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Find A Gene Project: Part 1

- 1) Name: Calcium/calmodulin-dependent protein kinase (CaMKII)
Accession: NP_524635.3
Species: *Drosophila melanogaster* (Fruit fly)
- 2) Method: TBLASTN (2.15.0) search against all except fruit fly ESTs
Database: Expressed Sequence Tags (est)
Organism: All except fruit fly

translated BLAST: tblastn

blastn blastp blastx **tblastn** tblastx

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) Clear

NP_524635.3

Query subrange [?](#)

From

To

Or, upload file No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database [?](#)

Organism ☒ exclude

Optional Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

Exclude ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Optional Limit to ☐ Sequences from type material

Optional Entrez Query

Optional Enter an Entrez query to limit search [?](#)

Search database est using Tblastn (search translated nucleotide databases using a protein query)

☐ Show results in a new window

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input type="checkbox"/>	WLA071C01full WLbrain Gallus gallus cDN...	Gallus g...	772	772	96%	0.0	71.65%	1882	CN210874.1
<input type="checkbox"/>	FP849438 mixed stages (KT0AAA) Oikople...	Oikople...	619	619	93%	0.0	60.20%	1696	FP849438.1
<input checked="" type="checkbox"/>	BX420151 Homo sapiens FETAL BRAIN Ho...	Homo s...	578	578	65%	0.0	83.28%	1066	BX420151.2
<input type="checkbox"/>	1099435177395 12-DrosW-norm-1P5Kb Dr...	Drosop...	572	572	59%	0.0	93.86%	903	EB493840.1
<input type="checkbox"/>	CLJ400-M11.y1d-s SHGC-CLJ2 Gasteroste...	Gastero...	553	553	62%	0.0	84.64%	1067	DW659903.1
<input type="checkbox"/>	AL553478 Homo sapiens PLACENTA COT...	Homo s...	551	551	63%	0.0	82.85%	984	AL553478.3

Chosen match: Accession BX420151.2, a 1066 base pair clone from homosapiens.

BX420151 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF024YB21 5-PRIME, mRNA sequenceSequence ID: [BX420151.2](#) Length: 1066 Number of Matches: 1Range 1: 20 to 988 [GenBank](#) [Graphics](#)[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
578 bits(1489)	0.0	Compositional matrix adjust.	269/323(83%)	294/323(91%)	0/323(0%)	+2
Query 1	MAAPAACTRFSDNYDIKEELGKGAFSIVKRCVQKSTGFEFAAKIINTKKLTARDFQKLER	60				
	MA CTRF+D Y + E++GK AFS+V+RCV+ TG E+AAKIINTKKL+ARD QKLER					
Sbjct 20	MATTVTCTRTFDEYQLYEDIGKXAFSVVRRVCVKLCTGHEYAAKIINTKKLSARDHQKLER	199				
Query 61	EARICRKLHHPNIVRLHDSIQEENYHYLVFDLVTGGELFEDIVAREFYSEADASHCIQQI	120				
	EARICR L H NIVRLHDSI EE +HYLVFDLVTGGELFEDIVARE+YSEADASHCIQQI					
Sbjct 200	EARICRLLKHSNIVRLHDSISEEGFHLYLVFDLVTGGELFEDIVAREYYSEADASHCIQQI	379				
Query 121	LESVNCHQNGVVRDLKPENLLLASKAKGAAVKLADFLAIEVQGDHQAQWFGFAGTPGY	180				
	LE+V HCHQ GVVHRDLKPENLLLASK KGAAVKLADFLAIEVQGD QAQWFGFAGTPGY					
Sbjct 380	LEAVLHCHQMVGVRDLKPENLLLASKCKGAAVKLADFLAIEVQGDQAQWFGFAGTPGY	559				
Query 181	LSPEVLKKEPYGKSVDIWACGVILYILLVGYPFFWDEDQHRLYSQIKAGAYDYPSPWD	240				
	LSPEVL+KE YGK VDIWACGVILYILLVGYPFFWDEDQH+LY QIKAGAYD+PSPWD					
Sbjct 560	LSPEVLRKEAYGKPVDIWACGVILYILLVGYPFFWDEDQHKLYQQIKAGAYDFPSPWD	739				
Query 241	VTPEAKNLINQMLTVNPNKRITAAEALKHPWICQRRERVASVVRQETVDCLKKFNARRKL	300				
	VTPEAKNLINQMLT+NP KRITA EALKHPW+CQR VAS++HRQETV+CLKKFNARRKL					
Sbjct 740	VTPEAKNLINQMLTINPAKRITAHEALKHPWCQRSTVASMMHRQETVECLKKFNARRKL	919				
Query 301	KGAILTTMLATRNFSRSRSMITKK	323				
	KGAILTTMLATR FS++S++T+K					
Sbjct 920	KGAILTTMLATRXFSAKSLTRK	988				

3) >XP_059790222.1

MAAGAGASAACAGPGRGCECWEQEWRERVQGAGAAVGAGLRCAARSWRAR
SAQISRALAARRSPARPLGAASRGVARARSVAVPASGSRSRRRPSAAERTPSPS
VAAMATTVTCTRTFDEYQLYEDIGKGAFSVVRRVCVKLCTGHEYAAKIINTKKLSA
RDHQKLREARICRLLKHSNIVRLHDSISEEGFHLYLVFDLVTGGELFEDIVAREYY
SEADASHCIQQILEAVLHCHQMVGVRDLKPENLLLASKCKGAAVKLADFLAIE
EVQGDQQAQWFGFAGTPGYLSPEVLRKEAYGKPVDIWACGVILYILLVGYPFFWDE
DQHKLYQQIKAGAYDFPSPWDVTPEAKNLINQMLTINPAKRITAAEALKHPW
VCQRSTVASMMHRQETVECLKKFNARRKLKGAILTTML
ATRNFSAKSLLNKKADGVKPQTNSTKNSAAATSPKGTLPAALEPQSTVIHNPVD
GIKESSDSTHTTIEDEDTKAPRPDILSSVRRGSGTPEGEGPPPCPPPAPISPLPTSP
RICDILSSVRRGSGTPEAEGPLPTPSLRISDILNTVRRGSGTPEAQGPPPCPPPALPG
SPPTLSRKQEIHKITEQLIEAVNNGDFEAYAKICDPGLTSFEPEALGNLVEGMDFH
YFENLLAKNSKPIHTTILNPHVHVIGEDAACIAYIRLTQYIDGQGRPRTSQSEETRV
WHRRDGKWQNVHFCGAPVAPLQ

Name: calcium/calmodulin-dependent protein kinase type II subunit beta isoform X5

Species: *Balaenoptera ricei*

- 4) A BLASTP search against NR database yielded a top hit result to a protein from *Balaenoptera acutorostrata* (common minke whale). This was a match with 100% identity, but to a different species than the one I started with (*Balaenoptera ricei*), hence I have this is likely a novel gene.

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase type II subunit beta isoform X5 [Balaeno...	Balaenopter...	1507	1507	100%	0.0	100.00%	731	XP_059790222.1
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase type II subunit beta isoform X4 [Balaeno...	Balaenopter...	1292	1292	84%	0.0	100.00%	620	XP_057405999.1
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase type II subunit beta isoform X4 [Balaeno...	Balaenopter...	1503	1503	100%	0.0	99.86%	732	XP_059790221.1
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase type II subunit beta isoform X3 [Balaeno...	Balaenopter...	1288	1288	84%	0.0	99.84%	621	XP_057405998.1
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase type II subunit beta isoform X4 [Balaeno...	Balaenopter...	1289	1289	84%	0.0	99.84%	620	XP_036719196.1
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase type II subunit beta isoform X3 [Balaeno...	Balaenopter...	1285	1285	84%	0.0	99.68%	621	XP_036719195.1