Table S4 Sequence similarity between the STKc_MEKK domain of AmphiMEKK2/3 and vertebrate MEKK subfamily members.

| **Species\gene** | **MEKK1** | **MEKK2** | **MEKK3** | **MEKK4** |
|---|---|---|---|---|
| *Homo sapiens* | 60.4 | 86.4 | 88.9 | 61.3 |
| *Mus musculus* | 60.4 | 87.1 | 88.9 | 60.9 |
| *Bos taurus* | 60.4 | 86.7 | 88.9 | 61.7 |
| *Ovis aries* | 60.0 | 86.7 | 88.9 | 61.7 |
| *Gallus gallus* | 60.8 | 87.1 | 89.3 | 60.9 |
| *Taeniopygia guttata* | 60.4 | 86.7 | 89.3 | 60.9 |
| *Chrysemys picta* | 60.8 | 87.1 | 88.9 | 60.9 |
| *Podarcis muralis* | 60.4 | 86.7 | 88.5 | 61.3 |
| *Xenopus laevis* | 59.3 | 36.3 | 87.7 | 61.3 |
| *Xenopus tropicalis* | 59.0 | 87.9 | 87.7 | 60.9 |
| *Danio rerio* | 59.0 | 87.9 | 88.5 | 61.3 |
| *Oncorhynchus mykiss* | 58.6 | 86.7 | 83.6 | 60.5 |
| *Callorhinchus milii* | 59.0 | 88.6 | 87.1 | 62.5 |
| *Mobula birostris* | 58.6 | 88.3 | 88.9 | 62.1 |