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Find A Gene

- 1) Name: Calcium/calmodulin dependant protein kinase type 1 (CAMK1)
Accession: Q14012
Species: Human
Function: CAMK1 acts as a signaling molecule when activated by calcium-calmodulin. It can phosphorylate various target proteins, influencing functions of gene expression, cell cycle regulation, neuronal activity, and muscle differentiation, among other functions.
- 2) Method: TBLASTN search against amphibian ESTs
Database: Expressed Sequence Tags (est)
Organism: amphibians (taxid: 8292)

The screenshot shows the NCBI TBLASTN search interface. At the top, there are tabs for different search types: blastn, blastp, blastx, **tblastn** (selected), and tblastx. Below the tabs, a header reads "TBLASTN search translated nucleotide databases using a protein query. more...".

The main form is divided into two sections: "Enter Query Sequence" and "Choose Search Set".

Enter Query Sequence:

- Input field: "Enter accession number(s), gi(s), or FASTA sequence(s) ? Clear". The value "sp|Q14012" is entered.
- Query subrange: "From" and "To" input fields.
- Or, upload file: "Choose File" button, "No file chosen" text.
- Job Title: "Q14012:RecName: Full=Calcium/calmodulin-dependent...". Below it, a prompt "Enter a descriptive title for your BLAST search ?".
- Checkbox: "Align two or more sequences ?".

Choose Search Set:

- Database: "Expressed sequence tags (est)" (selected from a dropdown).
- Organism: "amphibians (taxid:8292)". There is an "exclude" checkbox and an "Add organism" button. Below it, a prompt "Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown ?".
- Exclude: "Models (XM/XP)" and "Uncultured/environmental sample sequences" (both unchecked).
- Limit to: "Sequences from type material" (unchecked).
- Entrez Query: An empty input field with a "YouTube" icon and "Create custom database" link. Below it, a prompt "Enter an Entrez query to limit search ?".

At the bottom, there is a large blue "BLAST" button. To its right, there is a checkbox "Show results in a new window" and the text "Search database est using Tblastn (search translated nucleotide databases using a protein query)".

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	JGI_CABJ3685.fwd NIH_XGC_tropSki1 Xenopus tropicalis cDNA clone...	Xenopus tr...	506	506	74%	1e-180	87.77%	901	DT422254.1
<input type="checkbox"/>	AGENCOURT_10493284 NICHG_XGC_OO1 Xenopus laevis cDNA cl...	Xenopus l...	461	461	69%	2e-162	87.16%	946	BU915161.1
<input type="checkbox"/>	xl11007G08F_1289084 Xenopus ORFeome version 1.0 library Xenopu...	Xenopus l...	458	458	68%	3e-162	87.45%	794	JZ823559.1
<input type="checkbox"/>	BX726823 XGC-tadpole Xenopus tropicalis cDNA clone TTPA065I08 5'...	Xenopus tr...	450	450	65%	4e-159	89.26%	728	BX726823.1
<input type="checkbox"/>	BX714712 XGC-tadpole Xenopus tropicalis cDNA clone TTPA015p20 5'...	Xenopus tr...	442	442	65%	2e-155	88.07%	833	BX714712.1

Chosen match: Accession DT422254.1, a 901 base pair clone from *Xenopus tropicalis*.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Pipioidea; Pipidae; Xenopodinae; *Xenopus*; *Silurana*.

JGI_CABJ3685.fwd NIH_XGC_tropSki1 *Xenopus tropicalis* cDNA clone IMAGE:7869012 5', mRNA sequence

Sequence ID: [DT422254.1](#) Length: 901 Number of Matches: 1

Range 1: 66 to 899 [GenBank](#) [Graphics](#)

[Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
506 bits(1304)	1e-180	Compositional matrix adjust.	244/278(88%)	264/278(94%)	1/278(0%)	+3
Query 6	EGPRWKQ-AEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKEALEGKEGSME					
	+GP WK+ AEDIRDIY+FR+VLGTGAFSEV+LAE+K+TQKLVAIKCI K+ALEGKE S+E					
Sbjct 66	DGPSWKKRAEDIRDIYEFREVLGTGAFSEVLAEEKKTQKLVAIKCIPKKALEGKETSIE					
Query 65	NEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQ					
	NEIAVL KIKH NIV+L+DIYES HLYLIMQLVSGGELFDRIVEKGFYTE+DAS+LI Q					
Sbjct 246	NEIAVLRKIKHANIVSLEDIYESRSHLYLIMQLVSGGELFDRIVEKGFYTEKDASQLIKQ					
Query 125	VLDVAVKYLHDLGIVHRDLKPENLLYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGY					
	+LDVAVKYLHD+GIVHRDLKPENLLYYS+DEDSKIMISDFGLSK+E GSV+STACGTPGY					
Sbjct 426	ILDVAVKYLHDMGIVHRDLKPENLLYSIDESKIMISDFGLSKIEGSGSVMSTACGTPGY					
Query 185	VAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPYWDD					
	VAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPYWDD					
Sbjct 606	VAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPYWDD					
Query 245	ISDSAKDFIRHLMKDPKERTCEQALQHPWIAGDTAL 282					
	ISDSAKDFI+HLMKDP KR TC+QAL HPWIAGDTAL					
Sbjct 786	ISDSAKDFIQHLMKDPNKRNTCDQALXHPWIAGDTAL 899					

3) >DT422254.1_3 JGI_CABJ3685.fwd NIH_XGC_tropSki1 *Xenopus tropicalis* cDNA clone IMAGE:7869012 5', mRNA sequence

EPLLGLSGRCERDLRMPLDEDDGPSWKKRAEDIRDIYEFREVLGTGAFSEVVLAEE
 KKTQKLVAIKCIPKKALEGKETSIE NEIAVLRKIKHANIVSLEDIYESRSHLYLIMQL
 VSGGELFDRIVEKGFYTEKDASQLIKQILDAVKYLHDMGIVHRDLKPENLLYYSID
 EDSKIMISDFGLSKIEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAY
 ILLCGYPPFYDENDAKLFEQILKAEYEFDSPYWDDISDSAKDFIQHLMKDPNKR
 NTCDQALXHPWIAGDTALX

Name: Western clawed frog

Species: *Xenopus tropicalis*

4)

Standard Protein BLAST

blastn **blastp** blastx tblastn tblastx

BLASTP programs search protein databases using a protein query. more...

Enter Query Sequence

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

LYLIMQLVSGGELFDRIVEKGFYTEKDASQLIKQLDAVKYLHDMGIVHRDLK
PENLLYYSIDEDSKIMISDFGLSKIEGSGVMSTACGTPGYVAPEVLAQKPY
SKAVDCWSIGVIAYILLCGYPFYDENDAKLFEQILKAIEYFDSPYWDDISDS
AKDFIQHLMKDPNKRNTCDQALXHPWIAGDTALX

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

Databases ☒ Standard databases (nr etc.): New ☐ Experimental databases

[Try experimental clustered nr database](#)
For more info see [What is clustered nr?](#)

Compare ☐ Select to compare standard and experimental database ?

Standard

Database ?

Organism
Optional Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown ?

Exclude ☐ Models (XM/XP) ☐ Non-redundant RefSeq proteins (WP) ☐ Uncultured/environmental sample seq
Optional

Program Selection

Algorithm ☐ Quick BLASTP (Accelerated protein-protein BLAST)
☒ blastp (protein-protein BLAST)
☐ PSI-BLAST (Position-Specific Iterated BLAST)
☐ PHI-BLAST (Pattern Hit Initiated BLAST)
☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)
Choose a BLAST algorithm ?

BLAST | Search database nr using Blastp (protein-protein BLAST)

None of the results below match my sequence with 100%, making this protein novel:

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download

Select columns

Show

100

?

☐ select all

1 sequences selected

[GenPept](#)

[Graphics](#)

[Distance tree of results](#)

[Multiple alignment](#)

[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input type="checkbox"/>	hypothetical protein XENTR_v10012846 [Xenopus tropicalis]	Xenopus t...	582	582	94%	0.0	99.65%	419	KAE8612413.1
<input checked="" type="checkbox"/>	calcium/calmodulin-dependent protein kinase type 1 [Xenopus tropi...	Xenopus t...	581	581	94%	0.0	99.65%	383	NP_001016269.1
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase I L homeolog [Xenop...	Xenopus I...	577	577	94%	0.0	98.59%	382	NP_001082318.1
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase I L homeolog isoform...	Xenopus I...	576	576	94%	0.0	98.59%	382	XP_018112030.1
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase I S homeolog [Xenop...	Xenopus I...	573	573	94%	0.0	98.59%	378	NP_001080279.1
<input type="checkbox"/>	hypothetical protein GDO81_018368 [Engystomops pustulosus]	Engystom...	572	572	94%	0.0	98.23%	383	KAG8557225.1
<input type="checkbox"/>	calcium/calmodulin-dependent protein kinase type 1 [Microcaecilia ...	Microcaec...	571	571	94%	0.0	97.88%	383	XP_030064035.1

5) >Human|Q14012.1|Calcium/calmodulin-dependent protein kinase type

MLGAVEGPRWKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKEA
LEGKEGSMENEIAVLHKKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKG
FYTERDASRLIFQVLDAVKYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSK
MEDPGSVLSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDEN
DAKLFEQILKAEYEFDSPYWDDISDSAKDFIRHLMKDPKRFTCEQALQHPWIA
GDTALDKNIHQSVSEQIKKNFAKSKWKQAFNATAVVRHMRKLQLGTSQEGQGQ
TASHGELLTPVAGGPAAGCCCRDCCVEPGTELSPTLPHQL

>Western clawed frog | DT422254.1_3 calcium/calmodulin-dependent protein kinase
type 1 [Xenopus tropicalis]

EPLLGLSGRCERDLRMPLDEEDGPSWKKRAEDIRDIYEFREVLGTGAFSEVVLAEE
KKTQKLVAIKCIPKKALEGKETSIEINEIAVLRKIKHANIVSLEDIYESRSHLYLIMQL
VSGGELFDRIVEKGFYTEKDASQLIKQILDAVKYLHDMGIVHRDLKPENLLYYSID
EDSKIMISDFGLSKIEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAY
ILLCGYPPFYDENDAKLFEQILKAEYEFDSPYWDDISDSAKDFIQHLMKDPNKR
NTCDQALXHPWIAGDTALX

>Common spadefoot| XP_063282804.1 calcium/calmodulin-dependent protein kinase
type 1 [Pelobates fuscus]

MPLGDDGPSWKKRAEDIRDTYNFRDVLGTGAFSEVVLAEEKATQKLVAIKCIPK
KALEGKETSIEINEIAVLRKIKHANIVSLEDIYENRSHLYLIMQLVSGGELFDRIVEK
GFYTEKDASQLIKQILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSKIMISDFGLS
KIEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDEN
DAKLFEQILKAEYEFDSPYWDDISDSAKDFIQHLMKDPNKRKYTCQALQHPWI
AGDTALDKNIHESVSEQIRKNFAKSRWKQAFNATAVVRHMRKLQLGSSQEGPGQ
TTPTSPCHGNLLVPGDHHGSLSESCQDCCTQKSTENNSLSFSTHHCPQSNRV

>Sardinian treefrog| XP_056380675.1 calcium/calmodulin-dependent protein kinase type
1 [Hyla sarda]

MPLGEDGPSWKKRAEDIRDIYDFRDVLGTGAFSEVVLAEEKKTQKLVAIKCIPKK
ALEGKETSIEINEIAVLRKIKHTNIVSLEDIYESRSHLYLIMQLVSGGELFDRIVEKGF
YTEKDASQLIKQILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKI
EGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDEND
AKLFEQILKAEYEFDSPYWDDISDSAKDFIQHLMKDPNKRKYTCQALQHPWIA
GDTALDKNIHESVSEQIRKNFAKSRWKQAFNATAVVRHMRKLQLGTSQEGPGQT
TPTSPCHGNLLVPGDNHGSLSNQCQDRCSQKTPENNSLAYSTHHCPQSNRV

>Túngara frogs| KAG8557225.1 hypothetical protein GDO81_018368 [Engystomops pustulosus]

MPLGEDGPSWKKRAEDIRDIYEFRDVLGTGAFSEVVLAEKKKTQKLVAIKCIPKK
ALEGKETSIENEIAVLRKIKHANIVSLEDIYESRSHLYLIMQLVSGGELFDRIVEKGF
YTEKDASQLIKQILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKI
EGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDEND
AKLFEQILKAIEYEFDSPYWDDISDSAKDFIQHLMKDPNKRYTCDQALQHPWIA
GDTALDKNIHESVSEQIRKNFAKSRWKQAFNATAVVRHMRKLQLGTSQEGPGQT
TPTSPCHGNLLVPGDNHGSLSDSCQDRCSQKTPENNSLAYSAHHCPSNRV

>Tiny Cayenne Caecilian| XP_030064035.1 calcium/calmodulin-dependent protein kinase type 1 [Microcaecilia unicolor]

MPLEEDGPSWKKRAEDIRDIYEFREVLGTGAFSEVVLAEKKKTQKLVAIKCIPKK
ALEGKETSIENEIAVLRKIKHANIVSLEDIYESRSHLYLIMQLVSGGELFDRIVEKGF
YTEKDASQLIKQILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKI
EGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDEND
AKLFEQILKAIEYEFDSPYWDDISESAKDFIQHLMKDPNKRYTCDQALQHPWIAG
DTALDKNIHESVSEQMKKNFAKSKWKQAFNATAVVRHMRKLQLGTSQEGPGQT
TPTSPCHGPLLVPGDNHGSHKSDSCQDCCSRKSPEKTNNSLAAYCCHHSNRV

>Plains spadefoot toad| XP_053326075.1 calcium/calmodulin-dependent protein kinase type 1 [Spea bombifrons]

MPLEDDGPSWKKRAEDIRDKYEFRDVLGTGAFSEVVLAEKKTTQKLVAIKCIPKK
ALEGKETSIENEIAVLRKIKHANIVSLEDIYENRSHLYLIMQLVSGGELFDRIVEKG
FYTEKDASQLIRQILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSKIMISDFGLSK
IEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDEND
AKLFEQILKAIEYEFDSPYWDDISDSAKDFIQHLMKDPNKRYTCDQALQHPWIA
GDTALDKNIHESVSEQIRKNFAKSRWKQAFNATAVVRHMRKLQLGTSQEGPGQT
TPTSPCHGNLLTPGENHGSHHESCQDCYSQKSMENNSLSYSTHPCPQSNRV

CLUSTAL W (1.81) multiple sequence alignment

Human|Q14012.1|Calcium/calmoduli

-----MLGAVEGPRWKQ-AEDIRDIYDFRDVLGTGAFSEVILAEDKRTQK

Plains spadefoot toad

-----MPLEDDGPSWKKRAEDIRDKYEFRDVLGTGAFSEVVLAEKKTTQK

Common spadefoot

-----MPLGDDGPSWKKRAEDIRDTYNFRDVLGTGAFSEVVLAEKKATQK

Tiny Cayenne Caecilian

-----MPLEEDGPSWKKRAEDIRDIYEFREVLGTGAFSEVVLAEKKKTQK

EPLLGLSGRCERDLRMPLDEDGPSWKKRAEDIRDIYEFREVLGTGAFSEVVLAEKKKTQK

Sardinian treefrog

-----MPLGEDGPSWKKRAEDIRDIYDFRDVLGTGAFSEVVLAEKKKTQK

Túngara frogs

-----MPLGEDGPSWKKRAEDIRDIYEF RDVLGTGAFSEVVLAE EKKTKQ

* .*** ** . ***** *.***.*****.***.* ****

Human|Q14012.1|Calcium/calmodulin-dependent protein kinase II

LVAIKCIAKEALEGKEGSMENEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELF

Plains spadefoot toad

LVAIKCIPKKALEGKETSIENEIAVLRKIKHANIVSLEDIYENRSHLYLIMQLVSGGELF

Common spadefoot

LVAIKCIPKKALEGKETSIENEIAVLRKIKHANIVSLEDIYENRSHLYLIMQLVSGGELF

Tiny Cayenne Caecilian

LVAIKCIPKKALEGKETSIENEIAVLRKIKHANIVSLEDIYESRSHLYLIMQLVSGGELF

Western clawed frog

LVAIKCIPKKALEGKETSIENEIAVLRKIKHANIVSLEDIYESRSHLYLIMQLVSGGELF

Sardinian treefrog

LVAIKCIPKKALEGKETSIENEIAVLRKIKHTNIVSLEDIYESRSHLYLIMQLVSGGELF

Túngara frogs

LVAIKCIPKKALEGKETSIENEIAVLRKIKHANIVSLEDIYESRSHLYLIMQLVSGGELF

***** *.***** *.***** ***** *****.*.***** *****

Human|Q14012.1|Calcium/calmodulin-dependent protein kinase II

DRIVEKGFYTERDASRLIFQVLDAVKYLHDLGIVHRDLKPENLLYSLDEDSKIMISDFG

Plains spadefoot toad

DRIVEKGFYTEKDASQLIRQILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSKIMISDFG

Common spadefoot

DRIVEKGFYTEKDASQLIKQILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSKIMISDFG

Tiny Cayenne Caecilian

DRIVEKGFYTEKDASQLIKQILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSTIMISDFG

Western clawed frog

DRIVEKGFYTEKDASOLIKQILD AVKYLHDMGIVHRDLKPENLLYYSIDEDSKIMISDFG

Sardinian treefrog

DRIVEKGFYTEKDASQLIKQILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSKIMISDFG

Túngara frogs

DRIVEKGFYTEKDASOLIKOILDAVKYLHDMGIVHRDLKPENLLYYSLDEDSKIMISDFG

Human|Q14012.1|Calcium/calmoduli

LSKMEDPGSVLSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDA

Plains spadefoot toad

LSKIEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDA

Common spadefoot

LSKIEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDA

Tiny Cayenne Caecilian

LSKIEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDA

Western clawed frog

LSKIEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDA

Sardinian treefrog

LSKIEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDA

Túngara frogs

LSKIEGSGSVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDA

.* ***.**

Human|Q14012.1|Calcium/calmoduli

KLFEQILKAIEYFDSPYWDDISDSAKDFIRHLMKDPKRYTCDQALQHPWIAGDTALDK

Plains spadefoot toad

KLFEQILKAIEYFDSPYWDDISDSAKDFIQHLMKDPNKRYTCDQALQHPWIAGDTALDK

Common spadefoot

KLFEQILKAIEYFDSPYWDDISDSAKDFIQHLMKDPNKRYTCDQALQHPWIAGDTALDK

Tiny Cayenne Caecilian

KLFEQILKAIEYFDSPYWDDISESAKDFIQHLMKDPNKRYTCDQALQHPWIAGDTALDK

Western clawed frog

KLFEQILKAIEYFDSPYWDDISDSAKDFIQHLMKDPNKRNTCDQALXHPWIAGDTALX-

Sardinian treefrog

KLFEQILKAIEYFDSPYWDDISDSAKDFIQHLMKDPNKRYTCDQALQHPWIAGDTALDK

Túngara frogs

KLFEQILKAIEYFDSPYWDDISDSAKDFIQHLMKDPNKRYTCDQALQHPWIAGDTALDK

*****.* ***.*****

Human|Q14012.1|Calcium/calmoduli

NIHQSVSEQIKKNFAKSKWKQAFNATAVVRHMRKLQLGTSQEGQGQTA----SHGELLTP

Plains spadefoot toad

NIHESVSEQIRKNFAKSRWKQAFNATAVVRHMRKLQLGTSQEGPGQTTPTSPCHGNLLTP

Common spadefoot

NIHESVSEQIRKNFAKSRWKQAFNATAVVRHMRKLQLGSSQEGPGQTTPTSPCHGNLLVP

Tiny Cayenne Caecilian

NIHESVSEQMKNFAKSKWKQAFNATAVVRHMRKLQLGTSQEGPGQTTPTSPCHGPLLVP

Western clawed frog

Sardinian treefrog

NIHESVSEQIRKNFAKSRWKQAFNATAVVRHMRKLQLGTSQEGPGQTTPTSPCHGNLLVP

Túngara frogs

NIHESVSEQIRKNFAKSRWKQAFNATAVVRHMRKLQLGTSQEGPGQTTPTSPCHGNLLVP

Human

VAGGPAAGCCCRDCCVEPGTELSP-----TLPHQL

Plains spadefoot toad

GENHGSHHESCQDCYSQKSMENNSLSYSTHPCPQSNRV

Common spadefoot

GDHHGSLSESCQDCCTQKSTENNSLSFSTHHCPQSNRV

Tiny Cayenne Caecilian

GDNHGSHKDSCQDCCSRKSPEKTNNSLAAYCCHHSNRV

Western clawed frog

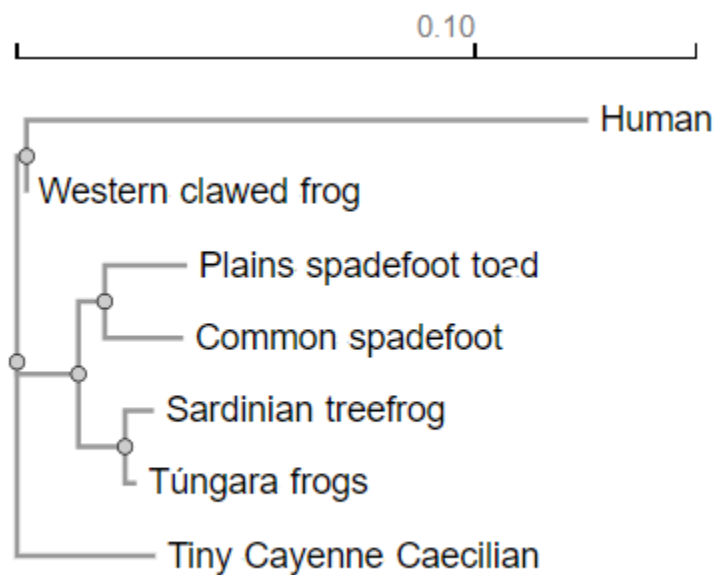
Sardinian treefrog

GDNHGSLSDNCQDRCSQKTPENNSLAYSTHHCPQSNRV

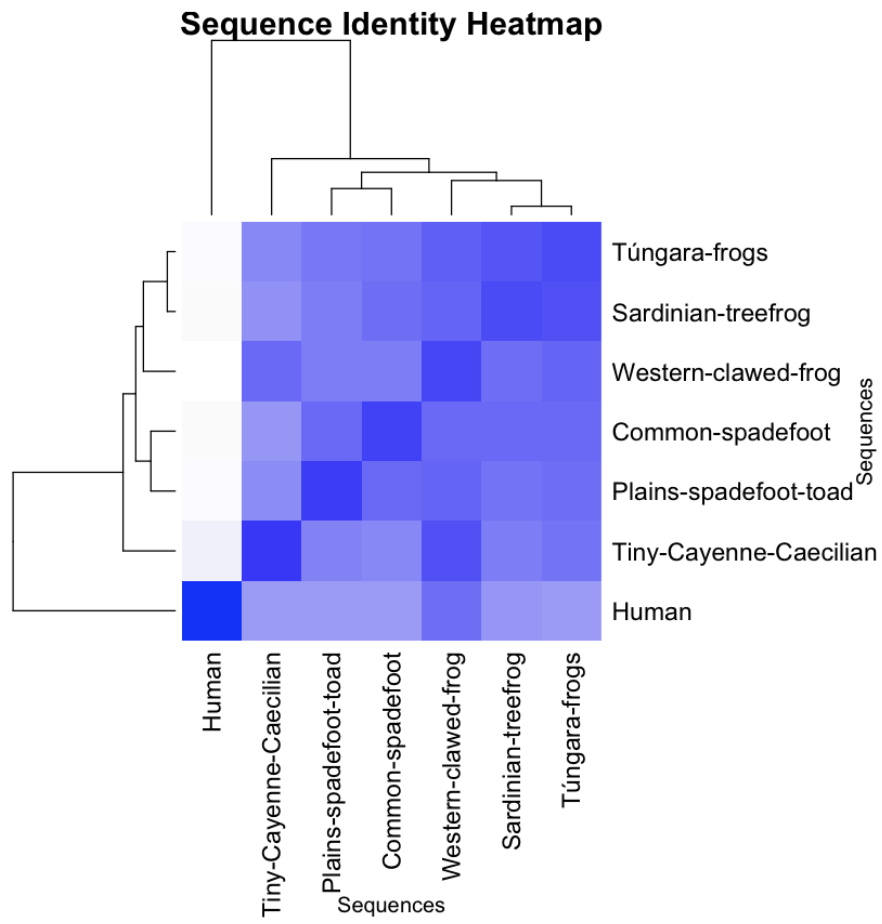
Túngara frogs

GDNHGSLSDSCQDRCSQKTPENNSLAYSAHHCPQSNRV

6)



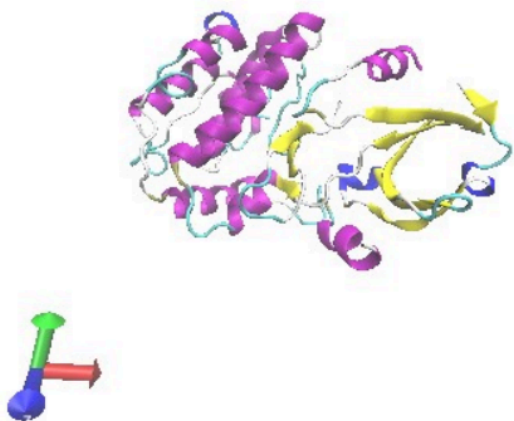
7)



8)

ID	Technique	Resolution	Source	E-value	Identity
1A06	X-ray Diffraction	2.5	Rattus norvegicus	0.0	87.58%
5IG1	X-ray Diffraction	2.9	Salpingoeca rosetta	3e-85	42.86%
2BDW	X-ray Diffraction	1.8	Caenorhabditis elegans	7e-77	41.36%

- 9) Given over 87% of their similarity, this structure is likely to be very similar to the novel protein. In the figure below the CAMK1 corresponds to the *Rattus norvegicus* subject of this report



- 10) ChEMBL details 209 Binding Assay (ChEMBL2493) and 1 Functional Assay. There are a total of 45 ligands in ligand efficiency data.

https://www.ebi.ac.uk/chembl/target_report_card/ChEMBL2493/

Binding assay linked to many different manuscripts, with most being under the category of inhibition of human CAMK1 assessed as residual activity at 25 μ M relative to control, and the concentration varies for each manuscript.

Huart AS, Saxty B, Merritt A, Nekulova M, Lewis S, Huang Y, Vojtesek B, Kettleborough C, Hupp TR.

<https://www.sciencedirect.com/science/article/pii/S0960894X13009864?via%3Dihub>

Ligand efficiency shows Average Binding Constant for CAMK1

Fabian MA, Biggs WH, Treiber DK, Atteridge CE, Azimioara MD, Benedetti MG, Carter TA, Ciceri P, Edeen PT, Floyd M, Ford JM, Galvin M, Gerlach JL, Grotzfeld RM, Herrgard S, Insko DE, Insko MA, Lai AG, Lélías JM, Mehta SA, Milanov ZV, Velasco AM, Wodicka LM, Patel HK, Zarrinkar PP, Lockhart DJ.

<https://www.nature.com/articles/nbt1068>