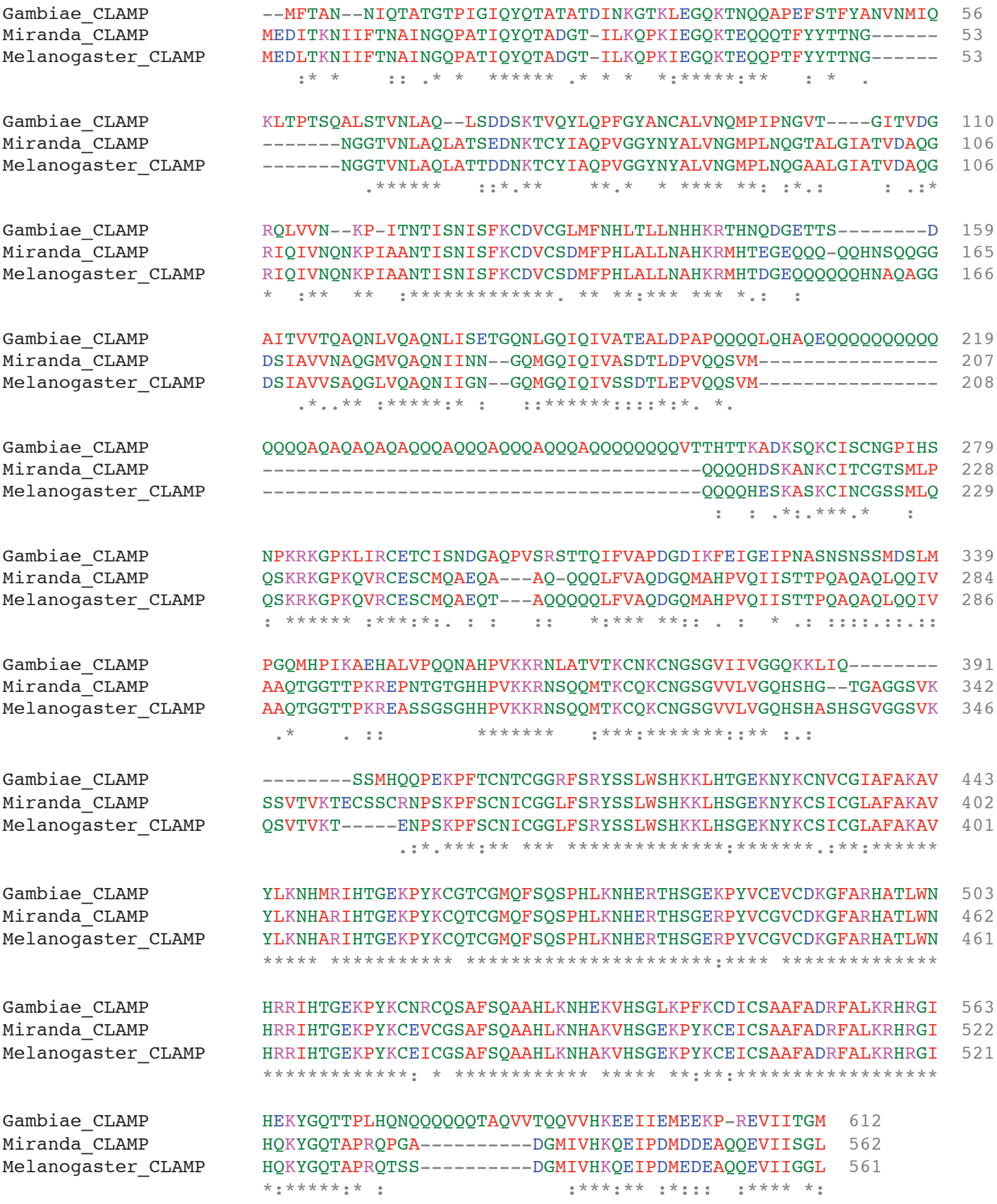
Gambiae_CLAMP --MFTAN--NIQTATGTPIGIQYQTATATDINKGTKLEGQKTNQQAPEFSTFYANVNMIQ 56
Miranda_CLAMP MEDITKNIIFTNAINGQPATIQYQTADGT-ILKQPKIEGQKTEQQQTFYYTTNG------ 53
Melanogaster_CLAMP MEDLTKNIIFTNAINGQPATIQYQTADGT-ILKQPKIEGQKTEQQPTFYYTTNG------ 53
Gambiae_CLAMP KLTPTSQALSTVNLAQ--LSDDSKTVQYLQPFGYANCALVNQMPIPNGVT----GITVDG 110
Miranda_CLAMP -------NGGTVNLAQLATSEDNKTCYIAQPVGGYNYALVNGMPLNQGTALGIATVDAQG 106
Melanogaster_CLAMP -------NGGTVNLAQLATTDDNKTCYIAQPVGGYNYALVNGMPLNQGAALGIATVDAQG 106
Gambiae_CLAMP RQLVVN--KP-ITNTISNISFKCDVCGLMFNHLTLLNHHKRTHNQDGETTS--------D 159
Miranda_CLAMP RIQIVNQNKPIAANTISNISFKCDVCSDMFPHLALLNAHKRMHTEGEQQQ-QQHNSQQGG 165
Melanogaster_CLAMP RIQIVNQNKPIAANTISNISFKCDVCSDMFPHLALLNAHKRMHTDGEQQQQQQHNAQAGG 166
Gambiae_CLAMP AITVVTQAQNLVQAQNLISETGQNLGQIQIVATEALDPAPQQQQLQHAQEQQQQQQQQQQ 219
Miranda_CLAMP DSIAVVNAQGMVQAQNIINN--GQMGQIQIVASDTLDPVQQSVM---------------- 207
Melanogaster_CLAMP DSIAVVSAQGLVQAQNIIGN--GQMGQIQIVSSDTLEPVQQSVM---------------- 208
Gambiae_CLAMP QQQQAQAQAQAQAQQQAQQQAQQQAQQQAQQQQQQQQVTTHTTKADKSQKCISCNGPIHS 279
Miranda_CLAMP ----------QQQQHDSKANKCITCGTSMLP 228
Melanogaster_CLAMP ----------QQQQHESKASKCINCGSSMLQ 229
Gambiae_CLAMP NPKRKGPKLIRCETCISNDGAQPVSRSTTQIFVAPDGDIKFEIGEIPNASNSNSSMDSLM 339
Miranda_CLAMP QSKRKGPKQVRCESCMQAEQA---AQ-QQQLFVAQDGQMAHPVQIISTTPQAQAQLQQIV 284
Melanogaster_CLAMP QSKRKGPKQVRCESCMQAEQT---AQQQQQLFVAQDGQMAHPVQIISTTPQAQAQLQQIV 286
Gambiae_CLAMP PGQMHPIKAEHALVPQQNAHPVKKRNLATVTKCNKCNGSGVIIVGGQKKLIQ-------- 391
Miranda_CLAMP AAQTGGTTPKREPNTGTGHHPVKKRNSQQMTKCQKCNGSGVVLVGQHSHG--TGAGGSVK 342
Melanogaster_CLAMP AAQTGGTTPKREASSGSGHHPVKKRNSQQMTKCQKCNGSGVVLVGQHSHASHSGVGGSVK 346
Gambiae_CLAMP --------SSMHQQPEKPFTCNTCGGRFSRYSSLWSHKKLHTGEKNYKCNVCGIAFAKAV 443
Miranda_CLAMP SSVTVKTECSSCRNPSKPFSCNICGGLFSRYSSLWSHKKLHSGEKNYKCSICGLAFAKAV 402
Melanogaster_CLAMP QSVTVKT-----ENPSKPFSCNICGGLFSRYSSLWSHKKLHSGEKNYKCSICGLAFAKAV 401
Gambiae_CLAMP YLKNHMRIHTGEKPYKCGTCGMQFSQSPHLKNHERTHSGEKPYVCEVCDKGFARHATLWN 503
Miranda_CLAMP YLKNHARIHTGEKPYKCQTCGMQFSQSPHLKNHERTHSGERPYVCGVCDKGFARHATLWN 462
Melanogaster_CLAMP YLKNHARIHTGEKPYKCQTCGMQFSQSPHLKNHERTHSGERPYVCGVCDKGFARHATLWN 461
Gambiae_CLAMP HRRIHTGEKPYKCNRCQSAFSQAAHLKNHEKVHSGLKPFKCDICSAAFADRFALKRHRGI 563
Miranda_CLAMP HRRIHTGEKPYKCEVCGSAFSQAAHLKNHAKVHSGEKPYKCEICSAAFADRFALKRHRGI 522
Melanogaster_CLAMP HRRIHTGEKPYKCEICGSAFSQAAHLKNHAKVHSGEKPYKCEICSAAFADRFALKRHRGI 521
Gambiae_CLAMP HEKYGQTTPLHQNQQQQQQTAQVVTQQVVHKEEIIEMEEKP-REVIITGM 612
Miranda_CLAMP HQKYGQTAPRQPGA----------DGMIVHKQEIPDMDDEAQQEVIISGL 562
Melanogaster_CLAMP HQKYGQTAPRQTSS----------DGMIVHKQEIPDMEDEAQQEVIIGGL 561