

Find a Gene Project (BGGN 213)

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May 15, 2019

Question 1: Name of the protein

Name: Sonic Hedgehog protein isoform 1 preprotein (SHH)

Accession: NP_000184.1

Species: Homo sapiens

Question 2: BLAST search

Method: TBLASTN search against Xenopus ESTs

Database: Expressed sequence tags (est)

Organism: Xenopus (Taxid: 8353)

Alignment details

Chosen match: Accession BX704643.1, a 874bp clone from *Xenopus tropicalis*.

>BX704643.1 BX704643 XGC-tadpole *Xenopus tropicalis* cDNA
clone TTpA011g13 5', mRNA sequence

cDNA clone TTpA011g13, mRNA sequence.
Length: 874

Score	Expect	Method	Identities
387 bits(994)	3e-132	Compositional matrix adjust.	197/285(69%)

Positives	Gaps	Frame
220/285(77%)	23/285(8%)	+2

Query	68	RNSERFKELTPNYPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEG	127
		RNS+RFKELTPNYPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEG	
Sbjct	41	RNSDRFKELTPNYPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEG	220
Query	128	WDEDGHHSEESLHYEGRAVDITTSRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSVKA	187
		WDEDGHHSEESLHYEGRAVDITTSRDRSKYGMLARLAVEAGFDWVY+ESKAHIHCSVKA	
Sbjct	221	WDEDGHHSEESLHYEGRAVDITTSRDRSKYGMLARLAVEAGFDWVYFESKAHIHCSVKA	400
Query	188	ENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFDLRDDG	247
		ENSVAAKSGGCFPGSA V +E GGTK V++L PGDRVL++D QG L+YSDFL F+D++	
Sbjct	401	ENSVAAKSGGCFPGSARVMVEPGGTKAVREL RPGRVLS S DPQGNLIYSDFLLFIDKEHD	580

```

Query 248 AKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATXXXXXXXXXXXXXXXXXXXXRALFAS 307
          KK++YVI+T + R R  +TAAHLLFVA  N + +                +++FAS
Sbjct 581 VKKLYYVIQTSQTRIR--MTAAHLLFVAQSNGTGS-----FKSVFAS 700

Query 308 RVRPGQRVYVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQG 352
          VRPG +Y   R D L A V V L EE G + P   G
Sbjct 701 NVRPGDVIYSADDR--DMTLREAMVEKVDL-EEDIGGFCPRNCPG 826

```

Translated BLAST: tblastn

blastn blastp blastx **tblastn** tblastx

TBLASTN search translated nucleotide databases using a protein query. [more...](#)

Enter Query Sequence

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

ref|NP_000184.1

Clear Query subrange [?](#)

From To

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

Job Title (2) - NP_000184:sonic hedgehog protein isoform 1... Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database [+](#) Expressed sequence tags (est) [?](#)

Organism Optional Xenopus (taxid:8353) ☐ exclude [+](#) Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

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

Limit to Optional ☐ Sequences from type material

Entrez Query Optional Enter an Entrez query to limit search [?](#) [YouTube](#) [Create custom database](#)

BLAST Search database Expressed sequence tags (est) using Tblastn (search translated nucleotide databases using a protein query) ☐ Show results in a new window

[Algorithm parameters](#) **Note:** Parameter values that differ from the default are highlighted in yellow and marked with [+](#) sign

Figure 1: BLAST parameters

Job Title

NP_000184:sonic hedgehog protein isoform 1...

RID

DT912J1E014

Search expires on 05-17 07:43 am

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Program

TBLASTN

Citation

Database

est

See details

Query ID

NP_000184.1

Description

sonic hedgehog protein isoform 1 preproprotein [Homo sapiens]

Molecule type

amino acid

Query Length

462

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Alignments

Taxonomy

Filter Results

Organism

only top 20 will appear

☐ exclude

Type common name, binomial, taxid or group name

+ Add organism

Percent Identity

to

E value

to

Filter

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Sequences producing significant alignments

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Show

100

☒ select all

37 sequences selected

GenBank

Graphics

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/>	DC124442 Yamamoto/Hyodo-Miura NIBB/NBRP Xenopus DMZ pCS2p+ cDNA library Xenopus laevis cDNA clone x1304x08 5' mRNA sequen	420	420	51%	4e-146	85.65%	DC124442.1
<input checked="" type="checkbox"/>	DC102103 Yamamoto/Hyodo-Miura NIBB/NBRP Xenopus DMZ pCS2p+ cDNA library Xenopus laevis cDNA clone x1228b16 5' mRNA sequen	394	394	43%	7e-136	91.63%	DC102103.1
<input checked="" type="checkbox"/>	BX704643 XGC-ladpole Xenopus tropicalis cDNA clone TTPA011g13 5' mRNA sequence	387	430	64%	3e-132	69.12%	BX704643.1

Figure 2: BLAST search results

Sequence ID: [BX704643.1](#) Length: 874 Number of Matches: 2

Score	Expect	Method	Identities	Positives	Gaps	Frame
387 bits(994)	3e-132	Compositional matrix adjust.	197/285(69%)	220/285(77%)	23/285(8%)	+2
Query	68	RNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEG		127		
Sbjct	41	RNSRFKELTPNYPNDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEG		220		
Query	128	WDEEDGHHSSEELSHYEGRAVDITTSDRDRSKYGMGLARLAVEAGFDWYYFESKAHIHCSVKA		187		
Sbjct	221	WDEEDGHHSSEELSHYEGRAVDITTSDRDRSKYGMGLARLAVEAGFDWYYFESKAHIHCSVKA		400		
Query	188	ENSVAASKSGGCFPGSATAHDLQGGTKLVKDLSPGDRVLRYSDFLFTLDRDDG		247		
Sbjct	401	ENSVAASKSGGCFPGSAVMYEPGGTKAVHLRPLRSDGRLVSSDPQGNLIYSDFLFLIKHED		580		
Query	248	AKKVYVIETREPRERLLLTAHLLFVAPHINDSTXXXXXXXXXXXXXXXXXXRRALFAS		307		
Sbjct	581	KK++YVI+T+R+R+TAHLLFVA+N++++FAS		700		
Query	308	VRPGRQRYVVAERDGRRLLPAAHVSYLTSEEAAGAYAPLTAQG		352		
Sbjct	701	VRPG+Y+RDLAVLVEEG+P+G		826		

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](#) [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
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 sequences

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 [?](#)

Figure 4: BLASTP parameters

Sequences producing significant alignments [Download](#) [Manage Columns](#) [Show](#) [?](#)

☐ select all 0 sequences selected [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#)

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	PREDICTED: sonic hedgehog protein [Xenopus tropicalis]	533	533	100%	0.0	97.71%	XP_017950257.1
<input type="checkbox"/>	RefName: Full=Sonic hedgehog protein; AltName: Full=Shh unprocessed N-terminal signaling and C-terminal autoprocessing domains; S	465	465	100%	7e-162	83.71%	Q92000.1
<input type="checkbox"/>	PREDICTED: sonic hedgehog protein-like [Xenopus laevis]	462	462	99%	7e-161	84.03%	XP_018124514.1
<input type="checkbox"/>	sonic hedgehog protein precursor [Xenopus laevis]	442	442	100%	1e-152	80.38%	NP_001081782.1
<input type="checkbox"/>	shh protein [Xenopus tropicalis]	423	423	80%	3e-147	97.14%	AAI66395.1
<input type="checkbox"/>	PREDICTED: sonic hedgehog protein [Nanorana parkeri]	424	424	100%	5e-146	76.32%	XP_018409491.1

Figure 5: BLASTP results page

[Download](#)
[GenPept](#)
[Graphics](#)

PREDICTED: sonic hedgehog protein [Xenopus tropicalis]

Sequence ID: [XP_017950257.1](#) Length: **416** Number of Matches: **1**

Range 1: 68 to 329
[GenPept](#)
[Graphics](#)

▼ Next Match
▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
533 bits(1373)	0.0	Compositional matrix adjust.	256/262(98%)	256/262(97%)	0/262(0%)
Query 1	RNSDRFKELTPNYPNDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEG				60
Sbjct 68	RNSDRFKELTPNYPNDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEG				127
Query 61	WDEGDHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYFESKAHIHCSVKA				120
Sbjct 128	WDEGDHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYFESKAHIHCSVKA				187
Query 121	ENSVAAKSGGCFPGSARVMVEPGGKAVRELPGDRVLSDDPQGNLIYSDFLLFIDKEHD				180
Sbjct 188	ENSVAAKSGGCFPGSARVMVEPGGKAVRELPGDRVLSDDPQGNLIYSDFLLFIDKEHD				247
Query 181	VKKLYYVIQTSQTRIRMTAAHLLFVAQSNGTGSFKSVFASNVRPGDVIYSADRRDRTLRE				240
Sbjct 248	VKKLYYVIQTSQTRIRMTAAHLLFVAQSNGTGSFKSVFASNVRPGDVIYSADRRDRTLRE				307
Query 241	AMVEKVDLEEDIGGFCPRNCPG		262		
	AMVEKVDLEEDIG F P G				
Sbjct 308	AMVEKVDLEEDIGAFAPVTAQG		329		

Figure 6: Alignment for top result

Question 5: Multiple sequence alignment

Relabeled sequences for alignment

```
>Xenopus_sonic_hedgehog (from BLAST result)
RNSDRFKELTPNYPNDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEG
WDEGDHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYFESKAHIHCSVKA
ENSVAAKSGGCFPGSARVMVEPGGKAVRELPGDRVLSDDPQGNLIYSDFLLFIDKEHD
VKKLYYVIQTSQTRIRMTAAHLLFVAQSNGTGSFKSVFASNVRPGDVIYSADRRDRTLRE
AMVEKVDLEEDIGGFCPRNCPG

>Human |Sonic hedgehog protein (NP_000184.1) [Homo sapiens]
MLLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGKISRNS
ERFKELTPNYPNDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEGDHSEESLH
YEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYFESKAHIHCSVKAENSVAAKSGGCFPGSATVHLEQG
GTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRDDGAKKVYVYIETREPRERLLLTAHLLFVAPHNDS
ATGEPEASSSGSPSGGALGPRAFASRVPRGQVRVYVVAERDGDRLLPAAVHSVTLSEEAAGAYAPLTA
QGTILINRVLASCYAVIEEHSWAHRAFAFPRLAHALLAALAPARTDRGDSGGGDRGGGGGRVALTAPGA
ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSS

>Mexican_walking_fish |sonic hedgehog [Ambystoma mexicanum] ARX70249.1
MGEMRLLLRLLLGTLVWALLVPSGLTCGPGRGIGKRRQPKKLTPLAYKQFIPNVAEKTLGASGRYEGKI
TRNSDRFKELTPNYPNDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEGDHSE
ESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYFESKAHIHCSVKAENSVAAKSGGCFPASAKVT
LEHGVTRPVKDLRPGDRVLAADGQGRLVYS DFLMFLDKEEAVTKVFYVYIETERPRQRLRLTAHLLFAA
RHPANSSSSSTGFQSIFASRVPRGHRVLTVDQEGRLQEATVTRVYLEEGAGAYAPVTSHGTVVIDKVLAS
CYAVIEEHSWAHWAFAPRLRLGYGILSIFSPQDYSHPSPAPSQKEGVHWYSEILYHIGTWVLHSDTIHPW
GMAAKSS
```

```
>Iberian_newt |sonic hedgehog-related protein [Pleurodeles waltl]
MGEMILLRRDLLGGFISTLLVPLGLGCGPGRGIGQRRRPQKLTPLAYKQFIPNVSEKTLGASGRYEVKITRNSERFQELT
PNYNPDIIFKVEENTGADRLMTQRCKDKLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSRDRRSK
YGMRLARLAVEAGFDWVYFESKAHIHCSVKAENSVAVKSGGCFPGSATVTLEQGVRIPVKGLKPGNRVLAVDVEGRLIYSD
FLLFMDEEETARKVIFYIETSLPRERLRLTAAHLLFVAQEHGPNASAGNFRSKFGHRRFRSMFASSVRPGRVLTEDREG
RGLREATVDVRVLEEATGAYAPVTAHGTVIDRVLASCYAVIEEHSWAHWAFAPLRVGFGLSFFSPQDYSSHSPAPSQ
AEGVHWYSEILYRIGTWVLQADTIHPLGMAAKSS
```

```
>African_clawed_frog |sonic hedgehog protein-like|XP_018124514.1 [Xenopus laevis]
MSVATGILLGLFTCSLLIPPGLSCGPGRGIGKRRHPKKLTPLVYKQFIPNVAEKTGASGRYEGKIASNSDRFKELTPNY
NPDIVFKDEENTGADRLMTQRCKDKLNSLAISVMNQWPGVKLRVTEGWDEDGHHLEESLHYEGRAVDITTSRDRRSKYGM
LARLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGGCFPAGAEVMVELGGTKAVKDLRPGDRVLSSDAQGNLLYSDFLL
FIDQQHDVKKLFYVIETSHPRRIRLTAHLLFVAQVNGSRFSKSVFASSIQPGDIIYSADPRAMALNEVKVEKVGLEED
TGAYAPLTAHGTVIDQVLSSCYALIEHTWAHLAFAPLRFGLSLSPYLFPKDSSPSPQSHHQLDSSPSPQSHHPEGIHW
WYSQLLYQLGTWLLDSNSLHPLGMATKSS
```

```
>Burmese_python |sonic hedgehog protein|XP_007433256.1 [Python bivittatus]
MLLRRRSGLLPLCLGALFLSAGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTGASGRYEGKISRNSERFKELTPN
YNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSRDRRSKYG
MLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGGCFPGSAWVNLEGGTKLVKDLRPGDRVLAADVHGQLFYSEFL
AFLDREDPPVHKLFYVIETQRPQTRLLTAHLLFVAPPQNHSHSQPQPIFASRVQPGQVYVLGQGGQTLLQAAVHSVS
LQEEASGAYAPLTAQGTILINQVLASCYAVIEEHSWAHWAFAPFRMAHAVLAMLDPEGLSSPLLFPAAAPEESSLAGVH
WYSRLLYHIGRWILDSETHMPLGMAS
```

```
>Tiger_snake |sonic hedgehog protein|XP_026536709.1 [Notechis scutatus]
MLLLRRTGLLPLCLGALFLSAGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTGASGRYEGKITRNSERFKELTPN
YNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSRDRRSKYG
MLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGGCFPGSAWVNLEGGTKLVKDLHPGDRVLAADVHGQLFYSEFL
AFLDREPPVHKLFYVIETQTPQARLLTAHLLFVAPPNHSHSQPQPIFASRVQPGQHVVYVLAQGGQTLLPAAVHSVS
LKEEASGAYAPLTAQGTILINQVLASCYAVIEEHSWAHWAFAPFRIHAALAVLNLEGLSSPLLFPAAVPEEGASLAGVH
WYSRLLYYIGRWILGSEMMHPLGMAS
```

Alignment

Using local MUSCLE (v3.8) program with `bio3d seqaln()`. The fasta output was converted to CLUSTALW format using `seaview`.

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

```
Iberian_newt      -MGEMILLRRDLLGGF-ISTLLVPLGLGCGPGRGIGQRRRPQKLTPLAYKQFIPNVSEKT
Mexican_walking_fish MGEMRLLLRLLLGTL-VWALLVPSGLTCGPGRGIGKRRQPKKLTPLAYKQFIPNVAEKT
African_clawed_frog ----MSVATGILLGLF-TCSLLIPPGLSCGPGRGIGKRRHPKKLTPLVYKQFIPNVAEKT
Xenopus_sonic_hedgehog -----
Burmese_python    ----MLLRRRSGLLPLCLGALFLSAGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKT
Tiger_snake       ----MLLLRRTGLLPLCLGALFLSAGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKT
Human            ----MLLLARCLLLVL-VSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKT
```

```
Iberian_newt      LGASGRYEVKITRNSERFQELTPNYNPDIIFKVEENTGADRLMTQRCKDKLNSLAISVMN
Mexican_walking_fish LGASGRYEGKITRNSDRFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMN
African_clawed_frog LGASGRYEGKIASNSDRFKELTPNYNPDIIVFKDEENTGADRLMTQRCKDKLNSLAISVMN
Xenopus_sonic_hedgehog -----RNSDRFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMN
Burmese_python    LGASGRYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMN
Tiger_snake       LGASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMN
```

Human LGASGRYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAI SVMN

Iberian_newt QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYF
Mexican_walking_fish QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYF
African_clawed_frog QWPGVKLRVTEGWDEDGHHLEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYY
Xenopus_sonic_hedgehog QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYF
Burmese_python QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYY
Tiger_snake QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYY
Human QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYY

Iberian_newt ESKAHIHCSVKAENSVAVKSGGCFPGSATVTLEQGVRI PVKGLKPGNRVLAVDVEGRLIY
Mexican_walking_fish ESKAHIHCSVKAENSVAAKSGGCFPASAKVTLEHGVTRPVKDLRPGDRVLAADGQGRLVY
African_clawed_frog ESKAHIHCSVKAENSVAAKSGGCFPAGAEVMVELGGTKAVKDLRPGDRVLSSDAQGNLLY
Xenopus_sonic_hedgehog ESKAHIHCSVKAENSVAAKSGGCFPGSARVMVEPGGTKAVREL RPGDRVLSSDPQGNLIY
Burmese_python ESKAHIHCSVKAENSVAAKSGGCFPGSAWVNLEEGGTKLVKDLRPGDRVLAADVHGQLFY
Tiger_snake ESKAHIHCSVKAENSVAAKSGGCFPGSAWVNLEGGGTKLVKDLHPGDRVLAADVHGQLFY
Human ESKAHIHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLY

Iberian_newt SDFLLFMDEEE-TARKVFYVIETSLPRERLRLTAAHLLFVAQEH PGNASAGNFRSKFGHR
Mexican_walking_fish SDFLMFLDKEE-AVTKV FYVIETERPRQLRLTAAHLLFAAR-HPANSSSST-----
African_clawed_frog SDFLLFIDQQH-DVKKLFYVIETSHPRRRIRL TAAHLLFVAQ----VNGSR S-----
Xenopus_sonic_hedgehog SDFLLFIDKEH-DVKKLYYVIQTS--QTRIRMTAAHLLFVAQ----SNGTGS-----
Burmese_python SEFLAFLDREDPPVHKLFYVIETQRPQTRLLLTAAHLLFVAP--PQN HSHSQ-----
Tiger_snake SEFLAFLDREEPPVHKLFYVIETQTPQARLLLTAAHLLFVAP--PHN HSHSQ-----
Human SDFLTFLDRDD-GAKKV FYVIETREPRERLLLTAAHLLFVAP--HNDSATGEPEASSGSG

Iberian_newt -----RFRSMFASSVRPGHRVLTEDR--EGRGLREATVDRVYL-EEATGAYAPVTAHG
Mexican_walking_fish -----GFQSIFASRV RPGHRVLTVDQ--EGRGLQEATVTRVYL-EEGAGAYAPVTS HG
African_clawed_frog -----FKSVFASSIQPDI IYSADP--RAMALNEVKVEKVGL-EEDTGAYAPLTAHG
Xenopus_sonic_hedgehog -----FKSVFASNVRPGDVIYSADR--RDMTLREAMVEKVDL-EEDIGGFCPRNCPG
Burmese_python -----PQPIFASRVQPQGQVYVLGQ--GGQTL LQA AVHSVSLQEEASGAYAPLTAQG
Tiger_snake -----PQPIFASRVQPQGHVYVLAQ--GGQTL LPA AVHSVSLKEEASGAYAPLTAQG
Human PPSGGALGPRALFASRV RPGQRVYVAERDGD RRL LPA AVHSVTLSEEAGAYAPLTAQG

Iberian_newt TVVIDRVLASCYAVIEEHSWAHWAFAPLRVGF GILSFFSPQ-----
Mexican_walking_fish TVVIDKVLASCYAVIEEHSWAHWAFAPLR LGYGILSIFSPQ-----
African_clawed_frog TLVIDQVLSSCYALIEETHWAHLAFAPLR FGLSLSPYLF PK-----DSSPSPQS
Xenopus_sonic_hedgehog -----
Burmese_python TILINQVLASCYAVIEEHSWAHWAFAPFRMAH AVLAML DPE-----GLS
Tiger_snake TILINQVLASCYAVIEEHSWAHWAFAPFRIAHAALAVLNLE-----GLS
Human TILINRVLASCYAVIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGGDRGGGGGR

Iberian_newt ---DYSSHSP PAPS-QAEGVHWYSEILYRIGTWVLQADTIHPLGMAAKSS
Mexican_walking_fish ---DYSPHSP PAPS-QKEGVHWYSEILYHIGTWVLHSDTIHPWGMAAKSS
African_clawed_frog HHQLDSSPSPQSHH-QPEGIHWYSQLLYQLGTWLLDSNSLHPLGMATKSS
Xenopus_sonic_hedgehog -----
Burmese_python SPLLFPAAAPEESS-SLAGVHWYSRLLYHIGRWILDSETMHPLGMAS---
Tiger_snake SPLLFPAAVPEEGA-SLAGVHWYSRLLYYIGRWILGSEMMHPLGMAS---

Human

VALTAPGAADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSS

Question 6: Phylogenetic tree

I used the simple phylogeny tool from EBI with the following parameters:

- Tree format: nj
- Distance correction: False
- Excludes Gaps: False
- Clustering Methods: Neighbor-joining
- Percent identity matrix: False

The resulting tree is this.



Figure 7: Phylogenetic tree derived from the sequence alignments in the previous section

Question 7: Heatmap of aligned sequences

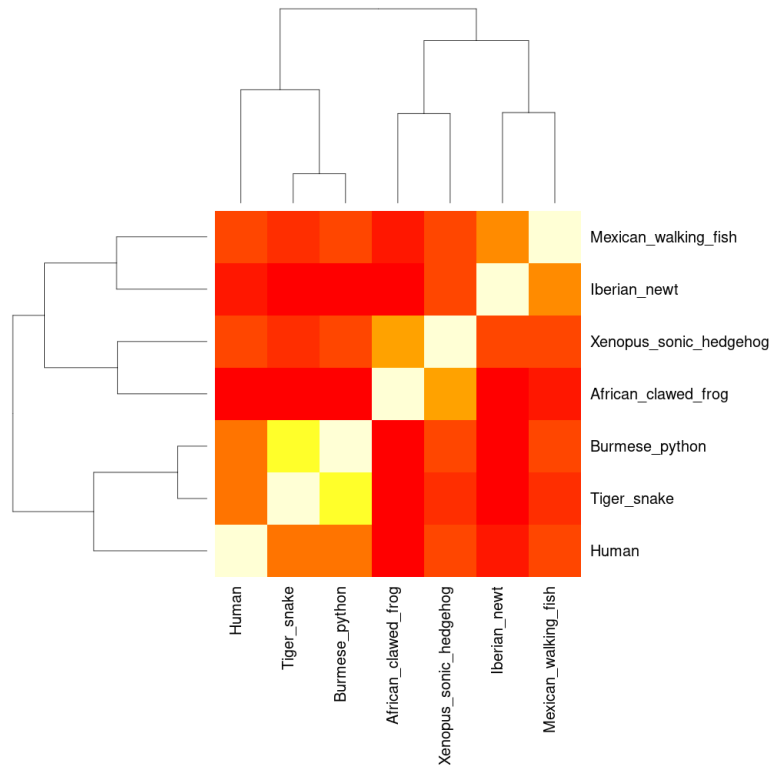


Figure 8: Heatmap derived from the sequence alignments.

Question 8: Protein Database Search