

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
F1LMV6	DESP_RAT	Rattus norvegicus	Desmoplakin	25.563465	NaN	S22;S62;T65;T70;S174;S175;S183;S1665;S1715;S2031;S2214;S2216;S232;S2817;S2822;T2824;S2827;S2831;S2855;T2859;S2874	34502162	MSCNGGSHPRINTLGRMTRAESGPD DLRYEMTYSGGGGGGGGGGTSTR MYYSRRCTVNDQNSDGYCQTGTMS RHQNQNTIQELLQNCADCLMRAELI AQPELKFGEQILAWNRELDYFTQ ANDQMEIIDGLIREMRQMGQPCDA YQKRLQLQEQMRALYKAISAPRVR RASSKGGYTCQSGSGWDEFTKRLTG ECLGWMRQRAEMDLMAWGVDSG SVEQHINSHRSIHNAIGDYRWQLDK IKADLREKSATYQLEEEYENLLKASF ERMDHLRQLQNIQATSREIMWIND CEEEELLYDWSKNTNIAQKOEAFS IRMSQLEVKKEKLNKQESDQLVL NQHPASDKIEAYMDTLQTQWSWIL QITKCIDVHLKENAAYFQFFEEAQST EAYLKGQDSIRKKYPCDKNMPLQH LLEQIKELEKEREKILEYKRQVQNLV NKSCKIVQLKPRNPYRSNKPILLRA LCDYKQDQKIVHKGDECILKDNNER SKWYVTGPGGVDMLVPSVGLIIPPPN PLAVDLSCKIEOYEAAILALWNQLYI NMKSLVSWHYCMIDIEKIRAMTIAK LKTMRQEDYMKTIEDLELHYQDFIK NSQSEMFGDDDKRRMQSQFTDA QKHQTLVQLPGHPQHQTVTKTEIT HVGTCQDVNHNKVIETNRENDKQE TWLLMELQKIRROMEHCEARMTLK NLLTDDQGSTHNITVKINELKSVQN DSQALAEVLNQLKDMLANFRGSEK YCYLQNEIFGLFQKLENINGVTDGYL NSLCSVRALLQAILQTEDMLKVYEA RLTEETVCLDLKVEAYRCGLKKIK NDLNLKKSLLATMKTQLQAQOIHS QSSQOYPLYDDLKGFTEKVTQLTD RWQKIDKQIDFRLWDLEKQIKQLRN YRDNYQSFCKWLYDAKRRQDSLES MKFGDSNTVMRFLNEQKLNHNEIS GKRDKSEEVHKAELCANSIKDYELQ LASYTSGLTLLNIPKRTMVQSPFG VILQEAADIHARYIELLTRSGDYRFL SEMLKSLEDLKLKNTKIEVLEELRL ARDANSENCKNKFQDLQNLQKYQA ECSQFKAKLVLEELKRQAEIDGKS AKQNLKCYGQIKELNEKITRLTYEI EDEKRRRTVDFRFDQKNDYDQL QKARQCEKESLQWQKLESEKAIKEA EYEIERLRVLLQEEGARKREYENELA KVRNHYNEMSNLRNKYETEINITK TTIKEISMQKEDDSKNLRNQLDRLS RENRLKDEIVRLNDSILQATEQRR RAEENALQKACGSEIMQKQHLE VELKQVIQORSEDNARHKQSLEEAA KTIQDNKEIERLKAQEYQEEAKRRW EYENELSKVRNSYDEEIIISLRNKFET EINITKTIHQLTMQKEEDTSGYRAQ IDNLTRENRLSEEVKRLKNTLAQTT ENLRRVEENVQQKASGSEMSQRK QQLEIELRQVSMRTEESMRKYQSL DDAAKTIQDNKEIERLQVLDKET NERKCLEDENSKLQRVQYDLQKAN NSATEAMSKLVQEQELTRLRIDYE RVSQERTVKDQDITRIQSSLDLQLO KQKAEELSRKRTASDESSKRKML EELEAMRRSLKEQAVKITNLQQL EQASIVKKRSEDDLROQRDVLGHHV REKQRTQEEELRRLSLDVEALRRQLV QEQENVKQAHLRNEHFQKAIEDKS RSLNESKIEIERLQSLTENLTKEHLM LEEELRNLRLEYDLRRGRSEADND KNSTISELRSQLOISNNRLELQGLI NDLQRERENLRQEIJEKFKQALEAS NRIQESKSQCTQVVQERESLLVKIKV LEQDKARLQRLDELELNRAKATLEAE TRVKQRLECEKQIQNDLNQWKTQ YSRKEETIRKIESEREKSEREKNSLR SEIERLQAEIKRIEERCRRKLEDSTR ETQSQLETERCLQKEIDKLRQRPY GSHRETQTEYEWTVDSSKLVDFGLR KKVTAMQLYECQLIDKTTLDKLLKG	False	True	2.704	1.98	1.464	1.677	1.086	4.449	1.848

KKSVEEVASEIQPFLRGAGAIAGASA  
SPKEYSLVEAKRKKFITPESTVMLL  
EAQAATGGIIDPHRNEKLTVDNAIAR  
DLIDFDDRQIYTAEKAITGFDDPFPS  
GKTVSVSEAIKKNLIDRETGMRLLEA  
QLASGGVVDPVNSVFLPKDVALARG  
LIDRDLYRSLNDPRDSQKNFVDPITK  
KKVSYMQLRERCRIEPTGLLLLSV  
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PSTVNELESGQISYDEVGERIKDFLQ  
GSSCIAGIYNETTKOKLGIYEMKIG  
LVRPGTALLEEAQAATGFIVDPVSN  
LRLPVEEAYKRGLVGIEFKEKLLSAE  
RAVTGYNDPETGNIISLQFAMNKELI  
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LPVDMAYKRGYFNEELSEILSDPSD  
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DEETGLCLLPLKEKKKQVQTSQKNT  
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DGSTRVVLVDRKTGSQYDIQDAIDKG  
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DSITGQRLLAQACTGGIHPPTGQK  
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RISTEEAIRKGFIDGRAAQRLQDISSY  
AKILTCPKTKLISYKDAMNRMVME  
DITGLRLLAASVSSKGLPSFYNMSA  
PGSRSGSRSGSRSGSRSGSRSGSRR  
GSFDTGNSSYSYSFSSSSIGY