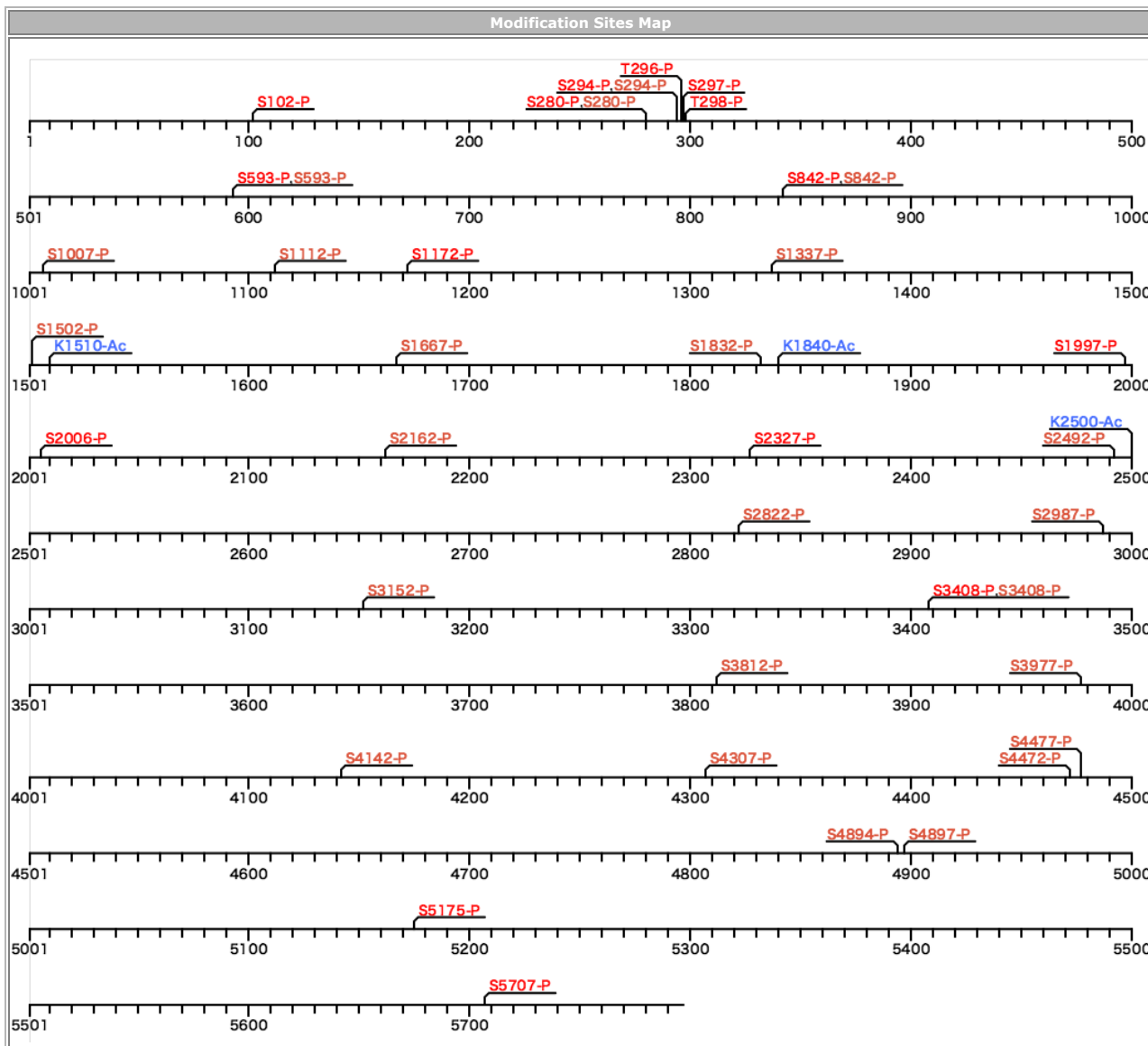


ID	Accession	GeneName	Chr.No.	Description
AHNM2_HUMAN	Q8IVF2	AHNAK2	14q32.33	105403581..105444694
				Protein AHNAK2



Click a modification site to display information in detail.

Site no	Amino acid	Type	Division	Detail
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**Protein Sequence**

MCDCFHMVLP TWPGTGPSVS GRQLQPGEPE AETEDDHSVT EGPADGIRP RPQGSSPVYE YTTEAADFGL QEDAPGRQGS AGRRRSWWKR DSGDSRTRFFR MSRPEAVQE  
 A TEVTLKTEVE AGASGYSVTG GGDQGIQFVKQ VLKDSAAKL FNLREGDQLL STTVFFENIK YEDALKIQY SEPYKVQFKI RRQLPAPQDE EWASSDAQHG PQGKEKEDTD V  
 ADGCRETPT KTLLEGDGDQE RLISKPRVGR GRQSQRERLS WPKFQSIKSK RGPQPQRSHS SSEAYEPRDA HDVSPITSTDT EAQLTVERQE QKAGPGSQRR RKFNLNLRFT GS  
 GQGPSSTG QPGRGFQSGV GRAGVLEELG PWGDSLEETG AATGSRREER AEQDREVMPA QSMPLTELG DPRLCEGTPQ EGGLRAARLH GKTLEGQAQE TAVARQKPRP Q  
 PTPGMSREG EGEGQLSLEI GIARLSLRDT TEGGTQIGPP EIRVRVHDLK TPKFAFSTEK EPERERRLST PQRGKRQDAS SKAGTGLKGE EVEGAGWMPG REPTTHAEAQ GDE  
 GDGEEGL QRTRITEEQD KGREDTEGQI RMPKFKIPSL GWSPSKHTKT GREKATEDTE QGREGEATAT ADRREQRTE EGLKDKEDSD SMTNNTTIQL IHDEKRLKKE QILTE  
 KEVAT KDSKFKMPKF KMPLFGASAP GKSMEASVDV SAPKVEADVS LLSMQGDLKT TDLSVQTPSA DLEVQDQVD VKLPEGLPE GASLKGHLPK VQRPSLKMMPK VDLKGP  
 KLDL KGPKAETAP DVKMSLSSME VDVQAPRAKL DGARLEGDLS LADKEVTAKD SKFKMPKFKM PSFGVSAPGK SMEDSDVSA PKVEADVLSL SMQGDLLKATD LSIQPP  
 SADL EVQAGQVDVK LPEGPVPEGA GPKVHLPKVE MPSFKMPKVD LKGPQIDVKG PKLDLKGPKA EVTAPDGEVS LPSMEVDVQA QKAKLDGAWL EGDLSLADKD VTAKDS  
 KFKM PKFKMPSFGV SAPGKSIALK VDVSAPKVEA DLSLPSMQGD LKTTDLSIQP ASTDLKQVAD QVDVLPKPEGH LPEGAGLKGH LPKVEMPSFK MPKVALKGPQ VDVKGPK  
 LDL KSPKAEVTAP DVEVSLPSVE VDVEAPGAKL DSARLEGELS LADKDVTAKE SRFKMPKFKM PSFGASAPGK SIEASVDVSA PKVEADVSLP SMQGDLLKATD LSIQPPSADL  
 EVHAGQVDVK LLEGHVPEGA GFKGHLPKVQ MPSLKMMPKVD LKGPQVEVRG PKLDLKGPKA EVTAHEVAVS LPSVEVDMQA PGAKLDGAQL DGDLSLADKD VTAKDSKFKM  
 PKFKMPSFGV SAPGKSIEAS VDLSAPKVEA DMSLPSMQGD LKTTDLSIQP PSTDLELQAG QLDVLPKPEGH VPEGAGLKGH LPKQMPSPK VPKVLDLKGPE IDIKGPKLDL KDP  
 KVEVTAP DVEVSLPSVE VDVEAPGAKL DGGRLLEDMS LADKDLTKD SKFKMPKFKM PSFGVSAPGK SIEASVDVSA PKVEADVSLP SMQGDLLKATD LSIQPPSADL EVQA  
 GQVDVK LPEGPVPEGA GLKGHLPKVD MPSFKMPKVD LKGPQIDVKG PKLDLKGPKA EVTAPDVEVS LPSMEVDVQA QKAKLDGARL EGDLSLADKD MTAKDSKFKM PKFKMPS  
 MPFGV SAPGKSIEAS VDVEAPKVEA DVSLPSMQGD LKTTDLSIQS PSADLQVQAG QVNVKLPKPEGH LPEGAGLKGH LPKQMPSPK MPKVALKGPQ MDVKGPKLDL KGPKA  
 EVMAP DVEVSLPSVE VDVEAPGAKL DSVRLEGDLS LADKDVTAKE SRFKMPKFKM PSFGVSAPGK SIEASVDVSA PKVEADVSLP SMQGDLLKATD LCIPLSADL VVQAGQV  
 DMK LPEGPVPEGA GLKGHLPKVD MPSFKMPKVD LKGPQIDVKG PKLDLKGPKA EVTAPDVEVS LPSMEVDVQA QKAKLDGARL EGDLSLADKD MTAKDSKFKM PKFKMPS  
 FGV SAPGRSIEAS VDVPAPKVEA DVSLPSMQGD LKTTDLSIQP PSADLQVQAG QVDVLPKPEGH VPEGAGLKGH LPKVEMPSLK MPKVALKGPQ VDIKGPKLDL KDPKVMR  
 VP DVEVSLPSME VDVQAPRAKL DSAHLQGDLT LANKDLTKD SKFKMPKFKM PSFGVSAPGK SIEASVDVSP PKVEADVSLP SMQGDLLKATD LSIQPLSADV KVQAGQVDV  
 K LLEGVPVEEV GLKGHLPKLV MPSFKMPKVD LKGPQIDVKG PKLDLKGPKA EVTAPDVEVS LPSMEVDVQA QKAKLDGARL EGDMSLADKD VTAKDSKFKM PKFKMPSFGV S

ALGKSIEAS ADVSALKVEA DVSLPSMQGD LKTTDLSVQP PSADLEVQAG QVDVKLPEGP VPEGAGLKGH LPKLQMPSEK MPKVDLKGQP IDVKGPKLKL KGPKTDMAP DV  
 EVSQPSVE VDVEAPGAKL DGAWLEGDLS VADKDVTTKD SRFKIPKFKM P<sup>S</sup>FGVSAPG<sup>K</sup> SIEASVDVSA PKVEADGSL SSMQGD<sup>L</sup>KATD LSIQPPSADL EVQAGQVDVK LPE  
 GVPVEGA GLKGHLPKVQ MPSEKMPKEMD LKGPQDVKG PKLDLKGPKA EVTAPDVEVS LSSMEVDVQA PRAKLDGARL EGDLSLADKG VTAKDSKFKM PKFKMPSFRV SAP  
 GESIEAL VDVSELKVEA DMSLPSMQGD LKTTDISIQP PSAQLEVQAG QVDVKLPEGH VPEGAGLKGH LPKLQMPSEK MPEVDLKGQP IDVKGPNVDL KGPKEVETAP DVKM  
 SLSSME VDVQAPRAKL DGARLEGDLS LADKGMTAKD SKFKMPKFKM P<sup>S</sup>FGVSAPGK SIEASVDVSE LKVEADGSFP SMQGD<sup>L</sup>KTTD IRIQPPSAQL EVQAGQVDVK LPEGH  
 VPEGA GLKGHLPKVQ MPSEKMPKVD LKGPQIDVKG PKLDLKGPKA EVTAPDVEVS LPSVEVDVQA PRAKLDGARL EGDLSLADKG VTAKDSKFKM PKFKMPSFRV SAPGKSI  
 EVS VDVSAKVEA EVSLPSMQGD LKTTDISIEP PSAQLEVQAG QVDVKLPEGH VPEGAGLKGH LPKLQMPSEK MPKVDLKGQP IDVKGPKLKL KGPKTDTVAP DVEVSQPG  
 ME VDVEAPGAKL DGARLEGDLS LADKDVTAKE SKFKMPKFKM P<sup>S</sup>FGVSAPGK SIEVLVDVSA PKVEADLSLP SMQGD<sup>L</sup>KNTD ISIEPPSAQL EVQAGQVDVK LPEGHVLEG  
 A GLKGHLPKLQ MPSEKMPKVD RKGQPIDIKG PKLDLKGPKM DVTAPDVEVS QPSMEVDVQA PGAKLDGARL EGDLSLADKG VTAKDSKFKM PKFKMPSYRA SAPGKSIQAS  
 VDVSAKVEA DVSLPSMQGD LKTTDLSIQL PSVDLEVQAG QVDVKLPEGH VPEGAGLKGH LPKVEMPSFK MPKVDLKG<sup>S</sup>PQ VDIKGP<sup>L</sup>KLKL KVPKAEVETVP DVEVSLPSVE VD  
 VQAPRAKL DGARLEGDLS LAEKDVTAKE SKFKMPKFKM P<sup>S</sup>FGVSAPGR SIEASLDVSA PKVEADVSL SSMQGD<sup>L</sup>KATD LSIQPPSADL EVQAVQVDVE LLEGVPEGA GLKG  
 HLPKVE MPSLTKPKVD LKGPQIDVKG PKLDLKGPKA EVRVPDVEVS LPSVEVDVQA PKAKLDAGRL EGDLSLADKG VTAKDSKFKM PKFKMPSFRV SAPGKSMEAS VDVSA  
 PKVEA DVSLPSMQGD LKTTDLSIQL PSADLVQAG QMDVKLPEGP VPEGAGLKEH LPKVEMPSLK MPKVDLKGQP VDIKGP<sup>L</sup>KLKL KVSKEVETAP DVEVSLPSVE VDVQAP  
 RAKL DSAQLEGDLS LADKDVTAKE SKFKMPKFKM P<sup>S</sup>FGVSAPGK SIEASVHVA PKVEADVSL SSMQGD<sup>L</sup>KTTD LSIQPHSADL TVQARQVDMK LLEGHVPEEA GLKGHL  
 KVQ MPSEKMPKVD LKGPEIDIKG PKLDLKDPKV EVTAPDVEVS LPSVEVDVQA PGAKLDGARL EGDLSLADKG VTAKDSKFKM PKFKMPS<sup>S</sup>FGV SAPGKSMEAS VDVTA  
 EA DVSLPSMQGD LKATDLSVQP PSADLEVQAG QVDVKLPEGP VPEGASLKGH LPKVQMPSEK MPKVDLKGQP IDVKGPKLKL KGPKEVETAP DVKMSLSSME VDVQAPRA  
 KL DGVQLEGDLS LADKDVTAKE SKFKMPKFKM P<sup>S</sup>FGVSAPGK SIEASVDVSE LKAKADVSL SSMQGD<sup>L</sup>KTTD LSIQSPSADL EVQAGQVDVK LPEGLPKGA GLKGHLPKV  
 Q MPCLKMPKVA LKGPQVDVKG PKLDLKGPKA DVMTPVVEVS LPSMEVDVQA PGAKLDSVRL EGDLSLADKG VTAKDSKFKM PKFKMPS<sup>S</sup>FGV SAPGKSIEAS LDVSAKVEA  
 DVSLPSMQGD LKTTLSIQL PSADLEVQAG QEDVKLPEGP VHEGAGLKGH LPKLQMPSEK VPKVDLKGQP IDVNVPKLKL KGPKEVETSP NLDVSLPSME VDIQAPGAKL DS  
 TRLEGDLS LADKDVTAKE SKFKMPKFKM P<sup>S</sup>FGML<sup>S</sup>PGK SIEVSDVSA PKMEADMSIP SSMQGD<sup>L</sup>KTTD LRIQAPSADL EVQAGQVDVK LPEGHMPEVA GLKGHLPKVE MPS  
 FKMPKVD LKGPQVDVKG PKLDLKGPKA EVMAPDVEVS LPSVETDVQA PGSMLD<sup>G</sup>ARL EGDLSLAHED VAGKDSK<sup>F</sup>QG PKLSTSGFEW SSKKVMSSS EIEGNVTFHE KTS  
 TFPIVES VVHEGDLHDP SRDGNLGLAV GEVGMDSKFK KLHFKVPKVS FSSTKTPKDS LVPGAKSSIG LSTIPLSSSE CSSFELQQVS ACSEPSMQMP KVGFAFPSS RDLT  
 PHFE SSILSPCEDV TLTKYQVTVP RAALAPELAL EIPSGSQADI PLPTECSTD LQPPEGVPTS QAESHSGPLN SMIPVSLGQV SFPKFKPKF VFSVPQMAVP EGD<sup>L</sup>HAAVGA  
 PVM<sup>S</sup>PL<sup>S</sup>PGE RVQCPLPSTQ LPSPGTCSVQ GPEELVASLQ TSVVAPGEAP SEDADHEGKG SPLKMPKIKL PSFRWSPKKE TGPKVDPECS VEDSKLSLVL DKDEVAPQSA IH  
 MDLPPERD GEKGRSTKPG FAMPKALPK MKASKGVSL QRDVDPSSL SATAGGSFQD TEKASSDGR GGLGATASAT GSEGVNLHRP QVHIPSGLGFA KPDLRSSKAK VE  
 VSQPEADL PLPKHDLSTE GDSRGCGLGD VPVSQPCGEG IAPTPEPLQ PSCRKPAEV LTV<sup>S</sup>PEEEA MTKYSQESWF KMPKFRMPSL RRSFRDRGGA GKLEVAQTQA PAA  
 TGGEEAAA KVKFELVSGS NVEAAMSLQL PEADA<sup>E</sup>VTA SSKSSTDILR CDLDSTGLKL HLSTAGMTGD ELSTSEVRIH PSKGLPLFQM PGMRLPETQV LPGEIDETPL SKPGHD  
 LASM EDKTEKWSSQ PEGPLK<sup>K</sup>AS STDMP<sup>S</sup>QISV VNV<sup>D</sup>QLWEDS VLVK<sup>F</sup>PKLM VPRFSFPAPS SEDDVFIPTV REVQCPEANI DTALCKESP LWGASILKAG AGVPGEQP  
 VD LNLPLEAPPI SKVRVHIQGA QVESQEVTHI SIVTPEFVDL SVPRTFSTQI VRESEIPTSE IQTPSYGFSL LKVKIPEPHT QARVYTTMTQ HSRTQEGTEE APIQATPGVD SISG  
 DLQPD<sup>T</sup> GEPFEMISSS VNLVGGQTLT FEVPSGHQLA DSCSDEEPAE ILEFPD<sup>S</sup>Q EATTP<sup>L</sup>ADEG RAPKDKPESK KSGLLWF<sup>W</sup>LP NIGFSSSVDE TGVDSKNDVQ R<sup>S</sup>APIQ  
 TQPE ARPEAELPKK QEKAGWFRFP KLGFS<sup>S</sup>PTK KSKSTEDGAE LEEQKLQEET ITFFDARESF SPEEKEEGEL IGPVGTGLDS RVMVTS<sup>A</sup>ART ELILPEQ<sup>D</sup>RK ADDESKGSGL  
 GPNE

Backcolor of amino acid : Yellow -> site of modification, gray -> in front of processing