Inverse ligand binding prediction provides insights into toxicity induced by Cyclosporine A

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Outline

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- Results
- computational analysis of putative targets
- binding assays
 enzymatic activity assays
- O such a since a currently
- Conclusions

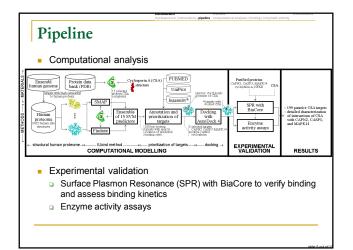
Introduction

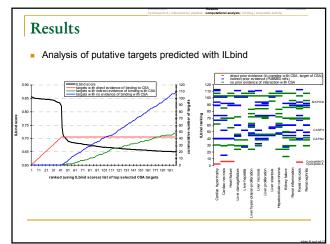
- Cyclosporin A (CSA)
 - cyclic nonribosomal peptide with 11 amino acids
 - immunosuppressant used in kidney, liver, bone marrow and pancreas transplantation; also used to treat heart failure, psoriasis, and rheumatoid arthritis
 - well understood mechanism of action
 - binds cyclophilin A & forms complex with calcineurin inhibiting its activity
 - this prevents dephosphorylation of nuclear factor of activated T-cells (NFAT), hampering their transit to the nucleus; thus immune response is shut down
 - also associated with severe side effects including nephrotoxicity, hepatotoxicity, and cardiotoxicity
 - mechanistic details behind these side effects remain unclear

Introduction

- Cyclosporin A (CSA)
 - interacts with many protein targets
 cyclophilin D, cyclophilin B, TGF-β, renin-angiotensin system, superoxide
 - dismutase, etc.

 these off-target interactions could be involved in the activation of
 - signaling pathways that lead to the toxic responses
- we use inverse ligand binding predictions to perform structural human proteome-wide determination of putative binding partners of CSA
 - these putative interactions are linked to toxicities
 - selected three are investigated experimentaly in vitro





Results

Analysis of putative targets predicted with ILbind

p-values	# targets
	9
9.31e-10	12
1.48e-09	12
p-values	# targets
3.91e-14 - 3.18e-04	64
7.76e-14 - 2.52e-04	53
5.04e-11 - 2.76e-04	50
1.55e-10 - 2.95e-04	42
4.47e-10 - 2.46e-04	45
p-values	# targets
	15
	12
2.10e-06 - 2.10e-06	8
6.43e-06 - 3.19e-02	9
2.36e-05 - 2.39e-01	8
	13
2.81e-05 - 1.88e-01	9
8.03e-05 - 1.50e-01	13
1.16e-04 - 1.16e-04	5
6.90e-04 - 8.09e-02	4
	12
	13
3.66e-08 - 3.19e-02	13
3.06e-06 - 1.93e-02	14
2.38e-04 - 2.38e-04	4
	$\begin{array}{c} 8.51e-10\\ 9.31e-10\\ 1.48e-09\\ \hline 9.31e-10\\ 3.16e-10\\ 3.16e-10\\ 3.16e-10\\ 3.16e-10\\ 3.16e-10\\ 3.16e-10\\ 3.16e-10\\ 3.16e-10\\ 3.16e-10\\ 3.16e-00\\ \hline 9.10e-10\\ 3.16e-00\\ 3.16e$

nal analysis |

