	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	extracellular region
0	Q9VCU9	DCR1_DROME	Drosophila melanogaster	Endoribonuclease Dcr-1	28.06426	S1312	S1423;S1877;S1880	40245499	MAFHWCDNNLHTTVFTPRDFQVEL LATAYERNTIICLGHRSSKEFIALKLL QELSRRARRHGRVSVYLSCEVGTST EPCSIYTMLTHLTDLRVWQEQPDM QIPFDHCWTDYHVSILRPEGFLYLLE TRELLLSSVELIVLEDCHDSAVYQRI RPLFENHIMPAPPADRPRILGLAGPL HSAGCELQQLSAMLATLEQSVLCQI ETASDIVTVLRYCSRPHEYIVQCAPF EMDELSLVLADVLNTHKSFLLDHRY DPYEIYGTDQFMDELKDIPDPKVDPL NVINSLLVVLHEMGPWCTQRAAHH FYQCNEKLKVKTPHERHYLLYCLVS TALIQLYSLCEHAFHRHLGSGSDSR QTIERYSSPKVRRLLQTLRCFKPEEV HTQADGLRRMRHQVDQADFNRLSH TLESKCRMVDQMDQPPTETRALVAT LEQILHTTEDRQTNRSAARVTPTPTP AHAKPKPSSGANTAQPRTRRRVYTR RHHRDHNDGSDTLCALIYCNQNHT ARVLFELLAEISRRDPDLKFLRCQYT TDRVADPTTEPKEAELEHRRQEEVL KRFRMHDCNVLIGTSVLEEGIDVPK CNLVVRWDPPTTYRSYVQCKGRARA APAYHVILVAPSYKSPTVGSVQLTDR SHRYICATGDTTEADSDSDDSAMPN SSGSDPYTFGTARGTVKILNPEVFSK QPPTACDIKLQEIQDELPAAAQLDTS NSSDEAVSMSNTSPSESSTEQKSRR FQCELSSLTEPEDTSDTTAEIDTAHS LASTTKDLVHQMAQYREIEQMLLSK CANTEPPEQEQSEAERFSACLAAYR PKPHLLTGASVDLGSAIALVNKYCAR LPSDTFTKLTALWRCTRNERAGVTL FQYTLRLPINSPLKHDIVGLPMPTQT LARRLAALQACVELHRIGELDDQLQ PIGKEGFRALEPDWECFELEPEDEQI VQLSDEPRPGTTKRRQYYYKRIASEF CDCRPVAGAPCYLYFIQLTLQCPIPE EQNTRGRKIYPPEDAQQGFGILTTKR IPKLSAFSIFTRSGEVKVSLELAKERV ILTSEQIVCINGFLNYTFTNVLRLQK FLMLFDPDSTENCVFIVPTVKAPAG GKHIDWQFLELIQANGNTMPRAVPD EERQAQPFDPQRFQDAVVMPWYRN QDQPQYFYVAEICPHLSPLSCFPGD NYRTFKHYYLVKYGLTIQNTSQPLLD VDHTSARLNFLTPRYVNRKGVALPT SSEETKRAKRENLEQKQILVPELCTV HPFPASLWRTAVCLPCILYRINGLLL ADDIRKQVSADLGLGRQQIEDEDFE WPMLDFGWSLSEVLKKSRESKQKE SLKDDTINGKDLADVEKKPTSEETQL DKDSKDDKVEKSAIELIIEGEEKLQE ADDFIEIGTWSNDMADDIASFNQED DDEDDAFHLPVLPANVKFCDQQTRY GSPTFWDVSNGESGFKGPKSSQNK QGGKGKAKGPAKPTFNYYDSDNSLG SSYDDDDNAGPLNYMHHNYSSDDD DVADDIDAGRIAFTSKNEAETIETAQ EVEKRQKQLSIIQATNANERQYQQT KNLLIGFNFKHEDQKEPATIRYEESI AKLKTEIESGGMLVPHDQQLVLKRS DAAEAQVAKVSMMELLKQLLPYVN EDVLAKKLGDRRELLLSDLVELNAD WVARHEQETYNVMGCGDSFDNYN DHHRLNLDEKQLKLQYERIEIEPPTS TKAITSAILPAGFSFDRQPDLVGHPG PSPSIILQALTMSNANDGINLERLETI GDSFLKYAITTYLYITYENVHEGKLS HLRSKQVANLNLYRLGRRKRLGEY MIATKFEPHDNWLPPCYYVPKELEK ALIEAKIPTHHWKLADLLDIKNLSSV QICEMVREKADALGLEQNGGAQNG QLDDSNDSCNDFSCFIPYNLVSQHS IPDKSIADCVEALIGAYLIECGPRGAL LFMAWLGVRVLPITRQLDGGNQEQ RIPGSTKPNAENVVTVYGAWPTPRS PLLHFAPNATEELDQLLSGFEEFEE	True	False	5.0	5.0	1.677	1.395	0.854	1.63	1.739

								SLGYKFRDRSYLLQAMTHASYTPNR LTDCYQRLEFLGDAVLDYLITRHLYE DPRQHSPGALTDLRSALVNNTIFASL AVRHGFHKFFRHLSPGLNDVIDRFV RIQQENGHCISEEYYLLSEEECDDAE DVEVPKALGDVFESIAGAIFLDSNMS LDVVWHVYSNMMSPEIEQFSNSVP KSPIRELLELEPETAKFGKPEKLADG RRVRVTVDVFCKGTFRGIGRNYRIAK CTAAKCALRQLKKQGLIAKKD								