

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q8WYP5	ELYS_HUMAN	Homo sapiens	Protein ELYS	4.589711	S1188;T1345;S1847;S1900;S2060	S509;S528;S1080;S1138;S1142;S1150;S1153;S1155;S1160;T1175;S1214;S1218;S1222;S1232;S1250;T1257;S1283;S1297;T1369;S1371;S1513;T1517;S1533;S1541;S1729;S1806;T1808;S1878;S1884;S1898;S1944;S1946;S1996;S2043;S2044;S2060;S2089;S2120;S2123;S2154;S2212;S2222;S2226	28411811;30379171;33214551;3219511;33465208;34019948	MRDLRAQVTSGLLPFPEVTLQALGE DEITLESVLRGKFAAGKNGLAACLAC GPQLEVNSITGERLSAYRFGVNE QPPVVLAVKEFSWQKRTGLLIGLEET EGSVLCLYDLGISKVVKAVVLPGRVT AIEPIINHGGASASTQHLHPSLRWLF GVAAVVTDVQGILLVDLCLDDLSCN QNEVEASDLEVLGTGIPAEVPHIRESV MRQGRHLCFQLVSPTGTAVSTLSYIS RTNQLAVGFSQGYLALWNMKSMMKR EYYIQLESGQVPVYAVTFQEPENDPR NCCYLWAVQSTQDSEGDVLSLHLL QLAFGNRKCLASGQILYEGLEYCEE RYTLDLTGGMFPLRGQTSNTKLLGC QSIEKFRSHGDREEGVNEALSPDTS VSVFTWQVNIYGQKPSVYLGFLDI NRWYHAQMPDLSRSGEYLHNC SYF ALWSLESVVSRTSPHGILDILVHERS LNRGVPPSYPPPEQFFNPSTYNFDA TCLLNSGVVHLTCTGFQKETLFLK KSGPSLNELIPDGYNRCLVAGLLSPR FVDVQPSLSQEEQLEAILSAAIQTS SLGLLTG YIRRWITEEQPNSATNLRF VLEWTWNKVVLTKEEFDRLCVPLFD GSCHFMDPQTIQSIQCYLLSNLNI VLSCFASEAREITERGLIDL SNKFVV SHLICQYAQVVLWFSHSGLLPEGID DSVQLSRLCYNYPVIQNYTSRRQKF ERLSRGKWNPDCLMIDGLVSQLGE RIEKLWKRDEGGTGKYPPASLHAVL DMYLLDGVTEAAKHSITYLLLDIMY SFPNKTDTPIESFPTVFAISWGQVKLI QGFWLIDHNDYESGLDLLFHPATAK PLSWQH SKIIQAFMSQGEHRQALRY IQTMKPTVSSGNDVILHLLTVLLFNRC MVEAWNFLRQHCNRLNIEELLKHM YEVCQEMGLMEDLLKLPFTDTEQEC LVKFLQSSASVQNEFLLVHHLQRA NYVPALKLNQTLKINVMNDRDPRLR ERSLARNSILDQYGKILPRVHRKLA ERAKPYHLSTSSVFRVSRPKPLSAV PKQVVTGTVLRSVFINNVLSKIGEV WASKEPINSTTPFNSSKIEEPSPIVYS LPAPELPEAFFGTPIKASQKISRLLD LVVQPVPRPSQCSEFIQQSSMKSPLY LVSRLPSSSQLKGSPOAISRASELH LLETPLVVKKAKSLAMSVTTSGFSEF TPQSILRSTLRSTPLASPSPPGRSPQ RLKETRISFVEEDVHPKWIPGAADD KLEVFTTPKKCAVPVETEWLKSADR TTSFFLNSPEKEHQEMDEGSQSLEK LDVSKGNSSVSITSDETTLEYQDAPS PEDLEETVFTASKPKSSSTALTNTVT EQTEKDGDKDVFASEVTPSDLQKQ MGNLEDAETKDLLVAEAFSELNHL SPVQGTASLCAPSVYEGKIFTQKSK VPVLDEGLTSVETYTPAIRANDNKS MADVLGDGGNSSLTISEGPIVSERRL NQEVALNLKEDHEVEVGVLKEVDL PEEKLPISDSPDQTQEIHVIEQEKLEA

QDSGEEARNLSFNELYPSGTLKLOQ
NFDTIDQQFCDLADNKDTAECDAE
VDGELFVAQSNFTLILEGEEGEVPEP
GDFASSDVLPKAANTATEEKLVCSG
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EITSDTMEQSIHETIPLVSQNMCP
KLVKSAFKTAQETSTMTMNVSQVD
DVVSSKTRTRGQRIQNVNVKSAQQE
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SEASENIYSDVRGLSQNQIPQNSV
TPRRGRRKKEVNQDILENTSSVEQE
LQITTGRESKRLKSSQLLEPAVEETT
KKEVKVSSVTKRTPRRIKRSVENQES
VEIINDLKVSTVTPSRMIRKLRSTN
LDASENTGNKQDDKSSDKQLRIKHV
RRVRGREVSPSDVREDSNLESSQLT
VQAEFDMSAIPRKRGRPRKINPSED
VGSKAVKEERSPKKKEAPSIRRRSTR
NTPAKSENVDVGKPALGKSILVPNE
ELSMVMSSKKLTKKTESQSQRSL
HSVSEERTDEMTHKETNEQEERLL
ATASFTKSSRSRTRSSKAILLPDLSE
PNNEPLFSPASEVPRKAKAKKIEVPA
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TSNKNKLEDELKDDAQSVETLGKPK
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IEIRLISPLASPADGVKSKPRKTTEVT
GTGLGRNRKLLSSYPKQILRRKML