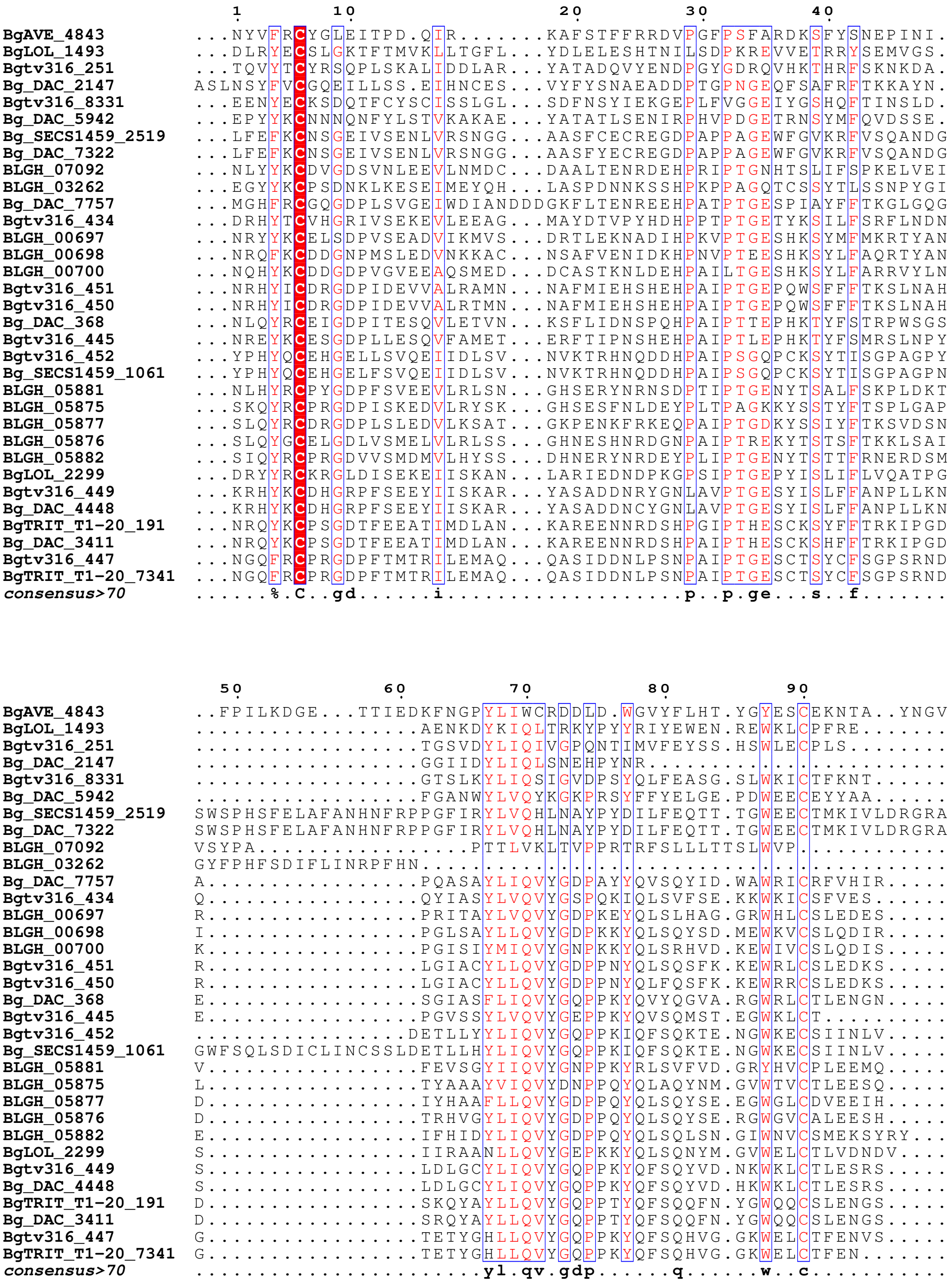
# Multiple sequence alignment (MSA) of AVR$_{A6}$ subfamily members



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                      1       10                20        30        40
                      .        .                 .         .         .
BgAVE_4843         ...NYVFRCYGLEITPD.QIR.......KAFSTFFRRDVPGFPSFARDKSFYSNEPINI.
BgLOL_1493         ...DLRYECSLGKTFTMVKLLTGFL...YDLELESHTNILSDPKREVVETRRYSEMVGS.
Bgtv316_251        ...TQVYTCYRSQPLSKALIDDLAR...YATADQVYENDPGYGDRQVHKTHRFSKNKDA.
Bg_DAC_2147        ASLNSYFVCGQEILLSS.EIHNCES...VYFYSNAEADDPTGPNGEQFSAFRFTKKAYN.
Bgtv316_8331       ...EENYECKSDQTFCYSCISSLGL...SDFNSYIEKGEPLFVGGEIYGSHQFTINSLD.
Bg_DAC_5942        ...EPYYKCNNNQNFYLSTVKAKAE...YATATLSENIRPHVPDGETRNSYMFQVDSSE.
Bg_SECS1459_2519   ...LFEFKCNSGEIVSENLVRSNGG...AASFCECREGDPAPPAGEWFGVKRFVSQANDG
Bg_DAC_7322        ...LFEFKCNSGEIVSENLVRSNGG...AASFYECREGDPAPPAGEWFGVKRFVSQANDG
BLGH_07092         ...NLYYKCDVGDSVNLEEVLNMDC...DAALTENRDEHPRIPTGNHTSLIFSPKELVEI
BLGH_03262         ...EGYYKCPSDNKLKESEIMEYQH...LASPDNNKSSHPKPPAGQTCSSYTLSSNPYGI
Bg_DAC_7757        ...MGHFRCGQGDPLSVGEIWDIANDDDGKFLTENREEHPATPTGESPIAYFFTKGLGQG
Bgtv316_434        ...DRHYTCVHGRIVSEKEVLEEAG...MAYDTVPYHDHPPTPTGETYKSILFSRFLNDN
BLGH_00697         ...NRYYKCELSDPVSEADVIKMVS...DRTLEKNADIHPKVPTGESHKSYMFMKRTYAN
BLGH_00698         ...NRQFKCDDGNPMSLEDVNKKAC...NSAFVENIDKHPNVPTEESHKSYLFAQRTYAN
BLGH_00700         ...NQHYKCDDGDPVGVEEAQSMED...DCASTKNLDEHPAILTGESHKSYLFARRVYLN
Bgtv316_451        ...NRHYICDRGDPIDEVVALRAMN...NAFMIEHSHEHPAIPTGEPQWSFFFTKSLNAH
Bgtv316_450        ...NRHYICDRGDPIDEVVALRTMN...NAFMIEHSHEHPAIPTGEPQWSFFFTKSLNAH
Bg_DAC_368         ...NLQYRCEIGDPITESQVLETVN...KSFLIDNSPQHPAIPTTEPHKTYFSTRPWSGS
Bgtv316_445        ...NREYKCESGDPLLESQVFAMET...ERFTIPNSHEHPAIPTLEPHKTYFSMRSLNPY
Bgtv316_452        ...YPHYQCEHGELLSVQEIIDLSV...NVKTRHNQDDHPAIPSGQPCKSYTISGPAGPY
Bg_SECS1459_1061   ...YPHYQCEHGELFSVQEIIDLSV...NVKTRHNQDDHPAIPSGQPCKSYTISGPAGPN
BLGH_05881         ...NLHYRCPYGDPFSVEEVLRLSN...GHSERYNRNSDPTIPTGENYTSALFSKPLDKT
BLGH_05875         ...SKQYRCPRGDPISKEDVLRYSK...GHSESFNLDEYPLTPAGKKYSSTYFTSPLGAP
BLGH_05877         ...SLQYRCDRGDPLSLEDVLKSAT...GKPENKFRKEQPAIPTGDKYSSIYFTKSVDSN
BLGH_05876         ...SLQYGCELGDLVSMELVLRLSS...GHNESHNRDGNPAIPTREKYTSTSFTKKLSAI
BLGH_05882         ...SIQYRCPRGDVVSMDMVLHYSS...DHNERYNRDEYPLIPTGENYTSTTFRNERDSM
BgLOL_2299         ...DRYYRCKRGLDISEKEIISKAN...LARIEDNDPKGPSIPTGEPYISLIFLVQATPG
Bgtv316_449        ...KRHYKCDHGRPFSEEYIISKAR...YASADDNRYGNLAVPTGESYISLFFANPLLKN
Bg_DAC_4448        ...KRHYKCDHGRPFSEEYIISKAR...YASADDNCYGNLAVPTGESYISLFFANPLLKN
BgTRIT_T1-20_191   ...NRQYKCPSGDTFEEATIMDLAN...KAREENNRDSHPGIPTHESCKSYFFTRKIPGD
Bg_DAC_3411        ...NRQYKCPSGDTFEEATIMDLAN...KAREENNRDSHPAIPTHESCKSHFFTRKIPGD
Bgtv316_447        ...NGQFRCPRGDPFTMTRILEMAQ...QASIDDNLPSNPAIPTGESCTSYCFSGPSRND
BgTRIT_T1-20_7341  ...NGQFRCPRGDPFTMTRILEMAQ...QASIDDNLPSNPAIPTGESCTSYCFSGPSRND
consensus>70       ......%.C..gd......i...................p..p.ge...s..f.......
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                     50           60        70         80         90
                      .            .         .          .          .
BgAVE_4843         ..FPILKDGE...TTIEDKFNGPYLIWCRDDLD.WGVYFLHT.YGYESCEKNTA..YNGV
BgLOL_1493         ..................AENKDYKIQLTRKYPYYRIYEWEN.REWKLCPFRE.......
Bgtv316_251        ..................TGSVDYLIQIVGPQNTIMVFEYSS.HSWLECPLS........
Bg_DAC_2147        ..................GGIIDYLIQLSNEHPYNR........................
Bgtv316_8331       ..................GTSLKYLIQSIGVDPSYQLFEASG.SLWKICTFKNT......
Bg_DAC_5942        ..................FGANWYLVQYKGKPRSYFFYELGE.PDWEECEYYAA......
Bg_SECS1459_2519   SWSPHSFELAFANHNFRPPGFIRYLVQHLNAYPYDILFEQTT.TGWEECTMKIVLDRGRA
Bg_DAC_7322        SWSPHSFELAFANHNFRPPGFIRYLVQHLNAYPYDILFEQTT.TGWEECTMKIVLDRGRA
BLGH_07092         VSYPA.................PTTLVKLTVPPRTRFSLLLTTSLWVP............
BLGH_03262         GYFPHFSDIFLINRPFHN..........................................
Bg_DAC_7757        A.................PQASAYLIQVYGDPAYYQVSQYID.WAWRICRFVHIR.....
Bgtv316_434        Q.................QYIASYLVQVYGSPQKIQLSVFSE.KKWKICSFVES......
BLGH_00697         R.................PRITAYLVQVYGDPKEYQLSLHAG.GRWHLCSLEDES.....
BLGH_00698         I.................PGLSAYLLQVYGDPKKYQLSQYSD.MEWKVCSLQDIR.....
BLGH_00700         K.................PGISIYMIQVYGNPKKYQLSRHVD.KEWIVCSLQDIS.....
Bgtv316_451        R.................LGIACYLLQVYGDPPNYQLSQSFK.KEWRLCSLEDKS.....
Bgtv316_450        R.................LGIACYLLQVYGDPPNYQLFQSFK.KEWRRCSLEDKS.....
Bg_DAC_368         E.................SGIASFLIQVYGQPPKYQVYQGVA.RGWRLCTLENGN.....
Bgtv316_445        E.................PGVSSYLVQVYGEPPKYQVSQMST.EGWKLCT..........
Bgtv316_452        .................DETLLYYLIQVYGQPPKIQFSQKTE.NGWKECSIINLV.....
Bg_SECS1459_1061   GWFSQLSDICLINCSSLDETLLHYLIQVYGQPPKIQFSQKTE.NGWKECSIINLV.....
BLGH_05881         V.................FEVSGYIIQVYGNPPKYRLSVFVD.GRYHVCPLEEMQ.....
BLGH_05875         L.................TYAAAYVIQVYDNPPQYQLAQYNM.GVWTVCTLEESQ.....
BLGH_05877         D.................IYHAAFLLQVYGDPPQYQLSQYSE.EGWGLCDVEEIH.....
BLGH_05876         D.................TRHVGYLIQVYGDPPQYQLSQYSE.RGWGVCALEESH.....
BLGH_05882         E.................IFHIDYLIQVYGDPPQYQLSQLSN.GIWNVCSMEKSYRY...
BgLOL_2299         S.................IIRAANLLQVYGEPKKYQLSQNYM.GVWELCTLVDNDV....
Bgtv316_449        S.................LDLGCYLIQVYGQPPKYQFSQYVD.NKWKLCTLESRS.....
Bg_DAC_4448        S.................LDLGCYLIQVYGQPPKYQFSQYVD.HKWKLCTLESRS.....
BgTRIT_T1-20_191   D.................SKQYAYLLQVYGQPPTYQFSQQFN.YGWQQCSLENGS.....
Bg_DAC_3411        D.................SRQYAYLLQVYGQPPTYQFSQQFN.YGWQQCSLENGS.....
Bgtv316_447        G.................TETYGHLLQVYGQPPKYQFSQHVG.GKWELCTFENVS.....
BgTRIT_T1-20_7341  G.................TETYGHLLQVYGQPPKYQFSQHVG.GKWELCTFEN.......
consensus>70       .......................yl.qv.gdp......q......w..c...........
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                 100
                    .
BgAVE_4843          TFGQLMNG
BgLOL_1493          ........
Bgtv316_251         ........
Bg_DAC_2147         ........
Bgtv316_8331        ........
Bg_DAC_5942         ........
Bg_SECS1459_2519    PY......
Bg_DAC_7322         PY......
BLGH_07092          ........
BLGH_03262          ........
Bg_DAC_7757         ........
Bgtv316_434         ........
BLGH_00697          ........
BLGH_00698          ........
BLGH_00700          ........
Bgtv316_451         ........
Bgtv316_450         ........
Bg_DAC_368          ........
Bgtv316_445         ........
Bgtv316_452         ........
Bg_SECS1459_1061    ........
BLGH_05881          ........
BLGH_05875          ........
BLGH_05877          ........
BLGH_05876          ........
BLGH_05882          ........
BgLOL_2299          ........
Bgtv316_449         ........
Bg_DAC_4448         ........
BgTRIT_T1-20_191    ........
Bg_DAC_3411         ........
Bgtv316_447         ........
BgTRIT_T1-20_7341   ........
consensus>70        ........
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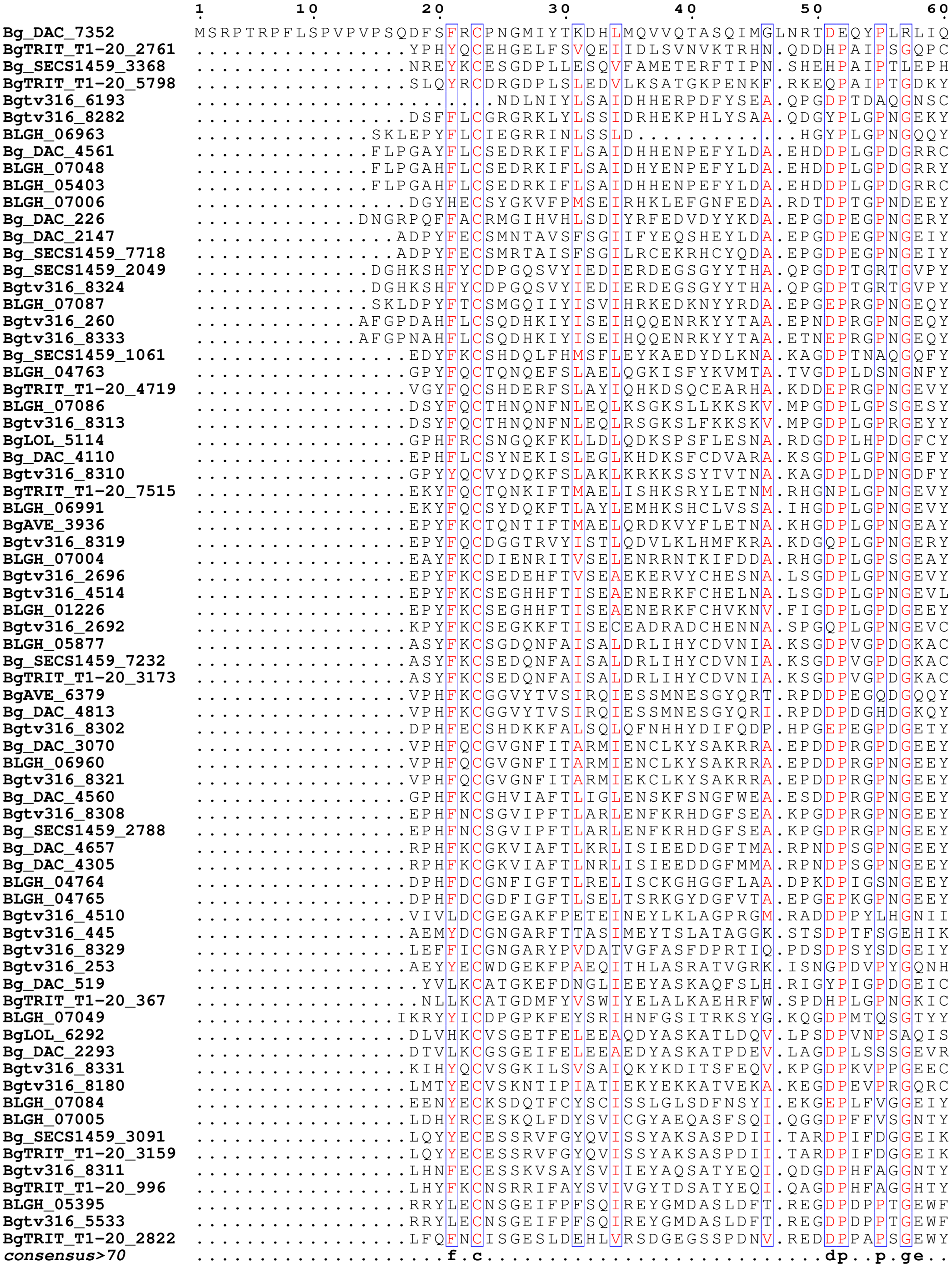
# Multiple sequence alignment (MSA) of AVR$_{A7}$ subfamily members



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                       1        10        20        30        40        50        60
Bg_DAC_7352            MSRPTRPFLSPVPVPSQDFSFRCPNGMIYTKDHLMQVVQTASQIMGLNRTDEQYPLRLIQ
BgTRIT_T1-20_2761      .................YPHYQCEHGELFSVQEIIDLSVNVKTRHN.QDDHPAIPSGQPC
Bg_SECS1459_3368       .................NREYKCESGDPLLESQVFAMETERFTIPN.SHEHPAIPTLEPH
BgTRIT_T1-20_5798      .................SLQYRCDRGDPLSLEDVLKSATGKPENKF.RKEQPAIPTGDKY
Bgtv316_6193           ........................NDLNIYLSAIDHHERPDFYSEA.QPGDPTDAQGNSC
Bgtv316_8282           .................DSFFLCGRGRKLYLSSIDRHEKPHLYSAA.QDGYPLGPNGEKY
BLGH_06963             ..............SKLEPYFLCIEGRRINLSSLD.............HGYPLGPNGQQY
Bg_DAC_4561            ..............FLPGAYFLCSEDRKIFLSAIDHHENPEFYLDA.EHDDPLGPDGRRC
BLGH_07048             ..............FLPGAHFLCSEDRKIFLSAIDHYENPEFYLDA.EHDDPLGPDGRRY
BLGH_05403             ..............FLPGAHFLCSEDRKIFLSAIDHHENPEFYLDA.EHDDPLGPDGRRC
BLGH_07006             .................DGYHECSYGKVFPMSEIRHKLEFGNFEDA.RDTDPTGPNDEEY
Bg_DAC_226             .............DNGRPQFFACRMGIHVHLSDIYRFEDVDYYKDA.EPGDPEGPNGERY
Bg_DAC_2147            ................ADPYFECSMNTAVSFSGIIFYEQSHEYLDA.EPGDPEGPNGEIY
Bg_SECS1459_7718       ................ADPYFECSMRTAISFSGILRCEKRHCYQDA.EPGDPEGPNGEIY
Bg_SECS1459_2049       ..............DGHKSHFYCDPGQSVYIEDIERDEGSGYYTHA.QPGDPTGRTGVPY
Bgtv316_8324           ..............DGHKSHFYCDPGQSVYIEDIERDEGSGYYTHA.QPGDPTGRTGVPY
BLGH_07087             ..............SKLDPYFTCSMGQIIYISVIHRKEDKNYYRDA.EPGEPRGPNGEQY
Bgtv316_260            .............AFGPDAHFLCSQDHKIYISEIHQQENRKYYTAA.EPNDPRGPNGEQY
Bgtv316_8333           .............AFGPNAHFLCSQDHKIYISEIHQQENRKYYTAA.ETNEPRGPNGEQY
Bg_SECS1459_1061       .................EDYFKCSHDQLFHMSFLEYKAEDYDLKNA.KAGDPTNAQGQFY
BLGH_04763             .................GPYFQCTQNQEFSLAELQGKISFYKVMTA.TVGDPLDSNGNFY
BgTRIT_T1-20_4719      .................VGYFQCSHDERFSLAYIQHKDSQCEARHA.KDDEPRGPNGEVY
BLGH_07086             .................DSYFQCTHNQNFNLEQLKSGKSLLKKSKV.MPGDPLGPSGESY
Bgtv316_8313           .................DSYFQCTHNQNFNLEQLRSGKSLFKKSKV.MPGDPLGPRGEYY
BgLOL_5114             .................GPHFRCSNGQKFKLLDLQDKSPSFLESNA.RDGDPLHPDGFCY
Bg_DAC_4110            .................EPHFLCSYNEKISLEGLKHDKSFCDVARA.KSGDPLGPNGEFY
Bgtv316_8310           .................GPYYQCVYDQKFSLAKLKRKKSSYTVTNA.KAGDPLDPNGDFY
BgTRIT_T1-20_7515      .................EKYFQCTQNKIFTMAELISHKSRYLETNM.RHGNPLGPNGEVY
BLGH_06991             .................EKYFQCSYDQKFTLAYLEMHKSHCLVSSA.IHGDPLGPNGEVY
BgAVE_3936             .................EPYFKCTQNTIFTMAELQRDKVYFLETNA.KHGDPLGPNGEAY
Bgtv316_8319           .................EPYFQCDGGTRVYISTLQDVLKLHMFKRA.KDGQPLGPNGERY
BLGH_07004             .................EAYFKCDIENRITVSELENRRNTKIFDDA.RHGDPLGPSGEAY
Bgtv316_2696           .................EPYFKCSEDEHFTVSEAEKERVYCHESNA.LSGDPLGPNGEVY
Bgtv316_4514           .................EPYFKCSEGHHFTISEAENERKFCHELNA.LSGDPLGPNGEVL
BLGH_01226             .................EPYFKCSEGHHFTISEAENERKFCHVKNV.FIGDPLGPDGEEY
Bgtv316_2692           .................KPYFKCSEGKKFTISECEADRADCHENNA.SPGQPLGPNGEVC
BLGH_05877             .................ASYFKCSGDQNFAISALDRLIHYCDVNIA.KSGDPVGPDGKAC
Bg_SECS1459_7232       .................ASYFKCSEDQNFAISALDRLIHYCDVNIA.KSGDPVGPDGKAC
BgTRIT_T1-20_3173      .................ASYFKCSEDQNFAISALDRLIHYCDVNIA.KSGDPVGPDGKAC
BgAVE_6379             .................VPHFKCGGVYTVSIRQIESSMNESGYQRT.RPDDPEGQDGQQY
Bg_DAC_4813            .................VPHFKCGGVYTVSIRQIESSMNESGYQRI.RPDDPDGHDGKQY
Bgtv316_8302           .................DPHFECSHDKKFALSQLQFNHHYDIFQDP.HPGEPEGPDGETY
Bg_DAC_3070            .................VPHFQCGVGNFITARMIENCLKYSAKRRA.EPDDPRGPDGEEY
BLGH_06960             .................VPHFQCGVGNFITARMIENCLKYSAKRRA.EPDDPRGPNGEEY
Bgtv316_8321           .................VPHFQCGVGNFITARMIEKCLKYSAKRRA.EPDDPRGPNGEEY
Bg_DAC_4560            .................GPHFKCGHVIAFTLIGLENSKFSNGFWEA.ESDDPRGPNGEEY
Bgtv316_8308           .................EPHFNCSGVIPFTLARLENFKRHDGFSEA.KPGDPRGPNGEEY
Bg_SECS1459_2788       .................EPHFNCSGVIPFTLARLENFKRHDGFSEA.KPGDPRGPNGEEY
Bg_DAC_4657            .................RPHFKCGKVIAFTLKRLISIEEDDGFTMA.RPNDPSGPNGEEY
Bg_DAC_4305            .................RPHFKCGKVIAFTLNRLISIEEDDGFMMA.RPNDPSGPNGEEY
BLGH_04764             .................DPHFDCGNFIGFTLRELISCKGHGGFLAA.DPKDPIGSNGEEY
BLGH_04765             .................DPHFDCGDFIGFTLSELTSRKGYDGFVTA.EPGEPKGPNGEEY
Bgtv316_4510           .................VIVLDCGEGAKFPETEINEYLKLAGPRGM.RADDPPYLHGNII
Bgtv316_445            .................AEMYDCGNGARFTTASIMEYTSLATAGGK.STSDPTFSGEHIK
Bgtv316_8329           .................LEFFICGNGARYPVDATVGFASFDPRTIQ.PDSDPSYSDGEIY
Bgtv316_253            .................AEYYECWDGEKFPAEQITHLASRATVGRK.ISNGPDVPYGQNH
Bg_DAC_519             ..................YVLKCATGKEFDNGLIEEYASKAQFSLH.RIGYPIGPDGEIC
BgTRIT_T1-20_367       ..................NLLKCATGDMFYVSWIYELALKAEHRFW.SPDHPLGPNGKIC
BLGH_07049             ................IKRYYICDPGPKFEYSRIHNFGSITRKSYG.KQGDPMTQSGTYY
BgLOL_6292             .................DLVHKCVSGETFELEEAQDYASKATLDQV.LPSDPVNPSAQIS
Bg_DAC_2293            .................DTVLKCGSGEIFELEEAEDYASKATPDEV.LAGDPLSSSGEVR
Bgtv316_8331           .................KIHYQCVSGKILSVSAIQKYKDITSFEQV.KPGDPKVPPGEEC
Bgtv316_8180           .................LMTYECVSKNTIPIATIEKYEKKATVEKA.KEGDPEVPRGQRC
BLGH_07084             .................EENYECKSDQTFCYSCISSLGLSDFNSYI.EKGEPLFVGGEIY
BLGH_07005             .................LDHYRCESKQLFDYSVICGYAEQASFSQI.QGGDPFFVSGNTY
Bg_SECS1459_3091       .................LQYYECESSRVFGYQVISSYAKSASPDII.TARDPIFDGGEIK
BgTRIT_T1-20_3159      .................LQYYECESSRVFGYQVISSYAKSASPDII.TARDPIFDGGEIK
Bgtv316_8311           .................LHNFECESSKVSAYSVIIEYAQSATYEQI.QDGDPHFAGGNTY
BgTRIT_T1-20_996       .................LHYFKCNSRRIFAYSVIVGYTDSATYEQI.QAGDPHFAGGHTY
BLGH_05395             .................RRYLECNSGEIFPFSQIREYGMDASLDFT.REGDPDPPTGEWF
Bgtv316_5533           .................RRYLECNSGEIFPFSQIREYGMDASLDFT.REGDPDPPTGEWF
BgTRIT_T1-20_2822      .................LFQFNCISGESLDEHLVRSDGEGSSPDNV.REDDPPAPSGEWY
consensus>70           ....................f.c...........................dp..p.ge..
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                                   70                          80        90
                                    .                           .         .
Bg_DAC_7352         PRYSVNG..N.....VWYHPIPGG.QH.................VQDFVVFNTDYEVVGV
BgTRIT_T1-20_2761   KSYTISGPAGP...........NGWFSQLSDICLINCSSLDETLLHYLIQVYGQPPKIQF
Bg_SECS1459_3368    KTYFSMRSLNP.............................YEPGVSSYLVQVYGEPPKYQV
BgTRIT_T1-20_5798   SSIYFTKSVDS.............................NDIYHAAFLLQVYGDPPQYQL
Bgtv316_6193        TAYRHTARV.............NG.VD.................VLILIQLSYEFPYNRV
Bgtv316_8282        PAFLHPIIGN............DG.GP.................MMTLVQLTPERPFNRV
BLGH_06963          RAYRYPVIGN............GG.VT.................IMTLIQEYDADPYNRV
Bg_DAC_4561         SAYRYSVIGN............DG.ST.................IMTLIQATSESPFNRV
BLGH_07048          SAYRYSVIGN............DG.ST.................IMTLIQATYESPFNRV
BLGH_05403          SAYRYSVIGN............DG.ST.................IMTLIQATYESPFNRV
BLGH_07006          FGMRFDMMPV............PE.VT.................VTYLIQIIYKAPYYRF
Bg_DAC_226          RARRLFKRTY............GG.SY.................GYILIQATDEYPFNRV
Bg_DAC_2147         PARRFTRVRR............DG.SD.................VLILIQSLDEYPLRRA
Bg_SECS1459_7718    SAYRFTKVRT............DG.SE.................VLILIQSTNEYPLCRV
Bg_SECS1459_2049    MAHRSAWVGN............NG.ET.................VPYLIQAYFEYPYYRV
Bgtv316_8324        MAHRSAWVGN............NG.ET.................VPYLIQAYFEYPYYRV
BLGH_07087          QAHIFKKCVV............NG.EE.................IRYLVQASNEHPFTRV
Bgtv316_260         SAHRFTREGF............NG.ET.................IRYLIQPAIEYPHNRV
Bgtv316_8333        SAHRFTREGL............NG.ET.................IRYLIQPAMEYPHNRV
Bg_SECS1459_1061    KTVRVTRMPE............RD.FF.................VKYLIQFIDETSTYRV
BLGH_04763          PTRQFSMIPR............PG.YK.................LSIPLLLLPHTILLGE
BgTRIT_T1-20_4719   RTTHIMTVPR............VG.FF.................VYYIIQVIDDSPTYRL
BLGH_07086          PTNRTTLILP............EG.VQ.................VSYIFQLIGGPQTFRV
Bgtv316_8313        PTNRTTLILP............EG.VQ.................VSYIFQLIGGPQTFRV
BgLOL_5114          PTHRLTKKSR............GG.QD.................TEYLFQLIDGKPTFHV
Bg_DAC_4110         RTRRYNLIPN............SG.YT.................TAYIVQLIDDTPTFRV
Bgtv316_8310        PTDRFTRKAW............RG.IK.................TEYLFQLIDEEPTFRV
BgTRIT_T1-20_7515   PSRQYSTVPI............GG.YT.................TTYLFQLIDEAPTFNV
BLGH_06991          PANRYRMIPK............DG.YT.................TTYLFQLVDEAPTFRV
BgAVE_3936          PTHRYSMIPI............RG.YT.................TTYLFQLVDEAPTFRV
Bgtv316_8319        MALIYDLAVG............PP.DS.................TAHFVQKIPEDPFFRV
BLGH_07004          IAWRHSFVTA............EG.YI.................IENLVQKIPEAPFIRV
Bgtv316_2696        KTIRFRRFTN............YG.GS.................IAYILQLIDIAPFFRV
Bgtv316_4514        KTSRSRRYRN............DG.SS.................IAYILQLIDLAPFFRV
BLGH_01226          KTSRFRRYRN............DG.SS.................IAYILQLIDLAPFFRV
Bgtv316_2692        KTYGLRQFTP............KG.SS.................VGYILQLIDIAPFFRV
BLGH_05877          KTNRWRQFTP............RG.SS.................VEYILQLIDIAPFFRI
Bg_SECS1459_7232    KTNRWRQFTP............RG.SS.................VEYILQLIDIAPFFRI
BgTRIT_T1-20_3173   KTYRWRQFTP............RG.SS.................VEYILQLIDIAPFFRI
BgAVE_6379          LSCRFNAAA..............G.DD.................SFCMAQRIDEHPNYRV
Bg_DAC_4813         LSCRFNAVAG............GG.DD.................SFCMAQRIDEHPNYRV
Bgtv316_8302        KSWVTFETYR............AG.SS.................VSYLVQLINEVPTFRV
Bg_DAC_3070         SSHRISATPE............GG.VE.................TPYLVQEIDEYPFIQV
BLGH_06960          WSHRISATPE............GG.VE.................TPYLVQEIDEYPFIQV
Bgtv316_8321        WSHRISATPE............GG.VE.................TPYLVQEIDEYPFIQV
Bg_DAC_4560         LSHRFRALPS............GG.K.................DTCYLAQLINEYPFFRV
Bgtv316_8308        LSYQFGATPP............GR.YS.................TSYLAQIIDEYPFFRA
Bg_SECS1459_2788    LSYQFGATPP............VS.YS..FDIAITKYASRCSDSTSYLAQIIDEYPFFRA
Bg_DAC_4657         LSHRYITVPE............GG.FS.................TTYLAQVIDEYPYFRA
Bg_DAC_4305         LSHRYITVPE............GG.FSSSFEITFTKHTSPCPDSTTYLAQVIDEYPYFRA
BLGH_04764          LSHRYSAIRY............GI.YS.................FSYLAQPINEYPYFRA
BLGH_04765          LSHRYRAMRS............II.YT.................TSYLAQPINEYPYFRA
Bgtv316_4510        GAYRMTV.............EIRG.NP.................RTFLIQRIDEIPYYRF
Bgtv316_445         GAFRFKRFSPTFHFAFANHPCLRA.VD.................RFFLVQSLLQYPFTRL
Bgtv316_8329        GVYRFQDTVQ............GN.TK.................RSFMMQSISRSPHFRL
Bgtv316_253         KTRKFTRV.P............SG.VI.................TTYLIQVDKVDSSIRL
Bg_DAC_519          KAYEFDIPLA............DTRDT.................DYYLVQVCGGMEGHRL
BgTRIT_T1-20_367    KAYPFTDPSA............YTGTT.................HHHLVQVCVGIEYFIL
BLGH_07049          PTYRFSTVYG............HE.YT.................YDYIVQEVDEVDSYRL
BgLOL_6292          GAHHFTRKTR............QN.EN.................GFYLVQYVGTLRLIQL
Bg_DAC_2293         GAYHFSRTTR............HN.ED.................GYYLVQLVGTLPSIVL
Bgtv316_8331        KATRFTKRLP............KG.VK.................MSYLLQATGTGPSYKL
Bgtv316_8180        KAKRFTVRLP............NR.ET.................MLYLLQVIGPQPSYQL
BLGH_07084          GSHQFTINSL............DG.TS.................LKYLIQSIGVDPSYQL
BLGH_07005          GAYRFTSHLP............DG.TP.................KNYLIQTVSVEPYRRL
Bg_SECS1459_3091    GAYRFTSNQP............DG.TP.................TTYLIQSVNVEPYQRL
BgTRIT_T1-20_3159   GAYRFTSNQP............DG.TP.................TTYLIQTVNVEPYQRL
Bgtv316_8311        RAYRFTDYLP............DG.SP.................RNYLVQMVNVNPYYRL
BgTRIT_T1-20_996    GAYRFTDYLP............DG.SP.................RNYLVQMVNVNPYYRL
BLGH_05395          GVYRFTSPAK............DG.RI.................IDYLVQSFSDYPYFTL
Bgtv316_5533        GVYGFTSPAK............DG.RI.................IDYLVQSFSDYPYFTL
BgTRIT_T1-20_2822   GVKKFKRQAQ............DG.RY.................IDYLVQRLQAYPNYIL
consensus>70        .......................g......................yl.q.....p..r.
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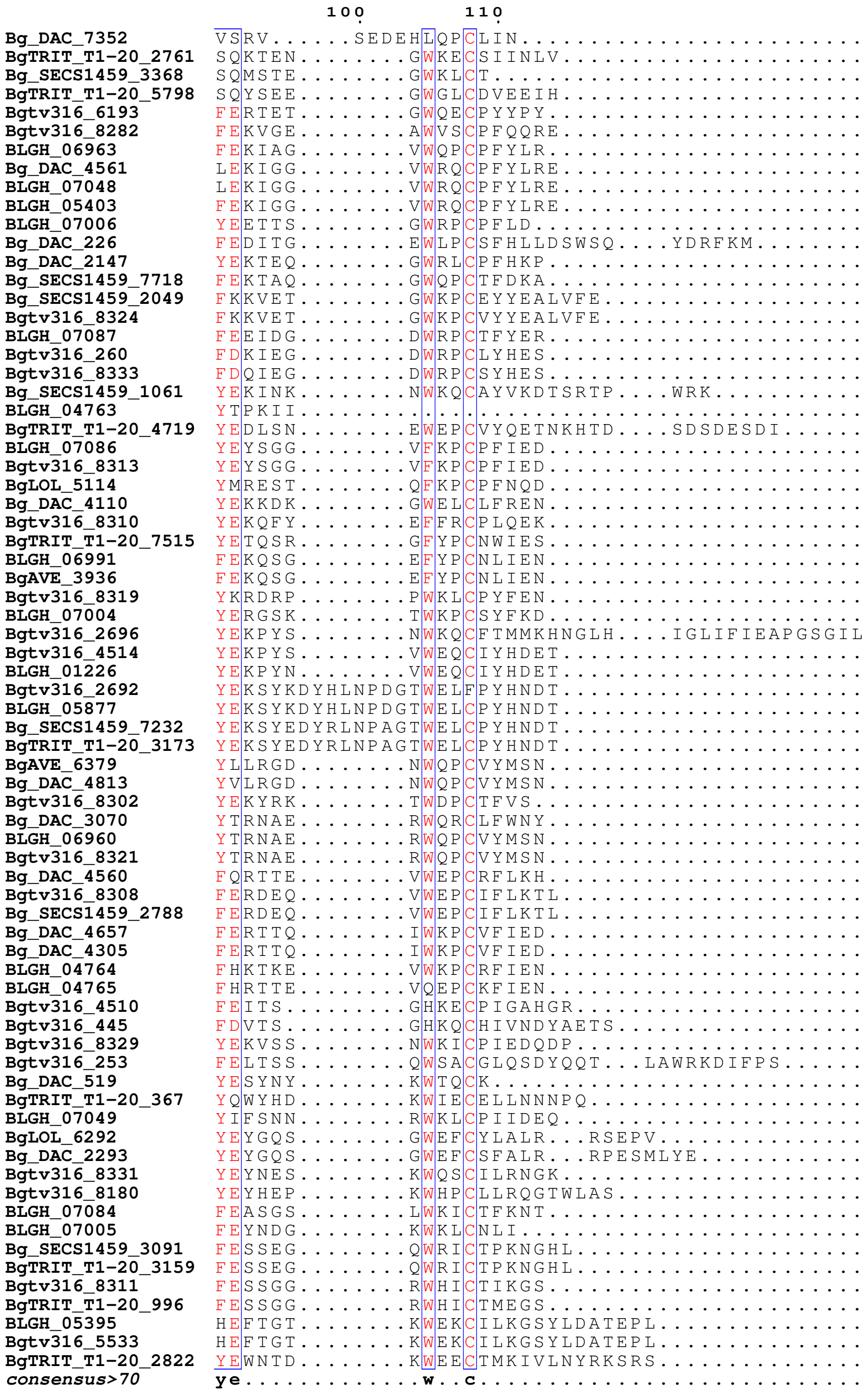

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                             100       110
                              .         .
Bg_DAC_7352         VSRV......SEDEHLQPCLIN.........................
BgTRIT_T1-20_2761   SQKTEN........GWKECSIINLV......................
Bg_SECS1459_3368    SQMSTE........GWKLCT...........................
BgTRIT_T1-20_5798   SQYSEE........GWGLCDVEEIH......................
Bgtv316_6193        FERTET........GWQECPYYPY.......................
Bgtv316_8282        FEKVGE........AWVSCPFQQRE......................
BLGH_06963          FEKIAG........VWQPCPFYLR.......................
Bg_DAC_4561         LEKIGG........VWRQCPFYLRE......................
BLGH_07048          LEKIGG........VWRQCPFYLRE......................
BLGH_05403          FEKIGG........VWRQCPFYLRE......................
BLGH_07006          YEETTS........GWRPCPFLD........................
Bg_DAC_226          FEDITG........EWLPCSFHLLDSWSQ....YDRFKM........
Bg_DAC_2147         YEKTEQ........GWRLCPFHKP.......................
Bg_SECS1459_7718    FEKTAQ........GWQPCTFDKA.......................
Bg_SECS1459_2049    FKKVET........GWKPCEYYEALVFE...................
Bgtv316_8324        FKKVET........GWKPCVYYEALVFE...................
BLGH_07087          FEEIDG........DWRPCTFYER.......................
Bgtv316_260         FDKIEG........DWRPCLYHES.......................
Bgtv316_8333        FDQIEG........DWRPCSYHES.......................
Bg_SECS1459_1061    YEKINK........NWKQCAYVKDTSRTP....WRK...........
BLGH_04763          YTPKII.........................................
BgTRIT_T1-20_4719   YEDLSN........EWEPCVYQETNKHTD....SDSDESDI......
BLGH_07086          YEYSGG........VFKPCPFIED.......................
Bgtv316_8313        YEYSGG........VFKPCPFIED.......................
BgLOL_5114          YMREST........QFKPCPFNQD.......................
Bg_DAC_4110         YEKKDK........GWELCLFREN.......................
Bgtv316_8310        YEKQFY........EFFRCPLQEK.......................
BgTRIT_T1-20_7515   YETQSR........GFYPCNWIES.......................
BLGH_06991          FEKQSG........EFYPCNLIEN.......................
BgAVE_3936          FEKQSG........EFYPCNLIEN.......................
Bgtv316_8319        YKRDRP........PWKLCPYFEN.......................
BLGH_07004          YERGSK........TWKPCSYFKD.......................
Bgtv316_2696        YEKPYS........NWKQCFTMMKHNGLH....IGLIFIEAPGSGIL
Bgtv316_4514        YEKPYS........VWEQCIYHDET......................
BLGH_01226          YEKPYN........VWEQCIYHDET......................
Bgtv316_2692        YEKSYKDYHLNPDGTWELFPYHNDT......................
BLGH_05877          YEKSYKDYHLNPDGTWELCPYHNDT......................
Bg_SECS1459_7232    YEKSYEDYRLNPAGTWELCPYHNDT......................
BgTRIT_T1-20_3173   YEKSYEDYRLNPAGTWELCPYHNDT......................
BgAVE_6379          YLLRGD........NWQPCVYMSN.......................
Bg_DAC_4813         YVLRGD........NWQPCVYMSN.......................
Bgtv316_8302        YEKYRK........TWDPCTFVS........................
Bg_DAC_3070         YTRNAE........RWQRCLFWNY.......................
BLGH_06960          YTRNAE........RWQPCVYMSN.......................
Bgtv316_8321        YTRNAE........RWQPCVYMSN.......................
Bg_DAC_4560         FQRTTE........VWEPCRFLKH.......................
Bgtv316_8308        FERDEQ........VWEPCIFLKTL......................
Bg_SECS1459_2788    FERDEQ........VWEPCIFLKTL......................
Bg_DAC_4657         FERTTQ........IWKPCVFIED.......................
Bg_DAC_4305         FERTTQ........IWKPCVFIED.......................
BLGH_04764          FHKTKE........VWKPCRFIEN.......................
BLGH_04765          FHRTTE........VQEPCKFIEN.......................
Bgtv316_4510        FEITS.........GHKECPIGAHGR.....................
Bgtv316_445         FDVTS.........GHKQCHIVNDYAETS..................
Bgtv316_8329        YEKVSS........NWKICPIEDQDP.....................
Bgtv316_253         FELTSS........QWSACGLQSDYQQT...LAWRKDIFPS......
Bg_DAC_519          YESYNY........KWTQCK...........................
BgTRIT_T1-20_367    YQWYHD........KWIECELLNNNPQ....................
BLGH_07049          YIFSNN........RWKLCPIIDEQ......................
BgLOL_6292          YEYGQS........GWEFCYLALR...RSEPV...............
Bg_DAC_2293         YEYGQS........GWEFCSFALR...RPESMLYE............
Bgtv316_8331        YEYNES........KWQSCILRNGK......................
Bgtv316_8180        YEYHEP........KWHPCLLRQGTWLAS..................
BLGH_07084          FEASGS........LWKICTFKNT.......................
BLGH_07005          FEYNDG........KWKLCNLI.........................
Bg_SECS1459_3091    FESSEG........QWRICTPKNGHL.....................
BgTRIT_T1-20_3159   FESSEG........QWRICTPKNGHL.....................
Bgtv316_8311        FESSGG........RWHICTIKGS.......................
BgTRIT_T1-20_996    FESSGG........RWHICTMEGS.......................
BLGH_05395          HEFTGT........KWEKCILKGSYLDATEPL...............
Bgtv316_5533        HEFTGT........KWEKCILKGSYLDATEPL...............
BgTRIT_T1-20_2822   YEWNTD........KWEECTMKIVLNYRKSRS...............
consensus>70        ye.............w..c............................
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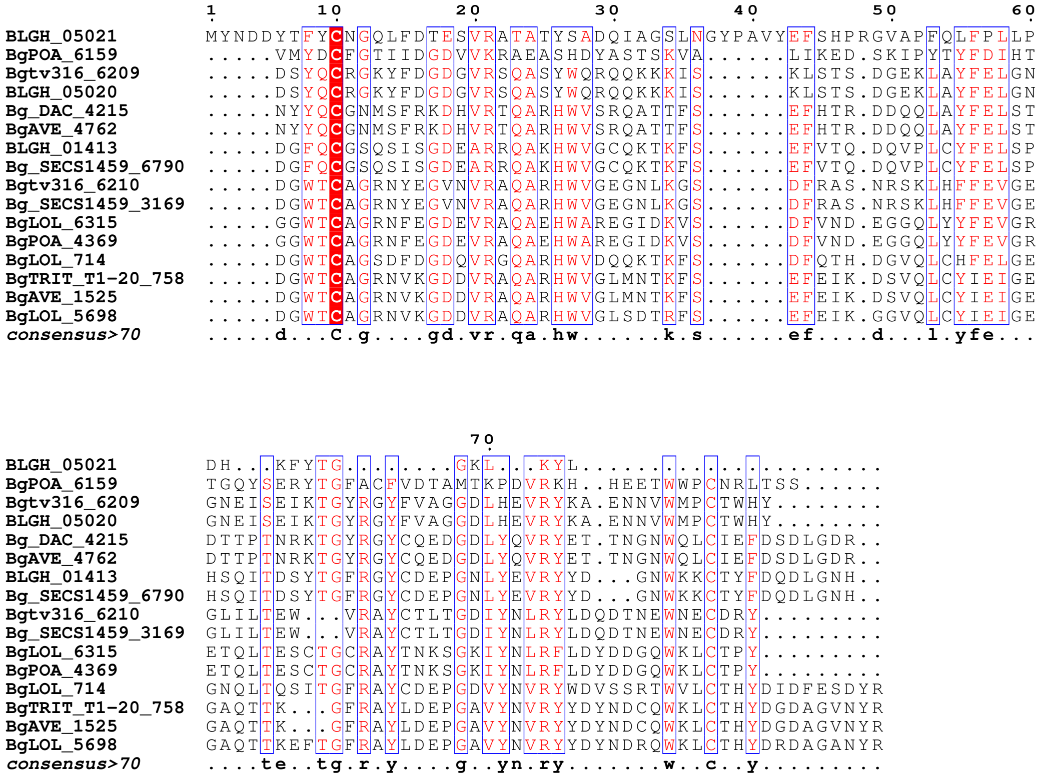
# Multiple sequence alignment (MSA) of $AVR_{A10}$/$AVR_{A22}$ subfamily members



```
                  1       10        20        30        40        50        60
BLGH_05021        MYNDDYTFYCNGQLFDTESVRATATYSADQIAGSLNGYPAVYEFSHPRGVAPFQLFPLLP
BgPOA_6159        .....VMYDCFGTIIDGDVVKRAEASHDYASTSKVA......LIKED.SKIPYTYFDIHT
Bgtv316_6209      .....DSYQCRGKYFDGDGVRSQASYWQRQQKKKIS......KLSTS.DGEKLAYFELGN
BLGH_05020        .....DSYQCRGKYFDGDGVRSQASYWQRQQKKKIS......KLSTS.DGEKLAYFELGN
Bg_DAC_4215       .....NYYQCGNMSFRKDHVRTQARHWVSRQATTFS......EFHTR.DDQQLAYFELST
BgAVE_4762        .....NYYQCGNMSFRKDHVRTQARHWVSRQATTFS......EFHTR.DDQQLAYFELST
BLGH_01413        .....DGFQCGSQSISGDEARRQAKHWVGCQKTKFS......EFVTQ.DQVPLCYFELSP
Bg_SECS1459_6790  .....DGFQCGSQSISGDEARRQAKHWVGCQKTKFS......EFVTQ.DQVPLCYFELSP
Bgtv316_6210      .....DGWTCAGRNYEGVNVRAQARHWVGEGNLKGS......DFRAS.NRSKLHFFEVGE
Bg_SECS1459_3169  .....DGWTCAGRNYEGVNVRAQARHWVGEGNLKGS......DFRAS.NRSKLHFFEVGE
BgLOL_6315        .....GGWTCAGRNFEGDEVRAQAEHWAREGIDKVS......DFVND.EGGQLYYFEVGR
BgPOA_4369        .....GGWTCAGRNFEGDEVRAQAEHWAREGIDKVS......DFVND.EGGQLYYFEVGR
BgLOL_714         .....DGWTCAGSDFDGDQVRGQARHWVDQQKTKFS......DFQTH.DGVQLCHFELGE
BgTRIT_T1-20_758  .....DGWTCAGRNVKGDDVRAQARHWVGLMNTKFS......EFEIK.DSVQLCYIEIGE
BgAVE_1525        .....DGWTCAGRNVKGDDVRAQARHWVGLMNTKFS......EFEIK.DSVQLCYIEIGE
BgLOL_5698        .....DGWTCAGRNVKGDDVRAQARHWVGLSDTRFS......EFEIK.GGVQLCYIEIGE
consensus>70      .....d...C.g....gd.vr.qa.hw......k.s......ef....d...l.yfe...

                                     70
BLGH_05021        DH...KFYTG........GKL...KYL......................
BgPOA_6159        TGQYSERYTGFACFVDTAMTKPDVRKH..HEETWWPCNRLTSS......
Bgtv316_6209      GNEISEIKTGYRGYFVAGGDLHEVRYKA.ENNVWMPCTWHY........
BLGH_05020        GNEISEIKTGYRGYFVAGGDLHEVRYKA.ENNVWMPCTWHY........
Bg_DAC_4215       DTTPTNRKTGYRGYCQEDGDLYQVRYET.TNGNWQLCIEFDSDLGDR..
BgAVE_4762        DTTPTNRKTGYRGYCQEDGDLYQVRYET.TNGNWQLCIEFDSDLGDR..
BLGH_01413        HSQITDSYTGFRGYCDEPGNLYEVRYYD...GNWKKCTYFDQDLGNH..
Bg_SECS1459_6790  HSQITDSYTGFRGYCDEPGNLYEVRYYD...GNWKKCTYFDQDLGNH..
Bgtv316_6210      GLILTEW...VRAYCTLTGDIYNLRYLDQDTNEWNECDRY.........
Bg_SECS1459_3169  GLILTEW...VRAYCTLTGDIYNLRYLDQDTNEWNECDRY.........
BgLOL_6315        ETQLTESCTGCRAYTNKSGKIYNLRFLDYDDGQWKLCTPY.........
BgPOA_4369        ETQLTESCTGCRAYTNKSGKIYNLRFLDYDDGQWKLCTPY.........
BgLOL_714         GNQLTQSITGFRAYCDEPGDVYNVRYWDVSSRTWVLCTHYDIDFESDYR
BgTRIT_T1-20_758  GAQTTK...GFRAYLDEPGAVYNVRYYDYNDCQWKLCTHYDGDAGVNYR
BgAVE_1525        GAQTTK...GFRAYLDEPGAVYNVRYYDYNDCQWKLCTHYDGDAGVNYR
BgLOL_5698        GAQTTKEFTGFRAYLDEPGAVYNVRYYDYNDRQWKLCTHYDRDAGANYR
consensus>70      ....te..tg.r.y....g..yn.ry.......w..c..y.........
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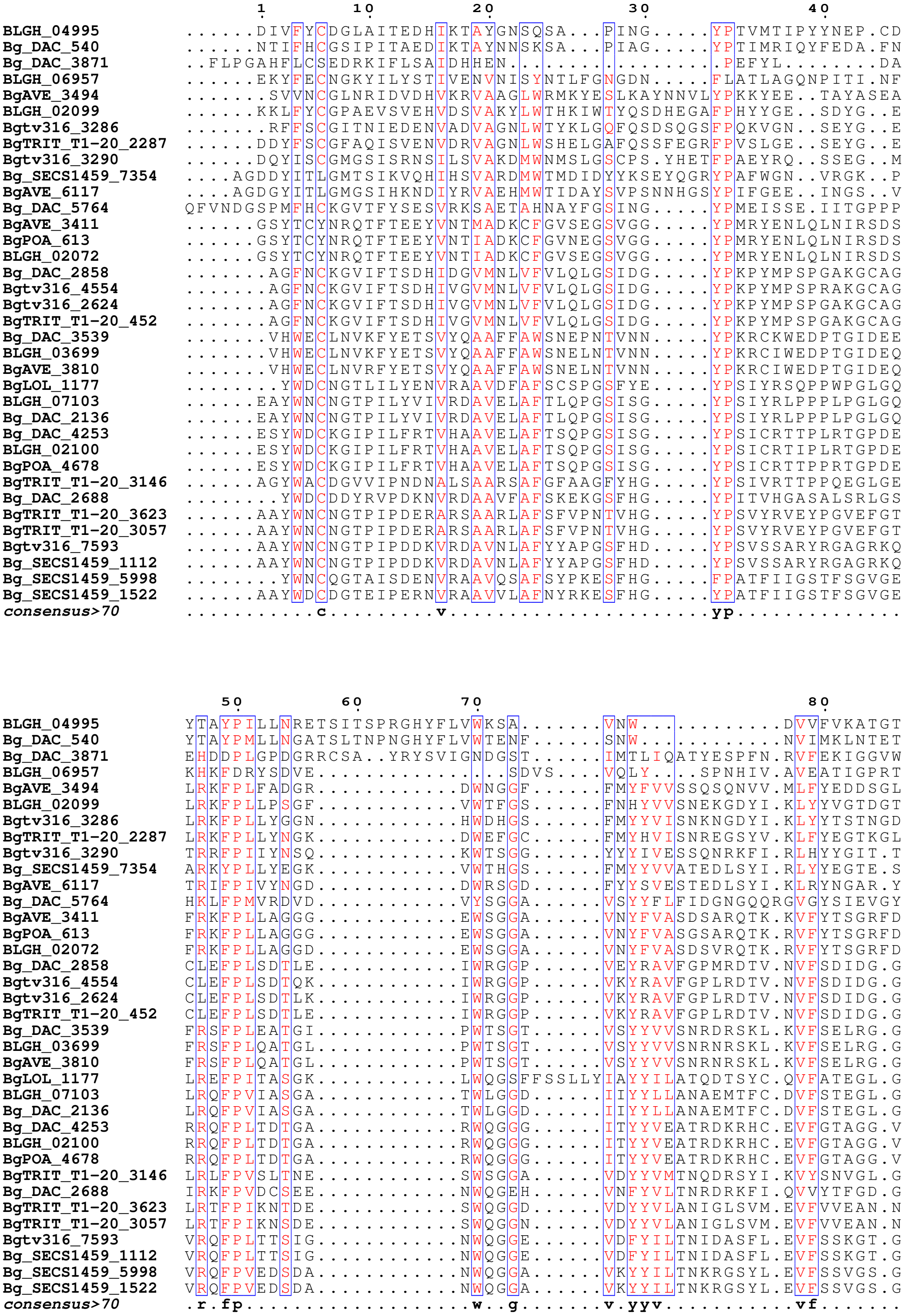
# Multiple sequence alignment (MSA) of AVR$_{PM2}$ subfamily members



```
                         1       10        20           30             40
                         .        .         .            .              .
BLGH_04995         ......DIVFYCDGLAITEDHIKTAYGNSQSA...PING.....YPTVMTIPYYNEP.CD
Bg_DAC_540         ......NTIFHCGSIPITAEDIKTAYNNSKSA...PIAG.....YPTIMRIQYFEDA.FN
Bg_DAC_3871        ..FLPGAHFLCSEDRKIFLSAIDHHEN...................PEFYL........DA
BLGH_06957         ......EKYFECNGKYILYSTIVENVNISYNTLFGNGDN.....FLATLAGQNPITI.NF
BgAVE_3494         .......SVVNCGLNRIDVDHVKRVAAGLWRMKYESLKAYNNVLYPKKYEE..TAYASEA
BLGH_02099         ......KKLFYCGPAEVSVEHVDSVAKYLWTHKIWTYQSDHEGAFPHYYGE..SDYG..E
Bgtv316_3286       .......RFFSCGITNIEDENVADVAGNLWTYKLGQFQSDSQGSFPQKVGN..SEYG..E
BgTRIT_T1-20_2287  ......DDYFSCGFAQISVENVDRVAGNLWSHELGAFQSSFEGRFPVSLGE..SEYG..E
Bgtv316_3290       ......DQYISCGMGSISRNSILSVAKDMWNMSLGSCPS.YHETFPAEYRQ..SSEG..M
Bg_SECS1459_7354   ....AGDDYITLGMTSIKVQHIHSVARDMWTMDIDYYKSEYQGRYPAFWGN..VRGK..P
BgAVE_6117         ....AGDGYITLGMGSIHKNDIYRVAEHMWTIDAYSVPSNNHGSYPIFGEE..INGS..V
Bg_DAC_5764        QFVNDGSPMFHCKGVTFYSESVRKSAETAHNAYFGSING.....YPMEISSE.IITGPPP
BgAVE_3411         ......GSYTCYNRQTFTEEYVNTMADKCFGVSEGSVGG.....YPMRYENLQLNIRSDS
BgPOA_613          ......GSYTCYNRQTFTEEYVNTIADKCFGVNEGSVGG.....YPMRYENLQLNIRSDS
BLGH_02072         ......GSYTCYNRQTFTEEYVNTIADKCFGVSEGSVGG.....YPMRYENLQLNIRSDS
Bg_DAC_2858        .......AGFNCKGVIFTSDHIDGVMNLVFVLQLGSIDG.....YPKPYMPSPGAKGCAG
Bgtv316_4554       .......AGFNCKGVIFTSDHIVGVMNLVFVLQLGSIDG.....YPKPYMPSPRAKGCAG
Bgtv316_2624       .......AGFNCKGVIFTSDHIVGVMNLVFVLQLGSIDG.....YPKPYMPSPGAKGCAG
BgTRIT_T1-20_452   .......AGFNCKGVIFTSDHIVGVMNLVFVLQLGSIDG.....YPKPYMPSPGAKGCAG
Bg_DAC_3539        .......VHWECLNVKFYETSVYQAAFFAWSNEPNTVNN.....YPKRCKWEDPTGIDEE
BLGH_03699         .......VHWECLNVKFYETSVYQAAFFAWSNELNTVNN.....YPKRCIWEDPTGIDEQ
BgAVE_3810         .......VHWECLNVRFYETSVYQAAFFAWSNELNTVNN.....YPKRCIWEDPTGIDEQ
BgLOL_1177         ........YWDCNGTLILYENVRAAVDFAFSCSPGSFYE.....YPSIYRSQPPWPGLGQ
BLGH_07103         ......EAYWNCNGTPILYVIVRDAVELAFTLQPGSISG.....YPSIYRLPPPLPGLGQ
Bg_DAC_2136        ......EAYWNCNGTPILYVIVRDAVELAFTLQPGSISG.....YPSIYRLPPPLPGLGQ
Bg_DAC_4253        ......ESYWDCKGIPILFRTVHAAVELAFTSQPGSISG.....YPSICRTTPLRTGPDE
BLGH_02100         ......ESYWDCKGIPILFRTVHAAVELAFTSQPGSISG.....YPSICRTIPLRTGPDE
BgPOA_4678         ......ESYWDCKGIPILFRTVHAAVELAFTSQPGSISG.....YPSICRTTPPRTGPDE
BgTRIT_T1-20_3146  ......AGYWACDGVVIPNDNALSAARSAFGFAAGFYHG.....YPSIVRTTPPQEGLGE
Bg_DAC_2688        ........YWDCDDYRVPDKNVRDAAVFAFSKEKGSFHG.....YPITVHGASALSRLGS
BgTRIT_T1-20_3623  ......AAYWNCNGTPIPDERARSAARLAFSFVPNTVHG.....YPSVYRVEYPGVEFGT
BgTRIT_T1-20_3057  ......AAYWNCNGTPIPDERARSAARLAFSFVPNTVHG.....YPSVYRVEYPGVEFGT
Bgtv316_7593       ......AAYWNCNGTPIPDDKVRDAVNLAFYYAPGSFHD.....YPSVSSARYRGAGRKQ
Bg_SECS1459_1112   ......AAYWNCNGTPIPDDKVRDAVNLAFYYAPGSFHD.....YPSVSSARYRGAGRKQ
Bg_SECS1459_5998   ........YWNCQGTAISDENVRAAVQSAFSYPKESFHG.....FPATFIIGSTFSGVGE
Bg_SECS1459_1522   ......AAYWDCDGTEIPERNVRAAVVLAFNYRKESFHG.....YPATFIIGSTFSGVGE
consensus>70       ...........c.........v......................yp..............

                      50        60        70                           80
                       .         .         .                            .
BLGH_04995         YTAYPILLNRETSITSPRGHYFLVWKSA.......VNW............DVVFVKATGT
Bg_DAC_540         YTAYPMLLNGATSLTNPNGHYFLVWTENF......SNW............NVIMKLNTET
Bg_DAC_3871        EHDDPLGPDGRRCSA..YRYSVIGNDGST......IMTLIQATYESPFN.RVFEKIGGVW
BLGH_06957         KHKFDRYSDVE................SDVS....VQLY....SPNHIV.AVEATIGPRT
BgAVE_3494         LRKFPLFADGR.............DWNGGF......FMYFVVSSQSQNVV.MLFYEDDSGL
BLGH_02099         LRKFPLLPSGF.............VWTFGS......FNHYVVSNEKGDYI.KLYYVGTDGT
Bgtv316_3286       LRKFPLLYGGN.............HWDHGS......FMYYVISNKNGDYI.KLYYTSTNGD
BgTRIT_T1-20_2287  LRKFPLLYNGK.............DWEFGC......FMYHVISNREGSYV.KLFYEGTKGL
Bgtv316_3290       TRRFPIIYNSQ.............KWTSGG......YYYIVESSQNRKFI.RLHYYGIT.T
Bg_SECS1459_7354   ARKYPLLYEGK.............VWTHGS......FMYYVVATEDLSYI.RLYYEGTE.S
BgAVE_6117         TRIFPIVYNGD.............DWRSGD......FYYSVESTEDLSYI.KLRYNGAR.Y
Bg_DAC_5764        HKLFPMVRDVD.............VYSGGA......VSYYFLFIDGNGQQRGVGYSIEVGY
BgAVE_3411         FRKFPLLAGGG.............EWSGGA......VNYFVASDSARQTK.KVFYTSGRFD
BgPOA_613          FRKFPLLAGGG.............EWSGGA......VNYFVASGSARQTK.RVFYTSGRFD
BLGH_02072         FRKFPLLAGGD.............EWSGGA......VNYFVASDSVRQTK.RVFYTSGRFD
Bg_DAC_2858        CLEFPLSDTLE.............IWRGGP......VEYRAVFGPMRDTV.NVFSDIDG.G
Bgtv316_4554       CLEFPLSDTQK.............IWRGGP......VKYRAVFGPLRDTV.NVFSDIDG.G
Bgtv316_2624       CLEFPLSDTLK.............IWRGGP......VKYRAVFGPLRDTV.NVFSDIDG.G
BgTRIT_T1-20_452   CLEFPLSDTLE.............IWRGGP......VKYRAVFGPLRDTV.NVFSDIDG.G
Bg_DAC_3539        FRSFPLEATGI.............PWTSGT......VSYYVVSNRDRSKL.KVFSELRG.G
BLGH_03699         FRSFPLQATGL.............PWTSGT......VSYYVVSNRNRSKL.KVFSELRG.G
BgAVE_3810         FRSFPLQATGL.............PWTSGT......VSYYVVSNRNRSKL.KVFSELRG.G
BgLOL_1177         LREFPITASGK.............LWQGSFFSSLLYIAYYILATQDTSYC.QVFATEGL.G
BLGH_07103         LRQFPVIASGA.............TWLGGD......IIYYLLANAEMTFC.DVFSTEGL.G
Bg_DAC_2136        LRQFPVIASGA.............TWLGGD......IIYYLLANAEMTFC.DVFSTEGL.G
Bg_DAC_4253        RRQFPLTDTGA.............RWQGGG......ITYYVEATRDKRHC.EVFGTAGG.V
BLGH_02100         RRQFPLTDTGA.............RWQGGG......ITYYVEATRDKRHC.EVFGTAGG.V
BgPOA_4678         RRQFPLTDTGA.............RWQGGG......ITYYVEATRDKRHC.EVFGTAGG.V
BgTRIT_T1-20_3146  LRLFPVSLTNE.............SWSGGA......VDYYVMTNQDRSYI.KVYSNVGL.G
Bg_DAC_2688        IRKFPVDCSEE.............NWQGEH......VNFYVLTNRDRKFI.QVVYTFGD.G
BgTRIT_T1-20_3623  LRTFPIKNTDE.............SWQGGD......VDYYVLANIGLSVM.EVFVVEAN.N
BgTRIT_T1-20_3057  LRTFPIKNSDE.............SWQGGN......VDYYVLANIGLSVM.EVFVVEAN.N
Bgtv316_7593       VRQFPLTTSIG.............NWQGGE......VDFYILTNIDASFL.EVFSSKGT.G
Bg_SECS1459_1112   VRQFPLTTSIG.............NWQGGE......VDFYILTNIDASFL.EVFSSKGT.G
Bg_SECS1459_5998   VRQFPVEDSDA.............NWQGGA......VKYYILTNKRGSYL.EVFSSVGS.G
Bg_SECS1459_1522   VRQFPVEDSDA.............NWQGGA......VKYYILTNKRGSYL.EVFSSVGS.G
consensus>70       .r.fp...................w..g.......v.yyv...........vf.......
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```
                     90         100
                      .         .
BLGH_04995         ESCWMAVPFLGRRLDSIVTM
Bg_DAC_540         KFCQMTSQYWGSSLQTILNL
Bg_DAC_3871        RQCPFYLRE...........
BLGH_06957         YPCYAVTIE...........
BgAVE_3494         HNCPLDQYYG..........
BLGH_02099         VECDIPRD............
Bgtv316_3286       VECDIYGP............
BgTRIT_T1-20_2287  EECVIVIPE...........
Bgtv316_3290       QECYVTGV............
Bg_SECS1459_7354   CDREVPSP............
BgAVE_6117         ETCMVSSPE...........
Bg_DAC_5764        QLCDAY..............
BgAVE_3411         DECAYTR.............
BgPOA_613          DECAYTR.............
BLGH_02072         DECAYTR.............
Bg_DAC_2858        QECVSA..............
Bgtv316_4554       QECVSA..............
Bgtv316_2624       QECVSA..............
BgTRIT_T1-20_452   QECVSA..............
Bg_DAC_3539        FLCNLIVTD...........
BLGH_03699         FLCNLKVTD...........
BgAVE_3810         FLCNLKVTD...........
BgLOL_1177         YECTHILG............
BLGH_07103         YRCDLVAS............
Bg_DAC_2136        YRCDLVAG............
Bg_DAC_4253        YKCTLVLRD...........
BLGH_02100         YKCTLVLLD...........
BgPOA_4678         YKCTLVLLD...........
BgTRIT_T1-20_3146  TMCGYYET............
Bg_DAC_2688        GNCAHVQD............
BgTRIT_T1-20_3623  KRCTKVAG............
BgTRIT_T1-20_3057  KRCTKVAG............
Bgtv316_7593       HKCTYFEG............
Bg_SECS1459_1112   HKCAYFEG............
Bg_SECS1459_5998   NECTFVEG............
Bg_SECS1459_1522   NKCTFVEG............
consensus>70       ..c.................
```