

Find a Gene Project (BGGN 213)

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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 RPGRVLSSDPQGNLIYSDFLLFIDKEHD	580

```

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

Query 308 RVRPGQRVYVVAERDGDRLLLPAAVHSVTLSEEAAGAYAPLTAQG 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 Download All ?
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
Other reports	?

Filter Results	
Organism <small>only top 20 will appear</small> <input type="checkbox"/> exclude	
Type common name, binomial, taxid or group name	
+ Add organism	
Percent Identity	E value
<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>
Filter	Reset

Descriptions	Graphic Summary	Alignments	Taxonomy
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Sequences producing significant alignments		Download ?	Manage Columns ?	Show 100 ?
<input checked="" type="checkbox"/> select all 37 sequences selected				
	Description	Max Score	Total Score	Query Cover
<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%
<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%
<input checked="" type="checkbox"/>	BX704643 XGC-ladpole Xenopus tropicalis cDNA clone TTPA011g13 5' mRNA sequence	387	430	64%

Figure 2: BLAST search results

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

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

Figure 3: Alignment details

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

A BLASTP search against the NR database yielded a top hit to a protein from *Xenopus tropicalis* with 100% coverage and 97.71% identity. The alignment details are given in the screenshots below.

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	ENSVAAKSGGCFPGSARVMVEPGGTKAVRELRPGDRVLSSDPQGNLIYSDFLLFIDKEHD				180	
Sbjct 188	ENSVAAKSGGCFPGSARVMVEPGGTKAVRELRPGDRVLSSDPQGNLIYSDFLLFIDKEHD				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
ENSVAAKSGGCFPGSARVMVEPGGTKAVRELRPGDRVLSSDPQGNLIYSDFLLFIDKEHD
VKKLYYVIQTSQTRIRMTAAHLLFVAQSNGTGSFKSVFASNVRPGDVIYSADRRDRTLRE
AMVEKVDLEEDIGGFCPRNCPG
```

>Human |Sonic hedgehog protein (NP_000184.1) [Homo sapiens]

```
MLLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGKISRNS
ERFKELTPNYPNDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEGDHSEESLH
YEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYFESKAHIHCSVKAENSVAAKSGGCFPGSATVHLEQG
GTLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRDDGAKKVYFVIETREPRERLLLTAHLLFVAPHNDS
ATGEPEASSSGSPSGGALGPRALFASRVRPGRVYVVAERDGDRLLPAAVHSVTLSEEAAGAYAPLTA
QGTILINRVLASCYAVIEEHSWAHRAFAFPRLAHALLAALAPARTDRGDSGGGDRGGGGGRVALTAPGA
ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSS
```

>Mexican_walking_fish |sonic hedgehog [Ambystoma mexicanum] ARX70249.1

```
MGEMRLLLRLLLGTLVWALLVPSGLTCGPGRGIGKRRQPKKLTPLAYKQFIPNVAEKTLGASGRYEGKI
TRNSDRFKELTPNYPNDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEGDHSE
ESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYFESKAHIHCSVKAENSVAAKSGGCFPASAKVT
LEHGVTRPVKDLRPGDRVLAADGQGRLVYS DFLMFLDKEEAVTKVFYVIETERPRQRLRLTAHLLFAA
RHPANSSSSSTGFQSIFASRVRPGRHRLTVDDQEGRLQEATVTRVYLEEGAGAYAPVTSHGTVVIDKVLAS
CYAVIEEHSWAHWAFAPRLRLGYGILSIFSPQDYSHPSPAPSQKEGVHWYSEILYHIGTWVLHSDTIHPW
GMAAKSS
```

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

```
>African_clawed_frog |sonic hedgehog protein-like|XP_018124514.1 [Xenopus laevis]
MSVATGILLGLFTCSLLIPPGLSCGPGRGIGKRRHPKCLTPLAYKQFIPNVAEKTGASGRYEGKIASNSDRFKELTPNY
NPDIVFKDEENTGADRLMTQRCKDKLNSLAISVMNQWPGVKLRVTEGWDEDGHHLEESLHYEGRAVDITTSRDRRSKYGM
LARLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGGCFPAGAEVMVELGGTKAVKDLRPGDRVLSSDAQGNLLYSDFLL
FIDQQHVDVKKLFYVIETSHPRRIRLTAHLLFVAQVNGSRFSKSVFASSIQPGDIIYSADPRAMALNEVKVEKVGLEED
TGAYAPLTAHGTVIDQVLSSCYALIEHTWAHLAFAPLRFGLSLSPYLFPKDSSPQSHHQLDSSPQSHHQPEGIH
WYSQLLYQLGTWLLDSNSLHPLGMATKSS
```

```
>Burmese_python |sonic hedgehog protein|XP_007433256.1 [Python bivittatus]
MLLRRRSGLLPLCLGALFLSAGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTGASGRYEGKISRNSERFKELTPN
YNPDIIIFKDEENTGADRLMTQRCKDKLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSRDRRSKYG
MLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGGCFPGSAWVNLEGGTKLVKDLRPGDRVLAADVHGQLFYSEFL
AFLDREDPPVHKLFYVIETQRPQTRLLTAHLLFVAPPQNHSHSQPQPIFASRVQPGQVYVLGQGGQTLLQAAVHSVS
LQEEASGAYAPLTAQGTILINQVLASCYAVIEEHSWAHWAFAPFRMAHAVLAMLDPGLSSPLLFPAAAPEESSLAGVH
WYSRLLYHIGRWILDSETHMPLGMAS
```

```
>Tiger_snake |sonic hedgehog protein |XP_026536709.1 [Notechis scutatus]
MLLLRRTGLLPLCLGALFLSAGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTGASGRYEGKITRNSERFKELTPN
YNPDIIIFKDEENTGADRLMTQRCKDKLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSRDRRSKYG
MLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGGCFPGSAWVNLEGGTKLVKDLRPGDRVLAADVHGQLFYSEFL
AFLDREPPVHKLFYVIETQTPQARLLTAHLLFVAPPNHSHSQPQPIFASRVQPGQHVVYVLAQGGQTLLPAAVHSVS
LKEEASGAYAPLTAQGTILINQVLASCYAVIEEHSWAHWAFAPFRIHAALAVLNLEGLSSPLLFPAAVPEEGASLAGVH
WYSRLLYYIGRWILGSEMMHPLGMAS
```

Alignment

Using MUSCLE at EBI:

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

```
Iberian_newt          -MGEMILLRRDLLGGF-ISTLLVPLGLGCGPGRGIGQRRRPQKLTPLAYKQFIPNVSEKT
Mexican_walking_fish  MGEMRLLLRLLLTGTL-VWALLVPSGLTCGPGRGIGKRRQPCKLTPLAYKQFIPNVAEKT
Xenopus_sonic_hedgehog -----
African_clawed_frog   ----MSVATGILLGLF-TCSLLIPPGLSCGPGRGIGKRRHPKCLTPLAYKQFIPNVAEKT
Burmese_python        ----MLLRRRSGLLPLCLGALFLSAGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKT
Tiger_snake           ----MLLLRRTGLLPLCLGALFLSAGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKT
Human                 ----MLLLARCLLLVL-VSSLLVCSGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKT
```

```
Iberian_newt          LGASGRYEVKITRNSERFQELTPNYPNDIIIFKVEENTGADRLMTQRCKDKLNSLAISVMN
Mexican_walking_fish  LGASGRYEGKITRNSDRFKELTPNYPNDIIIFKDEENTGADRLMTQRCKDKLNSLAISVMN
Xenopus_sonic_hedgehog -----RNSDRFKELTPNYPNDIIIFKDEENTGADRLMTQRCKDKLNSLAISVMN
African_clawed_frog   LGASGRYEGKIASNSDRFKELTPNYPNDIVFKDEENTGADRLMTQRCKDKLNSLAISVMN
Burmese_python        LGASGRYEGKISRNSERFKELTPNYPNDIIIFKDEENTGADRLMTQRCKDKLNSLAISVMN
Tiger_snake           LGASGRYEGKITRNSERFKELTPNYPNDIIIFKDEENTGADRLMTQRCKDKLNSLAISVMN
```

Human	LGASGRYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCKDKLNALAISVMN **:**:*****:** *****:*****
Iberian_newt	QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYF
Mexican_walking_fish	QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYF
Xenopus_sonic_hedgehog	QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYF
African_clawed_frog	QWPGVKLRVTEGWDEDGHHLEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYY
Burmese_python	QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYY
Tiger_snake	QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYY
Human	QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYY *****:*****:
Iberian_newt	ESKAHIHCSVKAENSVAVKSGGCFPGSATVTLEQGVRI PVKGLKPGNRVLAVDVEGRLIY
Mexican_walking_fish	ESKAHIHCSVKAENSVAAKSGGCFPASAKVTLEHGVTRPVKDLRPGDRVLAADGGQRLVY
Xenopus_sonic_hedgehog	ESKAHIHCSVKAENSVAAKSGGCFPGSARVMVEPGGTAKVRELPGDRVLSSDPQGNLIY
African_clawed_frog	ESKAHIHCSVKAENSVAAKSGGCFPAGAEVMVELGGTKAVKDLRPGDRVLSSDAQGNLLY
Burmese_python	ESKAHIHCSVKAENSVAAKSGGCFPGSAWNLEEGGTKLVKDLRPGDRVLAADVHGQLFY
Tiger_snake	ESKAHIHCSVKAENSVAAKSGGCFPGSAWNLEGGGTKLVKDLRPGDRVLAADVHGQLFY
Human	ESKAHIHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADQGRLLY *****.*****.* * : * * * . * ** : *** : * *.**
Iberian_newt	SDFLLFMDEEE-TARKVFYVIETSLPRERLRLTAHLLFVAQEHPGNASAGNFRSKFGHR
Mexican_walking_fish	SDFLMFLDKEE-AVTKVFYVIETERPRQRLRLTAHLLFAAR-HPANSSSST-----
Xenopus_sonic_hedgehog	SDFLLFIDKEH-DVKKLYYVIQTS--QTRIRMTAAHLLFVAQ----SNGTGS-----
African_clawed_frog	SDFLLFIDQQH-DVKKLFYVIETSHPRRRIRLTAHLLFVAQ----VNGSRS-----
Burmese_python	SEFLAFLDREDPPVHKLFYVIETQRPQTRLLLTAHLLFVAP--PQNHSQS-----
Tiger_snake	SEFLAFLDREPPVHKLFYVIETQTPQARLLLTAHLLFVAP--PHNHSQS-----
Human	SDFLTFLDRDD-GAKKVFYVIETREPRERLLLTAHLLFVAP--HNDSATGEPEASSGSG *: ** * : . *:***:* . *: :*****.* .
Iberian_newt	-----RFRSMFASSVRPGHRVLTEDR--EGRGLREATVDRVYL-EEATGAYAPVTAHG
Mexican_walking_fish	-----GFQSIFASVRPGHRVLTVDQ--EGRGLQEATVTRVYL-EEGAGAYAPVTSHG
Xenopus_sonic_hedgehog	-----FKSVFASNVVRPGDVIYSADR--RDMTLREAMVEKVDL-EEDIGGFCPRNCPG
African_clawed_frog	-----FKSVFASSIQPGDIIYSADP--RAMALNEVKVEKVGL-EEDTGAYAPLTAHG
Burmese_python	-----PQPIFASRVQPGQVYVLGQ--GGQTLLQAAVHSVSLQEEASGAYAPLTAQG
Tiger_snake	-----PQPIFASRVQPGQHVVYLAQ--GGQTLLPAAVHSVSLKEEASGAYAPL

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