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                         17          33  35 37 38
humART      1 MSSFEGQMAEYPTISIDRF-DRENLRA-RAYFLSHCHKDHMKGLRAPTLKRRLECSLKVY 58
muART       1 MSSFQGQMAEYPTISIDRF-DRENLKA-RAYFLSHCHKDHMKGLRAPSLKRRLECSLKVF 58
ratART      1 MSSFQGQMEEYPTISIDRF-DRENLKA-RAYFLSHCHKDHMKGLRAPSMKRRLECSLKVF 58
humSNM1   699 TCPFYKKIPG-TGFTVDAF-QYGVVEGCTAYFLTHFHSDHYAGLSKH-FTF----P---- 748
muSNM1    682 TCPFYKRIPG-TGFTVDAF-QYGEIEGCTAYFLTHFHSDHYAGLSKD-FTR----P---- 730
humSNM1B    1 MNGVL--IPH-TPIAVD-FWSLRRAGTARLFFLSHMSDHTVGLSST-WAR----P---- 47
muSNM1B     1 MNGVV--IPQ-TPIAVD-FWSLRRAGSARLFFLTHMHCDHTVGLSST-WAR----P---- 47
scSNM1              229 VVDGF 233     246 LSHFHSDHYI 255
smL1                72 LLDGG 76      103 LSHAHADHAG 112
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                                                                    115
humART     59 LYCSPVTKELLLTSPKYRFWKKRIISIEIETPTQISL-VDEASGEKEEIVVTLLPAGHCP 117
muART      59 LYCSPVTKELLLTSPKYRFWENRIITIEIETPTQISL-VDEASGEKEEVVVTLLPAGHCP 117
ratART     59 LYCSPVTKELLLTSPKYKFWENRIIAIEIETPTQVSL-VDEASGEKEEVVVTLLPAGHCP 117
humSNM1   749 VYCSEITGN-LLKN-KLHVQEQYIHPLPL--DTEC-I-VNGV---K--V-V-LLDANHCP 795
muSNM1    731 VYCSEITGN-LLKK-KLRVQEQYIRQLPM--DTEC-V-VDSV---K--V-V-FVDANHCP 778
humSNM1B   48 LYCSPITAH-LLHR-HLQVSKQWIQALEVG-ESHV-LPLDEIG--QETMVTLLDANHCP 101
muSNM1B    48 LYCSPITAC-LLHR-RLQVSKHWIRALEVG-ESHV-LPLDEIG--QETMVTLIDANHCP 101
scSNM1                                                        316 ANHCP 320
smL1                                                          179 AGHTP 183
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                           136                          165
humART    118 GSVMFLFQGNNGT-VLYTGDFRLAQGEAARMELLHSGGRVKDIQSVYLDTTFCDPRFYQI 176
muART     118 GSVMFLFQGSNGT-VLYTGDFRLAKGEASRMELLHSGGRVKDIQSVYLDTTFCDPRFYQI 176
ratART    118 GSVMFLFQGSNGT-VLYTGDFRLAKGEVSRMELLHSGGRVKDIQSVYLDTTFCDPRFYQI 176
humSNM1   796 GAVMILFYLPNGTVILHTGDFRAD-PSMER-SLLA-D---QKVHMLYLDTTYCSPEY-TF 848
muSNM1    779 GATMILFQLPNGAVILHTGDFRAD-PSMER-SRLA-G---RKVHTLFLDTTYCSPEY-TF 831
humSNM1B  102 GSVMFLFEGYFGT-ILYTGDFRYT-PSMLKEPALTLG---KQIHTLYLDNTNCNPAL-VL 155
muSNM1B   102 GSVMFLFEGYFGT-ILYTGDFRYT-PSMLKEPALILG---KQIHTLYLDNTNCNPAL-VL 155
scSNM1             345 TGDFR 349              374 YLDTT 378
smL1               203 YADSL 207
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humART    177 PSREECLS-GV-LELVRSWITRSPYHVVWLNCKAAYGYEYLFTN--L-SEE-L----GVQ 226
muART     177 PSREQCLR-GI-LELVRSWVTRSPHHVVWLNCKAAYGYEYLFTN--L-SEE-L----GVQ 226
ratART    177 PSREECLR-GV-LELVRSWITRSPKHVVWLNCKAAYGYEYLFTN--L-SEE-L----GVQ 226
humSNM1   849 PSQQEVIRFAINTAFEAV--TLNPHALV-V-C-GTYSIG-K-EKVFLAIADVLGSKVGMS 901
muSNM1    832 PSQQEVIQFAINTAFEAV--TLNPRALV-V-C-GTYCIG-K-EKVFLAIADVLGSKVGMS 884
humSNM1B  156 PSRQEAAH-QI-VQLIR---KHPQHNIK-I---GLYSLG-K-ES--L-LEQ-L----AL- 195
muSNM1B   156 PSRQEASQ-QI-VQLIR---QFPQHNIK-I---GLYSLG-K-ES--L-LEQ-L----AL- 195
scSNM1
smL1
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humART    227 VH-VNKLDMFRNMPEILHHLTT-DR-NTQIHACRHPKAEEYFQ-WS-KLP-CGITSRNRI 280
muART     227 VH-VDKLDMFKNMPDILHHLTT-DR-NTQIHACRHPKAEECFQ-WN-KLP-CGITSQNKT 280
ratART    227 VH-VDKLDMFKNMPDILHHLTT-DR-NTQIHACRHPKAEEYFQ-WN-KLP-CGMASKTKT 280
humSNM1   902 QEKYKTLQCL-NIPE-INSLITTDMCSSLVHLLPMMQ-IN-FKGLQSHLKKCG--GKYNQ 955
muSNM1    885 QEKYKTLQCL-NIPE-VSSLITTDMCDSLVHLLPMMQ-IN-FKGLQSHLKKCG--GKYDQ 938
humSNM1B  196 -E-FQTWVVL-SPRR-LE-LV--QL-LGLADVFTVEEKAGRIHAVD-HMEIC----H-SN 241
muSNM1B   196 -E-FRTWVVL-SPQR-LE-LV--QL-LGLADVFTVEEEAGRIHAVD-HTEIC----H-SA 241
scSNM1
smL1
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                                                   319
humART    281 PLHIISIKPSTMW-FGERSRKT-NVI--VRT-GESSYRACFSFHSSYSEIKDFLSYLCPV 335
muART     281 ALHTISIKPSTMW-FGERTRKT-NVI--VRT-GESSYRACFSFHSSFSEIKDFLSYICPV 335
ratART    281 VLHTISIKPSTMW-FGERTRKT-NVI--VRT-GESSYRACFSFHSSYSEIKDFLSYICPV 335
humSNM1   956 ILA---FRPTG-WTHSNKFTRIADVIPQTKG-NISIYGIPYSEHSSYLEMKRFVQWLKPQ 1010
muSNM1    939 ILA---FRPTG-WTHSNNITSTADIIPQTRG-NISIYGIPYSEHSSYLEMKRFVQWLKPQ 993
humSNM1B  242 ML-----R----WNQTHPTIAILPTSRKIHSSHPDIHVIPYSDHSSYSELRAFVAALKPC 292
muSNM1B   242 ML-----Q----WNQSHPTIAIFPTSRKVRSPHPSIYTVPYSDHSSYSELRAFVAALRPC 292
scSNM1                                          609 SEHSS 613
smL1                                           244 TPHPG 248
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humART    336 NAYPNVI--PVGT-TMDKVVEILKP-LCRSSQSTEPKYK 370
muART     336 NVYPNVI--PVGL-TVDKVMDVLKP-LCRSPQ-SVPKYK 370
ratART    336 NAYPNVI--PIGL-TVDKVMDFLKP-LCRSSQCAEPKYK 370
humSNM1  1011 KIIPTVN---VGT-WKSR-ST-MEK-YFREWK-LEAGY- 1040
muSNM1    994 KIIPTVN---VGS-FRSR-NT-MEK-YFKEWR-LEAGY- 1023
humSNM1B  293 QVVPIVSRRPCGG-FQDSLSPRISVPLIPD-S-VQQ-Y- 326
muSNM1B   293 QVVPIVHQKPCGEFFQDSLSPRLAMPLIPH-S-VQQ-Y- 327
scSNM1
smL1
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Figure Sup_1. The Human ARTEMIS Protein

Conserved Residues in the Metallo-β-lactamase/β-CASP Domain of ARTEMIS and Related Proteins. GenBank accession numbers of the sequences used were NM_022487 for human (hum) ARTEMIS, BAC34960 for murine (mu) ARTEMIS, AAM89124 for rat ARTEMIS, NM_014881 for human SNM1, AAF64472 for murine SNM1, NM_022836 for human SNM1B, BAC33550 for murine SNM1B, P30620 for yeast (sc) SNM1 and AJ251815 for *Stenotrophomonas maltophilia* (sm) L1. Highly conserved residues chosen for mutagenesis are indicated by black boxes. The numbering of mutagenized amino acids refers to positions in the human ARTEMIS protein (also see Callebaut et al. 2002).