

Protein Sequences Analyzed

Symbol	Protein	Organism	GenBank accession	Number of SCRs ^a	E-value of blastp comparison ^b	
					to C4bp α	to FH
VCP (C3L)	Vaccinia virus complement control protein	Vaccinia virus, strain WR	<u>P68638</u>	4	2×10^{-44}	1×10^{-21}
SPICE (D12L)	Smallpox inhibitor of complement enzymes	Variola major virus, strain India-1967	<u>NP_042056</u>	4	2×10^{-41}	4×10^{-20}
SPICE (D15L)	Smallpox inhibitor of complement enzymes	Variola major virus, strain Bangladesh-1975	<u>T28450</u>	4	2×10^{-41}	4×10^{-20}
IMP (C17L)	Inflammation modulatory protein	Cowpox virus, strain GRI-90	<u>CAA64102</u>	4	5×10^{-45}	9×10^{-24}
FH	Factor H	Human	<u>CAA68704</u>	20	1×10^{-37}	0.0
C4bp α	C4 binding protein, α chain	Human	<u>AAA36507</u>	8	0.0	3×10^{-36}
MCP	Membrane cofactor protein	Human	<u>P15529</u>	4	6×10^{-41}	2×10^{-19}
DAF	Decay accelerating factor	Human	<u>P08174</u>	4	4×10^{-37}	3×10^{-13}
CR1	Complement receptor type 1	Human	<u>P17927</u>	30	2×10^{-59}	4×10^{-77}
CR2	Complement receptor type 2	Human	<u>P20023</u>	15	3×10^{-66}	1×10^{-45}

^aThe number of SCRs listed for each sequence corresponds to the GenBank accession number provided. See text for the description of the allelic variation in the number of SCRs in the CR1 and CR2 proteins.

^bThe E-values are provided for blastp similarity searches at the National Center for Biotechnology Information BLAST server (www.ncbi.nlm.nih.gov/blast/) using as queries full length sequences of C4bp α and FH with accession numbers listed above. Due to the different number of SCRs in each protein, the E-values for the full length sequences do not directly correspond to the degree of sequence similarity between the individual SCRs.