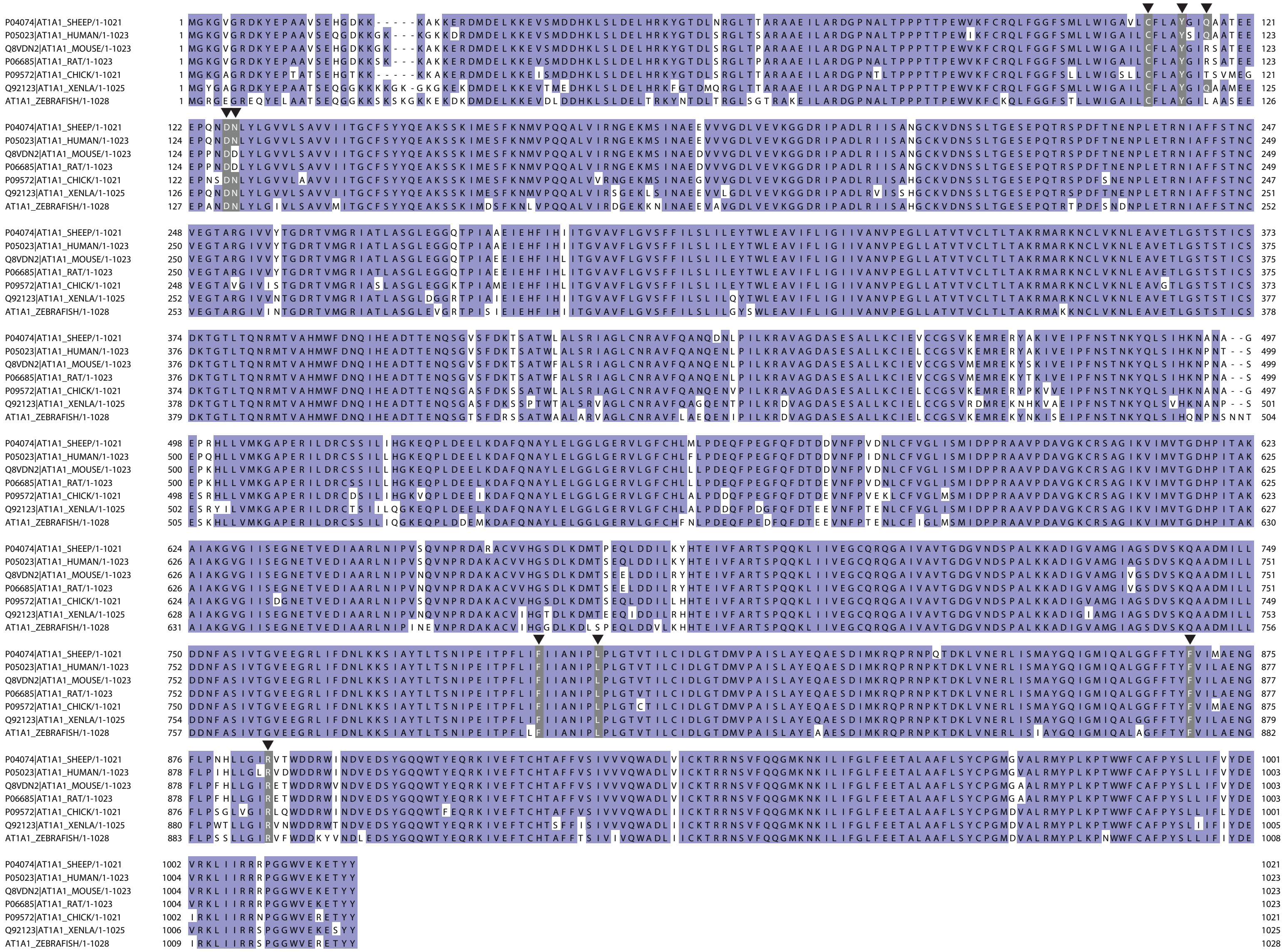

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Q8VDN2|AT1A1_MOUSE/1-1023       1 MGKGVGRDKYEPAAVSEHGDKKGK---KAKKERDMDELKKEVSMDDHKLSLDELHRKYGTDLSRGLTPARAAEILARDGPNALTPPPTTPEWVKFCRQLFGGFSMLLWIGAILCFLAYGIRSATEE 123
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P09572|AT1A1_CHICK/1-1021       1 MGKGAGRDKYEPTATSEHGTKK-----KKAKERDMDELKKEISMDDHKLSLDELHRKYGTDLSRGLTTARAAEILARDGPNTLTPPPTTPEWVKFCRQLFGGFSLLLWIGSLLCFLAYGITSVMEG 121
Q92123|AT1A1_XENLA/1-1025       1 MGYGAGRDKYEPAATSEQGGKKKKGK-GKGKEKDMDELKKEVTMEDHKLSLDELHRKFGTDMQRGLTTARAAEILARDGPNALTPPPTTPEWVKFCRQLFGGFSMLLWIGAILCFLAYGIQAAMEE 125
AT1A1_ZEBRAFISH/1-1028          1 MGRGEGREQYELAATSEQGGKKSKSKGKKEKDKDMDELKKEVDLDDHKLSLDELTRKYNTDLTRGLSGTRAKEILARDGPNALTPPPTTPEWVKFCKQLFGGFSTLLWIGAILCFLAYGILAASEE 126

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Q92123|AT1A1_XENLA/1-1025     126 EPQNDNLYLGVVLSAVVIITGCFSYYQEAKSSKIMESFKNMVPQQALVIRSGEKLSINAEEVVLGDLVEVKGGDRIPADLRVISSHGCKVDNSSLTGESEPQTRSPDFTNENPLETRNIAFFSTNC 251
AT1A1_ZEBRAFISH/1-1028        127 EPANDNLYLGIVLSAVVMITGCFSYYQEAKSSKIMDSFKNLVPQQALVIRDGEKKNINAEEVAVGDLVEVKGGDRIPADLRIISAHGCKVDNSSLTGESEPQTRTPDFSNDNPLETRNIAFFSTNC 252

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P06685|AT1A1_RAT/1-1023       250 VEGTARGIVVYTGDRTVMGRIATLASGLEGGQTPIAEEIEHFIHLITGVAVFLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICS 375
P09572|AT1A1_CHICK/1-1021     248 VEGTAVGIVISTGDRTVMGRIASLASGLEGGKTPIAMEIEHFIHLITGVAVFLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVGTLGSTSTICS 373
Q92123|AT1A1_XENLA/1-1025     252 VEGTARGIVVNTGDRTVMGRIATLASGLDGGRTPIAIEIEHFIHIITGVAVFLGVSFFILSLILQYTWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICS 377
AT1A1_ZEBRAFISH/1-1028        253 VEGTARGIVINTGDRTVMGRIATLASGLEVGRTPISIEIEHFIHIITGVAVFLGVSFFILSLILGYSWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMAKKNCLVKNLEAVETLGSTSTICS 378

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Q8VDN2|AT1A1_MOUSE/1-1023     376 DKTGTLTQNRMTVAHMWFDNQIHEADTTENQSGVSFDKTSATWFALSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIEVCCGSVMEMREKYSKIVEIPFNSTNKYQLSIHKNPNA--S 499
P06685|AT1A1_RAT/1-1023       376 DKTGTLTQNRMTVAHMWFDNQIHEADTTENQSGVSFDKTSATWFALSRIAGLCNRAVFQANQENLPILKRAVAGDASESALLKCIEVCCGSVMEMREKYTKIVEIPFNSTNKYQLSIHKNPNA--S 499
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Q92123|AT1A1_XENLA/1-1025     378 DKTGTLTQNRMTVAHMWFDNQIHEADTTENQSGASFDKSSPTWTALSRVAGLCNRAVFQAGQENTPILKRDVAGDASESALLKCIELCCGSVRDMREKNHKVAEIPFNSTNKYQLSVHKNANP--S 501
AT1A1_ZEBRAFISH/1-1028        379 DKTGTLTQNRMTVAHMWFDNQIHEADTTENQSGTSFDRSSATWAALARVAGLCNRAVFLAEQENIPILKRDVAGDASESALLKCIELCCGSVKEMREKYNKISEIPFNSTNKYQLSIHQNPNSNNT 504

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P04074|AT1A1_SHEEP/1-1021     750 DDNFASIVTGVEEGRLIFDNLKKSIAYTLTSNIPEITPFLIFIIANIPLPLGTVTILCIDLGTDMVPAISLAYEQAESDIMKRQPRNPQTDKLVNERLISMAYGQIGMIQALGGFFTYFVIMAENG 875
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P05023|AT1A1_HUMAN/1-1023     878 FLPIHLLGLRVDWDDRWINDVEDSYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFEETALAAFLSYCPGMGVALRMYPLKPTWWFCAFPYSLLIFVYDE 1003
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P05023|AT1A1_HUMAN/1-1023    1004 VRKLIIRRRPGGWVEKETYY 1023
Q8VDN2|AT1A1_MOUSE/1-1023    1004 VRKLIIRRRPGGWVEKETYY 1023
P06685|AT1A1_RAT/1-1023      1004 VRKLIIRRRPGGWVEKETYY 1023
P09572|AT1A1_CHICK/1-1021    1002 IRKLIIRRNPGGWVERETYY 1021
Q92123|AT1A1_XENLA/1-1025    1006 VRKLIIRRSPGGWVEKESYY 1025
AT1A1_ZEBRAFISH/1-1028       1009 IRKLIIRRSPGGWVERETYY 1028
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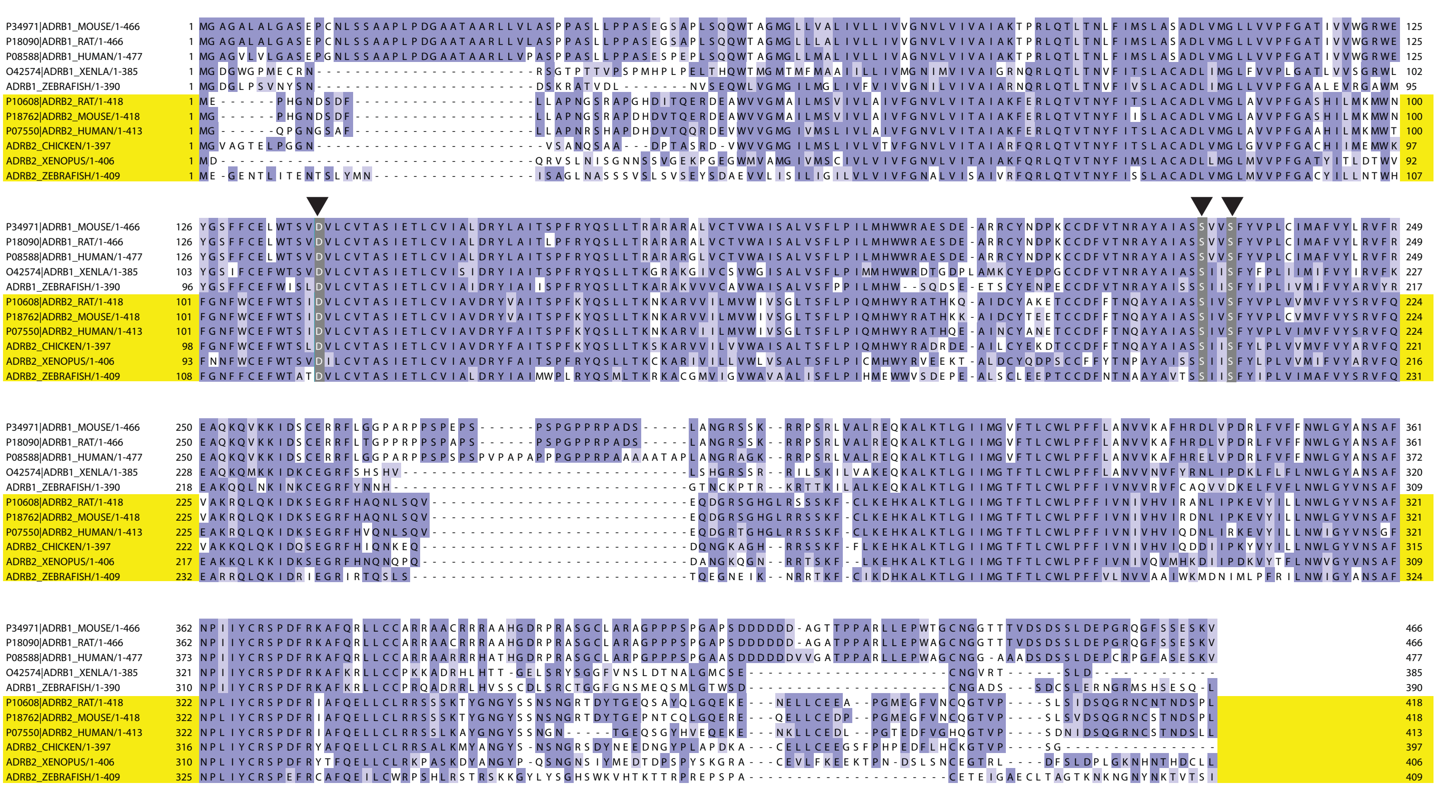

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P18090|ADRB1_RAT/1-466        1 MGAGALALGASEPCNLSSAAPLPDGAATAARLLVLASPPASLLPPASEGSAPLSQQWTAGMGLLLALIVLLIVVGNVLVIVAIAKTPRLQTLTNLFIMSLASADLVMGLLVVPFGATIVVWGRWE 125
P08588|ADRB1_HUMAN/1-477      1 MGAGVLVLGASEPGNLSSAAPLPDGAATAARLLVPASPPASLLPPASESPEPLSQQWTAGMGLLMALIVLLIVAGNVLVIVAIAKTPRLQTLTNLFIMSLASADLVMGLLVVPFGATIVVWGRWE 125
O42574|ADRB1_XENLA/1-385      1 MGDGWGPMECRN-----------------------RSGTPTTVPSPMHPLPELTHQWTMGMTMFMAAIILLIVMGNIMVIVAIGRNQRLQTLTNVFITSLACADLIMGLFVVPLGATLVVSGRWL 102
ADRB1_ZEBRAFISH/1-390         1 MGDGLPSVNYSN-----------------------DSKRATVDL-------NVSEQWLVGMGILMGLIVFVIVVGNILVIVAIARNQRLQTLTNVFIVSLACADLIMGLLVVPFGAALEVRGAWM 95
P10608|ADRB2_RAT/1-418        1 ME------PHGNDSDF-------------------LLAPNGSRAPGHDITQERDEAWVVGMAILMSVIVLAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGASHILMKMWN 100
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ADRB2_CHICKEN/1-397           1 MGVAGTELPGGN------------------------VSANQSAA---DPTASRD-VWVVGMGILMSLIVLVTVFGNVLVITAIARFQRLQTVTNYFITSLACADLVMGLGVVPFGACHIIMEMWK 97
ADRB2_XENOPUS/1-406           1 MD---------------------------------QRVSLNISGNNSSVGEKPGEGWMVAMGIVMSCIVLVIVFGNVLVITAIAKFQRLQTVTNYFIMSLACADLLMGLMVVPFGATYITLDTWV 92
ADRB2_ZEBRAFISH/1-409         1 ME-GENTLITENTSLYMN-----------------ISAGLNASSSVSLSVSEYSDAEVVLISILIGILVLVIVFGNALVISAIVRFQRLQTVTNYFISSLACADLVMGLMVVPFGACYILLNTWH 107

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P18090|ADRB1_RAT/1-466      126 YGSFFCELWTSVDVLCVTASIETLCVIALDRYLAITLPFRYQSLLTRARARALVCTVWAISALVSFLPILMHWWRAESDE-ARRCYNDPKCCDFVTNRAYAIASSVVSFYVPLCIMAFVYLRVFR 249
P08588|ADRB1_HUMAN/1-477    126 YGSFFCELWTSVDVLCVTASIETLCVIALDRYLAITSPFRYQSLLTRARARGLVCTVWAISALVSFLPILMHWWRAESDE-ARRCYNDPKCCDFVTNRAYAIASSVVSFYVPLCIMAFVYLRVFR 249
O42574|ADRB1_XENLA/1-385    103 YGSIFCEFWTSVDVLCVTASIETLCVISIDRYIAITSPFRYQSLLTKGRAKGIVCSVWGISALVSFLPIMMHWWRDTGDPLAMKCYEDPGCCDFVTNRAYAIASSIISFYFPLIIMIFVYIRVFK 227
ADRB1_ZEBRAFISH/1-390        96 YGSFFCEFWISLDVLCVTASIETLCVIAIDRYIAIISPFRYQSLLTKARAKVVVCAVWAISALVSFPPILMHW--SQDSE-ETSCYENPECCDFVTNRAYAISSSIISFYIPLIVMIFVYARVYR 217
P10608|ADRB2_RAT/1-418      101 FGNFWCEFWTSIDVLCVTASIETLCVIAVDRYVAITSPFKYQSLLTKNKARVVILMVWIVSGLTSFLPIQMHWYRATHKQ-AIDCYAKETCCDFFTNQAYAIASSIVSFYVPLVVMVFVYSRVFQ 224
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P07550|ADRB2_HUMAN/1-413    101 FGNFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIVSGLTSFLPIQMHWYRATHQE-AINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFVYSRVFQ 224
ADRB2_CHICKEN/1-397          98 FGNFWCEFWTSLDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKSKARVVILVVWAISALTSFLPIQMHWYRADRDE-AILCYEKDTCCDFFTNQAYAIASSIISFYLPLVVMVFVYARVFQ 221
ADRB2_XENOPUS/1-406          93 FNNFWCEFWTSVDILCVTASIETLCVIAVDRYFAITSPFRYQSLLTKCKARIVILLVWLVSALTSFLPICMHWYRVEEKT-ALDCYQDPSCCFFYTNPAYAISSSIISFYLPLVVMIFVYARVFQ 216
ADRB2_ZEBRAFISH/1-409       108 FGNFFCEFWTATDVLCVTASIETLCVIALDRYIAIMWPLRYQSMLTKRKACGMVIGVWAVAALISFLPIHMEWWVSDEPE-ALSCLEEPTCCDFNTNAAYAVTSSIISFYIPLVIMAFVYSRVFQ 231

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O42574|ADRB1_XENLA/1-385    228 EAQKQMKKIDKCEGRFSHSHV------------------------------LSHGRSSR--RILSKILVAKEQKALKTLGIIMGTFTLCWLPFFLANVVNVFYRNLIPDKLFLFLNWLGYANSAF 320
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P10608|ADRB2_RAT/1-418      225 VAKRQLQKIDKSEGRFHAQNLSQV---------------------------EQDGRSGHGLRSSSKF-CLKEHKALKTLGIIMGTFTLCWLPFFIVNIVHVIRANLIPKEVYILLNWLGYVNSAF 321
P18762|ADRB2_MOUSE/1-418    225 VAKRQLQKIDKSEGRFHAQNLSQV---------------------------EQDGRSGHGLRRSSKF-CLKEHKALKTLGIIMGTFTLCWLPFFIVNIVHVIRDNLIPKEVYILLNWLGYVNSAF 321
P07550|ADRB2_HUMAN/1-413    225 EAKRQLQKIDKSEGRFHVQNLSQV---------------------------EQDGRTGHGLRRSSKF-CLKEHKALKTLGIIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGF 321
ADRB2_CHICKEN/1-397         222 VAKKQLQKIDQSEGRFHIQNKEQ----------------------------DQNGKAGH--RRSSKF-FLKEHKALKTLGIIMGTFTLCWLPFFIVNIVHVIQDDIIPKYVYILLNWLGYVNSAF 315
ADRB2_XENOPUS/1-406         217 EAKKQLKKIDKSEGRFHNQNQPQ----------------------------DANGKQGN--RRTSKF--LKEHKALKTLGIIMGTFTLCWLPFFIVNIVQVMHKDIIPDKVYTFLNWVGYVNSAF 309
ADRB2_ZEBRAFISH/1-409       232 EARRQLQKIDRIEGRIRTQSLS-----------------------------TQEGNEIK--NRRTKF-CIKDHKALKTLGIIMGTFTLCWLPFFVLNVVAAIWKMDNIMLPFRILNWIGYANSAF 324

P34971|ADRB1_MOUSE/1-466    362 NPIIYCRSPDFRKAFQRLLCCARRAACRRRAAHGDRPRASGCLARAGPPPSPGAPSDDDDDD-AGTTPPARLLEPWTGCNGGTTTVDSDSSLDEPGRQGFSSESKV 466
P18090|ADRB1_RAT/1-466      362 NPIIYCRSPDFRKAFQRLLCCARRAACRRRAAHGDRPRASGCLARAGPPPSPGAPSDDDDDD-AGATPPARLLEPWAGCNGGTTTVDSDSSLDEPGRQGFSSESKV 466
P08588|ADRB1_HUMAN/1-477    373 NPIIYCRSPDFRKAFQRLLCCARRAARRRHATHGDRPRASGCLARPGPPPSPGAASDDDDDDVVGATPPARLLEPWAGCNGG-AAADSDSSLDEPCRPGFASESKV 477
O42574|ADRB1_XENLA/1-385    321 NPIIYCRSPDFRKAFKRLLCCPKKADRHLHTT-GELSRYSGGFVNSLDTNALGMCSE---------------------CNGVRT------SLD------------- 385
ADRB1_ZEBRAFISH/1-390       310 NPIIYCRSPDFRKAFKRLLCCPRQADRRLHVSSCDLSRCTGGFGNSMEQSMLGTWSD---------------------CNGADS---SDCSLERNGRMSHSESQ-L 390
P10608|ADRB2_RAT/1-418      322 NPLIYCRSPDFRIAFQELLCLRRSSSKTYGNGYSSNSNGRTDYTGEQSAYQLGQEKE---NELLCEEA--PGMEGFVNCQGTVP----SLSIDSQGRNCNTNDSPL 418
P18762|ADRB2_MOUSE/1-418    322 NPLIYCRSPDFRIAFQELLCLRRSSSKTYGNGYSSNSNGRTDYTGEPNTCQLGQERE---QELLCEDP--PGMEGFVNCQGTVP----SLSVDSQGRNCSTNDSPL 418
P07550|ADRB2_HUMAN/1-413    322 NPLIYCRSPDFRIAFQELLCLRRSSLKAYGNGYSSNGN-----TGEQSGYHVEQEKE---NKLLCEDL--PGTEDFVGHQGTVP----SDNIDSQGRNCSTNDSLL 413
ADRB2_CHICKEN/1-397         316 NPLIYCRSPDFRYAFQELLCLRRSALKMYANGYS-NSNGRSDYNEEDNGYPLAPDKA---CELLCEEGSFPHPEDFLHCKGTVP----SG---------------- 397
ADRB2_XENOPUS/1-406         310 NPLIYCRSPDFRYTFQELLCLRKPASKDYANGYP-QSNGNSIYMEDTDPSPYSKGRA---CEVLFKEEKTPN-DSLSNCEGTRL----DFSLDPLGKNHNTHDCLL 406
ADRB2_ZEBRAFISH/1-409       325 NPLIYCRSPEFRCAFQEILCWRPSHLRSTRSKKGYLYSGHSWKVHTKTTRPREPSPA---------------------CETEIGAECLTAGTKNKNGNYNKTVTSI 409
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CAC1C_CHICKEN/1-2144     1 MSVTGARTDFDLLMAK---EPPQ----------------------VSVNRSNYGSPRPAHA-NMNAN-------AAAGLAPEHIPTPGAALSWQAAIDAARQAKLMGSAGNATISTASSTQRKRQQYGKQ 97
CAC1C_Human/1-2138       1 MVNE----NTRMYIPE---ENHQ--------------------------GSNYGSPRPAHA-NMNAN-------AAAGLAPEHIPTPGAALSWQAAIDAARQAKLMGSAGNATISTVSSTQRKRQQYGKP 89
CAC1C_RAT/1-2169         1 MIRAFAQPSTPPYQPL---SSCLSEDTERKFKGKVVHEAQLNCFYISPGGSNYGSPRPAHA-NMNAN-------AAAGLAPEHIPTPGAALSWLAAIDAARQAKLMGSAGNATISTVSSTQRKRQQYGKP 119
CAC1C_MOUSE/1-2169       1 MIRAFVQPSTPPYQPL---SSHSSEETERKFKGKVVHEAQLNCFYISPGGSNYGSPRPAHA-NMNAN-------AAAGLAPEHIPTPGAALSWQAAIDAARQAKLMGSAGNATISTVSSTQRKRQQYGKP 119
CAC1C_DANIO/1-2168       1 MVNE----SKNMYIPEDTLENHQ--------------------------GSNYSSPSLAPVPSLNEDHVGGGGGVLGLAPKHIPTPGAPLSWQAAIFAARQAKLMGTTG-APISTASSTQRKRQHYTKP 99

CAC1C_CHICKEN/1-2144    98 KKQGTTTATRPPRALLCLTLKNPIRRACISIVEWKSFEIIILLTIFANCVALAIYIPFPEDDSNATNSNLERVEYLFLIIFTVEAFLKVIAYGLLFHPNAYLRNGWNLLDFIIVVVGLFSAILEQATKAD 227
CAC1C_Human/1-2138      90 KKQGSTTATRPPRALLCLTLKNPIRRACISIVEWKPFEIIILLTIFANCVALAIYIPFPEDDSNATNSNLERVEYLFLIIFTVEAFLKVIAYGLLFHPNAYLRNGWNLLDFIIVVVGLFSAILEQATKAD 219
CAC1C_RAT/1-2169       120 KKQGGTTATRPPRALLCLTLKNPIRRACISIVEWKPFEIIILLTIFANCVALAIYIPFPEDDSNATNSNLERVEYLFLIIFTVEAFLKVIAYGLLFHPNAYLRNGWNLLDFIIVVVGLFSAILEQATKAD 249
CAC1C_MOUSE/1-2169     120 KKQGGTTATRPPRALLCLTLKNPIRRACISIVEWKPFEIIILLTIFANCVALAIYIPFPEDDSNATNSNLERVEYLFLIIFTVEAFLKVIAYGLLFHPNAYLRNGWNLLDFIIVVVGLFSAILEQATKAD 249
CAC1C_DANIO/1-2168     100 KKQASTASTRPPRALLCLTLKNPIRRACINIVEWKPFEIIILMTIFANCVALAVYIPFPEDDSNATNSNLERVEYGFLIIFTVEAFLKVIAYGLLCHPNAYLRNGWNLLDFIIVVVGLFSAILEQATKGD 229

CAC1C_CHICKEN/1-2144   228 GGNSIGGKGAGFDVKALRAFRVLRPLRLVSGVPSLQVVLNSIIKAMVPLLHIALLVLFVIIIYAIIGLELFMGKMHKTCYHVQGGLIDTPAEDDPSPCAPQSAHGRQCQ--NGTECKAGWEGPKHGITNF 355
CAC1C_Human/1-2138     220 GANALGGKGAGFDVKALRAFRVLRPLRLVSGVPSLQVVLNSIIKAMVPLLHIALLVLFVIIIYAIIGLELFMGKMHKTCYN-QEGIADVPAEDDPSPCALETGHGRQCQ--NGTVCKPGWDGPKHGITNF 346
CAC1C_RAT/1-2169       250 GANALGGKGAGFDVKALRAFRVLRPLRLVSGVPSLQVVLNSIIKAMVPLLHIALLVLFVIIIYAIIGLELFMGKMHKTCYN-QEGIIDVPAEEDPSPCALETGHGRQCQ--NGTVCKPGWDGPKHGITNF 376
CAC1C_MOUSE/1-2169     250 GANALGGKGAGFDVKALRAFRVLRPLRLVSGVPSLQVVLNSIIKAMVPLLHIALLVLFVIIIYAIIGLELFMGKMHKTCYN-QEGIIDVPAEEDPSPCALETGHGRQCQ--NGTVCKPGWDGPKHGITNF 376
CAC1C_DANIO/1-2168     230 GGTSMGGKAAGFDVKALRAFRVLRPLRLVSGVPSLQVVLNSIIKAMVPLLHIALLVLFVIIIYAIIGLELFMGKMHRTCFFYKDGHKGHIAEEKPAPCAPSSAHGRHCSPPNITQCMMGWEGPNDGITNF 359

CAC1C_CHICKEN/1-2144   356 DNFAFAMLTVFQCITMEGWTDVLYWVNDAIGRDWPWIYFVTLIIIGSFFVLNLVLGVLSGEFSKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEDEGMDEEKPRNMSMPTSETESVNT 485
CAC1C_Human/1-2138     347 DNFAFAMLTVFQCITMEGWTDVLYWVNDAVGRDWPWIYFVTLIIIGSFFVLNLVLGVLSGEFSKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEDEGMDEEKPRNMSMPTSETESVNT 476
CAC1C_RAT/1-2169       377 DNFAFAMLTVFQCITMEGWTDVLYWMQDAMGYELPWVYFVSLVIFGSFFVLNLVLGVLSGEFSKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEDEGMDEDKPRNMSMPTSETESVNT 506
CAC1C_MOUSE/1-2169     377 DNFAFAMLTVFQCITMEGWTDVLYWMQDAMGYELPWVYFVSLVIFGSFFVLNLVLGVLSGEFSKEREKAKARGDFQKLREKQQLEEDLKGYLDWITQAEDIDPENEDEGMDEDKPRNMSMPTSETESVNT 506
CAC1C_DANIO/1-2168     360 DNFAFAMLTVFQCITMEGWTDVLYWMQDAMGYELPWVYFVSLVIFGSFFVLNLVLGVLSGEFSKEREKAKARGDFQKLRERQQLEEDLKGYLDWITQAEDIDPENDDEGLDDDKPRNLSMPASENESVNT 489

CAC1C_CHICKEN/1-2144   486 DNVPGTDIEGENCGARLAHRISKSKFSRYWRRWNRFCRRKCRAAVKSNVFYWLVIFLVFLNTLTIASEHYNQPDWLTEVQDTANKVLLALFTAEMLLKMYSLGLQAYFVSLFNRFDCFIVCGGILETILV 615
CAC1C_Human/1-2138     477 ENVAGGDIEGENCGARLAHRISKSKFSRYWRRWNRFCRRKCRAAVKSNVFYWLVIFLVFLNTLTIASEHYNQPNWLTEVQDTANKALLALFTAEMLLKMYSLGLQAYFVSLFNRFDCFVVCGGILETILV 606
CAC1C_RAT/1-2169       507 ENVAGGDIEGENCGARLAHRISKSKFSRYWRRWNRFCRRKCRAAVKSNVFYWLVIFLVFLNTLTIASEHYNQPHWLTEVQDTANKALLALFTAEMLLKMYSLGLQAYFVSLFNRFDCFIVCGGILETILV 636
CAC1C_MOUSE/1-2169     507 ENVAGGDIEGENCGARLAHRISKSKFSRYWRRWNRFCRRKCRAAVKSNVFYWLVIFLVFLNTLTIASEHYNQPHWLTEVQDTANKALLALFTAEMLLKMYSLGLQAYFVSLFNRFDCFIVCGGILETILV 636
CAC1C_DANIO/1-2168     490 DNAPAGDMEGETCCTRMANRISKSKFSRYSRRWNRLCRRKCRAAVKSNVFYWLVIFLVFLNTLTIASEHHQQPEWLTNVQDIANKVLLALFTGEMLLKMYSLGLQAYFVSLFNRFDSFVVCGGILETILV 619

CAC1C_CHICKEN/1-2144   616 ETKIMSPLGISVLRCVRLLRIFKITRYWNSLSNLVASLLNSVRSIASLLLLLFLFIIIFSLLGMQLFGGKFNFDEMQTRRSTFDNFPQSLLTVFQILTGEDWNSVMYDGIMAYGGPSFPGMLVCIYFIIL 745
CAC1C_Human/1-2138     607 ETKIMSPLGISVLRCVRLLRIFKITRYWNSLSNLVASLLNSVRSIASLLLLLFLFIIIFSLLGMQLFGGKFNFDEMQTRRSTFDNFPQSLLTVFQILTGEDWNSVMYDGIMAYGGPSFPGMLVCIYFIIL 736
CAC1C_RAT/1-2169       637 ETKIMSPLGISCWRCVRLLRIFKITRYWNSLSNLVASLLNSLRSIASLLLLLFLFIIIFSLLGMQLFGGKFNFDEMQTRRSTFDNFPQSLLTVFQILTGEDWNSVMYDGIMAYGGPSFPGMLVCIYFIIL 766
CAC1C_MOUSE/1-2169     637 ETKIMSPLGISVLRCVRLLRIFKITRYWNSLSNLVASLLNSVRSIASLLLLLFLFIIIFSLLGMQLFGGKFNFDEMQTRRSTFDNFPQSLLTVFQILTGEDWNSVMYDGIMAYGGPSFPGMLVCIYFIIL 766
CAC1C_DANIO/1-2168     620 ETKIMSPLGISVLRCVRLLRIFKITRYWNSLSNLVASLLNSVRSIASLLLLLFLFIIIFSLLGMQLFGGKFNFDE--TRRSTFDNFPQSLLTVFQILTGEDWNSVMYDGIMAYGGPSFPGMLVCIYFIIL 747

CAC1C_CHICKEN/1-2144   746 FICGNYILLNVFLAIAVDNLADAESLTSAQKEEEEEKERKKLARTASPEKKQEIEKTAVEEETKEEKIELKSITADGESPPATKINMDDYQPNENEEKSPYPTTE-APAEEDEEEPEMPVGPRPRPMSEL 874
CAC1C_Human/1-2138     737 FICGNYILLNVFLAIAVDNLADAESLTSAQKEEEEEKERKKLARTASPEKKQELVEKPAVGESKEEKIELKSITADGESPPATKINMDDLQPNENEDKSPYPNPE-TTGEEDEEEPEMPVGPRPRPLSEL 865
CAC1C_RAT/1-2169       767 FISPNYILLNLFLAIAVDNLADAESLTSAQKEEEEEKERKKLARTASPEKKQEVMEKPAVEESKEEKIELKSITADGESPPTTKINMDDLQPSENEDKSPHSNPD-TAGEEDEEEPEMPVGPRPRPLSEL 895
CAC1C_MOUSE/1-2169     767 FICGNYILLNVFLAIAVDNLADAESLTSAQKEEEEEKERKKLARTASPEKKQEVMEKPAVEESKEEKIELKSITADGESPPTTKINMDDLQPSENEDKSPHSNPD-TAGEEDEEEPEMPVGPRPRPLSEL 895
CAC1C_DANIO/1-2168     748 FICGNYILLNVFLAIAVDNLADAESLTSAQKEEEEEKERKKLARTASPEKRQNSEKPPLEDEKKEEKIELKSITSDGETPTATKINIDEYTGEDNEEKNPYPVNDFPAGEDDEEEPEMPVGPRPRPLSDI 877

CAC1C_CHICKEN/1-2144   875 HLKEKAVPMPDASAFFIFSPNNRFRVHCHRIVNDNIFTNLILFFILLSSISLAAEDPVRHLSFRNQVLFYFDIVFTVIFTIEIALKMTAYGAFLHKGSFCRNYFNILDLLVVSVSLISFGIQSSAINVVK 1004
CAC1C_Human/1-2138     866 HLKEKAVPMPEASAFFIFSSNNRFRLQCHRIVNDTIFTNLILFFILLSSISLAAEDPVQHTSFRNHILFYFDIVFTTIFTIEIALKMTAYGAFLHKGSFCRNYFNILDLLVVSVSLISFGIQSSAINVVK 995
CAC1C_RAT/1-2169       896 HLKEKAVPMPEASAFFIFSPNNRFRLQCHRIVNDTIFTNLILFFILLSSISLAAEDPVQHTSFRNHILFYFDIVFTTIFTIEIALKMTAYGAFLHKGSFCRNYFNILDLLVVSVSLISFGIQSSAINVVK 1025
CAC1C_MOUSE/1-2169     896 HLKEKAVPMPEASAFFIFSPNNRFRLQCHRIVNDTIFTNLILFFILLSSISLAAEDPVQHTSFRNHILGNADYVFTSIFTLEIILKMTAYGAFLHKGSFCRNYFNILDLLVVSVSLISFGIQSSAINVVK 1025
CAC1C_DANIO/1-2168     878 QLKEKAVPMPQAKAFFIFSPSNKFRVLCHKIVNHNIFTNLILFFILLSSISLAAEDPVKNDSFRNQILGYADYVFTGIFTIEIILKMTAYGAFLHKGSFCRNYFNILDLVVVSVSLISSGIQSSAINVVK 1007

CAC1C_CHICKEN/1-2144  1005 ILRVLRVLRPLRAINRAKGLKHVVQCVFVAIRTIGNIVIVTTLLQFMFACIGVQLFKGKLYSCTDSSKQTEAECRGYYITYKDGEVSQPMIQPRSWENSKFDFDNVLTAMMALFTVSTFEGWPELLYRSI 1134
CAC1C_Human/1-2138     996 ILRVLRVLRPLRAINRAKGLKHVVQCVFVAIRTIGNIVIVTTLLQFMFACIGVQLFKGKLYTCSDSSKQTEAECKGNYITYKDGEVDHPIIQPRSWENSKFDFDNVLAAMMALFTVSTFEGWPELLYRSI 1125
CAC1C_RAT/1-2169      1026 ILRVLRVLRPLR-INRAKGLKHVVQCVFVAIRTIGNIVIVTTLLQFMFACIGVQLFKGKLYTCSDSSKQTEAESKGNYITYKTGEVDHPIIQPRSWENSKFDFDNVLAAMMALFTVSTFEGWPELLYRSI 1154
CAC1C_MOUSE/1-2169    1026 ILRVLRVLRPLRAINRAKGLKHVVQCVFVAIRTIGNIVIVTTLLQFMFACIGVQLFKGKLYTCSDSSKQTEAECKGNYITYKDGEVDHPIIQPRSWENSKFDFDNVLAAMMALFTVSTFEGWPELLYRSI 1155
CAC1C_DANIO/1-2168    1008 ILRVLRVLRPLRAINRAKGLKHVVQCVFVAIRTIGNIVIVTSLLQFMFACIGVQLLKGKFFYCTDTSKQTQAECRGAYILYKDGNVGEPEKAQRSWENSDFNFDDVLQGMMALFAVSTFEGWPGLLYRAI 1137

CAC1C_CHICKEN/1-2144  1135 DSHMEDVGPIYNHRVEISIFFIIYIIIIAFFMMNIFVGFVIVTFQEQGEQEYKNCELDKNQRQCVEYALKARPLRRYIPKNQYQYKVWYVVNSTYFEYLMFVLILLNTICLAMQHYGQSCMFKEAMNILN 1264
CAC1C_Human/1-2138    1126 DSHTEDKGPIYNYRVEISIFFIIYIIIIAFFMMNIFVGFVIVTFQEQGEQEYKNCELDKNQRQCVEYALKARPLRRYIPKNQHQYKVWYVVNSTYFEYLMFVLILLNTICLAMQHYGQSCLFKIAMNILN 1255
CAC1C_RAT/1-2169      1155 DSHTEDKGPIYNYRVEISIFFIIYIIIIAFFMMNIFVGFVIVTFQEQGEQEYKNCELDKNQRQCVEYALKARPLPRYIPKNQHQYKVWYVVNSTYFEYLMFVLILLNTICLAMQHYGQSCLFKIAMNILN 1284
CAC1C_MOUSE/1-2169    1156 DSHTEDKGPIYNYRVEISIFFIIYIIIIAFFMMNIFVGFVIVTFQEQGEQEYKNCELDKNQRQCVEYALKARPLRRYIPKNQHQYKVWYVVNSTYFEYLMFVLILLNTICLAMQHYGQSCLFKIAMNILN 1285
CAC1C_DANIO/1-2168    1138 DSHAEDVGPIYNYRVVISIFFIIYIIIIAFFMMNIFVGFVIVTFQEQGEQEYKNCELDKNQRQCVEYALKARPLRRYIPKNPYQYKVWYVVNSTYFEYLMFTLILLNTICLAMQHHGQSQSFNKAMNILN 1267

CAC1C_CHICKEN/1-2144  1265 MLFTGLFTVEMVLKLIAFKPKHYFCDAWNTFDALIVVGSIVDIAITEVNPAENTQCSSS--------MNAEENSRISITFFRLFRVMRLVKLLSRGEGIRTLLWTFIKSFQALPYVALLIVMLFFIYAVI 1386
CAC1C_Human/1-2138    1256 MLFTGLFTVEMILKLIAFKPKHYFCDAWNTFDALIVVGSIVDIAITEVNPAEHTQCSPS--------MNAEENSRISITFFRLFRVMRLVKLLSRGEGIRTLLWTFIKSFQALPYVALLIVMLFFIYAVI 1377
CAC1C_RAT/1-2169      1285 MLFTGLFTVEMILKLIAFKPKHYFCDAWNTFDALIVVGSIVDIAITEVHPAEHTQCSPS--------MSAEENSRISITFFRLFRVMRLVKLLSRGEGIRTLLWTFIKSFQALPYVALLIVMLFFIYAVI 1406
CAC1C_MOUSE/1-2169    1286 MLFTGLFTVEMILKLIAFKPKGYFSDPWNVFDFLIVIGSIIDVILSETNPAEHTQCSPS--------MSAEENSRISITFFRLFRVMRLVKLLSRGEGIRTLLWTFIKSFQALPYVALLIVMLFFIYAVI 1407
CAC1C_DANIO/1-2168    1268 MLFTGLFTVEMILKLIAFKPRHYFVDAWNTFDALIVVGSVVDIAITEVNPADPSSSPPSSVVRPMGLQNTEDNARISITFFRLFRVMRLVKLLSRGEGIRTLLWTFIKSFQALPYVALLIVMLFFIYAVI 1397

CAC1C_CHICKEN/1-2144  1387 GMQVFGKIALNDTTEINRNNNFQTFPQAVLLLFRCATGEAWQEIMLACLPDKKCDPDSEPANSTEADHSCGSSFAVFYFISFYMLCAFLIINLFVAVIMDNFDYLTRDWSILGPHHLDEFKRIWAEYDPE 1516
CAC1C_Human/1-2138    1378 GMQVFGKIALNDTTEINRNNNFQTFPQAVLLLFRCATGEAWQDIMLACMPGKKCAPESEPSNSTEGETPCGSSFAVFYFISFYMLCAFLIINLFVAVIMDNFDYLTRDWSILGPHHLDEFKRIWAEYDPE 1507
CAC1C_RAT/1-2169      1407 GMQVFGKIALNDTTEINRNNNFQTFPQAVLLLFRCATGEAWQDIMLACMPGKKCAPESEPSNSTEGETPCGSSFAVFYFISFYMLCAFLIINLFVAVIMDNFDYLTRDWSILGPHHLDEFKRIWAEYDPE 1536
CAC1C_MOUSE/1-2169    1408 GMQVFGKIALNDTTEINRNNNFQTFPQAVLLLFRCATGEAWQDIMLACMPGKKCAPESEPSNSTEGETPCGSSFAVFYFISFYMLCAFLIINLFVAVIMDNFDYLTRDWSILGPHHLDEFKRIWAEYDPE 1537
CAC1C_DANIO/1-2168    1398 GMQMFGKIALRDNSQINRNNNFQTFPQAVLLLFRCATGEAWQEIMLACSPNRPCEKGSEINHSSE---DCGSHFAIFYFVSFYMLCAFLIINLFVAVIMDNFDYLTRDWSILGPHHLDEFKRIWAEYDPE 1524

CAC1C_CHICKEN/1-2144  1517 AKGRIKHLDVVTLLRRIQPPLGFGKLCPHRVACKRLVSMNMPLNSDGTVMFNATLFALVRTALRIKTEGNLEQANEELRAIIKKIWKRTSMKLLDQVVPPAGDDEVTVGKFYATFLIQEYFRKFKKRKEQ 1646
CAC1C_Human/1-2138    1508 AKGRIKHLDVVTLLRRIQPPLGFGKLCPHRVACKRLVSMNMPLNSDGTVMFNATLFALVRTALRIKTEGNLEQANEELRAIIKKIWKRTSMKLLDQVVPPAGDDEVTVGKFYATFLIQEYFRKFKKRKEQ 1637
CAC1C_RAT/1-2169      1537 AKGRIKHLDVVTLLRRIQPPLGFGKLCPHRVACKRLVSMNMPLNSDGTVMFNATLFALVRTALRIKTEGNLEQANEELRAIIKKIWKRTSMKLLDQVVPPAGDDEVTVGKFYATFLIQEYFRKFKKRKEQ 1666
CAC1C_MOUSE/1-2169    1538 AKGRIKHLDVVTLLRRIQPPLGFGKLCPHRVACKRLVSMNMPLNSDGTVMFNATLFALVRTALRIKTEGNLEQANEELRAIIKKIWKRTSMKLLDQVVPPAGDDEVTVGKFYATFLIQEYFRKFKKRKEQ 1667
CAC1C_DANIO/1-2168    1525 AKGRIKHLDVVTLLRRIQPPLGFGKLCPHRVACKRLVSMNMPLNSDGTVMFNATLFALVRTALRIETEGNLEQANEELRAIVKKIWKRTSMKLLDQVVPPAGDDEVTVGKFYATFLIQEYFRKFKKRKEQ 1654

CAC1C_CHICKEN/1-2144  1647 GLVGKPSQRNALSLQAGLRTLHDIGPEIRRAISGDLTAEEELDKAMKEAVSAASEDDIFRRAGGLFGNHVSYY-QSDGRSAFPQTFTTQRPLHINKSGNNQGDTESPSHEKLVDSTFTPSSYSSSGSNAN 1775
CAC1C_Human/1-2138    1638 GLVGKPSQRNALSLQAGLRTLHDIGPEIRRAISGDLTAEEELDKAMKEAVSAASEDDIFRRAGGLFGNHVSYY-QSDGRSAFPQTFTTQRPLHINKAGSSQGDTESPSHEKLVDSTFTPSSYSSTGSNAN 1766
CAC1C_RAT/1-2169      1667 GLVGKPSQRNALSLQAGLRTLHDIGPEIRRAISGDLTAEEELDKAMKEAVSAASEDDIFRRAGGLFGNHVSYY-QSDSRSNFPQTFATQRPLHINKTGNNQADTESPSHEKLVDSTFTPSSYSSTGSNAN 1795
CAC1C_MOUSE/1-2169    1668 GLVGKPSQRNALSLQAGLRTLHDIGPEIRRAISGDLTAEEELDKAMKEAVSAASEDDIFRRAGGLFGNHVTYY-QSDSRGNFPQTFATQRPLHINKTGNNQADTESPSHEKLVDSTFTPSSYSSTGSNAN 1796
CAC1C_DANIO/1-2168    1655 GLVAKIPPKTALSLQAGLRTLHDMGPEIRRAISGDLTVEEELERAMKETVCAASEDDIFRRSGGLFGNHVNYYHQSDGHVSFPQSFTTQRPLHISKSG-SPGEAESPSHQKLVDSTFTPSSYSSSGSNAN 1783

CAC1C_CHICKEN/1-2144  1776 INNANNTALC-RFPSPPSYPSTVSTVEGH-GTPLSPTIRVQEAPWKLPSKSSSSRDSQLAIVCQEEVSQDETY-DENLNEDIEYCSEPSLLSTEMLAYQDDENRQLTPP-ENNKGEDTRH--SP-KKGFL 1898
CAC1C_Human/1-2138    1767 INNANNTALG-RLPRPAGYPSTVSTVEGH-GPPLSPAIRVQEVAWKLSSNRCHSRESQAAMAGQEETSQDETY-EVKMNHDTEACSEPSLLSTEMLSYQDDENRQLTLP-EEDK-RDIRQ--SP-KRGFL 1888
CAC1C_RAT/1-2169      1796 INNANNTALG-RFPHPAGYSSTVSTVEGH-GPPLSPAVRVQEAAWKLSSKRCHSRESQGATVSQ-DMFPDETRSSVRLSEEVEYCSEPSLLSTDILSYQDDENRQLTCL-EEDK-REIQP--CP-KRSFL 1917
CAC1C_MOUSE/1-2169    1797 INNANNTALG-RFPHPAGYSSTVSTVEGH-GPPLSPAVRVQEAAWKLSSKRCHSRESQGATVNQ-EIFPDETR-SVRMSEEAEYCSEPSLLSTDMFSYQEDEHRQLTCP-EEDK-REIQP--SP-KRSFL 1917
CAC1C_DANIO/1-2168    1784 INNANNTAIGHRYPKP-----TVSTVDGQTGPPLT-TIPLPRPTWCFPNKSSDSSDSRLPIIRREEASTDETYDETFLDE-----RDQAMLSMDMLEFQDEESKQLAPMVEAEVGEERRPWQSPRRRAFL 1902

CAC1C_CHICKEN/1-2144  1899 CSSALGRRASFHLECLKRQKNQGVDVSQKTVLPLQMVHHQALAVAGLSPLLQRSHSPTTFSRLCATPPATPCSR--GWP-QQPIPTLRLEGAESSEKLNSSFPSVHCSSRFPDSSDCGSP----RRARPV 2021
CAC1C_Human/1-2138    1889 RSASLGRRASFHLECLKRQKDRGGDISQKTVLPLHLVHHQALAVAGLSPLLQRSHSPASFPRPFATPPATPGSR--GWP-PQPVPTLRLEGVESSEKLNSSFPSIHCGSW-AETTPGGGGSSAARRVRPV 2014
CAC1C_RAT/1-2169      1918 RSASLGRRASFHLECLKRQKDQGGDISQKTALPLHLVHHQALAVAGLSPLLQRSHSPSTFPRPRPTPPVTPGSR--GRP-LQPIPTLRLEGAESSEKLNSSFPSIHCSSWSEETTACSGGSSMARRARPV 2044
CAC1C_MOUSE/1-2169    1918 RSASLGRRASFHLECLKRQKDQGGDISQKTALPLHLVHHQALAVAGLSPLLQRSHSPTTFPRPCPTPPVTPGSR--GRP-LRPIPTLRLEGAESSEKLNSSFPSIHCSSWSEETTACSGSSSMARRARPV 2044
CAC1C_DANIO/1-2168    1903 CPTALGRRSSFHLECLRKHNRP--DVSQKTALPLHLVHHQALAVAGLSPLLRRSHSPTLFTRLCSTPPASPSGRSGGGPCYQPVPSLRLEGSGSYEKLNSSMPSVNCSSWYSDSNGNHSG----RAQRPV 2026

CAC1C_CHICKEN/1-2144  2022 SLTVPSPTAGSSRQF-HGSASSLVEAVLISEGLMQFAQDPKFIEVTTQELADACDMTIEEMENAADNILNGNSKQSPNGNLLPFVNCRD-----------------AGQDSAGEEEEE--VQNPDCXKSQ 2131
CAC1C_Human/1-2138    2015 SLMVPSQAGAPGRQF-HGSASSLVEAVLISEGLGQFAQDPKFIEVTTQELADACDMTIEEMESAADNILSGGAPQSPNGALLPFVNCRD-----------------AGQDRAGGEEDAGCVRARGR-PSE 2125
CAC1C_RAT/1-2169      2045 SLTVPSQAGAPGRQF-HGSASSLVEAVLISEGLGQFAQDPKFIEVTTQELADACDMTIEEMENAADNILSGGAQQSPNGTLLPFVNCRD-----------------PGQDRAVVPEDESCVYALGRGRSE 2156
CAC1C_MOUSE/1-2169    2045 SLTVPSQAGAPGRQF-HGSASSLVEAVLISEGLGQFAQDPKFIEVTTQELADACDMTIEEMENAADNILSGGAQQSPNGTLLPFVNCRD-----------------PGQDRAVAPEDESCAYALGRGRSE 2156
CAC1C_DANIO/1-2168    2027 SLTVPPVTRRDSISLAHGSAGSLVEAVLISEGLGRYAHDPSFIQVAKQEIAEACDMTMEEMENAADNILNANAPPNANGNLLPFIQCRDTGSQESRCSLSLGLSPATGSDGALEAELE---ESEGAGQRN 2153

CAC1C_CHICKEN/1-2144  2132 EELKDSRIY--ISSL 2144
CAC1C_Human/1-2138    2126 EELQDSRVY--VSSL 2138
CAC1C_RAT/1-2169      2157 EALPDSRSY--VSNL 2169
CAC1C_MOUSE/1-2169    2157 EALADSRSY--VSNL 2169
CAC1C_DANIO/1-2168    2154 SPLMEDEDMECVTSL 2168
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Supplemental Figures: Sequence alignments.

S1: AT1A1: the α1β1 subunit of Na/K ATPase; Extensive similarity is found in these proteins. Residues implicated in binding to the prototypic cardiac glycoside OUA (27) are highly conserved across the seven species presented here. S2: Adrenergic receptor; β1 receptors (no shading); β2 receptors (yellow shading). S3: Calcium Channel. Purple shading indicates amino acid conservation > 70% at each position; a black triangle or bar above a particular position, together with grey shading, denotes known drug binding residues or domains.