Table S2. Representative CID analysis of Ric-8A to identify specific phosphorylation sites after tryp

Tryptic Digestion

Phospho-Site	Peptide	# Peptide Hits
S30	(R)EHsQSFTFDDAQQEDR(K)	65
S32	(R)EHSQsFTFDDAQQEDR(K)	65
S298	(K)cLDVLLALELHEGsLEFMGVNMDVINALLAFLEK(R)	19
S435	(R)GLMAGGRPEGQYsEDEDtDTEEYR(E)	35

T440	(R)GLMAGGRPEGQYsEDEDtDTEEYR(E)	35

tic digest and MS analysis.

	Representitive Fragmentation						
#Phos-site Hits	B-Ions		Y-Ions		Total Peptide Mass	Predicted Mass	Differen
4	B2	267.11	Y14	1,753.67	2018.76	1939.93	78.83
	B3	434.11	Y13	1,586.67			
			Y12	1,458.61			
			Y11	1,371.58			
			Y10	1,224.51			
			Y9	1,123.47			
			Y8	976.4			
			Y7	861.37			
			Y6	746.34			
			Y5	675.31			
			Y4	547.25			
			Y3	419.19			
			Y2	290.15			
			Y1	175.12			
3	B2	267.1	Y14	1753.7	2018.76	1939.93	78.83
	B3	354.1	Y12	1538.6			
	B4	482.2	Y11	1371.6			
	B9	115.4	Y10	1224.5			
	B14	1730.6	Y9	1123.5			
			Y8	976.4			
			Y7	861.4			
			Y6	746.3			
			Y5	675			
			Y4	547.2			
			Y3	419.2			
			Y2	290.1			
			Y1	175.1			
1	B2	274.1	Y14	1590.9	3895.95	3761.46	134.49
	B3	389.1	Y12	1345.8			
	B4	488.2	Y11	1230.7			
	B5	601.3	Y10	1131.7			
	B9	1027.5	Y9	1018.6			
			Y8	904.6			
			Y7	833.5			
			Y6	720.4			
			Y5	607.3			
			Y4	536.3			
			Y2	276.2			
16	B7	643.3	Y15	1996.6	2864.81	2705.76	159.05
	B8	740.4	Y13	1811.6			
	B9	869.4	Y12	1648.5			
	B10	926.5	Y11	1481.5			
	B11	1054.5	Y10	1352.5			
	B12	1217.6	Y9	1237.4			

	B14	1513.6	Y8	1108.4			
	B15	1628.6	Y7	993.4			
	B16	1757.7	Y6	812.3			
	B17	1872.7	Y5	697.3			
			Y4	596.3			
			Y3	467.2			
13	B7	643.3	Y15	1996.6	2864.81	2705.76	159.05
	B8	740.4	Y13	1811.6			
	B9	869.4	Y12	1648.5			
	B10	926.5	Y11	1481.5			
	B11	1054.5	Y10	1352.5			
	B12	1217.6	Y9	1237.4			
	B14	1513.6	Y8	1108.4			
	B15	1628.6	Y7	993.4			
	B16	1757.7	Y6	812.3			
	B17	1872.7	Y5	697.3			
			Y4	596.3			
			Y3	467.2			

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1 Phosphorylation (+80)
1 Phosphorylation (+80)
1 Phosphorylation (+80) 1 Carbamidomethyl (+57)
2 Phosphorylation (+80)

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[2] Phosphorylation (+80)

Table S2. Representitive CID analysis of WT rat Ric-8A protein purified from *E. coli* and treated i
Tryptic & Chymotryptic digestion

Phospho-Site	Peptide	# Peptide Hits
S435	(R)PEGQYsEDEDtDTEEYREA(K)	20
T440	(R)PEGQYsEDEDtDTEEYREA(K)	20
S522	CETMEGQLssDPDsDPD	100
S523	CETMEGQLssDPDsDPD	100
S527	CETMEGQLssDPDsDPD	100

n vitro with CK2.

	Representitive Fragmentation						
#Phos-site Hits	B-Ions		Y-Ions		Total Peptide Mass	Predicted Mass	Differen
15	B2	227.1	Y10	1321.5	2549.9	2390.0	159.9
	B3	284.1	Y9	1140.5			
	B4	412.2	Y8	1025.5			
	B5	575.2	Y7	924.4			
	B8	986.3	Y6	795.4			
	B9	1115.4	Y5	666.4			
	B10	1230.4	Y4	503.3			
			Y3	347.2			
			Y2	218.1			
			Y1	147.1			
17	B2	227.1	Y10	1321.5	2549.9	2390.0	159.9
	B3	284.1	Y9	1140.5			
	B4	412.2	Y8	1025.5			
	B5	575.2	Y7	924.4			
	B8	986.3	Y6	795.4			
	B9	1115.4	Y5	666.4			
	B10	1230.4	Y4	503.3			
			Y3	347.2			
			Y2	218.1			
			Y1	147.1			
37	B2	290.1	Y7	840.2	2121.6	1824.7	296.9
	B3	391.1	Y6	725.2			
	B4	522.2	Y3	346.1			
	B5	651.2	Y2	231.1			
	B6	708.2					
	B7	836.3					
	B8	949.4					
	B11	1398.4					
63	B2	290.1	Y7	840.2	2121.6	1824.7	296.9
	B3	391.1	Y6	725.2			
	B4	522.2	Y3	346.1			
	B5	651.2	Y2	231.1			
	B6	708.2					
	B7	836.3					
	B8	949.4					
	B11	1398.4					
74	B2	290.1	Y7	840.2	2121.6	1824.7	296.9
	B3	391.1	Y6	725.2			
	B4	522.2	Y3	346.1			
	B5	651.2	Y2	231.1			

B6	708.2
B7	836.3
B8	949.4
B11	1398.4

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2 Phosphorylation (+80)

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3 Phosphorylation (+80)
1 Carbamidomethyl (+57)

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3 Phosphorylation (+80)
1 Carbamidomethyl (+57)