

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9Y3R5	DOP2_HUMAN	Homo sapiens	Protein dopey-2	24.917859	NaN	S556;S597;S1169	28411811	MDPEEQELLNDYRYSYSSVIEKAL RNFESSEWADLISLGLKLNKALQS NLRYSLPRLLISKRLAQCLHPALP SGVHLKALETYEIIFKIVGTKWLAKD LFLYSCGLFPLLAHAASVSRPVLLTL YEKYFLPLQKLLPSLQAFIVGLPLGL EEGSEISDRTDALLRLSLVVGKEVF YTALWGSVLASPSIRLPASVFFVGGHI NRDAPGREQKYMLGTNHQLTVKSL RASLLDSNVLVQRNNLEIVLFFFPFY TCLDSNERAIPLLRSDIVRILSAATQT LLRRDMSLNRRLYAWLLGSDIKGNT VPESEISNSYEDQSSYFFEKYSKDL LVEGLAEILHQKFIDADVEERHHAYL KPFRLVLSLLDKPEIGPVVGNLFLE VIRAFYSYCRDALGSDLKLSYTSQSGN SLISAIKENRNASEIVKTVNLLITSLS TDFLWDYMTRCFEECFRPVKQRYSV RNSVSPPTVSELALLVFLLDVIPL LYSEVQTQYLPQVLGCLVQPLAEDM EALSPELTHALKTCFKVLSKVQMP PSYLDTESTSGTSSPVKGENGKIILET KAVIPGDEDAFPPPKSEDSGIGLSA SSPELSEHLRVRVSLERDDVWKKG GSMQRTFLCIQELIANFASKNIFGVQ LTASGEESKSEEPAGKRDRDGTQSL AANDSSRKNSWEPKIPITVPQFKQML SDLFTARGSPFKTKSSESPSSPSSP ARKNGGEWDVEKVIDLGGREER REAFAAAACHLLDCATFPVYLSEET EQLCATLFLQPGAGDSSFPSWLKSL MTICCCVTDCYLQNVIAISTLEVINH SQSLALVIEDKMKRYKSSGHNPFPG KLQMVTVPPPIAPGILKVAEKTDFYQ RVARVLWNQLNKETREHHVTCVEL FYRLHCLAPTANICEDIICHALDPD KGTREALFRFVVIWHLTREIQGSRV TSHNRSFDRSLFVVLDLACTDGGAI GAAAQGWLVRLSLGDVARILEPVL LLLQPKTQRTSIHCLKQENSADDL HRWFNRKKTSFREACAVPEPQESGS EEHLPLSQFTTVDREAIWAEVEKEP EKYPLRGELSEELPYVVELPDRTAH GAPDSSEHTESADTSSCHTDSENTS SFSSPSHDLQELSNEENCCAPIPMG GRAYPKRSALLAAFQSESFKAGAKLS LVRVSDKTQASESFSSDEEADLEL QALTTSRLLKQORERQEAVALFKHI LLYLQPYDSRRVLYAFVLEAVLKTN PKEFIEAVSRTSMDTSSTAHLNLISN LLARHQEALIGQSFYQKLTQVQPNV CPHSLLELLTYLCLSLRYSYPCYL KVSHRDILGNRDVQVKSVEVLIRIM MQLVSVAKSSEGNVEFIHSLQRC KVQEFVLLSLSASMYTSQKRYGLAT AHHGRALPEDSLFEESLINLQGDQI WSEHPLQIELLKLLQVLIVLEHHLGR AHEEAENQPDLSREWQRALNFQQA ISALQYVQPHPLTSQGLLVSAVVRGL QPAYGYGMHPAWVSLVTHSLPYFGK SLGWTVPFVVQICKNLDDLKQYE SESVKLSVSTTSKRENISPDYPLTLE GLTTISHFCLEQANQNKTMAAGD PANLRNARNAILEELPRTVNTMALL WNVLRKEETQKRPVDLLGATKGSSS VYFKTTKTIRQKILDFLNPLTAHLGV QLTAAVAAVWSRKAQRHSMKMIIP TASASQLTLVDLVCALSTLQTDTLH LVKEVVKRPPQVKGDEKSPLDIPV LQFCYAFQRLPVPALQENFSSLLGV LKESVQLNLAPPGYFLLSMLNDFV TRTPNLENKKDQKDLQEITQKILEAV GNIAGSSLEQTSWLSRNLEVKAQPQ ASLEESDAEEDLYAAAAAMVSSS	False	False	2.697	1.062	0.996	0.643	3.545	3.237	4.166

APSVYSVQALSLLAEVLASLLDMVYR
SDEKEKAVPLISRLLYVFPYLRNHS
AYNAPSFragaQLLSSLSGYAYTKRA
WRKEVLELFLDPAFFQMDTSCVHW
KSHDHLLTHEKTMFKDLMNMQSSS
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LDQYHLYLPLIQERLTDNLRVGQTSI
VAAQMFLFFRVLLLRIPOHLSLW
PIMVSELIQTFTQLEEDLKDEDESLR
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SELILYLSACKFLDTALSFPDKMPL
FQIYRWAFIPEVDTEGPAFLSDVEEN
HQECKPHTVRILELLKLFGEISSSD
EITMKSEFLLRQHSVSSIRQLMPFF
MTLNGAFKTQRQLPADSPGTPFLDF
PVTDSRILKQLEECIEYDFLEHPEC