGTGGTAGTAGTGGTGGCAGTAGCAGTGG
TGCCGAGGTTCAGCTGGTGGAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTCCAACCCCTACTACTACG
GTGGTACGCACTGGGTGCGTCAGGCCCCGGGTGAGGAGCTGGAATGGGTTGCATCTATTGGTTCTTACCCTGGCTACACTGACTATGCCGATAGCGTCAAG
GGCCGTTTCACTATAAGCGCAGACACATCCAAAAACACAGCCTACCTACAAATGAACAGCTTAAGAGCTGAGGACACTGCCGTCTATTATTGTGCTCGCCA

TTACTACTGGTACGATGCTACTGACTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCG*GGAGGGGGCGGTTCC***CACCATCACCACCATCAC****TGATAG***

gWiz-LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK129-(Gly$_4$Ser)-His$_6$

ATGGACATGAGAGTGCCTGCTCAGCTGCTGGGCCTGCTGCTGCTGTGGCTGCCTGGTGCTAGATGCGAAGCACACAAGAGTGAGATCGCCCATCGGTATAA
TGATTTGGGAGAACAACATTTCAAAGGCCTAGTCCTGATTGCCTTTTCCCAGTATCTCCAGAAATGCTCATACGATGAGCATGCCAAATTAGTGCAGGAAG
TAACAGACTTTGCAAAGACGTGTGTTGCCGATGAGTCTGCCGCCAACTGTGACAAATCCCTTCACACTCTTTTTGGAGATAAGTTGTGTGCCATTCCAAAC
CTCCGTGAAAACTATGGTGAACTGGCTGACTGCTGTACAAAACAAGAGCCCGAAAGAAACGAATGTTTCCTGCAACACAAAGATGACAACCCCAGCCTACC
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GGCAGTAGCTCGTCTGAGCCAGACATTCCCCAATGCTGACTTTGCAGAAATCACCAAATTGGCAACAGACCTGACCAAAGTCAACAAGGAGTGCTGCCATG
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*GGTGGAGGAGGCTCTGGTGGAGGCGGTAGCGGAGGCGGAGGGTCG***GCTAGCGATATCCAGATGACCCAGTCCCCGAGCCCCCTGTCCGCCTCTGTGGGCGA**
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TATTACTGTCAGCGAGGTCATGCTCTGATCACGTTCGGACAGGGTACCAAGGTGGAGATCGAAGGTACTACTGCCGCTAGTGGTAGTAGTGGTGGCAGTAG
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CTTACGGTTCTATGCACTGGGTGCGTCAGGCCCCGGGTAAGGGCCTGGAATGGGTTGCATCTATTTACCCTTACTCTAGCTCTACTTACTATGCCGATAGC
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ATCACCACCATCAC**TGATAG**

gWiz-LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK138-ds1 (V$_L$100$^{Q>C}$ / V$_H$44$^{G>C}$)-(Gly$_4$Ser)-His$_6$

ATGGACATGAGAGTGCCTGCTCAGCTGCTGGGCCTGCTGCTGCTGTGGCTGCCTGGTGCTAGATGCGAAGCACACAAGAGTGAGATCGCCCATCGGTATAA

TGATTTGGGAGAACAACATTTCAAAGGCCTAGTCCTGATTGCCTTTTCCCAGTATCTCCAGAAATGCTCATACGATGAGCATGCCAAATTAGTGCAGGAAG
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CTCCGTGAAAACTATGGTGAACTGGCTGACTGCTGTACAAAACAAGAGCCCGAAAGAAACGAATGTTTCCTGCAACACAAAGATGACAACCCCAGCCTACC
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TCAGGTGTCAACCCCAACTCTCGTGGAGGCTGCAAGAAACCTAGGAAGAGTGGGCACCAAGTGTTGTACACTTCCTGAAGATCAGAGACTGCCTTGTGTGG
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AGGCGGCCATGCTTCTCTGCTCTGACAGTTGATGAAACATATGTCCCCAAAGAGTTTAAAGCTGAGACCTTCACCTTCCACTCTGATATCTGCACACTTCC
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*GGTGGAGGAGGCTCTGGTGGAGGCGGTAGCGGAGGCGGAGGGTCG*GCTATCCAGATGACCCGGTCCCCGAGCTCCCTGTCCGCCTCTGTGGGCGATAGGGT
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ACCTCTACTCTGGAGTCCCTTCCCGCTTCTCTGGTAGCCGTTCCGGGACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCGGAAGACTTCGCAACTTAT
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CAGTGGTGCCGAGGTTCAGCTGGTGGAGTCTGACGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTTCAACCTCTCTT
ACTACGGTATGCACTGGGTGCGTCAGGCCCCGGGTAAG*T*GCCTGGAATGGGTTGCATACATTGCTTCTTACCCTGGCTACACTTCTTATGCCGATAGCGTC
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*CC*CACCATCACCACCATCACTGATAG

gWiz-LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V_L-V_H) CK138-ds2 ($V_L43^{A>C}$ / $V_H105^{Q>C}$)-(Gly$_4$Ser)-His$_6$

ATGGACATGAGAGTGCCTGCTCAGCTGCTGGGCCTGCTGCTGCTGTGGCTGCCTGGTGCTAGATGCGAAGCACACAAGAGTGAGATCGCCCATCGGTATAA
TGATTTGGGAGAACAACATTTCAAAGGCCTAGTCCTGATTGCCTTTTCCCAGTATCTCCAGAAATGCTCATACGATGAGCATGCCAAATTAGTGCAGGAAG
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ACCATTTGAAAGGCCAGAGGCTGAGGCCATGTGCACCTCCTTTAAGGAAAACCCAACCACCTTTATGGGACACTATTTGCATGAAGTTGCCAGAAGACATC
CTTATTTCTATGCCCCAGAACTTCTTTACTATGCTGAGCAGTACAATGAGATTCTGACCCAGTGTTGTGCAGAGGCTGACAAGGAAAGCTGCCTGACCCCG

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gWiz-LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V_L-V_H) CK157-ds1 ($V_L100^{Q>C}$ / $V_H44^{E>C}$)-(Gly$_4$Ser)-His$_6$

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gWiz-LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V_L-V_H) CK157-ds2 ($V_L43^{A>C}$ / $V_H105^{Q>C}$)-(Gly$_4$Ser)-His$_6$

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gWiz-LS-mouse SA-(Gly$_4$Ser)-V$_L$ CK157-His$_6$

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gWiz-LS-mouse SA-(Gly$_4$Ser)-V_H CK157-His$_6$

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gWiz-LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V_L-V_H) CK129-ds1 ($V_L100^{Q>C}$ / $V_H44^{G>C}$)-(Gly$_4$Ser)-His$_6$

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gWiz-LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK129-ds2 (V$_L$43$^{A>C}$ / V$_H$105$^{Q>C}$)-(Gly$_4$Ser)-His$_6$

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TCTACTCTGGAGTCCCTTCTCGCTTCTCTGGTGGCCGTTCCGGGACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCGGAAGACTTCGCAACTTATTAC
TGTCAGCGAGGTCATGCTCTGATCACGTTCGGACAGGGTACCAAGGTGGAGATCGAAGGTACTACTGCCGCTAGTGGTAGTAGTGGTGGCAGTAGCAGTGG
TGCCGAGGTTCAGCTGGTGGAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTATCCTGTGCAGCTTCTGGCTTCAACATCTCTTCTTACG
GTTCTATGCACTGGGTGCGTCAGGCCCCGGGTAAGGGCCTGGAATGGGTTGCATCTATTTACCCTTACTCTAGCTCTACTTACTATGCCGATAGCGTCAAG
GGCCGTTTCACTATAAGCGCAGACACATCCAAAAACACAGCCTACCTACAAATGAACAGCTTAAGAGCTGAGGACACTGCCGTCTATTATTGTGCTCGTGG
TTACGGTCCGTGGTACGCTTACTCTTACTTCGCTTTGGACTACTGGGGT*TGC*GGAACCCTGGTCACCGTCTCCTCG*GGAGGGGGCGGTTCC*CACCATCACC
ACCATCACTGATAG

gWiz-LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V_H-V_L) sm3E-ds ($V_H44^{R>G}$ / $V_L100^{G>C}$)-(Gly$_4$Ser)-His$_6$

ATGGACATGAGAGTGCCTGCTCAGCTGCTGGGCCTGCTGCTGCTGTGGCTGCCTGGTGCTAGATGCGAAGCACACAAGAGTGAGATCGCCCATCGGTATAA
TGATTTGGGAGAACAACATTTCAAAGGCCTAGTCCTGATTGCCTTTTCCCAGTATCTCCAGAAATGCTCATACGATGAGCATGCCAAATTAGTGCAGGAAG
TAACAGACTTTGCAAAGACGTGTGTTGCCGATGAGTCTGCCGCCAACTGTGACAAATCCCTTCACACTCTTTTTGGAGATAAGTTGTGTGCCATTCCAAAC
CTCCGTGAAAACTATGGTGAACTGGCTGACTGCTGTACAAAACAAGAGCCCGAAAGAAACGAATGTTTCCTGCAACACAAAGATGACAACCCCAGCCTACC
ACCATTTGAAAGGCCAGAGGCTGAGGCCATGTGCACCTCCTTTAAGGAAAACCCAACCACCTTTATGGGACACTATTTGCATGAAGTTGCCAGAAGACATC
CTTATTTCTATGCCCCAGAACTTCTTTACTATGCTGAGCAGTACAATGAGATTCTGACCCAGTGTTGTGCAGAGGCTGACAAGGAAAGCTGCCTGACCCCG
AAGCTTGATGGTGTGAAGGAGAAAGCATTGGTCTCATCTGTCCGTCAGAGAATGAAGTGCTCCAGTATGCAGAAGTTTGGAGAGAGAGCTTTTAAAGCATG
GGCAGTAGCTCGTCTGAGCCAGACATTCCCCAATGCTGACTTTGCAGAAATCACCAAATTGGCAACAGACCTGACCAAAGTCAACAAGGAGTGCTGCCATG
GTGACCTGCTGGAATGCGCAGATGACAGGGCGGAACTTGCCAAGTACATGTGTGAAAACCAGGCGACTATCTCCAGCAAACTGCAGACTTGCTGCGATAAA
CCACTGTTGAAGAAAGCCCACTGTCTTAGTGAGGTGGAGCATGACACCATGCCTGCTGATCTGCCTGCCATTGCTGCTGATTTTGTTGAGGACCAGGAAGT
GTGCAAGAACTATGCTGAGGCCAAGGATGTCTTCCTGGGCACGTTCTTGTATGAATATTCAAGAAGACACCCTGATTACTCTGTATCCCTGTTGCTGAGAC
TTGCTAAGAAATATGAAGCCACTCTGGAAAAGTGCTGCGCTGAAGCCAATCCTCCCGCATGCTACGGCACAGTGCTTGCTGAATTTCAGCCTCTTGTAGAA
GAGCCTAAGAACTTGGTCAAAACCAACTGTGATCTTTACGAGAAGCTTGGAGAATATGGATTCCAAAATGCCATTCTAGTTCGCTACACCCAGAAAGCACC
TCAGGTGTCAACCCCAACTCTCGTGGAGGCTGCAAGAAACCTAGGAAGAGTGGGCACCAAGTGTTGTACACTTCCTGAAGATCAGAGACTGCCTTGTGTGG
AAGACTATCTGTCTGCAATCCTGAACCGTGTGTGTCTGCTGCATGAGAAGACCCCAGTGAGTGAGCATGTTACCAAGTGCTGTAGTGGATCCCTGGTGGAA
AGGCGGCCATGCTTCTCTGCTCTGACAGTTGATGAAACATATGTCCCCAAAGAGTTTAAAGCTGAGACCTTCACCTTCCACTCTGATATCTGCACACTTCC
AGAGAAGGAGAAGCAGATTAAGAAACAAACGGCTCTTGCTGAGCTGGTGAAGCACAAGCCCAAGGCTACAGCGGAGCAACTGAAGACTGTCATGGATGACT
TTGCACAGTTCCTGGATACATGTTGCAAGGCTGCTGACAAGGACACCTGCTTCTCGACTGAGGGTCCAAACCTTGTCACTAGATGCAAAGACGCCTTAGCC

*GGTGGAGGAGGCTCTGGTGGAGGCGGTAGCGGAGGCGGAGGGTCG*CAAGTTAAACTGGAACAGTCCGGTGCTGAAGTTGTCAAACCAGGTGCTTCCGTGAA
GTTGTCCTGTAAAGCCTCTGGTTTTAACATCAAGGATTCGTATATGCATTGGTTGAGACAAGGGCCAGGACAA*TGT*TTGGAATGGATTGGCTGGATTGATC
CAGAGAATGGTGATACCGAGTACGCTCCTAAATTTCAGGGAAAGGCTACTTTTACTACCGACACTTCCGCTAATACCGCATACTTGGGCTTATCTTCCTTG
AGACCAGAGGACACTGCCGTATACTACTGCAACGAAGGGACACCAACTGGTCCTTACTATTTCGACTACTGGGGACAAGGTACCTTAGTTACTGTCTCTAG
CGGTGGCGGAGGTTCAGGCGGTGGAGGGTCTGGAGGTGGCGGTAGTGAAAATGTGCTGACCCAATCTCCAAGCTCCATGTCTGTTTCTGTTGGCGATAGAG
TAACCATCGCTTGTAGCGCATCCTCTAGTGTCCCATATATGCACTGGCTTCAACAGAAGCCAGGTAAAAGCCCAAAGTTGTTGATTTATTTGACATCCAAC
TTGGCTTCTGGAGTGCCTTCAAGGTTTTCTGGTTCCGGCTCAGGAACCGATTATAGTTTGACTATTAGCTCAGTGCAGCCAGAGGATGCTGCAACCTACTA
TTGCCAGCAAAGGTCCTCATATCCACTGACTTTCGGG*TGT*GGAACGAAGTTGGAAATCAAG*GGAGGGGGCGGTTCC*CACCATCACCACCATCACTGATAG

Amino-acid sequences of antibody single-chain variable fragments (scFv) fused to the C-terminus of mouse serum albumin (SA): ^{N}SA-scFv^{C}

Amino acid sequences of translated polypeptides are shown. The sequences include the secretory leader peptide (LS, in grey underlined), the mouse serum albumin (SA, in grey), a long flexible $(Gly_4Ser)_3$ linker (in black italic and underlined), the antibody single-chain variable fragment (scFv, in blue bold), a short flexible (Gly_4Ser) linker (in black italic and underlined) and the hexa-histidine tag (His_6, in red bold). Cysteine residues introduced to form stabilizing intermolecular disulfide bridges (ds1 and ds2) are shown in in orange italic bold.

LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK138-(Gly_4Ser)-His_6

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA
*GGGGSGGGGSGGGGS*AS**AIQMTRSPSSLSASVGDRVTITCRASQYHDGSAAWYQQKPGKAPKLLIYGASYLYSGVPSRFSGSRSGTDFTLTISSLQPEDFA**
TYYCQQSSYSLITFGQGTKVEIKGTTAASGSSGGSSSGAEVQLVESDGGLVQPGGSLRLSCAASGFNLSYYGMHWVRQAPGKGLEWVAYIASYPGYTSYAD
SVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSGYSYSPYYSWFSAGMNYWGQGALVTVSS*GGGGS***HHHHHH**--

LS-mouse SA-$(Gly_4Ser)_3$-scFv (V_L-V_H) CK157-(Gly_4Ser)-His_6

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA
*GGGGSGGGGSGGGGS*AS**DIQMTQSPSSLSASVGDRVTITCRASQSYGGVAWYQQKPGKAPKLLIYSASYLYSGVPSRFSGSRSGTDFTLTISSLQPEDFAT**

YYCQQPSHLITFGQGTEVEIKGTTAASGSSGGSSSGAEVQLVESGGGLVQPGGSLRLSCAASGSNPYYYGGTHWVRQAPGEELEWVASIGSYPGYTDYADS
VKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARHYYWYDATDYWGQGTLVTVSS*GGGGS***HHHHHH**--

LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK129-(Gly$_4$Ser)-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA
*GGGGSGGGGSGGGGS*AS**DIQMTQSPSPLSASVGDRVTITCRASQYGGYVAWYQQKPGKAPKLLIYGASLLYSGVPSRFSGGRSGTDFTLTISSLQPEDFAT**
YYCQRGHALITFGQGTKVEIEGTTAASGSSGGSSSGAEVQLVESGGGLVQPGGSLRLSCAASGFNISSYGSMHWVRQAPGKGLEWVASIYPYSSSTYYADS
VKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGYGPWYAYSYFALDYWGQGTLVTVSS*GGGGS***HHHHHH**--

LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK138-ds1 (V$_L$100$^{Q>C}$ / V$_H$44$^{G>C}$)-(Gly$_4$Ser)-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA
*GGGGSGGGGSGGGGS*AS**AIQMTRSPSSLSASVGDRVTITCRASQYHDGSAAWYQQKPGKAPKLLIYGASYLYSGVPSRFSGSRSGTDFTLTISSLQPEDFA**
TYYCQQSSYSLITFG*C*GTKVEIKGTTAASGSSGGSSSGAEVQLVESDGGLVQPGGSLRLSCAASGFNLSYYGMHWVRQAPGK*C*LEWVAYIASYPGYTSYAD
SVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSGYSYSPYYSWFSAGMNYWGQGALVTVSS*GGGGS***HHHHHH**--

LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK138-ds2 (V$_L$43$^{A>C}$ / V$_H$105$^{Q>C}$)-(Gly$_4$Ser)-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA

GGGGSGGGGSGGGGSASAIQMTRSPSSLSASVGDRVTITCRASQYHDGSAAWYQQKPGKCPKLLIYGASYLYSGVPSRFSGSRSGTDFTLTISSLQPEDFA
TYYCQQSSYSLITFGQGTKVEIKGTTAASGSSGGSSSGAEVQLVESDGGLVQPGGSLRLSCAASGFNLSYYGMHWVRQAPGKGLEWVAYIASYPGYTSYAD
SVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSGYSYSPYYSWFSAGMNYWGCGALVTVSSGGGGSHHHHHH--

LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK157-ds1 (V$_L$100$^{Q>C}$ / V$_H$44$^{E>C}$)-(Gly$_4$Ser)-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA
GGGGSGGGGSGGGGSASDIQMTQSPSSLSASVGDRVTITCRASQSYGGVAWYQQKPGKAPKLLIYSASYLYSGVPSRFSGSRSGTDFTLTISSLQPEDFAT
YYCQQPSHLITFGCGTEVEIKGTTAASGSSGGSSSGAEVQLVESGGGLVQPGGSLRLSCAASGSNPYYYGGTHWVRQAPGECLEWVASIGSYPGYTDYADS
VKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARHYYWYDATDYWGQGTLVTVSSGGGGSHHHHHH--

LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK157-ds2 (V$_L$43$^{A>C}$ / V$_H$105$^{Q>C}$)-(Gly$_4$Ser)-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA
GGGGSGGGGSGGGGSASDIQMTQSPSSLSASVGDRVTITCRASQSYGGVAWYQQKPGKCPKLLIYSASYLYSGVPSRFSGSRSGTDFTLTISSLQPEDFAT
YYCQQPSHLITFGQGTEVEIKGTTAASGSSGGSSSGAEVQLVESGGGLVQPGGSLRLSCAASGSNPYYYGGTHWVRQAPGEELEWVASIGSYPGYTDYADS
VKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARHYYWYDATDYWGCGTLVTVSSGGGGSHHHHHH--

LS-mouse SA-(Gly$_4$Ser)-V$_L$ CK157-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE

RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA
*GGGGSGGGGSGGGGS*ASDIQMTQSPSSLSASVGDRVTITCRASQSYGGVAWYQQKPGKAPKLLIYSASYLYSGVPSRFSGSRSGTDFTLTISSLQPEDFAT
YYCQQPSHLITFGQGTEVEIK*GGGGS*HHHHHH--

LS-mouse SA-(Gly$_4$Ser)-V$_H$ CK157-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA
*GGGGSGGGGSGGGGS*ASAEVQLVESGGGLVQPGGSLRLSCAASGSNPYYYGGTHWVRQAPGEELEWVASIGSYPGYTDYADSVKGRFTISADTSKNTAYLQ
MNSLRAEDTAVYYCARHYYWYDATDYWGQGTLVTVSS*GGGGS*HHHHHH--

LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK129-ds1 (V$_L$100$^{Q>C}$ / V$_H$44$^{G>C}$)-(Gly$_4$Ser)-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA
*GGGGSGGGGSGGGGS*ASDIQMTQSPSPLSASVGDRVTITCRASQYGGYVAWYQQKPGKAPKLLIYGASLLYSGVPSRFSGGRSGTDFTLTISSLQPEDFAT
YYCQRGHALITFG*C*GTKVEIEGTTAASGSSGGSSSGAEVQLVESGGGLVQPGGSLRLSCAASGFNISSYGSMHWVRQAPGK*C*LEWVASIYPYSSSTYYADS
VKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGYGPWYAYSYFALDYWGQGTLVTVSS*GGGGS*HHHHHH--

LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V$_L$-V$_H$) CK129-ds2 (V$_L$43$^{A>C}$ / V$_H$105$^{Q>C}$)-(Gly$_4$Ser)-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
PLLKKAHCLSEVEHDTMPADLPAIAADFVEDQEVCKNYAEAKDVFLGTFLYEYSRRHPDYSVSLLLRLAKKYEATLEKCCAEANPPACYGTVLAEFQPLVE
EPKNLVKTNCDLYEKLGEYGFQNAILVRYTQKAPQVSTPTLVEAARNLGRVGTKCCTLPEDQRLPCVEDYLSAILNRVCLLHEKTPVSEHVTKCCSGSLVE
RRPCFSALTVDETYVPKEFKAETFTFHSDICTLPEKEKQIKKQTALAELVKHKPKATAEQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA

GGGGSGGGGSGGGGSASDIQMTQSPSPLSASVGDRVTITCRASQYGGYVAWYQQKPGKCPKLLIYGASLLYSGVPSRFSGGRSGTDFTLTISSLQPEDFAT
YYCQRGHALITFGQGTKVEIEGTTAASGSSGGSSSGAEVQLVESGGGLVQPGGSLRLSCAASGFNISSYGSMHWVRQAPGKGLEWVASIYPYSSSTYYADS
VKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGYGPWYAYSYFALDYWGCGTLVTVSSGGGGSHHHHHH--

LS-mouse SA-(Gly$_4$Ser)$_3$-scFv (V_H-V_L) sm3E-ds ($V_H44^{R>C}$ / $V_L100^{G>C}$)-(Gly$_4$Ser)-His$_6$

MDMRVPAQLLGLLLLWLPGARCEAHKSEIAHRYNDLGEQHFKGLVLIAFSQYLQKCSYDEHAKLVQEVTDFAKTCVADESAANCDKSLHTLFGDKLCAIPN
LRENYGELADCCTKQEPERNECFLQHKDDNPSLPPFERPEAEAMCTSFKENPTTFMGHYLHEVARRHPYFYAPELLYYAEQYNEILTQCCAEADKESCLTP
KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTKVNKECCHGDLLECADDRAELAKYMCENQATISSKLQTCCDK
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SNLASGVPSRFSGSGSGTDYSLTISSVQPEDAATYYCQQRSSYPLTFGCGTKLEIKGGGGSHHHHHH--