

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	e. r.
P49327	FAS_HUMAN	Homo sapiens	Fatty acid synthase	24.677425	T315;S595;S806;T980;S1534;T2204	S63;S207;S725;S1174;S1411;S1584;S1594;S2156;S2198;T2204;T2215;S2236	35132862;41550490;35008409;40307207;27185461;23301498;38665916;40684943;33214551;40596516;34019948;33465208;25367160;34229054;40914422;37340703;35138101;29351928;26853435;35083852;18369606;34725712;32119511	MEEVVIAGMSGKLPESENLQEFWDNLIGGVDMMVTDGRRWKAGLYGLP RRSGKLDLSRFDASFFGVHPKQAH TMDPQLRLLLEVYEAIVDGGINPDS LRGTHTGVVWVGSGETSEALSRRDP ETLVGYSMVGCCRAMMANRLSFFF DFRGPISALDTCSSSLMALQONAYO AIHSGQCPAAIVGGINVLKPNNTSVQ FLRLGMLSPGTCFAFDTAGNGYCR SEGVAVLLTKKSLARRVYATILNAG TNTDGFKEQGVTFPSGDIQEQLIRSL YQSAGVAPESFEYIEAHGTGTVKVGDP QELNGITRALCATROEPLIGSTKSN MGHPPEASGLAALAKVLLSLEHGLW APNLHFHSPNPEIPALLDGRLOQVVD QPLPVRGGNVGINSFVGGSNVHILL RPNTQPPAPAPHATLPRLLRASGRT PEAVQKLEQGLRHSQDLAFLSMLN DIAAVPATAMPFRGYAVLGGERRGP EVQQVPAGERPLWFICSGMGTQWR GMGLSLMRLDRFRDSILRSDEAVKP FGLKVSQLLSTDESTFFDIVHSFVS LTAIQIGLIDLLSCMGLRDPGIVGHSL GEVACGYADGCLSQEEAVLAAYWRG QCIKEAHLPPGAMAAVGLSWEECKQ RCPPGVVPACHNSKDTVTISGPQAP VFEFVEQLRKEGVFAKEVRTGGMAF HSYFMEAIAPLLQELKKVIREPKPR SARWLSTSIPEAQWHSSSLARTSSAE YNVNVLVSPVLFQAEALWHVPEHAV VLEIAPHALLQAVLKRGLKPSCTIPL MKKDHDRDNLEFFLAGIGRLHLSGID ANPNALFPVPEPAPRGTPLISPLIK WDHSLAWDVPAEEDFPNGSGSPSA AIYNIDTSSSEPDHYLVDHTLDGRVL FPATGYSIVWKTARALGLGVEQLP VVFEDVVLHQATILPKTGTVSLVRL LEASRAFEVSENGNLVVSQKVVQWD DPDPRLFDHPESPTPNPTEPLFLAQA EVYKELRLRGYDYGPHFQGLEASLE GDSGRLLWKNWVFMMDTMLQMS ILGSAKHGLYLPTRVTAIHIDPATHR OKLYTLQDKAQVADVVVSRWLRVTV AGGVHISGLHTESAPRRQEQQVPI LEKFCFTPHTEEGCLSERAAQLEEL QLCKGLVQALQTKVTQQLKMVVP GLDGAQIPRDPSPQELPRLLSAACRL QLNGNLQLELAQVLAQERPKLPEDP LLSGLDSPALKACLDTAVENMPSL KMKVVEVLAGHGHLYSRIPGLLSPH PLLQLSYATDRHPQALEAAQAELO QHDVAQGWDPADPAPSALGSADL LVCNCAVAALGDPASALSNMVAALR EGGFLLLHTLLRGHPLGDIVAFLLTST EPOYGQGILSODAWESLFSRVSLRL VGLKKSFGSTLFLCRRPTPQDSPIF LPVDDTSFRWVESLKGILADESSSRP VWLKAINCATSGVVGLVNLRRRPG GNRLRCVLLSNLSSTSHVPEVDPGS AELQKVLQGDLMNVYRDGAWGAF RHFLEEDKPEEPTAHAFVSTLTRG DLSSIRWVCSLRAHQPTCPGAOLC TVYYASLNFRDIMLATGKLSPDAIPG KWTSQDSSLGMEFSGRDASGKRV GLVPAKGLATSVLLSPDFLWVPSN WTLLEAAVSVVYSTAYALVVRGRV RPGETLLIHSGGVGGQAAIAIALSL GCRVFTTVGSAEKRAYLQARFPQLD STSFANSRDTSEFQHVWLWHTGGKG VDLVNLSLAEKLAQSVRCLATHGR FLEIGKFDLSQNHPLGMAIFLKNVT FHGVLLDAFFNESSADWREVWALV QAGIRDGVVRPLKCTVFHGAQVEDA FRYMAQGKHIGKVVVQVLAEEPEAV LKGAQKPLMSAISKTFCPAHKSYIIA GGLGGFGLAQLWLIQRGVQKLVLT SRSGIRTYQAKQVRRRWRQGVQV QVSTNISLLEGARGLIAEAAQLGPV GGVFNLAVVLRDGLLENQTEFFQD VCKPKYSGLNLDRTREACPELDY	True	True	4.894	2.997	3.122	2.

