

## Protein Family Summary

Filter    Significance threshold p <     Max. number of families  [\[help\]](#)  
 Ions score or expect cut-off     Dendrograms cut at

Proteins (8)    [Quantitation \(8\)](#)    [Unassigned \(1320\)](#)

### Protein families 1-8 (out of 8)

10 per page    1          
 Accession          Match case

▼ 2	gi 6978649	284	choline/ethanolamine kinase [Homo sapiens]				
1.1	gi 6978649	284	45242	37 (13)	22 (11)	1.50	choline/ethanolamine kinase [Homo sapiens]

▶ 1 sameset of gi|6978649

### ▼ 37 peptide matches (36 non-duplicate, 1 duplicate)

Auto-fit to window

Query Dupes	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
<a href="#">67</a>	388.2009	774.3872	774.3872	0.092	0	18	0.86	▶1	U	K.DGLQQSK.C
<a href="#">103</a>	416.2225	830.4304	830.4286	2.20	0	22	0.17	▶1	U	R.HYLAEAK.K
<a href="#">125</a>	435.7375	869.4604	869.4607	-0.25	0	1	4.1	▶3	U	R.VQPEELR.V
<a href="#">168</a> ▶1	468.6884	935.3622	935.3627	-0.45	1	27	0.11	▶1	U	R.RASSLSR.D + 2 Phospho (ST)
<a href="#">241</a>	<b>501.7458</b>	<b>1001.4770</b>	<b>1001.4778</b>	<b>-0.75</b>	<b>0</b>	<b>36</b>	<b>0.0022</b>	▶1	U	K.GQLTSVHSSS.-
<a href="#">248</a>	506.7555	1011.4964	1011.4975	-0.99	2	15	1.3	▶2	U	R.RASSLSR.D + Phospho (ST)
<a href="#">265</a>	513.7877	1025.5608	1025.5618	-0.90	1	21	0.42	▶1	U	R.VQPEELR.V
<a href="#">327</a>	<b>541.7293</b>	<b>1081.4440</b>	<b>1081.4441</b>	<b>-0.068</b>	<b>0</b>	<b>38</b>	<b>0.00096</b>	▶1	U	K.GQLTSVHSSS.- + Phospho (ST)
<a href="#">348</a>	546.7375	1091.4604	1091.4638	-3.05	2	4	1.2	▶4	U	R.RASSLSR.D + 2 Phospho (ST)
<a href="#">350</a>	546.7388	1091.4630	1091.4638	-0.67	2	7	1.1	▶2	U	R.RASSLSR.D + 2 Phospho (ST)
<a href="#">351</a>	364.8284	1091.4634	1091.4638	-0.37	2	16	1.3	▶2	U	R.RASSLSR.D + 2 Phospho (ST)
<a href="#">360</a>	550.3219	1098.6292	1098.6284	0.73	0	12	0.71	▶1	U	R.EPVLAAIATK.M
<a href="#">408</a>	568.2827	1134.5508	1134.5498	0.89	0	17	1.1	▶2	U	R.FQYFQOK.G
<a href="#">478</a>	586.2582	1170.5018	1170.5030	-0.98	1	15	1.3	▶2	U	R.ASSLRDAER.R + Phospho (ST)
<a href="#">487</a>	<b>588.7774</b>	<b>1175.5402</b>	<b>1175.5418</b>	<b>-1.34</b>	<b>0</b>	<b>56</b>	<b>0.00017</b>	▶1	U	K.GETLSQEEQR.K
<a href="#">591</a>	626.2416	1250.4686	1250.4693	-0.53	1	18	0.19	▶1	U	R.ASSLRDAER.R + 2 Phospho (ST)
<a href="#">592</a>	626.2424	1250.4702	1250.4693	0.75	1	0	1	▶1	U	R.ASSLRDAER.R + 2 Phospho (ST)
<a href="#">668</a>	<b>652.8253</b>	<b>1303.6360</b>	<b>1303.6368</b>	<b>-0.56</b>	<b>1</b>	<b>70</b>	<b>1.3e-005</b>	▶1	U	K.KGETLSQEEQR.K
<a href="#">669</a>	435.5532	1303.6378	1303.6368	0.76	1	24	0.057	▶1	U	K.KGETLSQEEQR.K
<a href="#">721</a>	448.5933	1342.7581	1342.7608	-2.07	0	9	1.2	▶2	U	R.LEQYIPSRPLK.T
<a href="#">722</a>	<b>672.3873</b>	<b>1342.7600</b>	<b>1342.7608</b>	<b>-0.60</b>	<b>0</b>	<b>36</b>	<b>0.019</b>	▶1	U	R.LEQYIPSRPLK.T
<a href="#">788</a>	704.2911	1406.5676	1406.5704	-1.97	2	10	2.4	▶3	U	R.RASSLSRDAER.R + 2 Phospho (ST)
<a href="#">789</a>	704.2917	1406.5688	1406.5704	-1.12	2	11	1.2	▶5	U	R.ASSLRDAER.R + 2 Phospho (ST)
<a href="#">790</a>	469.8636	1406.5690	1406.5704	-1.03	2	9	1.2	▶3	U	R.RASSLSRDAER.R + 2 Phospho (ST)
<a href="#">792</a>	704.2921	1406.5696	1406.5704	-0.55	2	15	0.29	▶1	U	R.RASSLSRDAER.R + 2 Phospho (ST)
<a href="#">811</a>	<b>715.3977</b>	<b>1428.7808</b>	<b>1428.7824</b>	<b>-1.07</b>	<b>1</b>	<b>67</b>	<b>8.6e-006</b>	▶1	U	R.KLEEDLLVEVSR.Y
<a href="#">867</a>	744.2761	1486.5376	1486.5367	0.61	2	5	0.82	▶1	U	R.RASSLSRDAER.R + 3 Phospho (ST)
<a href="#">900</a>	<b>760.3979</b>	<b>1518.7812</b>	<b>1518.7831</b>	<b>-1.21</b>	<b>0</b>	<b>49</b>	<b>0.00013</b>	▶1	U	R.SLGPQLYGVFPEGR.L
<a href="#">906</a>	<b>761.4261</b>	<b>1520.8376</b>	<b>1520.8351</b>	<b>1.67</b>	<b>0</b>	<b>41</b>	<b>0.00033</b>	▶1	U	R.VYPVSGGLSMLLFR.C
<a href="#">976</a>	534.8962	1601.6668	1601.6677	-0.56	0	20	0.4	▶1	U	K.HAQFHGHEMFFTK.E + 3 Oxidation (M)
<a href="#">977</a>	<b>801.8425</b>	<b>1601.6704</b>	<b>1601.6677</b>	<b>1.74</b>	<b>0</b>	<b>40</b>	<b>0.0018</b>	▶1	U	K.HAQFHGHEMFFTK.E + 3 Oxidation (M)
<a href="#">1012</a>	827.8621	1653.7096	1653.7070	1.63	1	30	0.012	▶1	U	K.DGLQQSKCPDTPK.R + Carbamidomethyl (C); Phospho (ST)
<a href="#">1058</a>	<b>564.9383</b>	<b>1691.7931</b>	<b>1691.7937</b>	<b>-0.38</b>	<b>0</b>	<b>31</b>	<b>0.0032</b>	▶1	U	R.CSLPDHLPVGEPR.E + Carbamidomethyl (C)
<a href="#">1059</a>	<b>846.9056</b>	<b>1691.7966</b>	<b>1691.7937</b>	<b>1.73</b>	<b>0</b>	<b>34</b>	<b>0.003</b>	▶1	U	R.CSLPDHLPVGEPR.E + Carbamidomethyl (C)
<a href="#">1084</a>	<b>863.9865</b>	<b>1725.9584</b>	<b>1725.9625</b>	<b>-2.33</b>	<b>1</b>	<b>46</b>	<b>6.9e-005</b>	▶1	U	K.TQELREPVLSAAIATK.M
<a href="#">1085</a>	576.3269	1725.9589	1725.9625	-2.08	1	18	0.16	▶1	U	K.TQELREPVLSAAIATK.H

**S1 Fig. Mass spectrometry analysis of phosphorylated CKβ.** Fifteen peptide fragments were found to be phosphorylated; the range of the ion score was from 4 to 38. A total of 13 peptide fragments covered the amino acid sequence Arg 36 to Arg 43 (RRASSLSR).