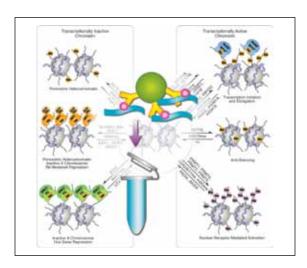
MethylScan® (Methylation Proteomics)

Step 1: MethylScan® Analysis

- 1. Experimental objectives and design consultation with scientists from Cell Signaling Technology (CST).
- 2. Determine samples and experimental parameters for study.
- 3. Methylated peptide immuno-affinity purification (IAP) with mono-methyl arginine antibody.
- 4. Tandem mass spectrometry (LC-MS/MS) analysis of enriched mono-methylated peptides for qualitative sequence and site identification.
- 5. Quantitative analysis of methylated peptide fold-change between study samples.



Step 2: MethylScan® Report and Consultation

- 1. MethylScan® report with qualitative and quantitative results.
- 2. Report contains sequence assignments in table format and detailed explanation of table contents and guidelines for data review.
- 3. Detailed discussion and review of report with CST scientists.
- 4. MethylScan® timeline: approximately 5 weeks; preliminary results delivery in 2–3 weeks; timeline will vary with project size.

o III	Methyls	can (Mono-Methyl-A	roinine) SAMPLE	RESULTS	1	,	-
	2000						
Table #1: Mouse Brain and Embryo; Trypsin Digest; Mono-Methyl-Arg Antibody (DSA12A3 & Me-R4-100) Samples: Sample 1 = Mouse Brain = CS13444, 13445; Sample 2 = Mouse Embryo = CS13450, 13451							
. 4	Legend	* - methylation, # -	oxidized methionin	e, § - published site, I	Blue Text - CST antibody a	ivaliable, no Fo	ild Change determined, Bold Intensity = manually rev
Η.	-7						
47			The second second				
1		-	Fold Change				
9	Index	Index in Betail	Brain Embrya	Gene Name	Protein Name	Site	Description
1	1	Activator protein		The second second second		0.40	Character ANALYSIA
6	1/2	The second secon	-317	6730463M24Rik	BONA *	316	proteit aurore boreals
VI.		Acapter/scattols		Salan Chip operation			
6	. 4	4	Dran	Abit; Abit	Abi-1, Abi-1 mo4	189; 184	atti interactor 1 isoform 1
p	. 5		- 4.5	Akapā	AKMIN	109	A-knale archor protein 8.
	- 6		Debrica	/Akapit	AKAPE	188	A-kinase anchor protein 8
9	,	12	Deliver.	Akap8i	HAP90	238	A kinese anchor protein 8-like
9	. 1	15	200	Ark1; Ark1	ANK1; ANK1 (652	1684; 1870	ankyrm-1 voform 1
1	. 9	19	-67	Ark3; Ark3; Ark3; Ark3	ANKS, ANKS INGS; ANKS INGT; AN	293, 293, 293, 293	ankyrin 3, epichelat isoform q
13	10	18	3.4	Chills	CN-R	13	E3 ubiquitin-protein ligate C8L-8
3.	11	19	Debras	Cris	C/k	50	adapter malecula ork
4	12	23	121.4	Digital	SAPARS	922	disks large-associated protein 3
5	23	26	127.8	Olgap4; Digap4	SAMPI SAMPI INZ	132; 132	disks large-accodated protein 4 isoform to
5	14	26	17.8	Disepti Disept	SAPAPH, SAPAPH INCO	132, 136; 132, 156	disks large-associated protein 4 softrim b
13	15	27	0941	Orgap4; Orgap4	SAPAPI; SAPAPI IIDZ	290; 290	daks large-associated protein 4 soform b
ı.	36	29	1.3	Owntg.	OVMEP	1397	dynamin-binding protein
N.	13	29	048.8	G38ps	6399-1	427	ras G19ss-activating protein-landing protein 1.
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ı.	20	48	57	G36p1	GRR-1	441	ras GTPsee-activating protein-binding protein 1
	21	54	330	G3691	G33P-1	445, 458	res GTPase-ectivating procein-binding protein 1
4	22	64	198.9	G3bp1	G38P-1	445, 458, 464	resi GTPese-activating protein-binding protein 1
	23	66	483	G3bp1	G35P-1	445, 464	ray GTPese-activating protein-binding protein 1
4	24	60	1888	Cisent	63.88P-1	418	rac GTPase-activating process-randing process 1
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		88			LM07; LM07 Isid4	1490, 950	LIM domain only 7
Ų.	26	99		Mpdz	HP02	1158	multiple PDZ domain protein
	30	90	60000	Ferd3to	MR3-beta	1179	partitioning defective 3 homolog B

