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Ag APN1 : MVRLL-LLVSLGLCCLLAS--ADRPPYKSSGIYEEEPQL-PGASDLSGGVASDEIGVAPAQA--VD-----ERYRLPTTSIPIHYDLHLRT :   80
Hs APN  : MAKGFYISKSLGILGILLGVAAVCTIIALSVVYSQEKNKNANSSPVASTTPSASATTNPASATTLDQSKAWNRYRLPNTLKPDSYRVTLRP :   91

Ag APN1 : EIHRNER---TFTGTVGIQLQVVQATDKLVMHNRGLVMSSAKVS-SLPNGVTGA-PTLIGDVQYSTDTTFEHITFTSPTILQPGTYLLEVA :  166
Hs APN  : YLTPNDRGLYVFKGSSTVRFTCKEATDVIIIHSKKLNYTLSQGHRVVLRGVGGSQPPDIDKTELVEPTEY-LVVHLKGSLVKDSQYEMDSE :  181

Ag APN1 : FQGRLATNDDGFYVSSYVADNGERRYLATTQFESTSARMAFPCYDEPGLKATFTVSITHSLSYKAISNM-PQKTTTDIETD--MRTTFFEK :  254
Hs APN  : FEGELADDLAGFYRSEYMEGN-VRKVVATTQMQAADARKSFPCFDEPAMKAEFNITLIHPKDLTALSNMLPKGPSTPLPEDPNWNVTEFHT :  271

Ag APN1 : TPAMSTYLLAFVVSDFQLRLSG-----AQRVYVRPNAFN--EATFALEAGVKILKVLDDHLGIPYDTYMPKLDQIAIPDFAAGAMENWGLV :  338
Hs APN  : TPKMSTYLLAFIVSEFDYVEKQASNGVLIRIWARPSAIAAGHGDYALNVTGPILNFFAGHYDTPY--PLPKSDQIGLPDFNAGAMENWGLV :  360

Ag APN1 : TYREQALLFNPAVSTYRGKTNVATTIAHEYAHQWFGNLVSPEWWEYIWLNEGFATLYEFYALDMAYPGQEYWELFNQQVIQYAMGQDGQAS :  429
Hs APN  : TYRENSLLFDPLSSSSSNKERVVTVIAHELAHQWFGNLVTIEWWNDLWLNEGFASYVEYLGADYAEPTWNLKDLMVLNDVYRVMAVDALAS :  451

Ag APN1 : TRPMNWN---AATPGEISALFDRVAYDKSGSVLNMMRHVLGDDNWKAGLKAYLTDRALQGAVDEQLYAGLQSAIEGKGVLPNGVTVAQIMR :  517
Hs APN  : SHPLSTPASEINTPAQISELFDAISYSKGASVLRMLSSFLSEDVFKQGLASYLHTFAYQNTIYLNLWDHLQEAVNNRSIQ-LPTTVRDIMN :  541

Ag APN1 : TWTNEAGYPVLNVRRSYDTGDVIISQERFYNDRK------VPNTNIWMIPYNYVHQAKADFNEFDDFQWLATKAARIETTVPANEWIVFNK :  602
Hs APN  : RWTLQMGFPVITVD----TSTGTLSQEHFLLDPDSNVTRPSEFNYVWIVPITSIRDGR----QQQDYWLIDVRAQNDLFSTSGNEWVLLNL :  624

Ag APN1 : QQVGYYRVNYDEHNWELITNALHENWASIHRLNRAQLIDDAYWLARSGRLDLRVALRFMTYLRNEREYAPWTAANVALTYFNNRLRGTAEY :  693
Hs APN  : NVTGYYRVNYDEENWRKIQTQLQRDHSAIPVINRAQIINDAFNLASAHKVPVTLALNNTLFLIEERQYMPWEAALSSLSYFKLMFDRSEVY :  715

Ag APN1 : HNFLIFVDALIEDIYSLLTI---DAVSPDDTLLHKY-LVQTISTWACSMGYTDCLMKTAALLKAEAS-GTGPAVHPDIASVTYCYGMRSAL :  779
Hs APN  : GPMKNYLKKQVTPLFIHFRNNTNNWREIPENLMDQYSEVNAIST-ACSNGVPECEEMVSGLFKQWMENPNNNPIHPNLRSTVYCNAIAQGG :  805

Ag APN1 : ESEFQYLYRKMMNSKNLAERTMLIDSLGCSNNKEFLKAFLTTALGSGTGVEINYRADERRRVVQAIYSGGRTGVDALIEFLMDPALVNEFV :  870
Hs APN  : EEEWDFAWEQFRNATLVNEADKLRAALACSKELWILNRYLSYTLNPDL----IRKQDATST------------IISITNNVIGQGLVWDFV :  880

Ag APN1 : S------------TLSTSTLNSALSAIASRTN---NVEEMNKLNALITALGSRVNSQTAANLRTTAQANLDWVNGFEGLMLSNFLAEFAA :  945
Hs APN  : QSNWKKLFNDYGGGSFSFSNLIQAVTRRFSTEYELQQLEQFKKDN-EETGFGSGTRALEQALE--KTKANIKWVKENKEVVLQWFTE---- :  964

Ag APN1 : ETLLTTTAAPETTTVTAGPTTTTTTPSSAVTTTTGPTSVTTTVVQTTTEEDDGAATIGLSIAALLVSITVHLLMG : 1020
Hs APN  : ------------------------------------------------------------------------NSK :  967
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Figure S3. Pairwise sequence alignment of full-length *Anopheles gambiae* APN1 (AGAP004809) and human alanyl (membrane) amino peptidase (NP_001141.2). The N-terminal 135 amino acid recombinant AnAPN1 protein fragment is underlined in black, the signal peptide is underlined in gray, and conserved amino acids are shaded in black. The alignment was performed using the proba_pair alignment algorithm on the T-Coffee (25) web-based server (www.tcoffee.org [1]) and edited with GeneDoc (http://www.nrbsc.org/gfx/genedoc/) and Adobe Illustrator.

References

1. **Notredame, C., D. G. Higgins, and J. Heringa**. 2000. T-Coffee: A novel method for fast and accurate multiple sequence alignment. J. Mol. Biol. **302:**205-217. Doi:10.1006/jmbi.2000.4042.