HA Gene

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          ************************************************************************************************************************************************************************************************************************
humanA    MNTQILAFIACMLIGTKGDKICLGHHAVANGTKVNTLTERGIEVVNATETVETVNIKKICTQGKRPTDLGQCGLLGTLIGPPQCDQFLEFDANLIIERREGTDVCYPGKFTNEESLRQILRGSGGIDKESMGFTYSGIRTNGATSACRRS
humanB    MNTQILAFIACMLIGTKGDKICLGHHAVANGTKVNTLTERGIEVVNATETVETVNIKKICTQGKRPTDLGQCGLLGTLIGPPQCDQFLEFDANLIIERREGTDVCYPGKFTNEESLRQILRGSGGIDKESMGFTYSGIRTNGATSACRRS
chickenA  MNTQILAFIACMLIGTKGDKICLGHHAVANGTKVNTLTERGIEVVNATETVETVNIKKICTQGKRPTDLGQCGLLGTLIGPPQCDQFLEFDANLIIERREGTDVCYPGKFTNEESLRQILRGSGGIDKESMGFTYSGIRTNGATSACRRS
chickenB  MNTQILAFIACMLIGTKGDKICLGHHAVANGTKVNTLTERGIEVVNATETVETVNIKKICTQGKRPTDLGQCGLLGTLIGPPQCDQFLEFDANLIIERREGTDVCYPGKFTNEESLRQILRGSGGIDKESMGFTYSGIRTNGATSACRRS
chickenE  MNTQILAFIACMLIGTKGDKICLGHHAVANGTKVNTLTERGIEVVNATETVETVNIKKICTQGKRPTDLGQCGLLGTLIGPPQCDQFLEFDANLIIERREGTDVCYPGKFTNEESLRQILRGSGGIDKESMGFTYSGIRTNGATSACRRS
ruler     1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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          ***********************************************************************************************.*****************************************.**************
humanA    GSSFYAEMKWLLSNSDNAAFPQMTKSYRNPRNKPALIIWGVHHSGSATEQTKLYGSGNKLITVGSSKYQQSFTPSPGARPQVNGQSGRIDFHWLLLDPNDTVTFTFNGAFIAPDRASFFRGESLGVQSDVPLDSGCEGDCFHSGGTIVSS
humanB    GSSFYAEMKWLLSNSDNAAFPQMTKSYRNPRNKPALIIWGVHHSGSATEQTKLYGSGNKLITVGSSKYQQSFTPSPGARPQVNGQSGRIDFHWLLLDPNDTVTFTFNGAFIAPDRASFFRGESLGVQSDVPLDSGCEGDCFHSGGTIVSS
chickenA  GSSFYAEMKWLLSNSDNAAFPQMTKSYRNPRNKPALIIWGVHHSGSATEQTKLYGSGNKLITVGSSKYQQSFTPSPGARPQVNGQSGRIDFHWLLLDPNDTVTFTFNGAFIAPDRASFFRGESLGVQSDVPLDSGCEGDCFHSGGTIVSS
chickenB  GSSFYAEMKWLLSNSDNAAFPQMTKSYRNPRNKPALIIWGVHHSGSATEQTKLYGSGNKLITVGSSKYQQSFTPSPGARPQVNGQSGRIDFHWLLLDPNDTVTFTFNGAFIAPDRASFFRGESLGVQSDVPLDSGSEGDCFHSGGTIVSS
chickenE  GSSFYAEMKWLLSNSDNAAFPQMTKSYRNPRNKPALIIWGVHHSGSATEQTKLYGSGNKLITVGSSKYQQSFTPSPGARPQVNGQSGRIDFQWLLLDPNDTVTFTFNGAFIAPDRASFFRGESLGVQSDVPLDSGCEGDCFHSGGTIVSS
ruler     .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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          ************************************      ***********************************************************************************************************************
humanA    LPFQNINPRTVGKCPRYVKQTSLLLATGMRNVPENPKQAYQKQMTRGLFGAIAGFIENGWEGLIDGWYGFRHQNAQGEGTAADYKSTQSAIDQITGKLNRLIDKTNQQFELIDNEFSEIEQQIGNVINWTRDSMTEVWSYNAELLVAMEN
humanB    LPFQNINPRTVGKCPRYVKQTSLLLATGMRNVPENPKQAYQKRMTRGLFGAIAGFIENGWEGLIDGWYGFRHQNAQGEGTAADYKSTQSAIDQITGKLNRLIDKTNQQFELIDNEFSEIEQQIGNVINWTRDSMTEVWSYNAELLVAMEN
chickenA  LPFQNINPRTVGKCPRYVKQTSLLLATGMRNVPENPK-------TRGLFGAIAGFIENGWEGLIDGWYGFRHQNAQGEGTAADYKSTQSAIDQITGKLNRLIDKTNQQFELIDNEFSEIEQQIGNVINWTRDSMTEVWSYNAELLVAMEN
chickenB  LPFQNINPRTVGKCPRYVKQTSLLLATGMRNVPENPKQAYRKRMTRGLFGAIAGFIENGWEGLIDGWYGFRHQNAQGEGTAADYKSTQSAIDQITGKLNRLIDKTNQQFELIDNEFSEIEQQIGNVINWTRDSMTEVWSYNAELLVAMEN
chickenE  LPFQNINPRTVGKCPRYVKQTSLLLATGMRNVPENPKQAYQKRMTRGLFGAIAGFIENGWEGLIDGWYGFRHQNAQGEGTAADYKSTQSAIDQITGKLNRLIDKTNQQFELIDNEFSEIEQQIGNVINWTRDSMTEVWSYNAELLVAMEN
ruler     .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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          ***************************************************************************************************************************************************
humanA    QHTIDLADSEMNKLYERVRKQLRENAEEDGTGCFEIFHKCDDQCMESIRNNTYDHTQYRTESLQNRIQIDPVKLSSGYKDIILWFSFGASCFLLLAIAMGLVFICIKNGNMRCTICI
humanB    QHTIDLADSEMNKLYERVRKQLRENAEEDGTGCFEIFHKCDDQCMESIRNNTYDHTQYRTESLQNRIQIDPVKLSSGYKDIILWFSFGASCFLLLAIAMGLVFICIKNGNMRCTICI
chickenA  QHTIDLADSEMNKLYERVRKQLRENAEEDGTGCFEIFHKCDDQCMESIRNNTYDHTQYRTESLQNRIQIDPVKLSSGYKDIILWFSFGASCFLLLAIAMGLVFICIKNGNMRCTICI
chickenB  QHTIDLADSEMNKLYERVRKQLRENAEEDGTGCFEIFHKCDDQCMESIRNNTYDHTQYRTESLQNRIQIDPVKLSSGYKDIILWFSFGASCFLLLAIAMGLVFICIKNGNMRCTICI
chickenE  QHTIDLADSEMNKLYERVRKQLRENAEEDGTGCFEIFHKCDDQCMESIRNNTYDHTQYRTESLQNRIQIDPVKLSSGYKDIILWFSFGASCFLLLAIAMGLVFICIKNGNMRCTICI
ruler     .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......
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M Gene (M1)

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          ************************************************************************************************************************************************************
humanA    MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALMEWLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRKLKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCAT
humanB    MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALMEWLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRKLKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCAT
chickenA  MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALMEWLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRKLKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCAT
chickenB  MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALMEWLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRKLKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCAT
chickenD  MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALMEWLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRKLKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCAT
chickenE  MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALMEWLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRKLKREITFHGAKEVALSYSTGALASCMGLIYNRMGTVTTEVAFGLVCAT
ruler     1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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          ***********************************************************************************************
humanA    CEQIADSQHRSHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRTIGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK
humanB    CEQIADSQHRSHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRTIGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK
chickenA  CEQIADSQHRSHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRTIGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK
chickenB  CEQIADSQHRSHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRTIGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK
chickenD  CEQIADSQHRSHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRTIGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK
chickenE  CEQIADSQHRSHRQMVTTTNPLIRHENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRTIGTHPSSSAGLKDDLLENLQAYQKRMGVQMQRFK
ruler     .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250..
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M Gene (M2)

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         ******************************************************************************************
  humanA MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILDRLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDSHFVNIELE
  humanB MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILDRLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDSHFVNIELE
chickenA MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILDRLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDSHFVNIELE
chickenB MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILDRLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDSHFVNIELE
chickenD MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILDRLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDSHFVNIELE
chickenE MSLLTEVETPTRNGWECKCSDSSDPLVIAASIIGILHLILWILDRLFFKCIYRRLKYGLKRGPSTEGVPESMREEYRQEQQSAVDVDDSHFVNIELE
    ruler 1.......10........20........30........40........50........60........70........80........90.......
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NA Gene

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         **********:*************************************************************************************************************************
  humanA MNPNQKIITIGVVNTTLSTIALHIGVGNLVFNTVIHEKIGDHQIVTHPTIMTPEVPNCSDTIITYNNTVINNITTTIITEAERPFKSPLPLCPFRGFFPFHKDNAIRLGENKDVIVTREPYVSCDNDNCWSFALAQGALLGTKHSNGTIK
  humanB MNPNQKIITIGVVNTTLSTIALLIGVGNLVFNTVIHEKIGDHQIVTHPTIMTPEVPNCSDTIITYNNTVINNITTTIITEAERPFKSPLPLCPFRGFFPFHKDNAIRLGENKDVIVTREPYVSCDNDNCWSFALAQGALLGTKHSNGTIK
chickenA MNPNQKIITIGVVNTTLSTIALLIGVGNLVFNTVIHEKIGDHQIVTHPTIMTPEVPNCSDTIITYNNTVINNITTTIITEAERPFKSPLPLCPFRGFFPFHKDNAIRLGENKDVIVTREPYVSCDNDNCWSFALAQGALLGTKHSNGTIK
chickenB MNPNQKIITIGVVNTTLSTIALLIGVGNLVFNTVIHEKIGDHQIVTHPTIMTPEVPNCSDTIITYNNTVINNITTTIITEAERPFKSPLPLCPFRGFFPFHKDNAIRLGENKDVIVTREPYVSCDNDNCWSFALAQGALLGTKHSNGTIK
chickenE MNPNQKIITIGVVNTTLSTIALLIGVGNLVFNTVIHEKIGDHQIVTHPTIMTPEVPNCSDTIITYNNTVINNITTTIITEAERPFKSPLPLCPFRGFFPFHKDNAIRLGENKDVIVTREPYVSCDNDNCWSFALAQGALLGTKHSNGTIK
    ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

         **********************************************************************************************************************************
  humanA DRTPYRSLIRFPIGTAPVLGNYKEICIAWSSSSCFDGKEWMHVCMTGNDNDASAQIIYGGRMTDSIKSWRKDILRTQESECQCIDGTCVVAVTDGPAANSADHRVYWIREGRIIKYENVPKTKIQHLEECSCYVDIDVYCICRDNWKGSN
  humanB DRTPYRSLIRFPIGTAPVLGNYKEICIAWSSSSCFDGKEWMHVCMTGNDNDASAQIIYGGRMTDSIKSWRKDILRTQESECQCIDGTCVVAVTDGPAANSADHRVYWIREGRIIKYENVPKTKIQHLEECSCYVDIDVYCICRDNWKGSN
chickenA DRTPYRSLIRFPIGTAPVLGNYKEICIAWSSSSCFDGKEWMHVCMTGNDNDASAQIIYGGRMTDSIKSWRKDILRTQESECQCIDGTCVVAVTDGPAANSADHRVYWIREGRIIKYENVPKTKIQHLEECSCYVDIDVYCICRDNWKGSN
chickenB DRTPYRSLIRFPIGTAPVLGNYKEICIAWSSSSCFDGKEWMHVCMTGNDNDASAQIIYGGRMTDSIKSWRKDILRTQESECQCIDGTCVVAVTDGPAANSADHRVYWIREGRIIKYENVPKTKIQHLEECSCYVDIDVYCICRDNWKGSN
chickenE DRTPYRSLIRFPIGTAPVLGNYKEICIAWSSSSCFDGKEWMHVCMTGNDNDASAQIIYGGRMTDSIKSWRKDILRTQESECQCIDGTCVVAVTDGPAANSADHRVYWIREGRIIKYENVPKTKIQHLEECSCYVDIDVYCICRDNWKGSN
    ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

         **********************************************************************************************************************************
  humanA RPWMRINNETILETGYVCSKFHSDTPRPADPSIMSCDSPSNVNGGPGVKGFGFKAGNDVWLGRTVSTSGRSGFEIIKVTEGWINSPNHVKSITQTLVSNNDWSGYSGSFIVKAKDCFQPCFYVELIRGRPNKNDDVSWTSNSIVTFCGLD
  humanB RPWMRINNETILETGYVCSKFHSDTPRPADPSIMSCDSPSNVNGGPGVKGFGFKAGNDVWLGRTVSTSGRSGFEIIKVTEGWINSPNHVKSITQTLVSNNDWSGYSGSFIVKAKDCFQPCFYVELIRGRPNKNDDVSWTSNSIVTFCGLD
chickenA RPWMRINNETILETGYVCSKFHSDTPRPADPSIMSCDSPSNVNGGPGVKGFGFKAGNDVWLGRTVSTSGRSGFEIIKVTEGWINSPNHVKSITQTLVSNNDWSGYSGSFIVKAKDCFQPCFYVELIRGRPNKNDDVSWTSNSIVTFCGLD
chickenB RPWMRINNETILETGYVCSKFHSDTPRPADPSIMSCDSPSNVNGGPGVKGFGFKAGNDVWLGRTVSTSGRSGFEIIKVTEGWINSPNHVKSITQTLVSNNDWSGYSGSFIVKAKDCFQPCFYVELIRGRPNKNDDVSWTSNSIVTFCGLD
chickenE RPWMRINNETILETGYVCSKFHSDTPRPADPSIMSCDSPSNVNGGPGVKGFGFKAGNDVWLGRTVSTSGRSGFEIIKVTEGWINSPNHVKSITQTLVSNNDWSGYSGSFIVKAKDCFQPCFYVELIRGRPNKNDDVSWTSNSIVTFCGLD
    ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

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  humanA NEPGSGNWPDGSNIGFMPK
  humanB NEPGSGNWPDGSNIGFMPK
chickenA NEPGSGNWPDGSNIGFMPK
chickenB NEPGSGNWPDGSNIGFMPK
chickenE NEPGSGNWPDGSNIGFMPK
    ruler .......460.........
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NP Gene

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          ************************************************************************************************:*************************************************
  humanA  MASQGTKRSYEQMETGGERQNATEIRASVGRMVGGIGRFYIQMCTELKLSDYEGRLIQNSITIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYKRRDGKWMRELILYDKEEIRRIWRQANNGEDATAGLTHLMIWHSNLNDATYQR
  humanB  MASQGTKRSYEQMETGGERQNATEIRASVGRMVGGIGRFYIQMCTELKLSDYEGRLIQNSITIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYKRRDGKWMRELILYDKEEIRRIWRQANNGEDATAGLTHLMIWHSNLNDATYQR
chickenA  MASQGTKRSYEQMETGGERQNATEIRASVGRMVGGIGRFYIQMCTELKLSDYEGRLIQNSITIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYRRRDGKWMRELILYDKEEIRRIWRQANNGEDATAGLTHLMIWHSNLNDATYQR
chickenB  MASQGTKRSYEQMETGGERQNATEIRASVGRMVGGIGRFYIQMCTELKLSDYEGRLIQNSITIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYKRRDGKWMRELILYDKEEIRRIWRQANNGEDATAGLTHLMIWHSNLNDATYQR
chickenD  MASQGTKRSYEQMETGGERQNATEIRASVGRMVGGIGRFYIQMCTELKLSDYEGRLIQNSITIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYKRRDGKWMRELILYDKEEIRRIWRQANNGEDATAGLTHLMIWHSNLNDATYQR
chickenE  MASQGTKRSYEQMETGGERQNATEIRASVGRMVGGIGRFYIQMCTELKLSDYEGRLIQNSITIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYKRRDGKWMRELILYDKEEIRRIWRQANNGEDATAGLTHLMIWHSNLNDATYQR
     ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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          ****************************************************************************************************************************************************************
  humanA  TRALVRTGMDPRMCSLMQGSTLPRRSGAAGAAVKGVGTMVMELIRMIKRGINDRNFWRGENGRRTRIAYERMCNILKGKFQTAAQRAMMDQVRESRNPGNAEIEDLIFLARSALILRGSVAHKSCLPACVYGLAVASGYDFEREGYSLVG
  humanB  TRALVRTGMDPRMCSLMQGSTLPRRSGAAGAAVKGVGTMVMELIRMIKRGINDRNFWRGENGRRTRIAYERMCNILKGKFQTAAQRAMMDQVRESRNPGNAEIEDLIFLARSALILRGSVAHKSCLPACVYGLAVASGYDFEREGYSLVG
chickenA  TRALVRTGMDPRMCSLMQGSTLPRRSGAAGAAVKGVGTMVMELIRMIKRGINDRNFWRGENGRRTRIAYERMCNILKGKFQTAAQRAMMDQVRESRNPGNAEIEDLIFLARSALILRGSVAHKSCLPACVYGLAVASGYDFEREGYSLVG
chickenB  TRALVRTGMDPRMCSLMQGSTLPRRSGAAGAAVKGVGTMVMELIRMIKRGINDRNFWRGENGRRTRIAYERMCNILKGKFQTAAQRAMMDQVRESRNPGNAEIEDLIFLARSALILRGSVAHKSCLPACVYGLAVASGYDFEREGYSLVG
chickenD  TRALVRTGMDPRMCSLMQGSTLPRRSGAAGAAVKGVGTMVMELIRMIKRGINDRNFWRGENGRRTRIAYERMCNILKGKFQTAAQRAMMDQVRESRNPGNAEIEDLIFLARSALILRGSVAHKSCLPACVYGLAVASGYDFEREGYSLVG
chickenE  TRALVRTGMDPRMCSLMQGSTLPRRSGAAGAAVKGVGTMVMELIRMIKRGINDRNFWRGENGRRTRIAYERMCNILKGKFQTAAQRAMMDQVRESRNPGNAEIEDLIFLARSALILRGSVAHKSCLPACVYGLAVASGYDFEREGYSLVG
     ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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          ****************************************************************************************************************************************************************
  humanA  IDPFRLLQNSQVFSLIRPNENPAHKSQLVWMACHSAAFEDLRVSSFIRGTRVVPRGQLSTRGVQIASNENMETMDSSTLELRSRYWAIRTRSGGNTNQQRASAGQISVQPTFSVQRNLPFERATIMAAFTGNTEGRTSDMRTEIIRMMEN
  humanB  IDPFRLLQNSQVFSLIRPNENPAHKSQLVWMACHSAAFEDLRVSSFIRGTRVVPRGQLSTRGVQIASNENMETMDSSTLELRSRYWAIRTRSGGNTNQQRASAGQISVQPTFSVQRNLPFERATIMAAFTGNTEGRTSDMRTEIIRMMEN
chickenA  IDPFRLLQNSQVFSLIRPNENPAHKSQLVWMACHSAAFEDLRVSSFIRGTRVVPRGQLSTRGVQIASNENMETMDSSTLELRSRYWAIRTRSGGNTNQQRASAGQISVQPTFSVQRNLPFERATIMAAFTGNTEGRTSDMRTEIIRMMEN
chickenB  IDPFRLLQNSQVFSLIRPNENPAHKSQLVWMACHSAAFEDLRVSSFIRGTRVVPRGQLSTRGVQIASNENMETMDSSTLELRSRYWAIRTRSGGNTNQQRASAGQISVQPTFSVQRNLPFERATIMAAFTGNTEGRTSDMRTEIIRMMEN
chickenD  IDPFRLLQNSQVFSLIRPNENPAHKSQLVWMACHSAAFEDLRVSSFIRGTRVVPRGQLSTRGVQIASNENMETMDSSTLELRSRYWAIRTRSGGNTNQQRASAGQISVQPTFSVQRNLPFERATIMAAFTGNTEGRTSDMRTEIIRMMEN
chickenE  IDPFRLLQNSQVFSLIRPNENPAHKSQLVWMACHSAAFEDLRVSSFIRGTRVVPRGQLSTRGVQIASNENMETMDSSTLELRSRYWAIRTRSGGNTNQQRASAGQISVQPTFSVQRNLPFERATIMAAFTGNTEGRTSDMRTEIIRMMEN
     ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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          ************************************************
  humanA  ARPEDVSFQGRGVFELSDEKATNPIVPSFDMSNEGSYFFGDNAEEYDN
  humanB  ARPEDVSFQGRGVFELSDEKATNPIVPSFDMSNEGSYFFGDNAEEYDN
chickenA  ARPEDVSFQGRGVFELSDEKATNPIVPSFDMSNEGSYFFGDNAEEYDN
chickenB  ARPEDVSFQGRGVFELSDEKATNPIVPSFDMSNEGSYFFGDNAEEYDN
chickenD  ARPEDVSFQGRGVFELSDEKATNPIVPSFDMSNEGSYFFGDNAEEYDN
chickenE  ARPEDVSFQGRGVFELSDEKATNPIVPSFDMSNEGSYFFGDNAEEYDN
     ruler .......460.......470.......480.......490........
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NS Gene (NS1)

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          ************************************************************************************************************************************************************
  humanA  MDSNTVSSFQVDCFLWHVRKRFADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILEEESDEALKMTIASVPASRYLTDMTLEEMSRDWFMLMPKQKVAGSLCIRMDQAIMNKNIILKANFSVIFDRLETLILLRAF
  humanB  MDSNTVSSFQVDCFLWHVRKRFADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILEEESDEALKMTIASVPASRYLTDMTLEEMSRDWFMLMPKQKVAGSLCIRMDQAIMNKNIILKANFSVIFDRLETLILLRAF
chickenA  MDSNTVSSFQVDCFLWHVRKRFADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILEEESDEALKMTIASVPASRYLTDMTLEEMSRDWFMLMPKQKVAGSLCIRMDQAIMNKNIILKANFSVIFDRLETLILLRAF
chickenB  MDSNTVSSFQVDCFLWHVRKRFADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILEEESDEALKMTIASVPASRYLTDMTLEEMSRDWFMLMPKQKVAGSLCIRMDQAIMNKNIILKANFSVIFDRLETLILLRAF
chickenD  MDSNTVSSFQVDCFLWHVRKRFADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILEEESDEALKMTIASVPASRYLTDMTLEEMSRDWFMLMPKQKVAGSLCIRMDQAIMNKNIILKANFSVIFDRLETLILLRAF
chickenE  MDSNTVSSFQVDCFLWHVRKRFADQELGDAPFLDRLRRDQKSLRGRGSTLGLDIETATRAGKQIVERILEEESDEALKMTIASVPASRYLTDMTLEEMSRDWFMLMPKQKVAGSLCIRMDQAIMNKNIILKANFSVIFDRLETLILLRAF
     ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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          ******:*************************************************************************
  humanA  TEEGAIIGEISPLPSLPGHTDEDVKNAIGVLIGGLEWNDNTVRVSETLQRFAWRSSNEDGRPPLPPKQKRKMARTIESEV
  humanB  TEEGAIIGEISPLPSLPGHTDEDVKNAIGVLIGGLEWNDNTVRVSETLQRFAWRSSNEDGRPPLPPKQKRKMARTIESEV
chickenA  TEEGAIVGEISPLPSLPGHTDEDVKNAIGVLIGGLEWNDNTVRVSETLQRFAWRSSNEDGRPPLPPKQKRKMARTIESEV
chickenB  TEEGAIIGEISPLPSLPGHTDEDVKNAIGVLIGGLEWNDNTVRVSETLQRFAWRSSNEDGRPPLPPKQKRKMARTIESEV
chickenD  TEEGAIIGEISPLPSLPGHTDEDVKNAIGVLIGGLEWNDNTVRVSETLQRFAWRSSNEDGRPPLPPKQKRKMARTIESEV
chickenE  TEEGAIIGEISPLPSLPGHTDEDVKNAIGVLIGGLEWNDNTVRVSETLQRFAWRSSNEDGRPPLPPKQKRKMARTIESEV
     ruler .......160.......170.......180.......190.......200.......210.......220.......230
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NS Gene (NS2)

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         ************************************************************************************************************
  humanA MDSNTVSSFQDILMRMSKMQLGSSSEDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQNRNGKWREQLSQKFEEIRWLIEEVRHRLKVTENSFEQITFMQALQLLLEVEQEIRTFSFQLI
  humanB MDSNTVSSFQDILMRMSKMQLGSSSEDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQNRNGKWREQLSQKFEEIRWLIEEVRHRLKVTENSFEQITFMQALQLLLEVEQEIRTFSFQLI
chickenA MDSNTVSSFQDILMRMSKMQLGSSSEDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQNRNGKWREQLSQKFEEIRWLIEEVRHRLKVTENSFEQITFMQALQLLLEVEQEIRTFSFQLI
chickenB MDSNTVSSFQDILMRMSKMQLGSSSEDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQNRNGKWREQLSQKFEEIRWLIEEVRHRLKVTENSFEQITFMQALQLLLEVEQEIRTFSFQLI
chickenD MDSNTVSSFQDILMRMSKMQLGSSSEDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQNRNGKWREQLSQKFEEIRWLIEEVRHRLKVTENSFEQITFMQALQLLLEVEQEIRTFSFQLI
chickenE MDSNTVSSFQDILMRMSKMQLGSSSEDLNGMITQFESLKLYRDSLGEAVMRMGDLHSLQNRNGKWREQLSQKFEEIRWLIEEVRHRLKVTENSFEQITFMQALQLLLEVEQEIRTFSFQLI
    ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.
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PA Gene

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  humanA MEDFVRQCFNPMIVELAEKAMKEYGEDPKIETNKFAAICTHLEVCFMYSDFHFIDERGESIIVESGDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTGVEKPKFLPDLYDYKENRFIEIGVTRREVHIYYLEKANKIKSEKTHIHIFSF
  humanB MEDFVRQCFNPMIVELAEKAMKEYGEDPKIETNKFAAICTHLEVCFMYSDFHFIDERGESIIVESGDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTGVEKPKFLPDLYDYKENRFIEIGVTRREVHIYYLEKANKIKSEKTHIHIFSF
chickenA MEDFVRQCFNPMIVELAEKAMKEYGEDPKIETNKFAAICTHLEVCFMYSDFHFIDERGESIIVESGDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTGVEKPKFLPDLYDYKENRFIEIGVTRREVHIYYLEKANKIKSEKTHIHIFSF
chickenB MEDFVRQCFNPMIVELAEKAMKEYGEDPKIETNKFAAICTHLEVCFMYSDFHFIDERGESIIVESGDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTGVEKPKFLPDLYDYKENRFIEIGVTRREVHIYYLEKANKIKSEKTHIHIFSF
chickenD MEDFVRQCFNPMIVELAEKAMKEYGEDPKIETNKFAAICTHLEVCFMYSDFHFIDERGESIIVESGDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTGVEKPKFLPDLYDYKENRFIEIGVTRREVHIYYLEKANKIKSEKTHIHIFSF
    ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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  humanA TGEEMATKADYTLDEESRARIKTRLFTIRQEMASRGLWDSFRQSERGEETIEERFEITGTMRRLADQSLPPNFSSLENFRAYVDGFEPNGCIEGKLSQMSKEVNARIEPFLKTTPRPLKLPDGSPCSQRSKFLLMDALKLSIEDPSHEGE
  humanB TGEEMATKADYTLDEESRARIKTRLFTIRQEMASRGLWDSFRQSERGEETIEERFEITGTMRRLADQSLPPNFSSLENFRAYVDGFEPNGCIEGKLSQMSKEVNARIEPFLKTTPRPLKLPDGSPCSQRSKFLLMDALKLSIEDPSHEGE
chickenA TGEEMATKADYTLDEESRARIKTRLFTIRQEMASRGLWDSFRQSERGEETIEERFEITGTMRRLADQSLPPNFSSLENFRAYVDGFEPNGCIEGKLSQMSKEVNARIEPFLKTTPRPLKLPDGSPCSQRSKFLLMDALKLSIEDPSHEGE
chickenB TGEEMATKADYTLDEESRARIKTRLFTIRQEMASRGLWDSFRQSERGEETIEERFEITGTMRRLADQSLPPNFSSLENFRAYVDGFEPNGCIEGKLSQMSKEVNARIEPFLKTTPRPLKLPDGSPCSQRSKFLLMDALKLSIEDPSHEGE
chickenD TGEEMATKADYTLDEESRARIKTRLFTIRQEMASRGLWDSFRQSERGEETIEERFEITGTMRRLADQSLPPNFSSLENFRAYVDGFEPNGCIEGKLSQMSKEVNARIEPFLKTTPRPLKLPDGSPCSQRSKFLLMDALKLSIEDPSHEGE
    ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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  humanA GIPLYDAIKCMKTFFGWKEPNIIKPHEKGINPNYLLAWKQVLAELQDLENEEKIPKTKNMKKTSQLKWALGENMAPEKVDFEDCKDVGDLKQYDSDEPEPRSLASWIQSEFNKACELTDSSWIELDEIGEDVAPIEHIASMRRNYFTAEV
  humanB GIPLYDAIKCMKTFFGWKEPNIIKPHEKGINPNYLLAWKQVLAELQDLENEEKIPKTKNMKKTSQLKWALGENMAPEKVDFEDCKDVGDLKQYDSDEPEPRSLASWIQSEFNKACELTDSSWIELDEIGEDVAPIEHIASMRRNYFTAEV
chickenA GIPLYDAIKCMKTFFGWKEPNIIKPHEKGINPNYLLAWKQVLAELQDLENEEKIPKTKNMKKTSQLKWALGENMAPEKVDFEDCKDVGDLKQYDSDEPEPRSLASWIQSEFNKACELTDSSWIELDEIGEDVAPIEHIASMRRNYFTAEV
chickenB GIPLYDAIKCMKTFFGWKEPNIIKPHEKGINPNYLLAWKQMLAELQDLENEEKTPKTKNMKKTSQLKWALGENMAPEKVDFEDCKDVGDLKQYDSDEPEPRSSASWIQSEFNKACELTDSSWIELDEIGEDVAPIEHIASMRRNYFTAEV
chickenD GIPLYDAIKCMKTFFGWKEPNIIKPHEKGINPNYLLAWKQVLAELQDLENEEKIPKTKNMKKTSQLKWALGENMAPEKVDFEDCKDVGDLKQYDSDEPEPRSLASWIQSEFNKACELTDSSWIELDEIGEDVAPIEHIASMRRNYFTAEV
    ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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  humanA SHCRATEYIMKGVYINTALLNASCAAMDDFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWEKYCVLEVGDMLLRTAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAES
  humanB SHCRATEYIMKGVYINTALLNASCAAMDDFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWEKYCVLEVGDMLLRTAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAES
chickenA SHCRATEYIMKGVYINTALLNASCAAMDDFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWEKYCVLEVGDMLLRTAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAES
chickenB SHCRATEYIMKGVYINTALLNASCAAMDDFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWEKYCVLEVGDMLLRTAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAES
chickenD SHCRATEYIMKGVYINTALLNASCAAMDDFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWEKYCVLEVGDMLLRTAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAES
    ruler .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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  humanA SVKEKDMTKEFFENKSETWPIGESPRGVEEGSIGKVCRTLLAKSVFNSLYASPQLEGFSAESRKLLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHALR
  humanB SVKEKDMTKEFFENKSETWPIGESPRGVEEGSIGKVCRTLLAKSVFNSLYASPQLEGFSAESRKLLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHALR
chickenA SVKEKDMTKEFFENKSETWPIGESPRGVEEGSIGKVCRTLLAKSVFNSLYASPQLEGFSAESRKLLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHALR
chickenB SVKEKDMTKEFFENKSETWPIGESPRGVEEGSIGKVCRTLLAKSVFNSLYASPQLEGFSAESRKLLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHALR
chickenD SVKEKDMTKEFFENKSETWPIGESPRGVEEGSIGKVCRTLLAKSVFNSLYASPQLEGFSAESRKLLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHALR
    ruler .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710......
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PB1 Gene

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  humanA MDVNPTLLFLKVPAQNAISTTFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEKGKWTTNTETGAPQLNPIDGPLPEDNEPSGYAQTDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVDKLTQGRQTYDWTLNRNQPAATALANTIEVF
  humanB MDVNPTLLFLKVPAQNAISTTFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEKGKWTTNTETGAPQLNPIDGPLPEDNEPSGYAQTDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVDKLTQGRQTYDWTLNRNQPAATALANTIEVF
chickenA MDVNPTLLFLKVPAQNAISTTFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEKGKWTTNTETGAPQLNPIDGPLPEDNEPSGYAQTDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVDKLTQGRQTYDWTLNRNQPAATALANTIEVF
chickenB MDVNPTLLFLKVPAQNAISTTFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEKGKWTTNTETGAPQLNPIDGPLPEDNEPSGYAQTDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVDKLTQGRQTYDWTLNRNQPAATALANTIEVF
   ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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  humanA RLNGLTANESGRLIDFLKDVMESMDKEEMEITTHFQRKRRVRDNMTKKMVTQRTIGKKKQMLNKRSYLIRALTLNTMTKDAERGKLKRRAIATPGMQIRGFVYFVETLARSICEKLEQSGLPVGGNEKKAKLANVVRKMMTNSQDTELSF
  humanB RLNGLTANESGRLIDFLKDVMESMDKEEMEITTHFQRKRRVRDNMTKKMVTQRTIGKKKQRLNKRSYLIRALTLNTMTKDAERGKLKRRAIATPGMQIRGFVYFVETLARSICEKLEQSGLPVGGNEKKAKLANVVRKMMTNSQDTELSF
chickenA RLNGLTANESGRLIDFLKDVMESMDKEEMEITTHFQRKRRVRDNMTKKMVTQRTIGKKKQRLNKRSYLIRALTLNTMTKDAERGKLKRRAIATPGMQIRGFVYFVETLARSICEKLEQSGLPVGGNEKKAKLANVVRKMMTNSQDTELSF
chickenB RLNGLTANESGRLIDFLKDVMESMDKEEMEITTHFQRKRRVRDNMTKKMVTQRTIGKKKQRLNKRSYLIRALTLNTMTKDAERGKLKRRAIATPGMQIRGFVYFVETLARSICEKLEQSGLPVGGNEKKAKLANVVRKMMTNSQDTELSF
   ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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  humanA TITGDNTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPVMFSNKMARLGKGYMFESKSMKLRTQIPAEMLANIDLKYFNESTKKKIEKIRPLLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQKRYTKTTYWWDGLQSSDDFALI
  humanB TITGDNTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPVMFSNKMARLGKGYMFESKSMKLRTQIPAEMLANIDLKYFNESTKKKIEKIRPLLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQKRYTKTTYWWDGLQSSDDFALI
chickenA TITGDNTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESKSMKLRTQIPAEMLANIDLKYFNESTKKKIEKIRPLLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQKRYTKTTYWWDGLQSSDDFALI
chickenB TITGDNTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESKSMKLRTQIPAEMLANIDLKYFNESTKKKIEKIRPLLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQKRYTKTTYWWDGLQSSDDFALI
   ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

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  humanA VNAPNHEGIQAGVDRFYRTCKLVGINMSKKKSYINRTGTFEFTSFFYRYGFVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGPNLYN
  humanB VNAPNHEGIQAGVDRFYRTCKLVGINMSKKKSYINRTGTFEFTSFFYRYGFVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGPNLYN
chickenA VNAPNHEGIQAGVDRFYRTCKLVGINMSKKKSYINRTGTFEFTSFFYRYGFVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGPNLYN
chickenB VNAPNHEGIQAGVDRFYRTCKLVGINMSKKKSYINRTGTFEFTSFFYRYGFVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGPNLYN
   ruler .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

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  humanA IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHREIESVNNAVVMPAHGPAKSMEYDAVATTHSWIPKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVSRARIDARIDFESGRIKKEEFAEIMKICSTI
  humanB IRNLHIPEVCLKWGLMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAVATTHSWIPKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVSRARIDARIDFESGRIKKEEFAEIMKICSTI
chickenA IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAVATTHSWIPKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVSRARIDARIDFESGRIKKEEFAEIMKICSTI
chickenB IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAVATTHSWIPKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVSRARIDARIDFESGRIKKEEFAEIMKICSTI
   ruler .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750

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  humanA EELRRQK
  humanB EELRRQK
chickenA EELRRQK
chickenB EELRRQK
   ruler .......
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PB2 Gene

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humanA    MERIKELRDLMSQSRTREILTKTTVDHMAIIKKYTSGRQEKNPALRMKWMMAMKYPITADKRIMEIIPERNEQGQTLWSKTNDAGSDRVMVSPLAVTWWNRNGPTTSTVHYPKVYKTYFEKVERLKHGTFGPVHFRNQVKIRRRVDTNPG
humanB    MERIKELRDLMSQSRTREILTKTTVDHMAIIKKYTSGRQEKNPALRMKWMMAMKYPITADKRIMEIIPERNEQGQTLWSKTNDAGSDRVMVSPLAVTWWNRNGPTTSTVHYPKVYKTYFEKVERLKHGTFGPVHFRNQVKIRRRVDTNPG
chickenA  MERIKELRDLMSQSRTREILTKTTVDHMAIIKKYTSGRQEKNPALRMKWMMAMKYPITADKRIMEIIPERNEQGQTLWSKTNDAGSDRVMVSPLAVTWWNRNGPTTSTVHYPKVYKTYFEKVERLKHGTFGPVHFRNQVKIRRRVDTNPG
chickenB  MERIKELRDLMSQSRTREILTKTTVDHMAIIKKYTSGRQEKNPALRMKWMMAMKYPITADKRIMEIIPERNEQGQTLWSKTNDAGSDRVMVSPLAVTWWNRNGPTTSTVHYPKVYKTYFEKVERLKHGTFGPVHFRNQVKIRRRVDTNPG
chickenD  MERIKELRDLMSQSRTREILTKTTVDHMAIIKKYTSGRQEKNPALRMKWMMAMKYPITADKRIMEIIPERNEQGQTLWSKTNDAGSNRVMVSPLAVTWWNRNGPTTSTVHYPKVYKTYFEKVERLKHGTFGPVHFRNQVKIRRRVDTNPG
chickenE  MERIKELRDLMSQSRTREILTKTTVDHMAIIKKYTSGRQEKNPALRMKWMMAMKYPITADKRIMEIIPERNEQGQTLWSKTNDAGSDRVMVSPLAVTWWNRNGPTTSTVHYPKVYKTYFEKVERLKHGTFGPVHFRNQVKIRRRADTNPG
ruler     1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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humanA    HADLSAKEAQDVIMEVVFPNEVGARILTSESQLTITKEKKEELQDCKIAPLMVAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQGTCWEQMYTPGGEVRNDDVDQSLIIAARNIVRRATVSADPLASLLEMCHSTQIGGIRMVDILRQ
humanB    HADLSAKEAQDVIMEVVFPNEVGARILTSESQLTITKEKKEELQDCKIAPLMVAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQGTCWEQMYTPGGEVRNDDVDQSLIIAARNIVRRATVSADPLASLLEMCHSTQIGGIRMVDILRQ
chickenA  HADLSAKEAQDVIMEVVFPNEVGARILTSESQLTITKEKKEELQDCKIAPLMVAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQGTCWEQMYTPGGEVRNDDVDQSLIIAARNIVRRATVSADPLASLLEMCHSTQIGGIRMVDILRQ
chickenB  HADLSAKEAQDVIMEVVFPNEVGARILTSESQLTITKEKKEELQDCKIAPLMVAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQGTCWEQMYTPGGEVRNDDVDQSLIIAARNIVRRATVSADPLASLLEMCHSTQIGGIRMVDILRQ
chickenD  HADLSAKEAQDVIMEVVFPNEVGARILTSESQLTITKEKKEELQDCKIAPLMVAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQGTCWEQMYTPGGEVRNDDVDQSLIIAARNIVRRATVSADPLASLLEMCHSTQIGGIRMVDILRQ
chickenE  HADLSAKEAQDVIMEVVFPNEVGARILTSESQLTITKEKKEELQDCKIAPLMVAYMLERELVRKTRFLPVAGGTSSVYIEVLHLTQGTCWEQMYTPGGEVRNDDVDQSLIIAARNIVRRATVSADPLASLLEMCHSTQIGGIRMVDILRQ
ruler     .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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humanA    NPTEEQAVDICKAAMGLRISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQTLKIRVHEGYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVFSQEDCMIKAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWG
humanB    NPTEEQAVDICKAAMGLRISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQTLKIRVHEGYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVFSQEDCMIKAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWG
chickenA  NPTEEQAVDICKAAMGLRISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQTLKIRVHEGYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVFSQEDCMIKAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWG
chickenB  NPTEEQAVDICKAAMGLRISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQTLKIRVHEGYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVFSQEDCMIKAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWG
chickenD  NPTEEQAVDICKAAMGLRISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQTLKIREHEGYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVFSQEDCMIKAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQDWG
chickenE  NPTEEQAVDICKAAMGLRISSSFSLGGFTFKRTSGSSVKREEEVLTGNLQTLKIRVHEGYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVFSQEDCMIKAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWG
ruler     .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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humanA    IEPIDNVMGMIGILPDMTPSTEMSLRGIRVSKMGVDEYSSTERVVVSIDRFLRVRDQRGNVLLSPEEVSETQGTEKLTITYSSSMMWEINGPESVLVNTYQWIIRNWETVKIQWSQDPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF
humanB    IEPIDNVMGMIGILPDMTPSTEMSLRGIRVSKMGVDEYSSTERVVVSIDRFLRVRDQRGNVLLSPEEVSETQGTEKLTITYSSSMMWEINGPESVLVNTYQWIIRNWETVKIQWSQDPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF
chickenA  IEPIDNVMGMIGILPDMTPSTEMSLRGIRVSKMGVDEYSSTERVVVSIDRFLRVRDQRGNVLLSPEEVSETQGTEKLTITYSSSMMWEINGPESVLVNTYQWIIRNWETVKIQWSQDPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF
chickenB  IEPIDNVMGMIGILPDMTPSTEMSLRGIRVSKMGVDEYSSTERVVVSIDRFLRVRDQRGNVLLSPEEVSETQGTEKLTITYSSSMMWEINGPESVLVNTYQWIIRNWETVKIQWSQDPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF
chickenD  IEPIDNVMGMIGILPDMTPSTEMSLRGIRVSKMGVDEYSSTERVVVSIDRFLRVRDQRGNVLLSPEEVSETQGTEKLTITYSSSMMWEINGPESVLVNTYQWIIRNWETVKIQWSQDPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF
chickenE  IEPIDNVMGMIGILPDMTPSTEMSLRGIRVSKMGVDEYSSTERVVVSIDRFLRVRDQRGNVLLSPEEVSETQGTEKLTITYSSSMMWEINGPESVLVNTYQWIIRNWETVKIQWSQDPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF
ruler     .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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humanA    QQMRDVLGTFDTVQIIKLLPFAAAPPEQSRMQFSSLTVNVRGSGMRILVRGNSPVFNYNKATKRLTVLGKDAGALTEDPDEGTAGVESAVLRGFLILGKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLVMKRKRDSSILTDSQTA
humanB    QQMRDVLGTFDTVQIIKLLPFAAAPPEQSRMQFSSLTVNVRGSGMRILVRGNSPVFNYNKATKRLTVLGKDAGALTEDPDEGTAGVESAVLRGFLILGKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLVMKRKRDSSILTDSQTA
chickenA  QQMRDVLGTFDTVQIIKLLPFAAAPPEQSRMQFSSLTVNVRGSGMRILVRGNSPVFNYNKATKRLTVLGKDAGALTEDPDEGTAGVESAVLRGFLILGKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLVMKRKRDSSILTDSQTA
chickenB  QQMRDVLGTFDTVQIIKLLPFAAAPPEQSRMQFSSLTVNVRGSGMRILVRGNSPVFNYNKATKRLTVLGKDAGALTEDPDEGTAGVESAVLRGFLILGKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLVMKRKRDSSILTDSQTA
chickenD  QQMWDVLGTFDTVQIIKLLPFAAAPPEQSRMQFSSLTVNVRGSGMRILVRGNSPVFNYNKATKRLTVLGKDAGALTEDPDEGTAGVESAVLRGFLILGKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLVMKRKRDSSILTDSQTA
chickenE  QQMRDVLGTFDTVQIIKLLPFAAAPPEQSRMQFSSLTVNVRGSGMRILVRGNSPVFNYNKATKRLTVLGKDAGALTEDPDEGTAGVESAVLRGFLILGKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLVMKRKRDSSILTDSQTA
ruler     .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750
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  humanA TKRIRMAIN
  humanB TKRIRMAIN
chickenA TKRIRMAIN
chickenB TKRIRMAIN
chickenD TKRIRMAIN
chickenE TKRIRMAIN
   ruler .........
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