

SAROTUP 2.0: a suite of web tools for finding potential target-unrelated peptides from phage display Jian Huang^{*}, Beibei Ru

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Introduction

MimoSearch

Phage display has made a great impact on modern medicine. It has been widely used for epitope mapping, analysis of protein-protein interactions, prediction of drug target, and identification of enzyme substrates and inhibitors.

- Some peptides derived from phage display have been developed into new drugs, such as romiplostim and peginesatide which are approved by FDA; others have shown promise for the development of diagnostics, vaccines, and the targeted delivery of therapeutics.
- However, phage display data are suffered from target-unrelated peptides (TUPs), which creep into or even dominate the experiment results through growing faster (propagation-related TUP), or binding to contaminants or other components of the screening system (selection-related TUP).
- In this poster, we present SAROTUP version 2.0, a suite of web tools that are helpful for cleaning phage display data. The tools are freely available at http://immunet.cn/sarotup.

TUPScan

This tool can check if your peptides are with known TUP motifs or identical to known TUP sequences.

SAROTUP: Target-Unrelated Peptides Scanners

This tool can check if any peptide in the MimoDB database is identical to your peptides, which indicates if any of your peptides "binds" multiple targets. If so, it might be a TUP rather than a mimotope.

SAROTUP: Target-Unrelated Peptides Scanners

UCSTC

Search HLAB

Home	Using the MimoDB database as a virtual and comprehensive control in background, the MimoSearch tool in the SAROTUP suite is designed to check if any submitted peptide has also				
TUPScan	been gained by other groups with various targets. If any, such peptide may be a target-unrelated peptide rather than a true target binder, because the chance of obtaining an identical peptide from a library having millions or billions of different peptides with completely different targets is extremely small. Here we go!				
MimoScan					
MimoSearch	Enter a set of peptide sequences in the text area below:				
MimoBlast	TESTPEPTIDES YLFSVHWPPLKA GEQRGEPSMITH				
Citation	SAHGTSTGVPWP MARIQHGEYSEN				
Help					
	Or upload a sequence file: Example Reset Scan				

MimoBlast

	Uestc			
Home TUPScan	The TUPScan tool in the SAROTUP suite is designed to check whether your peptides gained by phage display technology match any known TUP motif. If a peptide has a known TUP motif, this peptide is very likely to be a target-unrelated peptide rather than a true target binder. The tool will scan your peptides for all known TUP motifs, report possible	3	database is	can check if s highly similar
MimoScan	TUPs in a table, and produce a downloadable file in raw sequence format, of which the possible TUPs and redundant sequences are filtered. Here we go!		be a "binde	er" of multiple t
MimoSearch	Enter a set of peptide sequences in the text area below:		Enter a set of p	eptide sequences in th
MimoBlast	NMKLKLREMTQR A DARHSSSLQMLF MTRPTSLTQLTG		TESTPEPTIDES	Your Query Peptide
Citation	LHIRVNETAYRV GLTFQLHHQMRP DFLREHGMKNPR		YLFSVHWPPLKA SAHGTSTGVPWP	TESTPEPTIDES YLFSVHWPPLKA
Help	RSRPTNMTTLRD YTQTGWLNWHER			
	Or upload a sequence file: 浏览			
	Example Reset Scan			SAHGTSTGVPWP
				🕘 immunet.cn/sar

MimoScan

This tool can check if any peptide in the MimoDB database matches your mimotope motifs, which can indicate how specific your mimotope motifs are.

SAROTUP: Target-Unrelated Peptides Scanners				
Search HLAB				
Usersa	The MimoScan tool in the SAROTUP suite is designed to check if there is any peptide in the			

any peptide in the MimoDB r to your peptides. If so, it may argets.

Enter a set of p	Download result file			
TESTPEPTIDES You		ery Peptide	Similar Peptide in MimoDB	Blast Repor
YLFSVHWPPLKA	TESTPEPTIDES YLFSVHWPPLKA		No hits found!	Report 1 🍖
SAHGTSTGVPWP			YLFSVHWPPLKA in mimoset: 405	Report 2 🧶
			SAHGTSTGVPWP in mimoset: 1883	↑
			SAHGTSTGVPWP in mimoset: 1725	Read online
			SAHGTSTGVPWP in mimoset: 1524	
	SAHGT	STGVPWP	SAHGTSTGVPWP in mimoset: 1262	Report 3 🍖
		🕘 MimoBlast Alignme	ent Viewer - Mozilla Firefox	
Or upload a seque		🕙 immunet.cn/sarotup/cgi-bin/ViewAlignment.pl?File=MimoBlastResult1349765965651. 🏠 💉 🛩		
		> Mimoset ID: 1129; Peptide 1: SAHGTSTGVRGP Length=12		
Expect value: 10 Score = 21.6 bits (44), Expect = 0.72, Method: Compositional matrix adjus Identities = 10/12 (83%), Positives = 10/12 (83%), Gaps = 0/12 (0%)				
Coptimized particular Exam		Query 1 SAHG SAHG	memorration 10	e alignment on the fly

This tool can also be used to check if a known TUP has highly similar peptides in the MimoDB database, which can further be used to derive new TUP motifs. Possible TUPs similar with the notorious **SVSVGMKPSPRP** are found with MimoBlast and shown below.

Home	The MimoScan tool in the SAROTUP suite is designed to check if there is any peptide in the MimoDB database that matches patterns submitted. If any, the tool will list them for you to					
TUPScan	facilitate further analysis. The query can be consensus sequences, motifs or patterns derived from TUPs or your panning results. Besides the commonly used simple format, e.g. WXXW,					
MimoScan	patterns in PROSITE format are fully surpported. Here we go! Enter one or more peptide patterns in the text area below:					
MimoSearch	W-x-P(2)-F-[KR] F-[GSTV]-P-R-L-G					
MimoBlast	W-[TS]-[LI]-x(2)-H-[RK]					
Citation						
Help						
	Or upload a pattern file: 浏览…					
	Example Reset Scan					

Peptide	Target numbers	Mimoset numbers	Expect value	******
SVSVGMNPSPRP	1	1	0.14	
SVSVGLKPSPRP	1	1	0.15	
SVSVGMKPSHRP	1	1	0.16	
SVSVGMKPRPRP	2	2	0.17	
SVSVGMKPSPRK	1	1	0.17	
SVSVGKKPSPRP	1	1	0.24	
SVSGGMKPSPRP	1	1	0.26	
SVSVGMLPSPRP	1	1	0.32	
YVYVGMKPSPRP	1	1	0.32	

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