Figure S1

Domain II

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Pt_TFIIS1a     132  PSYVD--RVKYLNAISNLFILNIQKFK--NQ-NDLN-ASDRQTIKECVEKMENTIYY--KRQQDYTFRKAVEQDLKILAGFLK-DKNGSLTYSIFTKQFDPINAAQLRAADWVD
Pt_TFIIS1c     132  PAYAD--RIKYLKGINQMFIANIFTFK--KD-NVLN-DSEYQTIKECVEMMENTIYH--KRAKDHTPRKAVEQDLRILAGFLK-DKNGSLTYRIFTKAFDPVSAAQLRAADWVD
Pt_TFIIS2a     114  TGYVD--RIQNLNLISNLILHIFKNWN--QS-NKEQ-LISIDKVKEVTIGLEKEIYL--ENVFKDSKKLAVEMDIKTLVQFMK-RDKSGDVLIRVENKSLSYQQAAQLKSEDWID
Pt_TFIIS2b     114  TGYVD--RIQNLNLISNLILHIFKNWD--QT-NKEQ-LISIDKIKAVTIGLEKEIYL--RNFYKDSRKMTYEMDIKTLIQFMK-RDKTGDVLIRVFNKSLSYEQAAQLKSEDWID
Pt_TFIIS3      128  PQNFDPTRIKVLQT-------LIQKFT--NE-T----TPHQES-IKFCKKLEKEINQ--KFL-NKERQLQTAIREILKYLQ-NDRDGSVRNRMISGLVDIPTAAQLRSEDWTS
Pt_TFIIS4      137  -DQRDKIRAKLSEYLQKQLQQ---KQ--QQDLFQE-ENLVDKCNKLADAIENNIYN--KHYQTVAPGKNYSSDIKVLLYQYIG-DKDSGRVLHKIFAGFFTVNQACQLQLKDWLD
Tt_TFIIS       147  PTYKSDIRQKGLEANKIFMK---VK--DDINASP-----REWIELIVNLEKKIFS--RN---SQVVVYKSYIKEVLGMFSSNEVTTEVISKVLNKEISLQDVAEAKISVFLT
Ot_22233_0_g55 170  TQYRDSLRINFIKYMQIPE----ECV--EY--E-E-IVLTRAAQLGLQIEDELYK--SF----PRLAEYQNKARSLLFNLK-DPKNPDLRMSLIEGVIEPNQLVRLDSKSLAS
Ot_1015_0_g5   340  MTYRDQLRRKLVNIMRDSMKQIVYPCNSKAQLTDGE-KN---WATECGIRIEDQLNV--SY----SQVKTYSDKARSLLFNLS-DSKNFELRKIILNQELSAQQLVHTDVKKLAS
Ot_14486_0_g34 340  MTYRDQLRRKLVNIMRDSMKQIVYPCNSKAQLTDGE-KN---WATECGIRIEDQLNV--SY----SQVKTYSDKARSLLFNLS-DSKNFELRKIILNQELSAQQLVHTDVKKLAS
Mc_conN1       164  NETEDKVRNGIRKGLEKLICK----SN------EN-PK--KCKALSLKIENSVVL--RLG---THLKEYTNKCRSIIANLQ-R--SDEFRSKIINGIFIPDDLAAMNPRDFLE
Im_IMG5_116810  13  ------VRNKGLQAI---FMK---FK--E-CDQDK-----ADIVKISVNLEEKIAH--KN----SQVEVYKNIKEVLGMLSNYQVIQEVLKGILQEKISIKDVAECKSSVFML
Lm_TFIIS1-1    167  AAKRITLHQRWAALLHGVIMK---ER--PS--S---E--SERVMGLCVRIVESI------P---GDMEQTKDTFQTLLFNIK-DSKNGELRRKVVEGELLVERIVTMDDLEIAN
Lm_TFIIS2-1    257  PTQRKTFYDNVYQLLDSPIST---------T--R---Y--DDTVI---DEVARRL-----T---AEI-TDRDERQMLLRLR-EEELSFIRDHILSGEWTPKKYLDQPSEVFTT
Tb_TFIIS1       52  D----TRLTKWKTLLCKALMQ----CR--KE--E---D-EGRVADMAIRIVKAI------P---GGRSESADTFRMLIVHLG-DAKNRELRESLIEEKFSVEVLVRMKERDILN
Tb_TFIIS2-1    254  GGAQPQFVDRVQKLLL---QP----CD--PH--S---F--SVRSDLR-SVAEKI-----C---AEVT-RSEDRMYLLEHLS-KPGLSEIRRRIAMGELSGKDFLEISRWELMT
Hs_TCEA1       134  PSTSDSVRIKCREVIAAALRT---CD--DY--I----AI-GADEEELGSQIEDAIYQ--EIR---NTDMKYKNRVRSRISNLK-DAKNPNLRKNVICGNIPPDLFARMTAEEMAS
Hs_TCEA2       132  PVTCDAVRNKCREVIAALQT---DH--DH--V---AI-GADCERLSAQIEECIFR--DVG---NTDMKYKNRVRSRISNLK-DAKNPDLRRNVICGAITPQQLAVMTSEEMAS
Hs_TCEA3       181  YLTGDSVRDKCVEVLSAALKA---DD--DY--K---DY-GVNCDKMASEIEDHIYQ--ELK---STDMKYRNRVRSRISNLK-DPRNPGLRRNVISGAISAGLIAKMTAEEMAS
At_TFIIS       204  LKCNDPVRDKIREILVEALCRVAGEAD--DY--E-RESVNASDPLRVAVSVESLMFE--KLG---RSTGAQKLKYRSIMFNLR-DSNNPDLRRRVITGEISPEKIITLSAEDMAS
Ce_TFIIS       142  HLENDETRIKSAQLILSALRF---CD--MP--Q---G--TLDPEELAVQIEEKLYS--VHR---DTNKSYSAAVRSRIFNLR-DKKNLALRENVLTGVVRAEKEATVISEEMAS
Dm_TFIIS       147  GGMTDAVRIKCREMLATALKI---EE--VP--E---G--CGEPEDMAAEIEDAIYS--EFN---NTDMKYKNRIRSRVANLK-DPKNPGLRRFLQGAVTAKQLAKMTPEEMAS
Dm_CG8117        6  ------RIKCREMLATALKS---GN--MP--P---G--CGDPDDMAAKLEDAIYG--DLN---GCKVKYKNRLNSRLANLR-DPKNPELRQKFLLQGIGLSKMTPEEMAS
Sp_tfs1        127  NVTDDKIRNNCIGLMYNALV----IDS--DE--S-S-----SLIIAKAKETDAQVLA-RAAG---KTGSEYRNRMRSLYMNLK-DKNNPKLRASVIRNEIIPQRLSTMTSAELAS
Sc_Dst1        142  AIYHHKLRDQVLKALYDVLA----KES--EH--P-P-----QSILHTAKAIESEMNKVNNCD---TNEAAYKARYRIIYSNVI-SKNNPDLKHKILANGDITPEFLATCDAKDLAP
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α1   α2   α3   α4   α5   α6

Linker & Domain III

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Pt_TFIIS1a     238  DETKQEQSRIIREKMEAEQIGFYKDLSK-REMEGVEGKTCGGQKKVYLVDEKQTRASDEPTTKFFECYNCGD-KFRIC
Pt_TFIIS1c     238  DETKQEQARIIKEKMEAEQIGFYKDLSK-REMEGIEGKTCGCGQKKVYLVDEKQTRCADFPTIKFFECYNCGD-KFRIC
Pt_TFIIS2a     220  EKTKLNQKAAQKEELEINQIGFYKEVSK-REMDGVEGKQCKGCHQKKVYLVEEKQTRCADFPTIKFFECFNCGD-KFR-I
Pt_TFIIS2b     220  EKTKLNQQAAQKEFLEINQIGFYKEISK-REMDGVEGKQCRGCHQKKVYLVDEKQTRCADFPTIKFFECFNCGD-KFR-V
Pt_TFIIS3      222  ATRLAIAGGVGREILSANIMNHNKYIAQ-AINKDVAILGLONNCGQKQMKLVNEIQTRASDFPSIKFYECINCGIGETTNG
Pt_TFIIS4      241  EEVIRELENRKISEVKDDDADYYRQIRI-KEMTQSKGQECPRCHNNYLYIIETKQIRRADEPATIFYECFACQH-RYK-V
Tt_TFIIS       245  DRQRAQQKKAVEDQLATSDPDFYNNMRR-QRLQGLEGELCKGCKKKTAFLVKELQTRSSDEPMTRFMECNSGCK-SWK-D
Ot_22233_0_g55 266  KAIQDDERNKTQQANLNARRSDWFIENAA--KKGNKGFETCKKCHSKNTTY-FQMQTRGADFPMTNFITCLDCKN-QWK-C
Ot_1015_0_g5   444  EWMKQKREESILRTLSMKRTDWDVQETL-SQGEFQGMEQCE-CGSQKTGY-IQLQIERADFPMTNFVYCYCDGEN-RWK-C
Ot_14486_0_g34 444  EWMKQKREESILRTLSMKRTDWDVQETL-SQGEFQGMEQCE-CGSQKTGY-IQLQIERADFPMTNFVYCYCDGEN-RWK-C
Mc_conN1       256  DSLKKKRAKKETRIIDSKRS---DYTLA-NSKIKEGMYTCEKCKSKKTTF-YEQQTRSADFPMTTFVQCLMCSH-NMK-F
Im_IMG5_116810 101  QKEKEENLQQLQTEFEVLDPEFYNKLRR-KNLVGLEGEKCRNCKKLTAFLVKELQTRAADFPMTRFMECNCCKK-KWK-E
Lm_TFIIS1-1    259  PELRKHIEEKIEERSKDTNL---SEIRKAMRTSNSTLEKCRVCGARDSSW-EQRQTRSGDFPMTVIITCNKCNT-QWRKY
Lm_TFIIS2-1    342  KSEKARQEQRIQEKMKAIEA---A---DNAMLNITSLEKCGRCGKRHCTF-YEQQTRSADFPTTKYITCLDCKN-TWTQE
Tb_TFIIS1      140  PEERERQEAAFLARSRDTDL---TEIRK-ATSITSTLEPCPCSCKAKNCTY-TQKQTRSADFPMTIFCICNICEH-KWRRY
Tb_TFIIS2-1    341  QEEKEDAERRTTEKLRNLE---ETER-SLLHTTSLEECPECHGRECEW-RELQIRSADFPTTKFIKCIKCKH-NWSEN
Hs_TCEA1       231  DELKEMRKNLTKEAIREH------QMAK-TGGQTQTDLFTCGKCKRKNCTY-TQVQTRSADFPMTTFVVCNCDGN-RWKFC
Hs_TCEA2       229  DELKEIRKAMTKEAIREH------QMAR-TGGQTQTDLFTCGKCKRKKNCTY-TQVQTRSADFPMTTFVVCNECGN-RWKFC
Hs_TCEA3       278  DELRELRNAMTQEAIREH------QMAK-TGGITTDLEQCGSKCKKKNCTY-NQVQTRSADFPMTTFVLCNECGN-RWKFC
At_TFIIS       308  DKRKQENNQIKEKALFDC----ERGL-AAKASTDEKCGRCGQRKCTY-YQMQTRSADFPMTTYVTCVNCDN-HWKFC
Ce_TFIIS       238  AEIREMRDKFTKEAILEH------QMSV-QQGTPSDMEKCGKCGKNCTY-TQLQTRSSDFPMTTFVFCLECGN-RWKFC
Dm_TFIIS       243  DEMKKLREKFVKEAINDA------QLAT-VQGIKTDLLKCAKCKKRNCTY-NQLQTRSADFPMTTFVMCNECGN-RWKFC
Dm_CG8117       95  DDMKQMRQKYVQDSINAA------QMAK-VQGIKTDEFKCERCDKRNCS---QLHIRDGDFPIITFVICDECGN-RWK-S
Sp_tfs1        223  EDRRKEDAKLEQELLFHA------QGAK-PQKAVTDLETCGKCQKKVSY-YQLQTRSADFPLTTFCECTVCGN-RWKFS
Sc_Dst1        239  APLKQKIEEIAKQNLYNA------QGAT-IERSVTDRETCGKCQKKSY-YQLQTRSADFPLTTFCEDCGN-RWKFS
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α7   C   C   β1   DF   β2   C   C   β3