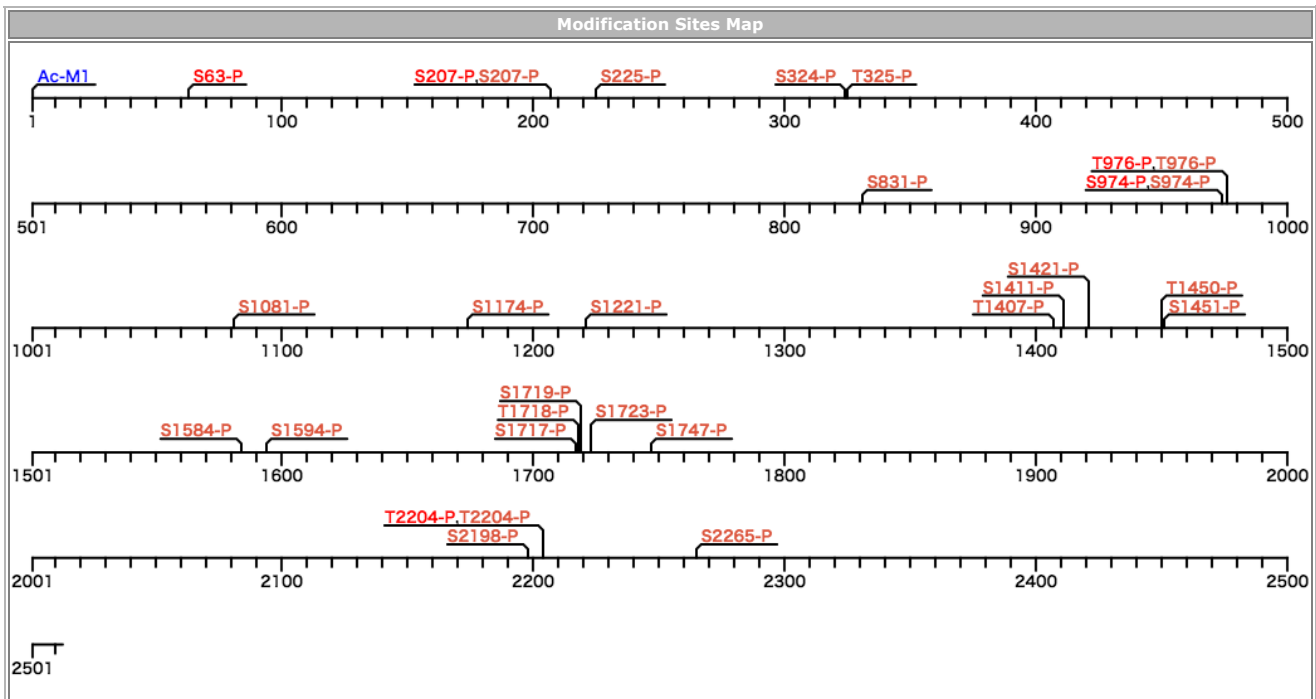


ID	Accession	GeneName	Chr.No.		Description
FAS_HUMAN	P49327	FASN	17q25.3	80036214..80056208	Fatty acid synthase



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
207	S	P	Lab	110711_titania_LNCaP_AI_2.mgf[F017442]
207	S	P	Lab	110711_titania_LNCaP_AI_3.mgf[F017444]
207	S	P	Lab	110711_titania_LNCaP_AI_5.mgf[F017446]
207	S	P	Lab	110711_titania_LNCaP_2.mgf[F017434]
207	S	P	Lab	100520-GIST-IM2.mgf[F017512]
207	S	P	Lab	100520-GIST-W2.mgf[F017522]
207	S	P	Lab	100520-GIST-W3.mgf[F017524]
207	S	P	Paper	Sci Signal 2011, 4(179), rs5

**Protein Sequence**

MEEVVIAGMS GKLPESENQ EFDWNLIGGV DMVTDDRRW KAGLYGLPRR SGKLDLSRF DASFFGVHPK QAHTMDPQLR LLEVTYEA IVDGGINPDSL RGHTTGWVWG VSGSETSEAL SRDPETLVGY SMVGCQRAMM ANRLSFFDF RGPSIALDTA CSSLMALQN AYQAIHSGQC PAAIVGGINV LLKPNTSVQF LRLGMLSPEG TCKAFDTAGN GY CRSEGVVA VLLTKKSLAR RVYATILNAG TNDTGFKEQG VTFPSGDIQE QLIRSLYQSA GVAPESFEYI EAHGTGTVKG DPQELNGITR ALCATRQPEL LIGSTKSNMG HPEPAS GLAA LAKVLLSLEH GLWAPNLHFH SPNPEIPALL DGRLQVVDQP LPVRGGNVGI NSFGFGGSNV HIILRPNTQP PPAPAPHATL PRLLRASGRV PEAVQKLEQ GLRHSQDLAF LSMLNDIAAV PATAMPFRGY AVLGGERGGP EVQQVPAGER PLWFICSGMG TQWRGMGLSL MRLDRFRDSI LRSDEAVKPF GLKVSQLLS TDESTFDDIV HSFVSLTAIQ IG LIDLSCM GLRPDGVIGH SLGEVACGYA DGCLSQEEAV LAAYWRGQCI KEAHLPPGAM AAVGLSWEEC KQRCPPGVVP ACHNSKDTVT ISGPQAPVFE FVEQLRKEGV FAK EVRTGGM AFHSYFMEAI APPLQELKK VIREPKRSA RWLSTSIPEA QWHSSLRATS SAEYVNNLV SPVLFQEALW HVPEHAVVLE IAPHALLQAV LKRGLKPSCT IIPLMKK DHR DNLEFFLAGI GRLHLSGIDA NPNALFPVPE FPAPRGTPLI SPLIKWDHSL AWDVPAEADF PNGSGSPSAA IYNIDTSES PDHYLDVHTL DGRVLPATG YLSIVWKTLA R ALGLGVEQL PVVFEVDVLLH QATILPKTGT VSEVRLLEA SRAFEVSENG NLVVSQVYQ WDDPDPRLFD HPESPTNPT EPLFLAQEV YKELRLRGYD YGPHFQGILE ASLEG DSGRL LWKDNWVSFM DTMLQMSILG SAKHGLYLPT RVTAIHDPA THRQKLYTLQ DKAQVADV VV SRWLRTVAG GVHISGLHTE SAPRRQEQEQ VPILEKFCFT PHTEEG CLSE RAALQEELQK CKGLVQALQT KVTQQLKMW VPGLDGAQIP RDPSQQLPR LLSAACRLQL NGNLQLELAQ VLAQERPKLP EDPLLSGLLD SPALKACLDT AVENMPSLK M KVVEVLAGHG HLYSRIPGLL SPHPLLQSY TATDRHPQAL EAAQAEQV DVAQGWDPD DPAPSALGSA DLLVCNCAVA ALGDPASALS NMVAALREGG FLLHLLTRG HPLGDIVAVL TSTEPQYGG ILSQDAWESL FSRVSLRVG LKFSYFGSTL FLCRRPTPQD SPIFLPDDT SFRWVESLKG ILADEDSSRP VWLKAINCATSGVVGLVNL RREP GGNNLR CVLLSNLSST SHVPEVDPGS AELQKVLQGD LVMNVYRDGA WGAFRHFLE EDKPEEPTAH AFVSTLTRGD LSSIRWVCS LRHAQPTCPG AQLCTVYAS LNFRDI MLAT GKLSPAIIPG KWTSQDSSLG MEFSGRDASG KRVMGLVPAK GLATSVLLSP DFLWLVPSNW TLEEAAVSPV VYSTAYALV VRGRVRPGET LLIHSGSGV GQAAIAIA LS LGCRVFTTVG SAEKRAYLQA RFPQLDSTSF ANSRDTSFEQ HVLWHTGGGK VDLVLNSLAE EKLAQSVRCL ATHGRFLEIG KFDLSQNHPL GMAIFLNKNT FHVGLLDAFF NESSADWREV WALVQAGIRD GVVRLKCTV FHGAQVEDAF RYMAQGHIG KVVVQVLAEE PEAVLKGAKP KLMSAISKTF CPAHKSYIIA GGLGGFLEL AQLLIQRGVQ K LVLTSRSGI RTGYQAKQVR RWRQGVQVQ VSTSNISSE GARGLIAEAA QLGPVGGVFN LAVVLRDGLL ENQTEFFQD VCKPKYSGTL NLDRTVREAC PELDYFVVS SVS CGRGNAG QSNYGFANSA MERICEKRRH EGLPGLAVQW GAIGDVGILV ETMSTNDTIV SGTLPQRMAS CLEVLDFLN QPHMVLSSVF LAEAAAYRD RDSQRDLVEA VAHI LGIRDL AAVNLDSSLA DLGLDSLMSV EVRQTLREL NLVLSVREVR QLTLRKLQEL SSKADEASEL ACTPKEDGL AQQTQLNLR LLLVNPGEPT LMRLNSVQSS ERPLFLVH PI EGSTTVFHSI ASRLSIPTYG LQCTRAAPLD SIHSLAAYI DCIRQVQPEG PYRVAGYSYG ACVAFEMCSQ LQAQSPAPT HNSLFLFDGS PTYVLAYTQS YRAKLTGPCE AE AETEAICF FVQQFTDMEH NRVLEALLPL KGLEERVAAA VDLIIKSHQG LDRQELFAA RSFYKLRAA EQYTPKAKYH GNVMLLRAKT GGAYGEDLGA DYNLSQVCDG KSVV HVIEGD HRTLLESGSL ESIISIIHSS LAEPRVSVRE G

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