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Revisiting the evolution of the somatostatin family: already five genes in the gnathostome ancestor

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Abstract

The somatostatin (SST) family members are a group of neuropeptides that are best known for their role in the regulation of growth, development and metabolism. The occurrence of six paralogous SST genes named *SST1*, *SST2*, *SST3*, *SST4*, *SST5* and *SST6* has been reported in vertebrates. It has been proposed that *SST1*, *SST2* and *SST5* arose in 2R from a common ancestral gene. *SST3* and *SST6* would have been subsequently generated by tandem duplications of the *SST1* and *SST2* genes respectively, at the base of the actinopterygian lineage. *SST4* is thought to have appeared more recently from *SST1*, in teleost-specific 3R.

In order to gain more insights into the SST gene family in vertebrates, we sought to identify which paralogs of this family are present in cartilaginous fish. For this purpose, we first searched the recently available genome and transcriptome databases from the catshark *Scyliorhinus canicula*. In a previous study, three *S. canicula* SST genes, called at that time *SSTa*, *SSTb* and *SSTc*, were identified and proposed to correspond to *SST1*, *SST5* and *SST2* respectively. In the present work, two additional SST genes, called *SSTd* and *SSTe*, were found in *S. canicula* plus two other chondrichthyan species, elephant shark (*Callorhinchus milii*) and whale shark (*Rhincodon typus*). Phylogeny and synteny analyses were then carried out in order to reveal the evolutionary relationships of *SSTd* and *SSTe* with other vertebrate SSTs. We showed that *SSTd* and *SSTe* correspond to *SST2* and *SST3* respectively, while *SSTc* corresponds to *SST6* and not to *SST2* as initially proposed. Our investigations in other vertebrate species also led us to find that the so-called *SST2* gene in chicken, lungfish, sturgeons and teleosts actually corresponds to *SST6*. Conversely, the so-called *SST6* gene in actinopterygians corresponds to *SST2*.

Taken together, our results suggest that: *i*) *SST3* and *SST6* were already present in the gnathostome ancestor, much earlier than previously thought; *ii*) *SST6* was also present in the tetrapod ancestor and still occurs in living birds; with this respect, it is likely that *SST6* was independently lost several times during evolution: in euteleosts, amphibians, squamates and mammals; *iii*) *SST2*, *SST3* and *SST5* were probably lost in euteleosts, sarcopterygians and tetrapods, respectively.

Introduction

Somatostatin (currently known as somatostatin 1 or SST1) was originally isolated from ovine hypothalamus and found to inhibit the release of growth hormone from the rat pituitary (Brazeau *et al.* 1973). It has been subsequently shown that SST1 is widely distributed in the central nervous system and in various peripheral organs where it plays important roles in the regulation of growth, development and metabolism (Günther *et al.* 2018). The occurrence of SST1 was reported in all vertebrate species investigated so far. Moreover, most species were shown to possess additional SST forms. In gnathostomes (jawed vertebrates), it was demonstrated that all these SST variants are the products of at least six paralogous genes named *SST1*, *SST2* (also known as *Cortistatin* in mammals) *SST3*, *SST4*, *SST5* and *SST6* (de Lecea *et al.* 1996, Liu *et al.* 2010, Tostivint *et al.* 1996, 2008, 2013, 2014). SST-related peptides are thought to act through at least six SST receptor subtypes (Ocampo Daza *et al.* 2012). In lampreys, three *SST* genes have been characterized but their phylogenetic status is still unclear (Tostivint *et al.*, 2016), while in the hagfish *Myxine glutinosa*, the occurrence of only one *SST* gene, encoding a SST1-like peptide, is attested to date (Conlon *et al.*, 1988).

It is currently well accepted that the evolution of the *SST* gene family, as that of many other neuropeptides (Elphick *et al.* 2018), was strongly shaped by the different rounds of whole-genome duplications that took place in the vertebrate history, especially the two basal rounds of vertebrate genome doubling (2R) and the teleost fish-specific genome doubling (3R) (Dehal & Boore 2005, Putnam *et al.* 2008, Sacerdot *et al.* 2018). Thus, *SST1*, *SST2* and *SST5* seem to have been generated during 2R from a common ancestral gene, while *SST4* is likely to have appeared during 3R from *SST1*. Impact of 2R on the early evolution of *SST* gene family is notably supported by synteny analysis showing that *SST* genes are located on a same tetraparalogon that contains paralogous genes of at least ten other families (Liu *et al.* 2010, Tostivint *et al.*, 2013, 2014). For their part, *SST3* and *SST6* would have been independently generated by tandem duplications of *SST1* and *SST2* respectively, at the base of the actinopterygian lineage (Liu *et al.* 2010, Tostivint *et al.* 2004, 2008). Some of these genes could have been subsequently lost explaining their absence in some lineages. For example, *SST5* is believed to have been lost in tetrapods.

Cartilaginous fish (chondrichthyans) are of particular interest in evolutionary studies because of their key phylogenetic position at the base of the gnathostome lineage. They consist of two major groups: elasmobranchii (sharks and skates/rays) and holocephali (chimaeras). Until 2013, SST-related peptides were characterized in only a very few species of cartilaginous fish: *SST1* from the ray *Torpedo marmorata* (Conlon *et al.* 1985), a SST1-like peptide exhibiting a serine residue at position 5 from the ratfish *Hydrolagus colliei* (Conlon 1990), a SST2-like sequence from the elephant shark *Callorhinchus milii* (Tostivint *et al.* 2008) and finally a totally atypical SST-related sequence from both the little skate *Leucoraja erinacea* and *C. milii* (Liu *et al.* 2010). In 2013, three *SST* genes, called *SSTa*, *SSTb* and *SSTc*, were identified in the common dogfish (today referred to as small-spotted catshark, *Scyliorhinus canicula*) and proposed to correspond to *SST1*, *SST5* and *SST2*, respectively (Quan *et al.* 2013). Surprisingly, none of these genes appeared as the apparent ortholog of the atypical SST-like gene found in *C. milii* and *L. erinacea*. Nevertheless, these findings were regarded as in good agreement with the model described above since they support the existence of these three *SST* genes in the gnathostome ancestor (Liu *et al.* 2010, Tostivint *et al.* 2013, 2014). However, due to the lack of a fully sequenced and assembled *S. canicula* genome, this view could not be confirmed (Quan *et al.* 2013).

The first goal of the present study was to determine the complete repertoire of the *SST* gene family in cartilaginous fish. For this purpose, we searched the newly available *S. canicula* genome and transcriptome databases (unpublished data). We also took the opportunity to explore or reexplore the genome and transcriptome databases from two additional species, the

whale shark, *Rhincodon typus* (Read *et al.* 2017) and the elephant shark, *C. milii* (Venkatesh *et al.* 2014). We found two novel *S. canicula* SST genes that we propose to provisionally call *SSTd* and *SSTe* (according to the nomenclature initially proposed in Quan *et al.* 2013). *S. canicula* *SSTd* was shown to be the ortholog of the *L. erinacea* and *C. milii* atypical SST-like gene above-mentioned, while *S. canicula* *SSTe* appeared as a totally new SST gene. In both *R. typus* and *C. milii*, four SST genes were found that correspond *SSTa*, *SSTc*, *SSTd* and *SSTe*.

Taking advantage of the genome assembly of various representative species from other vertebrate groups, we then carried out phylogeny and synteny analyses in order to reveal the evolutionary relationships of chondrichthyan *SSTd* and *SSTe* with other vertebrates SSTs. From our investigations, it appeared that *SSTd* and *SSTe* correspond to *SST2* and *SST3*, respectively, while *SSTc* corresponds to *SST6* but not to *SST2* as initially proposed (Quan *et al.* 2013).

The major implication of these results is that the repertoire of the SST gene family in the gnathostome ancestor was already composed of five paralogs namely *SST1*, *SST2*, *SST3*, *SST5* and *SST6*. Our observations also led us to revisit the phylogenetic status of *SST2* and *SST6*. As a result, the nomenclature of these genes had to be corrected in some species.

Material and methods

Nomenclature

In this article, *S. canicula* SSTs, as well as their counterparts from other chondrichthyans, will be first described as *SSTa*-*SSTe*, according to the provisionnal nomenclature proposed by Quan *et al.* (2013), without prejudice to their evolutionary relationships with other vertebrates SSTs. Thereafter, in the light of the phylogeny and synteny data, they will be renamed according to the phylogenetic nomenclature, *SST1*-*SST6*, initially introduced by Tostivint *et al.* (2008) then extended by Liu *et al.* (2010). Nevertheless, the correspondence between the two nomenclatures will be regularly reminded throughout the article as follows: *SSTa* = *SST1*; *SSTb* = *SST5*; *SSTc* = *SST6*; *SSTd* = *SST2* and *SSTe* = *SST3*. Note that in Quan *et al.* (2013) *SSTc* was initially but mistakenly referred to as *SST2*.

Identification of *SSTd* and *SSTe* sequences from cartilaginous fish

S. canicula *SSTd* and *SSTe* genes were sought by TBLASTN (Altschul *et al.* 1990) using the *C. milii* and *L. erinacea* SST2-like sequences (AGCKLFFWKTFSHC and APCKLFFWKTFSHC) as queries against the *S. canicula* genome draft assembly (version 1, unpublished). *S. canicula* full-length *SSTd* cDNA (but not *SSTe* cDNA) was also retrieved from *S. canicula* Illumina transcriptome (version 1, unpublished).

The SST repertoire of SST genes in *R. typus* and *C. milii* was sought by TBLASTN using the *S. canicula* SST cDNA sequences as queries against the *R. typus* and *C. milii* genome assembly databases (Read *et al.* 2017; Venkatesh *et al.* 2014).

Protein sequences were predicted by using consensus splice donor and acceptor site and by sequence identity comparison with related SST genes. The signal peptide cleavage site was determined using SignalP (<http://www.cbs.dtu.dk/services/SignalP/>) (Petersen *et al.* 2011).

Molecular cloning of the coding sequence of *S. canicula* *SSTe* cDNA

5'RACE-ready cDNAs used for this procedure were constructed as previously described (Gaillard *et al.* 2018). The coding sequence of the *S. canicula* *SSTe* cDNA was amplified by nested PCR using the Advantage 2 PCR kit (Clontech). Nested PCR was carried out in a MyCycler thermal cycler (Bio-Rad, Marne la Coquette, France) with the following primers, csSSTe Rev x Universal Primer A Mix (UPM) then csSSTe Rev Nest x Nested Universal Primer A Mix (NUP) (see **Table S1**) using the manufacturer's procedure. PCR amplifications were carried out for 35 cycles (denaturation 94°C, 30 sec; annealing between 57 and 60°C depending on the T_m of the primers, 30 sec; and extension 72°C, 30 sec) and a final extension

of 72°C for 7 min. The product of the nested PCR was subcloned into the pGEM-T vector (Promega, Charbonnières-les-Bains, France) and sequenced (Value Read Sequencing at MWG Biotech, Ebersberg, Germany).

Synten analysis

To generate synten maps, genes flanking *C. milii* and *R. typus* *SST* genes were obtained from the NCBI database. Non-protein coding genes and genes coding unknown proteins were excluded from further analysis. Note that *SSTb* was not included in the study since it is absent in both *C. milii* and *R. typus*, while in *S. canicula*, it is located on a very short scaffold that did not contain any other genes. Genes flanking the *SST* genes in eight additional osteichthyan species, namely human, chicken (*G. gallus*), green anole lizard (*A. carolinensis*), Western clawed frog (*X. tropicalis*), coelacanth (*L. chalumnae*), spotted gar (*L. oculatus*), zebrafish (*Danio rerio*) and medaka (*Oryzias latipes*), were obtained from Genomicus (version 92.01) (Muffato *et al.* 2010).

Phylogeny analysis

A set of 147 vertebrate *SST* precursor sequences was primarily collected from Yun *et al.* (2015) and Tostivint *et al.* (2016) and supplemented by the chondrichthyan sequences characterized in the present study. All these sequences were aligned using the Muscle algorithm (Edgar 2004) then manually adjusted. The phylogeny of *SST* precursors was inferred by Maximum Likelihood using PhyML (Guindon & Gascuel 2003) with the LG model of substitution combined to the neighbor-joining interchange (NNI) method on Seaview browser (Gouy *et al.* 2010). The robustness of the tree was assessed by the approximate likelihood test (aLRT) SH-like branch support and by bootstrapping procedure from 500 data set replicates. The Genbank accession numbers for all sequences used in the analysis are listed in **Figure S1**. The alignment is presented in **Figure S2**.

Tissue expression of *S. canicula* *SSTd* and *SSTe* genes by reverse transcriptase-polymerase chain reaction (RT-PCR) amplification

The expression profiles of *S. canicula* *SSTd* and *SSTe* genes were examined by RT-PCR, as previously described (Quan *et al.* 2013, Gaillard *et al.* 2018). Total RNA was extracted from various tissues, including telencephalon, diencephalon, mesencephalon, cerebellum, brain stem, spinal cord, skeletal muscles, heart, spleen, gills, stomach, duodenum, valvular intestine, pancreas, liver, kidney, ovary and testis and purified by using RNAeasy Plus Mini kit (Qiagen, Courtabœuf, France). For each tissue, ~330 ng of total RNA were reverse transcribed using ImProm-II Reverse Transcription System (Promega, Charbonnières, France). Gene-specific primers of *S. canicula* *SSTd* and *SSTe* were designed according to the predicted sequences (**Table S1**). PCR amplifications were carried out for 35 cycles (denaturation 94°C, 30 sec; annealing between 57 and 60°C depending on the T_m of the primers, 30 sec; and extension 72°C, 30 sec) and a final extension of 72°C for 7 min. The *S. canicula* *Egfl* gene was amplified in parallel with specific primers (**Table S1**) to verify the quality and quantity of all cDNAs samples. Negative controls were performed without cDNA template. All PCR products were electrophoresed through 2.0% agarose gel and stained with ethidium bromide and then detected under UV light with the ChemiDoc Touch Imaging System (BioRad). Three independent PCR amplifications were performed to check the consistency of amplification.

Results

Structure of *S. canicula* *SSTd* (*SST2*) and *SSTe* (*SST3*) precursor cDNAs and genes

The nucleotide and deduced amino acid sequences of *S. canicula* SSTs including *SSTd* and *SSTe* are shown in **Figure S3**. The coding region of the *SSTd* cDNA consists of 315 nucleotides (nt) that encode a 105-amino acid (aa) protein (PSSTd) including a 20-residue potential signal sequence (Petersen *et al.* 2011). The primary structure of PSSTd contains a monobasic processing site at position 91 (Lys) potentially yielding the mature 14-aa peptide SSTd (SST2), TPCKLFFWKTFSHC, plus one dibasic and one monobasic processing sites at positions 87-88 (Arg-Arg) and 79 (Arg) respectively, potentially yielding 17- and 26-aa NH₂-extended forms of SSTd.

The coding region of the *SSTe* cDNA consists of 321 nt that encode a 106-aa protein with a 18-residue potential signal sequence. The *SSTe* sequence is flanked by a pair of basic residues (Arg-Lys) at position 92-93 potentially yielding the mature 14-aa peptide *SSTe* (SST3), NCKNFFWKTYTLC, plus two monobasic processing sites at positions 85 (Arg) and 90 (Arg) respectively, potentially yielding 17- and 22-aa NH₂-extended forms of *SSTe*.

Comparison of the cDNAs with genomic sequences revealed that *SSTd* and *SSTe* genes are each composed of two exons and one intron (**Figure S4**). For each gene, exon 1 encodes the 5' UTR, the signal peptide and the N-terminus of the prepro-peptide while exon 2 encodes the C-terminus of the precursor, including the putative mature peptide.

Repertoire of SST cDNAs and/or genes in cartilaginous fish

The entire repertoire of SST cDNAs and/or genes found from *S. canicula*, *R. typus* and *C. milii* databases is shown in **Figures S3-S8**. *S. canicula* SST family appears as the richest with no less than five SST genes: the three genes previously reported in Quan *et al.* (2013), namely *SSTa*, *SSTb* and *SSTc*, plus two additional genes characterized in the present study, *SSTd* and *SSTe*. All these genes, with the exception of *SSTb*, were retrieved from *R. typus* and *C. milii*. Only a partial sequence of the *SSTd* gene could be detected from *L. erinacea* (already reported in Liu *et al.* 2010).

General organization of the chondrichthyan SST genes and SST precursors

The molecular organization of the SST precursors is the same in all species examined, with a signal peptide followed by a long central segment, a conserved pair of basic residues and, finally, the SST sequence at their C-terminus (**Figure 1**). All putative SST possess a cyclic conformation ensured by the presence of two Cys residues, and their cyclic region encompasses the Phe-Trp-Lys motif. The structure of the corresponding genes is also very well conserved with two exons and one intron (**Figures S4, S5, S7**). Note that the first exon of *S. canicula* *SSTd* and that of *S. canicula* *SSTa* (*SST1*) exhibit almost the same nucleotide sequence (**Figure S4**). This sequence identity was also found in the corresponding cDNA identified by RT-PCR ruling out an artefact of genome assembly (**Figure S3**).

Structural features of the chondrichthyan putative SST tetradecapeptides

- SSTa (SST1)

The primary structure of SSTa is AGCKNFFWKTFSTSC both in *S. canicula* and *R. typus*. In *C. milii*, it exhibits one substitution, Ser vs Asn, at position 5, as previously reported in the ratfish *H. colliei* (Conlon 1990) (**Table S2**). It is to note that the genomic *SSTa* sequence encodes for a Leu in place of Phe at position 6 that was not retrieved in the cDNAs (**Figures S3 and S4**). Chondrichthyan prepro-SSTa exhibit high sequence identity (ranging from 66.3 to 74.1% between one another) (**Table S3**).

- SSTb (SST5)

As mentioned above, the SSTb sequence could only be found in *S. canicula* (see Quan 2013 for a complete description of the precursor). Just as a reminder, *S. canicula* SSTb exhibits the same primary structure as SSTa (SST1) (**Table S2**).

- SSTc (SST6)

SSTc exhibits two substitutions at positions 1 and 2 when compared to SSTa (**Table S2**). The residue at position 2 is a Pro, except in *R. typus*. The residue at position 1 is more variable. Chondrichthyan prepro-SSTc exhibit high sequence identity (ranging from 53.8 to 86.7% between one another) (**Table S3**).

- SSTd (SST2)

When compared to that of SSTa, the primary structure of SSTd can be distinguished by the Ser-His-Cys (SHC) motif at its C-terminus (**Table S2**). Variable residues are present at position 1 and 2. However, the residue at position 2 is generally a Pro, except in *C. milii*. Chondrichthyan prepro-SSTd exhibit high sequence identity (ranging from 51.9 to 76% between one another) (**Table S3**).

- SSTe (SST3)

In all species examined, the primary structure of SSTe exhibits the unique Tyr-Thr-Leu-Cys (YTLC) motif at its C-terminus (**Table S2**). Only the residue at position 1 is different depending on the species. *S. canicula* and *C. milii* prepro-SSTe exhibit only 38.1% identity (**Table S3**).

Synteny analysis of SST genomic regions

In both *R. typus* and *C. milii*, *SSTe* (SST3) and *SSTa* (SST1) are tandemly arranged on the same scaffold (**Figure 2, Table S4**). However, this scaffold is very short and does not contain any other genes. On the basis of our previous results suggesting that *SSTa* probably corresponds to *SST1* (Quan *et al.* 2013), we aligned the chondrichthyan *SSTa-SSTe* scaffold with the *SST1* locus from the other species analyzed. In teleosts, *SST3* is localized in tandem with *SST1*, as *SSTe* and *SSTa* in cartilaginous fish.

In spotted gar, the *SST1-SST3* locus bears a third *SST* gene, here called *SST4*, surrounded by *Nyap2* and *Irs1* (**Figure 2, Table S4**). In teleosts, the *SST* known as *SST4* is located on a different chromosome than that bearing *SST1* and *SST3*. Its closest neighbors are *Nyap2b* and *Fgf12a* (**Figure 2, Table S4**). The co-orthologs of these two latter genes, *Nyap2a* and *Fgf12b*, are present in the vicinity of both *SST1* and *SST3*. Thus, the teleost *SST4* can be viewed as either an ortholog to gar *SST4* (as this is what its name implies) or a 3R duplicate of either *SST1* or *SST3*. These three possibilities are illustrated in **Figure 2**.

R. typus and *C. milii* *SSTd* (named *SST2* in **Figure 3**) were found in a genomic region containing several genes, *Kif1b*, *Pgb*, *Cenps* and *Dffa*, that are also present in the vicinity of the human *SST2* gene (**Figure 3, Table S4**). It is to note that the gar and zebrafish *SST* genes present in the syntenic region correspond to genes previously known as *SST6*.

The neighborhood of the *R. typus* and *C. milii* *SSTc* (named *SST6* in **Figure 3**) is composed of several genes, *Tardbp*, *Masp2* and *Srm*, that, in the other species examined, were present in the vicinity of *SST* genes previously known as *SST2*, notably in chicken, spotted gar, zebrafish and medaka (**Figure 3, Table S4**).

Phylogeny analysis of SST precursors

Figure 4 displays an unrooted tree constructed from 147 selected vertebrates *SST* precursor sequences using maximum likelihood phylogeny analysis. In the resulting tree, osteichthyan *SST* sequences cluster into six main clades, *SST1-SST6*. Bootstrap support values for these six groups were 53, 10, 94, 29, 68 and 75%, respectively. The only discrepancy of this patterning is the presence of the gar *SST4* sequence into the *SST3* clade. It is to note that the actinopterygian *SST* sequences belonging to the *SST2* clade were previously known as *SST6*. Likewise, chicken, lungfish, sturgeon and teleost *SST* sequences included in the *SST6* clade were previously known as *SST2*.

Chondrichthyan *SSTb*, *SSTc* and *SSTd* branch at the base of the *SST5*, *SST6* and *SST2* clades, respectively. Gnathostome *SST2-SSTd* and *SST6-SSTc* appeared as two sister groups as well

as osteichthyan SST1 and SST3. For their part, chondrichthyan SSTa and SSTe formed a monophyletic group that branch at the base of the osteichthyan SST1-SST3 clade.

As previously reported (Tostivint *et al.* 2016), lamprey SST sequences did not group to any of the gnathostome SST clades.

Tissue-specific expression of *S. canicula* SSTd (SST2) and SSTe (SST3) genes

The distribution of *S. canicula* SSTd and SSTe mRNAs in various tissues was examined by RT-PCR. **Figure 5** shows the results of one representative experiment out of three performed with identical results. SSTd mRNA was detected primarily in the brain (notably in the diencephalon, mesencephalon and brainstem) and spinal cord. In contrast, SSTe mRNA appeared particularly abundant in the central nervous system (in all subdivisions examined except in the cerebellum) as well as in the intestinal tract and pancreas. Note that traces of SSTd mRNA were also seen in the spleen, gills, pancreas and gonads.

Discussion

The main aim of the present study was to determine the repertoire of the SST gene family in cartilaginous fish. For this purpose, the genome and/or transcriptome databases from three representative chondrichthyan species were examined, namely the small-spotted catshark *S. canicula* (unpublished, see Gaillard *et al.* 2018 for more details), the whale shark, *R. typus* (Read *et al.* 2017) and the elephant shark *C. milii* (Venkatesh *et al.* 2014). In *S. canicula*, two new SST genes, named SSTd and SSTe were found, in addition to the three SST genes, SSTa, SSTb and SSTc, previously identified (Quan *et al.* 2013). All these genes, with the exception of SSTb, were retrieved from *R. typus* and *C. milii*. It is noteworthy that the occurrence of partial sequences of the SSTc (Tostivint *et al.* 2008) and SSTd genes (Liu *et al.* 2010) were already reported in both *L. erinacea* and/or *C. milii*. In contrast, SSTe appeared as a totally novel gene. The nomenclature used above (SSTa-SSTe) was initially (and provisionally) proposed to designate the *S. canicula* SSTs without prejudice to their evolutionary relationships with other vertebrate SSTs (Quan *et al.* 2013). Synteny comparisons and phylogeny analysis were subsequently carried out in order to reveal the phylogenetic status of all these genes.

Synteny comparisons suggest that SSTd is the chondrichthyan counterpart of SST2 since both *S. canicula* and *C. milii* SSTd reside in the same chromosomal environment as that of human SST2. For the same reasons, SSTc can be legitimately viewed as the chondrichthyan counterpart of SST6. These conclusions are quite consistent with our phylogeny analysis because SSTd and SSTc precursor sequences branch at the base of the SST2 and SST6 clades, respectively, although the bootstrap support values of the new clades are extremely weak (4% and 37% respectively).

Our investigations on the chondrichthyan SSTc and SSTe also led us to redefine the relationships between SST2 and SST6. The SST2 gene was been first characterized in frog (Tostivint *et al.* 1996) and mammals (de Lecea *et al.* 1996, 1997a), then in most other vertebrates, including chicken (Trabucchi *et al.* 2003), lungfish (Trabucchi *et al.* 1999) and sturgeons (Trabucchi *et al.* 2002, Li *et al.* 2009) (see Tostivint *et al.* 2008 for review). All peptides encoded by SST2 possessed a Pro residue at position 2 and most of them exhibited the APCKNNFWKTFTSC sequence (Quan *et al.* 2013), except in mammals and some other species such as frog (Vaudry *et al.* 1992; Tostivint *et al.* 2008 for review) (**Table S2**). As for, the SST6 gene was initially characterized in only one teleost species, the zebrafish (Liu 2010), then in spotted gar (Tostivint *et al.* 2013) and coelacanth (Yun *et al.* 2015) (**Table S2**). In the present study, we found an ortholog of this gene in several other teleost species belonging to various groups (particularly from otocephala) but not from euteleosts. Peptides encoded by SST6 also shared a Pro at position 2, suggesting a common origin with SST2. In support of this latter view, in both zebrafish and gar, SST2 and SST6 are closely linked on the same chromosome, indicating that

they most likely arose by tandem duplication. Our phylogeny and synteny analyses showed that most of the non-mammalian *SST* sequences previously referred as to *SST2* are not orthologous to *cortistatin* (the other name of the mammalian *SST2*) but actually correspond to *SST6*. Such is notably the case for birds (chicken) and fish (lungfish, sturgeons, bony and cartilaginous fish), but not for reptiles (lizard) and amphibians (marsh frog). Conversely, all *SST* sequences previously referred to as *SST6* appeared to correspond to *SST2*. As a result, all the *SST* genes concerned with these observations were renamed accordingly. It is to note that the nomenclature adopted in the present article was already proposed in Yun *et al.* (2015) but without explicit justification.

In *R. typus* and *C. milii*, *SSTe* and *SSTa* are tandemly arranged suggesting that both genes arose by local duplication of a common ancestral gene. Synteny analysis of the *SSTa*-*SSTe* locus was inhibited by the fact that *SSTa* and *SSTe* were the only genes present on their scaffold. However, based on previous results showing that *SSTa* probably corresponds to *SST1* (Quan *et al.* 2013), the most credible assumption is that *SSTe* corresponds to *SST3* because in all species possessing both *SST1* and *SST3*, these genes are systematically localized in tandem (Tostivint *et al.* 2004, 2008, 2013, 2014). Phylogeny analysis is in agreement with close evolutionary relationships between *SSTa* and *SSTe*, on the one hand, and *SST1* and *SST3*, on the other hand. However, it does not fully support the orthology between *SST1* and *SSTa*, on one hand, and *SST3* and *SSTe*, on the other hand, since chondrichthyan *SSTa* and *SSTe* sequences did not strictly group with osteichthyan *SST1* and *SST3*, respectively. One explanation to reconcile these contradictory results would be that *SST1*/*SSTa* and *SST3*/*SSTe* genes were subjected to concerted evolution, a genetic process that leads to homogenize repetitive DNA sequences over time (Liao 1999). Indeed, the major hallmark of concerted evolution is that paralogous genes within species are more similar to one another than they are to their orthologous counterparts in closely related species (Liao 1999). DNA recombination mechanisms, especially unequal crossover and gene conversion, are responsible for concerted evolution (Liao 1999). Interestingly, we have shown that nucleotide sequences of the first exon of *S. canicula* *SSTa* and *S. canicula* *SSTe* are almost identical (93.5% of identity), while those of the second exon are much more divergent (only 61% of identity). Such level of similarity may be a good indicator of a recent recombination event occurring between the two genes.

The phylogenetic status of the *S. canicula* *SSTd* and *SSTe* genes suggested by synteny and phylogeny analyses is consistent with their tissue expression pattern since *SSTd*, as *SST2*, is primarily expressed in the central nervous system (SNC) (de Lecea *et al.* 1997b, Lin *et al.* 1999, Trabucchi *et al.* 1999, 2003), while *SSTe*, as *SST3*, is expressed both in the SNC and the gastrointestinal tract (Moore *et al.* 1995, Xing *et al.* 2005). Further studies at the cellular level will be needed to speculate about the functions of the corresponding peptides.

In contrast to the other *SST* genes found in cartilaginous fish, *SSTb* was detected only in *S. canicula* and not in *R. typus* and *C. milii*. Phylogeny analysis showed that *SSTb* grouped into the *SST5* clade, as previously reported (Quan *et al.* 2013). However, the orthology relationships between *SSTb* and osteichthyan *SST5* could not be confirmed by synteny analysis since the *S. canicula* *SSTb*-bearing scaffold was too short.

Among the six *SST* paralogs characterized so far in gnathostomes, *SST4* is the only one not to exist in cartilaginous fish. Up to now, the *SST4* gene was considered as a *SST1* paralog generated by 3R (Liu *et al.* 2010), in agreement with the fact that it was found only in teleosts (**Figure S9A**). Recently, however, Yun *et al.* (2015) reported the occurrence of a so-called *SST4* ortholog in spotted gar. This finding is clearly in conflict with the Liu's view since the gar lineage is known to have diverged from teleosts before the 3R (**Figure S9B**) (Braasch *et al.* 2016). In the present study, synteny analysis showed that teleost *SST4* can be equally viewed as orthologous to the gar *SST4*, or co-orthologous to either teleost *SST1* or teleost *SST3*, without

the possibility to decide between these three conceptions. Indeed, in both zebrafish and medaka, the *SST4*-bearing chromosome block contains only very few paralogs of the neighboring genes of *SST1* and *SST3* (such as *Fgf12* and *Nyap2*), making it impossible to precisely place the teleost *SST4* in relation to gar *SSTs*. Examination of other teleost species whose genome is available in Ensembl failed to resolve the problem (data not shown). What is clear, however, is that phylogeny analysis absolutely does not support the orthology of gar *SST4* and teleost *SST4* since gar *SST4* groups within the gnathostome *SST3* clade, thus without any obvious relationships with the teleost *SST4* clade. Rather, the very high level of sequence similarity between gar *SST3* and gar *SST4* (91 % nucleotide identity) strongly suggests that gar *SST4* arose very recently by tandem duplication of *SST3*. It therefore appears unlikely that gar *SST4* and teleost *SST4* are orthologous unless gar *SST4* and *SST3* were subjected to concerted evolution, as shown above for *S. canicula* *SST1/SSTa* and *SST3/SSTe*.

Concluding remarks

Over the past few years, significant advances have been made in the understanding of the evolution of the *SST* family. One of the most important results has been the demonstration that the current diversity of the family was initially caused by 2R (Liu *et al.* 2010, Tostivint *et al.* 2013, 2014). According to this view, the last common ancestor of vertebrates possessed four *SST* genes, three of which, *SST1*, *SST2* and *SST5*, are still present in all extant vertebrate species. A fourth *SST* gene (referred to as *SST?* in **Figure 6**) is likely to have been generated by 2R but since this gene has never been found in extant vertebrate species, it is assumed to have been lost very early after 2R. Conversely, the rest of the diversity of the family, represented by *SST3*, *SST4* and *SST6*, was considered restricted to only some groups of bony fish (Tostivint *et al.* 2013, 2014): actinopterygians for *SST3* and *SST6* and teleosts for *SST4*.

The principal result of the present study is the demonstration of an unexpected diversity of *SST* genes in cartilaginous fish. Thus, in *S. canicula*, not less than five *SST* genes, *SST1*, *SST2*, *SST3*, *SST5* and *SST6*, have been identified, while only three of them were characterized so far (Quan *et al.* 2013). Therefore, contrary to what was previously thought, it is likely that all these five genes were already present in the gnathostome ancestor (**Figure 6**).

It is to note that our study did not provide any new data supporting the impact of 2R in the evolution of the *SST* gene family due to the small size of the scaffolds from the three chondrichthyan species examined. Thus, within the regions containing *SST* genes, *Masp 1* and *Masp 2* were the only genes indicating that *SST1* and *SST3*, on the one hand and *SST2* and *SST6*, on the other hand, belong to the same paralogon. In contrast, our study confirms the idea that *SST3* and *SST6* likely arose by tandem duplications from *SST1* and *SST2*, respectively (**Figure 6**). In strict logic, however, we must admit that it is currently impossible to know which of *SST1* and *SST3*, on the one hand and *SST2* and *SST6*, on the other hand are the ancestral genes. The uncertainty on this matter will remain as long as the phylogenetic status of lamprey *SSTs* is unsolved (Tostivint *et al.* 2016) because the lamprey *SST* sequences are the only ones that could be currently used as outgroups. Thus, in **Figure 6**, *SST1* and *SST2* are displayed as ancestral genes in a totally arbitrary manner.

Another important result of the present study was the finding that *SST6* was not totally lost in sarcopterygians, as previously thought, because it is still present in coelacanth and birds (**Figure 6**). In this context, it is noteworthy that chicken *SST6* was initially but mistakenly reported as *SST2* (Trabucchi *et al.* 2002), now refuted by synteny and phylogeny analysis. In a general way and for the same reasons, all teleost genes previously known as *SST6* had to be renamed *SST2*, and *vice versa*. Notably, the true *SST2* is also present in amphibians (but not in *Xenopus*), sauropsids (but not in birds) and mammals (**Figure 6**). Taken together, our results show that *SST2* and *SST6* have been lost independently and repeatedly during evolution: in euteleosts, birds and some amphibians for *SST2* and amphibians and mammals for *SST6* (**Figure 6**). After

their appearance, *SST3* and *SST5* were also secondarily lost in sarcopterygians and tetrapods, respectively.

Finally, the present work was unable to precisely determine the phylogenetic status of teleost *SST4*. In particular, whether teleost *SST4* and gar *SST4* are truly orthologous or not remains to be investigated. Further studies in other species than those examined here will be needed to address this issue.

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Legends to figures

Figure 1. Alignment of the amino acid sequences of prepro-SST1 (PSSTa), -SST2 (PSSTd), -SST3 (PSSTd) and -SST6 (PSSTc) characterized from cartilaginous fish. (*) denotes conserved residues. SST peptide sequences are in red. Potential cleavage sites are in bold. Signal peptides are in grey. (p), partial sequences. Sequences of *S. canicula* SST2 (SSTd) and SST3 (SSTe) cDNAs have been deposited in the GenBank database under the accession numbers MK491629 and MK491630, respectively.

Figure 2. Synteny of genes in the SST1-SST3 locus in *R. typus* and *C. milii* plus eight selected bony vertebrate species (human, chicken, anole lizard, western clawed frog, coelacanth, spotted gar, zebrafish and medaka). Genes are represented by block arrows. Genes with conserved synteny are coloured. For the teleost SST4 gene, three possible positions are proposed with respect to the gar SSTs (see the text for more details). Position of the genes (in megabases -Mb) is displayed below each box, according to the Ensembl database. Empty circles indicate the end of scaffolds. Letters inside the boxes refer to the specific and provisional nomenclature of *S. canicula* SSTs initially proposed in Quan (2013). The detailed chromosomal locations of genes displayed in this map are included in **Table S4**.

Figure 3. Synteny of genes in the SST2-SST6 locus in *R. typus* and *C. milii* plus eight selected bony vertebrate species (human, chicken, anole lizard, western clawed frog, coelacanth, spotted gar, zebrafish and medaka). Letters inside the boxes refer to the nomenclature of *S. canicula* SSTs proposed in Quan (2013), while numerals refer to the previous nomenclature of vertebrate SST genes (Tostivint 2013, 2014). Legends are the same as in the **Figure 3**.

Figure 4. Phylogenetic tree of vertebrate SST precursor sequences. Phylogenetic analysis of 147 vertebrate SST amino acid sequences was performed using Maximal Likelihood, with 500 bootstrap replicates. The number shown at each branch node indicates in percentage the bootstrap value. Sequence references and alignment are given in **Figure S1** and **Figure S2**, respectively

Figure 5. Tissue distribution of *S. canicula* SST2 (SSTd) and SST3 (SSTe) mRNAs using RT-PCR. Parallel amplification of dogfish *Egf1* mRNA served as internal control. NC, non-template control.

Figure 6. A proposed evolutionary scheme for the evolution of the SST gene family in gnathostomes with special emphasis on chondrichthyan species (in red). The names of the different paralogous genes are given in the boxes. Note the unresolved status of the teleost SST4. Gar SST4 is shown here to have arisen independently of teleost SST4. Boxes connected by a vertical line represent linked genes. Crossed-out boxes represent lost genes. Double-headed arrows represent local duplications. R, rounds of whole genome duplication.

Supplementary data

Table S1. Sequences of the oligonucleotides used for PCR amplifications.

Table S2. Primary structure of SST-related peptides from different vertebrate species. Peptides from chondrichthyan species are in red. Conserved residues are in bold.

Table S3. Pair-wise comparison of full-length SST protein sequences from *S. canicula*, *R. typus*, *L. erinacea* and *C. milii*. Values represent percentage of amino acid identity.

Table S4. Chromosomal locations of gene orthologs in the synteny analysis of the *SST* loci. All human gene names in the table are approved HGNC symbols and the genes from other species have been given the name of their human orthologs. Chromosomal locations of genes are expressed in bp. Blanks represent genes that have not been found in the current genome databases. Non-syntenic genes are in grey.

Figure S1. Protein sequences of prepro-SSTs used for phylogenetic analysis and their accession numbers. Chondrichthyan sequences are in red.

Figure S2. Amino acid sequence alignment of the SST family used for the phylogenetic analysis. The alignment was made using Muscle and then manually optimized. Conserved residues between all orthologs are in black bold. Characteristic residues of each ortholog are colored.

Figure S3. Nucleotide sequence and deduced amino acid sequence of *S. canicula* cDNAs. Nucleotides are numbered 5' to 3' and amino acids N-terminal to C-terminal from the putative starting methionine. Signal peptides are in grey. SST peptide sequences are in red. Potential cleavage sites are in bold. Polyadenylation signals, when detected, are underlined. Nucleotide sequence (almost) identical between *SST1* and *SST3* is in red.

Figure S4. Sequence of *S. canicula* *SST* genes, inferred from the cDNA sequences given in **Figure S3**. Exons are indicated by colored boxed. The exon/intron boundary consensus sequences (GT/AG) are highlighted in red. Initiation (ATG) and stop codons are boxed. Polyadenylation signals are underlined. The identity of the scaffolds containing the sequences is indicated. Nucleotide sequence (almost) identical between *SST1* and *SST3* is in red.

Figure S5. Predicted sequence of *R. typus* *SST* genes, inferred from the *SST* cDNA sequences given in **Figure S6**. Legends are the same as in the **Figure S4**.

Figure S6. Nucleotide and deduced amino acid sequences of *R. typus* *SST* cDNAs. Legends are the same as in the **Figure S3**.

Figure S7. Predicted sequence of *C. milii* *SST* genes, inferred from the *SST* cDNA sequences given in **Figure S8**. Legends are the same as in the **Figure S4**.

Figure S8. Nucleotide and deduced amino acid sequences of *C. milii* *SST* cDNAs. Legends are the same as in the **Figure S3**.

Figure S9. Two alternative conceptions regarding the phylogenetic status of the teleost *SST4* gene. **A.** Conception from Liu *et al.*, (2010). **B.** Conception from Yun *et al.* (2015).

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Figure 1

PSST1 (PSSTa)

C. milii MSCGRVQCALALLSIALTVLSVTSAPAHDRYREILQRLAAAGARSKPELTKYSLAQLLA
S. canicula MWCSRLQLSLALLSIALAVLSVSSAPTDNRYREILQRAMAATGSGGKAEITKYSLAQLLS
R. typus MWCSRVQCALALLSIALAVLSAGAAPADRYRELLQTSMAGAEPRSKAELIKYNLVQLLA
* * * * * ***** ** * * * * *

C. milii ELANAENEALEAEDMARATAQDEVVLELRSANPNLAQRE**RKAGCKSFFWKFTFTSC**
S. canicula ELANAENEALETDAM---GGRNEVRLELERSINPNLANRE**RKAGCKNFFWKFTFTSC**
R. typus ELANAENEVLGDGLPRMAKQDEVVLDLRSANPNSPQRE**RKAGCKNFFWKFTFTSC**
** ***** * * * * * * * * * * *

PSST2 (PSSTd)

C. milii MQWQAFASVVCLLFIVTVQGVEPQEERMGLQLNREMKDKKRLIAKLLAGLLDVEDNLL
L. erinacea (p) -----MEDRT---TLQELTKNRKSLILKLLAGLLDVEDHLLGE
S. canicula MKWLMTVSLMSLLYLLRVEGTDLLEERMKLQVNREMTKSRKNLIVKLLAGLLETDDNLL
R. typus ----MTVCLMSLLLLLSVEAADPLEERMKLQVNREVTKSRYLMKLLSGLLDPDDNLL
* * * * *

C. milii SVIAPLGLSKEEGTDFEERSAAGEIPPRKP**KAGCKLFFWKTFSHC**
L. erinacea (p) SGYTYSNTEEAGERSLEERAVVAVIPPREQ**KAPCKLFFWKTFSHC**
S. canicula NGFAPLKPEEAEGTLFEERSVNAGIPPREQ**KTPCKLFFWKTFSHC**
R. typus NDFTSLSPGEEES-SLEERSVNAGIPRPQ**KAPCKLFFWKTFSHC**
* * * * *

PSST3 (PSSTe)

C. milii -MQARCTLTAL--LSLAALGLSALPHTLRDQVLVLQGSFAMELRDGVVRELIAVADAES
S. canicula MWCSRLQLSLALLSIALAVLSVSSAPTDNHREILQRALDQELLKDTMMKLLPLVTDVDT
R. typus (p) -----DFLKDTIIQLLHVADADK
* * *

C. milii KPQSEEAEDF-APDEKAE---LRLALAP**RWRKDKNFFWKTYTLC**
S. canicula EAGTLDVSNAETSEENTTPMKFQHRQLGM**RMRKNCNFFWKTYTLC**
R. typus DAVEVNASQVETPPXNKIPMKFQQRQLGT**RMRKNCNFFWKTYTLC**
* * * * *

PSST6 (PSSTc)

C. milii MQIL--VALISTLFLVSGVSTTTASLDDRFNLQSSREMNQERKEMILKLLSGLLDNAVS
S. canicula MQLLGTASLLSMLLIV-SSVRATAPLEDRLSLRANQELNKERKEVILKLLSGLLDSS--S
R. typus MQLLGSASXVSILLIV-SSVKATAPLEDRLSLRANQELNKERKEVVLLKLLSALLDSS--S
* * * * *

C. milii GQTGSEAGYPEPADGGPVMLEERS**RYSQLPQRSRKVPCKNFFWKFTFTSC**
S. canicula NQIAIENTFPDPEDVEEMKVEERS**RFSQLPQRERKAPCKNFFWKFTFTSC**
R. typus NQMGIENTFPDQEDMEEMKVEDRS**RFSQLPQREKTSCKNFFWKFTFTSC**
* * * * *

Whale shark (*R. typus*)

Elephant shark (*C. milii*)

Human (*H. sapiens*)

Chicken (*G. gallus*)

Anolis (*A. carolinensis*)

Xenopus (*X. laevis*)

Coelacanth (*L. chalumnae*)

Spotted gar (*L. occulatus*)

Zebrafish (*D. rerio*)

Medaka (*O. latipes*)

Figure 2

Figure 3

Whale shark (*R. typus*)

Elephant shark (*C. milii*)

Human (*H. sapiens*)

Chicken (*G. gallus*)

Anolis (*A. carolinensis*)

Xenopus (*X. tropicalis*)

Coelacanth (*L. chalumnae*)

Spotted gar (*L. occulatus*)

Zebrafish (*D. rerio*)

Medaka (*O. latipes*)

Figure 4

Figure 5

Figure 6

Figure S1

Somatostatin 1

Primates

>Human (*Homo sapiens*) SST1 (BC032625)

MLSCRLQCALAALSIVLALGCVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTENDALEPEDLSQAAEQDEMRLQLQRSANSNPAMAPRERKAGCKNFFWKTFTSC

>Monkey (*Macaca fascicularis*) SST1 (XP_005545499)

MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTENDALEPEDLSQAAEQDEMRLQLQRSANSNPAMAPRERKAGCKNFFWKTFTSC

Other mammals

>Bovine (*Bos taurus*) SST1 (NP_776385.1)

MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTEIDALEPEDLSQAAEQDEMRLQLQRSANSNPAMAPRERKAGCKNFFWKTFTSC

>Dog (*Canis lupus familiaris*) SST1 (NP_001003307.1)

MLSCRLQCALAALSIVLALGGVTCAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTENDALEPEDLSQAAEQDEMRLQLQRSANSNPAMAPRERKAGCKNFFWKTFTSC

>Mouse (*Mus musculus*) SST1 (NP_033241.1)

MLSCRLQCALAALCIVLALGGVTGAPSDPRLRQFLQKSLAAATGKQELAKYFLAELLSEPN
QTENDALEPEDLPQAAEQDEMRLQLQRSANSNPAMAPRERKAGCKNFFWKTFTSC

>Pig SS1 (*Sus scrofa*) SST1 (AAT02532.1)

MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTENDALEPEDLSQAAEQDEMRLQLQRSANSNPAMAPRERKAGCKNFFWKTFTSC

Birds

>Flycatcher (*Ficedula albicollis*) SST1 (ENSFALT00000007767.1)

MLSCRLQCALALLSIALALGTVSAAPSDPRLRQFLQKSLGGGGGGGELAKYFLAELLSEPSQ
TENEAESEDLRGAEQDEVRLQLERSANSNPALAPRERKAGCKNFFWKTFTSC

>Chicken (*Gallus gallus*) SST1 (CN210817.1)

MLSCRLQCALALLSIALAVGTVSAAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPSQ
TENEAESEDLRGAEQDEVRLQLERSANSNPALAPRERKAGCKNFFWKTFTSC

>Turkey (*Meleagris gallopavo*) SST1 (ENSMGAT00000008507.2)

KELAKYFLAELLSEPSQTENEAESEDLRGAEQDEVRLQLERSANSNPALAPRERKAGCKN
FFWKTFTSC

Reptiles

>Anole lizard (*Anolis carolinensis*) SST1 (XP_003228868)

MLPCRLPCALALLSLALALGSGAAAPADPRLRQFLQKSLAAAAAGKQELAKYFLAELLSEP
GQAENEALEPEELSRGGGAEQDEVRLQLERSASLNPALAPRERKAGCKNFFWKTFTSC

>Chinese softshell turtle (*Pelodiscus sinensis*) SST1 (ENSPSIT00000016437.1)

MLSCRLQCALALLSLALAVSSVSGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLAEPS
QPENEALEPEDLSRGPEQDEVRLQLERSANPNPALAPRERKAGCKNFFWKTFTSC

Amphibians

>Marsh frog (*Pelophylax ridibundus*) SST1 (P87384.1)

MQSCRVCALTLALLSLALAINSISAAPTDPRRLRQFLQKSLASAGKQELAKYFLAELLSEPSQTD
NEALESDDLPRGAEQDEVRLQLERSANSSPALAPRERKAGCKNFFWKTFTSC

Lobe-finned fish

>Coelacanth (*Latimeria chalumnae*) SST1 (XP_005992512.1)

MLSSRLQCAFAFLSLALVVSNIASAAPSDLRLRQLLQKSLAAAAGKQEVSKYSLAELLAELAQ
AENEAELESDDFSKTSQDEVRLQLERSANGNPALAPRERKAGCKNFFWKTFTSC

>African lungfish (*Protopterus annectens*) SST1 (AAD39138.1)

MLSCRFQCALVLLSLAVVFSKVSAAPSDLRLRQLLQRSLAAAAGKQELTKYSLAELLSELA
QSENDALDSSDLRGADQDEVRLLEDRSANSSPLAARERKAGCKNFFWKTFTSC

Euteleosts

>Orange-spotted grouper (*Epinephelus coioides*) SST1 (AAU93565.1)
MKMVSSSRLRCLLLLLSLTASISCSAAQRDSKLRLLLHRTPLLGSQDMSRASLAELLSD
LLQVENEALEEENFPLAEGEPEDVHVDLERAAGSGPLLAPRERKAGCKNFFWKTFTSC
>Killifish (*Fundulus heteroclitus*) SST1 (EV461374.1)
MKMFSSLSLRCLLLLLCLASISCSAAQRDSKLRLLLHRTPLLSSQQDVSRSSLAELLSD
LLQMENEALEEDGFTLPEGEPEDIRVDLERAASSGPLLAPRERKAGCKNFFWKTFTSC
>Atlantic cod (*Gadus morhua*) SST1 (AAZ85702.1)
MMSVRSTLLLLSCAAMLSGSSAAPSDTKLRQLLQRSLLAPMPGQEETVRYTLAQLLSELAQ
AENEALGTDDQDDERMDLERAAGPMMAPRERKAGCKNFFWKTFTSC
>Stickleback (*Gasterosteus aculeatus*) SST1 (KT235748)
MVSSRLRCLLLLLSLTASISCSSTAQRDGKLHLLHRTPLLSSKQDMSRASLVELLLSDLLQ
VQNEALEEENLAPAGGEPEEVHLDLERAADAGPLLGPRLERKAGCKNFFWKTFTSC
>African cichlidfish (*Haplochromis burtoni*) SST1 (AAS97964.1)
MNSSSRLRCLLLLLVSLTASISCTSAQRDSKLRLLLHRTPLLGSQDMSRSSLAEALLSDLL
QVENEALEEENFPLADGEPEDIRVDLERAAGSGPLLAPRERKAGCKNFFWKTFTSC
>American anglerfish (*Lophius americanus*) SST1 (P01169.1)
MKMVSSSRLRCLLVLLSLTASISCSFAGQRDSKLRLLLHRYPLQGSQDMTRSALAELLSD
DLLQGENEALEEENFPLAEGGPEDAHADLERAASGGPLLAPRERKAGCKNFFWKTFTSC
>Rainbow trout (*Oncorhynchus mykiss*) SST1 (CA364601.1)
MLSTRVQCALALLSLALAISSVSAAPSDAKLRQLLQRSLLMAPAGKQELARNTLVELLSELAH
VENEAIELDDMSHGVEQEDVDLELERAPGPVLAPRERKAGCKNFFWKTFTSC
>Tilapia (*Oreochromis niloticus*) SST1 (ENSONIT00000001338.1)
MNSSSRLRCLLLLLVSLTASISCTSAQRDSKLRLLLHRTPLLGSQDMSRSSLAEALLSDLL
QVENEALEEENFPLADGEPEDIRVDLERAAGSGPLLAPRERKAGCKNFFWKTFTSC
>Medaka (*Oryzias latipes*) SST1 (XP_004084505.1)
MMSSSSRLLLLLSLTASISCSAAQRDSKLRLLLQRTPLLGSQDMSRSSLAEALLSDLLQM
ENEVLEEDGFPLSDGEPEDVRVDLERAAGSGPLLAPRDRKAGCKNFFWKTFTSC
>Amazon molly (*Poecilia formosa*) SST1 (ENSPFOT00000005658.1)
MKMLSSLSLRCLLLLLSLASISCSAAQRDSKLRLLLHRTPLLSSKQDASRSSLAEALLSDL
LQMENEALEEDGFGLPEGEPEDIRVDLERAAGSGPLLAPRERKAGCKNFFWKTFTSC
>Atlantic salmon (*Salmo salar*) SST1 (CB509644.1)
MLSTRVQCALALLSLALAISSVSAAPSDAKLRQLLQRSLLMAPAGKQELARYTLAELLSELAQ
AENEAIESDDLDRGVEQEDVRLELERAAGPVLAPRERKAGCKNFFWKTFTSC
>Takifugu (*Takifugu rubripes*) SST1 (ENSTRUG00000010048)
MFSSNSMCLLMLLLSLSASFSCSSAAHRDFKLPLLQSNALMGNKQEMTRSSLANLLSDLL
QVGNEALEENLALAEGEPEEVHIDMERAAGIGPFLTPRERKAGCKNFFWKTFTSC
>Tetraodon (*Tetraodon nigroviridis*) SST1 (KT235747)
MKMFSNSCCLLMLLLSLSASFSCSSAAHRDSKLALMLPPNPLLGHRQEMSRSSLADLLSDL
LQVENQALDENFPLVEGEPEEVHVDMERAADAGIGPFLTPRERKAGCKNFFWKTFTSC
>Platyfish (*Xiphophorus maculatus*) SST1 (ENSXMAT00000014478.1)
MKMLSSLSLRCLLLLLSLASISCSAAQRDSKLRLLLHRTPLLSSKQDASRSSLAEALLSDL
LQMENEALEEDGFPEGEPEDIRVDLERAAGSGPLLPRERKASCKNFFWKTFTSC

Other teleosts

>Mexican tetra (*Astyanax mexicanus*) SST1 (ENSAMXT00000006698.1)
MLSTRVQCALALLSIALAVGSVSGAPSDAKLRQFLQRSLLIGSAGKQELARYTLAELLSELAQ
AENEALEDDVPRGAEQEDVRMELERAAGPVLAPRERKAGCKNFFWKTFTSC

>Goldfish (*Carassius auratus*) SST1 (Q9YGH5.1)

MLSTRIQCALALLSLALAVCSVSAAPSDAKLRQLLQRSLLNPAGKQELARYTLADLLSELVQ
AENEALEPEDLSRAVEKDEVRLERLERAAGPMLAPRERKAGCKNFFWKTFTSC

>Clown knife fish (*Chitala chitala*) SST1 (AAK97070.2)

MLSTRIQCALALLSLALAVSSVYAAPSDLKLRQLLQRSIIAPASKQELARYTLAELLSELAQV
ENEALSDDLRSGADQEEVRLERLERAAGPPLAPRERKAGCKNFFWKTFTSC

>Atlantic herring (*Clupea harengus*) SST1 (XP_012673158.1)

MLSLRLQCALALLSIVLAISCISAAPTDVKLRQLLQRSILFAPGGKQELARLTAEELLSELAQA
ENEALSEDMSRGAEGEDVRYELERSAGSMLAPRERKAGCKNFFWKTFTSC

>Grass carp (*Ctenopharyngodon idella*) SST1 (ACB69423.1)

MLSTRIQCALALLSLALAVCSVSAAPSDAKLRQLLQRSLLNPAGKQELARYTLADLLSDLV
QAENEALEPEDLSRAVEKDDVRLERLERAAGPMLAPRERKAGCKNFFWKTFTSC

>Zebrafish (*Danio rerio*) SST1 (AAH76254.1)

MLSTRIQCALALLSLALAVSSVSAAPSDAKLRQLLQRSLLSPAGKQELARYTLADLLSDLVQ
AENEALEPEDLSRGAEKDDVRLERLERAAGPMLAPRERKAGCKNFFWKTFTSC

>Elephant nose fish (*Gnathonemus petersii*) SST1 (AF292652)

MLSSRIQCALALLSLALAVSSVSAAPSDLKLRQLLQRSLLAPASKQDLARNPLEELLSEMVR
VENEALPDLLSRGADQEEVRLERLERAAGPALAPRERKAGCKNFFWKTFTSC

>Channel catfish (*Ictalurus punctatus*) SST1 (CAA23877.1)

MPSTRIQCALALLAVALSVCSVSGAPSDAKLRQFLQRSILAPSVKQELTRYTLAELLAELAQ
AENEVLDSDEVSRAAESEGARLEMERAAAGPMLAPRERKAGCKNFFWKTFTSC

>Megalobrama (*Megalobrama pellegrini*) SST1 (AAO92644.1)

MLSTRIQCALALLSLALAVSSVSAAPSDAKLRQLLQRSLLNPAGKQELARYTLTDLLSDLVQ
AENEVLEPEDLSRAVEKDEVRLERLERAAGPMLAPRERKAGCKNFFWKTFTSC

>Fathead minnow (*Pimephales promelas*) SST1 (DT100930)

MLSTRIQCALALLSLALAISSVSAAPSDAKLRQLLQRSLLNPAGKQELARYTLADLLSELVQ
AENEALEPEDLSRAVEKDDVRLERLERAAGPMLAPRERKAGCKNFFWKTFTSC

>Red-bellied piranha (*Pygocentrus nattereri*) SST1 (XP_017539070.1)

MLSTRVQCALALLSLALALSSVSGAPSDAKLRQFLQRSILGPSGKQELARYTLAELLSELAQ
AENEALAEADMPRGAEQEDVRMELERAAGPVLAPRERKAGCKNFFWKTFTSC

Other ray-finned fish

>White sturgeon (*Acipenser transmontanus*) SST1 (AAL13248.1)

MLSSRLQCALAFLSLALAVSSVSAAPSDPRLRQLLQRTLAASAGKQELLKYSIAELLSELAQS
ENDALASDELSRAAEQNDVRLERLERSANGNPAMAPRERKAGCKNFFWKTFTSC

>Chinese sturgeon (*Acipenser sinensis*) SST1 (FJ792687.1)

MLSSRLQCALALLSLALAVSSVSAATSEPRIRQLLQRLVASAGKQDLLKYSIAELLSELAQ
SENDALASDELSRAAEQNDVRLERLERSANGNPAMAPRERKAGCKNFFWKTFTSC

>Spotted gar (*Lepisosteus oculatus*) SST1 (XP_006637937.1)

MLSSRVQCALALLCLALAVSSVSAAPSDLRQLLQRSILASAGKQELARYTLAELLSELA
QSENEALSDDLRRAAEQDEVRLERLERSANPALAPRERKAGCKNFFWKTFTSC

Cartilagonous fish

>Elephant shark (*Callorhynchus milii*) SSTa (XP_007910586.1)

MSCGRVQCALALLSIALTVLSVTSAPAHDRYREILQRSILAAAGARSKPELTKYSLAQLLAEL
ANAENEALAEADMARATAQDEVRLERLERSANPNLAQRERKAGCKSFFWKTFTSC

>Whale shark (*Rhincodon typus*) SSTa (XP_020365362.1)

MWCSRVCALALLSIALAVLSAGAAPTADRYRELLQTSMAGAEPRSKAELIKYNLVQLLAE
LANAENEVLDDGEDLPRMAKQDEVRLERLERSANPNPQRRERKAGCKNFFWKTFTSC

>Catshark (*Scylorhinus canicula*) SSTa (JX964750)

MWCSRLQLSLALLSIALAVLSVSSAPTNDNRYREILQRAMAATGSGGKAELTKYSLAQLLSEL
ENAENEALETDAMGGRNEVRLERLERSINPNLANRERKAGCKNFFWKTFTSC

Somatostatin 2

Primates

>Human (*H. sapiens*) SST2 (AAB66895.1)

MPLSPGLLLLLLSGATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQAS
AGPLIGEEAREVARRQEGAPPQQSARRDRMPCRNFFWKTFSCK

> Monkey (*M. fascicularis*) SST2 (XP_015298230)

MPLPPGLLLLLLSGATATAALPLEGSPTGPDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASA
GPLIGEEAREVARRQEGAPPQQSARRDRTPCKNFFWKTFSCK

Other mammals

> Bovine (*B. taurus*) SST2 (NP_001191825)

MLPLCLLLPLLLLPSGATTALSPEGGLAGHESGHMQEVAEIKTNSLLTFLAWWYEWASQAR
AVPFVGGAEAREVSKRQEGAPLHQSTRQDKTPCKNFFWKTFSCK

>Mouse (*M.musculus*) SST2 (AAD51127.1)

MMGGRGTGGKWPSAFGLLLLWGVAASALPLESGPTGQDSVQEATEGRSGLLTFLAWWHE
WASQASSSTPVGGGTPGLSKSQERPPPQQPPHLDKKPCKNFFWKTFSCK

> Pig (*S. scrofa*) SST2 (NP_001191865)

MLPPLCLLLLLLLPPLGATTALPLEGGLTSHDRDSGHMQEVAEIKKNSLLTFLAWWHEWMS
QAREVPFVGGETREMPKKQEGLPRQQASRGDRTPCGNFFWKTFSCK

Reptiles

>Anole lizard (*A. carolinensis*) SST2 (XP_008119733.1)

MAFLVHPPPSAPFLALLSFSRLMGAAPAAVLPIPGGLAWKHNEGSADLGRDELLAFLSGLV
DRASRRHGMPLSKQEKVVRSPREERVFFRHPVREKAPCKNFFWKTFSCK

Amphibians

> Marsh Frog (*P. ridibundus*) SST2 (AAC60094.1)

MLGSAGTLLLLLLAWGARALSQPDDNRITTGRNQDLNAIQDLLLLKLLSGWTDRESNLVE
VERNVPDPPEPKIPPSVKFPRLSLRERKAPCKNFFWKTFTMC

Lobe-finned fish

>Coelacanth (*L. chalumnae*) SST2 (NW_005819697)

MQPLILLVPLVLMAWNLGVAAPVKEERLMLYDKVNRETTGFGEERKQFLSNMLDALIGLN
TLENDTPLLGTKEQEEHNLSESAFKYSSLKKAPCRNFFWKTFSCK

Teleosts

>Mexican tetra (*A. mexicanum*) SST2 (ENSAMXT00000013558.1)

MALSGGGDTCGAADGGMFIMRMLLSLVPLLLIAWSGTNTDALPIDNKLPQSKEVLTKEQKD
LLIKIMSDLAELNMTLKDLDGALDLEQLLNGKLGERSVEKSPCTNFFWKTFSAC

>Atlantic herring (*C. harengus*) SST2 (XP_012681486.1)

MGVLARVDPCSVAQSARITMRVLTSVLPLILIVWSGSQTGALPVREKPLRNESLADEERILL
KILAGLTEKNLTEENLTGHDLEGLLNGTLKGGSVPTPQERSPCKNFFWKTFSCK

>Zebrafish (*D. rerio*) SST2 (ENSADART00000146411.2)

MFLMRVLLSLFPLVFVIWNGEALPIQDKQSQTNEILSKEEDGLKMITYVAELNLTSKELADL
DAELLNGKLWEKSDKPSKDKSPCKLFFWKTFSCK

>Channel catfish (*I. punctatus*) SST2 (XP_017341959.1)

MALGGRINLYQAVDSPMFTMRVLLSLIPLLFVAWSANNADALPVQDKLPNSNEVLTKEQK
DFMTQFLANLAELNMTIKDLETMDHEQLSKLSERAAFGLPAREKSQCENFFWKTFSCK

> Red-bellied piranha (*P. nattereri*) SST2 (XM_017706353.1)

MALAVGGTSCGGADGGMFIMRMLLSLVPLLLIAWSGTSTDALPVENKLPQSNEVLTKEQK
DLLIKIMSDLAELNMTVKDLGALDLEQLLSGKLGERSVFGLPAQEKSCKNFFWKTFSACQ

H

Other ray-finned fish

>Spotted gar (*L. oculatus*) SST2 (NC_023203.1)

MHLLSSLVPLALLVWSLKCAAAPSEERRALQSNGLAKERKDVLLKVL SGLLVSNLLRKE
QSAVDSEQLKSSLMGERSVFGPSVSRERTPCKNFFWKTFS SC

Cartilaginous fish

>Elephant shark (*C. milii*) SSTd (XP_007900347.1)

MQWQAFASVVCLLFIVTVQGVEPQEERMGLQLNREMVKDKKRLIAKLLAGLLDVDDN LLE
SVIAPLGLSKEEGTDFEERSAAGEIPPRKPKAGCKLFFWKTFS HC

>Whale shark (*R. typus*) SSTd (XP_020390988.1)

MTVCLMSLLLLLSVEAADPLEERMKLQVNREVTKSRYLMLKLLSGLLDPDDN LLENDFTS
LSPGEEESSLEERSVNAGIPRRPQKAPCKLFFWKTFS HC

>Catshark (*S. canicula*) SSTd (MK491629)

MKWLMTVSLMSLLYLLRVEGTDLLEERMKLQVNREMTKS RKNLIVKLLAGLLETDDN LLE
NGFAPLKPEEAEGTLFEERSVNAGIPRREQKTPCKLFFWKTFS HC

Somatostatin 3

Euteleosts

>Orange-spotted grouper (*E. coioides*) SST3 (AAU93566.1)

MQCIRCPTILVLVALVLCSPGVFSQPDRDQDQYQNQDL DLELRHHRL LQRARSAGLLS QEW
SKRAVEDLLAQMSLPEADTQREAEVVS MATGGRMN LERSVDPPNN LPPRERKAGCKNFY W
KGFTSC

>Stickleback (*G. aculeatus*) SST3 (KT235756)

MQYTRCPAILVLVGLVLCGPGVSSQRNRDQDQDQYQNQ DLDPRPHLL LQRARGAGLLS QD
WSKRAVEDLLAQMSLPEADSQLGAEVVS AATGGRLHLERSVDPPNN LPARERKAGCKNFY
WKGFTSC

>American anglerfish (*L. Americanus*) SST3 (P01170.2)

MQCIRCPAILALLALVLCGPSVSSQLDREQSDNQDL DLELRQHWLLERARSAGLLS QEW SK
RAVEELLAQMSLPEADVQREAE DASMATGGRMN LERSVDSTNN LPPRERKAGCKNFY WK
GFTSC

>Rainbow trout (*O. mykiss*) SST3 (Q91194.1)

MKVCRIHCALALLGLALAICSQGAASQPDLDLRSRLLQRARAAAWPHRSGV SERWRTFYP
NCPCLRPRKVKCPAGAKEDLRVELERSVGNPNN LPPRERKAGCKNFY WKGFTSC

>Medaka (*O. latipes*) SST3 (AU168379.1)

MQHARGPAFVVLAALALSSLGVSSQSDRDQDQFQNHDL DLELRHHRL LQRARSAGLLS QD
WSKRAIENMLARMPDPEAEAEAEVGRNNMERSVDANVPPRNRKD GCKNFY WKGFTSC

>Amazon molly (*P. formosa*) SST3 (ENSPFOT00000005672.2)

MHHARCPTILVLAALAALS LGVSSQADRDQDPYQNQNLDLDLELRHHRL LQRARSAGLLS
QDWSKRAVEDLLAQMSRSAVEAQDDPEAASKGTDSRLNLERSVETTARERKAGCKNFY
WKGLTSC

>Atlantic salmon (*S. salar*) SST3a (DW531645.1)

MKFSQIHCALALLGLALAICSQGAASQPDLDLRSRLLQRARAAASIATQEWSKRVMEDVLS
KLSLPDVEAQKSVGSTADAKEDLERSVDNSNN LPPRERKAGCKNFY WKGFTSC

>Atlantic salmon (*S. salar*) SST3b (CB505007.1)

MKVCRIHCALALLGLALAICSQGAASQPDLDLRSRLLQRARAAGIATQEWSKRAVEDILS
 QLSWPEAQESEVSPAGAKEDLRVELERSVGNNPNNLPPRERKAGCKNFYWKGFTSC
 >Takifugu (*T. rubripes*) SST3 (ENSTRUT00000025350.1)
 MQRIHSSTILMLTTLVLCIQGVSSQPDRDLNQNQDLEMEVRHHRLQLHVHGAGLLSQEWSK
 RAVEDLIAQMSMPEGTGQRDTEVVSMATGGRMNLERSVDTTNNLSPPERKAGCKNFYWK
 GPTSC
 >Tetraodon (*T. nigroviridis*) SST3 (ENSTNIT00000001563.1)
 MPGVRSSSTILVLTALVLSIQAVSSQPDRDLNQNQDLDQEVRRHRLQLRAHGAGLLSQDWSK
 RAVEDLIAQMSLPEGTGQRDTEVVSMATGGRMNLERSVDTTNNLPPRKAGCKNFYWKGFT
 SC
 >Platyfish (*X. maculatus*) SST3
 MHHARYPAILVLAALAALSLGVSSQADRDQDPYQNQNLDLDLELRHHRLQLRARSAGLLS
 QDWSKRAVEDLLAQMSRSEVEAQDGPAAASRGTSRLNERSVETTARERKAGCKNFY
 WKGLTSC
 Other teleosts
 >Mexican tetra (*A. mexicanum*) SST3 (ENSAMXT00000006711.1)
 MKVCVLQCGLVLLGLALVLCSSGASSQPDLDLDLVDLRRHRLQLRARALGIAAQEWKKR
 EMEDLLSQLTLPESEFQESEISTLGSKQDVRVEMDRSAENPNSLPPRERKAGCKNFYWKGFT
 SC
 >Goldfish (*C. auratus*) SST3 (AAF15306.1)
 MRLCELHCYLALLGLSLVLCGRCANSQLPDLDFRHHRLQLRASATGQATRWDFTKRDVE
 KLLSLLSIPEMEMREKGLSMAGESEDRLLEQERSAESSNQLPTRVRKEGCKNFYWKGFTSC
 >White sucker (*Catostomus commersonii*) SST3 (AAK97071.2)
 MRLCELHCYLALLGLSLVLCDRGADSQLEPDMDFRHHRLQLRARAIGLATQDWTCKDIEEL
 LSQSLPEIEARENGVSTTGGNDDLHLELERSAENTNQLYPRERKAGCKNFYWKGFTSC
 >Clown knife fish (*C. chitala*) SST3 (AAV48555.1)
 MKNCQAQCILALMGLFLGLCWPSDASQPDLRYRSLQLRAHSAPASPQDWTRRTVEDLLAR
 LPPPEGEFTPVEDVPAADEGEEVRVELERSVDPNNLPPRERKAGCKNFYWKGFTSC
 >Atlantic herring (*C. harengus*) SST3 (XP_012693360.1)
 MMRFSGIHCSLALLGLSLVLCSHSASSQPDLDLDLRHHRLQLRARAAGMSTQEWSKRAV
 EDLLSQLSLPEEETQDREVSTVGAAKDDLHMERSAETNNIPPKDRKSGCKNFFWKGRITSC
 >Grass carp (*C. idella*) SST3 (ACB69424.1)
 MRLCELQCYLALLGLSLVLCGRSANSQLEPDLDFRHHRLQLRARAIGQATQDWTCKDVEEL
 LSLLSMPMEMRENDISTVDENEDLRVELERSAESSNHIPARERKAGCKNFYWKGFTSC
 >Zebrafish (*D. rerio*) SST3 (XP_694143.1)
 MRLCELQCYLALLGLSLVLCGRSANSQLEPEMDFRHHRLQLRARAIGQAQEWTKKDVEEL
 LSLLSMPMEMQMRSDLSTTDENEDLRVELERSAESSNHIPARERKAGCKNFYWKGFTSC
 >Channel catfish (*I. punctatus*) SST3 (CK424149.1)
 MRTCVLQCCLTLLGLSLVLCNGVSSQPDLDLRHHRLQLRVQALGVAAQEWTKNDLKAIL
 AQLTMPSEFQESDVSTLGTQDLTVELERSAEDPNSLPPRERKAGCKNFYWKGFTSC
 >Elephant nose fish (*G. petersii*) SST3 (AAV48556.1)
 MKTCQVHCVLVLLGLVLGLCYPSAASQPDLRYRSFMQRAHTAAMSPQDWSRRVVEDLLSR
 LAPPEDDTPQSEMSTAEEGEETRVELERSVEPNNLPPRERKAGCKNFYWKGFTSC
 >Silver arowana (*Osteoglossum bicirrhosum*) SST3 (AAK97067.1)
 MKICQIHCTLVLLGLVLGLYCPSAASQPDLRYRSFLQRAHAAAMSPQDWSKQAVEELLSRL
 APAQGEVPQGAVSAADEEEDVRVDLERSLELNNLPPRERKAGCKNFYWKGFTSC
 >Freshwater butterfly fish (*Pantodon buchholzi*) SST3 (AAK97068.2)
 MKLCQVHCILALLGLVLGMCGSSSATQLDSRYRSLVQRARAASMGPQQDWGKLSVEDLSL
 LAATEADMPFGDMSAAEESEGAHLDLERSVEPGNVPPRERKAGCKNFYWKGFTSC

> Red-bellied piranha (*P. nattereri*) SST3 (XP_017539071.1)

MRVCVLQCCLALLGLSLVLCGNGASSQPDLDMDVDVDLDPRYHRLQLQRARALGMAAQD
WRKREMEDLLSQLTLPESEFKSEITSLGAKHDVRVELERSAENPNNLPPRERKAGCKNFY
WKGFTSC

Other ray-finned fish

>Spotted gar (*L. oculatus*) SST3 (ENSLOCT00000011545.1)

MLSYRVHCTLALFGLVLAFFCCVSAVSHSDLRFRRLQKAKAAGLNKQDSSKYAIEDLISQL
VQSDSEALENEMSVLDENSDARLELERSTEIGKEIPPRERKAGCRNFYWKTFSTC

Cartilaginous fish

>Elephant shark (*C. milii*) SSTe (XP_007910587.1)

MQARCTLTLALLSLAALGLSALPHTLRDQLVLQGGSPAMELRDGVVRELIQAVADAESKPQS
EEAAEDFAPDEKAELRLALAPRWKDCCKNFFWKTYTLC

>Whale shark (partial) (*R. typus*) SSTe (XP_020365363.1)

DFLKDTIIQLLHVADADKDAVEVNASQVETPPXNKIPMKFQQRQLGTRMRKNCKNFFWK
TYTLC

>Catshark (*S. canicula*) SSTe (MK491630)

MWCSRLQLSLALLSIALAVLSVSSAPTNRHREILQRALDQELLKDTMMKLLPLVTDVDE
AGTLDVSNAETSEENTTPMKFQHRQLGMRMRKNCKNFFWKTYTLC

Somatostatin 4

Euteleosts

>Stickleback (*G. aculeatus*) SST4 (KT235754)

MAHILCVFALLCFAFCAAQDGETQRGFKDNRLQRDSLPLWLDKLQDEQDSTKKLNLIWLYS
FYKFDNGNIVKGPTDAEEPEKNRRGLGKTTRRFGCRVFFWKSWSPC

>Medaka (*O. latipes*) SST4 (KT235752)

MANVLCVLAFLCFAVCVVQNTIMVESEDLPAGQGGLSSFDRIQDFQSVETGILMNLLYKL
SRPDSAITLQQVRDSEKQEKNNRGVEIATQRPCRVPFYWKSWSAKC

>Atlantic salmon (*S. salar*) SST4 (CA039604.1)

MALTGIWCAFVLVCVTLCQMGKVDSFVNEDKPTWLETLDQKQVSAADDKYNLVWLLYKL
SQSHHDNTFKINFPPHGPESVGKPESTRRETIPQDSRVRKEGCKVFFWKSWSWAC

>Takifugu (*T. rubripes*) SST4 (NC_018911.1)

MARALCILVLLCFAPCCAENSKTEHRFNDLQVQEDLLSWLKPQEKWEPSKRQTLEDLLYKL
TNYKSENRIPLQQPGDTENQEKNNRDLDNLRVQQRQFGCRMFFWKSWSWYC

>Tetraodon (*T. nigroviridis*) SST4 (KT235753)

MARALCFLVLLCFASRCAGNSKTEHRLKDLQVEEDVLPWLNSQEKWEPSKGGQNLEDLLYK
LTNYRSENRIVSQQPSDTNQEKNNRGGLDNLKVQQRQAGCRIFFWKSWSWTC

Other teleosts

>Zebrafish (*D. rerio*) SST4 (NP_571802.1)

MASSQLHLTATLLCLAMMAGIICGRSHMLLNSALQASRGTSADDEEIPERYSLSELEWLLSNS
DPAVFQPDSSSLGSLHSGLELMRRDTKEERKTGCKNYFWKSRTAC

>Channel catfish (*I. punctatus*) SST4 (P01172.1)

MSSSPLRLALALMCLVSAVGVISGRPHVVLNSALEEARNVPFGEEVPERLTLPELQWMLS
NNELTPVQVEEAPRSRLELVRRDNTVTSKPLNCMNYFWKSRTAC

Other ray-finned fish

>Spotted gar (*L. oculatus*) SST4 (ENSLOCT00000011651.1)

MLSYRVHCTLALFGLVFAFCCVSAVSNSDLRFRRLQKAKAASLSTRDSSKYALEDLISQIA
QSDNEALENEMSVLDENSDARLELERSADMVKVIPPRERKAGCRNYYYWKTTSC

Somatostatin 5

Lobe-finned fish

>Coelacanth (*L. chalumnae*) SST5 (XP_005999859.1)

MMCSHVQSLAVLSASLLLVGVGGLPKGEVLTDLFQGGGAEGKEDFSRMLMLKMOVSNLL
KSENDVLVPSAEDTASQDELTRRLAPSRERKAGCKNFFWKTFTSC

Euteleosts

>Stickleback (*G. aculeatus*) SST5 (ALD51533.1)

MQVLLVALFSSVLLVQVSGAPRGDMPTQRGDPADNKDLAYSMLLKFVSELTAARGGETLL
VPEQEEEEAEGRQEVMMRRHLPLTQREKAGCRNFFWKTFTSC

>Rainbow trout (*O. mykiss*) SST5 (BX909872.3)

MLCSQLQVLLVALSASVFLARVSAAPHRDMLAELLRADSTKGNEDLSRTLLLKMMSDLMS
AAVGENEVLPDLEEALGVREEVVRQLPLSHRERKAGCRNFFWKTFTSC

>Sockeye (*Oncorhynchus nerka*) SST5 (EV380196.1)

MLCSQLQVLLVALSASVFLARVSAAPHRDMLAELLRADTTKGNEDLSRTLLLKMMSDLMS
TAVGENEVLPDLEEALGVREEVVRQLPLSHRERKAGCRNFFWKTFTSC

>Tilapia (*O. niloticus*) SST5 (XP_005464163.1)

MLRSQVLLVALGLSVLLVRVSTAPYSDMLTETLRADLTNDKDLTHWLLLKFMALMAARG
DETRRGREEVTRRHLSSLQREKAGCRNFFWKTFTSC

>Medaka (*O. latipes*) SST5 (XP_020567335.1)

MLLAALGLSLLMACVSGAPQRNPLTHTKQLQLLKSEVDPTRLLLMKLVLELVALRRQEML
QELEEELGGRERLMKRHIRFTQREKAGCRNFFWKTFTSC

>Amazon molly (*P. formosa*) SST5 (XP_007551472.1)

MLCSQMKVLFVALCSSMLALHVSSAPQMDDELTTQLAELISDKDLTGLLLLRFMSELMASR
GEEMLRKQEEEEELGGRQRLMRRHIRFSHRERKAGCRNFFWKTFTSC

>Takifugu (*T. rubripes*) SST5 (N.D.)

MLSQVQLLLVTSFSSMLLMEVSSAPRKHMPSELLPADPLKDKDLAILILLRISEVMAAEREM
LLLPQEGEEEAGVREGEVMMRRQVPFSQRDRKAGCRNFFWKTFTSC

>Tetraodon (*T. nigroviridis*) SST5 (ALD51532.1)

MTRSQLLLAASFSLLLMEAGGTPRKHKFLPADSVKDKDLALVTSCLKFAFEGTAAQREMLL
LLQEDEEDAGVREMMMMMRRQIPFSQRERKAGCRNFFWKSFTSC

>Platyfish (*X. maculatus*) SST5 (XP_005804860.3)

MLCSQMKVLVVALCSSMLALHVSSAPQMDDELTTQLAELISDKDLTGLLLLRLMSELTASR
GEEMLRQEEEEDELGGRQRLMRRHIRFTHRERKAGCRNFFWKTFTSC

Other teleosts

> Mexican tetra (*A. mexicanum*) SST5 (XP_007243346.1)

MCSQLQVVVLVALSVLVSRVSAAPRGDVLTQLLQNEADTKENEDISRMLMLKLLSELEVA
GENEVLSGADVVRNDVVRQLPFSQRERKTGCRNFFWKTFTSC

>Zebrafish (*D. rerio*) SST5 (XP_001333082.1)

MFSRLQVVVVTLWVSLLLCRVSSAPRGDLLFQLLRSQVDPKENELQDLSRLLLLKQLSESVT
PEEKDALDSIDELDVRNEVVRQIPVSQRERKAGCRNFYWKTFTSC

> Channel catfish (*I. punctatus*) SST5 (XP_017327476.1)

MSSQMQUIVVLAVSLLVLVSRVRTAPRTDLLAHMLQNEADGKEDLSRILLKLISELKIPDEN
DTLSDDDMELNRILRHLPLTTREKAGCRNFFWKTFTSC

>Fathead minnow (*P. promelas*) SST5 (DT105503.1)

MFSPLQMVAATLSLSLLCSVSSAPGGDMLIQLLRSEVEPKEIELQDFFRLLLLKQLSESAAP
EEKQPRESIDDDPEVHNEVVRQIPLSHRERKTGCRNFYWKTFTSC

> Red-bellied piranha (*P. nattereri*) SST5 (XP_017578562.1)

MNFEVKSSLLSRAAGRSASTPVIQTFFEEFYFKSICLLNHLITRVSAAPRGDILAQLQADPKG
NEELSRMLILKLLSDLEIPGDNEVLSGTDVRSMDVVRQLPFPQRERKTGCRNFFWKTFTSC

Other ray-finned fish

>Spotted gar (*L. oculatus*) SST5 (XP_006627411.2)

MSTGQPSLPPAPAPNQGFQQHKLQVLLVALSVSVLLARVSGVPQRDRDLADLLRAEVPEGKE
DLSRMLLLKIFSDLLRAENEIPPGSAEDAGIRSDVPRQLPLAQRERKAGCRNFFWKTFTSC

Cartilaginous fish

>Catshark (*S. canicula*) SSTb (JX964751)

MPRSQTQVLLTLVTVALLLRGSSSTARVQGLPDILQERNDEGTEELSRTMVLNLLSELLHAG
DKGLPSTERRGLPQAEIVRRWNSPRDRKAGCKNFFWKTFTSC

Somatostatin 6

Birds

>Duck (*Anas platyrhynchos*) SST6

MQLVASLVSVLLLWWSVRATALPGEERLALQNSREQTKLRKDAILKMLAGLLESVDVASPD
LEEEGKLEERATLGRLAQLSQRDRKAPCKNFFWKTFTSC

>Chicken (*G. gallus*) SST6 (DQ279789)

MQLVASLVSVLLLWWSVRATALPGEERLALQNSREQTKLRDALLKMLAGLLESSDVASP
DLEEEGKLEEERAAALGRLAQLSQRDRKAPCKNFFWKTFTSC

>Zebra finch (*Taeniopygia guttata*) SST6

MQLVASLASVLLLWWSVRATALPGQEGQLSTREQSTARKDVILKMLAGLLGSVDAGAEVA
FPAGQEKARLEEDQAALGRLAQLSQRDRKAPCKNFFWKTFTSC

Lobe-finned fish

>Coelacanth (*L. chalumnae*) SST6 (XP_005994063.1)

MQLTSLVSFLLVWWSVRATALPIEEKLM SHNNVELTKERKELMLKMIAGLLEGIDSPPMG
GEVGSM DLEEPVEPKLEERAAFNRLPQLPQRDRKAPCKNFFWKTFTSC

>African lungfish (*P. annectens*) SST6 (Q9W7E9.1)

MQFLASLVSFLLVWWSVKATALPVEDRLSVHSNRDLTREREEMILKMISGLLDGSDNSLFG
GEVTSMDIEEPL ENKLEERAAYNALPQLPQRDRKAPCKNFFWKTFTSC

Euteleosts

>Orange-spotted grouper (*E. coioides*) SST6 (AAU93567.1)

MQLLVVLAALMGVLFVRAAAVLPVEDRSSIHVNRELSKERKELILKLVSGLLDGALDTNM
LPGEAAPVDLEEPLESRL EERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Atlantic cod (*G. morhua*) SST6

MQLMVVLAALMGVLFVRAAALLPVEDRSNFHSSRELSKERKELILKLVSGLLEGSPDSNM
LPGELSPVELEEPLESRL EERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Stickleback (*G. aculeatus*) SST6 (ENSGACG00000007077)

MQLLVVLAATLMGVLFVRAAAVLPMEDRSSINVNRELSKERKELILKLVSGLLDGAADAN
MLPGEAAPVD FEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Rainbow trout (*O. mykiss*) SST6 (CX153272.1)

MQLLVILASLMGVLYSVRAAAVLPVEERSPLL NRELSKERKELILKLVSGLLDGATDTNMLP
GEGVSPVDLEEPLESRL EERAAYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Medaka (*O. latipes*) SST6 (BJ885293.1)

MQLLVVLAALMGVLFVRAAAVLPVEDRSSIHVNRELSKERKELILKLVSGLLDGSLDTNM
LPGEAAPVD FEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Rainbow smelt (*Osmerus mordax*) SST6 (EL519905.1)

MQLLVVLAALMGVLYSARAAVLPVEERSPIQANRELSTERKQLILKLVSGLLDGASDSNM
LPGDVSPLDLEEPLESRL EERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Amazon molly (*P. formosa*) SST6

MQLLVVLAALMGVLFVRAAAVLPLED RSPIHANRELSKERKELILKLVSGLLDGALDTNM
LPGEAAPVDLEEPLESRL EERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Takifugu (*T. rubripes*) SST6 (ENSTRUG00000012370)

MQLLVVLAALTGVLLSIRAAAVLPVEERSPVHLNRELSKERKELILKLVSGLLDGALDTNML
PMETVDLEEPLESRL EERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Tetraodon (*T. nigroviridis*) SST6 (ENSTNIG00000015178)

MQLLVVLAALTGVLLSVRAAAVLPVEERIPLHLNRELSKERKELMLKLVSGLLDGALDTNM
LPMEAVDLEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Platyfish (*X. maculatus*) SST6

MQLLVVLAALMGVLFVRAAAVLPLEDRSPIHANRELSKERKELILKLVSGLLDGALDTNM
LPGEAAPVDLEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

Other teleosts

> Mexican tetra (*Astyanax mexicanus*) SST6 (ENSAMXT00000013526.1)

MQILASLVSLLLVLYSVRAAAVLPVEERSPAHTRELSKERKELILKLVSGLLDGVDNSVLGG
DLVPMEAEPELESRLERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Goldfish (*C. auratus*) SST6 (AAD09631.1)

MQLLSSLVSLLLVLYSVRAAAVLPVEERNPAQSRELSKERKELILKLISGLLDGVDNSVLDG
EIAPVPFDAEPELESRLERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

> Atlantic herring (*Clupea harengus*) SST6 (XP_012681579.1)

MQLLASLVSLMLVLYSIRAAAVLPVDERSPAHAARELSKERKELILKLVSGLLDGVESNMLPG
DEAPLDLEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Grass carp (*C. idella*) SST6 (ACB69425.1)

MQLLASLVSLLLVLYSVRAAAVLPVEERNLAQSRELSKERKELILKLISGLLDGVDNNVLAG
EIAPVPLDVEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Zebrafish (*D. rerio*) SST6 (BG307388)

MQLLASLVSLLLVLYSVRAAAVLPLEERNPAQSRELSKERKELILKLISGLLDGVDNSVLAG
EIAPVPLDVEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

> Channel catfish (*I. punctatus*) SST6

MQLLASLVSLLLVLYSVRAAAVLPAAEERSPAHTREPSKERKEMILKMVSSLLDGVDNNMLA
GDLLPLEEEEPIDSRLEERAVYNRLAQLPQRDRKAPCKNFFWKTFTSC

>Fathead minnow (*P. promelas*) SST6 (DT250237.1)

MQLLASLVSLMLVLYSVRAAALLPVEERNLAQSRELSKDRKELILKLISGLLDGVDNSVLAG
EIAQVPMDAEPELESRLERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

Other ray-finned fish

>White sturgeon (*A. transmontanus*) SST6 (AAL13249.1)

MQLRARLVSLMLVVYSLRVVAVLPGEERLSVHSNRELSKERKEGFLKLLSGLLDREVDSVV
LGEDVSPMDLEEPLDSRLERAIYNRLSQLPLRARKAPCKNFFWKTFTSC

>Chinese sturgeon (*A. sinensis*) SST6 (FJ792688.1)

MQLRASLVSLMLVVYSLRVVAVLPGEERLSVHSNRELSKERKEGFLKLLSGLLDGVDSSVV
LGEDVSPMDLEEPLDSRLERAVYNRLSQLPQRARKAPCKN

>Spotted gar (*L. oculatus*) SST6 (XP_006642047.1)

MQLLASLASMLVVYSVRAAAVLPGEERATLHTKELSKDRKELILKLISGLLDGADSAMLA
GDVASVDLEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

Cartilaginous fish

>Elephant shark (*C. milii*) SSTc (XP_007895974.1)

MQILVALISTLFLVSGVSTTTASLDDRNLQSSREMNERKEMILKLLSGLLDNAAVSGQTG
SEAGYPEPADGGPVMLEERSRYSQLPQRSRKVPCKNFFWKTFTSC

>Whale shark (*R. typus*) SSTc (XP_020368528.1)

MQLLGASXVSILLIVSSVKATAPLEDRLSLRANQELNKERKEVVLKLLSALLDSSSNQMGIE
NTFPDQEDMEEMKVEDRSRFSQLPQRERKTSCKNFFWKTFTSC

> Catshark (*S. canicula*) SSTc (JX964752) = SST6

MQLLGASLLSMLLIVSSVRATAPLEDRLSLRANQELNKERKEVILKLLSGLLDSSSNQIAIE
NTFPDPEDVEEMKVEERSRFSQLPQRERKAPCKNFFWKTFTSC

Other somatostatins

Lampreys

>Japanese lamprey (*Lethenteron japonicum*) SSTa (KU522234)

MPAMPTTCVLLLFSLGVTALLPRPLGASPFRRPAEGSSLAGLGAWALGPGAGXGGAGLIDD
RLQQRVEAVLTQELSREERALVGRLLAELAAGGAGLGALPPLGWGPGSSSDEEGGEEGEG
AGGDGGRGERALSARVRKAGCKNFFWKTFTSC

>River lamprey (*Lampetra fluviatilis*) SSTb (KX345282)

MKISRATTTTTSTFSSTLSTSSTSSCRAVRLLFVLPMLSVVLGSVTADVRPLHVRMALERVM
DGPGMENLDQDQKQFLVRLLAIDSSADETNELNHSEDGSLPEVLVARALRAAAAPGAAG
GAQLPLGNRERKAGCKNFFWKTFFSSC

>Japanese lamprey (*Lethenteron japonicum*) SSTb (KU522235)

MKISRATTSTTSTFSSTLSTSSTTSSCRAVRLLFLLSVLSVVLGSVTADVRPLHARMALERVM
DGLGMENLDQDQKLFLVRLLAIDSSADETNELNHSEDGSLPEALVARALRAAAAPGAAG
GAQLPLGNRERKAGCKNFFWKTFFSSC

>Japanese lamprey (*Lethenteron japonicum*) SSTc (KU522236)

MKATAAICCSLALVLVATGGRRGGGLHAASIGRSAILRAPASYRQLEAHPDLQMGDQDDSQ
MLLMIVEAMRMRDAGPETDGPGEGEAARVVDGLPEFPREEVRALGPNERPFVVPVLSPRD
RKANCRMFYWKTMAAC

>Sea lamprey (*Petromyzon marinus*) SSTc (KU529940)

MKATAAICCSLALVLVASGGRRSGLHAASIGRSAILRAPASFRQLEAHPDLQMGDQDDSQIL
LNMIVEAMRMRDAGPETDGPGEGEATRVDGLPEFPREEARALVPNERPFVPGALSPRDRK
ANCRMFYWKTMAAC

1Clown_knife_fish	-----	-----	MLST-RI	Q	CALAL	-----
1Orange-spotted_grouper	-----	-----	MKMOVSSSR	R	CLLLL	-----
1Anglerfish	-----	-----	MKMOVSSSR	R	CLLVL	-----
1Megalobrama	-----	-----	MLST-RI	Q	CALAL	-----
1African_cichlid_fish	-----	-----	MNSSSR	R	CLLLL	-----
1Cod	-----	-----	MMSV-R	-	STLLL	-----
1Zebrafish	-----	-----	MLST-RI	Q	CALAL	-----
1Medaka	-----	-----	MMSSSR	-	LLLLL	-----
1Stickleback	-----	-----	MVSS-RL	R	CLLLL	-----
1Takifugu	-----	-----	MFSSNSM	-	CLLML	-----
1Tetraodon	-----	-----	MKMFNSC	-	CLLML	-----
1Trout	-----	-----	MLST-RV	Q	CALAL	-----
1Fathead_minnow	-----	-----	MLST-RI	Q	CALAL	-----
1Killifish	-----	-----	MKMFSSL	R	CLLLL	-----
1Salmon	-----	-----	MLST-RV	Q	CALAL	-----
1Pygocentrus	-----	-----	MLST-RV	Q	CALAL	-----
1Ictalurus	-----	-----	MPST-RI	Q	CALAL	-----
1Astyanax	-----	-----	MLST-RV	Q	CALAL	-----
1Clupea	-----	-----	MLSL-RL	Q	CALAL	-----
1Amazon_molly	-----	-----	MKMLSSL	R	CLLLL	-----
5Coelacanth	-----	-----	MMC	SHVQ	-	SLLAV
5Zebrafish	-----	-----	MFSRLQ	-	VVVVT	-----
5Stickleback	-----	-----	-	-	MOVLL	-----
5Takifugu	-----	-----	MLSQVQ	-	LLLV	-----
5Tetraodon	-----	-----	MTRSQ	-	LLLAA	-----
5Medaka	-----	-----	-	-	MLLAA	-----
5Sockeyess	-----	-----	MLCSQLQ	-	VLLVA	-----
5Trout	-----	-----	MLCSQLQ	-	VLLVA	-----
5Fathead_minnow	-----	-----	MFSPLQ	-	MVVAT	-----
5Amazon_molly	-----	-----	MLCSQMK	-	VLFVA	-----
5Platyfish	-----	-----	MLCSQMK	-	VLVVA	-----
5Tilapia	-----	-----	MLRSQVL	-	LVAL	-----
5Lepisosteus	MSTG	QPSLPPAPAP	NQGFQCHKLQ	-	VLLVA	-----
5Astyanax	-----	-----	MCSQLQ	-	VVLVA	-----
5Ictalurus	-----	-----	MSSQMQ	-	IVVLA	-----
5Pygocentrus	-----	MNFE	VKSSLLSRAA	GR	SASTP	VIQ
Catshark5	-----	-----	MPRSQTQ	-	VLLTL	-----
6Chicken	-----	-----	MQLV	-	ASLVS	-----
6Zebra_finch	-----	-----	MQLV	-	ASLAS	-----
6Duck	-----	-----	MQLV	-	ASLVS	-----
6Lungfish	-----	-----	MQFL	-	ASLVS	-----
6Coelacanth	-----	-----	MLNMQLL	-	TSLVS	-----
6White_sturgeon	-----	-----	MQLR	-	ARLVS	-----
6Chinese_sturgeon	-----	-----	MQLR	-	ASLVS	-----
6Lepisosteus	-----	-----	MQLL	-	ASLAS	-----
6Carp	-----	-----	MQLL	-	ASLVS	-----
6Goldfish	-----	-----	MQLL	-	SSLVS	-----
6Orange-spotted_grouper	-----	-----	MQLL	-	VVLAA	-----
6Zebrafish	-----	-----	MQLL	-	ASLVS	-----
6Stickleback	-----	-----	MQLL	-	VVLAT	-----
6Takifugu	-----	-----	MQLL	-	VVLAA	-----
6Tetraodon	-----	-----	MQLL	-	VVLAA	-----
6Rainbow_smelt	-----	-----	MQLL	-	VVLAA	-----
6Trout	-----	-----	MQLL	-	VILAS	-----
6Medaka	-----	-----	MQLL	-	VVLAA	-----
6Fathead_minnow	-----	-----	MQLL	-	ASLVS	-----
6Astyanax	-----	-----	MQIL	-	ASLVS	-----
6Pygocentrus	-----	-----	MQLL	-	ASLVS	-----
6Clupea	-----	-----	MQLL	-	ASLVS	-----
6Ictalurus	-----	-----	MQLL	-	ASLVS	-----
6Amazon_molly	-----	-----	MQLL	-	VVLAA	-----
6Cod	-----	-----	MQLM	-	VVLAA	-----
6Platyfish	-----	-----	MQLL	-	VVLAA	-----
Catshark6	-----	-----	MQLL	-	GTASL	-----
Elephant_shark6	-----	-----	MQILVALI	-	STLFL	-----
whale_shark6	-----	-----	MQLLGSASX	-	VSILL	-----
4Lepisosteus	-----	-----	MLS	YRVH	-	CTLAL
4Zebrafish	-----	-----	MASSQLH	-	LTATL	-----
4Takifugu	-----	-----	MARAL	-	CILVL	-----
4Medaka	-----	-----	MANVL	-	CVLAF	-----
4Tetraodon	-----	-----	MARAL	-	CFLVL	-----
4Channel_catfish	-----	-----	MSSSP	LR	-	LALAL
4Stickleback	-----	-----	MAHIL	-	CVFAL	-----
4Atlantic	-----	-----	MALTGIW	-	CAFVL	-----

2Human	---	---	SGAT	ATAALPL	---	---	EG	---
2Mouse	---	---	LLL-WGVA	ASALP	---	---	---	---
2Pig	---	---	LLL-PPLG	ATTALPL	---	---	EG	GL
2Bovine	---	---	LLL-LPSG	ATTALSP	---	---	EG	GLA
2Monkey	---	---	LLL-SGAT	ATAALPL	---	---	EG	---
2Lizard	---	---	LLSFS-RLMG	AAPAAVL	---	---	PI	PGGLA
2Frog	---	---	LL- -LAW	GARALSO	---	---	PD	DNRIT
2Coelacanth	---	---	LVLMAWNLG	-VAAVPK	---	---	EE	RLMLYD
2Lepisosteus	---	---	LALLVWSLK	CAAAVPS	---	---	EE	RRALQ
2Astyanax	---	---	LLLIAWSGT	NTDALPI	---	---	DN	KLPQ
2Pygocentrus	---	---	LLLIAWSGT	STDALPV	---	---	EN	KLPQ
2Clupea	---	---	LILIV-WSGS	QTGALPV	---	---	---	REKPL
2Ictalurus	---	---	LLFVA-WSAN	NADALPV	---	---	QD	KL-PN
2Zebrafish	---	---	LVFVI-WNGE	- -ALPI	---	---	QD	KQ-SQ
Catshark2	---	---	MSLL-YLLR	VEGTDLL	---	---	EE	RMKLO
Whale_shark2	---	---	MSLL-LLLS	VEAADPL	---	---	EE	RMKLO
Elephant_shark2	---	---	VCLL-FIVT	VQGVPEQ	---	---	EE	RMGLQ
Skate2	---	---	---	---	---	---	QE	---
aLethenteron	PFRP	AE	LAGL	GAWALG	PGAGXGG	---	AG	LIDDR
bLethenteron	---	---	LSVLSVVLG	SVTADVR	---	---	PL	HARMA
bLampetra	---	---	LPMLS-VVLG	SVTADVR	---	---	PL	HVRMA
cPetromyzon	---	---	LVLV-ASGG	RRSGLHA	---	ASIGR	SA	ILRAPA
cLethenteron	---	---	LVLVA-TGGR	RGGGLHA	---	ASIGR	SA	ILRAPA
3Lepisosteus	---	---	FGLV-LAFC	CVSAVSH	---	S	DL	RFRRF
3Astyanax	---	---	LGLA-LVLC	SSGASSQ	---	PDLDDL	DVDLRHRR	---
3Clupea	---	---	LGLS-LVLC	SHSASSQ	---	PDL	DLDLDRHHR	---
3Ictalurus	---	---	LGLS-LVLC	SNGVSSQ	---	P	DLDLRHRR	---
3Pygocentrus	---	---	LGLS-LVLC	GNGASSQ	P	DLDMDVDVDL	DL	RYHRL
3Amazon_molly	---	---	AALAALSLG	VSSQADR	DQ	DPYQNQNLDL	DP	ELRHHR
3Platyfish	---	---	AALAALSLG	VSSQADR	---	DQDPYQNQN	DLDLELRHHR	---
3Rainbow_trout	---	---	LGLA-LAIC	SQGAASQ	---	P	DLDLRSRRL	---
3Freshwater_butterfly	---	---	LGLV-LGMC	GSSSATQ	---	L	DS	RYRSL
3Grass_carp	---	---	LGLS-LVLC	GRSANSQ	---	LEP	DLDLFRHRR	---
3Goldfish	---	---	LGLS-LVLC	GRCANSQ	---	L	EPDLDFRHR	---
3Clown_knifefish	---	---	MGLF-LGLC	WPSDASQ	---	P	DL	RYRSL
3Orange-spotted	---	---	VALV-LCSP	GVFSQPD	---	RDQDQYQNQ	DLDLELRHHR	---
3American_anglerfish	---	---	LALVL-CGPS	VSSQLDR	---	EQSDNQDL	DL	ELRQHW
3Silver_aronana	---	---	LGLV-LGLY	CPSAASQ	---	P	DL	RYRSF
3White_sucker	---	---	LGLS-LVLC	DRGADSQ	---	LEP	DMDLFRHRR	---
3Elephant_nose_fish	---	---	LGLV-LGLC	YPSAASQ	---	P	DL	RYRSF
3Zebrafish	---	---	LGLS-LVLC	GRSANSQ	---	L	EPDMDFRHHR	---
3Stickleback	---	---	VGLV-LCGP	GVSSQRNRDQ	---	DQDQYQNQDL	DP	RPHLL
3Takifugu	---	---	TTLV-LCIO	GVSSQPD	---	RDLNQNQ	DLEMEVRHHR	---
3Tetraodon	---	---	TALV-LSIQ	AVSSQPD	---	RDLNQNQ	DLDQEVRRHR	---
3Medaka	---	---	LALSSLGVS	SQSDRDQ	---	DQFQNH	DLDLELRHHR	---
3aAtlantic_salmon	---	---	LGLA-LAIC	SQGAASQ	---	P	DLDLRSRRL	---
3bAtlantic_salmon	---	---	LGLA-LAIC	SQGAASQ	---	P	DLDLRSRRL	---
Elephant_shark3	---	---	LS	LAAL	GLSALPT	---	---	HLRDQLV
Whale_shark3	---	---	---	---	---	---	---	---
catshark3	---	---	LSIA-LAVL	SVSSAPT	---	---	DN	RHREI
Catshark1	---	---	LSIA-LAVL	SVSSAPT	---	---	DN	RYREI
Whale_shark1	---	---	LSIA-LAVL	SAGAAPT	---	---	AD	RYREI
Elephant_shark1	---	---	LSIA-LTVL	SVTSAPA	---	---	HD	RYREI
1Human	---	---	LSIV-LALG	CVTGAPS	---	---	DP	RLRQF
1Mouse	---	---	LCIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Monkey	---	---	LSIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Bovine	---	---	LSIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Pig	---	---	LSIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Dog	---	---	LSIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Chicken	---	---	LSIA-LAVG	TVSAAPS	---	---	DP	RLRQF
1Flycatcher	---	---	LSIA-LALG	TVSAAPS	---	---	DP	RLRQF
1Turkey	---	---	---	---	---	---	---	---
1Anole_lizard	---	---	LSLA-LALG	SGAAAPA	---	---	DP	RLRQF
1Chinese_softshell_turtle	---	---	LSLA-LAVS	SVSGAPS	---	---	DP	RLRQF
1Frog	---	---	LSLA-LAIN	SISAAPT	---	---	DP	RLRQF
1Lungfish	---	---	LSLA-VVFS	KVSAAPS	---	---	DL	RLRQL
1Coelacanth	---	---	LSLA-LVVS	NISAAPS	---	---	DL	RLRQL
1Lepisosteus	---	---	LCLA-LAVS	SVSAAPS	---	---	DL	RLRQL
1White_sturgeon	---	---	LSLA-LAVS	SVSAAPS	---	---	DP	RLRQL
1Chinese_sturgeon	---	---	LSLA-LAVS	SVSAATS	---	---	EP	RLRQL
1Platyfish	---	---	LLSL-ASIS	CSSAAQR	---	---	DS	KLRL
1Tilapia	---	---	LVSLT-ASIS	CTSAAQR	---	---	DS	KLRL
1Elephant_nose_fish	---	---	LSLA-LAVS	SVSAAPS	---	---	DL	KLRL
1Carp	---	---	LSLA-LAVC	SVSAAPT	---	---	DA	KLRL
1Goldfish	---	---	LSLA-LAVC	SVSAAPT	---	---	DA	KLRL
1Clown_knife_fish	---	---	LSLA-LAVS	SVYAAPS	---	---	DL	KLRL
1Orange-spotted_grouper	---	---	LLSLT-ASIS	CSSAAQR	---	---	DS	KLRL
1Anglerfish	---	---	LLSLT-ASIS	CSFAGQR	---	---	DS	KLRL

1Megalobrama	-----	-LSLA-LAVS	SVSAAPS	-----	DA	-KLRQL
1African_cichlid_fish	-----	LVSLT-ASIS	CTSAAQR	-----	DS	-KLRLL
1Cod	-----	-LSCA-AMLS	GSSAAPS	-----	DT	-KLRQL
1Zebrafish	-----	-LSLA-LAVS	SVSAAPS	-----	DA	-KLRQL
1Medaka	-----	-LSLT-ASIS	CSSAAQR	-----	DS	-KLRLL
1Stickleback	-----	LLSLT-ASIS	CSSTAQR	-----	DG	-KLHLL
1Takifugu	-----	LLSLS-ASFS	CSSAAHR	-----	DF	-KLPLL
1Tetraodon	-----	LLSLS-ASFS	CSSAAHR	-----	DS	-KLALM
1Trout	-----	-LSLA-LAIS	SVSAAPS	-----	DA	-KLRQL
1Fathead_minnow	-----	-LSLA-LAIS	SVSAAPS	-----	DA	-KLRQL
1Killifish	-----	LLCLS-ASIS	CSAAAQR	-----	DS	-KLRLL
1Salmon	-----	-LSLA-LAIS	SVSAAPS	-----	DA	-KLRQL
1Pygocentrus	-----	-LSLA-LALS	SVSGAPS	-----	DA	-KLRQF
1Ictalurus	-----	-LAVA-LSVC	SVSGAPS	-----	DA	-KLRQF
1Astyanax	-----	-LSIA-LAVG	SVSGAPS	-----	DA	-KLRQF
1Clupea	-----	-LSIV-LAIS	CISAAPT	-----	DV	-KLRQL
1Amazon_molly	-----	LLSLS-ASIS	CSSAAQR	-----	DS	-KLRLL
5Coelacanth	-----	-LSAS-LLLV	GVGGLPK	-----	GE	-VLTDL
5Zebrafish	-----	-LWVS-LLLC	RVSSAPR	-----	GD	---LLF
5Stickleback	-----	VALFSSVLLV	QVSGAPR	-----	GD	---
5Takifugu	-----	---SFSSMLLM	EVSSAPR	-----	KH	---
5Tetraodon	-----	---SFSFLLLM	EAGGTPR	-----	KH	---
5Medaka	-----	-IGLS-LLMA	CVSGAPQ	-----	R	NP
5Sockeyess	-----	-LSAS-VFLA	RVSAAPH	-----	RD	-MLAEL
5Trout	-----	-LSAS-VFLA	RVSAAPH	-----	RD	-MLAEL
5Fathead_minnow	-----	-LSLS-LLLC	SVSSAPG	-----	GD	-MLIQ
5Amazon_molly	-----	-LCSSMLALH	VSSAPQM	-----	DE	---
5Platyfish	-----	LCSSM-LALH	VSSAPQM	-----	DE	---
5Tilapia	-----	---GLS-VLLV	RVSTAPY	-----	SD	-MLTET
5Lepisosteus	-----	-LSVS-VLLA	RVSGVPQ	-----	RD	-RLADL
5Astyanax	-----	-LSVL-VLVS	RVSAAPR	-----	GD	-VLTQL
5Ictalurus	-----	-VSLL-VLVS	RVRTAPR	-----	TD	---
5Pygocentrus	IFEEFEYFKS	ICLLN-HLIT	RVSAAPR	-----	GD	-ILAQL
Catshark5	---	V-TVA-LLLL	RGSSTAR	-----	VQ	-GLPDI
6Chicken	-----	VLLLV-WSVR	A-TALPG	-----	EE	-RLALQ
6Zebra_finch	-----	VLLLL-WSVR	ATALPGQ	-----	EG	---
6Duck	-----	VLLLV-WSVR	A-TALPG	-----	EE	-RLALQ
6Lungfish	-----	FLLVV-WSVK	A-TALPV	-----	ED	-RLSVH
6Coelacanth	-----	FLLVV-WSVR	A-TALPI	-----	EE	-KLM
6White_sturgeon	-----	LMLVV-YSLR	VVAVLPG	-----	EE	-RLSVH
6Chinese_sturgeon	-----	LMLVV-YSLR	VVAVLPG	-----	EE	-RLSVH
6Lepisosteus	-----	LMLVV-YSVR	AAAVLPG	-----	EE	-RATLH
6Carp	-----	-LLLVLYSVR	AAAVLPV	-----	EE	-RNLAQ
6Goldfish	-----	LLLVL-YSVR	AAAVLPV	-----	EE	-RNPAQ
6Orange-spotted_grouper	-----	LMGVL-FSVR	AAAVLPV	-----	ED	-RSSIH
6Zebrafish	-----	-LLLVLYSVR	AAAVLPL	-----	EE	-RNPAQ
6Stickleback	-----	LMGVL-FSVR	AAAVLPM	-----	ED	-RSSIN
6Takifugu	-----	LTGVL-LSIR	AAAVLPV	-----	EE	-RSPVH
6Tetraodon	-----	LTGVL-LSVR	AAAVLPV	-----	EE	-RIPLH
6Rainbow_smelt	-----	LMGVL-YSAR	AAAVLPV	-----	EE	-RSPIQ
6Trout	-----	LMGVL-YSVR	AAAVLPV	-----	EE	-RSPL
6Medaka	-----	LMGVL-FSVR	AAAVLPV	-----	ED	-RSSIH
6Fathead_minnow	-----	LMLVL-YSVR	AAALLPV	-----	EE	-RN
6Astyanax	-----	LLLVL-YSVR	AAAVLPV	-----	EE	-RSPAH
6Pygocentrus	-----	-LLLVLYSVR	AAAVLPV	-----	EE	-RSPTH
6Clupea	-----	LMLVL-YSIR	AAAVLPV	-----	DE	-RSPAH
6Ictalurus	-----	LLLVL-YSVR	AAVVLPA	-----	EE	-RSPAH
6Amazon_molly	-----	LMGVL-FSVR	AAAVLPL	-----	ED	-RSPIH
6Cod	-----	LMGVL-FSVR	AAALLPV	-----	ED	-RSNFH
6Platyfish	-----	LMGVL-FSVR	AAAVLPL	-----	ED	-RSPIH
Catshark6	-----	-LSMLLIVSS	VRATAPL	-----	ED	-RLSLR
Elephant_shark6	-----	---VSGV	STTTASL	-----	DD	-RFNLQ
whale_shark6	-----	---IVSS	VKATAPL	-----	ED	-RLSLR
4Lepisosteus	-----	-FGLV-FAFC	CVSAVSN	-----	S	DL
4Zebrafish	-----	-LCLA-MMAG	IICG	-----	---	-RSHML
4Takifugu	-----	-LC-FAFC	CAENSKI	-----	EH	-RFNDL
4Medaka	-----	-LCFAVCVQ	NTEIMVE	-----	SE	-DLPAGQ
4Tetraodon	-----	-LC-FASR	CAGNSKI	-----	EH	-RLKDL
4Channel_catfish	-----	-MCLV-SAVG	VISCGRP	-----	---	-HVVLSN
4Stickleback	-----	-LCFA-FCAA	QDGETQR	-----	---	-GFKDNR
4Atlantic	-----	V-CVTLQMG	KVDSFVN	-----	ED	-KPTWLE

2Human	-GPTGRDSEH	MQEAAAGI	---	RKSSLLT	-FL	AWWFWEWS	--	QASAGPLI	--
2Mouse	-LESGETGQD	SVQEATE	---	GRSGLLT	-FL	AWWHEWAS	--	QASSSTPV	--
2Pig	-TSHDRDSEH	MQEVAEI	---	KNNSLLT	-FL	AWWHEWMS	--	QAREVPFV	--
2Bovine	---GHESGH	MQEVAEI	---	KTNSLLT	-FL	AWWYEWAS	--	QARAVPFV	--
2Monkey	-SPTGPDSEH	MQEAAAGI	---	RKSSLLT	-FL	AWWFWEWS	--	QASAGPLI	--
2Lizard	-WKHNEGSA	---	DL	GRDELLA	-FL	SGLVDRASRR	---	HGMPLSK	---
2Frog	-TGRNQDLN	---	AI	QQDLLLK	-LL	SGWTD	-SRE	SN	-LVE
2Coelacanth	-KVNRETTGF	---	GEE	RKQFLSN	-ML	DALIGL	---	NTLENDTP	---
2Lepisosteus	-SNGGLAKE	---	---	RKDVLK	-VL	SGLLV	---	NLLRKEQS	---
2Astyanax	-SKEVLTK	---	---	QKDLLIK	-IM	SDLAELNMTI	---	KDLGALDL	---
2Pygocentrus	-SNEVLTK	---	---	QKDLLIK	-IM	SDLAELNMTV	---	KDLGALDL	---
2Clupea	-RNESLADE	---	---	ERILLK	-IL	AGLTEKNL	---	ENLTGHDL	---
2Ictalurus	-SNEVLTK	---	---	QKDFMTQ	-FL	ANLAELNMTI	---	KDLETMDH	---
2Zebrafish	-TNEILSKE	---	---	EDGL	-K	MI	---	KELADLDA	---
Catshark2	-VNREMTKS	---	---	RKNLIVK	-LL	AGLLETDD	---	NLLENGFA	---
Whale_shark2	-VNREMTKS	---	---	RKYLMLK	-LL	SGLLDVDD	---	NLLENGFA	---
Elephant_shark2	-LNREMTKD	---	---	KKRLIAK	-LL	AGLLDVDD	---	NLLESVIA	---
Skate2	-LTKN	---	---	RKSLILK	-LL	AGLLDVDD	---	HLGESGYT	---
aLethenteron	-LQORVEAVL	TQELSRE	---	ERALVGR	-LL	AELAAGGAGL	---	GGALPPLGWG	---
bLethenteron	-LERVMDGLG	MENLDQD	---	QKLFLVR	-LL	AAIDSSADET	---	NELNHSDE	-G
bLampetra	-LERVMDGPG	MENLDQD	---	QKQFLVR	-LL	AAIDSSADET	---	NELNHSDE	-G
cPetromyzon	-SFRQLEAHPD	LQMGDQD	---	DSQILLN	-MI	VEAMRMRDAG	---	PETDGPGE	---
cLethenteron	-SYRQLEAHPD	LQMGDQD	---	DSQMLLN	-MI	VEAMRMRDAG	---	PETDGPGE	---
3Lepisosteus	-LQAKAAG	-LNKQDS	---	SKYAIED	-LI	SQVQSDS	---	EALNEMS	---
3Astyanax	-LQARALG	-IAAQEW	---	KKREMED	-LL	SQTLPESEF	---	QESISTL	---
3Clupea	-LQARARAAG	-MSTQEW	---	SKRAVED	-LL	SQSLPEEET	---	QDREVSTV	---
3Ictalurus	-LQRVQALG	-VAAQEW	---	TKNDLKA	-IL	AQTLPESEF	---	QENDVSTL	---
3Pygocentrus	-LQARALG	-MAAQDW	---	KKREMED	-LL	SQTLPESEF	---	QESISTL	---
3Amazon_molly	-LQARARSAG	-LLSQDW	---	SKRAVED	-LL	AQMSRSV	---	EAQQDDPE	---
3Platyfish	-LQARARSAG	-LLSQDW	---	SKRAVED	-LL	AQMSRSEV	---	EAQQDGPE	---
3Rainbow_trout	-LQARAAA	P	---	HRSGVSE	---	-RWRTFYPNC	---	PCLRPRKV	---
3Freshwater_butterfly	-VORARAAS	MGPQDQD	---	GKLSVED	-L	SLLAATEA	---	DMPFGDMS	---
3Grass_carp	-LQARARAIG	-QATQDW	---	TKKDVEE	-LL	SLLSMPEM	---	EMRENDIS	---
3Goldfish	-LQARASATG	-QATRWDF	---	TKRDVEK	-LL	SLLSIPEM	---	EMREKGLS	---
3Clown_knifefish	-LQRAHSAP	-ASPQDW	---	TRRTVED	-LL	ARLPPPEG	---	EFTPTVEDV	---
3Orange-spotted	-LQARARSAG	-LLSQEW	---	SKRAVED	-LL	AQMSLPEA	---	DTQREAEV	---
3American_anglerfish	-LQERARSAG	-LLSQEW	---	SKRAVEE	-LL	AQMSLPEA	---	DVQREAEV	---
3Silver_aronana	-LQRAHAAA	-MSPQDW	---	SKQAVEE	-LL	SRLAPAQG	---	EVPQGAVS	---
3White_sucker	-LQARARAIG	-LATQDW	---	TKKDIEE	-LL	SQSLPEI	---	EARENGVS	---
3Elephant_nose_fish	-MQRAHTAA	-MSPQDW	---	SRRVED	-LL	SRLAPPED	---	DTQSEMS	---
3Zebrafish	-LQARARAIG	-QAQEW	---	TKKDVEE	-LL	SLLSMPEM	---	QMRESLDS	---
3Stickleback	-LQARAGAG	-LLSQDW	---	SKRAVED	-LL	AQMSLPEA	---	DSQLGAEV	---
3Takifugu	-LQHVHAG	-LLSQEW	---	SKRAVED	-LI	AQMSMPEG	---	TGQRDTEV	---
3Tetraodon	-LQRAHAG	-LLSQDW	---	SKRAVED	-LI	AQMSLPEG	---	TGQRDTEV	---
3Medaka	-LQARARSAG	-LLSQDW	---	SKRAIEN	-ML	ARMPDPEA	---	EAEREAEV	---
3aAtlantic_salmon	-LQARARAAS	-IATQEW	---	SKRMED	-VL	SKLSLPDV	---	EAQKS	---
3bAtlantic_salmon	-LQARARAAG	-IATQEW	---	SKRAVED	-IL	SQSLWPEA	---	QSEVSPA	---
Elephant_shark3	-LQGSPA	---	MEL	RDGVVRE	-LI	QAVADAESKP	---	QSEAAE	---
Whale_shark3	---	---	DF	LKDTIIC	-LL	HVVADADKDA	---	VEVNASQV	---
catshark3	-LQR	-ALD	---	LKDTMMK	-LL	PLVTDVDTA	---	GTLDVSNA	---
Catshark1	-LQRAMAATG	SGGKAEL	---	TKYSLAQ	-LL	SELENAEN	---	EALETDAM	---
Whale_shark1	-LQTSMAAG	PRSKAEL	---	TKYNLVC	-LL	AELANAEN	---	EVLDGEDL	---
Elephant_shark1	-LQSLAAG	ARSKPEL	---	TKYSLAQ	-LL	AELANAEN	---	EALAEADM	---
1Human	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Mouse	-LQKSLAAA	-TGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Monkey	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Bovine	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEI	---	DALEPEDL	---
1Pig	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Dog	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Chicken	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPSQTEN	---	EALASEDL	---
1Flycatcher	-LQKSLGGG	-GGGGEL	---	AKYFLAE	-LL	SEPSQTEN	---	EALASEDL	---
1Turkey	---	---	KEL	AKYFLAE	-LL	SEPSQTEN	---	EALASEDL	---
1Anole_lizard	-LQKSLAAA	-AAGKQEL	---	AKYFLAE	-LL	SEPGQEN	---	EALPEEL	---
1Chinese_softshell_turtle	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	AEPSPQEN	---	EALPEEDL	---
1Frog	-LQKSLASA	-GKQEL	---	AKYFLAE	-LL	SEPSQTDN	---	EALSSDDL	---
1Lungfish	-LQKSLAAA	-AGKQEL	---	TKYSLAE	-LL	SELAQSEN	---	DALDSSDL	---
1Coelacanth	-LQKSLAAA	-AGKQEV	---	SKYSLAE	-LL	AELAQAEN	---	EALSSDDL	---
1Lepisosteus	-LQKSLAAS	-AGKQEL	---	ARYTLAE	-LL	SELAQSEN	---	EALSSDDL	---
1White_sturgeon	-LQRTLAAS	-AGKQEL	---	LKYSIAE	-LL	SELAQSEN	---	DALASDEL	---
1Chinese_sturgeon	-LQRTLAAS	-AGKQEL	---	LKYSIAE	-LL	SELAQSEN	---	DALASDEL	---
1Platyfish	-LHRTPLLS	---	SKQDA	SRSSLAELLL	---	SDLLQMEN	---	EALSEEDG	---
1Tilapia	-LHRTPLLG	---	SKQDM	SRSSLAELLL	---	SDLLQVEN	---	EALSEENF	---
1Elephant_nose_fish	-LQKSLAP	-ASKQDL	---	ARNPLEE	-LL	SEMVREN	---	EALPEDDL	---
1Carp	-LQKSLNLP	-AGKQEL	---	ARYTLAD	-LL	SDLVQAEN	---	EALPEEDL	---
1Goldfish	-LQKSLNLP	-AGKQEL	---	ARYTLAD	-LL	SELVQAEN	---	EALPEEDL	---
1Clown_knife_fish	-LQKSLIAP	-ASKQEL	---	ARYTLAE	-LL	SELAQVEN	---	EALSSDDL	---
1Orange-spotted_grouper	-LHRTPLLG	---	SKQDM	SRSSLAELLL	---	SDLLQVEN	---	EALSEENF	---
1Anglerfish	-LHRYPLQG	---	SKQDM	TRSLAEELLL	---	SDLLQGEN	---	EALSEENF	---

1Megalobrama	-LQ RSLNLP-	-AGKQEL---	ARYTLTD-LL	SDLVQAE--	EVLEPEDL--
1African_cichlid_fish	-LHRTPLLG-	--SKQDM---	SRSSLAE LLL	SDLLQVEN--	EALEEENF--
1Cod	-LQ RSL LAP-	MPGQEET---	VRYTLAQ-LL	SELAQAEN--	EALGTD DQ--
1Zebrafish	-LQ RSL LSP-	-AGKQEL---	ARYTLAD-LL	SDLVQAE--	EALEPEDL--
1Medaka	-LQ RTPLLG-	--SKQDM---	SRSSLAE LLL	SDLLQMEN--	EVLEEDGF--
1Stickleback	-LHRTPLLS-	--SKQDM---	SRASLVELLL	SDLLQVQN--	EALEEENL--
1Takifugu	-LQSNALMG-	--NKQEM---	TRSSLAN LLL	SDLLQVGN--	EALEENLA--
1Tetraodon	-LPPNPLLG-	--HRQEM---	SRSSLAD LLL	SDLLQVEN--	QALDENFP--
1Trout	-LQ RSL MAP-	-AGKQEL---	ARNTLVE-LL	SELAHVEN--	EAIELDDM--
1Fathead_minnow	-LQ RSL LNP-	-AGKQEL---	ARYTLAD-LL	SELVQAE--	EALEPEDL--
1Killifish	-LHRTPLLS-	--SQQDV---	SRSSLAE LLL	SDLLQMEN--	EALEEDGF--
1Salmon	-LQ RSL MAP-	-AGKQEL---	ARYTLAE-LL	SELAQAEN--	EAIESDDL--
1Pygocentrus	-LQ RSL IGP-	-SGKQEL---	ARYTLAE-LL	SELAQAEN--	EALEAEDM--
1Ictalurus	-LQ RSL IAP-	-SVKQEL---	TRYTLAE-LL	AELAQAEN--	EVLD SDEV--
1Astyanax	-LQ RSL IGS-	-AGKQEL---	ARYTLAE-LL	SELAQAEN--	EALEDDVP--
1Clupea	-LQ RSL FAP-	-GGKQEL---	ARLT LAE-LL	SELAQAEN--	EALE SEDM--
1Amazon_molly	-LHRTPLLS-	--SKQDA---	SRSSLAE LLL	SDLLQMEN--	EALEEDGF--
5Coelacanth	-FQGQGAEG-	--KEDF---	SRMLMLK-MV	SNLLKSEN--	DVLVPSAE--
5Zebrafish	QLLR SQVDPK	ENELQDL---	SRLLLLK-QL	SESVTPEEK	DALDSIDE--
5Stickleback	-MPTQRGDP-	-ADNKDL---	AYSMLLK-FV	SELTAARGGE	TLLVPEQE--
5Takifugu	-MPSEL LPAD-	PLKDKDL---	AILILLR-II	SEVMAAER--	EMLLLPQE--
5Tetraodon	-----KFLPAD	SVKDKDL---	ALVTS LK-FA	FEGTAAQR--	EMLLLLQE--
5Medaka	-LTHTKQLQL	LKSEVDP---	TRLLLLM-LV	LELVALRR--	QEMLQELE--
5Sockeyess	-LRADTTKG-	--NEDL---	SRTL LK-MM	SDLMSTAVGE	NEVL PDLE--
5Trout	-LRADSTKG-	--NEDL---	SRTL LK-MM	SDLMSAAVGE	NEVL PDLE--
5Fathead_minnow	-LLRSEVEPK	EIELQDF---	FRLLLLK-QL	SESAAPE---	EKQPRESI--
5Amazon_molly	-LTETLQAE-	LISDKDL---	TGLLLLR-FM	SELMASRG--	EEMLREKQ--
5Platyfish	-LTETLQAE-	LISDKDL---	TGLLLLR-LM	SELTASRGEE	MLREQEEE--
5Tilapia	-LRADLTND-	-----KDL---	THWLLK-FM	AELMAAR---	-----
5Lepisosteus	-LRAEVPEG-	-----KEDL---	SRML LK-IF	SDLLRAEN--	---EIPPG--
5Astyanax	-LQNEADTK-	-----ENEDI---	SRMLMLK-LL	SELEVAGEN--	EVL SGADV--
5Ictalurus	-LLAHMLQNE	ADGKEDL---	SRIL LK-LI	SELKIPDEN--	DTLSDDDM--
5Pygocentrus	-----QAD	PKGNEEL---	SRMLILK-LL	SDLEIPGD-N	EVLSGTDV--
Catshark5	-LQERNDEG-	-----TEEL---	SRTMVLN-LL	SELLHAGD--	-----
6Chicken	-NSREQTKL-	-----	RRDALLK-ML	AGLLESSD--	---VASPDL--
6Zebra_finch	-LQSTREQS-	-----TA---	RKDVILK-ML	AGLLGSVD--	AGAEVAF--
6Duck	-NSREQTKL-	-----	RKDAILK-ML	AGLLESVD--	--VASPDL--
6Lungfish	-SNRDLTRE-	-----	REEMILK-MI	SGLLDGSD--	NSLFGGEV--
6Coelacanth	-SHNNVELT-	-----KE---	RKELMLK-MI	AGLLEGID--	SPPMGGEV--
6White_sturgeon	-SNRELSKE-	-----	RKEGFLK-LL	SGLLD RVS-	SVVLGEDV--
6Chinese_sturgeon	-SNRELSKE-	-----	RKEGFLK-LL	SGLLDGVS-	SVVLGEDV--
6Lepisosteus	-TKELSKD-	-----	RKELILK-LI	SGLLDGVD--	SAMLAGDV--
6Carp	-SRELSKE-	-----	RKELILK-LI	SGLLDGVD--	NNVLAGEIAP
6Goldfish	-SRELSKE-	-----	RKELILK-LI	SGLLDGVD--	NSVLDGEIAP
6Orange-spotted_grouper	-VNRELSKE-	-----	RKELILK-LV	SGLLDGALDT	NMLPGEAA--
6Zebrafish	-SRELSKE-	-----	RKELILK-LI	SGLLDGVD--	NSVLAGEIAP
6Stickleback	-VNRELSKE-	-----	RKELILK-LV	SGLLDGAADA	NMLPGEAA--
6Takifugu	-LNRELSKE-	-----	RKELILK-LV	SGLLDGALDT	NMLPME TV--
6Tetraodon	-LNRELSKE-	-----	RKELMLK-LV	SGLLDGALDT	NMLPMEAV--
6Rainbow_smelt	-ANRELSTE-	-----	RKQLILK-LV	SGLLDGASDS	NMLPGDVS--
6Trout	-LNRELSKE-	-----	RKELILK-LV	SGLLDGATDT	NMLPGEV--
6Medaka	-VNRELSKE-	-----	RKELILK-LV	SGLLDGSLDT	NMLPGEAA--
6Fathead_minnow	-LAQSRELS-	-----KD---	RKELILK-LI	SGLLDGVD--	NSVLAGEIAQ
6Astyanax	-TKRELSKE-	-----	RKELILK-LV	SGLLDGVD--	NSVLGGDL--
6Pygocentrus	-TRELSKE-	-----	RKELILK-LI	TGLLDGVD--	SSVLAGDL--
6Clupea	-ARELSKE-	-----	RKELILK-LV	SGLLDGVE--	SNMLPGDE--
6Ictalurus	-TREPSKE-	-----	RKEMILK-MV	SSLLDGVD--	NNMLAGDL--
6Amazon_molly	-ANRELSKE-	-----	RKELILK-LV	SGLLDGALDT	NMLPGEAA--
6Cod	-SSRELSKE-	-----	RKELILK-LV	SGLLEGSPDS	NMLPGELS--
6Platyfish	-ANRELSKE-	-----	RKELILK-LV	SGLLDGALDT	NMLPGEAA--
Catshark6	-ANQELNKE-	-----	RKEVILK-LL	SGLLDSSS--	NQIAIENT--
Elephant_shark6	-SSREM NQE-	-----	RKEMILK-LL	SGLLDNAAVS	GQTGSEAG--
whale_shark6	-ANQELNKE-	-----	RKEVVLK-LL	SALLDSSS--	NQMGIENT--
4Lepisosteus	-LQKAKAAS-	-LSTRDS---	SKYALED-LI	SQIAQSDN--	EALENEMS--
4Zebrafish	-LNSALQASR	GTSADEEIP-	ERYSLSE--L	FWLLSNSD--	PAVFQPDSSS
4Takifugu	-QVQEDLLSW	LKPQEKWEPS	KRQTL ED-LL	YKLTNYKSEN	RILPQQPG--
4Medaka	GLLSSFDR I-	SDFQQSV---	ETGILMN-LL	YKLSRPDSAI	TLQQVRDS--
4Tetraodon	-QVEEDVL PW-	LNSQEKWEPS	KGQNL ED-LL	YKLTNYRSEN	RIVSQQPS--
4Channel_catfish	-ALEEARNVP-	-FGEEVP---	ERLTLP E--L	QWMLSN----	NELTPVQV--
4Stickleback	-LQ RDSL PWL-	DKLQDEQDST	KKLN LIE-WL	YSFYKFDNG-	NIVKGPTD--
4Atlantic	TLQDKQVSA-	-----AD---	DKYNLVW-LL	YKLSQSHHD-	NTFKINFPPH

2Human	---	GEEARE	VARR	-QEG	---	APPOQS	---	ARRDRM	PCRNFFWKTF
2Mouse	---	GGGTPG	LSKS	-QER	---	PPPQQP	---	PHLDKK	PCKNFFWKTF
2Pig	---	GGETRE	MPKK	-QEG	---	LPRQQA	---	SRGDRT	PCGNFFWKTF
2Bovine	---	GGEARE	VSKR	-QEG	---	APLHQS	---	TRQDKT	PCKNFFWKTF
2Monkey	---	GEEARE	VARR	-QEG	---	APPOQS	---	ARRDRT	PCKNFFWKTF
2Lizard	QEKVVRSPRE	ERVP	-FFR	---	---	H	---	PVREKA	PCKNFFWKTF
2Frog	VERNVPDPPE	PKIPP	-SVK	---	FPRL	S	---	LRERKA	PCKNFFWKTF
2Coelacanth	LLGTKEQEE	HNLS	-ER	---	SAFKY	---	SSLKKA	PCRNFFWKTF	
2Lepisosteus	AVDSEQ	LKSSLMGER	---	SVFGPSVS	---	---	RERT	PCKNFFWKTF	
2Astyanax	EQLLN	GKLG	-ER	---	---	---	SVEKS	PCTNFFWKTF	
2Pygocentrus	EQLLS	GKLG	-ER	---	SVFGL	---	PAQEKs	PCKNFFWKTF	
2Clupea	EGLLN	GTLK	---	---	GGSVP	---	TPQERS	PCKNFFWKTF	
2Ictalurus	EQL-S	-KLS	-ER	---	AAFG-LP	---	PAREKS	QCN-FFWKTF	
2Zebrafish	E-LLN	GKLW	-EK	---	SDK	---	PSKDKS	PCKLFFWKTF	
Catshark2	PLKPEEAEG	TLFE	-ER	---	SVNAGIP	---	RREQKT	PCKLFFWKTF	
Whale_shark2	SLSPGEE	SSLE	-ER	---	SVNAGIP	---	RRPKA	PCKLFFWKTF	
Elephant_shark2	PLGLSKEEG	TDFE	-ER	---	SAAGEIP	---	PRKPKA	GCKLFFWKTF	
Skate2	YSNTEEAGE	RSLE	-ER	---	AVVAVIP	---	RREQKA	PCKLFFWKTF	
aLethenteron	PGSSSDEEGG	EEGE	-GAGG	DGGRGERALS	---	ARVRKA	GCKNFFWKTF		
bLethenteron	SLPEALVARA	LRAA	-AAPG	AAGGAQLPLG	---	NRERKA	GCKNFFWKTF		
bLampetra	SLPEVLVARA	LRAA	-AAPG	AAGGAQLPLG	---	NRERKA	GCKNFFWKTF		
cPetromyzon	ATRVVDGLPE	FPRE	-EARA	LVPNERPFVP	GALS	SPDRKA	NCRMFWKTM		
cLethenteron	AARVVDGLPE	FPRE	-EVRA	LGPNERPFVP	VVLS	SPDRKA	NCRMFWKTM		
3Lepisosteus	VLDENS	ARLE	-LER	STEIGKEIP	---	PRERKA	GCRNFWKTF		
3Astyanax	GSKQD	VRVE	-MDR	SAENPNSLP	---	PRERKA	GCKNFWKGF		
3Clupea	GAAKDD	LHME	---	RSAETINNIP	---	PKDRKS	GCKNFFWKGR		
3Ictalurus	GTKQD	LTVE	-LER	SAEDPNTLP	---	PRERKA	GCKNFWKGF		
3Pygocentrus	GAKHD	VRVE	-LER	SAENPNNLP	---	PRERKA	GCKNFWKGF		
3Amazon_molly	AASKGTD	SRLN	-LER	SVETT	---	ARERKA	GCKNFWKGL		
3Platyfish	AASRGTTG	SRLN	-LER	SVETT	---	ARERKA	GCKNFWKGL		
3Rainbow_trout	KCPAGAKED	LRVE	-LER	SVGNPNNLP	---	PRERKA	GCKNFWKGF		
3Freshwater_butterfly	AAEESEG	AHLD	-LER	SVEPGNVP	---	PRERKA	GCKNFWKGF		
3Grass_carp	TVDENED	LRVE	-LER	SAESSNHIP	---	ARERKA	GCKNFWKGF		
3Goldfish	MAGESED	LRLE	-QER	SAESSNQLP	---	TRVRKE	GCKNFWKGF		
3Clown_knifefish	PAADEGEE	VRVE	-LER	SVDPNNLP	---	PRERKA	GCKNFWKGF		
3Orange-spotted	VSMATG	GRMN	-LER	SVDPPNNLP	---	PRERKA	GCKNFWKGF		
3American_anglerfish	ASMATG	GRMN	-LER	SVDSTNNLP	---	PRERKA	GCKNFWKGF		
3Silver_aronana	AADEEED	VRVD	-LER	SLELNNLP	---	PRERKA	GCKNFWKGF		
3White_sucker	TTGGNDD	LHLE	-LER	SAENTNQLY	---	PRERKA	GCKNFWKGF		
3Elephant_nose_fish	TAEEGEE	TRVE	-LER	SVEPNNLP	---	PRERKA	GCKNFWKGF		
3Zebrafish	TTDENED	LRVE	-LER	SAESSNHIP	---	ARERKA	GCKNFWKGF		
3Stickleback	VSAATG	GRLH	-LER	SVDPPNNLP	---	ARERKA	GCKNFWKGF		
3Takifugu	VSMATG	GRMN	-LER	SVDTTNNLS	---	PPERKA	GCKNFWKGP		
3Tetraodon	VSMATG	GRMN	-LER	SVDTTNNLP	---	PR-KA	GCKNFWKGF		
3Medaka	---	GRNN	-MER	SVDANVP	---	PRNRKD	GCKNFWKGF		
3aAtlantic_salmon	VGSTAD	AKED	-LER	SVDNSNNLP	---	PRERKA	GCKNFWKGF		
3bAtlantic_salmon	GAKED	LRVE	-LER	SVGNPNNLP	---	PRERKA	GCKNFWKGF		
Elephant_shark3	DFAPD	EKAE	-LRL	A- LA	---	PRWRK	DCKNFFWKTY		
Whale_shark3	ETPPX	NKIP	-MKF	Q- QROLG	---	TRMRK	NCKNFFWKTY		
catshark3	ETSEE	NTTP	-MKF	QH- RQLG	---	MRMRK	NCKNFFWKTY		
Catshark1	GGRNE	VRLE	-LER	SINPNLA	---	NRERKA	GCKNFFWKTF		
Whale_shark1	PRMAKQDE	VRVD	-LER	SANPNSP	---	QERKA	GCKNFFWKTF		
Elephant_shark1	ARATAQDE	VRVE	-LER	SANPNLA	---	QERKA	GCKSFFWKTF		
1Human	SQAAEQDE	MRLE	-LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Mouse	PQAAEQDE	MRLE	-LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Monkey	SQAAEQDE	MRLE	-LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Bovine	SQAAEQDE	MRLE	-LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Pig	SQAAEQDE	MRLE	-LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Dog	SQAAEQDE	MRLE	-LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Chicken	SRGAEQDE	VRLE	-LER	SANSNPALA	---	PRERKA	GCKNFFWKTF		
1Flycatcher	SRGAEQDE	VRLE	-LER	SANSNPALA	---	PRERKA	GCKNFFWKTF		
1Turkey	SRGAEQDE	VRLE	-LER	SANSNPALA	---	PRERKA	GCKNFFWKTF		
1Anole_lizard	SRGGGAEQDE	VRLE	-LER	SASLNPAL	---	PRVRKA	GCKNFFWKTF		
1Chinese_softshell_turtle	SRGPEQDE	VRLE	-LER	SANPNPALA	---	PRERKA	GCKNFFWKTF		
1Frog	PRGAEQDE	VRLE	-LER	SANSSPALA	---	PRERKA	GCKNFFWKTF		
1Lungfish	SRGADQDE	VRLE	-LDR	SANSSPLA	---	ARERKA	GCKNFFWKTF		
1Coelacanth	SKTSDQDE	VRLE	-LER	SANGNPALA	---	PRERKA	GCKNFFWKTF		
1Lepisosteus	SRAAEQDE	VRLE	-LER	SANPALA	---	PRERKA	GCKNFFWKTF		
1White_sturgeon	SRAAEQND	VRLE	-LER	SANGNPAMA	---	PRERKA	GCKNFFWKTF		
1Chinese_sturgeon	SRAAEQND	VRLE	-LER	SANGNPAMA	---	PRERKA	GCKNFFWKTF		
1Platyfish	PEGEPE	IRVD	-LER	AASSGPLL	---	PRERKA	GCKNFFWKTF		
1Tilapia	PLADGEPED	IRVD	-LER	AAGSGPLLA	---	PRERKA	GCKNFFWKTF		
1Elephant_nose_fish	SRGADQEE	VRLE	-LER	AAGPALA	---	PRERKA	GCKNFFWKTF		
1Carp	SRAVEKDD	VRLE	-LER	AAGPMLA	---	PRERKA	GCKNFFWKTF		
1Goldfish	SRAVEKDE	VRLE	-LER	AAGPMLA	---	PRERKA	GCKNFFWKTF		
1Clown_knife_fish	SRGADQEE	VRLE	-LER	AAGPPLA	---	PRERKA	GCKNFFWKTF		
1Orange-spotted_grouper	PLAEGEPED	VHVD	-LERA	AAAGSGPLLA	---	PRERKA	GCKNFFWKTF		
1Anglerfish	PLAEGGPED	AHAD	-LER	AAAGSGPLLA	---	PRERKA	GCKNFFWKTF		

1Megalobrama	-SRAVEKDE	VRLE	-LER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF	
1African_cichlid_fish	-PLADGEPED	IRVD	-LER	---	AAGSGPLLA	----	PRERKA	GCKNFFWKTF	
1Cod	-----	DD	ERMD	-LER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF
1Zebrafish	-SRGAEKDD	VRLE	-LER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF	
1Medaka	-PLSDGEPED	VRVD	-LER	---	AAASGPLLA	----	PRDRKA	GCKNFFWKTF	
1Stickleback	-APAGEPEE	VHLD	-LER	---	AADAGPLL	----	PRERKA	GCKNFFWKTF	
1Takifugu	-LAEGEPEE	VHID	-MERA	---	AAAGIGPFLT	----	PRERKA	GCKNFFWKTF	
1Tetraodon	-LVEGEPEE	VHVD	-MERA	---	ADAGIGPFLT	----	PRERKA	GCKNFFWKTF	
1Trout	-SHGVEQED	VDLE	-LER	---	APGPVLA	----	PRERKA	GCKNFFWKTF	
1Fathead_minnow	-SRAVEKDD	VRLE	-LER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF	
1Killifish	-TLPEGEPEE	IRVD	-LER	---	AASSGPLLA	----	PRERKA	GCKNFFWKTF	
1Salmon	-SRGVEQED	VRLE	-LER	---	AAGPVLA	----	PRERKA	GCKNFFWKTF	
1Pygocentrus	-PRGAEQED	VRME	-LER	---	AAGPVLA	----	PRERKA	GCKNFFWKTF	
1Ictalurus	-SRAAESEG	ARLE	-MER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF	
1Astyanax	-RGAEQED	VRME	-LER	---	AAGPVLA	----	PRERKA	GCKNFFWKTF	
1Clupea	-SRGAEGED	VRYE	-LER	---	SAGSMLA	----	PRERKA	GCKNFFWKTF	
1Amazon_molly	-GLPEGEPEE	IRVD	-LER	---	AASSGPLLA	----	PRERKA	GCKNFFWKTF	
5Coelacanth	-DTASQDE	LTRR	-LAP	-----	-----	-----	SERKA	GCKNFFWKTF	
5Zebrafish	-----	LD	VRNE	-VVR	-----	QIPVS	-----	QERKA	GCRNFFWKTF
5Stickleback	-----	EEEEAG	GRQE	-VMR	-----	RHLPLT	-----	QERKA	GCRNFFWKTF
5Takifugu	-----	GEEEAG	VREGEVMMR	-----	-----	ROVPFS	-----	QRDRKA	GCRNFFWKTF
5Tetraodon	-----	DEEDAG	VREMMMMR	-----	-----	ROIPFS	-----	QERKA	GCRNFFWKS
5Medaka	-----	EEELG	GRER	-LMK	-----	RHIRFT	-----	QERKA	GCRNFFWKTF
5Sockeyess	-----	EALG	VREE	-VVR	-----	QLPLS	-----	HRERKA	GCRNFFWKTF
5Trout	-----	EALG	VREE	-----	-----	VRQLPLS	-----	HRERKA	GCRNFFWKTF
5Fathead_minnow	-----	DDDP	VHNE	-VVR	-----	QIPLS	-----	HRERKA	GCRNFFWKTF
5Amazon_molly	-----	EEEEEEELG	GRQR	-LMR	-----	RHIRFS	-----	HRERKA	GCRNFFWKTF
5Platyfish	-----	EEDELG	GRQR	-LMR	-----	RHIRFT	-----	HRERKA	GCRNFFWKTF
5Tilapia	-----	GDETRR	GRE	-VTR	-----	RHLSLS	-----	QERKA	GCRNFFWKTF
5Lepisosteus	-----	SAEDAG	IRSD	-VPR	-----	QLPLA	-----	QERKA	GCRNFFWKTF
5Astyanax	-----	-----	RND	-VVR	-----	QLPFS	-----	QERKA	GCRNFFWKTF
5Ictalurus	-----	-----	E	-LNR	-----	ILRHLPLT	-----	TRERKA	GCRNFFWKTF
5Pygocentrus	-----	-----	RSD	-MVR	-----	QLPFP	-----	QERKA	GCRNFFWKTF
Catshark5	-----	KGLPST	ERRG	-LPC	-----	AEIVRRWNS	-----	PRDRKA	GCKNFFWKTF
6Chicken	-----	EEE	GKLE	-EER	-----	AALGRLAQLS	-----	QRDRKA	PCKNFFWKTF
6Zebra_finch	-----	AGQEK	ARLE	-EDQ	-----	AALGRLAQLS	-----	QRDRKA	PCKNFFWKTF
6Duck	-----	EEE	GKLE	-EER	-----	ATLGRLAQLS	-----	QRDRKA	PCKNFFWKTF
6Lungfish	-----	TSMDIEEPLE	NKLE	-ER	-----	AAYNALPQLP	-----	QRDRKA	PCKNFFWKTF
6Coelacanth	-----	GSMDLPEEPVE	PKLE	-ER	-----	AAFNRLLPQLP	-----	QRDRKA	PCKNFFWKTF
6White_sturgeon	-----	SPMDLEEPLE	SRLE	-ER	-----	AIYNRLSQLP	-----	LRARKA	PCKNFFWKTF
6Chinese_sturgeon	-----	SPMDLEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRARKA	PCKNFFWKTF
6Lepisosteus	-----	ASVDLEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Carp	-----	VPLDVEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Goldfish	-----	VPFDAEPEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Orange-spotted_grouper	-----	PVDLEEPLE	SRLE	-ER	-----	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF
6Zebrafish	-----	VPLDVEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Stickleback	-----	PVDFEPEEPLE	SRLE	-ER	-----	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF
6Takifugu	-----	DLEEPLE	SRLE	-ER	-----	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF
6Tetraodon	-----	DLEEPLE	SRLE	-ER	-----	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF
6Rainbow_smelt	-----	PLDLEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Trout	-----	SPVDLEEPLE	SRLE	-ER	-----	AAYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Medaka	-----	PVDFEPEEPLE	SRLE	-ER	-----	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF
6Fathead_minnow	-----	VPMDAEPEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Astyanax	-----	VPMEAEPEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Pygocentrus	-----	VNMEVEPEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Clupea	-----	APLDLEEPLE	SRLE	-ER	-----	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF
6Ictalurus	-----	LPLEEEEEPID	SRLE	-ER	-----	AVYNRLAQLP	-----	QRDRKA	PCKNFFWKTF
6Amazon_molly	-----	PVDLEEPLE	SRLE	-ER	-----	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF
6Cod	-----	PVELEEPLE	SRLE	-ER	-----	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF
6Platyfish	-----	PVDLEEPLE	SRLE	-ER	-----	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF
Catshark6	-----	FDPDPEDVEE	MKVE	-ER	-----	SRFSQLP	-----	QERKA	PCKNFFWKTF
Elephant_shark6	-----	YPEPADGGP	VMLE	-ER	-----	SRYSQLP	-----	QSRKV	PCKNFFWKTF
whale_shark6	-----	FDPQEDMEE	MKVE	-DR	-----	SRFSQLP	-----	QERKA	PCKNFFWKTF
4Lepisosteus	-----	VLDENSD	ARLE	-LER	-----	SADMGKVIP	-----	PRERKA	GCRNFFWKTF
4Zebrafish	-----	LGLSLHSGLEL	MRRD	-----	-----	T	-----	KEERKA	GCRNFFWKTF
4Takifugu	-----	DTNQEK	NRRD	-LDN	-----	LR	-----	VQQRQF	GCRNFFWKTF
4Medaka	-----	EKQEK	NRRG	-VEI	-----	ATQR	-----	ATQR	GCRNFFWKTF
4Tetraodon	-----	DTNQEK	NRRG	-LDN	-----	LK	-----	VQQRQA	GCRNFFWKTF
4Channel_catfish	-----	EEAPR	SRLE	-LVRR	-----	DNTVTSKPLN	-----	-----	GCRNFFWKTF
4Stickleback	-----	AEEPEK	NRRG	-----	-----	LG	-----	KTTRRF	GCRNFFWKTF
4Atlantic	-----	GPESVGKPE	RRET	-IPQ	-----	D	-----	SRVRKE	GCKVFFWKTF

2Human	SSCK--
2Mouse	SSCK--
2Pig	SSCK--
2Bovine	SSCK--
2Monkey	SSCK--
2Lizard	SSC--
2Frog	TMC--
2Coelacanth	SSC--
2Lepisosteus	SSC--
2Astyanax	SAC--
2Pygocentrus	SACQH
2Clupea	SSC--
2Ictalurus	SSC--
2Zebrafish	SSC--
Catshark2	SHC--
Whale_shark2	SHC--
Elephant_shark2	SHC--
Skate2	SHC--
aLethenteron	TSC--
bLethenteron	SSC--
bLampetra	SSCX--
cPetromyzon	AAC--
cLethenteron	AAC--
3Lepisosteus	TSC--
3Astyanax	TSC--
3Clupea	TSC--
3Ictalurus	TSC--
3Pygocentrus	TSC--
3Amazon_molly	TSC--
3Platyfish	TSC--
3Rainbow_trout	TSC--
3Freshwater_butterfly	TSC--
3Grass_carp	TSC--
3Goldfish	TSC--
3Clown_knifefish	TSC--
3Orange-spotted	TSC--
3American_anglerfish	TSC--
3Silver_aronana	TSC--
3White_sucker	TSC--
3Elephant_nose_fish	TSC--
3Zebrafish	TSC--
3Stickleback	TSC--
3Takifugu	TSC--
3Tetraodon	TSC--
3Medaka	TSC--
3aAtlantic_salmon	TSC--
3bAtlantic_salmon	TSC--
Elephant_shark3	TLC--
Whale_shark3	TLC--
catshark3	TLC--
Catshark1	TSC--
Whale_shark1	TSC--
Elephant_shark1	TSC--
1Human	TSC--
1Mouse	TSC--
1Monkey	TSC--
1Bovine	TSC--
1Pig	TSC--
1Dog	TSC--
1Chicken	TSC--
1Flycatcher	TSC--
1Turkey	TSC--
1Anole_lizard	TSC--
1Chinese_softshell_turtle	TSC--
1Frog	TSC--
1Lungfish	TSC--
1Coelacanth	TSC--
1Lepisosteus	TSC--
1White_sturgeon	TSC--
1Chinese_sturgeon	TSC--
1Platyfish	TSC--
1Tilapia	TSC--
1Elephant_nose_fish	TSC--
1Carp	TSC--
1Goldfish	TSC--
1Clown_knife_fish	TSC--
1Orange-spotted_grouper	TSC--
1Anglerfish	TSC--

1Megalobrama	TSC	--
1African_cichlid_fish	TSC	--
1Cod	TSC	--
1Zebrafish	TSC	--
1Medaka	TSC	--
1Stickleback	TSC	--
1Takifugu	TSC	--
1Tetraodon	TSC	--
1Trout	TSC	--
1Fathead_minnow	TSC	--
1Killifish	TSC	--
1Salmon	TSC	--
1Pygocentrus	TSC	--
1Ictalurus	TSC	--
1Astyanax	TSC	--
1Clupea	TSC	--
1Amazon_molly	TSC	--
5Coelacanth	TSC	--
5Zebrafish	TSC	--
5Stickleback	TSC	--
5Takifugu	TSC	--
5Tetraodon	TSC	--
5Medaka	TSC	--
5Sockeyess	TSC	--
5Trout	TSC	--
5Fathead_minnow	TSC	--
5Amazon_molly	TSC	--
5Platyfish	TSC	--
5Tilapia	TSC	--
5Lepisosteus	TSC	--
5Astyanax	TSC	--
5Ictalurus	TSC	--
5Pygocentrus	TSC	--
Catshark5	TSC	--
6Chicken	TSC	--
6Zebra_finch	TSC	--
6Duck	TSC	--
6Lungfish	TSC	--
6Coelacanth	TSC	--
6White_sturgeon	TSC	--
6Chinese_sturgeon	TSC	--
6Lepisosteus	TSC	--
6Carp	TSC	--
6Goldfish	TSC	--
6Orange-spotted_grouper	TSC	--
6Zebrafish	TSC	--
6Stickleback	TSC	--
6Takifugu	TSC	--
6Tetraodon	TSC	--
6Rainbow_smelt	TSC	--
6Trout	TSC	--
6Medaka	TSC	--
6Fathead_minnow	TSC	--
6Astyanax	TSC	--
6Pygocentrus	TSC	--
6Clupea	TSC	--
6Ictalurus	TSC	--
6Amazon_molly	TSC	--
6Cod	TSC	--
6Platyfish	TSC	--
Catshark6	TSC	--
Elephant_shark6	TSC	--
whale_shark6	TSC	--
4Lepisosteus	TSC	--
4Zebrafish	TAC	--
4Takifugu	TYC	--
4Medaka	AKC	--
4Tetraodon	TSC	--
4Channel_catfish	TAC	--
4Stickleback	SPC	--
4Atlantic	TAC	--

Figure S3

A. Catshark SST1 (SSTa)

gctgtccacagagccagtgtctgaaaccaccgccaatcttcaaagcgtttgtaa
atgtggtgcagccgccttcagttgagcctggctctcctctccatcgccctggcagtagt
M W C S R L Q L S L A L L S I A L A V L
agtgtcagctcagcaccacagacaacaggtatcgcgaaatcctgcagagagccatggca
S V S S A P T D N R Y R E I L Q R A M A
gccacaggaagcggagggaaagcggagttgacgaaatattccctcgcccaactgctctcc
A T G S G G K A E L T K Y S L A Q L L S
gaactggaaaacgcggagaatgaagctctggaaacggatgcaatggcgagcgaacgag
E L E N A E N E A L E T D A M G G R N E
gtgcggctcgaactggagagatcgataaatcccaacctggcgaaacagggagcgaaaagcg
V R L E L E R S I N P N L A N R E R K A
ggatgtaagaacttcttttggaaaaccttcacatcctgttaactctccgaattctccata
G C K N F F W K T F T S C -
gcaaccacacactcagaatgtggcattcagataactaaataaatcatgtggtgaatgat
tctatttgaattatgtaagagaagacaattgggttgaattgtccaatagcaggccagttt
gaatggtgactggatagagtcgctatttttcttaaatctgttgcaataaaatctctgttt
gaaattg

B. Catshark SST2 (SSTd)

tttagcattttgtccaggagtgtctcgaagattcagc
atgaagtggctaattgacagtgagcctgatgtctctgtctgtaccttctgagagtcgaggggt
M K W L M T V S L M S L L Y L L R V E G
actgacctactggaagaaagaatgaaacttcaggtaaacagagaaatgacaaaaagcagg
T D L L E E R M K L Q V N R E M T K S R
aagaatctgattgtaaagctactggctggcttggaggagactgatgataatctcttggag
K N L I V K L L A G L L E T D D N L L E
aatggctttgcacctttgaaaccagaagaggcagaagggactttgttcgaagagaggtcg
N G F A P L K P E E A E G T L F E E R S
gttaacgctggaattccacgcagggagcaaaaaaccccatgcaaactgttcttctggaaa
V N A G I P R R E Q K T P C K L F F W K
accttttccactgttaataaccgtgttagcggatttttctaaagcagtgaggagtatgaaa
T F S H C -
gaaaaatgggtgtaaaggcttaacttttaaaactatcgaaaatacactgcaatcatgtttt
tctctatcccaaataatttaattcaaatttacaggaaatgcttgcaataaagttaacctga
aagttacaccttttaagacatgtgaaattattgtgttttaaatgagatagcaatccagtt
aaactttctcagtttcttatcatgcctgttatttccctgttttccagcattgtttt
cttctctcagttcctcgctttcctttggcatgttagccccctctcttcccacagaatgct
cctgggattccgtactctccccctcgctttacctttccctcttctcgctagacgaatgttt
ctgaaagattgcacctgccccctgacacagccggctgggacttctggaagcacttgaattt
tgccagacacaatttgggatattttctgagttaaagcctatatatatgttgacagtgacc
tttctcttgatcgtagatctgagcatattgtaatgggtgttaattgttttgaccagttct
atctgcatacaatgtacatacttatctcgaaatatcctgtgagtaatgctaacaataaaa
agaca

C. Catshark SST3 (SSTe)

acatgg
ggagagacagtgctgaaacgcctctccactttccgtcggttcttctgccttgtgcagag
atgtggtgcagccgccttcagttgagcctggctctcctctccatcgccctggcagtagt
M W C S R L Q L S L A L L S I A L A V L
agtgtcagctcagccccacagacaacaggcatcgcgaaatcctgcagagagccttggat
S V S S A P T D N R H R E I L Q R A L D
caggaacttctgaaggacacaatgatgaaactgttgcccttgggttactgatgtagacact
Q E L L K D T M M K L L P L V T D V D T
gaggccggaacactggatgtttccaatgctgagacttcagaagaaaacacaacaccgatg
E A G T L D V S N A E T S E E N T T P M
aaattccagcatcgtagttgggaatgagaatgcggaaaaactgcaagaacttcttttgg
K F Q H R Q L G M R M R K N C K N F F W

aaaacctacacttttatgctaatccactgtacccagtgagcccttctcactggaccctgct
K T Y T L C -
gtacccac

D. Catshark SST5 (SSTb)

tcgaccctcgcgctccggagcagttacacagagaagctcgccctctgcccacactgcccga
cgagacagtttgccaatcgttcccatctcccactccgcagtaagaaaatcagagctcgag
atgccgagatcgagactcaagtcctcctcactctgggtcactgtcgctctgctgttactg
M P R S Q T Q V L L T L V T V A L L L L
cggggatcgagtacagccagagtgcaggggctgccgatatcttacaggagaggaacgac
R G S S T A R V Q G L P D I L Q E R N D
gaggggactgaggagctgtccaggaccatgggtgctgaacctcctctccgagctgctccat
E G T E E L S R T M V L N L L S E L L H
gctggggacaaggggttgcccagcaccgagagacgggagcttccccaggtgagatcgtc
A G D K G L P S T E R R E L P Q A E I V
cgccggtggaactcaccgcgggaccgcaaagcaggctgcaagaacttcttttgaaaacc
R R W N S P R D R K A G C K N F F W K T
ttcacctcttgtaacgtgcgagagagagaggggaaagagaaagtgagccggcgggggga
F T S C -
gagatataaagagaattcctccctctcccaaaaccatcttcagctcctgaaggaggca
aaaaaaaaatcaattgcctctaactttagattttaagattcacaaatcccaaccacctcc
gtccctcgaaagattgcctccccctttgggctgcctctccgctgaggatttctctgtgtc
tttatccaaggtgtttgtaaattgattgacttgtttgctttgttctctgagcatggacttg
ctctcacatcataaaatatctttatttctcagcaaaaaaaaaaaaaaaaa

E. Catshark SST6 (SSTc)

tcgaccctcgcgctccgccaaggctcgaggcaca
ttgagaagatctcgccaggctccgcttcattccaacttcacaagatcgagagtgtcagc
atgcagttgctgggaacggcgagcctcctgtccatgctgctcatcggtgtccagtgtgagg
M Q L L G T A S L L S M L L I V S S V R
gccacggcaccttttgaagatcggtgtgagtctgcgggcaaatacaggagctgaacaaagaa
A T A P L E D R L S L R A N Q E L N K E
aggaaagagggtcattttgaagctgttatccggactgcttgactccagcagcaatcaaatac
R K E V I L K L L S G L L D S S S N Q I
gcgattgagaacactttcccgatccagaggatgtggaggagatgaaagtggaggagagg
A I E N T F P D P E D V E E M K V E E R
tcccgttccagccagttaccgcagagagagcgcaaggctccctgcaaaaacttcttttgg
S R F S Q L P Q R E R K A P C K N F F W
aaaaccttcacctcctgctgacgacagacaatgccacctggctgccactaaagccgccg
K T F T S C -
agaaaggaactgatttagcactgtacataagctgctttttattttattcatctgtgaggg
gtggtggagggtggggggggggttaatatcttctgtcgtgcacaagaaaaataaaaagagc
atgattgtgtgatttcaccgcaacctgtatgtattttattttcttccagtaatgttgtc
gcgctcaacctgccagagcaataaagtggatccgagataaaaaaaaaaaaaa

Figure S4

A. Catshark SST1 = SSa (scaffold122178)

AACAGAAGTAAAATGATACCTGGTCCCAGTGTGTAAATCTGTAACAGCCCCATTTCTGTGGCATTTC AAT
GAAAAGCTAGTTTAAACCTGACGAATACAGTGGAGTTATTGAGATGAACACATTGCAGATTGGCACATGT
GGGCCACAAAGAGAACACGCTGTAAAATCACAACTACACACAATTATTGAGATGGCAGCGAGTCTTTC
CCCAGGAAACATTTCCTTTATTCTGTCTCACTCAGTCTCTAACTTTGTACATTGAGTTCACTGGGATTACC
CAACCCATTCCCCACTGATCCAGTGTGTTCAATGCTCAAGGAAGATTGAGATTTATGGATGAGGGTGTTT
ACTGGGGATTGATGTTCACTTTTTCCACGGATTTTCTAGTTGAAGACTTGGCTGCATTTCATTTTGTGATC
GACACGAACCAATACAATCGTAGGGCCAGCTGCCAACACGCGATAGGGTGTCCACATTGAGACTCCATGG
ATCTATCTCAATCTTCCTCATGGGTAATGGGTTGGTTGAGGATGTGACTGGGTTGTGCGTAAATACTCGT
CATCTCCTGGGACCCTCCTCCCAACGTGTGAGCTGGTGTGAAGGCGGCTTTAAAAGGAGCTTCCCCGATT
GCAGGGACAGAAGGAGCGGAGCTGTCCACAGAGCCAGTGTGAAACCACCGCCAATTTCAAAGCGTTTGG
AAACTGCTCTCCTTCTCGCTGTCTCTCCCGTTGATCTTCGCTTGTGCAGAGATGTTGGTGCAGCCGCTT
M W C S R L
CAGTTGAGCCTGGCTCTCCTCTCCATCGCCCTGGCAGTACTGAGTGTGAGCTCAGCACCCACAGACAACA
Q L S L A L L S I A L A V L S V S S A P T D N
GGTATCGCGAAATCCTGCAGAGAGCCATGGCAGCCACAGGAAGCGGAGGGAAAGCGCTAAGGACCCAGCA
R Y R E I L Q R A M A A T G S G G K A
AAAAGTCACATTCAATAGAAATGGTAGTTTGTGTTTCATCCCGTTCACCTCGAATAGAAACAGGGACTGGG
AAATAACTGGTTCAATTCTGATCTAGTGAGAAGACCCACTTTTAACAGGACTATAATATTGAGAGTGAAT
TGGCTTTGTTTAGTGTGGGGATCATTTTCATTGGTTTAGAAAGGTTTCTGAGCGCGTTGATCCAAATTAC
TGGATTTCTCGTGCATCGAGTAAAATCTCGTCCTCTCCAATCCATAGCCACTCTGCACAAAGAGTAACAG
ACAAGAAGTAGACATCGTTCCACAATCCCAGAGAACTTACTGCTCTTCTCTCTTCCCAAACCTGCCTCTCC
CATCTTAACCCCAACCCCTCCTCTCTCCCCAAATCCCGTCTCCCATCCCAACCCCAACCCCTCCTCTCTCC
CAAATCCCCTCTCCTGTCCCAACCCCAACCCCTCCTCTCTCCCCAAGCTCCCAACCCCCCTCTCCCATCC
CAACCCCAATCCCCCTTTCTCCCCAAACCCCCCTCTCCCCACCCCAACCCCAACCCCTCTCTCTCCCCAAAC
CCTCTCTCCCCACCCCAACCCCAACCCCTCCTCTCTCCCCACCCCTGGGACTCTGACCAAGGCTCAT
TTGGTCCTGTTTATCATTTGAAGACGAGCACCTGAGTCTCTCTCAGTCACCTCCAATAACCATCTAGAAT
GGGGCAGCTGAATCAAATCTTGCAACCAAGTCATTTCAGTTTGAAAGAAATATTCATTACAATTATGTTTT
CAATTGCCTTCATGTTGAAAAGAACTCCGAGCACGGGGATTGGTTCTTCCAGAGATTTTCTCGCTCTT
TCCAATGTCCACCTCCCTTTGAAGGGTTCAGAATTGTGGTGGATGGAATGGAGTTTCGGGGTGGAGTGGGA
GGGGGTTTGGGCAGTTCAGGTCTCTATTTGCGAATTGGGATCTTCCCGCCGGTTGCAATGGAGAAATAT
GAAGATAAATGAAGATAATTTACAAAGTTGAATTTAATTCATTGTAGATTTATTTCGGGGAGTTTGCAA
CTTTTCGTTTGCAAAACAAACGTAAATATAGCGTCAATTGGCGGAAATTTCTCCCCTAATCTATTTCCTGT
TGTTCTCAGGAGTTGACGAAATATTCCTCGCCCCAAGTCTCTCCGAACTGGAAAACCGCGGAGAATGAAG
E L T K Y S L A Q L L S E L E N A E N
CTCTGGAACGGATGCAATGGGCGGACGCAACGAGGTGCGGCTCGAACC GGAGAGATCGAGAAATCCCAA
E A L E T D A M G G R N E V R L E P E R S N P N
CCTGCCGAACAGGGAGCGAAAAGCGGGATGTAAGAACTTATTTTGGAAAACCTTCACATCCTGTAACTC
L P N R E R K A G C K N L F W K T F T S C -
TCCGAATTCTCCATAGCAACCCACACACTCAGAATGTGGCATTTCAGATAACTAAATAAATCATGTGGTGA
ATGATTCTATTTGAATTATGTAAGAGAAGACAATTGGTTTGAATTGTCCAATAGCAGGCCAGTTTGAATG
GTGACTGGATAGAGTCGCTATTTTTTCAATTAATCTGTTGCAATAAAATCTCTGTTTGAAAGTGGACCATTT
GTTGGATTTTGTCTCTGGGAGATGGGGCAATATAACAAGGGACAGAATTAACCTCGGCTAGTTTCAACA
CCAGTCTGTGTCCAAAGGTACAGAGCGAGGGGAGTCATTTTCCACAGTTGTGACTTTGTAAATCAGCTCT
GGGTGGAATCGCTCTGGGTCACTGTCTCTGATCTGGAATGTGTTGCTGGAAGTTCCCTCCGCGTATTCA
AACTCAGAGGAGACAATGAATGGACGGATATTAAAGGGGGTTCTGCTCTGTCCAATGCAACCGTGCTCTG
TGAGTGCTGTAATCTGCAGGAGAGCAAACTATTACCTGCATCACACTGGTAAAAGTCTAACCCCTGGTCA
ATGAAAGCATCAATCCACAAATCACAAACCTGCTTCCAGCCTTCCCTTGTAAGCCGGTTTCCATTCTAA
CCTAGCGGCACGGTAGCACAGTGGTTAGCACTGCTACTTCACAGCGGCAGGGTCCGGGGTTTCGATTCCCA
CTTGGGTCACTGTCCATGCGGAGTCTGCACGTTCTCCCCGTGTCTGCGTGGGTTTCTCCGGGTGCTCCG
GTTTCTCTCCACAAGTCCCGAAAGACGTGCTGTTGGGTAATTTGGACATTTCGGAATTCTCCCTCTCTGTT
CCCGGACAGGCACCAGAATGTGGCGACTAGGGGCTTTTTCACAGTGGAAATGTCAGTGGAGGTTCTGTACA
ATACCAATGTTCCGTACAGGTGTTGAATTGTGTTCTACACAGGAAATTGCCTTCCATCATCCCCATTAT
GTCTAGAAACATAGAAAATAGGTGCAGGAGGAGGTCATTTGGCCCTTTGAGCCTGTTCTGCCATTCAATTA
TGATCATGGCTGATCATCCAGCTCAATAGCCTTCTCCAGCGTTCCCCCATATCCTTTGATCTCCTTCACC
ATAAGTGCTATATCTAACTGCTTCTTGAAAATATATTGAGAGGGATTCTCCATCCTGCCACACCAGGAGC
TGGATTCTCTGCCGTGCGGATTCTCTATTTTGGCAGAAGCACGGGGGTTTCCCAACAGCGTAGGGTGGCC
CCACAAGGAGAAACCCCGTTGACCAGCTGGCGAAACGGAGAATCCCGATGGCATATGGTGGGACAGAGAA

ACCCGCCCCAGATTTCTGATGCGGCATGTCTGTCGGGATTCTCCATTTTCGCCGACTGGTCAATGGGGTTTC
CCATCATGGGGCAGCCCCATGTCTGTCGGAACCCCTTGGGCTGGGGGTAAAATGGAAAATCATGATGGC...

B. Catshark SST2
(scaffold 83887)

...CACTCTTTCTCAAAAAGCAGTGGACGCAGTCTTAAATATGTTCAAGACAGAGGTAGATAGATTCTTGAA
AGGTAATGGGGTGCAAGGTTGTTGGGGGTAGGCGGGAGATTACAGTCCGATGGGCCATGATCTTATTGAA
TGGCAGATCAGGCTCGAAGGGCCGAGTGGCCTACACGTGCTCTTAGTTCTATGTCTGTAACATCCGACA
CTTTGGAGAAGAATATTTTTGATTGTGTGTCAGGAATCCAGCCCTCCCAGAATTTTCCAGGGTGCTAATAAT
CAGTTTTTACTTAGATTTCTAGTCAACCTACAGGTTTTAGATTTTCTTATACTGCATTGGAGGG
TCAGTTGTTGAACAGCATCCATCCAATTCACCTTTTATAACTTCTAAAAATATAATTTGTTTAAATGGC
TGGAACATTCTTGGATTGGAGGCTATAAAGCTCTTTAATGGCTGCTTCATTCAAATTGAACTGCAATTTT
AACTGTCCACATTACAGATCCTTCATCTACTTGCCCATAAATTTACAGAACGTAAAAGTGTAATATAATC
AGTCAGGTATGTTCTTCTGAATTAATATTCCTCCATTTACGATAACGCAAACCTGTTACTCCTTATATA
CATATTGTTTTAGGCTGTATTGGGTAAATGATGCACACTGGCTATTAGGCTTTGATTGTATCATTAAT
TTTGTGCGTCAGAGTTGCTTCTGCTGTGCTATAAAGAGCTGGAAACACTTTCGGAAAAATAGATTGAGG
AGTTCACAATACATTTAGCATTTTGTCCAGGAGTGTCTGAAGATTACAGC

ATGAAGTGGCTAATGACAGTGM K W L M T V

AGCCTGATGTCTCTGCTGTACCTTCTGAGAGTCGAGGGTACTGACCTACTGGAAGAAAGAATGAAACTTC
S L M S L L Y L L R V E G T D L L E E R M K L

AGGTAAACAGAGTGTAGTAGAAAGATCATTACTAAATGCACAGAGGTGGCGGCAGTGTGGTGAAAGGGGTG
Q V N R

GGAGGGACGAAATCCACAGCCATAAGGAGAGAATTGACGTAAAAATATTGGGAAAATTATGTAGAGAGAT
GAGAGACAATGGGATTGTTCTCTCTAATGCTAGGAGATTAAGGGAAGACTTAATAGAGGTGTTCAAAAATA
ATGAGAAAGCGTTTTCCACAGGCAGATGGGCCGGTGACCACGAGGAGAACATTTTAAACTAATTGATAAAA
GAGCAAGAGGGAGCGATGAGGAAAATTGTTTTTTACATCGTCAATCATTATAATCTGAAACGTGTTGCCT
GAAAGTTGATGGAAGCAGATTCAATAGTAACTTTTCAAAGGACTTAGATATATACTTGAAGGTTGGAAA
CTTGCGAAGTATCAGGAAGAGGGGAGGGAGCACTATAAATTCTGCACTGTAAATTCTATGATTACGTTA
AGGCAGGAAAATGGAAGTAATTGAGTAGCTCTTTACAAAGGGCTGGTATAGATGTGATGGGATGAATGGC
CTTTTTTGCTGTAAAGTTCCATGAAAGCCAACATCAGCAATAATCAGACTTTCAGATTTCCAGCATCCAC
ACTATTTTGCTTTAATCAGCATTAAATATATCATCAAGGGATCTGGTAGTGGGTAGTTGTCTTACTGGACA
AGATTAATAATCAGGAGAATTTGAGTTCAAAAACCACCATGGCAGTTTGAGAACTCGAATTTGGTTTGAA
AATAAAATCTGGAACAAGAAACTGGTTTTAGTCAAAAGACGTAAACTGTCTGGATTGTCTATAAACCCCTCAA
CTGGTTTCGTCAATACCTTTTTTTAATATAAGTTTAGAGTTCCCAATTAATTTTTTTTCCAATTAAGGGGCA
ATTTAGCGTGGCCAATCCACCAACCCTGCACATCTTTTGGGTTGTGGGGGTGAGACCCACGCAGACACGG
GGAGAATGTGCAAACTCCACACGGACAGTGACCCGGGGCTGGGATCGAACCTGGGGCCTTGGCGCTGTGA
GGCAGCAGTGTCAACCACTGCGCCACCGTGTCTGCCCTGGCCAATACCTTCTAAGGAAGGAAACTGATCT
GCCAGGTATCCTGGGCCATAGCAATCTGTTTGGCTGTTAACAGAGATTTCTTAGTGACCTAACGAGCCACAC
AGGTTTAACAGGATGGCAATAATGTGCCAGTCGGACTTGAATTCTGTGAAAAGATCAGAAAACCCGGC
GCAGACTGTTCTTCGGGAAAAATTGCTGATTAAAGTTTGGTGGATTACTTTAAACTAGTGGAACATTAT
TGAAAGGACCTGTGGACCTGAACAAGCTCGACACTCATTTTTTGCCTTTAATCTAATGTCTTCAGGGAAT
GAAATCTGCCGTCTTACCTGGTCTGGCCTACATGTGACTCCAGATCCACAGCAATGTGGTTGGACTCTT
AACTGCCCCCTCAAGGGCAATTAGATATGGGCAATAAATGCTGCCAGCCTGCGACGCCCATGTCCCTTG
AGCGAATAAAAAATAAATCAGGCCAAGTACAAAAATATATTGAGGGAACAGAAAGATTTAGGCTTAGGGAT
GTTTCGAGTTGGCAAGATATGCAGAGGGTAGCAACGAGTAAACTGTAACAAAACCTGGGTCAATGGTGGGAA
TAATGGTTGGAAATAAAGTGTAAGACAATAAAGAGCTGAGCTAGATCTGAGTGAGTGATTATGTT
TGGCATCAACAAACAAGTGCCTTGCAATGAAATGAAAACGAAAGCTTTCTATTCTCTGTTTATCCACAAG
GAAATGACAAAAGCAGGAAGAATCTGATTGTAAAGCTACTGGCTGGCTTGTTGGAGACTGATGATAATC

E M T K S R K N L I V K L L A G L L E T D D L
TCTTGGAGAATGGCTTTGCACCTTTGAAACCGGAAGAGGCAGAAGGGACTTTGTTGGAAGAGAGGTCCGGT

D L L E N G F A P L K P E E A E G T L F E E R S
TAACGCTGGAATTCACGCAGGGAGCAAAAAACCCCATGCAAACTGTTCTTCTGGAAAACCTTTTCCCAC

V N A G I P R R E Q K T P C K L F F W K T F S
TGTAAATAACCGTGTAGCGGATTTTTCTAAAGCAGTGGGAGTATGAAAGAAAAATGGGTGTAAAGGCTTA

H C -

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C. Catshark SST3
(scaffold121269)

TTAGATTCTGGCTTGGGTCCTGCTGTGCGGAGTCTGCACGTTCTCCCCGTGTGTGCGTGGGTTTCCT
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CTNN
NN
NN
NN
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M W C S R L Q L S L

CTCTCCTCTCCATCGCCCTGGCAGTACTGAGTGTGAGCTCAGCCCCACAGACAACAGGCATCGCGAAAT

A L L S I A L A V L S V S S A P T D N R H R E I

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L Q R A L D Q

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(scaffold 604248)

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E L L K D

CACAATGATGAACTGTTGCCTTTGGTTACTGATGTAGACACTGAGGCCGGAACACTGGATGTTTCCAAT

T M M K L L P L V T D V D T E A G T L D V S N

GCTGAGACTTCAGAAGAAAACACAACACCGATGAAATTCAGCATCGTCAGTTGGGAATGAGAATGCGGA

A E T S E E N T T P M K F Q H R Q L G M R M R

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K N C K N F F W K T Y T L C -

ACTGGACCCTGCTGTACCCCACTGCACCCCACTGACTCCATCCCACTGTACCC

D. Catshark SST5 = SSb

(scaffold 888145)

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M P R S Q T Q V
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L L T L V T V A L L L L R G S S T A R V Q G L P
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D I L Q E R N D E G T E
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(scaffolds 316000)

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E L S R T M V L N L L S E L L H A G
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D K G L P S T E R R E L P Q A E I V R R W N S
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P R D R K A G C K N F F W K T F T S C -
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E. Catshark SST6 = SSc

(scaffold 66610)

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M Q L L G T A S L L S M L L I V S S V R A
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T A P L E D R L S L R A N Q

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A. Whale shark SST1/3 (NW_018029766.1)

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B. Whale shark SST2 (NW_018077477.1)

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 AGGAGGATCAGGGTTTAAGGAAGTGTTCATTGGCAAAGAGCAGTGAGGAGTTTTATTTATTCATTTTGTG
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 GTTTGGAAGGAGCTACGTGAGGATCTTTGATTTTCTGCAGTGCATCTTGTAGATAGTACACACTGCTGCA
 ACTGCAGTAACTGCAATAAAGCAGGTGATGGTGGGGAAGGTGCTGCTATAAACTATGAAAAGCATTCA
 GGACAACCTGAGCACAATTTGAGTAAGCAAATGATGCTTGCATCAATGGACAAATGGCTTGTGTTGTATAA
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 E V T K S R K Y L
ATGTTAAACTGCTGTCTGGGCTGTTGGATCCTGATGATAATCTCTTGGAAAATGACTTCACGTCTTTGA
 M L K L L S G L L D P D D N L L E N D F T S L
GCCCAGGAGAGGAAGAGAGTTTCGCTTGAAGAGAGGTTCGGTTAACGCTGGCATCCCTCGTAGACCCGAGAA
 S P G E E E S S L E E R S V N A G I P R R P Q **K**
GGCACCGTGTAATTTGTTCTTCTGGAACATTCTCGCACTGT**TAA**TTATTGATGGATTTCTAAACCAAGT
A P C K L F F W K T F S H C -
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 TCATGCTGCTTGGCCTGCTGTGTTTCATCCAGCTCTACACCTTGTATCTCTGTTTTCTGTAAAGGCTTA
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C. Whale shark SST6 (NW_018032490.1)

...CCTTGGCATAGGAAAGGGAGAATGTACTTATTTCCAGGTTCTAACTGCTACACAGTAATGCCTAGTG
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TGCAGCTACTGGGGTCAGCGAGCTTKGTGTCTATACTGCTCATTGTGTCCAGTGTGAAGGCCACAGCACC

M Q L L G S A S X V S I L L I V S S V K A T A P

TTTGGGAAGACAGACTGAGTCTTCGGGCAAATCAGGTGAGTAAAGTCTTAAATGTGGGAGCAGTACGTGA

L E D R L S L R A N Q

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ACTTCCACAGTTCTTTTCGGTTTTTGTGAATGAGTTTCGTGTTTGTCTTTAACAGGAGCTGAATAAAGAAA

E L N K E

GGAAAGAGGTTGTTCTCAAGCTGTTATCTGCACTGCTTGACTCCAGCAGCAATCAAATGGGGATTGAGAA
R K E V V L K L L S A L L D S S S N Q M G I E N
CACGTTCCAGATCAGGAGGACATGGAAGAGATGAAAGTGAAGACAGGTCCCGCTTCAGTCAGTTACCA
T F P D Q E D M E E M K V E D R S R F S Q L P

CAACGAGAGCGGAAGACATCCTGCAAAAACCTTCTTCTGGAAAACCTTCACCTCCTGCTAAACGTCAGACGA

Q R E R K T S C K N F F W K T F T S C -

TGACATGTCGCTAGGAACTGATTTAGCACTGTACATAAGCTGGTGTTGTTTATTTTCTTTGTTTCTTGGG
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GGAATTTGAATTCAGTATAAAGAAAAATCTAGCTGGTGCTCTGGTTTCCTCCCACAGCCCAAAGATGTGC
AGGCTAGGTGGATTGGCCATGCTAAATTGCCTATAGTGTTCAAGGGTGTGTAGATTAGGTCGGTTATAG...

Figure S6

A. Whale shark SST1 (SSTa)

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M W C S R V Q C A L A L L S I A L A V L
agtgcgggcgccgctcccaccgcccagaggtatcgcgaaactcctccagacatcaatggct
S A G A A P T A D R Y R E L L Q T S M A
ggcgcagagccccggagtaaagcggagctgatcaaatacaatctcgtccaattgctcgcg
G A E P R S K A E L I K Y N L V Q L L A
gagctggcaaacgcccagagaacgaagttttggatggggaggatttgccgcggatggcgaaa
E L A N A E N E V L D G E D L P R M A K
caggatgaggtacgggttgatctggaacgatccgccaacccaattcgccccagagggaa
Q D E V R V D L E R S A N P N S P Q R E
cgcaaagcgggctgcaaaaacttcttctggaaaaccttcacatcctgttaa
R K A G C K N F F W K T F T S C -
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B. Whale shark SST2 (SSTd)

```
gaagtggcaa
atgacagtgtgcctgatgtccctgctgcttcttctaagtgttgaggcagcagaccactg
M T V C L M S L L L L L S V E A A D P L
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E E R M K L Q V N R E V T K S R K Y L M
ttaaaactgctgtctgggctgttggatcctgatgataatctcttggaaaatgacttcacg
L K L L S G L L D P D D N L L E N D F T
tctttgagcccaggagaggaagagaggttcgcttgaagagaggtcggttaacgctggcatc
S L S P G E E E S S L E E R S V N A G I
cctcgtagaccgcagaaggcaccgtgtaaattgttcttctggaaaacattctcgcactgt
P R R P Q K A P C K L F F W K T F S H C
taattat
-
```

C. Whale shark SST3 (SSTe) (exon 2 only)

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gactttctgaaggacacaattatccaacttctacatgtgggtcgcggatgcagacaaggat
D F L K D T I I Q L L H V V A D A D K D
gctgtggaagtgaatgcttctcaagttgagactccaccagwtaacaagattccaatgaaa
A V E V N A S Q V E T P P X N K I P M K
ttccagcagcgtcaattgggaacaagaatgcggaaaaactgcaagaatttcttctggaaa
F Q Q R Q L G T R M R K N C K N F F W K
acatacactttatgttaa
T Y T L C -
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D. Whale shark SST6 (SSTc)

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aaccacacagagacttcaagggtcgaggcacattg
caaagatctcgaaaaggcaccacttcaatccaattccaagcgactgagagaagaggcagc
atgcagctactggggtcagcgagcttkgtgtctatactgctcattgtgtccagtgtgaag
M Q L L G S A S X V S I L L I V S S V K
gccacagcacctttggaagacagactgagtccttcgggcaaatacaggagctgaataaagaa
A T A P L E D R L S L R A N Q E L N K E
aggaaagaggttggttctcaagctgttatctgcactgcttgactccagcagcaatcaaatag
R K E V V L K L L S A L L D S S S N Q M
gggattgagaacacgttcccagatcaggaggacatggaagagatgaaagtggaagacagg
G I E N T F P D Q E D M E E M K V E D R
tcccgttctcagtcagttaccacaacgagagcggaagacatcctgcaaaaacttcttctgg
S R F S Q L P Q R E R K T S C K N F F W
aaaaccttcacctcctgctaacgtcagacgatgacatgtcgttaggaactgatttagcac
K T F T S C -
```

tgtacataagctggtggttggtttatcttctttggttcttgggggttacatttctttcatgc
acaagaaa

Figure S7

A. Elephant shark SST1 (Sc_821)

...TTTAGTGGATGGTATGTTGTGGATGCTGTATAGGGGATTGTGTGTAATGGATTGTGTGTAAGGGATGGT
GTGTAGTGGTTGGTGTGTAGAGGATAGTGTGTAGTGGATGGTGTGTGGTGGTTGGTTTGTAGAGGATAGT
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CGTGAGGCGGCTTTATAAGGCGAGTCTATGGACACCAGGACCAGAAGATCCAGACGAGGCAGAGCGTCCA
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M S C G R V Q C A L A L L S I A L T V L
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S V T S C A P A H D R Y R E I L Q R S L A A A G A
CAGGAGTAAACCGTAAGACAGCCGATTCCACACTGGGTAATTAATATCTGACAAGGTTGCTAAATACAC
R S K P
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E L T K Y S L A Q L L A E L A N A E N
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E A L E A E D M A R A T A Q D E V R V E L E R
TCGGCCAAACCCAACTGGCGCAGAGAGAGCGCAAAGCGGGCTGTAAAAGCTTCTTCTGGAAAACCTTCA
S A N P N L A Q R E R K A G C K S F F W K T F
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T S C -
CCACCCCTCCCATCCCCACCCTACACACAAAGTTTTCCCGATCCCCCGCCACACACACACACACACAT
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B. Elephant shark SST2 (Sc_58)

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A A G E I P P R K P K A G C K L F F W K T F S H
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C. Elephant shark SST3 (Sc_821)

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P R W R K D C K N F F W K T Y T L C -

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 AAAAAATTATCATTTTGGTCACGACTGTTTGTGGGACGCTGCTGTGCGCATTTCTGCCCAACAAACATACAG
 TCAATTCACTTTACAGTATATACTGTGAAGCGCTTTGAGACATATAGAAGACGTGATAAGGCGCTGTATC
 AAATGCAAGGATTATTATTATTATTATGCTTTCTCTCTCACACTCTTTCTCTCTCTGCTGCTTCTCTCTCT

[illegible]

A. Elephant shark SST1 (SSTa)

agactgtttgtagaggatgctgt
gcagtgaaggggtgtgttggggatgaaggtggcgtgagggcgtttataaggcgagtcctat
ggacaccaggaccagaagatccagacgaggcagagcgtccagagagccggtgctgaacca
cgagcgttcctccgttcctctctcgtcctcctttgacagtttggtgccgtcgccccgag
atgtcgtgcggccgagtgcagtgcgccttggtgtgtctccatcgccctgacagtgctg
M S C G R V Q C A L A L L S I A L T V L
agtgtcacctcggcgccagcacacgacaggtaccgcgaaatcctgcagcgatcactggcc
S V T S A P A H D R Y R E I L Q R S L A
gcgggcgaggagccaggagtaaacggagctgaccaagtacagcctggctcagctgttggtg
A A G A R S K P E L T K Y S L A Q L L A
gaattggccaacgcggagaacgagggcgtggaggcgaggacatggcccgagcaaccgca
E L A N A E N E A L E A E D M A R A T A
caggacgaagtaaggggtgaattggagagatcggccaaaccccaacctggcgagagagag
Q D E V R V E L E R S A N P N L A Q R E
cgcaaagcgggctgtaaaagcttcttctggaacaccttcaacttctgtaactctgagca
R K A G C C K S F F W K T F T S C -
ccccccaccctctctcacacacactcctcctgacccccaccctcc
catccccaccctacacacaaagttttcccgatcccccgccacacacacacacacacat
tgtatgtgtcttacgctacgtgggtctgttctgattttaacatactgtaaataaaaacacat
ggtgatgataattcaacctaatatttattgtgacagaaccttttagatgggggtgtgactgta
tagttaccactctttctggctagaggtgtatgtattatttttaatttgtatgtcgcaat
gaaatacatgtttgaaactgaaa

B. Elephant shark SST2 (SSTd)

a
tatcaaagcaaggattattattatattgatattgagacgtcttcccgatgtgaaaagca
ctatacgaatgtaatcttcttgtggaaatgttacaaaactcagagctggctaaatgtttg
ttctacagacaaaattccccatgaagagtcaccaatcccataagctgctgaacccttatt
tagtaaaactggaggtcaatcatgtaatactgtggacctttctgggtcatgtatcagatcg
cccaacgagagctctatcaaagagaattgtctcagctccactagtcagtttagattggtgt
tggcatcaccctttctcagagttgtcccatgacatcaattctctccgcaaactcaggct
tcagcctcactgattccttatcagtccttgaaaacaatgactttctgagttgtgaaaatc
ttatgttctgtaacaggcattattttcctgttaggggtcatcaagtggatttgccaagggga
gccacttttttaatatagatcagatgacagattgggttaatgtctcatttgaggacagat
gattcatggtaagacgaaaaagtttcatttcttgtggatttctagagctggaacaatttc
tacctccacttttaattcgtagaagtgttttttgtgtgttggatattatagaagattgatg
ttgaaagctctatacaaaacacacaaagactgactcattctaaattggaaagctctttta
attatcagtggttctaattctttgatgcaaactcgaaattggaaaatataaaataaacaatt
atgatctttctaaattaacattttttccagttgttgactttgtcatttttttaattgttc
cagttaatgggttctcattgtatattagtgtctgattatagcactaattttgcacgtcagc
gagtgctataattgtgctgcattataaaagcaggacaattagagttttctcagcaaaaca
gggaaagagtcagtgaaagctcgacagatccattgaaaagagagaaagtttgagtccagc
atgcagtggaagcatttcgaagtgtcgtgtgtctgttgttcattgtaactgttcaggga
M Q W Q A F A S V V C L L F I V T V Q G
gttgaaccacaggaggaacgaatgggtcttcagctgaacagggagatggtaaggacaag
V E P Q E E R M G L Q L N R E M V K D K
aaacgcctgattgcgaagctgctggcgggattgttggacgtggatgacaatctgttagaa
K R L I A K L A G L L D V D D N L L E
agtgtcatcgccccattgggtctgagcaaagaagaggggactgatttcgaggagagatca
S V I A P L G L S K E E G T D F E E R S
gctgccggtgaaatccctcccagaaaaccgaaggcaggggtgcaaactgttcttctggaaa
A A G E I P P R K P K A G C K L F F W K
accttctcgactgttagtggtttgtcaaagataaacatttttttaaaatccagtttgt
T F S H C -
gttttctgttgatgtgaaacacttccccccccccact

C. Elephant shark SST3 (SSTe)

gcagca
atgcaggctcgggtgcaccctcactctagccctcctctccctggcagcgcttggcctcagt
M Q A R C T L T L A L L S L A A L G L S
gctttgcccacacacctcagggaccagctcgttctccagggatcaccagcaatggagctg
A L P T H L R D Q L V L Q G S P A M E L
cgggatgggtgtgggtccgggagctgatacaggcagtgggccgatgcagagagcaaaccacag
R D G V V R E L I Q A V A D A E S K P Q
agtgaggaggcagcagaggacttcgctccagatgaaaaggctgaactacggcttgcgctg
S E E A A E D F A P D E K A E L R L A L
gctccacgggtggcggaagattgtaaaaatttcttctggaaaacttacactttgtgctaa
A P R W **R K D C K N F F W K T Y T L C** -
tcctgtgccagcggttaaagcctgactgaaccacaaccgtctggctggcgagaggtcttaa
ttaatgtgtaatatgaattgtttgctatttagcatgcctcaattattgttaatcctttac
tcattgtgaattcttaatcaagtgtttactgttacg

D. Elephant shark SST6 (SSTc)

cgctctccc
tcactcgccctgctcctgttccctctcgcctctctctcgcctcgccttcgctccgctcacacc
atgcagatcctcgtcgcctcttatctccactctcttccctcgtgtccggggtgagcaccacc
M Q I L V A L I S T L F L V S G V S T T
actgcctcgcctggacgacagattcaacctccagagcagccgggagatgaatcaggaaagg
T A S L D D R F N L Q S S R E M N Q E R
aaagagatgatcctcaagctgttgtcaggtctcctggacaatgccgcggtgagtgggcag
K E M I L K L L S G L L D N A A V S G Q
acggggagcgaggccggttacccctgagcccgcggatggggggccggtgatgttggaggaa
T G S E A G Y P E P A D G G P V M L E E
cgatctcgctacagccaactgccccagcgaagccgcaaagtcctcctgtaagaacttcttc
R S R Y S Q L P Q R S **R K V P C K N F F**
tgaaaaacattcacctcctgttgacgataaacagtacagacctcctacacccccctctcc
W K T F T S C -
ccgtccctctttccctcctcttccccccacccccacccccacacctaagcacgggatg
aaaccaccagtaactaaactgttttagcactgtacatttgcctgctgctgtttttatTTTT
attcatctgtgaagtgaattcctttcttgggcacggaaataattaaagaaagcataacc
atacgttcactgcctgggtgtttctttcttctggtgacagagcgcgagggagggaggat
ggagggagagagagagaggggggaaggagagagggaggtggtacctgagctcatagcatct
cccatttacaggggagcggatatctcaatcgcacctacacacaatcgcacacactcaca
ctcgctcac

Figure S9

Table S1.

Molecular cloning		
Catshark SST3 (SSTe)	CshSSTe Rev	CAGTGGGATGGAGTCAGTGGGGTGCA
	CshSSTe Rev Nest	GGAGTCAGTGGGGTGCAGTGGGGTAC
Tissue distribution analysis		
Catshark SST2 (SSTd)	CshSSTd For	TTGTCCAGGAGTGCTCGAAGA
	CshSSTd Rev	GTCCCTTCTGCCTCTTCTGGT
Catshark SST3 (SSTe)	CshSSTd For	ATGTAGACACTGAGGCCGGA
	CshSSTd Rev	AGAAGGGCTCACTGGGTACA
Egf1	Egf1 For	CTTTCGCTCACCTACCCAAG
	Egf1 Rev	GGTCAAAGTGCTCCCAGAAG

Table S2

Name	Sequence	Species
SST1	AGCKN FFWK TF TSC	Most vertebrates, including <i>catshark (SSTa)</i>
	AGCK SFFWK TF TSC	<i>Elephant shark, ratfish (SSTa)</i>
SST2 (*previously known as SST6)	MP CRNFFWK TFSSCK	Human
	P CKNFFWK TFSSCK	Mouse, rat
	TP CKNFFWK TFSSCK	Bovine, monkey
	TP CGNFFWK TFSSCK	Pig
	AP CKNFFWK TF TMC	Frog
	AP CKNFFWK TFSSC	Anolis
	AP CRNFFWK TFSSC	Coelacanth
	SP CTNFFWK TF SAC	Mexican tetra*
	SP CKNFFWK TF SAC	Piranha*
	TP CKNFFWK TFSSC	Spotted gar*
	SP CKLFFWK TFSSC	Zebrafish*
	SP CKNFFWK TFSSC	Herring*
	AP CKLFFWK TF SHC	<i>Whale shark, skate (SSTd)</i>
	TP CKLFFWK TF SHC	<i>Catshark (SSTd)</i>
	AG CKLFFWK TF SHC	<i>Elephant shark (SSTd)</i>
SST3	AGCK NFYWK G FTSC	Most teleosts
	AGCK NFYWK G LFTSC	Tilapia
	AGCK NFYWK G PFTSC	Takifugu
	DGCK NFYWK G FTSC	Medaka
	AG CRNFYWK TF TSC	Spotted gar
	SGCK NFFWK G RTSC	Herring
	NCK NFFWK TY TLC	<i>Whale shark, catshark (SSTe)</i>
	DCK NFFWK TY TLC	<i>Elephant shark (SSTe)</i>
SST4	FG CRVPFFWK S WSPC	Stickleback
	PC RVFYWK S WAKC	Medaka
	QF GCRMFFWK S WTYC	Takifugu
	QAG CRIFFWK S WTSC	Tetraodon
	TG CKNYFWK S RTAC	Zebrafish
	PL NCMNYFWK S RTAC	Catfish
SST5	AG CRNFFWK TF TSC	Most actinopterygians
	AG CRNFFWK SY TSC	Tetraodon
	TG CRNFFWK TF TSC	Piranha, mexican tetra*
	AG CRNFFWK TF TSC	Zebrafish
	AG CKNFFWK TF TSC	Coelacanth, <i>catshark (SSTb)</i>
SST6 (*previously known as SST2)	AP CKNFFWK TF TSC	Chicken*, lungfish*, coelacanth*, actinopterygians*, <i>catshark (SSTc)*</i>
	TS CKNFFWK TF TSC	<i>Whale shark (SSTc)</i>
	VP CKNFFWK TF TSC	<i>Elephant shark (SSTc)</i>
Others		
SSTa	AGCKN FFWK TF TSC	Lampreys
SSTb	AGCKN FFWK TFSSC	
SSTc	ANCR MFYWK TMAAC	

Table S3

SST1 (SSTa)	Csh	Wsh	Esh
Catshark		66.37	73.45
Whale shark			74.14
Elephant shark			

SST2 (SSTc)	Csh	Wsh	Sk	Esh
Catshark		76.0	62.03	58.1
Whale shark			62.82	53.0
Skate				51.9
Elephant shark				

SST3 (SSTe)	Csh	Wsh
Catshark		38.14
Elephant shark		

SST6 (SSTc)	Csh	Wsh	Esh
Catshark		86.79	58.65
Whale shark			53.85
Elephant shark			

Table S4

Gene	Designation	Species	Ensembl ID	Chromosome location	Position (Mb)
Mb21d2	Mab-21 domain containing 2	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000180611	3	192,796,815 - 192,918,161
		<i>G. gallus</i>	ENSGALG00000007218	9	13,300,318 - 13,348,379
		<i>X. tropicalis</i>	ENSXETG00000002143	GL127217.1	276,599 - 277,885
		<i>A. carolinensis</i>			
		<i>L. chalumnae</i>	ENSLACG000000017691	JH126687.1	2,299,815 - 2,301,095
		<i>I. oculatus</i>	ENSLOGG00000009364	LG14	18,861,293 - 18,899,827
		<i>D. rerio</i>	ENSODARG00000077316	15	45,527,281 - 45,538,773
		<i>O. latipes</i>	ENSODARG00000077690	2	5,563,077 - 5,581,772
Fgf12	Fibroblast growth factor 12	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000114279	3	192,139,395 - 192,767,764
		<i>G. gallus</i>	ENSGALG000000036973	9	13,360,379 - 13,557,972
		<i>X. tropicalis</i>	ENSXETG00000002144	GL127217.1	393,833 - 521,969
		<i>A. carolinensis</i>	ENSACAG000000000000	GL142086.1	262,716 - 190,480
		<i>L. chalumnae</i>	ENSLACG000000017275	JH126687.1	2,003,413 - 2,283,293
		<i>I. oculatus</i>	ENSLOGG000000009371	LG14	18,996,717 - 19,055,889
		<i>D. rerio</i>	ENSODARG000000113525	15	45,414,883 - 45,510,977
		<i>O. latipes</i>	ENSODARG000000027957	2	5,587,495 - 5,681,658
Il1rap	Interleukin 1 receptor accessory protein	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000196083	3	190,514,051 - 190,659,750
		<i>G. gallus</i>	ENSGALG000000007253	9	13,905,930 - 13,926,342
		<i>X. tropicalis</i>	ENSXETG000000015044	GL127217.1	998,488 - 1,097,171
		<i>A. carolinensis</i>			
		<i>L. chalumnae</i>	ENSLACG000000016241	JH126687.1	1,498,996 - 1,521,106
		<i>I. oculatus</i>	ENSLOGG000000009378	LG14	19,120,504 - 19,150,963
		<i>D. rerio</i>	ENSODARG000000114719	15	45,338,623 - 45,356,635
		<i>O. latipes</i>	ENSODARG000000016010	17	24,782,508 - 24,802,926
Gmc	Geminin coiled-coil domain containing	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000196083	3	190,514,051 - 190,659,750
		<i>G. gallus</i>	ENSGALG000000007253	9	13,905,930 - 13,926,342
		<i>X. tropicalis</i>	ENSXETG000000015044	GL127217.1	998,488 - 1,097,171
		<i>A. carolinensis</i>			
		<i>L. chalumnae</i>	ENSLACG000000016241	JH126687.1	1,498,996 - 1,521,106
		<i>I. oculatus</i>	ENSLOGG000000009378	LG14	19,120,504 - 19,150,963
		<i>D. rerio</i>	ENSODARG000000114719	15	45,338,623 - 45,356,635
		<i>O. latipes</i>	ENSODARG000000016010	17	24,782,508 - 24,802,926
Ostn	Osteonin	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000188729	3	191,199,241 - 191,265,615
		<i>G. gallus</i>	ENSGALG000000007226	9	13,761,297 - 13,772,476
		<i>X. tropicalis</i>	ENSXETG000000015042	GL127217.1	750,574 - 755,484
		<i>A. carolinensis</i>			
		<i>L. chalumnae</i>	ENSLACG000000016886	JH126687.1	1,792,819 - 1,800,129
		<i>I. oculatus</i>	ENSLOGG000000009421	LG14	19,280,012 - 19,292,855
		<i>D. rerio</i>	ENSODARG000000054055	15	36,128,853 - 36,249,087
		<i>O. latipes</i>			
Masp1	Mannan binding lectin serine peptidase 1	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000127241	3	187,217,285 - 187,292,022
		<i>G. gallus</i>	ENSGALG000000007419	9	14,910,864 - 14,927,972
		<i>X. tropicalis</i>	ENSXETG000000019757	GL127217.1	2,406,583 - 2,454,003
		<i>A. carolinensis</i>	ENSACAG000000006732	GL343730.1	51,210 - 227,647
		<i>L. chalumnae</i>	ENSLACG000000011850	JH127453.1	641,714 - 706,681
		<i>I. oculatus</i>	ENSLOGG000000009432	LG14	19,284,195 - 19,341,321
		<i>D. rerio</i>	ENSODARG000000068726	15	36,187,434 - 36,223,417
		<i>O. latipes</i>			
SST1	Somatostatin 1	<i>R. typos</i>	XM_020509773.1	NW_018029766	122,014 - 124,407
		<i>C. milli</i>	XM_007912395.1	Sc_821	7,008 - 9,515
		<i>H. sapiens</i>	ENSG00000157909	3	187,668,906 - 187,670,399
		<i>G. gallus</i>	ENSGALG000000007361	9	14,852,386 - 14,853,973
		<i>X. tropicalis</i>	ENSXETG000000019777	GL127217.1	2,228,041 - 2,229,578
		<i>A. carolinensis</i>	ENSACAG000000006722	GL343730.1	4,342 - 23,375
		<i>L. chalumnae</i>	ENSLACG000000003574	JH126687.1	88,278 - 90,189
		<i>I. oculatus</i>	ENSLOGG000000009439	LG14	19,459,762 - 19,467,399
		<i>D. rerio</i>	ENSODARG000000040799	15	36,156,986 - 36,158,851
		<i>O. latipes</i>	ENSODARG000000019152	scaffold660	2,344 - 3,701
SST3	Somatostatin 3	<i>R. typos</i>	XM_020509774.1	NW_018029766	131,096 - 160,273
		<i>C. milli</i>	XM_007912396.1	Sc_821	17,287 - 22,746
		<i>H. sapiens</i>			
		<i>G. gallus</i>			
		<i>X. tropicalis</i>			
		<i>A. carolinensis</i>			
		<i>L. chalumnae</i>			
		<i>I. oculatus</i>	ENSLOGG000000009445	LG14	19,441,987 - 19,443,409
		<i>D. rerio</i>	ENSODARG000000033161	15	36,115,955 - 36,120,277
		<i>O. latipes</i>	ENSODARG000000019158	scaffold660	8,674 - 10,556
Col4a3	Collagen type IV alpha 3 chain	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000169031	2	227,164,565 - 227,314,792
		<i>G. gallus</i>	ENSGALG000000038612	9	9,384,943 - 9,430,089
		<i>X. tropicalis</i>			
		<i>A. carolinensis</i>	ENSACAG000000004217	3	23,464,166 - 23,573,541
		<i>L. chalumnae</i>	ENSLACG000000009918	JH126709.1	458,799 - 547,615
		<i>I. oculatus</i>	ENSLOGG000000009454	LG14	19,454,926 - 19,507,683
		<i>D. rerio</i>	ENSODARG00000003395	15	36,054,864 - 36,112,794
		<i>O. latipes</i>			
Col4a4	Collagen type IV alpha 4 chain	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG000000081052	2	227,002,711 - 227,164,453
		<i>G. gallus</i>	ENSGALG000000004946	9	9,318,986 - 9,370,173
		<i>X. tropicalis</i>			
		<i>A. carolinensis</i>	ENSACAG000000003770	3	23,583,599 - 23,670,714
		<i>L. chalumnae</i>	ENSLACG000000012078	JH126709.1	673,429 - 787,527
		<i>I. oculatus</i>	ENSLOGG000000009493	LG14	19,522,370 - 19,590,210
		<i>D. rerio</i>	ENSODARG000000002831	15	35,951,888 - 36,055,401
		<i>O. latipes</i>			
Rhbd1	Rhomboid domain containing 1	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000144458	2	226,835,581 - 226,999,215
		<i>G. gallus</i>	ENSGALG00000004957	9	9,276,974 - 9,300,051
		<i>X. tropicalis</i>	ENSXETG000000020986	GL127898.1	177,755 - 505,839
		<i>A. carolinensis</i>	ENSACAG000000003827	3	23,670,816 - 23,710,982
		<i>L. chalumnae</i>	ENSLACG000000013155	JH126709.1	816,263 - 961,871
		<i>I. oculatus</i>	ENSLOGG000000009504	LG14	19,592,741 - 19,635,912
		<i>D. rerio</i>	ENSODARG000000021046	15	35,933,094 - 35,944,902
		<i>O. latipes</i>			
Irs1	Insulin receptor substrate 1	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000169047	2	226,731,317 - 226,799,759
		<i>G. gallus</i>	ENSGALG00000004959	9	9,244,127 - 9,248,454
		<i>X. tropicalis</i>	ENSXETG000000020086	GL127898.1	560,083 - 563,337
		<i>A. carolinensis</i>	ENSACAG000000003830	3	23,742,830 - 23,746,420
		<i>L. chalumnae</i>	ENSLACG000000014111	JH126709.1	963,541 - 1,032,531
		<i>I. oculatus</i>	ENSLOGG000000017412	LG14	19,644,120 - 19,647,336
		<i>D. rerio</i>	ENSODARG000000054087	15	35,888,549 - 35,930,070
		<i>O. latipes</i>			
SST4	Somatostatin 4	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>			
		<i>G. gallus</i>			
		<i>X. tropicalis</i>			
		<i>A. carolinensis</i>			
		<i>L. chalumnae</i>			
		<i>I. oculatus</i>	ENSLOGG000000009520	LG14	19,696,596 - 19,698,886
		<i>D. rerio</i>	ENSODARG000000014190	2	5,726,353 - 5,728,843
		<i>O. latipes</i>	NO	17	24,768,840 - 24,769,036
Nyp2b	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	<i>R. typos</i>			
		<i>C. milli</i>			
		<i>H. sapiens</i>	ENSG00000144460	2	225,399,710 - 225,654,018
		<i>G. gallus</i>	ENSGALG000000004986	9	8,727,389 - 8,844,775
		<i>X. tropicalis</i>	ENSXETG000000005150	GL127898.1	945,276 - 992,671
		<i>A. carolinensis</i>	ENSACAG000000003843	3	24,114,255 - 24,276,004
		<i>L. chalumnae</i>	ENSLACG000000016098	JH126709.1	1,453,451 - 1,537,668
		<i>I. oculatus</i>	ENSLOGG000000009528	LG14	19,821,041 - 19,871,639
		<i>D. rerio</i>	ENSODARG000000079581	15	35,698,508 - 35,895,161
		<i>O. latipes</i>	ENSODARG000000093357	2	5,734,870 - 5,776,030
		<i>O. latipes</i>	ENSODARG000000016004	17	24,738,491 - 24,749,441