

Additional file 1

Putative substrate recognition sites (SRSs) 1 to 6.

P/G-rich

Tribolium Spo-CYP307A1 1 MLALLCLCVLLVWVFSRPKKSPS-----TIPGFRPWFLIGSMHLLAGH
Daphnia Spo-CYP307A1 1 MADSLFTRIKSKAQRLLVRSHLAKSSAAKASAAAATAVPVVTPAAATSAGTSAGVVAKPTSPFPGEVGVWPVIGSIHLLQY
Drosophila Spo-CYP307A1 1 MLAAALTYTILATLLSVIATSYICIIYG-----VKRRVLQPVKTKNSTEINHAYQKTTQAPGFRPWFTIGNLHLLDRY
Drosophila Spok-CYP307A2 1 MLTSVFYVLFATAITILISYVFLLLK-----CKQKAFVVIGLLYQEKK---YQCEQDQAPGHPWFTIGNLHLLRF

SRS1

45 -ETPFQAF TALSRVYGDIFSIHLGSASCVVNNFKLIKEVLI AKGGDFGGRPDEFREHKLEGGDRNNSLALCDWSSLQKT
81 -EVPPFAFSELSKIYGDIFSTLTGSTPCVVVNSFKLIKEVLT KGPFGGRENFTRYDILFGGDRDNSLALCDWSYLQD
74 RLSPFAFTALAQYGDIVSLTFCHTRCLVVNNLELIEVLNQNGKVMSSGRPDEFTRYHKLEGGDRNNSLALCDWSQLQK
70 QYNPFYCFGTLTTKYGDIVSLSLGHTRCTIVVNNVDLIKEVLNKGKYEFGGRPDEFTRYHKLEGGDRNNSLALCDWSQLQK

124 RRSLARTYCSPRFTLQYDRVNNVGEETKSFHQLDQLP---HGQPCNVKPAVLMVCANMFTQYMCSTSEAYEDKGFQ
160 RRSLARHWCPRVDSMQFDTLSRMLTSBSDLMLNELSLMTAAAAAGKIDUKTTMMTCANVFTHYMCSTREDYNNKEFG
154 RRNLARRHCSPREFSCTFYMKMSQTGCCEMEHWNRELGNQLVP---GEFINIKPLILKACANMFTQYMCSLREDYDDVDFQ
150 RRNLARRHCSPRESSSYFSKMSEITGGLEVNQLLDQLTN-ISS---GYPCDVKPLILAAASANMFTQYMCVVRNYSRKGFG

SRS2/3

200 KIVRYFDEIFWEINQGYAVDFLPWLLFVVTGHHKKTISNWAETIRQFILLSRIIDKFRATLITNSPERDFTDALIMHLEEDP
240 KIVRLFDQIFWIDINQGYAVDFLPWLMFVRRHMQQLKSWGTDIRQFIVKTIIDEFRSTMDVNNP-RDFTDVLSSLGNEK
231 QIVQYFDEIFWEINQGHPLDFLPWLIFEFYQRHLNKIINWSSITRGFIMERIIRHIELSVLDLEEDRDFTDALIKSLLEDK
226 KILEYFDEIFWEINQGYSEDYIPWLVEFYCNHLSRIVHWSASIRKFTILERIVNHRRESNININEEDKDFTDALLKSLKEDK

SRS4 Helix-I

280 N-----MNVCHTIFELEDFLGGHSAIGNLVMTLAAVVDHPEVAKRIQEEVDQVTG-GTRCPNLFKAA
319 NNGENVQAADHNDNEKQLDWNHVLYLEDFLGGHSAIGNLIMRAVGELCSSPHVMANIQEEIRRVTCDNSRPVLEDRPS
311 D-----VSRNTTIFMLEDFLGGHSAVGNLVMIVLAYIAKNVDICERRIQEEIDATIEEENRSDNLLLMNA
306 N-----VSRNTTIFMLEDFLGGHSAVGNLVMIALAYIAKNETIALHIREVDIVSAGGIRBICLYVMNV

Helix-K SRS5

343 MPYTEATILETLRTASSPIVPHVASKDTEIDGHEVSKGTIVFINNYELNQCLAYWDEEGL-FKEERFLSST-----
399 MPYTEATILETLRLSSSPIVPHVAMQNTSVAGDIVQEGTIVFINNYELNISPDVWGQALTFDEARFLIQ-----
375 MPYTMATIFEVLRYSSSPIVPHVATEDTVISGNGVTKGTIVFINNYVLNTSEKEFWNEKE-FNELRFLFP----SKEQSP
370 MPYTMASISEVLRYSSSPIVPHVAMEDTVIKGGVVRKGTIVFINNYVLNMESEFWNHPEQ-FDERFLENFTNNKESGL

Heme-binding

413 -----GNIVKPAH-----FIPFSTGKRTCIGQLVQCFSEFVVLATLLQYDVSTKE
469 -----GKIVKPEY-----FIPFSTGKRACMGYRLVQHVSEFVTLATLLQNEDVSAE
450 K-----NSKGSDSGIESDNEKLQ---LKRNIPIHFLPFSTGKRTCIGQLVRCFGFLVVVNVNQRYNISSHNP
449 KCDDNKRTEFIRKNDNDSGTSKSKYGKQNLNNKLLKKSIPQFLPFSSVGKRTCIGQLVRGFGFLLLANLIQNNVNSADP

SRS6

459 SVKVQP-GCVAVPEPDCFKLVLTTPRK-----
515 DWIHLPKACVAVPEPDAFRVVLTPRPSPAPASY
514 STIKTSPESLALPADCFPLVLTTPREKIGPL-
529 SKIKLEKSSIALPKKCFKLSLRPRT-----

P/G-rich

Apis Phm-CYP306A1 1 -----MILDHYIAIFVLP---FLLLLVVRK--NRKARRLPPGPWQLFLLGYLFWIDAEKPHHTLTRLSR

Drosophila Phm-CYP306A1 1 MSADIVDIG--HTGWMPSVQSLSIILVPGALVIVILYLCEQCNDLMGAFPPGPWGLFELGYLFFLDARAPHKSLQKLAK

Tribolium Phm-CYP306A1 1 -----MAPLWSVLLS----FLLFTIAYTWLRRSRNLPPGPWNLPVIGYLAWLNPPQFFYYTLTSLSK

Daphnia Phm-CYP306A1 1 MEEGVLEEEEARSVGVWAWLSLSSILLGLLALWLRHSQQNRQLLLLPPGPBSGLFWLGYLFWIDSRAPYBTFAELSR

SRS1 **Helix-C**

61 VYGPVCGFRMGSVYTVLLSDPQLLRQSFADKSTINRAPLYLTHGIMKGYGLICAEGEQWKDQRKFISNCLNFGMVKHEG

79 RYGGIEELKMGRVFTVVLSDAALVRDFERRDVMIGRAPLYLTHGIMGGFGLICAEQEDINWHARRETIDWLKALGMTRRPG

58 KYGPIVGLYLGSIYTVVISDAKLTKKTENKTDASSGRAPILHHTHGIMKGFGLICAEQEDLWKDQRKFVHNTLRLTGASVVS-

81 RYGRITSLKLGDMIAVFISDPQLVRQAFSRPVFSGRAPLYLTHGIMKGHGLICAEGESWREHREFVMNVMKQLGMAGR-

141 AKRDKMEERTSDAVNECVSVLR---DRGANGPIDPLDTHHCLGNLVNSTVFGKTYEESIRIMKWLRLHQEEGVKQIGVA

159 ELRARLERRIARGVDECVRLFDEAKKSCASEVNPLPALHHSILGNTINDLVFGITTKRDPFDWLYLQRLQEEGVKLGIVS

137 PNRPTMEALTLHHVSLVQHIIK---SLGESVTLDPDLSLRHSLGSAINQMVFGKCSRDATWKLQHLQEEGTHKHGVA

160 -GASVMESRMMAGVLEFVHCQVT--DGVGGGVLDLPGLRHCTIGNIINGVVFGRTYAADPTTWLWQLHLLDQGVKQVAVA

SRS2/3

218 GELNFLFLRLFLQYGRVIRSVTDGKDKTHEIYRQILDEHRARVDS-----GNGCKII

239 GVVNFLEWLRHLBANVNTIRFLLGKAKTHAIYDRIVEACGQRIKEKQKVFKEQLQEQRKLQRQLEKEQLRQSKEADPSQE

214 GELNFLFLRLFLPKSKQTINFLTEGIRDTHQIYREIIEQKNSSNE-----TVSNVI

237 GEINFLVLRLFLPSYRKIMSEILDGQAETHRHYQEIILQRLNLISANQG-----PDYTSVV

SRS4 **Helix-I**

270 DSELAAFDEQMRKKD-----GAESGYTEEPQLYHLLADLFGAGTDTLTLTLRWFLFLMAAHPMEEQEKIQS

319 QSEADDDDEESDEEDTYEPECILEHFLAVRDTDSQLVDDQLRHLLADLFGAGVDTSLATLRWFILYLAREQRCQRLH-

266 QAEFLAEKFKRKNEDS-----VKFYNDQQEFLYLLADIFGASLDTLTLTLRWVVLVMAVHQDVQKKVR-

293 EAYLLDMQRQSAGIP-----PETETTVQLHHVLADMFAGTDALTITIKWIVLYILYIPDVQERTHE

Helix-K **SRS5**

335 EMDLCIREGEQP----TINRIVMERLEAATAEVQIRSVTPLGIPHGTSSELVEIGGYDIPCSAMIVEMQWALHTDAYW

398 --ELLPLGPSP----TLELEPLAYLRACISFTMRIRSVVPLGIPHGCKBNFVVGDFYIKGGSIMIVCSEWAIHMDVAV

327 -----SLNDL-----TLEQIAMVPYFEATIAEVQIRFVVFVGIPIHGSVEELEIAQYKIPPGSMIVPLQWAVHMDANIW

356 EIERVVGQLDQGRIPCYATARRMEWTEATICEVQRLKTIPLGVPHGTLQDCELAGYRIEKSAMVVFVWAMNLDFTLW

"PERF" **Heme-binding**

411 RIPLEFRPDRFLSEDG---TEFFKPESTLPFQNGRRVCVGEELARMITILEFAGRIILAFSVRVPAGEIADLEG-----ECG

472 EPEEEFRPERFLTAG---AYQAEPEQFIPFSSGYRMCPEGEEIARMILITLETGRILRREHIELEBSGTEVDMAG-----ESG

397 DEPEVFRPERFLINEEG---KEFKPEAFIPFQAGKRMCMVGDELARMELYLEGAAVLRNEATSCMG--EVDLTG-----DCG

436 EPELQFRPERFLIEEKEKWRVEKPEHFLPFQCGRRMCTGDDLGRITLIELEFVTTLQHFRLSFEPQFTDYSATNFPQPIYG

483 ITLVFPHHRLAEVGRDR-----

544 ITLTETPHMLRFTKLPAVEMRHAPDGAVVQD

467 ITLTETPHELIETSL-----

516 ITLVPHHYPVALHPR-----

Daphnia Dib-CYP302A1 1 MFSKQIPWTLCLPSRLCGGQKCVDKQVYYFNQTTCLNCPHQFPTSESTK---EMRPFSGSIPGKPLPVVGNLWRYA--I
Tribolium Dib-CYP302A1 1 -----MCLFS-----KKSVMHYLLTIRTRNYYYRGRFLTAVD---PKKSEKPIPGELSLPLVGTLYLYEEFI
Apis Dib-CYP302A1 1 -----MCTLL-----KKCNQSIRKKLFIKFYSNEFTTKIKIKINHSQKAFYDIIPGPKSLPIIGTLYKYLEFI
Drosophila Dib-CYP302A1 1 -----MLTKL-----LKISCTSRQCTFAKEYQ-----AIPGRGPFPGMGNLYNYLEGI

P/G-rich

SRS1

76 GQYSEFDQLHVTGLKKYLQEGPTVREEILPGVNLILLYRPEDIERTYQVEG-RYFSRRSHTALEFYRLQRPHTYNSGGLLF
60 GRYQFDRLHKNAKNEQLYGPITREEIVPGEHIVWLGLEDDIAKMEHTEG-TYPYRKSHLTLERYRLDRPHIYNSGGLLF
63 GBYSEFNLYESGKKKLLKCGPLVREEILPNVNIWIYRPEDIAELKAEESGLHPERRSHLALLRYRKDRPNINYNTGGLLF
44 GSYSMLRLHQAGQDKNEKYGATVRETIIVPGQDIVWLYLEKDIALLLNERD--CPGRSHLALAQYRKSRPDYKTTGLLF

Helix-C

155 TNGPEWTRLRQALQEPINMMENTROYIPGIDNISSEFAEQIAISIKNKTSDFDFEDLSKVFLEFIGLMTFETRLGSLR-
139 TNGPEWSRIRKVFQKGLSGTEALSFIKGSDDVISEWLDTRFKKIHKETSNDMFLQELSRFLLELIGVAAFTRFQSEHD
143 TNGSEWWRLRKEFQKVSSKEQDVINYLKETDCVIQEFVE--LCNNEK---FADFPLLSRLFLLELTCLVVFETRLNSES
122 TNGPEWRRIRAQVQKELSAKSVRNFRQVDGVTKETIR--FLQESNNGGAIMLPKLTRLNLELTSLLTGARGLOSETA

SRS2/3

234 TLPGDSCPNKLTQAASDTNSEILLRTDNGLOFWRKKNTPAYKRITRSCQYERVAESEFNAKNAELRSENGQDQSQKTL
219 DELDPOSKSKLLESFVNTSTILKTDNGEQLRWRKEETPAYRRLRKAQELMESVAIDLVALKLTFTFKETS---NPTILL
218 PERCENSISSKLIKAAAFATNSAILKLDNGLQLWRLEETELYRKLRACTYMEMIALELVSRKKNNMKIRYN-----KSF
200 CRQDPSSRSTHMDAAETNSCILPTDGLQLWRFLFTPSERKLSQAQSYMEGVAMELVEENVVRNGSVGS-----SLI

SRS4 Helix-I

314 EVYLTSKDLVDKDVVTIVSDMLLAGIDTTSYTMSEFILYHLAENFLKQEKVYQEVNRFVPNSTSEVTTQGILA-ELKYLKAA
296 ERYLASASLDEKDIIGVVDPELLAGMDTTYSSSFILYHLATNPSTODALYEEAGRILPNPAAPLTTEKYK-QAEYAKCA
293 LAYLENFVLDIKDIVGMACDMLLAGIDTTSYSTAYILYHLAENQNIQEKLRIEATQLLKNHNEPISINILR-NASYTKAV
273 SAYVKNFELDRSDVVGTAADLLLAGIDTTSYASAFILYHLAENPEVQCKLHEEAKRVLPKAKDELSDMALRTDITYTRA

Helix-K

SRS5

"PERF"

393 VKESFRLNPISIGVGRILPEDSSFSGYHCPKNTILVSONQVSCKLRYFKNELLVPERWMKGDAAYEKT-----HPY
375 VKESLRLRPISIGVGRQLTDDVVFESGYKVPESGTVVVTINQVLSRMEKYFPPEPDSKPERWMKNDPFSYVQT-----HPY
372 VKESLRLNPISIGVGRILQTDVVLGSYRVPKGSVVVTQNTICRLPEYFESPNLTPERWLREYSENNNKINYKKTVHPY
353 VKESLRLNPITAVGVGRILNQDAIFSGYFVPGGTIVVTQNMVRCRLQHFQDPLRQCFDRWLQHRSALE-----PY

Heme-binding

SRS6

466 LVLPFGHGPRACIARRLAEQNHILLRLVKRSTEWNG--AELDVRSQLINRPDAPLKFNFVERRNC---
448 LVLPFGHGQRSCIARRFAEQNMVILLKLARKYKLRWNG--SEIDSKSLLINKPDAPILLSEFPR-----
452 VILPFGHGPRSCIARRFAEQNMQILLRLCRRLKISWHG--DDLGMISLLINKPNALLKFNFDHILNNSV
423 LVLPFGHGMRACIARRLAEQNHILLRLRETELINSGSDDMGVKTLLINKPDAPVLIDLR--LRRE--

Apis Sad-CYP315A1 1 -MNLAQNILKSGKSVLSNNVIALKYNIPGCGYAGASQTSRIDDLSDISKSTDGGNRSKIEITEKLDRDNYGTAVATSE
Tribolium Sad-CYP315A1 1 -----MLFRRVIAQLSTRP-----KSS-----LVSANTV
Drosophila Sad-CYP315A1 1 MTEKRERPGPLRWLRHLLDQLIVRILSLIS-----LFRSR-----CDPPPLQRFPA TELPPAVA
Daphnia Sad-CYP315A1 1 -----MASYL RHP IRRISLIER-----RCYTAKS

P/G-rich

80 SILQEMHEPFGTIFVEGTILFSFILSGGPKIQHEYVDKRHKELGFIYKERIG-PTTAVFVNSIHEERKIERLEGSTPKHELP
 25 LHEDEIFSPKGLPLVGTTLALIAHGSTPKLHDYVDKRHKQLGPIFKEKLG-PVSAVFVADPDEIRAVEDHEGKHPLHWLP
 54 AKYVPIHRVKGLPVVGTIIVDLIAAGGATHLHKYIDARHKQYGPPIFRERLGGTQDAVFVSSANLMRGVFOHEGQYFQEBLP
 25 QPEDSTIAPKGLPLVGTLDVIRAGGVSOIHRYLDDRHRLQLGPIFKEKLG-HVEAVWLADPALYEQVQKEGTCPRFMLP

SRS1

Helix-C

159 EAWTLTYNEILKRCRRGLLFMNGEEWYFRILNKMVLLPDPTNLMIAPCQEWAIETKRWKQIKT--NNIISN-----
 104 DAWVAYNQMYSCPRLFFMDGANWYHREIMNRLLLKGDFR-WIEGACECVSDKLT--DSLME--SDYCGN-----
 134 DAWTLYNQOQACQRLFFMEGAEWIHNRRILNRLLLNGNLN-WMDVHIESCTRRMVDQWRRTAE--AAAIPLAESGEIR
 104 EEWLILNKKHAYKRGLEFFMOGEWLRYSKILSPLLKTATLHRHIESFYDADRLLDKMEHTENGLITH-----

SRS2/3

230 -----LQVQLYQWSIEAMMATLMGSYWYSYKH-QLSRDFEILAEITLHEITFEYSANLSITPVKLAMNRLFLVWKKFVASA
 171 -----LEATLYKWSLDVIVSILLGSGSYSQLCGELEPKVQKLAQVTHLVEQTSANLALIPASBASKFKIPQWRRFVDSV
 211 SYELPLLEQQLYRWSTEVLCCEIMFGTS--VLTCFKIQSSLDYFTQIVHKVEHSSELMTFPPRLAQILILELHWRFDEANV
 173 -----LEGDLYCMFVQVFKNEILKTK-----ITCWASIGSARLTLLPPALAAKNLDAWRCEEQSA

SRS4 Helix-I

303 ITAFEIVRMLVPEMA-----KLGNGLLKMMDEGIRAEIAICIVTDETLAAGDTTATTLQWILLLLCNHEKEEEL
 245 DNALAQNALMDTLTEK-----KPHSDGLLPKLLAEQITLEDIKRIIVDLVLAAGDTTAVAMEMWMLVLAASFQICEKL
 289 DEVLREGAALIDHCHRVQEDQR-KPHDEALYHNLQAADVPGEMIKRIFFVDLVLAAGDTTAFSSQWALFALSKEERLQORL
 229 LSAQLANQLTQTCLEKLPQDDNNEDECTIVSSLRQQKMKVKSIDIQRIVADFLAAADTTSHTTQWVLLLLARHEEVONKI

Helix-K

SRS5

375 FHLKDLSDQEDILR-----LPLKGIITKESLRLYPTAPFTISRYLPEDSVIGNYFVFKGELLVLSLYSSGRDAANFPQPN
 319 RENPD-----FVKHVEKETLRLYPVAPFLTRILPEDAILGGYGVPKGTLVVMMSIYTSGRDGRYFKNPG
 368 AMERATNDSR-----LMHGLTIKESLRLYPVAPFTIGRYLFDQAQLGGHFEKDTMVLISLYTAGRDPSEHEPE
 309 FYEIELVQSSKQRIGDEWQHPTIKGSVKEALRLYPVATFLTRIMQEOCTEGGYNIPEPDTLMLMSAYTSGRDERYEFWNAQ

"PERF"

Heme-binding

SRS6

449 BERPERWIRTQKGIYQGVVHPHASLPFALCARSCIGRKLAETQTSFALAEILKSEKTECINKNQVKLILHLISVFSQSITK
 382 DEQPERWDRKDE--FYSSEMKKASLPFANGLRACVGRKVAETQLQMTLLKIVNKEVEELGNQREVEIVLKMVAVPSEPLL
 436 RVLPERWCIGET---EQVHKSHGSLPFALGQRSCIGRRVALKQLHSILGRCAAQFEMSCINEMFVDSVLRMTVPEDRTLRL
 389 DEIPERWNRHGFSNGGMVMDPFASLPFCHGRRCIGRRLAESQMYITLLYKATPRETFQABN--HVKMIMRLIGTVDQPVQ

529 LKLMERN-
 460 LKFRKL--
 513 LALRERTE
 467 LELRTES-

