

HBP-5: A Leading Heparin-Binding Peptide with Remarkable Activity against Gram-negative Bacteria

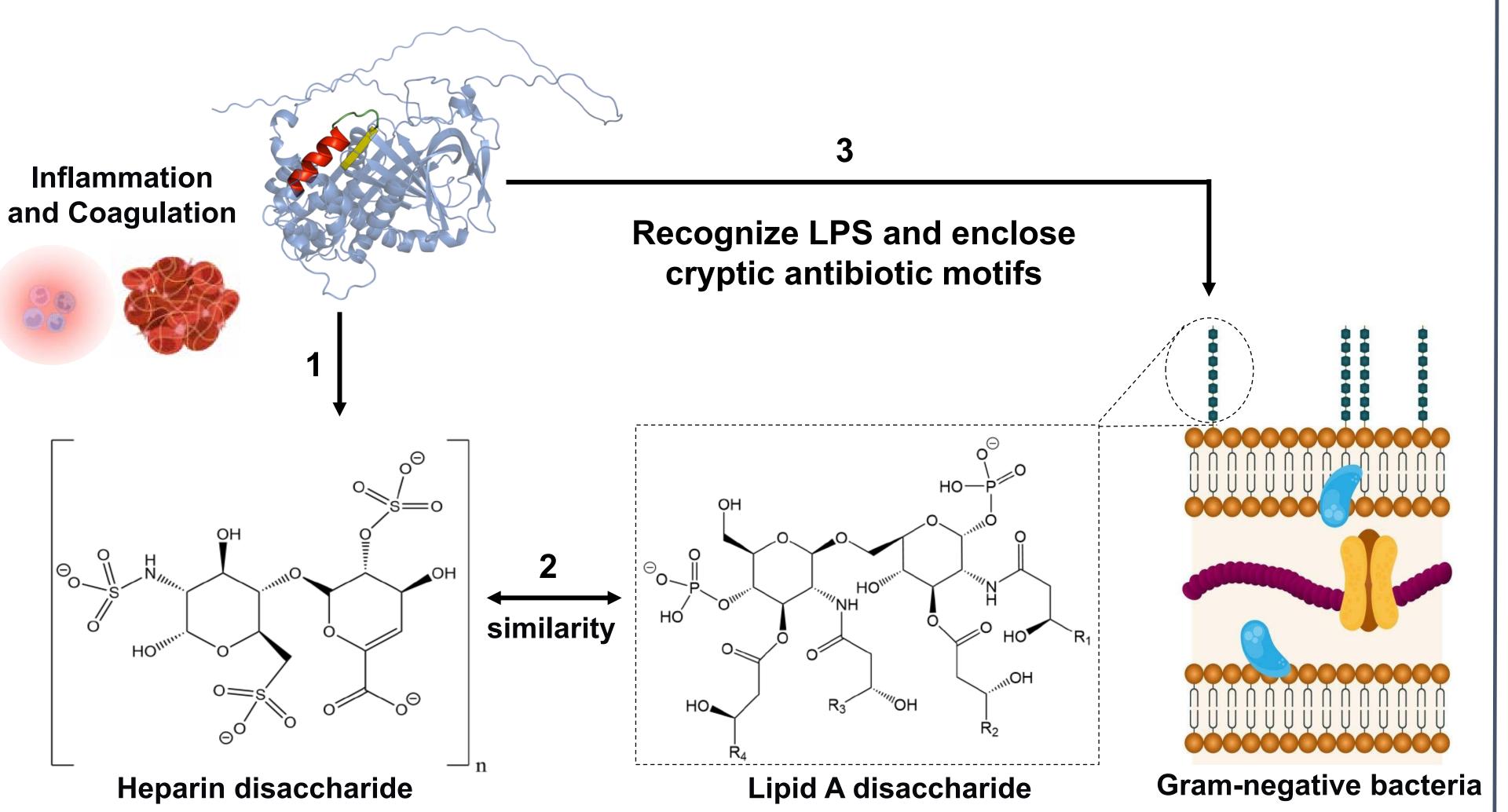


Roberto Bello Madruga ¹, Daniel Sandín ¹, Javier Valle ², David Andreu ² and Marc Torrent ¹ roberto.bello@uab.cat

Systems Biology of Infection Lab, Department of Biochemistry and Molecular Biology, UAB, Cerdanyola del Vallès 08193. Spain ² Universitat Pompeu Fabra, Department of Medicine and Life Sciences, Barcelona Biomedical Research Park, Barcelona 08003. Spain

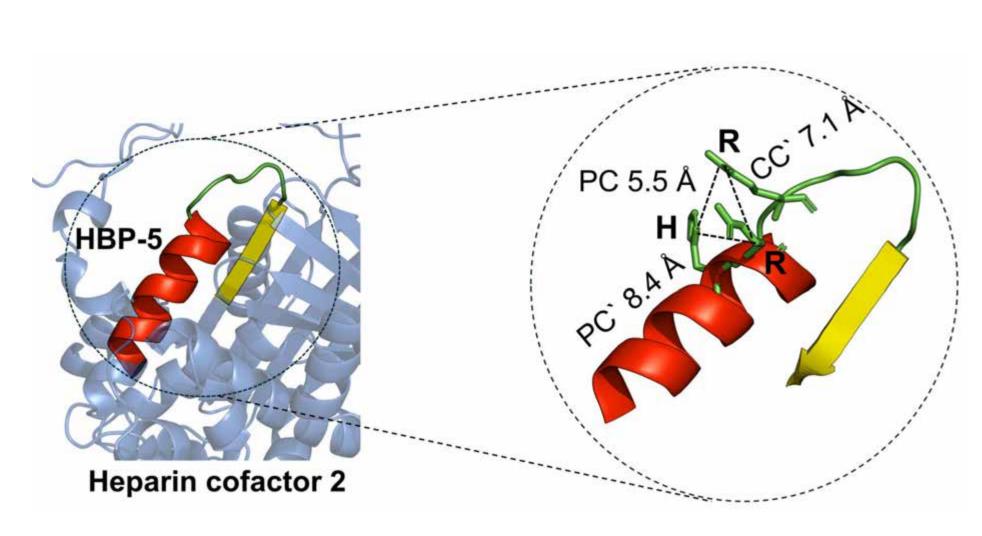
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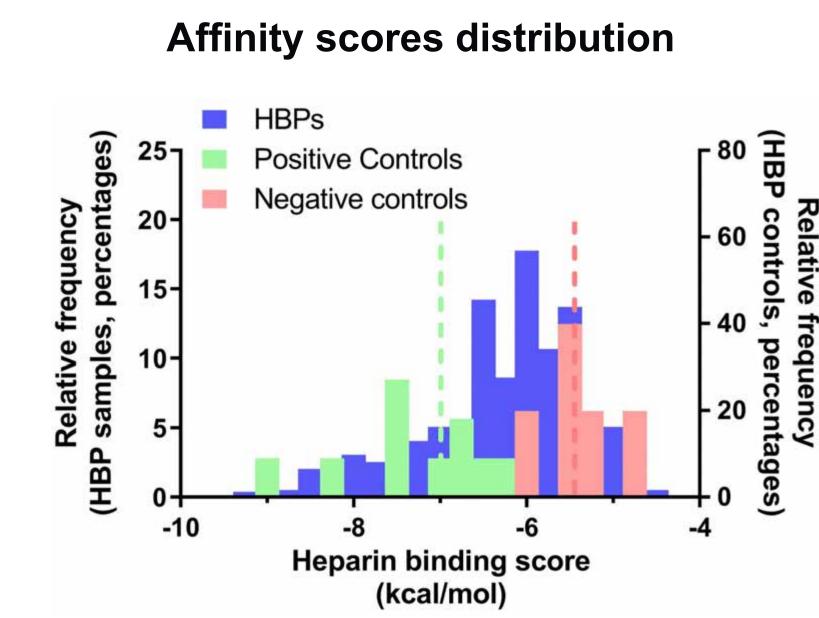
BACKGROUND



METHODOLOGY

- > Use the AMPA predictor to identify antimicrobial regions in Heparin-Binding Proteins (HBPs).
- > Identification of Heparin Binding sites (CPC) motif) in cryptic peptides and evaluation of their affinity by molecular docking.
- > Synthesis and validation of the best candidates corresponding to the regions with the highest AMPA and Heparin-binding score.





MRC-5 cytotoxicity

RESULTS

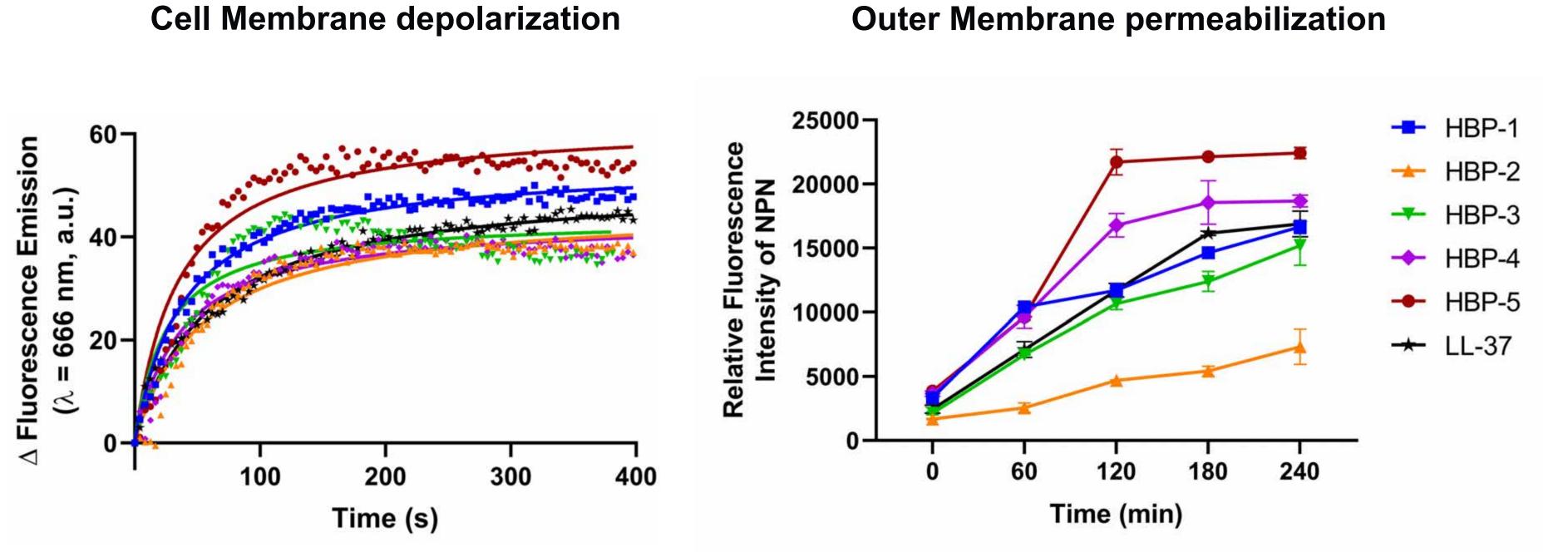
Antimicrobial Activity, Heparin-LPS Affinity and Toxicity of HBPs peptides

Minimum Inhibitory Concentration (uM)

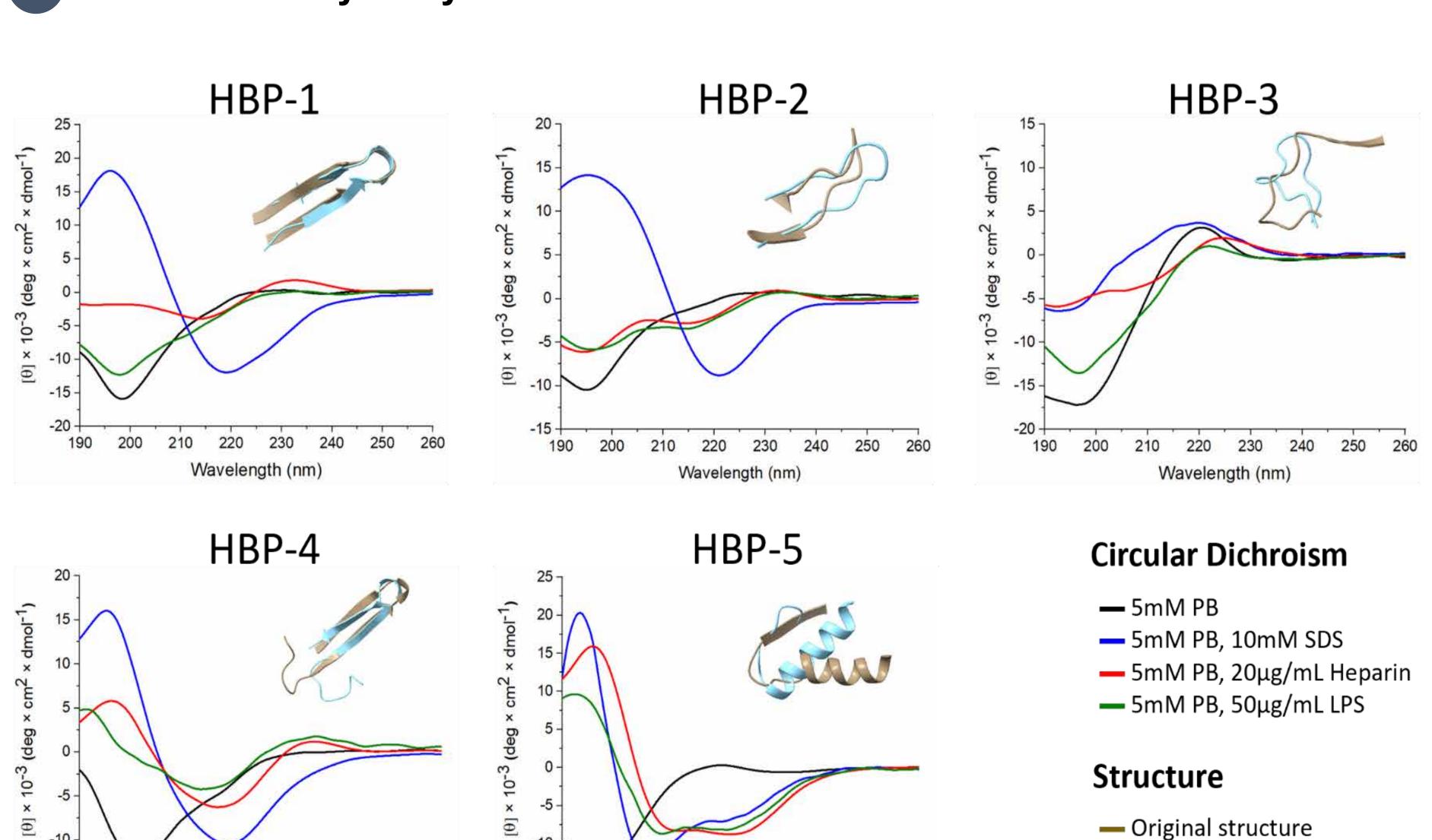
			Minimum Inhibito	ry Concentra	Heparin, LPS Affinity and Toxicity					
	E. coli	A. baumannii	P. aeruginosa	S. aureus	E. faecium	L. monocytogenes	Heparin Affinity (% Elution buffer)	LPS Affinity (EC50, μM)	Hemolysis % (125 µM of peptide)	
P-1	1.6	1.6	3.1	50	100	6.3	60	42 ± 16	4.6 ± 0.6	

	E. COII	A. Daumamm	P. aeruginosa	S. aureus	E. laeciulli	L. monocytogenes	(% Elution buffer)	(EC50, µM)	(125 µM of peptide)	(IC50, μM)
HBP-1	1.6	1.6	3.1	50	100	6.3	60	42 ± 16	4.6 ± 0.6	>200
HBP-2	12.5	50	25	>100	>100	37.5	59	1500 ± 600	2 ± 1	>200
HBP-3	3.1	0.8	6.3	25	>100	6.3	68	7 ± 5	4 ± 1	>200
HBP-4	0.2	0.8	8.0	3.1	12.5	1.6	82	0.7 ± 0.6	15.5 ± 0.1	35 ± 1
HBP-5	0.4	0.2	0.8	6.3	25	1.6	98	0.9 ± 0.7	10.3 ± 0.2	69 ± 2
LL-37	1.6	6.3	0.8	25	0.8	8.0	50	0.9 ± 0.8	32.7 ± 0.7	26 ± 3

Mechanism of Action of HBP-derived Antimicrobial Peptides

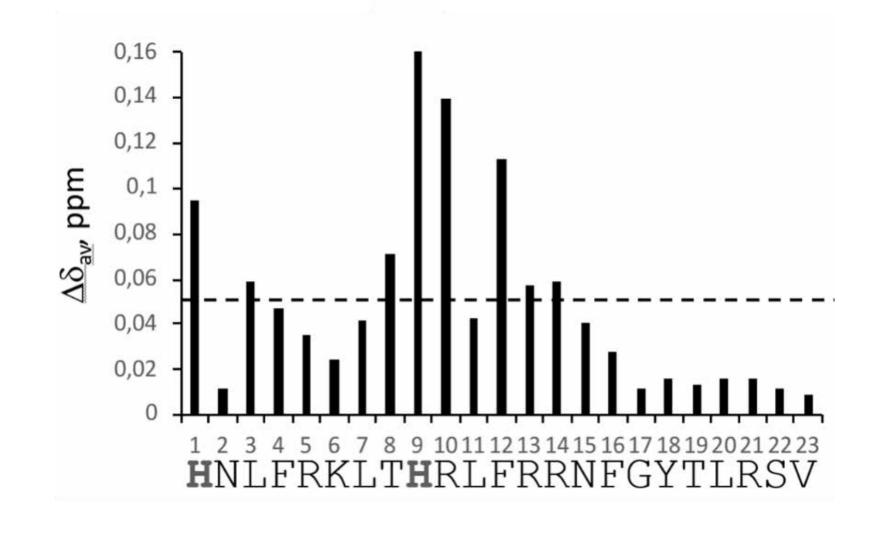


3 Structural Analysis by Circular Dichroism



Characterization of HBP-5 peptide

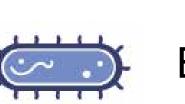
Chemical shifts induced by Heparin



involved in Heparin binding

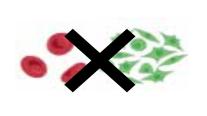
Distances between CPC' residues

Why HBP-5 is a leading peptide?

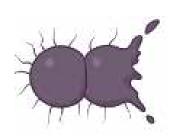


Broad spectrum of antibacterial activity

Time (ns)



Non-cytotoxic and non-hemolytic



Bacterial cell depolarization and permeabilization



High affinity for LPS

Conclusions

- > We have shown that Glycosaminoglycans-binding proteins can be a source of new AMPs, some with remarkable activity, particularly against Gram-negative bacteria.
- > The fact that these peptides can bind to both Heparin and LPS is consistent with the structural similarity hypothesis.

What's next

- > Investigate the structural determinants of HBP-5 and their implication on the antibacterial mechanism.
- > Optimize and evaluate HBP-5 peptide in an *in vivo* infection model.



Wavelength (nm)



210 220 230 240 250 260

Wavelength (nm)



PepFold prediction



