

MATRIX **SCIENCE** Mascot Search Results

Protein View

Match to: PP2AB_MOUSE Score: 63 Expect: 0.012

Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Mus musculus GN=Ppp2cb PE=1 SV=1

Nominal mass (M_r): 36123; Calculated pI value: 5.21

NCBI BLAST search of [PP2AB_MOUSE](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Mus musculus](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 55

Number of mass values matched: 8

Sequence Coverage: 36%

Matched peptides shown in **Bold Red**

```
1 MDDKAFTEKEL DQWVEQLNEC KQLNENQVRT LCEKAKEILT KESNVQEVRC
51 PVTVCGDVHG QFHDLMELEFR IGGKSPDTNY LFMGDYVDRG YYSVETVTL
101 VALKVRYPER ITILRGNHES RQITQVYGFY DECLRKYGNA NVWKYFTDLF
151 DYLPALTALVD GQIFCLHGGL SPSIDTLDHI RALDRLQEVV HEGPMC DLLW
201 SDPDDRGGWG ISPRGAGYTF GQDISETFNH ANGLTLVSRA HQLVMEGYNW
251 CHDRNVVTIF SAPNYCYRCG NQAAIMELDD TLKYSFLQFD PAPRRGEPHV
301 TRRTPDYFL
```

Show predicted peptides also

Sort Peptides By

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
22 - 29	1000.5300	999.5227	999.5097	0.0130	0	K.QLNENQVR.T
75 - 89	1808.7482	1807.7409	1807.7723	-0.0314	0	K.SPDTNYLFMGDYVDR.G Oxidation (M)
90 - 106	1910.9869	1909.9797	1910.0877	-0.1080	1	R.GYYSVETVTLVVALKVR.Y
122 - 135	1791.8034	1790.7962	1790.8298	-0.0336	0	R.QITQVYGFYDECLR.K
137 - 144	951.4625	950.4553	950.4610	-0.0057	0	K.YGNANVWK.Y
215 - 239	2655.2424	2654.2351	2654.2725	-0.0374	0	R.GAGYTFGQDISETFNHANGTLVSR.A
255 - 268	1703.7961	1702.7888	1702.8137	-0.0249	0	R.NVVTIFSAPNYCYR.C
284 - 294	1340.6349	1339.6276	1339.6561	-0.0285	0	K.YSFLQFDPAPR.R

MATRIX SCIENCE Mascot Search Results

Protein View

Match to: SPEE_MOUSE Score: 69 Expect: 0.003
Spermidine synthase OS=Mus musculus GN=Srm PE=2 SV=1

Nominal mass (M_r): 34543; Calculated pI value: 5.31

NCBI BLAST search of SPEE_MOUSE against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Mus musculus

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 33

Number of mass values matched: 7

Sequence Coverage: 26%

Matched peptides shown in **Bold Red**

```

1  MEPGPDGPAA PGPAAIREGW FRETCSLWPG QALSLQVEQL LHHRRSRYQD
51 ILVFRSKTYG NVLVLDGVIQ CTERDEFSYQ EMIANLPLCS HPNPRKVLII
101 GGGDGGVLR VVKHPSVESV VQCEIDEDVI EVSKKFLPGM AVGFSSSKLT
151 LHVGDGFEFM KQNQDAFDVI ITDSSDPMGP AESLFKESYY QLMKTALKED
201 GILCCQGECQ WLHLDLIKEM RHFCKSLFPV VDYAYCSIPT YPSGQIGFML
251 CSKNPSTNFR EPVQQLTQAQ VEQMLKYIN SDMHRAAFVL PEFTRKALND
301 IS
  
```

Show predicted peptides also

Sort Peptides By

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 22	2279.0984	2278.0911	2278.0953	-0.0042	1	-.MEPGPDGPAAPGPAAIREGWFR.E	
48 - 55	1053.5476	1052.5403	1052.5655	-0.0252	0	R.YQDILVFR.S	
58 - 74	1936.9450	1935.9378	1935.9724	-0.0347	0	K.TYGNVLVLDGVIQCTER.D	
96 - 109	1353.7764	1352.7691	1352.8140	-0.0449	1	R.KVLIIGGGDGGVLR.E	
97 - 109	1225.7058	1224.6985	1224.7190	-0.0206	0	K.VLIIGGGDGGVLR.E	
278 - 295	2233.0896	2232.0823	2232.0422	0.0401	1	K.YYNSDMHRAAFVLPEFTR.K	Oxidation (M)
286 - 295	1150.6021	1149.5948	1149.6182	-0.0234	0	R.AAFVLPEFTR.K	

MATRIX SCIENCE Mascot Search Results

Protein View

Match to: HS90B MOUSE Score: 71 Expect: 0.0021
Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2

Nominal mass (M_r): 83615; Calculated pI value: 4.97
NCBI BLAST search of [HS90B MOUSE](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Mus musculus](#)

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 71
Number of mass values matched: 12
Sequence Coverage: 23%

Matched peptides shown in **Bold Red**

```
1 MPEEVHHGEE EVETFAFQAE IAQLMSLIIN TFYSNKEIFL RELISNASDA
51 LDKIRYESLT DPSKLDSGKE LKIDILPNPQ ERTLTLVDTG IGMTKADLIN
101 NLGTIAKSGT KAFMEALQAG ADISMIGQFG VGFYSAYLVA EKVVVITKHN
151 DDEQYAWESS AGGSFTVRAD HGEPIGRGTK VILHLKEDQT EYLEERRVKE
201 VVKKHSQFIG YPITLYLEKE REKEISDDEA EEEKGEKEEE DKEDEEKPKI
251 EDVGSDEEDD SGKDKKKKTK KIKEKYIDQE ELNKTKPIWT RNPDDITQEE
301 YGEFYKSLTN DWEDHLAVKH FSVEGQLEFR AFLFIPRRAP FDLFENK KKK
351 NNIKLYVRRV FIMDSCDELI PEYLNFI RGV V DSEDLPLNI SREMLQQSKI
401 LKVIRKNIVK KCLELFSELA EDKENYKKFY EAFSKNLKLG IHEDSTNRRR
451 LSELLRYHTS QSGDEMTSL S EYVSRMKETQ KSIYYITGES KEQVANPAFV
501 ERVRKRGFEV VYMTEPID EY CVQQLK EFDG KSLVSVTKEG LELPEDEEEK
551 KKMEESKAKF ENLCKLMKEI LDKKVEKVTI SNRLVSSPCC IVTSTYGWTA
601 NMERIMKAQA LRDNSTMGY M MAKKHLEINP DHPIVETLRQ KAEADKNDKA
651 VKDLVLLFE TALLSSGFSL EDPQTHSNRI YRMIKLGLGI DEDEVTAEEP
701 SAAVPDEIPP LEGDEDASRM EEVD
```

Show predicted peptides also

Sort Peptides By

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
73 - 82	1194.6427	1193.6354	1193.6404	-0.0050	0	K.IDILPNPQER.T
149 - 168	2256.0970	2255.0898	2254.9516	0.1382	0	K.HNDDEQYAWESSAGGSFTVR.A
205 - 219	1808.9492	1807.9419	1807.9509	-0.0090	0	K.HSQFIGYPITLYLEK.E
320 - 330	1348.6543	1347.6471	1347.6572	-0.0101	0	K.HFSVEGQLEFR.A
320 - 337	2193.0609	2192.0536	2192.1531	-0.0995	1	K.HFSVEGQLEFRAFLFIPR.R
338 - 347	1236.6249	1235.6177	1235.6299	-0.0122	1	R.RAPFDLFENK.K
360 - 378	2390.1382	2389.1309	2389.1334	-0.0025	0	R.VFIMDSCDELIPEYLNFI R.G Oxidation (M)
379 - 392	1513.7753	1512.7680	1512.7784	-0.0103	0	R.GV DSEDLPLNISR.E
613 - 623	1264.6385	1263.6312	1263.4934	0.1379	0	R.DNSTMGYMAK.K Oxidation (M)
624 - 639	1911.0228	1910.0155	1910.0374	-0.0218	1	K.KHLEINPDHPIVETLR.Q
625 - 639	1782.9488	1781.9416	1781.9424	-0.0008	0	K.HLEINPDHPIVETLR.Q
686 - 719	3535.6461	3534.6388	3534.6373	0.0015	0	K.LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR.M

MATRIX SCIENCE Mascot Search Results

Protein View

Match to: CALB2_MOUSE Score: 55 Expect: 0.081
Calretinin OS=Mus musculus GN=Calb2 PE=1 SV=3

Nominal mass (M_r): 31467; Calculated pI value: 4.94

NCBI BLAST search of [CALB2_MOUSE](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Mus musculus](#)

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 41
Number of mass values matched: 7
Sequence Coverage: 32%

Matched peptides shown in **Bold Red**

1 MAGPQQPPY LHLAELTASQ FLEIWKHFDA DNGYIEGKE **LENFFQELEK**
51 ARKGGMMSK SDNFGEKMK FMOQYDKNSD **GKIEMAEFAQ ILPTEENFLL**
101 **CFRQHVGSAA EFMEAWRKYD** TDRSGYIEAN ELKGFLSDLL **KKANRPYDEP**
151 **KLQEYQTIL RMFDLNGDGK** LGLSEMSRL **PVQENFLLK** QGMKLTSEEF
201 NAIFTFYDKD GSGYIDENEL DALLKDLYEK **NKKEMNIQQL TTYRKSVM**SL
251 AEAGKLYRKD LEIVLCSEPP V

Show predicted peptides also

Sort Peptides By

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
40 - 50	1425.6827	1424.6755	1424.6823	-0.0069	0	K.ELENFFQELEK.A
83 - 103	2553.2423	2552.2350	2552.2654	-0.0304	0	K.IEMAEFAQILPTEENFLLCFR.Q Oxidation (M)
104 - 117	1650.8507	1649.8434	1649.7256	0.1178	0	R.QHVGSAAEFMEAWR.K Oxidation (M)
134 - 142	1020.5924	1019.5851	1019.6015	-0.0164	1	K.GFLSDLLKK.A
152 - 161	1264.6918	1263.6845	1263.6823	0.0022	0	K.LQEYQTILR.M
179 - 189	1313.7619	1312.7546	1312.7755	-0.0208	0	R.LLPVQENFLLK.F
234 - 244	1412.6853	1411.6781	1411.6765	0.0015	0	K.EMNIQQLTTYR.K Oxidation (M)