

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrar
094762	RECQ5_HUMAN	Homo sapiens	ATP-dependent DNA helicase Q5	21.144273	T456;T898	S488;S491;S727;S815;T839	40596516;30379171;38253038	MSSHHTTFFPDPERRVRSTLKKVFG FDSFKTLPQESATMAVVKGNKDVV CMPTGAGKSLCYQLPALLAKGITTV SPLIALIQDQVDHLLTLKVRVSSLNS KLSAQERKELLADLEREKPTKILYI TPEMAASSSFQPTLNSLVSRLHLLSYL VVDEAHCVSQWGHDFRPDYLRLGA LRSRLGHAPCVALTATATPQVQEDV FAALHLKKPVAIFKTPCFRANLFYDV QFKELISDPYGNLKDFFCLKALGQEA DKGLSGCGIVYCRTRREACEQLAIELS CRGVNAKAYHAGLKASERTLVQND WMEEKVPVIVATISFGMGVDKANVR FVAHWNIKSMAGGYQESGRAGR GKPSWCRLYYSRNDRDQVSFLIRKE VAKLQEKRGNKASDKATIMAFDALV TFCEELGCRHAAIAKYFGDALPACAK GCDHCQNPTAVRRRLEALERSSSW SKTCIGPSQNGFDPPELYEGGRKGY GDFSRYDEGSGSGDEGRDEAHKR EWNLFYQKQMLRKGKDPKIEEFV PPDENCPLKEASSRRIPRLTVKAREH CLRLLEALSSNRQSTRTADADLR AKAVELEHETFRNAKVANLYKASVL KKVADIHRASKDGGPYDMGGSKSC SAQAEPPEPNEYDIPPASHVYSLKPK RVGAGFPKGSFPQTATELMTETRI REQAPQPERGGEHEPPSRPCGLLDE DGSEPLPGRGEVPGGSAHYGGPSP EKKAKSSSGSSLAKGRASKQQLL ATAAHKDSQSIARFFCRRVESPALLA SAPEAEGACPSCEGVQGPMAPEKY TGEEEDGAGGHSAPPQTEECLRERP STCPPRDQGTPEVQPTPAKDTWKGK RPRSQQENPESQPKRPRPSAKPSV VAEVKGSVSASEQGLNPTAQDPFO LSAPGVSLKEAANVVVKCLTPFYKEG KFASKELFKGFARHLSHLLTQKTSP GRSVKEEAQNLRHFFHGRARCESE ADWHGLCGPQR	True	False	4.331	5.0	0.375	False	False	False