



Figure S2. Multiple sequence alignment with selected species and bioinformatics analysis of three Es-Caspases. A1-C1. The prediction of 2D-structure of three Es-Caspases. A2-C2. Sequence alignments of Es-Caspases. Consensus residues are in yellow (identical), blue (conservative) and green (block of similar) colour, the conservative region is in red box. A3-C3. The phylogenetic trees of three Es-Caspases. A4-C4. The predicted 3D-structure of three Es-Caspases.

Table 1. Primers and probes used in this article.

Name	Sequences	application
Caspase 3-mf-F	CTTCDTCCAGTTTTGCCGDGGA	Middle-fragment cloning
Caspase 3-mf-R	CAAGAACTTGCTGCCTCTGAG	
Caspase 7-mf-F	AGTAVGTCCGNACGKCYCC	
Caspase 7-mf-R	CGCHCANGDASTGGATGAA	
Caspase 8-mf-F	CATYCTNTCGCATGGNGA	
Caspase 8-mf-R	NGACYTTCTTYTTCTCRAAN	
Caspase 3-3R-F1	GCTGTTCTCTTCAACTTTTGTGCGA	3'RACE cloning
Caspase 3-3R-F2	AAGTCGGTGGACCAAGATGC	
Caspase 7-3R-F1	GTGCTGACTTGCCACCTTGCTTTTAC	
Caspase 7-3R-F2	ATGCGTAAAGTCTACTTCCCTGTGA	
Caspase 8-3R-F1	ACAGAAGACTCGCCAGAGCCTAAAG	
Caspase 8-3R-F2	CTTAATAGCCCGCTTTGAATTATCTT	
3'RACE Outer primer	TACCGTCGTTCCACTAGTGATTT	
3'RACE Inner primer	CGCGGATCCTCCACTAGTATTTCACTATAGG	
Caspase 3-5R-R1	GACAAAAGTTGAAGAGGAACAG	5'RACE cloning
Caspase 3-5R-R2	CTCAGGCTGGGGCACTGCTC	
Caspase 7-5R-R1	TGTACACCTTTGTCAGTGCGCATAACC	
Caspase 7-5R-R2	CGCATACCCTGCATGCCTGGATG	
Caspase 8-5R-R1	CTAACAAAGGTTTCTTCAAGGGGTCG	
Caspase 8-5R-R2	CGACCTGTCTCTGAATACCAATCCCT	
Long primer	TAATACGACTCACTATAGGGCAAGCAGTGGTA TCAACGCAGAGT	
Short primer	CTAATACGACTCACTATAGGGC	
Caspase 3-rt-F	GGGCTATCTCGTGACTGTGTGGGT	Semi-quantitative RT-PCR &ISH probes
Caspase 3-rt-R	GTGAGTTTTTGTGCTGGTTCCTTG	
Caspase 7-rt-F	TTCATGTTGAGGAATCTTGG	
Caspase 7-rt-R	CTTATTGACTGGGTGGTAGG	
Caspase 8-rt-F	AGAGAGGAGGAGTAGAGCCAGAC	
Caspase 8-rt-R	GGTTATCAAAATGCAACACATGA	
β -actin-rt-F	TCGTGCTCGACTCTGGTG	
β -actin-rt-R	GCAGCTCGTAAGACTTCTCC	
Caspase 3-fl-F	ATGAAGCGGCAGGAAGAGGCTACA	
Caspase 3-fl-R	CTACTGGCTTAGCAGCTGTGTTGGGT	