

NP_001004605_ZF	DNCPSR-----
ARRDC3_HUMAN	SCPSR-----
Q6TEM6_ZFISH	MTC-----
ARRDC2_HUMAN	MTC-----
ARRDC4_HUMAN	VSFIL-----
XP_683827_ZFISH	-----
Txnip_ZFISH	PVC-----
TXNIP_HUMAN	-----
NP_001017785_ZF	-----
NP_001017889_ZF	PDQPEKS-----
XP_695840_ZFISH	PNAPY-----
Q6ZM71_ZFISH	MPSSASVPPSYRSSAYPQEAPPSYEDSFNT-----
ARRDC1_HUMAN	TTSTLILPPEYSSWGYPYEAPPSYEQSCGGVEPSLTPES
ARRDC5_HUMAN	-----
NP_999846_ZFISH	C-----
Arrb2_ZFISH	HFC-----
ARRB2_HUMAN	QLC-----
Arrb1_ZFISH	-----
ARRB1_HUMAN	EDGTGSPQLNNR-----
AAX69083_ZFISH	-----
NP_001002405_ZF	-----
Arr3_ZFISH	-----
ARR3_HUMAN	GDEGS-----
Zgc-66109_ZFISH	NANIEENV-----
SAG_HUMAN	RDKNDADE-----

*Arr3 struct
interactions*

*TXNIP
Phyre consensus
consens probab*

Arrestin domain

Additional file 4. Human arrestin family compared to select fish arrestins. We include all the high confidence zebrafish arrestins that we could identify, but there may be more [see Additional file 2]. Positions that may be conserved in both classes of vertebrate arrestins are shaded yellow, those specific to alphas are blue, beta are red, potentially notable are light gray, and PY motifs are black. A candidate class I SH3-binding motif (RXXPXXP) conserved in a loop near the center of the C domain of ARRDC2/3/4 is shown by dark gray shading of white letters. The arrestin domains are given at the bottom, n for N domain, c for C and t for Tail; italics show sequence not considered as part of the N and C domains according to Pfam. Shading on that line maps secondary structure elements on ARR3 (cone arrestin) – beta strands in gray and the one alpha helix in black (adapted from Sutton et al. 2005). Below the ARR3 structural elements, the predicted secondary structure of TXNIP is shown [see Additional file 2]. Underlining highlights regions involved in receptor specificity. Asterisks (*) show residues involved in the “three-element interaction”; number symbols (#) mark residues that make up the “polar core”.