

# **CCK reduces the food intake mainly through CCK1R in Siberian sturgeon (*Acipenser baerii* Brandt)**

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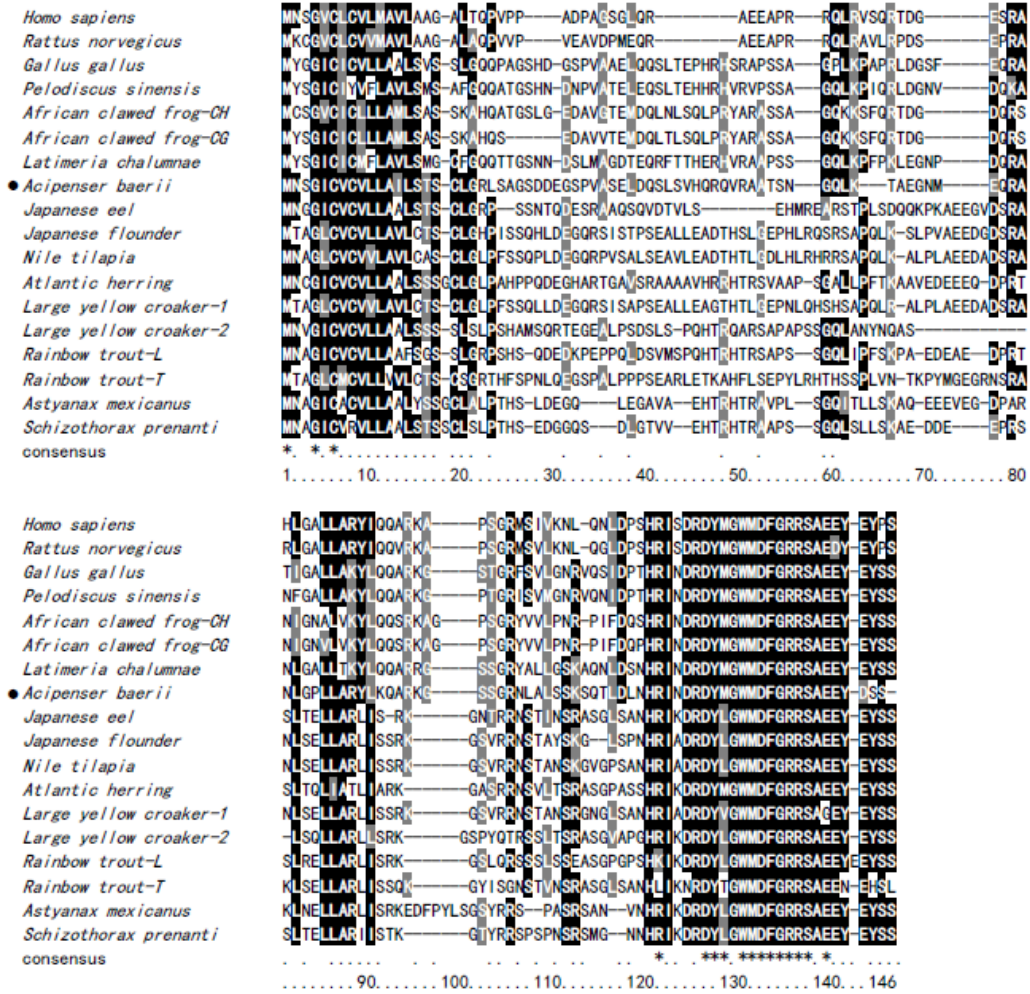
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**Supplementary Fig. 1** Amino acid sequence alignment of Siberian sturgeon CCK with other vertebrates, including Human (*Homo sapiens*, AH002739), Rat (*Rattus norvegicus*, NM\_012829), Chicken (*Gallus gallus*, NM\_001001741), Chinese soft-shelled turtle (*Pelodiscus sinensis*, XM\_006131816), African clawed frog (*Xenopus laevis*, Z47558/ Z47557), Coelacanth (*Latimeria chalumnae*, XM\_006013037), rainbow trout (*Oncorhynchus mykiss*, NM\_001124611/ NM\_001124345), *Schizothorax prenanti* (KJ194185), *Astyanax mexicanus* (XM\_007250428), Nile tilapia (*Oreochromis niloticus*, NM\_001279730), Large yellow croaker (*Larimichthys crocea*, KC899121/ KF938690), Atlantic herring (*Clupea harengus*, NM\_001309836), Japanese eel (*Anguilla japonica*, AB109556) and Japanese flounder (*Paralichthys olivaceus*, AB009281). The colored amino acids highlight the differences in conservation of the amino acids between species of CCK.

**Supplementary Fig. 2** Phylogenetic analysis of CCK amino acid sequences was performed using MEGA 7.0 software of maximum likelihood method with default settings. Scale bar indicates the substitution rate per residue. Numbers at nodes indicate the bootstrap value, as percentages, obtained for 1000 replicates. GenBank accession numbers were listed in the legend of Supplementary Fig.1.

# Supplementary Fig. 1



Supplementary Fig. 2

