

A

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mSAA1 1: ATGAAGCTACTCACCAGCCTGGTCTTCTGCTCCCTGCTCCTGGGAGTCTGCCATGGAGGGGTTTTTTTCAT 70
mSAA2 1: ..... 70
mSAA3 1: ..... CTTC.. TTGC. A. CA. TC. T.. AT. T.. A..... TGA. AGCCA. A. A. GGG. CCAG. 70

mSAA1 71: TTGTTACAGAGGCTTTCCAAGGGGCTGGGGACATGTGGCGAGCCTACACTGACATGAAGGAAGCTAACTG 140
mSAA2 71: ..A..GGG.....A..... 140
mSAA3 71: .CA.GA.A.A...GGT.....T..A.A.....T.....A..... 140

mSAA1 141: GAAAAACTCAGACAAATACTTCCATGCTCGGGGAACTATGATGCTGCTCAAAGGGGTCCCGGGGAGTC 210
mSAA2 141: ....G.TGG.....C..... 210
mSAA3 141: .....C.GG.....C. 210

mSAA1 211: TGGGCTGCTGAGAAAATCAGTGATGGAAGAGAGGCCTTTCAGGAATTCTTCGGCAGAGGACATGAGGACA 280
mSAA2 211: .....C.....AG.....C..... 280
mSAA3 211: .....A.AGTC.....C....CC.....TG.....A.G...ACG..ACAT...GCA.....T 280

mSAA1 281: CCATTGCTGACCAGGAAGCCAACAGACATGGCCGAGTGGCAAAGACCCCAATTACTACAGACCTCTGG 350
mSAA2 281: ....G..... 350
mSAA3 281: .A.GA.....TTT.....TGAGTGG.....G.....CC...T.C....G.... 350

mSAA1 351: ACTGCCTGACAAATACTGA 369
mSAA2 351: .....C..... 369
mSAA3 351: C.....A.A.G..... 369
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B

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mSAA1 1: MKLLTSLVFCSLLLGVCHGGGFFSFVHEAFQAGDMWRAYTDMKEANWKNSDKYFHARGNYDAAQRGPGGV 70
mSAA2 1: .....IG.....G..DG..... 70
mSAA3 1: .. PSIAIIL. I. I... DSQRWVQ.MK..G..SR.....S...K.....R.....A 70

mSAA1 71: WAAEKISDGREAFQEFFGRGHEDTIADQEANRHGRSGKDPNYYRPPGLPKY 122
mSAA2 71: .....A..S.....M.....A.. 122
mSAA3 71: ...KV...A...V.K.T.H.A..SR...F..EW.....HF..A...KR. 122
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Supplemental Fig. S1. Alignment of nucleotide and amino acid sequences of murine SAA1, SAA2 and SAA3. (A) Alignment of nucleotide sequences of murine SAA1 (BC087933), SAA2 (M11130) and SAA3 (NM011315). (B) Alignment of amino acid sequences of murine SAA1, SAA2 and SAA3. Recombinant murine SAA1 (rSAA1) and SAA3 (rSAA3) were constructed from amino acids 20 to 122, excluding signal sequences. Signal sequence regions are shown in bold (nucleotides 1 to 57 and amino acids 1 to 19). Consensus nucleotides and amino acids are shown by dots.