

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P17927	CR1_HUMAN	Homo sapiens	Complement receptor type 1	13.589521	NaN	NaN	37217939	MGASSPRSPEVGPAPGLPFCCGG SLLAVVLLALPVAWGQNAPEWLP FARPTNLTDEFEFPIGTYLNYECRPG YSGRPFSIICLNKNSVWTGAKDRCCRK SCRNPPDPVNGMVHVIKGIQFGSQI KYSCTKGYRLIGSSSATCIISGDTVIV DNETPICDRIPCGLPPTITNGDFISTN RENFHYGSVVTYRCNPGSGGRKVFE LVGEPYICTSNDDQVGIWSPAPQ CIIPNKCTPPNVENGILVSDNRSLS LNEVVEFRCQPGFVMKGPRRVKQC ALNKWEPELPSCSRVCQPPDVLHA ERTQRDKDNFSPGQEVFYSCEPGYD LRGAASMRCTPQGDWSPAAPTCEV KSCDDFMGQLLNGRVLFPVNLQLG AKVDFVCDEGFQLKGSSASYCVLAG MESLWNSSVPVCEQIFCSPPPVIPN GRHTGKPLEVFPFGKTVNYTCDPHP DRGTSFDLIGESTIRCTSDPQNGV WSSPAPRCGILGHCQAPDHFLFAKL KTQTNASDFPIGTSKLYECRPEYYGR PFSITCLDNLVWSSPKDVCKRKSC TPPDPVNGMVHVITDIQVGSRINYSC TTGHRILIGHSSAECILSGNAAHWST KPPICQRIPCGLPPTIANGDFISTNRE NFHYGSVVTYRCNPGSGGRKVFEV GEPYICTSNDDQVGIWSPAPQCII PNKCTPPNVENGILVSDNRSLSL EVVEFRCQPGFVMKGPRRVKQC NKWEPELPSCSRVCQPPDVLHAER TQRDKDNFSPGQEVFYSCEPGYDLR GAASMRCTPQGDWSPAAPTCEVKS CDDFMGQLLNGRVLFPVNLQLGAK VDFVCDEGFQLKGSSASYCVLAGME SLWNSSVPVCEQIFCSPPPVIPNGRH TGKPLEVFPFGKAVNYTCDPHPDRG TSFDLIGESTIRCTSDPQNGVWSSP APRCGILGHCQAPDHFLFAKLKTQ NASDFPIGTSKLYECRPEYYGRPFSIT CLDNLVWSSPKDVCKRKSCKTPPDP VNGMVHVITDIQVGSRINYSC RLIGHSSAECILSGNTAHWSTKPPIC QRIPCGLPPTIANGDFISTNRENFHY GSVVTYRCNLGSRGRKVFELVGEPSI YCTSNDDQVGIWSPAPQCIIIPNKCT PPNVENGILVSDNRSLSLNEVVEF RCQPGFVMKGPRRVKQCALNKWEP ELPSCSRVCQPPPEILHGEHTPSHQ DNFSPGQEVFYSCEPGYDLRGAASL

							HCTPQGDWSPEAPRCAVKSCDDFL GQLPHGRVLFPLNLQLGAKVSFVCD EGFRLKGSVSHCVLVGMRLWNN SVPVCEHIFCPNPPAILNGRHTGTPS GDIPYGKEISYTCDPHPDRGMTFNL GESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFPFASPTIPINDF EFPVGTSLNYECPGYFGKMFSISCL ENLVWSSVEDNCRKSCGPPPEPF NGMVHINTDTQFGSTVNYSCNEGF RLIGSPSTTCLVSGNNVTWDKKAPIC EISCEPPPTISNGDFYSNNRTSFHN GTVVTYQCHTGPDGEQLFELVGERS IYCTSKDDQVGWSSPPPRCISTNKC TAPEVENAIRVPGNRSFFSLTEIIRFR CQPGFVMVGSHTVQCQTNGRWGPK LPHCSRVCQPPPEILHGEHTLSHQD NFSPGQEVFYSCEPSYDLRGAASLH CTPQGDWSPEAPRCTVKSCDDFLGQ LPHGRVLLPLNLQLGAKVSFVCD FRLKGRSASHCVLAGMKALWNSSV PVCEQIFCPNPPAILNGRHTGTPFGD IPYGKEISYACDTHPDRGMTFNLIGE SSIRCTSDPQNGVWSSPAPRCELS VPAACPHPPKIQNGHYIGGHVSLYLP GMTISYICDPGYLLVGKGFIFCTDQGI WSQLDHYCKEVNCSFPLFMNGISK ELEMKKVYHYGDYVTLKCEDGYTLE GSPWSQCQADDRWDPPLAKCTSRT HDALIVGTLSGTIFFILLIIFLSWILK HRKGNNAHENPKEVAIHLHSQGGG SVHPRTLQTNEENSRVLP
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