

1. Query using text or sequence search

Search

2. Explore results and add constraints

Set minimum prediction values

CA (Cancer) 0.5

CVD (Cardiovascular disease) 0

DM (Diabetes) 0

APO (Apoptosis) 0

ANG (Angiogenesis) 0.5

MI (Molecular imaging) 0

BD (Binding data available) 0

Details

Results 1 - 20 of 32

CA	CVD	DM	APO	ANG	MI	BD		Peptide	Sequence	Interactor	Reference	Score
							<input type="checkbox"/>	YWKV	YWKV	unknown	11026536	0.49
							<input type="checkbox"/>	RGDYK	RGDYK	unknown	11216533	0.49
							<input type="checkbox"/>	YRGDY	YRGDYK	unknown	11216533	0.49
							<input type="checkbox"/>	YRGDY	YRGDYV	unknown	11216533	0.49
							<input type="checkbox"/>	ATWLP	ATWLPPR	KDR	10747021	0.77
							<input type="checkbox"/>	RLVSY	RLVSYNGIIFFLK	unknown	15256450	0.5
							<input type="checkbox"/>	RGD	RGD	unknown	16391196	0.68
							<input type="checkbox"/>	RGDFV	RGDFV	unknown	10452325	0.49
							<input type="checkbox"/>	YRADY	YRADYV	unknown	10452325	0.49
							<input type="checkbox"/>	YRGDY	YRGDYV	unknown	10452325	0.49
							<input type="checkbox"/>	YRGDF	YRGDFY	unknown	10452325	0.49
							<input type="checkbox"/>	SYSPY	SYSPYDMLSEIK	unknown	12453439	0.49
							<input type="checkbox"/>	SLYYI	SLYYIQQDTK	unknown	12453439	0.5
							<input type="checkbox"/>	HTMYY	HTMYHHYQHHL	KDR	12183450	0.75
							<input type="checkbox"/>	SFLLR	SFLLRNPNDKYEPE	unknown	14521590	0.49

3. Review and vote

Classification incorrect?
 Click the corresponding button to vote. Your vote is used to improve the automatic classification.

"Yes, abstract is *related*."
 "No, abstract is *not related*."

CA	CVD	DM	APO	ANG	MI	BD	Vote
<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Yes
<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	No

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Template-constrained cyclic peptide analogues of somatostatin: subtype-selective binding to somatostatin receptors and antiangiogenic activity.

Suich DJ, Mousa SA, Singh G, Liapakis G, Reisine T, DeGrado WF

Beta-turns are a common secondary structure motif found in proteins that play a role in protein folding and stability and participate in molecular recognition interactions. Somatostatin, a peptide hormone possessing a variety of therapeutically-interesting biological activities, contains a beta-turn in its bioactive conformation. The beta-turn and biological activities of somatostatin have been successfully mimicked in cyclic hexapeptide analogues. Two novel, structured, non-peptidic molecules were developed that are capable of holding the bioactive tetrapeptide sequence of somatostatin analogues in a beta-turn conformation, as measured by somatostatin receptor (SSTR) binding. Template-constrained cyclic peptides in which the ends of the **-Tyr-D-Trp-Lys-Val-tetrapeptide** were linked by scaffolds based on either an N,N'-dimethyl-N,N'-diphenylurea or a substituted biphenyl system (DJS631 and DJS811, respectively), bound selectively to mouse SSTR2B and rat and human