Supplementary Information

The Modules of *trans*-Acyltransferase Assembly Lines Redefined with a Central Acyl Carrier Protein

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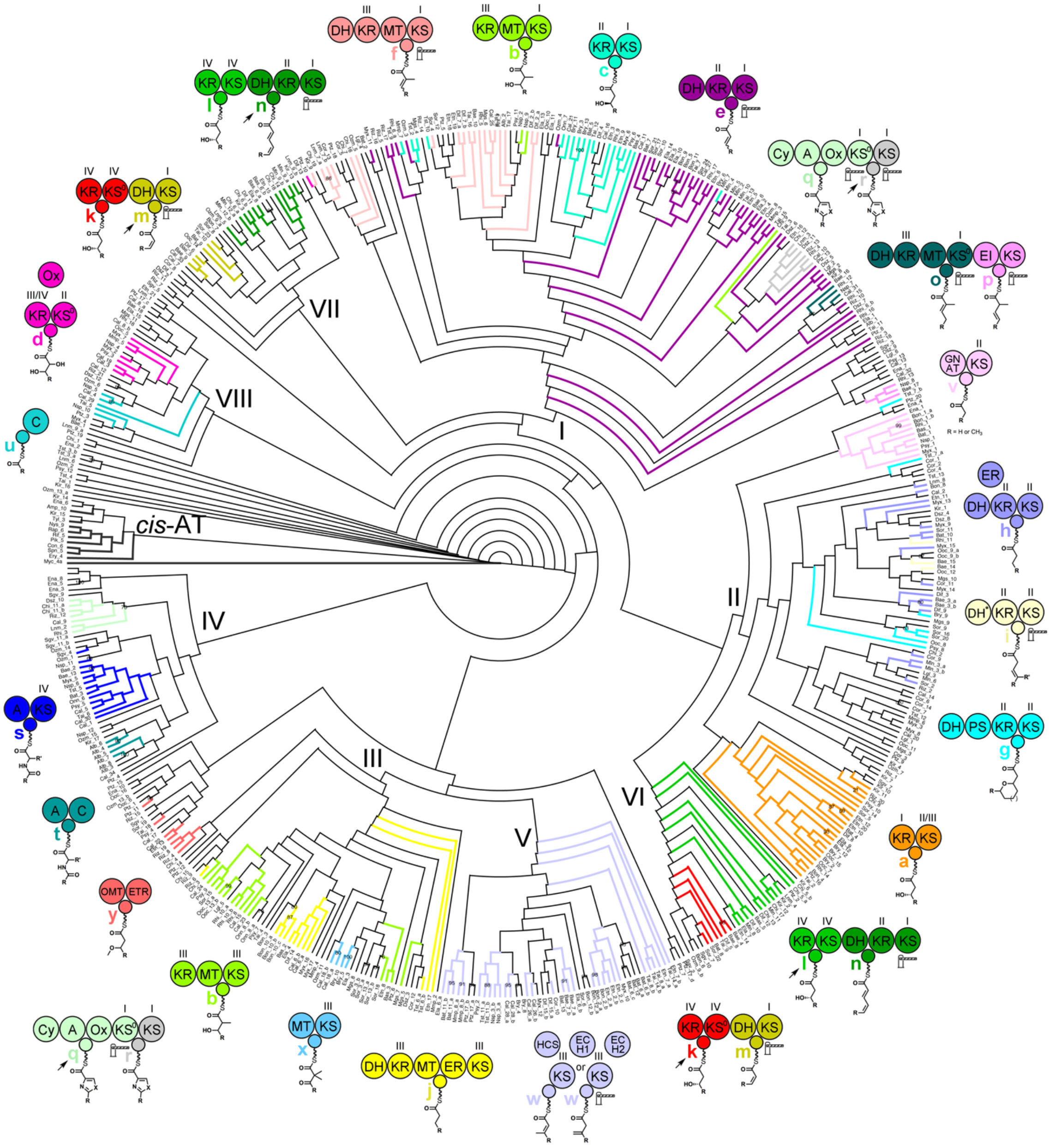


Figure S1. Cladogram of 526 ACPs from 33 *trans*-AT Assembly Lines. ACPs from similar types of modules were observed to clade together. They were colored by the module types shown in the cartoons surrounding the cladogram ("module type" is defined by both the chemical moiety a module adds and the classes of enzyme contained in the module). Only the colored ACPs appear in Figure 2. Uncolored ACPs within or adjacent to a clade are often from modules that are very similar to the module type of those ACPs. Next to the cartoons, bold letters (**a-y**) represent module types, and Roman numerals indicate KS and KR clades as defined in Figures S2 and S3. ACP Families contain ACPs from similar module types and are indicated by large Roman numerals within the cladogram.

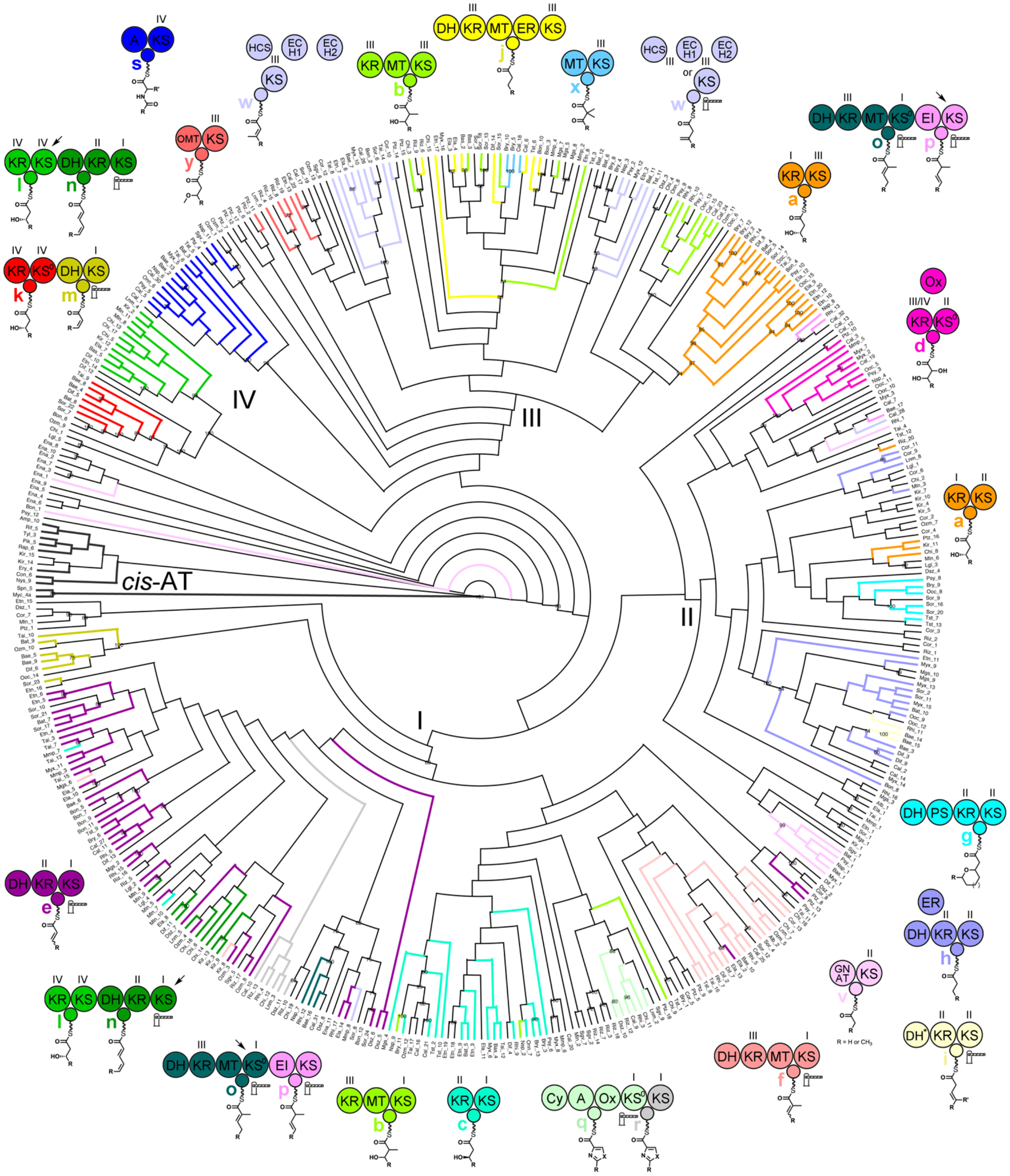


Figure S2. Cladogram of 423 KSs from 33 *trans*-AT Assembly Lines. KSs are colored by the module types of preceding ACPs as in Figure S1 (**a-y**). KSs that are not colored are usually in undefined module types (**z**) similar to the module types of KSs nearby in the cladogram. The bottom cladogram in Figure 3 only shows KSs associated with **a-y** modules and *cis*-AT modules. KS clades I-IV are defined here. Most KS$_{I}$s gatekeep for intermediates with α/β-double bonds, as indicated by the gate icon.

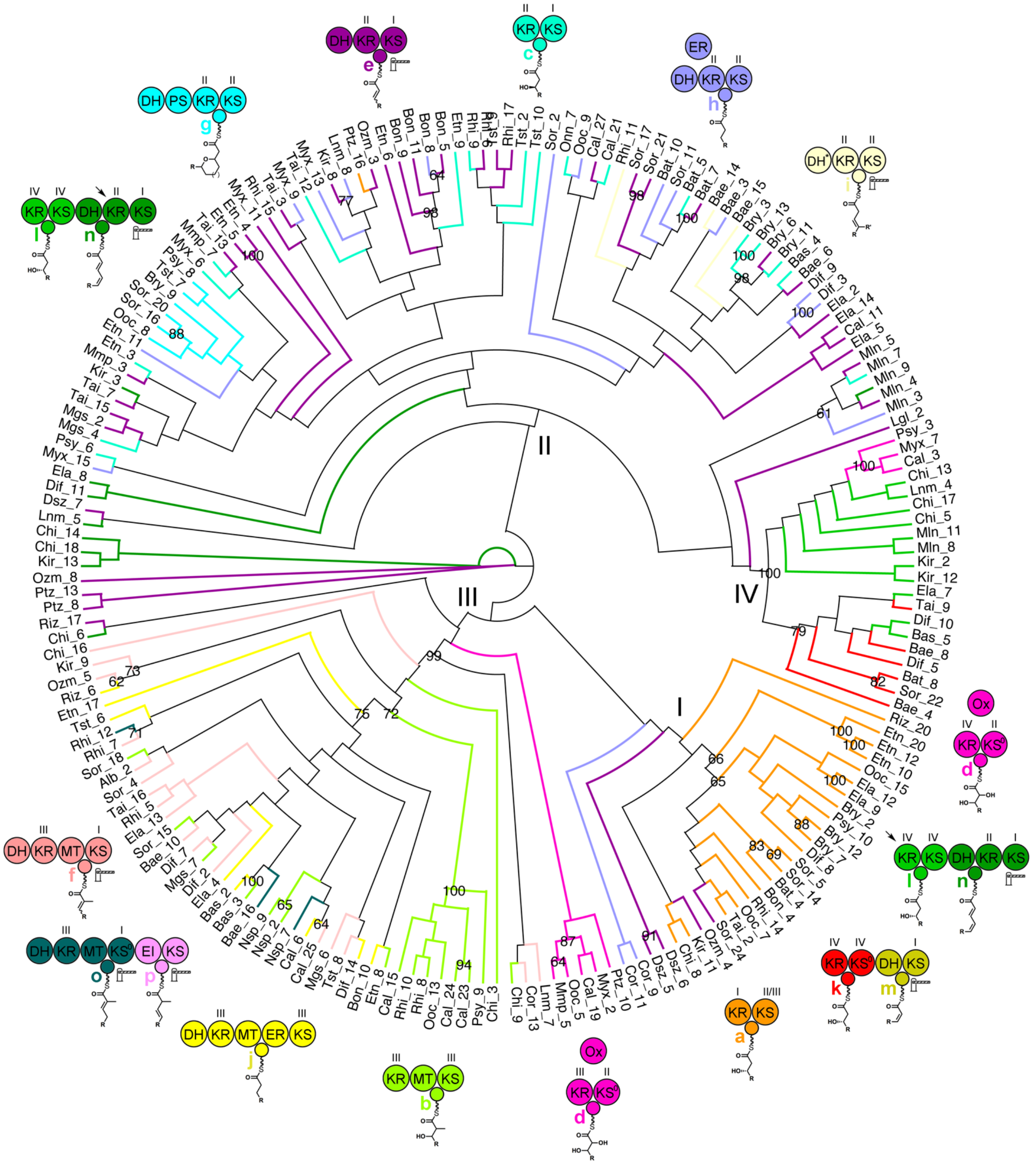
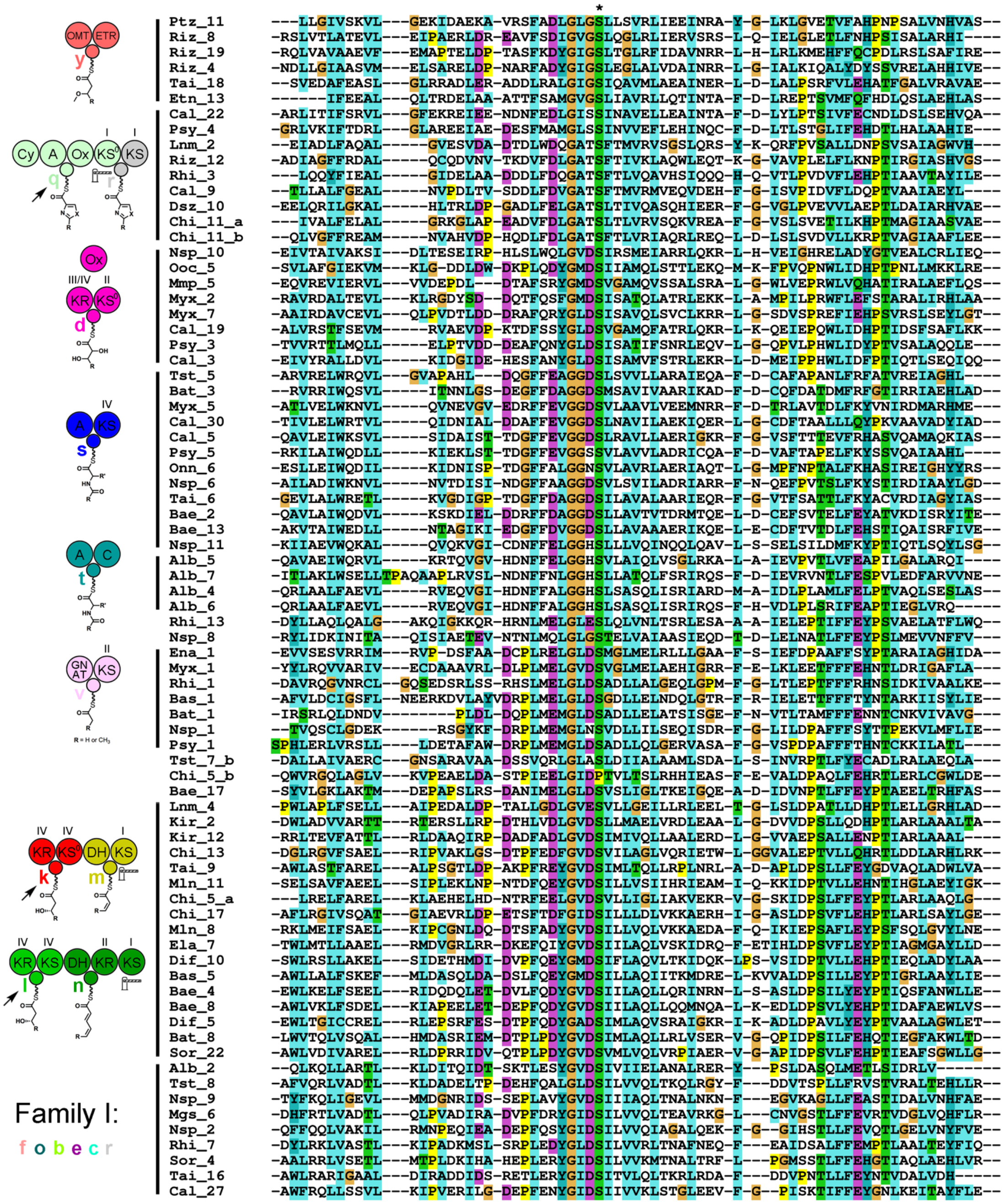


Figure S3. Cladogram of KRs from defined module types. The catalytic subdomains of KRs from defined module types are compared. From this analysis, KRs are observed to generally fall into one of four clades (I-IV). The KR_{I} clade contains KRs that are from methyltransferase (MT)-less modules and generally A-type, the KR_{II} contains KRs that are from MT-less modules and generally B-type, the KR_{III} clade contains KRs that are from MT-containing modules and can be A-type or B-type, and the KR_{IV} clade contains KRs that are from the first module of dehydrating bimodules as well as some α-oxidizing modules and are A-type.



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                                               *
Ptz_11      ---LLGIVSKVL---GEKIDAEKA-VRSFADLGLGSLLSVRLIEEINRA-Y-G-LKLGVETVFAHPNPSALVNHVAS--
Riz_8       -RSLVTLATEVL---EIPAERLDR-EAVFSDIGVGSLQGLRLIERVSRS-L-Q-IELGLETLFNHPSISALARHI----
Riz_19      -RQLVAVAAEVF---EMAPTELDP-TASFKDYGIGSLTGLRFIDAVNRR-L-H-LRLKMEHFFQCPDLRSLSAFIRE--
Riz_4       -NDLLGIAASVM---ELSARELDP-NARFADYGIGSLEGLALVDAINRR-L-G-IALKIQALYDYSSVRELAHHIVE--
Tai_18      --SVEDAFEASL---GLRRADLER-ADDLRALGIGSIQAVMLAEAINER-L-D-LALPSRFVLEHATFGALVRAVAE--
Etn_13      ------IFEEAL---QLTRDELAA-ATTFSAMGVGSLIAVRLLQTINTA-F-D-LREPTSVMFQFHDLQSLAEHLAS--
Cal_22      -ARLITIFSRVL---GFEKREIEE-NDNFEDLGISSINAVELLEAINTA-F-D-LYLPTSIVFECNDLDSLSEHVQA--
Psy_4       -GRLVKIFTDRL---GLAREEIAE-DESFMAMGLSSINVVEFLEHINQC-F-D-LTLSTGLIFEHDTLHALAAHIE---
Lnm_2       --EIADLFAQAL-----GVESVDA-DTDLWDQGATSFTMVRVSGSLQRS-Y-K-QRFPVSALLDNPSVSAIAGWVH---
Riz_12      -ADIAGFFRDAL-----QCQDVNV-TKDVFDLGATSFTIVKLAQWLEQT-K-G-VAVPLELFLKNPTIRGIASHVGS--
Rhi_3       ---LQQYFIEAL-----GIDELAA-DDDLFDQGATSFTLVQAVHSIQQQ-H-Q-VTLPVDVFLEHPTIAAVTAYILE--
Cal_9       --TLLALFGEAL-----NVPDLTV-SDDLFDVGATSFTMVRMVEQVDEH-F-G-ISVPIDVFLDQPTVAAIAEYL----
Dsz_10      -EELQRILGKAL-----HLTRLDP-GADLFELGATSLTIVQASQHIEER-F-G-VGLPVEVVLAEPTLDAIARHVAE--
Chi_11_a    ---IVALFELAL-----GRKGLAP-EADVFDLGATSLTLVRVSQKVREA-F-G-VSLSVETILKHPTMAGIAASVAE--
Chi_11_b    --QLVGFFREAM-----NVAHVDP-HQDLFDLGATSFTLVRIAQRLREQ-L-D-LSLSVDVLLKRPTVAGIAAFLEE--
Nsp_10      -EIVTAIVAKSI---DLTESEIRP-HLSLWQLGVDSIRSMEIARRLQKR-L-H-VEIGHRELADYGTVEALCRLIEQ--
Ooc_5       -SVLAFGIEKVM---KLG-DDLDW-DKPLQDYGMDSIIAMQLSTTLEKQ-M-K-FPVQPNWLIDHPTPNLLMKKLRE--
Mmp_5       -EQVREVIERVL---VVDEPDL---DTAFSRYGMDSVGAMQVSSALSRA-L-G-WLVEPRWLVQHATIRALAEFLQS--
Myx_2       -RAVRDALTEVL---KLRGDYSD--DQTFQSFGMDSISATQLATRLEKK-L-A-MPILPRWFLEFSTARALIRHLAA--
Myx_7       -AAIRDAVCEVL---QLPVDTLDD-DRAFQRYGLDSISAVQLSVCLKRR-L-G-SDVSPREFIEHPSVRSLSEYLGT--
Cal_19      -ALVRSTFSEVM-----RVAEVDP-KTDFSSYGLDSVGAMQFATRLQKR-L-K-QEIEPQWLIDHPTIDSFSAFLKK--
Psy_3       -TVVRTTLMQLL-----ELPTVDD-DEAFQNYGLDSISATIFSNRLEQV-L-G-QPVLPHWLIDYPTVSALAQQLE---
Cal_3       -EIVYRALLDVL-----KIDGIDE-HESFANYGLDSISAMVFSTRLEKR-L-D-MEIPPHWLIDFPTIQTLSEQIQQ--
Tst_5       -ARVRELWRQVL---GVAPAHL---DQGFFEAGGDSLSVVLLARAIEQA-F-D-CAFAPANLFRFATVREIAGHL----
Bat_3       --RVRRIWQSVL-----ITNNLGS-DEGFFDAGGDSMSAVIVAARIKAD-F-D-CQFDATDMFRFGTIRRIAEHLAD--
Myx_5       -ATLVELWKNVL-----QVNEVGV-EDRFFEVGGDSVLAAVLVEEMNRR-F-D-TRLAVTDLFKYVNIRDMARHME---
Cal_30      -TIVLELWRTVL-----QIDNIAL-DDAFFEVGGDSLNAVILAEKIQER-L-G-CDFTAALLLQYPKVAAVADYIAD--
Cal_5       -QAVLEIWKSVL-----SIDAIST-TDGFFEVGGDSLRAVLLAERIGKR-F-G-VSFTTTEVFRHASVQAMAQKIAS--
Psy_5       -RKILAIWQDLL-----KIEKLST-TDGFFEVGGSSVLAVVLADRICQA-F-D-VAFTAPELFKYSSVQAIAAHL----
Onn_6       -ESLLEIWQDIL-----KIDNISP-TDGFFALGGNSVLAVRLAERIAQT-L-G-MPFNPTALFKHASIREIGHYYRS--
Nsp_6       -AILADIWKNVL-----NVTDISI-NDGFFAAGGDSVLSVILADRIARR-F-N-QEFPVTSLFKYSTIRDIAAYLGD--
Tai_6       -GEVLALWRETL-----KVGDIGP-TDGFFDAGGDSILAVALAARIEQR-F-G-VTFSATTLFKYACVRDIAGYIAS--
Bae_2       -QAVLAIWQDVL-----KSKDIEL-DDRFFDAGGDSLLAVTVTDRMTQE-L-D-CEFSVTELFEYATVKDISRYITE--
Bae_13      -AKVTAIWEDLL-----NTAGIKI-EDGFFDVGGDSLLAVAAAERIKQE-L-E-CDFTVTDLFEHSTIQAISRFIVE--
Nsp_11      -KIIAEVWQKAL-----QVQKVGI-CDNFFELGGHSLLLVQINQQLQAV-L-S-SELSILDMFKYPTIQTLSQYLSG--
Alb_5       -QAVAEIWQRVL-----KRTQVGV-HDNFFELGGHSVLAIQLVSGLRKA-L-A-IEVPVTLVFEAPILGALARQI----
Alb_7       -ITLAKLWSELLTPAQAAPLRVSL-NDNFFNLGGHSLLATQLFSRIRQS-F-D-IEVRVNTLFESPVLEDFARVVNE--
Alb_4       -QRLAALFAEVL-----RVEQVGI-HDNFFALGGHSLSASQLISRIARD-M-A-IDLPLAMLFELPTVAQLSESLAS--
Alb_6       -QRLAALFAEVL-----RVEQVGI-HDNFFALGGHSLSASQLISRIRQS-F-H-VDLPLSRIFEAPTIEGLVRQ-----
Rhi_13      -DYLLAQLQALG---AKQIGKKQR-HRNLMELGLESLQLVNLTSRLESA-A-A-IELEPTIFFEYPSVAELATFLWQ--
Nsp_8       -RYLIDKINITA---QISIAETEV-NTNLMQLGLGSTELVAIAASIEQD-T-D-LELNATLFFEYPSLMEVVNFFV---
Ena_1       -EVVSESVRRIM---RVP-DSFAA-DCPLRELGLDSMGLMELRLLLGAA-F-S-IEFDPAAFFSYPTARAIAGHIDA--
Myx_1       -YYLRQVVARIV---ECDAAAVRL-DLPLMELGVDSVGLMELAEHIGRR-F-E-LKLEETFFFEHNTLDRIGAFLA---
Rhi_1       -DAVRQGVNRCL--GQSEDSRLSS-RHSLMELGLDSADLLALGEQLGPM-F-G-LTLEPTFFFRHNSIDKIVAALKE--
Bas_1       -AFVLDCIGSFL--NEERKDVLAYVDRPLMELGLDSGDLLELNDQLGTR-F-R-IELETTFFFTYNTARKIISYLIE--
Bat_1       -IRSRLQLDNDV--------PLDL-DQPLMEMGLDSADLLELATSISGE-F-N-VTLTAMFFFENNTCNKVIVAVG---
Nsp_1       --TVQSCLGDEK-------RSGYKF-DRPLMEMGLNSVDLLILSEQISDR-F-G-LILDPAFFFSYTTPEKVLMFLIE--
Psy_1       SPHLERLVRSLL-----LDETAFAW-DRPLMEMGLDSADLLQLGERVASA-F-G-VSPDPAFFFTHNTCKKILATL----
Tst_7_b     -DALLAIVAERC---GNSARAVAA-DSSVQRLGLASLDIIALAAMLSDA-L-S-INVRPTLFYECADLRALAEQLA---
Chi_5_b     -QWVRGQLAGLV---KVPEAELDA-STPIEELGIDPTVLTSLRHHIEAS-F-E-VALDPAQLFEHRTLERLCGWLDE--
Bae_17      -SYVLGKLAKTM---DEPAPSLRS-DANIMELGLDSVSLIGLTKEIGQE-A-D-IDVNPTLFFEYPTAEELTRHFAS--
Lnm_4       -PWLAPLFSELL---AIPEDALDP-TALLGDLGVESVLLGEILLRLEEL-T-G-LSLDPATLLDHPTLELLGRHLAD--
Kir_2       -DWLADVVARTT---RTERSLLRP-DTHLVDLGVDSLLMAELVRDLEAA-L-G-DVVDPSLLQDHPTLARLAAALTA--
Kir_12      -RRLTEVFATTL---RLDAAQIRP-DADFADLGVDSIMIVQLLAALERD-L-G-VVAEPSALLENPTIARLAAAL----
Chi_13      -DGLRGVFSAEL---RIPVAKLGS-DTPFEDFGVDSVILAGLVQRIETW-L-GGVALEPTVLLQHRTLDDLARHLRK--
Tai_9       -AWLASTFAREL---ALPSGTLDP-AKPFREYGVDSIMLTQLLRPLNRL-A-D-APLDPSLLFEYGDVAQLADWLVA--
Mln_11      -SELSAVFAEEL---SIPLEKLNP-NTDFQEYGVDSILLVSIIHRIEAM-I-Q-KKIDPTVLLEHNTIHGLAEYIGK--
Chi_5_a     ---LRELFAREL---KLAEHELHD-NTRFEELGVDSVLLIGLIAKVEKR-V-G-SKIDPSLFFEYPTLARLAAQLG---
Chi_17      -AFLRGIVSQAT---GIAEVRLDP-ETSFTDFGIDSILLLDLVKKAERH-I-G-ASLDPSVFLEHPTLARLSAYLGE--
Mln_8       -RKLMEIFSAEL---KIPCGNLDQ-DTSFADYGVDSILLVQLVKKAEDA-F-Q-IKIEPSAFLEYPSFSQLGVYLNE--
Ela_7       -TWLMTLLAAEL---RMDVGRLRR-DKEFQIYGVDSIILAQLVSKIDRQ-F-ETIHLDPSVFLEYPTIAGMGAYLLD--
Dif_10      -SWLRSLLAKEL---SIDETHMDI-DVPFQEYGMDSIFLAQVLTKIDQK-LPS-VSIDPTVLLEHPTIEQLADYLAA--
Bas_5       -AWLLALFSKEF---MLDASQLDA-DSLFQEYGMDSILLAQIITKMDRE-L-KVVALDPSILLEYPTIGRLAAYLIE--
Bae_4       -EWLKELFSEEL---RIDQDQLET-DVLFQDYGVDSIILAQLLQRINRN-L-S-ASLDPSILYEYPTIQSFANWLLE--
Bae_8       -AWLVKLFSDEL---KIAPEELET-DEPFQDYGVDSIILAQLLQQMNQA-L-K-EDLDPSVLYEHPTIDAFAEWLVS--
Dif_5       -EWLTGICCREL---RLEPSRFES-DTPFQDYGADSIMLAQVSRAIGKR-I-K-ADLDPAVLYEYPTVAALAGWLET--
Bat_8       -LWVTQLVSQAL---HMDASRIEM-DTPLPDYGVDSIMLAQLLRLVSER-V-G-QPIDPSILFEHQTIEGFAKWLTD--
Sor_22      -AWLVDIVAREL---RLDPRRIDV-QTPLPDYGVDSVMLVQLVRPIAER-V-G-APIDPSVLFEHPTIEAFSGWLLG--
Alb_2       --QLKQLLARTL---KLDITQIDT-SKTLESYGVDSIVIIELANALRER-Y---PSLDASQLMETLSIDRLV-------
Tst_8       -AFVQRLVADTL---KLDADELTP-DEHFQALGLDSILVVQLTKQLRGY-F---DDVTSPLLFRVSTVRALTEHLLR--
Nsp_9       -TYFKQLIGEVL---MMDGNRIDS-SEPLAVYGVDSIIIAQLTNALNKN-F---EGVKAGLLFEASTIDALVNHFAE--
Mgs_6       -DHFRTLVADTL---QLPVADIRA-DVPFDRYGIDSILVVQLTEAVRKG-L---CNVGSTLFFEVRTVDGLVQHFLR--
Nsp_2       -QFFQQLVAKIL---RMNPEQIEA-DEPFQSYGIDSILVVQIAGALQEK-F-G--GIHSTLLFEVQTLGELVNYFVE--
Rhi_7       -DYLRKLVASTL---KIPADKMSL-SRPLEDYGLDSILVVRLTNAFNEQ-F---EAIDSALFFEMPTLAALTEYFIQ--
Sor_4       -AALRRLVSETL---MTPLDKIHA-HEPLERYGIDSILVVKMTNALTRF-L---PGMSSTLFFEHGTIAQLAEHLVR--
Tai_16      -AWLRARIGAAL---DIRADDIDS-RETLERYGIDSITVLQLTKRLRDA-F---DDVPNTLLFEYNTVDALVDH-----
Cal_27      -AWFRQLLSSVL---KIPVERILG-DEPFENYGIDSIIVVKLSTGLEEV-F-G--PISKTIFFEYGNLKEITAYFLE--
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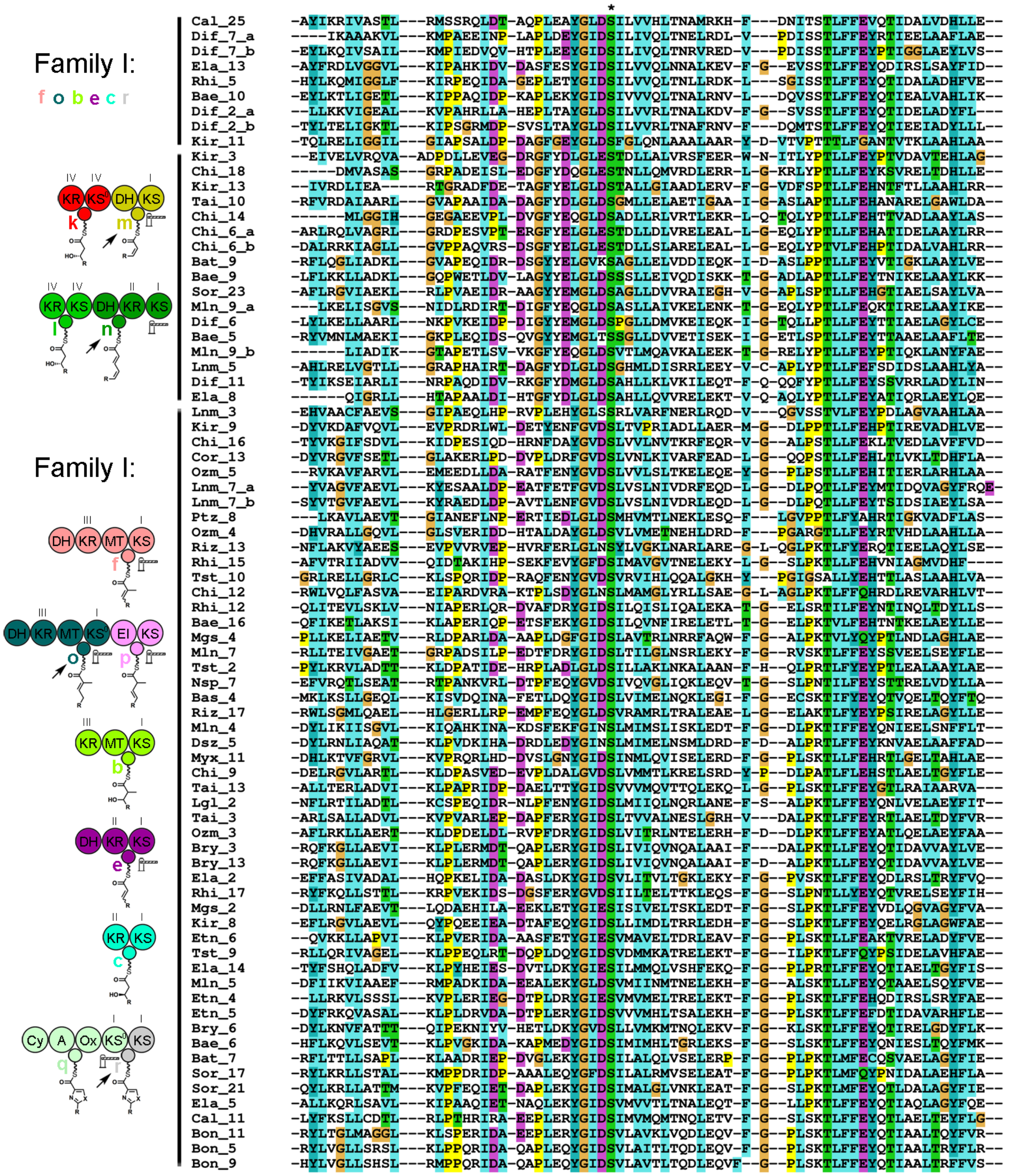

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Cal_25     -AYIKRIVASTL---RMSSRQLDT-AQPLEAYGLDSILVVHLTNAMRKH-F---DNITSTLFFEVQTIDALVDHLLE--
Dif_7_a    ----IKAAAKVL---KMPAEEINP-LAPLDEYGIDSILIVQLTNELRDL-V---PDISSTLFFEYRTIEELAAFLAE--
Dif_7_b    -EYLKQIVSAIL---KMPIEDVQV-HTPLEEYGIDSILIVQLTNRVRED-V---PDISSTLFFEYPTIGGLAEYLVS--
Ela_13     -AYFRDLVGGVL---KIPAHKIDV-DASFESYGIDSILVVQLNNALKEV-F-G--EVSSTLFFEYQDIRSLSAYFID--
Rhi_5      -HYLKQMIGGLF---KIRPEQIDA-GEPLETYGIDSILVVQLTNLLRDK-L---SGISSTLFFEYQTIDALADHFVE--
Bae_10     -EYLKTLIGETL---KIPPAQIDP-KAPLEKYGIDSIVVVQLTNALRNV-L---DQVSSTLFFEYQTIEALVAHLIK--
Dif_2_a    --LLKKVIGEAL---KVPAHRLLA-HEPLTAYGLDSILVVRLTNALKDV-F-G--SVSSTLFFEYQTIDELADYFL---
Dif_2_b    -TYLTELIGKTL---KIPSGRMDP-SVSLTAYGLDSILVVRLTNAFRNV-F---DQMTSTLFFEYQTIEEIADYLLL--
Kir_11     -TQLRELIGGIL---GIAPSALDP-DAGFGEYGLDSFGLQNLAAALAAR-Y-D-VTVPTTTLFGANTVTKLAAHLAA--
Kir_3      --EIVELVRQVA--ADPDLLEVEG-DRGFYDLGLESTDLLALVRSFEER-W-N-ITLYPTLLFEYPTVDAVTEHLAG--
Chi_18     -----DMVASAS---GRPADEISL-EDGFYDQGLESTNLLQMVRDLERR-L-G-KRLYPTLLFEYKSVRELTDHLLE--
Kir_13     --IVRDLIEA-----RTGRADFDE-TAGFYELGLDSTALLGIAADLERV-F-G-VDFSPTLLFEHNTFTLLAAHLRR--
Tai_10     -RFVRDAIAARL---GVAPAAIDA-DAGFYDLGLDSGMLLELAETIGAA-I-G-ASLAPTLLFEHANARELGAWLDA--
Chi_14     ------MLGGIH---GEGAEEVPL-DVGFYEQGLDSADLLRLVRTLEKR-L-Q-TQLYPTLLFEHTTVADLAAYLAS--
Chi_6_a    -ARLRQLVAGRL---GRDPESVPT-ERGFYELGLESTDLLDLVRELEAL-L-G-EQLYPTLLFEHATIDELAAYLRR--
Chi_6_b    -DALRRKIAGLL---GVPPAQVRS-DSGFYELGLESTDLLSLARELEAL-L-G-EQLYPTVLFEHPTIDALVAHLRR--
Bat_9      -RFLQGLIADKL---GVAPEQIDR-DSGYYELGVKSAGLLELVDDIEQK-I-D-ASLPPTLLFEYVTIGKLAAYLVE--
Bae_9      -LFLKKLLADKL---GQPWETLDV-LAGYYELGLDSSSLLEIVQDISKK-T-G-ADLAPTLLFEYTNIKELAAYLKK--
Sor_23     -AFLRGVIAEKL---RLPVAEIDR-AAGYYEMGLDSAGLLDVVRAIEGH-V-G-APLSPTLLFEHGTIAELSAYLVA--
Mln_9_a    ---LKELISGVS---NIDLRDIRT-DIGFYEQGLDSASLLAIVKELENK-T-G-EQLYPTLLFEQKTIRELAAYIKE--
Dif_6      -LYLKELLAARL---NKPVKEIDP-DIGYYEMGLDSPGLLDMVKEIEQK-I-G-TQLLPTLLFEYTTIAELAGYLCE--
Bae_5      -RYVMNLMAEKI---GKPLEQIDS-QVGYYEMGLTSSGLLDVVETISEK-I-G-ETLSPTLLFEYTTAAELAAFLTE--
Mln_9_b    ------LIADIK---GTAPETLSV-VKGFYEQGLDSVTLMQAVKALEEK-T-G-RELYPTLLFEYPTIQKLANYFAE--
Lnm_5      -AHLRELVGTLL---GRAPHAIRT-DAGFYDLGLDSGHMLDISRRLEEY-V-C-APLYPTLLFEFSDIDSLAAHLYA--
Dif_11     -TYIKSEIARLI---NRPAQDIDV-RKGFYDMGLDSAHLLKLVKILEQT-F-Q-QQFYPTLLFEYSSVRRLADYLIN--
Ela_8      ------QIGRLL---HTAPAALDI-HTGFYDLGLDSAHLLQVVRELEKT-V-Q-AQLYPTLLFEYATIQRLAEYLQE--
Lnm_3      -EHVAACFAEVS---GIPAEQLHP-RVPLEHYGLSSRLVARFNERLRQD-V---QGVSSTVLFEYPDLAGVAAHLAA--
Kir_9      -DYVKDAFVQVL---EVPRDRLWL-DETYENFGVDSLTVPRIADLLAER-M-G--DLPPTLLFEHPTIREVADHLVE--
Chi_16     -TYVKGIFSDVL---KIDPESIQD-HRNFDAYGVDSLVVLNVTKRFEQR-V-G--ALPSTLLFEKLTVEDLAVFFVD--
Cor_13     -DYVRGVFSETL---GLAKERLPD-DVPLDRFGVDSLVNLKIVARFEAD-L-G--QQPSTLLFEHLTLVKLTDHFLA--
Ozm_5      --RVKAVFARVL---EMEEDLLDA-RATFENYGVDSLVVLSLTKELEQE-Y-G--PLPSTLLFEHITIERLARHLAA--
Lnm_7_a    --YVAGVFAEVL---KYESAALDP-EATFETFGVDSLVSLNIVDRFEQD-L-G--DLPQTLLFEYMTIDQVAGYFRQE-
Lnm_7_b    -SYVTGVFAEVL---KYRAEDLDP-AVTLENFGVDSLVSLNIVDRLEQD-L-G--DLPQTLLFEYTSIDSIAEYLSA--
Ptz_8      ---LKAVLAEVT---GIANEFLNP-ERTIEDLGLDSMHVMTLNEKLESQ-F---LGVPPTLFYAHRTIGKVADFLAS--
Ozm_4      -DHVRALLGQVL---GLSVERIDD-HTALDAYGLDSVLVMETNEHLDRD-F---PGARGTLLFEYRTVHDLAAHLLA--
Riz_13     -NFLAKVYAEES---EVPVVRVEP-HVRFERLGLNSYLVGKLNARLARE-G-L-QGLPKTLFYERQTIEELAQYLSE--
Rhi_15     -AFVTRIIADVV---QIDTAKIHP-SEKFEVYGFDSIMAVGVTNELEKY-L-G--SLPKTLLFEHVNIAGMVDHF----
Tst_10     -GRLRELLGRLC---KLSPQRIDP-RAQFENYGVDSVRVIHLQQALGKH-Y---PGIGSALLYEHTTLASLAAHLVA--
Chi_12     -RWLVQLFASVA---EIPARDVRA-KTPLSDYGLNSLMAMGLYRLLSAE-G-L-AGLPKTLFFQHRDLREVARHLVT--
Rhi_12     -QLITEVLSKLV---NIAPERLQR-DVAFDRYGIDSILQISLIQALEKA-T-G--ELSRTILFEYNTINQLTDYLLS--
Bae_16     -QFIKETLAKSI---KLAPERIQP-ETSFEKYGIDSILQVNFIRELETL-T-G--ELPKTVLFEHTNTKELAEYLLE--
Mgs_4      -PLLKELIAETV---RLDPARLDA-AAPLDGFGIDSLAVTRLNRRFAQW-F-G--ALPKTVLYQYPTLNDLAGHLAE--
Mln_7      -RLLTEIVGAET---GRPADSILP-EDTFDRYGIDSLTILGLNSRLEKY-F-G--RVSKTLFFEYSSVEELSEYFLE--
Tst_2      -PYLKRVLADTT---KLDPATIDE-HRPLADLGLDSILLAKLNKALAAN-F-H--QLPRTLFYEYPTLEALAAYLAE--
Nsp_7      -EFVRQTLSEAT---RTPANKVRL-DTPFEQYGVDSIVQVGLIQKLEQV-T-G--SLPNTILFEYSTTRELVDYLLA--
Bas_4      -MKLKSLLGEQL---KISVDQINA-FETLDQYGIDSLVIMELNQKLEGI-F-G--ECSKTIFYEYQTVQELTQYFTQ--
Riz_17     -RWLSGMLQAEL---HLGERLLRP-EMPFEQYGLDSVRAMRLTRALEAE-L-G--ELAKTLFYEYPSIRELAGYLLE--
Mln_4      -DYLIKIISGVL---KIQAHKINA-KDSFEKFGINSLMIMSLISKLEDT-F-G--DLPKTIFFEYQNIEELSNFFLT--
Dsz_5      -DYLRNLIAQAT---KLPVDKIHA-DRDLEDYGINSLMIMELNSMLDRD-F-D--ALPRTLFFEYKNVAELAAFFAD--
Myx_11     -DHLKTVFGRVL---KVPRQRLHD-DVSLGNYGIDSINMLQVISELERD-F-G--PLSKTLLFEHRTLGELTAHLAE--
Chi_9      -DELRGVLARTL---KLDPASVED-EVPLDALGVDSLVMMTLKRELSRD-Y-P--DLPATLFLEHSTLAELTGYFLE--
Tai_13     -ALLTERLADVI---KLPAPRIDP-DAELTTYGIDSVVVMQVTTQLEKQ-L-G--PLSKTLFFEYGTLRAIAARVA---
Lgl_2      -NFLRTILADTL---KCSPEQIDR-NLPFENYGIDSLMIIQLNQRLANE-F-S--ALPKTLFFEYQNLVELAEYFIT--
Tai_3      -ARLSALLADVL---KVPVARLEP-DAPFERYGIDSLTVVALNESLGRH-V---DALPKTLFFEYRTLAELTDYFVR--
Ozm_3      -AFLRKLLAERT---KLDPDELDL-RVPFDRYGIDSLVITRLNTELERH-F-D--DLPKTLFFEYATLQELAEYFAA--
Bry_3      -RQFKGLLAEVI---KLPLERMDT-QAPLERYGIDSLIVIQVNQALAAI-F---DALPKTLLFEYQTIDAVVAYLVE--
Bry_13     -RQFKGLLAEVI---KLPLERMDT-QAPLERYGIDSLIVIQVNQALAAI-F-D--ALPKTLLFEYQTIDAVVAYLVE--
Ela_2      -EFFASIVADAL---HQPKELIDA-DASLDKYGIDSVLITVLTGKLEKY-F-G--PVSKTLFFEYQDLRSLTRYFVQ--
Rhi_17     -RYFKQLLSTTL---KRPVEKIDS-DGSFERYGVDSIILTELTTKLEQS-F-G--SLPNTLLYEYQTVRELSEYFIH--
Mgs_2      -DLLRNLFAEVT---LQDAEHILA-EEKLETYGIESISIVELTSKLEDT-F-G--SLPKTLFFEYVDLQGVAGYFVA--
Kir_8      -EFLRGVLAEVL---QYPQEEIEA-DTAFEQYGIDSLLIMDLTRRLEDH-F-G--SLPKTLFFEYQELRGLAGWFAE--
Etn_6      --QVKKLLAPVI---KLPVERIDA-AASFETYGIESVMAVELTDRLEAV-F-G--PLSKTLLFEAKTVRELADYFVE--
Tst_9      -RLLQRIVAGEL---KLPPEQLRT-DQPLDQYGIDSVDMMKATRELEKT-F-G--ILPKTLFFQYPSIDELAVHFAE--
Ela_14     -TYFSHQLADFV---KLPYHEIES-DVTLDKYGIESILMMQLVSHFEKQ-F-G--PLPRTLFFEYQTIAELTGYFIS--
Mln_5      -DFIIKVIAAEF---RMPADKIDA-EEALEKYGLDSVMIINMTNELEKH-F-G--ALSKTLLFEYQTAAELSQYFVE--
Etn_4      --LLRKVLSSSL---KVPLERIEG-DTPLDRYGIESVMVMELTRELEKT-F-G--PLSKTLFFEHQDIRSLSRYFAE--
Etn_5      -DYFRKQVASAL---KLPLDRVDA-DTPLERYGIDSVVVMHLTSALEKH-F-G--PLSKTLFFEFDTIDAVARHFLE--
Bry_6      -DYLKNVFATTT---QIPEKNIYV-HETLDKYGVDSLLVMKMTNQLEKV-F-G--KLSKTLFFEYQTIRELGDYFLK--
Bae_6      -HFLKQVLSEVT---KLPVGKIDA-KAPMEDYGIDSIMIMHLTGRLEKS-F-G--SLSKTLFFEYQNIESLTQYFMK--
Bat_7      -RFLTTLLSAPL---KLAADRIEP-DVGLEKYGIDSILALQLVSELERP-F-G--PLPKTLMFECQSVAELAGYFIE--
Sor_17     -RYLKRLLSTAL---KMPPDRIDP-AAALEQYGFDSILALRMVSELEAT-F-G--PLPKTLMFQYPNIDALAEHFLA--
Sor_21     -QYLKRLLATTM---KVPFEQIET-DAPLEKYGIDSIMALGLVNKLEAT-F-G--SLPKTLMFEYQTLDALAGYFIE--
Ela_5      -ALLKQRLSAVL---KIPAAQIET-NAQLEKYGIDSVMVVTLTNALEQT-F-G--LLPKTLFFEYQTIAQLAGYFQE--
Cal_11     -LYFKSLLCDTL---RLPTHRIRA-EEPLERYGIDSIMVMQMTNQLETV-F-G--SLSKTLFFEYQTLAELTEYFLG--
Bon_11     -RYLTGLMAGGL---KLSPERIDA-EEPLERYGIDSVLAVKLVQDLEQV-F-G--PLSKTLFFEYQTIAALTQYFVR--
Bon_5      -RYLVGLLSRSL---KLPPQRIDA-QAPLEQYGIDSVLAITLTQDLEQV-F-G--PLSKTLFFEYQTIAALTRYFLR--
Bon_9      -HYLVGLLSHSL---RMPPQRIDA-QAPLEQYGIDSVLAVTLTQDLEQVF--G--PLSKTLFFEYQTIAALTRFFVS--
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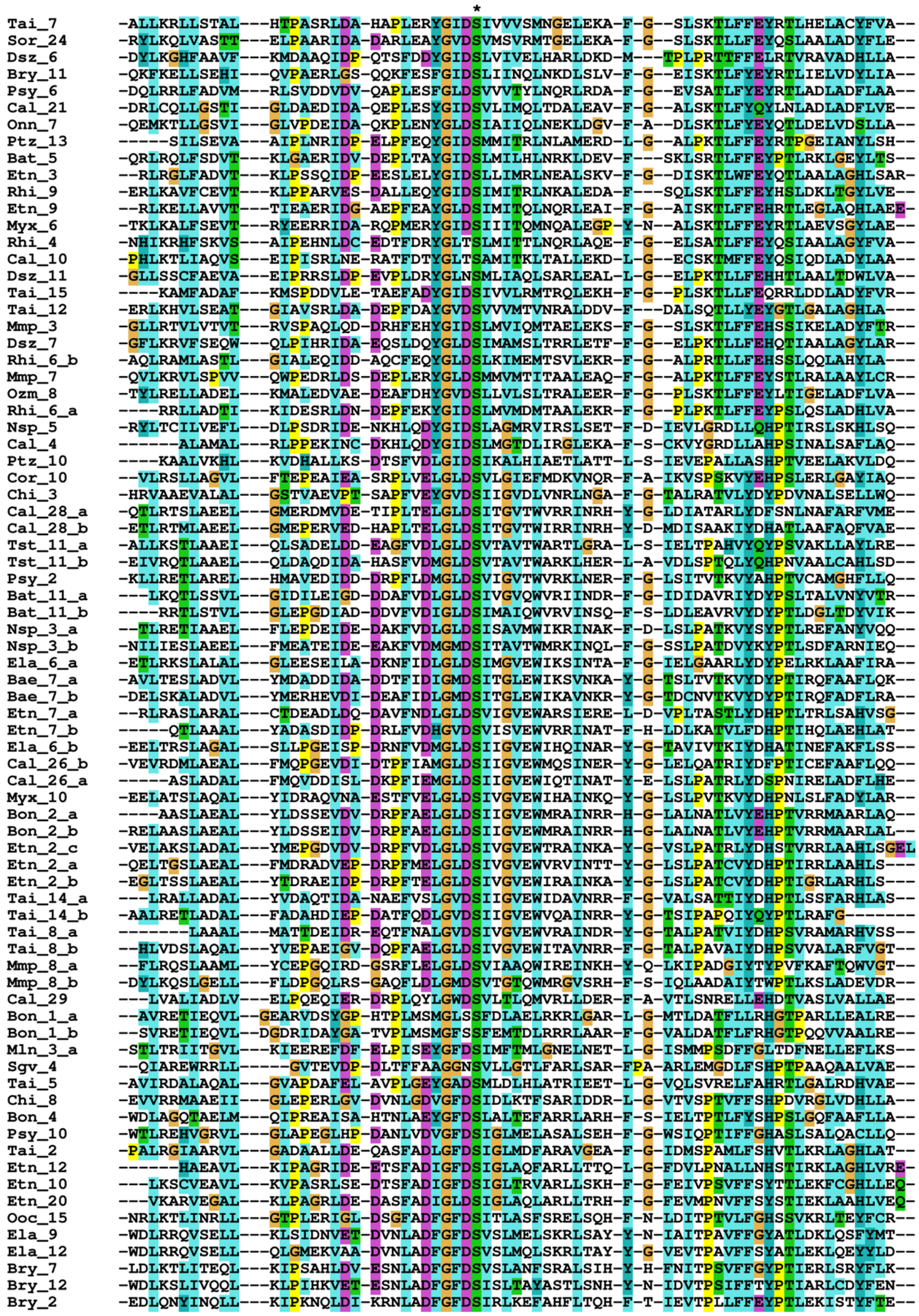
Family I:

f o b e c r



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Tai_7     -ALLKRLLSTAL---HTPASRLDA-HAPLERYGIDSIVVVSMNGELEKA-F-G--SLSKTLFFEYRTLHELACYFVA--
Sor_24    -RYLKQLVASTT---ELPAARIDA-DARLEAYGVDSVMSVRMTGELEKA-F-G--SLSKTLLFEYQSLAALADYFLE--
Dsz_6     -DYLKGHFAAVF---KMDAAQIDP-QTSFDDYGIDSLVIVELHARLDKD-M---TPLPRTTFFELRTVRAVADHLLA--
Bry_11    -QKFKELLSEHI---QVPAERLGS-QQKFESFGIDSLIINQLNKDLSLV-F-G--EISKTLFYEYRTLIELVDYLIA--
Psy_6     -DQLRRLFADVM---RLSVDDVDV-QAPLESFGLDSVVVTYLNQRLRDA-F-G--EVSATLFYEYRTLADLADFLAA--
Cal_21    -DRLCQLLGSTI---GLDAEDIDA-QEPLESYGIDSVLIMQLTDALEAV-F-G--ALSKTLFYQYLNLADLADFLVE--
Onn_7     -QEMKTLLGSVI---GLVPDEIDA-QKPLENYGLDSIAIIQLNEKLDGV-F-A--DLSKTLFYEYQTLDELVDSLLA--
Ptz_13    -----SILSEVA---AIPLNRIDP-ELPFEQYGIDSMMITRLNLAMERD-L-G--ALPKTLFFEYRTPGEIANYLSH--
Bat_5     -QRLRQLFSDVT---KLGAERIDV-DEPLTAYGIDSLMILHLNRKLDEV-F---SKLSRTLFFEYPTLRKLGEYLTS--
Etn_3     --RLRGLFADVT---KLPSSQIDP-EESLELYGIDSLLIMRLNEALSKV-F-G--DISKTLWFEYQTLAALAGHLSAR-
Rhi_9     -ERLKAVFCEVT---KLPPARVES-DALLEQYGIDSIMITRLNKALEDA-F---SQLSKTLFFEYHSLDKLTGYLVE--
Etn_9     --RLKELLAVVT---TIEAERIDG-AEPFEAYGLDSIMITQLNQRLEAI-F-G--AISKTLFFEHRTLEGLAQHLAEE-
Myx_6     -TKLKALFSEVT---RYEERRIDA-RQPMERYGIDSIIITQMNQALEGP-Y-N--ALSKTLFFEYRTLAEVSGYLAE--
Rhi_4     -NHIKRHFSKVS---AIPEHNLDC-EDTFDRYGLTSLMITTLNQRLAQE-F-G--ELSATLFFEYQSIAALAGYFVA--
Cal_10    -PHLKTLIAQVS---EIPISRLNE-RATFDTYGLTSAMITKLTALLEKD-L-G--ECSKTMFFEYQSIQDLADYLAA--
Dsz_11    -GLLSSCFAEVA---EIPRRSLDP-EVPLDRYGLNSMLIAQLSARLEAL-L-G--ELPKTLLFEHHTLAALTDWLVA--
Tai_15    ----KAMFADAF---KMSPDDVLE-TAEFADYGIDSIVVLRMTRQLEKH-F-G--PLSKTLLFEQRRLDDLADYFVR--
Tai_12    -ERLKHVLSEAT---GIAVSRLDA-DEPFDAYGVDSVVVMTVNRALDDV-F---DALSQTLLYEYGTLGALAGHLA---
Mmp_3     -GLLRTVLVTVT---RVSPAQLQD-DRHFEHYGIDSLMVIQMTAELEKS-F-G--SLSKTLFFEHSSIKELADYFTR--
Dsz_7     -GFLKRVFSEQW---QLPIHRIDA-EQSLDQYGLDSIMAMSLTRRLETF-F-G--ELPKTLLFEHQTIAALAGYLAR--
Rhi_6_b   -AQLRAMLASTL---GIALEQIDD-AQCFEQYGLDSLKIMEMTSVLEKR-F-G--ALPRTLLFEHSSLQQLAHYLA---
Mmp_7     -QVLKRVLSPVV---QWPEDRLDS-DEPLERYGLDSMMVMTITAALEAQ-F-G--ALPKTLFFEYSTLRALAAYLCR--
Ozm_8     -TYLRELLADEL---KMALEDVAE-DEAFDHYGVDSLLVLSLTRALEER-F-G--PLSKTLFFEYLTIGELADFLVA--
Rhi_6_a   ----RRLLADTI---KIDESRLDN-DEPFEKYGIDSLMVMDMTAALEKR-F-G--PLPKTLFFEYPSLQSLADHLVA--
Nsp_5     -RYLTCILVEFL---DLPSDRIDE-NKHLQDYGIDSLAGMRVIRSLSET-F-D-IEVLGRDLLQHPTIRSLSKHLSQ--
Cal_4     ------ALAMAL---RLPPEKINC-DKHLQDYGIDSLMGTDLIRGLEKA-F-S-CKVYGRDLLAHPSINALSAFLAQ--
Ptz_10    ----KAALVKHL---KVDHALLKS-DTSFVDLGIDSIKALHIAETLATT-L-S-IEVEPALLASHPTVEELAKVLDQ--
Cor_10    --VLRSLLAGVL---FTEPEAIEA-SRPLVELGLDSVLGIEFMDKVNQR-F-A-IKVSPSKVYEHPSLERLGAYIAQ--
Chi_3     -HRVAAEVALAL---GSTVAEVPT-SAPFVEYGVDSIIGVDLVNRLNGA-F-G-TALRATVLYDYPDVNALSELLWQ--
Cal_28_a  -QTLRTSLAEEL---GMERDMVDE-TIPLTELGLDSITGVTWVRRINRH-Y-G-LDIATARLYDFSNLNAFARFVME--
Cal_28_b  -ETLRTMLAEEL---GMEPERVED-HAPLTELGLDSITGVTWIRRINRH-Y-D-MDISAAKIYDHATLAAFAQFVAE--
Tst_11_a  -ALLKSTLAAEI---QLSADELDD-EAGFVDLGLDSVTAVTWARTLGRA-L-S-IELTPAHVYQYPSVAKLLAYLRE--
Tst_11_b  -EIVRQTLAAEL---QLDAQDIDA-HASFVDMGLDSVTAVTWARKLHER-L-A-VDLSPTQLYQHPNVAALCAHLSD--
Psy_2     -KLLRETLAREL---HMAVEDIDD-DRPFLDMGLDSVIGVTWVRKLNER-F-G-LSITVTKVYAHPTVCAMGHFLLQ--
Bat_11_a  ---LKQTLSSVL---GIDILEIGD-DDAFVDLGLDSIVGVQWVRIINDR-F-G-IDIDAVRIYDYPSLTALVNYVTR--
Bat_11_b  ----RRTLSTVL---GLEPGDIAD-DDVFVDIGLDSIMAIQWVRVINSQ-F-S-LDLEAVRVYDYPTLDGLTDYVIK--
Nsp_3_a   --TLRETIAAEL---FLEPDEIDE-DAKFVDLGLDSISAVMWIKRINAK-F-D-LSLPATKVYSYPTLREFANYVQQ--
Nsp_3_b   -NILIESLAEEL---FMEATEIDE-EAKFVDMGMDSITAVTWMRKINQL-F-G-SSLPATDVYKYPTLSDFARNIEQ--
Ela_6_a   -ETLRKSLALAL---GLEESEILA-DKNFIDLGLDSIMGVEWIKSINTA-F-G-IELGAARLYDYPELRKLAAFIRA--
Bae_7_a   -AVLTESLADVL---YMDADDIDA-DDTFIDIGMDSITGLEWIKSVNKA-Y-G-TSLTVTKVYDYPTIRQFAAFLQK--
Bae_7_b   -DELSKALADVL---YMERHEVDI-DEAFIDLGMDSITGLEWIKAVNKR-Y-G-TDCNVTKVYDYPTIRQFADFLRA--
Etn_7_a   --RLRASLARAL---CTDEADLDQ-DAVFNDLGLDSVIGVEWARSIERE-L-D-VPLTASTLYDHPTLTRLSAHVSG--
Etn_7_b   -----QTLAAAL---YADASDIDP-DRLFVDHGVDSVISVEWVRRINAT-F-H-LDLKATVLFDHPTIHQLAEHLAT--
Ela_6_b   -EELTRSLAGAL---SLLPGEISP-DRNFVDMGLDSIIGVEWIHQINAR-Y-G-TAVIVTKIYDHATINEFAKFLSS--
Cal_26_b  -VEVRDMLAEAL---FMQPGEVDI-DTPFIAMGLDSIIGVEWMQSINER-Y-G-LELQATRIYDFPTICEFAAFLQQ--
Cal_26_a  -----ASLADAL---FMQVDDISL-DKPFIEMGLDSIIGVEWIQTINAT-Y-E-LSLPATRLYDSPNIRELADFLHE--
Myx_10    -EELATSLAQAL---YIDRAQVNA-ESTFVELGLDSIVGVEWIHAINKQ-Y-G-LSLPVTKVYDHPNLSLFADYLAR--
Bon_2_a   ----AASLAEAL---YLDSSEVDV-DRPFAELGLDSIIGVEWMRAINRR-H-G-LALNATLVYEHPTVRRMAARLAQ--
Bon_2_b   -RELAASLAEAL---YLDSSEIDV-DRPFAELGLDSIIGVEWMRAINRR-H-G-LALNATLVYEHPTVRRMAARLAL--
Etn_2_c   -VELAKSLADAL---YMEPGDVDV-DRPFVDLGLDSIVGVEWTRAINKA-Y-G-VSLPATRLYDHSTVRRLAAHLSGEL
Etn_2_a   -QELTGSLAEAL---FMDRADVEP-DRPFMELGLDSIVGVEWVRVINTT-Y-G-LSLPATCVYDHPTIRRLAAHLS---
Etn_2_b   -EGLTSSLAEAL---YTDRAEIDP-DRPFTELGLDSIVGVEWIRAINKA-Y-G-LSLPATCVYDHPTIGRLARHLS---
Tai_14_a  ---LRALLADAL---YVDAQTIDA-NAEFVSLGVDSIIGVEWIDAVNRR-F-G-VALSATTIYDHPTLSSFARHLAS--
Tai_14_b  -AALRETLADAL---FADAHDIEP-DATFQDLGVDSIIGVEWVQAINRR-Y-G-TSIPAPQIYQYPTLRAFG-------
Tai_8_a   -------LAAAL---MATTDEIDR-EQTFNALGVDSIVGVEWVRAINDR-Y-G-TALPATVIYDHPSVRAMARHVSS--
Tai_8_b   --HLVDSLAQAL---YVEPAEIGV-DQPFAELGLDSIVGVEWITAVNRR-F-G-TALPAVAIYDHPSVVALARFVGT--
Mmp_8_a   --FLRQSLAAML---YCEPGQIRD-GSRFLELGLDSVIAAQWIREINKH-Y-Q-LKIPADGIYTYPVFKAFTQWVGT--
Mmp_8_b   -DYLKQSLGELL---FLDPGQLRS-GAQFLDLGMDSVTGTQWMRGVSRH-F-S-IQLAADAIYTWPTLKSLADEVDR--
Cal_29    ---LVALIADLV---ELPQEQIER-DRPLQYLGWDSVLTLQMVRLLDER-F-A-VTLSNRELLEHDTVASLVALLAE--
Bon_1_a   --AVRETIEQVL--GEARVDSYGP-HTPLMSMGLSSFDLAELRKRLGAR-L-G-MTLDATFLLRHGTPARLLEALRE--
Bon_1_b   --SVRETIEQVL--DGDRIDAYGA-TVPLMSMGFSSFEMTDLRRRLAAR-F-G-VALDATFLFRHGTPQQVVAALRE--
Mln_3_a   -STLTRIITGVL---KIEEREFDF-ELPISEYGFDSIMFTMLGNELNET-L-G-ISMMPSDFFGLTDFNELLEFLKS--
Sgv_4     --QIAREWRRLL-----GVTEVDP-DLTFFAAGGNSVLLGTLFARLSAR-FPA-ARLEMGDLFSHPTPAAQAALVAE--
Tai_5     -AVIRDALAQAL---GVAPDAFEL-AVPLGEYGADSMLDLHLATRIEET-L-G-VQLSVRELFAHRTLGALRDHVAE--
Chi_8     -EVVRRMAAEII---GLEPERLGV-DVNLGDVGFDSIDLKTFSARIDDR-L-G-VTVSPTVFFSHPDVRGLVDHLLA--
Bon_4     -WDLAGQTAELM---QIPREAISA-HTNLAEYGFDSLALTEFARRLARH-F-S-IELTPTLFYSHPSLGQFAAFLLA--
Psy_10    -WTLREHVGRVL---GLAPEGLHP-DANLVDVGFDSIGLMELASALSEH-F-G-WSIQPTIFFGHASLSALQACLLQ--
Tai_2     -PALRGIAARVL---GADAALLDE-QASFADLGFDSIGLMDFARAVGEA-F-G-IDMSPAMLFSHVTLKRLAGHLAT--
Etn_12    ------HAEAVL---KIPAGRIDE-ETSFADIGFDSIGLAQFARLLTTQ-L-G-FDVLPNALLNHSTIRKLAGHLVRE-
Etn_10    ---LKSCVEAVL---KVPASRLSE-DTSFADIGFDSIGLTRVARLLSKH-F-G-FEIVPSVFFSYTTLEKFCGHLLEQ-
Etn_20    ---VKARVEGAL---KLPAGRLDE-DASFADIGLDSIGLAQLARLLTRH-F-G-FEVMPNVFFSYSTIEKLAAHLVEQ-
Ooc_15    -NRLKTLINRLL---GTPLERIGL-DSGFADFGFDSITLASFSRELSQH-F-N-LDITPTVLFGHSSVKRLTEYFCR--
Ela_9     -WDLRRQVSELL---KLSIDNVET-DVNLADFGFDSVSLMELSKRLSAY-Y-N-IAITPAVFFGYATLDKLQSFYMT--
Ela_12    -WDLRRQVSELL---QLGMEKVAA-DVNLADFGFDSVSLMQLSKRLTAY-Y-G-VEVTPAVFFSYATLEKLQEYYLD--
Bry_7     -LDLKTLITEQL---KIPSAHLDV-ESNLADFGFDSVSLANFSRALSIH-Y-H-FNITPSVFFGYPTIERLSRYFLK--
Bry_12    -WDLKSLIVQQL---KLPIHKVET-ESNLADFGFDSISLTAYASTLSNH-Y-N-IDVTPSIFFTYPTIARLCDYFEN--
Bry_2     -EDLQNYINQLL---KIPKNQLDI-KRNLADFGFDSIRLKEFAHFLTQH-F-T-IEVTPLLFFEYPTLEKISTYFTE--
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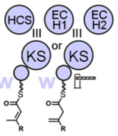

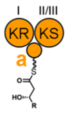

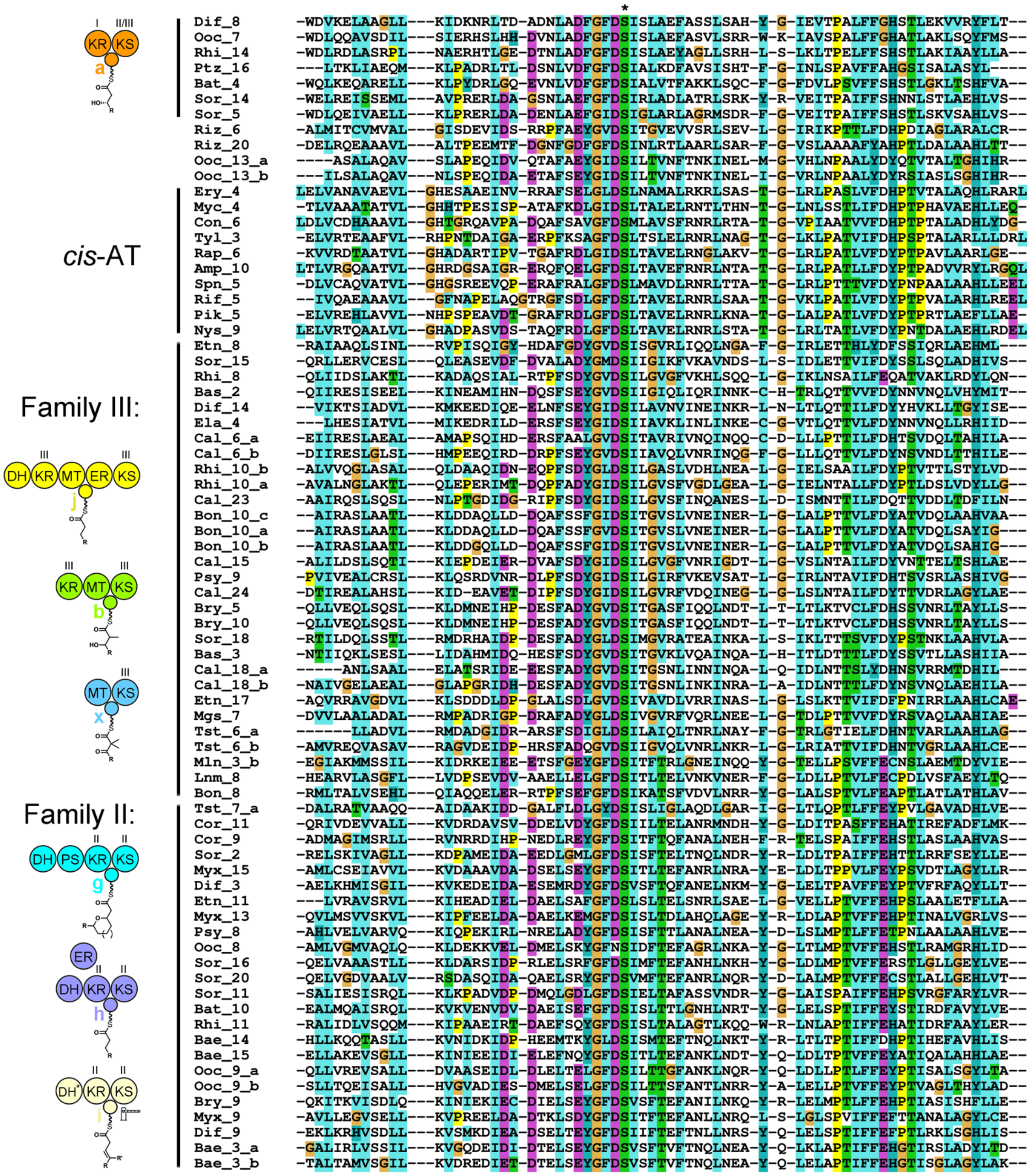

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Dif_8     -WDVKELAAGLL---KIDKNRLTD-ADNLADFGFDSISLAEFASSLSAH-Y-G-IEVTPALFFGHSTLEKVVRYFLT--
Ooc_7     -WDLQQAVSDIL---SIERHSLHH-DVNLADFGFDSISLAEFASVLSRR-W-K-IAVSPALFFGHATLAKLSQYFMS--
Rhi_14    -WDLRDLASRPL---NAERHTLGE-DTNLADFGFDSISLAEYAGLLSRH-L-S-LKLTPELFFSHSTLAKIAAYLLA--
Ptz_16    ---LTKLIAEQM---KLPADRLTL-DSNLVDFGFDSIALKDFAVSISHT-F-G-INLSPAVFFAHGSISALASYL----
Bat_4     -WQLKEQARELL---KLPYDRLGQ-EVNLVDFGFDSIALVTFAKKLSQC-F-G-FDVLPSVFFSHSTLGKLTSHFVA--
Sor_14    -WELREISSEML---AVPRERLDA-GSNLAEFGFDSIRLADLATRLSRK-Y-R-VEITPAIFFSHNNLSTLAEHLVS--
Sor_5     -WDLQEIVAELL---KLPRERLDA-DENLAEFGIDSIGLARLAGRMSDR-F-G-VEITPAIFFSHSTLSKVSAHLVS--
Riz_6     -ALMITCVMVAL---GISDEVIDS-RRPFAEYGVDSITGVEVVSRLSEV-L-G-IRIKPTTLFDHPDIAGLARALCR--
Riz_20    -DELRQEAAAVL---ALTPEEMTF-DGNFGDFGFDSINLRTLAARLSAR-F-G-VSLAAAAFYAHPTLDALAAHLTT--
Ooc_13_a  ----ASALAQAV---SLAPEQIDV-QTAFAEYGIDSILTVNFTNKINEL-M-G-VHLNPAALYDYQTVTALTGHIHR--
Ooc_13_b  ---ILSALAQAV---NLSPEQIDA-ETAFSEYGIDSILTVNFTNKINEL-I-G-VRLNPAALYDYRSIASLSGHIHR--
Ery_4     LELVANAVAEVL--GHESAAEINV-RRAFSELGLDSLNAMALRKRLSAS-T-G-LRLPASLVFDHPTVTALAQHLRARL
Myc_4     -TLVAAATATVL--GHHTPESISP-ATAFKDLGIDSLTALELRNTLTHN-T-G-LNLSSTLIFDHPTPHAVAEHLLEQ-
Con_6     LDLVCDHAAAVL--GHTGRQAVPA-DQAFSAVGFDSMLAVSFRNRLRTA-T-G-VPIAATVVFDHPTPTALADHLYDG-
Tyl_3     -ELVRTEAAFVL--RHPNTDAIGA-ERPFKSAGFDSLTSLELRNRLNAG-T-G-LKLPATVIFDHPSPTALARLLLDRL
Rap_6     -KVVRDTAATVL--GHADARTIPV-TGAFRDLGIDSLTAVELRNGLAKV-T-G-LRLPATLVFDYPTPAVLAARLGE--
Amp_10    LTLVRGQAATVL--GHRDGSAIGR-ERQFQELGFDSLTAVEFRNRLNTA-T-G-LRLPATLLFDYPTPADVVRYLRGQL
Spn_5     -DLVCAQVATVL--GHGSREEVQP-ERAFRALGFDSLMAVDLRNRLTTA-T-G-LRLPTTTVFDYPNPAALAAHLLEEL
Rif_5     --IVQAEAAAVL---GFNAPELAQGTRGFSDLGFDSLTAVELRNRLSAA-T-G-VKLPATLVFDYPTPVALARHLREEL
Pik_5     -ELVREHLAVVL--NHPSPEAVDT-GRAFRDLGFDSLTAVELRNRLKNA-T-G-LALPATLVFDYPTPRTLAEFLLAE-
Nys_9     LELVRTQAALVL--GHADPASVDS-TAQFRDLGFDSLTAVELRNRLSTA-T-G-LRLTATLVFDYPNTDALAEHLRDEL
Etn_8     -RAIAAQLSINL---RVPISQIGY-HDAFGDYGVDSISGVRLIQQLNGA-F-G-IRLETTHLYDFSSIQRLAEHML---
Sor_15    -QRLLERVCESL---QLEASEVDF-DVALADYGMDSIIGIKFVKAVNDS-L-S-IDLETTVIFDYSSLSQLADHIVS--
Rhi_8     -QLIIDSLAKTL---KADAQSIAL-RTPFSDYGVDSILGVGFVKHLSQQ-L-G-IKLNSAILFEQATVAKLRDYLQN--
Bas_2     -QIIRESISEEL---KINEAMIHN-DQSFSEYGVDSIIGIQLIQRINNK-C-H-TRLQTTVVFDYNNVNQLVHYMIT--
Dif_14    --VIKTSIADVL---KMKEEDIQE-ELNFSEYGIDSILAVNVINEINKR-L-N-LTLQTTILFDYYHVKLLTGYISE--
Ela_4     ---LHESIATVL---MIKEDRILD-ERSFSEYGIDSIIAVKLINLINKE-C-G-VTLQTTVLFDYNNVNQLLRHIID--
Cal_6_a   -EIIRESLAEAL---AMAPSQIHD-ERSFAALGVDSITAVRIVNQINQQ-C-D-LLLPTTILFDHTSVDQLTAHILA--
Cal_6_b   -DIIRESLGLSL---HMPEEQIRD-DRPFSEYGVDSIIAVQLVNRINQG-F-G-LLLQTTVLFDYNSVNDLTTHILE--
Rhi_10_b  -ALVVQGLASAL---QLDAAQIDN-EQPFSDYGLDSILGASLVDHLNEA-L-G-IELSAAILFDYPTVTTLSTYLVD--
Rhi_10_a  -AVALNGLAKTL---QLEPERIMT-DQPFADYGIDSILGVSFVGDLGEA-L-G-IELNTALLFDYPTLDSLVDYLLG--
Cal_23    -AAIRQSLSQSL---NLPTGDIDG-RIPFSDYGIDSILGVSFINQANES-L-D-ISMNTTILFDQTTVDDLTDFILN--
Bon_10_c  --AIRASLAATL---KLDDAQLLD-DQAFSSFGIDSITGVSLVNEINER-L-G-LALPTTVLFDYATVDQLAAHVAA--
Bon_10_a  --AIRASLAATL---KLDDAQLLD-DQAFSSFGVDSITGVSLVNEINER-L-G-LALPTTVLFDYATVDQLSAYIG---
Bon_10_b  --AIRASLAATL---KLDDGQLLD-DQAFSSFGIDSITGVSLVNEINER-L-G-LALPTTVLFDYATVDQLSAHIG---
Cal_15    -ALILDSLSQTI---KIEPDEIER-DVAFSDYGIDSILGVGFVNRIGDT-L-G-VSLNTAILFDYVNTTELTSHLAE--
Psy_9     -PVIVEALCRSL---KLQSRDVNR-DLPFSDYGIDSILGIRFVKEVSAT-L-G-IRLNTAVIFDHTSVSRLASHIVG--
Cal_24    -DTIREALAHSL---KID-EAVET-DIPFSDYGIDSILGVRFVDQINEG-L-G-LSLNTAILFDYTTVDRLAGYLAE--
Bry_5     -QLLVEQLSQSL---KLDMNEIHP-DESFADYGVDSITGASFIQQLNDT-L-T-LTLKTVCLFDHSSVNRLTAYLLS--
Bry_10    -QLLVEQLSQSL---KLDMNEIHP-DESFADYGVDSITGASFIQQLNDT-L-T-LTLKTVCLFDHSSVNRLTAYLLS--
Sor_18    -RTILDQLSSTL---RMDRHAIDP-DESFADYGLDSIMGVRATEAINKA-L-S-IKLTTTSVFDYPSTNKLAAHVLA--
Bas_3     -NTIIQKLSESL---LIDAHMIDQ-HESFSDYGVDSITGVKLVQAINQA-L-H-ITLDTTTLFDYSSVTLLASHIIA--
Cal_18_a  -----ANLSAAL---ELATSRIDE-EESFADYGVDSITGSNLINNINQA-L-Q-IDLNTTSLYDHNSVRRMTDHIL---
Cal_18_b  -NAIVGELAEAL---GLAPGRIDH-DESFADYGVDSITGSNLINKINRA-L-A-IDLNTTTLFDYNSVNQLAEHILA--
Etn_17    -AQVRRAVGDVL---KLSDDDLDP-GLALSDLGVDSIVAVDLVRRINAS-L-G-LSLKTTVIFDFPNIRRLAAHLCAE-
Mgs_7     -DVVLAALADAL---RMPADRIGP-DRAFADYGLDSIVGVRFVQRLNEE-L-G-TDLPTTVVFDYRSVAQLAAHIAE--
Tst_6_a   ------LLADVL---RMDADGIDR-ARSFSDIGLDSILAIQLTNRLNAY-F-G-TRLGTIELFDHNTVARLAAHLAG--
Tst_6_b   -AMVREQVASAV---RAGVDEIDP-HRSFADQGVDSIIGVQLVNRLNKR-L-G-LRIATTVIFDHNTVGRLAAHLCE--
Mln_3_b   -EGIAKMMSSIL---KIDRKEIEE-ETSFGEYGFDSITFTRLGNEINQQ-Y-G-TELLPSVFFECNSLAEMTDYVIE--
Lnm_8     -HEARVLASGFL---LVDPSEVDV-AAELLELGFDSITLTELVNKVNER-F-G-LDLLPTVLFECPDLVSFAEYLTQ--
Bon_8     -RMLTALVSEHL---QIAQQELER-RTPFSEFGFDSIKATSFVDVLNRR-Y-G-LALSPTVLFEAPTLATLATHLAV--
Tst_7_a   -DALRATVAAQQ---AIDAAKIDD-GALFLDLGYDSISLIGLAQDLGAR-I-G-LTLQPTLFFEYPVLGAVADHLVE--
Cor_11    -QRIVDEVVALL---KVDRDAVSV-DDELVDYGFDSIILTELANRMNDH-Y-G-LDITPASFFEHATIREFADFLMK--
Cor_9     -ADMAGIMSRLL---RVNRRDIHP-NEDLREYGFDSITFTQFANALNEH-F-R-TELSPAIFFEHSTLASLAAHVAS--
Sor_2     -RELSKIVAGLL---KDPAMEIDA-EEDLGMLGFDSISFTELTNQLNDR-Y-R-LDLTPAIFFEHTTLRRFSEYLLE--
Myx_15    -AMLCSEIAVVL---KVDAAAVDA-DSELSEYGFDSITLTEFANRLNRA-Y-E-LDLTPPVLFEYPSVDTLAGYLLR--
Dif_3     -AELKHMISGIL---KVKEDEIDA-ESEMRDYGFDSVSFTQFANELNKM-Y-G-LELTPAVFFEYPTVFRFAQYLLT--
Etn_11    ---LVRAVSRVL---KIHEADIEL-DAELSAFGFDSLSLTELSNRLSAE-L-G-VELLPTVFFEHPSLAALETFLLA--
Myx_13    -QVLMSVVSKVL---KIPFEELDA-DAELKEMGFDSISLTDLAHQLAGE-Y-R-LDLAPTVFFEHPTINALVGRLVS--
Psy_8     -AHLVELVARVQ---KIQPEKIRL-NRELADYGFDSISFTTLANALNEA-Y-D-LSLMPTLFFETPNLAALAAHLVE--
Ooc_8     -AMLVGMVAQLQ---KLDEKKVEL-DMELSKYGFNSIDFTEFAGRLNKA-Y-G-LTLMPTVFFEHSTLRAMGRHLID--
Sor_16    -QELVAAASTLL---KLDARSIDP-RLELSRFGFDSIMFTEFANHLNKH-Y-G-LDLMPTVFFERSTLGLLGEYLVE--
Sor_20    -QELVGDVAALV---RSDASQIDA-QAELSRYGFDSVMFTEFANRLNQR-Y-D-LALMPTVFFECSTLALLGEHLVT--
Sor_11    -SALIESISRQL---KLKPADVDP-DMQLGDLGFDSIELTAFASSVNDR-Y-G-LAISPAIFFEHPSVRGFARYLVR--
Bat_10    -EALMQAISRQL---KVKVENVDV-DAEISEFGFDSISLTTLGNHLNRT-Y-G-LELSPTIFFEYSTIRDFAVYLVE--
Rhi_11    -RALIDLVSQQM---KIPAAEIRT-DAEFSQYGFDSISLTALAGTLKQQ-W-R-LNLAPTIFFEHATIDRFAAYLER--
Bae_14    -HLLKQQTASLL---KVNIDKIDP-HEEMTKYGLDSISMTEFTNQLNKT-Y-R-LTLTPTIFFDHPTIHEFAVHLIS--
Bae_15    -ELLAKEVSGLL---KINIEEIDI-ELEFNQYGFDSITLTEFANKLNDT-Y-Q-LDLTPTVFFEYATIQALAHHLAE--
Ooc_9_a   -QLLVREVSALL---DVAASEIDL-DLELTELGFDSILTTGFANKLNQR-Y-Q-LDLLPTLFFEYPTISALSGYLTA--
Ooc_9_b   -SLLTQEISALL---HVGVADIES-DMELSELGFDSILTTSFANTLNRR-Y-A-LELLPTVFFEYPTVAGLTHYLAD--
Bry_9     -QKITKVISDLQ---KINIEKIEC-DIELSEYGFDSVSFTEFANILNKQ-Y-R-LELMPTLFFEHPTIASISHFLLE--
Myx_9     -AVLLEGVSELL---KVPREELDA-DTKLSDYGFDSITFTEFANLLNRQ-L-S-LGLSPVIFFEFTTANALAGYLCE--
Dif_9     -EKLKRHVSDLL---KVSMKDIEA-DSELTEYGFDSIIFTEFTNLLNRS-Y-Q-LELSPTIFFEFPTLRKLSGHLIS--
Bae_3_a   -GALIRLVSSIL---KVGQDEIDI-DTELSEYGFDSVSFTVFTNQLNEA-Y-Q-LKLAPTIFFEHGTIRSLADYLTD--
Bae_3_b   -TALTAMVSGIL---KVDREDIET-DTELSEYGFDSVSFTVFTNQLNEA-Y-Q-LELAPTIFFEHGTISGLAGYLAK--
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Figure S4. Sequence Alignment of 526 ACPs from 33 *trans*-AT Assembly Lines. A ClustalX sequence alignment performed on the ACP domains show that they largely group with others from their module type or ACP family (Figures S1 and 2). Relative gaps and insertions are observed and described in Figure 4. The serine that becomes phosphopantetheinylated is indicated with an asterisk.