

Table SIV. A total of 23 differentially abundant phosphorylated proteins belong to the six candidate Gene Ontology terms between the sham and CIBP groups.

Accession	Gene name	Description	Sequence	Average CIBP/Sham	P-value
P34926	Map1a	Microtubule-associated protein 1A	aELEEmEETHPsDEEGEETk	1.218449	0.004873
			tPPAQk	1.211517	0.025277
			aELEEMEETHPsDEEGEETk	1.206755	0.046310
			kVAELEEESQsQGSSSYSDW	0.806445	0.038922
			Vk		
Q62936	Dlg3	Disks large homolog 3	gVTSNTsDsESSSk	1.288081	0.016595
			ekREsVAsGDDR	1.324898	0.000023
			qPGVQsPSR	1.221849	0.010812
			esVAsGDDRAEEDMDEALE	1.3423	0.019607
P15025	Map1b	Microtubule-associated protein 1B	k		
			gEAEQsEEEEEEEEEDkAEDA	1.685242	0.032947
			R		
			dENERSsIsPMDEPVPDSEsPI	1.229505	0.035904
			Ek		
			ekREsVAsGDDR	1.324898	0.000023
			qPGVQsPSR	1.221849	0.010812
			esVAsGDDRAEEDMDEALE	1.3423	0.019607
F1LRL9	Map1b	Microtubule-associated protein 1B	k		
			gEAEQsEEEEEEEEEDkAEDA	1.685242	0.032947
			R		
			dENERSsIsPMDEPVPDSEsPI	1.229505	0.035904
			Ek		
			kIAELEEEERSQGSStNSDWM	0.766251	0.027879
			k		
			kIAELEEEERSQGSStNSDWM	0.742905	0.046295

			k		
			sPAEAkSPASV	1.736638	0.001647
			sPAEAkSPASVksPGEAk	1.411921	0.003365
			sPAEAkSPAsVksPGEAk	1.709063	0.003860
			sPAEAkSPAsV	1.644461	0.017441
			sPAEAkSPAEVksPVEAk	1.833923	0.030742
			sPAsVksPGEAkSPAEAk	1.659234	0.045356
P16884	Nefh	Neurofilament heavy polypeptide	sPAEVksPVEAk	1.791695	0.047290
			sPAEAkSPASV	0.806932	0.0000007
			sPATVksPGEAkSPAEAk	0.788244	0.000916
			sPASVksPGEAk	0.780776	0.012463
			sPASVksPGEAkSPAEAk	0.792127	0.030177
			sPATVksPGEAk	0.8133	0.041132
			sPMkEEAkPEk	0.805671	0.046242
A0A0G2K1X6	Bsn	Protein bassoon	hsDSGsDSk	1.332851	0.018862
			mAGTmETSEMVNGAAEQR	1.213448	0.013202
			TSskEssPVPsPTSDR		
Q5D002	Sptbn1	Sptbn1 protein (Fragment)	tSskEssPVPsPTSDR	1.367144	0.037730
			tsskEssPVPsPTSDRk	1.241235	0.041324
			tSskEsSPVPSPTSDRk	0.761075	0.026971
			sDQAEEGGsEkEGSSEk	1.389471	0.028813
			gsGQEEEk	1.357906	0.033204
G3V7S2	Nefm	Neurofilament medium polypeptide	eGssEkDEGEQEEEGETEAE	1.663831	0.042216
			GEGEEAEAk		
			eEEPEVEksPVksPEAk	1.95233	0.043710
			sPVPksPVEEVkPkPEAk	0.811632	0.007093
G3V874	Epb4113	Erythrocyte membrane protein	hEGkDsER	1.334197	0.042372

		band 4.1-like 3			
		Calcium/calmodulin-d	ssSSVHLmEPQTTVVHNAT		
		ependent protein	DGIk	1.306945	0.016160
P11730	Camk2g	kinase type II subunit			
		gamma	gSTEscNtttEDEDLk	1.667428	0.027277
		SRC kinase signaling			
Q9QXY2	Srcin1	inhibitor 1	IPPSsPQk	0.831671	0.017739
		Calcium/calmodulin-d	eSSEStNttIEDEDTk	1.27198	0.003455
		ependent protein			
P11275	Camk2a	kinase type II subunit	nDGVkEssEstNttIEDEDTk	1.375954	0.022220
		alpha			
			aSYDSVEDSsEsENsPVVR	1.387626	0.017806
Q9JKS6	Pclo	Protein piccolo	dSFSQESSPsPSDLAk	1.269353	0.021622
		Amyloid beta A4			
		precursor			
O35430	apba1	protein-binding family	qDIspTR	1.213466	0.039330
		A member 1			
			dAATEEPGsPVkstPASPVQS		
F8WFS9	Add2	Beta-adducin	PTR	1.276839	0.017977
Q4KM62	Palmd	Palmdelphin	sGPQcSsPIcQEEADV	0.748617	0.026192
O35867	Ppp1r9a	Neurabin-1	sNRGsSDsLDsLsPR	1.30774	0.004587
		Potassium			
		voltage-gated channel			
P10499	Kcna1	subfamily A member	rsSSTISk	0.799317	0.022709
		1			
		Tumor protein			
A0A0G2K27			dTVDSAGtsPTAVLAAGEDA		
2	Tprg11	p63-regulated gene	GAGR	1.202368	0.005073
		1-like protein			
P63142	Kcna2	Potassium	kSRsAsTISk	0.828529	0.003808

		voltage-gated channel			
		subfamily A member			
		2			
P61765	Stxbp1	Syntaxin-binding protein 1	INkTDEEIsS	0.832581	0.019192
P51111	Htt	Huntingtin	asPGR	0.791498	0.025317
		Adaptor-related			
B5DFK6	Ap3d1	protein complex 3, delta 1 subunit	hSsLPtEsDEDIAPAQR	1.231754	0.031886
Q63564	Sv2b	Synaptic vesicle glycoprotein 2B	gNEQNPEEDAQsDVTEGHD EEDEIYEGEYQGIPHPDDV	1.260401	0.036579

A 1.2-fold cut-off for hypophosphorylation and hyperphosphorylation events ($P < 0.05$) was used. CIBP, cancer-induced bone pain.