	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ext reg
0	Q9H583	HEAT1_HUMAN	Homo sapiens	HEAT repeat-containing protein 1	23.508671	NaN	S516;S1190;S1492	23301498;34725712;40914422;34019948;28510447	MTSLAQQLQRLALPQSDASLLSRDE VASLLFDPKEAATIDRDTAFAIGCTG LEELLGIDPSFEQFEAPLFSQLAKTL ERSVQTKAVNKQLDENISLFLIHLSP YFLLKPAQKCLEWLIHRFHIHLYNQ DSLIACVLPYHETRIFVRVIQLLKINN SKHRWFWLLPVKQSGVPLAKGTLIT HCYKDLGFMDFICSLVTKSVKVFAE YPGSSAQLRVLLAFYASTIVSALVAAE DVSDNIIAKLFPYIQKGLKSSLPDYRA ATYMIICQISVKVTMENTFVNSLASQ IIKTLTKIPSLIKDGLSCLIVLLQRQKP ESLGKKPFPHLCNVPDLITILHGISET YDVSPLLHYMLPHLVVSIIHHVTGEE TEGMDGQIYKRHLEAILTKISLKNNL DHLLASLLFEEYISYSSQEEMDSNK VSLLNEQFLPLIRLLESKYPRTLDVV LEEHLKEIADLKKQELFHQFVSLSTS GGKYQFLADSDTSLMLSLNHPLAPV RILAMNHLKKIMKTSKEGVDESFIK EAVLARLGDDNIDVVLSAISAFEIFK EHFSSEVTISNLLNLFQRAELSKNG EWYEVLKIAADILIKEEILSENDQLS NQVVVCLLPFMVINNDDTESAEMKI AIYLSKSGICSLHPLLRGWEEALENV IKSTKPGKLIGVANQKMIELLADNIN LGDPSSMLKMVEDLISVGEEESFNL KQKVTFHVILSVLVSCCSSLKETHFP FAIRVFSLLQKKIKKLESVITAVEIPSE WHIELMLDRGIPVELWAHYVEELNS TQRVAVEDSVFLVFSLKKFIYALKAP KSFPKGDIWWNPEQLKEDSRDYLHL LIGLFEMMLNGADAVHFRVLMKLFI KVHLEDVFQLFKFCSVLWTYGSSLS NPLNCSVKTVLQTQALYVGCAMLSS QKTQCKHQLASISSPVVTSLLINLGS PVKEVRRAAIQCLQALSGVASPFYLII DHLISKAEEITSDAAYVIQDLATLFEE LQREKKLKSHQKLSETLKNLLSCVY SCPSYIAKDLMKVLQGVNGEMVLSQ LLPMAEQLLEKIQKEPTAVLKDEAM VLHLTLGKYNEFSVSLLNEDPKSLDI FIKAVHTTKELYAGMPTIQITALEKIT KPFFAAISDEKVQQKLLRMLFDLLV NCKNSHCAQTVSSVFKGISVNAEQV RIELEPPDKAKPLGTVQQKRRQKMQ QKKSQDLESVQEVGGSYWQRVTLIL ELLQHKKKLRSPQILVPTLFNLLSRC LEPLPQEQGNMEYTKQLILSCLLNIC QKLSPDGGKIPKDILDEEKFNVELIV QCIRLSEMPQTHHHALLLLGTVAGI FPDKVLHNIMSIFTFMGANVMRLD DTYSFQVINKTVKMVIPALIQSDSGD SIEVSRNVEEIVVKIISVFVDALPHVP EHRRLPILVQLVDTLGAEKFLWILLIL LFEQYVTKTVLAAAYGEKDAILEADT EFWFSVCCEFSVQHQIQSLMNILQY LLKLPEEKEETIPKAVSFNKSESQEE MLQVFNVETHTSKQLRHFKFLSVSF MSQLLSSNNFLKKVVESGGPEILKG LEERLLETVLGYISAVAQSMERNAD KLTVKFWRALLSKAYDLLDKVNALL PTETFIPVIRGLVGNPLPSVRRKALDL LNNKLQQNISWKKTIVTRFLKLVPD LLAIVQRKKKEGEEEQAINRQTALYT LKLLCKNFGAENPDPFVPVLNTAVK LIAPERKEEKNVLGSALLCIAEVTSTL EALAIPQLPSLMPSLLTTMKNTSELV SSEVYLLSALAALQKVVETLPHFISPY LEGILSQVIHLEKITSEMGSASQANI RLTSLKKTLATTLAPRVLLPAIKKTYK QIEKNWKNHMGPFMSILQEHIGVM KKEELTSHQSQLTAFFLEALDFRAQ HSENDLEEVGKTENCIIDCLVAMVV KLSEVTFRPLFFKLFDWAKTEDAPK DRLLTFYNLADCIAEKLKGLFTLFAG HLVKPFADTLNQVNISKTDEAFFDS ENDPEKCCLLLQFILNCLYKIFLFDT QHFISKERAEALMMPLVDQLENRLG GEEKFQERVTKHLIPCIAQFSVAMA	True	False	1.178	5.0	4.424	0.519	False	3.346	Fal

									DDSLWKPLNYQILLKTRDSSPKVRF AALITVLALAEKLKENYIVLLPESIPF LAELMEDECEEVEHQCQKTIQQLET VLGEPLQSYF										