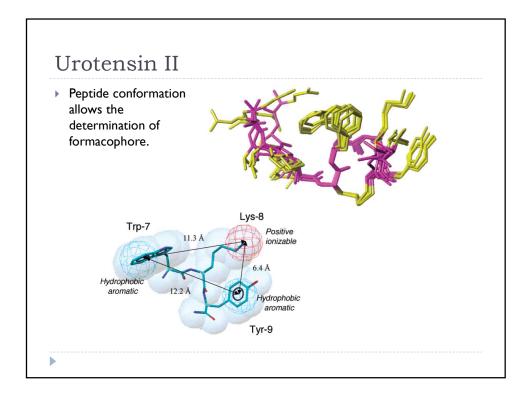
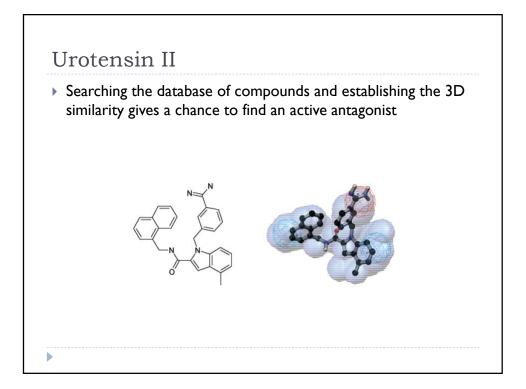
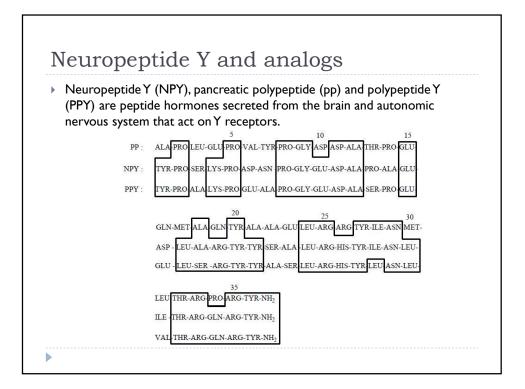
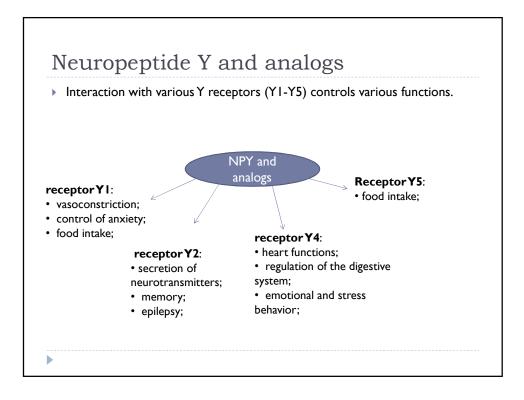


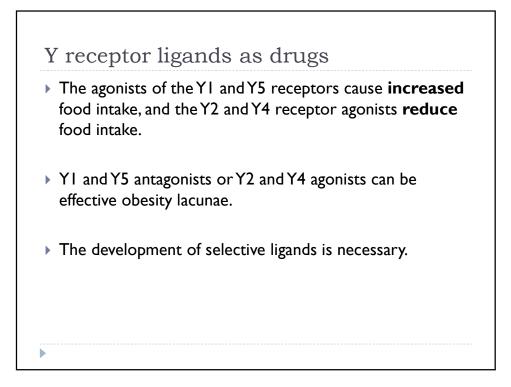
•	The alanine scan and		<u></u>					
	the study of short		no.	peptide	sequen	ce	EC ₅₀ (nM)	Emax
	•		1	U-II (1-11)	ETPDCFW		2.5 ± 0.2	100
	peptides allow to find		2	U-II (2-11)	TPDCFWK		2.4 ± 0.1	$103 \pm 3.$
	the motif responsible		3	U-II (3-11)	PDCFWKY		3.6 ± 0.6	$100 \pm 5.$
	for activity.		4	U-II $(4-11)$	DCFWKYC		3.0 ± 0.9	$102 \pm 4.$
	for accivicy.		5	U-II (5-11) U-II (1-10)	CFWKYCV ETPDCFW		1.8 ± 0.3 1.8 ± 0.1	$106 \pm 4.99 \pm 3.000$
	The key motive is		7	U-II (1 - 10) U-II (5-10)	CFWKYC	KIC .	2.3 ± 1.1	$95 \pm 6.$
	Trp-Lys-Tyr.		÷	80 199				
		no.		sequence	е	EC	₅₀ (nM)	Emax
		8	ATPDCFWKYCV EAPDCFWKYCV ETADCFWKYCV		V		1.8 ± 0.3	101 ± 1.7
		9			V		3.3 ± 0.8	101 ± 0.7
		10			V		1.9 ± 0.8	102 ± 3
	11 ETPACFWK		PACFWKYC	V		2.7 ± 0.5	101 ± 3	
		12	ETPDAFWKYCV (linear)		V (linear)	23	3 ± 16	96 ± 4
		13	ET	PDCAWKYC	V		5.7 ± 0.3	98 ± 1
		14		PDCFAKYC	Charles and Charles an	1,30	3 ± 98	45 ± 2
		15	ET	PDCFWAYC	V	14,80	0 ± 800	ND
		16		PDCFWKAC			3 ± 9	75 ± 3
		17	ET	PDCFWKYC	A		3.2 ± 0.3	99 ± 2

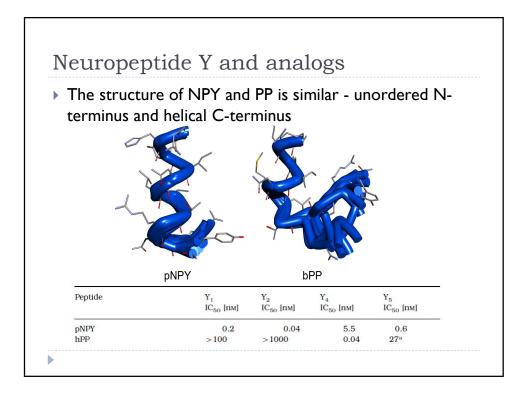


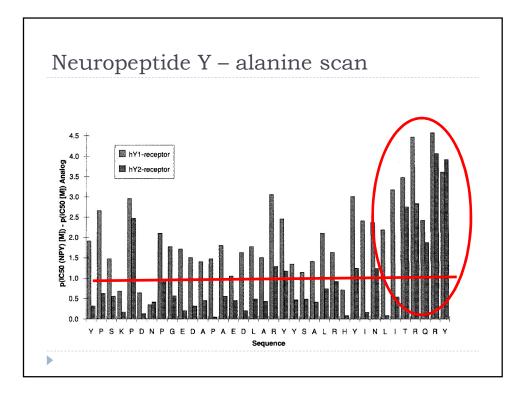












The C-terminal NPY fragment retains significant biological activity					
compound	rat brain (Y ₂) IC_{50} (μM				
1, NPY	0.00045 ± 0.00005				
2 , NPY(13-36)	0.015 ± 0.002				
3, PheMetArgPhe-NH $_2$	$\begin{array}{c} 40 \pm 1.4 \\ > 100 \\ 2.95 \pm 1.7 \\ 0.4 \pm 0.01 \\ 0.31 \pm 0.01 \end{array}$				
4, ThrArgGlnArgTyr-NH ₂					
5, IleTyrArgLeuArgTyr-NH ₂					
6, LeuIleTyrArgLeuArgTyr-NH ₂					
7, AsnLeulleTyrArgLeuArgTyr-NH ₂					
8, IleAsnLeuIleTyrArgLeuArgTyr-NH ₂	0.037 ± 0.006				
9, TyrlleAsnLeulleTyrArgLeuArgTyr-NH ₂	$\begin{array}{c} 0.008 \pm 0.003 \\ 0.012 \pm 0.002 \end{array}$				
10, HisTyrlleAsnLeulleTyrArgLeuArgTyr-NH ₂ 11, ArgHisTyrlleAsnLeulleTyrArgLeuArgTyr-NH ₂	0.012 ± 0.002 0.012 ± 0.007				

	Neuropeptide Y									
(dir shc	aple modification merization, subs ort peptides can ectivity.	titution) of	Ile-Asn-Pro-Ile-Tyr-Arg-Leu-Arg-Tyr-NH ₂ Ile-Asn-Pro-Ile-Tyr-Arg-Leu-Arg-Tyr-OMe Ile-Asn-Pro-Cys-Tyr-Arg-Leu-Arg-(CH ₂ -NH)-Tyr-NH Ile-Asn-Pro-Cys-Tyr-Arg-Leu-Arg-Tyr-OMe Ile-Asn-Pro-Cys-Tyr-Arg-Leu-Arg-(CH ₂ -NH)-Tyr-N Ile-Asn-Pro-Cys-Tyr-Arg-Leu-Arg-(CH ₂ -NH)-Tyr-N Ile-Asn-Pro-Cys-Tyr-Arg-Leu-Arg-(CH ₂ -NH)-Tyr-N Ile-Glu-Pro-Dpr-Tyr-Arg-Leu-Arg-(CH ₂ -NH)-Tyr-N							
peptide	Y1	Y2	\sim							
NPY	0.52 ± 0.02	0.23 ± 0.02	Ile–Glu-Pro-Dpr-Tyr-Arg-Leu-Arg-Tyr-NH ₂							
1 ^c	5.0 ± 0.46	11.3 ± 3.8	lle-Glu-Pro-Dpr-Tyr-Arg-Leu-Arg-Tyr-OMe							
2	25.7 ± 5.9	1420 ± 191	\sim							
3	34.8 ± 5.8	1650 ± 114								
4	4.8 ± 1.1	1120 ± 15	Ile-Glu-Pro-Dpr-Tyr-Arg-Leu-Arg-Tyr-OMe							
	2.3 ± 0.5	822 ± 78	Ile-Glu-Pro-Dpr-Tyr-Arg-Leu-Arg-(CH2-NH)-Tyr-NH2							
5	0.07 1.0.01									
5 6 ^c 7	0.07 ± 0.01 0.27 ± 0.01	55 ± 21 1036 + 116	\sim							

