# Results colour-coded for amino acid conservation

The current colourscheme of the alignment is for **amino acid conservation**.

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position. The colour assignments are:

**Unconserved** 0 1 2 3 4 5 6 7 8 9 10 **Conserved**

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                 .........10........20........30........40........50
Arcyptera_corea  ---MLILSMS IMISFTMPMI VMLIATILSK KII-N-DREK SSPFECGFDP
Teleogryllus_co  --MILIISII ISFTLILSII LMFLSLTL-S KKS-LLDREK ISPFECGFDP
Drosophila_mela  --MFSIIFIA LLILLITTIV MFLASILS-K KAL-I-DREK SSPFECGFDP
Culex_pipiens_p  MILILLIMS CIIFIITIVV MMLATFLS-K KTI-I-DREK SSPFECGFDP
Phlaeoba_albone  ---MLILSLS ILISFIIPMI VMLIATTLSK KLI-N-DREK SSPFECGFDP
Anopheles_darli  ---MLMLSTM TLIIMIITIV VMILATLLSK KTL-T-DREK CSPFECGFDP
Gastrimargus_ma  ---MMMLMTT IIISFLLPMI IMLMATML-S KKS-N-DWKK GSPFECGFDP
Anoplophora_gla  --MLIIFLLI IMILLIIFIL IIMLNLIS-K KSF-S-DREK SSPFECGFDS
Chorthippus_chi  ---MLTLSTS ILISFTMPMM IMLIATILSK KLI-N-NREK SSPFECGFDP
Thrinchus_schre  --MMTLSVTF MISFLVPMLV MLLATILS-K KII-N-DREK SSPFECGFDP
Oxya_chinensis_  ---MLTLFSS MTICFIIPMI VMLIATMLSK KLI-N-DREK SSPFECGFDP
Teleogryllus_em  MMITSTINYF QPLFYTIIMN TLIINFTKKK DFKMEKNSSH LS-WGIWIQK
Consistency      0016667444 5574665377 6776656518 8450408788 5*89888997

                 .........60........70........80........90.......100
Arcyptera_corea  KSSARMPFSL RFFLIAVIFL IFDVEIALIL PIVIIMKTSN IMVWTMSSMF
Teleogryllus_co  KSSARLPFSL RFFLIAVIFL IFDVEIALIM PAMIIQMSSN PLYWIFTLMF
Drosophila_mela  KSSSRLPFSL RFFLITIIFL IFDVEIALIL PMIIIMKYSN IMIWTITSII
Culex_pipiens_p  MNYSRLPFSL RFFLIAIIFL IFDVEIALIL PMILIIKSSN LLNWSITSLF
Phlaeoba_albone  KSSARMPFSL RFFLIAVIFL IFDVEIALIL PIVIIMKTSN IMMWTLSTMF
Anopheles_darli  MNSSRLPFSL RFFLIAIIFL IFDVEIALLL PMIMIIKSSN LINWTITSLF
Gastrimargus_ma  KSSARMPFLI QFFLSAVIFL IFDVEIALIL PILIIMKTSN IMMWTLSTML
Anoplophora_gla  KNSARLPFSL QFFLIAVIFL IFDVEITLLF PLIITLKISN MNYSIIFIF-
Chorthippus_chi  KSPARMPFSL RFFLIAVIFL IFDVEIVMIL PIVIIMKTSN IMMWTMSTMF
Thrinchus_schre  KSSARMPFSL RFFLIAVIFL IFDIEIALIL PIVIIMKSSN LMIWTSATLF
Oxya_chinensis_  KSSARMPFSL RFFLIAVIFL IFDVEIALIL PIVIIMKTSN IFVWTMSTMF
Teleogryllus_em  SGGS----VT DFLLWE--YL SKSSEI---F SCNGGENLRY NSRGQYWWGS
Consistency      7768878878 7*9*78789* 8898**6777 8677767588 6547655565

                 .........110........120......
Arcyptera_corea  FIMILLLG-- --LYYEWNQG ALQWAE
Teleogryllus_co  FILILLLG-- --LYHEWNQG ALQWAE
Drosophila_mela  FILILLIG-- --LYHEWNQG MLNWSN
Culex_pipiens_p  FIFILLIG-- --LYHEWNQG ALEWNN
Phlaeoba_albone  FIMVLLGG-- --LYHEWNQG ALQWAE
Anopheles_darli  FIFILIVG-- --LYHEWNQG ALEWNE
Gastrimargus_ma  FIILLLIG-- --LYYEWNQG AFKWAK
Anoplophora_gla  FIMILIFG-- --LFHEWNQG ALNWAY
Chorthippus_chi  FILVLLSG-- --LYYEWNQG ALQWAD
Thrinchus_schre  FILVLLGG-- --LYHEWNQG ALQWAE
Oxya_chinensis_  FIIVLLGG-- --LYFEWNQG ALKWAE
Teleogryllus_em  LFPTHYYGGV PPVILEWNQG VLQWAE
Consistency      9958883*00 00986***** 896*76
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