

Sequest Summary

Sample: Berne, M. (K6) 1 mb
 DataFiles: K6 (02/27/04-02/27/04)
 Database: rat (01/05/2004)
 Directory: mbernek6 View Info
 Diff Mods: 16 M 57.02 C 0.000 X
 OutFiles: 12831944
 Enzyme: Trypsin_Strict
 Mass: ±1.5 (Mono)
 Max list: 1000
 Intensity: 3.569 MS2 DTA VCR

#	GBU	TIC	File	z	dm	MH+	XC	dCn	Sp	RSP	Ions	Sf	Ref	Sequence	Prob	Consensus	Depth:
A gi133591997 ref NP_112319.1 246 401E:9.7e8 28% avg:2.4e7 f37.3,0.1,1.1 methylmalonate semialdehyde dehydrogenase gene [Rattus norvegicus] gi1400269 sp Q02253 MMSA_RAT Methylmalonate-semialdehyde dehydrogenase [acylating] (EC 1.2.1.2)																	
429		7.9e7	1844-1888	2	0.8	1962.4	5.90	0.59	889	889	1	22/38	gi133591997	(-)VNAGDQPGADLGPLITPQAK			
528		7.3e6	2123-2152	2	0.5	1888.6	5.59	0.59	1933	970	1	23/32	gi133591997	(-)AISFVGSNOAGEYTFER			
422		6.6e7	1818-1840	2	0.6	1721.3	4.42	0.56	970	970	1	21/28	gi133591997	(-)WIDHNPATNEVGR			
416		6.9e5	1791-1806	2	0.5	2051.7	4.32	0.44	883	883	1	18/34	gi133591997	(-)SDKWLIDHNPATNEVGR			
439		2.0e6	1893-1898	2	0.8	1962.4	4.28	0.52	772	772	1	18/38	gi133591997	(-)VNAGDQPGADLGPLITPQAK			
395		2.3e7	1754-1778	2	0.0	1465.8	4.16	0.48	1145	1145	1	19/26	gi133591997	(-)C#M*ALSTAVLVEBAK			
428		2.9e6	1824	3	-0.9	1722.8	4.07	0.35	2031	2031	1	30/56	gi133591997	(-)WIDHNPATNEVGR			
294		1.5e7	1519-1539	2	-0.3	1923.2	4.02	0.54	655	655	1	17/34	gi133591997	(-)EEDATLSSPAVVM*PTM*GR			
352		1.7e7	1649-1680	2	0.0	1194.3	3.97	0.47	1107	1107	1	17/20	gi133591997	(-)TLADAEGDVFR			
482		1.3e6	2033-2038	2	-0.6	2721.0	3.64	0.59	307	307	1	17/48	gi133591997	(-)GLOVEEHAC#SVNLSM*LGETM*PSITK			
414		3.1e7	1790-1816	2	0.1	1226.3	3.34	0.33	702	702	1	15/18	gi133591997	(-)OGIQEYFQAK			
555		3.3e6	2184-2207	2	0.3	1435.3	3.15	0.47	1025	1025	1	19/24	gi133591997	(-)AFPAWADTILSR			
299		3.7e7	1545-1575	2	0.4	1030.8	3.02	0.37	1253	1253	1	16/18	gi133591997	(-)EGASILLDGR			
288		8.0e7	1481-1516	2	-0.4	1017.0	3.01	0.44	514	514	1	15/18	gi133591997	(-)VPGATM*LLAK			
129		1.7e7	0750-0801	2	-0.4	1197.9	2.90	0.45	724	724	1	14/20	gi133591997	(-)NHGVVM*PDANK			
248		3.8e7	1329-1353	2	-0.2	1078.6	2.90	0.32	866	866	1	13/14	gi133591997	(-)TLADAEGDVFR			
356		5.5e5	1689-1691	2	0.6	1193.7	2.82	0.53	575	575	1	13/20	gi133591997	(-)DM*DLYSYR			
154		5.5e6	0855-0883	2	0.0	1166.5	2.79	0.48	1457	1457	1	16/20	gi133591997	(-)TLADAEGDVFR			
351		3.4e7	1646-1687	1	0.4	1193.9	2.72	0.46	197	197	1	11/20	gi133591997	(-)AEM*EAAVAAC#K			
541		5.8e5	2168	2	0.5	1888.5	2.66	0.39	482	482	1	13/32	gi133591997	(-)TLADAEGDVFR			
230		3.0e7	1235-1267	2	-0.7	1077.2	2.58	0.11	583	583	6	13/18	gi133591997	(-)AISFVGSNOAGEYTFER			
176		1.3e6	0990	2	0.0	902.0	2.27	0.35	324	324	1	14/14	gi133591997	(-)VC#NLLIDSGAK			
466		2.0e6	1961-1968	2	-1.5	2693.7	2.20	0.27	175	175	1	14/46	gi133591997	(-)GDTNFFYK			
242		3.1e6	1296	2	0.1	902.0	2.18	0.32	310	310	2	9/14	gi133591997	(-)GYENGNFVGPILLISNVKPSM*TC#YK			
456		1.5e6	1925	2	0.1	1042.1	2.09	0.32	368	368	2	11/14	gi133591997	(-)LITLLEQK			
232		1.2e7	1236-1270	1	-0.3	1076.8	2.05	0.14	625	625	1	12/18	gi133591997	(-)WDEPVEYR			
240		3.9e7	1283-1326	1	0.2	692.7	1.97	0.07	537	537	14	8/10	gi133591997	(-)WDEPVEYR			
316		4.0e5	1601-1606	1	0.2	1062.9	1.94	0.24	307	307	7	9/14	gi133591997	(-)VC#NLLIDSGAK			
471		3.9e5	1982-1995	2	-0.5	2281.0	1.94	0.20	399	399	1	14/42	gi133591997	(-)LITLLEQK			
418		1.0e7	1792-1817	1	0.5	1225.9	1.94	0.17	84	84	3	11/18	gi133591997	(-)DMDLFSYR			
238		1.1e8	1276-1332	1	0.2	901.9	1.84	0.03	487	487	1	10/14	gi133591997	(-)IVNDNPPYGNQVAIFTTNGATAR			
306		3.3e5	1589	2	0.2	1031.0	1.83	0.34	425	425	2	10/18	gi133591997	(-)OGIQEYFQAK			
173		5.3e7	0962-1010	1	0.2	901.8	1.76	0.22	151	151	2	7/14	gi133591997	(-)LITLLEQK			

Flicka

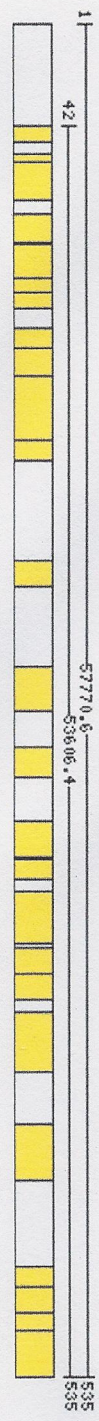
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Sample: Berne, M. K6 1

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>gi|13591997|ref|NP_112319.1| methylmalonate semialdehyde dehydrogenase gene [Rattus norvegicus]
 gi|400269|sp|Q02253|MMSA_RAT Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor (MMSDH) gi|347034|pir|A44097 methylmalonate-semialdehyde dehydrogenase (acylating) (EC 1.2.1.27) - rat
 gi|205526|gb|AA441638.1| methylmalonate semialdehyde dehydrogenase [MASS=57808] [MASS=57808]
 MAAAVVAAAA VRSRILQVSS KVNSTWYPAS SFSSSVPTV KLFDGKFEV SKSDKWTIDH NPATNEVYGR VPOSTKAEME
AAVAACKRAF PAWADTSILS ROOVLIRYQQ LIKENLIKETA RLITTEQKKT IADAEQDVER GLOVEHACS VTSIMLGETM
PSITKMDILY SYRLPLGVCA GIAPENFPAM IPLMFPVAM VCGNTFLMKP SERVPGATML IAKLIQDSGA PDGTLNIIHG
 OHEAVNFI CD HPDIKAISFV GSNQAGEYIF ERGRNNGKRV QANMGAKNHG VMPPDANKEN TLNQLVGAAL GAAGQRSMAL
STAVLVGEAK KWLPELVERA KNLRVYAGDQ PGADIGPLIT PQAKEYCNL IDSGAKEGAS ILLDGRKIKV KGYENGNFTVG
PTIISNVKES MTCYKEEIFG PVLVLELET IDEAIKIVND NRYGNGLAIF TINGAIAKRY AHMVDVGQYG VNVPIVPLP
 MEFSTGSRSS FRGDTNFFYGK QGIGFTYQLK TITTSQKKEED ATLISSPAYVM PTMGR

Mass (mono): 57770.6 Identifier: gi|13591997 Database: C:/database/rat.fasta
 Protein Coverage: 301/535 = 56.3% by amino acid count, 32467.4/57770.6 = 56.2% by mass



Sort by: Sequence Position

Sequence	Position
PERSTAT AEEMEAAVAACK	77 - 87
PERSTAT AAFPAMADTSILSR	89 - 101
PERSTAT AISFVGSNOAGEYIFER	256 - 272
PERSTAT CMALSTAVLVGEAK	317 - 330
PERSTAT DMDLYSYR	166 - 173
PERSTAT EEDATLISSPAYVMPTMGR	518 - 535
PERSTAT EGASILLDGR	377 - 386
PERSTAT GDTNFFYGK	493 - 500
PERSTAT	141 - 165

Sequest Summary

Sample: Berne, M. (K7) 1 mb

Datafiles: KZ (03/01/04-03/01/04)

Database: rat (01/05/2004)

Directory: mbernek7 View Info

Diff Mods: 16 M 57.02 C 0.000 X

Outfiles: 13801925

Enzyme: Trypsin_Strict

Mass: ±1.5 (Mono)

Max list: 1000

Intensity: 8.4e9

MS2

DTA VCR

File Select Sequest Protein Utilities Help

#	GBU	TIC	File	z	DM	MH+	XC	dcn	Sp	RSP	Ions	Sf	Ref	Sequence	Prob	Consensus	Depth:
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228 421X:2.8e9|33%|avg:6.6e7|37.320013

argininosuccinate synthetase 1 [Rattus norvegicus] |gi114291|sp|P09034|ASSY_RAT_Argininosuccinate synthase (Citruiline--aspartate ligase)

arg168637|p|ir||AARTRs_argininosuccinate synthase (EC 6.3.4.5) - rat |gi155767|emb|CAA30999.1| unnamed protei

921	1.2e7	2715-2751	2	-0.6	2315.7	5.65	0.61	1249	1	22/40	1	22/40	gi 25453414	(-) DGTTHSTSLDLEFM*YLNEVAGK			
924	5.3e7	2716-2741	3	-0.7	2315.8	5.59	0.54	1806	1	32/80	1	32/80	gi 25453414	(-) DGTTHSTSLDLEFM*YLNEVAGK			
761	2.2e8	2329-2370	3	-0.4	2693.6	5.43	0.52	2136	1	39/88	1	39/88	gi 25453414	(-) SPWSM*DENIM*HISYBAGILENPK			
658	1.1e8	2049-2079	3	0.5	1601.3	5.43	0.50	1110	1	28/52	1	28/52	gi 25453414	(-) APNTPDYLEIEFFK			
883	1.4e8	2613-2655	2	0.8	1782.2	5.38	0.57	1432	1	21/30	1	21/30	gi 25453414	(-) EOGYDVIAYLANIGOK			
851	7.3e6	2501-2514	3	-0.7	2677.9	4.91	0.14	1133	1	29/88	1	29/88	gi 25453414	(-) SPWSM*DENIM*HISYBAGILENPK			
868	2.3e7	2577-2614	2	-0.7	2374.8	4.72	0.51	1079	1	18/36	1	18/36	gi 25453414	(-) SPWSM*DENIM*HISYBAGILENPK			
762	1.3e7	2338-2352	2	-1.1	2694.3	4.59	0.47	645	1	18/44	1	18/44	gi 25453414	(-) EOGYDVIAYLANIGOK			
887	2.8e6	2622-2650	3	0.5	1782.5	4.56	0.34	1442	1	29/60	1	29/60	gi 25453414	(-) SPWSM*DENIM*HISYBAGILENPK			
938	3.3e5	2779-2791	2	0.8	2299.8	4.24	0.54	1152	1	19/40	1	19/40	gi 25453414	(-) EOGYDVIAYLANIGOK			
655	6.1e7	2044-2082	2	1.4	1600.5	4.15	0.47	630	1	17/26	1	17/26	gi 25453414	(-) APNTPDYLEIEFFK			
733	5.9e6	2259-2260	2	0.7	1472.9	3.88	0.53	848	1	17/24	1	17/24	gi 25453414	(-) APNTPDYLEIEFFK			
719	5.9e8	2207-2254	2	0.3	1473.3	3.76	0.40	649	1	17/24	1	17/24	gi 25453414	(-) APNTPDYLEIEFFK			
1007	6.5e6	3030-3034	3	-1.5	2851.9	3.28	0.23	381	1	26/96	1	26/96	gi 25453414	(-) GIYEPBAGTIIYHAHDIEAFTM*DR			
534	1.1e8	1811-1835	2	-1.2	995.4	3.23	0.20	867	1	15/16	1	15/16	gi 25453414	(-) YLGTSLAR			
439	7.0e7	1420-1456	2	0.4	1064.8	3.04	0.39	725	1	14/16	1	14/16	gi 25453414	(-) KVFIEDVSK			
454	3.5e7	1517-1537	2	0.1	937.0	2.82	0.26	443	1	12/14	1	12/14	gi 25453414	(-) VFIEDVSK			
475	8.7e7	1588-1621	2	0.0	906.1	2.66	0.37	718	1	14/18	1	14/18	gi 25453414	(-) GQVYTIIGR			
366	5.9e6	1162	2	-0.4	1213.0	2.55	0.43	564	1	14/18	1	14/18	gi 25453414	(-) GRNDLM*EYAK			
274	2.6e7	0845-0868	2	-1.1	973.3	2.44	0.10	531	1	11/14	1	11/14	gi 25453414	(-) KOVELAOR			
374	8.7e7	1183-1219	2	-0.8	1000.2	2.37	0.23	901	1	13/14	1	13/14	gi 25453414	(-) NDLM*EYAK			
441	1.6e6	1429-1447	1	0.9	1064.4	2.29	0.29	596	1	11/16	1	11/16	gi 25453414	(-) KVFIEDVSK			
389	7.3e7	1225-1255	2	-0.5	972.9	2.16	0.32	698	1	12/12	1	12/12	gi 25453414	(-) M*PEFYNR			
456	7.3e7	1525-1543	2	0.1	806.9	2.15	0.08	410	1	11/12	1	11/12	gi 25453414	(-) VOVSVER			
452	5.7e7	1506-1540	1	0.6	936.5	2.11	0.21	645	2	10/14	1	10/14	gi 25453414	(-) VFIEDVSK			
453	1.5e8	1512-1555	1	0.1	806.8	2.08	0.15	792	1	10/12	1	10/12	gi 25453414	(-) VOVSVER			
395	1.5e7	1267-1273	2	-0.8	973.2	2.03	0.15	474	1	10/12	1	10/12	gi 25453414	(-) M*PEFYNR			
306	2.8e7	1003-1031	2	0.6	895.3	2.00	0.17	580	1	11/12	1	11/12	gi 25453414	(-) EDPEEAR			
492	1.1e6	1656-1669	1	0.9	1186.5	1.95	0.39	93	1	10/20	1	10/20	gi 25453414	(-) OHGIPIPVTPK			
212	1.5e7	0520-0543	2	0.4	845.6	1.92	0.02	359	3	9/10	1	9/10	gi 25453414	(-) LKEYHR			
491	1.7e8	1650-1681	3	-0.1	1187.5	1.87	0.02	471	1	18/40	1	18/40	gi 25453414	(-) OHGIPIPVTPK			
473	1.7e8	1581-1627	1	0.2	905.9	1.78	0.08	208	44	9/14	1	9/14	gi 25453414	(-) GQVYTIIGR			
488	8.9e7	1649-1684	2	0.2	1187.2	1.77	0.07	293	1	14/20	1	14/20	gi 25453414	(-) OHGIPIPVTPK			

296	3.8e7	0941-0970	2	0.4	843.6	1.61	----	445	1	12/12	--	gi 25453414	(-) QVEIAOR
359	2.2e7	1139-1210	1	-0.1	999.6	1.58	0.12	104	3	9/14	--	gi 25453414	(-) NDLM*ETAK
298	2.3e7	0946-0972	1	0.1	843.9	1.57	0.02	83	1	9/12	--	gi 25453414	(-) QVEIAOR
458	2.5e7	1541-1573	1	0.5	741.4	1.32	----	138	72	6/10	--	gi 25453414	(-) VIAPWR
532	6.5e7	1807-1843	1	0.2	994.0	1.26	0.11	68	13	9/16	--	gi 25453414	(-) YLLGTSIAR
397	3.5e6	1272-1290	1	0.8	1088.4	1.03	----	234	1	11/18	--	gi 25453414	(-) NOAPPGLYTK
393	1.5e7	1241-1253	1	0.0	972.4	1.09	0.15	46	4	7/12	--	gi 25453414	(-) M*PEFYNR
311	5.9e7	1020-1059	1	0.0	615.8	0.93	----	62	1	8/10	--	gi 25453414	(-) OGLGLK
206	2.5e5	0502	1	0.6	627.2	0.77	----	102	19	4/10	--	gi 25453414	(-) KGVPEVK

<p>B gi 18392833 ref NP_058682.1 132 18 E:2.6e8 3% avg:1.5e7 15.0,2.0,0.2 </p> <p>acetyl-coenzyme A dehydrogenase, medium chain; Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain [Rattus norvegicus] gi 113018 sp P08503 ACDM_RAT Acyl-Coa dehydrogenase, medium-chain specific, mitochondrial precursor (MCAD) gi 66079 pir DERTCM acyl-CoA dehydrog</p>													
767	3.4e7	2351-2380	2	0.6	1873.6	5.31	0.62	1981	1	24/34	--	gi 8392833	(-) AFTGFTVEADTPGIHIGK
459	6.4e7	1547-1577	2	0.2	1468.5	4.55	0.48	1202	1	22/28	--	gi 8392833	(-) TRPTVAAGVGLAOR
736	5.4e7	2265-2307	2	0.5	1838.5	4.33	0.52	671	1	23/30	--	gi 8392833	(-) QEPGLGESFELLTEQOK
738	8.8e5	2266-2280	2	-0.9	2049.0	4.13	0.55	716	1	19/34	--	gi 8392833	(-) LVEHOGVSELLAEM*AM*K
466	2.3e7	1553-1570	3	0.7	1468.0	3.94	0.23	1015	1	26/56	--	gi 8392833	(-) TRPTVAAGVGLAOR
346	7.5e6	1115-1146	2	0.2	1251.2	3.94	0.32	1509	1	16/20	--	gi 8392833	(-) KGEVYINGOK
530	2.9e6	1806	2	0.7	1583.1	3.69	0.39	1512	1	19/24	--	gi 8392833	(-) IYQIYEGTAQIQR
741	1.9e6	2267	3	-1.1	2049.2	3.01	0.25	568	1	21/68	--	gi 8392833	(-) LVEHOGVSELLAEM*AM*K
765	1.0e6	2347	2	0.4	1170.0	2.75	0.51	1120	1	14/16	--	gi 8392833	(-) ANWYFVTR
688	2.8e7	2130-2154	2	-0.1	1151.5	2.44	0.25	484	1	13/18	--	gi 8392833	(-) SGEYPPFLIK
407	4.5e6	1330-1356	2	-0.3	991.3	2.43	0.33	963	2	14/16	--	gi 8392833	(-) AAMEVDSGR
536	3.6e6	1839	2	0.4	1234.0	2.42	0.33	461	1	15/22	--	gi 8392833	(-) ENVLIGEGAFK
770	9.4e5	2353-2376	3	0.4	1873.8	2.09	0.10	246	1	17/68	--	gi 8392833	(-) AFTGFTVEADTPGIHIGK
813	6.0e5	2448	2	-2.0	1876.1	1.86	0.14	280	1	11/34	--	gi 8392833	(-) AFTGFTVEADTPGIHIGK
214	1.6e7	0525-0555	1	0.1	747.7	1.70	0.06	377	2	8/12	--	gi 8392833	(-) ALDEATK
494	1.3e7	1668-1687	1	0.5	1014.7	1.67	0.20	369	1	11/16	--	gi 8392833	(-) NTFYFASIAK
391	5.9e6	1231-1237	1	0.6	864.4	1.37	----	144	21	8/12	--	gi 8392833	(-) EFQTIAR
1258	1.8e5	3792	2	-1.3	1929.5	1.14	----	137	9	10/32	--	gi 8392833	(-) ALDEATRYALDRKTFK

<p>C gi 1730519 sp P50310 PGK_CRIGR 134 18 E:1.1e8 1% avg:6.3e6 14.4,0.0,0.0 </p> <p>phosphoglycerate kinase gi 2117894 pir 148074 phosphoglycerate kinase (EC 2.7.2.3) - Chinese hamster gi 987048 emb CAA86028.1 phosphoglycerate kinase [Crickettulus griseus] [MASS=44563] [MASS=44563]</p>													
570	1.0e7	1913-1935	2	0.8	1741.2	4.84	0.62	1620	1	25/34	--	gi 1730519	(-) VSHVSTGGASLELLEEK
782	3.3e6	2401-2424	2	0.9	2023.3	4.75	0.36	1102	1	21/34	--	gi 1730519	(-) ITLPPVDFVTADKEDENAK
553	2.3e7	1879-1894	3	0.2	1635.6	4.49	0.46	1231	1	29/56	--	gi 1730519	(-) LGDVIYVNDAFGTAHR
847	8.3e6	2494-2512	2	0.2	1769.9	4.42	----	1277	1	21/32	--	gi 1730519	(-) ALESPPERPELAILGGAK
842	1.0e7	2487-2511	3	0.7	1769.4	4.34	0.24	1689	1	37/64	--	gi 1730519	(-) ALESPPERPELAILGGAK
550	1.7e7	1878-1895	2	0.6	1635.2	4.04	0.36	1497	1	20/28	--	gi 1730519	(-) LGDVIYVNDAFGTAHR
575	3.7e6	1925-1932	3	0.1	1741.9	3.66	0.48	1466	1	30/68	--	gi 1730519	(-) VSHVSTGGASLELLEEK
538	9.9e5	1840-1861	2	-1.0	2000.0	3.45	0.33	526	1	16/34	--	gi 1730519	(-) VLNMM*EIGTSLIYDEEGAK
425	6.9e6	1375-1385	2	0.1	1383.6	3.30	----	1142	1	17/24	--	gi 1730519	(-) AHSMM*VGVNLPQK
218	1.6e6	0548	2	0.1	1102.1	2.96	0.12	881	1	14/16	--	gi 1730519	(-) NNQITNNOR
606	8.5e6	1972-1985	2	-0.8	1221.2	2.79	0.36	492	1	15/20	--	gi 1730519	(-) YSLEPVADELK
509	6.6e5	1740-1747	2	-0.5	2067.5	2.28	0.06	193	1	14/36	--	gi 1730519	(-) SVVLM*SHLGRPDGVPVPM*PDK
554	1.0e7	1885-1908	1	0.5	734.4	1.78	----	494	3	8/10	--	gi 1730519	(-) DVLFLK
785	7.9e6	2411-2417	3	-0.9	2025.1	1.72	0.11	360	1	20/68	--	gi 1730519	(-) ITLPPVDFVTADKEDENAK

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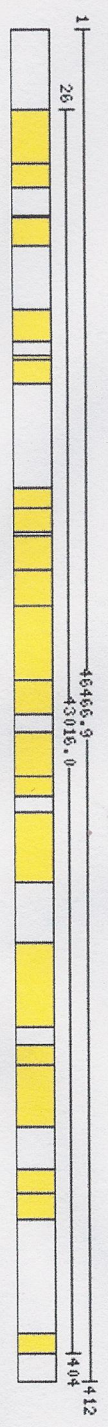
- [Setup](#)
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Sample: Berne, M. K7 1

Send to: [PEPQUT](#) [PEPSTRT](#) [BLAST](#) [NCBI: SEQUENCE](#) [HE STRUCT](#)

```
>gi|25453414|ref|NP_037289.1| argininosuccinate synthetase; argininosuccinate synthetase 1 [Rattus norvegicus]
gi|114291|sp|P09034|ASSY_RAT Argininosuccinate synthase (Citruulline--aspartate ligase) gi|68637|pir||AJRTRS
argininosuccinate synthase (EC 6.3.4.5) - rat gi|55767|emb|CAA30999.1| unnamed protein product [Rattus
norvegicus] gi|203016|gb|AAA40771.1| argininosuccinate synthetase [Rattus norvegicus] [MASS=46496] [MASS=46496]
MSSKGSVWLA YSGGLDITSCI IVMLEQGYD VIAYLANIGQ KEDEFEARKK ALKIGAKKVF LEDVSKELFVE EPIWPAVQSS
ALYEDRYLLG TSLARPCIAR KOVEIAQREG AKYVSHGATG KANDQVRBEL TCYSLAPQIK VIAPWMPDEF YNRFKGRNDL
MEYAKQHGIP IPVTPKSPWS MDENIMHSY EAGILENPKN QAPPGIYTKI QDPAKADNTP DVLEIEFKKG VEVKVTNVKD
GTHSTSLIDL FMYLINEVAKG HGVGRIDIVE NRFIGMKSRG IYETPAGTILL YHAHLIDIEAF TMDREVRKIK QGLGLKEAEL
VYTGFWHSPE CEFVRHCIDK SQERVEGKVQ VSVFKGQVYI LGRESPLSLY NEELVSMNVQ GDYEPIIDATG FININSLRLK
EYHRLQSKVT AK
```

Mass (mono): 46466.9 Identifier: gi|25453414 Database: C:/database/rat.fasta
 Protein Coverage: 227/412 = 55.1% by amino acid count, 25899.2/46466.9 = 55.7% by mass



Sort by:	Sequence	Position
<input type="checkbox"/>	APNTPDVLEIEFK	216 - 228
<input type="checkbox"/>	APNTPDVLEIEFK	216 - 229
<input type="checkbox"/>	DGTTHTSTSLIDLFMYLINEVAKG	240 - 260
<input type="checkbox"/>	EDFEEAR	42 - 48
<input type="checkbox"/>	EOGYDVIAIYLANIGQK	26 - 41
<input type="checkbox"/>	FAELVYTGFWHSPECFVR	317 - 335
<input type="checkbox"/>	GIYETTPAGTILYHAHLIDIEAFITMDR	280 - 304
<input type="checkbox"/>	GOVYILGR	356 - 363
<input type="checkbox"/>	GRNDIMEYAK	156 - 165

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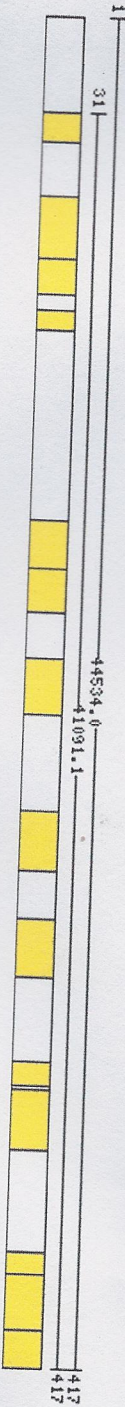
Sample: Berne, M. K7 1

Send to: [PEPQT](#) [PEPSTRT](#) [BLAST](#) [NCBI: SEQUENCE](#) [RETRACT](#)

>gi11730519|sp|P50310|PGK_CRIGR Phosphoglycerate kinase gi12117894|pir||I48074 phosphoglycerate kinase (EC 2.7.2.3) - Chinese hamster gi1987048|emb|CAA86028.1| phosphoglycerate kinase [Cricetulus griseus] [MASS=44563]

MSLSNKLTLID KLDVKGKRRVV MRVDENVPMK **NNQITNNQR**I KAAVPSIKFC LDNGAK**SVVL** **MSHLGRPDGV** **PMPDKYSLEP**
VAAELIKSLIG **KDVLFLKDCV** GPEVENACAN PAAGTVILLE NLRFHVEEFG KGDASGNKI KAEPKIDAF RASLSK**LGDV**
YVNDAFGTAH **RAHSSMWGVN** **LPQKAGGFIM** KKEINYE**FAKA** **IESPERFLIA** **ILGGAKVADK** IQLINMLDK VNEMI**IGGM**
AFTFLKVLNN **MEIGTSLYDE** **EGAKIVKDIM** AKAEKNGV**KI** **TLPVDFVTAD** **KFDENAKTGQ** ATVASSGIPAG WMGLDCG**TES**
SKRYAEAVAR **AKQIVWNGPV** **GVFEWEAFAR** GTKSIMDEVV KATSRGCITI IGGDTATCC AK**WNTEDKVS** **HVSTGGGASL**
ELLEGKVLPG **VDALSNV**

Mass (mono): 44534.0 Identifier: gi11730519 Database: C:/database/rat.fasta
Protein Coverage: 186/417 = 44.6% by amino acid count, 20121.3/44534.0 = 45.2% by mass



Sort by: Sequence

Position

Sequence	Position
AHSSSMVGVN LPQK	172 - 184
AL ESPERFLIA ILGGAK	200 - 216
DVL FLK	92 - 97
ITL LPVDFVTADK FDENAK	280 - 297
LG DDVYYNDA FGTAHR	157 - 171
NNQITNNQR	31 - 39
Q IVWNGPVGVFEWEA FAFAR	333 - 350
SVV IMSHLGRPDGV MPDK	57 - 75
V LNNMEIGTSLYDE FGAK	247 - 264
V LPGVDA LSNV	407 - 417

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Sample: Berne, M. K7 1

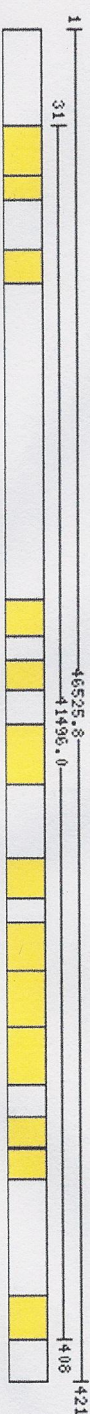
Send to: [PEPSTAT](#) [PERSTAT](#) [BLFAST](#) [NCBI: SEQUENCE](#) [RESTRFACCT](#)

>gi|8392833|ref|NP_058682.1| acetyl-coenzyme A dehydrogenase, medium chain; Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain [Rattus norvegicus] gi|113018|sp|P08503|ACDM_RAT Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor (MCAD) gi|66079|pir|DERTCM acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, medium-chain-specific, mitochondrial - rat gi|202689|gb|AAA40670.1| acyl-CoA dehydrogenase medium subunit (EC 1.3.99.3) [MASS=46555] [MASS=46555]

MAAALRRGYK VLRSVSHFEC RAQHTKPSLK **QEPGLGFSFE** **LTEQOKEFQT** IARKFARFEI IPVAPDYDKS **GEYFPPLIKR**
 AWELGLINTH IPESCGLGL GFEDACLITE ELAYGCTGVQ TAIKANSLGQ MPVITAGNDQ QKKKYLGRMT EQPMCAVCV
 TEPASGSDVA GIKTKAEKKG **DEYVINGQKM** WITNGKAKNW **YFVLTRSNPD** PKVPASKAFT **GFIVEADTPG** IHIGKELNM
 GQRCSDTRGI TFEDEVVPKE **NVLIGEGAGF** KIAMGAFDRT **RPTVAAGAVG** **LAQRALDEAT** KYALDRKTFG **KLIVEHQGVS**
FLIAEMAMKV ELARLSYQRA **AMEVDSGRN** **TYFASIAKAF** AGDIANQLAT DAVQIFGGYG FNTTEYVEKLI MRDAKIYQIY
EGTAQIQRLI IAREHIEKYYK N

Mass (mono): 46525.8 Identifier: gi|8392833 Database: C:/database/rat.fasta

Protein Coverage: 164/421 = 39.0% by amino acid count, 18149.4/46525.8 = 39.0% by mass



Sort by:	Sequence	Position
PERSTAT	AAAEVDSGR	340 - 348
PERSTAT	AFTGFIVEADTPGIHIGK	218 - 235
PERSTAT	ALDEATK	295 - 301
PERSTAT	ALDEATKYALDRKTFGK	295 - 311
PERSTAT	ANWYFVLTTR	198 - 206
PERSTAT	EFQTIAR	47 - 53
PERSTAT	ENVLIGEGAGFK	260 - 271
PERSTAT	IYQIYEGTAQIQIR	396 - 408
PERSTAT		179 - 189

Sequest Summary

Sample: Berne, M. (K11) 1 mb
 Datafiles: [K11 \(03/02/04-03/02/04\)](#)
 Database: [rat \(01/05/2004\)](#)
 Directory: [mbermek11](#) [View Info](#)
 Diff Mods: 16 M 57.02 C 0.000 X

Outfiles: [11421754](#)
 Enzyme: [Trypsin_Strict](#)
 Mass: [±1.5 \(Mono\)](#)
 Max list: [1000](#)
 Intensity: [1.4e10](#) [MS2](#) [DTA VCR](#)

#	GBU	TIC	File	z	DM	MH+	XC	dCn	Sp	RSP	Ions	Sf	Ref	Q	Sequence	Prob	Consensus	Depth:	
<p>A gill2119726 p I156581 302 611E:4.9e9 35% avg 8.0e7 {54.6,1.0,2.4}</p>																			
<p>dnk-type molecular chaperone grp75 precursor - rat gill1000439 g I AAB34982.1 grp75 [Rattus sp.] [MASS=73745] [MASS=73745]</p>																			
462	2.5e7	1838-1849	2	-0.1	1810.1	5.71	0.56	2171	1	24/32	1	24/32	g 2119726	+1	(-)SÖVFSTPAADGÖTÖVEIK	V		3	
566	4.0e8	2188-2229	2	0.3	1646.6	5.52	----	1241	1	24/30	1	24/30	g 2119726	+3	(-)VINEPFAAALAYGLDK	V		3	
476	2.7e7	1887-1918	2	0.6	1809.4	5.44	0.54	2342	1	24/32	1	24/32	g 2119726	+1	(-)SÖVFSTPAADGÖTÖVEIK	V		3	
491	1.0e7	1930-1958	2	0.6	1809.4	5.25	0.52	1533	1	22/32	1	22/32	g 2119726	+1	(-)SÖVFSTPAADGÖTÖVEIK	V		3	
514	3.8e8	2013-2053	2	-0.8	1873.7	4.57	0.51	1472	1	21/32	1	21/32	g 2119726	+1	(-)VEAVNM*AEGIHDETEK	V		3	
649	1.9e7	2440-2464	2	-0.3	2642.6	4.45	0.62	606	1	20/46	1	20/46	g 2119726	+2	(-)C#ELSSVÖTDINLPYLTM*DASGPK	V		3	
509	1.7e8	1992-2024	2	0.1	1243.3	4.33	0.35	1174	1	20/22	1	20/22	g 2119726	+2	(-)DAGÖISGINVLR	V		3	
385	7.3e7	1624-1654	2	0.6	1474.1	4.20	0.51	1460	1	22/26	1	22/26	g 2119726	+1	(-)EQÖIYÖSSGGLSK	V		3	
667	1.4e8	2510-2542	2	-0.1	1569.9	4.13	0.48	1130	1	20/26	1	20/26	g 2119726	+2	(-)IYSPSÖIGAFVIM*K	V		3	
362	2.4e7	1570-1582	2	-0.6	1870.4	4.05	0.53	1147	1	21/28	1	21/28	g 2119726	+1	(-)M*EEFKDÖLPADFC#MK	V		3	
672	3.4e8	2534-2571	2	0.2	1334.4	4.04	0.42	1541	1	19/22	1	19/22	g 2119726	+5	(-)AQFEGIVTDLIK	V		3	
739	6.1e5	2773-2776	2	0.9	2309.7	4.02	0.56	957	1	21/42	1	21/42	g 2119726	+1	(-)GVPEIETFDIDANGIVHSAK	V		3	
500	2.9e8	1956-1994	2	0.6	1290.9	3.99	0.45	1426	1	17/20	1	17/20	g 2119726	+1	(-)VÖQFVÖDILFGR	V		3	
533	3.4e8	2077-2112	2	-0.4	1463.2	3.89	0.32	786	1	18/26	1	18/26	g 2119726	+2	(-)SDIGEVILVGM*TR	V		3	
322	8.4e6	1383-1389	2	0.0	1334.4	3.88	0.47	975	1	16/22	1	16/22	g 2119726	+3	(-)ETAENYLGHTAK	V		3	
517	1.2e8	2025-2055	3	-1.0	1874.0	3.83	0.43	688	1	29/64	1	29/64	g 2119726	+1	(-)VEAVNM*AEGIHDETEK	V		3	
713	7.1e7	2637-2656	2	0.5	1593.5	3.81	0.55	766	1	21/28	1	21/28	g 2119726	+1	(-)LLGÖFTLLIGIPPPAPR	V		3	
310	2.6e7	1310-1330	2	-0.8	1609.6	3.81	0.49	1291	1	20/26	1	20/26	g 2119726	+3	(-)M*KETAEMLYLGHTAK	V		3	
358	3.6e7	1528-1533	2	0.3	1569.4	3.80	0.45	644	1	17/26	1	17/26	g 2119726	+2	(-)QAVTNPNTFYAFK	V		3	
528	1.2e7	2062-2073	2	-0.7	1244.2	3.70	0.26	1384	1	20/22	1	20/22	g 2119726	+2	(-)DAGÖISGINVLR	V		3	
316	3.8e7	1353-1370	2	0.0	1232.4	3.69	0.43	806	1	17/22	1	17/22	g 2119726	+2	(-)QAASSLQÖASLK	V		3	
303	1.0e7	1292-1298	2	0.1	1342.3	3.65	0.42	1129	1	18/24	1	18/24	g 2119726	+2	(-)ASNGDAWEAHHK	V		3	
466	4.0e8	1846-1885	2	0.5	1477.1	3.55	0.61	695	1	17/26	1	17/26	g 2119726	+2	(-)TTPSVVAFPTPDGER	V		3	
728	3.3e7	2742-2775	2	0.1	1593.4	3.46	0.36	734	1	20/28	1	20/28	g 2119726	+1	(-)LLGÖFTLLIGIPPPAPR	V		3	
718	1.8e8	2692-2737	2	0.6	1593.9	3.49	0.45	577	1	19/28	1	19/28	g 2119726	+1	(-)LLGÖFTLLIGIPPPAPR	V		3	
204	1.6e8	0954-0993	2	-0.2	959.2	3.28	0.34	661	1	14/16	1	14/16	g 2119726	+2	(-)VLENAEHAR	V		3	
557	4.3e8	2155-2192	2	0.3	1695.6	3.23	0.09	577	1	20/28	1	20/28	g 2119726	+2	(-)NAVITVPAYFNDSÖR	V		3	
695	4.9e6	2606-2612	2	-0.6	1335.1	3.17	0.34	1325	1	17/22	1	17/22	g 2119726	+5	(-)AQFEGIVTDLIK	V		3	
469	1.1e7	1862-1876	1	0.6	1477.0	3.08	0.39	337	1	16/26	1	16/26	g 2119726	+2	(-)TTPSVVAFPTPDGER	V		3	
432	1.4e6	1744	2	0.4	1474.2	3.08	0.39	661	1	16/26	1	16/26	g 2119726	+1	(-)EQÖIYÖSSGGLSK	V		3	
524	8.8e6	2060-2068	2	-1.5	1293.6	3.02	0.30	1422	1	15/26	1	15/26	g 2119726	+1	(-)VÖQFVÖDILFGR	V		3	
391	1.5e6	1636	1	1.0	1473.6	2.98	0.47	434	1	13/16	1	13/16	g 2119726	+1	(-)EQÖIYÖSSGGLSK	V		3	
214	1.6e8	0990-1022	2	0.0	1150.2	2.92	0.23	502	1	13/16	1	13/16	g 2119726	+2	(-)RYDDPEVÖK	V		3	
569	6.2e6	2206-2217	2	0.1	1695.8	2.85	----	387	1	14/28	1	14/28	g 2119726	+2	(-)NAVITVPAYFNDSÖR	V		3	

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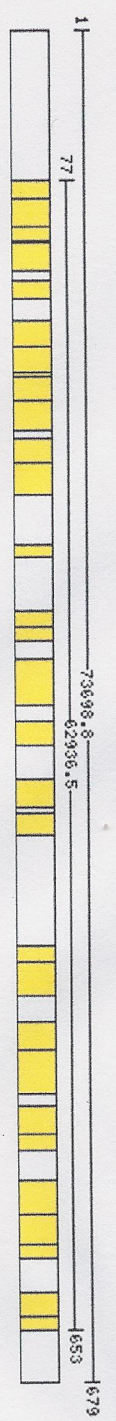
Sample: Berne, M. K11 1

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 NCBI: [SEQUENCE](#) [RESTRIC](#)

>gi|2119726|pir|I156581 dnaK-type molecular chaperone grp75 precursor - rat gi|1000439|gb|AAB34982.1| grp75

[Rattus sp.] [MASS=73745] [MASS=737451]
 MISASRAAA RLYGTTASRS PAARHQDGM NGLSHEAFRF VSRRDYASEA IKGAVVGIDL GTTNSCVAVM EGKQAKYLEN
 AEGARTPSV VAFPTDGERL VGMPAKQAV TNPNTFYAT KRLIGRRYDD PEVQKDTKNV PFKIVRASNG DAWVEAHGKL
 YSPSQIGAFV IMKKEETAEN YLGHTAKNAV ITVPAYFNDS QROATKDAQO ISGLNVLRLI NEPTAALAY GIDKSEDKVI
 AVYDLGGTF DISILEIQK VFEVKSTNGD TFLGGEFDDQ ALLRHIVKEF KRETGVDLTK DNMALQVRE AAERKAKCELS
 SSVQTDINLP YLTMDASGPK HLNMKLTAAQ FEGIVTDLIK RTIAPCCOKAM QDAEVSXSDI GEVILVGGMT RMPKVOQITVQ
 DLFRAPSKA VNPDEAVAIG AAIQGGVLAG DVTVDVLLLDV TPLSLGIETL GGVFTKLINK NTTIIPTKKSQ VFSTAADGQT
 QVEIKVCCGE REMAGDNKLL GQFTLIGIPP APRGVPOIEV TFDIDANGIV HVSAKDKGTG REQIVIVQSS GGLSKDDIEN
 MVKNAEKYAE EDRRKKERVE AVNMAEGTIH DTETKMEEFK DQLPADECNK IKELISKMRE LLARKDSEITG ENIRQAASSL
 QQASIKLLEM AYKMASERE GSSSSSTGEQ KEDQKEEKQ

Mass (mono): 73698.8 Identifier: gi|2119726 Database: C:/database/rat.fasta
 Protein Coverage: 361/679 = 53.2% by amino acid count, 39119.9/73698.8 = 53.1% by mass



Sort by: Sequence Position

PEPSTRT	Sequence	Position
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PEPSTRT	ASNGDAWVEAHGK	147 - 159
PEPSTRT	CELISSSVQTDINLPYLTMDASGPK	317 - 340
PEPSTRT	DAGQISGINVLIR	207 - 218
PEPSTRT	DDIENMVK	556 - 563
PEPSTRT	DNMALQVRE	301 - 307
PEPSTRT	EQQIVIVQSSGGLSK	542 - 555
PEPSTRT	ETAENYLLGHTAK	176 - 187
PEPSTRT		293 - 300

Sequest Summary

Sample: Berne, M. (K301) 1 mb

DataFiles: K301 (04/05/04-04/05/04)

Database: rat (01/05/2004)

Directory: mbernek301 View Info

Diff Mods: 16 M 57.02 C 0.000 X

OutFiles: 13191895

Enzyme: Trypsin_Strict

Mass: ±1.5 (Mono)

Max list: 1000

Intensity: 9.4e9

MS2

DTA VCR

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#	GBU	TIC	File	z	DM	MH+	XC	dCn	Sp	RSP	Ions	SF	Ref	Sequence	Prob	Consensus	Depth:
---	-----	-----	------	---	----	-----	----	-----	----	-----	------	----	-----	----------	------	-----------	--------

A g 16729936 pdb 1MAB G +1.76 1612.7 1e8 8% avg:4.5e7 {3.0,0.0,0}																	
Chain G	Rat Liver F1-Atypase	g 1310190 gb AAA41776.1	ATP synthase gamma-subunit [Rattus norvegicus] [MASS=29933] [MASS=29933]														
1025	1.4e8	3383-3402	2	-2.2	3651.3	4.82	0.55	1181	1	22/64	--		g 167229936	(-) KPPTEGDASVIALPELLNSGYEFDEGSIIENQFK			
1021	3.3e8	3368-3416	2	1.2	3647.9	4.50	0.57	1066	1	23/64	--		g 167229936	(-) KPPTEGDASVIALPELLNSGYEFDEGSIIENQFK			
683	5.2e6	2149-2168	2	-0.5	1755.4	3.27	0.48	677	1	17/28	--		g 167229936	(-) NASDM+IDKLTITENR			
557	4.5e7	1972-2008	2	0.0	1309.4	3.16	0.53	741	1	16/20	--		g 167229936	(-) THSDQFLVSEFK			
291	8.3e7	1123-1170	2	0.2	1078.4	3.11	0.39	1262	1	17/20	--		g 167229936	(-) NDM*AAITTAAGK			
563	4.5e6	1980-2002	3	-0.7	1310.2	3.09	0.27	568	2	21/40	--		g 167229936	(-) THSDQFLVSEFK			
1050	3.1e6	3480-3495	2	-0.4	3649.5	3.02	0.58	473	1	17/64	--		g 167229936	(-) KPPTEGDASVIALPELLNSGYEFDEGSIIENQFK			
1034	1.0e7	3431-3465	2	-2.3	3651.4	3.00	0.41	276	1	13/64	--		g 167229936	(-) KPPTEGDASVIALPELLNSGYEFDEGSIIENQFK			
568	1.4e6	1988-1993	1	1.1	1308.4	2.26	0.43	627	1	13/20	--		g 167229936	(-) THSDQFLVSEFK			
802	9.1e6	2480-2531	1	0.6	1314.9	2.25	0.25	245	10	9/24	--		g 167229936	(-) ELTEIISGAALD			
462	4.5e7	1752-1781	2	-0.7	1091.3	2.05	0.29	454	1	13/18	--		g 167229936	(-) EVM*IVGIGEK			
502	1.5e7	1847-1867	2	0.1	865.0	1.83	----	303	3	9/12	--		g 167229936	(-) ILETFENR			
467	4.5e6	1759-1777	1	0.1	1090.5	1.84	0.27	142	1	12/18	--		g 167229936	(-) EVM*IVGIGEK			
803	2.6e6	2484-2513	1	-1.0	1316.5	1.56	0.17	293	2	10/24	--		g 167229936	(-) ELTEIISGAALD			
804	5.2e5	2489-2507	2	0.7	1314.8	1.46	----	261	12	11/24	--		g 167229936	(-) ELTEIISGAALD			
306	1.1e7	1225-1249	1	0.5	696.3	0.94	----	207	1	6/10	--		g 167229936	(-) SVTSYK			

B g 127700611 ref XP_230019.1 36 415:1.2e6 0% avg:3.1e5 {3.0,1.0,1.6}																	
ftin	[Rattus norvegicus]	[MASS=1297407]	[MASS=1297407]														
30	3.5e5	0253-0282	3	-0.4	1415.9	1.37	0.15	154	50	10/44	--		g 127700611	(-) VDM+NDAENFTC#R			
181	4.5e5	0460	2	-1.5	875.5	1.09	0.03	153	50	6/14	--		g 127700611	(-) NTINKAGR			
47	2.5e5	0283	2	-0.9	934.4	1.06	0.01	107	27	5/14	--		g 127700611	(-) IGSIC#LR			
1133	1.8e5	3730	2	1.1	3250.7	0.92	----	96	27	9/56	--		g 127700611	(-) YVCOIKNDAGMRCESALLITVLEPARIVEK			

C g 127666086 ref XP_222242.1 30 315:1.9e2 0% avg:6.3e6 {3.0,0.0,0.0}																	
similar to	mKIAA0219 protein	[Mus musculus]	[Rattus norvegicus]	[MASS=313138]	[MASS=313138]												
951	9.6e6	3128-3138	2	0.9	2782.3	1.72	0.03	51	376	7/50	--		g 127666086	(-) TVVNSHKVLPLEFIVTDAGEVMEFGK			
567	1.9e6	1987-2006	3	-1.2	2020.2	1.72	0.08	133	265	14/60	--		g 127666086	(-) EM+IQQMDKKAQTRR			
1210	1.4e5	3935	2	-1.1	2811.6	0.93	0.08	99	12	8/48	--		g 127666086	(-) RLQELDGELEFAALGLLDATM*FRNPR			

D g|17380501|sp|P16086|SPCN_RAT +1.42 515:3.8e2|0%|avg:7.5e6 {2.2,1.0,1.0}

Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin) (Fodrin alpha chain) g|13462887|gb|AAC33127.1| alpha-fodrin [Rattus norvegicus] [MASS=284637] [MASS=284637]

543 1.8e7 1949-1970 2 1.3 1524.3 2.26 ---- 407 12 11/22 -- g|17380501 +4 (-) DMDEESWIKEK

http://localhost/cgi-bin/runsummary.pl?directory=mbenek301&PULL_TO_TOP.x=1&max_rank=3&max_list=1000&sort=cons... 4/5/2004

Flicka

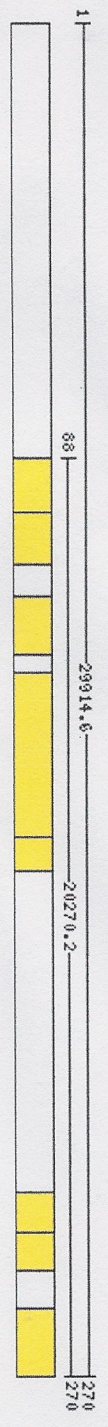
[Setup](#)
 [Create DTA](#)
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Sample: Berne, M. K301 1

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 [NCBI: SEQUENCE](#)
 [ABSTRACT](#)

>gi|6729936|pdb|1MAB|G Chain G, Rat Liver Fl-Atpase gi|310190|gb|AAA41776.1| ATP synthase gamma-subunit [Rattus norvegicus] [MASS=29933] [MASS=29933]
 RDITRLKSI KNIQKITKSM KMVAAAKYAR AERELKPARV YGTGSLALYE KAEIKGPEDK KKHLLIIGVSS DRGLCGAIHS
 SVAKQKNDM **AALTAAGKEV** **MIVGIGEKIK** SILYR**THSDQ** **FLVSEKDVGR** **KPPTFGDASV** **IALELLNSGY** **EFDEGSIIFN**
QFKSVISYKT EEKPIFSFST VVAENMSIY DDIDADVLQN YQEYNLANII YYSIKESTTS EQSARMTAMD NASKNASDMI
DKLTLTFNRT RQAVIT**KELI** **EISGAALD**

Mass (mono): 29914.6
 Identifier: gi|6729936
 Database: C:/database/rat.fasta
 Protein Coverage: 99/270 = 36.7% by amino acid count, 10727.5/29914.6 = 35.9% by mass



Sort by: Sequence Position

Sequence	Position
ELIEIISGAAALD	258 - 270
EVMIVGIGEK	99 - 108
KPPTFGDASVIALELLNSGYEFDEGSIIFNQFK	131 - 163
LTLTFNR	243 - 249
NASDMIDKLTLLTFNR	235 - 249
NDMAALLTAAGK	88 - 98
SVISYK	164 - 169
THSDQFLVSEK	116 - 126