

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
P56715	RP1_HUMAN	Homo sapiens	Oxygen-regulated protein 1	16.682301	S155	NaN	30379171;37217939	MSDTPSTGFSIIHPTSSEGVPPPRH LSLTHPVVAKRISFYKSGDQFQGGVR VVVNPFRSFKSDALDNLNLSRQVPLP FGVRNISTPRGRHSITRLELEDGES YLCSHGRKVQVVDLKDARRRPRPWL SSRAISAHSPPHPVVAAPGMPRPPR SLVFRNGDPKTRRAVLLSRRVTQS FEAFQLHLTEVMQRPVVKLYATDGR RVPSLQAVILSSGAVVAAGREPFKPG NYDIQKYLPLARLPGISQRVYPKGNA KSESRKISTHMSSSSRSQIYSVSSEK THNNDCYLDYSFVPEKYLALAKNDS QNLPIYPSIEDIEKSIIFNQDGTMTV EMKVRFRIKEEETIKWTTTVSKTGPS NNDEKSEMSFPGRTESRSSGLKLA CSFSADVSPMERSSNQEGSLAEINI QMTDQVAETCSSASWENATVDTDII QGTQDQAKHRFYRPPTPGLRRVRQK KSVIGSVTLVSETEVQEKMIGQFYS EERESGENKSEYHMFTHSCSKMSS VSNKPVLVQINNNDQMEESSLERK KENSLLKSSAISAGVIEITSQKMLEM SHNNGLPSTISNNSIVEEDVDCVV LDNKTGKKNFKTYGNTNDRFSPISA DATHFSSNNSGTDKNISEAPASEAS STVTARIDRLINEFAQCGLTKLPKNE KKILSSVASKKKKSRQAINSRYQD GQLATKGILNKNERINTKGRITKEMI VQSDSPLKGGILCEEDLQKSDTVIE SNTFCSKSNLNTISKNFHRNKLNT TQNSKVQGLLTKRKSRLNKLGLGAP KKREIQQRDKVPHNESKYCKSTFE NKSFLHFVFNILEQPKDFYAPQSQ EVASGYLRGMAKKSLSVSKVTDSHITL KSQKRRKGDKVASAILSKQHATTR ANSLASLKKPDFPEAIAHHSIQNYIQ SWLQININPYPTLKPISAPVCRNETS VVNCSNNSFSGNDPHTNSGKISNFV MESNKHITKIAAGLTGDNLCKEGDKS FIANDTGEEDLHETQVGSNDAYLV PLHEHCTLSQSAINDHNTKSHIAAE KSGPEKLVYQFQINLARKRQSVAAI QVDPIEETPKDLLPVLMLHQLQAS VPGIHKTONGVVQMPGSLAGVFPFHS AICNSSTNLLLAWLLVNLKGMNS FCQVDAHKATNKSSETLALLEILKHI AITEEADDLKAANLVESTTSHFGL SEKEQDMVPIDLSANCTVNIQSV KCSNERTQGISSLDGGCSASEACA PEVCVLEVTCSPECMTVNKAYSPK ETCNPSDTFFPSDGYGVDQTSMNKA CFLGEVCSLTDVFSKAKAQAQENH TYEGACPIDETYVPVNVNTIDFLNS KENTYTDNLDSTEELERGGDDIQKDL NILDPEYKNGFNTLVSHQNVSNLS SCGLCLSEKEAELDKKSSLDDEFEN CSLRKFQDENAYTSFDMEEPRTSEE PGSITNSMTSSERNISELESFELEN HDTDIFNTVVNGGEQATEELIQEEV EASKTLELIDISSKNIMEEKRNGIY EIIKRLATPPSLDFCYDSKQNSEKE TNEGKTMVMMVKMTMETGSYSES SPDLKCKIKSPVTSWSDYRPSDS EQPKYKSSDDPNDSGELTQEKYNI GFVKRAIEKLYGKADIIKPSFFPGSTR KSQVCPYNSVEFQCRRKASLYDSEG QSFQSSEQVSSSSMLQEFQEEERQD KCDVSAVRDNYCRGDIVPEPGTKQND DSRILTDIEEGLIDKGGWLLKENHL LRMSENPGMCGNADTTSVDTLLD NNSSEVPYSHFGNLAPGPTMDELSS SELEELTQPLELKCNYFNMPHGS EPFHEDLLDVRNETCAKERIANHHT EEKGSHQSERVCTSVTHSFISAGNK VYPVSDDAIKNQPLPGSNMIGTLQ EADSLDKLYALCGQHCPILT VIIQPM NEEDRGFAYRKESDIENFLGFYLWM	None	None	None	None	None	None	None	None	

								KIHPYLLQTDKNV FREENNKASMRQ NLIDNAIGDIFDQFYFSNTFDLMGK RRKQKRINFLGLEEEGNLKKFPDL KERFCMNFLHTSLLVVGNVDSNTQ DLSGQTNEIFKAVDENNNLLNNRF QGSRTNLNQVRENINCHYFFEML GQACLLDICQVETS LNISNRNILELC MFEGENLFIWEEEDILNLTDESSR EQEDL						
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