# **Supplementary Information**

# A Gly-zipper motif mediates homo-dimerization of the transmembrane domain of the mitochondrial kinase ADCK3

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**Supplementary Table S1, summary of CATM Model 1 of ADCK3**

| **Model 1** | | |
|---|---|---|
| Total CATM score | −59.8 | |
| Van der Waals component | −43.3 | |
| Hydrogen Bonding component | −16.6 | |
| Quadrant of closest approach | G219-L224 | |
| *d* (inter-helical distance) | 6.6 Å | |
| θ (crossing angle) | −27.1 º | |
| *Z*’ (crossing point, axial shift) | 4.2 Å | |
| ω’ (crossing point, axial rotation) | 51.9 º | |
| Number of inter-helical H-bonds | 12 | |
| **Donor** | **Acceptor** | **Distance** |
| B 216 Asn HA | A 215 Ala O | 3.25251 |
| B 219 Gly HA1 | A 216 Asn OD1 | 2.51865 |
| B 219 Gly HA1 | A 216 Asn O | 2.94603 |
| B 220 Leu HA | A 219 Gly O | 2.37817 |
| B 223 Gly HA1 | A 220 Leu O | 3.03996 |
| B 224 Leu HA | A 223 Gly O | 3.37371 |
| A 216 Asn HA | B 215 Ala O | 3.25251 |
| A 219 Gly HA1 | B 216 Asn OD1 | 2.51865 |
| A 219 Gly HA1 | B 216 Asn O | 2.94603 |
| A 220 Leu HA | B 219 Gly O | 2.37817 |
| A 223 Gly HA1 | B 220 Leu O | 3.03996 |
| A 224 Leu HA | B 223 Gly O | 3.37371 |

## Supplementary Table S2, summary of CATM Model 2 of ADCK3

| Model 2 | | |
|---|---|---|
| Total CATM score | −50.8 | |
| Van der Waals component | −28.3 | |
| Hydrogen Bonding component | −22.4 | |
| Quadrant of closest approach | G219-L224 | |
| $d$ (inter-helical distance) | 6.3 Å | |
| $\theta$ (crossing angle) | −42.2 º | |
| $Z'$ (crossing point, axial shift) | 0.6 Å | |
| $\omega'$ (crossing point, axial rotation) | 42.8 º | |
| Number of inter-helical H-bonds | 12 | |
| **Donor** | **Acceptor** | **Distance** |
| B 216 Asn HA | A 216 Asn OD1 | 3.04807 |
| B 219 Gly HA1 | A 216 Asn OD1 | 3.13004 |
| B 220 Leu HA | A 219 Gly O | 2.83268 |
| B 223 Gly HA1 | A 220 Leu O | 2.41331 |
| B 224 Leu HA | A 223 Gly O | 2.34205 |
| B 227 Gly HA1 | A 224 Leu O | 3.11619 |
| A 216 Asn HA | B 216 Asn OD1 | 3.04807 |
| A 219 Gly HA1 | B 216 Asn OD1 | 3.13004 |
| A 220 Leu HA | B 219 Gly O | 2.83268 |
| A 223 Gly HA1 | B 220 Leu O | 2.41331 |
| A 224 Leu HA | B 223 Gly O | 2.34205 |
| A 227 Gly HA1 | B 224 Leu O | 3.11619 |

**Supplementary Table S3, summary of CATM Model 3 of ADCK3**

| **Model 3** | | |
|---|---|---|
| Total CATM score | −47.7 | |
| Van der Waals component | −32.2 | |
| Hydrogen Bonding component | −15.5 | |
| Quadrant of closest approach | A215-L220 | |
| *d* (inter-helical distance) | 6.3 Å | |
| θ (crossing angle) | −44.0 º | |
| *Z*’ (crossing point, axial shift) | 0.9 Å | |
| ω’ (crossing point, axial rotation) | 46.1 º | |
| Number of inter-helical H-bonds | 10 | |
| **Donor** | **Acceptor** | **Distance** |
| B 216 Asn HA | A 215 Ala O | 2.75854 |
| B 219 Gly HA2 | A 216 Asn OD1 | 3.03411 |
| B 219 Gly HA1 | A 216 Asn O | 2.35013 |
| B 220 Leu HA | A 219 Gly O | 2.40005 |
| B 223 Gly HA1 | A 220 Leu O | 3.32438 |
| A 216 Asn HA | B 215 Ala O | 2.75854 |
| A 219 Gly HA2 | B 216 Asn OD1 | 3.03411 |
| A 219 Gly HA1 | B 216 Asn O | 2.35013 |
| A 220 Leu HA | B 219 Gly O | 2.40005 |
| A 223 Gly HA1 | B 220 Leu O | 3.32438 |

## Supplementary Table S4, summary of CATM Model 4 of ADCK3

| **Model 4** | | |
|---|---|---|
| Total CATM score | −31.4 | |
| Van der Waals component | −23.3 | |
| Hydrogen Bonding component | −8.0 | |
| Quadrant of closest approach | G223-A227 | |
| *d* (inter-helical distance) | 6.7 Å | |
| θ (crossing angle) | −49.9 º | |
| *Z*’ (crossing point, axial shift) | 2.8 Å | |
| ω’ (crossing point, axial rotation) | 47.0 º | |
| Number of inter-helical H-bonds | 4 | |
| **Donor** | **Acceptor** | **Distance** |
| B 224 Leu HA | A 223 Gly O | 2.73165 |
| B 227 Gly HA1 | A 224 Leu O | 2.65991 |
| A 224 Leu HA | B 223 Gly O | 2.73165 |
| A 227 Gly HA1 | B 224 Leu O | 2.65991 |

**Supplementary Table S5, summary of CATM Model 5 of ADCK3**

| **Model 5** | | |
|---|---|---|
| Total CATM score | −29.6 | |
| Van der Waals component | −17.9 | |
| Hydrogen Bonding component | −11.7 | |
| Quadrant of closest approach | A215-L220 | |
| *d* (inter-helical distance) | 6.9 Å | |
| θ (crossing angle) | −25.0 º | |
| *Z*' (crossing point, axial shift) | 4.8 Å | |
| ω' (crossing point, axial rotation) | 50.3 º | |
| Number of inter-helical H-bonds | 6 | |
| **Donor** | **Acceptor** | **Distance** |
| B 216 Asn HA | A 215 Ala O | 2.69118 |
| B 216 Asn HD21 | A 215 Ala O | 2.1257 |
| B 219 Gly HA1 | A 216 Asn O | 3.42358 |
| A 216 Asn HA | B 215 Ala O | 2.69118 |
| A 216 Asn HD21 | B 215 Ala O | 2.1257 |
| A 219 Gly HA1 | B 216 Asn O | 3.42358 |

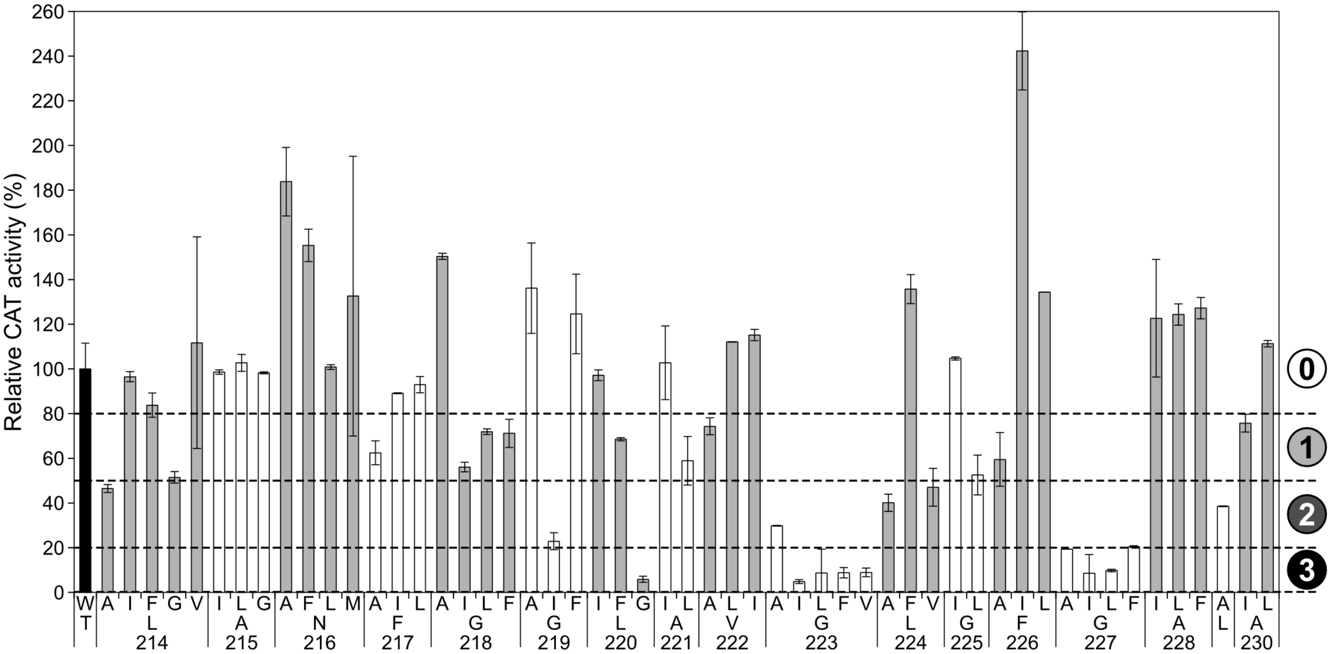

**Fig. S1 Mutagenesis of the TM helix of ADCK3.** The figure shows the TOXCAT result for each of the point mutants of the TM domain of ADCK3 schematically summarized in Fig. 5. The CAT activity (left axis) is normalized to that of the wild type sequence, shown in black. The mutations at each position are visually grouped by color. Each mutation has been categorized relative to the wild type activity (back bar) as “WT-like” (0: >80% of WT), “Mild” (1: 50-80%), “Severe” (2: 20-50%) or “Disruptive” (3: 0-20%), as indicated on the right axis and by the dashed lines.

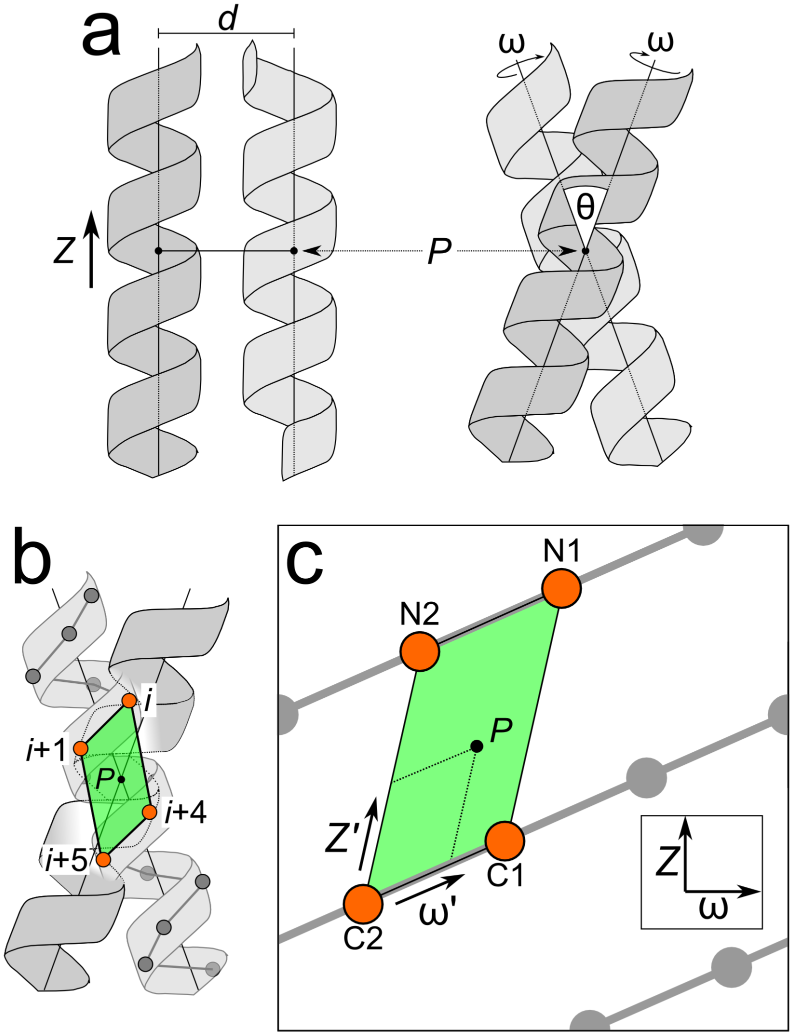

**Fig. S2 Definition of 4 parameters that define the geometry of a symmetrical dimer.** a) $d$: inter-helical distance; $\theta$: crossing angle; $\omega$: rotation of the helix around its axis; $Z$: vertical position of the point of closest approach between the two helical axes (the crossing point $P$). b) The coordinates can be redefined by expressing them as a function of the unit cell (green) on the helical lattice that contains the point of closest approach $P$. The four interfacial positions that surround the the point of closest approach are designated as N1 (relative position $i$), N2 ($i$+1), C1($i$+4) and C2 ($i$+5). The principal axes are the rotation along the helical screw ($\omega'$) and the vector between C2 and C2 ($Z'$)[1].

## Supplementary Text S1, sequence alignment of ADCK3 homologs

The sequence logo of Fig. 2c was created using homologous sequence of ADCK3 obtained with Blast[2] (http://blast.ncbi.nlm.nih.gov), which queried with the sequence of human ADCK3 and standard parameters. The top 400 hits were aligned using ClustalW[3] (http://www.ebi.ac.uk/Tools/msa/clustalw2). The web logo was produced using WebLogo (http://weblogo.berkeley.edu)[4]. The identifiers of the sequence used in the alignment are the following:

gi|556101431|gb|ESO90083.1| hypothetical protein LOTGIDRAFT_218121 [Lottia gigantea]
gi|524869263|ref|XP_005091427.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Aplysia californica]
gi|405957185|gb|EKC23415.1| Chaperone activity of bc1 complex-like, mitochondrial [Crassostrea gigas]
gi|340375939|ref|XP_003386491.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Amphimedon queenslandica]
gi|32565180|ref|NP_498014.2| Protein COQ-8 [Caenorhabditis elegans]
gi|341896229|gb|EGT52164.1| CBN-COQ-8 protein [Caenorhabditis brenneri]
gi|268574088|ref|XP_002642021.1| C. briggsae CBR-COQ-8 protein [Caenorhabditis briggsae]
gi|308487612|ref|XP_003106001.1| CRE-COQ-8 protein [Caenorhabditis remanei]
gi|560117677|emb|CDJ97685.1| ABC-1 domain containing protein [Haemonchus contortus]
gi|560123355|emb|CDJ92014.1| ABC-1 domain containing protein [Haemonchus contortus]
gi|568281227|gb|ETN74063.1| ABC1 family protein [Necator americanus]
gi|170572278|ref|XP_001892048.1| chaperone-activity of bc1 complex-like, mitochondrial [Brugia malayi]
gi|393904834|gb|EJD73810.1| atypical/ABC1/ABC1-A protein kinase [Loa loa]
gi|541042808|gb|ERG81884.1| ubiquinone biosynthesis protein coq-8 [Ascaris suum]
gi|339240355|ref|XP_003376103.1| ubiquinone biosynthesis protein coq-8 [Trichinella spiralis]
gi|555930212|emb|CDJ07330.1| ABC domain containing protein kinase [Hymenolepis microstoma]
gi|556521987|emb|CDJ25289.1| ABC domain containing protein kinase [Echinococcus granulosus]
gi|256074523|ref|XP_002573574.1| ABC transporter [Schistosoma mansoni]
gi|18859849|ref|NP_572836.1| CG32649 [Drosophila melanogaster]
gi|195352724|ref|XP_002042861.1| GM11527 [Drosophila sechellia]
gi|194895760|ref|XP_001978335.1| GG19534 [Drosophila erecta]
gi|195478070|ref|XP_002100397.1| GE16192 [Drosophila yakuba]
gi|194764011|ref|XP_001964125.1| GF20885 [Drosophila ananassae]
gi|125980843|ref|XP_001354442.1| GA17042 [Drosophila pseudoobscura pseudoobscura]
gi|195173652|ref|XP_002027601.1| GL22961 [Drosophila persimilis]
gi|195133048|ref|XP_002010951.1| GI16276 [Drosophila mojavensis]
gi|195397037|ref|XP_002057135.1| GJ16920 [Drosophila virilis]
gi|195059807|ref|XP_001995703.1| GH17620 [Drosophila grimshawi]
gi|195425895|ref|XP_002061196.1| GK10272 [Drosophila willistoni]
gi|498984706|ref|XP_004530431.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Ceratitis capitata]
gi|498984710|ref|XP_004530432.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X2 [Ceratitis capitata]
gi|557776089|ref|XP_005187688.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Musca domestica]
gi|557776091|ref|XP_005187689.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X2 [Musca domestica]
gi|157103279|ref|XP_001647906.1| hypothetical protein AaeL_AAEL000003 [Aedes aegypti]
gi|170063784|ref|XP_001867254.1| ubiquinone biosynthesis protein coq-8 [Culex quinquefasciatus]
gi|347968821|ref|XP_311995.4| AGAP002906-PA [Anopheles gambiae str. PEST]
gi|568251291|gb|ETN60854.1| ubiquinone biosynthesis protein coq-8 [Anopheles darlingi]
gi|189236501|ref|XP_001815964.1| PREDICTED: similar to GA17042-PA [Tribolium castaneum]
gi|270005327|gb|EFA01775.1| hypothetical protein TcasGA2_TC007376 [Tribolium castaneum]
gi|478262769|gb|ENN81291.1| hypothetical protein YQE_02295, partial [Dendroctonus ponderosae]
gi|546675371|gb|ERL86581.1| hypothetical protein D910_03988 [Dendroctonus ponderosae]
gi|357627323|gb|EHJ77059.1| hypothetical protein KGM_21488 [Danaus plexippus]
gi|512933841|ref|XP_004932891.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Bombyx mori]
gi|322798371|gb|EFZ20095.1| hypothetical protein SINV_02598 [Solenopsis invicta]
gi|332021879|gb|EGI62215.1| Chaperone activity of bc1 complex-like, mitochondrial [Acromyrmex echinatior]
gi|307167954|gb|EFN61320.1| Uncharacterized aarF domain-containing protein kinase 4 [Camponotus floridanus]
gi|307194680|gb|EFN76939.1| Uncharacterized aarF domain-containing protein kinase 4 [Harpegnathos saltator]
gi|328782774|ref|XP_624948.3| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X5 [Apis mellifera]
gi|571571172|ref|XP_006563062.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X4 [Apis mellifera]
gi|572301426|ref|XP_006616772.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like [Apis dorsata]
gi|380021104|ref|XP_003694414.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Apis florea]
gi|340725065|ref|XP_003400895.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Bombus terrestris]
gi|350398351|ref|XP_003485168.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Bombus impatiens]
gi|383865801|ref|XP_003708361.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Megachile rotundata]
gi|345483054|ref|XP_001605712.2| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Nasonia vitripennis]

gi|193584682|ref|XP_001951205.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Acyrthosiphon pisum]
gi|156379799|ref|XP_001631643.1| predicted protein [Nematostella vectensis]
gi|241651014|ref|XP_002411257.1| conserved hypothetical protein [Ixodes scapularis]
gi|196007476|ref|XP_002113604.1| hypothetical protein TRIADDRAFT_26675 [Trichoplax adhaerens]
gi|321478972|gb|EFX89928.1| hypothetical protein DAPPUDRAFT_300027 [Daphnia pulex]
gi|391343550|ref|XP_003746072.1| PREDICTED: uncharacterized protein LOC100906274 [Metaseiulus occidentalis]
gi|449665263|ref|XP_002161433.2| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Hydra vulgaris]
gi|22760302|dbj|BAC11143.1| unnamed protein product [Homo sapiens]
gi|34147522|ref|NP_064632.2| chaperone activity of bc1 complex-like, mitochondrial [Homo sapiens]
gi|120538499|gb|AAI29931.1| CABC1 protein [Homo sapiens]
gi|332812087|ref|XP_514248.3| PREDICTED: aarF domain containing kinase 3 isoform 2 [Pan troglodytes]
gi|410034536|ref|XP_003949756.1| PREDICTED: aarF domain containing kinase 3 [Pan troglodytes]
gi|395728943|ref|XP_003775463.1| PREDICTED: LOW QUALITY PROTEIN: chaperone activity of bc1 complex-like, mitochondrial [Pongo abelii]
gi|426333991|ref|XP_004028547.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Gorilla gorilla gorilla]
gi|397487825|ref|XP_003814979.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform 1 [Pan paniscus]
gi|52546036|emb|CAH56132.1| hypothetical protein [Homo sapiens]
gi|397487827|ref|XP_003814980.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform 2 [Pan paniscus]
gi|402857025|ref|XP_003893074.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform 1 [Papio anubis]
gi|402857027|ref|XP_003893075.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform 2 [Papio anubis]
gi|384475947|ref|NP_001245119.1| chaperone activity of bc1 complex-like, mitochondrial [Macaca mulatta]
gi|194375033|dbj|BAG62629.1| unnamed protein product [Homo sapiens]
gi|296230259|ref|XP_002760620.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Callithrix jacchus]
gi|403277369|ref|XP_003930337.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Saimiri boliviensis boliviensis]
gi|193786848|dbj|BAG52171.1| unnamed protein product [Homo sapiens]
gi|348577083|ref|XP_003474314.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Cavia porcellus]
gi|533118786|ref|XP_005374854.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Chinchilla lanigera]
gi|507627177|ref|XP_004626878.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Octodon degus]
gi|351707065|gb|EHB09984.1| Chaperone activity of bc1 complex-like, mitochondrial [Heterocephalus glaber]
gi|512883071|ref|XP_004895646.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X1 [Heterocephalus glaber]
gi|512983100|ref|XP_004853533.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X1 [Heterocephalus glaber]
gi|512983104|ref|XP_004853535.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X3 [Heterocephalus glaber]
gi|478530930|ref|XP_004439621.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Ceratotherium simum simum]
gi|562857623|ref|XP_006157308.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Tupaia chinensis]
gi|532081710|ref|XP_005326605.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X1 [Ictidomys tridecemlineatus]
gi|291402048|ref|XP_002717679.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Oryctolagus cuniculus]
gi|504132582|ref|XP_004578904.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Ochotona princeps]
gi|395852655|ref|XP_003798850.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Otolemur garnettii]
gi|344278579|ref|XP_003411071.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Loxodonta africana]
gi|471370985|ref|XP_004376003.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Trichechus manatus latirostris]
gi|507634746|ref|XP_004700024.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Echinops telfairi]
gi|586481609|ref|XP_006871324.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Chrysochloris asiatica]
gi|586562148|ref|XP_006914332.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Pteropus alecto]
gi|507971753|ref|XP_004690821.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Condylura cristata]
gi|26380702|dbj|BAB29459.2| unnamed protein product [Mus musculus]
gi|70778882|ref|NP_075830.2| chaperone activity of bc1 complex-like, mitochondrial [Mus musculus]
gi|148681213|gb|EDL13160.1| chaperone, ABC1 activity of bc1 complex like (S. pombe) [Mus musculus]
gi|568911100|ref|XP_006497026.1| PREDICTED: aarF domain containing kinase 3 isoform X4 [Mus musculus]
gi|354490267|ref|XP_003507280.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Cricetulus griseus]
gi|537166611|gb|ERE73576.1| chaperone activity of bc1 complex-like protein [Cricetulus griseus]
gi|524956468|ref|XP_005078200.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Mesocricetus auratus]
gi|61557218|ref|NP_001013203.1| chaperone activity of bc1 complex-like, mitochondrial [Rattus norvegicus]
gi|532010464|ref|XP_005349032.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Microtus ochrogaster]
gi|507538935|ref|XP_004653481.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Jaculus jaculus]
gi|505789979|ref|XP_004605582.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Sorex araneus]
gi|114051798|ref|NP_001039884.1| chaperone activity of bc1 complex-like, mitochondrial [Bos taurus]
gi|555962731|ref|XP_005893453.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Bos mutus]
gi|426239559|ref|XP_004013687.1| PREDICTED: LOW QUALITY PROTEIN: chaperone activity of bc1 complex-like, mitochondrial [Ovis aries]
gi|556740431|ref|XP_005965760.1| PREDICTED: LOW QUALITY PROTEIN: chaperone activity of bc1 complex-like, mitochondrial-like [Pantholops hodgsonii]
gi|548498106|ref|XP_005690657.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Capra hircus]
gi|466014904|ref|XP_004271020.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Orcinus orca]
gi|470647744|ref|XP_004327582.1| PREDICTED: LOW QUALITY PROTEIN: chaperone activity of bc1 complex-like, mitochondrial [Tursiops truncatus]
gi|545852349|ref|XP_003130598.4| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform 1, partial [Sus scrofa]
gi|560923968|ref|XP_006188176.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Camelus ferus]
gi|560952717|ref|XP_006198884.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Vicugna pacos]
gi|530668235|gb|EQB78536.1| chaperone activity of bc1 complex-like, mitochondrial [Camelus ferus]
gi|281348093|gb|EFB23677.1| hypothetical protein PANDA_015361 [Ailuropoda melanoleuca]
gi|301780770|ref|XP_002925802.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Ailuropoda melanoleuca]
gi|511873470|ref|XP_004756948.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Mustela putorius furo]

gi|511962401|ref|XP_004799377.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X1 [Mustela putorius furo]
gi|511962403|ref|XP_004799378.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X2 [Mustela putorius furo]
gi|511962405|ref|XP_004799379.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X3 [Mustela putorius furo]
gi|472347789|ref|XP_004393611.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Odobenus rosmarus divergens]
gi|585182226|ref|XP_006742744.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Leptonychotes weddellii]
gi|587017724|ref|XP_006942676.1| PREDICTED: aarF domain containing kinase 3 [Felis catus]
gi|545506130|ref|XP_005623029.1| PREDICTED: aarF domain containing kinase 3 [Canis lupus familiaris]
gi|554576731|ref|XP_005880198.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X1 [Myotis brandtii]
gi|584071606|ref|XP_006756105.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Myotis davidii]
gi|432113956|gb|ELK36021.1| Chaperone activity of bc1 complex-like, mitochondrial [Myotis davidii]
gi|126307154|ref|XP_001377083.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Monodelphis domestica]
gi|395531486|ref|XP_003767809.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Sarcophilus harrisii]
gi|149641637|ref|XP_001513165.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Ornithorhynchus anatinus]
gi|313661454|ref|NP_001186342.1| chaperone activity of bc1 complex-like, mitochondrial [Gallus gallus]
gi|326914963|ref|XP_003203792.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Meleagris gallopavo]
gi|529444353|ref|XP_005241891.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Falco peregrinus]
gi|541956581|ref|XP_005434055.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Falco cherrug]
gi|543732775|ref|XP_005507410.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X1 [Columba livia]
gi|543732777|ref|XP_005507411.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X2 [Columba livia]
gi|449276751|gb|EMC85172.1| Chaperone activity of bc1 complex-like, mitochondrial, partial [Columba livia]
gi|514758667|ref|XP_005022606.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Anas platyrhynchos]
gi|524990363|ref|XP_005043064.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X1 [Ficedula albicollis]
gi|524990367|ref|XP_005043066.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X3 [Ficedula albicollis]
gi|524990365|ref|XP_005043065.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X2 [Ficedula albicollis]
gi|542159593|ref|XP_005488529.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Zonotrichia albicollis]
gi|543277692|ref|XP_005427071.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Geospiza fortis]
gi|543358942|ref|XP_005523340.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Pseudopodoces humilis]
gi|449495964|ref|XP_002194924.2| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Taeniopygia guttata]
gi|527267587|ref|XP_005151915.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Melopsittacus undulatus]
gi|465951733|gb|EMP24538.1| Chaperone activity of bc1 complex-like protein [Chelonia mydas]
gi|530591945|ref|XP_005289615.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Chrysemys picta bellii]
gi|558139018|ref|XP_006118119.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Pelodiscus sinensis]
gi|557262176|ref|XP_006016618.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Alligator sinensis]
gi|564253057|ref|XP_006265537.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Alligator mississippiensis]
gi|327262641|ref|XP_003216132.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Anolis carolinensis]
gi|565315927|gb|ETE67702.1| Chaperone activity of bc1 complex-like, mitochondrial [Ophiophagus hannah]
gi|147900195|ref|NP_001091311.1| aarF domain containing kinase 3 [Xenopus laevis]
gi|301618993|ref|XP_002938888.1| PREDICTED: aarF domain containing kinase 3 [Xenopus (Silurana) tropicalis]
gi|147899712|ref|NP_001088525.1| uncharacterized protein LOC495397 [Xenopus laevis]
gi|47219134|emb|CAG01797.1| unnamed protein product [Tetraodon nigroviridis]
gi|410916387|ref|XP_003971668.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Takifugu rubripes]
gi|432946141|ref|XP_004083788.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Oryzias latipes]
gi|551513801|ref|XP_005808412.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Xiphophorus maculatus]
gi|498940545|ref|XP_004542084.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Maylandia zebra]
gi|548345351|ref|XP_005725088.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Pundamilia nyererei]
gi|583996053|ref|XP_006793141.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Neolamprologus brichardi]
gi|583996055|ref|XP_006793142.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X2 [Neolamprologus brichardi]
gi|554813655|ref|XP_005917659.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X2 [Haplochromis burtoni]
gi|554813653|ref|XP_005917658.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Haplochromis burtoni]
gi|498940549|ref|XP_004542085.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X2 [Maylandia zebra]
gi|498940554|ref|XP_004542086.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X3 [Maylandia zebra]
gi|548345353|ref|XP_005725089.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X2 [Pundamilia nyererei]
gi|548345355|ref|XP_005725090.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X3 [Pundamilia nyererei]
gi|542219606|ref|XP_005449721.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Oreochromis niloticus]
gi|542219608|ref|XP_005449722.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X2 [Oreochromis niloticus]
gi|75570792|sp|Q5RGU1.1|ADCK3_DANRE RecName: Full=Chaperone activity of bc1 complex-like, mitochondrial; Short=Chaperone-ABC1-like; AltName: Full=aarF domain-containing protein kinase 3; Flags: Precursor
gi|210147448|ref|NP_001002728.2| chaperone activity of bc1 complex-like, mitochondrial [Danio rerio]
gi|573875685|ref|XP_006626150.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Lepisosteus oculatus]
gi|498932179|ref|XP_004540126.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Maylandia zebra]
gi|548392780|ref|XP_005736748.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Pundamilia nyererei]
gi|348510987|ref|XP_003443026.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Oreochromis niloticus]
gi|554872385|ref|XP_005946136.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Haplochromis burtoni]
gi|551495531|ref|XP_005799326.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Xiphophorus maculatus]
gi|410930426|ref|XP_003978599.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Takifugu rubripes]
gi|432954567|ref|XP_004085541.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Oryzias latipes]
gi|326675425|ref|XP_002665174.2| PREDICTED: si:dkey-36g24.3 [Danio rerio]

gi|556954625|ref|XP_005988940.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X1 [Latimeria chalumnae]
gi|556954628|ref|XP_005988941.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial isoform X2 [Latimeria chalumnae]
gi|530642535|ref|XP_005307970.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Chrysemys picta bellii]
gi|530642537|ref|XP_005307971.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X2 [Chrysemys picta bellii]
gi|465954273|gb|EMP25824.1| Chaperone activity of bc1 complex-like protein [Chelonia mydas]
gi|558223105|ref|XP_006136616.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Pelodiscus sinensis]
gi|61354508|gb|AAX41012.1| aarF domain containing kinase 4 [synthetic construct]
gi|217416386|ref|NP_001136027.1| aarF domain-containing protein kinase 4 isoform b [Homo sapiens]
gi|397482626|ref|XP_003812521.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 2 [Pan paniscus]
gi|530417278|ref|XP_005259327.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Homo sapiens]
gi|27363457|ref|NP_079152.3| aarF domain-containing protein kinase 4 isoform a [Homo sapiens]
gi|397482624|ref|XP_003812520.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 1 [Pan paniscus]
gi|441653776|ref|XP_003270391.2| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 1 [Nomascus leucogenys]
gi|297704826|ref|XP_002829281.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Pongo abelii]
gi|296233847|ref|XP_002762184.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 1 [Callithrix jacchus]
gi|296233849|ref|XP_002762185.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 2 [Callithrix jacchus]
gi|403305330|ref|XP_003943220.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Saimiri boliviensis boliviensis]
gi|388454683|ref|NP_001252874.1| uncharacterized aarF domain-containing protein kinase 4 [Macaca mulatta]
gi|544511478|ref|XP_005589349.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Macaca fascicularis]
gi|544511480|ref|XP_005589350.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X2 [Macaca fascicularis]
gi|402905602|ref|XP_003915605.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 2 [Papio anubis]
gi|402905600|ref|XP_003915604.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 1 [Papio anubis]
gi|544511482|ref|XP_005589351.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X3 [Macaca fascicularis]
gi|426388803|ref|XP_004060822.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Gorilla gorilla gorilla]
gi|301776655|ref|XP_002923742.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like isoform 1 [Ailuropoda melanoleuca]
gi|301776657|ref|XP_002923743.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like isoform 2 [Ailuropoda melanoleuca]
gi|281340735|gb|EFB16319.1| hypothetical protein PANDA_012945 [Ailuropoda melanoleuca]
gi|345785025|ref|XP_541612.3| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Canis lupus familiaris]
gi|472353458|ref|XP_004396399.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 1 [Odobenus rosmarus divergens]
gi|472353460|ref|XP_004396400.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 2 [Odobenus rosmarus divergens]
gi|585199774|ref|XP_006750848.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Leptonychotes weddellii]
gi|511913667|ref|XP_004776163.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Mustela putorius furo]
gi|410983006|ref|XP_003997835.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Felis catus]
gi|478534964|ref|XP_004441612.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Ceratotherium simum simum]
gi|545175623|ref|XP_001499301.2| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Equus caballus]
gi|358416778|ref|XP_001790539.3| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Bos taurus]
gi|528919554|ref|XP_005195382.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X4 [Bos taurus]
gi|359075501|ref|XP_002695038.2| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Bos taurus]
gi|528991909|ref|XP_005219173.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X4 [Bos taurus]
gi|296477723|tpg|DAA19838.1| TPA: CG32649-like [Bos taurus]
gi|555957046|ref|XP_005890661.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Bos mutus]
gi|440910287|gb|ELR60096.1| Putative aarF domain-containing protein kinase 4 [Bos mutus]
gi|555957048|ref|XP_005890662.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X2 [Bos mutus]
gi|556735916|ref|XP_005963563.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Pantholops hodgsonii]
gi|556735918|ref|XP_005963564.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X2 [Pantholops hodgsonii]
gi|426242907|ref|XP_004015310.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Ovis aries]
gi|548504237|ref|XP_005692475.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Capra hircus]
gi|560927453|ref|XP_006189892.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Camelus ferus]
gi|528757664|gb|EPY77323.1| aarF domain containing kinase 4-like protein [Camelus ferus]
gi|560985733|ref|XP_006215065.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Vicugna pacos]
gi|466016349|ref|XP_004271313.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Orcinus orca]
gi|470617903|ref|XP_004317662.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Tursiops truncatus]

gi|507980581|ref|XP_004693955.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Condylura cristata]
gi|586524116|ref|XP_006905482.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X2 [Pteropus alecto]
gi|586524114|ref|XP_006905481.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Pteropus alecto]
gi|521027530|gb|EPQ09318.1| Putative aarF domain-containing protein kinase 4 [Myotis brandtii]
gi|554548625|ref|XP_005868851.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X6 [Myotis brandtii]
gi|554548615|ref|XP_005868846.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Myotis brandtii]
gi|584078231|ref|XP_006759254.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Myotis davidii]
gi|584078239|ref|XP_006759258.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X5 [Myotis davidii]
gi|558187491|ref|XP_006102683.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Myotis lucifugus]
gi|558187509|ref|XP_006102687.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X5 [Myotis lucifugus]
gi|58865696|ref|NP_001012065.1| aarF domain-containing protein kinase 4 [Rattus norvegicus]
gi|149056534|gb|EDM07965.1| rCG53591 [Rattus norvegicus]
gi|148692246|gb|EDL24193.1| aarF domain containing kinase 4, isoform CRA_a [Mus musculus]
gi|148692247|gb|EDL24194.1| aarF domain containing kinase 4, isoform CRA_b [Mus musculus]
gi|81882352|sp|Q566J8.1|ADCK4_MOUSE RecName: Full=AarF domain-containing protein kinase 4
gi|124244100|ref|NP_598531.2| aarF domain-containing protein kinase 4 [Mus musculus]
gi|532057885|ref|XP_005371641.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Microtus ochrogaster]
gi|507573610|ref|XP_004670390.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Jaculus jaculus]
gi|533203123|ref|XP_005414084.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Chinchilla lanigera]
gi|533203139|ref|XP_005414092.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X9 [Chinchilla lanigera]
gi|533203127|ref|XP_005414086.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X3 [Chinchilla lanigera]
gi|533203125|ref|XP_005414085.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X2 [Chinchilla lanigera]
gi|533203129|ref|XP_005414087.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X4 [Chinchilla lanigera]
gi|507713992|ref|XP_004648033.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Octodon degus]
gi|348552480|ref|XP_003462055.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoformX1 [Cavia porcellus]
gi|351715414|gb|EHB18333.1| hypothetical protein GW7_03562 [Heterocephalus glaber]
gi|512940021|ref|XP_004909014.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X3 [Heterocephalus glaber]
gi|512939977|ref|XP_004909012.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Heterocephalus glaber]
gi|512940005|ref|XP_004909013.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X2 [Heterocephalus glaber]
gi|532101764|ref|XP_005336498.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Ictidomys tridecemlineatus]
gi|532101766|ref|XP_005336499.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X2 [Ictidomys tridecemlineatus]
gi|444732041|gb|ELW72365.1| Putative aarF domain-containing protein kinase 4 [Tupaia chinensis]
gi|562821230|ref|XP_006140531.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Tupaia chinensis]
gi|395859756|ref|XP_003802198.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Otolemur garnettii]
gi|344298217|ref|XP_003420790.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Loxodonta africana]
gi|471418854|ref|XP_004390922.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Trichechus manatus latirostris]
gi|586482135|ref|XP_006871583.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Chrysochloris asiatica]
gi|488534652|ref|XP_004459036.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 1 [Dasypus novemcinctus]
gi|488534658|ref|XP_004459039.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 4 [Dasypus novemcinctus]
gi|488534656|ref|XP_004459038.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 3 [Dasypus novemcinctus]
gi|488534654|ref|XP_004459037.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform 2 [Dasypus novemcinctus]
gi|505854734|ref|XP_004620788.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Sorex araneus]
gi|585714667|ref|XP_006901010.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Elephantulus edwardii]
gi|291412188|ref|XP_002722364.1| PREDICTED: aarF domain containing kinase 4 [Oryctolagus cuniculus]
gi|504178057|ref|XP_004598133.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Ochotona princeps]
gi|507680869|ref|XP_004710559.1| PREDICTED: LOW QUALITY PROTEIN: uncharacterized aarF domain-containing protein kinase 4 [Echinops telfairi]
gi|126329345|ref|XP_001371518.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Monodelphis domestica]
gi|149517884|ref|XP_001517948.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4, partial [Ornithorhynchus anatinus]
gi|564259209|ref|XP_006268530.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 [Alligator mississippiensis]
gi|47224869|emb|CAG06439.1| unnamed protein product [Tetraodon nigroviridis]
gi|410931113|ref|XP_003978940.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Takifugu rubripes]
gi|499024141|ref|XP_004562829.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like isoform X1 [Maylandia zebra]
gi|499024143|ref|XP_004562830.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like isoform X2 [Maylandia zebra]
gi|554832150|ref|XP_005926629.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like isoform X1 [Haplochromis burtoni]
gi|554832152|ref|XP_005926630.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like isoform X2 [Haplochromis

burtoni]
gi|542231740|ref|XP_005454356.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Oreochromis niloticus]
gi|542231744|ref|XP_005454358.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X3 [Oreochromis niloticus]
gi|542231742|ref|XP_005454357.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X2 [Oreochromis niloticus]
gi|551506177|ref|XP_005804621.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Xiphophorus maculatus]
gi|432891020|ref|XP_004075509.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Oryzias latipes]
gi|125845977|ref|XP_001336310.1| PREDICTED: aarF domain containing kinase 3 [Danio rerio]
gi|573878944|ref|XP_006627695.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like [Lepisosteus oculatus]
gi|301618935|ref|XP_002938863.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Xenopus (Silurana) tropicalis]
gi|512861086|ref|XP_004917145.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X2 [Xenopus (Silurana) tropicalis]
gi|148237982|ref|NP_001087459.1| aarF domain containing kinase 4 [Xenopus laevis]
gi|327276355|ref|XP_003222935.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like [Anolis carolinensis]
gi|260803936|ref|XP_002596845.1| hypothetical protein BRAFLDRAFT_237511 [Branchiostoma floridae]
gi|390340728|ref|XP_791783.2| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Strongylocentrotus purpuratus]
gi|443693751|gb|ELT95038.1| hypothetical protein CAPTEDRAFT_4776 [Capitella teleta]
gi|555698322|gb|ESO01555.1| hypothetical protein HELRODRAFT_185687 [Helobdella robusta]
gi|198433434|ref|XP_002126787.1| PREDICTED: Chaperone, ABC1 activity of bc1 complex like (S. pombe)-like [Ciona intestinalis]
gi|70984246|ref|XP_747640.1| molecular chaperone (ABC1) [Aspergillus fumigatus Af293]
gi|159122426|gb|EDP47547.1| molecular chaperone (ABC1), putative [Aspergillus fumigatus A1163]
gi|119467674|ref|XP_001257643.1| molecular chaperone (ABC1), putative [Neosartorya fischeri NRRL 181]
gi|121703680|ref|XP_001270104.1| molecular chaperone (ABC1), putative [Aspergillus clavatus NRRL 1]
gi|83771723|dbj|BAE61853.1| unnamed protein product [Aspergillus oryzae RIB40]
gi|317148885|ref|XP_001822986.2| molecular chaperone (ABC1) [Aspergillus oryzae RIB40]
gi|391872361|gb|EIT81488.1| ABC (ATP binding cassette) 1 protein [Aspergillus oryzae 3.042]
gi|115386302|ref|XP_001209692.1| protein ABC1, mitochondrial precursor [Aspergillus terreus NIH2624]
gi|134082149|emb|CAK42263.1| unnamed protein product [Aspergillus niger]
gi|317035315|ref|XP_001396633.2| molecular chaperone (ABC1) [Aspergillus niger CBS 513.88]
gi|350636116|gb|EHA24476.1| hypothetical protein ASPNIDRAFT_210041 [Aspergillus niger ATCC 1015]
gi|358369687|dbj|GAA86301.1| molecular chaperone [Aspergillus kawachii IFO 4308]
gi|255945845|ref|XP_002563690.1| Pc20g12040 [Penicillium chrysogenum Wisconsin 54-1255]
gi|584407182|emb|CDM37491.1| Protein kinase-like domain [Penicillium roqueforti]
gi|425773941|gb|EKV12266.1| Molecular chaperone (ABC1), putative [Penicillium digitatum PHI26]
gi|525582383|gb|EPS28633.1| hypothetical protein PDE_03579 [Penicillium oxalicum 114-2]
gi|557729936|dbj|GAD91447.1| molecular chaperone (ABC1), putative [Byssochlamys spectabilis No. 5]
gi|67540804|ref|XP_664176.1| hypothetical protein AN6572.2 [Aspergillus nidulans FGSC A4]
gi|212546311|ref|XP_002153309.1| molecular chaperone (ABC1), putative [Talaromyces marneffei ATCC 18224]
gi|242823783|ref|XP_002488129.1| molecular chaperone (ABC1), putative [Talaromyces stipitatus ATCC 10500]
gi|303322252|ref|XP_003071119.1| ABC1 family protein [Coccidioides posadasii C735 delta SOWgp]
gi|320034974|gb|EFW16916.1| hypothetical protein CPSG_06184 [Coccidioides posadasii str. Silveira]
gi|119196625|ref|XP_001248916.1| hypothetical protein CIMG_02687 [Coccidioides immitis RS]
gi|258569513|ref|XP_002543560.1| ABC1 [Uncinocarpus reesii 1704]
gi|296810398|ref|XP_002845537.1| ABC1 [Arthroderma otae CBS 113480]
gi|225554743|gb|EEH03038.1| ABC1 protein [Ajellomyces capsulatus G186AR]
gi|325095075|gb|EGC48385.1| molecular chaperone [Ajellomyces capsulatus H88]
gi|240276886|gb|EER40397.1| molecular chaperone [Ajellomyces capsulatus H143]
gi|154272561|ref|XP_001537133.1| hypothetical protein HCAG_08242 [Ajellomyces capsulatus NAm1]
gi|239613160|gb|EEQ90147.1| molecular chaperone [Ajellomyces dermatitidis ER-3]
gi|327354767|gb|EGE83624.1| molecular chaperone [Ajellomyces dermatitidis ATCC 18188]
gi|261190961|ref|XP_002621889.1| molecular chaperone [Ajellomyces dermatitidis SLH14081]
gi|531984034|gb|EQL34621.1| Atypical/ABC1/ABC1-A protein kinase [Ajellomyces dermatitidis ATCC 26199]
gi|225678532|gb|EEH16816.1| ubiquinone biosynthesis protein coq-8 [Paracoccidioides brasiliensis Pb03]
gi|295668939|ref|XP_002795018.1| molecular chaperone (ABC1) [Paracoccidioides sp. 'lutzii' Pb01]
gi|226294759|gb|EEH50179.1| molecular chaperone (ABC1) [Paracoccidioides brasiliensis Pb18]
gi|378728060|gb|EHY54519.1| aarF domain-containing kinase [Exophiala dermatitidis NIH/UT8656]
gi|565939386|gb|ETI28492.1| hypothetical protein G647_00941 [Cladophialophora carrionii CBS 160.54]
gi|568122948|gb|ETN45538.1| hypothetical protein HMPREF1541_09370 [Cyphellophora europaea CBS 101466]
gi|189190186|ref|XP_001931432.1| ubiquinone biosynthesis protein coq-8 [Pyrenophora tritici-repentis Pt-1C-BFP]
gi|330935611|ref|XP_003305048.1| hypothetical protein PTT_17791 [Pyrenophora teres f. teres 0-1]
gi|576923973|gb|EUC38086.1| hypothetical protein COCCADRAFT_22435 [Bipolaris zeicola 26-R-13]
gi|578492995|gb|EUN30391.1| hypothetical protein COCVIDRAFT_90496 [Bipolaris victoriae FI3]
gi|451854432|gb|EMD67725.1| hypothetical protein COCSADRAFT_179327 [Bipolaris sorokiniana ND90Pr]
gi|576933723|gb|EUC47246.1| hypothetical protein COCMIDRAFT_90666 [Bipolaris oryzae ATCC 44560]
gi|482812665|gb|EOA89384.1| hypothetical protein SETTUDRAFT_183445 [Setosphaeria turcica Et28A]
gi|526193171|gb|EPS35371.1| hypothetical protein H072_11228 [Dactylellina haptotyla CBS 200.50]
gi|549049527|emb|CCX11368.1| Similar to Protein ABC1 homolog, mitochondrial; acc. no. Q92338 [Pyronema omphalodes CBS 100304]
gi|85101761|ref|XP_961212.1| hypothetical protein NCU03823 [Neurospora crassa OR74A]
gi|336472939|gb|EGO61099.1| hypothetical protein NEUTE1DRAFT_76825 [Neurospora tetrasperma FGSC 2508]
gi|576046376|ref|XP_006697061.1| hypothetical protein CTHT_0067700 [Chaetomium thermophilum var. thermophilum DSM 1495]

gi|475667257|gb|EMT65046.1| Protein ABC1 like protein, mitochondrial [Fusarium oxysporum f. sp. cubense race 4]
gi|517313371|emb|CCT65584.1| probable abc1 protein precursor [Fusarium fujikuroi IMI 58289]
gi|500252321|gb|EON96167.1| putative abc1 family protein [Togninia minima UCRPA7]
gi|573057179|gb|ETS77054.1| hypothetical protein PFICI_10928 [Pestalotiopsis fici W106-1]
gi|346974573|gb|EGY18025.1| ABC1 protein [Verticillium dahliae VdLs.17]
gi|353244349|emb|CCA75757.1| related to ABC1-ubiquinol--cytochrome-c reductase complex assembly protein [Piriformospora indica DSM 11827]
gi|540383897|gb|AFR95375.2| Atypical/ABC1/ABC1-A protein kinase [Cryptococcus neoformans var. grubii H99]
gi|384494254|gb|EIE84745.1| hypothetical protein RO3G_09455 [Rhizopus delemar RA 99-880]
gi|511009067|gb|EPB90317.1| Atypical/ABC1/ABC1-A protein kinase [Mucor circinelloides f. circinelloides 1006PhL]
gi|3087737|emb|CAA04557.1| ABC1 protein [Arabidopsis thaliana]
gi|15234260|ref|NP_192075.1| ABC transporter 1 [Arabidopsis thaliana]
gi|297814165|ref|XP_002874966.1| ABC1 protein [Arabidopsis lyrata subsp. lyrata]
gi|565458552|ref|XP_006287275.1| hypothetical protein CARUB_v10000471mg [Capsella rubella]
gi|567161086|ref|XP_006396362.1| hypothetical protein EUTSA_v10028510mg [Eutrema salsugineum]
gi|225437742|ref|XP_002273486.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial [Vitis vinifera]
gi|508703589|gb|EOX95485.1| Ubiquinone biosynthesis protein coq-8 [Theobroma cacao]
gi|462418300|gb|EMJ22749.1| hypothetical protein PRUPE_ppa002977mg [Prunus persica]
gi|255548205|ref|XP_002515159.1| Ubiquinone biosynthesis protein coq-8, putative [Ricinus communis]
gi|567904304|ref|XP_006444640.1| hypothetical protein CICLE_v10019335mg [Citrus clementina]
gi|356501819|ref|XP_003519721.1| PREDICTED: uncharacterized aarF domain-containing protein kinase 4-like isoform X1 [Glycine max]
gi|356533503|ref|XP_003535303.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like isoform X1 [Glycine max]
gi|561018272|gb|ESW17076.1| hypothetical protein PHAVU_007G208100g [Phaseolus vulgaris]
gi|502117517|ref|XP_004495848.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Cicer arietinum]
gi|449449246|ref|XP_004142376.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Cucumis sativus]
gi|449487112|ref|XP_004157500.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Cucumis sativus]
gi|527203960|gb|EPS70264.1| hypothetical protein M569_04492, partial [Genlisea aurea]
gi|460366560|ref|XP_004229149.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Solanum lycopersicum]
gi|586684890|ref|XP_006841526.1| hypothetical protein AMTR_s00003p00150920 [Amborella trichopoda]
gi|242052821|ref|XP_002455556.1| hypothetical protein SORBIDRAFT_03g013060 [Sorghum bicolor]
gi|514777156|ref|XP_004968647.1| PREDICTED: chaperone activity of bc1 complex-like, mitochondrial-like [Setaria italica]
gi|302783410|ref|XP_002973478.1| hypothetical protein SELMODRAFT_99295 [Selaginella moellendorffii]
gi|302809972|ref|XP_002986678.1| hypothetical protein SELMODRAFT_42234 [Selaginella moellendorffii]
gi|159489070|ref|XP_001702520.1| ubiquinone biosynthesis protein [Chlamydomonas reinhardtii]
gi|545376077|ref|XP_005652152.1| ubiquinone biosynthesis protein, partial [Coccomyxa subellipsoidea C-169]
gi|299116986|emb|CBN75090.1| Protein required for ubiquinone (coenzyme Q) biosynthesis and for respiratory growth [Ectocarpus siliculosus]
gi|530737183|gb|EQC35425.1| aarF domain-containing kinase [Saprolegnia diclina VS20]

## Supplementary References

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