

nn

ARRB1 2ry struc. PAPEDKK-PLTRLQERLIKKLG-EHAYPFTFEIPPNLPCS-VTLQP
 BPS CCCCCC-**HHHHHHHHHHH**CCCC-CCC**EEEE**CCCCCCCCCCCCCCCC
 D_R CCCCCC-CCC**HHHHHHHHH**CHC-CC**H**CCCCCCCCCCCCCCCC**H**CCCC
 DSC CCCCCC-CHHHHHHHHHHHHHHC-CCCCC**EEEE**CCCCCCCC**EEEE**CC
 GGR CCCCCC-CHHHHHHHHHHHHHHC-CCCCCC**EEEE**CCCCCCCC**EEEE**CC
 GOR CCCCCC-**HHHHHHHHHHHHHHH**-CCCCCC**B**CCCCCCCCCCCC**EE**CC
 H_K CCCCCC-CC**HHHHHHHHHHHHH**-CCCCCCCCCCCCCCCCCCCC**EE**CC
 K_S CCCCCC-CCCC**HHHHHHHHHHH**-**H**CCCCCCCCCCCCCCCCCCCCC
 JOI CCCCCC-CHHHHHHHHHHHHHHC-CCCCCC**B**CCCCCCCCCCCC**EE**CC

PD--TGE-----TTTL-PPG-RHEFLFSFQLP--PTL-VTSFE
CC--CCC-----CCCC-CCC-CCCCCCCCCE--EEE-EEEEC
CC--CCC-----CCCC-CCC-CHHHHBEFCCC--CEE-EEEEC
CC--CCC-----EEEC-CCC-CEEEEEEECCC--CEE-EEEEC
CC--CCC-----CEEC-CCC-CCCEEECCC-CEE-EEEEC
CC--CCC-----EEEE-CCC-CHHHHHHHCCC--CEE-EEEEC
CC--CCC-----EEEC-CCC-CCCEEECCC-CEE-EEEEC
CC--CCC-----CCCC-CCC-CCCECCCCC-CEE-EECCCC
CC--CCC-----CEEC-CCC-CCCEEECCC-CEE-EEEEC

Additional file 6. Visual/beta arrestin helix I is absent in alpha arrestins. The multiple sequence alignment shows visual/beta arrestins (red/top) and alpha arrestins (blue/bottom) from zebrafish and humans. Positions that may be conserved in both vertebrate subfamilies are shaded yellow, those specific to alphas are blue, visual/betas are red, and potentially notable are light gray. Below, is the ARRB1 sequence duplicated from the alignment, but with the secondary structure features determined by crystallography (adapted from Han et al. 2001) mapped – beta strand in gray and helix in black. Below that are the ARRB1 secondary structure predictions made by eight algorithms (PELE, UCSD Biology Workbench [see Additional file 2]). The helix is predicted to be absent in all human alpha arrestins. Below that is the ARRDC2 sequence duplicated, shown with its secondary structure predictions. The top line shows the aligned region is within the Arrestin N domain.