

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P49327	FAS_HUMAN	Homo sapiens	Fatty acid synthase	24.255257	T315;T980;S1534	S63;S207;S725;S1174;S1411;S1584;S1594;S2156;S2198;T2204;T2215;S2236	34229054;34019948;25367160;18369606;29351928;33214551;32119511;23301498;34725712;26853435;27185461;35138101;35083852;33465208;35132862;35008409	MEEVVIAGMSGKLPESENLQEFWD NLIGGVDMVTDDRRRWKAGLYGLP RRSGKLDLSRFDFASFFGVHPKQAH TMDPQLRLLLEVTYEAIVDGGINPDS LRGTHTGWVWVGVSGSETSEALSRDP ETLVGYSMVGCQRAMMANRLSFFF DFRGPISALDTACSSSLMALQNAVYQ AIHSGQCPAAIVGGINVLLKPNTSVQ FLRLGMLSPGTCFAFDTAGNGYCR SEGVVAVLLTKKSLARRVYATILNAG TNTDGFKEQGVTFPSGDIQEQLIRSL YQSAGVAPESFEYIEAHGTGTVKVGDP QELNGITRALCATRQEPLIGSTKSN MGHPEPASGLAALAKVLLSLEHGLW APNLHFHSPNPEIPALLDGRLLQVVD QPLPVRGGNVGINSFGFGGSNVHIL RPNTQPPAPAPHATLPRLLRASGRT PEAVQKLEQGLRHSQDLAFLSMLN DIAAVPATAMPFRGYAVLGGGERGGP EVQVQVAGERPLWFICSGMGTQWR GMGLSLMRLDRFRDSILRSDEAVKP FGLKVSQLLLSTDESTFDDIVHSFVS LTAIQIGLIDLLSCMGLRPDGIVGHSL GEVACGYADGCLSQEEAVLAAYWRG QCIKEAHLPPGAMAAGLSWEECKQ RCPFGVVPACHNSKDTVTISGPQAP VFEFVEQLRKEGVFAKEVRTGGMAF HSYFMEAIAPPLLQELKKVIREPKPR SARWLSTSIPEAQWHSSLARTSSAE YVNNLVSPVLFQEALWHVPEHAV VLEIAPHALLQAVLKRGLKPSCTIIP MCKDHRDNLEFFLAGIGRLHLSGID ANPNALFPPVEFPAPRGTPPLISPLIK WDHSLAWDVPAAEDFPNGSGSPSA AIYNIDTSSSPDHVLDHTLDGRVL FPATGYLSIVWKTLLARALGLGVEQLP VVFEDVVLHQATILPKTGTVSLVRL LEASRAFEVSENGNLVVSQKVVYQWD DPDPRFLFDHPESPTPNPTEPLFLAQA EVYKELRLRGYDYGPHFQGILEASLE GDSGRLWLDNWNVFMMDTMLQMS ILGSAKHGLYLPTRVTAIHIDPATHR QKLYTLQDKAQVADVVVSRWLRVTV AGGVHISGLHTESAPRRQEQVPI LEKFCFTPHTEEGCLSERAAEQEEL QLCKGLVQALQTKVTQQGLKMVVP GLDGAQIPRDPSQQELPRLLSAACRL QLNGNLQLELAQVLAQERPKLPEDP LLSGLLDSPALKACLDTAVENMPSL KMKVVEVLAGHGHLYSRIPGLLSPH PLLQLSYTATDRHPQALEAAQAEQ QHDVAQQQWDPADPAPSALGSADL LVCNCAVAALGDPASALSNMVAALR EGGFLLLHTLLRGHPLGDIVAFLTST EPQYGGILSQDAWESLFSRVSLRL VGLKKSFYGSTLFLCRRPTPQDSPIF

LPVDDTSFRWVESLKGILADESSRP  
VWLKAINCATSGVVGLVNCLRREPG  
GNRLRCVLLSNLSSTSHVPEVDPGS  
AELQKVLQGDLMNVYRDGAWGAF  
RHFLLLEEDKPEEPTAHAFVSTLTRG  
DLSSIRWVCSSLRHAQPTCPGAQLC  
TVYYASLNFRDIMLATGKLSFDAIPG  
KWTSQDSSLGMEFSGRDASGKRV  
GLVPAKGLATSVLLSPDFLWDVPSN  
WTLEEAASVPVVYSTAYYALVVRGRV  
RPGETLLIHSGSGGQAAIAIALSL  
GCRVFTTVGSAEKRAYLQARFPQLD  
STSFANSRDTSEFQHVLTWHTGGKG  
VDLVLNSLAEEKLQASVRCLATHGR  
FLEIGKFDLSQNHPLGMAIFLKNVT  
FHGVLLDAFFNESSADWREVVWALV  
QAGIRDGVVRPLKCTVFHGAQVEDA  
FRYMAQGGKHIGKVVVQVLAEEPEAV  
LKGAKPKLMSAISKTFCPAHKSYIIA  
GGLGGFGLELAQWLIQRGVQKLVLT  
SRSGIRTGYQAKQVRRWRRQGVQV  
QVSTSNISLEGARGLIAEAAQLGPV  
GGVFNLAVVLRDGLLENQTPEFFQD  
VCKPKYSGTLNLDRTVREACPELDY  
FVVFSSVSCGRGNAGQSNYGFANSA  
MERICEKRRHEGLPGLAVQWGAIGD  
VGILVETMSTNDTIVSGTLPQRMAS  
CLEVLDLFLNQPMLVLSFVLAEKA  
AAYRDRDSQRDLVEAVAHILGIRDLA  
AVNLDSSLADLGLDSLMSVEVRQTL  
ERELNLVLSVREVRQLTLRKLQELSS  
KADEASELACPTPKEDGLAQQQTQL  
NLRSLLVNPEGPTLMRLNSVQSSER  
PLFLVHPIEGSTTVFHSLASRLSIPTY  
GLQCTRAAPLDSIHSALAAYYIDCIRQ  
VQPEGPYRVAGYSYGACVAFEMCSQ  
LQAQQSPAPTHNSLFLFDGSPTYVL  
AYTQSYRAKLTGCEAEAETEAIKFF  
VQQFTDMEHNRVLEALLPLKGLEER  
VAAAVDLIKSHQGLDRQELSFARS  
FYYKLRAAEQYTPKAKYHGNVMLLR  
AKTGAYGEDLGADYNLSQVCDGKV  
SVHVIEGDHRTLLEGSGLESIIHS  
SLAEPRVSVREG