The 2.8 Å crystal structure of visual arrestin : a model for arrestin's regulation

> Hirsch JA *etc. Cell* 97:257-269 (1999)

> > Presented by Liang



Active state: monomer;

Inactive state: heterodimer;

High concentration: tetramer.

chain A-alpha, BLUE; chain B-beta, CYAN; chain C-alpha, GREEN; chain D-beta, YELLOW.



Arrestin: desensitize GPCR*p



The binding of an arrestin to the phosphorylated receptor prevents the receptor from binding to its G protein and can direct its endocytosis.

Structure of arrestin-alpha



Topology of arrestin



3		
	α	β
1	10-16	11-16
11	22-26	22-26
111	30-33	30-33
IV	41-47	41-47
h	-	49-52
V	56-67	56-67
VI	79-89	79-91
hl	102-111	102-109
VII	115-120	115-120
VIII	130-132	130-132
IX	143-154	143-157
h**	155-163	-
S	-	161-163
h*	-	165-167
X	169-178	169-178
XI	191-198	189-194
XII	201-208	203-209
XIII	213-215	213-215
XIV	220-228	220-228
XV	234-247	234-247
XVI	254-264	254-263
XVII	272-280	272-280
h*ll	283-287	283-287
h*III	317-321	317-321
XVIII	323-335	323-335
h*	337-341	-
XIX	345-356	347-356
XX	375-379	375-379

s: strand;
h: alpha-helix;
h*: 3₁₀ helix;
h**: helical conformation.

C tail: restrain arrestin inactive



Critical residues are conserved

	ARABARA MARAARAA				II.I.I.I		*
1222	1						20
Vis.	MKANKPAPNHVIFKKISRDKS	VTIYLGRADYIDHVE	RVEPVDGVVLVDPELVKG.	KRVYVSLTCAFRYGQEDID	VMGLSFRRDLYFSQVQVFPPVG	ASGATTRLQESLIKKLGANTYPFLL	TFPDYLPCSVMLQPAPQDVG
Hu MAA	SGKTSKSEPNHVIFKKISRDKS	SVTIYLGNRDYIDHVS	QVQPVDGVVLVDPDLVKG.	KKVYVTLTCAFRYGQEDID	VIGLTFRROLYFSRVQVYPPVG	ASTPTKLOESLLKKLGSNTYPFLL	TFPDYLPCSVHLQPAPQDSG
Cone	MAESSKVFKKSSGDGK	LAIYLAKRDYVDHVD	HVEPVDGMIIIDPEYQKD.	KEVEVTLACTERYGRODHE	LIGLSFKKELCFLHCQVYPPLP	EDKKPTPLOEKLSKKLGVNAFPECE	NMTTDLPCSVTLOPGPEDTG
DroA	MVVNFKVFKKCSPNNM	ITLYMNRRDFVDSVT	QVEPIDGIIVLDDEYVRQN	REIFVOLVCNFRYGREDDE	MIGLRFOKELTLVSOQVCPPQK	DIQLIMMOERLLKKLGSNAYPEVM	OMPPSSPASVVLQQKASDES
DroB	MVVSVKVFKKATPNGK	(VTFYLGRRDFIDHID)	YCDPVDGVIVVEPDYLKN.	REVFGQLATTYRYGREEDE	VMGVKFSKELILCREQIVPMTN	PNMEMT PMQEKLVRKLGS . SAPFTF	HFPPNSPSSVTLQQEGDDNG
Barr1	MGDKGTRVFKKASPNGK	LTVYLGKRDFVDHID	LVDPVDGVVLVDPEYLKE.	RRVYVTLTCAFRYGREDLD	VLGLTFRKDLFVANVQSFPPAP	DKKPTRLQERLIKKLGEHAYPFTF	EIPPNLPCSVTLQPGPEDTG
Arr3	MGEKPGTRVFKKSSPNCK	LTVYLGKRDFVDHLD	KVDPVDGVVLVDPDYLKD.	REVEVILITCAFRYGREDLD	VLGLSFRKOLFIANYQAFPPTP	IPPRPTRLQERLLRKLGQHAHPFFF	TIPONLPCSVTLOPGPEDTG
trout	MGDKAGTRVFKKSSPNCK	VTVYLGKRDFVDHLD	OVDPVDGVILVDPEYLKD.	REVEVTLTCAFRYGREDLD	VLGLSFREDLYISTFOAFPPIA	ERKASRLOERLLKKLGQQAHPFYF	TIPONLPCSVTLOPGPEDTG
c.ele.	MVDEDKKSGTRVFKKTSPNGR	(ITTYLGKRDFIDRGD	YVD *** GHVLIDEEYIKDN	REVTAHLLAAFRYGREDLD	VLGLTERKOLISETFOVYPOTO	C. ***SRLQERLKRKLGANAFPFWF	EVAPKSASSVTLQPAPGDTG

	18	A second at the second second	411	211		XIV	10V		XVI >	XVII
				.200	210	220	230			
Vis.	KSCGVDFEIKAFATHSTDVEEDKIPK	KSSVRLLIRKVQHAPR	DMGPQPRAEASWQFF	SDKPLRLAVSI	SKEIYYHGE	PIPVTVAVTNS	TEKTVKKIKVLVEQ	VTNVVLYSSDYYIK	TVAAEEAQEKVPPNS:	SLTKTLTL
Hu	KSCGVDFEVKAFATDSTDAEEDKIPK	KSSVRLLIRKVQHAPL	EMGPOPRAEAAWOFF	SOKPLHLAVSI	NKEIYFHGER	PIPVTVTVTNN	TEKTVKKIKAFVEQ	VANVVLYSSDYYVK	PVAMEEAQEKVPPNS:	TLTKTLTL
Cone	KKCGVDFEVKGF WADNVEEKISR	KNSVQLIIRKVQFAPE	ATGTASCVQTTRQEM	SDKPLQVEVSI	DKEVYYHGE	VGIKLKINNN	TSKIVKKIKITVEQ	LTDVVLYSLDKYTK	IVCCEEINETVAANAN	NFSGSYSL
DroA	QPCGVQYFVKIF TGDSDCDRSHR	RSTINLGIRKVQYAPT	KQGIQPCTVVRKDFLL	SPGELELEVTI	DKQLYHHGEN	ISVNICVENN	SNKVVKKIKAMVQQ	GVDVVLFQNGQFRN	TIAFMETSEGCPLNS	SLOKVHYL
DroB	KPLGVEYTIRAF VGDSEDDRQHK	RSMVSLVIKKLQYAPL	NRGRLPSSLVSKGFT	SNGKISLEVTI	DREIYYHGEN	TAATVQVSNN	SKKSVKSIKCFIVO	HTEITHV . NAQFSK	HVAQLETKEGCPITA	NLTKTFYL
Barr1	KACGVDYEVKAF CAENLEEKIHK	RNSVRLVIRKVQYAPE	RPGPOPTAETTROFIL	SOKPLHLEASI	DKEIYYHGE	ISVNVHVTNN	INKTVKKIKISVRO	YADICLENTAQYKC	PVAMEEADDTVAPSS:	TFCKVYTL
Arr3	KACGVDFEIRAF CAKSLEEKSHK	RNSVRLVIRKVQFAPE	KPGPQPSAETTRHFLM	SDRSLHLEASI	DKELYYHGE	LNVNVHVTNN	STKTVKKIKVSVRQ	YADICLESTAQYKC	PVAQVEQDDQVSPSS	TECKVYTI
Trout	KACGVDFEIRAF CAKSIEEKIHK	RNSVRLVIRKVQYAPE	KPGPQPMVETTRSFL	SDRSLHLEASI	DKELYYHGE	ISVNVHVTNN	TKTVKRLKISVRQ	YADICLESTAQYKC	PVAQVEADDQVSSSS	TECKVYTL
c ala	KOCOUNTELETEVAUTOGSSCER PR	ROTUPLATERLTVAPE	RSPROPMUTUSKY	SCILLHMEVEL	DREMYVHORS	TRUNUHTONN	SNETVERLETYTTO	VADICLETTASYSC	EVARTESNEGEPPGC	TLSEVEAV

290.300 310.320 330.340 350 360.370.2859 2000 2000 2000 2000 2000 2000 2000 20		a a Juria a construction and Halten and a stilling a statistical frame. It was a statistical statistical statis
Vis. VPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDKTVMGILVSVQIKVKLTVSGLIGELTSSEVATEVPFRLMHPQPEDPT. KESYQDENEVPEEPARQKLKAGEYKEEKTOQEAAMOE Hu LPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDRTVLGILVSYQIKVKLTVSGFLGELTSSEVATEVPFRLMHPQPEDPT. KESYQDENEVPEEPARQKLKGAGEXEEGKRDNDADE Come TPLLANNKERRGIALDGKIKHEDTNLASSTIIRPGKKEVLGALVSYVVVGILGDLTSSDVSVELPPTLMHPKPSPDQTIEDVVIREPARQKLQGAEGEDOKDDA DroA VPTLVANCDRAGIAVEGDIKRKDTALASTTLIASQDARDAFGIIVSYAVKVKLFLGALGGELCAELPFILMHPKPSRKAQ FARSTI TPFLANNRERRGIALDGKIKHEDTNLASSTTLRPGKDKEVLGILVSYVVVGILGDLTSSDVSVELPPTLMHPKPSRKAQ Barri TPFLANNRERRGIALDGKIKHEDTNLASSTTLRPGKDKEVLGILVSYVVKVKLVVSRG*GDLASSDVAVELPFTLMHPKPDDDIVFEDFARQRLKGMKDNNMAD Arr3 TPLSNNRERRGIALDGKIKHEDTNLASSTIVKEGANKEVLGILVSYKVKVKVVSRG*GDLASSDVAVELPFTLMHPKPDDDIVFEDFARQRLKGMKDKDEDDGTGSPHLNNI Arr3 TPLLSNNRERRGIALDGKLKHEDTNLASSTIVKOVTNKEVLGILVSYKVKVKVVSRG*GDVSVELPFVLMHPKPDDDIVFEDFARQRLKGMADDKDDDC c.ele. CPLLSNNKDKRGIALDGQLKHEDTNLASSTILDSKTSKESLGIVVQVRVKVRAVLGPLNGELFAELPFTLTHSKPDDDLIFEDFARMRLHGNDSEDQPSPSANLPPSLL insertion: DroB: GTIEKKRSNAMKKMKSIEQKR VKGYYQDN Barr1: Arr3: HDHIALPRPQSAATHPFTLPSAVEESTP DTNLIEFTNYAT trout: C.ele.: PESPERTVGSAVPDSDPP DTNLIEFTNYAT trout: C.ele.: PESPERTVGSAVPDSDPP DTNLIEFTNYAT		290
Hu LPLANNKERRGIALDGKIKHEDTNLASSTIIKEGIORTVLGILVSVQIKVKLTVSGFLGELTSSEVATEVPFRLMHPQEEDP. KESYQDANLVFEFARHNLKDAGEAEEGKRDKNDADE Cone TPLLANNKERRGIALDGKIKHEDTNLASSTIIRPGMDKVLGNLVSYVVRUSLV*GILGDLTSSDVSVELPFTLMHPKPSPDQT IEDVINEPFARKUQGAEGEDDKDDA Dro& VPTLVANCDRAGIAVEGDIKKKDTALASTTLIASQDADAFGIVSYVVRUSLV*GILGDLTSSDVSVELPFTLMHPKPSPDQT IEDVINEPFARKUQGAEGEDDKDDA DroB IPLAANNKDRHGIALDGHLKDEDVNLASSTMVQEGKSTGDCGIVISYSVRIKLNCGTLGGEMQTDVPFKLLQPAP DDDIVFEDFARQALKGKDKHEDTNLASSTILRPGAMEFILDIIVSYKVKVKUVSRG*GGLASSDVAVELPFTLMHPKP Arr3 TPLLSNNREKRGIALDGKLKHEDTNLASSTIVKEGAMKEVLGILVSYRVKVKUVSRG*GDV.SVELPFVLMHPKP DDDIVFEDFARQALKGKDKDEEDDGTGSPHLNNI Arr3 TPLLSNNREKRGIALDGKLKHEDTNLASSTIVKEGAMKEVLGILVSYRVKVKUVISRG*GDV.SVELPFVLMHPKP DDDIVFEDFARQALKGKDDDCC c.ele. CPLLSNNKDKRGIALDGQLKHEDTNLASSTILDSKTSKESLGIVVQYRVKVRAVLGPLNGELFAELPFTLTHSKP DDDIVFEDFARLKLKGKADDKDDCC c.ele. CPLLSNNKDKRGIALDGQLKHEDTNLASSTILDSKTSKESLGIVVQYRVKVRAVLGPLNGELFAELPFTLTHSKP DDDLIFEDFARMRLHGNDSEDQPSPSANLPPSLL insertion: DroB: GTIEKKRSNAMKKMKSIEQRR KEEPPHREVPESETP DTNLIELDTN Arr3: HDHIALPRQSAATHPPTLPSAVFETDAP DTNLIEFTNYAT trout: C.ele.: PESPERTORGLPSIEATNGSE.P DIDLILFETNYAT	Vis.	VPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDKTVMGILVSYQIKVKLTVSGLLGELTSSEVATEVPFRLMHPQPEDPDT KESFQDENFVFEEPARQNLKDAGEYKEEKTDQEAAMDE
Cone TPLLANNKEKRGLALDGKLKHGDTNLASSTILREGAMDKEVLCALUSYKVRVSUV*GILGDLTSSDVSVELPPTLMHPKPSPDQT IEDVVIREPARQKLQGAEGEDDKDDA Drok VPTLVANCDRAGIAVEGDIKRKDTALASTTLIASQDARDAPGIVSYAVKVKLFLGALGGELCAELPFILMHPKPSRKQ EAEGSIEA Drob IPLAANNKERGLALDGKLKHEDTNLASSTLIASQDARDAPGIVSYAVKVKLFLGALGGELQAELPFILMHPKPSRKQ DDNIVPEDPAKMRMNNVNMAD Arr3 TPFLANNREKRGLALDGKLKHEDTNLASSTLIKEGAME ILDIVSYKVKVKLVVSRG*GDLASSDVAVELPFTLMHPKP DDDIVPEDPARQELKGMKDKDEEDDGTGSPHLNNI Arr3 TPLLSNNREKRGLALDGKLKHEDTNLASSTLVKEGANKEVLGIVSYRVKVKLVVSRG*GDV SVELPPVLMHPKP DDDIVPEDPARQELKGMKDDKDEEDDGTGSPHLNNI Arr3 TPLLSNNREKRGLALDGKLKHEDTNLASSTIVKEGANKEVLGILVSYRVKVKLVSRG*GDV SVELPPVLMHPKP DDDIVPEDPARQELKGAMDDKDDDC c.ele CPLLSNNKDKRGLALDGQLKHEDTNLASSTIVDYTMKEVLGILVSYRVKVRLVISRG*GDV SVELPPVLMHPKP DDDIVPEDPARQELKGAMDDKDDCC c.ele CPLLSNNKDKRGLALDGQLKHEDTNLASSTILDSKTSKESLGIVVQYRVKVRAVLGPLNGEL FAELPFTLTHSKP DDDLIPEDFARMELHGNDSEDQPSPSANLPPSLL insertion: GTIEKKRSNAMKMKSIEQHR VKGYYQDN garr1: KEEPPHREVPESETP DTNLIELDTN Arr3: HDHIALPPQSAATHPPTLHPSAVETDAP DTNLIELTNN YKGYYQDN TELPISRPQSAVPDSDPP DTNLIEFTNSFSQ c.ele: PESPERTDRGLPSLATHEPTNEFTNSFSQ	Hu	LPLLANNRERRGIALDCKIKHEDTNLASSTIIKEGIDRTVLCILVSYQIKVKLTVSCFLGELTSSEVATEVPFRLMHPQPEDPKESYQDANLVFEEFARHNLKDAGEAEEGKRDKNDADE
DroA VPTLVANCORAGIAVEGDIKRKOTALASTTLIASQDARDAFGIIVSVAVKVKLFLGALGGELCA. ELPFILMHPKPSRKAQ EAEGSIEA DroB IPLANNKORHGIALDGKLKHEDTNLASSTWVQEGKSTGOCGIVSSVSRIKLNCGTLGGEMQT. DVPFKLQPAPDONIVFEDFAKMRMONVNMAD #arr1 TPFLANNREKRGLALDGKLKHEDTNLASSTLLREGANKEVLGILVSYKVKVVSRG*GDLASSDVAVELPFTLMHPKPDODIVFEDFAKMRMONVNMAD Arr3 TPLLSNNREKRGLALDGKLKHEDTNLASSTIVKEVLGILVSYKVKVVSRG GOV. SVELPFVLMHPKPDODIVFEDFAKMRMONVDMAD c.ele. CPLLSNNREKRGLALDGKLKHEDTNLASSTIVKDVTNKEVLGILVSYRVKVKLVISRG GOV. SVELPFVLMHPKPDDDIVFEDFARLRLKGLADDKDDDQFC c.ele. CPLLSNNKDKRGLALDGQLKHEDTNLASSTILDSKTSKESLGIVVQYRVKVRAVLGPLNGEL. FAELPFTLTHSKFDDDLIFEDFARMRLHGNDSEDQPSPSANLPPSLL insertion: DroB: GTIEKKRSNAMKKMKSIEQHR KEEPFRREVFESETP DTNLIELDCTN Arr3: HDHIALPRPQSAATHPPTLLPSAVPETDAP DTNLIELDCTN Arr3: TELPISRPQSAVPEDAP DTNLIEFTNYAT trout: TELPISRPQSAVPEDAP DTNLIEFTNYAT	Cone	TPLLANNKEKRGLALDGKLKHGDTNLASSTILRPGNDKEVLGHLVSYKVRVSLVV*GILGDLTSSDVSVELPPTLMHPKPSPDQTIEDVVIREPARQKLQGAEGEDDKDDA
DroB IPLANNKORHGIALDGHLKDEDVNLASSTMVQEGKSTGDCGIVISYSVRIKLNCGTLGGEMQT. DVPFKLLQPAP parr1 TPFEANNREKRGIALDGKLKHEDTNLASSTLLREGANEILDIVSYKVKVKLVVSRG GDLASSDVAVELPFTLMHPKP Arr3 TPLLSNNREKRGIALDGKLKHEDTNLASSTLVKEGANKEVLGILVSYKVKVKLVISRG GDV. SVELPFVLMHPKP DDDIVFEDFARQALKGKDKDEDDDCC c.ele. CPLLSNNKEKRGIALDGKLKHEDTNLASSTIVKDYNKEVLGILVSYKVKVKLVISRG GDV. SVELPFVLMHPKP DDDIVFEDFARLALKGLKDGKDCC c.ele. CPLLSNNKEKRGIALDGKLKHEDTNLASSTIVKDYNKEVLGILVSYKVKVKLVISRG GDV. DDDIVFEDFARLALKGLKDGKLKHEDTNLASSTIVKDYNKEVLGILVSYKVKVKLVISRG GDV. c.ele. CPLLSNNKDKRGIALDGKLKHEDTNLASSTIVLDYNKEVLGILVSYKVKVKLVISRG GDV. DDDIVFEDFARLALKGLKDGKDCC c.ele. CPLLSNNKDKRGIALDGQLKHEDTNLASSTILDSKTSKESLGIVVQYRVKVRAVLGPLNGEL. FAELPFTLTHSKP DDDLIFEDFARLALKGKAGNDSEDQPSPSANLPPSLL insertion: DroB: GTIEKKRSNAMKKMKSIEQKR KEEPPHREVPESETP DTNLIELDTN Arr3: HDHIALPRQSAATHPPTLPSAVPETDAP DTNLIEFTNYAT trout: C.ele.: PESPERTORGLPSIEATNGSE.P DIDLIQLKEELPRY	DroA	VPTLVANCDRAGIAVEGDIKRKDTALASTTLIASQDARDAFGIIVSYAVKVKLFLGALGGELCAELPFILMHPKPSRKAQ
\$arr1 TPFLANNREKRGLALDGKLKHEDTNLASSTLLREGANREILGIIVSYKVKVKLVVSRG*GDLASSDVAVELPFTLMHPKPDDDIVFEDFARQRLKGHXDDKDEEDDGTGSPHLNNI Arr3 TPLLSNNREKRGLALDGKLKHEDTNLASSTIVKEGANREVLGILVSYKVKVKLVVSRG.GDVSVELPFVLMHPKPDDDIVFEDFARQRLKGHXDDKDEEDDGTGSPHLNNI C.ele. CPLLSNNKDKRGLALDGQLKHEDTNLASSTIVKDVTNKEVLGILVSYRVKVKLVISRG.GDVSVELPFVLMHPKPDDDIVFEDFARQRLKGHXDDKDEDDQFC insertion: DroB: GTIEKKRSNAMKKMKSIEQHR VKGYYQDN \$arr1: KEEPPHREVPESETP DTNLIEFTNAT Trout: TELPISRPQSAVTHOPSDAP C.ele.: PESPERTORGLPJSTATHGSE.P	DroB	IPLAANNKORHGIALDGHLKDEDVNLASSTMVQEGKSTGDCGIVISYSVRIKLNCGTLGGEMQTDVPFKLLQPAPDDNIVFEDFAKMRMNNNMAD
Arr3 TPLLSNNREKRGLALDGKLKHEDTNLASSTIVKEGANKEVLGILVSYRVKVKLVVSRG.GDVSVELPFVLMHPKPDDDIVFEDPARLRLKGLADDQPC Trout TPTLDKNREKRGLALDGKLKHEDTNLASSTIVKDVTNKEVLGILVSYRVKVKLVISRG.GDVSVELPFVLMHPKPDDDIVFEDPARLRLKGLADDKDDDC c.ele. CPLLSNNKDKRGLALDGQLKHEDTNLASSTILDSKTSKESLGIVVQYRVKVRAVLGPLNGELFAELPFTLTHSKPDDDLIFEDFARMRLHGNDSEDQPSPSANLPPSLL insertion:	Barr1	TPFLANNRENRGLALDGKLKHEDTNLASSTLLREGANREILGIIVSYKVKLVVSRG*GDLASSDVAVELPFTLMHPKPDDDIVFEDFARGRLKGMKDDKDEEDDGTGSPHLNNR
Trout TPTLDKNREKRGLALDGKLKHEDTNLASSTIVKDVTNKEVLGILVSYRVKVKLVISRG.GDVSVELPFVLMHPKP c.ele. CPLLSNNKDKRGLALDGQLKHEDTNLASSTILDSKTSKESLGIVVQYRVKVRAVLGPLNGELFAELPFTLTHSKP insertion: DroB: GTIEKKRSNAMKKMKSIEQKR KEEPPHREVESETP DTNLIELDTN Arr3: HDHIALPRQSAATHPPTLLPSAVPETDAP DTNLIEFETNSFSQ c.ele.: PESPERTORGLPSIEATNGSE.P DIDLIQLWEELEPRY	Arr3	TPLLSNNREKRGLALDGKLKHEDTNLASSTIVKEGANKEVLGILVSYRVKVKLVVSRG.GDVSVELPPVLMHPKDDDDIVFEDFARLRLKGLKDEDYDDOFC
c.ele. CPLLSNNKDKRGLALDGOLKHEDTNLASSTILDSKTSKESLGIVVOYRVKVRAVLGPLNGELFAELPFTLTHSKPDDDLIFEDFARMRLHGNDSEDQPSPSANLPPSLL insertion: DroB: GTIEKKRSNAMKKMKSIEQRR KEEPPHREVPESETP DTNLIELDTN Arr3: HDHIALPRPQSAATHPPTLLPSAVPETDAP DTNLIEFETNYAT trout: c.ele.: PESPERTORGLPSIEATNGSE.P DIDLIQLWEELEPRY	Trout	TPTLOKNREKRGLALOGKLKHEDTNLASSTIVKDVTNKEVLGILVSYRVKVKLVISRG.GDV. SVELPFVLMHPKP. DDDFVFEDFARLRLKGMADOKDDDC
insertion: DroB: Barrl: Arr3: trout: c.ele.: DroB: DroB: GTIEKKRSNAMKKMKSIEQHR KEEPPHREVPESETP DTNLIELDTN KEEPPHREVPESETP DTNLIEFTNYAT TELPISRPQSAVPETDAP DTNLIEFETNSFSQ PESPERTORGLPSIEATNGSE.P DIDLIQLHEELEPRY	c.ele.	CPLLSNNKDKRGLALDGQLKHEDTNLASSTILDSKTSKESLGIVVQYRVKVRAVLGPLNGELFAELPFTLTHSKPDDDLIFEDFARMRLHGNDSEDQPSPSANLPPSLL
DroB: GTIEKKRSNAMKKMKSIEQHR VKGYYQDN βarr1: KEEPPHREVPESETP DTHLIELDTH Arr3: HDHIALPRQSAATHPPTLLPSAVPETDAP DTHLIEFTNYAT trout: TELPISRPQSAVPESDPP DTNLIEFTNSFSQ c.ele.: PESPERTORGLPSIEATNGSE.P DIDLIQLWEELEPRY	insert	
βar1: KEEPPHREVPESETP βar1: KEEPPHREVPESETP DTNLIEFTNYAT HDHIALPRPQSATHPTLLPSAVPETOP trout: TELPISRPQSAVPDSDPP c.ele.: PESPERTORGLPSIEATNGSE.P	DroB.	CATE PURCHASHING TRANSPORT
pari: Distribution Arr3: HDHIALPRQSAVFPTLPSAVPETDAP trout: TELPISRPQSAVPDSDPP c.ele.: PESPERTORGLPSIEATNGSE.P	Barri.	
AFF3: HDHIALPRQSAATAPPTLPSAVETDAR DTALLEFITATAT trout: TELPISRPQSAVPSDPP DTALLEFITASFSQ c.ele.: PESPERTORGLPSIEATAGSE.P DIDLIQLHEELEPRY	parrii	REAPPREVESSIP DIALIELDIA
c.ele.: TELPISRPQSAVPDSDPP DTNLIEFETNSFSQ PESPERTDRGLPSIEATNGSE.P DIDLIQLHEELEPRY	ATT3:	HDHIALPRPQSAATHPPTLLESAVPETDAP DINLLEPETRIAT
c.ele.: PESPERTDRGLPSIEATNGSE.P DIDLIQLHEELEPRY	trout:	TELPISRPQSAVPDSDPP DTNLIEPETNSFSQ
	c.ele.	PESPERTORGLPSIEATNGSE, P DIDLIQLHEELEPRY



Plasticity of Arrestin



- A, helical conformation of residues 155-165;
- B, strand-turn-strand conformation;
- C, dimer interface between alpha and beta (residues 68-79);
- D, interface between alpha and beta (residues 337-347);
- E, dimer interface between alpha and beta.

A. residues 155-165



arresin-alpha: **helix**

arresin-beta: strand-turn-strand

C. interface between alpha and beta



D. interface between alpha and beta



Polar core: energetic un-favor









- charged side chains are buried;
- forming charge-charge interaction to keep neutrality;





Cleavage C tail actives arrestin





Model for arrestin's activation

- C tail & balanced polar core maintains basal state of arrestin
- Rho*p destabilize polar core
- Arrestin rearranges into active state
- Form arrestin-receptor complex



Thanks.

Oct. 21, 2003