	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi appara
	P58107	EPIPL_HUMAN	Homo sapiens	Epiplakin	36.900231	T1624;T3157	T34;T1543;S2422;S2508;S2718;S2958;S3044;S3249;S3489;S3575;S3783;S4023;S4109;S4317;S4557;S4645;S4850	33465208;23301498;30397120;41350704;26374642;33214551;40596516	MSGHTLPPLPVPGTNSTEQASVPRAMAATLGAGTPPRPQARSIAGVYVEASGQAQSVYAAMEQGLLPAGLGQALLEAQAATGGLVDLARGQLLPVSKALQQGLVGLELKEKLLAAERATTGYPDPYGGEKLALFQAIGKEVVDRALGQSWLEVQLATGGLVDPAQGVLVAPEPACHQGLLDRETWHKLSELEPGTGDLRFLDPNTLERLTYHQLLERCVRAPGSGLALLPLKITFRSMGGAVSAAELLEVGILDEQAVQGLREGRLAAVDVSARAEVRRYLEGTGSVAGVVLLPEGHKKSFFQAATEHLLPMGTALPLLEAQAATHTLVDPITGQRLWVDEAVRAGLVSPELHEQLLVAEQAVTGHHDPFSGSQIPLFQAMKKGLVDRPLALRLLDAQLATGGLVCPARRLRLPLEAALRCGCLDEDTQRQLSQAGSFSDGTHGGLRYEQLLALCVTDPETGLAFLPLSGGPRGGEPQGPPFIKYSTRQALSTATATVSVGKFRGRPVSLWELLFSEAISSEQRAMLAQQYQEGTLSVEKLAAKLSATLEQAAATARVTFSGLRDTVTPGELLKAEIIDQDLYERLEHGQATAKDVGSLASVQRYLQGTGCIAGLLLPGSQERLSIYEARCKGLLRPGTALILLEAQAATGFIIDPKANKGHSVEEALRAAVIGPDVFAKLLSAERAVTGYTDPYTGQQISLFQAMQKGLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYRRGYFDQMLNLILLDPSDDTKGFFDPNTHENLTYLQLLERCVRDPETGLYLLPLSSTQSPLVDSATQQAFQNLLLSVKYGRFQGQRVSAWELINSEYFSEGRRRQLLRRYRQREVTLGQVAKLLEAETQRQADIMLPALRSRVTVHQLLEAGIIDQQLLDQVLAGTISPEALLLMDGVRRYLCGLGAVGGVRLLPSGQRLSLYQAMRQKLLGPRVALALLEAQAATGTIMDPHSPESLSVDEAVRRGVVGPELYGRLKRAEGAIAGFRDPFSGKQVSVFQAMKKGLIPWEQAARLLEAQVATGGIIDPTSHHHLPMPVAIQRGYVDQEMETALSSSSETFPTPDGQGRTSYAQLLEECPRDETSGLHLLPLPESAPALPTEEQVQRSLQAVPGAKDGTSLWDLLSSCHFTEEQRRGLLEDVQEGRTTVPQLLASVQRWVQETKLLAQARVMVPGPRGEVPAVWLLDAGIITQETLEALAQGTQSPAQVAEQPAVKACLWGTGCVAGVLLQPSGAKASIAQAVRDGLLPTGLGQRLLEAQVASGFLVDPLNNQRLSVEDAVKVGLVGRELSEQLGQAERAAAGYPDPYSRASLSLWQAMEKGLVPQNEGLPLLQVQLATGGVVDPVHGVHLPQAAACRLGLLDTQTSQVLTAVDKDNKFFFDPSARDQVTYQQLRERCVCDSETGLLLLPLPSDTVLEVDDHTAVALRAMKVPVSTGRFKGCSVSLWDLLLSEYVGADKRRELVALCRSGRAAALRQVVSAVTTLVEAAERQPLQATFRGLRKQVSARDLFRAQLISRKTLDELSQGTTTVKEVAEMDSVKRSLEGGNFIAGVLIQGTQERMSIPEALRRHILRPGTALVLLEAQAATGFIIDPVENRKLTVEEAFKAGMFGKETYVKLLSAERAVTGYTDPYTGQQISLFQAMQKDLIVREHGIRLLEAQIATGGIIDPVHSHRVPVDVAYRCGYFDEEMNRILADPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLYLLQIIKKGENYVYINEATRHVLQSRTAKMRVGRFADQVVSFWDLLSSPYFTEDRKRELIQEYGAQSGGLEKLLEIITTTIEETETQNQGIKVAAIRGEVTAADLFNSRVIDQKTLHTLRVGRTGGQALSTLECVKPYLEGSGCIAGVTVPSTREVMSLHEASRKELIPAAFATWLLEAQAATGFLLDPCTRQKLSVDEAVDVGLVNEELRERLLKAERAATGYRDPATGLYLLPLETAY

									TMEVKVGRLRGRAVPVWDVLASGY VSRAAREELLAEFGSGTLDLPALTRR LTAIIEEAEEAPGARPQLQDAWRGPR EPGPAGRGDGDSGRSQREGQGEGE TQEAAAATAAARRQEQTLRDATMEV QRGQFQGRPVSVWDVLFSSYLSEAR RDELLAQHAAGALGLPDLVAVLTRVI EETEERLSKVSFRGLRRQVSASELH TSGILGPETLRDLAQGTKTLQEVTEM DSVKRYLEGTSCIAGVLVPAKDQPG HQEKMSIYQAMWKGVLRPGTALVL LEAQAATGFVIDPVRNLRLSVEEAVA AGVVGGEIQEKLLSAERAVTGYTDPY TGQQISLFQAMQKDLIVREHGIRLLE AQIATGGVIDPVHSHRVPVDVAYRRG YFDEEMNRVLAHPSDDTKGFFDPN THENLTYVQLLRRCVPDPDTGLYML QLAGRGSAVHQLSEELRCALRDARV MPGSGALQGQSVSVWELLFYREVSE DRRQDLLSRYRAGTLTVEELGATLTS LLAQAQAQARAEAEAEAGSPRPDPR EALRAATMEVKVGRLRGRAVPVWD VLASGYVSGAAREELLAEFGSGTLDL PALTRRLTAIIEEAEEAPGARPQLQD AWRGPREPGPAGRGDGDSGRSQRE GQGEGETQEAAAAARRQEQTLRDAT MEVQRGQFQGRPVSVWDVLFSSYL SEAHRDELLAQHAAGALGLPDLVAV LTRVIEETEERLSKVSFRGLRRQVSA SELHTSGILGPETLRDLAQGTKTLQE VTEMDSVKRYLEGTSCIAGVLVPAK DQPGRQEKMSIYQAMWKGVLRPGT ALVLLEAQAATGFVIDPVRNLRLSVE EAVAAGVVGGEIQEKLLSAERAVTGY TDPYTGQQISLFQAMQKDLIVREHGI RLLEAQIATGGVIDPVHSHRVPVDVA YRRGYFDEEMNRVLADPSDDTKGFF DPNTHENLTYLQLLQRATLDPETGL LFLSLSLQ							