

## Review

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### Complement evasion by human pathogens

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#### Summary

The human complement system has a pivotal role in the recognition, opsonization and elimination of microbial intruders. This functionality is maintained by a well-balanced interaction network of serum proteins and cell-surface receptors.

Over thousands of years of co-evolution, many microorganisms have developed specific complement-evasion strategies to escape the attack of the immune system. Although some of these strategies are highly specific for a single species, others are shared more broadly among bacteria, viruses, fungi and parasites.

The most prevalent complement-evasion mechanism seems to be the capture of soluble host complement regulators on the microbial surface or the expression of their structural mimics. However, the inactivation of complement components by proteolytic degradation or specific inhibition of essential functional sites is also frequently observed.

*Staphylococcus aureus* has a particularly wide and diverse arsenal of complement-evasion proteins, many of which have been discovered only recently. These numerous evasion strategies could contribute to the high virulence of this bacterium.

Structural biology is an indispensable tool for characterizing the structure and function of complement-evasion proteins. Recent publications of the co-crystal structures of evasion proteins with their human targets have allowed an even deeper insight into the molecular basis of these escape mechanisms.

The rapid increase in the structural and functional understanding of complement evasion could serve as an important starting point for the development of antimicrobial or complement-targeting therapeutics.

## About the authors

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John D. Lambris is the Dr Ralph and Sallie Weaver Professor of Research Medicine at the department of Pathology and Laboratory Medicine of the University of Pennsylvania, Philadelphia, USA. After earning his Ph.D. in biochemistry from the University of Patras, Greece, he dedicated his research to various aspects of the complement system. In his laboratory at the University of Pennsylvania, he applies ideas and methods that are embodied in engineering, computer science, physics, chemistry and other fields to address today's challenges in complement research. His current research efforts include the development of small-size complement inhibitors, the crosstalk of complement with other pathways and complement evasion by bacteria and viruses. He has been the president of the International Complement Society and is the founder and executive director of the Aegean Conferences.

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Daniel Ricklin is a postdoctoral researcher at the University of Pennsylvania, Philadelphia, USA, in the research group of John D. Lambris. He earned his M.Sc. in pharmaceutical sciences from the Swiss Federal Institute of Technology in Zurich, Switzerland, and his Ph.D. in pharmaceutical chemistry from the University of Basel, Switzerland. His current research is centred on the structure, function and interaction network of complement proteins and the therapeutic intervention of complement-related diseases.

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**Supplementary information S1 (table): Microbial complement-targeting proteins**

Pathogen Protein	Target	Action	Ref
<b>Bacteria</b>			
<b><i>Actinobacillus</i> spp.</b>			
Omp100	fh	Recruitment of regulators	1
<b><i>Bordetella</i> spp.</b>			
FHA	C4BP, (fh, FHL-1)	Recruitment of regulators	2
<b><i>Borrelia</i> spp.</b>			
CRASP	fh, FHL-1	Recruitment of regulators	3
Erp	fh	Recruitment of regulators	4, 5
n/a	C8, C9	Prevents MAC formation	6
<b><i>Escherichia</i> spp.</b>			
OmpA	C4BP	Recruitment of regulators	7
StcE	C1-INH	Recruitment of C1-INH	8
TraT	C5b6	Prevents MAC formation	9
<b><i>Fusobacterium</i> spp.</b>			
n/a	fh	Recruitment of regulators	10
<b><i>Haemophilus</i> spp.</b>			
n/a	C4BP, fh	Recruitment of regulators	11, 12
<b><i>Moraxella</i> spp.</b>			
UspA1/2	C4BP	Recruitment of regulators	13
<b><i>Neisseria</i> spp.</b>			
LOS	fh, FHL-1	Recruitment of regulators	14
GNA1870	fh, FHL-1	Recruitment of regulators	15, 16
Por	C4BP, fh, FHL-1	Recruitment of regulators	17
n/a	MCP	Attachment to epithelial cells	
<b><i>Porphyromonas</i> spp.</b>			
prtH	C3, IgG	Degrades C3 and IgG	18

<b><i>Pseudomonas</i> spp.</b>			
PaE	Pseudomonas elastase	C1q, C3	Degrades C1q and C3
PaAP	Pseudomonas alkaline protease	C1q, C3	Degrades C1q and C3
Tuf	Elongation factor	fH, FHL-1	Recruitment of regulators
<b><i>Serratia</i> spp.</b>			
n/a	56 kDa protease	C5a, C1-INH	Degrades C5a, degrades C1-INH
<b><i>Staphylococcus</i> spp.</b>			
CHIPS	Chemotaxis inhibitory protein of <i>S. aureus</i>	C5aR	Antagonizes C5a
Efb	Extracellular fibrinogen-binding protein	C3/C3b/C3d	Inhibition of C3 and C3b-containing convertases
Ehp <sup>a</sup>	Efb-homologous protein	C3/C3b/C3d	Inhibition of C3 and C3b-containing convertases
SAK	Staphylokinase	C3b, IgG (via Plasmin) IgG	Cleaves complement proteins, removes C3b from surface Inhibits Ig interaction with C1q
Sbi	<i>S. aureus</i> IgG-binding protein	C3 Convertases	Inhibits C3 activation to C3a/C3b
SCIN	Staphylococcal complement inhibitor	Ig's, gC1q-R	Inhibits Ig interaction with C1q
SpA	<i>S. aureus</i> protein A	C5	Prevents C5 cleavage
SSL-7	Staphylococcal superantigen-like protein 7		
<b><i>Streptococcus</i> spp.</b>			
Bac	-Protein	IgA, fH	Recruitment of regulators
Fba	Fibronectin-binding protein	fH, FHL-1	Recruitment of regulators
Hic <sup>b</sup>	Factor H-binding inhibitor of complement	fH	Recruitment of regulators
IdeS	IgG-degrading Enzyme of <i>S. pyogenes</i>	IgG	Cleaves IgG, no interaction with C1q
M <sup>b</sup>	Surface proteins M family (Acp, Sir, etc.)	fH, C4BP, FHL, FHR, MCP	Recruitment of regulators
PLY	Pneumolysin	IgG, C1q	Complement activation / depletion
PspA	Pneumococcal surface protein A	unknown	Potential impairing of AP and complement receptors
PspC <sup>c</sup>	Pneumococcal surface protein C	fH (C3, IgA)	Recruitment of regulators.
scpA/B	Streptococcal C5a peptidase	C5a	Potential degradation of C3/C3b
SIC	Streptococcal inhibitor of complement	C5b-7, C5b-8	Degrades C5a, Disrupts signaling
SPE B	Streptococcal pyrogenic exotoxin B	Properdin, Ig's	Prevention of MAC formation
SpG	Streptococcus protein G	Ig's	Degrades Properdin, Ig's Inhibits Ig interaction with C1q

<b><i>Yersinia</i> spp.</b>					
YadA	Yersinia adhesin A	fH		Recruitment of regulators	52
<b>Viruses</b>					
<b>Herpes viruses</b>					
gC1/2	Transmembrane glycoproteins C1,C2 (HSV)	C3b		Binds to C3b, decay acceleration (only AP), inhibits binding of properdin & C5	53
gE+gI	Glycoproteins E+I (HSV)	IgG		Fc-receptor, less activation	54, 55
gp34,68	Glycoproteins 34, 68 (HCMV)	IgG		Fc-receptors, less activation	56, 57
gpl+gpIV	Glycoproteins I+IV (VZV)	IgG		Fc-receptor, less activation	58
KCP <sup>d</sup>	Kaposi's sarkoma-associated complement control protein (KSHV)	C3b		Mimics regulators (cofactor/decay acceleration)	59
<b>Retroviruses</b>					
gp41	Envelope glycoprotein 41 (HIV)	C1q, fH, CD59		Direct CP activation, Recruitment of regulators, decrease CD59 expression	60-62
gp120	Envelope glycoprotein 120 (HIV)	MBL, fH		Direct LP activation, Recruitment of regulators	62, 63
Tat	Transactivator of transcription (HIV)	C1-INH		Induces C1-INH expression	64
<b>Poxviruses</b>					
IMP	Cowpox control inflammation modulatory protein (Cowpox Virus)	C3b, Convertases		Mimics regulators (cofactor/decay acceleration)	65
MOPICE	Monkeypox inhibitor of complement enzymes (monkeypox virus)	C3b		Mimics regulators (only cofactor activity)	66
SPICE	Smallpox inhibitor of complement enzymes (variola virus)	C3b, Convertases		Mimics regulators (cofactor/decay acceleration)	67
VCP	Vaccinia virus complement control protein (vaccinia virus)	C3b, Convertases		Mimics regulators (cofactor/decay acceleration)	68
<b>Filoviruses</b>					
NS1	Non-structural protein 1 (West Nile virus)	fH		Recruitment of regulators	69
<b>Fungi</b>					
<b><i>Aspergillus fumigatus</i></b>					
n/a	Unknown factor	fH, FHL-1, C4BP		RCA recruitment	83

<b><i>Candida albicans</i></b>				
CRASP-1	Complement regulator-acquiring surface protein 1	fH, FHL-1, C4BP	Recruitment of regulators	84, 85
Gpm1p	Phosphoglycerate mutase	fH, FHL-1	Recruitment of regulators	86

**Parasites**

<b><i>Echinococcus</i> spp.</b>				
n/a	Hydatid cyst wall	fH	Recruitment of regulators	70
<b><i>Ixodes</i> spp.</b>				
IRAC	<i>Ixodes ricinus</i> anti-complement protein	AP convertase	Decay acceleration	71
ISAC	<i>Ixodes scapularis</i> anti-complement protein	AP convertase	Decay acceleration	72
<b><i>Onchocerca</i> spp.</b>				
mf	Microfilariae	fH	Recruitment of regulators	73
<b><i>Ornithodoros</i> spp.</b>				
OmCl	<i>Ornithodoros moubata</i> complement inhibitor	C5	Binds to C5 (potentially blocks binding to C5 convertase)	74
<b><i>Schistosoma</i> spp.</b>				
CRIT	Complement C2 receptor trispanning	C2	Inhibits CP convertase formation	75
m28	28kDa membrane serine protease	iC3b	Cleaves iC3b, restricts CR3 binding	76, 77
Pmy <sup>e</sup>	Paramyosin	C8, C9, C1q, IgG	Prevents MAC formation Decreases AP activation	78-81
<b><i>Trypanosoma</i> spp.</b>				
CRIT	Complement C2 receptor trispanning	C2	Inhibits CP convertase formation	75
T-DAF	Trypanosoma decay-accelerating factor	Convertase	Destabilizes convertase	82

<sup>a</sup>Ehp has also been termed extracellular complement-binding protein (Ecb). <sup>b</sup>As Hic is not a member of the classical PspC family but a PspC-like protein, it is listed as separate protein. <sup>c</sup>Former names: cholin-binding protein (CbpA), *Streptococcus pneumoniae* secretory IgA-binding protein (SpsA) and pneumococcal C3-binding protein A (PbcA). <sup>d</sup>KPC has also been termed kaposica. <sup>e</sup>Paramyosin has previously been described as Schistosome complement inhibitor protein 1 (SCIP-1). AP, alternative pathway; C1-INH, C1 esterase inhibitor; C4BP, C4-binding protein; C5aR, C5a receptor; CP, classical pathway; DAF, decay accelerating factor; fH, factor H; FHL, factor H-like protein; Ig, immunoglobulin; MBL, mannose-binding lectin; MCP, membrane cofactor protein.

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