

Supplementary Materials

Hepatitis C virus infection and intrinsic disorder in the signaling pathways induced by toll-like receptors

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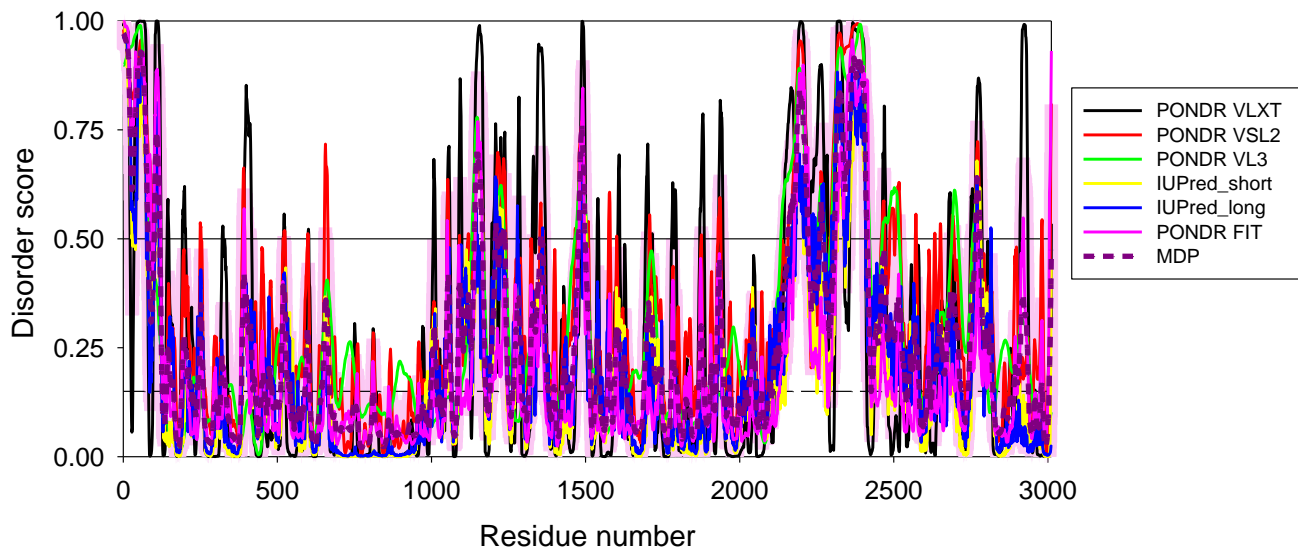
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Supplementary Figure S1. Amino acid sequences, structural and intrinsic disorder-based features of HCV proteins, human TLRs, and major players of the TLR-regulated downstream signaling pathways. With exception for HCV proteins, information for each protein includes amino acid sequence in FASTA format, disorder profile generated based on the outputs of RIDAO, functional disorder profile generated by D²P², protein-protein interaction network generated by STRING, and a model of 3D structure generated by AlphaFold. For HCV polyprotein and mature individual proteins, amino acid sequences and disorder profile generated based on the outputs of RIDAO are shown.

HCV proteins

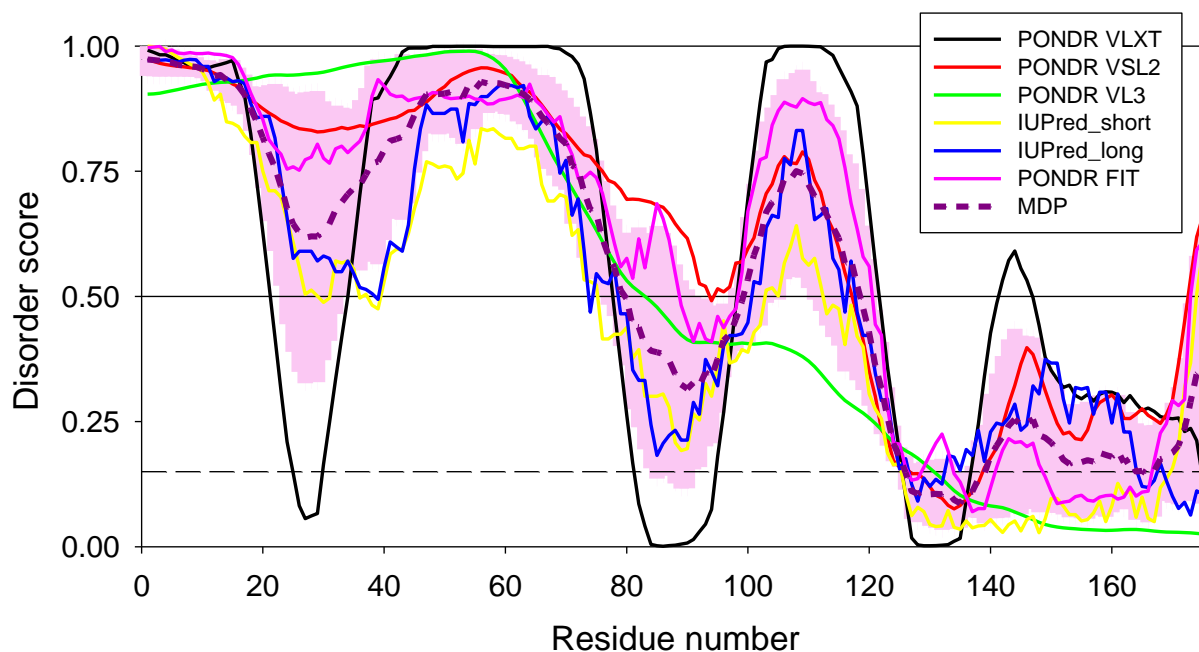
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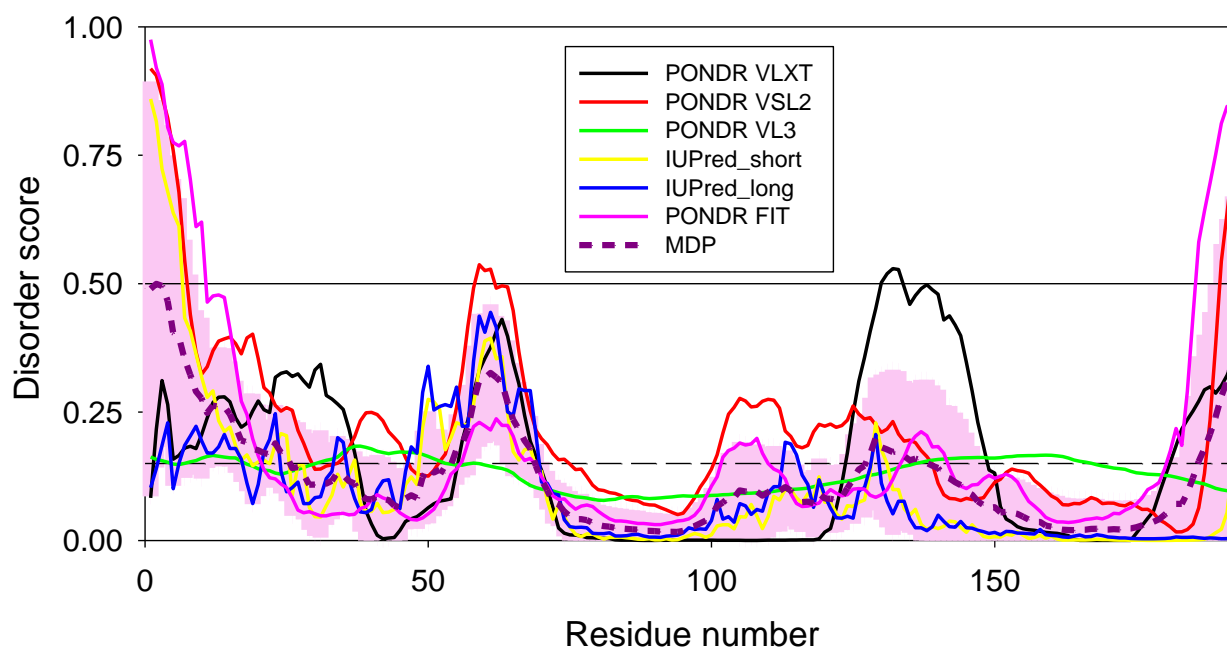
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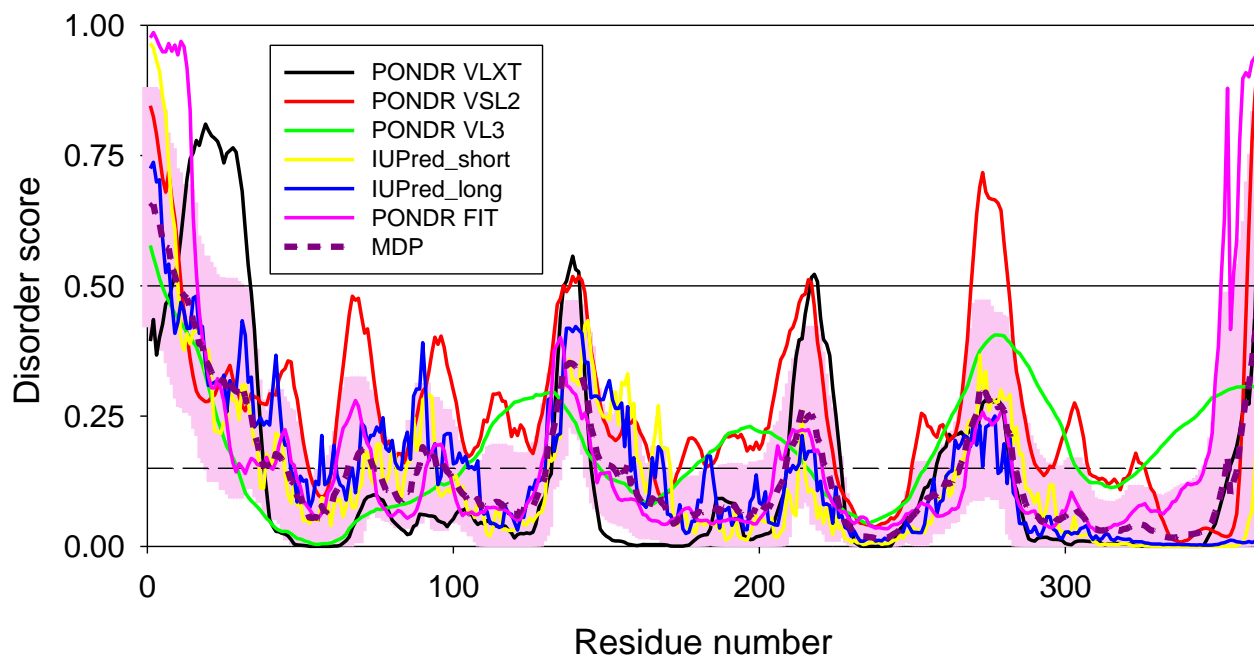
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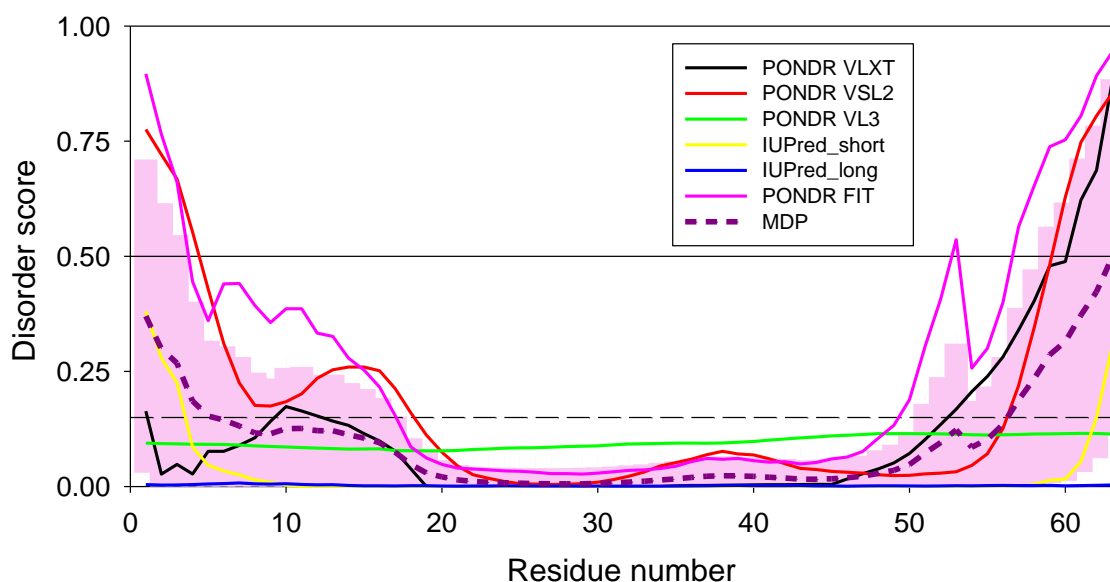
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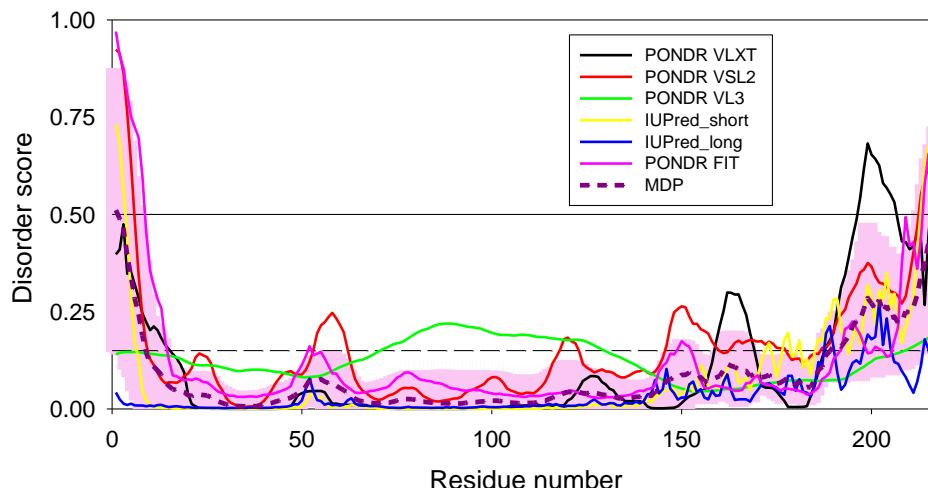
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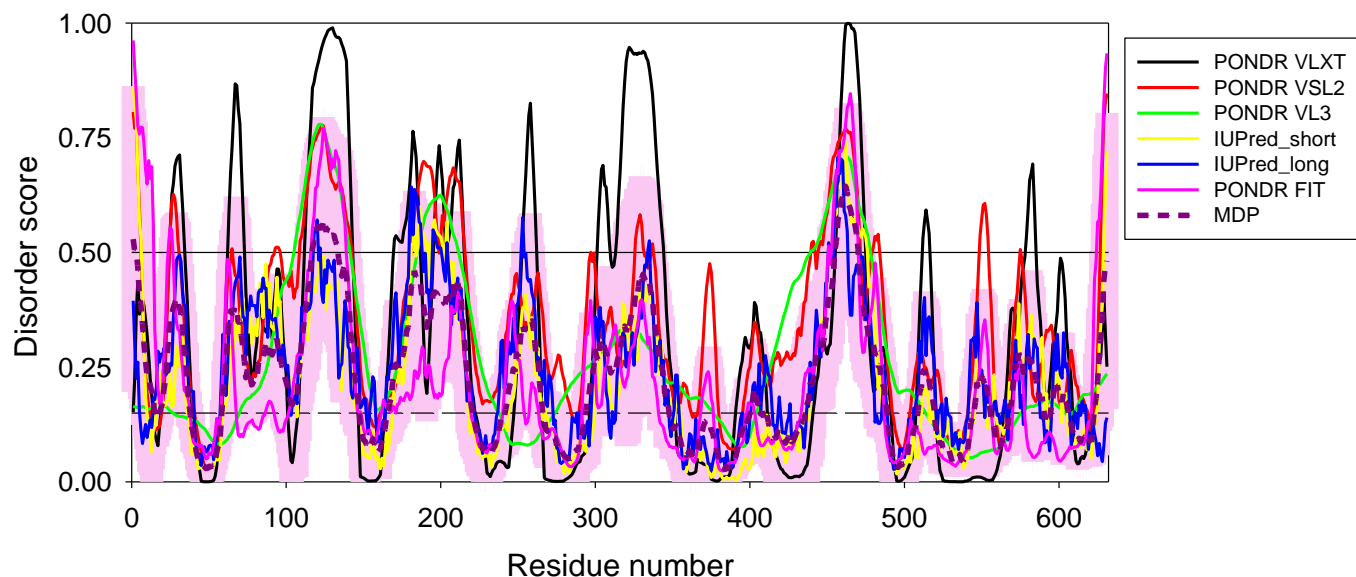
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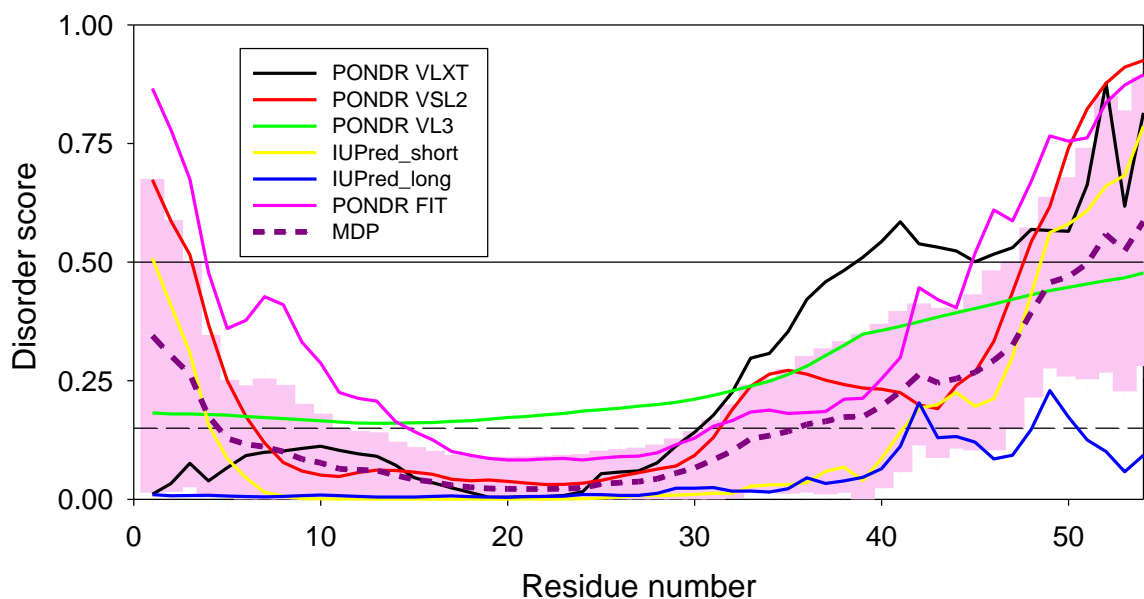
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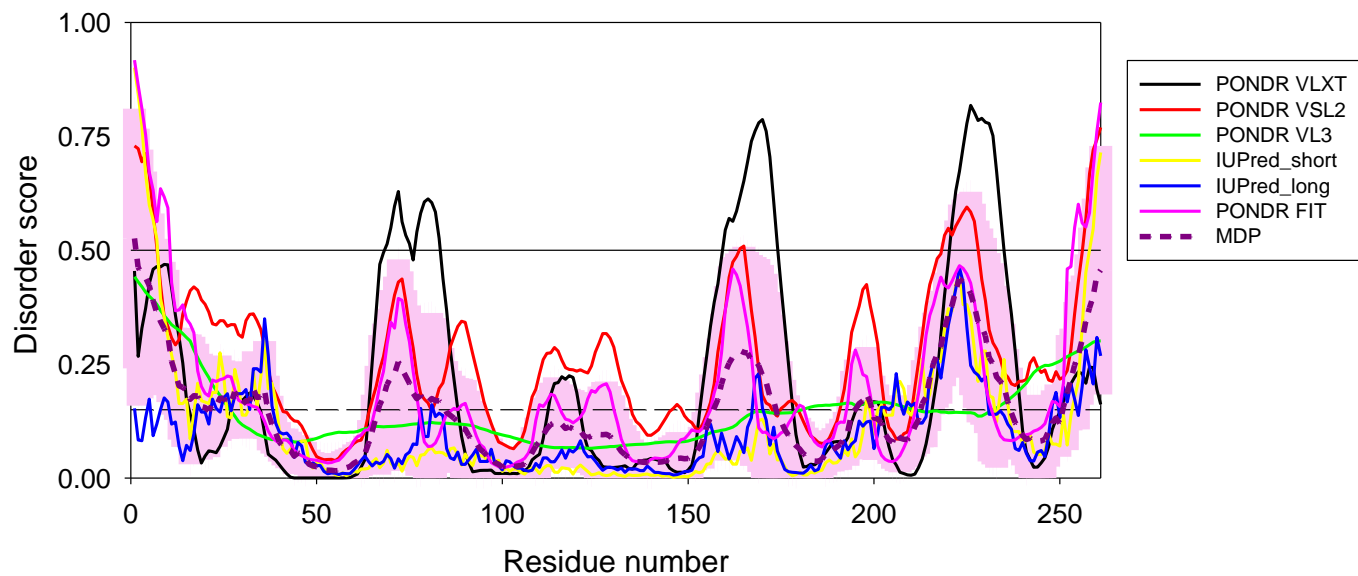
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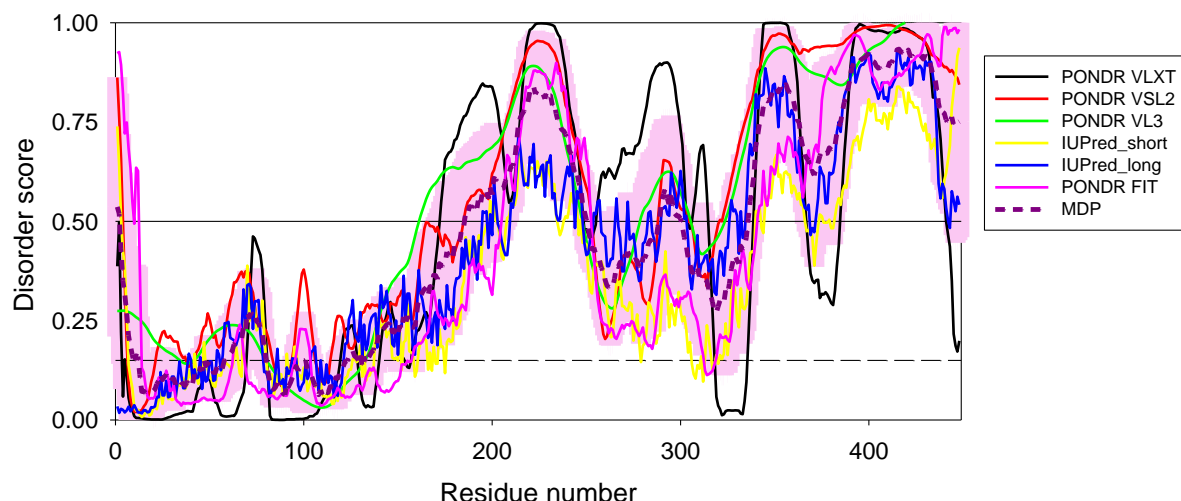
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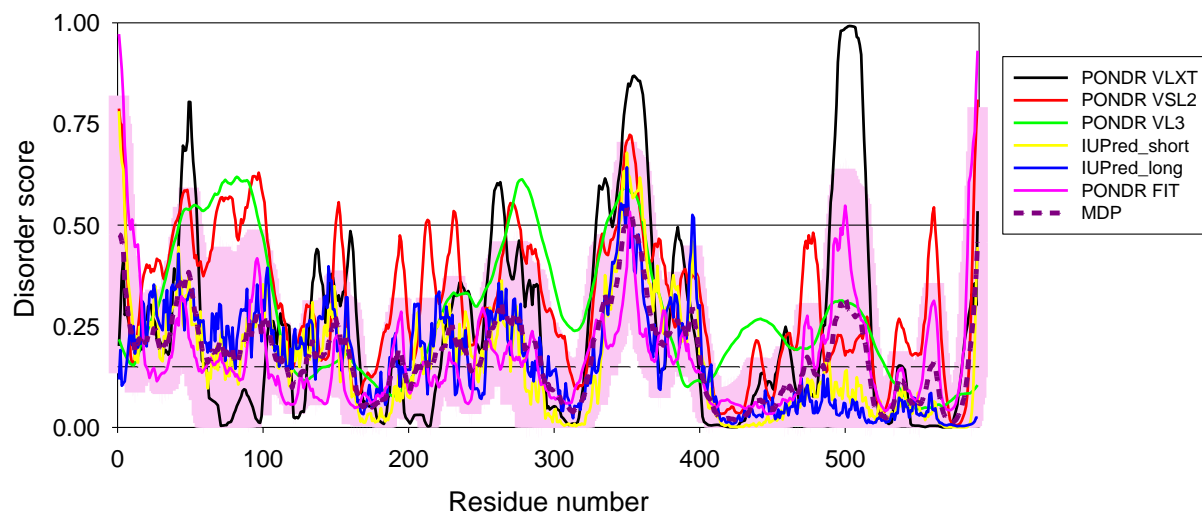
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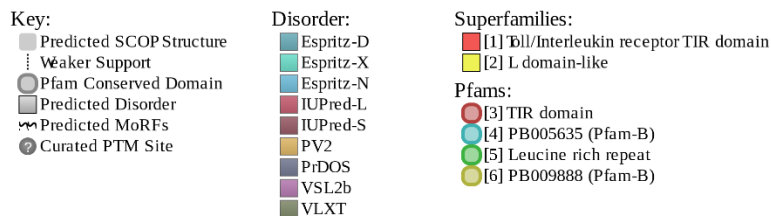
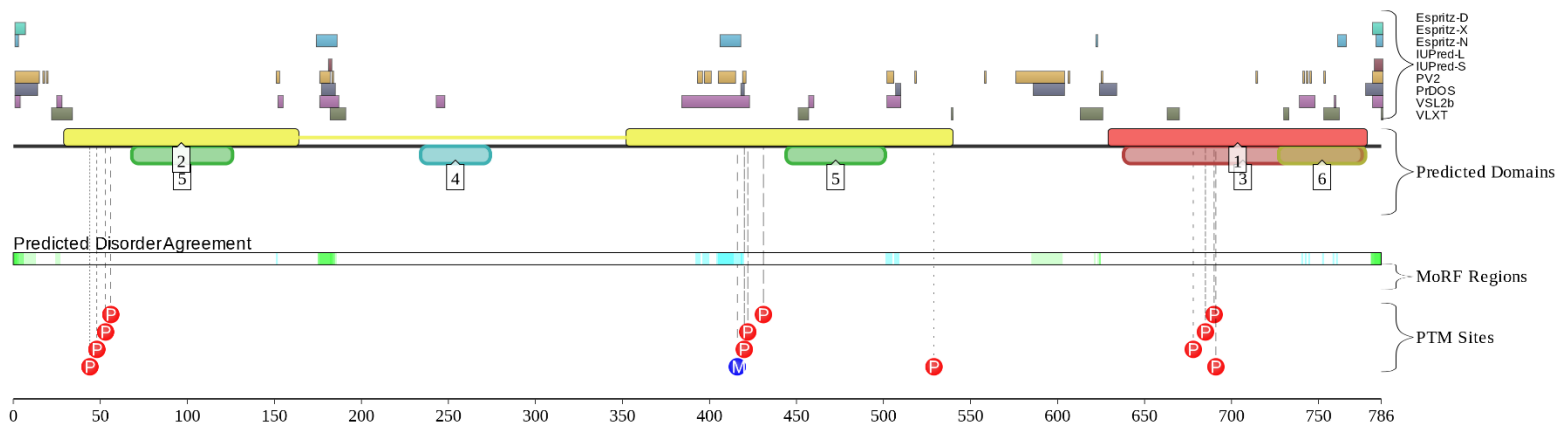
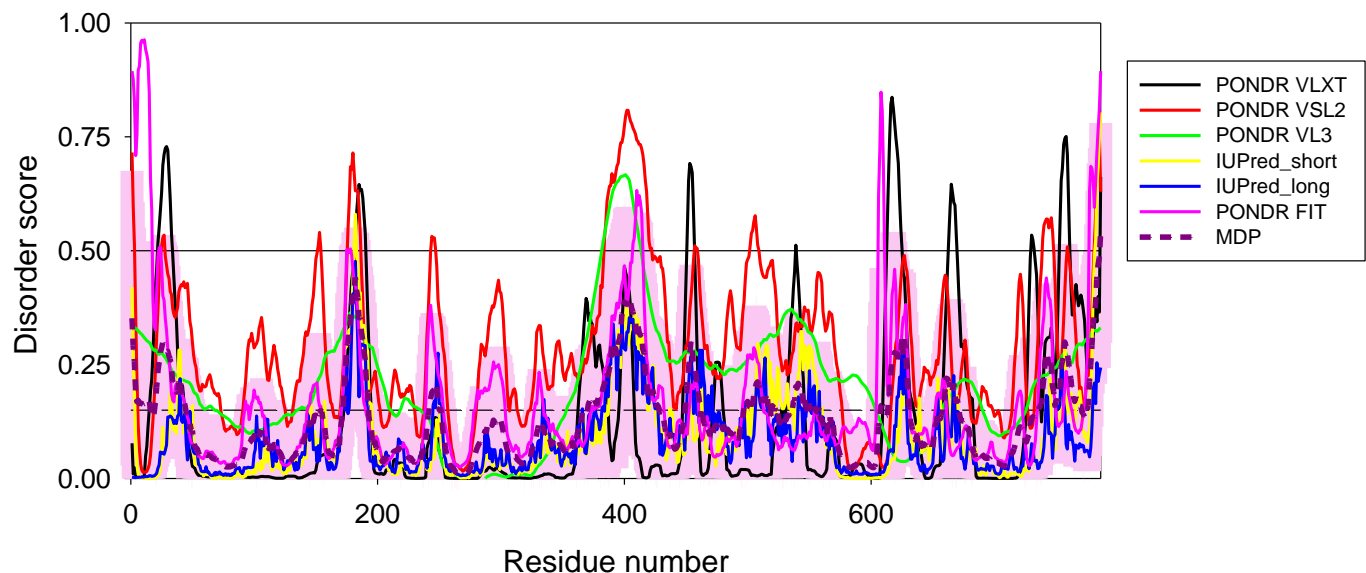
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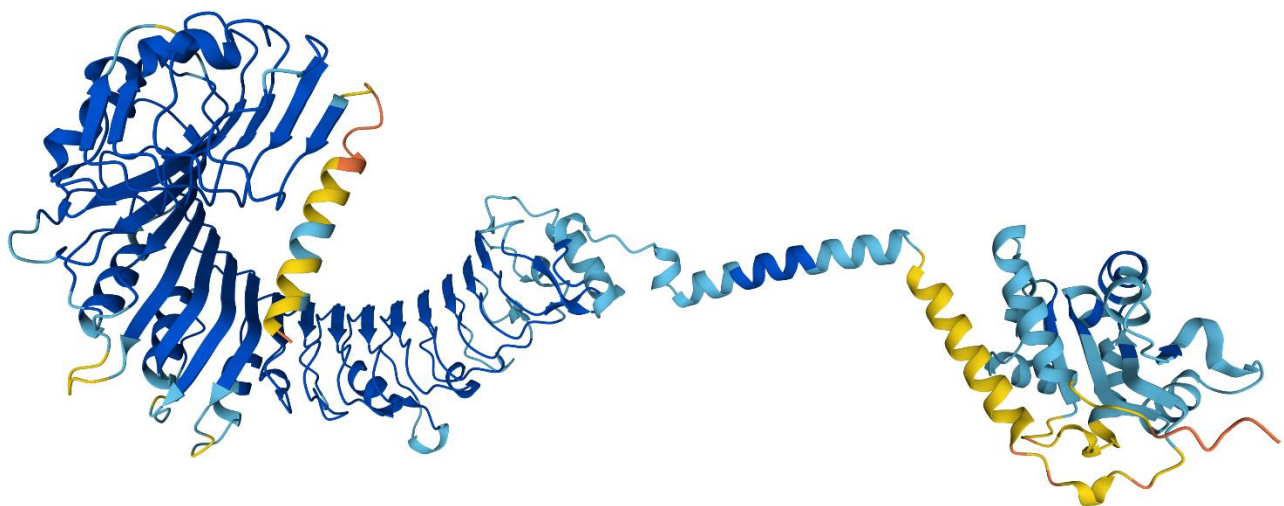
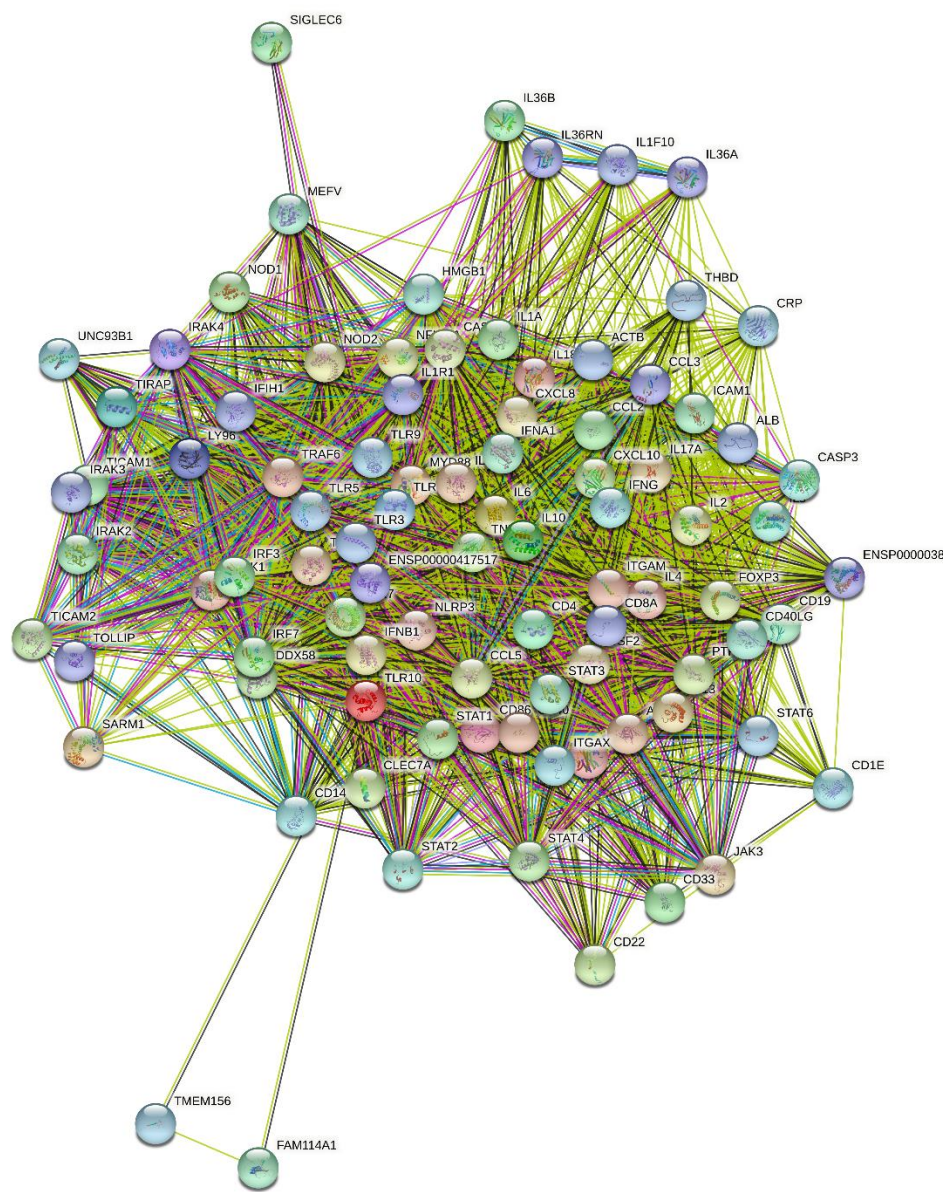
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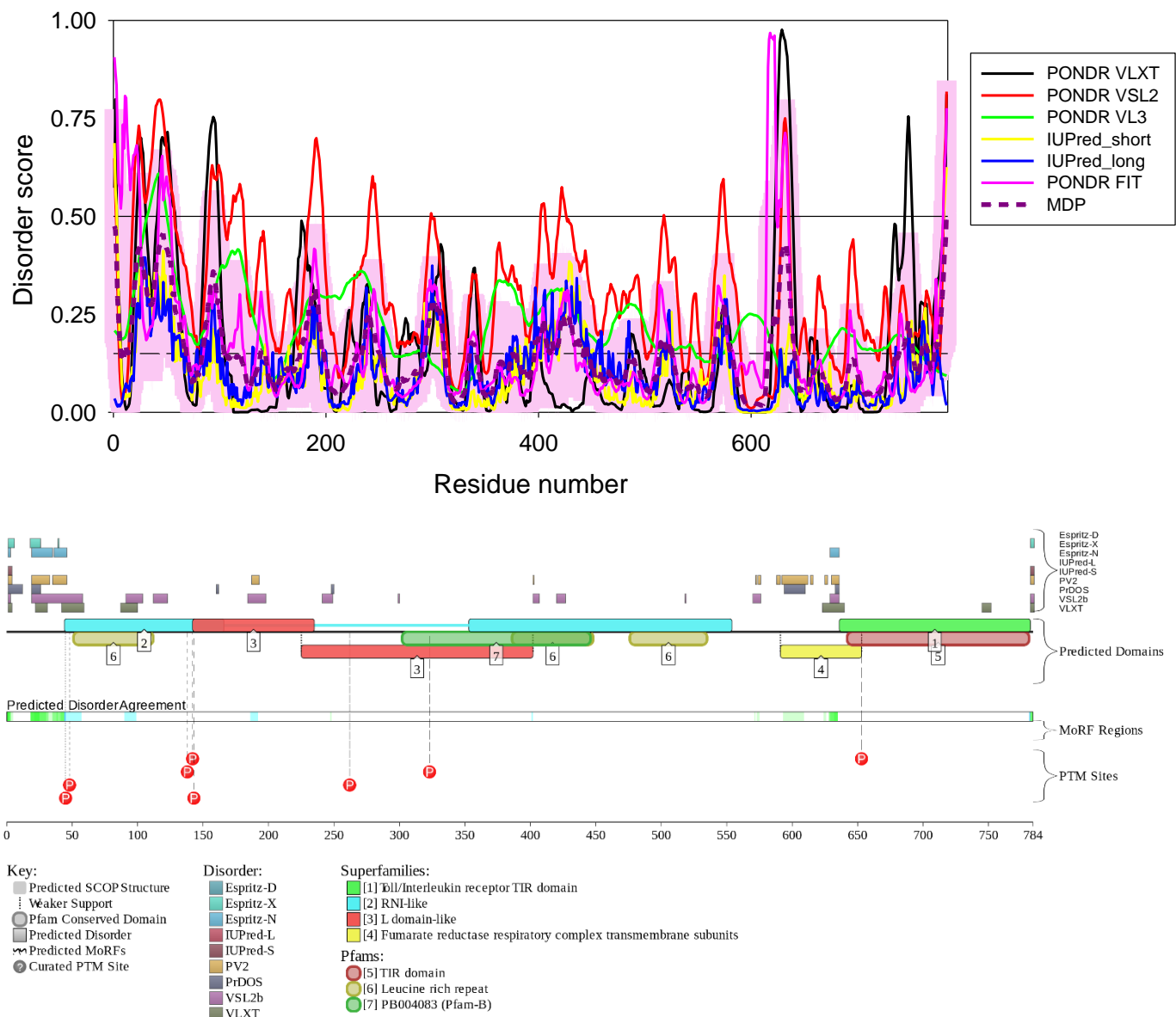
Human TLRs

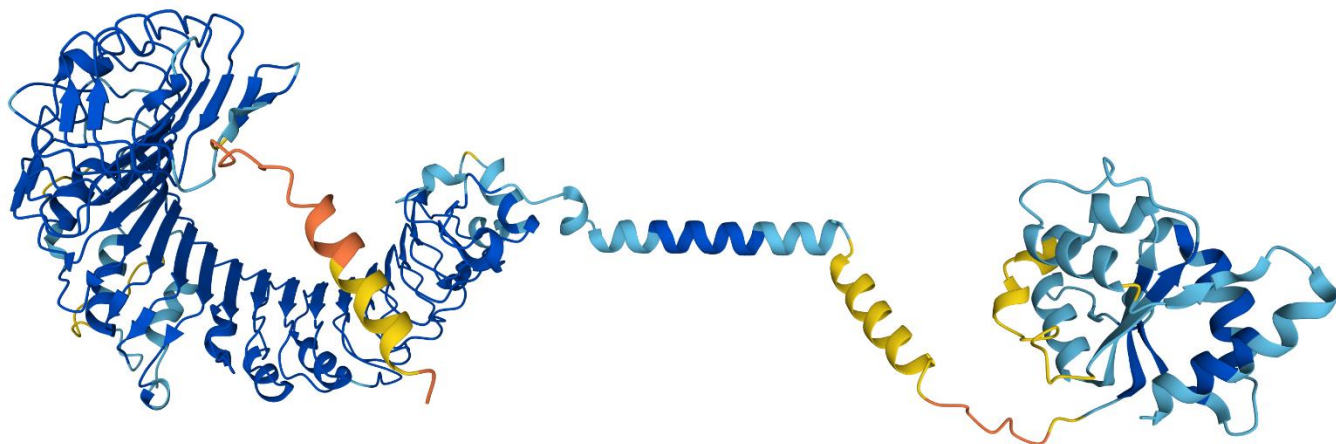
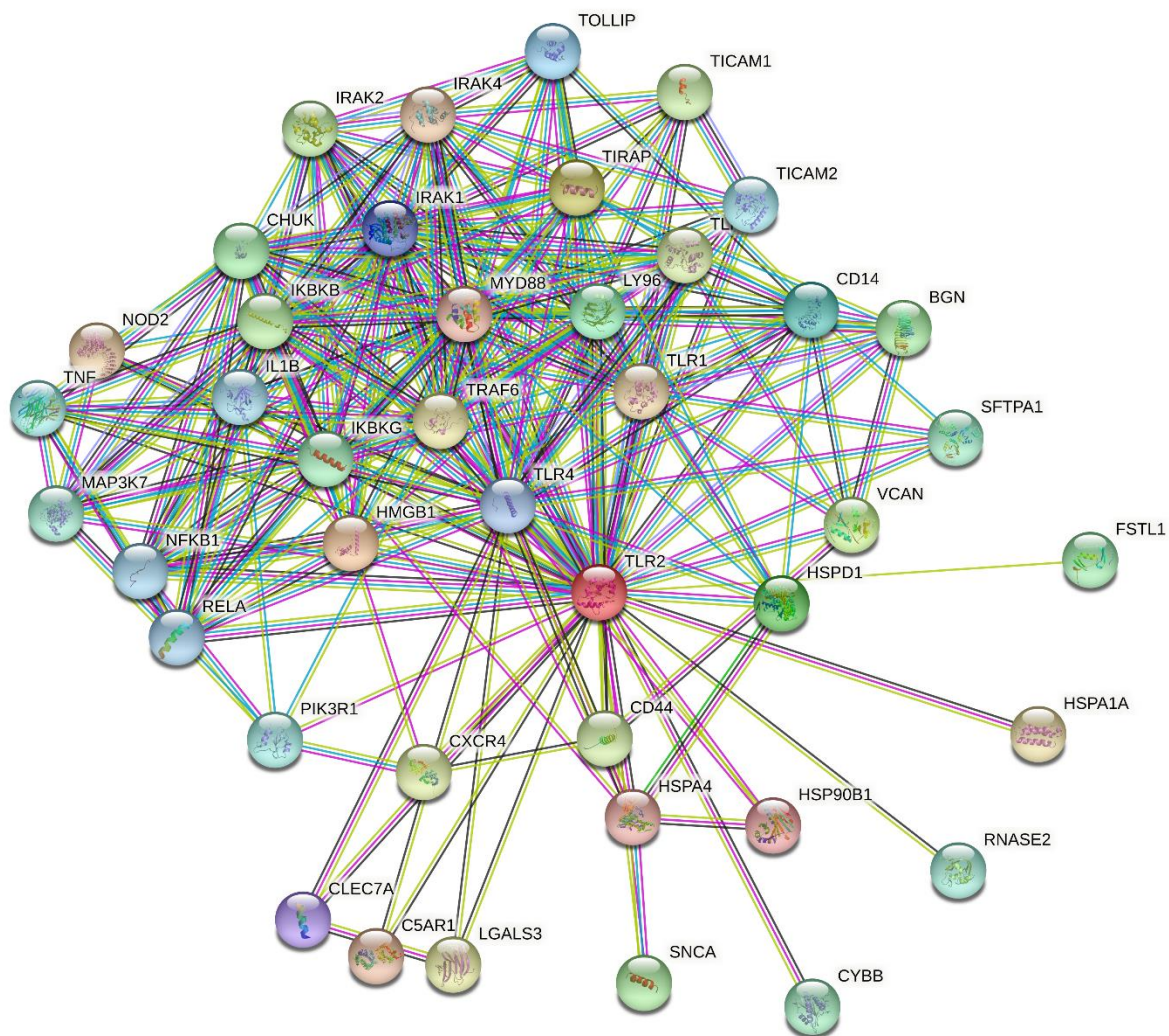
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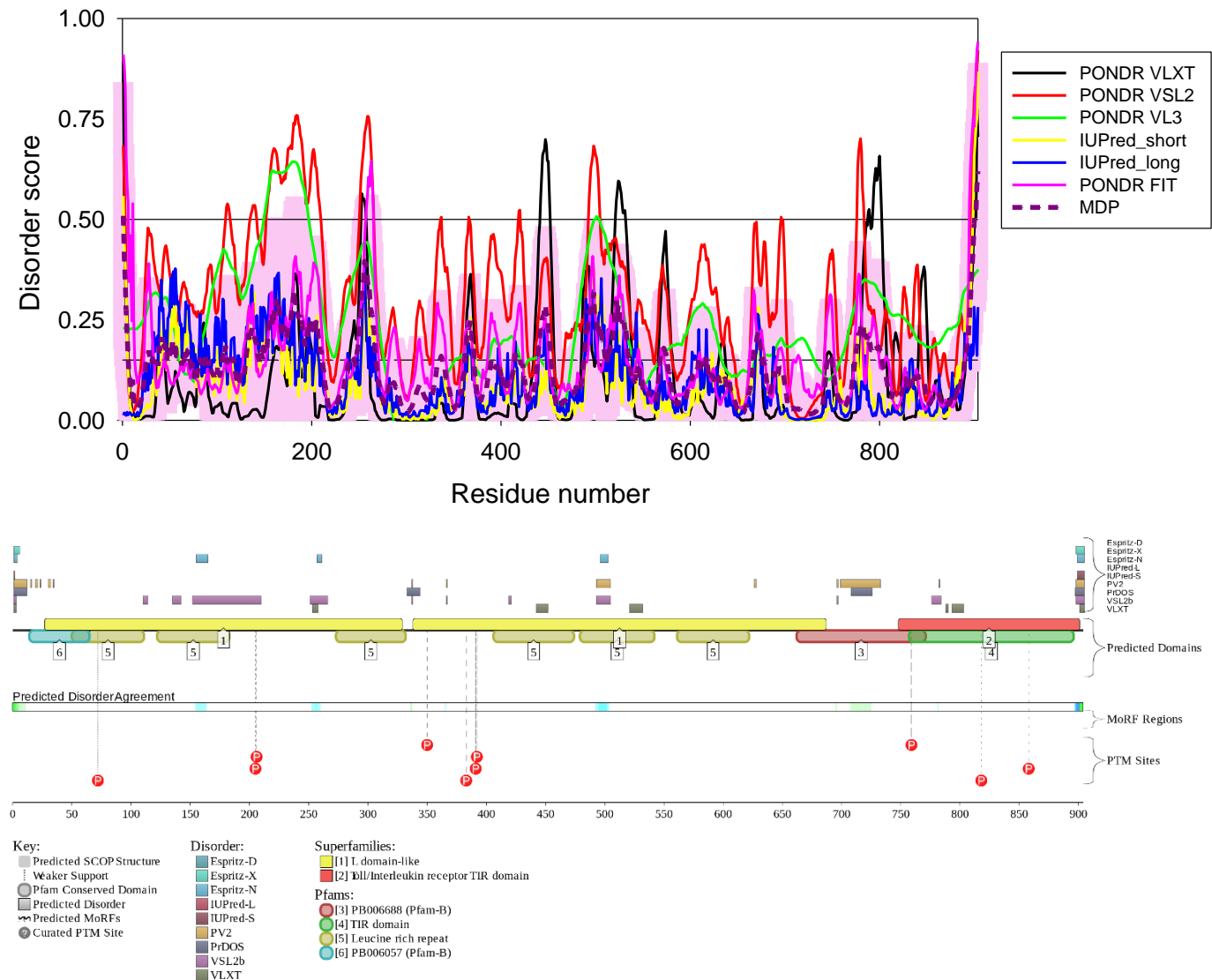


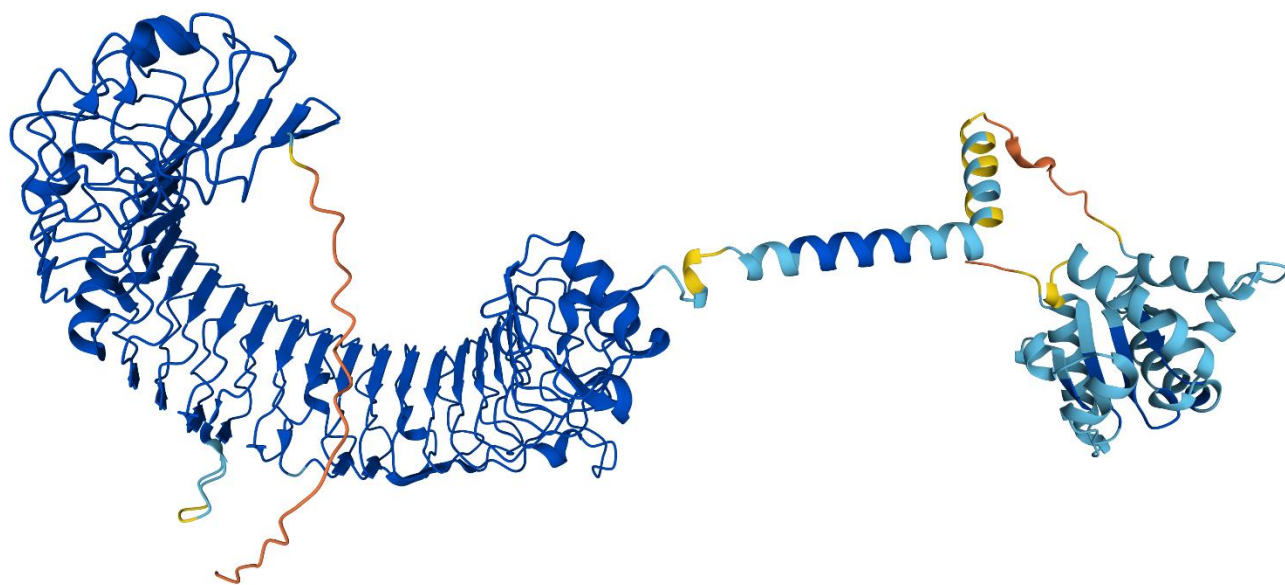
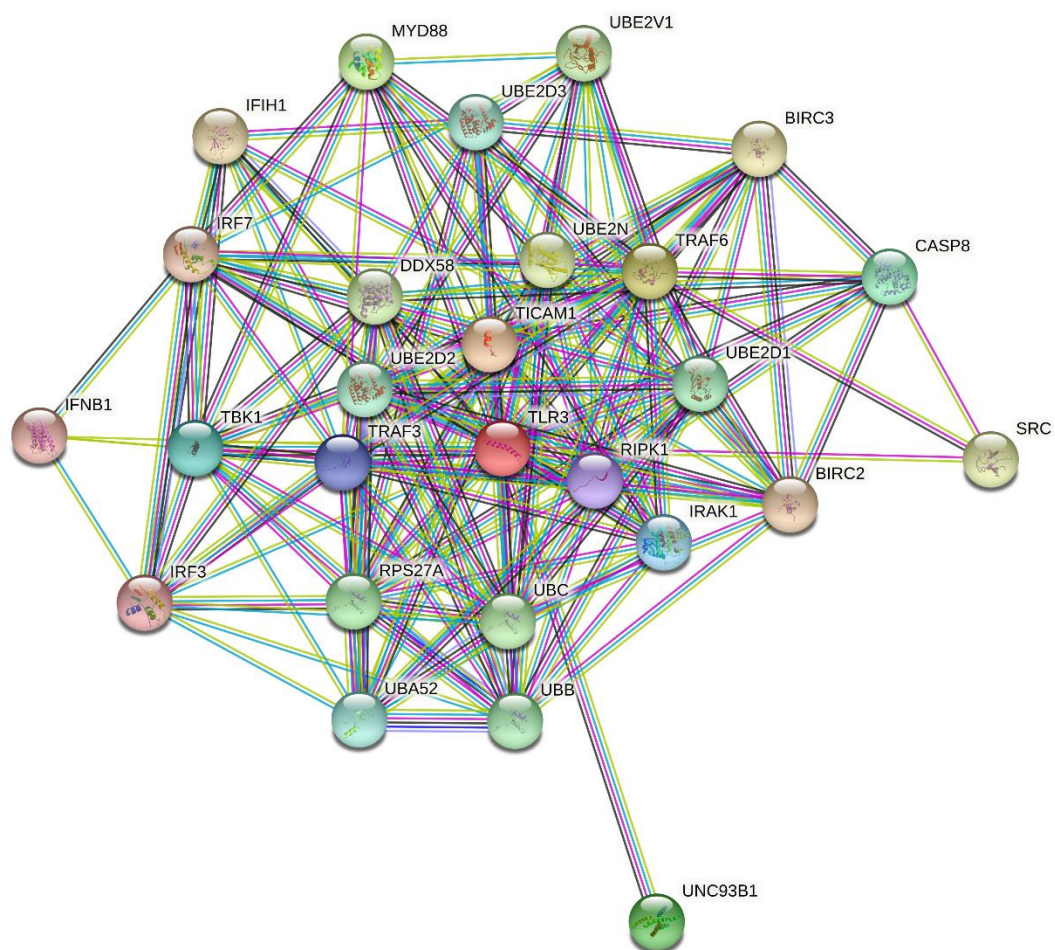


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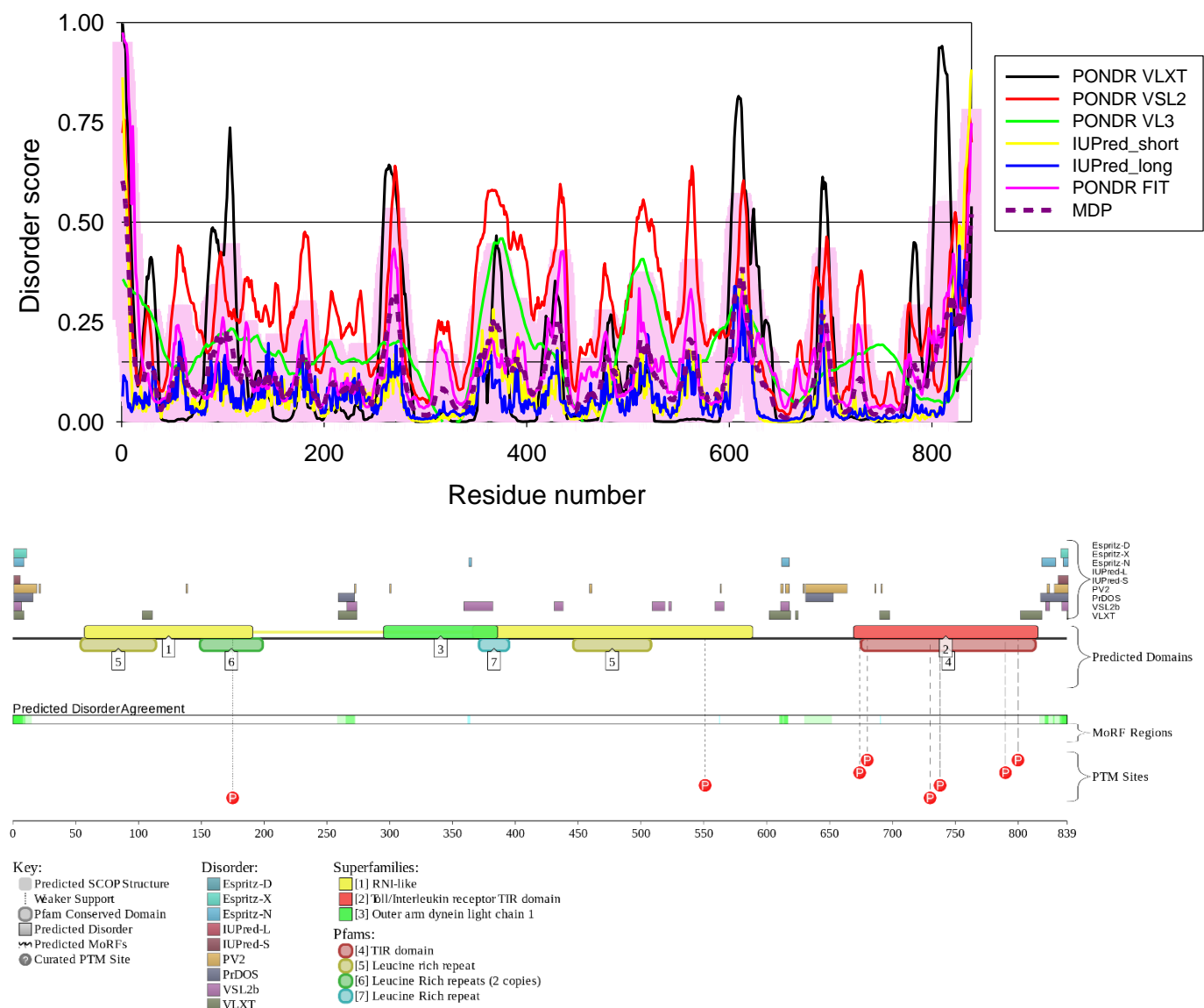
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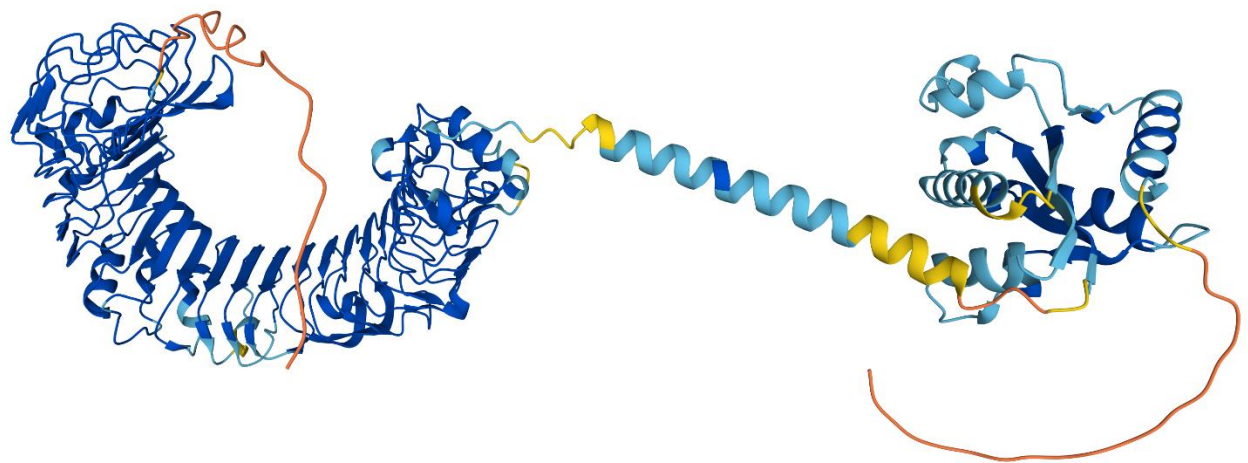
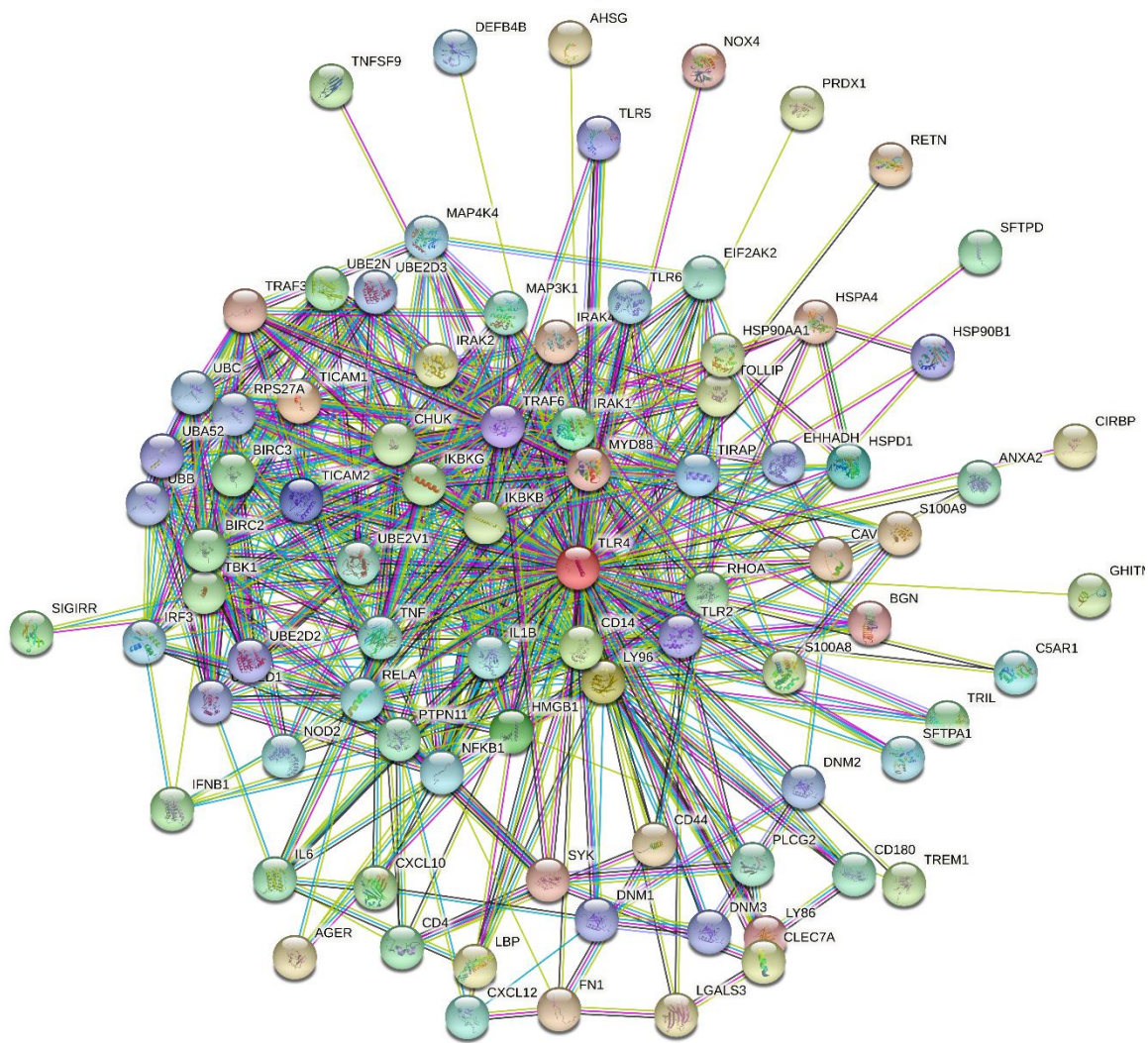
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HLD FQH S NLK Q M SEFSV FL S R N LI Y L D I S H T H R V A F N G I F N G L S S L E V L K M A G N S F Q E N F L P D I F T E L R N L T F L D L S Q C Q L E Q
L S P T A F N S L S S L Q V L N M S H N N F F S L D T F P Y K C L N S L Q V L D Y S L N H I M T S K K Q E L Q H F P S S L A F L N L T Q N D F A C T C E H Q S F L Q W I K
D Q R Q L L V E V E R M E C A T P S D K Q G M P V L S L N I T C Q M N K T I I G V S V L S V L V V S V V A V L V Y K F Y F H L M L L A G C I K Y G R G E N I Y D A F V I Y
S S Q D E D W V R N E L V K N L E E G V P P F Q L C L H Y R D F I P G V A I A A N I I H E G F H K S R K V I V V S Q H F I Q S R W C I F E Y E I A Q T W Q F L S S R A G
I I F I V L Q K V E K T L L R Q Q V E L Y R L L S R N T Y L E W E D S V L G R H I F W R R L R K A L L D G K S W N P E G T V G T G C N W Q E A T S I
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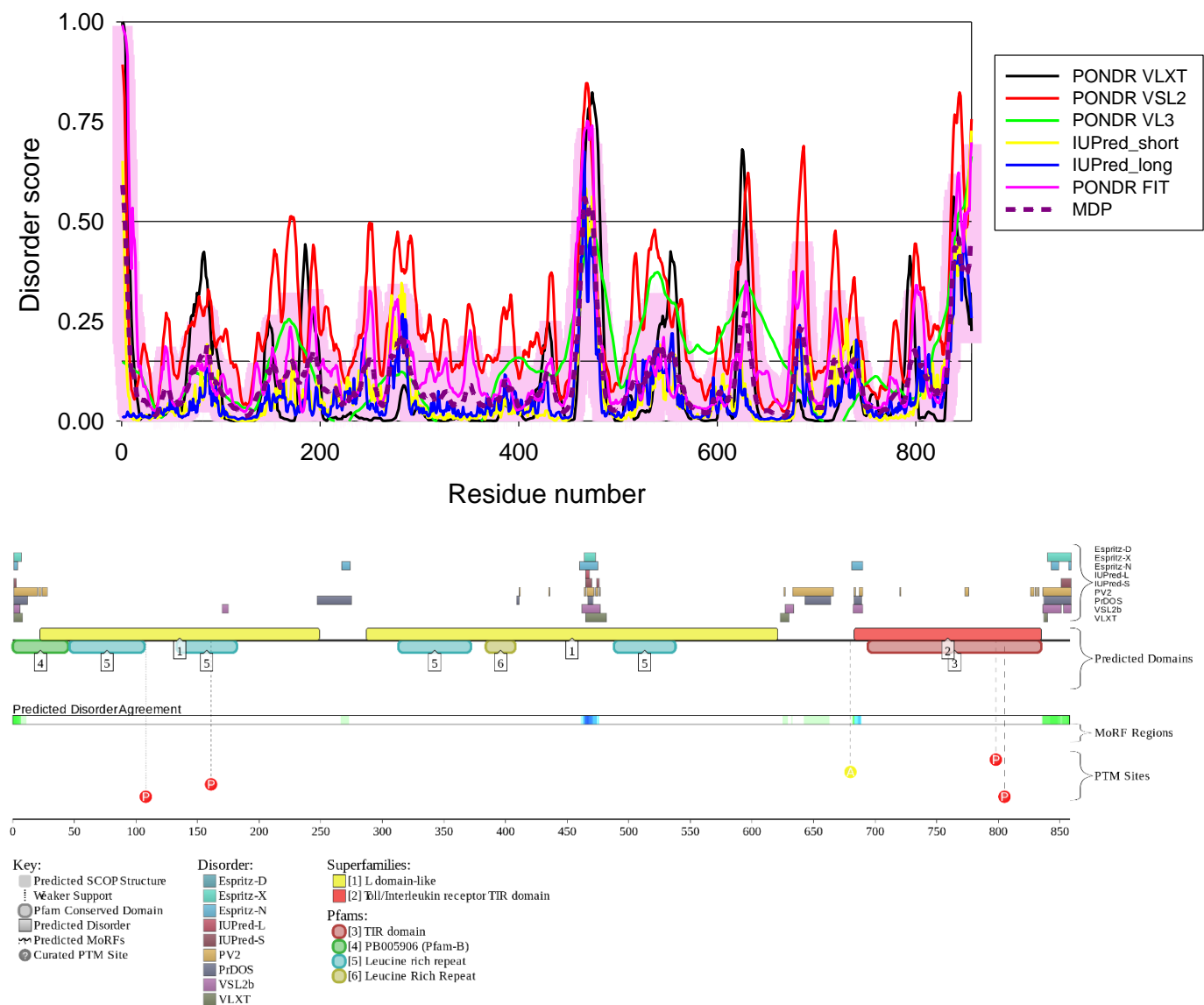


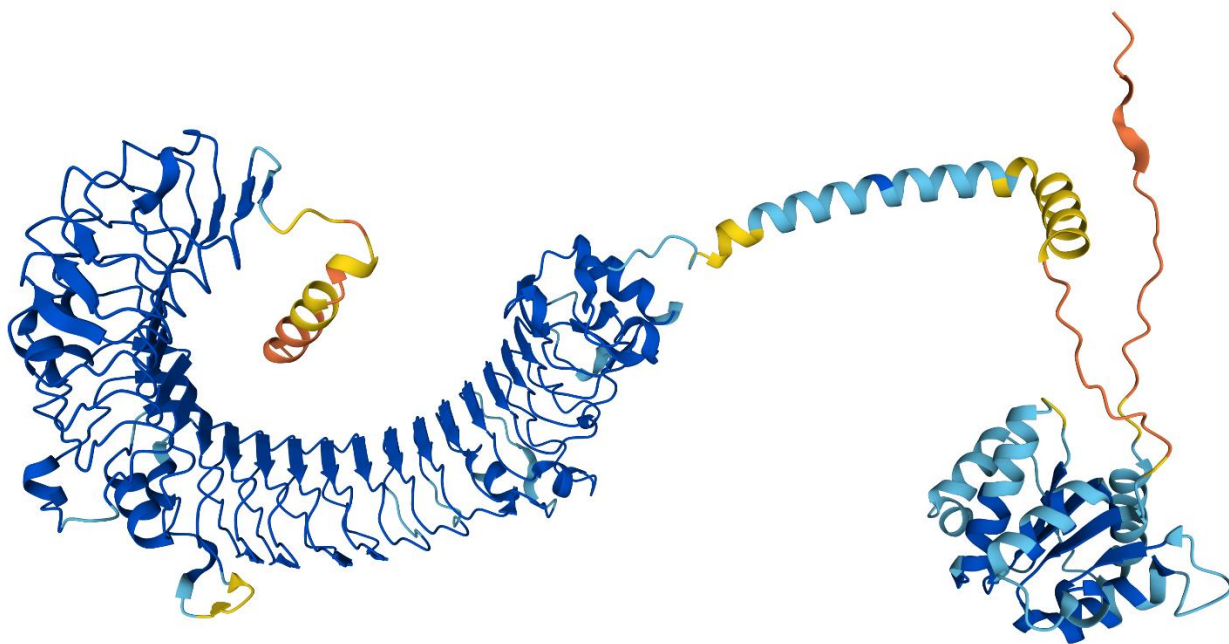
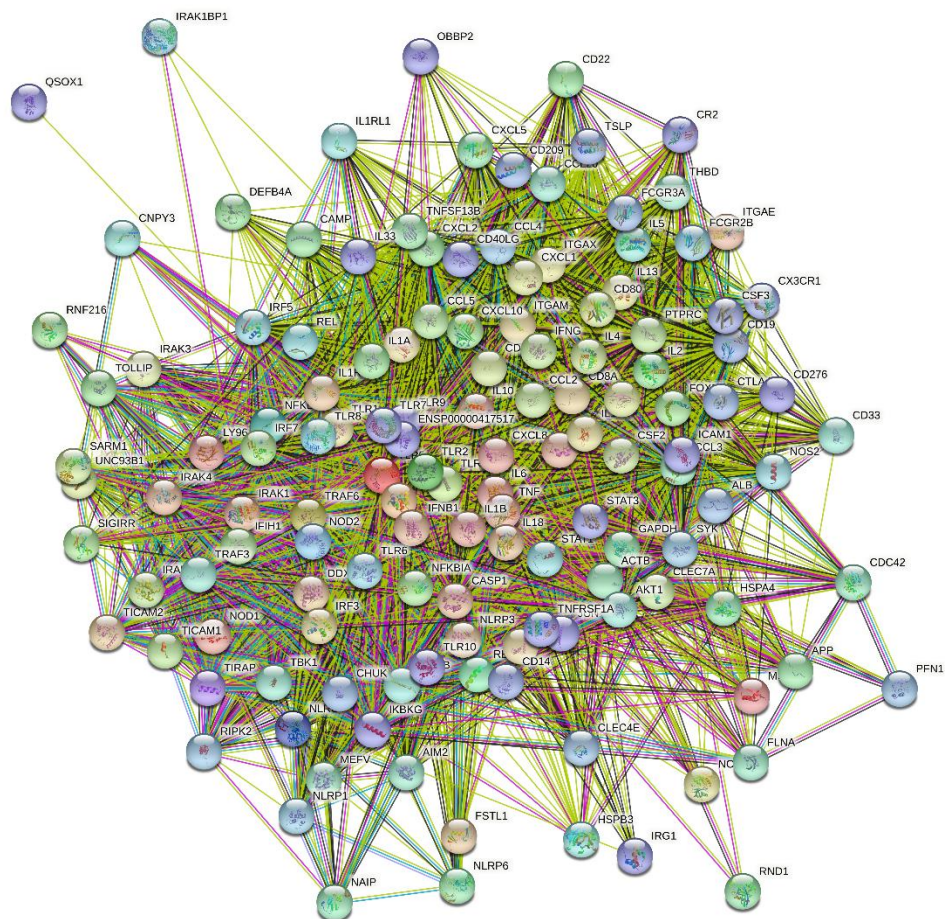


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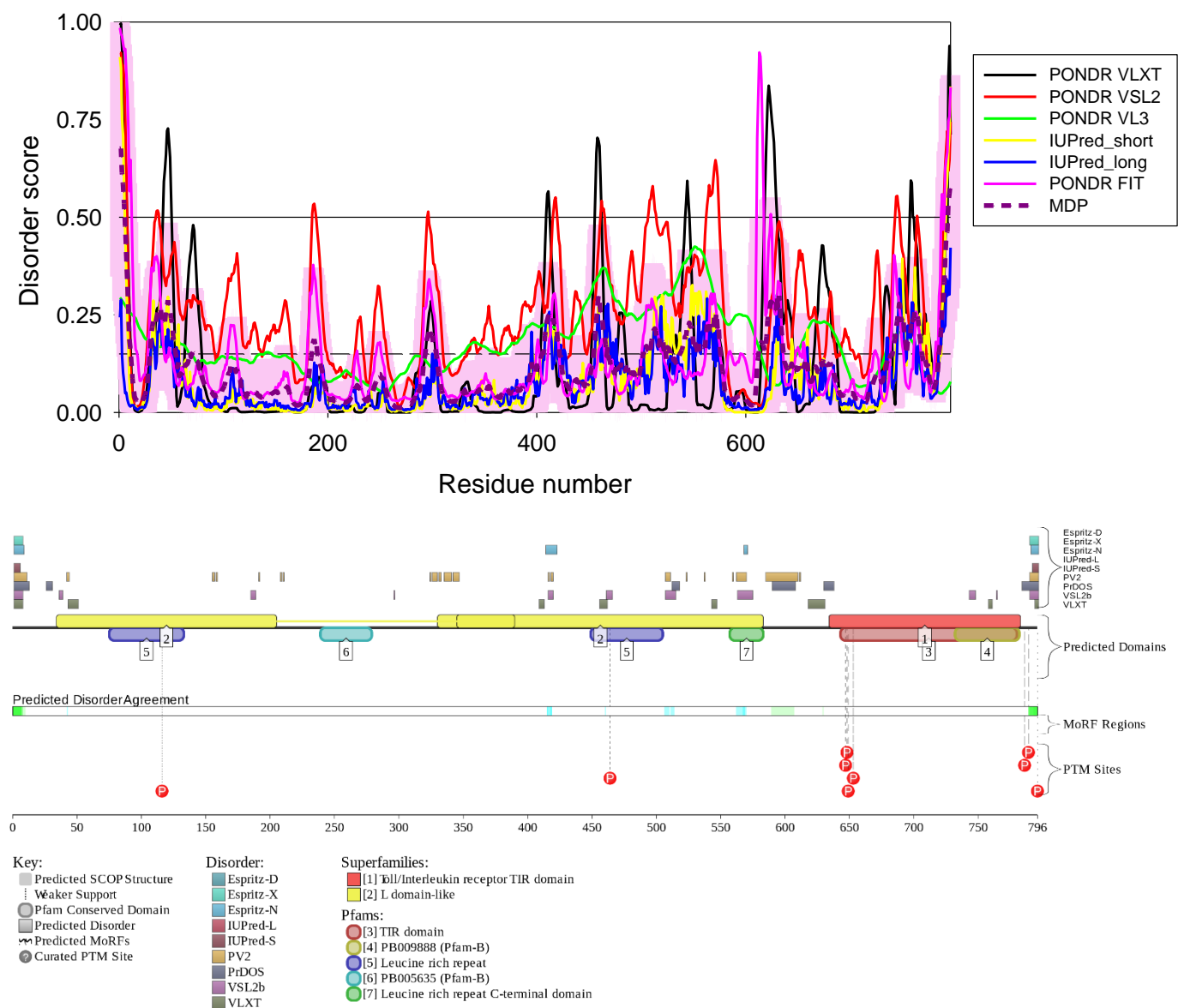
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LNLSYNLLGELYSSNFYGLPKVAYIDLQKNHIAIIQDQTFKFLEKLQTLDLRDNALTTIHFIPIPDIFLSGNKLVLTLPKINLTA
NLIHLSNRLENLDILYFLLRVPHLQILILNQNRFS SCSDQTPSENPSLEQLFLGENMLQLAWETELCWDVFEGLSHLQVLYLN
HNYLNSLPPGVFSLHTALRGLSLNSNRLTVLSHNDLPANLEILDISR NQLLAPNPDV FVSVLSVLDITHNKFICECELSTFINWLN
HTNVTIAGPPADIYCVYPDSFSGVSLFSLSTEGCDEEEVLKSLKFSLFIVCTVTLTLFLMTILT VTKFRGFCFICYKTAQR L VFK
DHPQGTEPD MYKYDAYLCFSSKDFTWVQNALLKHLDTQYS DQNRFNLCFEERDFVPGENRIANIQDAIWN SRKIVCLVSRHFLRD
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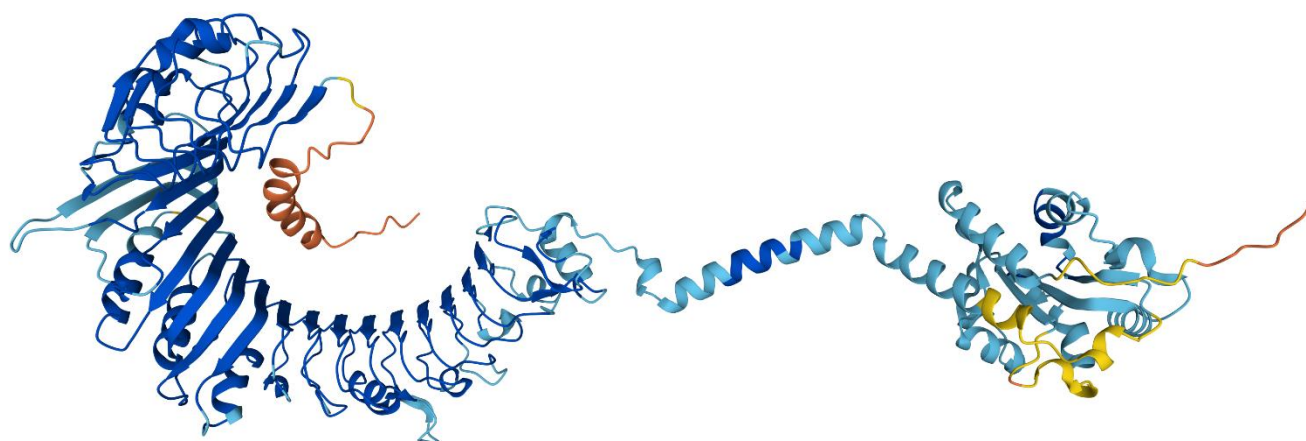
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NRIQLLDLSVFKFNQDLEYLDLSHNQLQKISCHPIVSFRHLDLSFNDFKALPICKEFGNLSQLNFLGLSAMKLQKLDLLPIAHLH
LSYILLDLRNYIYIKENETESLQILNAKTLHLVFHPTSLFAIQVNISVNTLGCLQLTNIKLNDNCQVFIKFLSELTRGSTLLNFT
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TPFIHMLCPHAPSTFKFLNFTQNVFTDSIFEKCS TLVKLET LILQKNGLKDLFKVGLMTKDMPSLEILDVSWNSLESGRHKENCT
WVESIVVLNLSSNMLTDSVFRCLPPRIKVLDLHSNKIKSVPKQVVKLEALQELNVAFNSLTDLPGCGSFSSLSVLIIDHNSVSH
SADFFQSCQKMRSIKAGDNPFQCTCELREFVKNIDQVSSEVLEGWPD SYKCDY P ESYRGSPLKDFHMSSELSCNITLLIVTIGATM
LVLAVTVTSLCIYLDLPWYLRMVCQWTQTRRRARNIPLLEELQRNLQFHAFISYSEHDSAWVKSELVPYLEKEDIQICLHERNFVP
GKSIVENIINCIEKSYKSIFVLSPNFVQSEWCHYELYFAHHNLFHEGSGNNLILILLEPIPQNSIPNKYHKLKALMTQRTYLQWPK
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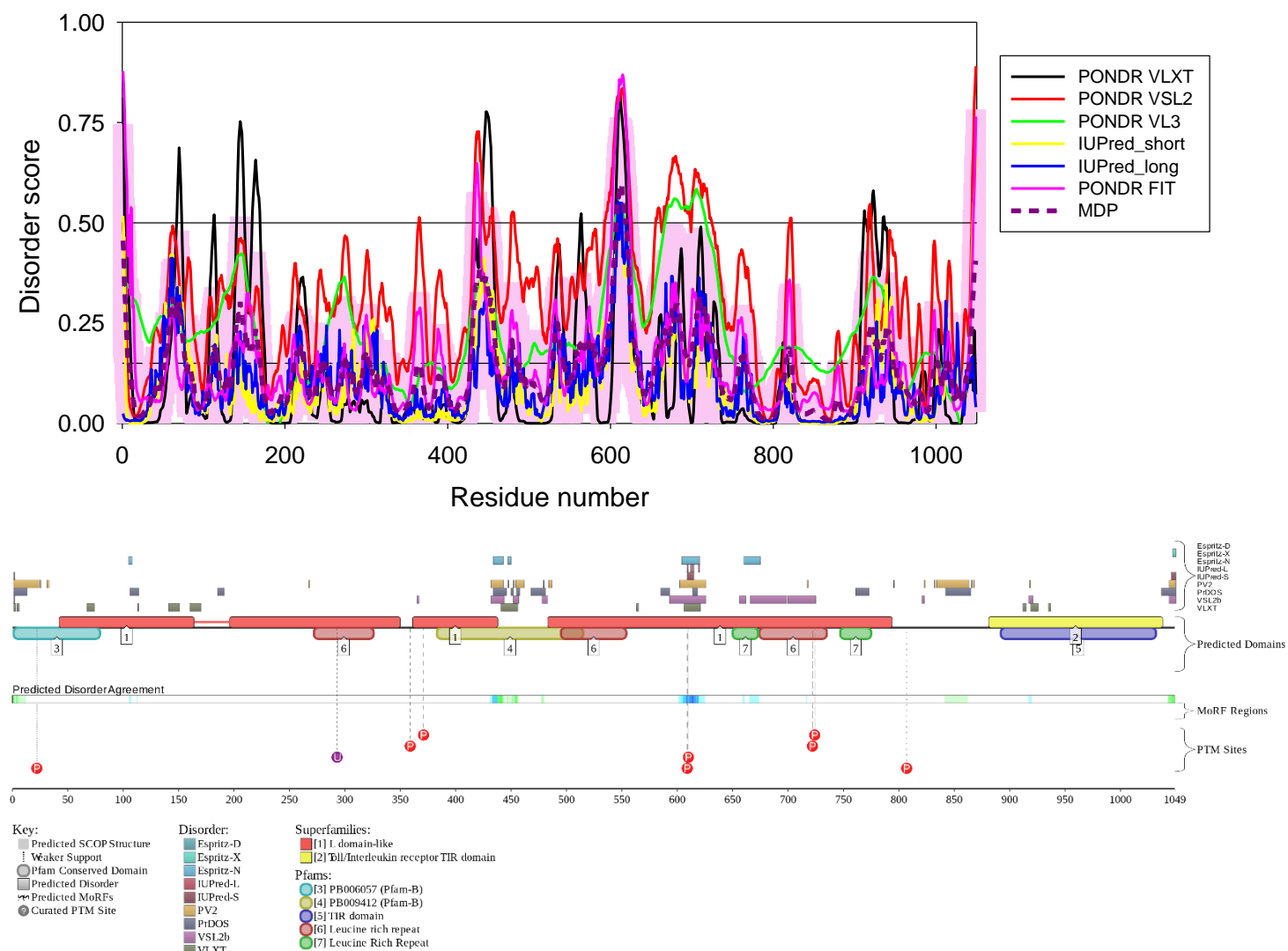


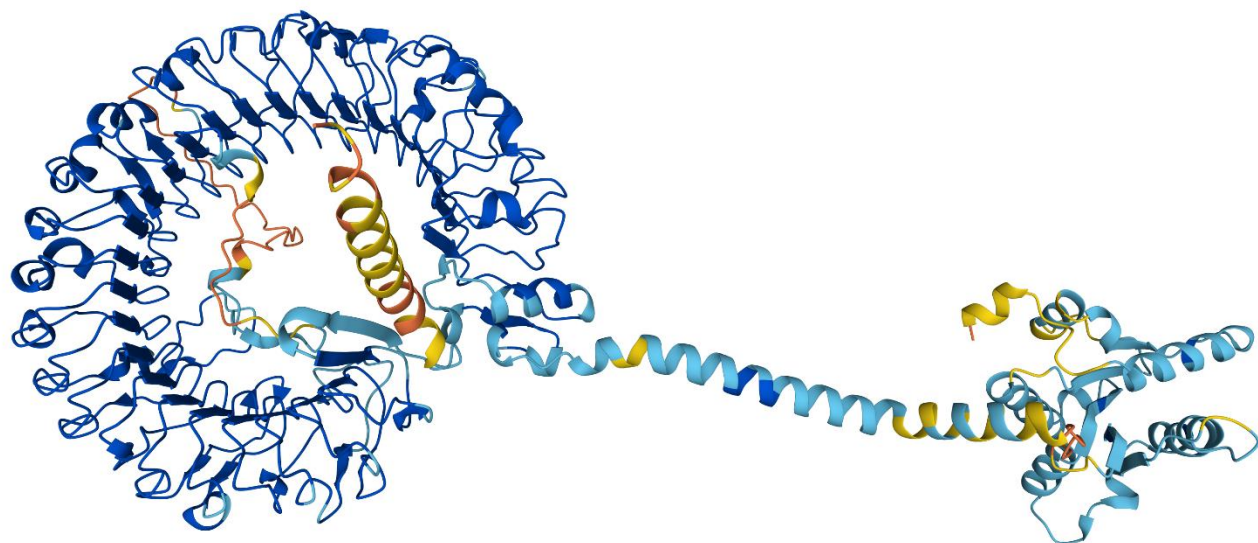
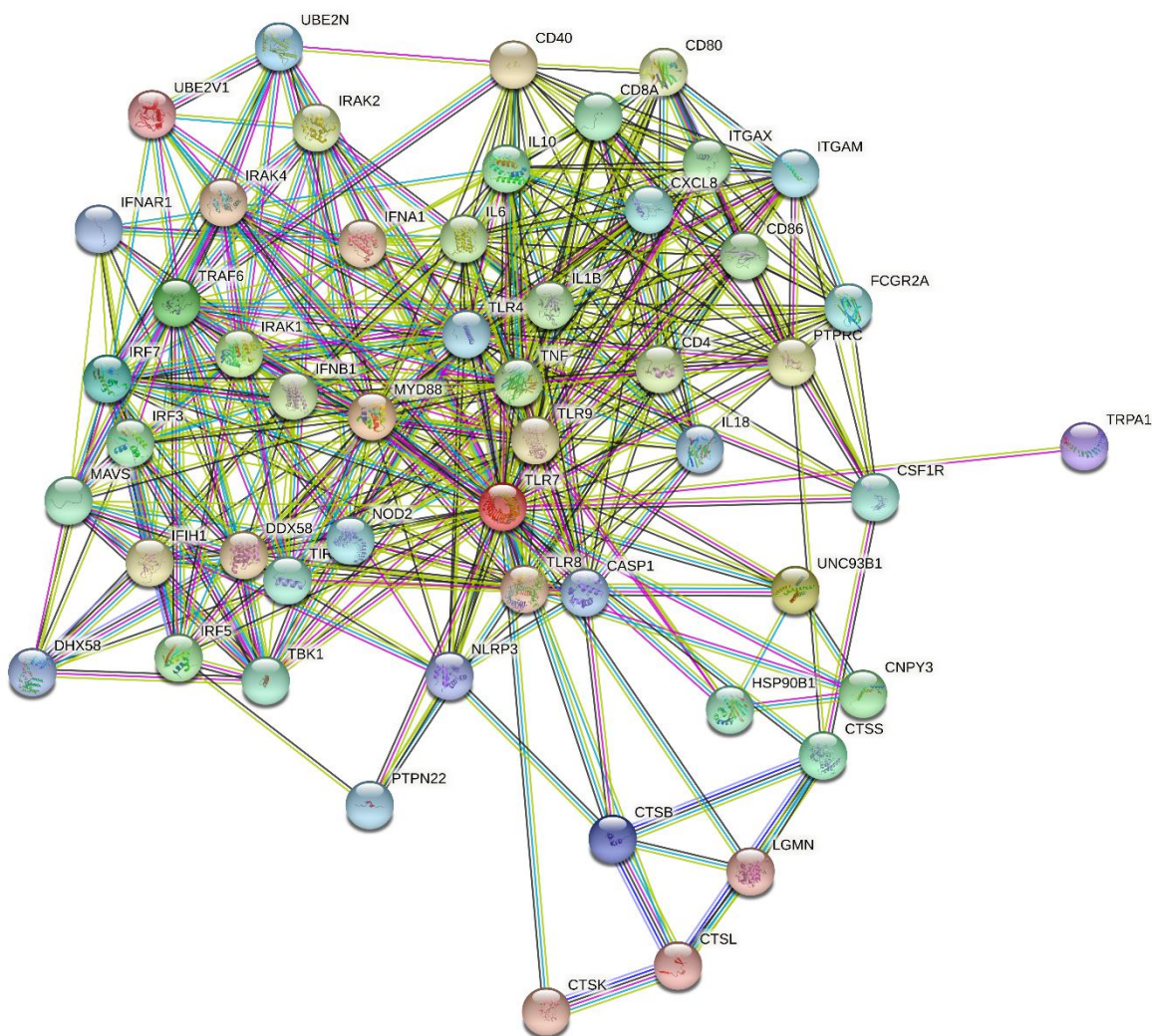


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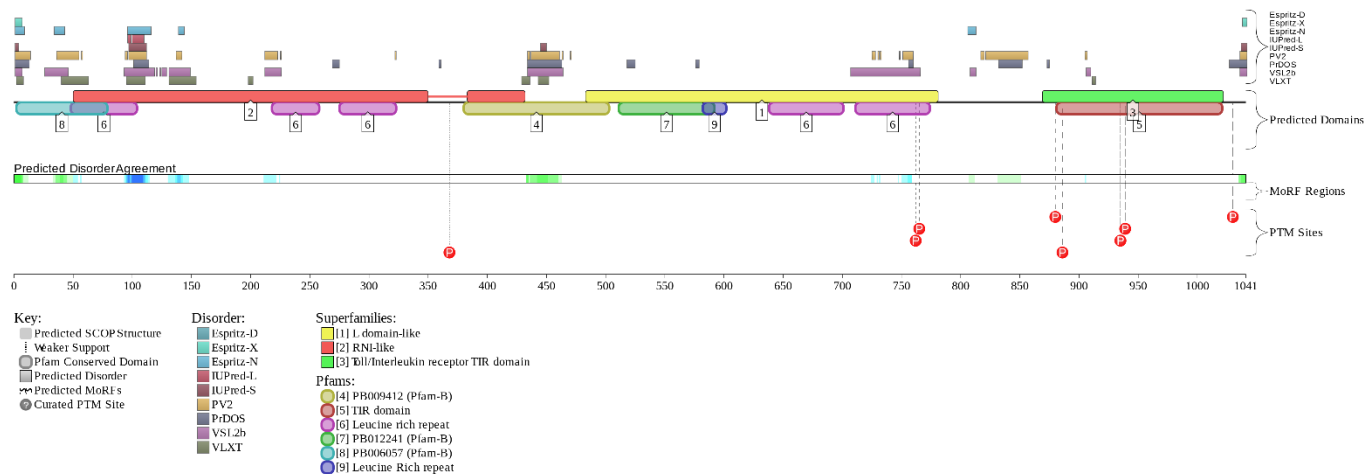
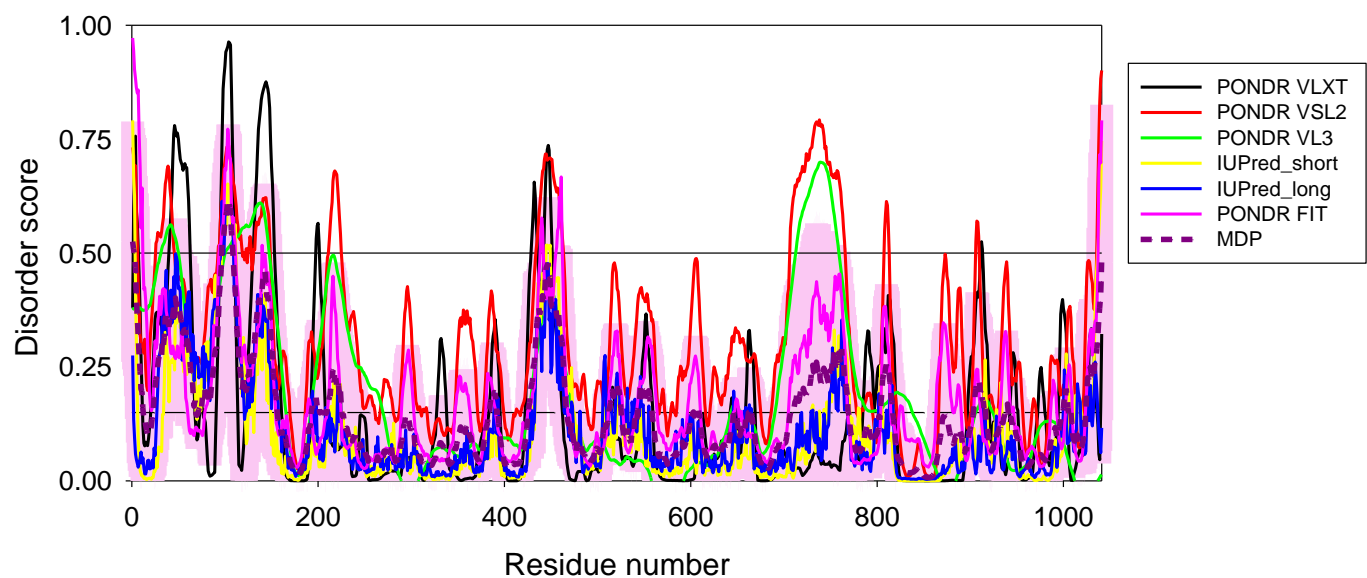
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LANIEILYLGQNCYRNPICYVSYSIEKDAFLNLTCLKVLSLKDNVNTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNLNQLQILD
LSGNCPRCYNAPFPAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWFKNINKLQELDLSQNF LAKEIGDAKFLHFLP
SLIQDLDSFNLFELQVYRASMNLSQAFSSLSKILIRIGYVFKEKLSFNLSPLHNLQNLEVLDTGTNFIKIANLSMFKQFKRLKV
IDLSVNKISPSGDSSEVGFCNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDSLKNSIFFVKS
SDFQHLSTFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRLDLLHSTAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNL
KVLQKLMMDNDISSSTSRMTSESLRTELEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSFLPSGVFDGMPPNLKNL
SLAKNGLKSFWSKKLQCLKNLETLDSLHNQLTTVPERLSNCSRSLSKNLILKNNQIRSLTKYFLQDAFQLRYLDLSSNKIQMIQKT
SFPENVLNNLKMLLLHHNRFLCTCDAVWFVWVNHTTEVTIPYLATDVTVCVGPAGHKQSVISLDLYTCELDLTNLILFSLISVS
LFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCEERDWLP
GQPVLENLSQSIQLSKKTVMFMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQ
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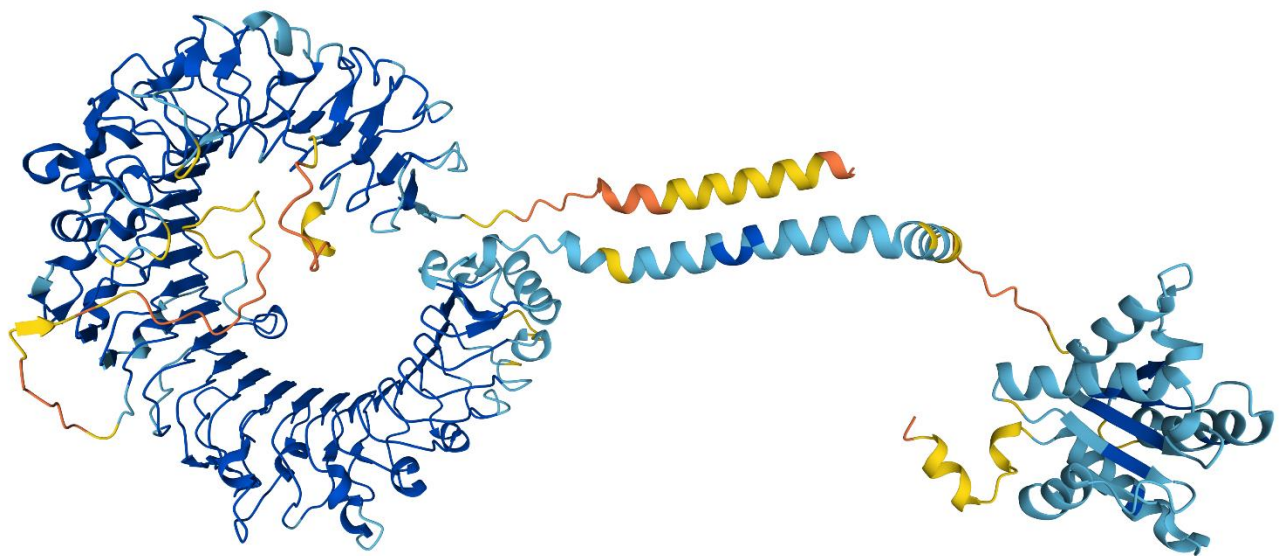
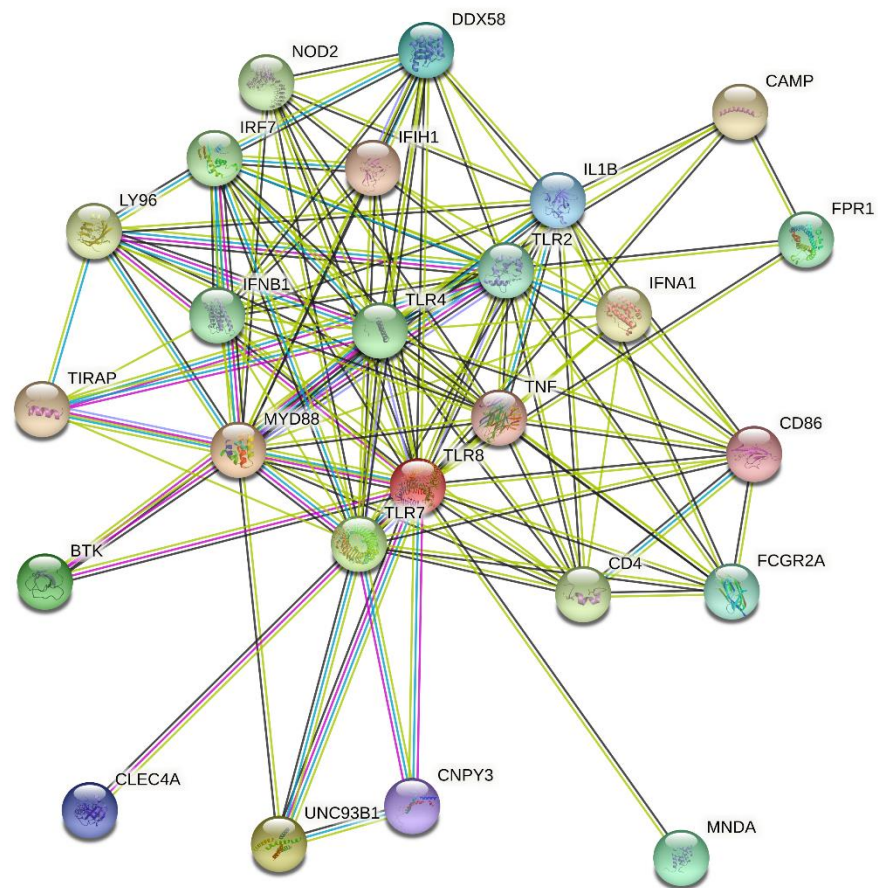
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LQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNLKLNRELLLEDNQLPQIPSGLPESLTELSQLNNIYNITKEGISRLI
NLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFSLNTQIKYISEEDFKGLINLTLLDLG
NCPRCFNAPFPCVPCDGGASINIDRFAFQNLTLQLRYLNLSSTSLRKINAAWFKNMPHLKVLDLEFNLYLVEIASGAFLTMLPRLE
ILDLSFNLIKGSYPQHINISRNFSKLLSLRALHLRGYVFQELREDDFQPLMQPLNLSTINLGINFIKQIDFKLFQNFNSLEIIYL
SENRI SPLVKDTRQSYANSSSFQRHIRKRRSTD FEFDPHSNFYHFT RPLIKPQCAAYGKALDLSLSIFFIGPNQFENLPDIACL
NLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDEVLDSLNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNN
IYTLTDKYNLESKSLVELVFSGNRLDILWNDDDNRYISIFKGLKNLTRLDLNLRLKHIPNEAFLNLPASLTELHINDNMLKFFN
WTL LQQFPRLLELLDLRGNKLLFLTDLSLSDFTSSRLTLLLSHNRISHLPSGFLSEVSSSLKHLDLSSNLLKTINKSALETKT TTKLS
MLELHG NPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASPGDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVLAALAH
LFYWDVWFIYNVCLAKVKGRSLSTSQTfyDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLGLAIDNLMQS
INQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVIFILLEPVLQHSQYLRLRQRICKSSILQWPDNPKAEGFLWQTLRN
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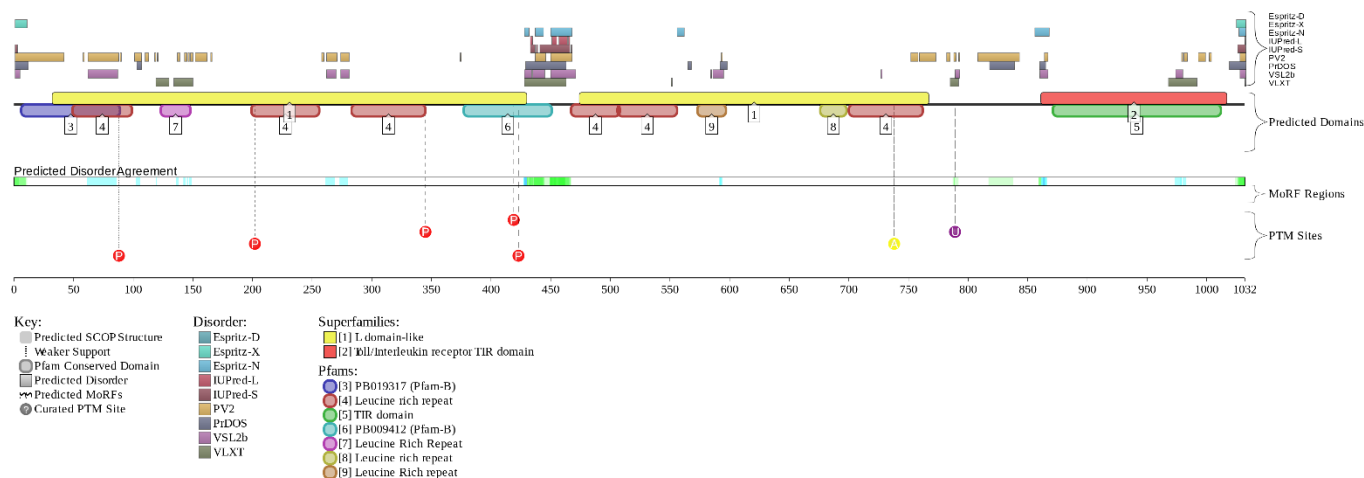
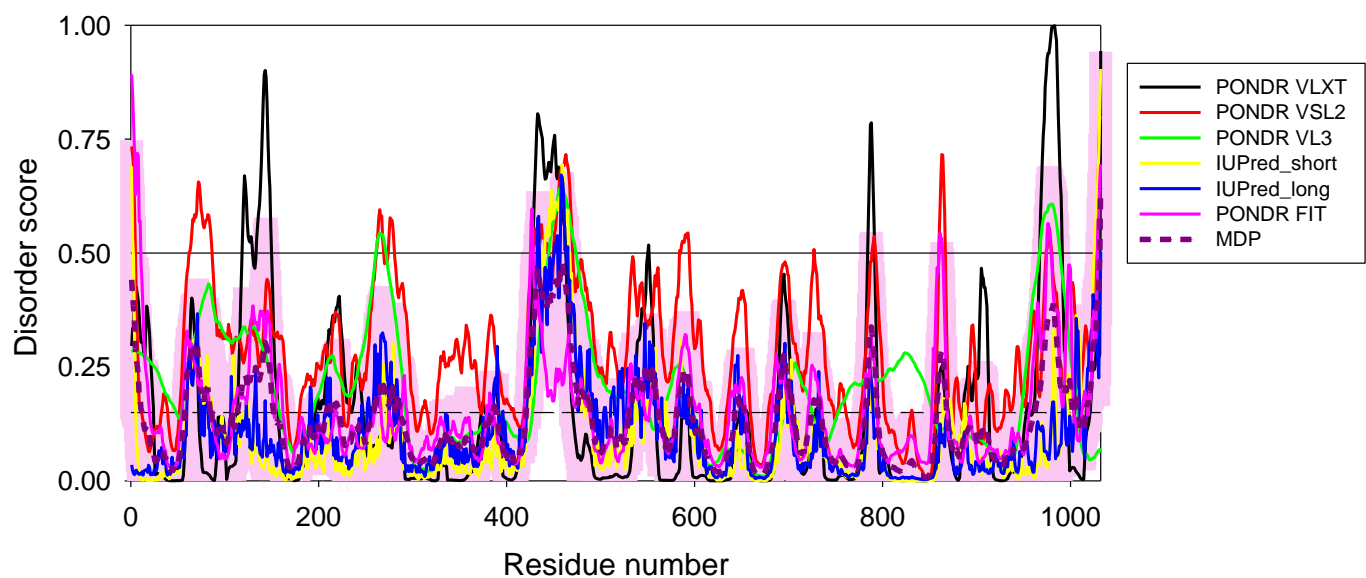


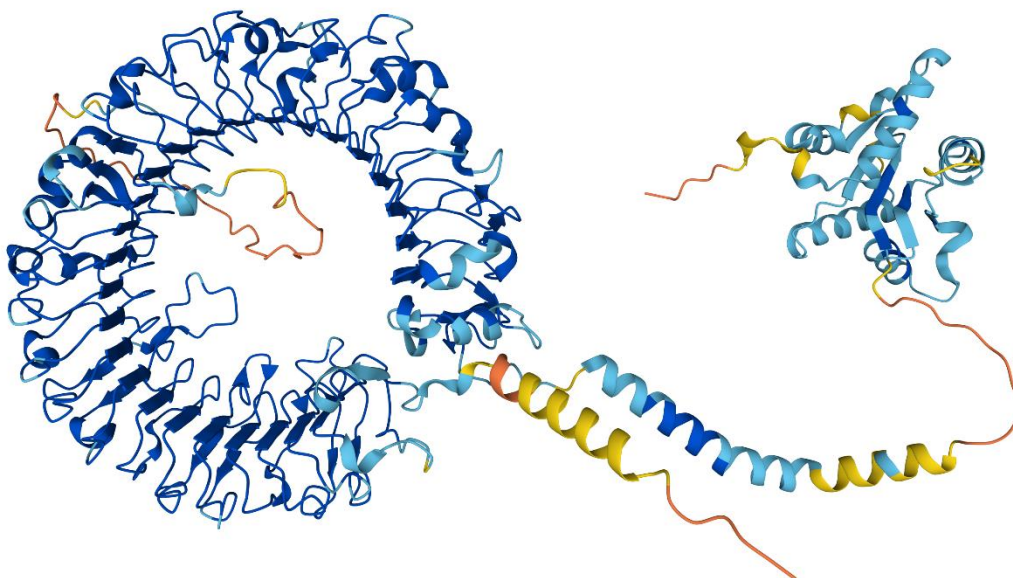



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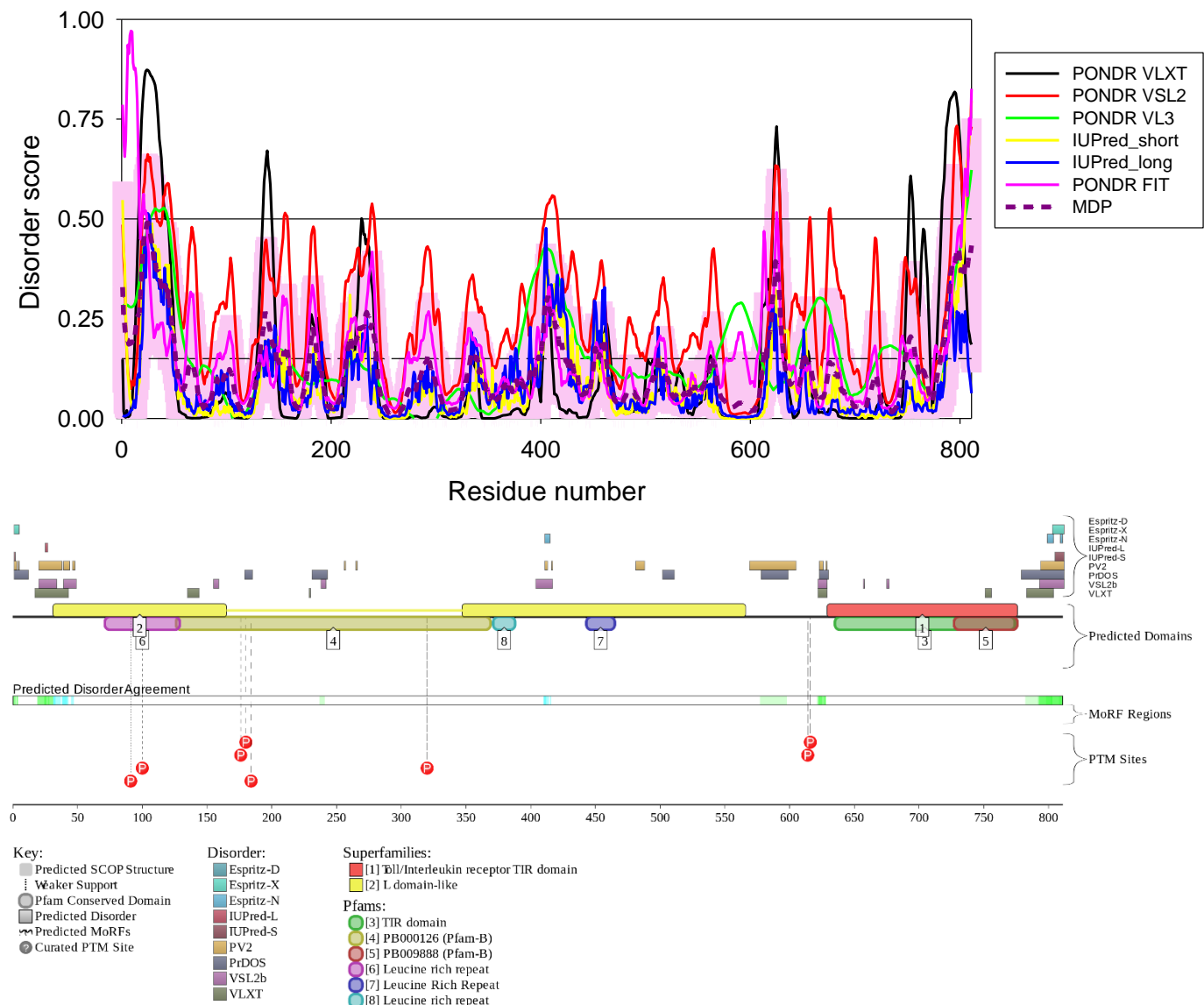
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FLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNTLVVPRNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGNC
RRCDHAPNPMCMECPRHFPQLHPDTFSSHLSRLEGLVLKDSLSWLNASWFRGLGNLRVLDLSENFYKCI TKTKAFQGLTQLRKLN
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RISGASELTATMGEADGGEKVWLQPGDLAPAPVDTFSSSEDFRPNCSLTNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQ
AVNGSQFLPLTGLQVLDLSHNKLDLYHEHSFTLPRLEALDLSYNSQPFQMVGHNFSFVAHLRRTLRLHLSLAHNNIHSQVSQQL
CSTSLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSONRLHTLLPQTLRNLPKSLQVLRRLRDNYLAFFKWWSLHFLPKLE
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CGAAMDFLLEVQAAPVGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCAFSLSLAVALGLGVPMHLHLCGWDLYWCFHLC
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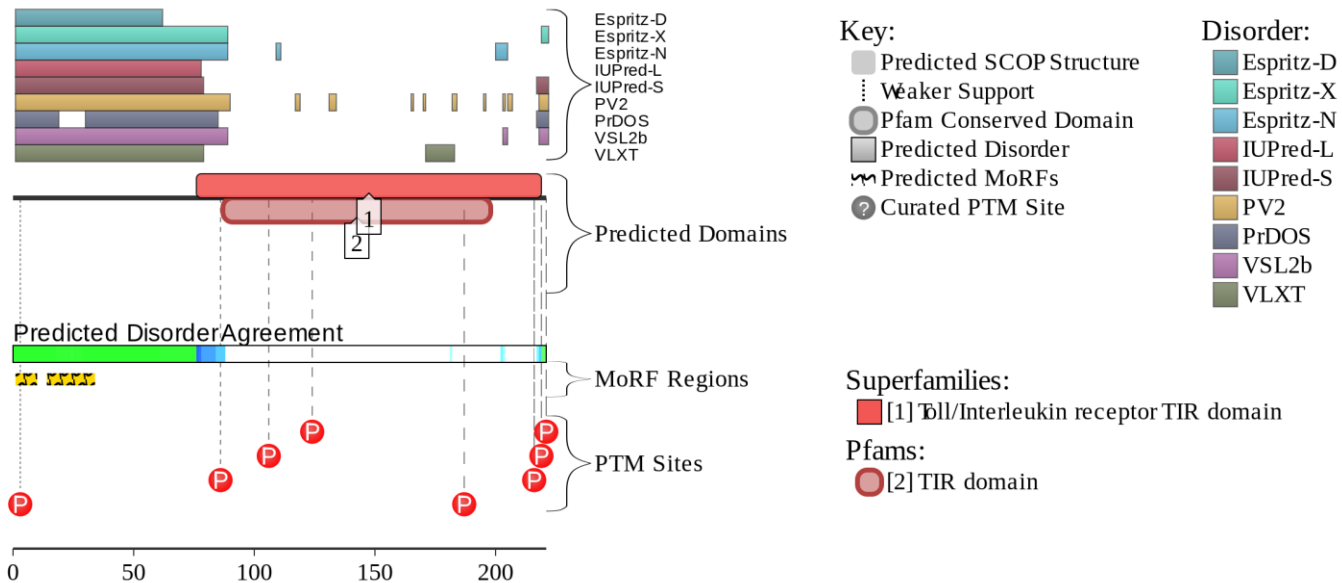
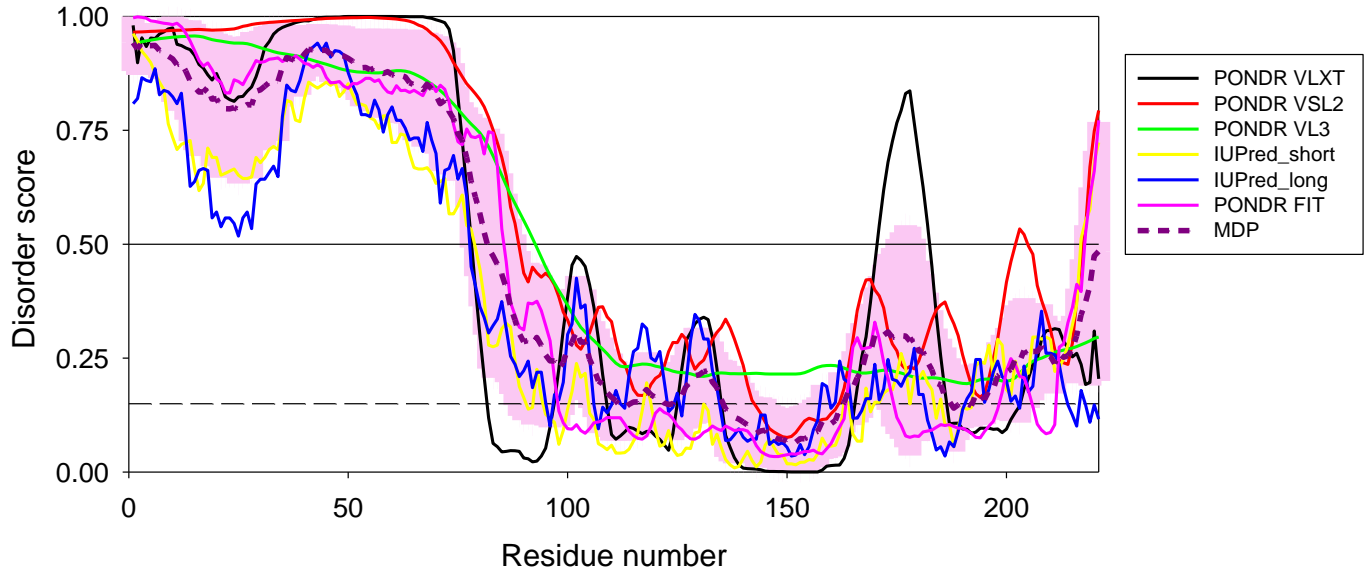


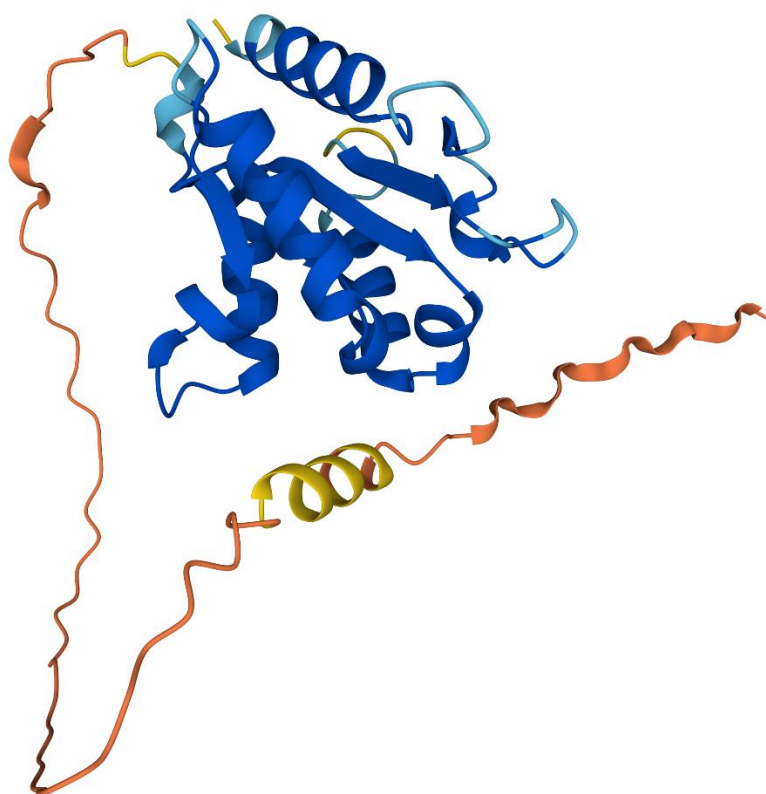
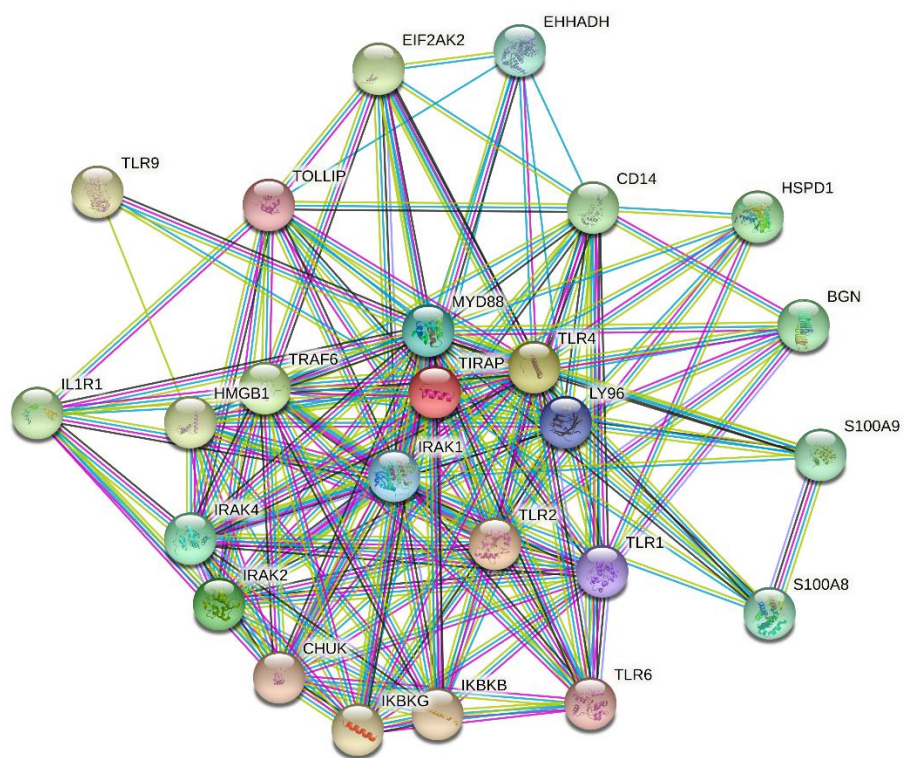
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QLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGRLYLDLSFNDFDTPMICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTV
FLGFRTLPHYEEGSLPILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNKVDLL
WDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFIYIQDKIYLLLTAKMDIENLTISNAQMPH
MLFPNYPYTKFQYLNLFANNILTDELFRKTIQLPHLKTILNNGNKLETLSLVSCFANNTPLEHLDLSQLNLLQHKNDENCSPWETVNV
MNLSTYKLSDSVFRCLPKSIQILDNLNNQIQVTPKETIHLMALRELNIAFNFLTDLPGCSEHFSRLSVLNIEMNFILSPSLDFVQS
CQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMVGWSDSYTCEYPLNLRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVA
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NIVSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLFHENS DHIIILILEPIPFYCIPTRYHKLKALLEKKAYLEWPKDRKCG
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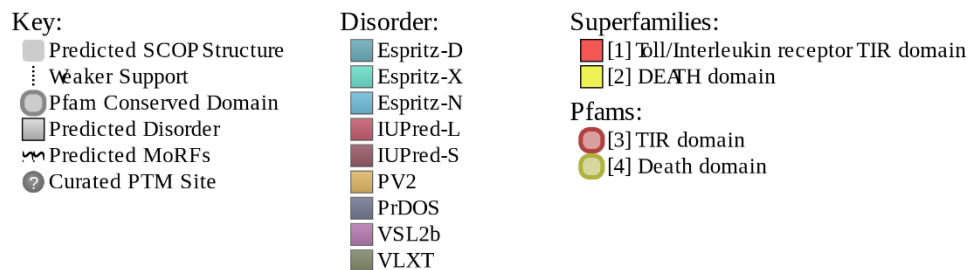
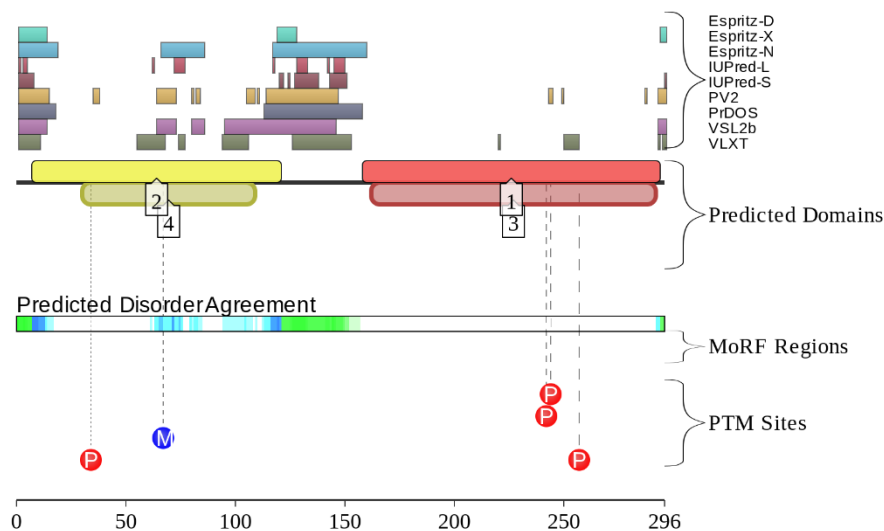
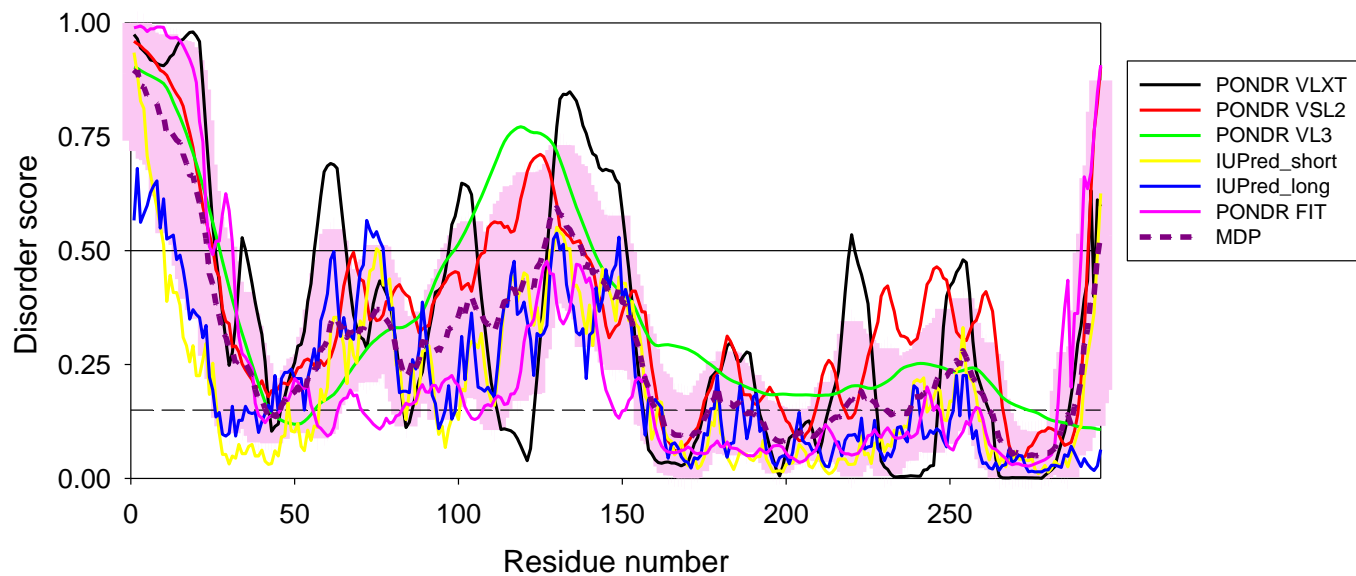
Proteins in TLR-related signaling pathways

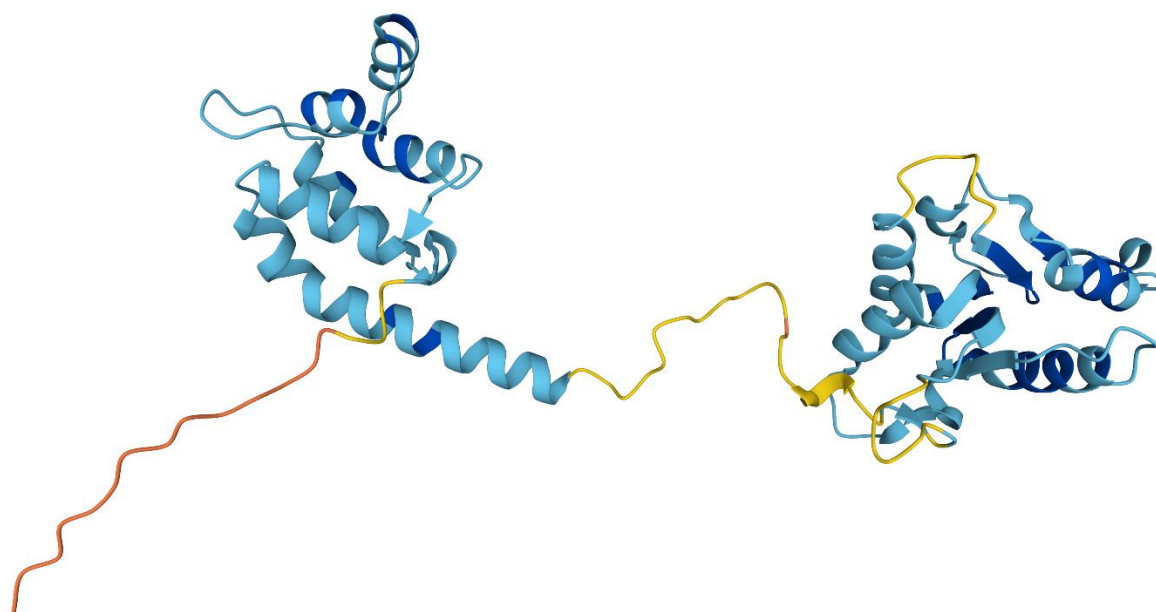
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YDVCVCHSEEDLVAAQDLVSYLEGSTASLRCLQLRDATPGGAIVSELQALSSSHCRVLLITPGFLQDPWCKYQMLQALTEAPG
AEGCTIPLLSSGLSRAAYPPELRFMYYVDGRGPDGGFRQVKEAVMRYLQTL
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sapiens OX=9606 GN=MYD88 PE=1 SV=1
MAAGGPGAGSAAPVSSTSSLPLAALNMRVRRRLSLFLNVRTQVAADWTALAEEMDFEYLEIRQLETQADPTGRLLDAWQGRPGAS
VGRLLLELLTKLGRDDVLLLELGPSTIEEDCQKYILKQQQEEAEKPLQVAAVDSSVPTAELAGITTLDLPLGHMPERFDAFICYCPS
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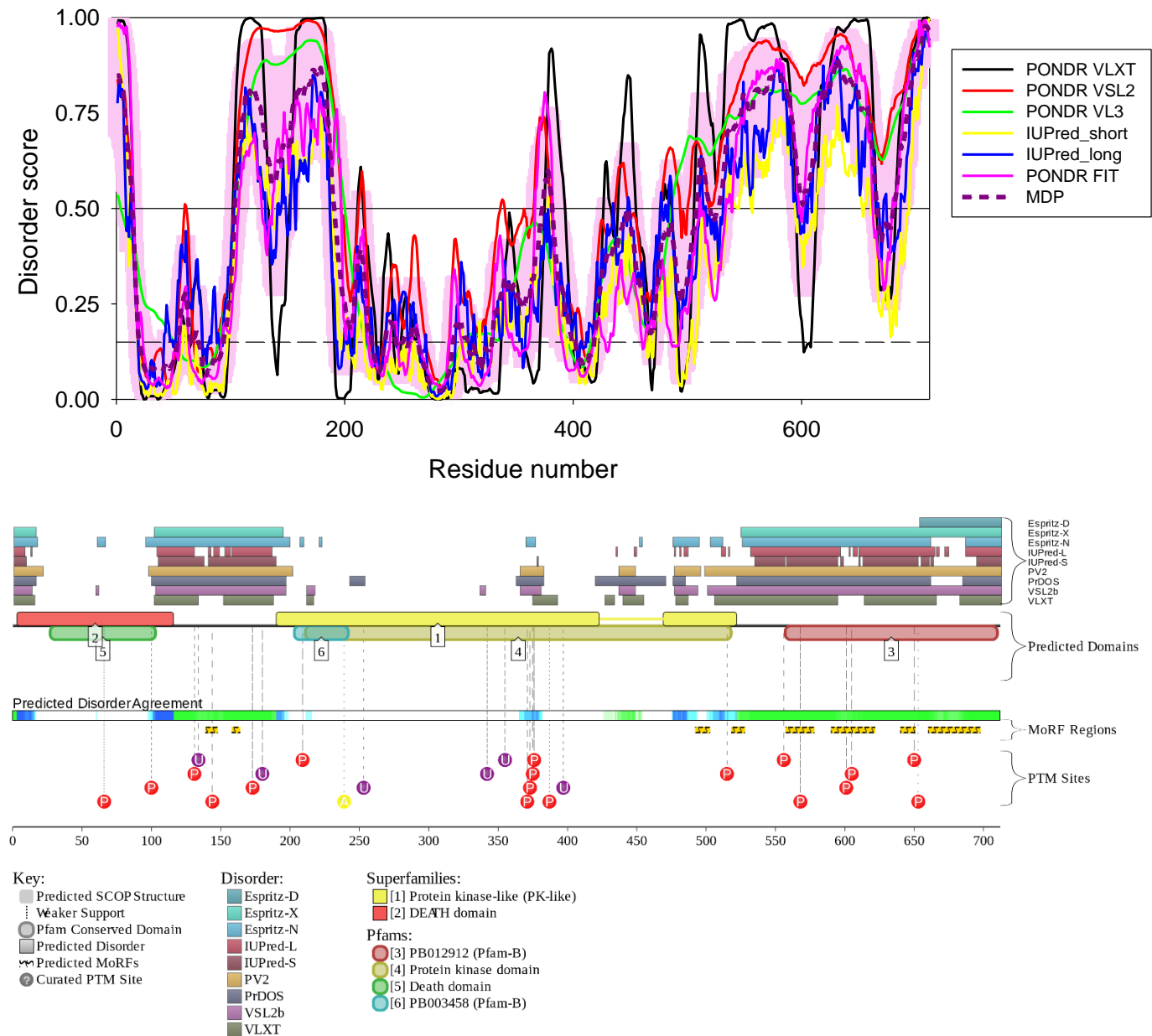




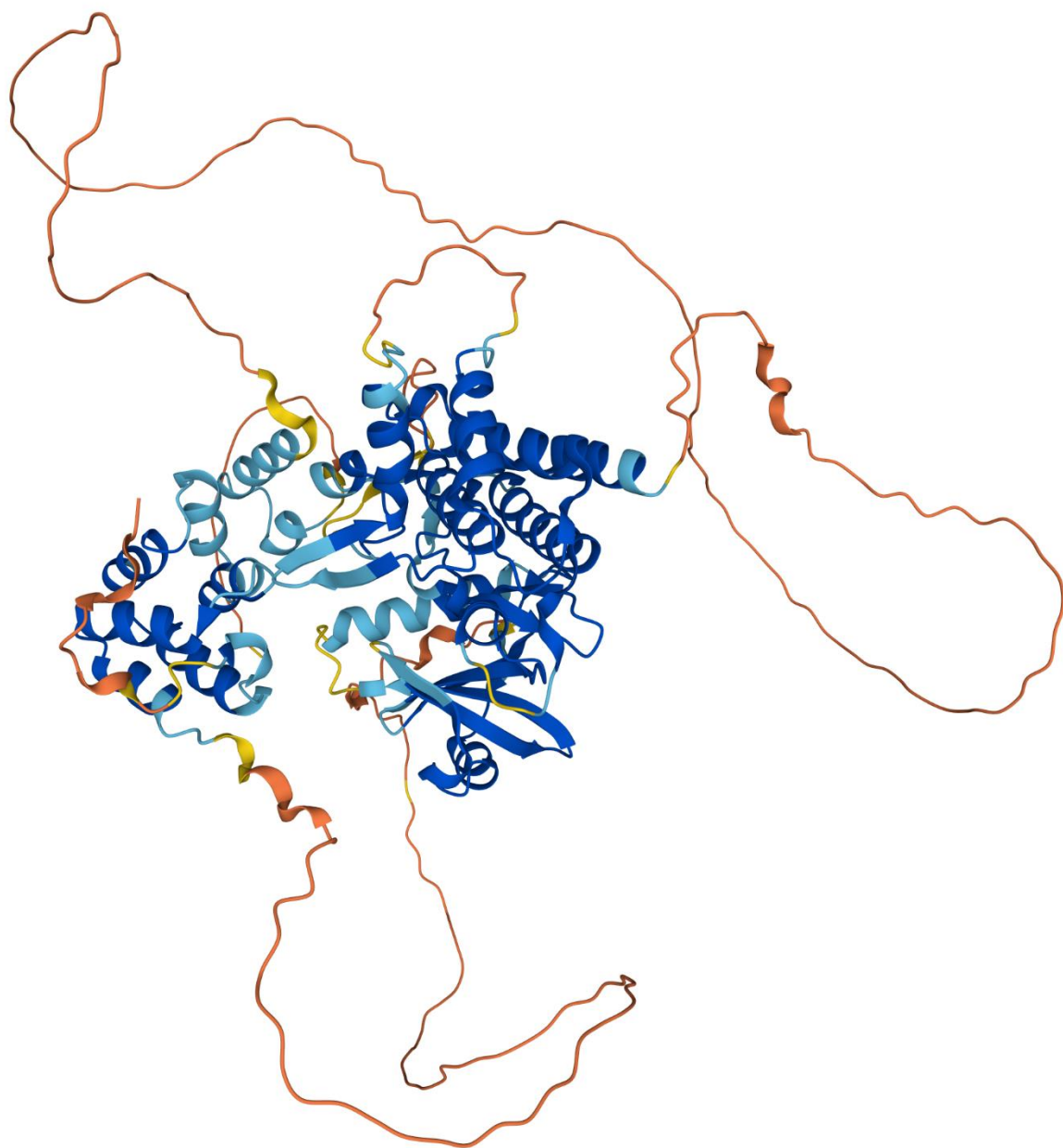
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ILTHLQLLRARDIITAWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSASTFLSPAFFPGSQTHSGPELGLVPSPASLWPP
PPSPAPSSTKPGPESSVSLQGARFPFFCWPLCEISRGTNHFSEELKIGEGGFGCVYRAVMRNTVYAVKRLKENADLEWTAVKQS
FLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGLSLEDRLHCQTQACPLSWPQRLDILLGTARAIQFLHQDSPSLIHGD
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THGARTKYLKDLVEEEAEAEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDP RP GPCPELGLGLGQLACCLHRRRAKRRPP
MTQVYERLEKLQAVVAGVPGHSEAASCI PPSPQENS YV SSTGRAHSGAAPWQPLAAPSGASAAEQ LQRGPNQPVESDES LGGL
SAALRSWHLTPSCPLDPAPLREAGCPQGD TAGESSWGSGPGSRPTAVEGLALGSSASSSSEPPQII INPARQKMVQKLALYEDGA
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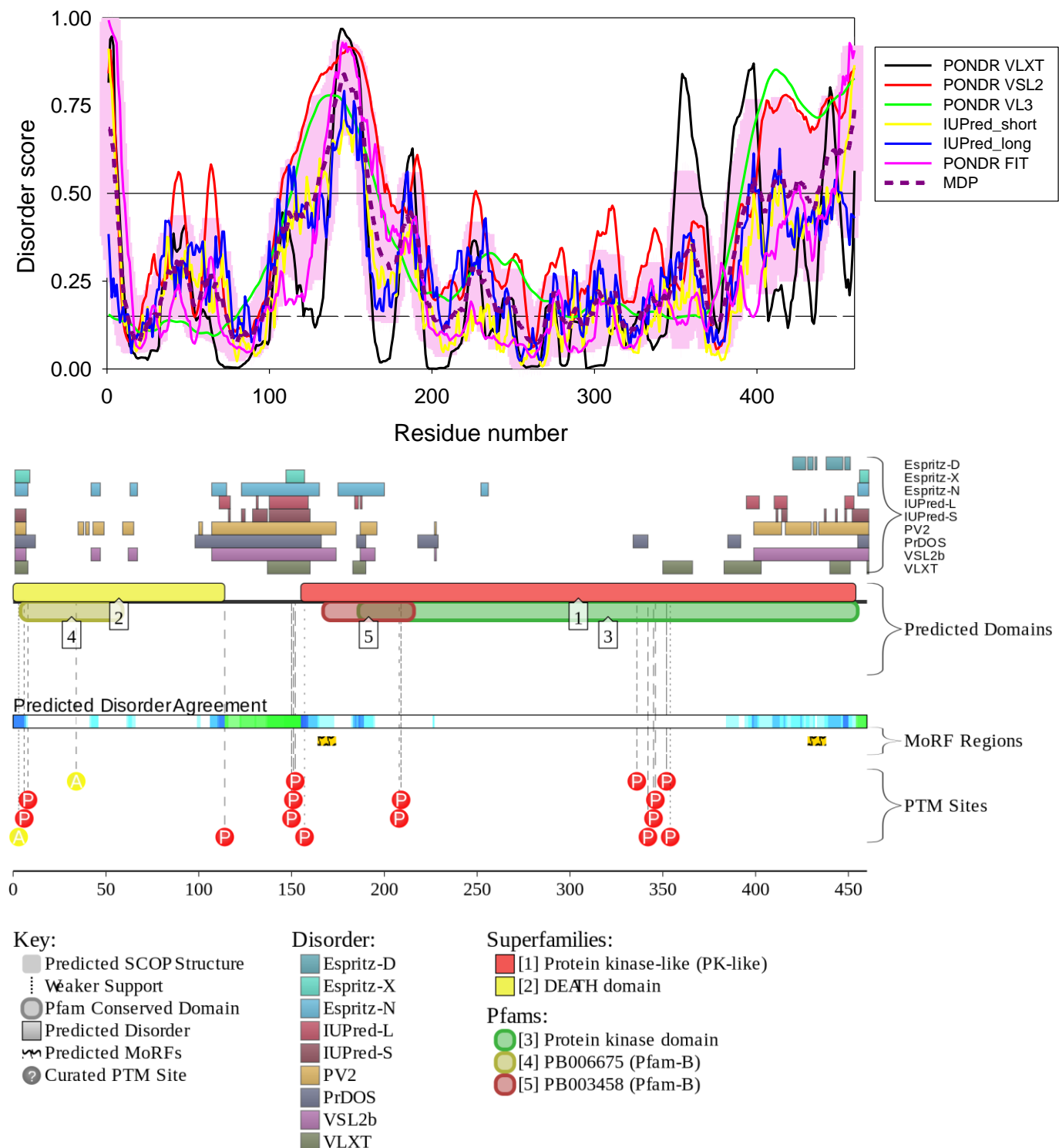
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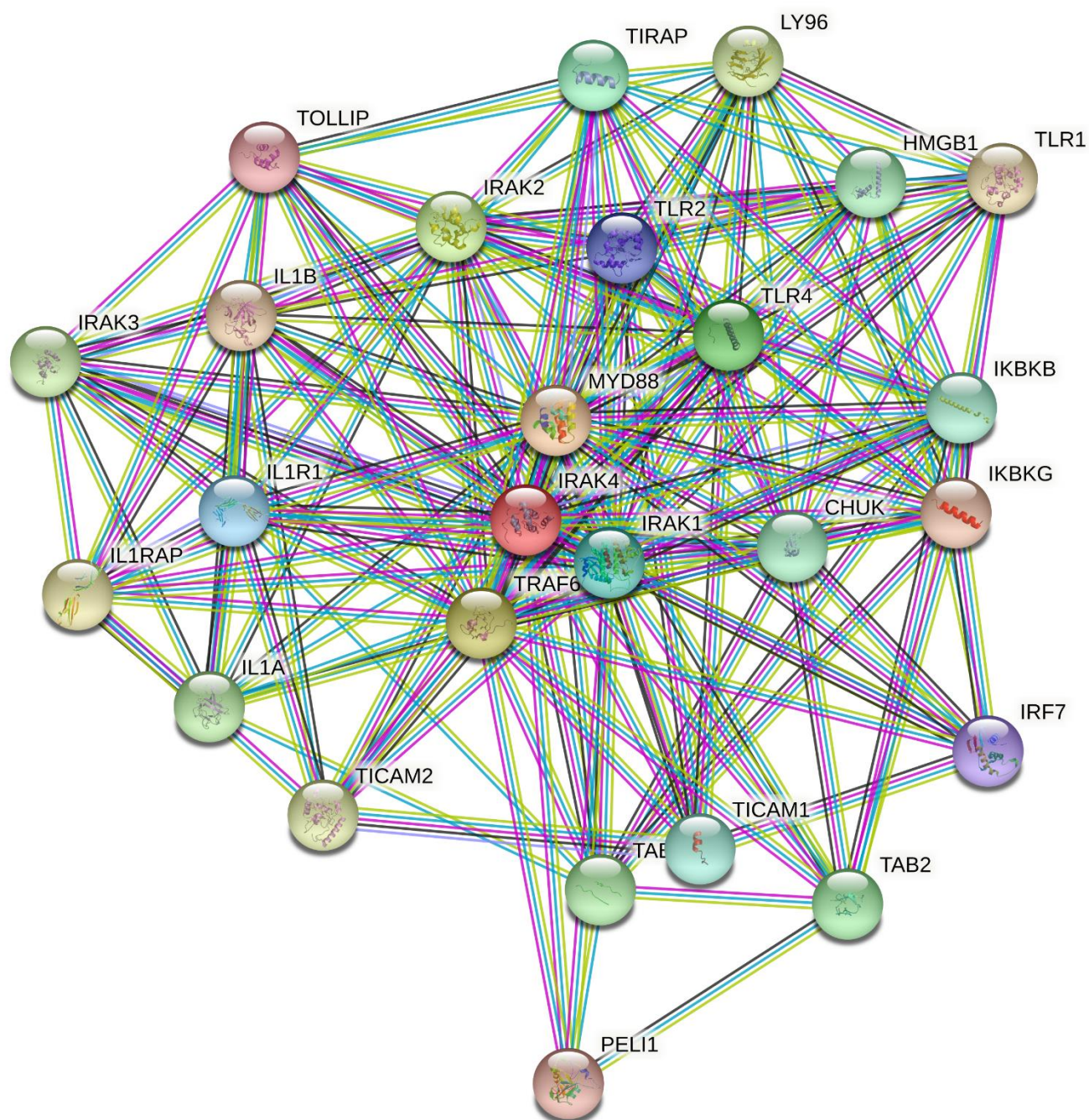


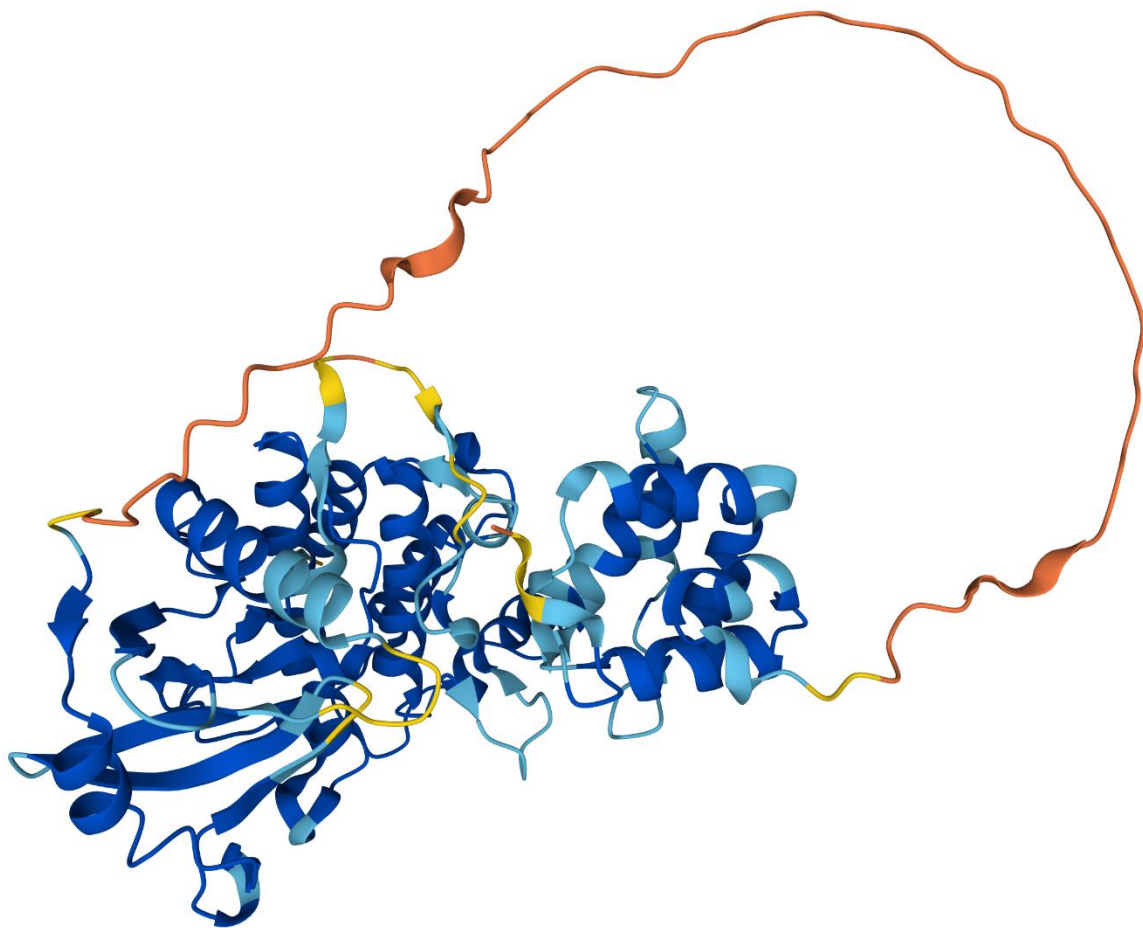




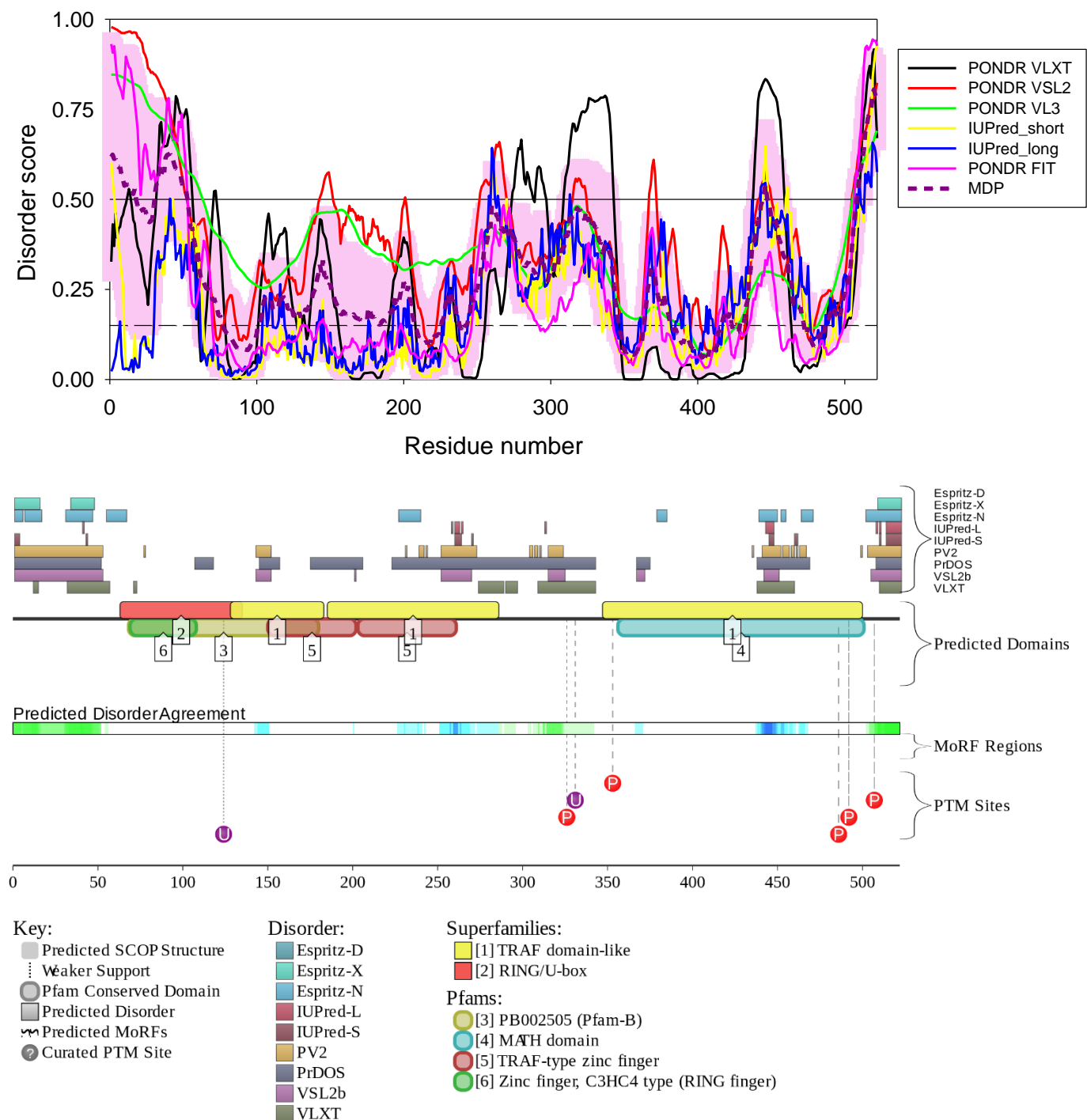

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YELKNVTNNFDERPISVGGNKMGEFGVYKGYVNNTTVAVKKLAAMVDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDG
DDLCLVYVYMPNGSLDLRLSCLDGTPLPSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLARASEKFA
QTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHREPQLLLDIKEEIEDEEKTIEDYIDKKMNDADSTS
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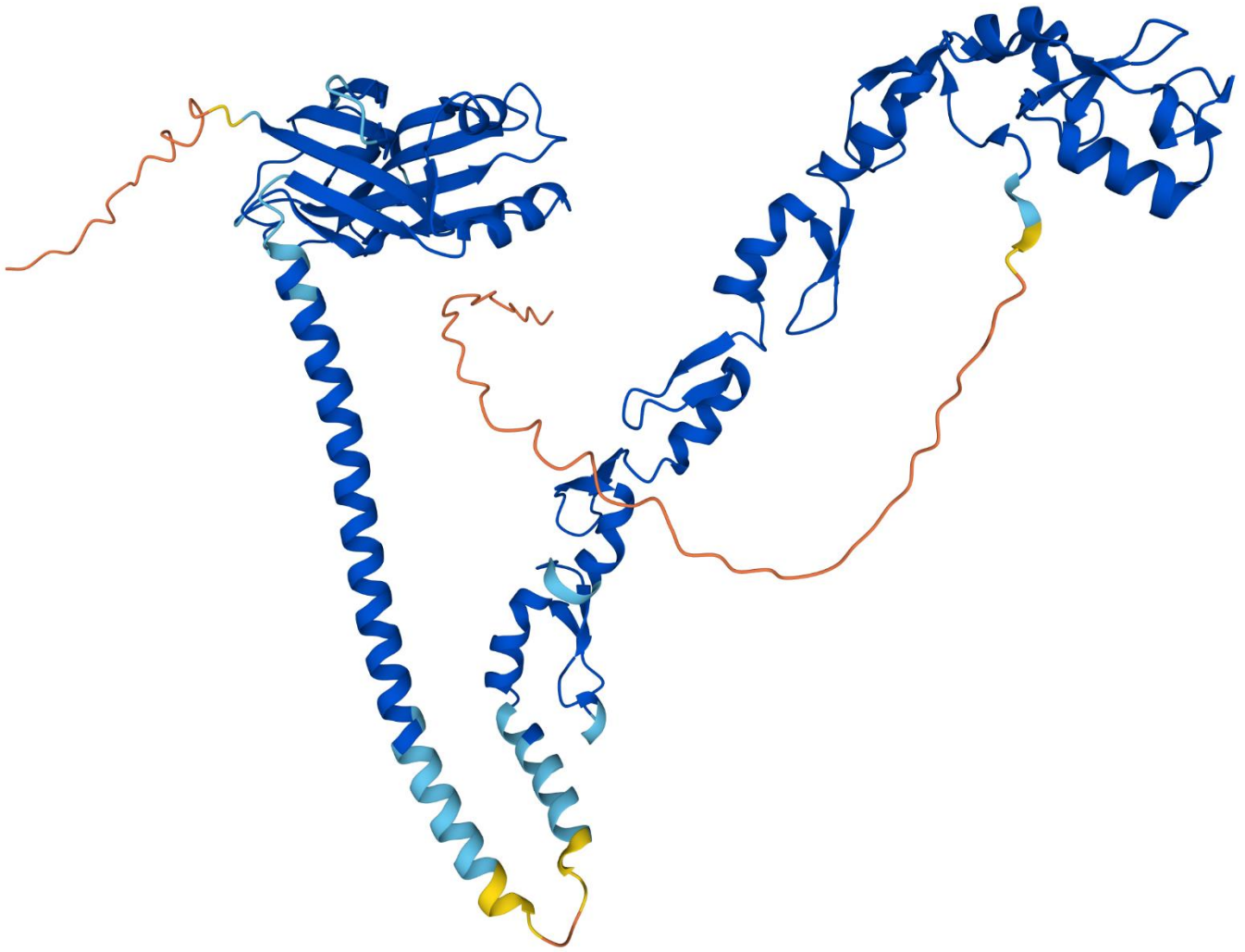




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NHLARHLQENTQSHMRMLAQAVHLSVIPDSGYISEVRNFQETIHQLEGLRQVLDHQLIRELTAKMETQSMYVSELKRTIRTLEDK
VAEIEAQQCNGIYIWKIGNFGMHLKCEEEKPVVIHSPGFYTGKPGYKLCMRLHLQLPTAQRCANYISLFVHTMQGEYDShLPWP
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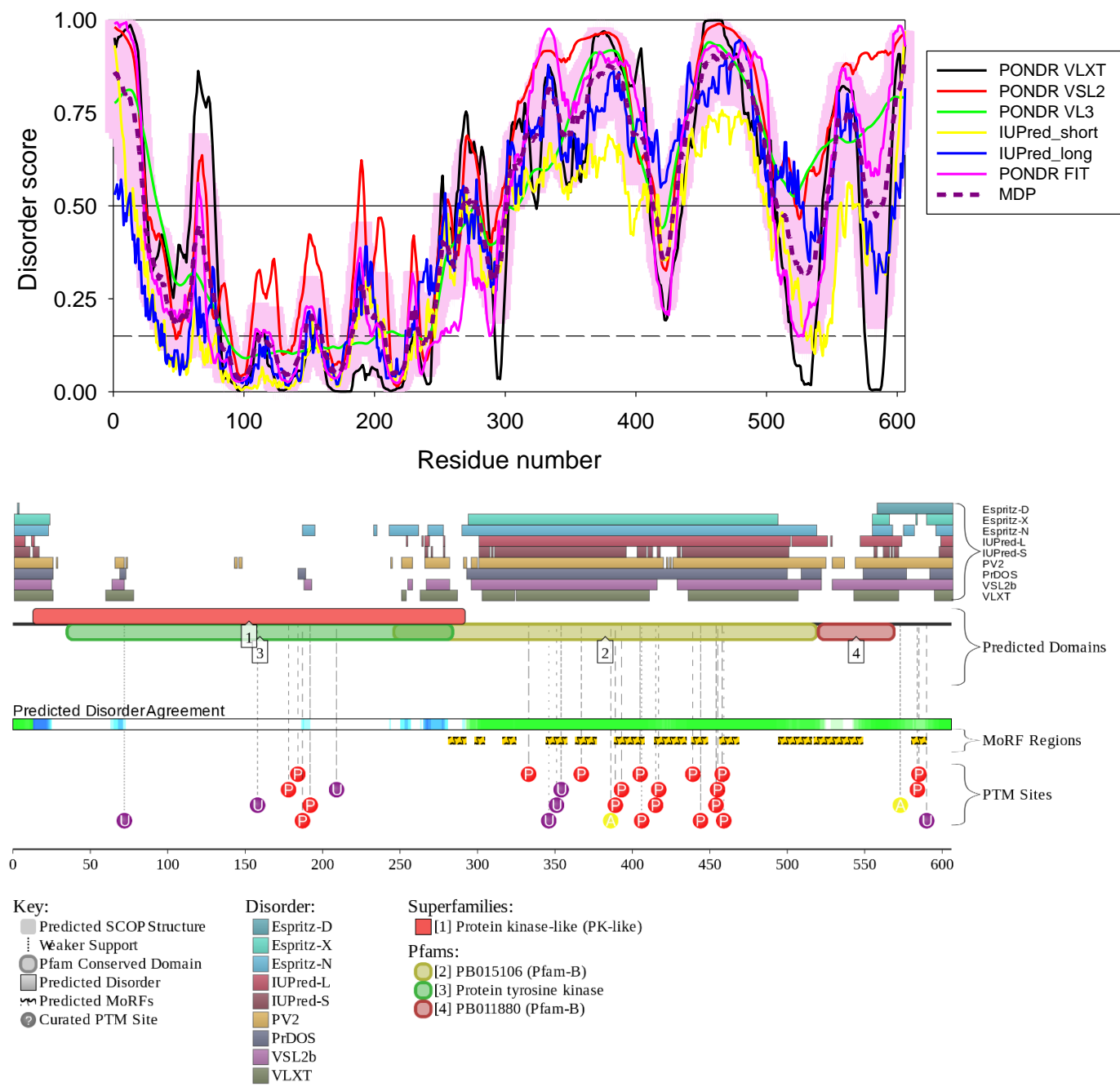


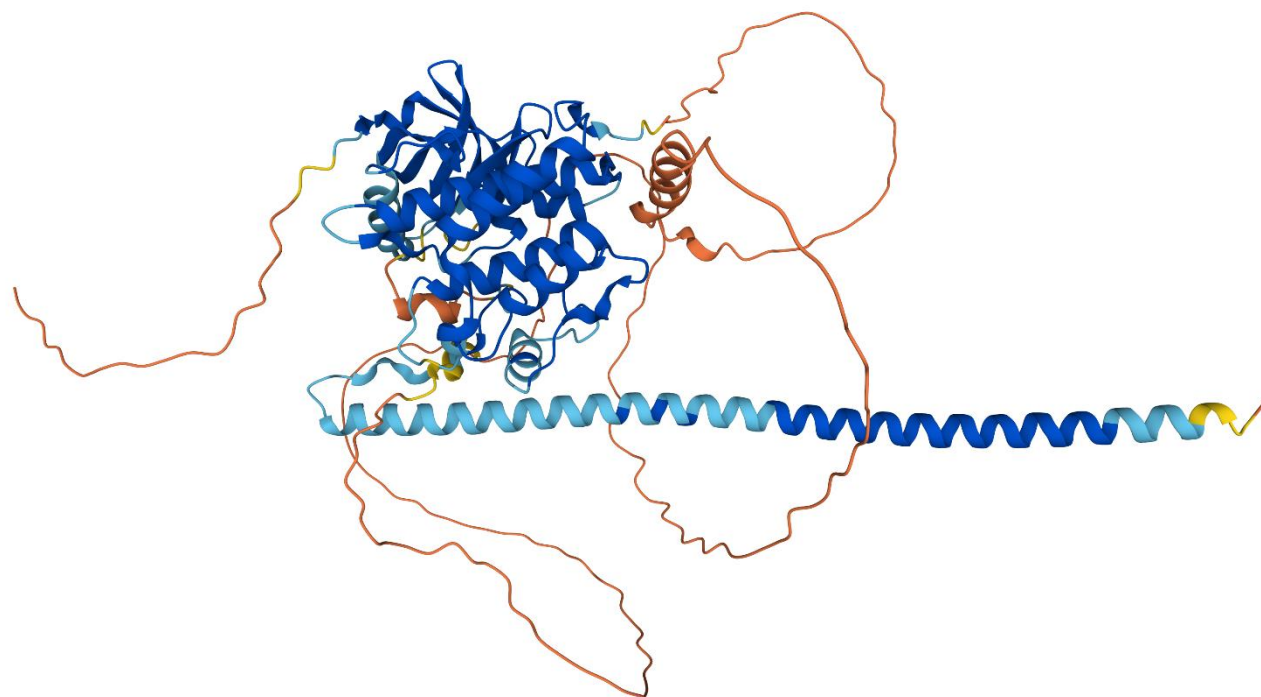


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sapiens OX=9606 GN=MAP3K7 PE=1 SV=1
MSTASAASSSSSSSAGEMIEAPSQVLNFEEIDYKEIEVEEVVGRGAFGVVCKAKWRAKDVAIKQIESESERKAFIVELRQLSRVN
HPNIVKLYGACLNPFVCLVMEYAEGGSLYNVLHGAEPYPYTAAHAMSWCLQCSQGVAYLHSMQPKALIHRLDKPPNLLLAVAGGTV
LKICDFGTACDIQTHMTNNKGSAAWMAPEVFEGSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKNL
PKPIESLMTRCWSKDPSQRPMSMEEIVKIMTHLMRYFPGADEPLQYPCQYSDEGQSN SATSTGFSFMDIASTNTSNKSDTNMEQVPA
TNDTIKRLESKLLKNQAKQQSESGRLSLGASRGSSVESLPPTSEGKRMSADMSEIEARIAATTAYSKPKRGHRKTASF GNILDVP
EIVISGNGQPRRRSIQDLTVTGTEPGQVSSRSSSPSVRMITTS GPTSEKPTRSHPWTPDDSTD TNGSDNSIPMAYLTLDHQLQPL
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RSQQQKRQGT S

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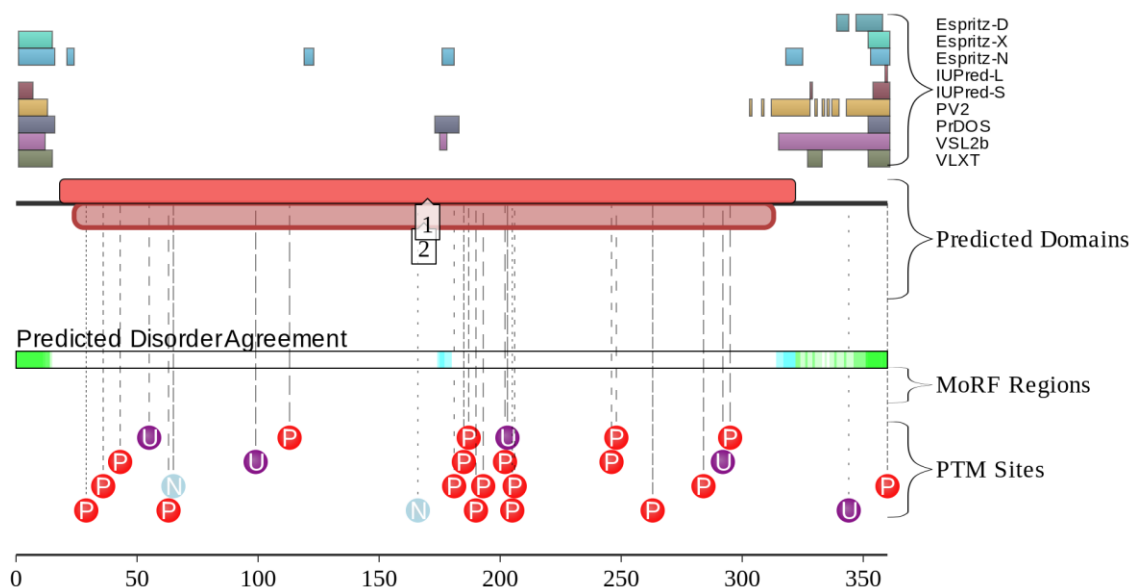
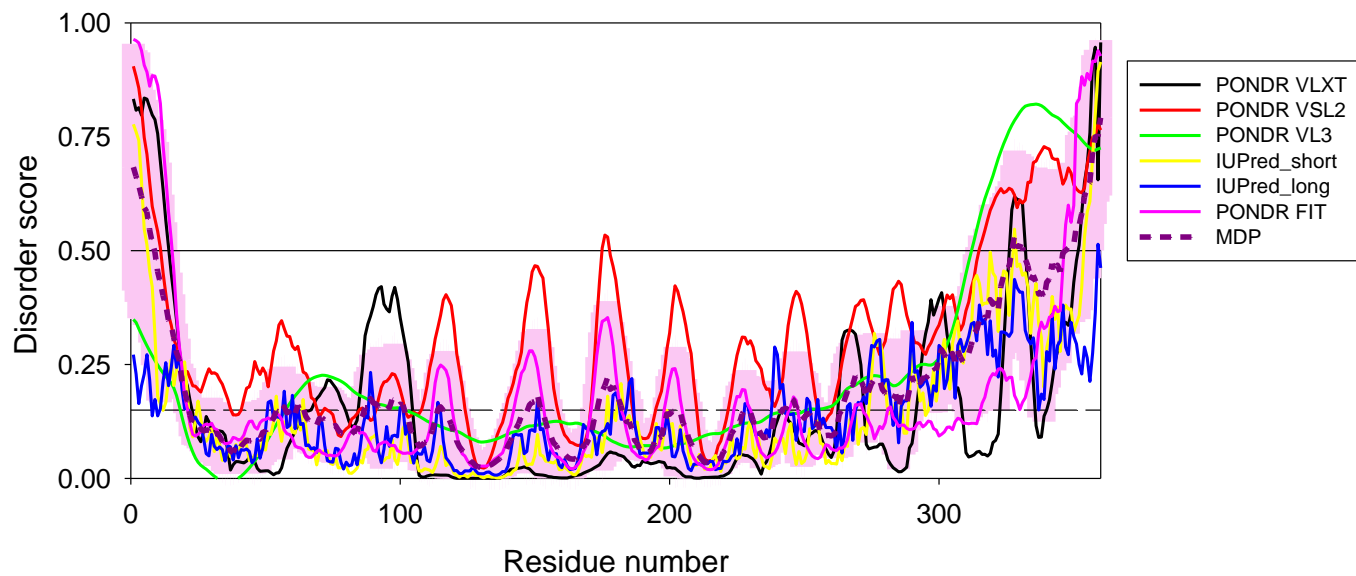




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GN=MAPK1 PE=1 SV=3
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INDIIRAPTIEQMKDVYIVQDLMETDLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLLNTTCDLKICDFGL
ARVADPDHDHTGFLTEYVATRWRAP EIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPKGHYLDQLNHILGILGSPSQEDLNCI
INLKARNYLLSLPHKNKVPWNRLFPNADSKALDLDKMLTFNPHKRIEVEQALAHPPYLEQYYDPSDEPIAEAPFKFDMELDDLPK
EKLKELIFEETARFQPGYRS

```



Key:

- Predicted SCOP Structure
- Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:

- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

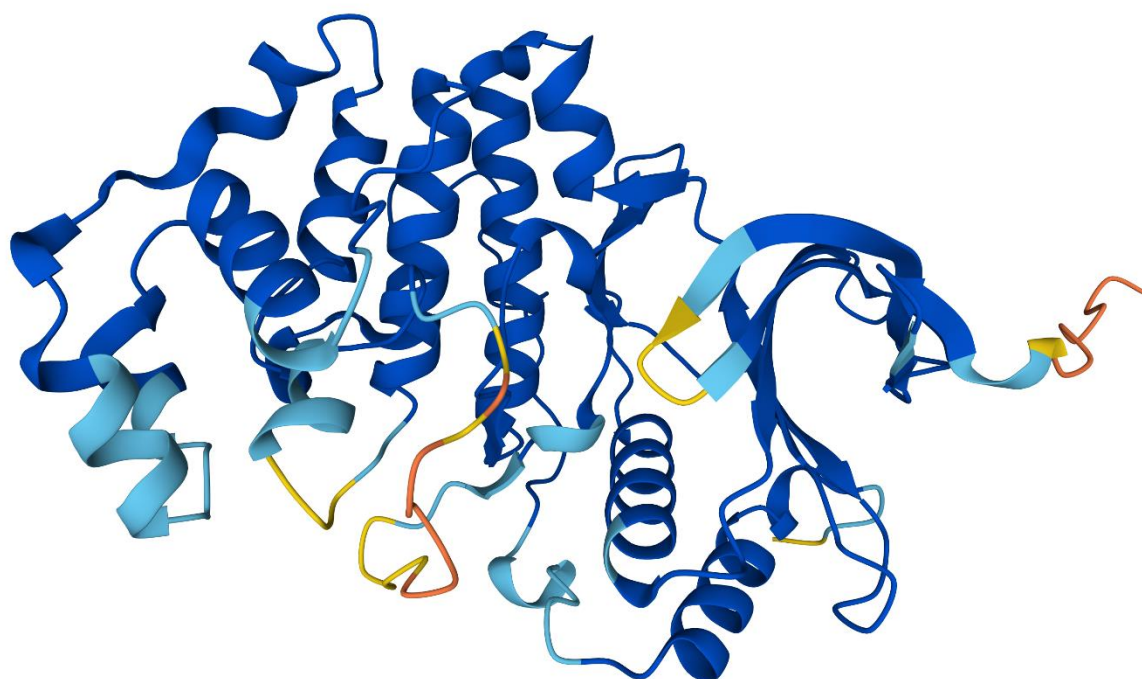
Superfamilies:

- [1] Protein kinase-like (PK-like)

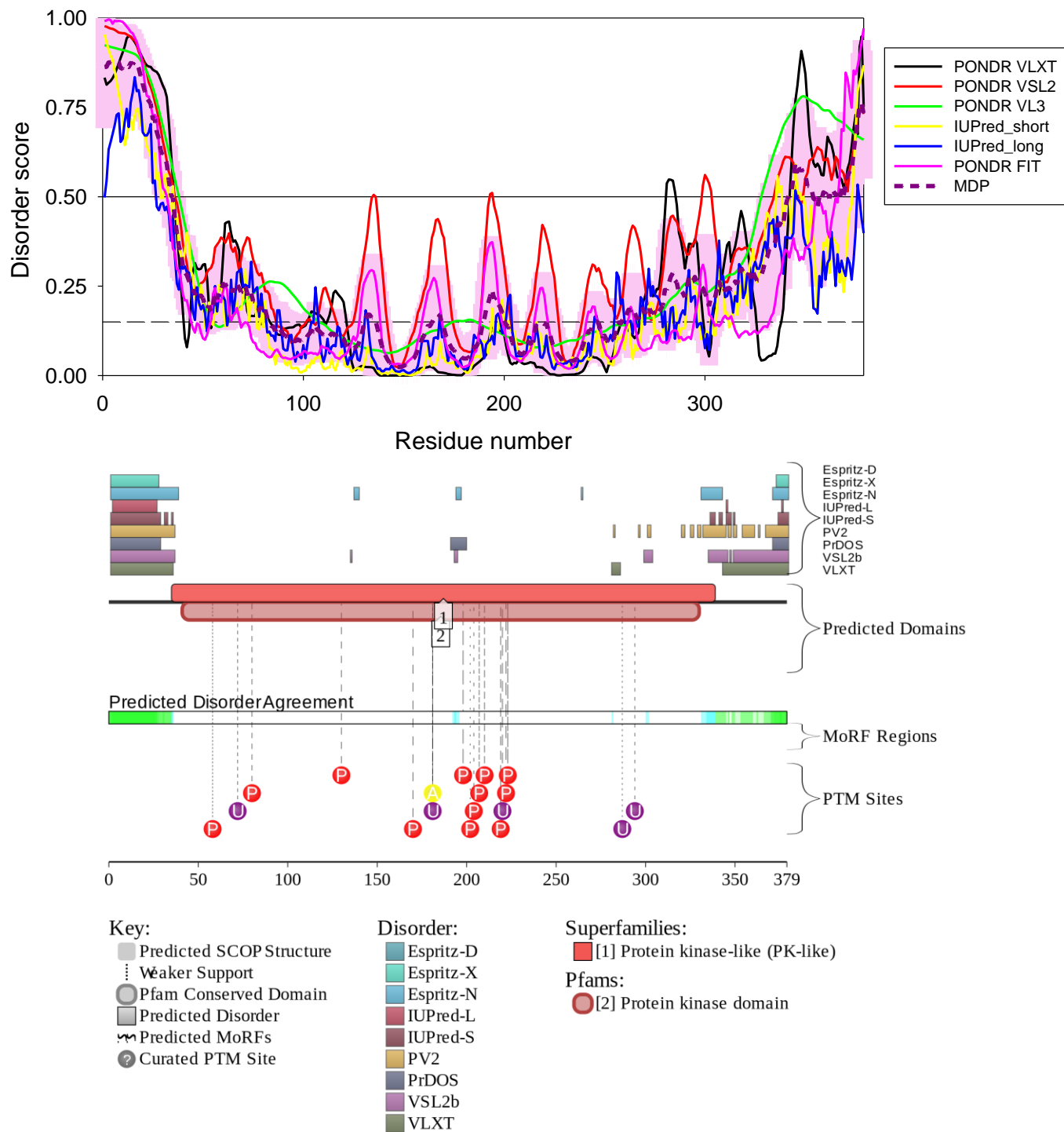
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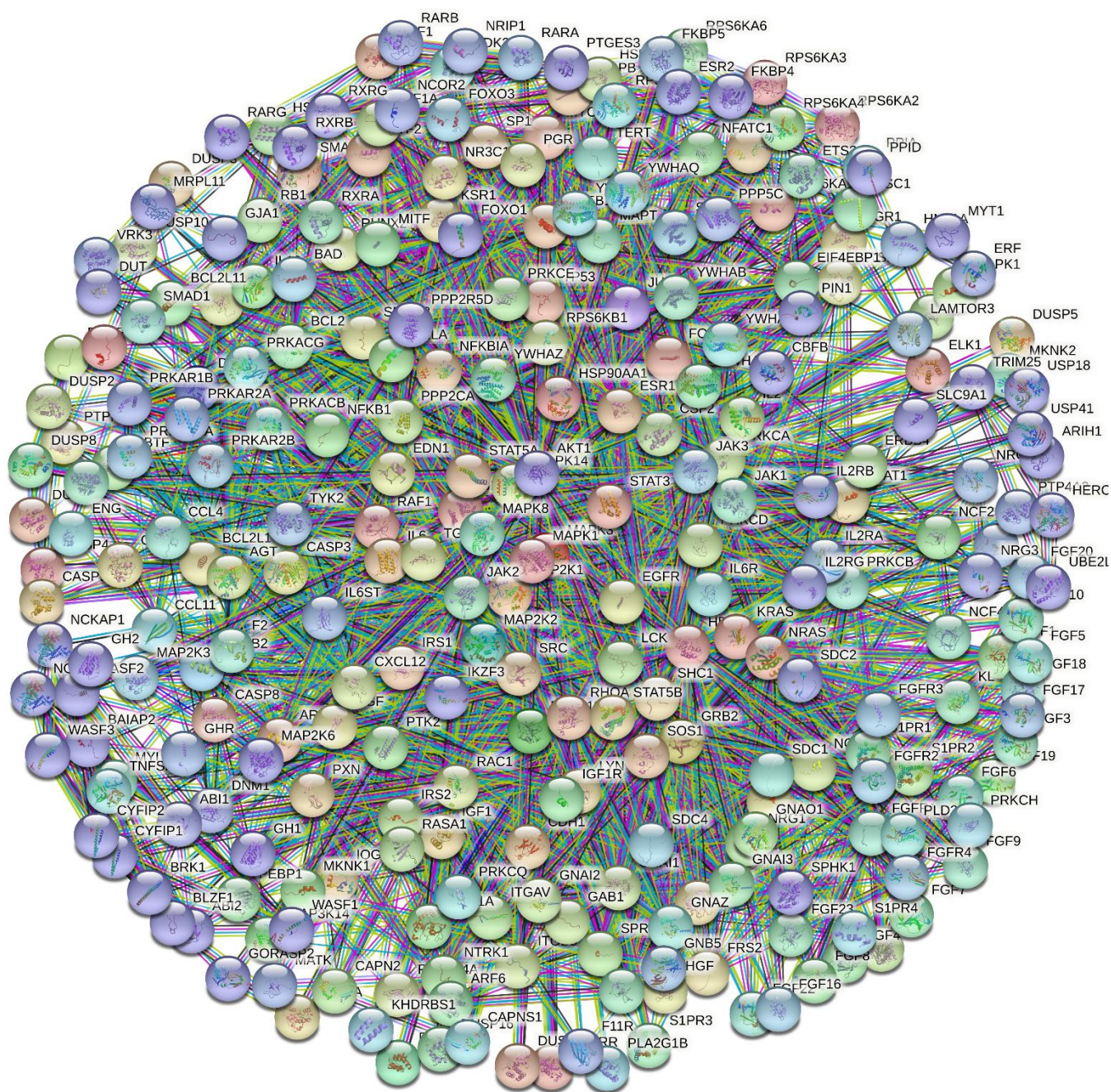
- [2] Protein kinase domain

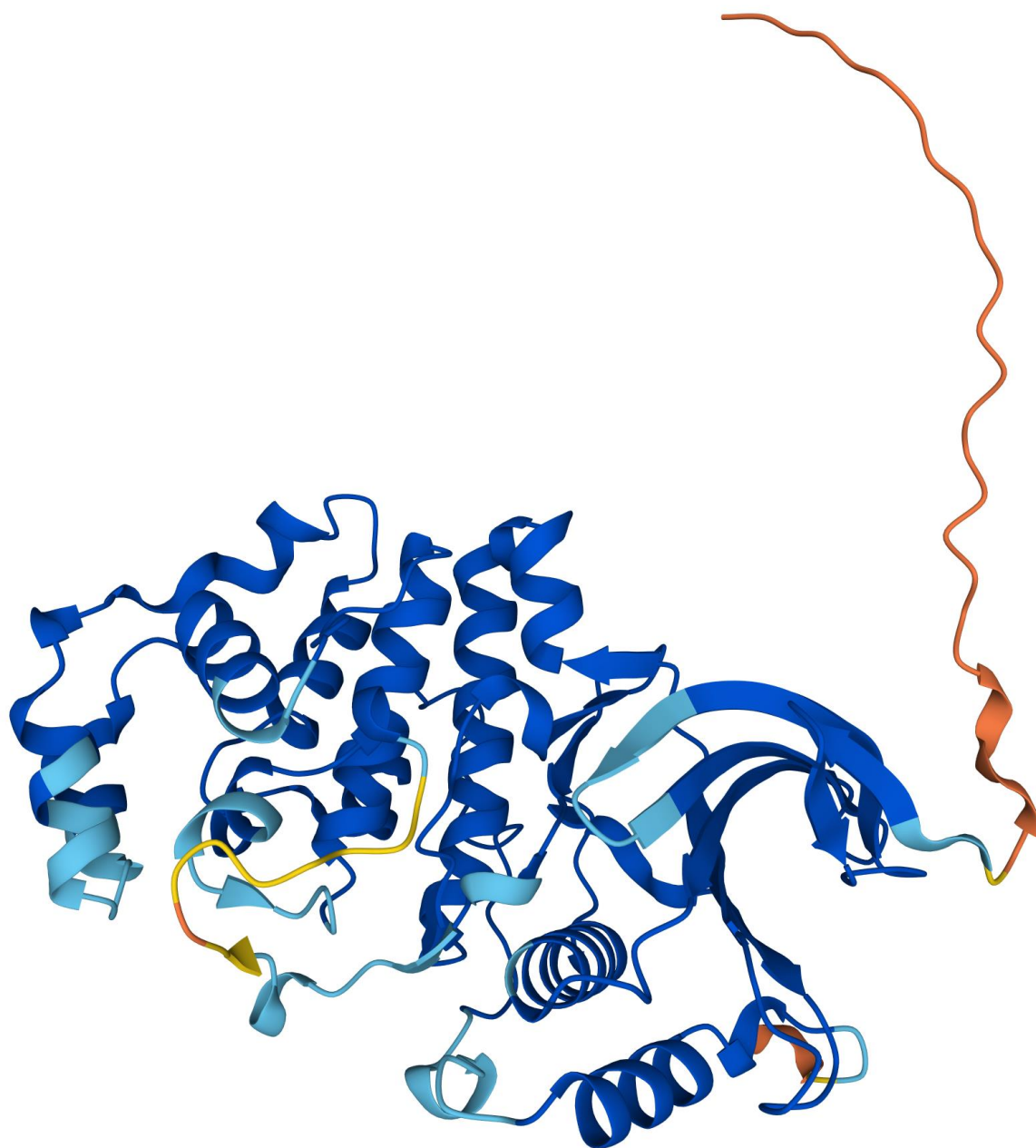




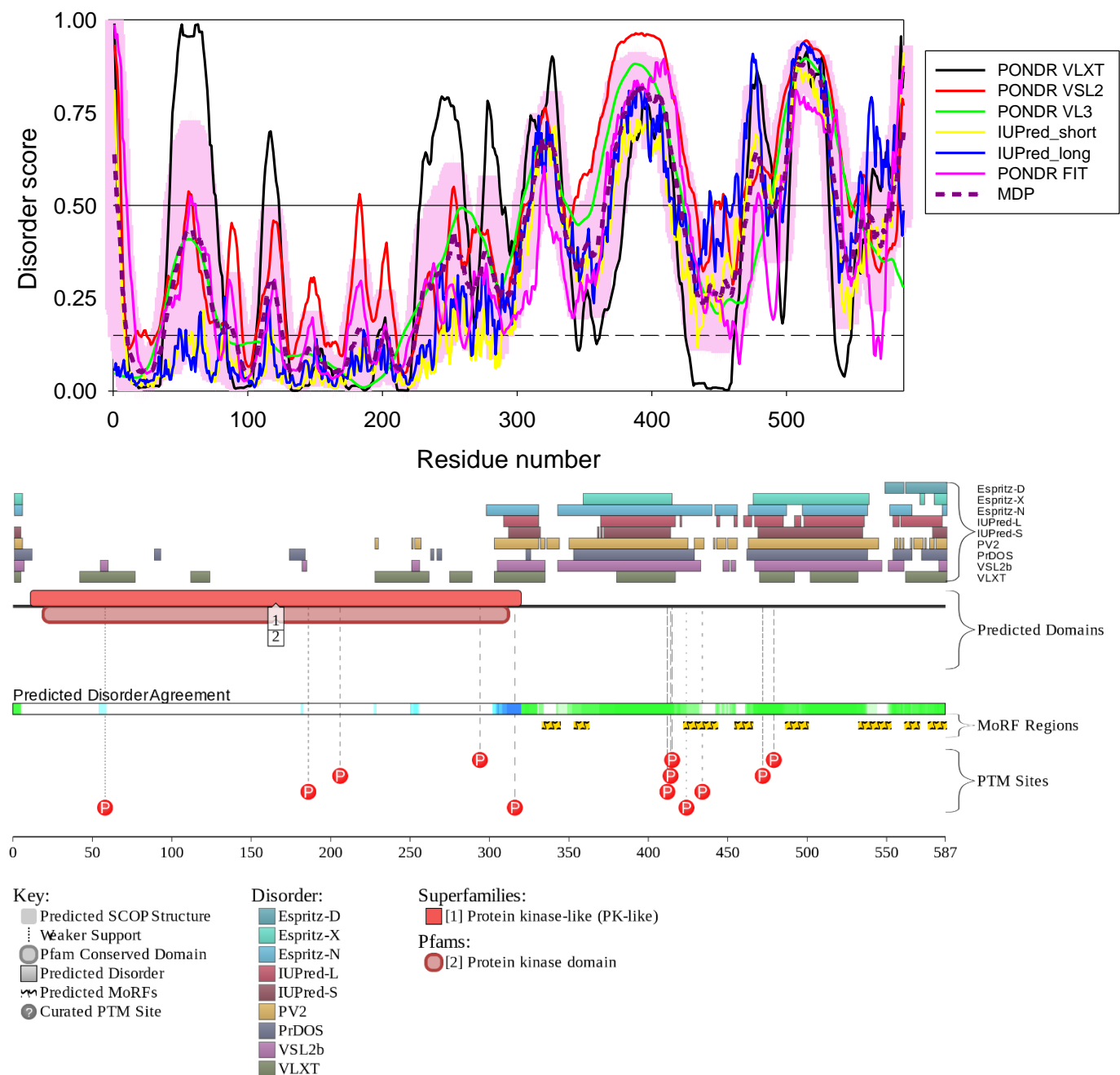

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NLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPKGHYLDQLN
HILGILGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLDRLMTFNPKNKRITVEEALAHPPYLEQYYDPTDEP
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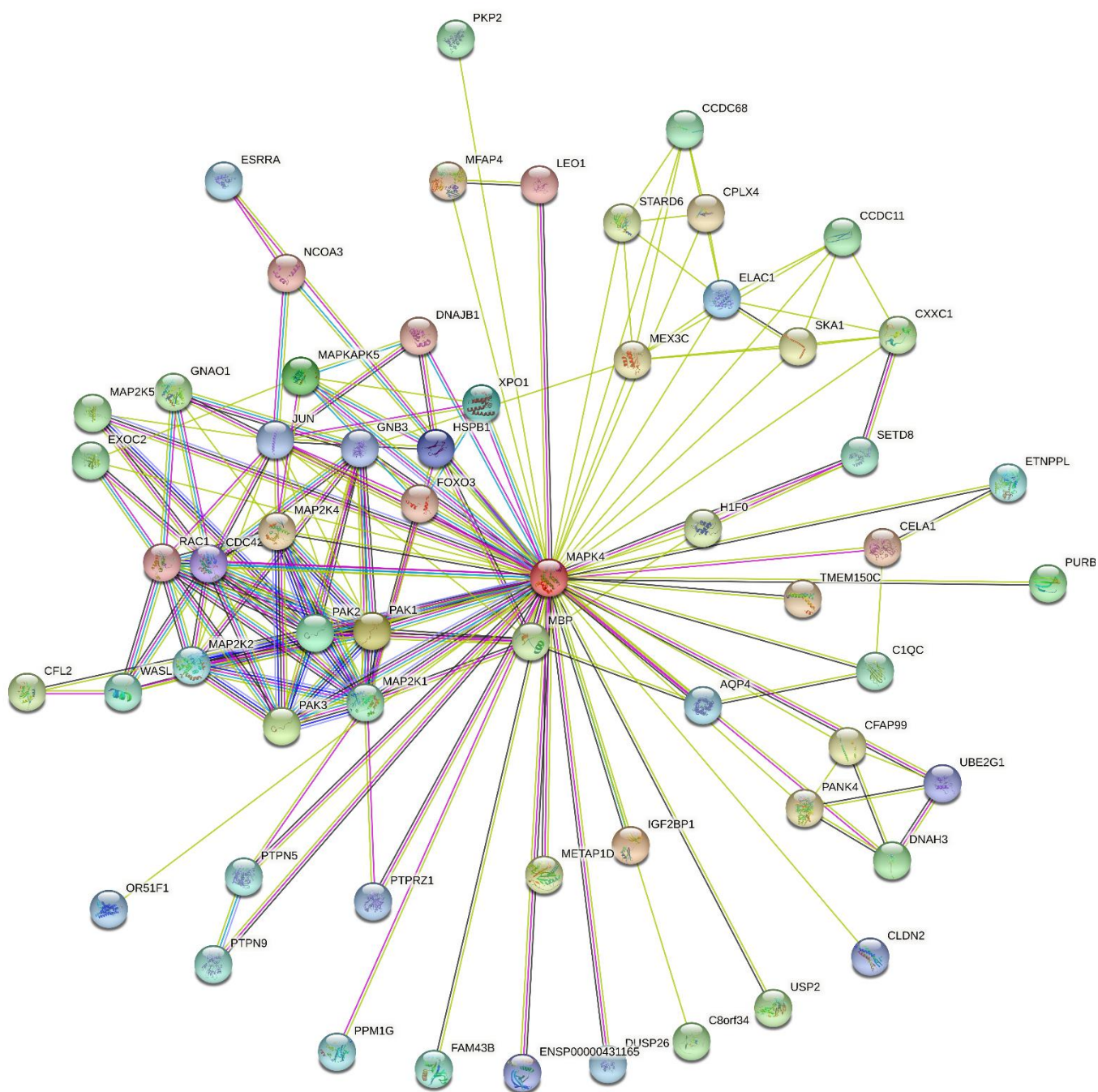


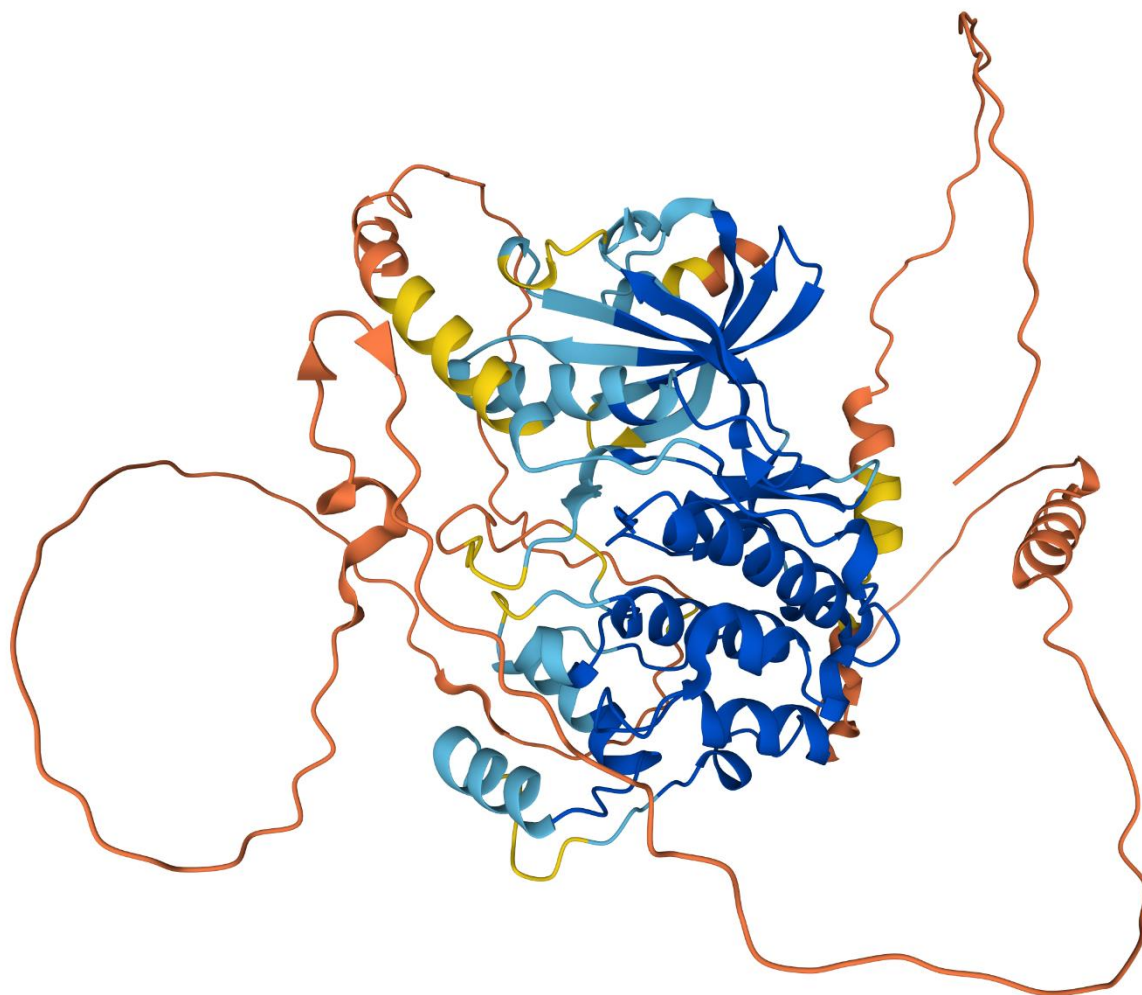




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PKGTDLQGELFKFSVAYIVQEYMETDLARLLEQGTAEHAKLFMYQLLRGLKYIHSANVLHRDLKPANIFISTEDLVLKIGDFG
LARIVDQHYSHKGYLSEGLVTKWYRSPRLLSSPNNTKAIDMWAAGCILAEMLTGRMLFAGAHELEQMQLILETIPVIREEDKDE
LLRVMPFSFVSSTWEVKRPLRKLLEPVNSEAIDFLEKILTFNPMDRDLTAEMGLQHPYMSPYSCPEDEPTSQHPFRIEDEIDDIVLM
AANQSQLSNWDTCCSRYPVSLSSDLEWRPDRCQDASEVQRDPAGSAPLAEDVQVDPKDSHSSSERFLEQSHSSMERAFEADYG
RSCDYKVGSPSYLDKLLWRDNKPHHYSEPKLILDLSHWKQAAGAPPTATGLADTGAREDEPASLFLEIAQWVKSTQGGPEHASPP
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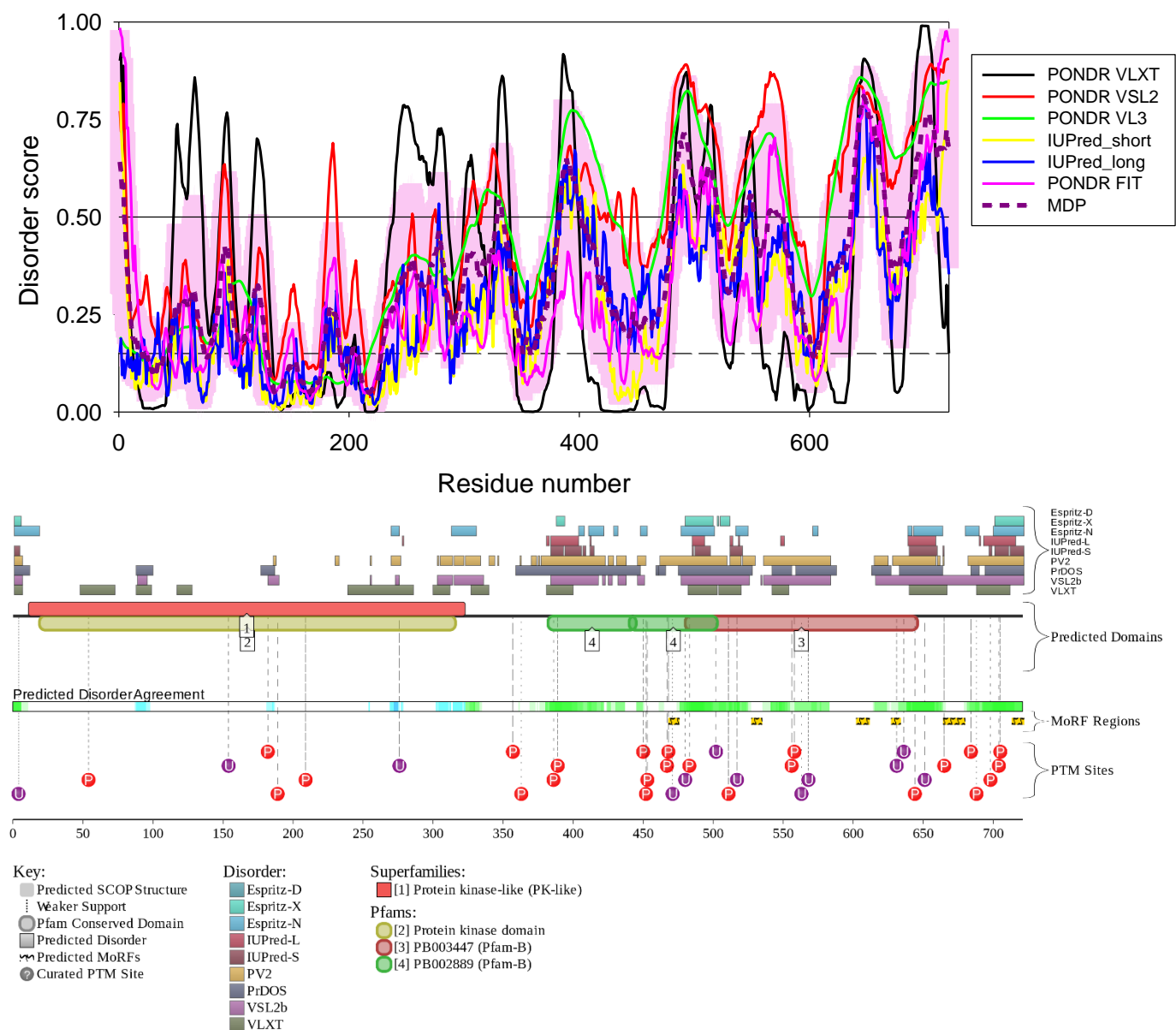


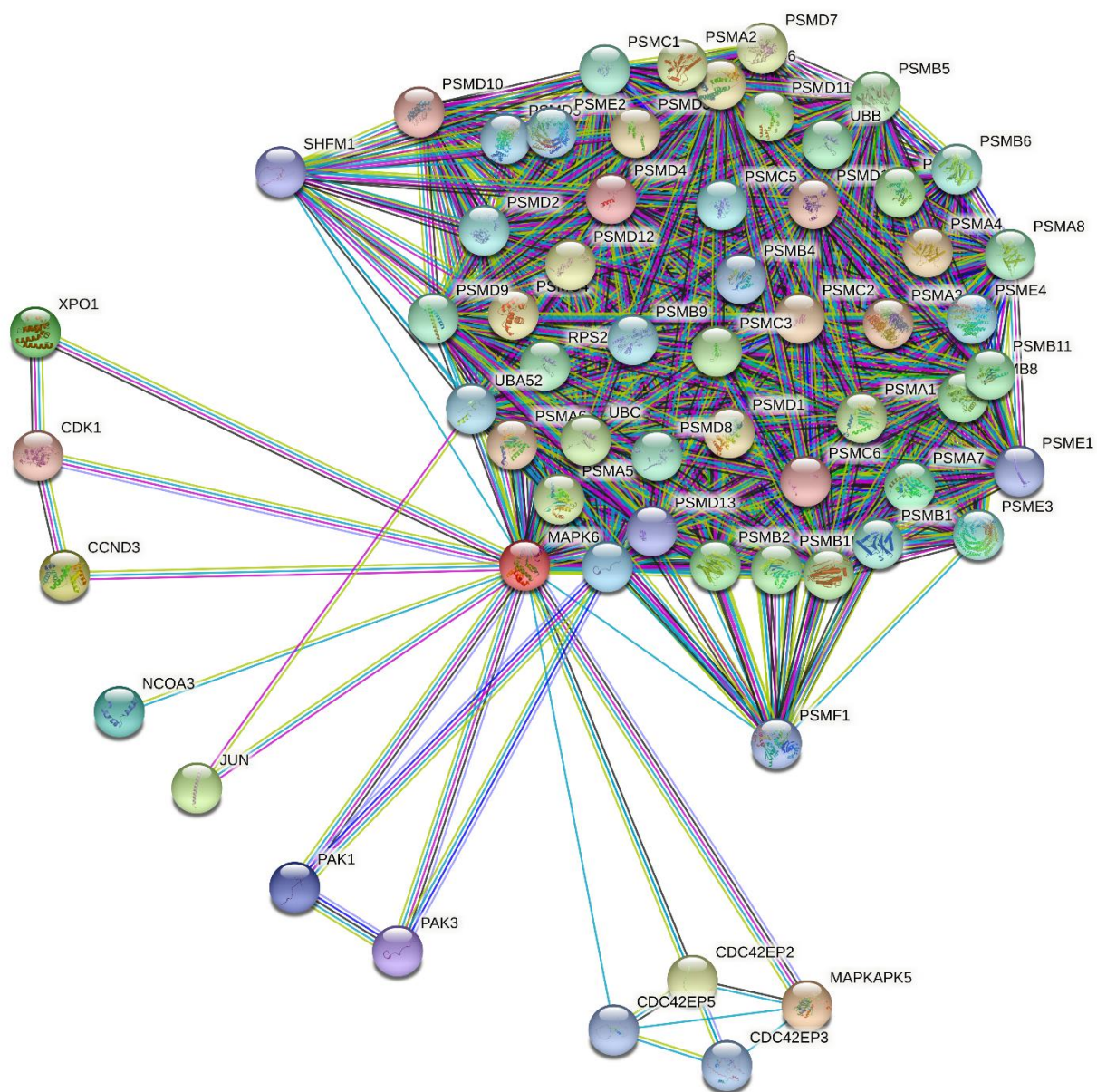


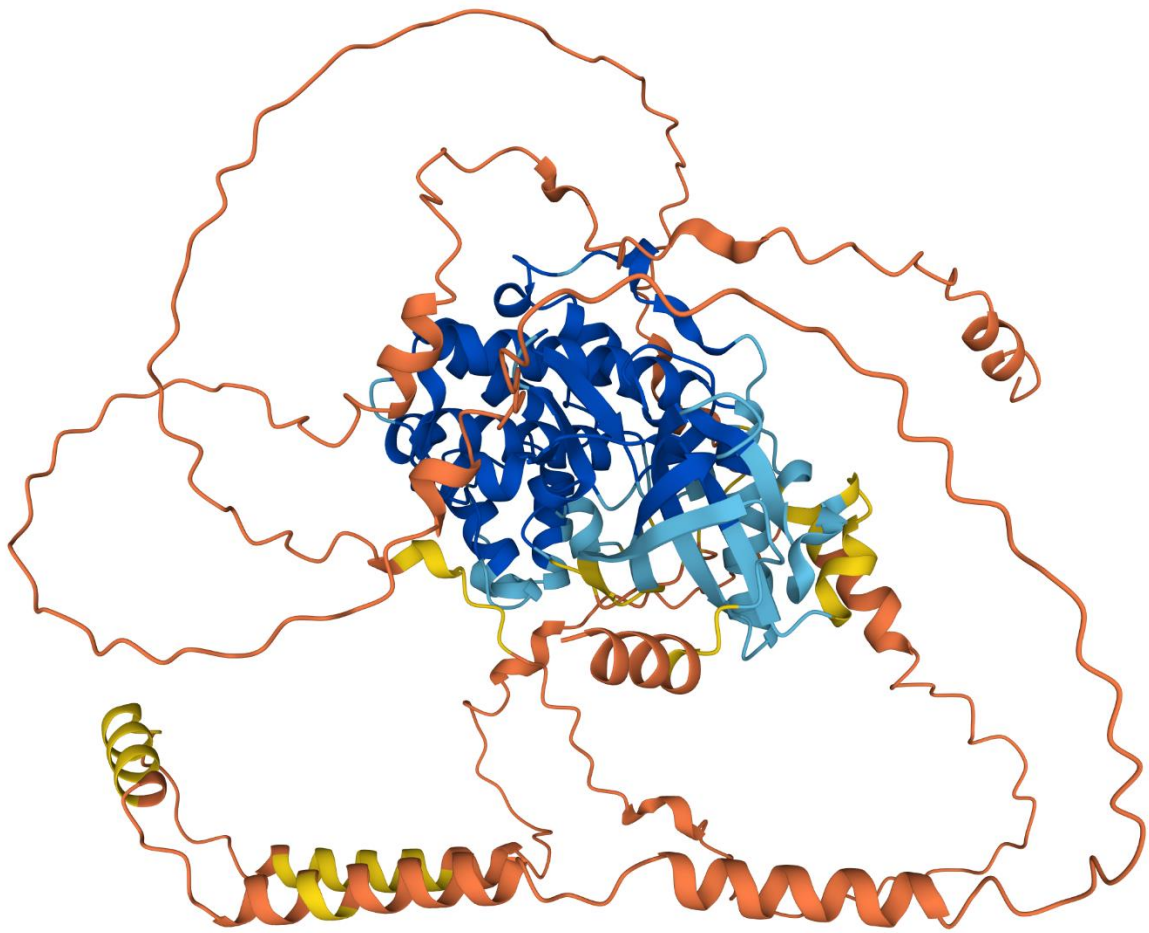
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PSGSQLTDDVGSLELNSVYIVQEYMETDLANVLEQGPLLEEHLRFMYQLLRGLKYIHSANVLHRDLKPANLFINTEDLVLKIG
DFGLARIMDPHYSHKGLHSEGLVTKWYRSPRLLLSPNNYTKAIDMWAAGCIFAEMLTGKTLFAGAHELEQMQLILESIPVVHEED
RQELLSVIPVYIRNDMTEPHKPLTQLLPGISREALDFLEQILTFSPMDRLTAEALSHPYMSIYSFPMDEPISSHPFHIEDEVDD
IILMDETHSHIYNWERYHDCQFSEHDWPFVHNNFDIDEVQLDPRALSDVTDEEEVQVDPKRYLDGDREKYLEDPAFDTNYPEPCW
QYSDHHENKYCDLECSHTCNKYKTRSSSYLDNLVWRESEVNHYEYEPKLIIDLSNWKEQSKEKSDKKGKSKCERNGLVKAQIALEEA
SQQLAGKEREKNQGFDFDSFIAGTIQLSSQHEPTDVVDKLNLDLNSSVSQLELKSLSKSVSQEKQEKGMANLAQLEALYQSSWDS
QFVSGGEDCFFINQFCEVRKDEQVEKENTYTSYLDKFFSRKEDTEMLETEPVEDGKLGERGHEEGFLNNSGEFLFNKQLESIGIP
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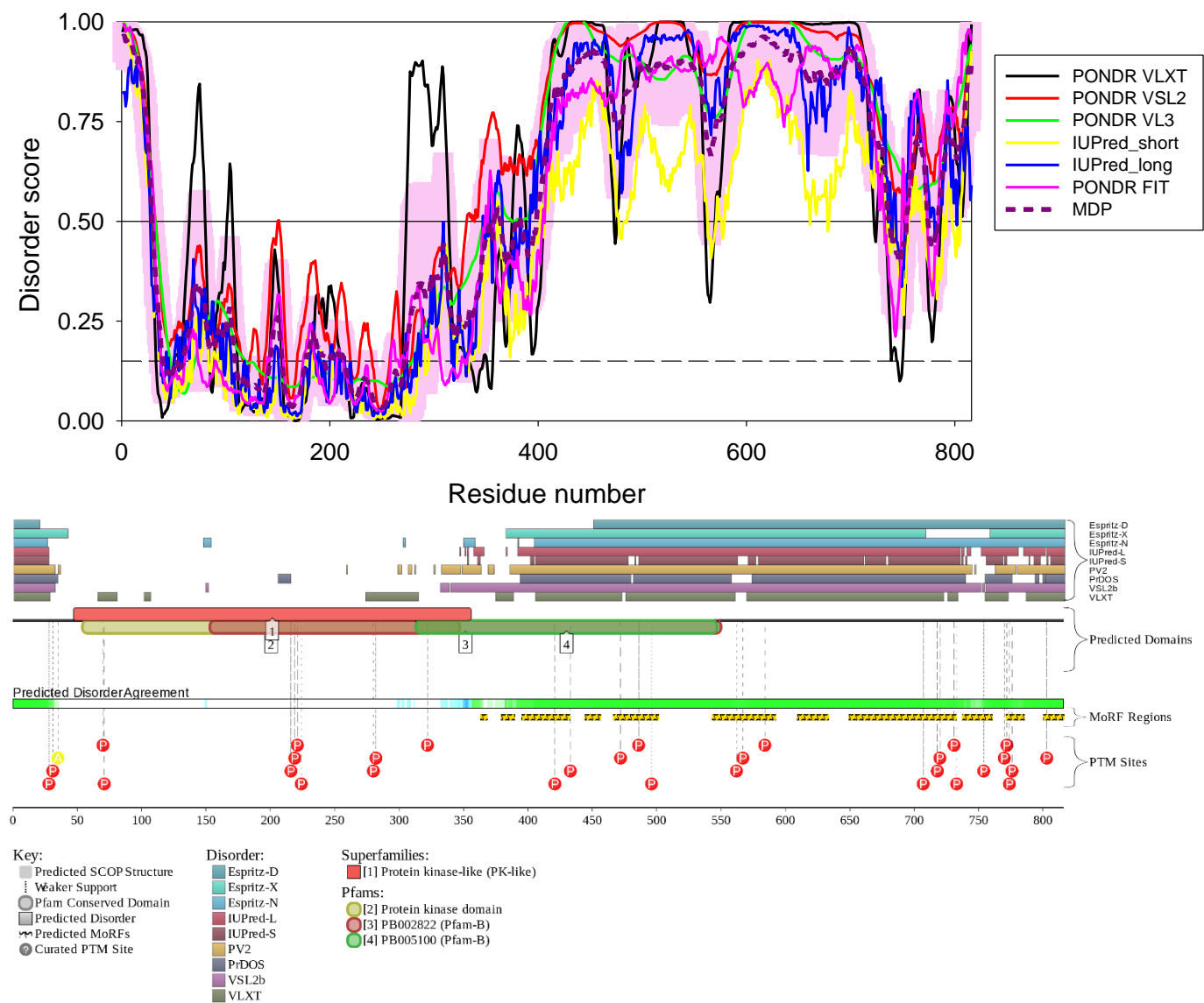




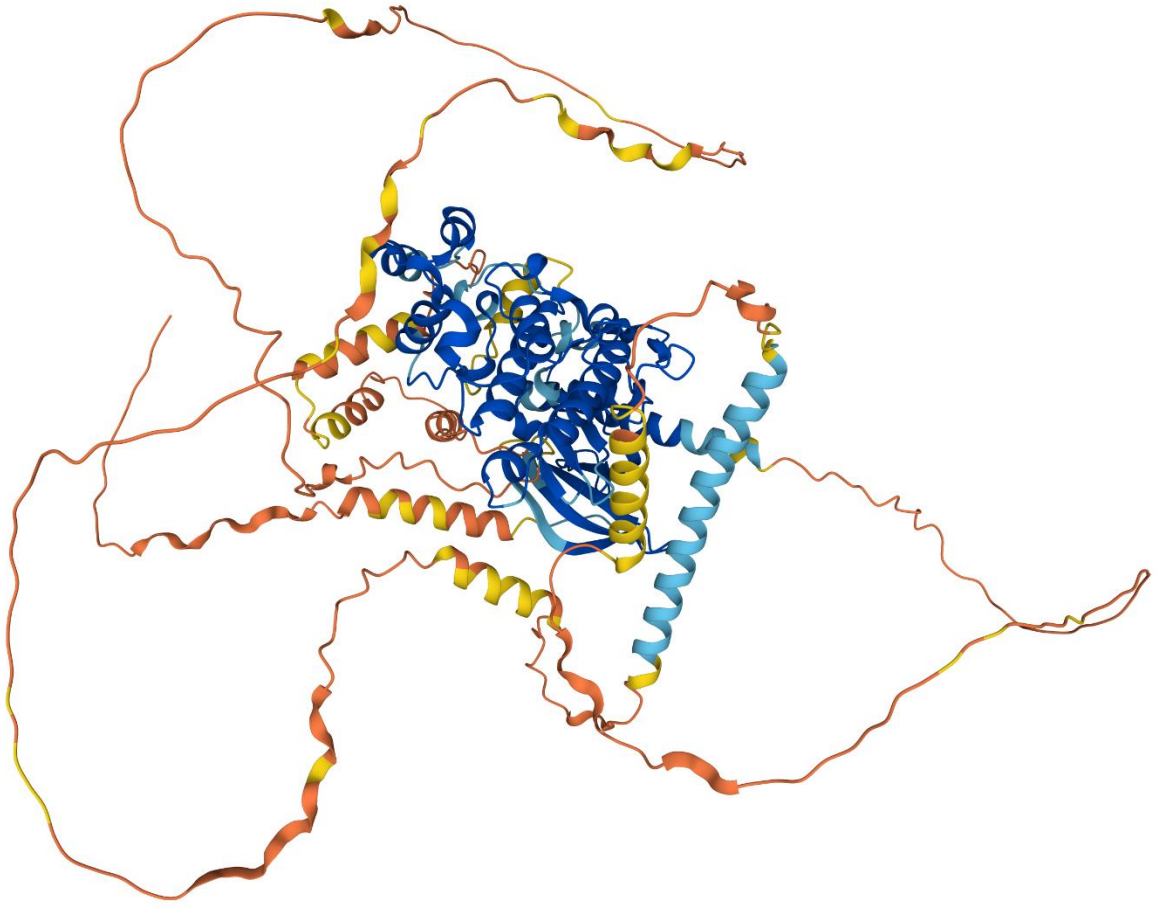
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IPNAFVVTNAKRTLRELKILKHFKHDNIIAIKDILRPTVPYGEFKSVYVVLDMESDLHQIIHSSQPLTLEHVRYFLYQLLRGL
KYMHSAQVIHRDLKPSNLLVNENCELKIGDFGMARGLCSPAHEQYFMTEYVATRWYRAPELMLSLHEYTQAIDLWSVGCIFGEM
LARRQLFPGKKNYVHQLQLIMMVLTGTPSPAVIQAVGAERVRAIYQSLPPRQPVWETVYPGADRQALSLLGRMLRFEP SARISAAA
ALRHPFLAKYHDPDDEPDCAFPDFDAFDREALTRERIKEAIVAEIEDFHARREGIRQQIRFQPSLQPVASEPGCPDVEMPSPWAP
SGDCAMESPPPPPPPCPGPAPDTIDLTLQPPPPVSEPPPKKDGAI SDNTKAALKAALLKSLRSRLRDGPSAPLEAPEPRKPVTA
QERQREREKRRRRQERAKEREKRRQERERKERGAGASGGPSTDPLAGLVLSNDNRSLLERWTRMARPAAPALTSVPAPAPAPT
TPTPVQPTSPPPGPVAQPTGPPQPSAGSTSGPVPQPACPPPGPAPHPTGPPGPIPVAPPQIATSTSLAAQSLVPPPGPLPGSST
PGVLPYFPPGLPPPDAAGAPQSSMSESPDNLVTQQLSKSQVEDPLPPVFSGTPKSGAGYGVGFDLEEFNLQSFDMGVADGPDQD
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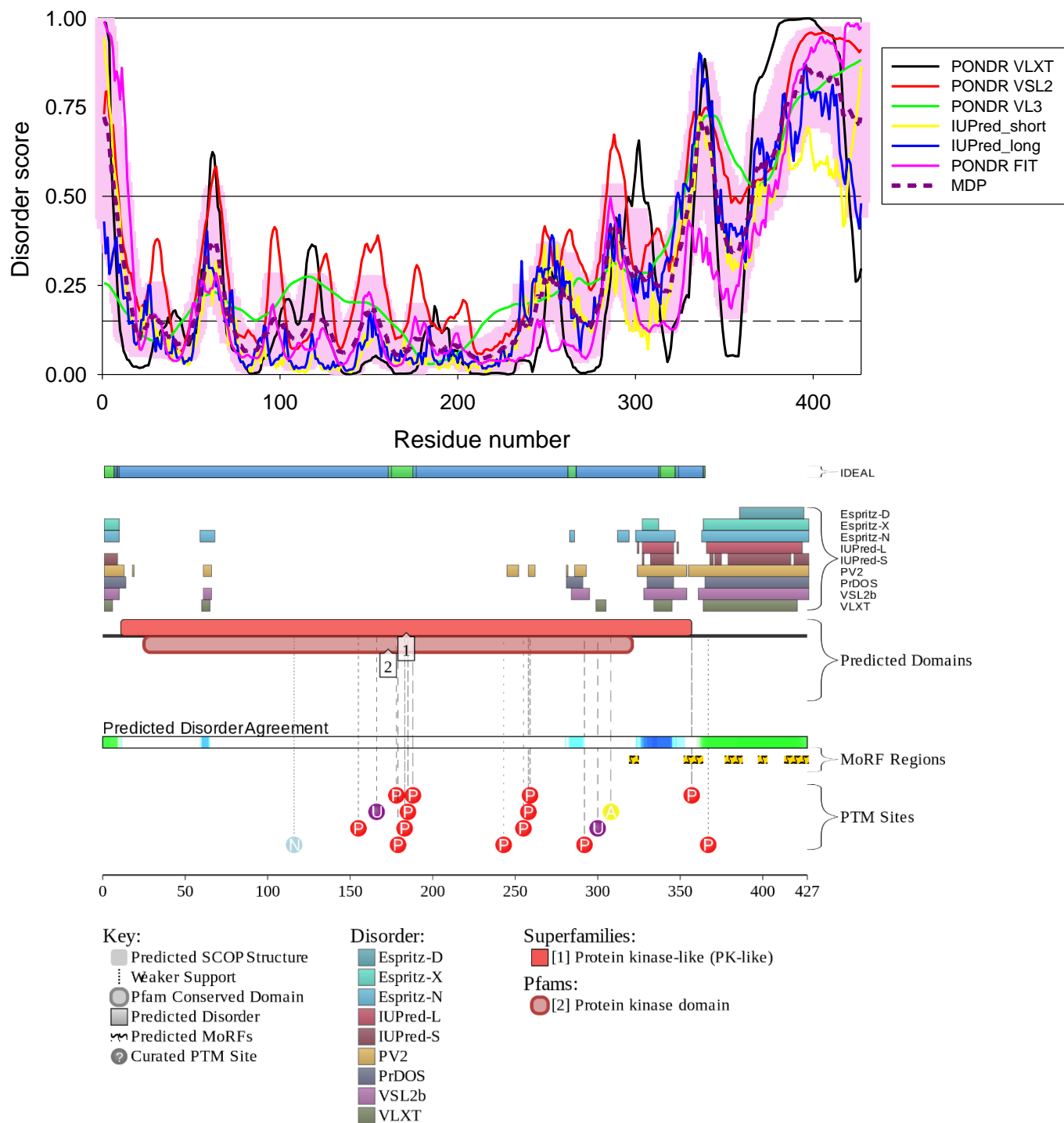
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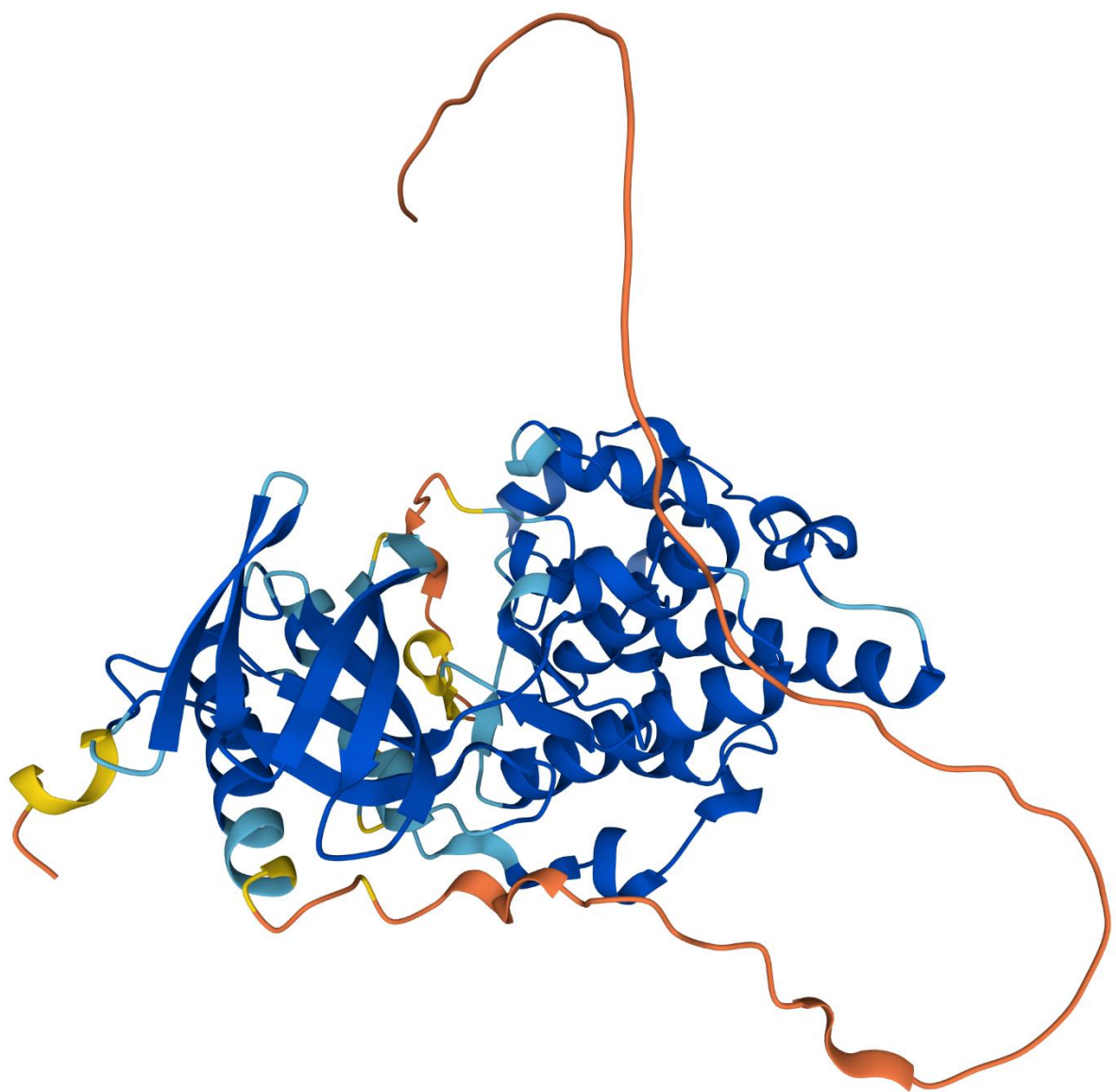




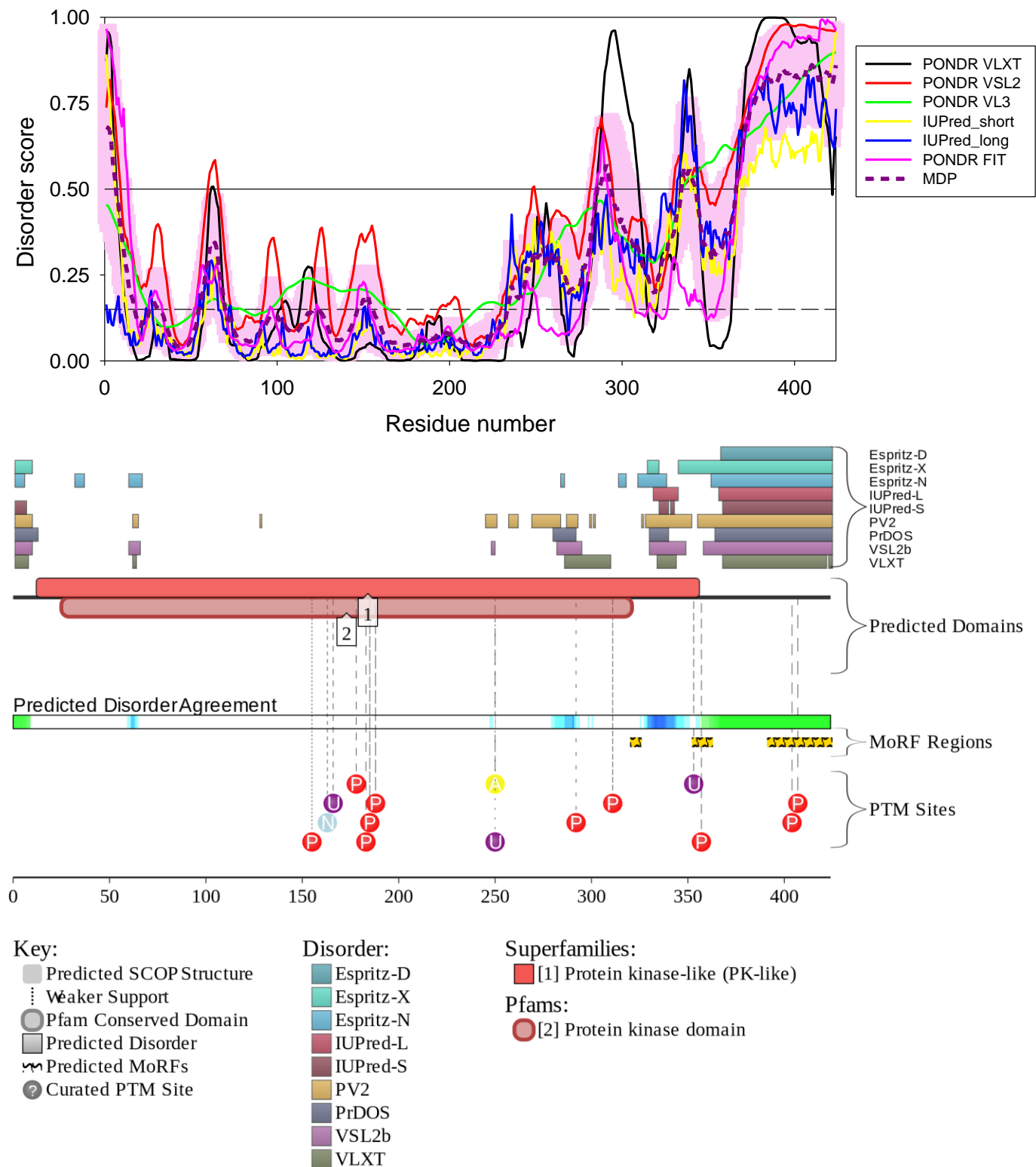

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IGLLNVFTFPQKSLEEFQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDF
GLARTAGTSFMMTPYVVTRYRAPEVILGMGYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCFEFMKKLQPT
VRTYVENRPKYAGYSFEKLFDPDLFPADSEHNKLKASQARDLLSKMLVIDASKRISVDEALQHPYINVWYDPSEAEAPPPKIPDK
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CR
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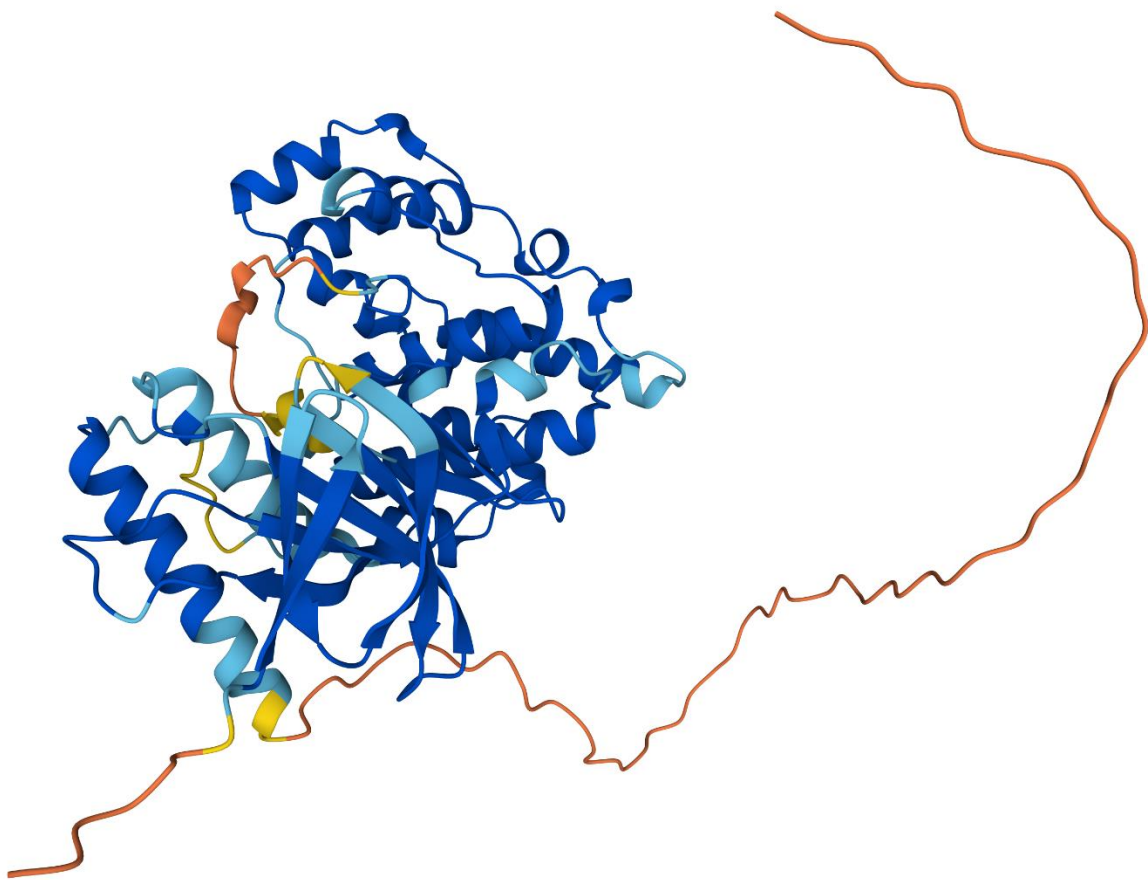




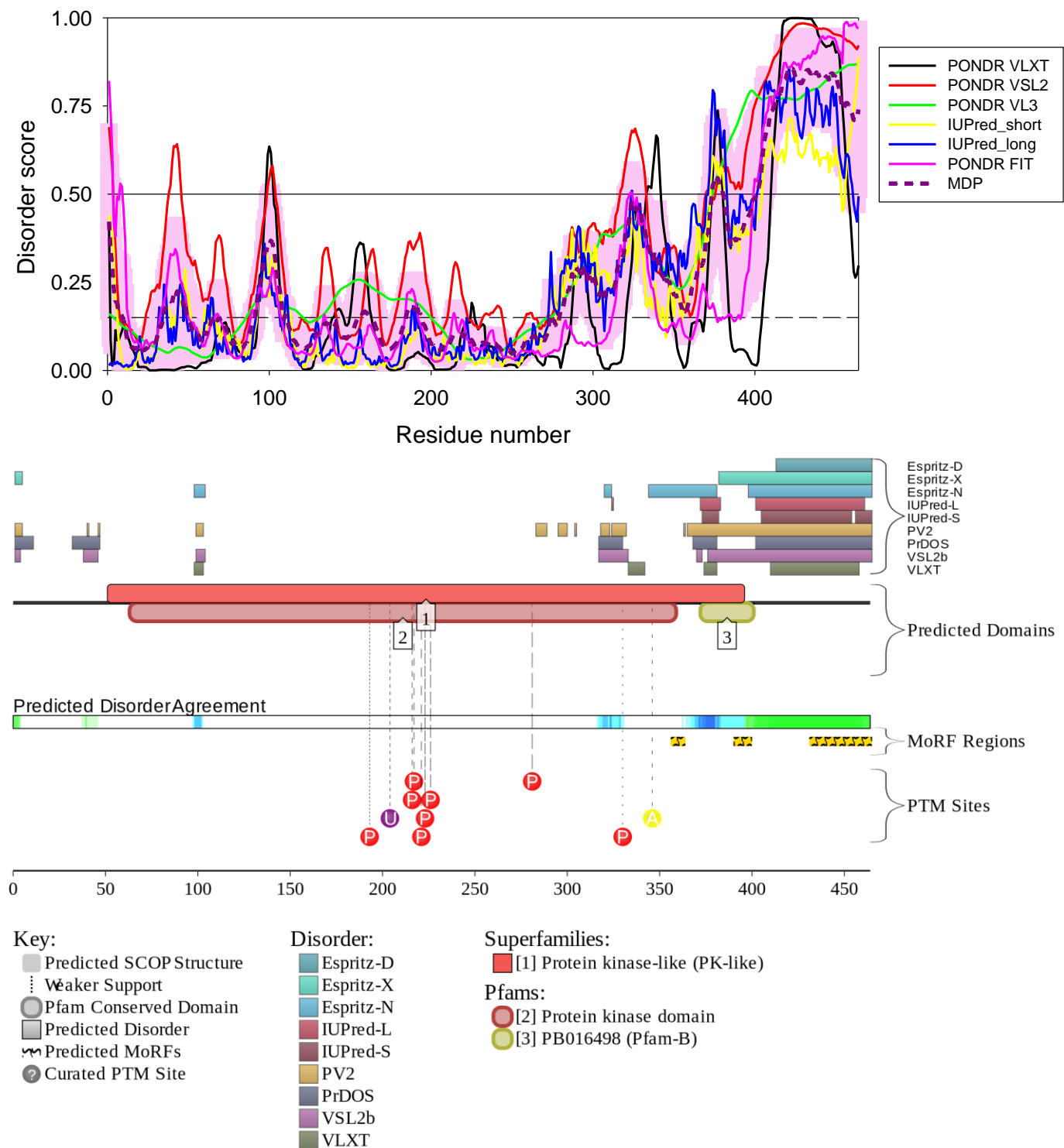


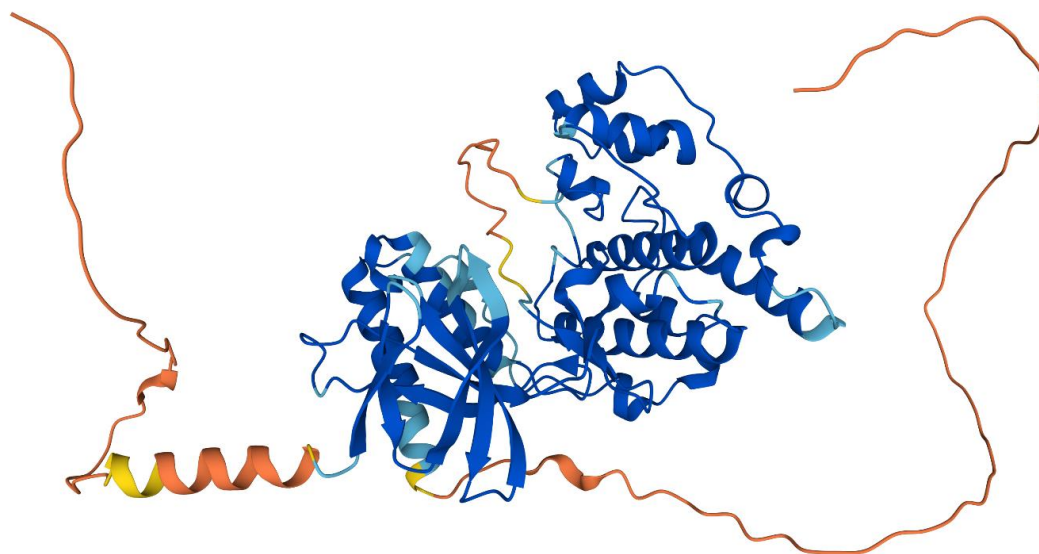
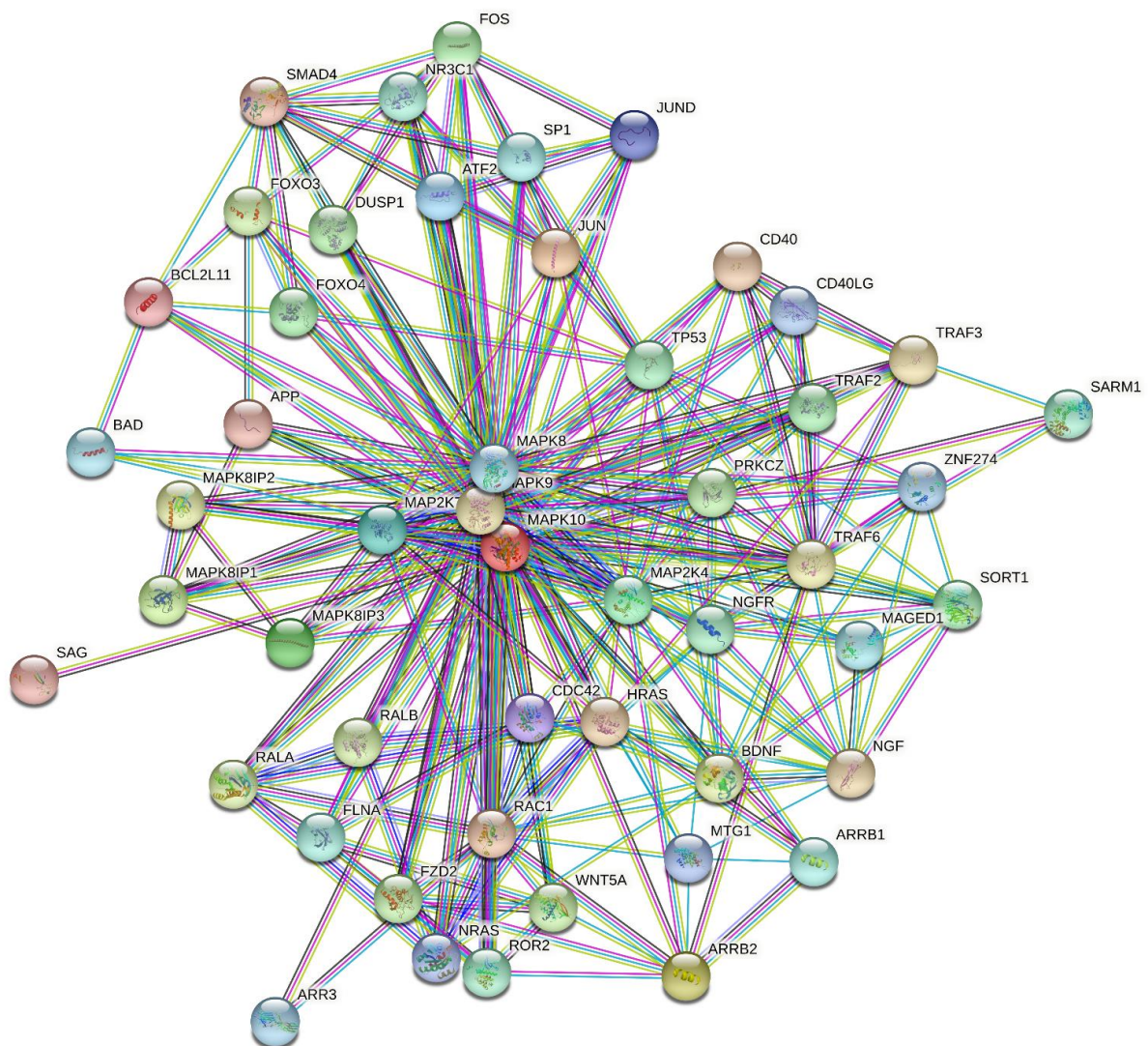

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ISLLNVFTFPQKTLEEFQDVYLVMEELMDANLCQVIHMELDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDF
GLARTACTNFMMPYPYVVTRYRAPEVILGMGYKENVDIWSVGCIMGELVKGCVIFQGTDHIDQWNKVIEQLGTPSAEFMKKLQPT
VRNYVENRPKYPGIKFEELFPDWIFPSESERDKIKTSQARDLLSKMLVIDPDKRISVDEALRHPYITVWYDPAEAEAPPPQIYDA
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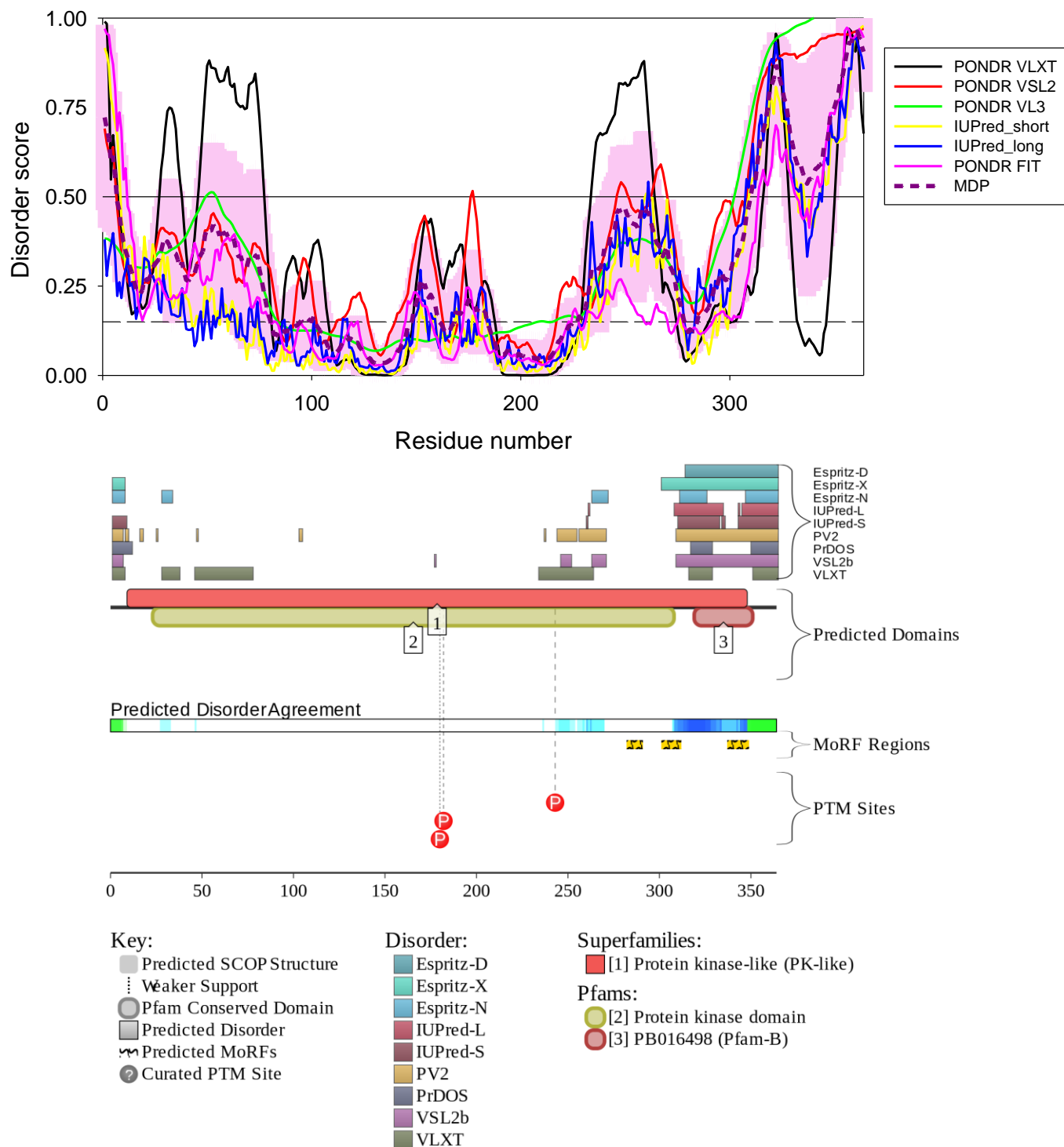


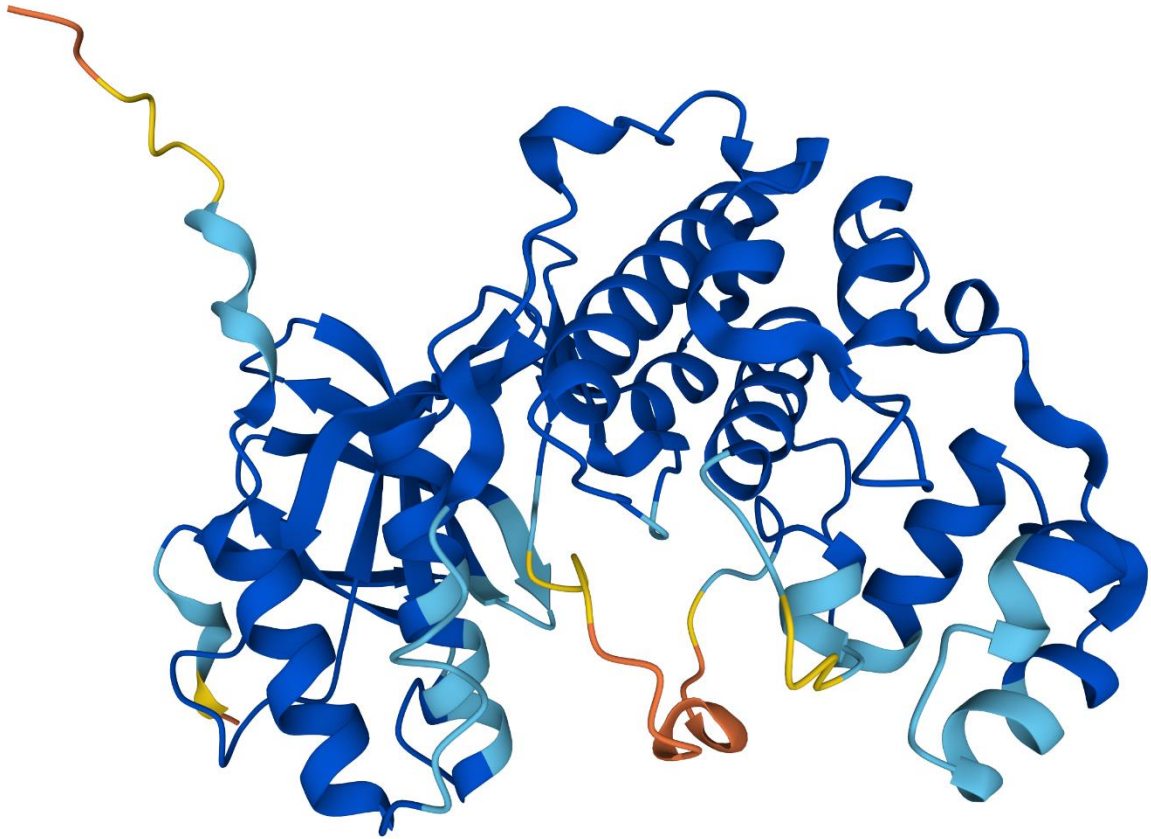
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 LDRNVAIKKLSRPFQNTAKRAYRELVL MKCVNHKNIISLLNVFTPQKTLEEFQDVYLVME LMDANLCQVIQMELDHERMSYLL
 YQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGMGYKENVDIWSVGCIMGE
 MVRHKILFPGRDYIDQWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFFPKLFPDSLFPADSEHNK LKASQARDLLSKML
 VIDPAKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKELIYKEVMNSEEKTKNGVVKGQPSPSGA AVNSSE
 SLPPSSSVNDISSMSTDQTLASDTDS SLEASAGPLGCCR



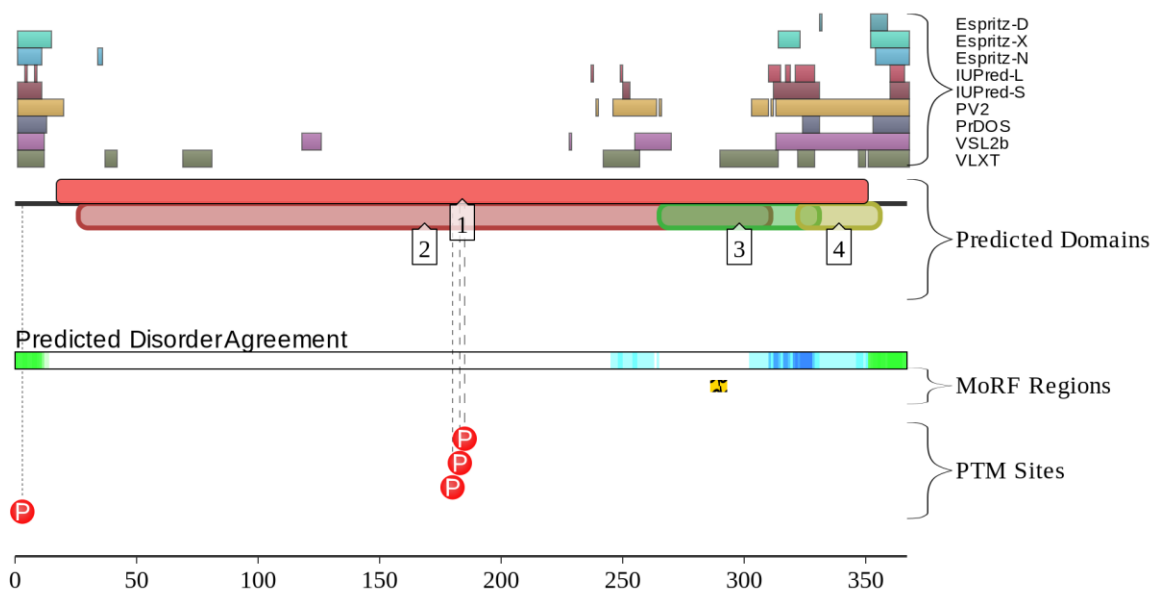
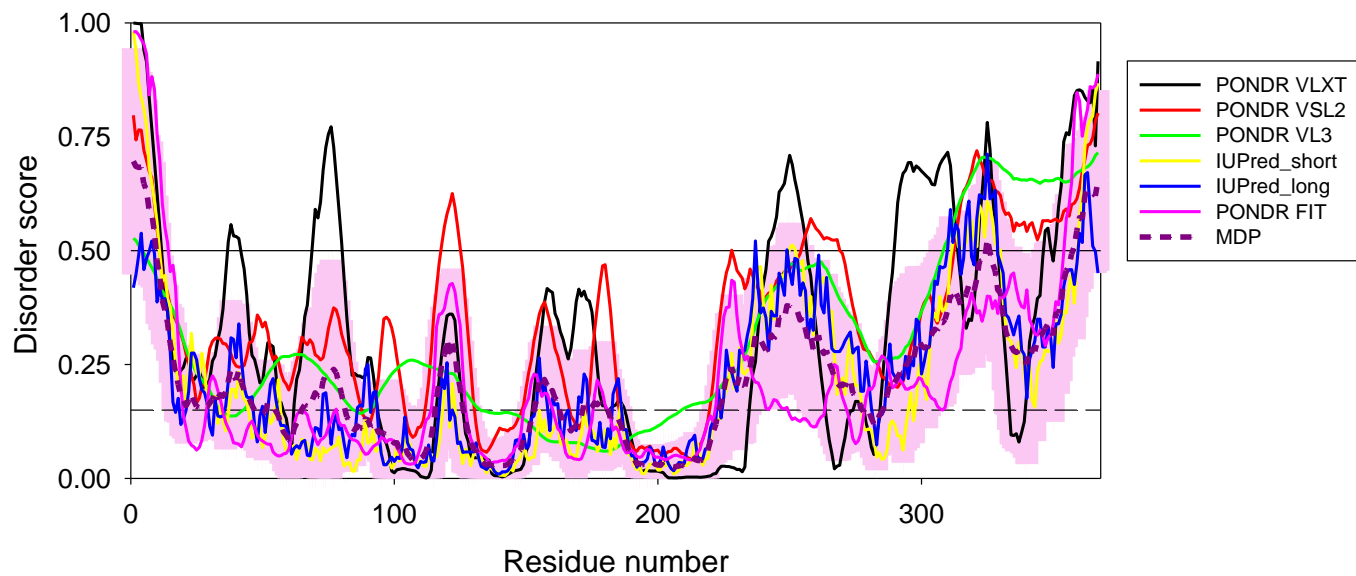



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LLDVFTPATSIEDFSEVYLVTTLMGADLNNIVKCQALSDEHVQFLVYQLLRGLKYIHSAGIIHRDLKPSNVAVNEDCELRIIDFG
LARQADEEMTGYVATRWYRAPEIMLNWMHYNQTVDIWSVGCIMAE LLQGKALFPGSDYIDQLKRIMEVVGTPSPEVLAKISSEHA
RTYIQSLPPMPQKDLSSIFRGANPLAIDLLGRMLVLVLDSDQRVSA AEALAHAYFSQYHDPEDPEPEAEPYDESVEAKERTLEEWKEL
TYQEVLSFKPPEPPKPPGSLEIEQ
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VIGLLDVFTPD ETLDDFTDFYLVM PFMGTD LGKLMKHEKLGEDRIQFLVYQMLKGLRYIHAAGIIHRDLKPGNLAVNEDCELKIL
DFGLARQADSEMTGYVVTRWYRAPEVILNWMRYTQTVDIWSVGCIMAEMITGKTLFKGSDHLDQLKEIMKVTGTPPAEFVQRLQS
DEAKNYMKGLPELEKKDFASILTNASPLAVNLLKMLVLDAEQRV TAGEALAH P YFESLHDTEDEPQVQKYDDSFDDVDRTLDEW
KRVTYKEVLSFKPPRQLGARVSKETPL
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Key:

- Predicted SCOP Structure
- ⋯ Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- ⋯ Predicted MoRFs
- ⊙ Curated PTM Site

Disorder:

- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

- [1] Protein kinase-like (PK-like)

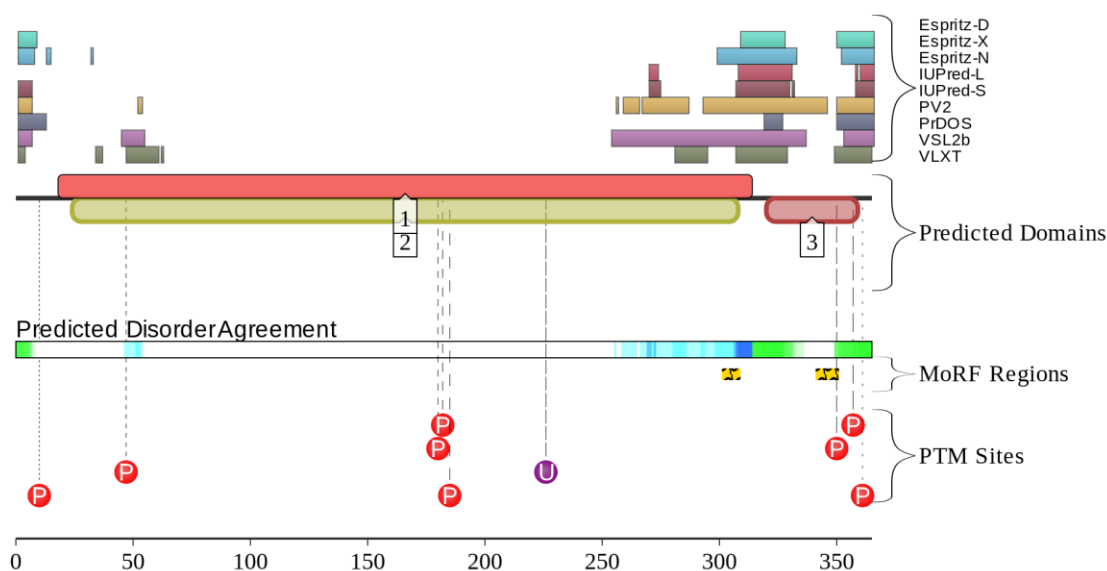
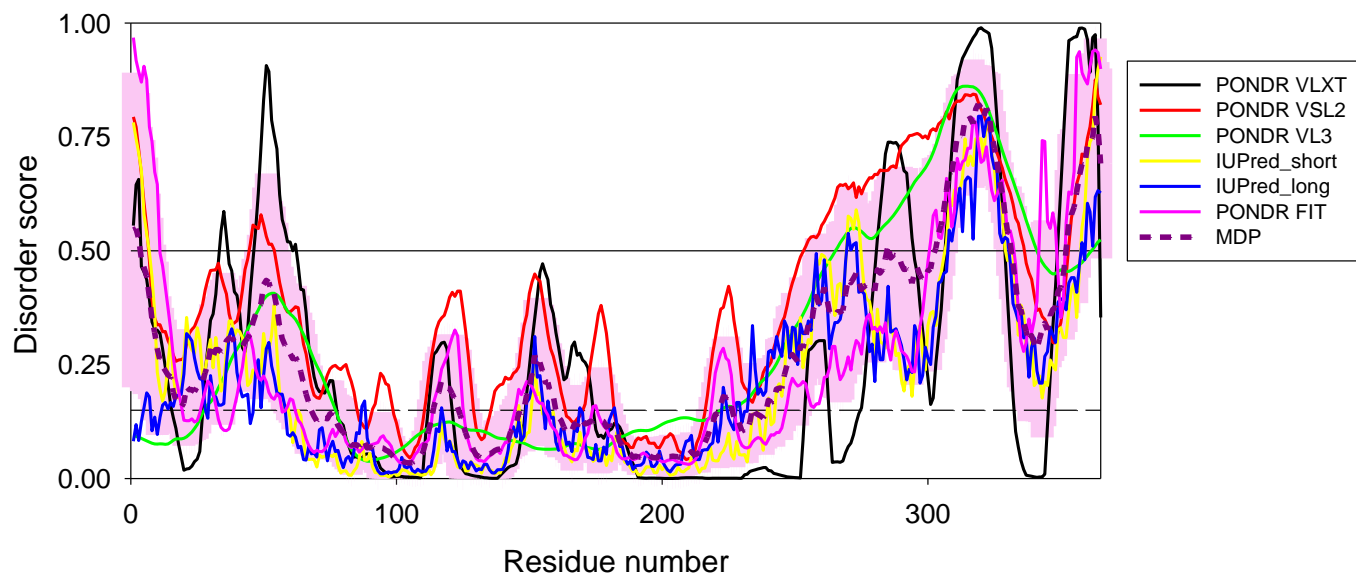
Pfams:

- [2] Protein kinase domain
- [3] PB012322 (Pfam-B)
- [4] PB016498 (Pfam-B)






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GLLDVFTPASSLRNFYDFYLVMPFMQTDLQKIMGMEFSEEKIQYLVIYQMLKGLKYIHSAGVVHRDLKPGNLAVNEDCELKILDFG
LARHADAEMTGYVVTRWYRAPEVILSWMHYNQTVDIWSVGCIMAEMLTGKTLFKGKDYLDQLTQILKVTGVPGTEFVQKLNDKAA
KSYIQSLPQTPRKDFTQLFPRASPQAADLLEKMLELDVDKRLTAAQALTHPFFEPFRDPEEETEAAQQPFDDSL EHEKLTVD EWKQ
HIYKEIVNFSPIARKDSRRRSGMKL
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Key:

- Predicted SCOP Structure
- Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:

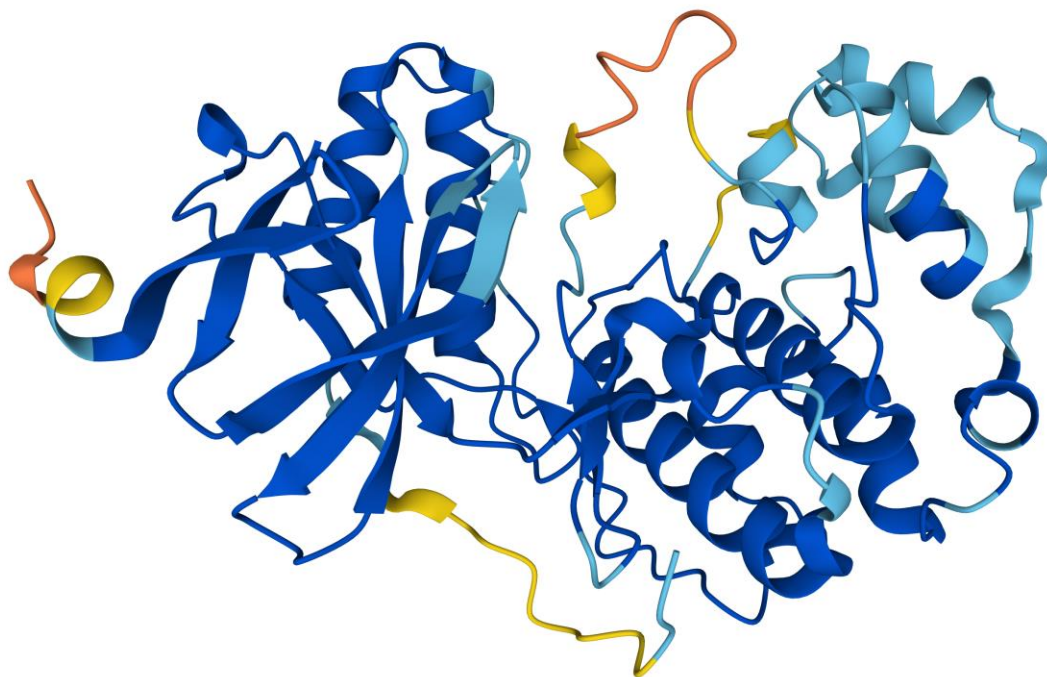
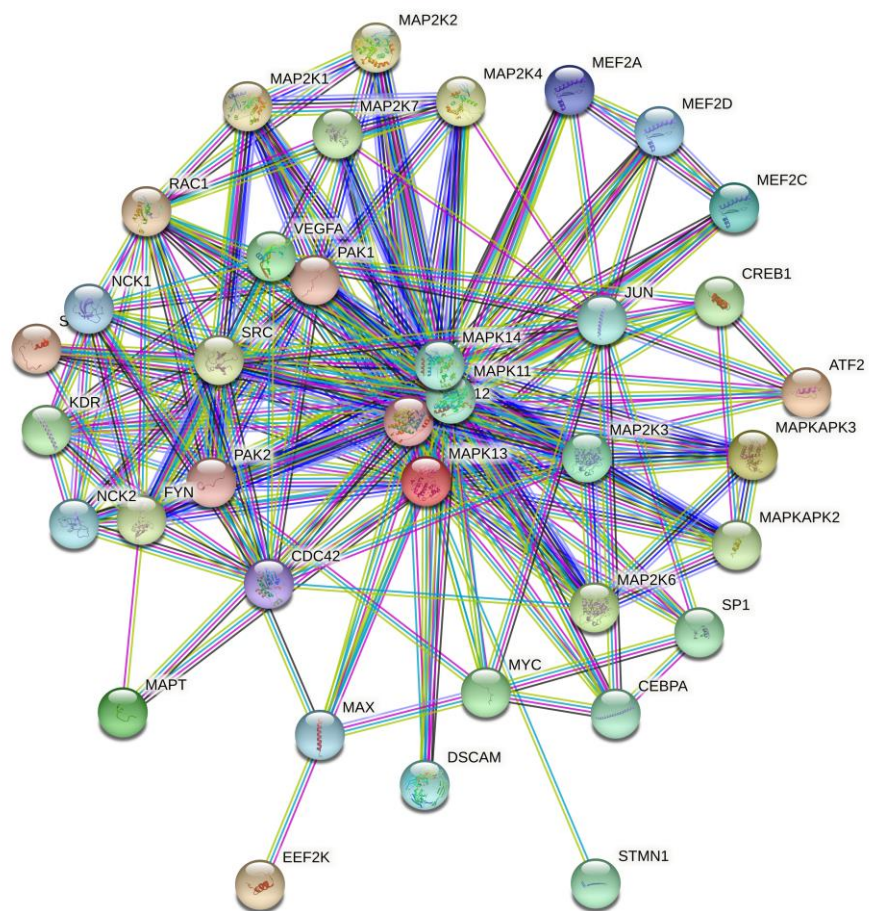
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

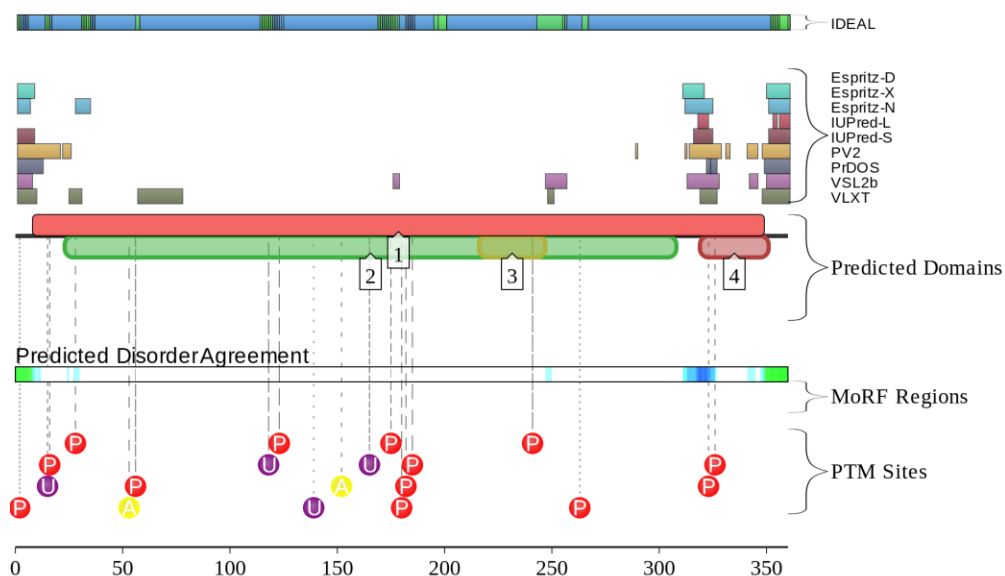
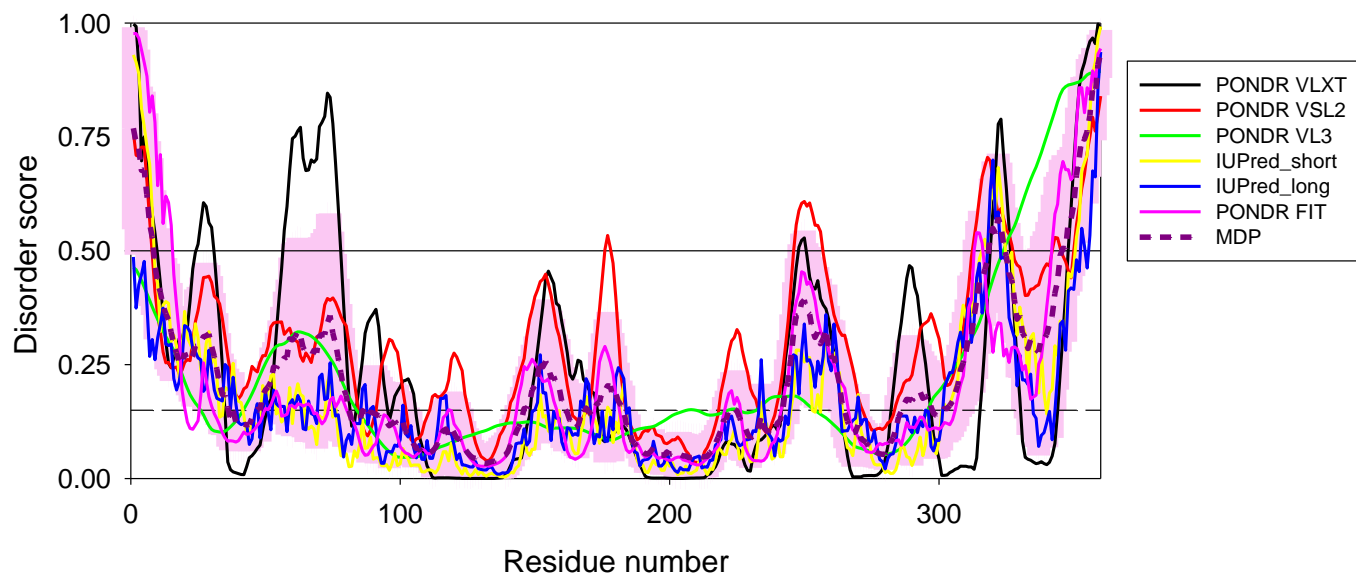
[1] Protein kinase-like (PK-like)

Pfams:

- [2] Protein kinase domain
- [3] PB016498 (Pfam-B)



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LLDVFTPARSLEEFNDVYLVTHLMGADLNNIVKQCQLTDDHVQFLIYQILRGLKYIHSADIIHRDLKPSNLAVNEDCELKILDFG
LARHTDDEMTGYVATRWYRAPEIMLNWMHYNQTVDIWSVGCIMAEELLTGRTLFPGTDHIDQLKLILRLVGTPGAELLKKISSESA
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Key:

- Predicted SCOP Structure
- Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:

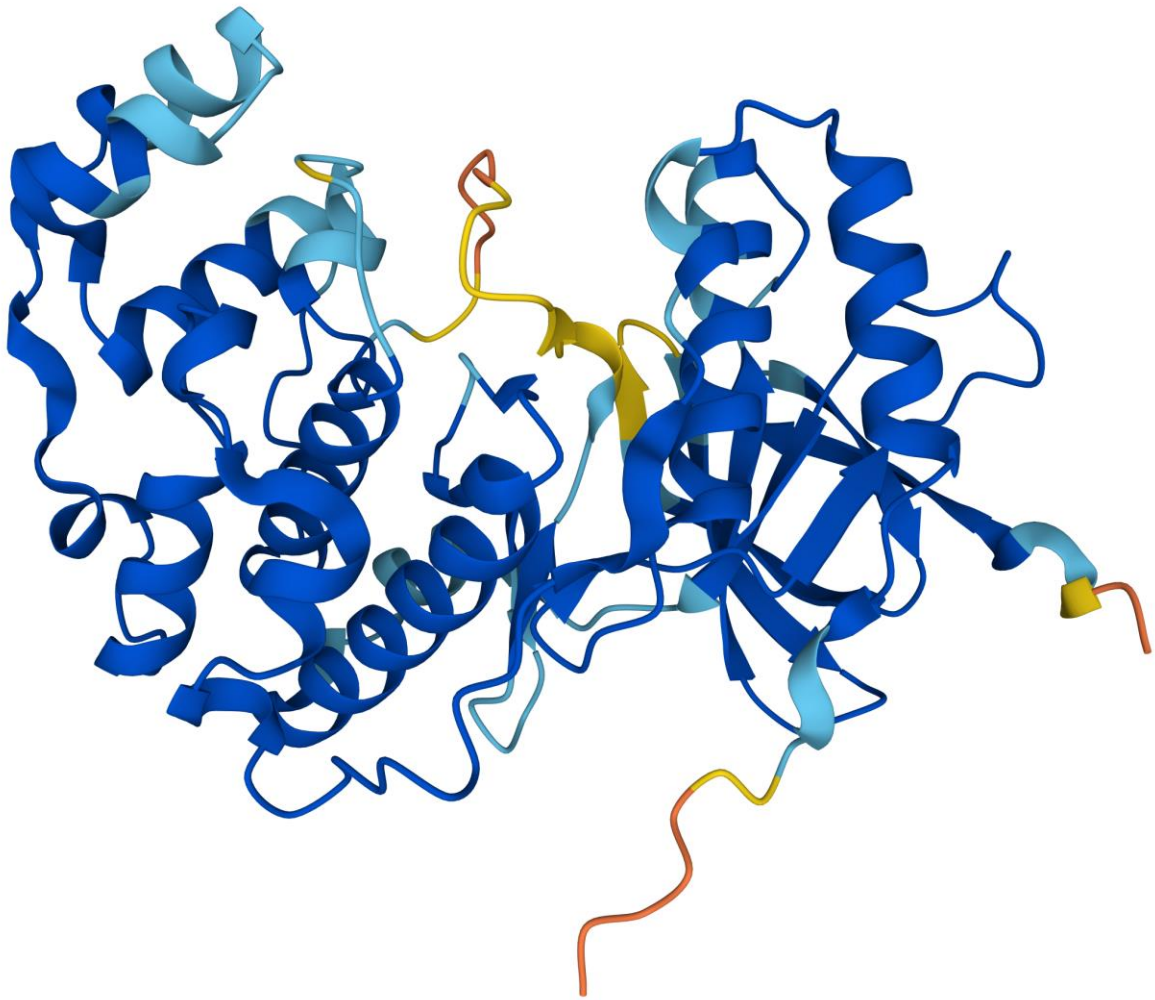
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

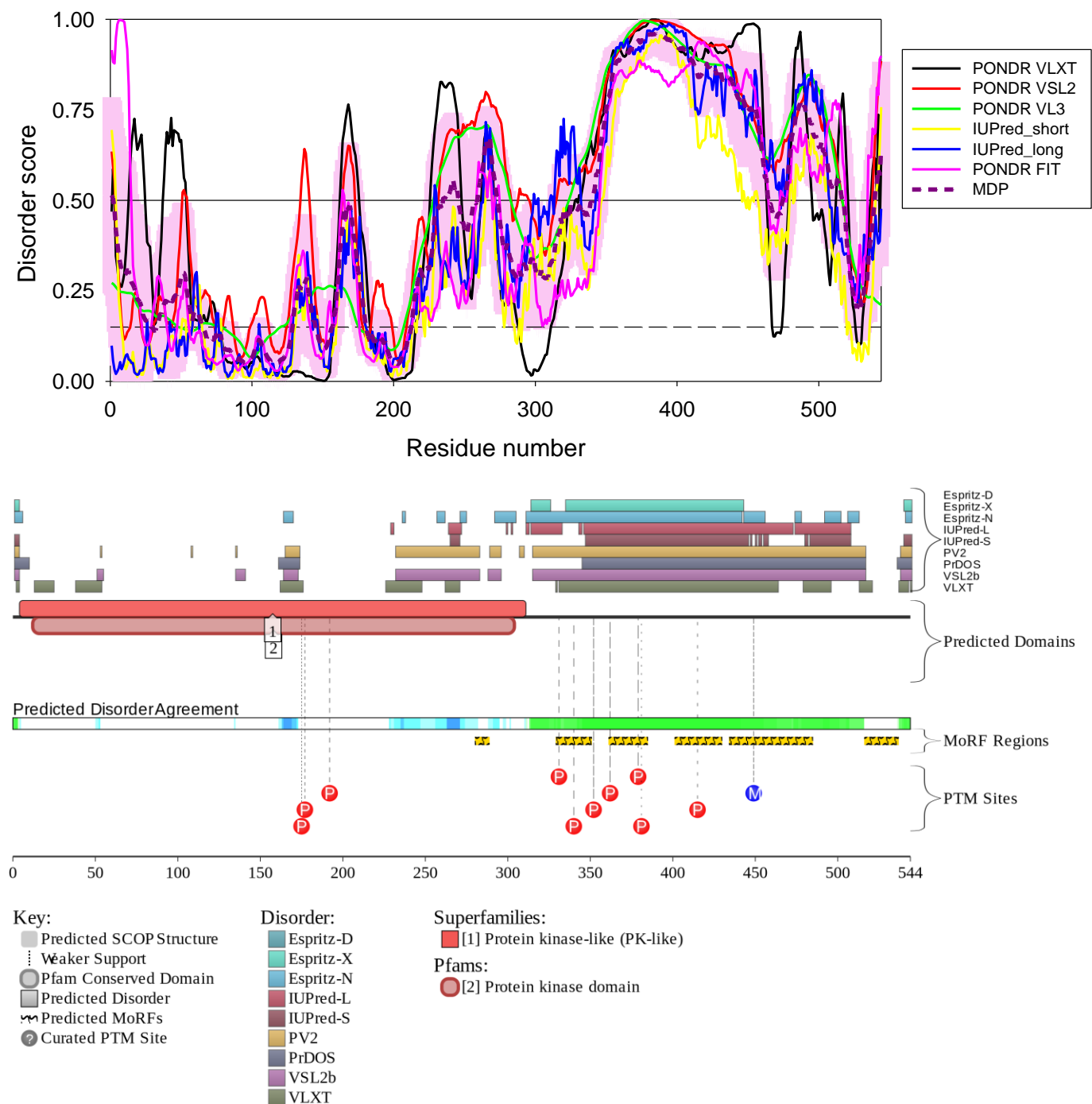
- [1] Protein kinase-like (PK-like)

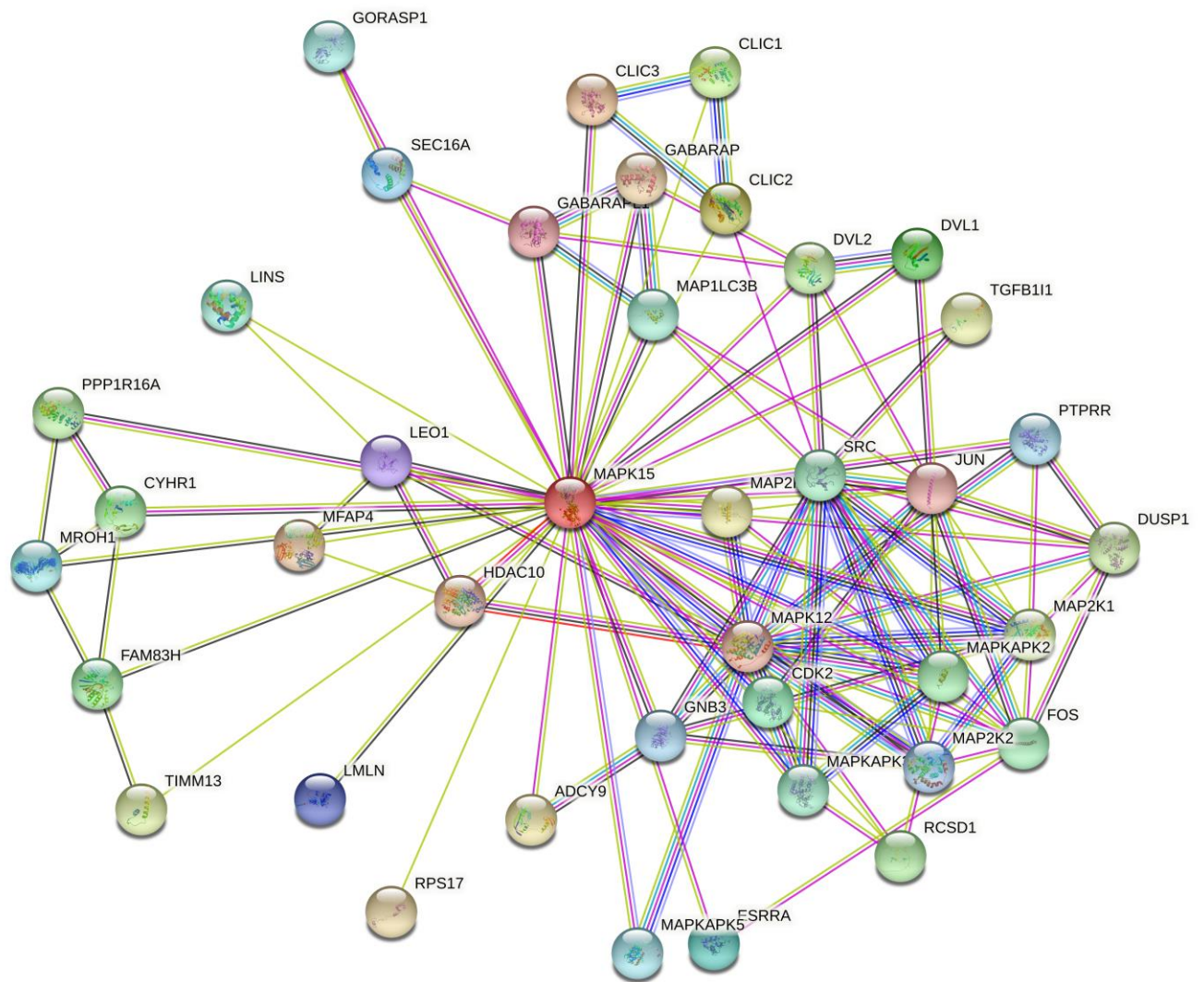
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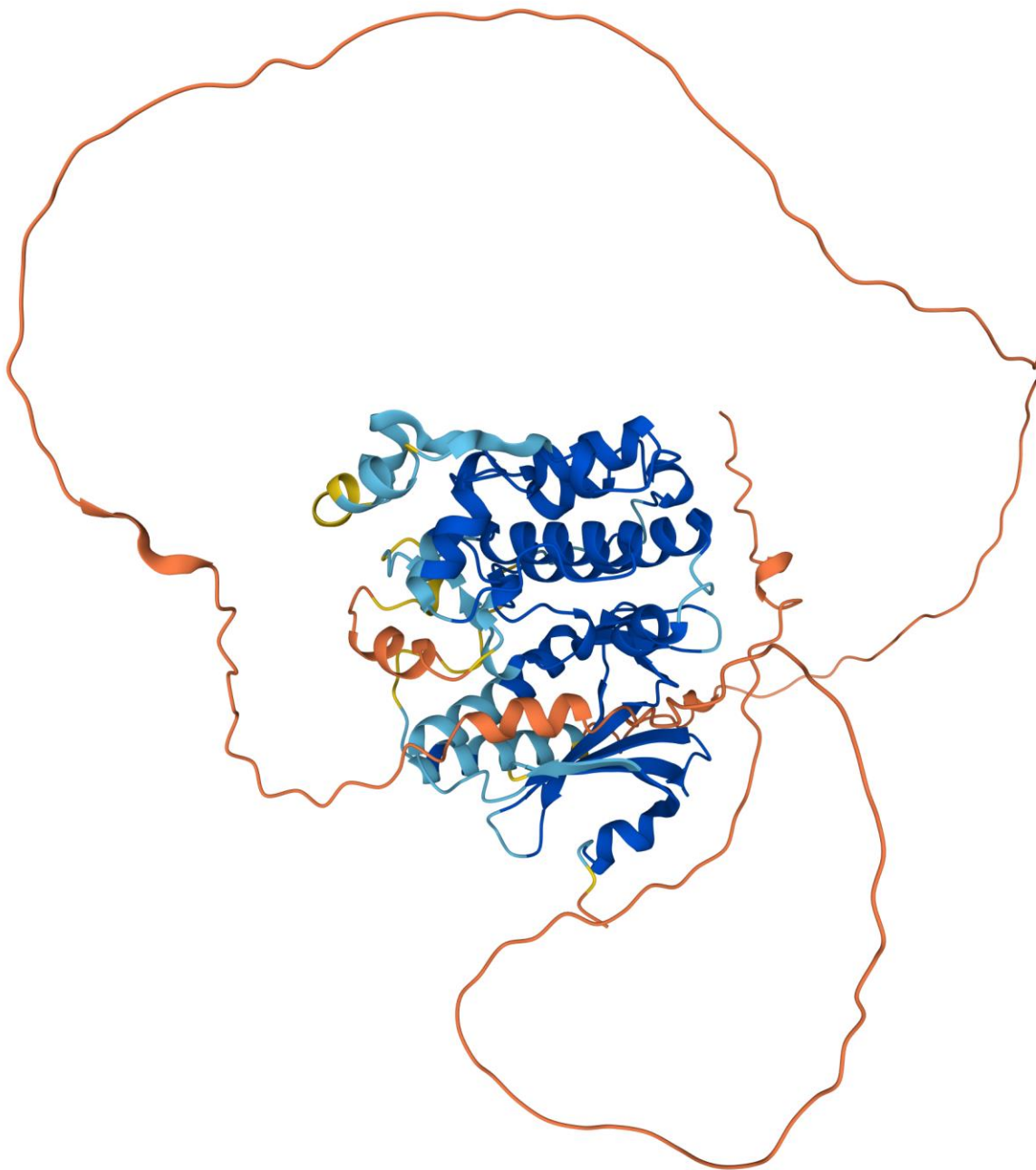
- [2] Protein kinase domain
- [3] PB019783 (Pfam-B)
- [4] PB016498 (Pfam-B)



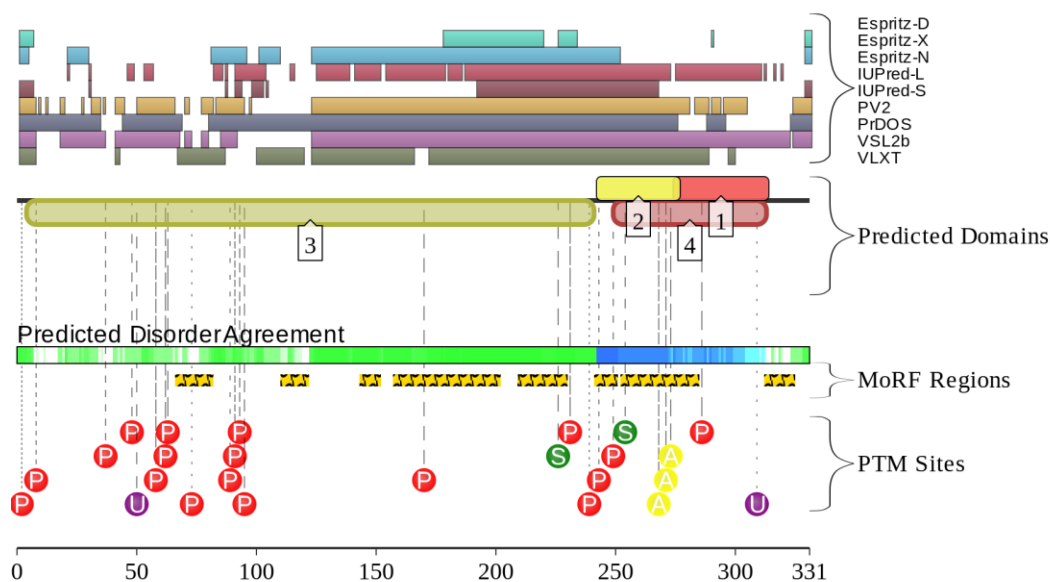
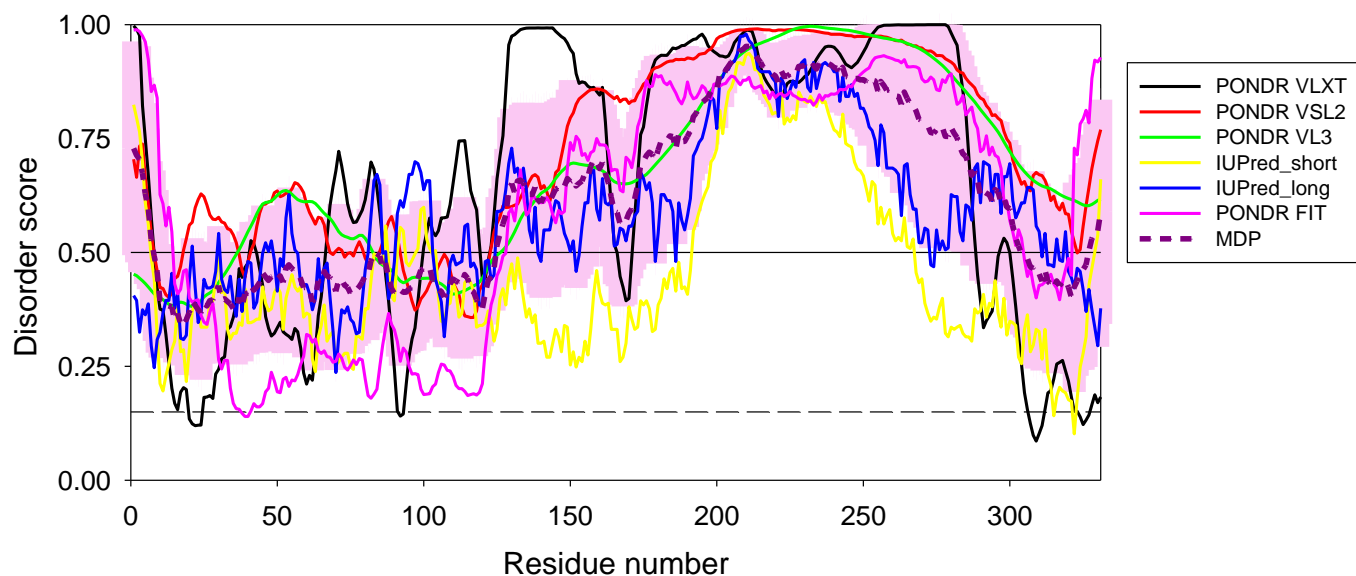
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GN=MAPK15 PE=1 SV=1
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RDIYLVFEFMDTDLNAVIRKGGLLQDVHVSIFYQLLRATRFLLHSGHVVRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEGPE
DQAVTEYVATRWYRAPEVLLSSHRYTLGVDMWSLGCILGEMLRGRPLFPGTSTLHQLELILETIPPPSEEDLLALGSGCRASVLH
QLGSRPRQTL DALLPPDTSPEALDLLRRLLVFAPDKRLSATQALQHPYVQRFHCPSEDEAREADVPRPRAHEGVQLSVPEYRSRVY
QMILECGGSSGTSREKGPPEGVSPSQAHLHKPRADPQLPSRTPVQGP RPQPSSPGHDP AEHESPRAAKNVPRQNSAPLLQTALLG
NGERPPGAKEAPPLTSLVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV RVASVQQVPPRLPPEARPGRRMFST SALQGA
QGGARALLGGYSQAYGTVCHSALGHLPLLEGGHV
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SV=2
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GHITTTPTPTQFLCPKNVTDEQEGFAEGFVRALAEHLHSQNTLPSVTSAAQPVNGAGMVAPAVASVAGGSGSGGFSASLHSEPPVY
ANLSNFPNGALSSGGGAPSYGAAGLAFFPAQPPQQQQPPHHLPPQMPVQHPRLQALKEEPQTVPEMPGETPPLSPIDMESQERIK
ERKMRNRNRIAAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQKVMNHVNSGCQLMLTQQLQTF
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Key:

- Predicted SCOP Structure
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- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:

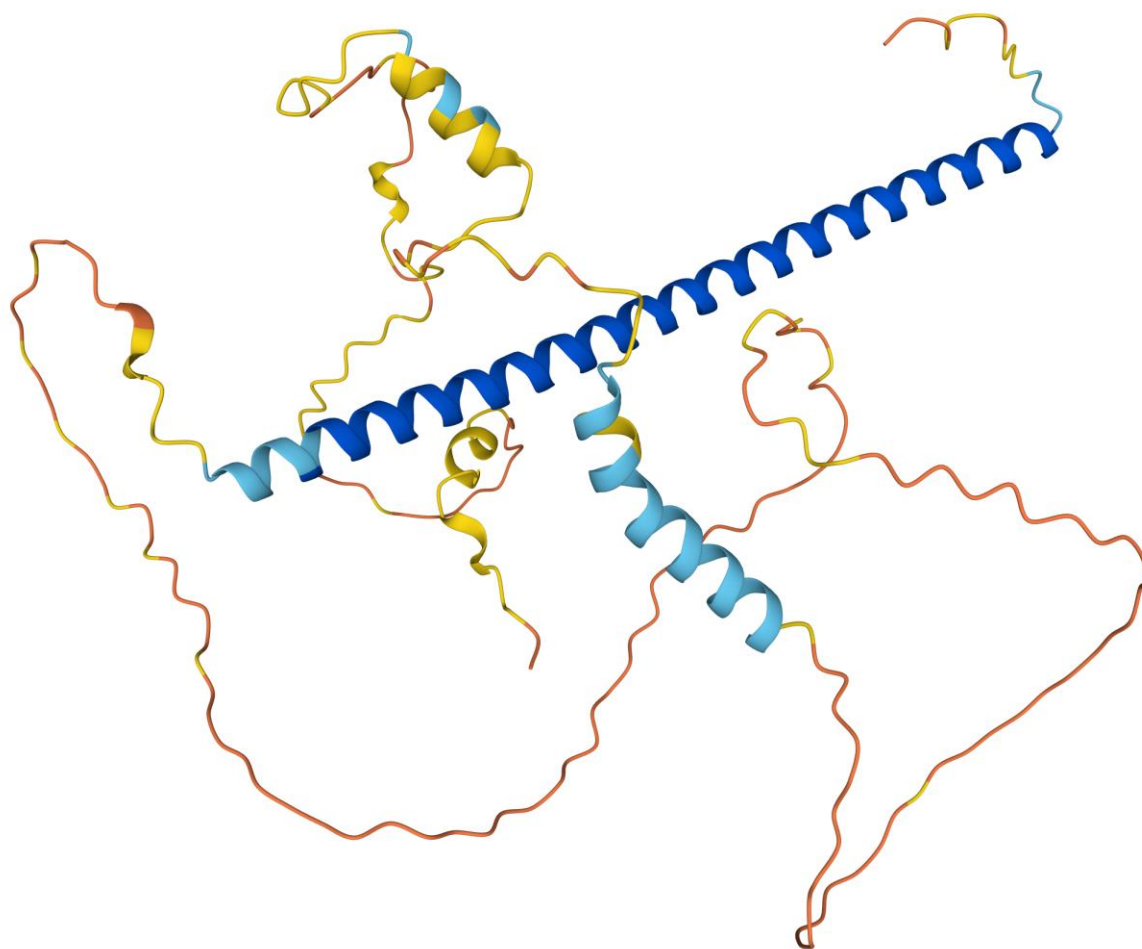
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

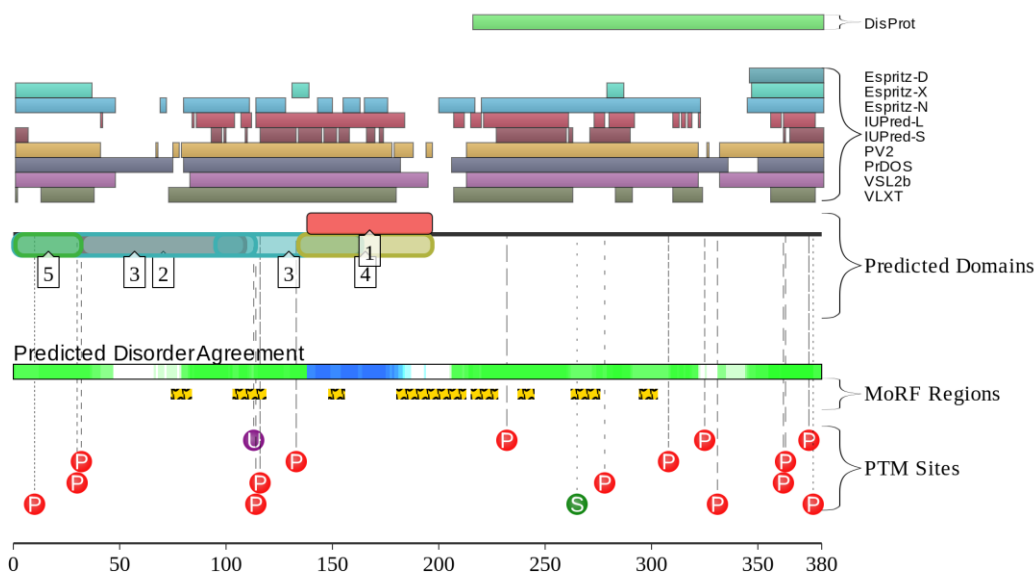
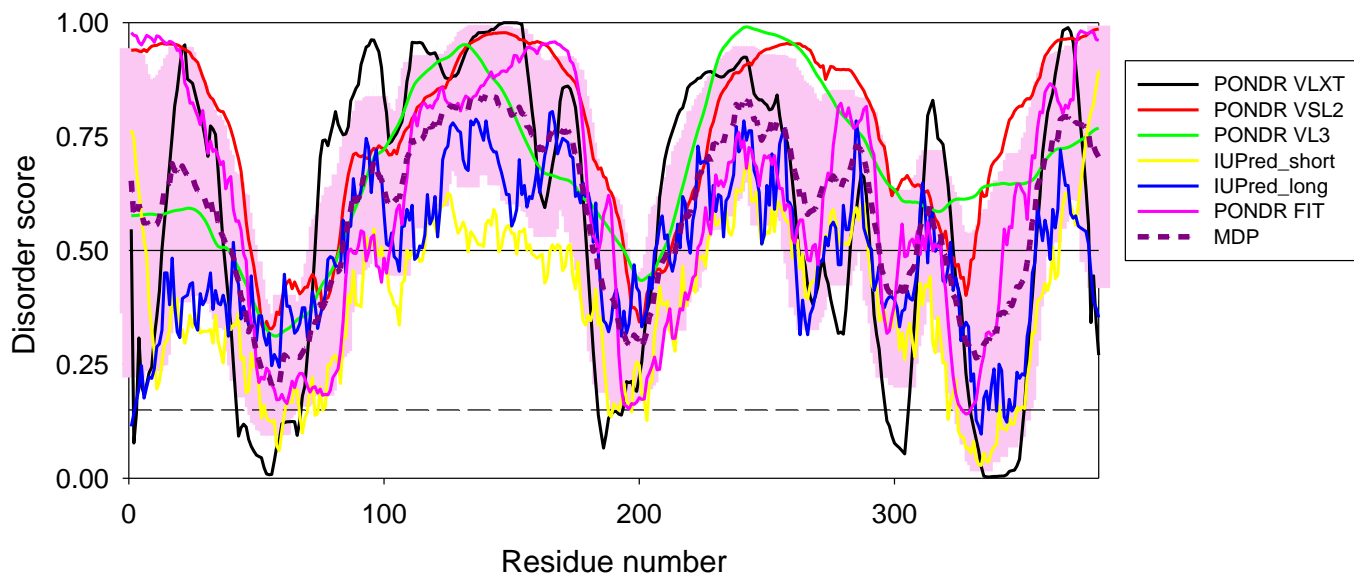
- [1] Leucine zipper domain
- [2] ADNA-binding domain in eukaryotic transcription factors

Pfams:

- [3] PF03957.8 (Family)
- [4] bZIP transcription factor



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APSQTRAPHFPFGVPAPSAGAYSRAAGVVKMTGTGGAQSIGRRGKVEQLSPEEEEKRRIRRRERNKMAAAKCRNRRELTDTLQAETD
QLEDEKSALQTEIANLLKEKEKLEFILAAHRPACKIPDDLGFPEEMSVASLDLTGGLPEVATPESEEAFITPLLLNDPEPKPSVEP
VKSISSEMELKTEPFDDFLFPASSRPSGSETARSVPDMDLSGSFYAADWEPLHSGSLGMGPMALETELEPLCTFPVVTCTPSCCTAYTSS
FVFTYPEADSFPSCAAHRKGSSSNPESSDSLSSPTLLAL
```



Key:

- Predicted SCOP Structure
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Disorder:

- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

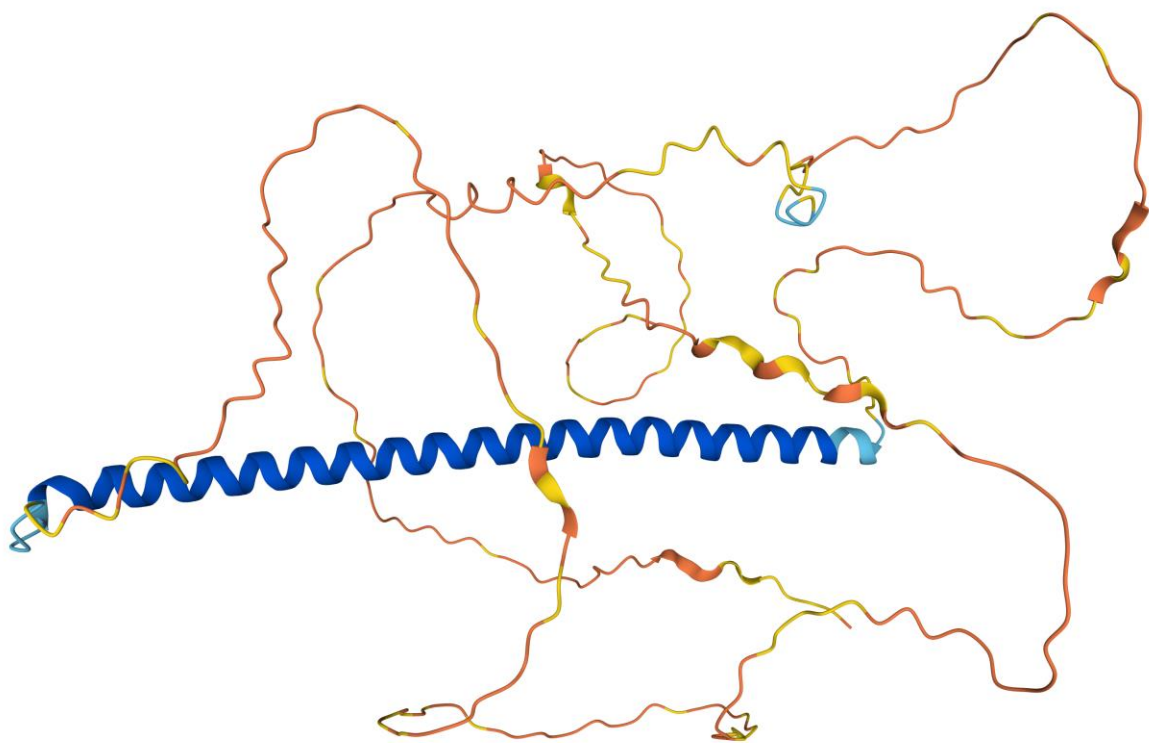
Superfamilies:

- [1] Leucine zipper domain

Pfams:

- [2] PB013236 (Pfam-B)
- [3] PB015196 (Pfam-B)
- [4] bZIP transcription factor
- [5] PB016094 (Pfam-B)

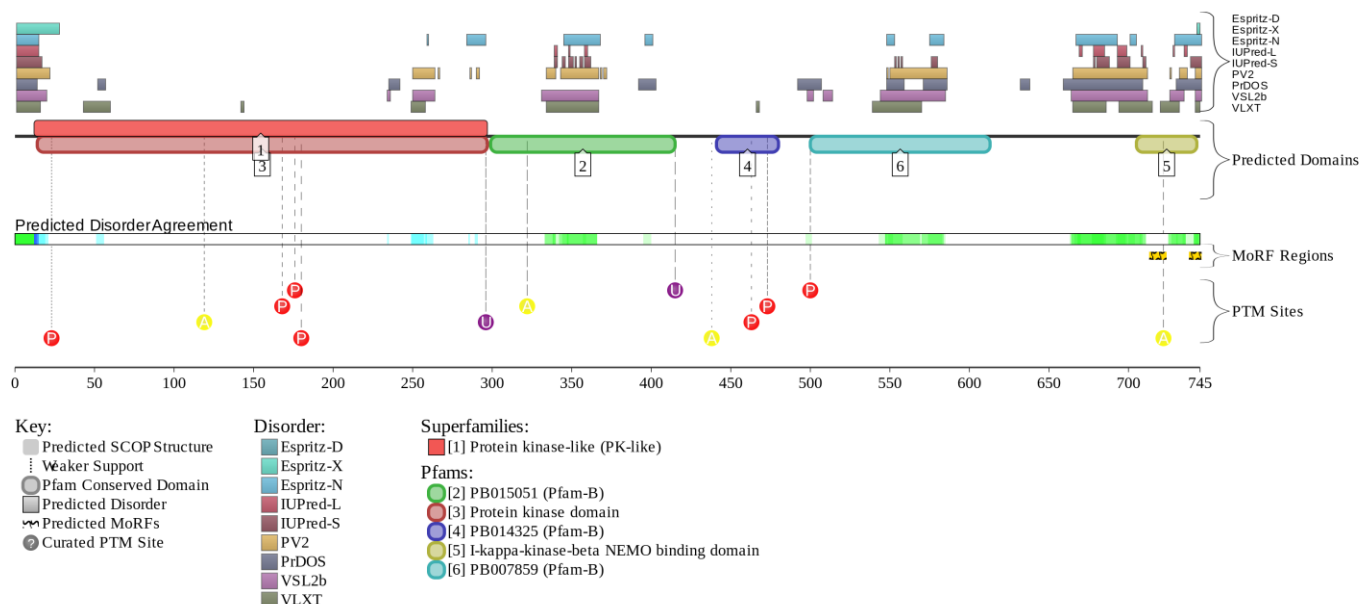
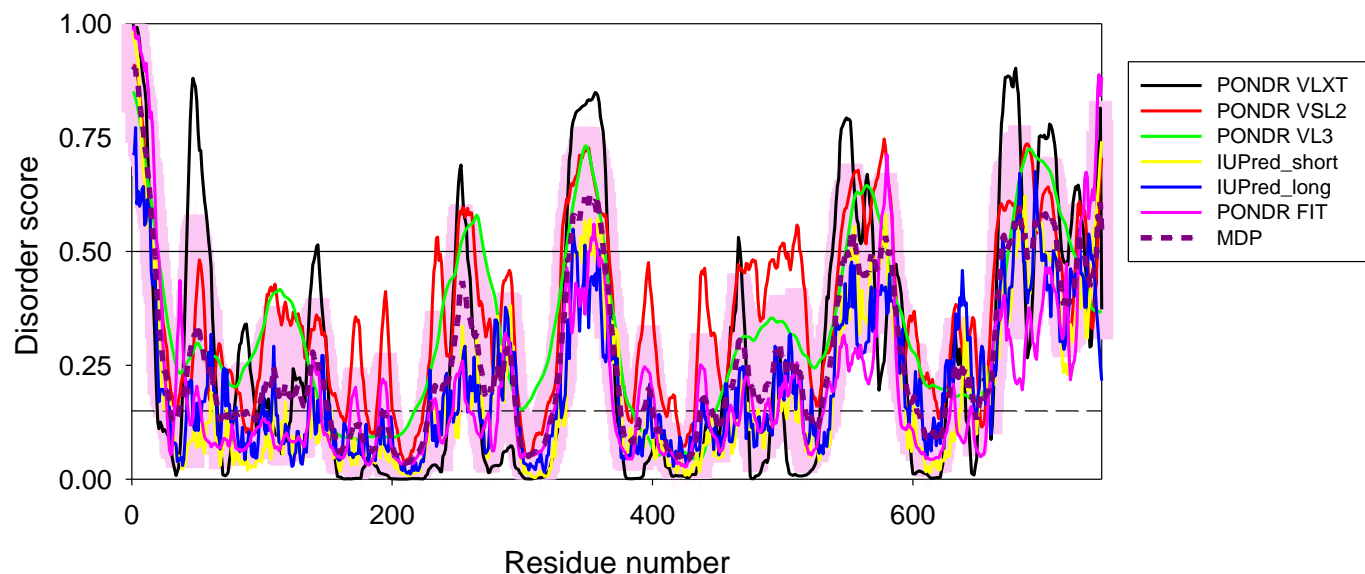


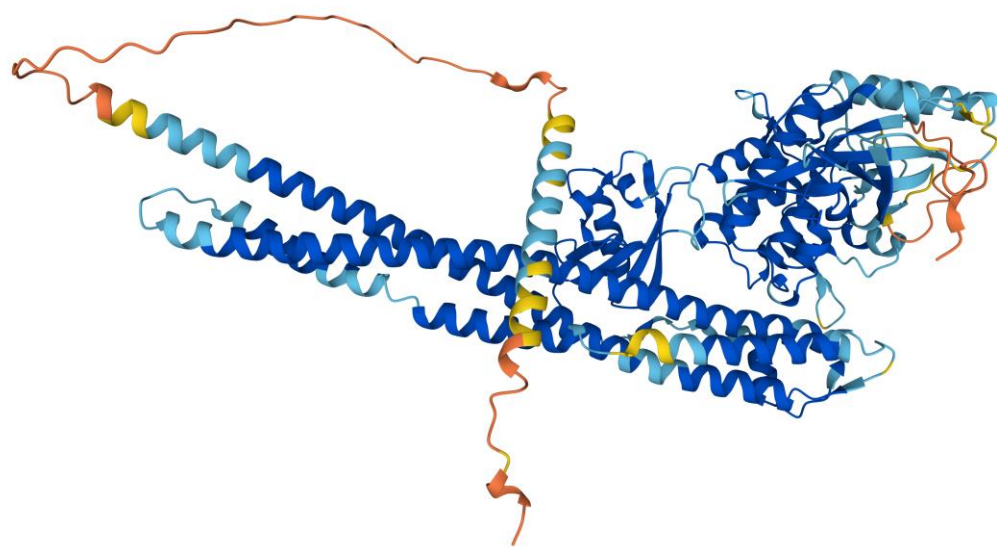


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LIHDVPLLAMEYCSGGDLRKLNLNKPENCCGLKESQILSLSDIGSGIRYLHENKIIHRDLKPENIVLQDVGGKIIHKIIDLGYAK
DVDQGSCLTSFVGTLTQYLAPELFENKPYTATVDYWSFGTMVFECIAGYRPFLLHHLQPFTHWEKIKKKDKPCIFACEEMSGEVRF
SHLPQPNLCLSLVVEPMENWLQMLNWDPPQRRGGPVDLTCLKQPRCFVLMHDHILNLKIVHILNMTSAKIIISFLLPPDESLSLQSR
IERETGINTGSQELLSETGISLDPRKPASQCVDLDGVRGCDSYMVYLFDKSKTVYEGPFAFSRSLSDCVNYIVQDSKIQLPIIQLRK
VWAEAVHYVSGLKEDYSRLFQGGQRAAMLSLLRYNANLTKMKNTLISASQQLKAKLEFFHKSIIQLDLERYSEQMTYGISSEKMLKA
WKEMEKAIIHYAEVGVIGYLEDQIMSLHAEIMELQKSPYGRQGDLMESLEQRAIDLKYLKLRPSDHSYSDSTEMVKIIVHTVQ
SQDRVLKELFGHLSKLLGCKQKIIDLLPKVEVALSNIKEADNTVMFMQGRQKEIWHLLKIACTQSSARSLVGSLEGAVTPQTS
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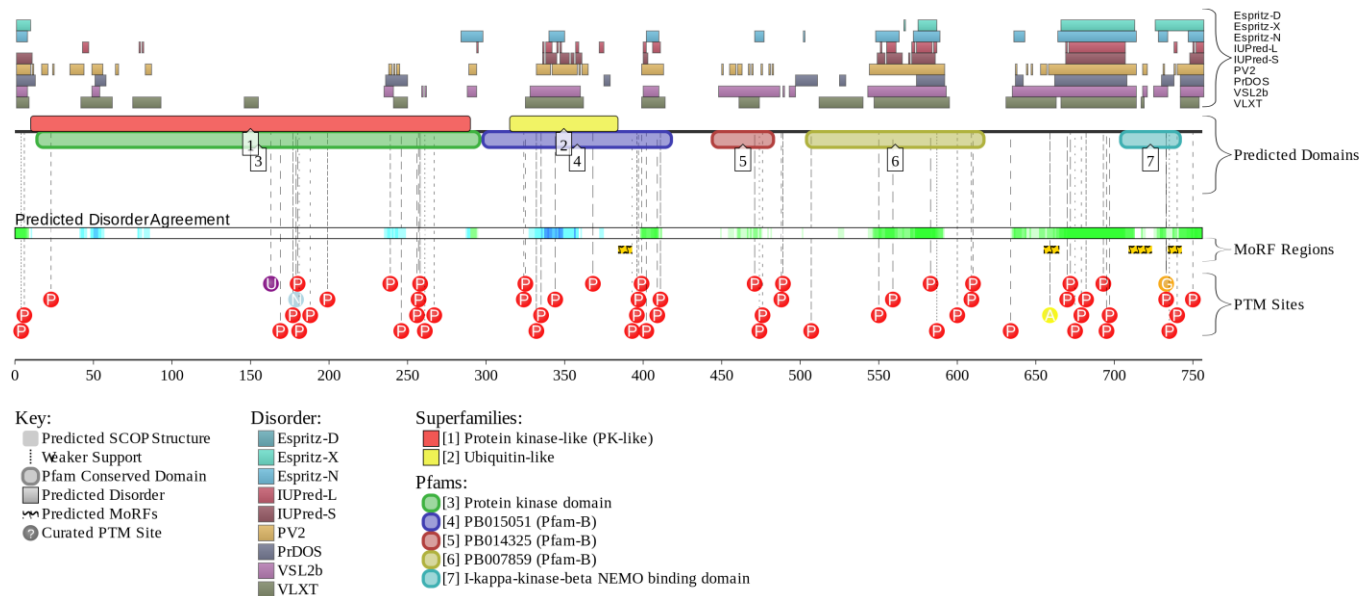
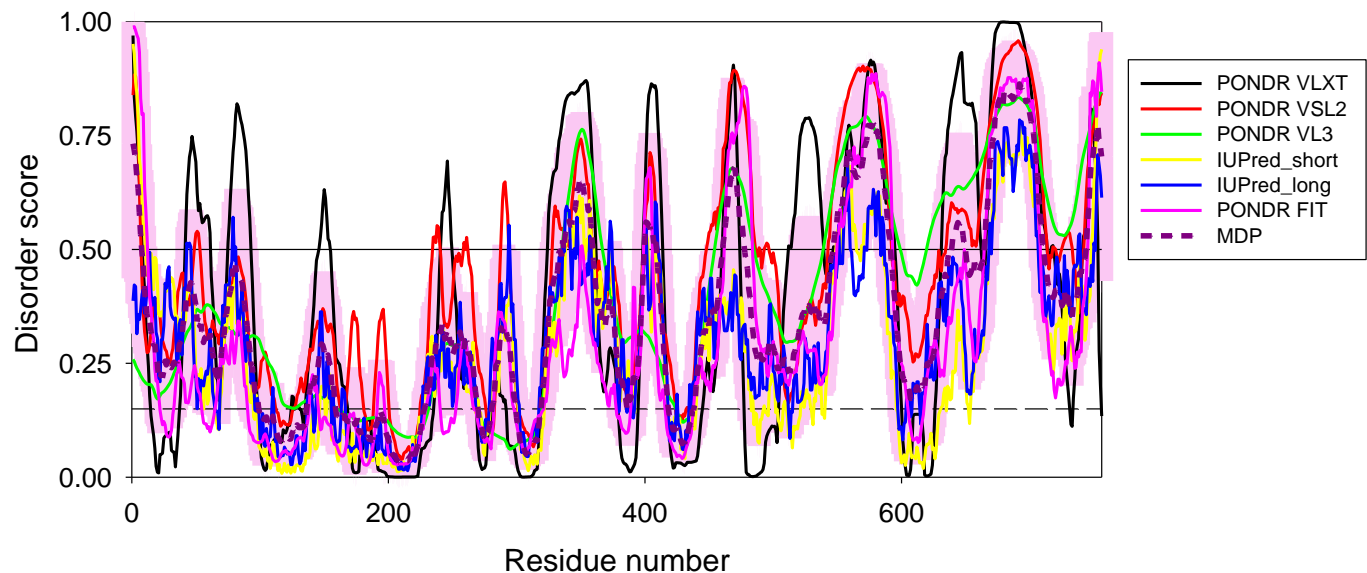


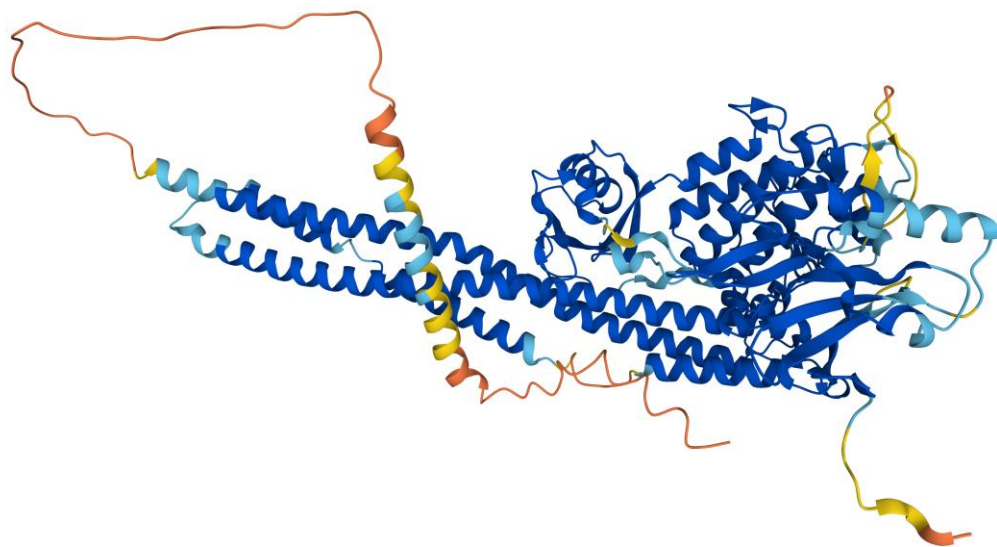
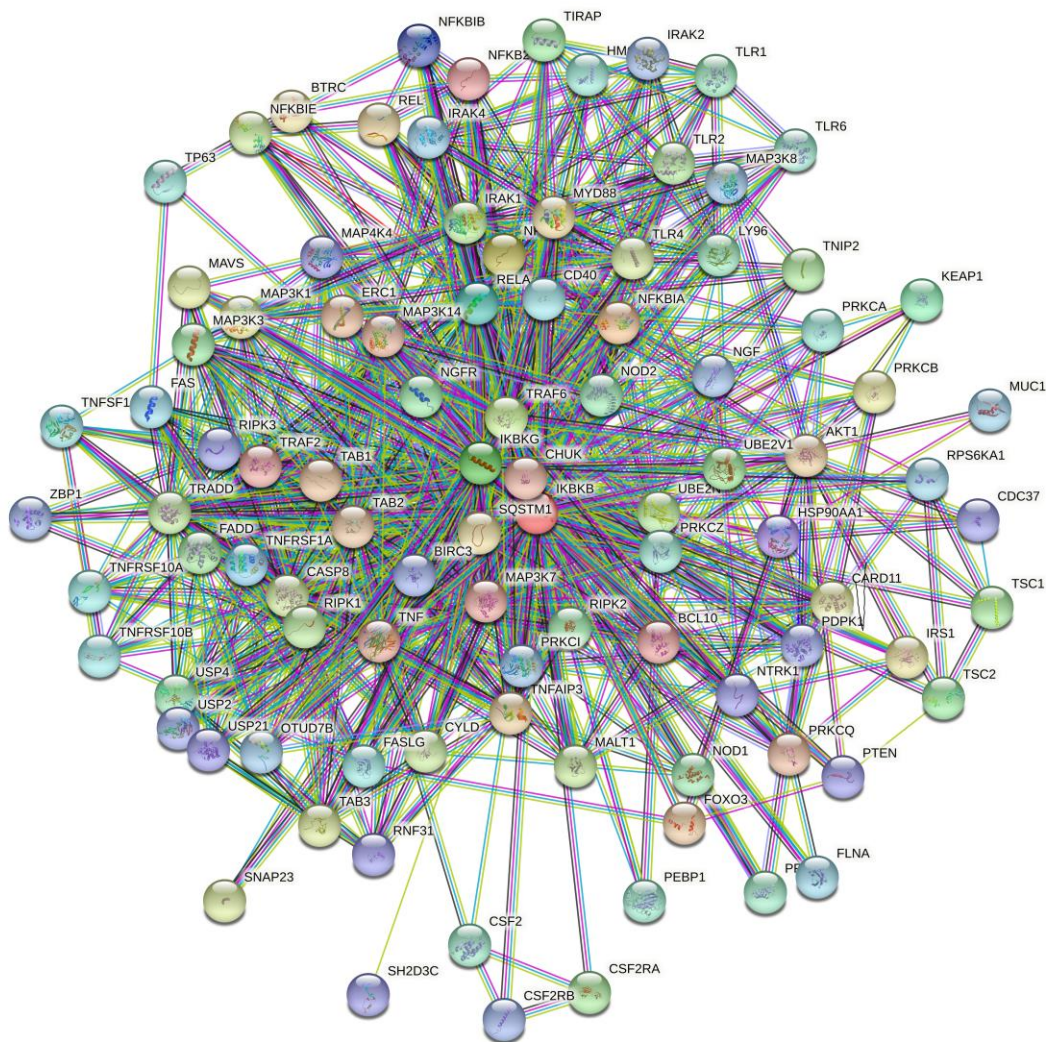


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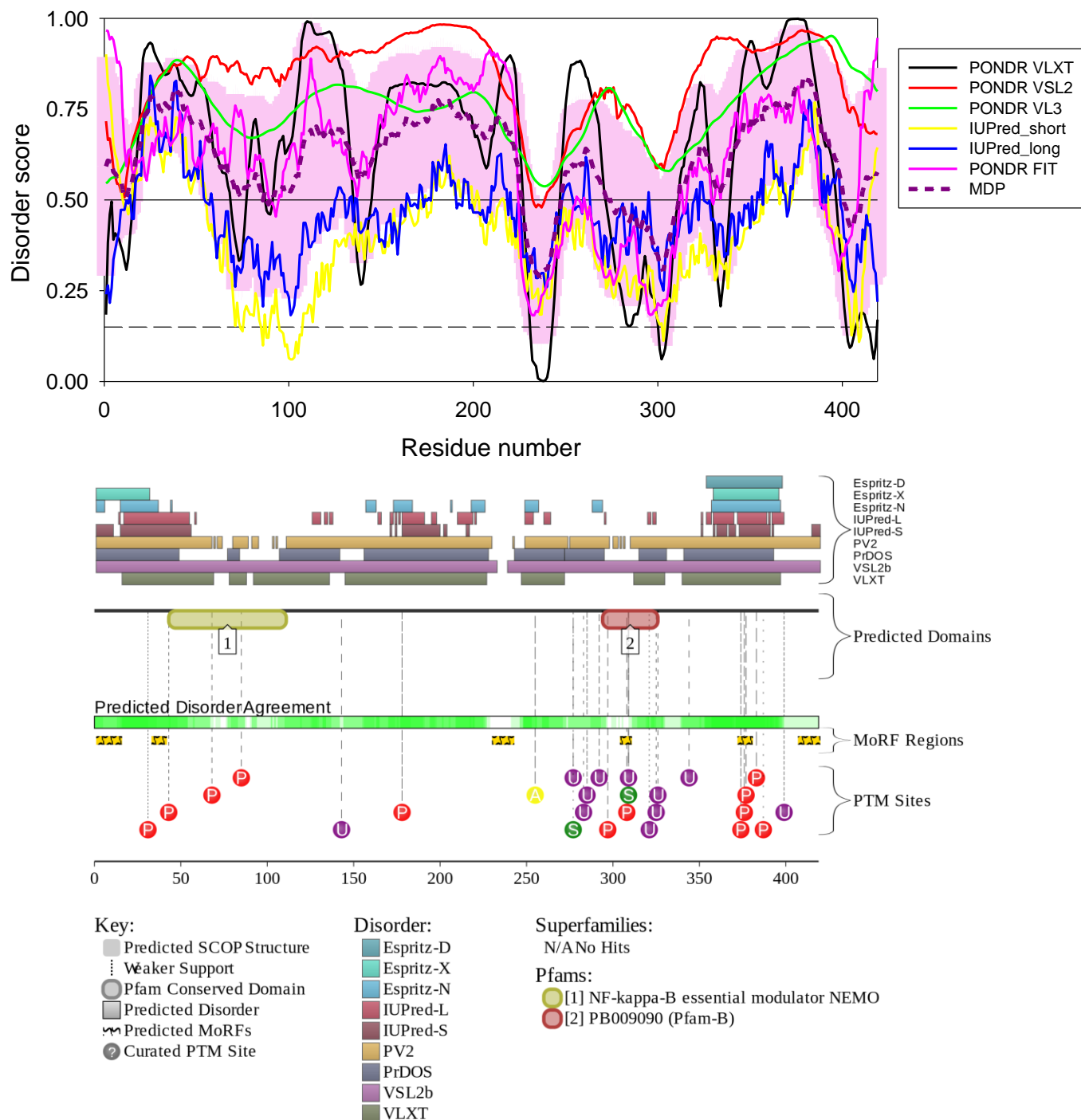
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sapiens OX=9606 GN=IKKB PE=1 SV=1
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LAPNDLPLAMEYCQGGDLRKYLNQFENCCGLREGAILTLLSDIASALRYLHENRIIHRDLKPENIVLQQGEQRLIHKIIDLGYA
KELDQGSLCTSFVGTQLQYLAPELLEQQKYTVTVDYWSFGTLAFECITGFRPFLPNWQPVQVHWSKVRQKSEVDIVVSEDLNGTVKF
SSSLPYPNLNSVLAERLEKWLQLMLMWHPRQRGTDPTYGPNCGCFKALDDIILNLKLVHILNMVTGTIHTYPTVEDESLQSLKARI
QQDTGIPEEDQELLQEAGLALIPDKPATQCISDGKLNIGHTLDMDLVFLFDNSKITIYETQISPRQPESVSCILQEPKRNLAFFQ
LRKVWGQVWHSIQTLKEDCNRLQQGQRAAMNLLRNNSCLSKMKNSMASMSQQLKAKLDFFKTSIQIDLEKYSEQTEFGITSDKL
LLAWREMEQAVELCGRENEVKLLVERMMALQTDIVDLQRSMPGRKQGGTLDDLEEQARELYRRLREKPRDQRTEGDSQEMVRLLL
QAIQSFEKKVRVIYITQLSKTVVCKQKALELLPKVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACSKVRGPVSGSPDSMNASR
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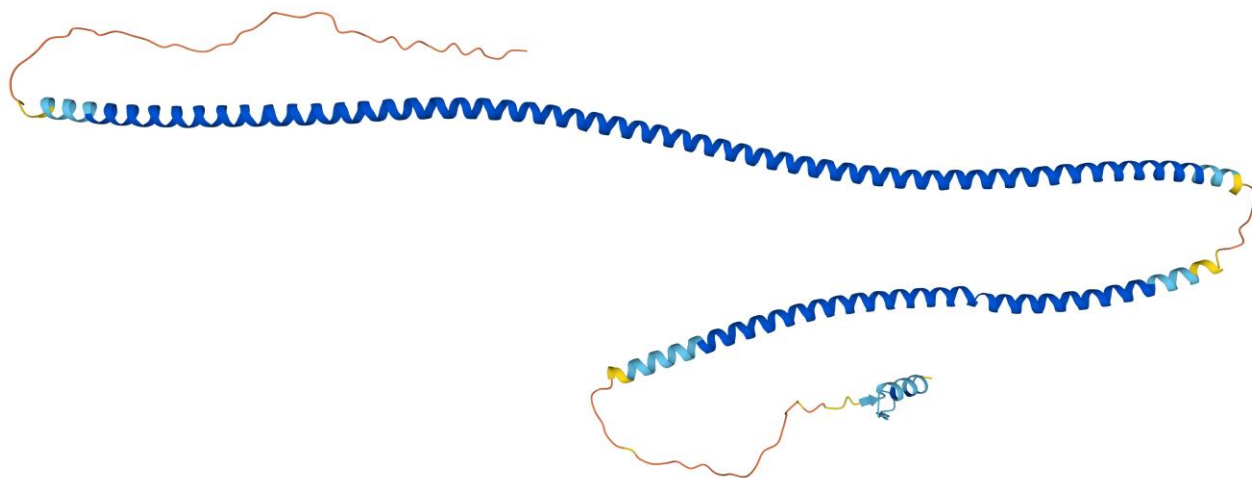
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PE=1 SV=2
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QREEKEFLMCKFQEARKLVERLGLLEKLDLKRQKEQALREVEHLKRCQQQMAEDKASVKAQVTSLLGELQESQSRLEAATKECQAL
EGRARAASEQARQLESEREALQQQHSVQVDQLRMGGQSVEAALRMRQAASEEKRLAQQLQVAYHQLFQEYDNHIKSSVVGSEK
RGMQLEDLQQLQQAEEALVAKQEVIDKLKEEAQHKIVMETVPVLKAQADIYKADFQAERQAREKLAIEKKELLQEQLQQLQREY
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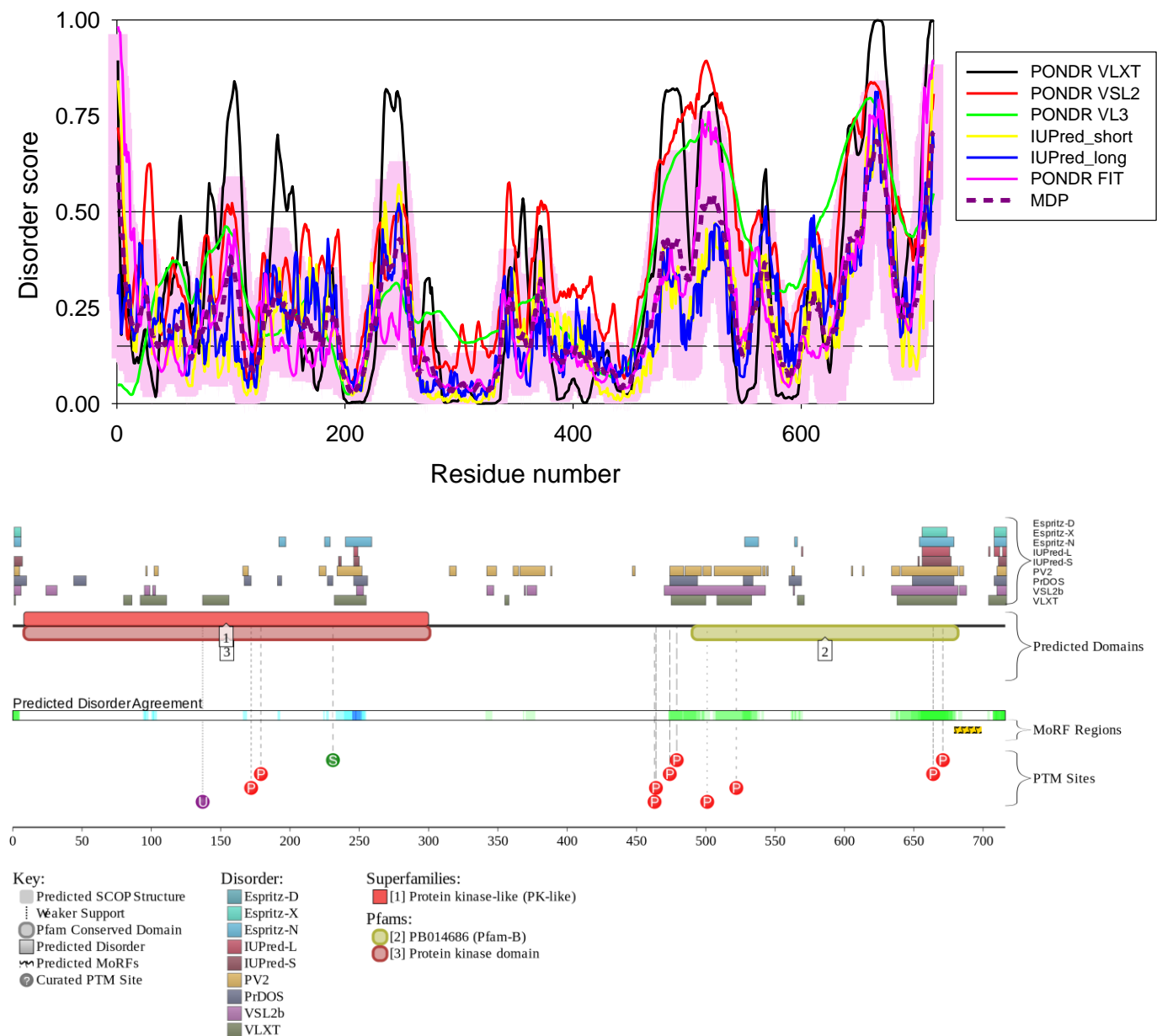


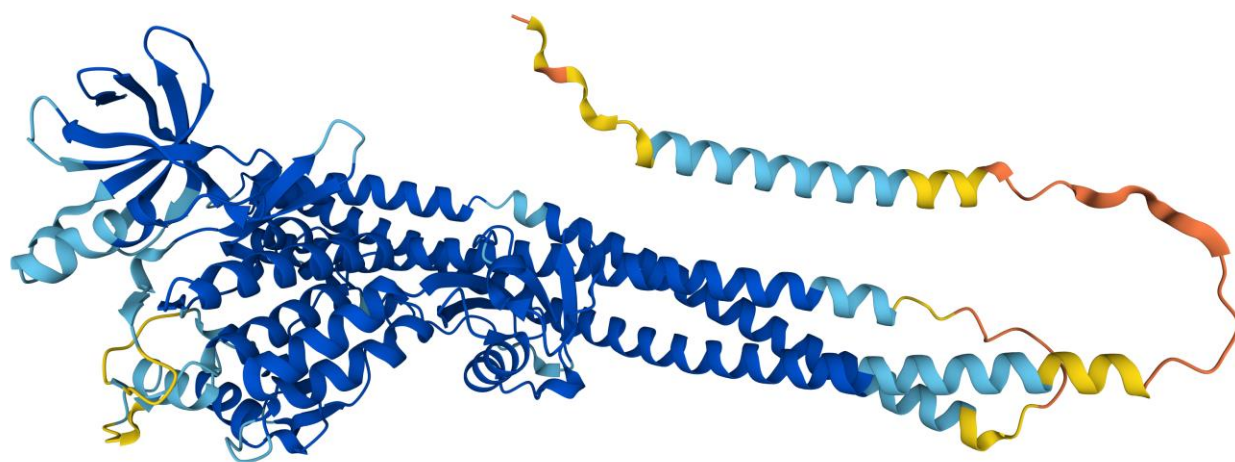
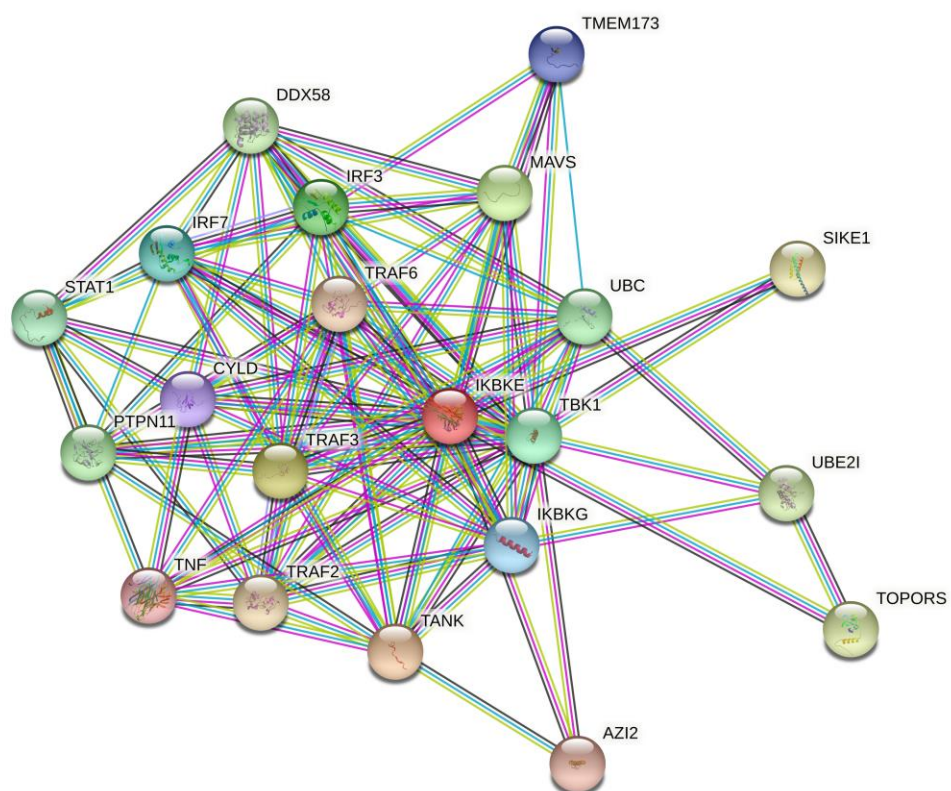


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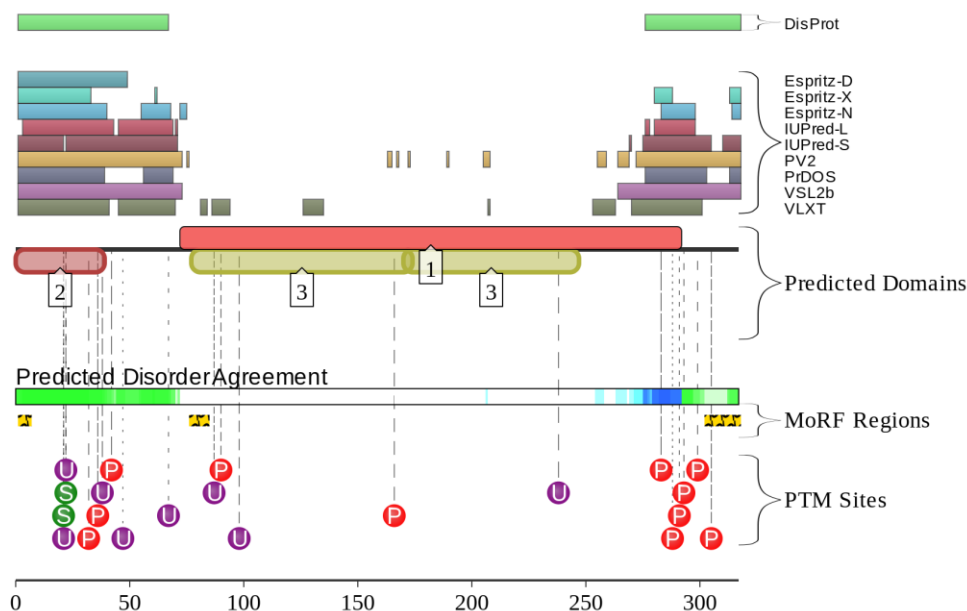
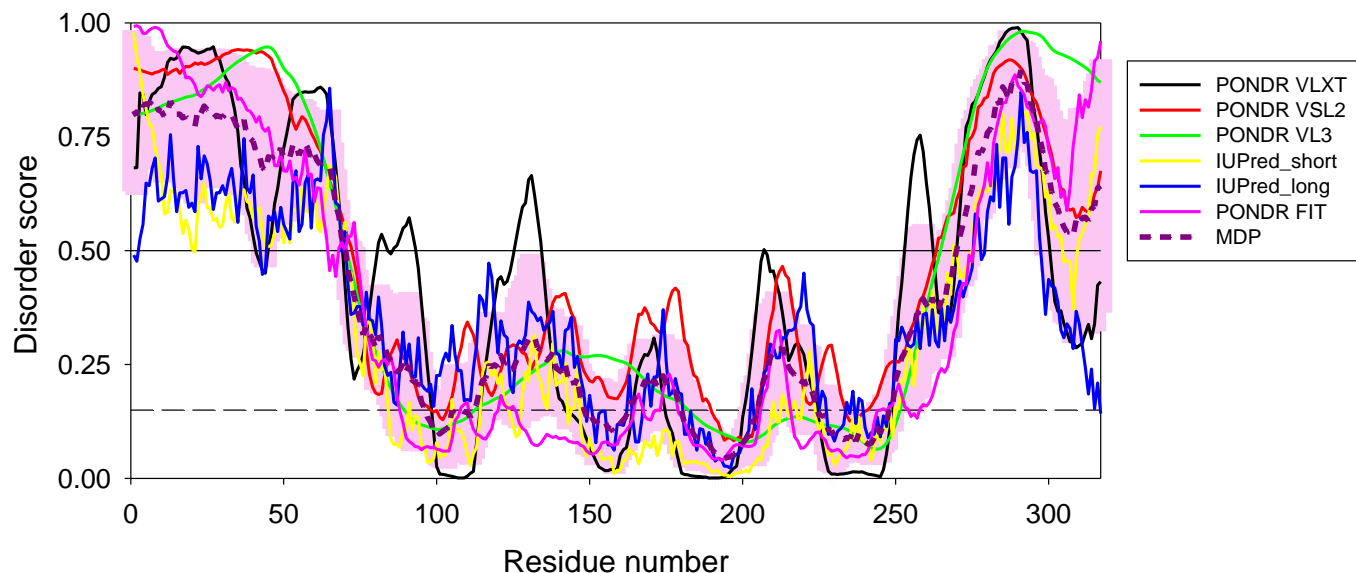
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VSVYGTTEEYLHPDMYERAVLRKPQQKAFGVTVDLWSIGVTLYHAATGSLPFIPIFGGPRRNKEIMYRITTEKPAGAIAGAQRRENG
PLEWYSYTLPTICQLSLGLQSQLVPILANILEVEQAKCWGFDQFFAETSDILQRVVHVFSLSQAVLHHIYIHAHNTIAIFQEAVH
KQTSVAPRHQEYLFEGHLCVLEPSVSAQHIAHTTASSPLTLFSTAIPKGLAFRDPALDVPKFVPKVDLQADYNTAKGVLGAGYQA
LRLARALLDGOELMFRGLHWVMEVLQATCRRTLEVARTSLLYLSSSLGTERFSSVAGTPEIQELKAAAEELRSRLRTLAEVL SRC S
QNITETQESLSSLNRELVKSRDQVHEDRSIQQIQCCLDKMNFIYKQFKKSRMRPGLGYNEEQIHKLDKVNFSHLAKRLLQVVFQEE
CVQKYQASLVTHGKRMRVVHETRNHLRLVGCSVAACNTEAQGVQESLSKLLLEELSHQLLQDRAKGAQASPPPIAPYPSPTRKDLL
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```
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PE=1 SV=1
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EKALTMEVIRQVKGDIAFLNFQNNLQQTPLHLAVITNQPEIAEALLGAGCDPELRDFRGNTPLHLACEQGCLASVGLTQSCTTP
HLHSILKATNYNGHTCLHLASIHGYLGIVELLVSLGADVNAQEPNCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQGYSPYQ
LTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFTEFTEDELDPYDDCVFGGQRLTL
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Key:

- Predicted SCOP Structure
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- Curated PTM Site

Disorder:

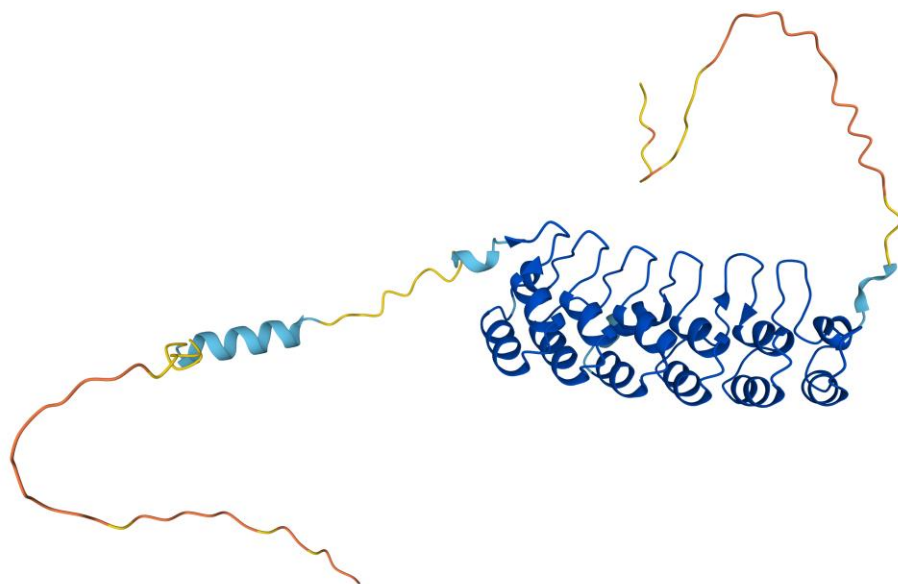
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

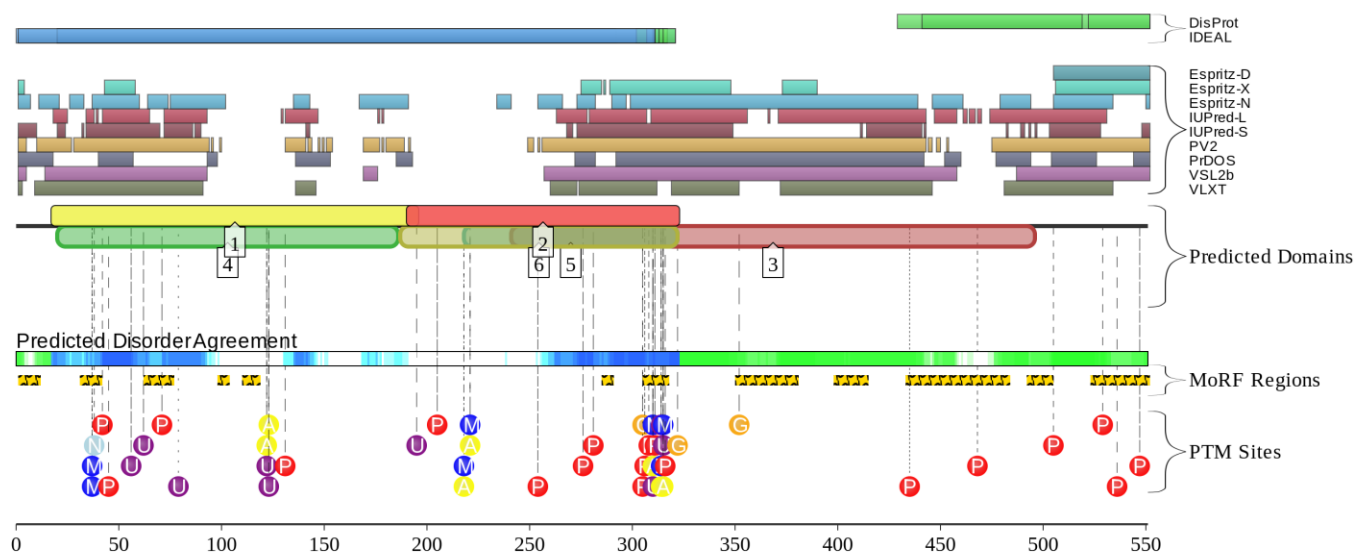
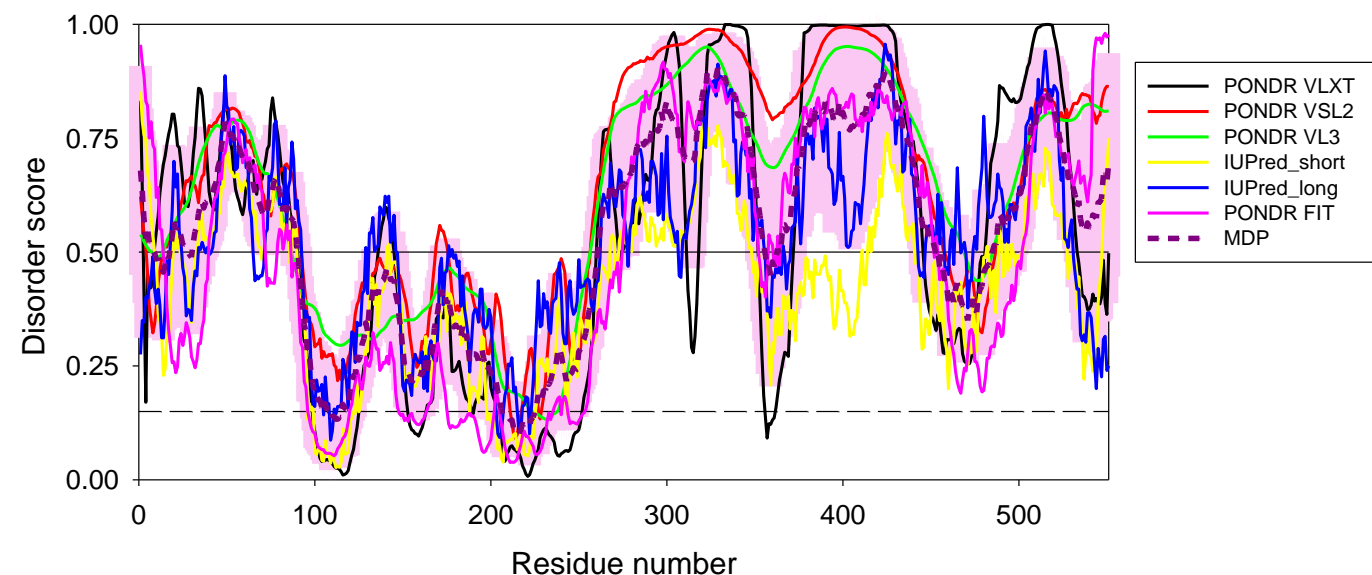
- [1]Ankyrin repeat

Pfams:

- [2] PB016960 (Pfam-B)
- [3]Ankyrin repeats (3 copies)




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HPHELVGKDCRDGFEAEELCPDRCIHSFQNLGIQCCKRDLEQAISQRIQTNNNPFQVPIEEQRGDYDLNAVRLCFQVTVRDP SG
RPLRLPPVLSHPIFDNRAPNTAELKICRVNRNSGSLGGDEIFLLCDKVQKEDI EYFTGPGWEARGSFSSQADVHRQVAIVFRT P
PYADPSLQAPVRVSMQLRRPSDRELSEPMFQYLPD TDDRHRIEEKRKRTYETFKSIMKKS PFSGPTDPRPPPRRIAVPSRSSAS
VPKPAPQPYPF TSSSLSTINYDEFPTMVFP SGQISQASALAPAPPQVLPQAPAPAPAPAMVSALAQA PAPVPVLAPGPPQAVAPPA
PKPTQAGEGTLSEALLQLQFDD ELDGALLGNSTDPAVF TDLASVDNSEFQQLLNQGI PVAPHTTEPMLMEYPEAITRLVTGAQRP
PDPAPAPL GAPGLPNGLLSGDEDFSSIADMDFSALLSQISS
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Key:

- Predicted SCOP Structure
- Waker Support
- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:

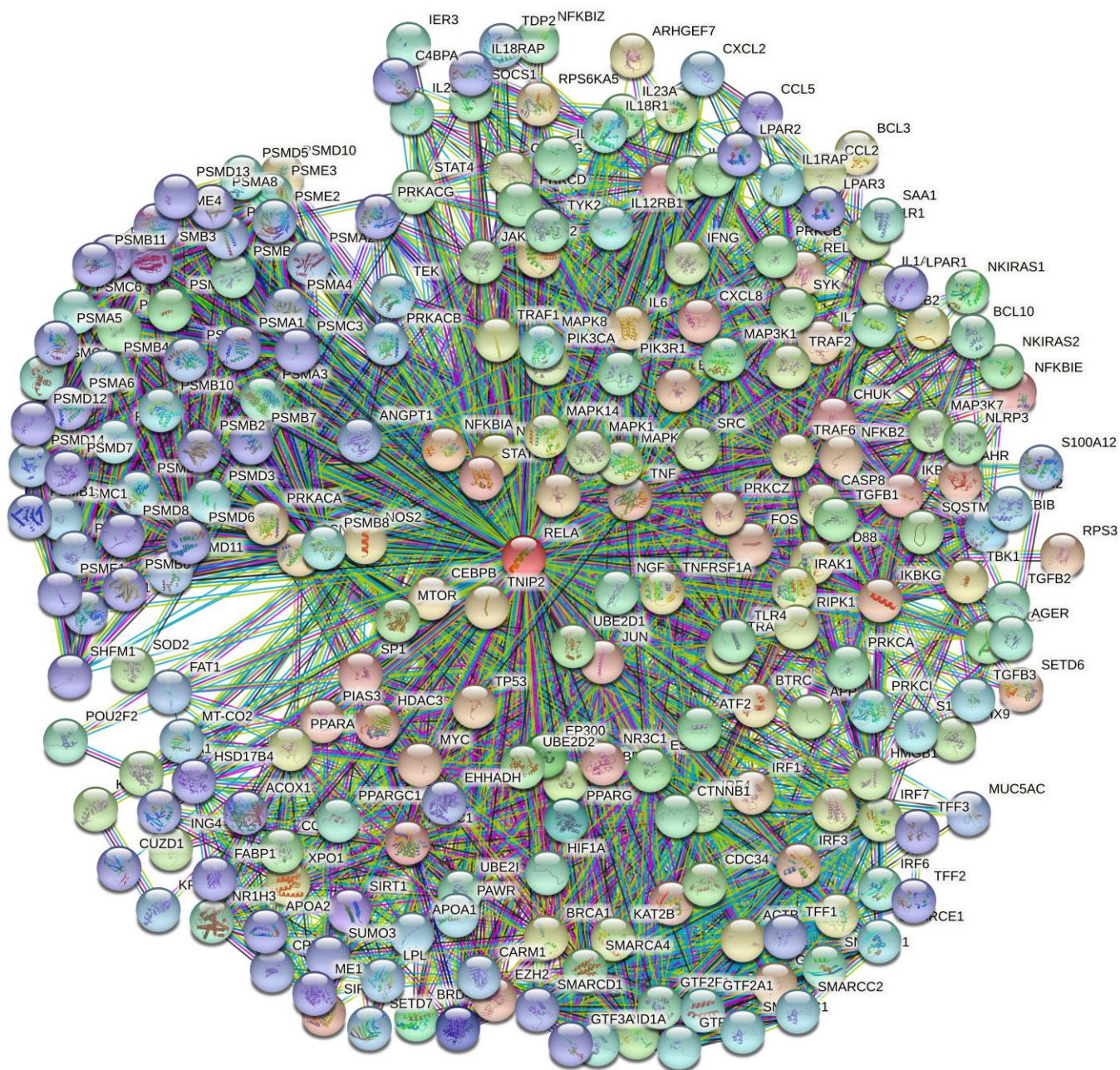
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

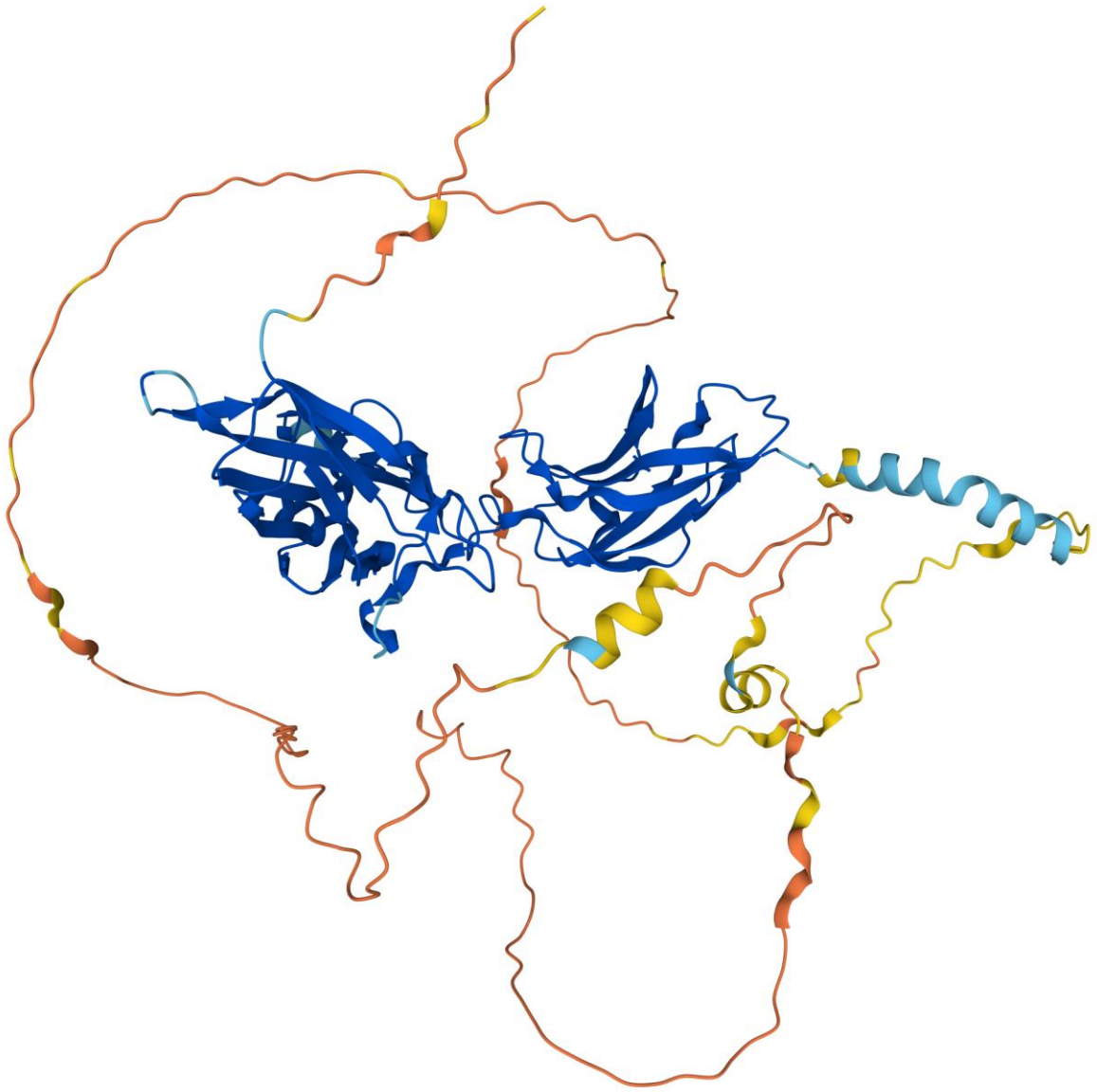
Superfamilies:

- [1] p53-like transcription factors
- [2] E set domains

Pfams:

- [3] PB018191 (Pfam-B)
- [4] Rel homology domain (RHD)
- [5] PB012675 (Pfam-B)
- [6] PB003008 (Pfam-B)

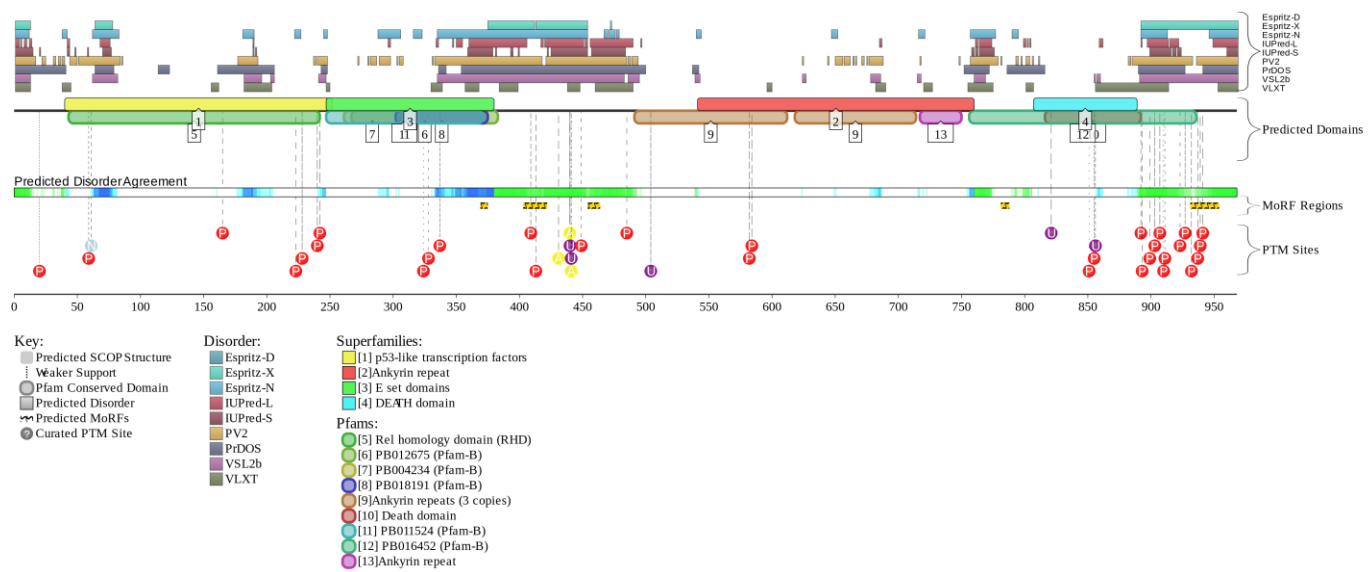
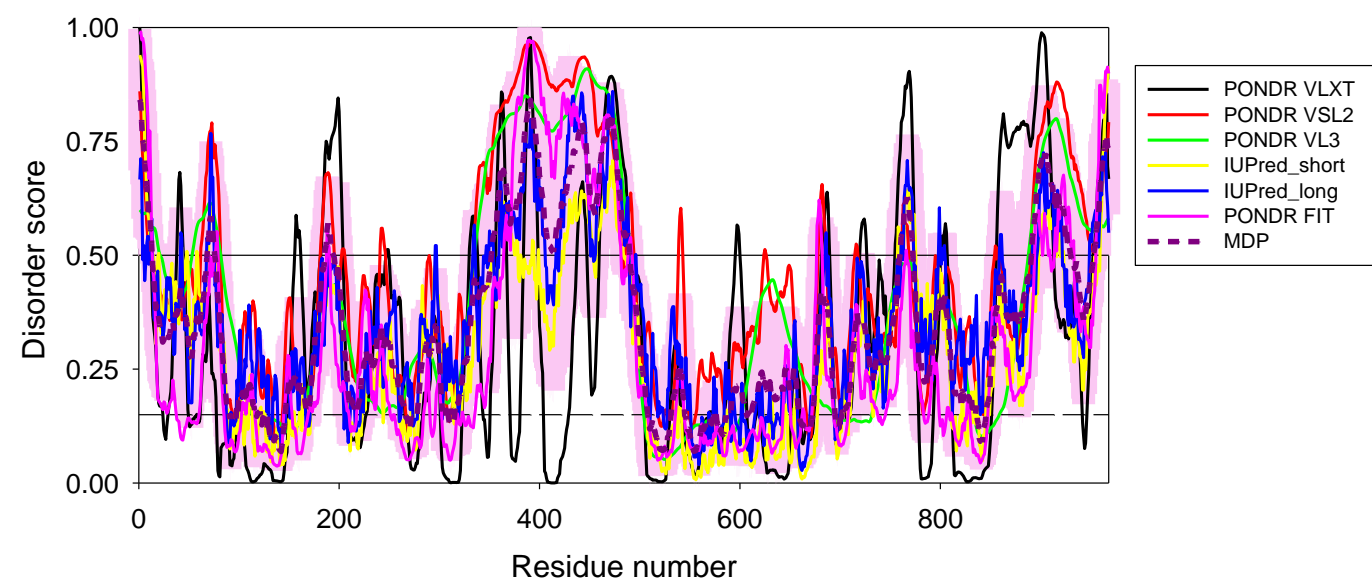




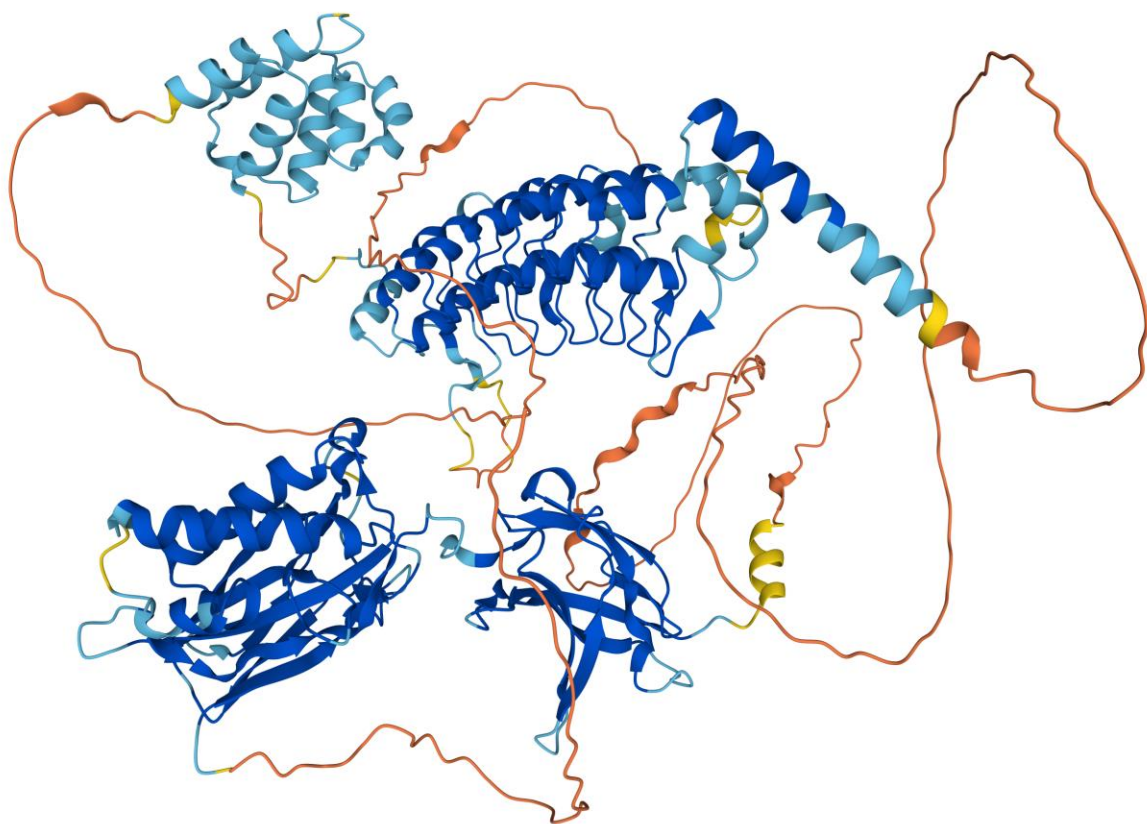

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ICNYVGPAAKIVIVQLVTNGKNIHLHAHSLVGKHCEDGICTVTAGPKDMVVGAFANLILHVTKKKVFETLEARMTEACIRGYNPGLL
VHPDLAYLQAEGGGDRQLGDREKELIRQAALQQTKEMDLSVVRLMFTAFLPDSTGSFTRRLEPVVSDAIYDSKAPNASNLKIVRM
DRTAGCVTGGEIYLLCDKVQKDDIQIRFYEEEEENGGVWEGFGDFSPTDVHRQFAIVFKTPKYKDINITKPASVVFVQLRRKSDLE
TSEPKPFLYYPEIKDKKEEVQRKRQKLMFNFSDSFGGSGAGAGGGGMFGSGGGGGGTGSTGPGYSFPHYGFPTYGGITFHPGTTK
SNAGMKHGTMDTESKKDPEGCDKSDDKNTVNLFGKVIETTEQDQEPSEATVGNGEVTLTYATGTKEESAGVQDNLFLEKAMQLAK
RHANALFDYAVTGDVKMLLAVQRHLTAVQDENGDSVLHLAI IHLHSQLVRDLLEVTSGLISDDI INMRNDLYQTPHLHAVITKQE
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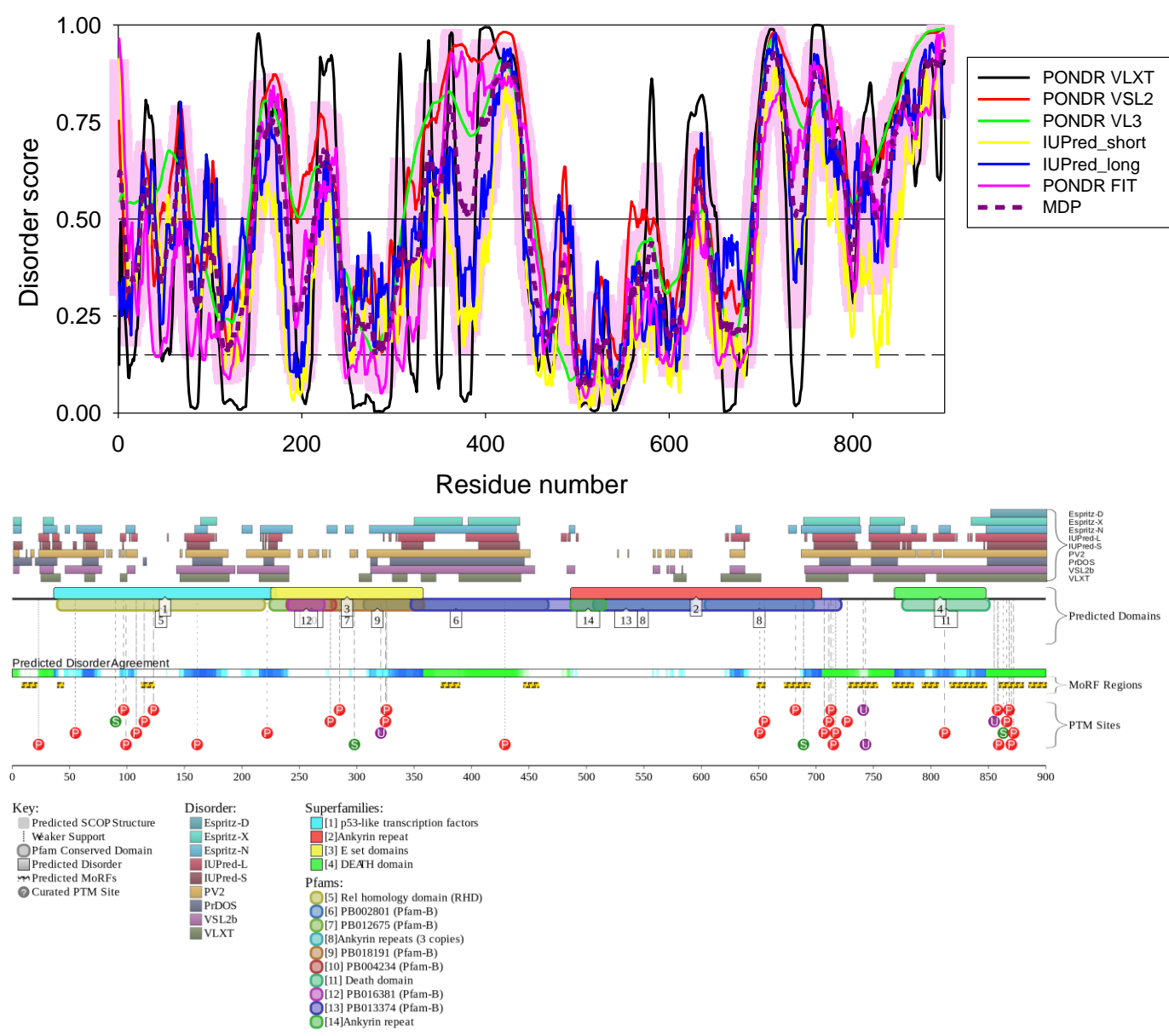


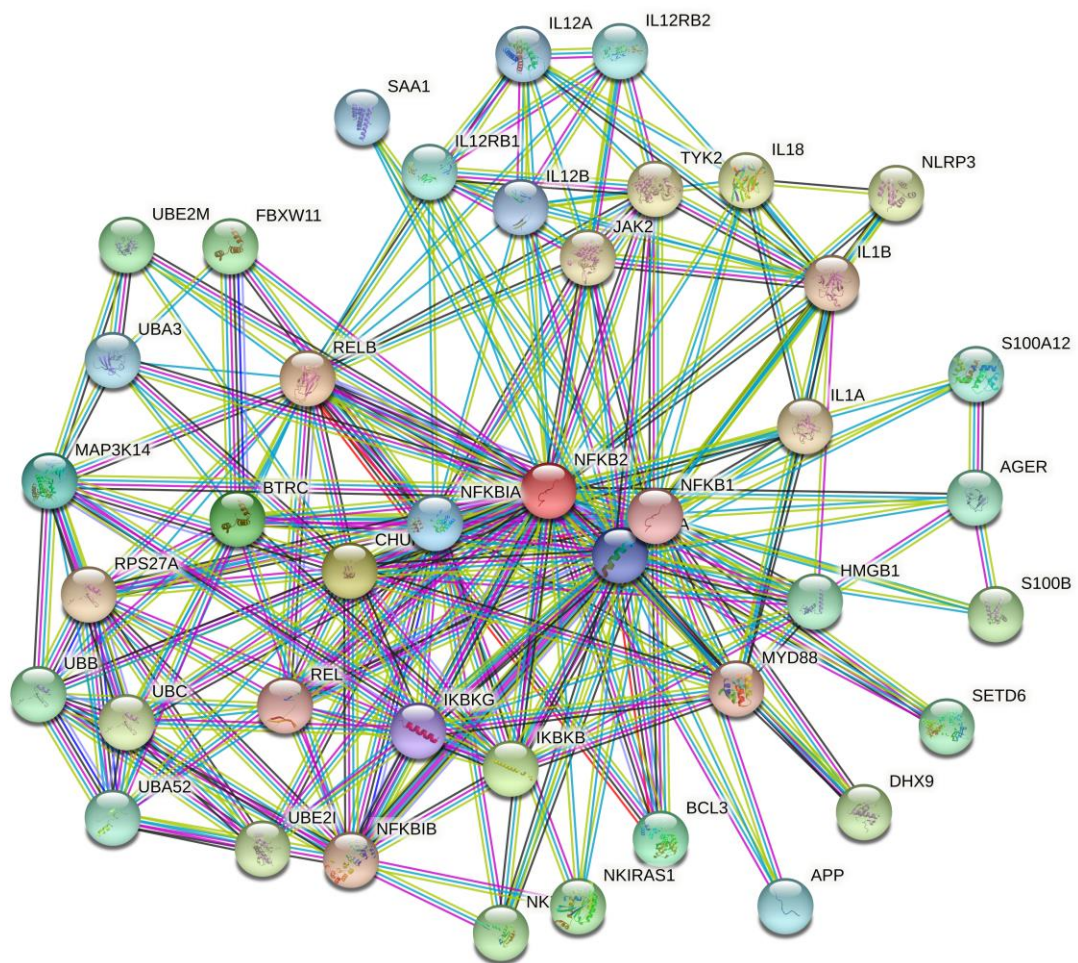


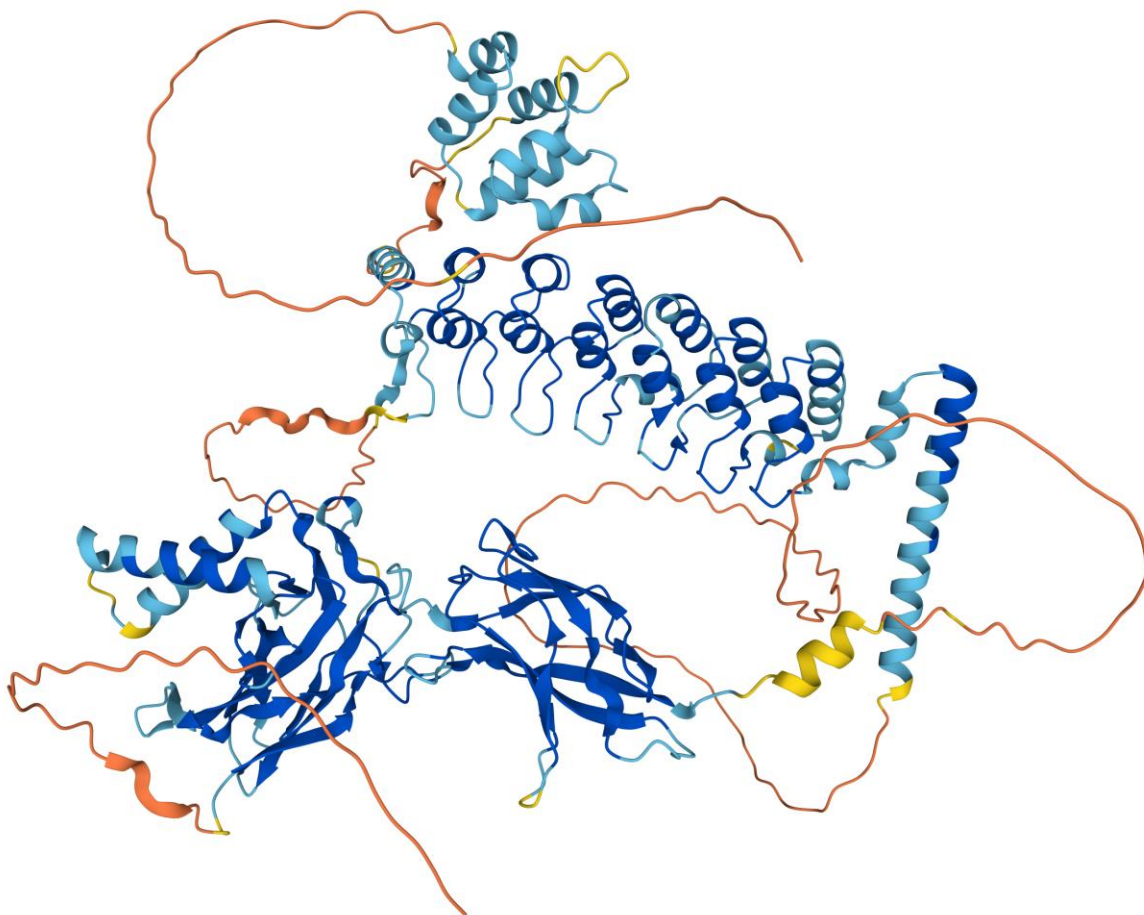

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EGPAKIEVDLVTHSDPPRAHAHSLVGKQCSELGICAVSVGPKDMTAQFNNLGVLVHTKKNMMGMTMIQKLQRQRLSRPQGLTEAE
QRELEQEAKELKKVMDLSIVRLRFS AFLRASDGSFSLPLKPVISQPIHDSKSPGASNLKISRMDKTAGSVRGGDEVYLLCDKVQK
DDIEVRFYEDDENGWQAFGDFSPTDVHKQYAI VFRTPPYHKMKIERPVTVFLQLKRKRGGDVSDSKQFTYYPLVEDKEEVQRKR
KALPTFSQPFGGGSHMGGGSGGAAGGYGGAGGGGSLGFFPSSLAYSPYQSGAGPMGCYPGGGGGAQMAATVPSRDSGEEAAEPSA
PSRTPQCEPQAP EMLQRAREYNARLFLGLAQRSARALLDYGVTDARALLAGQRHLLTAQDENGDTPLHLAI IHGQTSVIEQIVYV
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PGLSLGDTALQNLEQLLDGPEAQGSWAELAERLGLRSLVDTYRQTTSPSGSLLSYELAGGDLAGLLEALSMDMGLEEGVRLLRGP
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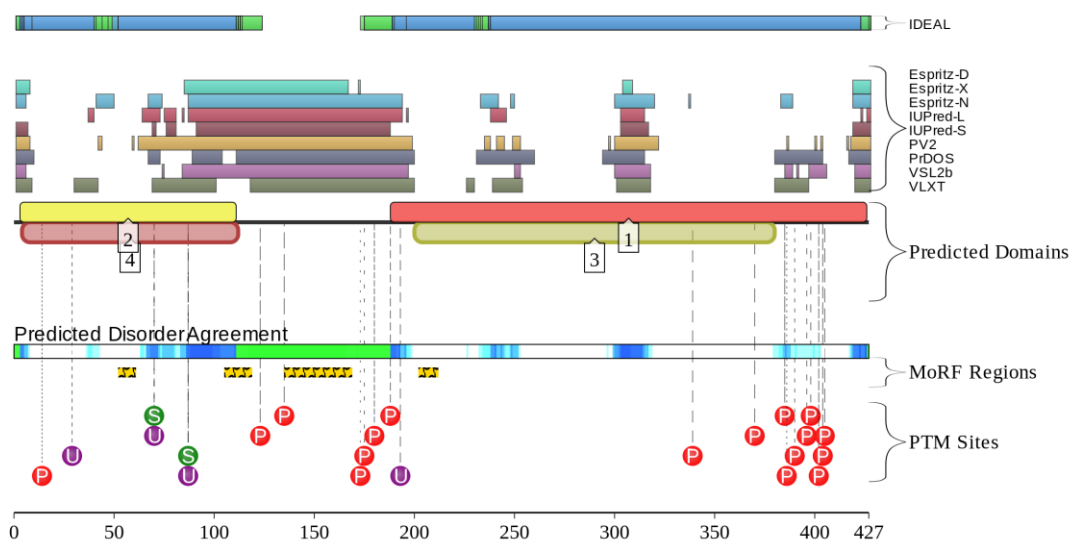
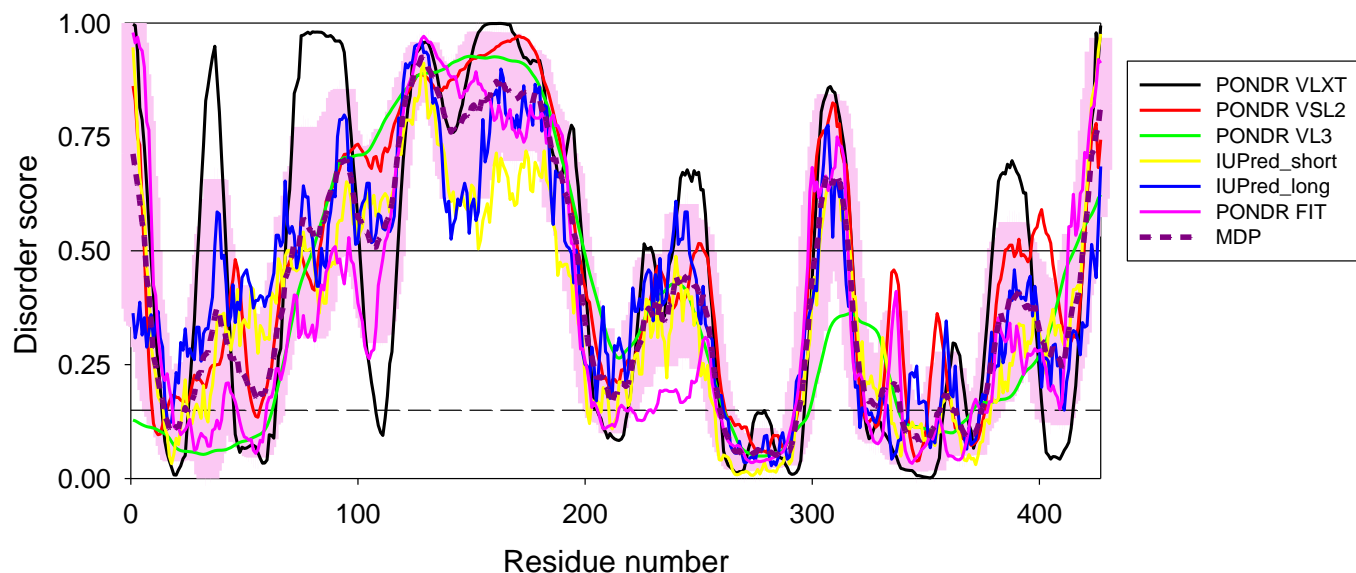
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RKEGLRLAEDRSKDPHPHKIYEFVNSGVGDFSQPDTSPTDNGGGSTSDTQEDILDLLGNMVLAPLPDPGPPSLAVAPEPCQP
LRSPSLDNPTFPFNLGPSENPLKRLLLVPGEWEFEVTAIFYRGRQVFQQTISCPEGLRLVGSEVGDRTLPGWFPVTLDPGMSLTDR
GVMSYVRHVLSCGGGLALWRAGQWLWAQRLGHCHTYWAVSEELLPSNGHGPDPGEVPKDKEGGVFDLGPFIVDLITFTEGSGRSP
RYALWFCVGESWPQDQDPWTKRLVMKVVPVPTCLRALVEMARVGGASSLENTVDLHISNSHPLSLTSDQYKAYLQDLVEGMDFQGGP
ES
```



Key:

- Predicted SCOP Structure
- Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:

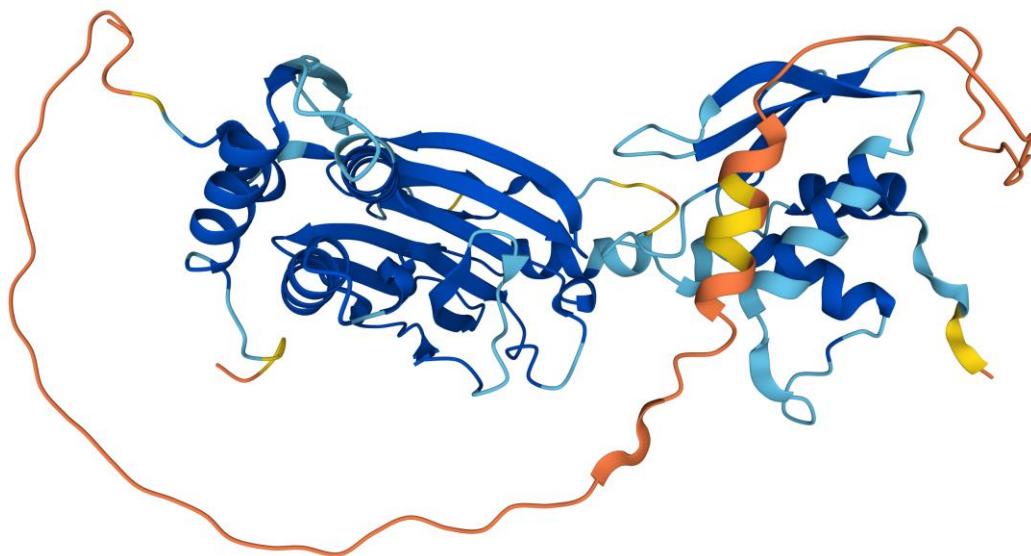
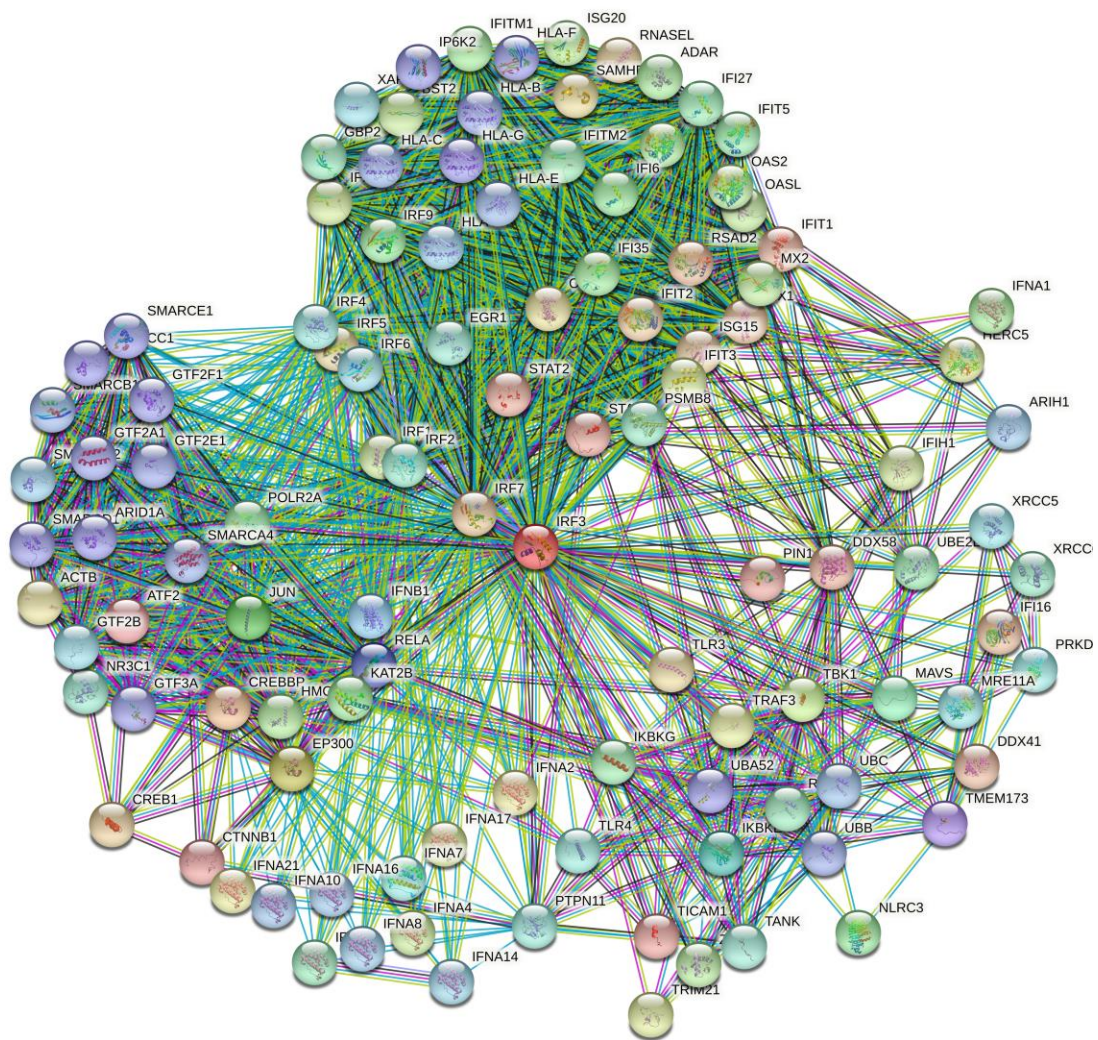
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

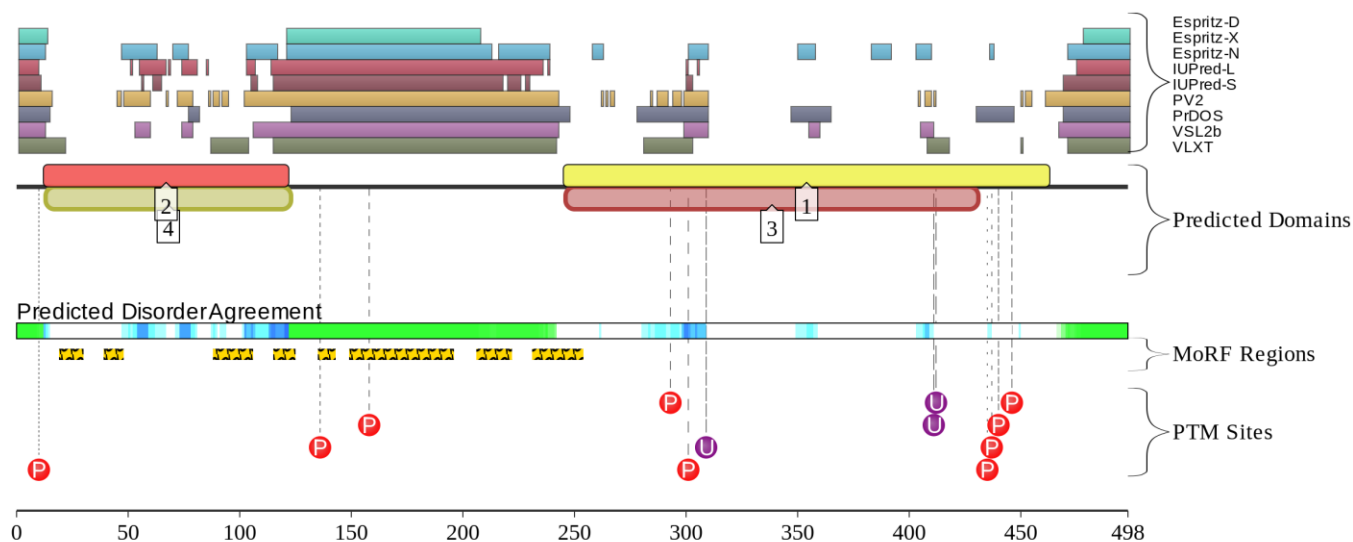
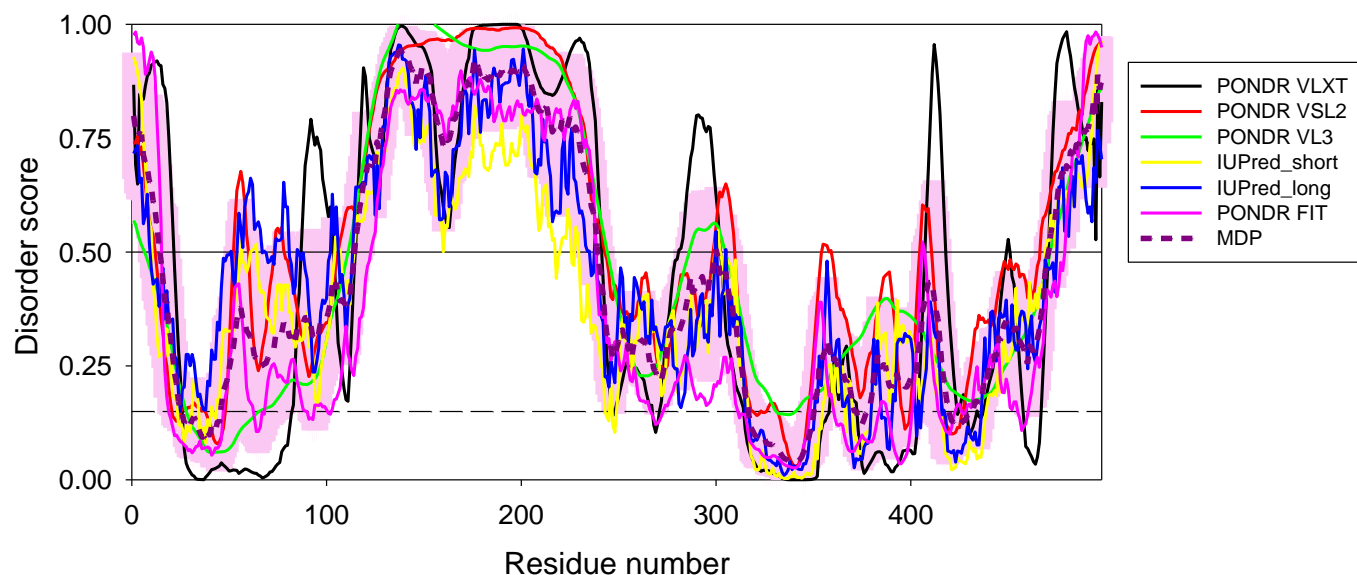
- [1] SMAD/FHA domain
- [2] "Winged helix" DNA-binding domain

Pfams:

- [3] Interferon-regulatory factor 3
- [4] Interferon regulatory factor transcription factor



```
>sp|Q13568|IRF5_HUMAN Interferon regulatory factor 5 OS=Homo sapiens OX=9606 GN=IRF5
PE=1 SV=2
MNQSIPVAPTPPRRVRLKPWLVAQVNSCQYPGLQWVNGEKKLFCIPWRHATRHGPSQDGDNTIFKAWAKETGKYTEGVDEADPAK
WKANLRCALNKS RDRFLIYDGRDMPPQPYKIYEVCNSGPAPTDSQPPEDYSFGAGEEEEEEEELQRM LPSLSLTEDVKWPPTLQ
PPTLRPPTLQPPTLQPPVVLGPPADPSP LAPP PGNPAGFRELLSEVLEPGPLPASLP PAGEQLLPDLLISPHMLPLTDLEIKFQ
YRGRPPRALTISNPHGCR LFYSQLEATQE QVELFGPI SLEQVRFPSPEDIPSDKQRFYTNQLLDVLDRLILQLQGQDLYAIRLC
QCKVFWSGPCASAH DSCPNPIQREVKT KLFSL EHF LNELILFQKGQTNTPPPFEIFFCFGE EWPDRKPREKKLITVQVVPVAARL
LLEMFSGELSW SADSIRLQISNPDLKDRMVEQFKELHHIWQSQQRLQPV AQAPP GAGLGVGQGPWPMHPAGMQ
```



Key:

- Predicted SCOP Structure
- ⋯ Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- ⋯ Predicted MoRFs
- ⊙ Curated PTM Site

Disorder:

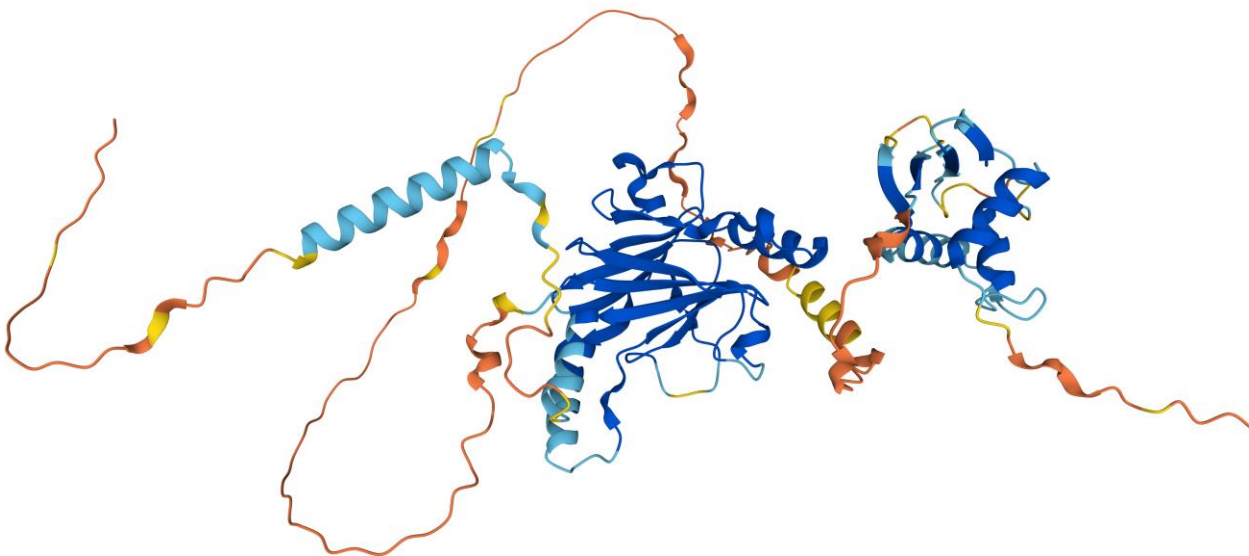
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

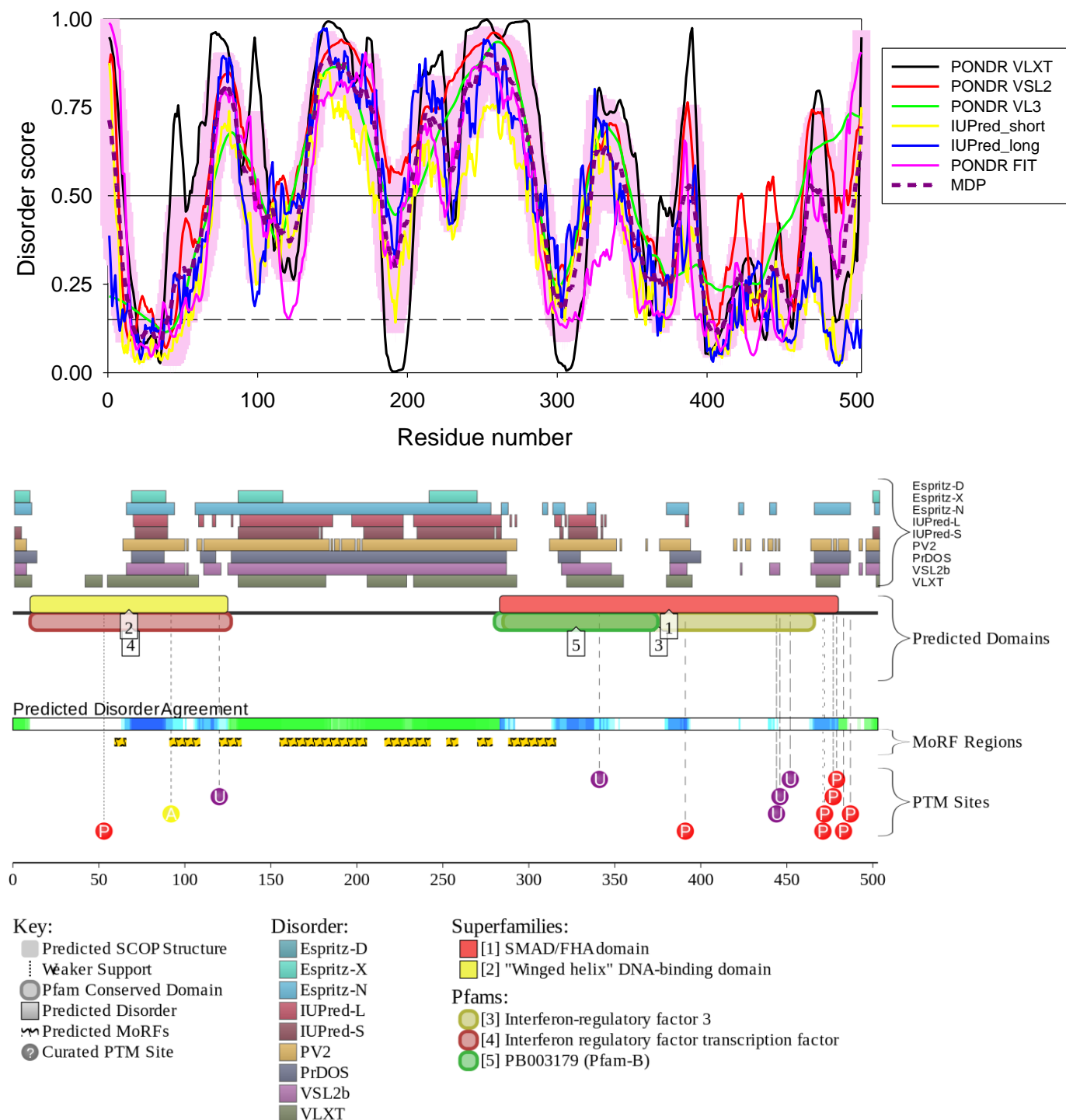
- [1] SMAD/FHA domain
- [2] "Winged helix" DNA-binding domain

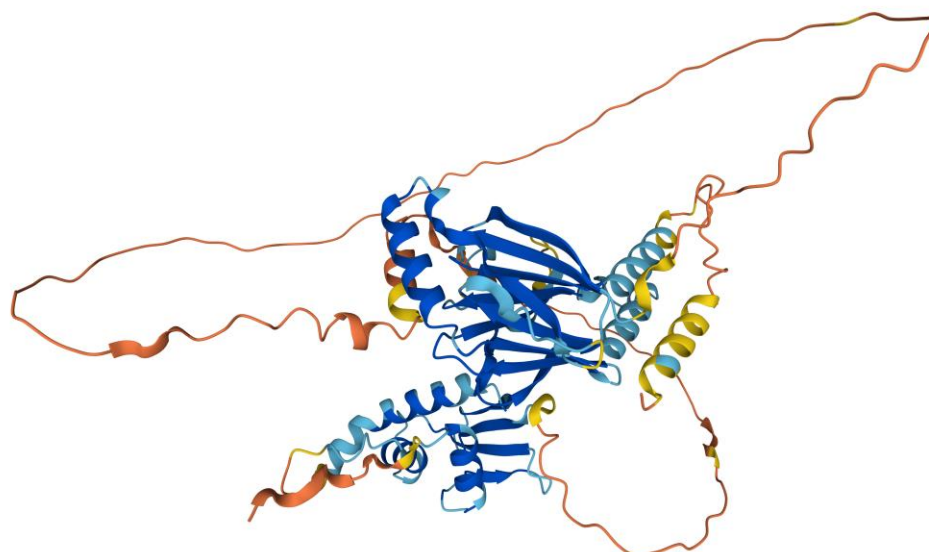
Pfams:

- [3] Interferon-regulatory factor 3
- [4] Interferon regulatory factor transcription factor

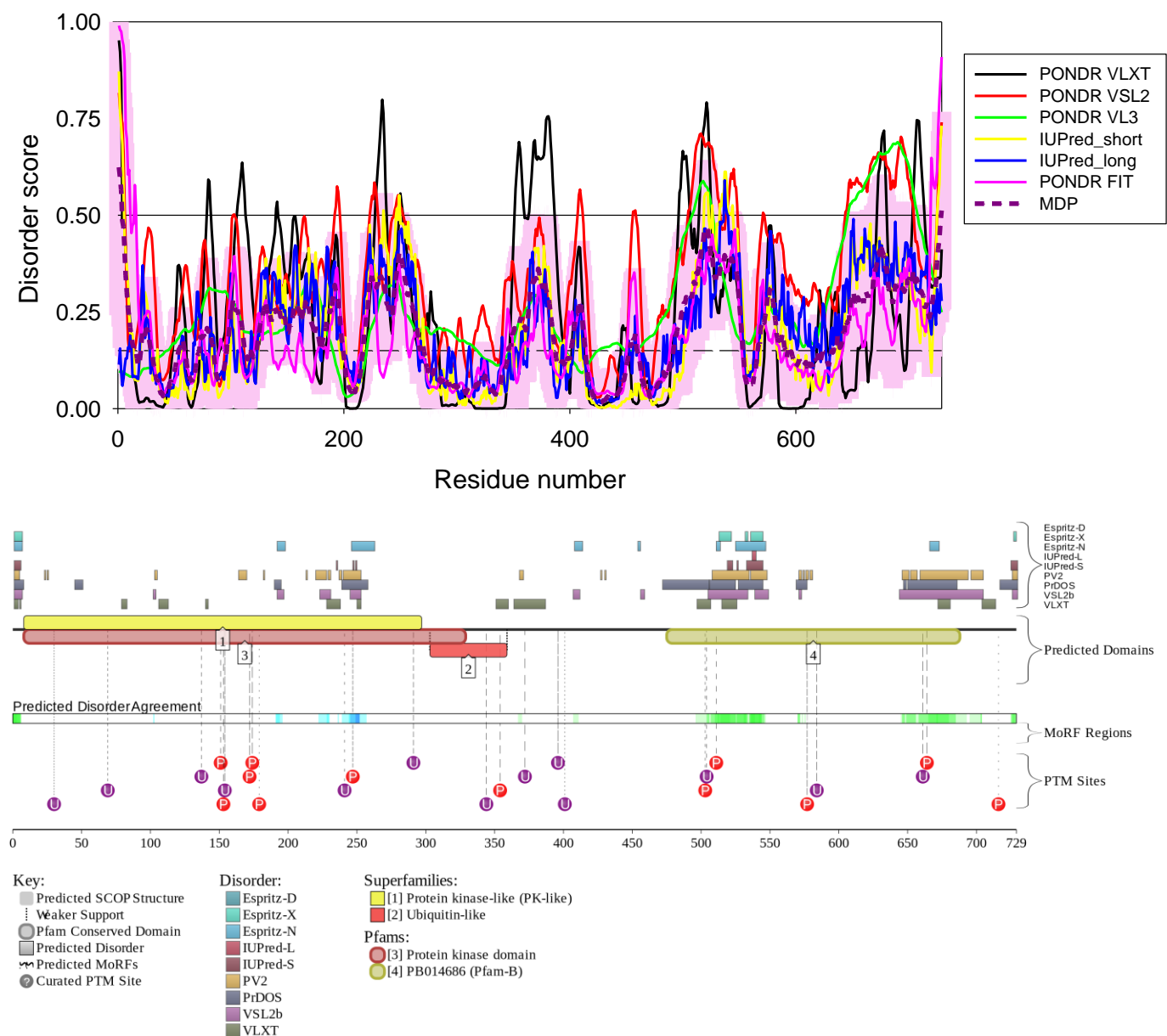


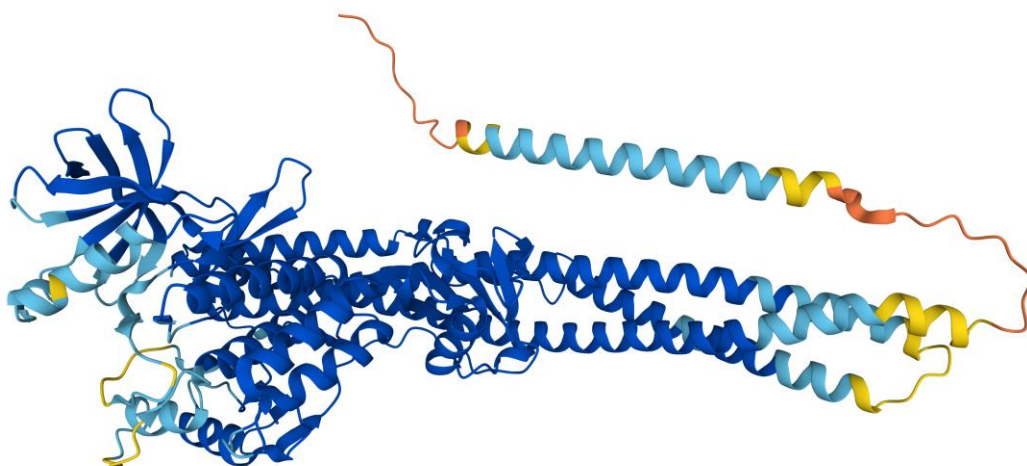
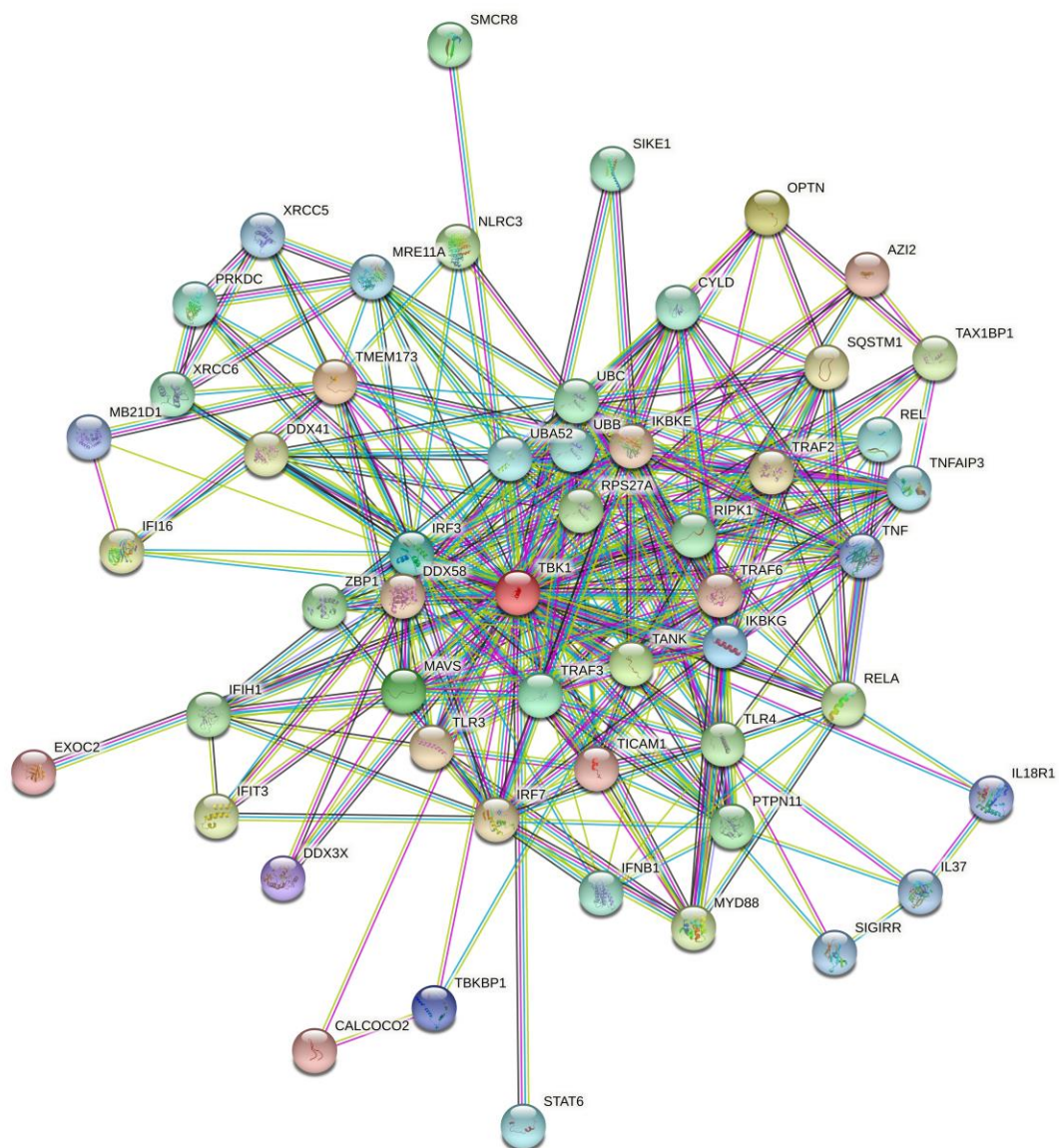
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PE=1 SV=2
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AERAGWKTNFRCALRSTRRFVMLRDN SGDPADPHKVYALSRELWCWREGPGTDQTEAEAPAAVPPPQGGPPGPF LAHTHAGLQAPG
PLPAPAGDKGDL LLQAVQQSCLADHLLTASWGADFPVPTKAPGEGQEGLPLTGACAGGPGLPAGELYGWAVETTPSPGPQPAALTT
GEAAAPESPHQAEPYLSPPSACTAVQEPSPGALDVTIMYKGRITVLQKVVGHPSCFTLYGPPDPAVRATDPQQVAFPSPAELPDQ
KQLRYTEELLRHVAPGLHLELRGPQLWARRMGKCKVYWEVGGPPGSASPSTPACLLPRNCDTPIFD FRVFFQELVEFRARQRRGS
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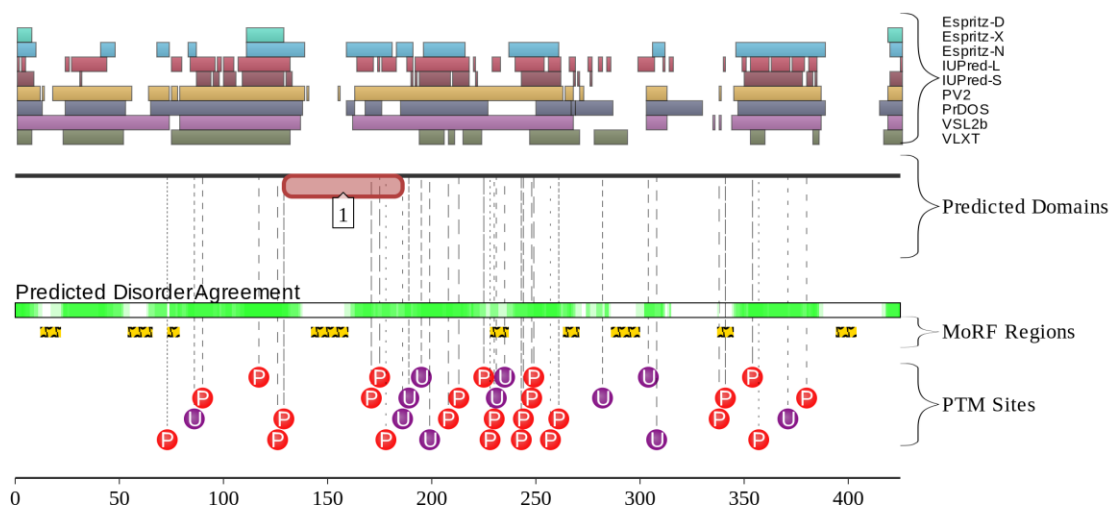
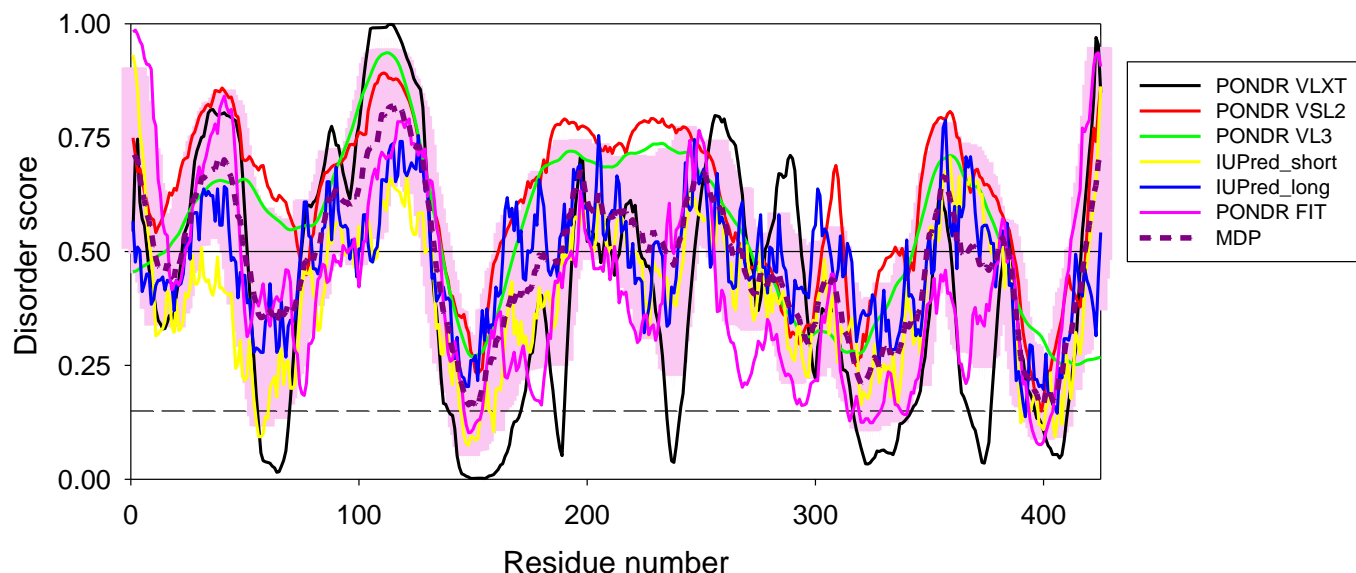



```
>sp|Q9UHD2|TBK1_HUMAN Serine/threonine-protein kinase TBK1 OS=Homo sapiens OX=9606
GN=TBK1 PE=1 SV=1
MQSTSNHLWLLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLKKLNHKNIVKLFAIEEETTTRHKVLI
MEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVVGGMNLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQF
VSLYGTEEYLHPDMYERAVLRKDHQKKYGATVDLWSIGVTIFYHAATGSLPFRPFEGPRRNKEVMIKIITGKPSGAISGVQKAENG
PIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEKCWGFDQFFAETSDILHRMVIHVFSLQQMTAHKIYIHSYNTATIFHELVI
KQTKIISNQELIYEGRRLVLEPGRLAQHFPKTTEENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLGDASMAKAITGVVCYA
CRIAFTLLLYQELMRKGIRWLIELIKDDYNETVHKKTEVVITLDFCIRNIEKTVKVYEKLMKINLEAAELGEISDIHTKLLRLSS
SQGTIETSLQDIDSRLSPGGSGLADAWAHQEGTHPKDRNVEKLQVLLNCMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYHAT
KAMTHFTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQKMFTASSGIKHTMTPIYPSS
NTLVEMTLGMKKLKEEMEGVVKELAENNHILERFGSLTMDGGLRNVDCL
```





```
>sp|Q92844|TANK_HUMAN TRAF family member-associated NF-kappa-B activator OS=Homo
sapiens OX=9606 GN=TANK PE=1 SV=2
MDKNIGEQLNKAYEAFRQACMDRDSAVKELQQKTENYEQRIREQQEQLSLQQTIIIDKLKSQLLLNVNSTQDNNYGCVPILLEDSETR
KNNLTLDQPQDKVISGIAREKLPKVRREQEVSSPRKETSARSLSGSPLLHERGNIEKTFWDLKEEFHKICMLAKAQKDHLKLNIPD
TATETQCSVPIQCTDKTDKQEALFKPQAKDDINRGAPSITSVTPRGLCRDEEDTSFESLSKFNVKFPPMDNDSTFLHSTPERPGI
LSPATSEAVCQEKFNMEFRDNPNGNFVKTEETLFEIQGIDPIASAIQNLKTTDKTKPSNLVNTCIRTTLDRACLPPGDHNLALYVN
SFPLLDPSDAPFPSPDPSGKAIRGPPQPIWKPFNPQDSDSVVLSGTDSELHIPRVCEFCQAVFPPSITSRGDFLRHLNHSFNGET
```



Key:

- Predicted SCOP Structure
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- Curated PTM Site

Disorder:

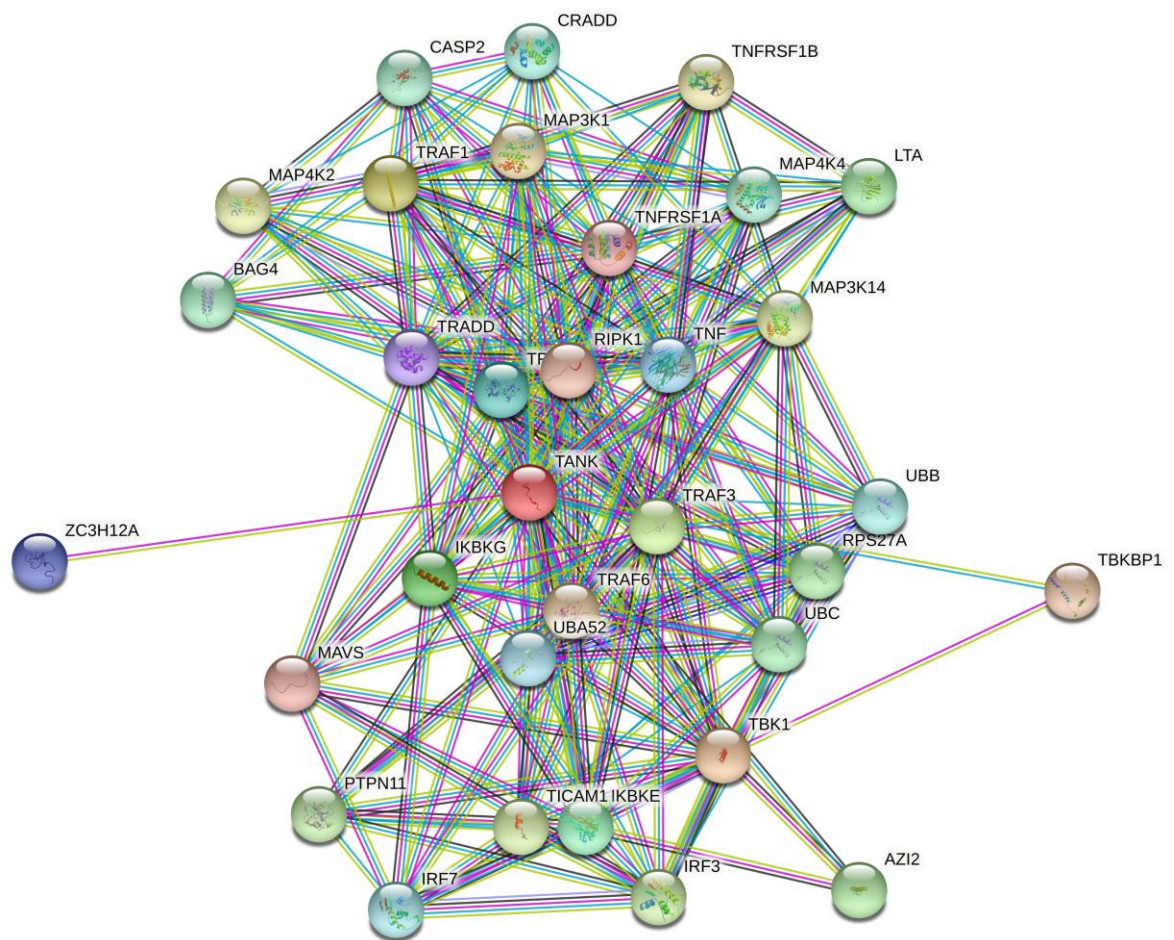
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

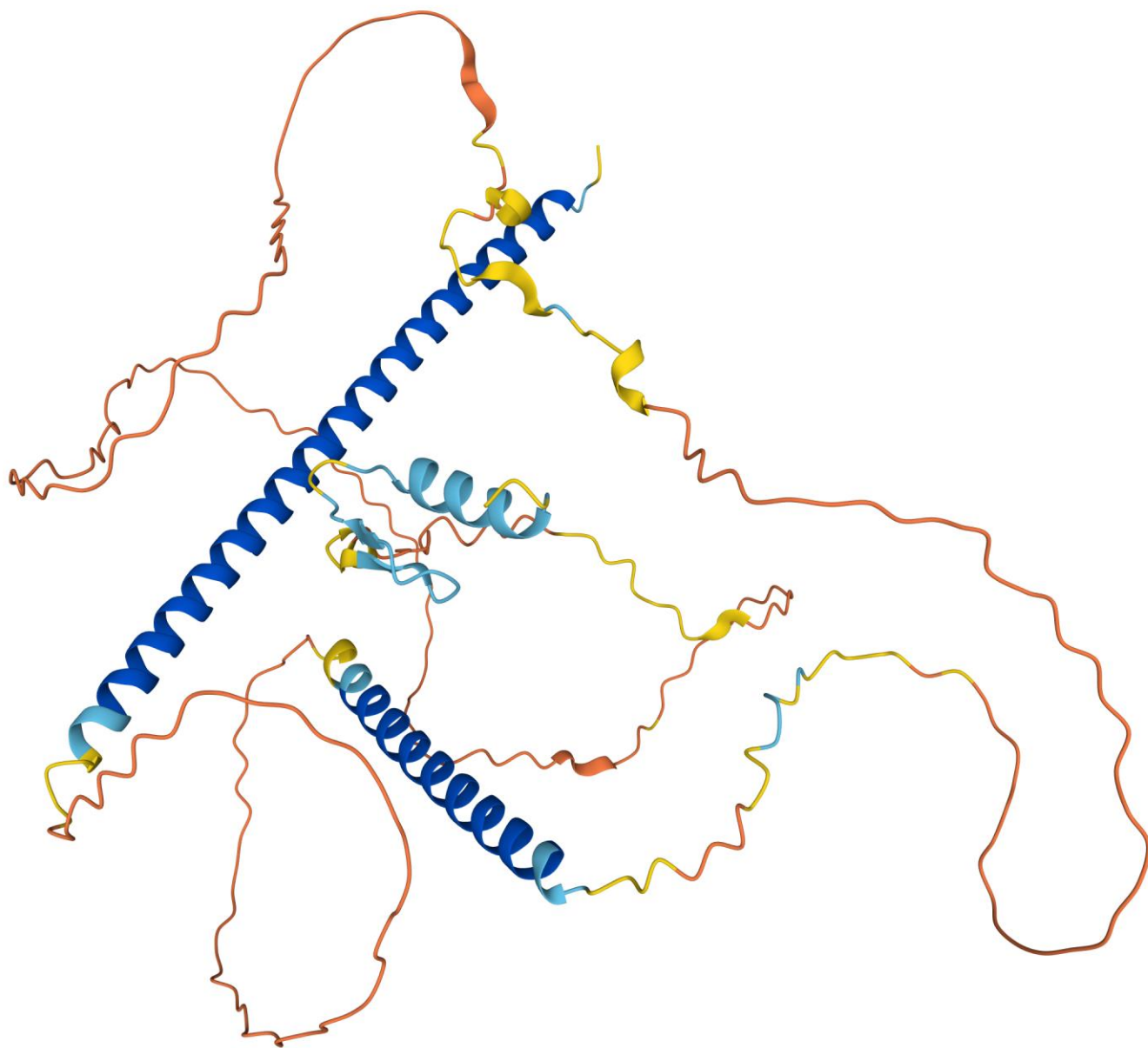
Superfamilies:

N/A No Hits

Pfams:

[1] PF12845.2 (Family)

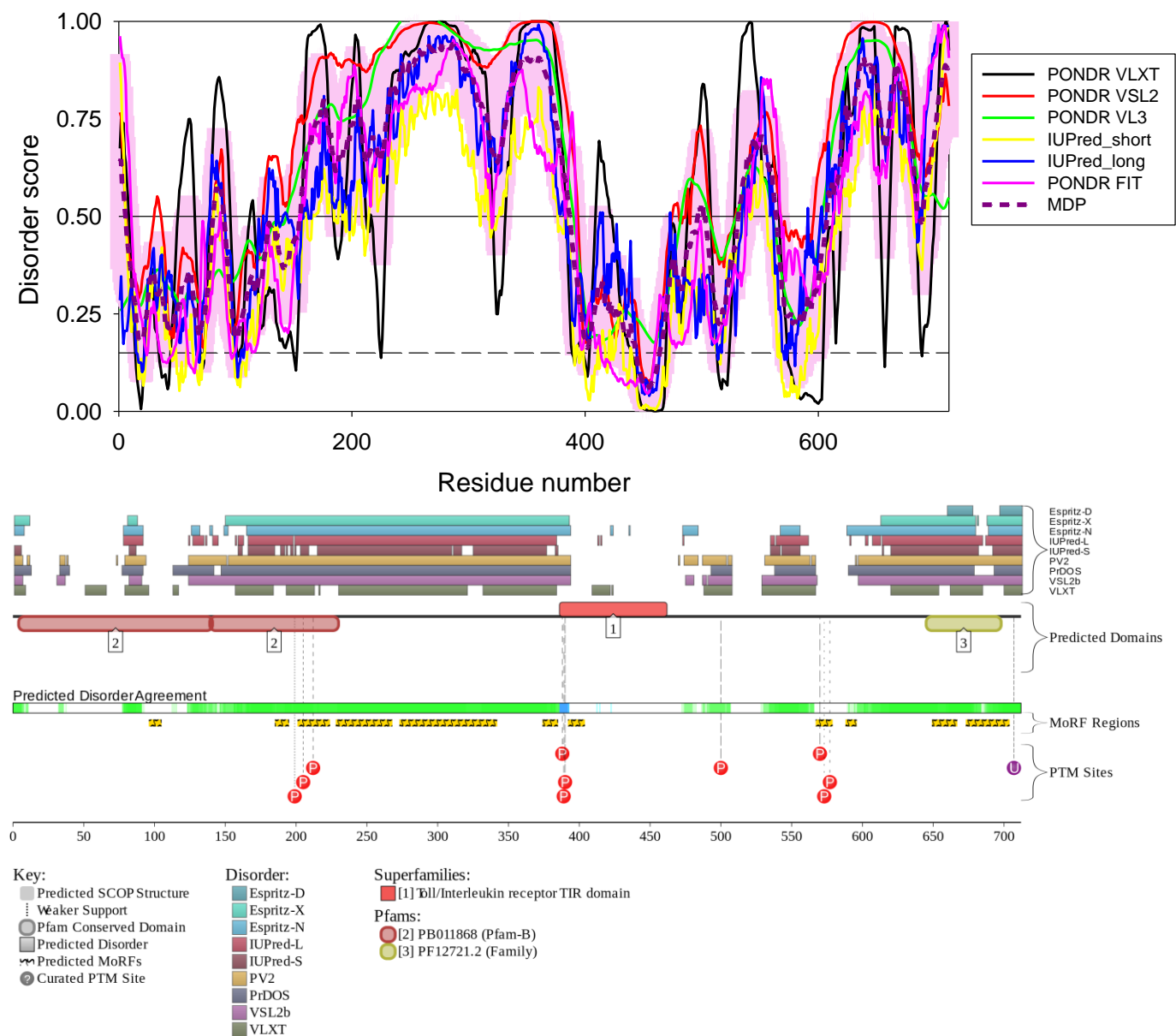


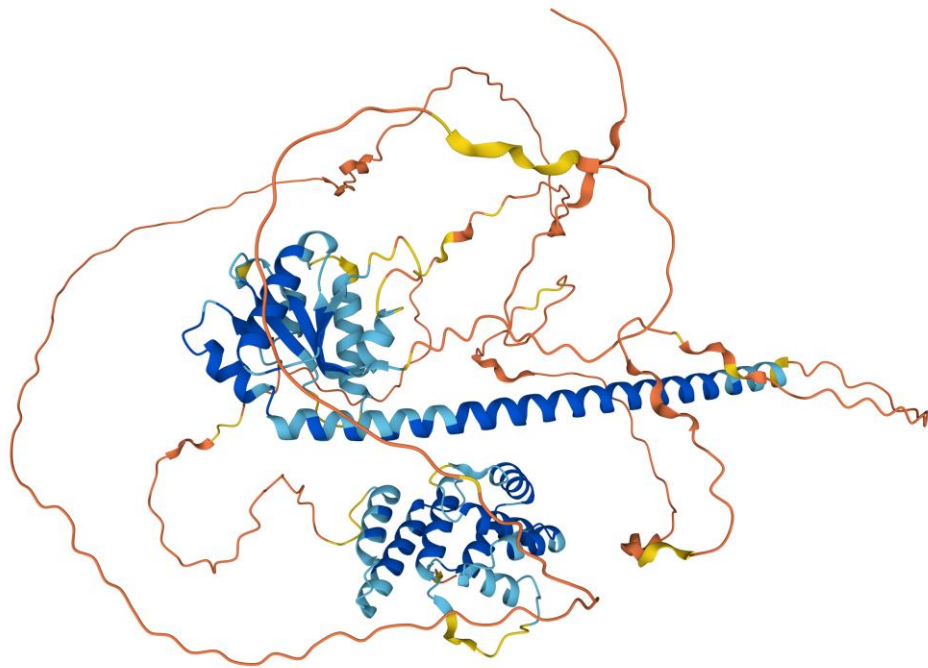
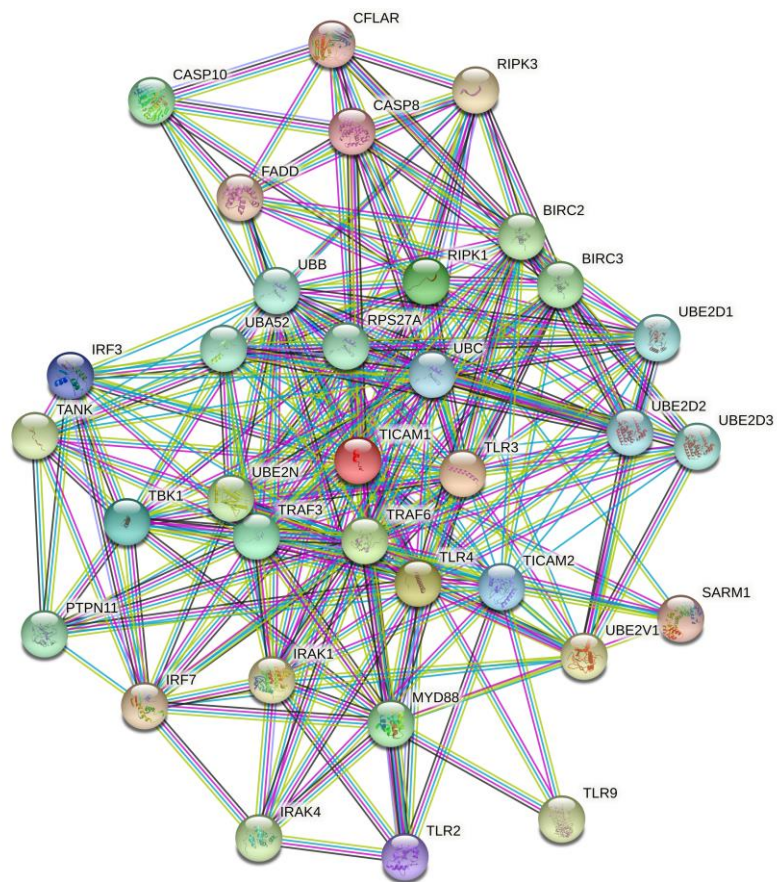


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>sp|Q8IUC6|TCAM1_HUMAN TIR domain-containing adapter molecule 1 OS=Homo sapiens
OX=9606 GN=TICAM1_TRIF PE=1 SV=1
MACTGPSLPSAFDILGAAGQDKLLYLKHKLKTPRPGCQGQDLLHAMVLLKLGQETEARISLEALKADAVARLVARQWAGVDSTED
PEEPPDVSWAVARLYHLLAEKLCPASLRDVAYQEAVRTLSSRDDHRLGELQDEARNRCGWDIAGDPGSIRTLQSNLGLCLPPSSA
LPSGTRSLPRPIDGVSDWSQGC SLRSTGSPASLASNLEISQSPTMPFSLSLHRS PHGPSKLCDDPQASLVPEFVPGGCQEPPEMSW
PPSGEIASPPELPSSPPPPGLPEVAPDATSTGLPDTAAPETSTNYPVECTEGSAGPQSLPLPILEPVKNPCSVKDQTPQLSVED
TTSPTNTKPCPPTPTTPETSPPPPPPPSSTPCSAHLTPSSLFPSSLESSEQKFYNFVILHARADEHIALRVREKLEALGVDPGA
TFCEDFQVPGRGELSCLQDAIDHSAFIILLTNSNFDCLSLHQVNQAMMSNLTRQGS PDCVIPFLPLESSPAQLSSDTASLLSGL
VRLDEHSQIFARKVANTFKPHRLQARKAMWRKEQDTRALREQS QHLDGERMQAAALNAAYSAYLQSYLSYQAQMEQLQVAFGSHM
SFGTGAPYGARMPFGGQVPLGAPPPFPTWPGCPQPPPLHAWQAGTPPPPSPQPAAFPQSLPFPQSPAFPTASPAPPQSPGLQPLI
IHHAQMVLQGLNNHNMWNQRGSQAPEDKTQEAE

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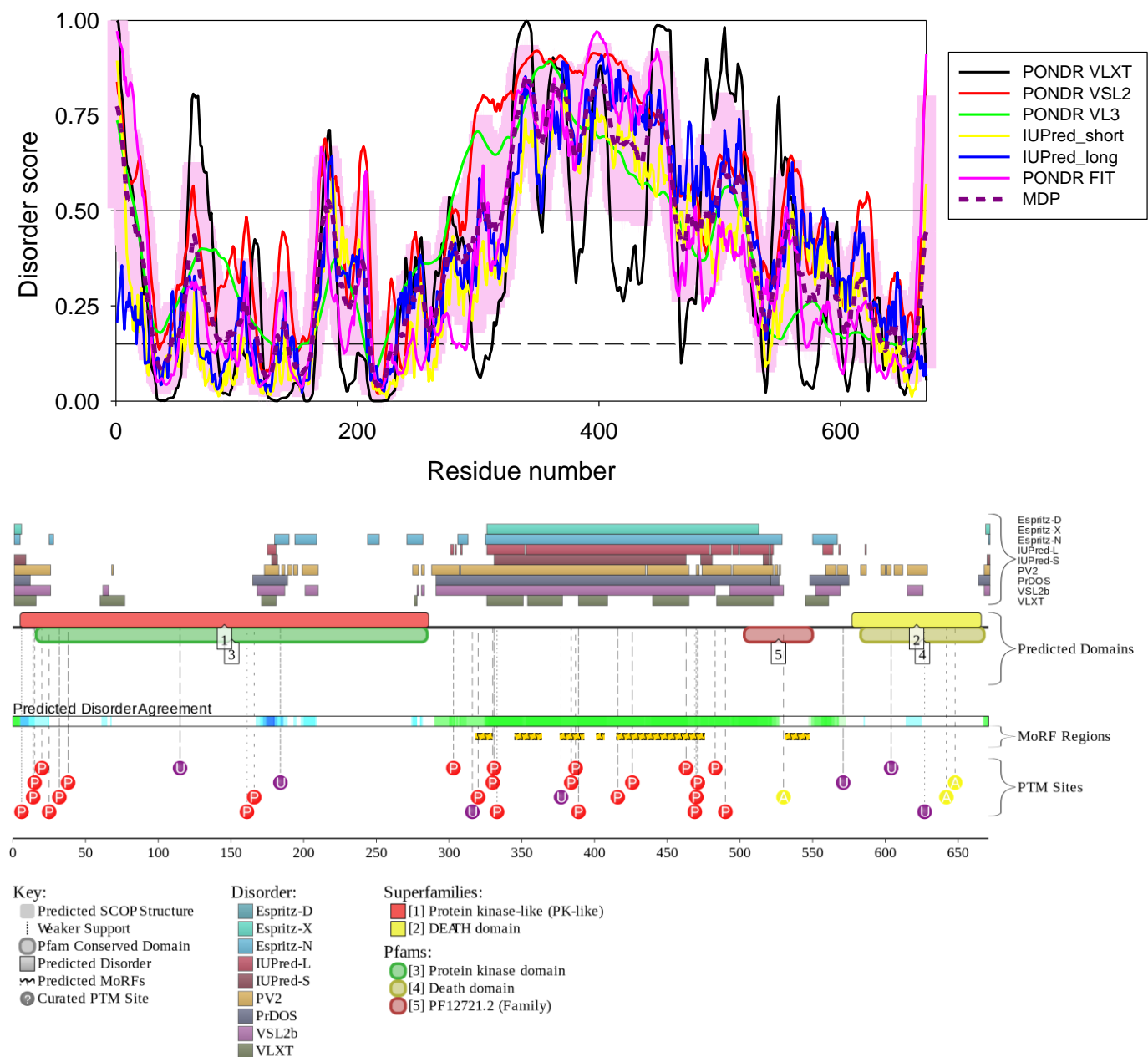


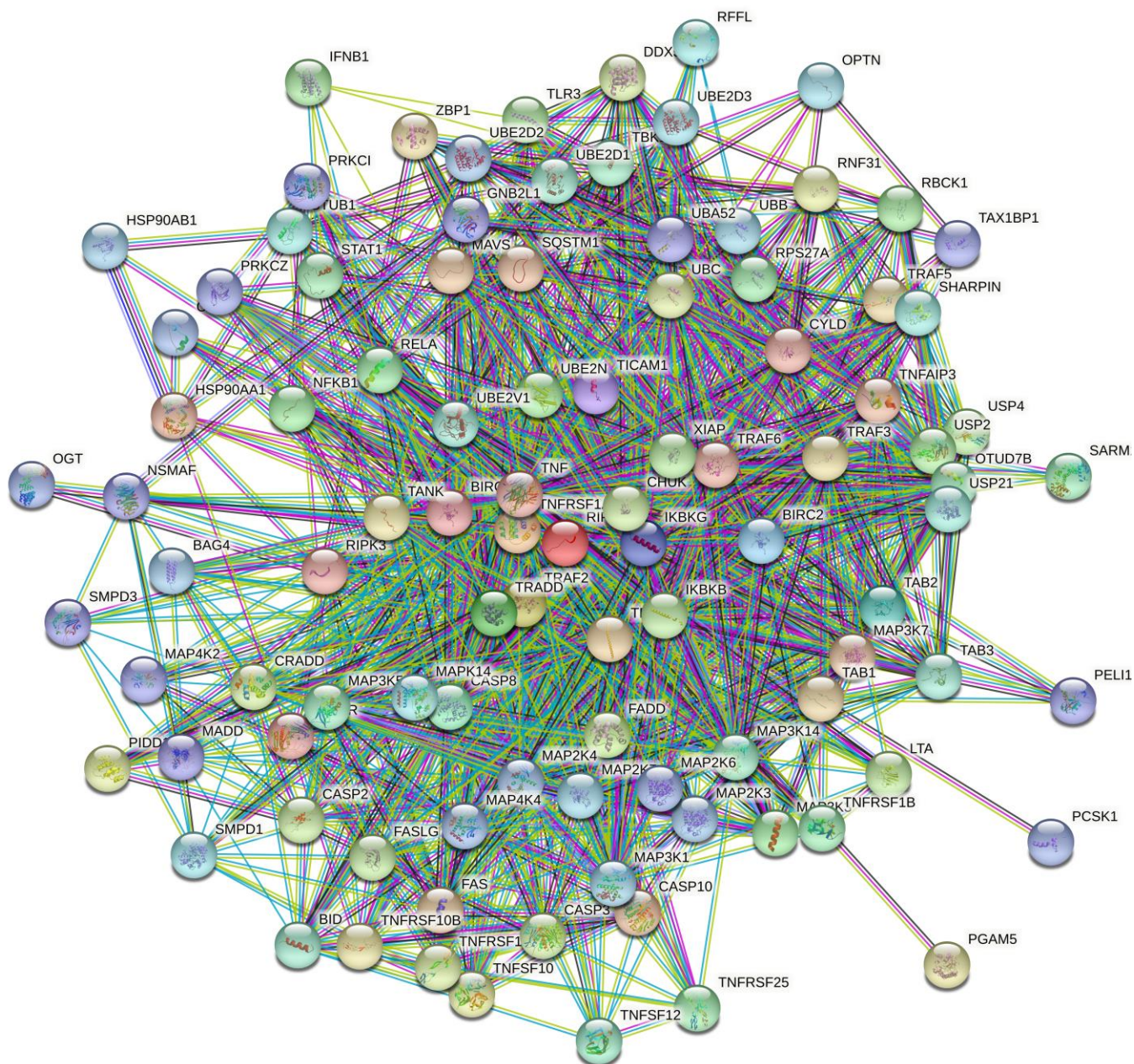


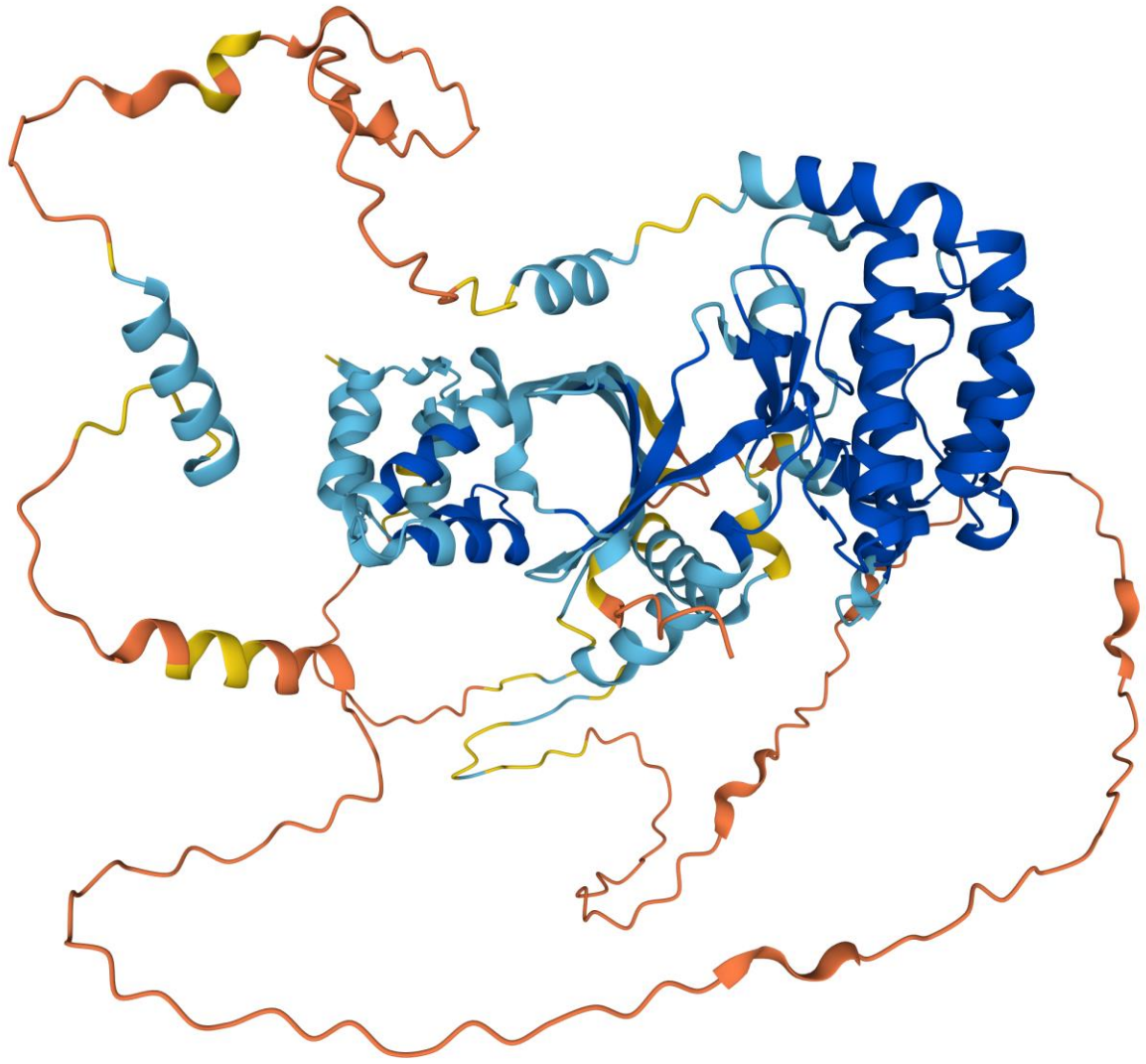
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>sp|Q13546|RIPK1_HUMAN Receptor-interacting serine/threonine-protein kinase 1 OS=Homo
sapiens OX=9606 GN=RIPK1 PE=1 SV=3
MQPDMSLNVIKMKSSDFLESAELDSGGFGKVS LCFHRTQGLMIMKTVYKGPNCIEHNEALLEEAKMMNRLRHSRVVKLLGVIIIE
GKYS LVM EYMEKGNLMHVLKAEMSTPLSVKGRIILEIIEGMCYLHGKGV I HKDLKPENILVDNDFHIKIADLGLASF KMW SKLNN
EEHNELREVDGTAKKNGGTLYYMAPEHLNDVNAKPTKSDVYSFAVVLWAI FANKEPYENAICEQQ LIMCIKSGNRPD VDDITEY
CPREIISLMKLCWEANPEARPTFFPGIEEKFRFPYLSQLEESVEEDVKS LKKEYSNENAVVKRMQSLQLDCVAVPSSRSNSATEQP
GSLHSSQGLGMGPVEESWFAPSLEHPQEENEPSLQSKLQDEANYHLYGSRMDRQTKQQPRQNVAYNREEERRRRVSHDPFAQQRP
YENFQNTGKGTAYSSAASHGNAVHQPSGLTSQPQVLYQNNGLYSSHGFGTRPLDPGTAGPRVWYRPIPSHMPSLHNI PVPETNY
LGNTPTMPFSSLPPTDESIKYTIYNSTGIQIGAYNYMEIGGTSSSLDSTNTNFKEEPAAKYQAIFDNTTSLTDKHLDP IRENLG
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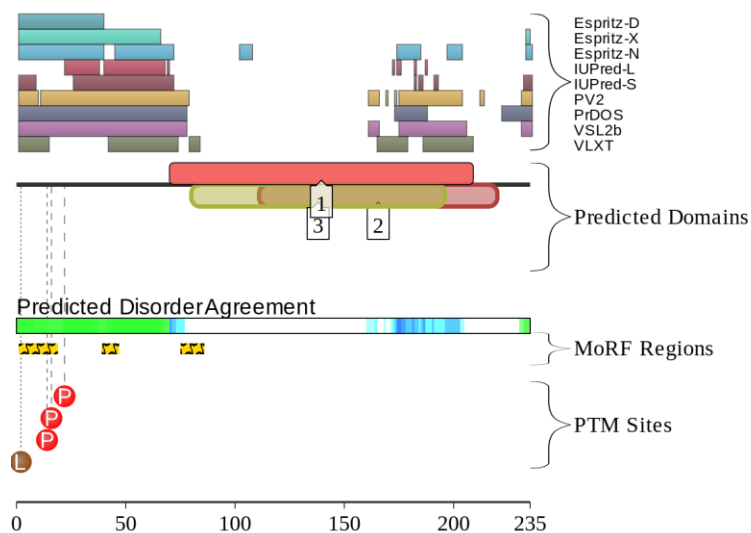
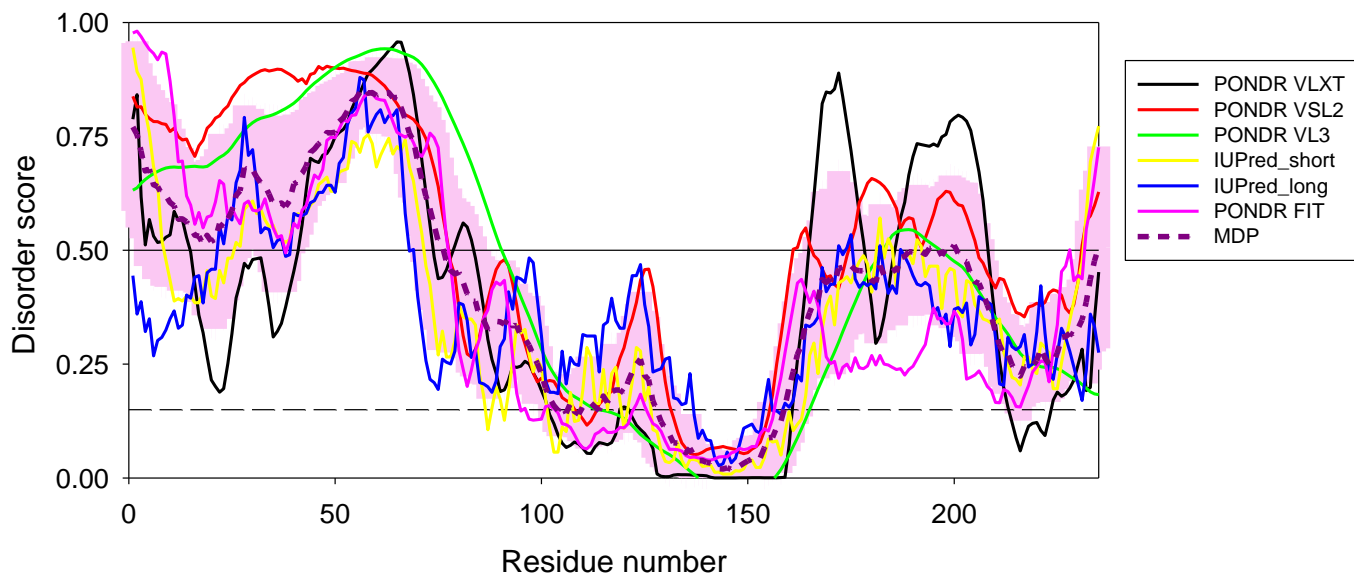




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>sp|Q86XR7|TCAM2_HUMAN TIR domain-containing adapter molecule 2 OS=Homo sapiens
OX=9606 GN=TICAM2 PE=1 SV=1
MGIGKSKINSCPLSLSWGKRHSVDTSPTYHESDSKKSSEDLNVAEHSNTTEGPTGKQEGAQSVEEMFEEEEAEVFLKFVILH
AEDDTDEALRVQNLQDDFGIKPGIIFAEMPCGRQHLQNLDDAVNGSAWTILLTLENFLRDTWCNFFQFYTSLMNSVNRQHKYNSV
IPMRPLNNPLPRERTPFALQNTINALEEESRGFTQVERIFQESVYKTQQTIIWKETRNMVQRQFIA

```



Key:

- Predicted SCOP Structure
- Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:

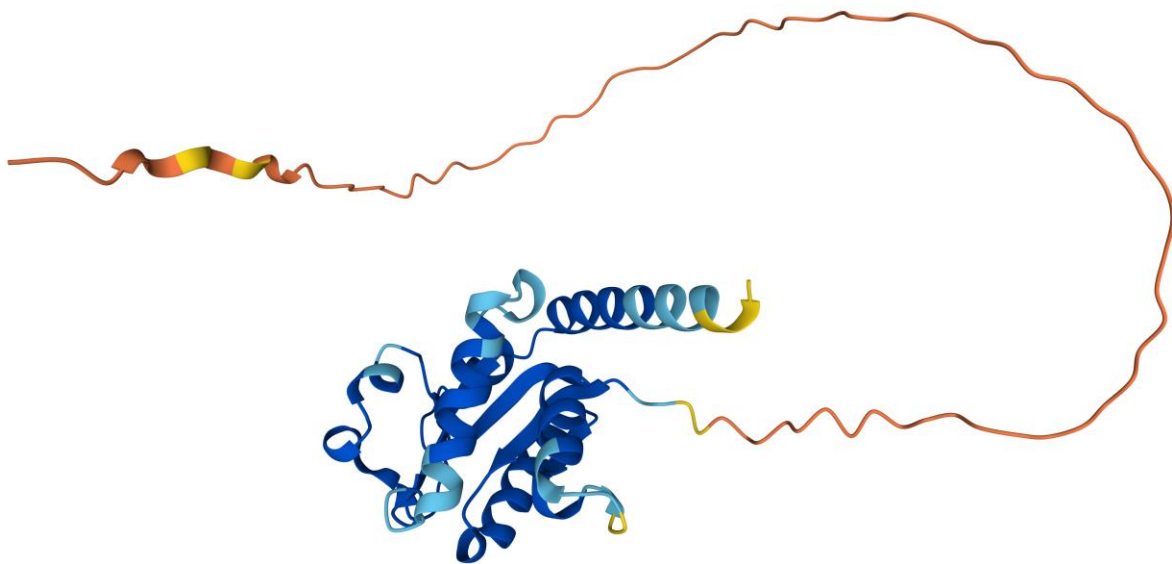
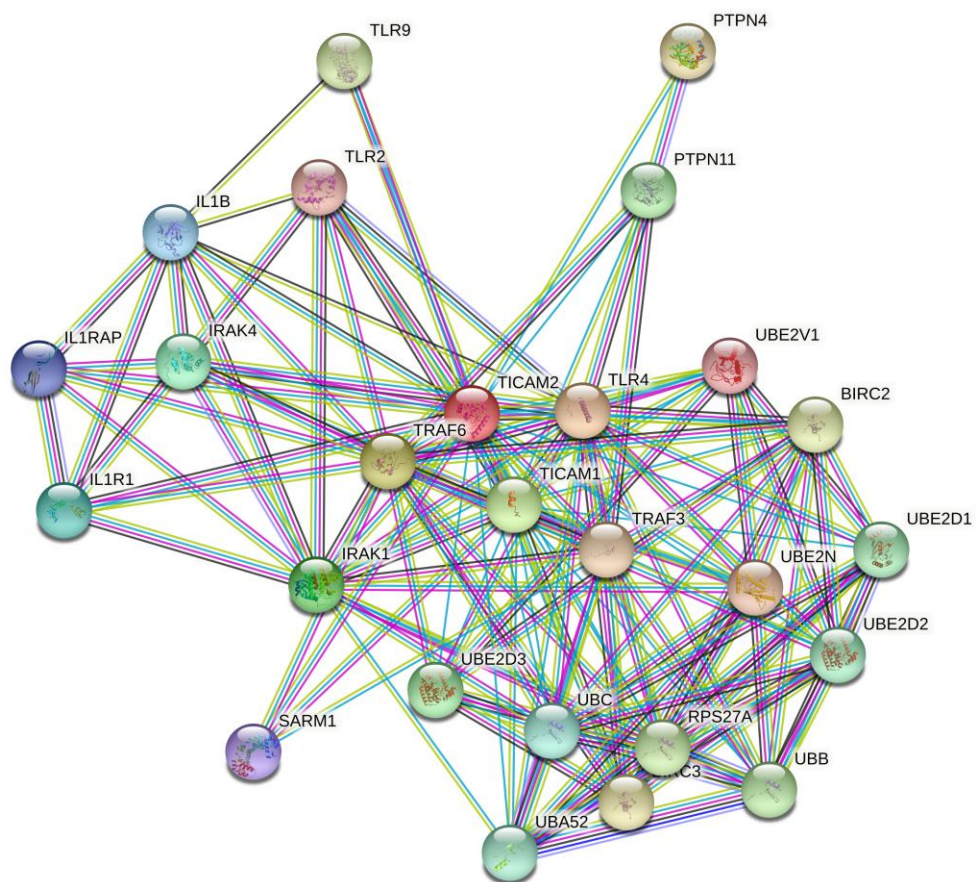
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

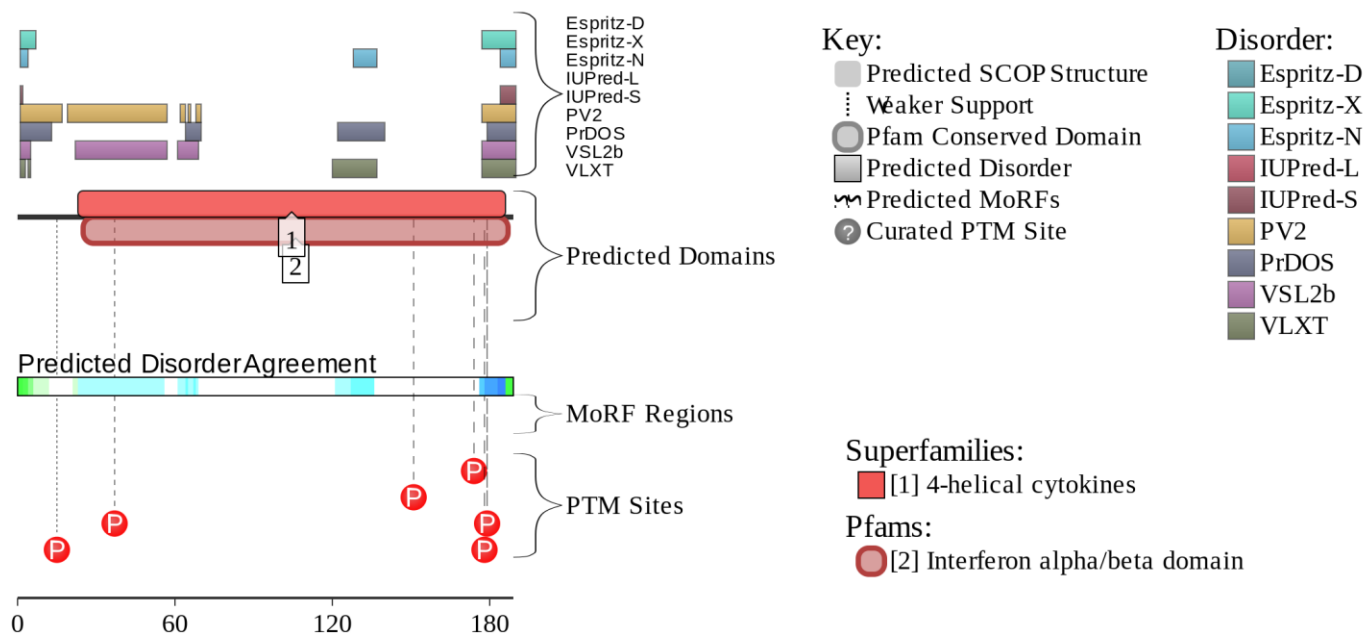
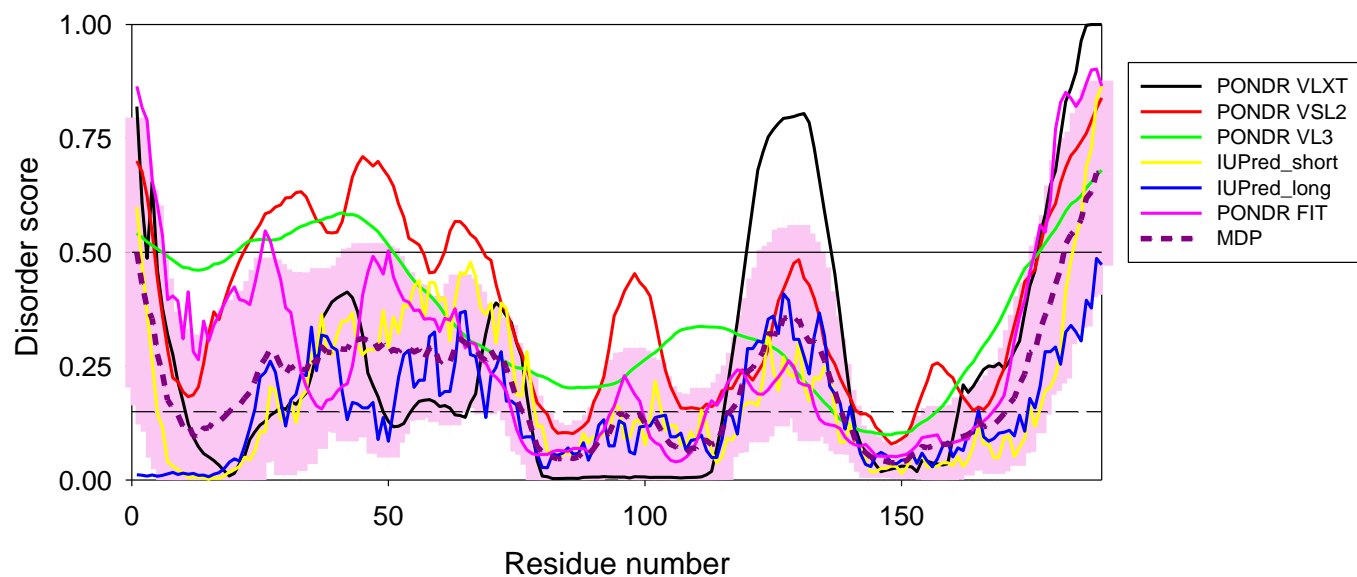
- [1] Toll/Interleukin receptor TIR domain

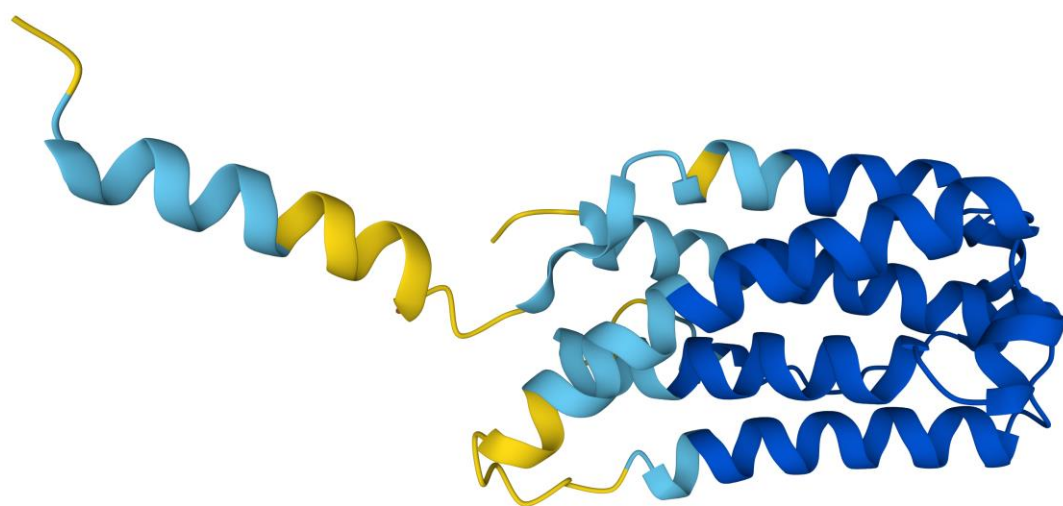
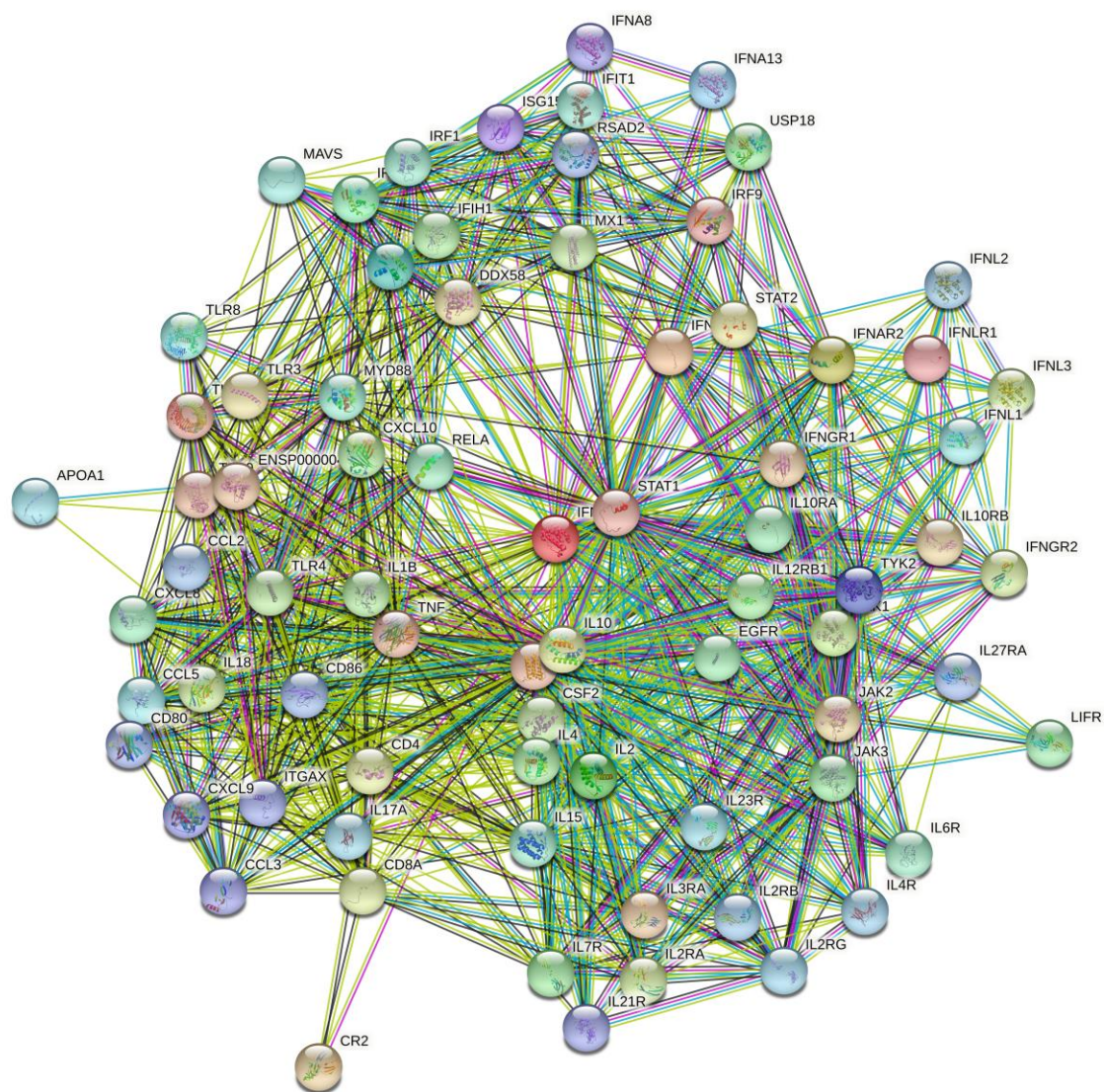
Pfams:

- [2] PB011868 (Pfam-B)
- [3] TIR domain

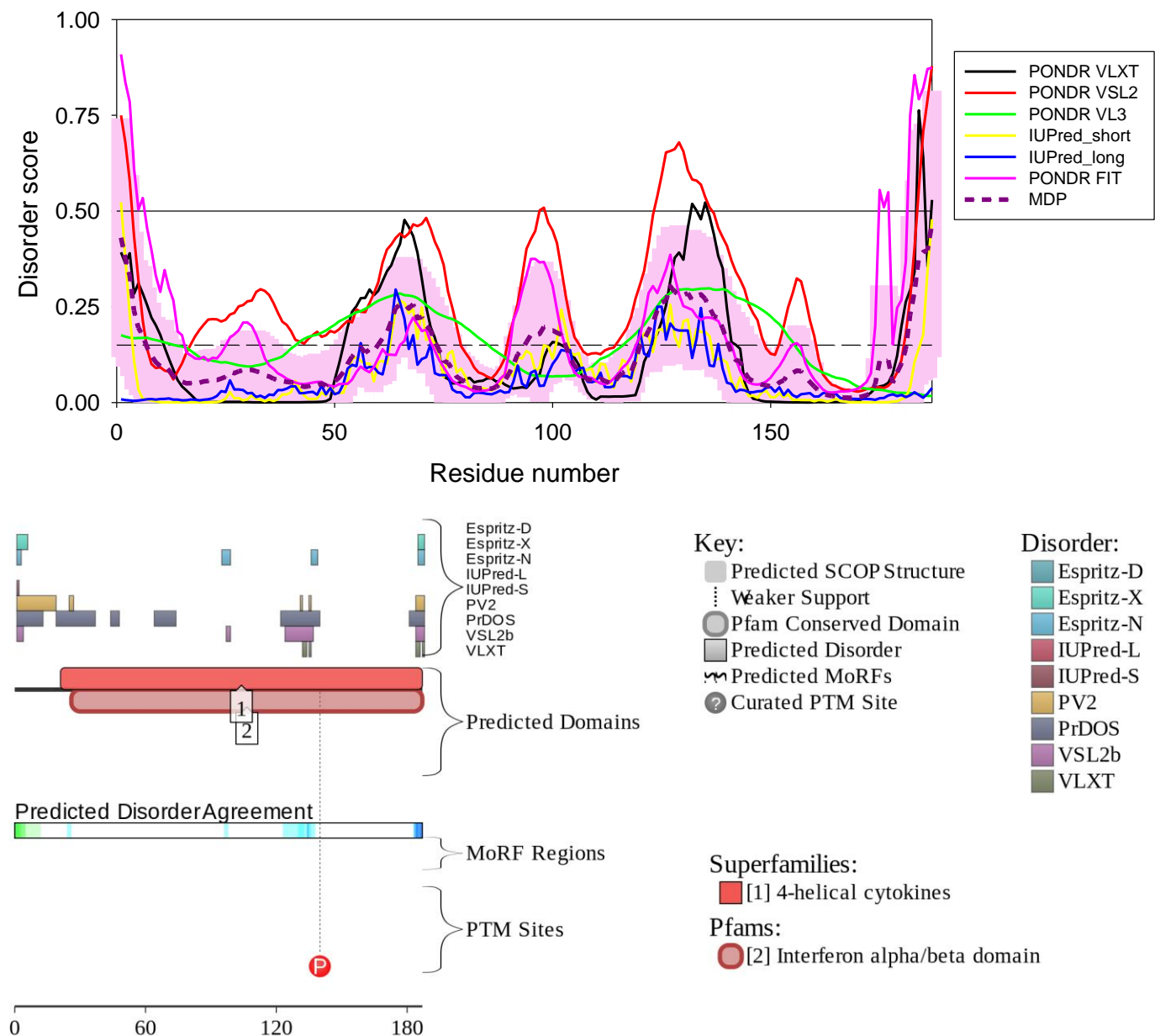


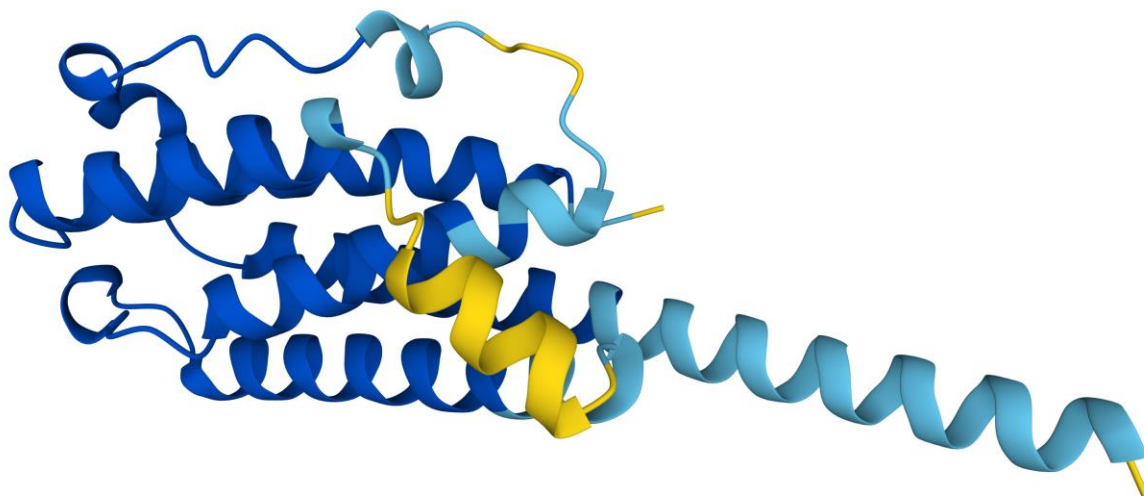
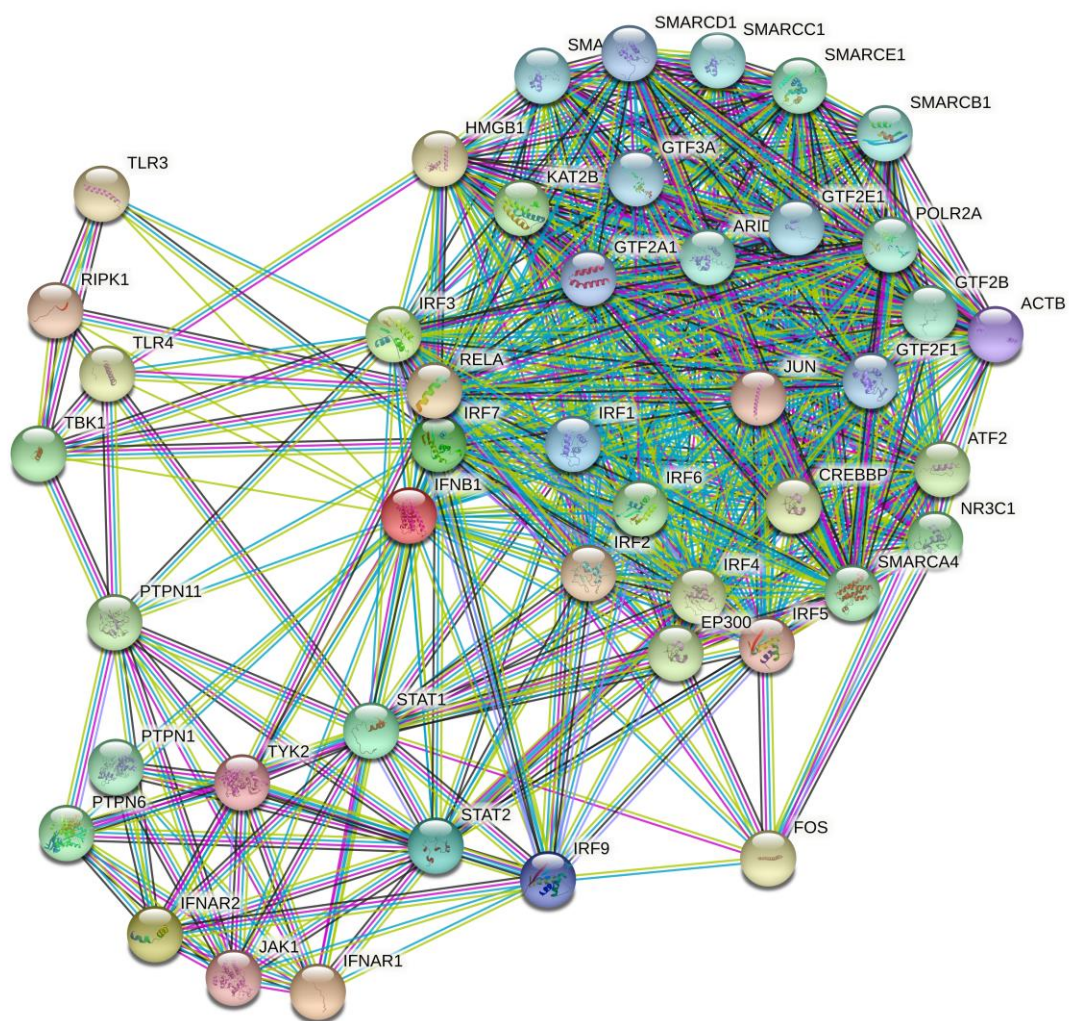

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>sp|P01562|IFNA1_HUMAN Interferon alpha-1/13 OS=Homo sapiens OX=9606 GN=IFNA1 PE=1
SV=1
MASPFALLMVLVVLSCKSSCSLGCGLPETHSLDNRRTLMLLAQMSRISPSSCLMDRHDGFGFPQEEFDGNQFQKAPASVLHELIO
QIFNLFTTKDSSAAWDEDLLDKFCTELYQQLNLEACVMQEERVGETPLMNADSIKAVKKYFRRITLYLTEKKYSPCAWEVVRAE
IMRSLSLSTNLQERLRKE
```



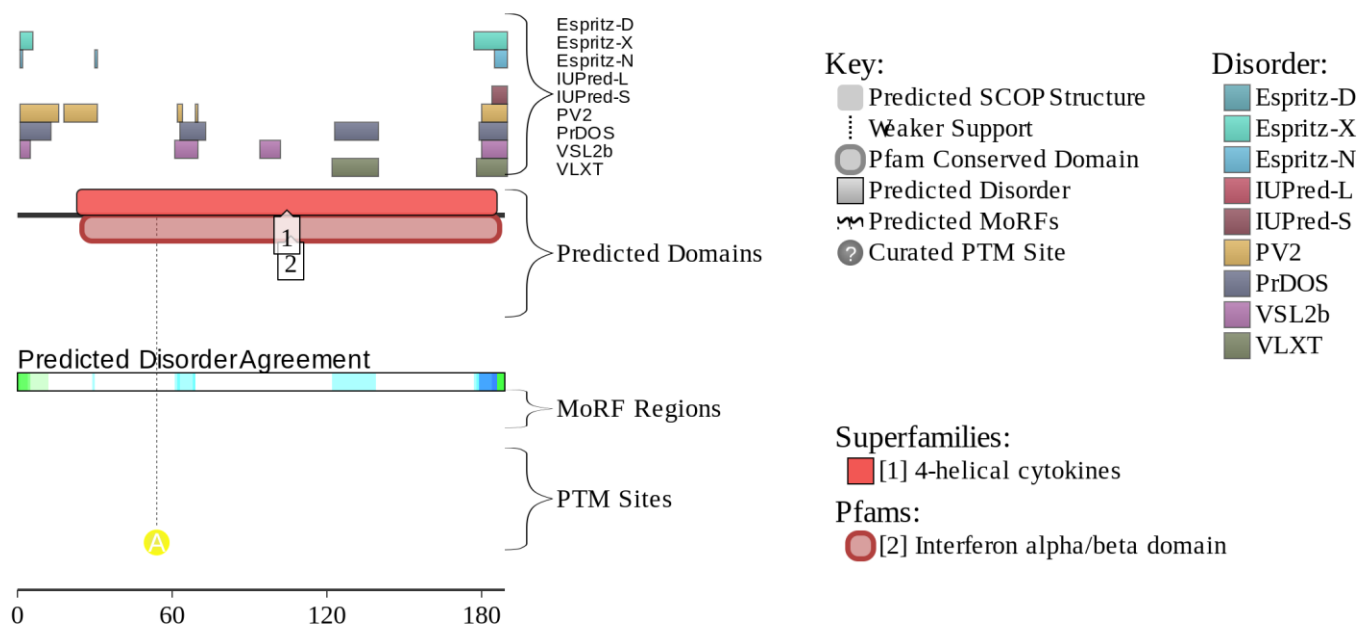
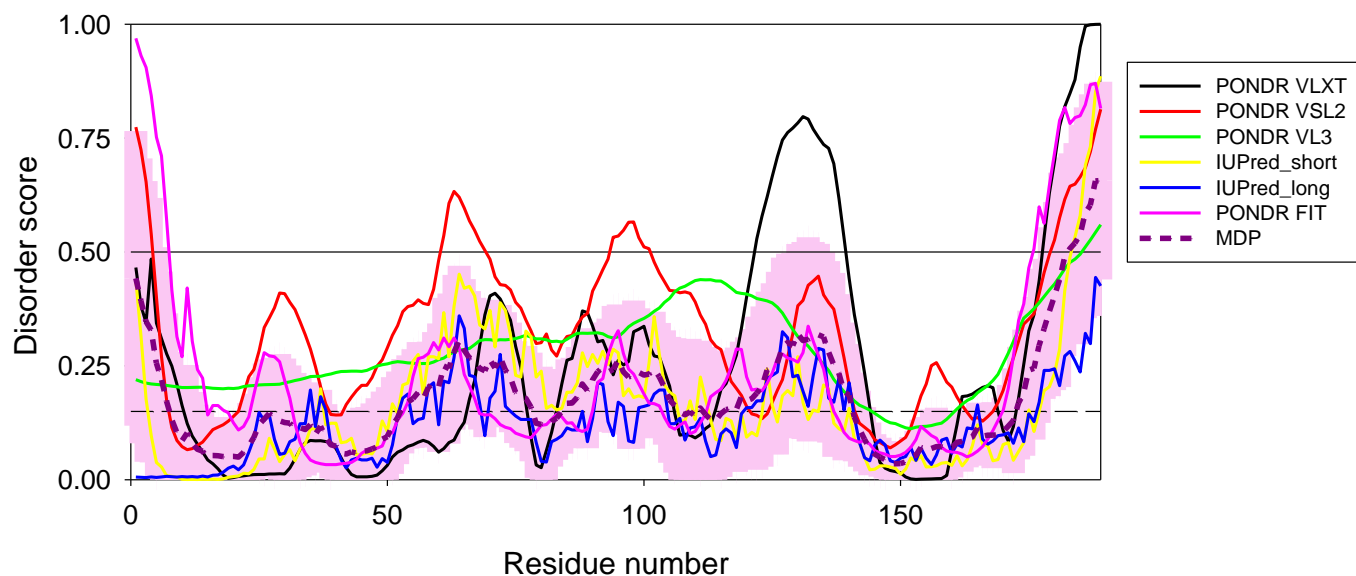


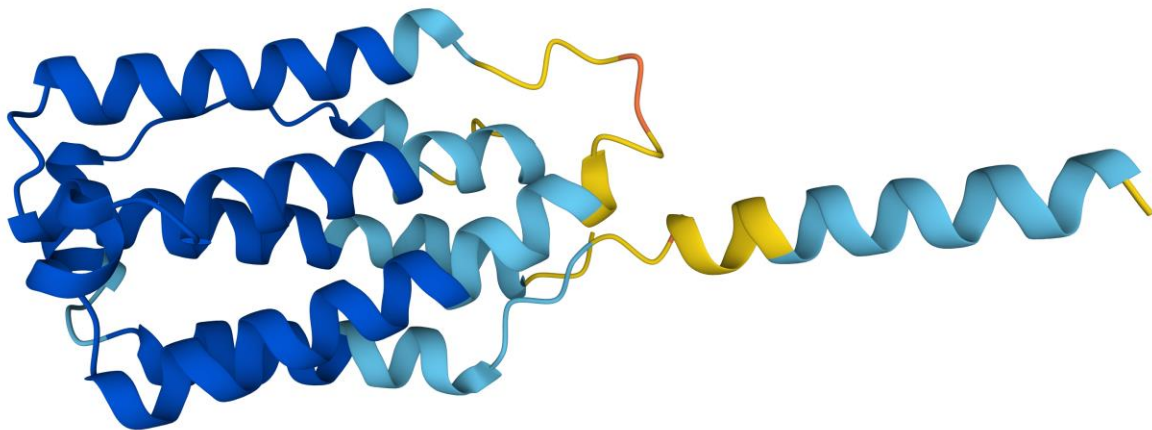
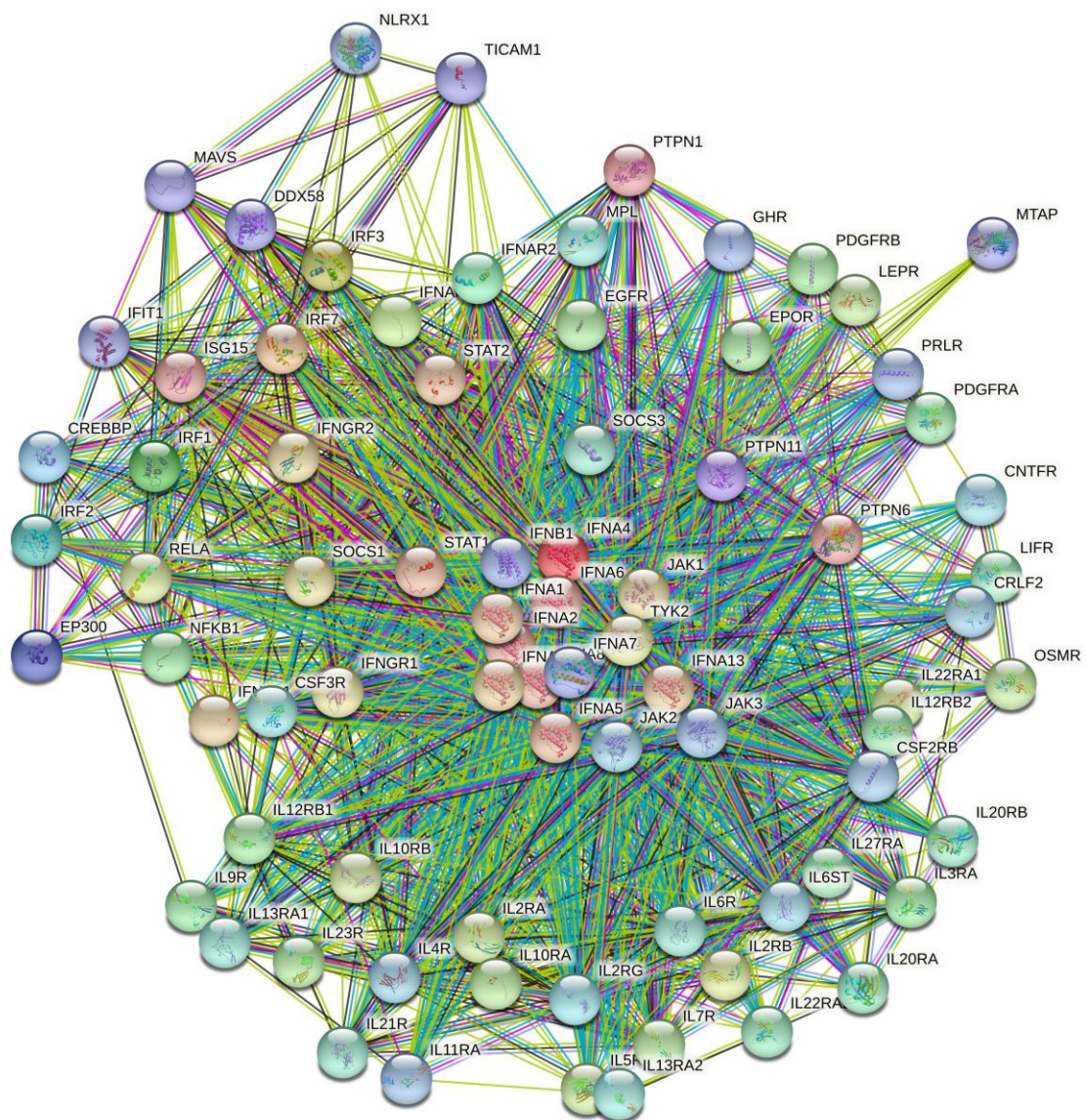
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>sp|P01574|IFNB_HUMAN Interferon beta OS=Homo sapiens OX=9606 GN=IFNB1 PE=1 SV=1
MTNKCLLQIALLLCFSTTALSMSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQ
NIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYYGRIHLHYLKAKEYSHCAWTIVRVE
ILRNFYFINRLTGylRN
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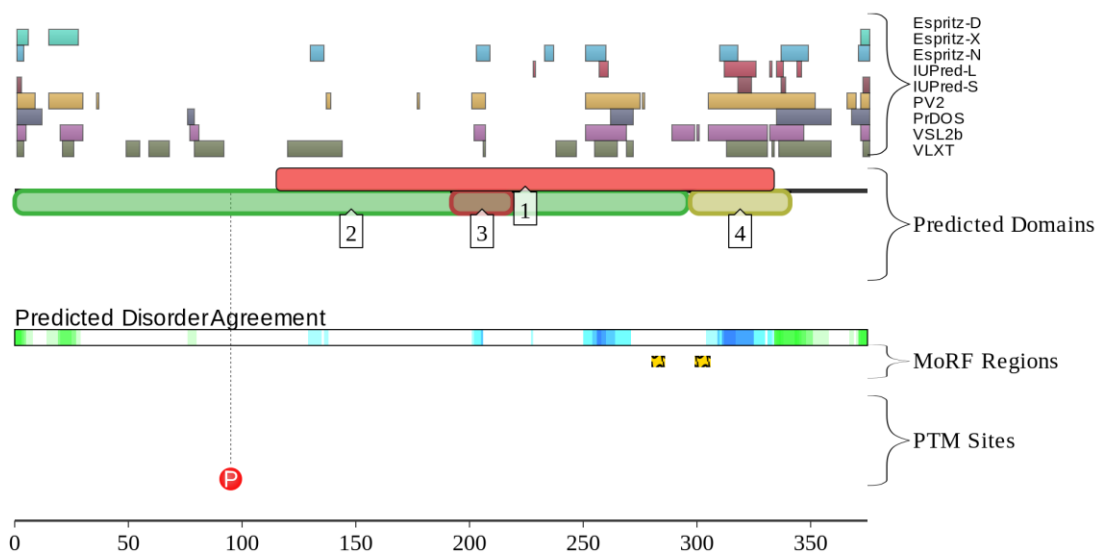
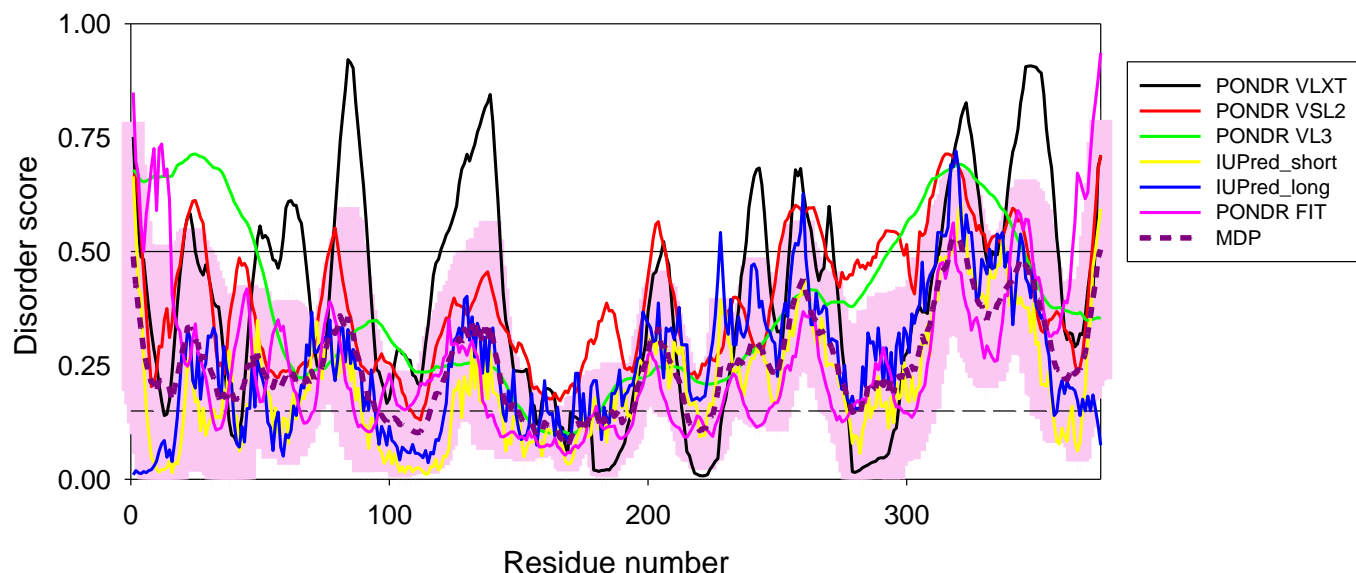


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>sp|P05014|IFNA4_HUMAN Interferon alpha-4 OS=Homo sapiens OX=9606 GN=IFNA4 PE=1 SV=2
MALSFSLMAVLVLSYKSLGCDLPQTHSLGNRRALILLAQMGRISHFSLKDRHDFGFPPEEEFDGHQFQKAQAISVLHEMIQ
QTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNDLEACVIEVGVVEETPLMNEDSILAVRKYFQRITLYLTEKKYSPCAWEVVRAE
IMRSLSFSTNLQKRLRRKD
```






```
>sp|P08571|CD14_HUMAN Monocyte differentiation antigen CD14 OS=Homo sapiens OX=9606
GN=CD14 PE=1 SV=2
MERASCLLLLLLPLVHVSATTPEPCELDDDEFRCVCNCFSEPPQPDWSEAFQCVS AVEVEIHAGGLNLEPFLKRVDADADPRQYADT
VKALRVRLTVGAAQVPAQLLVGALRVLAYSRKELTLEDLKITGTMPPPLPLEATGLALSSLRLRNVSATGRSWLAELQQWLKP
GLKVLISIAQAHSPAFCSEQVRAFPALTSLDLSDNPGGLGERGLMAALCPHKFFAIQNALARNRNTGMETPTGVCAALAAAGVQPHSLD
LSHNSLRATVNPSPAPRCMWSSALNSLNLSFAGLEQVPKGLPAKLRVLDLSCNRLNRAPQPDDELPEVDNLTLDGNPFLVPGTALPH
EGSMNSGVVPACARSTLSVGVSGTLVLLQGARGFA
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Key:

- Predicted SCOP Structure
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Disorder:

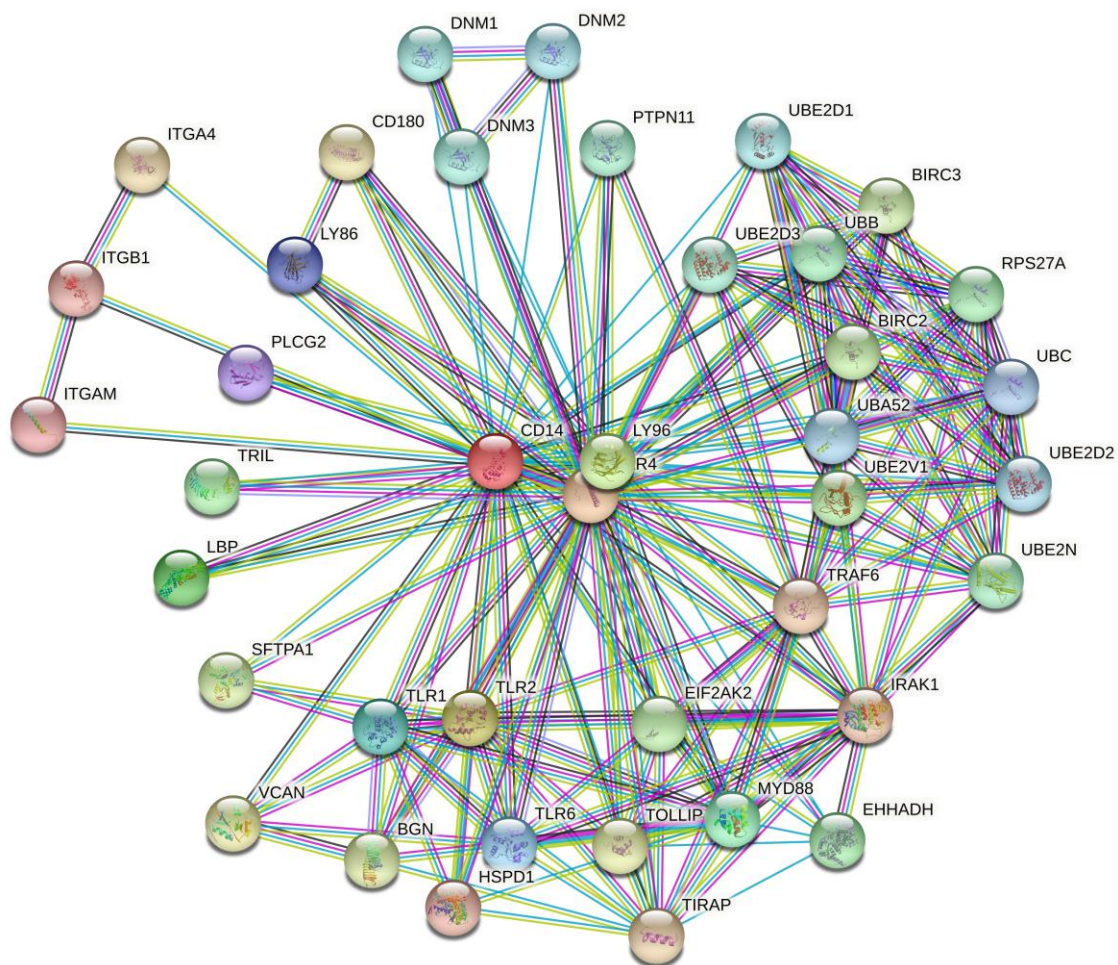
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

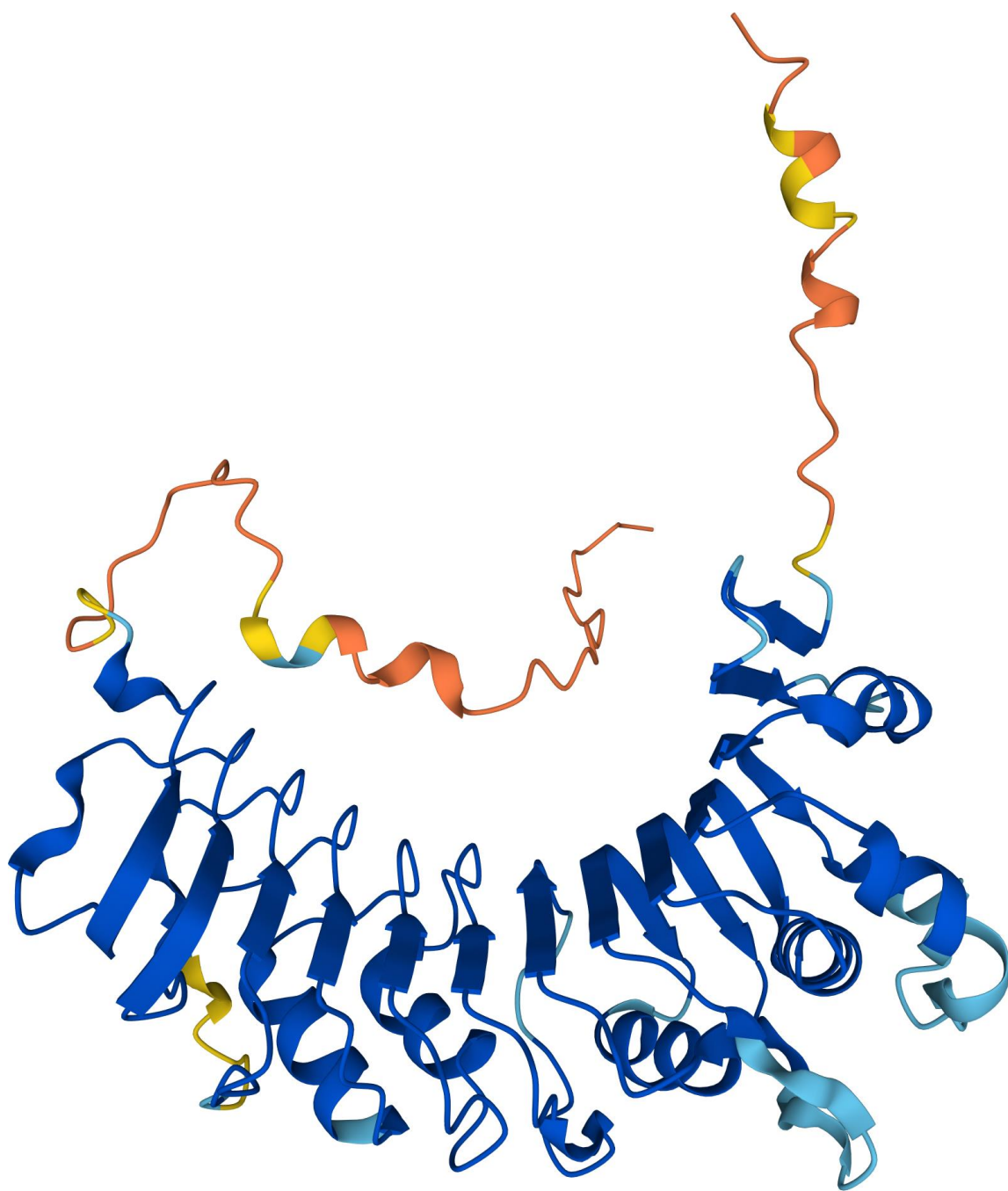
Superfamilies:

- [1] L domain-like

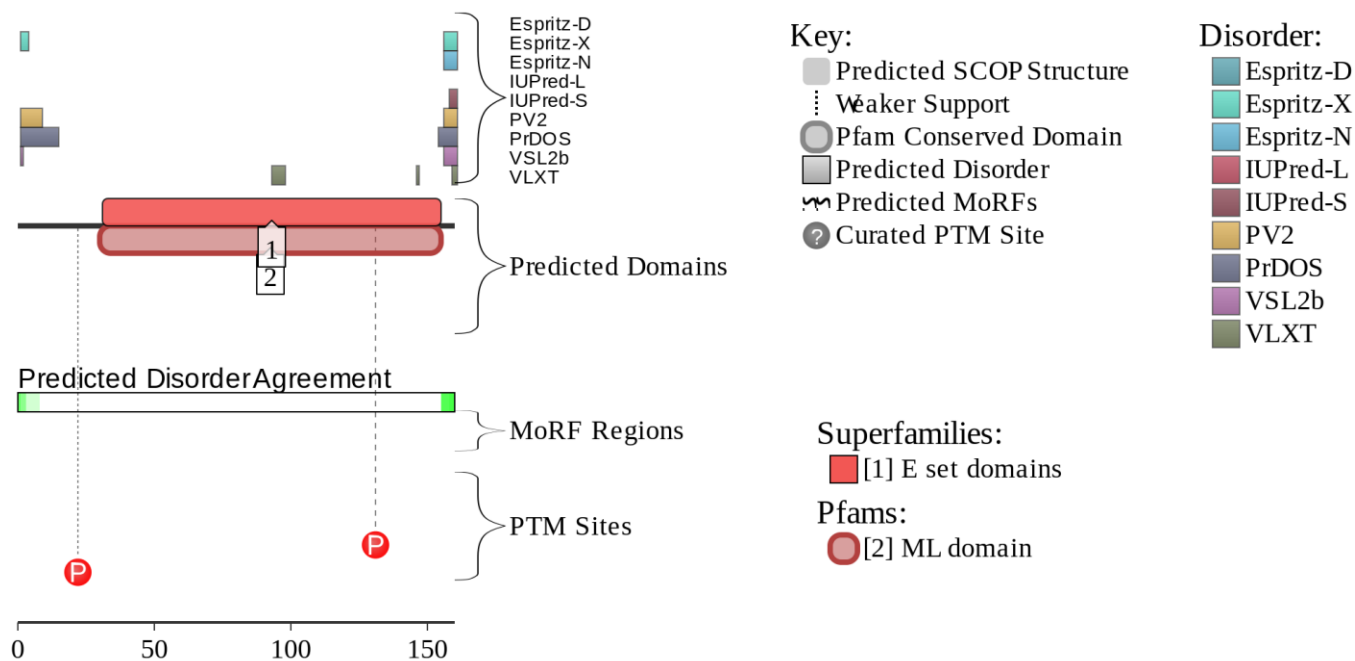
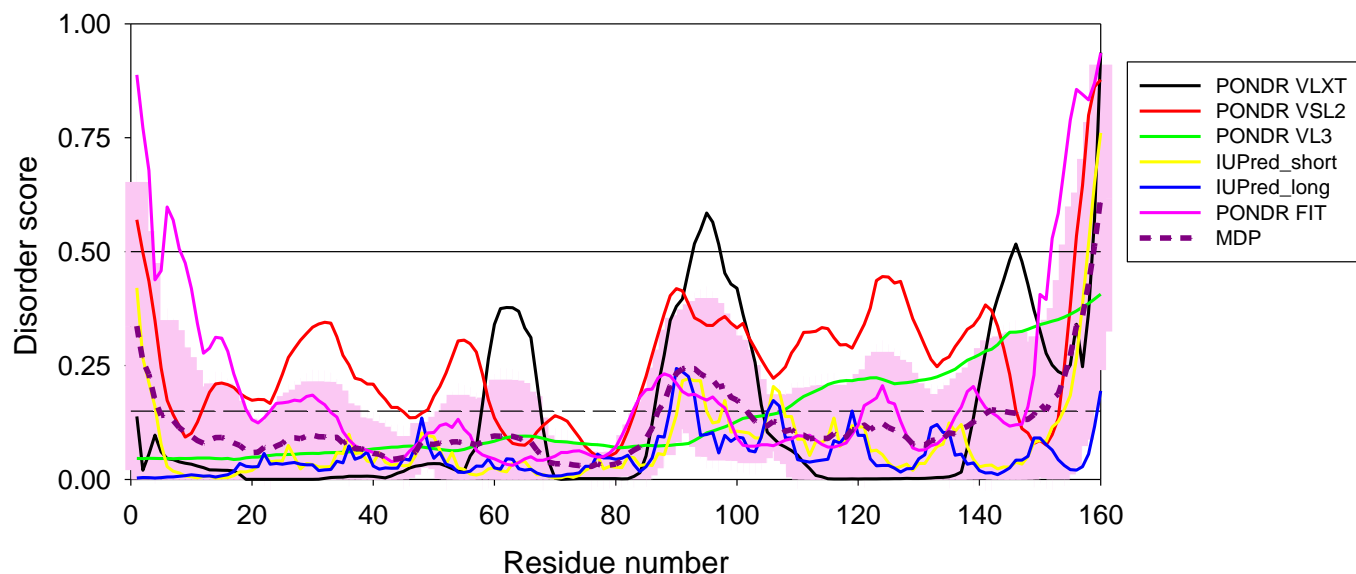
Pfams:

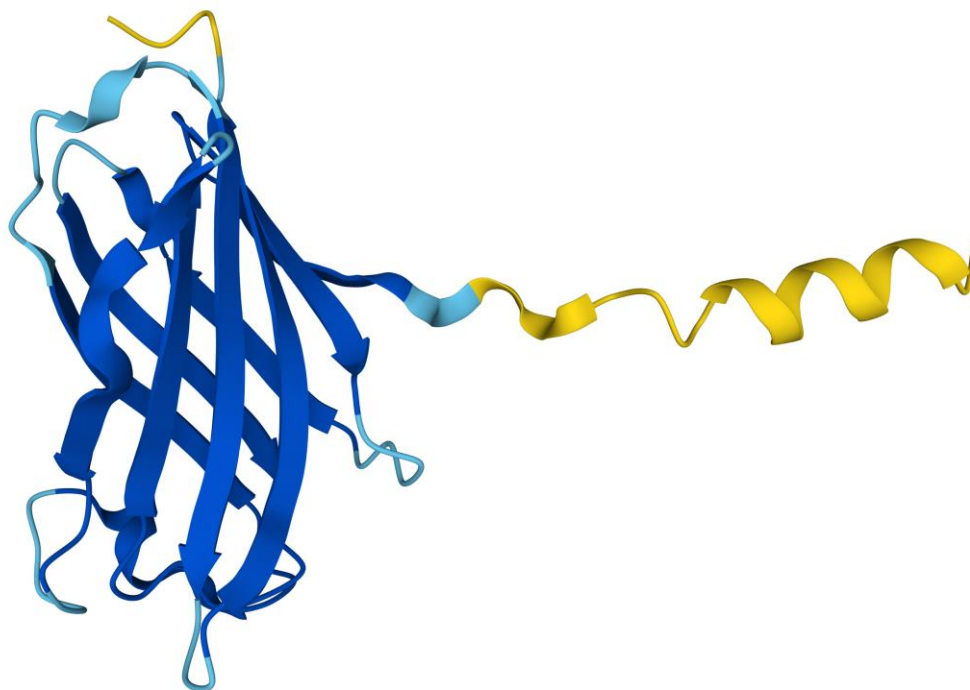
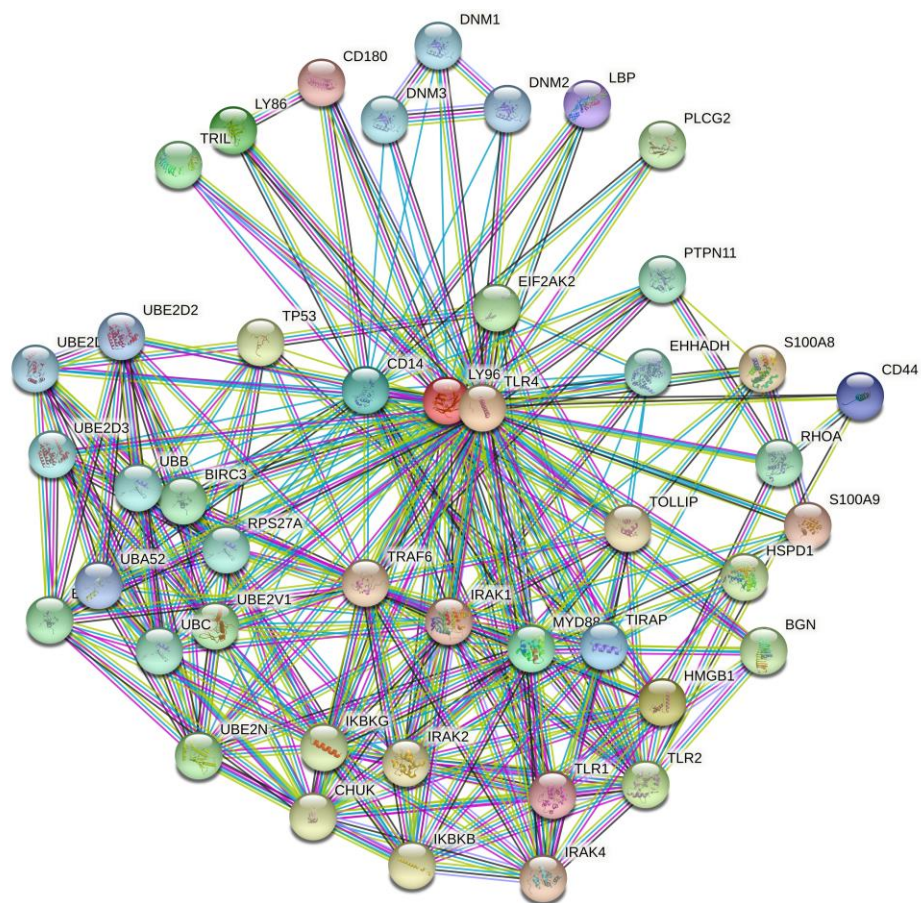
- [2] PB002723 (Pfam-B)
- [3] Leucine Rich repeat
- [4] Leucine Rich Repeat





>sp|Q9Y6Y9|LY96_HUMAN Lymphocyte antigen 96 OS=Homo sapiens OX=9606 GN=LY96 PE=1 SV=2
MLPFLFFSTLFFSSIFTEAQKQYWVCNSSDASISYTYCDKMQYPISINVNPCIELKRSKGLLHIFYIPRRDLKQLYFNLYITVNTM
NLPKRKEVICRGSDDDYSFCRALKGETVNTTISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPNSN





Supplementary Table S1. Some physico-chemical and intrinsic disorder-related features of HCV proteins, human TLRs, and major players of the TLR-regulated downstream signaling pathways

Protein name (UniProt ID)	Protein function	Length	PPIDR	ADS	Number of IDRs	Longest IDR	MoRFs	Number of interactors
HCV proteome								
HCV genome polyprotein (P27958)	Genome polyprotein, processed to individual viral proteins at maturation	3011	19.46	0.3224	40	2295-2417 (123)	1-52 (52) 76-94 (19) 2174-2213 (40) 2222-2234 (13) 2290-2301 (12) 2330-2412 (83)	259 (IntAct)
Core (2-177)	Mature core protein; packages viral RNA	176	68.18	0.6242	3	1-93 (93)	1-51 (51) 75-95 (21)	112 ^a
E1 (192-383)	Envelope glycoprotein E1; mediates virus attachment to the host cell	192	6.77	0.2159	3	1-7 (7)	N/P	10 ^a
E2 (384-746)	Envelope glycoprotein E2; mediates virus attachment to the host cell	363	9.37	0.2593	6	270-281 (12)	N/P	31 ^a
p7 (747-809)	Viroporin; ion channel protein that acting in the assembly, envelopment and secretion of viral particles	63	12.70	0.1848	2	1-4 (4) 60-63 (4)	N/P	2 (UniProt)
NS2 (810-1026)	Cysteine protease; required for the proteolytic auto-cleavage	217	4.61	0.1579	2	1-5 (5) 213-217 (5)	N/P	31 ^a
NS3 (1027-1657)	Serine protease/ helicase with three enzymatic activities: serine protease with a chymotrypsin-like fold, NTPase and RNA helicase	631	22.03	0.3442	16	109-142 (34)	N/P	242 ^a
NS4A (1658- 1711)	Non-structural protein 4A; non- covalent peptide cofactor of NS3 serine protease	54	18.52	0.2504	2	48-54 (7)	N/P	11 ^a

NS4B (1712-1972)	Non-structural protein 4B; induces membrane alterations serving as a scaffold for the virus replication complex	261	9.20	0.2621	4	219-228 (10)	N/P	16 ^a
NS5A (1973-2420)	Non-structural protein 5A; indispensable for viral replication and assembly	448	47.99	0.5411	6	323-448 (126)	202-241 (40) 250-262 (13) 318-329 (12) 358-448 (91)	139 ^a
NS5B (2421-3011)	RNA-directed RNA polymerase; performs primer-template recognition and RNA synthesis during viral replication	591	15.40	0.3120	11	85-102 (18)	N/P	66 ^a
Human toll-like receptors								
TLR1 (Q15399)	Toll-like receptor 1	786	11.58	0.2904	11	384-422 (39)	N/P	89 (0.400) ^b
TLR2 (O60603)	Toll-like receptor 2	784	14.92	0.3074	13	19-57 (39)	N/P	41 ^c
TLR3 (O15455)	Toll-like receptor 3	904	13.05	0.3050	12	152-209 (58)	N/P	26
TLR4 (O00206)	Toll-like receptor 4	839	9.30	0.2670	10	359-381 (23)	N/P	84
TLR5 (O60602)	Toll-like receptor 5	858	7.11	0.2458	7	462-476 (15) 836-850 (15)	N/P	134 (0.400)
TLR6 (Q9Y2C9)	Toll-like receptor 6	796	7.16	0.2550	11	763-574 (12)	N/P	132 (0.400)
TLR7 (Q9NYK1)	Toll-like receptor 7	1049	12.77	0.3055	11	593-625 (33) 666-698 (33)	N/P	51 (0.700) ^d
TLR8 (Q9NR97)	Toll-like receptor 8	1041	18.64	0.3135	13	707-765 (59)	N/P	24 (0.700)
TLR9 (Q9NR96)	Toll-like receptor 9	1032	11.05	0.2857	14	62-86 (25)	N/P	54 (0.700)
TLR10 (Q9BXR5)	Toll-like receptor 10	811	9.12	0.2587	9	793-811 (19)	N/P	89 (0.400)
Members of the signaling pathways induced by the toll-like receptors								
MAL/ TIRAP (P58753)	MYD88 adapter-like; Toll/ interleukin-1 receptor domain-containing adapter protein	221	42.53	0.5508	3	1-88 (88)	1-9 (9) 14-33 (20)	24
MYD88 (Q99836)	Myeloid differentiation primary response protein MyD88	296	19.93	0.3572	3	109-130 (30)	N/P	66
IRAK1 (P51617)	IL-1 receptor-associated kinase 1	712	52.67	0.5516	9	501-712 (212)	139-147 (9) 158-163 (6) 492-502 (11)	67

							518-527 (10) 557-577 (21) 590-621 (32) 640-650 (11) 660-697 (38)	
IRAK4 (Q9NWZ3)	IL-1 receptor-associated kinase 4	460	33.48	0.4224	7	107-173 (67)	164-173 (10) 428-437 (10)	25
TRAF6 (Q9Y4K3)	TNF receptor-associated factor 6	522	23.37	0.3888	8	1-52 (52)	N/P	152
TAK1/ MAP3K7 (O43318)	Transformation growth factor- β (TGF- β)-activated kinase; Mitogen-activated protein kinase kinase kinase 7	606	57.10	0.5751	8	296-415 (120)	281-292 (12) 298-304 (7) 316-324 (9) 344-357 (14) 363-376 (14) 388-407 (20) 414-434 (21) 438-448 (11) 456-468 (13) 494-515 (22) 517-548 (32) 580-589 (10)	92
MAPK1 (P28482)	Mitogen-activated protein kinase 1; Extracellular signal-regulated kinase 2	350	16.67	0.3075	3	315-360 (46)	N/P	271
MAPK3 (P27361)	Mitogen-activated protein kinase 3; Extracellular signal-regulated kinase 1	379	22.96	0.3569	7	1-36 (36)	N/P	277
MAPK4 (P31152)	Mitogen-activated protein kinase 4	587	41.06	0.4576	11	467-546 (90)	333-344 (12) 353-362 (10) 422-443 (22) 454-465 (12) 486-500 (15) 532-552 (21)	59 (0.400)

							561-570 (10) 576-587 (12)	
MAPK6 (Q16659)	Mitogen-activated protein kinase 6	721	43.13	0.4644	16	616-721 (106)	468-475 (8) 527-534 (8) 602-611 (10) 627-633 (7) 664-679 (16) 713-721 (9)	61
MAPK7 (Q13164)	Mitogen-activated protein kinase 7	816	63.24	0.6389	6	340-751 (412)	363-368 (6) 379-389 (11) 395-432 (38) 444-456 (13) 466-501 (36) 543-592 (50) 609-633 (25) 649-732 (84) 737-760 (24) 771-785 (15) 800-816 (17)	187 (0.400)
MAPK8/JNK1 (P45983)	Mitogen-activated protein kinase 8; c-Jun N-terminal kinase 1	427	27.63	0.3735	5	361-427 (67)	319-324 (6) 352-363 (12) 377-387 (11) 397-402 (6) 413-427 (15)	162
MAPK9/JNK2 (P45984)	Mitogen-activated protein kinase 9; c-Jun N-terminal kinase 2	424	27.36	0.3783	6	358-424 (67)	320-325 (6) 352-362 (11) 391-424 (34)	65
MAPK10/JNK3 (P53779)	Mitogen-activated protein kinase 10; c-Jun N-terminal kinase 3	464	26.72	0.3747	6	376-464 (89)	356-363 (8) 390-399 (10) 431-464 (34)	49
MAPK11 (Q15759)	Mitogen-activated protein kinase 11; Mitogen-activated protein kinase p38 beta	364	21.15	0.3771	5	309-364 (56)	282-290 (9) 301-311 (11) 337-348 (12)	139

MAPK12 (P53778)	Mitogen-activated protein kinase 12; Mitogen-activated protein kinase p38 gamma	367	24.52	0.3432	5	311-367 (55)	286-293 (7)	43
MAPK13 (O15264)	Mitogen-activated protein kinase 13; Mitogen-activated protein kinase p38 delta	365	30.68	0.3859	4	254-336 (83)	301-308 (8) 341-350 (10)	36
MAPK14 (Q16539)	Mitogen-activated protein kinase 14; Mitogen-activated protein kinase p38 alpha	360	13.89	0.2952	6	313-327 (15)	N/P	207
MAPK15 (Q8TD08)	Mitogen-activated protein kinase 15	544	53.31	0.5137	8	315-516 (302)	280-288 (9) 329-350 (22) 361-384 (24) 401-429 (29) 434-484 (51) 516-536 (21)	39 (0.400)
AP-1/C-JUN (P05412)	Transcription factor Jun	331	82.78	0.7235	8	123-322 (200)	66-81 (16) 110-121 (12) 143-151 (9) 157-201 (45) 209-229 (21) 241-250 (10) 252-284 (33) 312-324 (13)	209
AP-1/C-FOS (P01100)	Protein c-FOS	380	83.42	0.7553	4	213-321 (112)	74-83 (10) 103-118 (16) 148-155 (8) 180-212 (33) 215-227 (13) 237-244 (8) 262-275 (14) 294-302 (9)	131
IKK α (O15111)	Inhibitor of nuclear factor- κ B (NF- κ B) kinase subunit alpha	745	24.56	0.3623	10	664-711 (48)	71-723 (11) 738-745 (8)	104

IKK β (O14920)	Inhibitor of nuclear factor- κ B (NF- κ B) kinase subunit beta	756	35.45	0.4382	16	635-713 (79)	394-392 (9) 655-664 (10) 709-723 (15) 734-742 (9)	95
IKK γ (Q9Y6K9)	Inhibitor of nuclear factor- κ B (NF- κ B) kinase subunit gamma; NF-kappa-B essential modulator (NEMO)	419	98.57	0.8288	2	1-232 (232)	1-15 (15) 33-41 (9) 230-242 (13) 304-310 (7) 372-380 (9) 407-419(13)	116
IKK ϵ (Q14164)	Inhibitor of nuclear factor- κ B (NF- κ B) kinase subunit epsilon	716	23.88	0.3811	13	470-542 (73)	679-698 (20)	20
NFKBIA/IKBA (P25963)	NF-kappa-B inhibitor alpha; I-kappa-B-alpha	317	39.75	0.4695	2	1-72 (72)	1-6 (6) 78-84 (9) 302-317 (16)	133
p65/RELA/NFKB3 (Q04206)	Transcription factor p65; Nuclear factor NF-kappa-B p65 subunit	551	64.61	0.6443	5	257-457 (201)	1-11 (11) 31-41 (11) 62-75 (15) 98-103 (6) 110-113 (9) 285-290 (6) 305-317 (13) 350-380 (31) 398-414 (17) 433-483 (51) 492-504 (13) 523-551 (29)	235
p50/NFKB1 (P19838)	Nuclear factor NF-kappa-B p105 subunit	968	33.16	0.4490	15	335-482 (148)	369-374 (6) 403-421 (19) 454-463 (10) 781-787 (7) 931-953 (23)	156
p52/NFKB2 (Q00653)	Nuclear factor NF-kappa-B p100 subunit	900	59.89	0.5837	14	690-900 (211)	8-21 (14) 39-44 (6)	41

							112-123 (12) 373-389 (17) 445-458 (14) 648-655 (8) 672-694 (23) 728-753 (26) 766-784 (19) 792-806 (15) 816-848 (33) 859-880 (22) 885-900 (16)	
IRF3 (Q14653)	Interferon regulatory factor 3	427	37.94	0.4565	9	84-196 (113)	52-60 (9) 105-118 (14) 135-168 (34) 202-211 (10)	109
IRF5 (Q13568)	Interferon regulatory factor 5	498	43.17	0.5151	8	106-242 (137)	19-29 (11) 39-47 (9) 88-105 (18) 115-124 (10) 135-142 (8) 149-195 (47) 206-221 (16) 231-253 (23)	68
IRF7 (Q92985)	Interferon regulatory factor 7	503	58.05	0.5520	12	125-268 (162)	59-65 (7) 91-108 (18) 120-132 (13) 155-205 (51) 216-242 (27) 252-258 (7) 270-278 (9) 288-315 (28)	104
TBK1 (Q9UHD2)	Serine/threonine-protein kinase TBK1; TANK-binding kinase 1	729	10.62	0.3349	12	644-704 (61)	N/F	52

CD14 (P08571)	Cluster of differentiation 14; Monocyte differentiation antigen CD14	375	25.87	0.2891	10	305-330 (26)	280-285 (6) 299-305 (7)	39
TANK (Q92844)	TRAF family member-associated NF-kappa-B activator	425	70.35	0.6059	8	162-267 (106)	12-21 (10) 54-65 (12) 73-78 (6) 142-159 (18) 228-236 (9) 263-270 (8) 286-299 (14) 337-344 (8) 394-403 (10)	32
TRIF/TICAM1	Toll-interleukin-1 receptor domain-containing adapter protein inducing interferon beta; TIR domain-containing adapter molecule 1	712	66.29	0.6621	9	124-393 (270)	96-104 (9) 185-194 (10) 201-223 (23) 228-267 (40) 273-341 (69) 374-384 (11) 392-403 (12) 567-578 (12) 588-595 (8) 649-666 (18) 673-703 (31)	34
RIP1/RIPK1 (Q13546)	Receptor-interacting protein 1; Receptor-interacting serine/threonine-protein kinase 1	671	47.84	0.4978	11	291-482 (192)	318-329 (12) 345-363 (19) 376-392 (17) 401-406 (6) 415-475 (61) 531-547 (17)	99
TRAM/TICAM2 (Q86XR7)	TRIF related adapter molecule; TIR domain-containing adapter molecule 2	235	50.21	0.5112	4	1-77 (77)	1-18 (18) 39-46 (8) 75-85 (11)	25
IFNA1 (P01562)	Interferon alpha	189	31.75	0.3759	4	22-56 (36)	N/P	74 (0.700)
IFNA4 (P05014)	Interferon alpha 4	189	16.40	0.3241	4	180-189 (10)	N/P	78 (0.400)

IFNB1 (P01574)	Interferon beta	187	11.76	0.2695	4	124-136 (13)	N/P	44
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^a Data on protein-protein interactions for HCV proteins are derived from [1]

^b Interaction data are derived from STRING-based analysis using medium confidence (0.400) for a minimum required interaction score

^c Interaction data are derived from STRING-based analysis using highest confidence (0.900) for a minimum required interaction score

^d Interaction data are derived from STRING-based analysis using high confidence (0.700) for a minimum required interaction score

References

1. Fan, X.; Xue, B.; Dolan, P.T.; LaCount, D.J.; Kurgan, L.; Uversky, V.N. The intrinsic disorder status of the human hepatitis C virus proteome. *Molecular bioSystems* **2014**, *10*, 1345-1363, doi:10.1039/c4mb00027g.