


Año	Título de la Publicación	Nombre de la Revista / Libro	Vínculo o DOI	Indexador	Autoría
2010	[Aproximaciones globales para el estudio de interacciones proteína-proteína entre virus y hospedero]	Future Microbiol	https://dx.doi.org/10.2217/fmb.10.7	SCOPUS	PA,AC
Importancia: Uso de la bioinformática para predecir interacciones proteínicas utilizando información de similitud de las secuencias proteicas.					

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SPECIAL FOCUS ISSUE: ON THE ROAD TO SYSTEMS BIOLOGY OF HOST-PATHOGEN INTERACTIONS - REVIEW  normal

Global approaches to study protein–protein interactions among viruses and hosts

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While high-throughput protein–protein interaction screens were first published approximately 10 years ago, systematic attempts to map interactions among viruses and hosts started only a few years ago. HIV–human interactions dominate host–pathogen interaction databases (with approximately 2000 interactions) despite the fact that probably none of these interactions have been identified in systematic interaction screens. Recently, combinations of protein interaction data with RNAi and other functional genomics data allowed researchers to model more complex interaction networks. The rapid progress in this area promises a flood of new data in the near future, with clinical applications as soon as structural and functional genomics catches up with next-generation sequencing of human variation and structure-based drug design.

Keywords: hepatitis C virus • herpes viruses • HIV • mass spectrometry • protein interaction networks • protein purification • RNAi • yeast two-hybrid screens