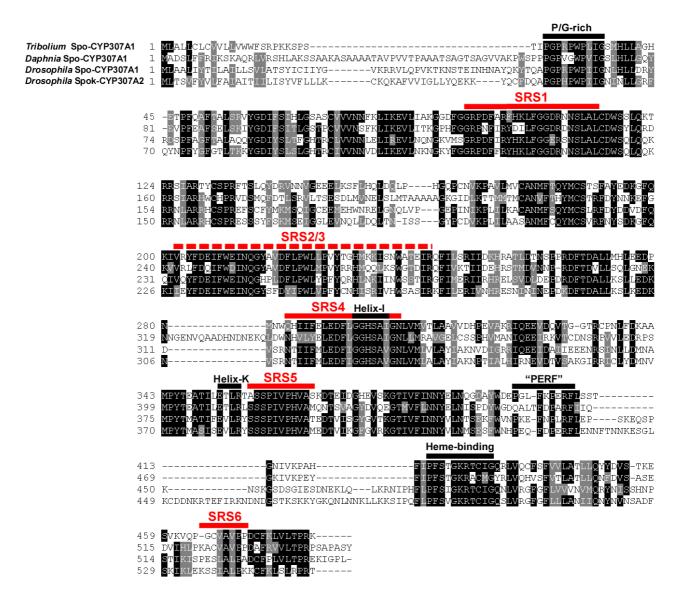
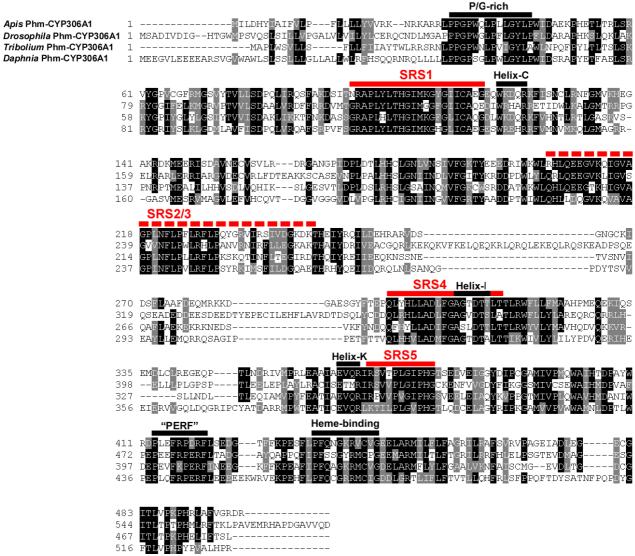
Additional file 1

Putative substrate recognition sites (SRSs) 1 to 6.





P/G-rich 1 MFSKQIPWTLCLPSRLCGGQKCVDKQVYYFNQTTCIHNCPHQFPTSESTK---EMKPEGSTPGP 1 -----MCLFS-----KKSVHYLLTIRTRNYYYRGRFLTTAVD---PPKSEKEIPGP 1 -----MCTLL-----KKCNQSIRKKLFIKFYSNEFTKSKIKINHSQPKABYDIPGP 1 ------MLTKL-----LKISCTSRQCTFAKPYQ-----AIPGP PLPЪP ATPGPRGPE SRS1 76 GQYSEDQLHVTGLKKYLQFGPIVREEILEGVNLILLYRPEDIERMYQVEG-RYPSRSHTALEFYRLQREHIYNSGGLLP
60 GRYQEDRLHKNALKNEQLYGPIIREEIVPGEHIVWLGDPDDIAKMFHTEG-TYPYRKSHLTLEKYRLIRPHIYNSGGLLP
63 GEYSETNLYESFKKKLKCFGPIVREEIIPNVNVIWTYRPEDIAEIFKAESGLHPERRSHLALLKYRKDRPNIYNTGGLLP
44 GSYSWLRLHQAGQDKYEKYGAIVRETIVEGQDIVWLYDEKDIALLLNERD--CPQRRSHLALLAGYRKSRPDVYKTTGLLP Helix-C 155 TIGPEWERLRQALQREINMMENIRQYIEGIDNISSEFAEQIAISIKKNKTSPDFLEDLSKVFLEFIGLVIETTRLGSLR-139 TIGPEWSRIRKVFQKGISGETEALSFIKGSDDVISEWLDTRFKKIHKETSNMOFLQELSRLFLELIGVAAETIRFOSFHD 143 TIGSEWWRLRKEFQKVSSKFQDVINYLKETDCVIQEFVE-LCNNEK--FADFLELLSRLFLELTCLVVFDIRLNSFSK 122 TIGPEWWRLRQVQKELSAEKSVRNFVRQVDGVTKEFIR-FLQESENGGAIDMIPKLTRLNLELTSLIFFGARLQSFTA SRS 3 TDLPGDSCPNKLTQAASDTNSEILRTDNGLQFWRKANTFAYKRITFSQEYEERVASSEVNAKNAELRSRNGQDQSQKTLL
DELDPCSKSTKLLESAFVTNSTILKTDNGPQLWRKEETFAYRRLRKAQELMESVAIDLVALKLSTFKEKTS---NPFTLL
BERCENSISSKLIKAAFATNSAILKIDNGLQLWRFETFLYRKLRKAQTYMEMIALELVSRKKNNMKIRYN-----KSFL
QEQDPSSRSTRLMDAAETTNSCILFTDQGLQLWRFLETESFRKLSQAQSYMEGVAMELVEENVRNGSVGS------SLI SRS4 Helix-I 314 EVYLTSKDLDVKDVTLVSDMLLAGIDTSSYTMSFILYHLARNELKOEKVYQEVNREVENSISEVIQGILA-ELKYLKAA 296 ERYLASASLDFKDIIGVVCDFLLAGNDTITYSSSELYHLATNESICIALYEEACRILENPAAELITEKYK-QAEYAKCA 293 DAYLENEVLDIKDIVGMACDMLLAGIDTISYSTAYILYHLAKNONIOEKLRIEATQILKNHNEEISINILR-NASYTKAV 273 SAYVKNEELDRSDVVGTAADLLLAGIDTISYASAFLLYHIARNEEVQQKLHEEAKRVLESAKDELSMDALRIDITYTRAV SRS5 "PERF" Helix-K 393 VKESERLNPISIGVGRILPEDSSFSGYHCPKNTILVSCNQVSCKLDRYFKNPLLEVPERWMKGDAAYEKT-----HPY
375 VKESERLRPISIGVGRQLTDVVFSGYKVFSGVVVTINQVLSRMEKYFPEPDSEKPERWMKNDPSYVQT-----HPY
372 IKESERLNPISIGIGRILQTDVVLSGYKVFKGSVVVTQNQIICRLPEYFEEPNLFIPERWLREYSENNNKINYKKTVHPY
353 LKESERLNPIAVGVGRILNQDAIFSGYFVFKGTVVTQNMVRCRLEQHEQDELREQEDRWLQHRSALN------PY Heme-binding SRS6 LDVRS<mark>CLINR</mark>PDAPLKFNEVERRNC---IDSKSLLINKPDEPILLSEEPR-----LGM<mark>ISLLINKPNAL</mark>LKFNEHDILNNNSV MGVKTLLINKPDAPVLIDLR--LRRE--
 466
 LVLPFGHGERACIARRIAEQNLYILLSRLVKRESTEWNG

 448
 LVTPFGHGCRSCIARRFAEQNMVILLLKLARKYKIRWNG

 452
 VLLPFGHGERSCIARRFAEQNMQILLLRICRRLKTSWHG

 423
 LVLPFGHGMRACIARRIAEQNMHILLLRLRETELIWSG
 --SEIDS --DDLGM

 Daphnia Dib-CYP302A1
 1
 MFSKQIPW

 Tribolium Dib-CYP302A1
 1

 Apis Dib-CYP302A1
 1

 Drosophila Dib-CYP302A1
 1

