A

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CaArf1       1 MG--LTISKLFASLLG-RREMRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVE
CaArf2       1 MG--LSFSKLFANLFG-NKEMRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVE
CaArl1       1 MGQAFSFGNIFSKLWGTNKEIRILILGLDGAGKTTILYRLQMGEVVTTKPTIGFNVETLK
CaArf3       1 MG------GLVSKLFK-NREMRILMLGLDNAGKTTILYKLKLGKTSKTVPTVGFNVETVK
consensus    1 **  ....... .*.. ..*.***..***.********.*..*....*.**.******.

CaArf1      58 YKNISFTVWDVGGQDKIRPLWRYYFQNTQGIIFVVDSNDRDRINEAREELQSMLNEDELK
CaArf2      58 YKNISFTVWDVGGQDKIRPLWRYYFQNTQGIIFVVDSNDRDRIAEAREELQQMLNEDELR
CaArl1      61 YKNITLNIWDLGGQTSIRPYWRCYYSNTSAVIFVVDSTDKDRIDTACKELHQMLKEEELQ
CaArf3      54 HKNVSFAVWDCGGQERIRPLWRHYFTGTNALIYVVDSSDVDRLEESKQELFRIVTDKELT
consensus   61 .**.....**.***..***.**.*...*...*.****.*.**......**.......**.

CaArf1     118 DAVLLVLANKQDLPNAMNAAEITEKMGLHSIR-NRPWFIQATCATTGDGLYEGLEWLSNQ
CaArf2     118 DALLLVFANKQDLPNAMNAAEITEKLGLHSIR-QRPWYIQATCATTGDGLYEGLEWLSTN
CaArl1     121 DSALLVFANKQDQPGAMTAAEVSQALSLTDLK-DRSWSIVASSAIKGEGLTEGLDWLMDV
CaArf3     114 NCLLVVLANKQDVDGAVKPKDLIERFQLNKLTGEHTWSVIPTIAIDGTGLVETLNWISSH
consensus  121 ...*.* *****.. *...........*....  ..*......* .*.**.*.*.*....

CaArf1     177 VGK---  179
CaArf2     177 LKNSS-  181
CaArl1     180 IKDEQL  185
CaArf3     174  SK---- 175
consensus  181 ...   .*
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B

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CaArl3       1 MFHLASSLYTQYTKREQYNILILGLDNAGKTTFLEHLKLLYSSSTESANKNQLSKNSTTS
ScArl3       1 MFHLVKGLYNNWNKKEQYSILILGLDNAGKTTFLETLKKEYSLAFKALEK----------
HsARFP1      1 MYTLLSGLYKYMFQKDEYCILILGLDNAGKTTFLEQSKTRFNKNYKGMSLS---------

CaArl3      61 DDQPRSTSDVIKSKRILPTVGQNTTTIKFESKDSDSPLASQFKNINLKFWDLGGQKSLRN
ScArl3      51 --------------IQPTVGQNVATIPVDSKQ------------ILKFWDVGGQESLRS
HsARFP1     52 --------------KITTTVGLNIGTVDVGKAR-------------LMFWDLGGQEELQS

CaArl3     121 MWSRYFKQCHGIIFIIDSTDTERFQECYETLIDIAHDDIWMQIDDDDDNDNDNSNVDGTV
ScArl3      84 MWSEYYSLCHGIIFIVDSSDRERLDECSTTLQSVVMD----------------EEIEG--
HsARFP1     85 LWDKYYAECHGVIYVIDSTDEERLAESKQAFEKVVTS----------------EALCG--

CaArl3     181 NVPILMMANKQDLPQAVDLVSLKTGVFIKLVSELEATDSKLLPVSVLENQGLQESLEWLV
ScArl3     126 -VPILMLANKQDRQDRMEVQDIKE-VFNKIAEHISARDSRVLPISALTGEGVKDAIEWMI
HsARFP1    127 -VPVLVLANKQDVETCLSIPDIKT-AFSDCTSKIGRRDCLTQACSALTGKGVREGIEWMV

CaArl3     241 TRLIYNKRNKKPEYK---
ScArl3     184 VRLERNKKSRPPIYK---
HsARFP1    185 KCVVRN-VHRPPRQRDIT
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