

Supplementary Materials

Looking at the Pathogenesis of the Rabies Lyssavirus Strain Pasteur Vaccins through a Prism of the Disorder-Based Bioinformatics

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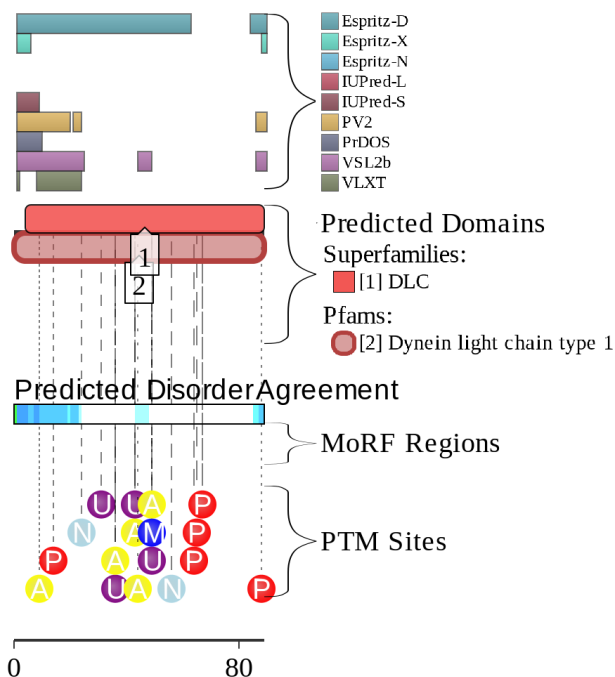
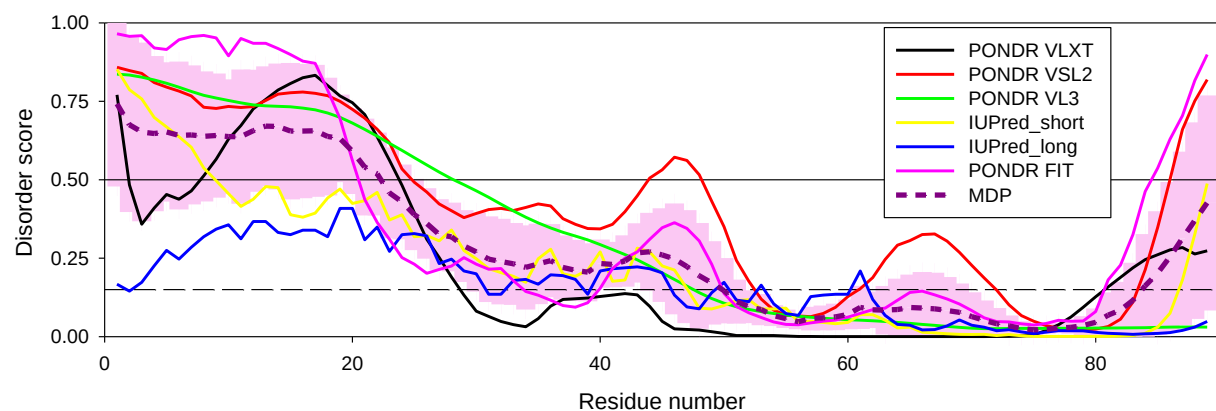
* Correspondence: vuversky@usf.edu

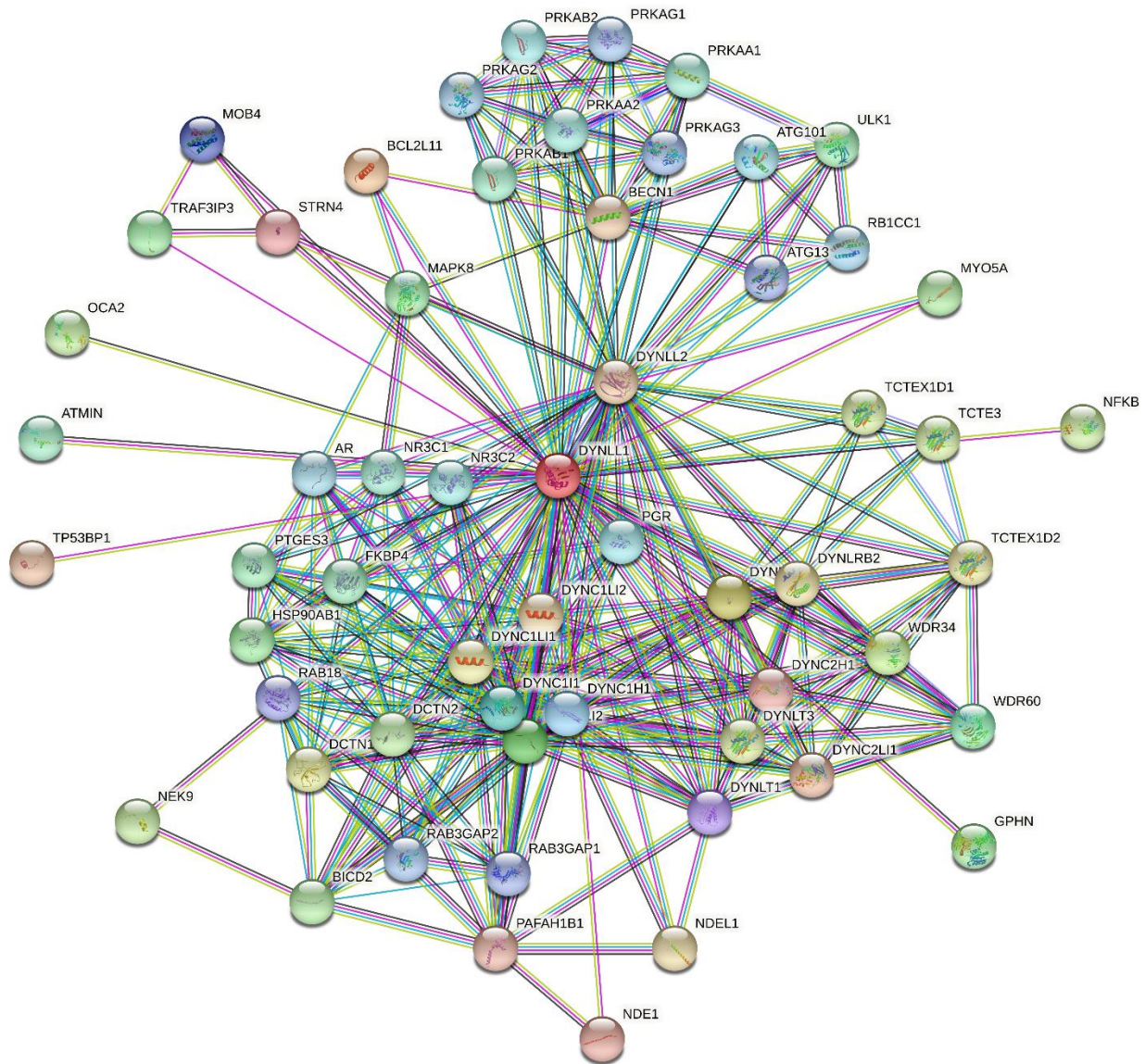
Supplementary Figure S1. Functional disorder in human proteins interacting with the RABV P-protein. For each protein, an amino acid sequence in FASTA format is shown followed by the disorder profile generated by RIDAO, D²P²-generated functional disorder profile, modeled 3D structure generated by AlphaFold, and STRING-based protein-protein interaction network.

DYNLL1 (UniProt ID: P63167)

>sp|P63167|DYL1_HUMAN Dynein light chain 1, cytoplasmic OS=Homo sapiens OX=9606
GN=DYNLL1 PE=1 SV=1

MCDRKAVIKNADMSEEMQQDSVECATQALEKYNIEKDIAAHIKKEFDKKYNPTWHCIV
GRNFGSYVTHETKHFIFYFLGQVAILLFKSG





minimum required interaction score: highest confidence (0.900)

number of nodes: 58

number of edges: 338

average node degree: 11.7

avg. local clustering coefficient: 0.828

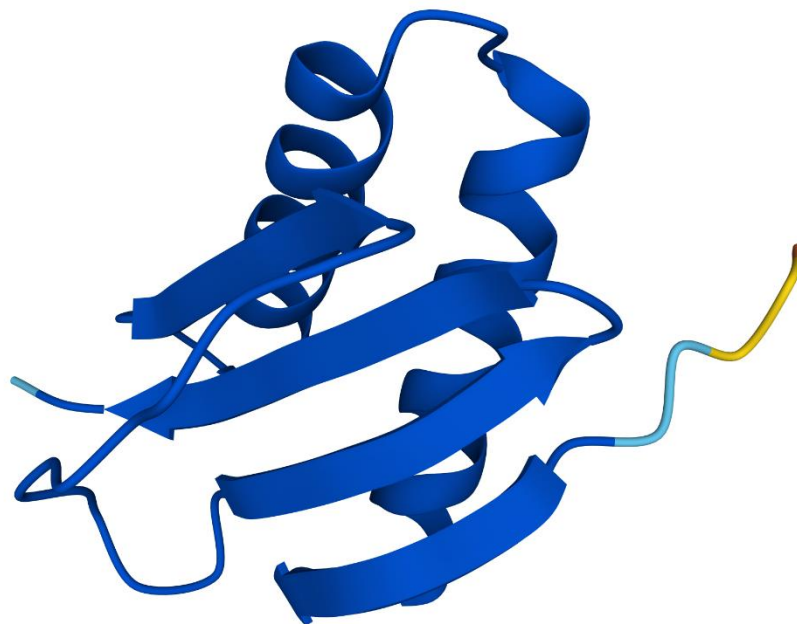
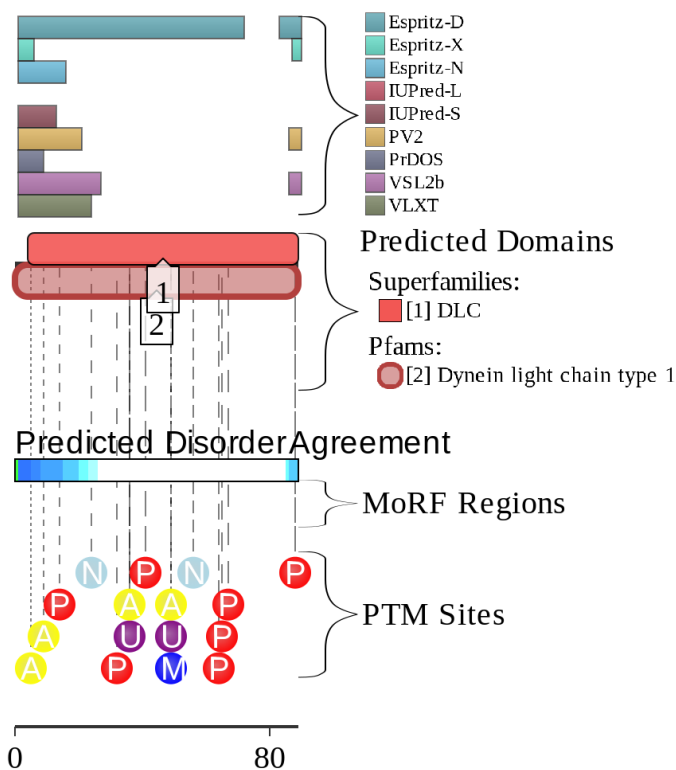
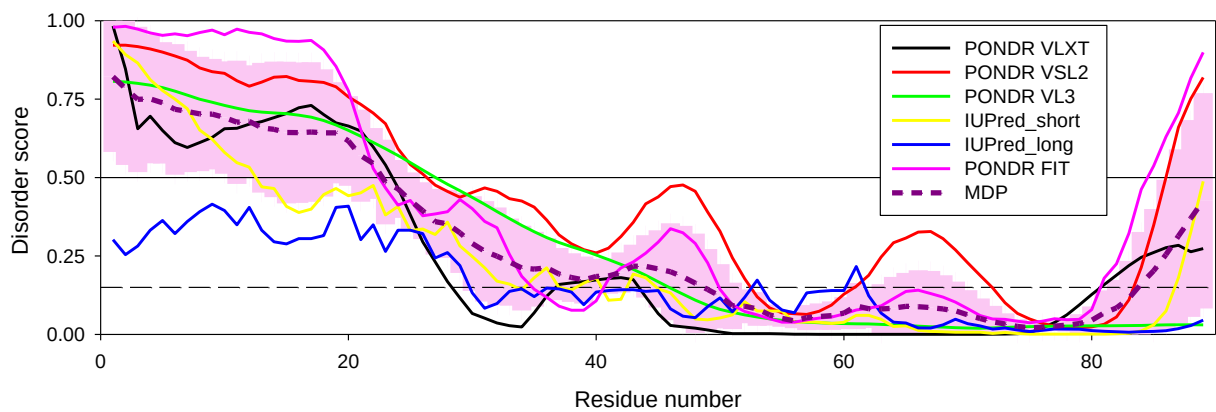
expected number of edges: 68

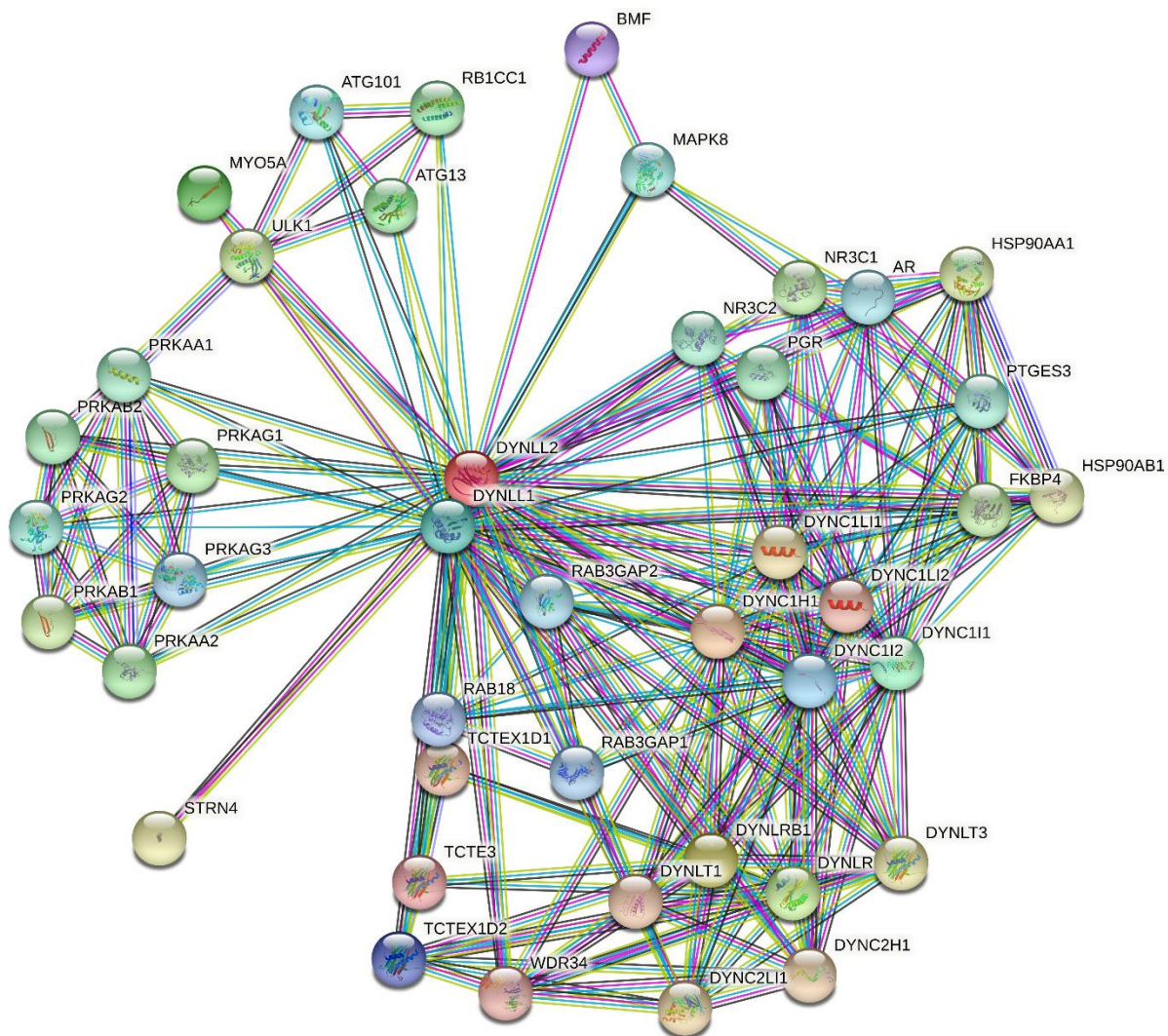
PPI enrichment p-value: $< 1.0e-16$

DYNLL2 (UniProt ID: Q96FJ2)

>sp|Q96FJ2|DYL2_HUMAN Dynein light chain 2, cytoplasmic OS=Homo sapiens OX=9606
GN=DYNLL2 PE=1 SV=1

MSDRKAVIKNADMSQDAVDCATQAMEKYNIEKDIAAYIKKEFDKKYNPTWHCI
VGRNFGSYVTHETKHFIYFYLGQVAILLFKSG





minimum required interaction score: highest confidence (0.900)

number of nodes: 43

number of edges: 257

average node degree: 12

avg. local clustering coefficient: 0.847

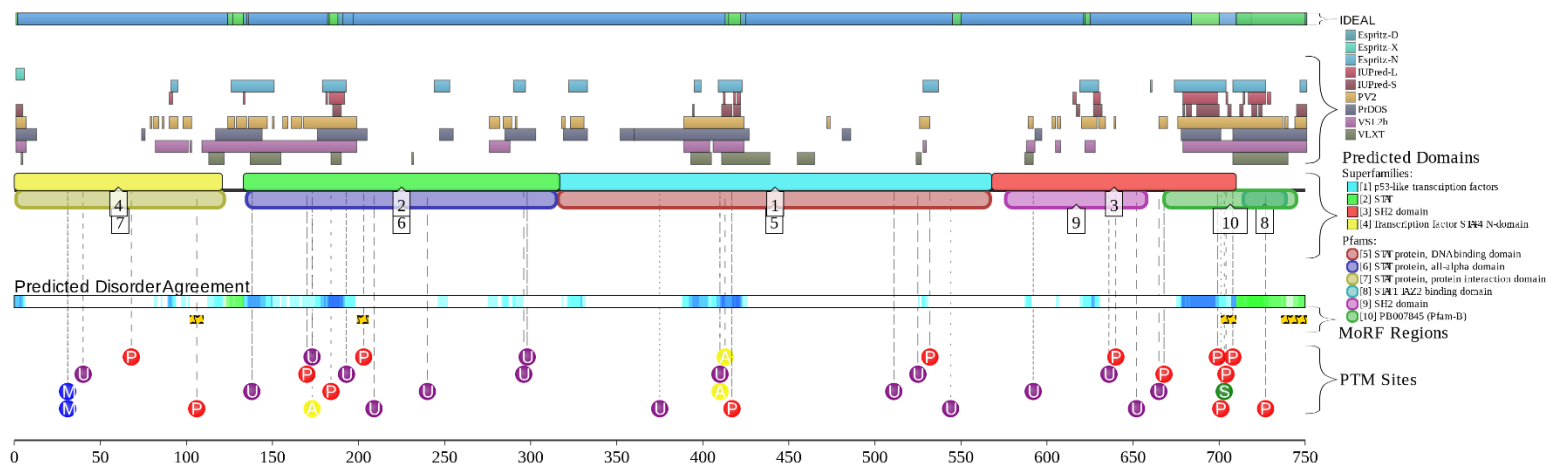
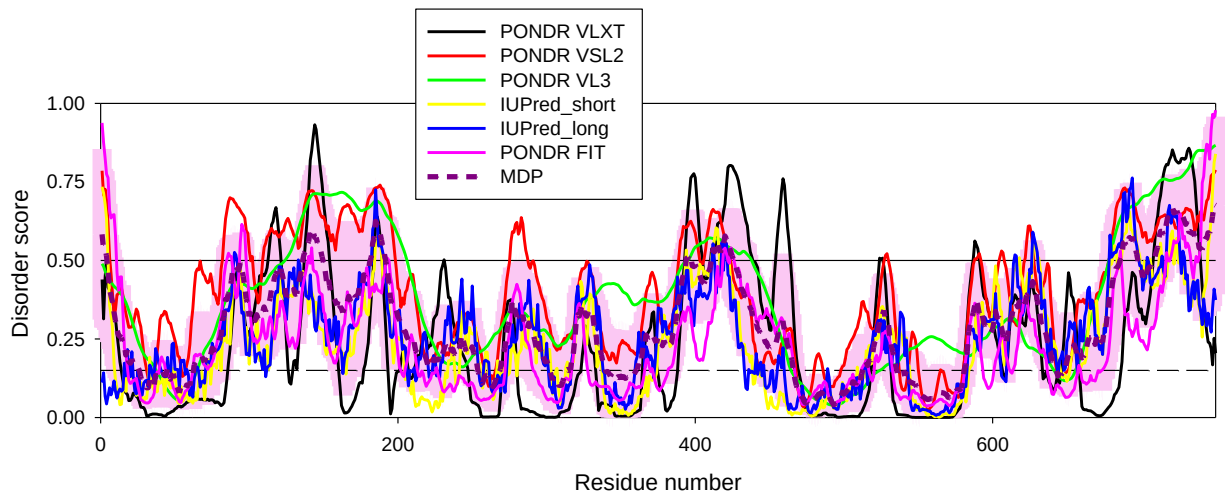
expected number of edges: 50

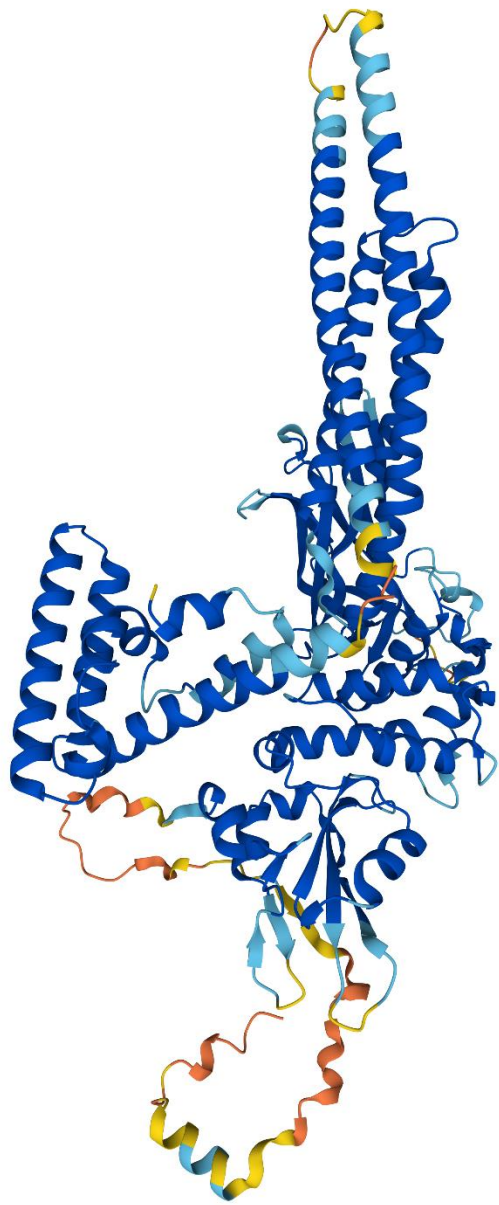
PPI enrichment p-value: $< 1.0e-16$

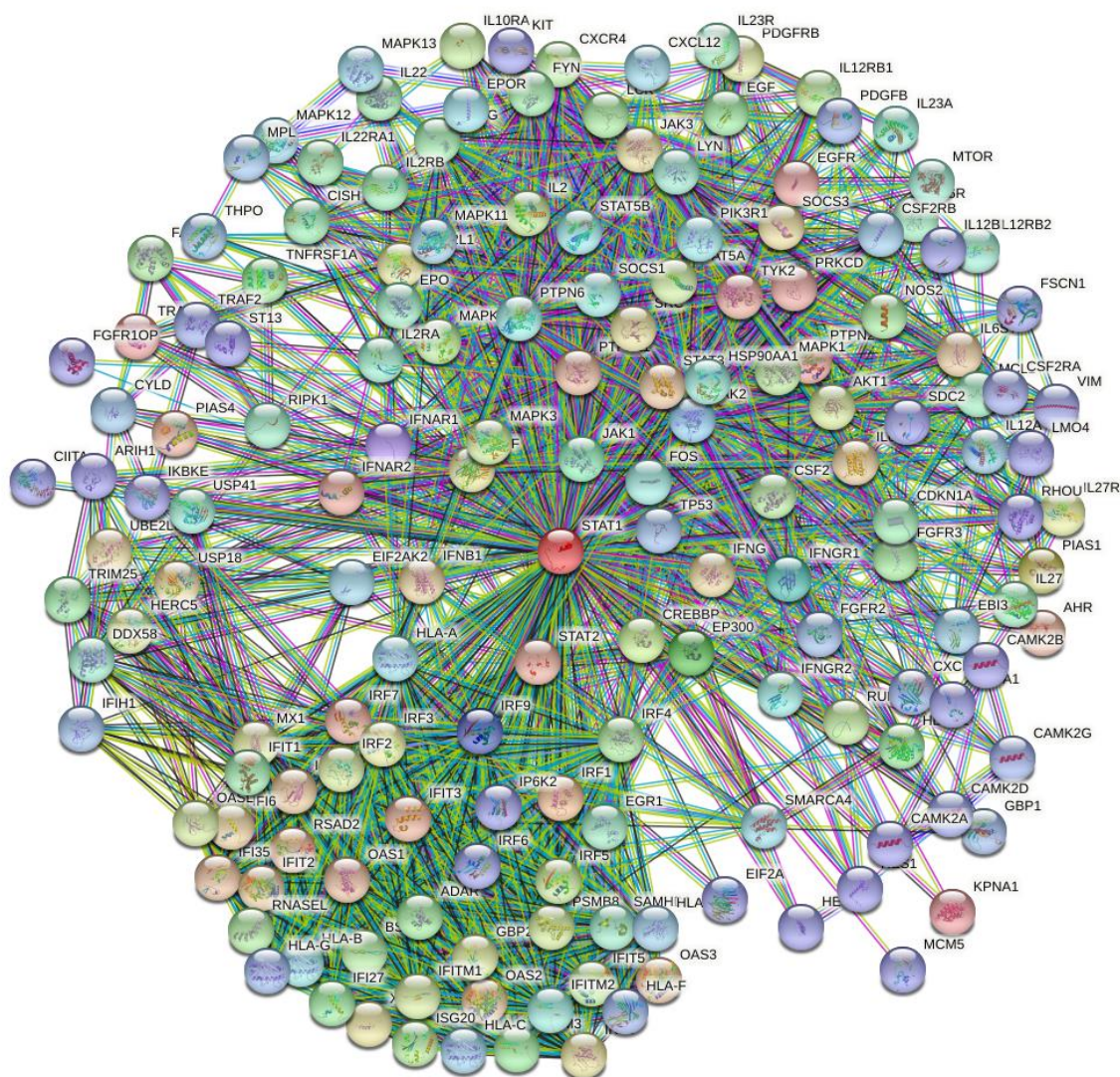
STAT1 (UniProt ID: P42224)

>sp|P42224|STAT1_HUMAN Signal transducer and activator of transcription 1-alpha/beta
OS=Homo sapiens OX=9606 GN=STAT1 PE=1 SV=2

MSQWYELQQLDSKFLEQVHQLYDDSFPMERQYLAQWLEKQDWEHAANDVSFATIRF
HDLLSQLDDQYSRFSLENNFLLQHNIRKSKRNLQDNFQEDPIQMSMIIYSCLKEERKILEN
AQRFNQAQSGNIQSTVMLDKQKELDSKVRNVKDKVMCIEHEIKSLEDLQDEYDFKCKT
LQNREHETNGVAKSDQKQEQLLLKKMYLMLDNKRKEVVKHIIELNVTTELQNALIND
ELVEWKRRQQSACIGGPPNACLDQLQNWFTIVAESLQQVRQQLKKLEELEQKYTYEHD
PITKNKQVLWDRTFSLFQQLIQSSFVVERQPCMPHTHPQRPLVLKTGVQFTVKLRLLVKL
QELNYNLKVKVLFDKDVNERNTVKGFRKFNILGHTTKVMNMEESTNGSLAAEFRHLQL
KEQKNAGTRTNEGPLIVTEELHSLSFETQLCQPGLVIDLETTSLPVVVISNVSQLP
SGWAS ILWYNMLVAEPRNLSFFLTPPCARWAQLSEVLSWQFSSVTKRGLNVDQLNMLGEKLLG
PNASPDGLIPWTRFCKENINDKNFPFWLWIESILELIKHHLLPLWNDGCIMGFISKERERA
LLKDQQPGTFLLRFSESSREGAITFTWVERSQNGGEPDFHAVEPYTKKELSAVTFPDIIRN
YKVMAAENIPENPLKYLYPNIDKDHAFGKYYSRPKEAPEPMELDGPKGTYIKTELISVS
EVHPSRLQTTDNLLPMSPEEFDEVSRIVGSVEFDSMMNTV







minimum required interaction score: highest confidence (0.900)

number of nodes: 43

number of edges: 257

average node degree: 12

avg. local clustering coefficient: 0.847

expected number of edges: 50

PPI enrichment p-value: $< 1.0e-16$

number of nodes: 164

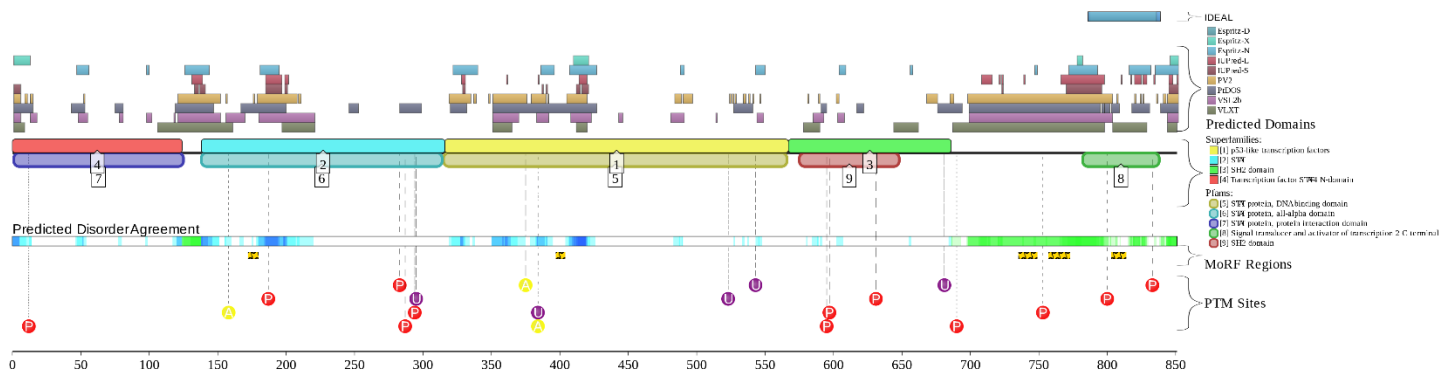
number of edges: 2126

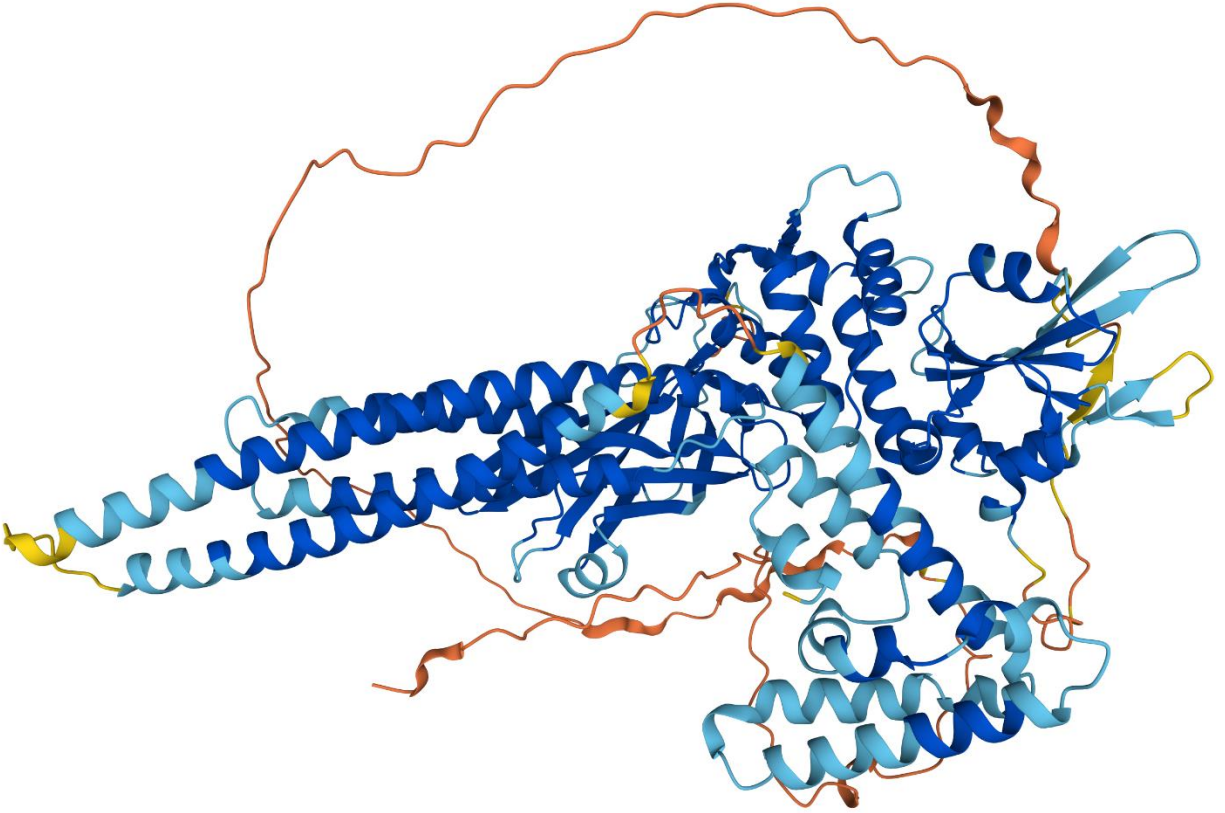
average node degree: 25.9

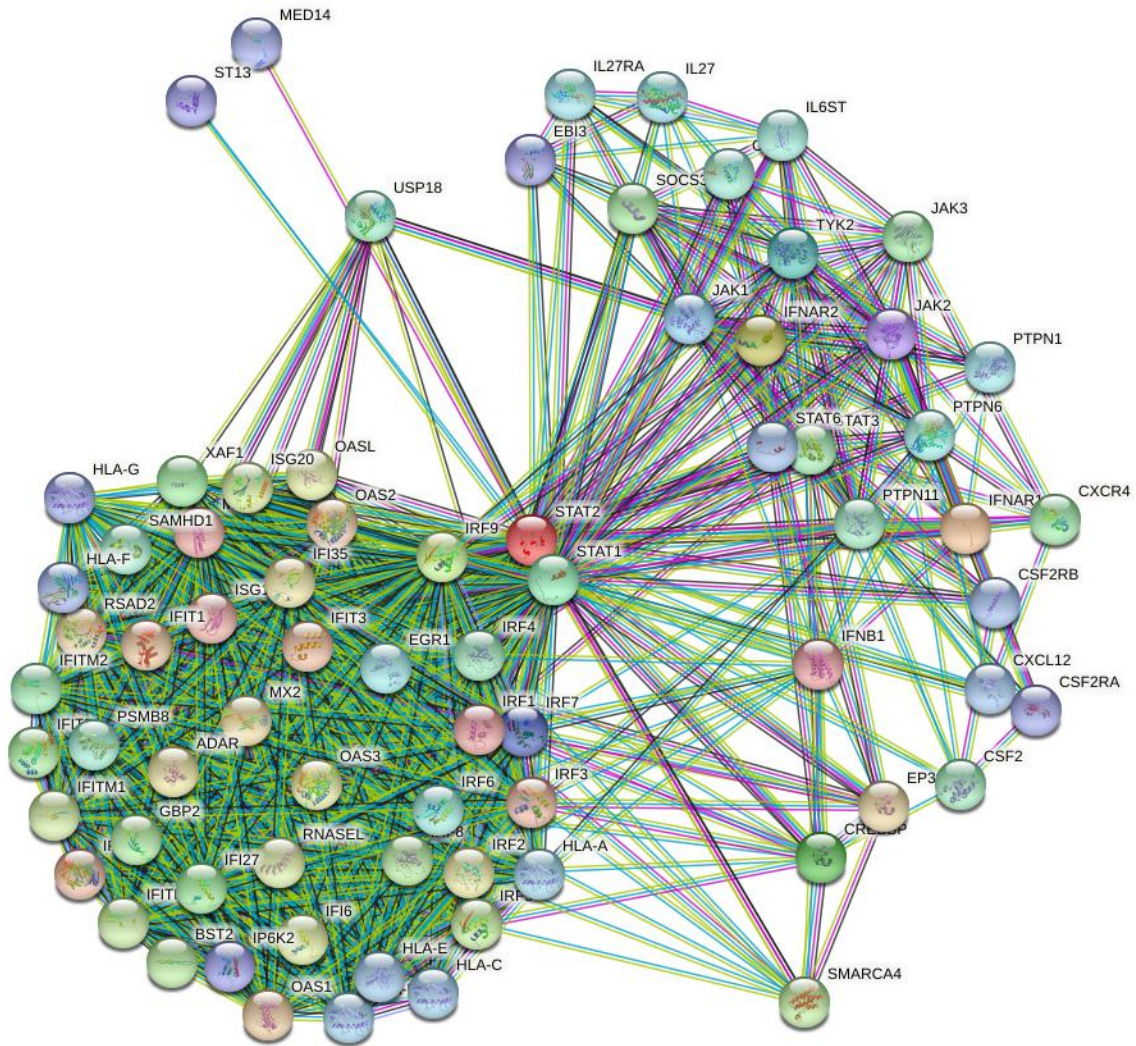
avg. local clustering coefficient: 0.733

expected number of edges: 507

PPI enrichment p-value: $< 1.0e-16$







minimum required interaction score: highest confidence (0.900)

number of nodes: 74

number of edges: 1198

average node degree: 32.4

avg. local clustering coefficient: 0.872

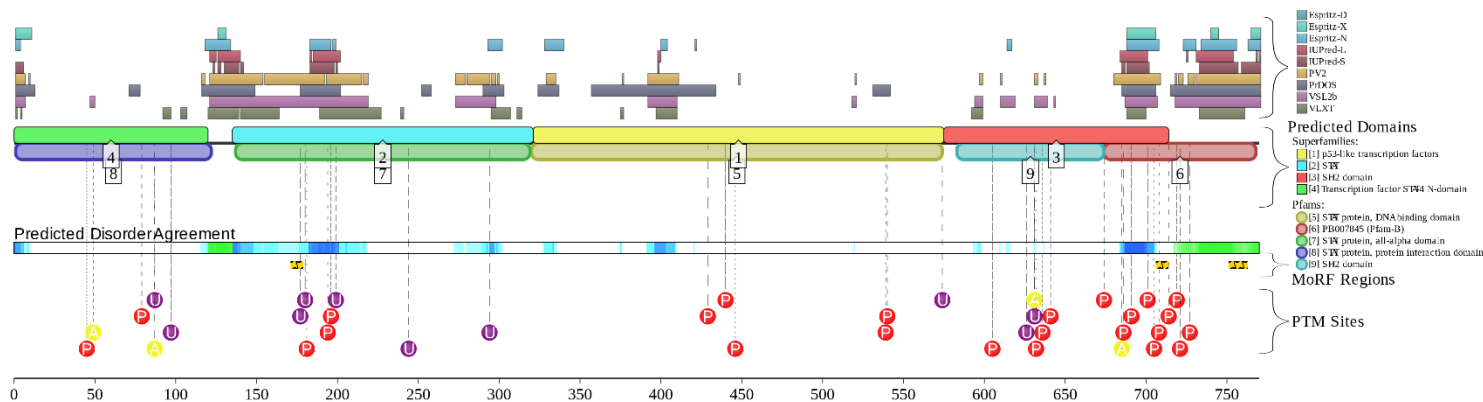
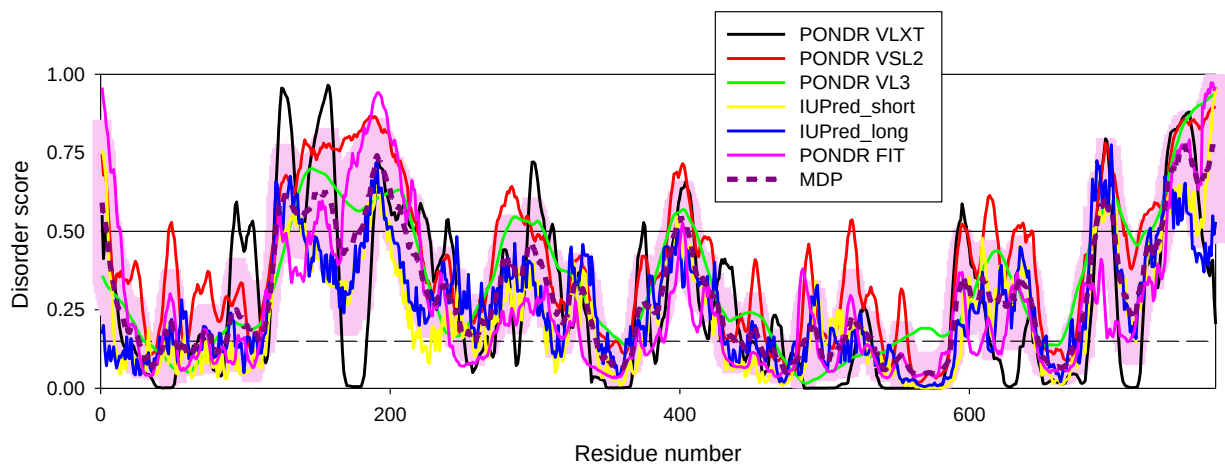
expected number of edges: 128

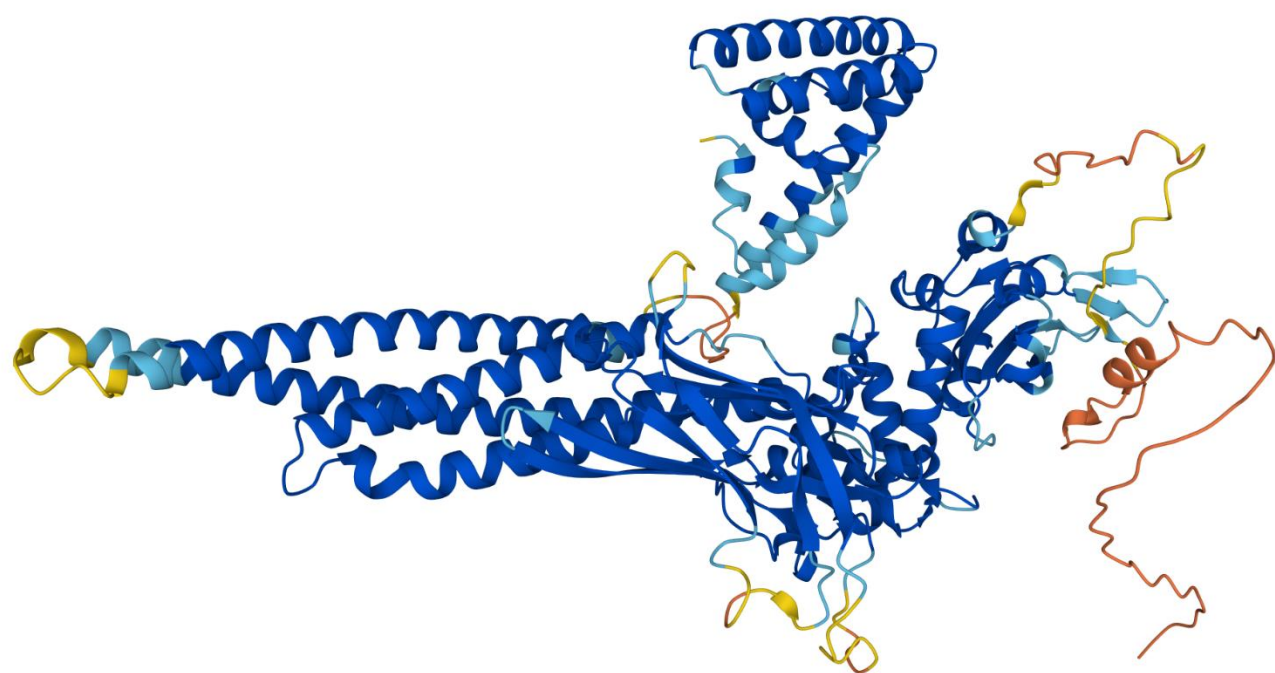
PPI enrichment p-value: $< 1.0e-16$

STAT3 (UniProt ID: P40763)

>sp|P40763|STAT3_HUMAN Signal transducer and activator of transcription 3 OS=Homo sapiens OX=9606 GN=STAT3 PE=1 SV=2

MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWAYAASKESHATLVF
HNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIARIVARCLWEESRLQ
TAATAAQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFD
FNYKTLKSQGDMQDLNGNNSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEY
VQKTLTDEELADWKRRQIACIGGPPNICLDRLNWTSLAESQLQTRQQIKKLEELQKQ
VSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKV
RLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEF
KHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVISNICQ
MPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLWSQFSSTTKRGLSIEQLTTL
AEKLLGPGVNYSGCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIM
GFISKERERAILSTKPPGTFLLRFSSESKEGGVTFWVEKDISGKTQIQSVEPYTKQQLNN
MSFAEIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLK
TKFICVTPTTCSNTIDLPMSPRTLDSLMLQFGNNGEGAEPSSAGGQFESLTFDMELTSECATS
PM

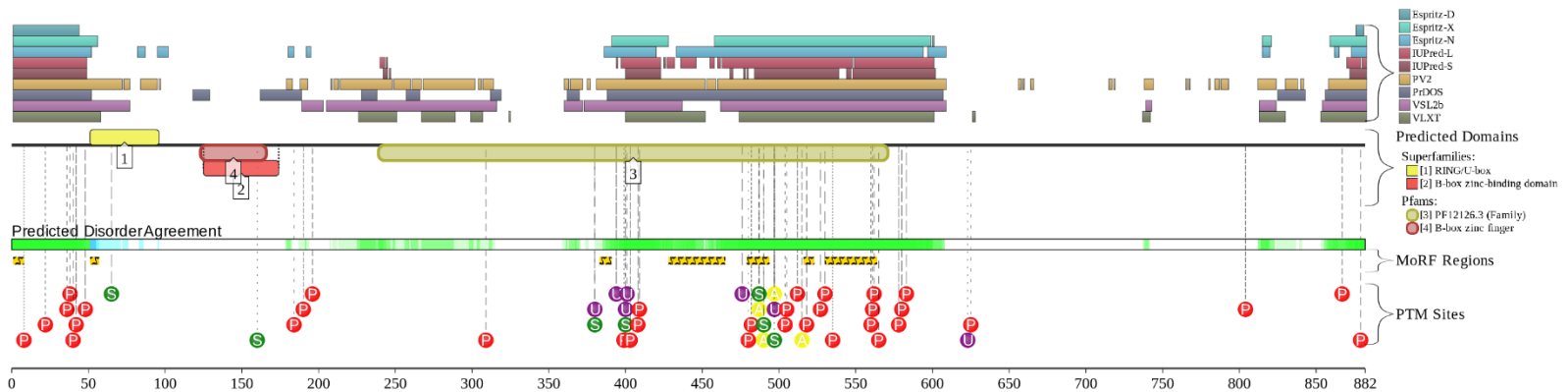
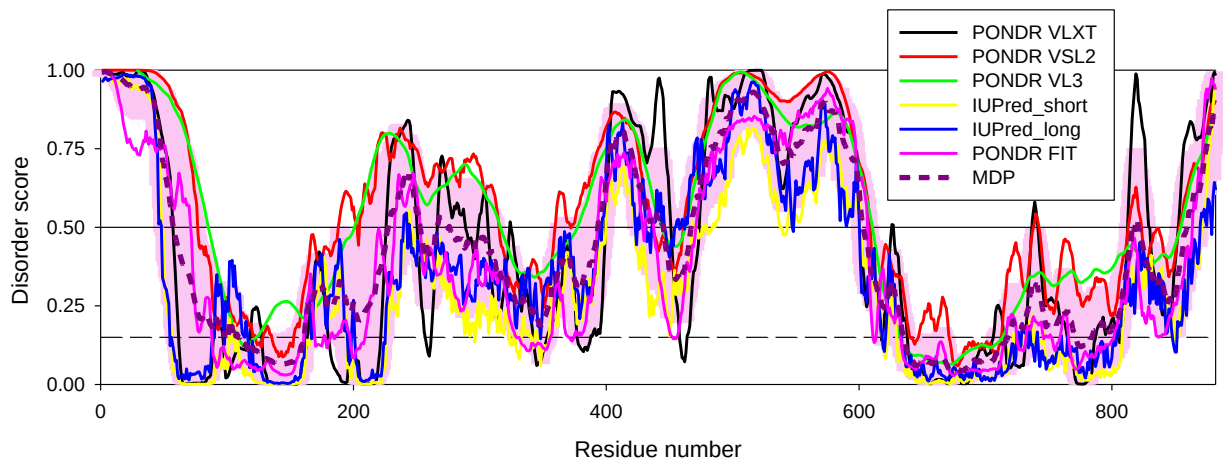


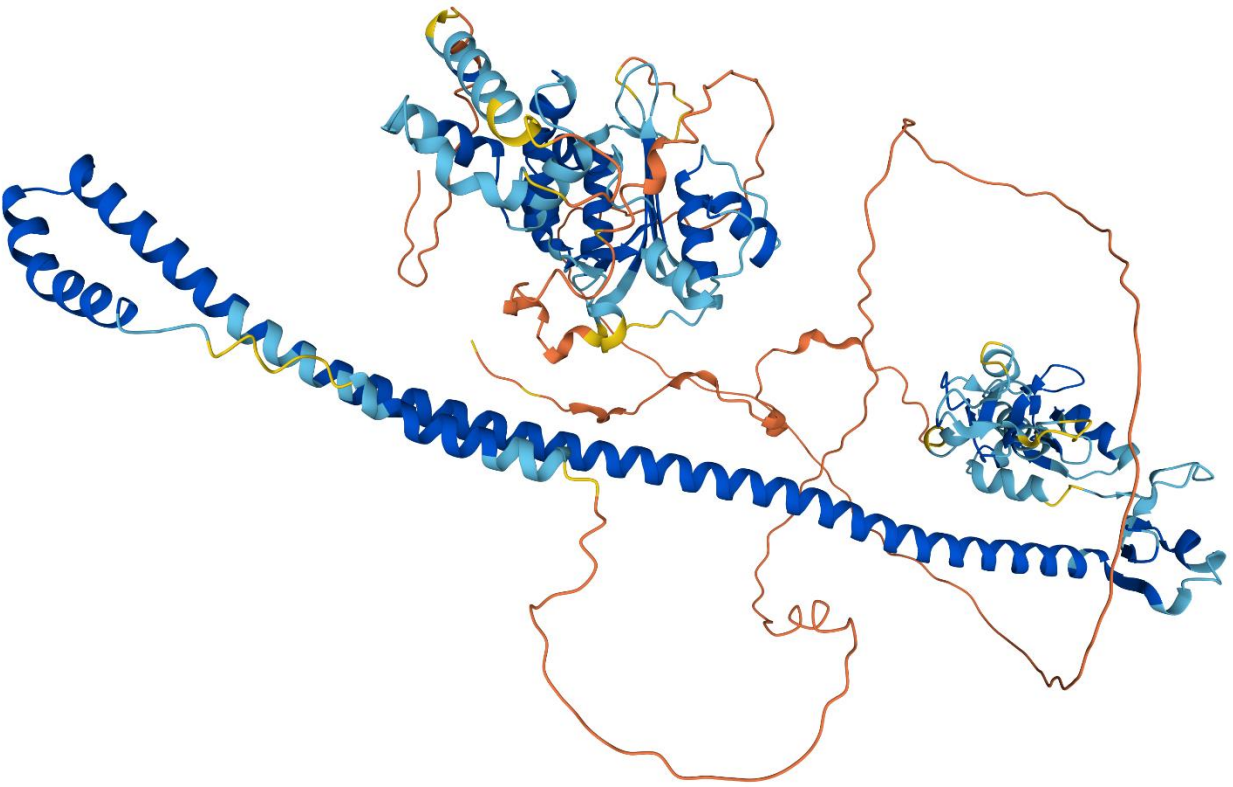


PML protein (UniProt ID: P29590)

>sp|P29590|PML_HUMAN Protein PML OS=Homo sapiens OX=9606 GN=PML PE=1 SV=3

MEPAPARSPRPQQDPARPQEPTMPPPETPSEGRQPSPSPSPTERAPASEEEFQFLRCQQCQ
AEAKCPKLLPCLHTLCSGCLEASGMQCPICQAPWPLGADTPALDNVFFESLQRRLSVYR
QIVDAQAVCTRCKESADFWCFECEQLLCAKCFEAHQWFLKHEARPLAELRNQSVREFL
DGTRKTNNIFCSNPNHRTPTLTISIYCRGCSKPLCCSCALLDSSHSELKCDISAEIQQRQEEL
DAMTQALQEQDSAFGAVHAQMHAAVGQLGRARAETEELIRERVVRQVVAHVRAQEREL
LEAVDARYQRDYEEMASRLGRLDAVLQRIRTGSALVQRMKCYASDQEVLDMHGFLRQ
ALCRLRQEEPQSLQAAVRTDGFDEFKVRLLDLSSCITQGKDAAVSKKASPEAASTPRDPI
DVDLPEEAERVKAQVQALGLAEAQPMMAVVSQVPGAHPVPVYAFSIKGPSYGEDVSNNTT
TAQKRKCSQTQCPRKVIKMESEEGKEARLARSSPEQPRPSTSKAVSPPHLDGPPSPRSPVI
GSEVFLPNSNHVASGAGEAEERVVVISSSESDAENSSSRELDSSSESSDLQLEGPSTLR
VLDENLADPQAEDRPLVFFDLKIDNETQKISQLAAVNRESKFRVVIQPEAFFSIYSKAVSL
EVGLQHFLSFLSSMRRPILACYKLWGPGLPNFFRALEDINRLWEFQEASGFLAALPLIRE
RVPGASSFKLKNLAQTYLARNMSERSAMA AVLAMRDLCLLLEVSPGPQLAQHVYPFSS
LQCFASLQPLVQAAVLPRAEARLLALHNVSFMELLSAHRDRDQGGGLKKYSRYLSLQTT
TLPPAQPAFNLQALGTYFEGLLLEGPALARAEGVSTPLAGRGLAERASQQS

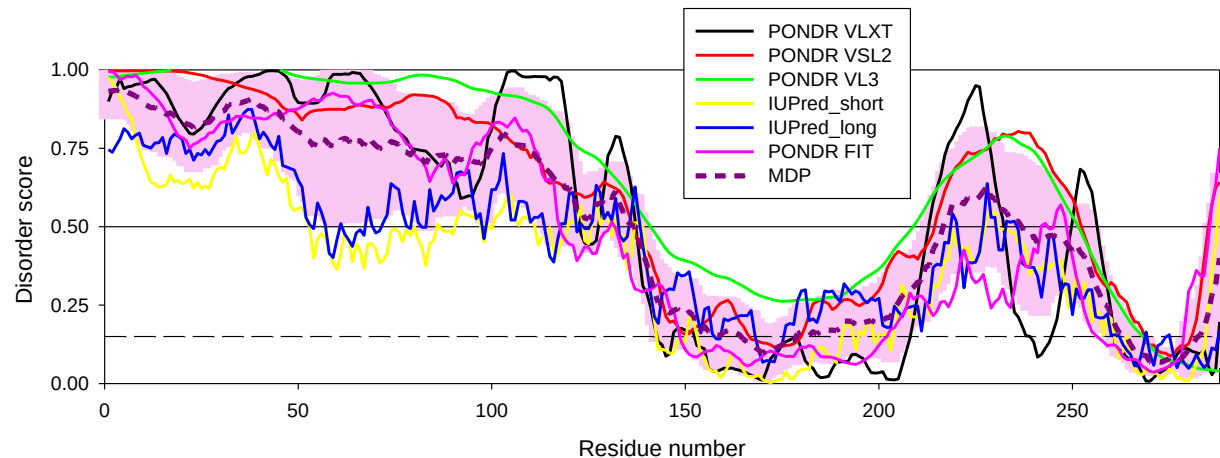


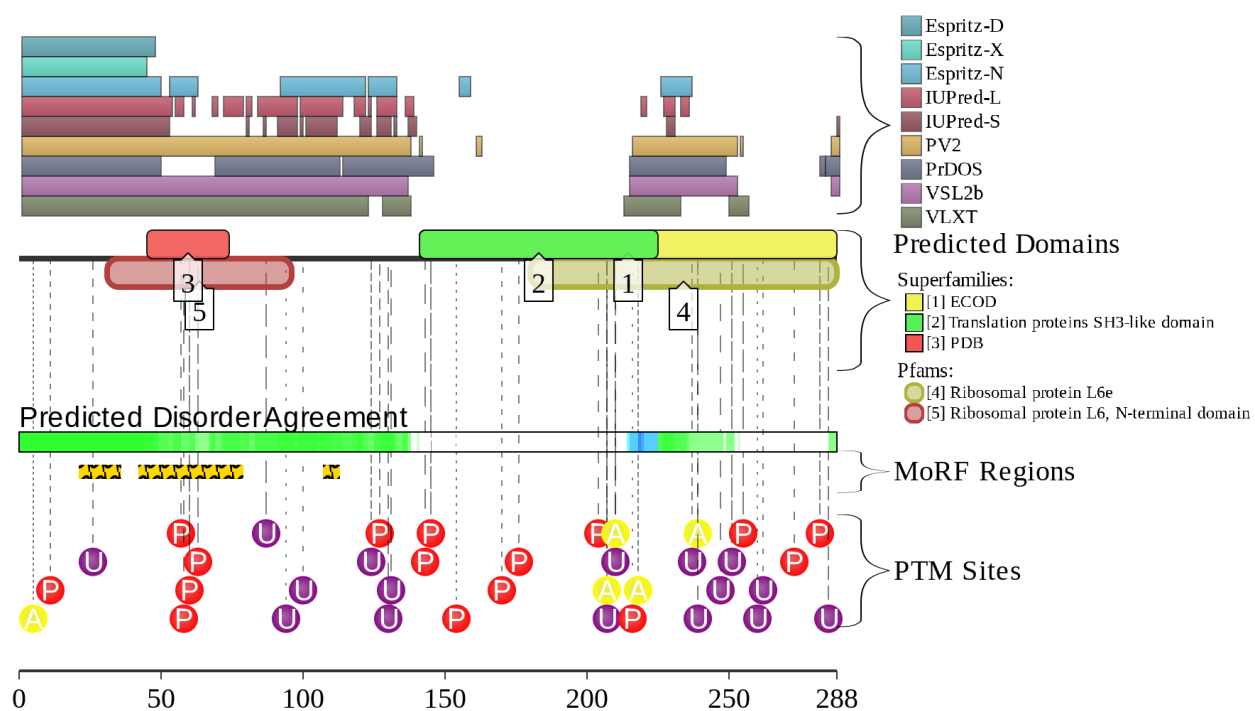


Ribosomal protein L9 (UniProt ID: Q02878)

>sp|Q02878|RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6
PE=1 SV=3

MAGEKVEKPD~~TKEKKPEAKKVDAGGKVKKGNLKA~~KKPKKGKPHCSRN~~PVLVRGIGRY~~
SRSAMYSRKAMYKRKYSAAKSKVEKKKKEKVLATVTKPVGGDKNGGTRVVKLRKMP
RYYPTEDVPRKLLSHGKKPFSQHVRKLRASITPGTILILTGRHRGKRVVFLKQLASGLLL
VTGPLVLNRVPLRRTHQKFVIATSTKIDISNVKIPKHLTDAYFKKKKLRKPRHQEGEIFDT
EKEKYEITEQRKIDQKA~~VDSQILPKIAIPQLQGYLRSVFALTNGIYPHKL~~VF

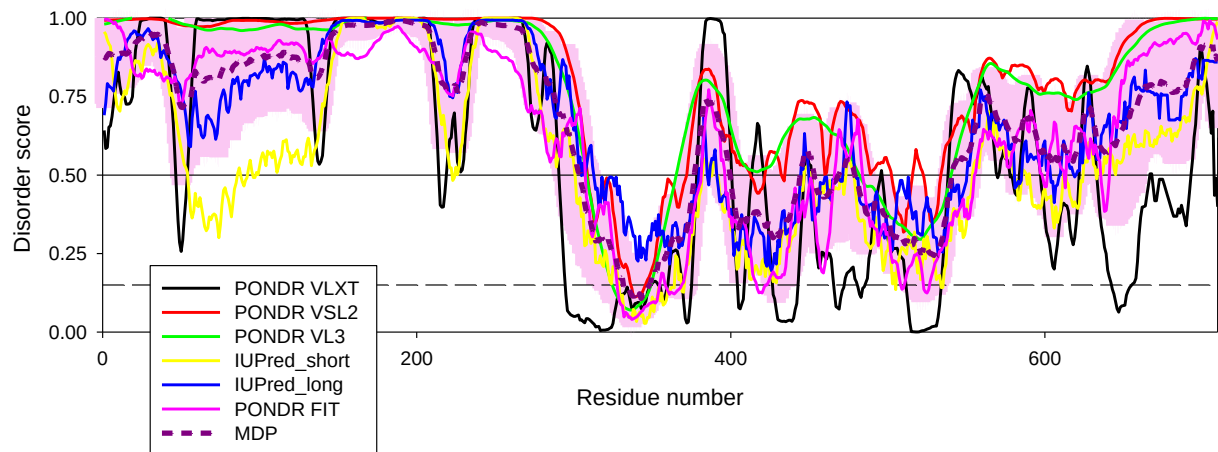


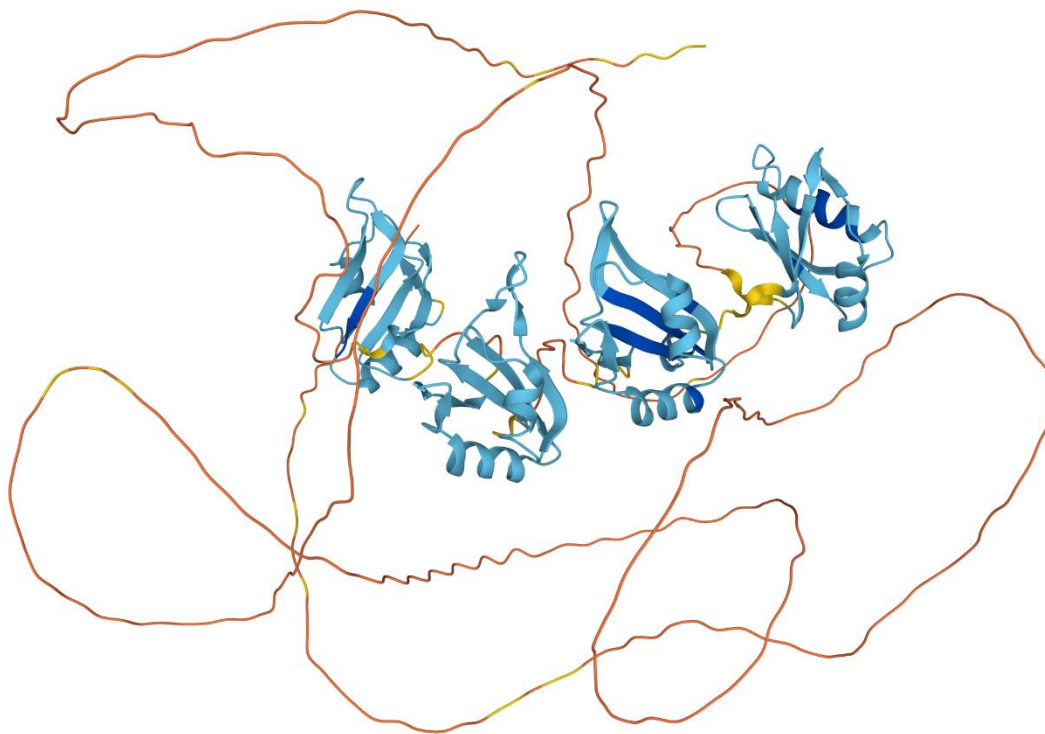
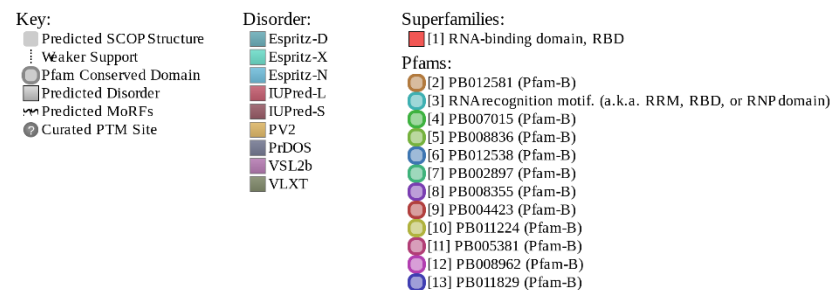
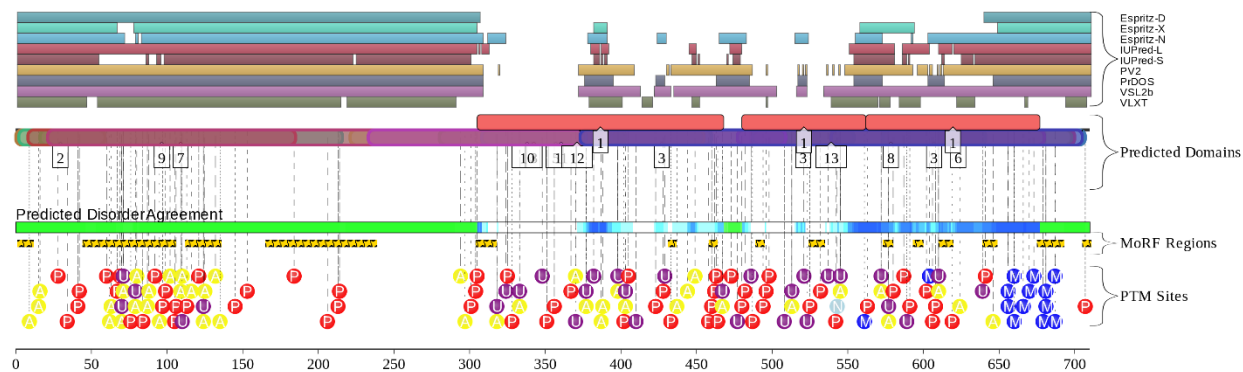


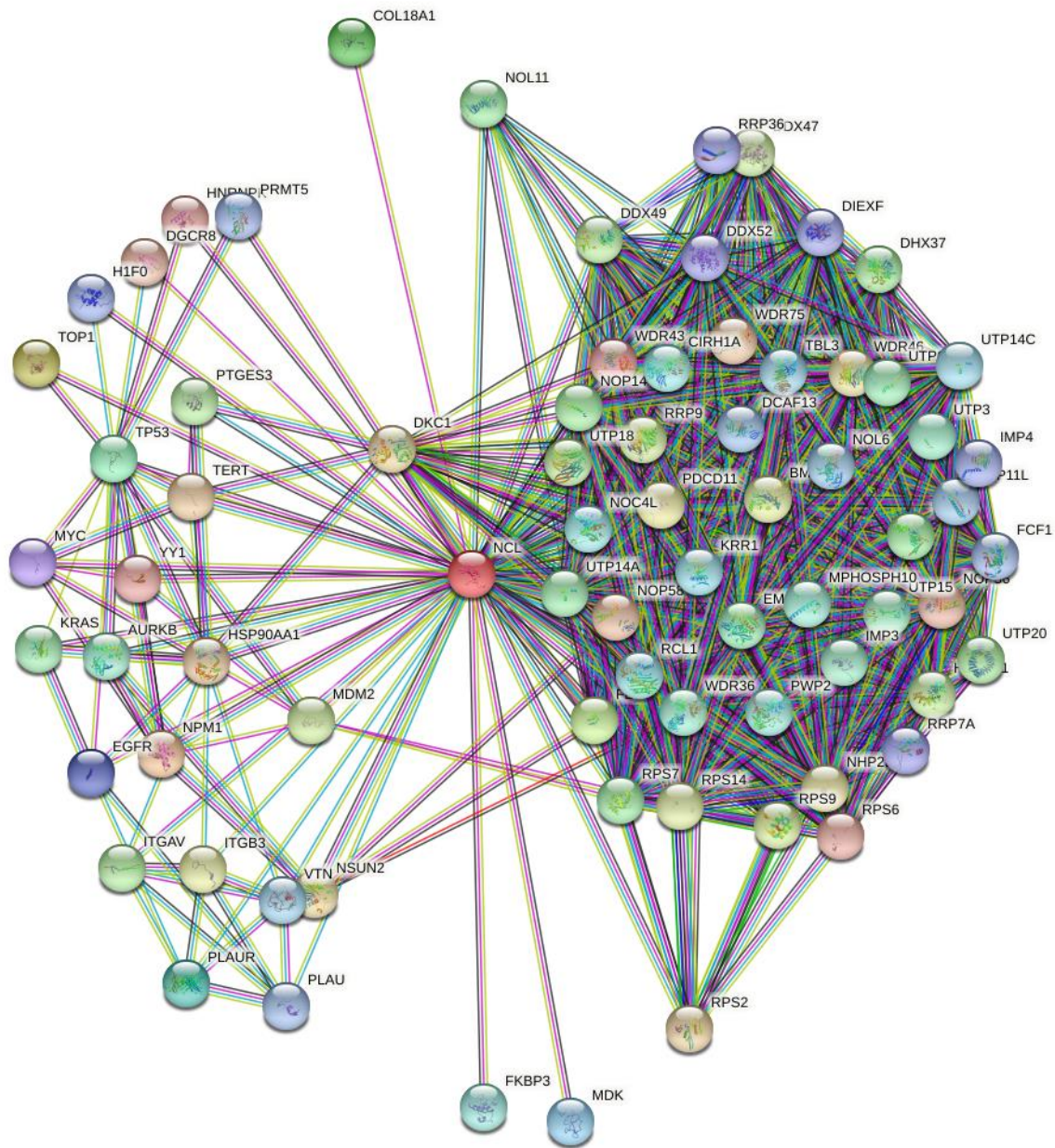
NCL (UniProt ID: P19338)

>sp|P19338|NUCL_HUMAN Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3

MVKLAKAGKNQGDPKKMAPPPKEVEEDSEDEEMSEDEEDDSSGEEVVIPQKKGKKAA
ATSAKKVVVSPTKKVAVATPAKKA AVTPGKKAAATPAKKT VTPAKAVTTPGKKGATP
GKALVATPGKKGAAIPAKGAKNGKNAKKEDSDEEEDDDSEDEEDEDDEDEDEDEIEP
AAMKAAAAAPASEDEDEDDEDDEDDEDDDDDEEDDSEEEAMETTPAKGKKAAKVVPVK
AKNVAEDEDEEEDDEDDEDDEDDDDDEDDEDDEDEEEEEEEEEEPVKEAPGKRKKEMA
KQKAAPEAKKQKVEGTEPTTAFNLFVGNLFNFKSAPELKTGISDVFAKNDLAVVDVRIG
MTRKFGYVDFESAEDLEKALELTGLKVFGNEIKLEKPKGKDSKKERDARTLLAKNLPY
KVTQDELKEVFEDAAEIRLVSKDGKSKGIAYIEFKTEADA EKTFE EKQGTEIDGRSISLYY
TGEKGQNQDYRGGKNSTWSGESKTLVLSNLSYSATEETLQEVFEKATFIKVPQNQNGKS
KGYAFIEFASFEDA KEALNSCNKREIEGRAIRLELQGPRGSPNARSQPSKTLFVKGLSED
TEETLKESFDGSVRARI VTDRETGSSKGFGFVDFNSEEDAKAAKEAMEDGEIDGNKVTL
DWAKPKGEGGFGRGGGRGGFGGRGGGRGGFGGRGGGRGGFGGRGGFRGGRGGG
GDHKPQGKKTKFE







minimum required interaction score: highest confidence (0.900)

number of nodes: 75

number of edges: 1128

average node degree: 30.1

avg. local clustering coefficient: 0.882

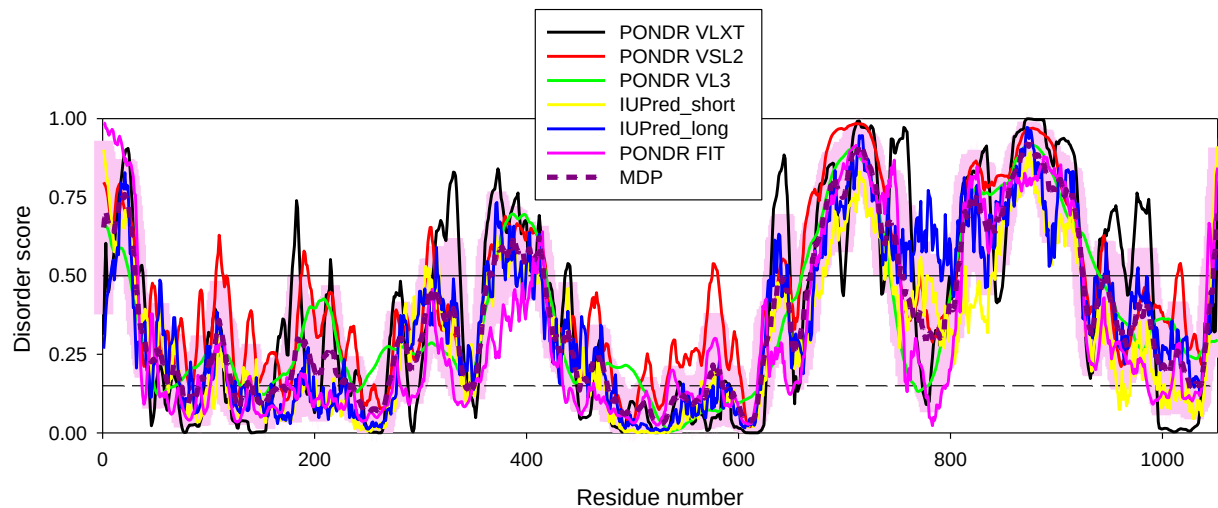
expected number of edges: 200

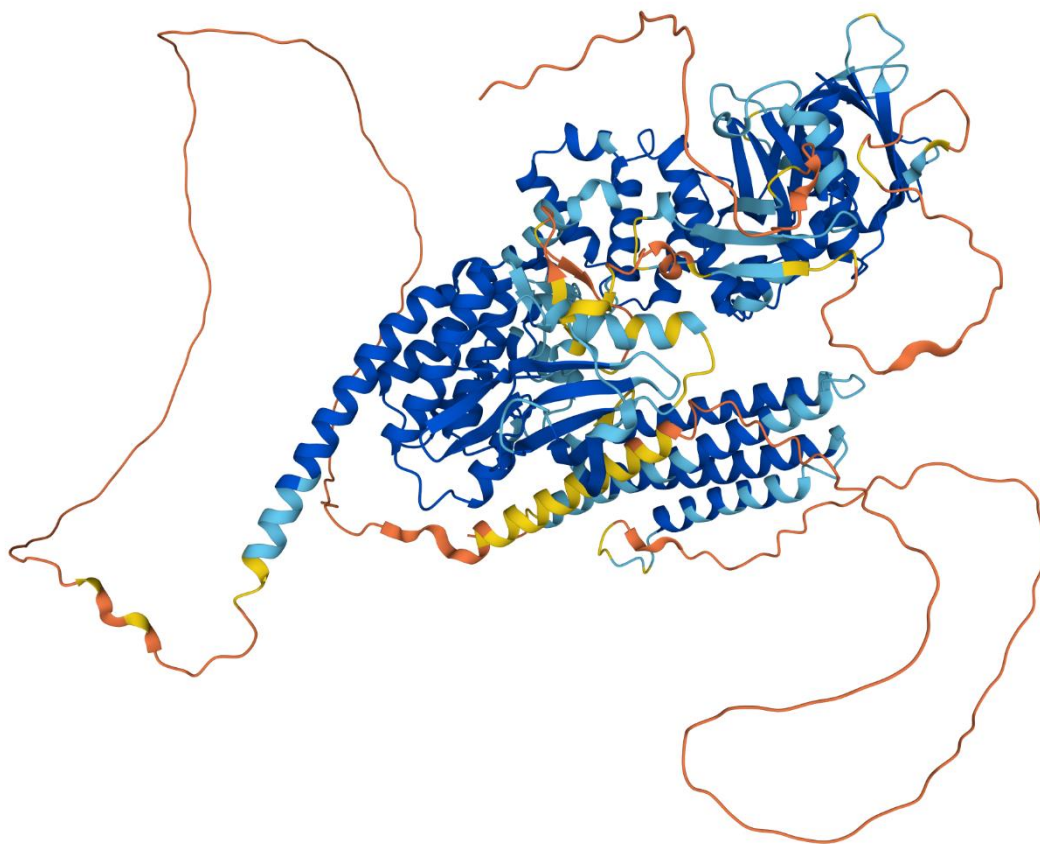
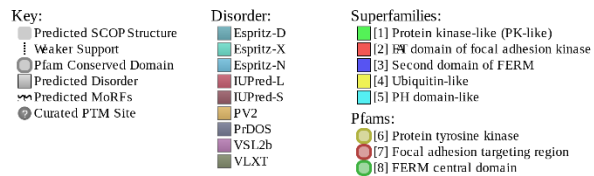
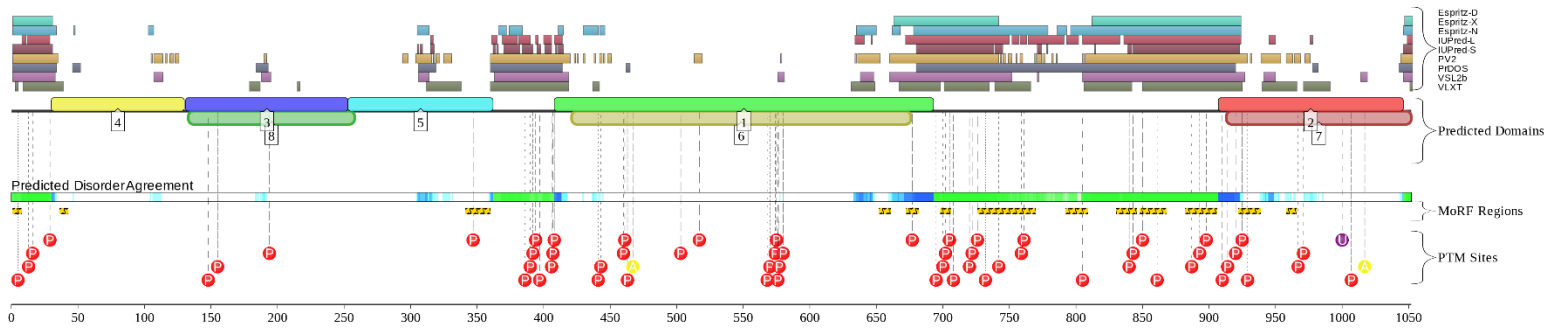
PPI enrichment p-value: $< 1.0e-16$

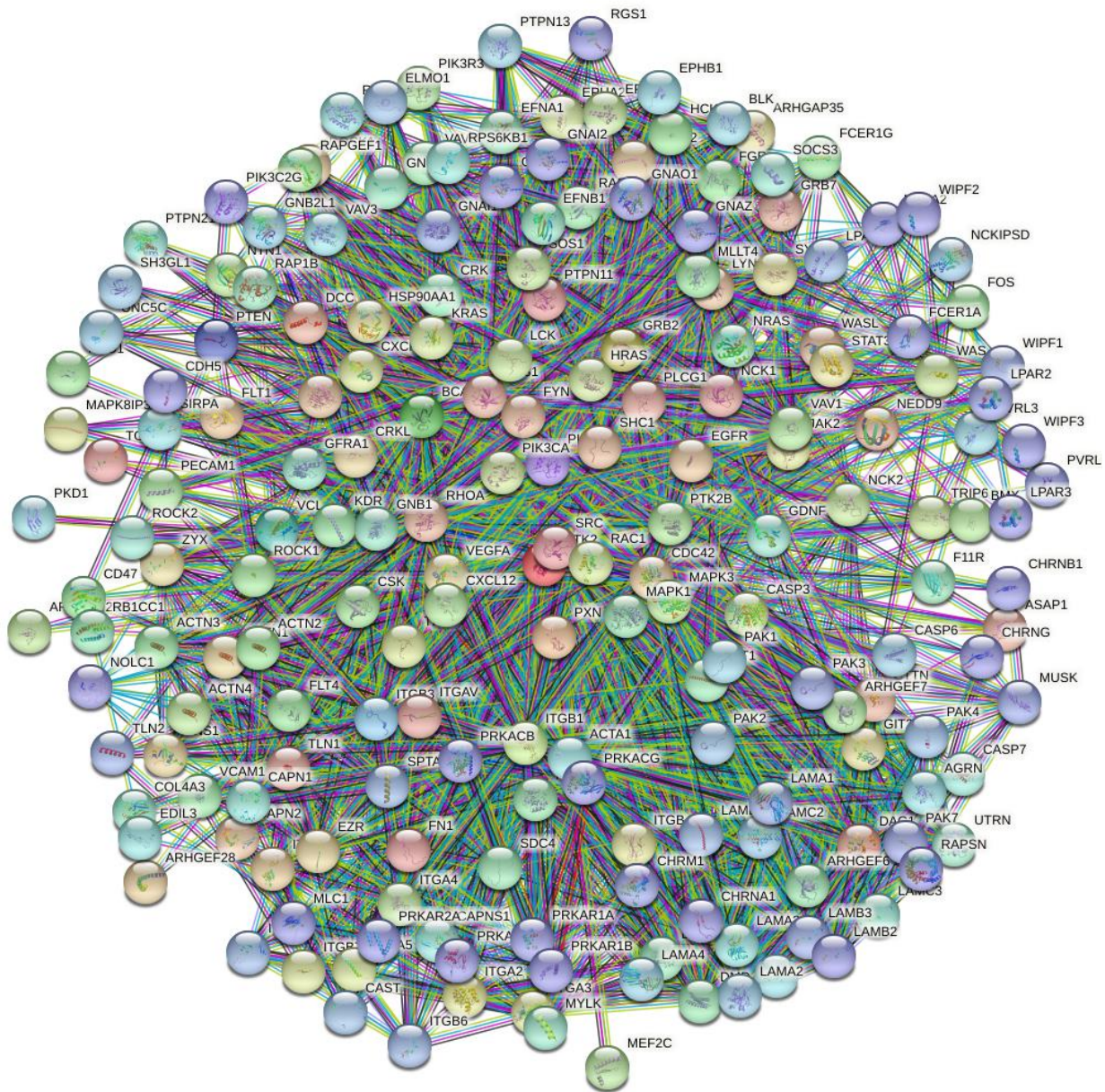
FAK (UniProt ID: Q05397)

>sp|Q05397|FAK1_HUMAN Focal adhesion kinase 1 OS=Homo sapiens OX=9606 GN=PTK2
PE=1 SV=2

MAAAYLDPNLNHTPNSSSTKTHLGTGMERSPGAMERVLKVFHYFESNSEPTTWASIIRHG
DATDVRGIIQKIVDSHKVKHVACYGFRLSHLRSEEVHWLHVDMGVSSVREKYELAHPP
EEWKYELRIRYLPKGFLNQFTEDKPTLNFFYQQVKSDYMLEIADQVDQEIALKLGCLEIR
RSYWEMRGNAL EKKS NYEVLEKDVGLKRFFPKSLLDSVKAKTLRKL IQQTFRQFANLN
REESILKFFEILSPVYRFDKECFKCALGSSWISVELAIGPEEGISYLTDKGCNPTHADFT
QVQTIQYSNSEDKDRKGMLQLKIAGAPEPLTVTAPSLTIAENMADLIDGYCRLVNGTSQ
SFIIRPQKEGERALPSIPKLANSEKQGMRTHAVSVSETDDYAEIIDEEDTYTMPSTRDYEI
QRERIELGRCIGEGQFGDVHQGIYMSPENPALAVA IKTCKNCTSDSVREKFLQEAL TMR
QFDHPPHIVKLIGVITENPVWII MELCTLGELRSFLQVRKYSLDLASLILYAYQLSTALAYL
ESKR FVHRDIAARNVLVSSNDCVKLGDFGLSRYMEDSTYYKASKGKLP IKWMA PESINF
RRFTSASDVWMFGVCMWEILMHGVKPFQGVKNNDVIGRIENGERLPMPPNCPPTLYSL
MTKCWAYDPSRRPRFTELKAQLSTILEEEKAQQEERM RMESRRQATVSWDSGGSDEAP
PKPSRPGYPSPRSSEGFYPSQHMVQTNHYQVSGYPGSHGITAMAGSIYPGQASLLDQTD
SWNHRPQEIAMWQPNVEDSTVLDLRGIGQVLP THLMEERLIRQQQEMEEDQRWLEKEE
RFLKPDVRLSRGSIDREDGSLQGPIGNQHIYQPVGKPDPAAPPKKPPRPGAPGHLGLSLAS
LSSPADSYNEGVKLQPQEISPPPTANLDRSNDKVYENV TGLVKAVIEMSSKIQPAPPEEY
VPMVKEVGLALRTL LATVDETIPLLPASTHREIEMAQKLLNSDLGELINKMKLAQQYVM
TSLQQEYKKQMLTAAHALAVDAKNLLDVIDQARLKMLGQTRPH







minimum required interaction score: highest confidence (0.900)

number of nodes: 196

number of edges: 2816

average node degree: 28.7

avg. local clustering coefficient: 0.676

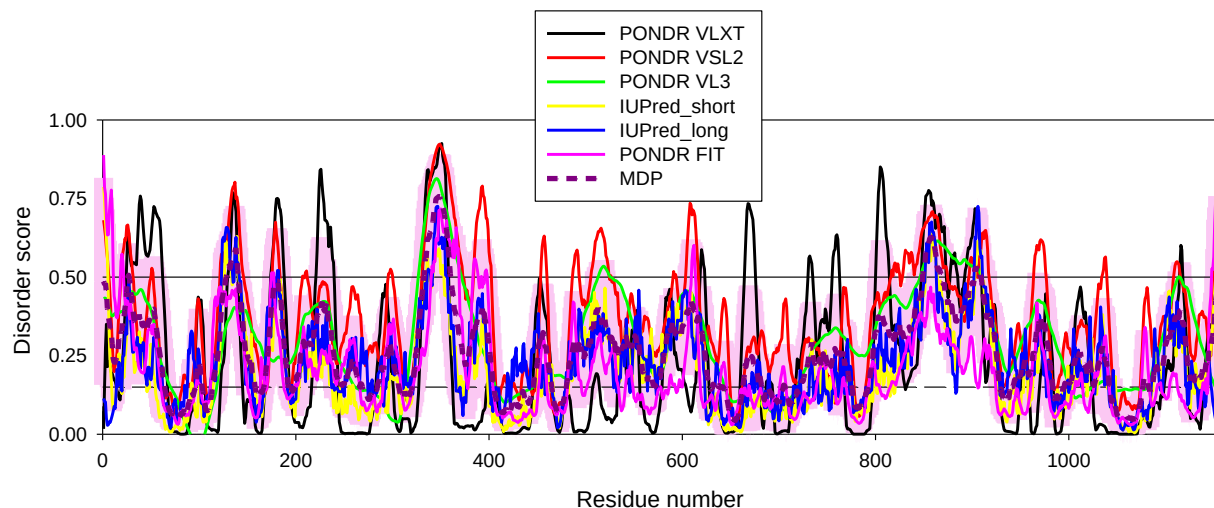
expected number of edges: 664

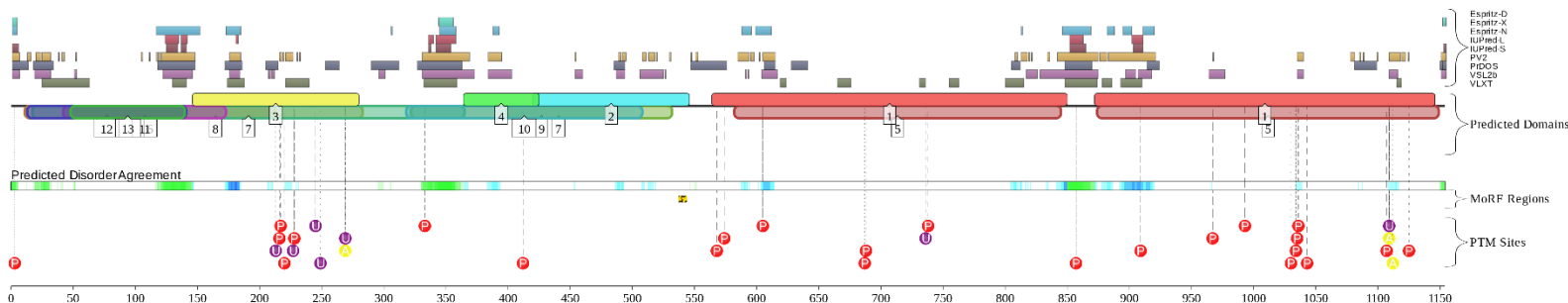
PPI enrichment p-value: $< 1.0e-16$

JAK1 (UniProt ID: P23458)

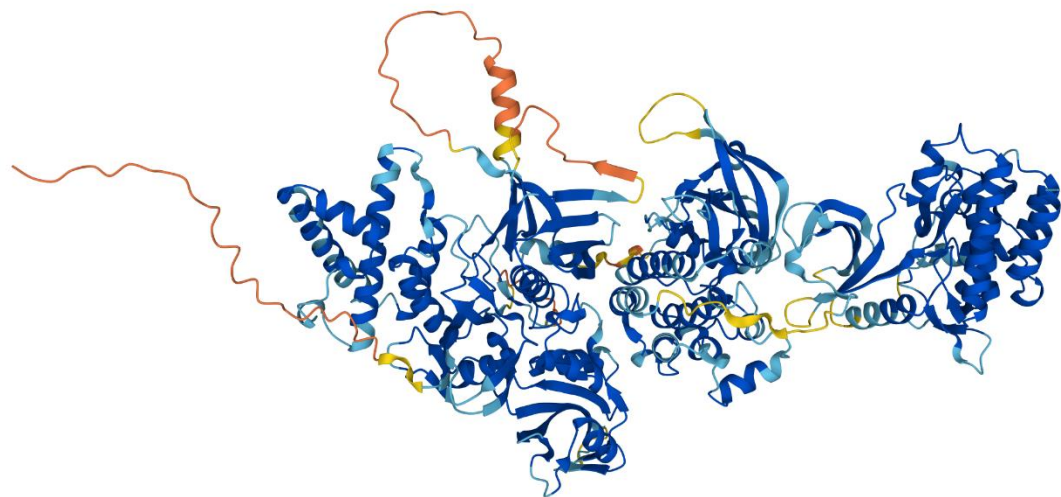
>sp|P23458|JAK1_HUMAN Tyrosine-protein kinase JAK1 OS=Homo sapiens OX=9606
GN=JAK1 PE=1 SV=2

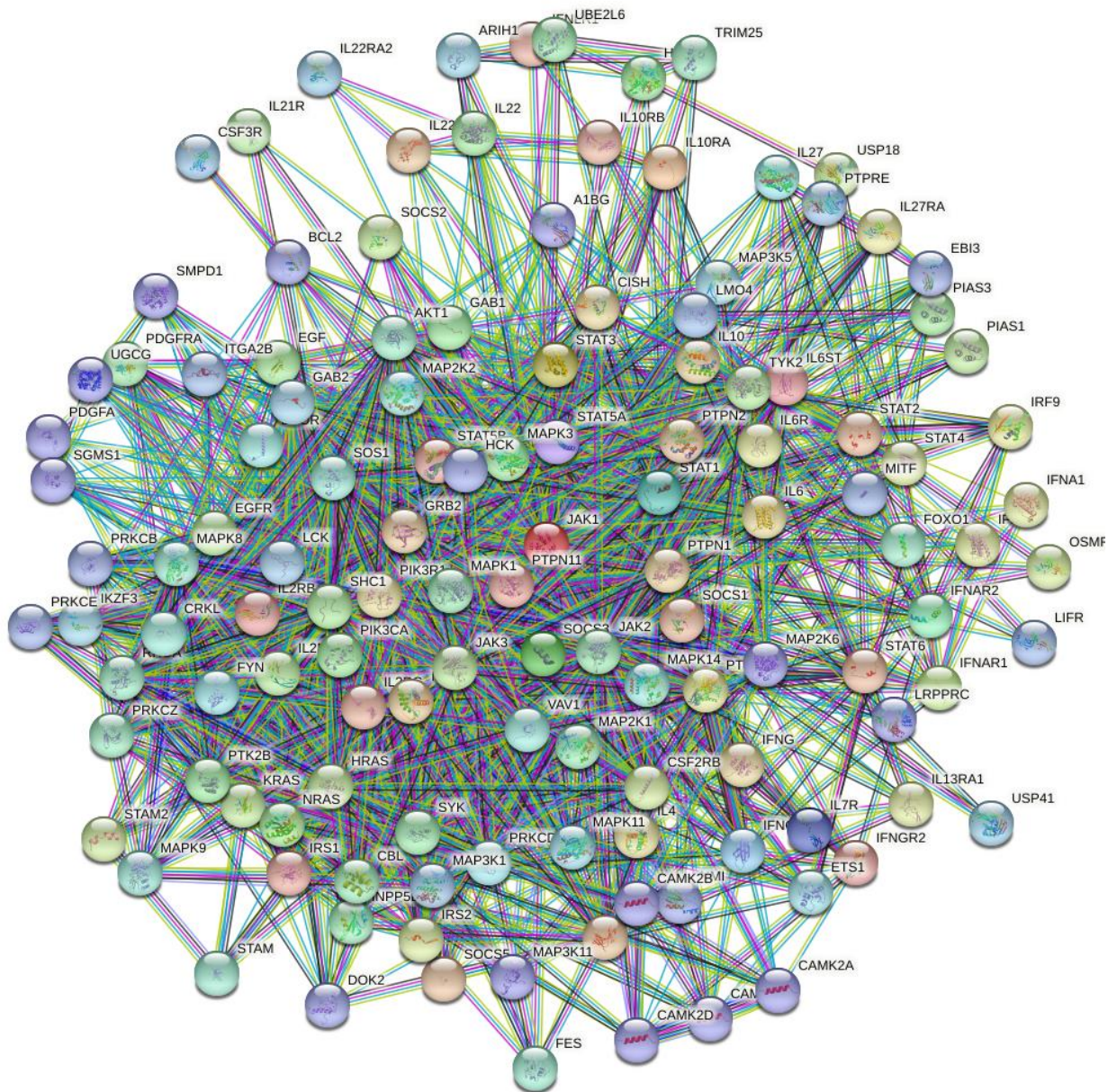
MQYLNIEDCNAMAFCAKMRSSKKTEVNLEAPEPGVEVIFYLSDREPLRLGSGEYTAEE
LCIRAAQACRISPLCHNLFALYDENTKLWYAPNRTITVDDKMSLRLHYRMRFYFTNWH
GTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQGQYDLVKCLAPIRD
PKTEQDGHDIENECLGMAVLAISHYAMMKKMQLPELPKDISYKRYIPETLNKSIRQRNL
LTRMRINNFKDFLKEFNNTICDSSVSTHDLKVLYLATLETTLTKHYGAEIFETSMLLISS
ENEMNWFHSNDGGNVLYYEVMVTGNLGIQWRHKPNVVSVEKEKNKLKRKKLENKHK
KDEEKNKIREEWN NFSYFPEITHIVIKESVVSINKQDNKKMELKLSSHEEALS FVSLVDG
YFRLTADAHHYLCTDVAPPLIVHNIQNGCHGPICTEYAINKLRQEGSEEGMYVLRWSCT
DFDNILMTVTCFEKSEQVQGAQKQFKNFQIEVQKGRYSLHGSDRSFPSLGLMSHLKKQ
ILRTDNISFMLKRCCQPKPREISNLLVATKKAQEWQPVYPMSQLSFDRILKKDLVQGEHL
GRGTRTHIYSGTLM DYKDDEGTSEEKKIKVILKVLDPSHRDISLAFFEAASMMRQVSHK
HIVLYYGVCVRDVENIMVEEFVEGGPLDLFMHRKSDVLTTPWKFKVAKQLASALSYLE
DKDLVHGNVCTKNLLLAREGIDSECGPFIKLSDPGIPITVLSRQECIERIPWIAPECVEDSK
NLSVAADKWSFGTTLWEICYNGEIPLKDKTLIEKERFYESRCRPVTPSCKELADLMTRC
MNYDPNQRPFFRAIMRDINKLEEQNPDIVSEKKPATEVDP THFEKRFLKRIRDLGEGHFG
KVELCRYDPEGDNTGEQVAVKSLKPESGGNHIADLKKEIEILRNLYHENIVKYKGICTED
GGNGIKLIMEFLPSGSLKEYLPKNKNKINLKQQLKYAVQICKGMDYLGSRQYVHRDLA
ARNVLVESEHQVKIGDFGLTKAIETDKEYYTVKDDRDSPVFWYAPECLMQSKFYIASDV
WSFGVTLLHELLTYCSDSSPMALFLKMIGPTHGQMTVTRLVNTLKEGKRLPCPPNCPDE
VYQLMRKCWEFQPSNRTSFQNLIEGF EALLK





- Key:**
- Predicted SCOP Structure
 - Weak 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)
 - [2] SH2 domain
 - [3] Second domain of FERM
 - [4] PH domain-like
- Pfams:**
- [5] Protein tyrosine kinase
 - [6] PB012686 (Pfam-B)
 - [7] PB004056 (Pfam-B)
 - [8] PB004639 (Pfam-B)
 - [9] PB000991 (Pfam-B)
 - [10] PB001288 (Pfam-B)
 - [11] PB015196 (Pfam-B)
 - [12] PB002501 (Pfam-B)
 - [13] PB005821 (Pfam-B)





minimum required interaction score: highest confidence (0.900)

number of nodes: 128

number of edges: 1555

average node degree: 24.3

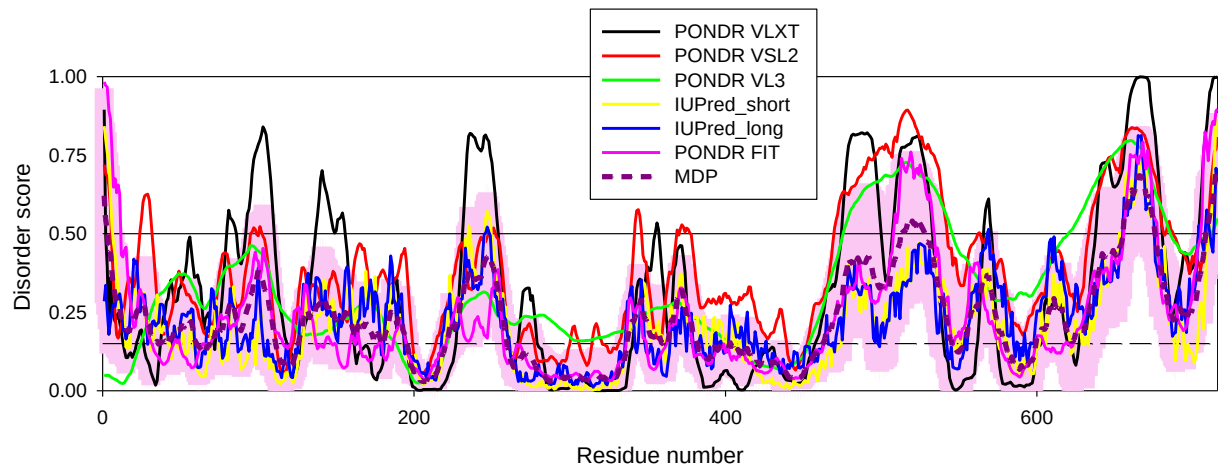
avg. local clustering coefficient: 0.668

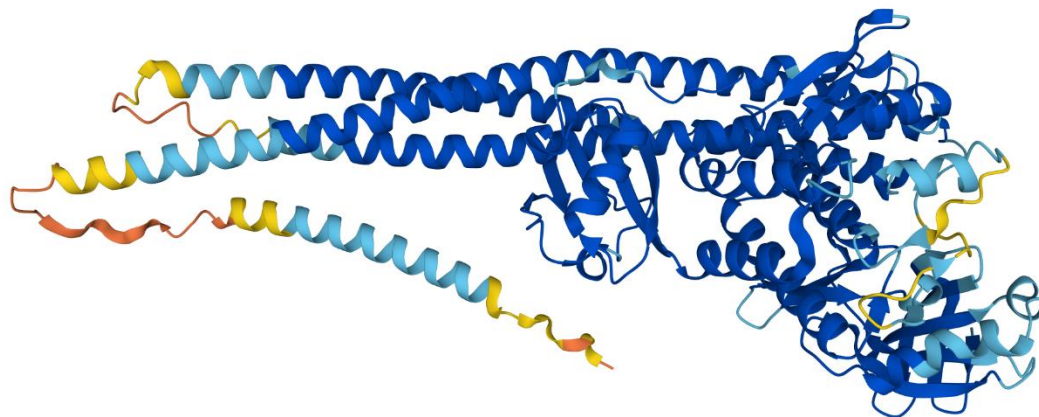
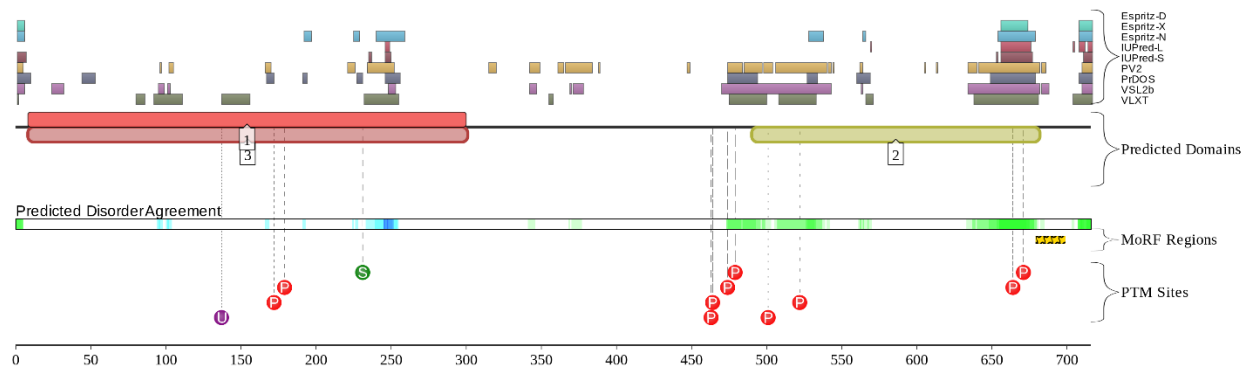
expected number of edges: 333

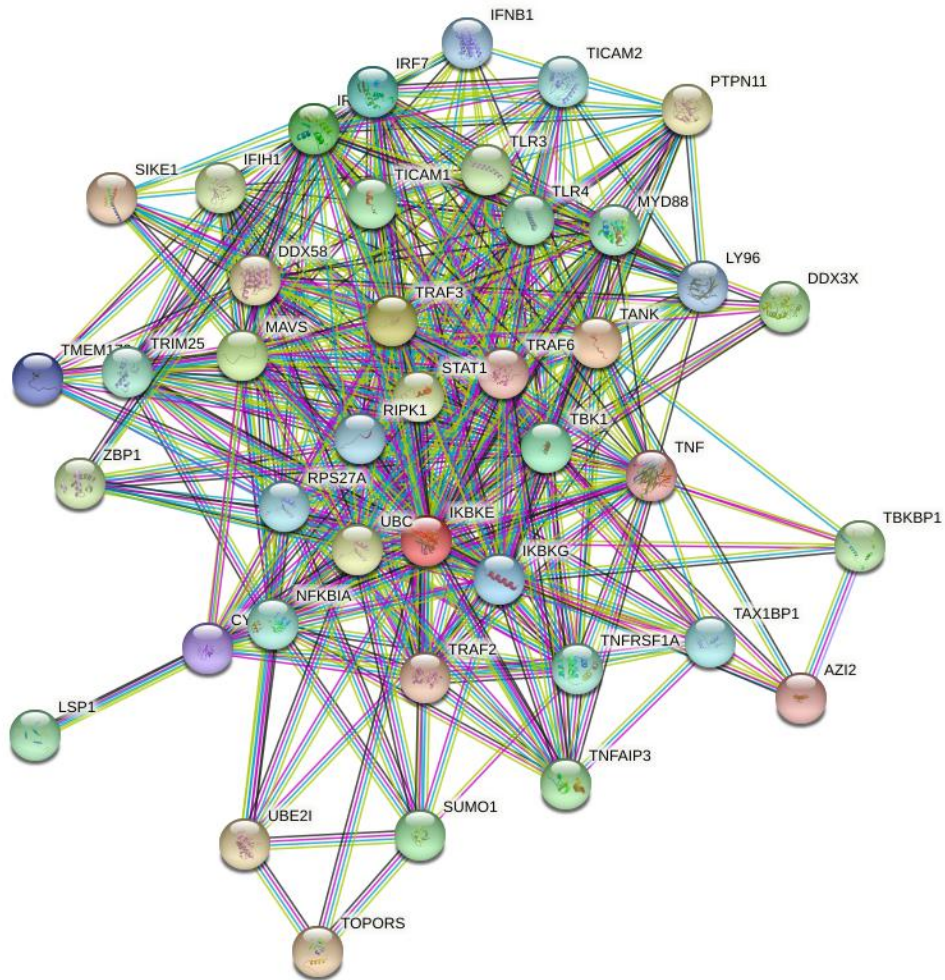
PPI enrichment p-value: $< 1.0e-16$

>sp|Q14164|IKKE_HUMAN Inhibitor of nuclear factor kappa-B kinase subunit epsilon
OS=Homo sapiens OX=9606 GN=IKBKE PE=1 SV=1

MQSTANYLWHTDDLLGQGATASVYKARNKKSSELVAVKVFNNTTSYLRPREVQVREFE
VLRKLNHQNIVKLF AVEETGGS RQKVLVMEYCSSGSLLSVLESPENAFGLPEDEFLVVL
RCVVAGMNHLENGIVHRDIKPGNIMRLVGEEGQSIYKLTDFGAARELDDDEKFVSVY
GTEEYLHPDMYERAVLRKPQKAFGVTVDLWSIGVTLYHAATGSLPFIPFGGPRRNKEI
MYRITTEKPAGAIAGAQRRENGPLEWSYTLPTCQLSLGLQSQLVPILANILEVEQAKCW
GFDQFFAETSDILQRVVVHVFSLSQAVLHHIYIHAHNTIAIFQEAVHKQTSVAPRHQEYL
FEGHLCVLEPSVSAQHIAHTTASSPLTLFSTAIPKGLAFRDPALDVPKFVPKVDLQADYN
TAKGVLGAGYQALRLARALLDGQELMFRGLHWVMEVLQATCRRTLEVARTSLLYLSS
SLGTERFSSVAGTPEIQELKAAAE LRSRLRTLAEVLSRCSQNITETQESLSSLNREL VKSR
DQVHEDRSIQQIQCCLDKMNFYKQFKKSRMRPGLGYNEEQIHKLDKVNFSHLAKRLLQ
VFQEECVQKYQASLVTHGKRMRVVHETRNHLRLVGCSVAACNTEAQGVQESLSKLL
ELSHQLLQDRAKGAQASPPPIAPYPSPTRKDLLLHMQELCEGMKLLASDLLDNNRIIERL
NRVPAPPDV







minimum required interaction score: high confidence (0.700)

number of nodes: 41

number of edges: 380

average node degree: 18.5

avg. local clustering coefficient: 0.769

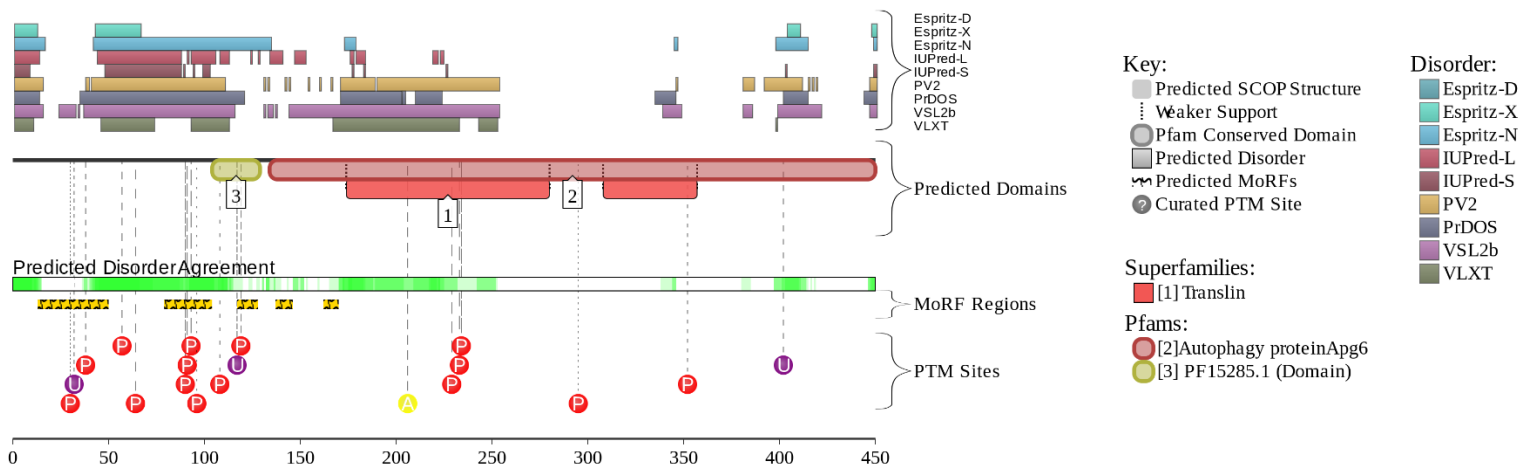
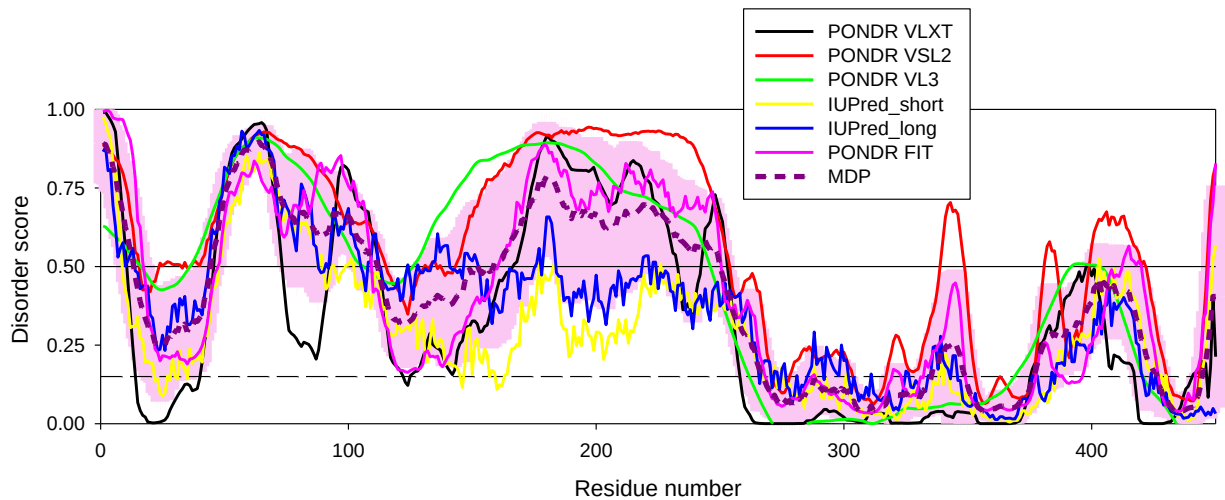
expected number of edges: 70

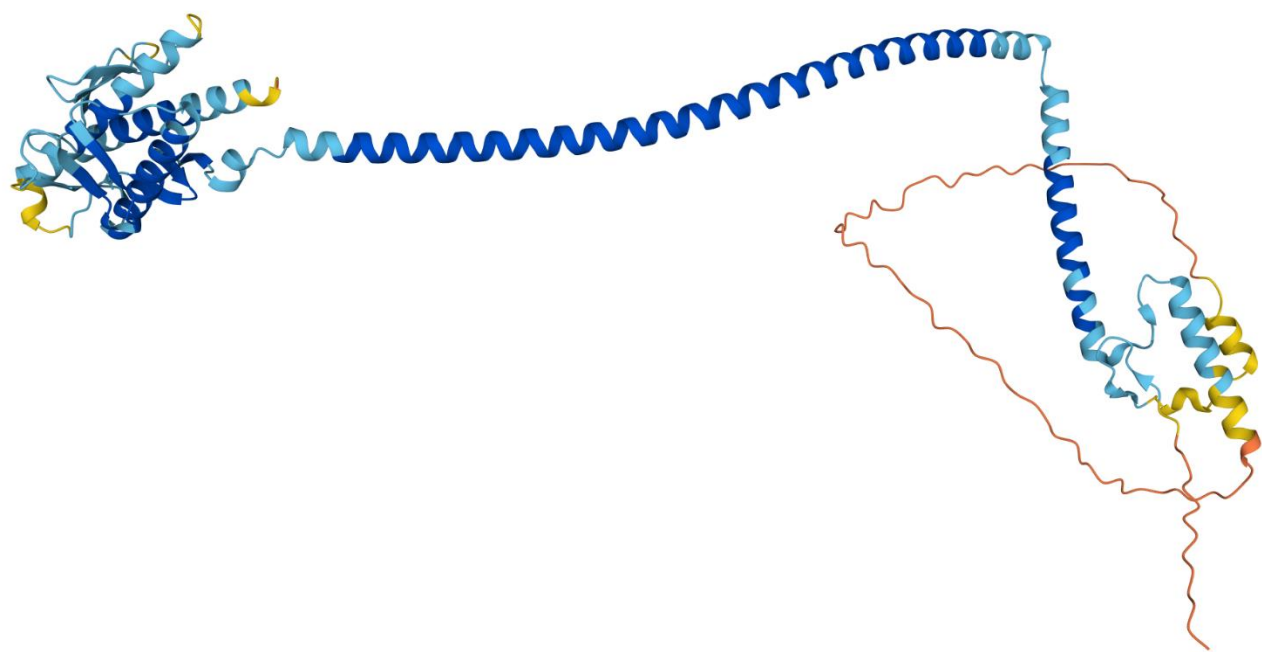
PPI enrichment p-value: $< 1.0e-16$

BECN1 (UniProt ID: Q14457)

>sp|Q14457|BECN1_HUMAN Beclin-1 OS=Homo sapiens OX=9606 GN=BECN1 PE=1 SV=2

MEGSKTSNNSTMQVSFVCQRCSQPLKLDTSFKILDRVTIQELTAPLLTTAQAQKPGETQEE
ETNSGEEPFIETPRQDGVSRRFIPPARMMSTESANSFTLIGEASDGGTMENLSRRLKVTGD
LFDIMSGQTDVDHPLCEECDTLLDQLDTQLNVTENECQNYKRCLEILEQMNEDDSEQL
QMELKELALEEERLIQELEDVEKNRKIVAENLEKVQAEAEERLDQEAAQYQREYSEFKRQ
QLELDDELKSVENQMRYAQTQLDKLKKTNVFNATFHIWHSGQFGTINNFRLGRLPSVPV
EWNEINAAWGQTVLLHALLANKMGLKFQRYRLVPYGNHSYLESLTDKSKELPLYCSGG
LRFWDNKFHAMVAFLDCVQQFKEEVEKGETRFCLPYRMDVEKGKIEDTGGSGGSYS
IKTQFNSEEQWTKALKFMLTNLKWGLAWVSSQFYNK

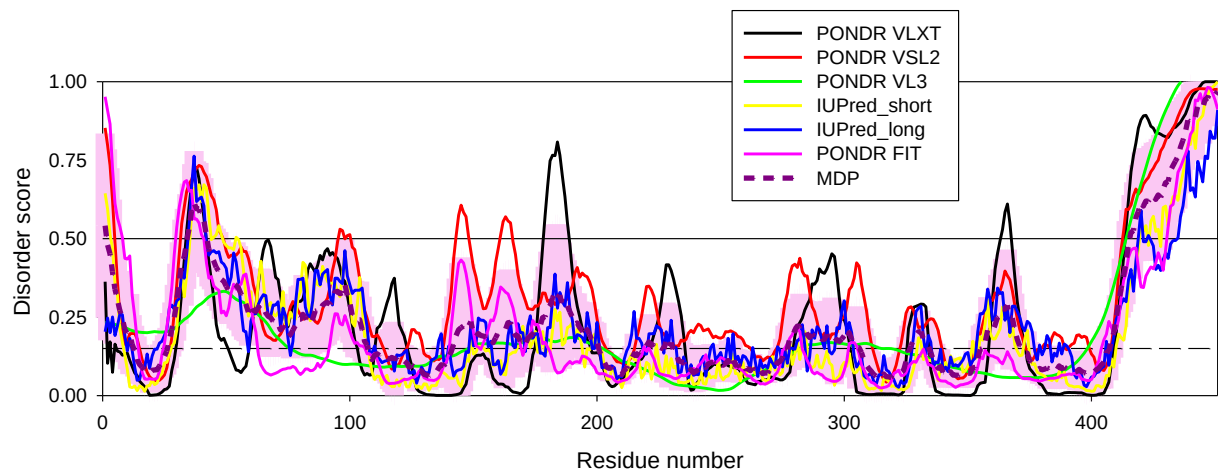


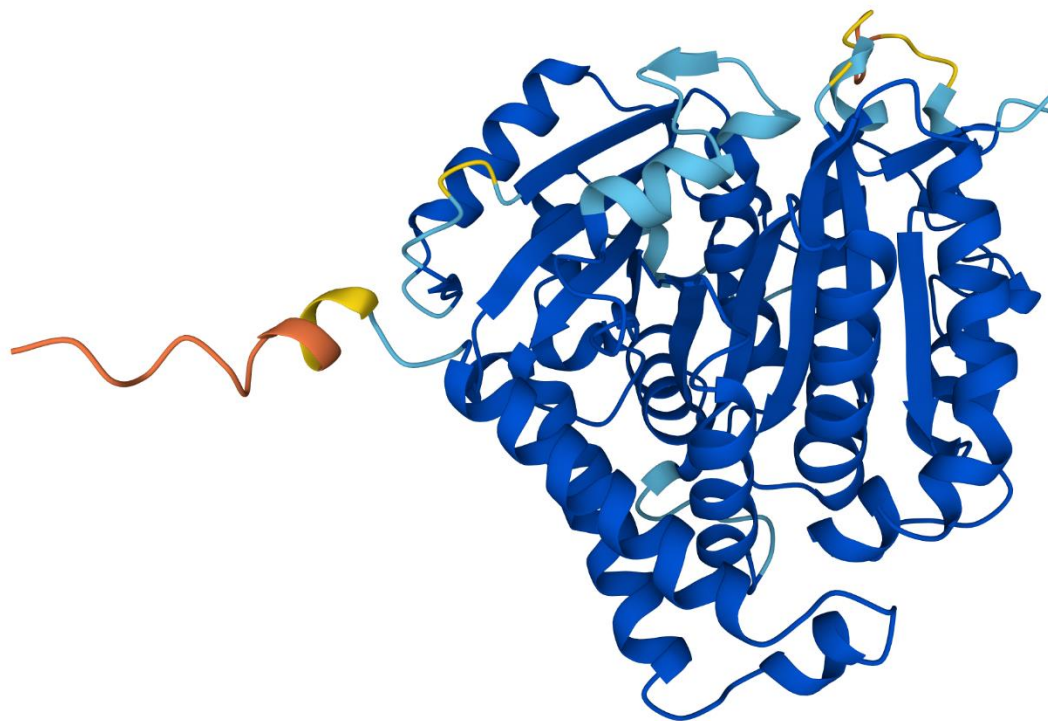
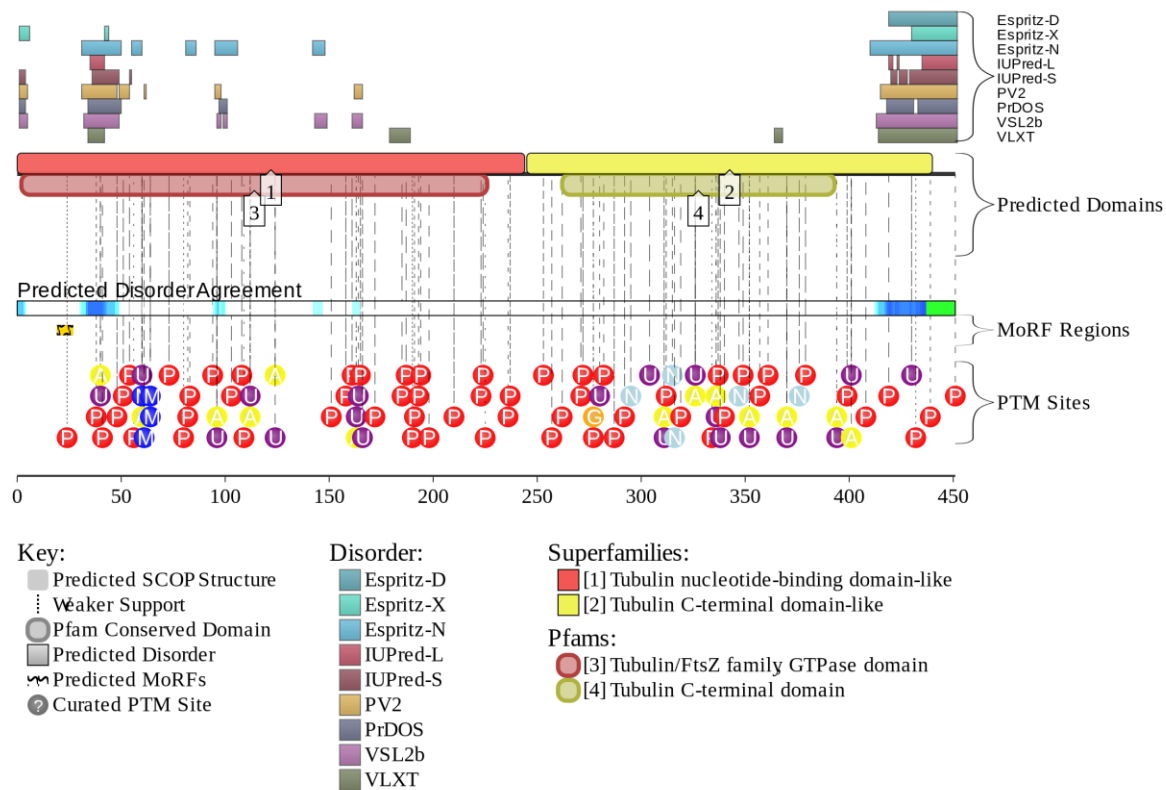


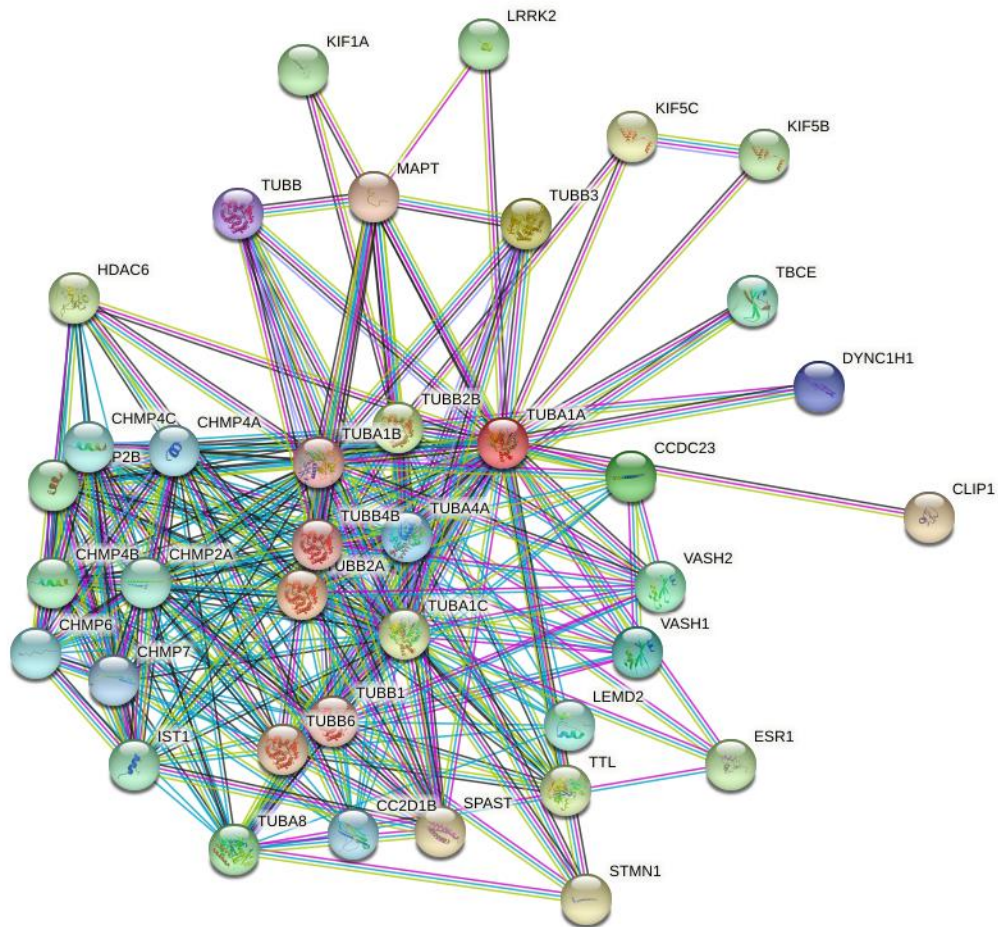
TUB- α (UniProt ID: Q71U36)

>sp|Q71U36|TBA1A_HUMAN Tubulin alpha-1A chain OS=Homo sapiens OX=9606
GN=TUBA1A PE=1 SV=1

MRECISIHVGQAGVQIGNACWELYLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAG
KHVPRAVFVDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVL
DIRKCLADQCTGLQGFLVFHSFGGGTSGSGFTSLLMERLSVDYGGKSKLEFSIYPAPQVST
AVVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLLIGQIVSSITAS
LRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISA EKAYHEQLSVAEITNACFEPANQ
MVKCDPRHGKYM ACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQP
PTVVPGGDLAKVQRAVCMLSNTTAIAEAWARLDHKFDL MYAKRA FVHWYVGEGMEE
GEFSEAREDMAALEKDYEEVGVD SVEGE GEEEGEEY







minimum required interaction score: highest confidence (0.900)

number of nodes: 38

number of edges: 254

average node degree: 13.4

avg. local clustering coefficient: 0.755

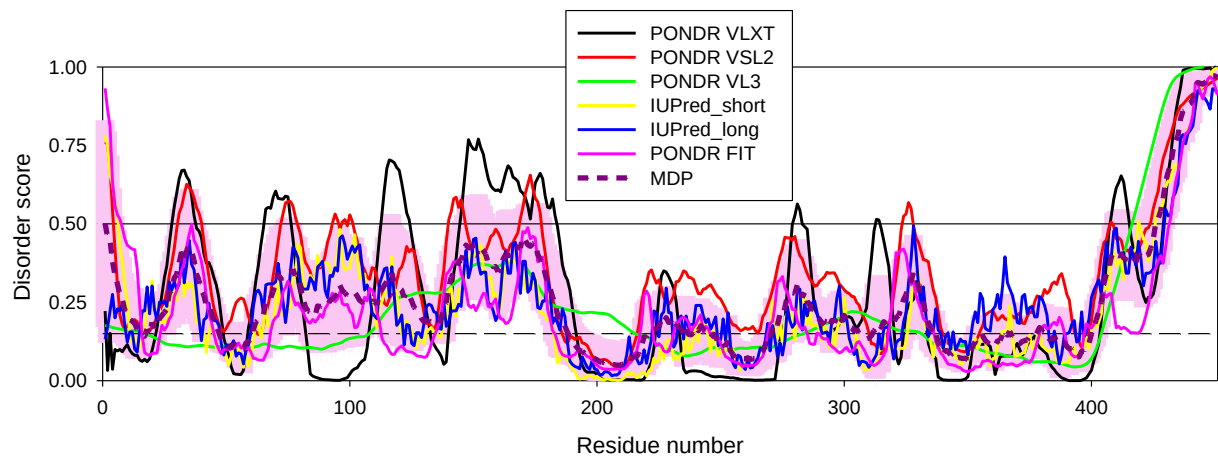
expected number of edges: 40

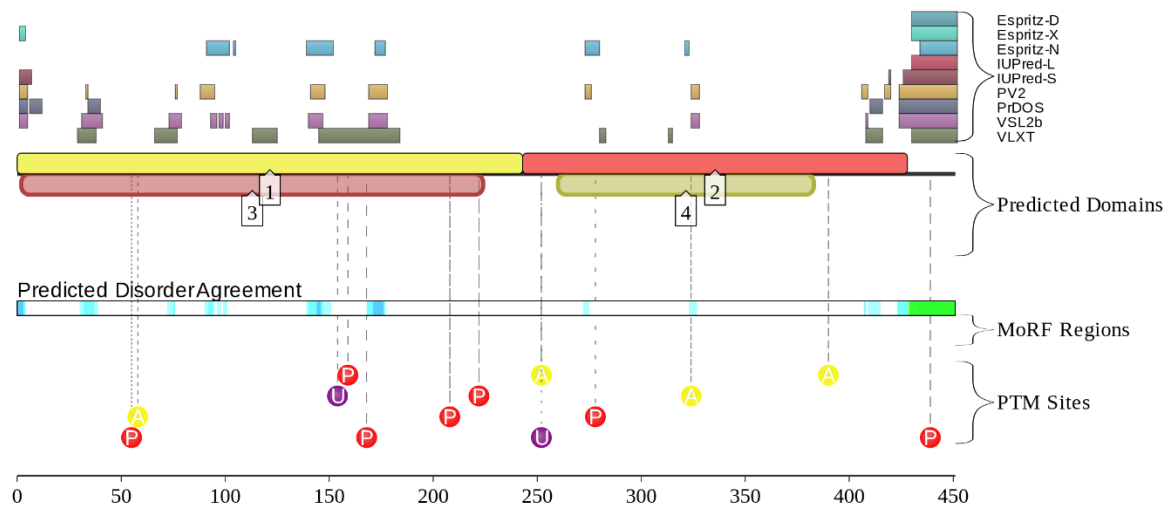
PPI enrichment p-value: $< 1.0e-16$

TUB- β (UniProt ID: Q9H4B7)

>sp|Q9H4B7|TBB1_HUMAN Tubulin beta-1 chain OS=Homo sapiens OX=9606 GN=TUBB1
PE=1 SV=1

MREIVHIQIGQCGNQIGAKFWEMIGEEHGIDLAGSDRGASALQLERISVYYNEAYGRKY
VPRAVLVDLEPGTMDSIRSSKLGALFQPDFVHGNSGAGNNWAKGHYTEGAELIENVL
EVVRHESESCDCLQGFQIVHSLGGGTGSGMGTLTMNKIREEYPDRIMNSFSVMPSPKVS
DTVVEPYNAVLSIHQLIENADACFCIDNEALYDICFRTLKLTPTTYGDLNHLVSLTMSGIT
TSLRFPGQLNADLRKLA VNMVFPRLHFFMPGFAPLTAQGSQQYRALSVAELTQQMFD
ARNTMAACDLRRGRYLTVACIFRGKMSTKEVDQQLSVQTRNSSCFVEWIPNNVKVAV
CDIPPRGLSMAATFIGNNTAIQEIFNRVSEHFSAMFKRKA FVHWYTSEGMDINEFGEAEN
NIHDLVSEYQQFQDAKAVLEEDEEVTEEAEMEPEDKGH





Key:

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

Disorder:

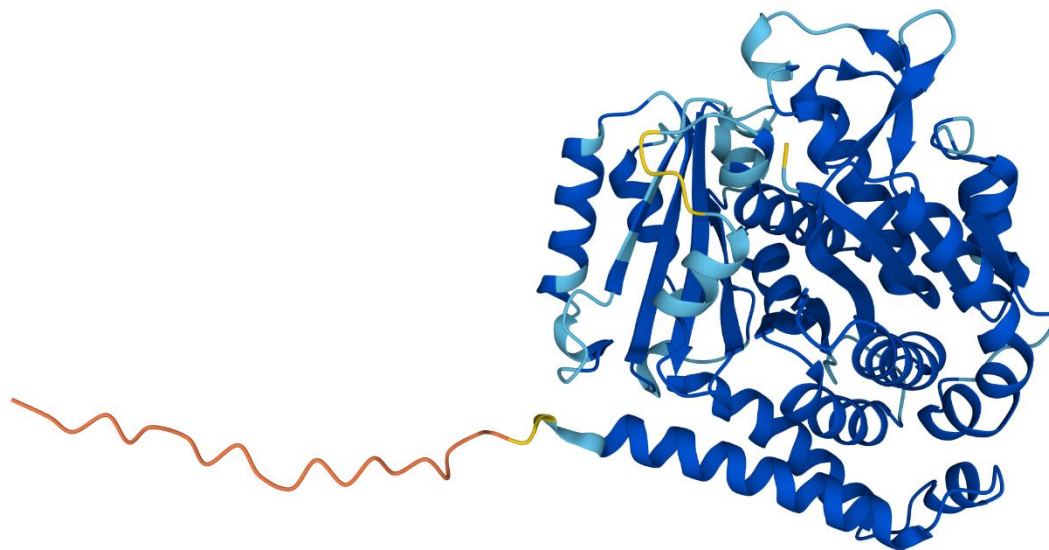
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

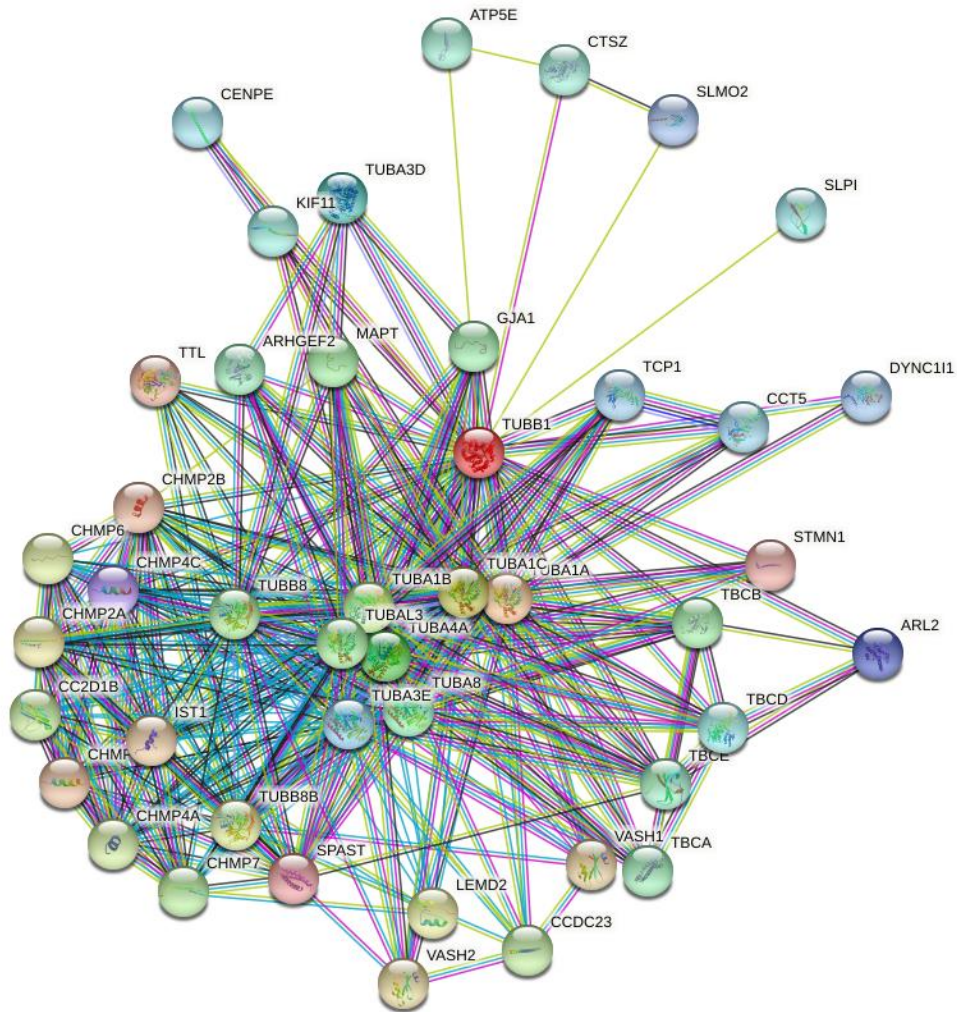
Superfamilies:

- [1] Tubulin nucleotide-binding domain-like
- [2] Tubulin C-terminal domain-like

Pfams:

- [3] Tubulin/FtsZ family GTPase domain
- [4] Tubulin C-terminal domain





minimum required interaction score: high confidence (0.700)

number of nodes: 44

number of edges: 325

average node degree: 14.8

avg. local clustering coefficient: 0.757

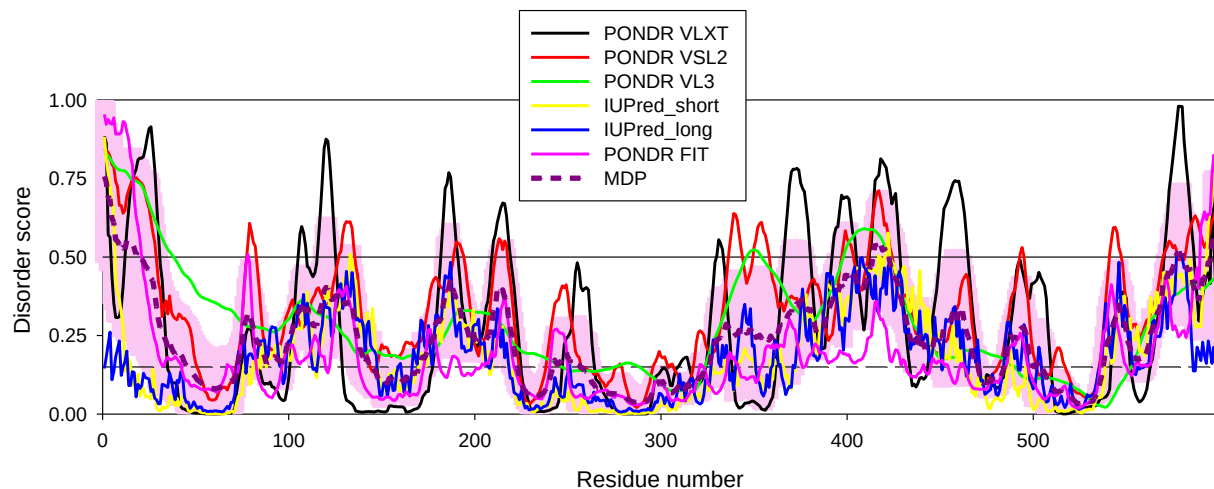
expected number of edges: 49

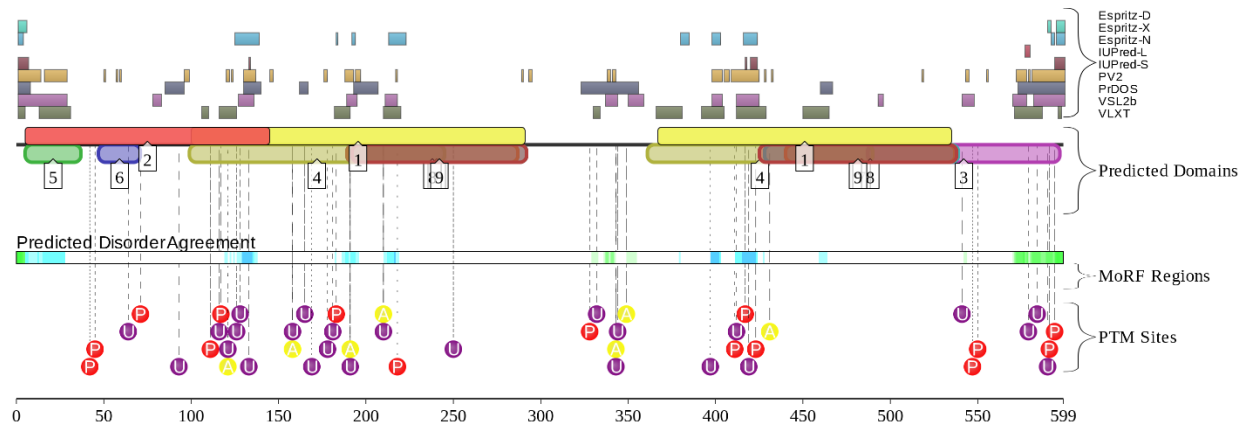
PPI enrichment p-value: $< 1.0e-16$

ABCE1 (UniProt ID: P61221)

>sp|P61221|ABCE1_HUMAN ATP-binding cassette sub-family E member 1 OS=Homo sapiens
OX=9606 GN=ABCE1 PE=1 SV=1

MADKLTRIAIVNHDKCKPKKCRQECKKSCPVVRMGKLCIEVTPQSKIAWISSETLCIGCGI
CIKKCPFGALSIVNLPSNLEKETTHRYCANAFKLHRLPIPRPGEVLGLVGTNGIGKSTALK
ILAGKQKPNLGKYDDPPDWQEILTYFRGSELQNYFTKILEDDLKAIKPQYVDQIPKAAK
GTVGSILDRKDETKTQAIVCQQLDLTHLKERNVEDLSGGELQRFACAVVCIQKADIFMF
DEPSSYLDVKQRLKAAITIRSLINPDRIIVVEHDLVLDYLSDFICCLYGVP SAYGVVTM
PFSVREGINIFLDGYVPTENLRF RDASLVFKVAETANEEEVKKMCMYKYPGMKKKMGE
FELAIVAGEFTDSEIMVMLGENGTGKTTFIRMLAGRLKPDEGGGEVPVLNVSYKPQKISPK
STGSVRQLLHEKIRDAYTHPQFVTDVMKPLQIENIIDQEVQTLSSGGELQRVALALCLGKP
ADVYLIDEPSAYLDSEQRLMAARVVKR FILHAKKTA FVVEHDFIMATYLA DRVIVFDGV
PSKNTVANSPQTLLAGMKNKFLSQLEITFRRDPNNYRPRINKLNSIKDVEQKKSGNYFFLD
D





Key:

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

Disorder:

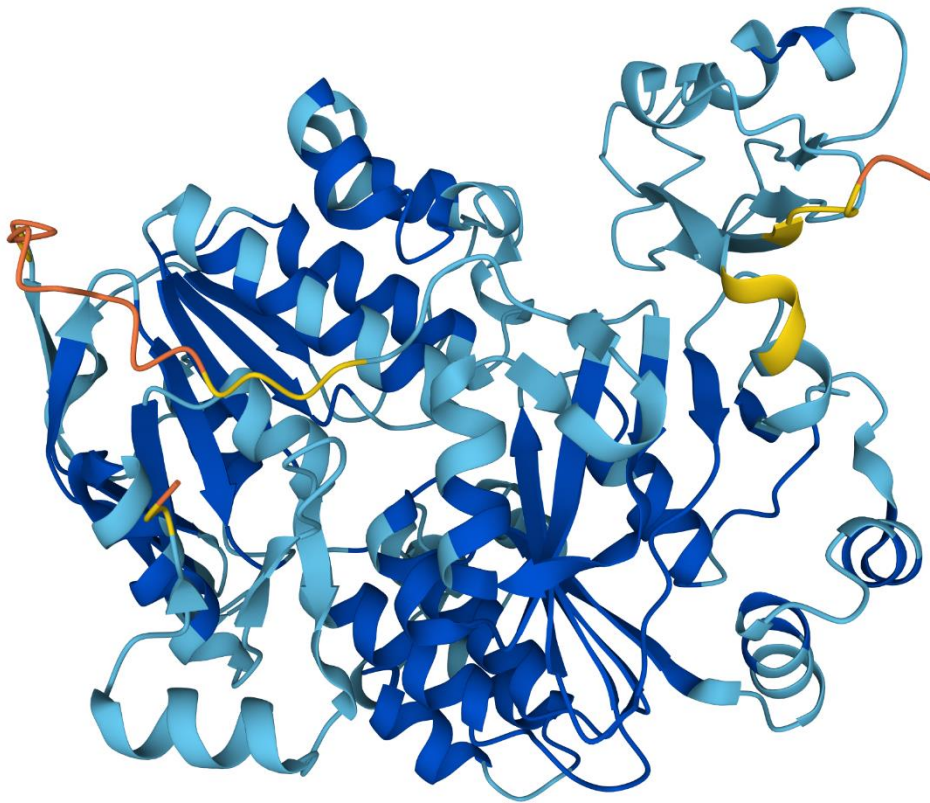
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

- [1] P-loop containing nucleoside triphosphate hydrolases
- [2] 4Fe-4S ferredoxins

Pfams:

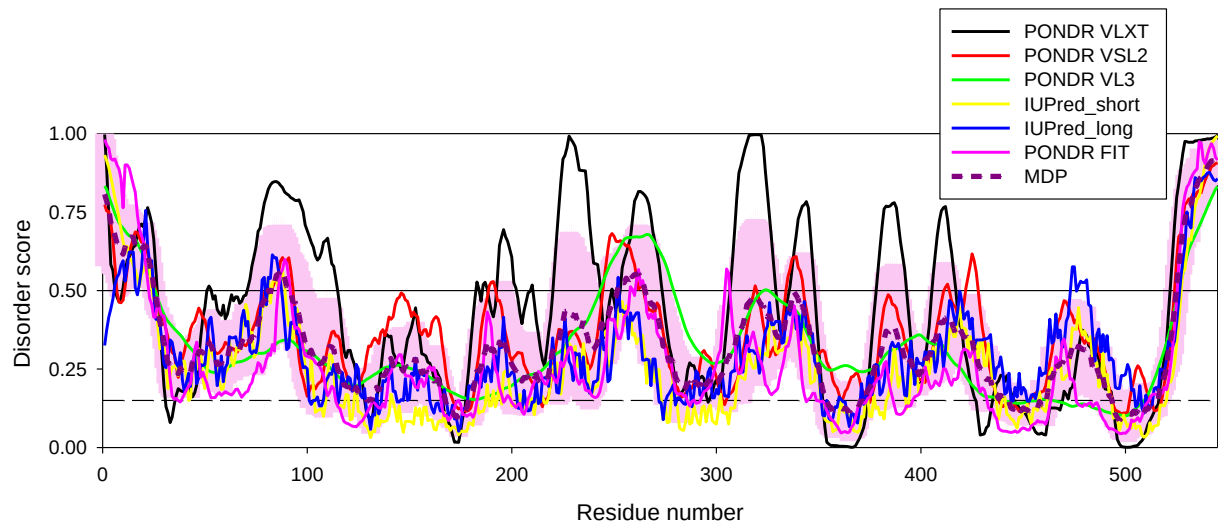
- [3] PB008974 (Pfam-B)
- [4] ABC transporter
- [5] Possible Fer4-like domain in RNase L inhibitor, RLI
- [6] 4Fe-4S binding domain
- [7] PB018733 (Pfam-B)
- [8] PB000671 (Pfam-B)
- [9] PB012404 (Pfam-B)

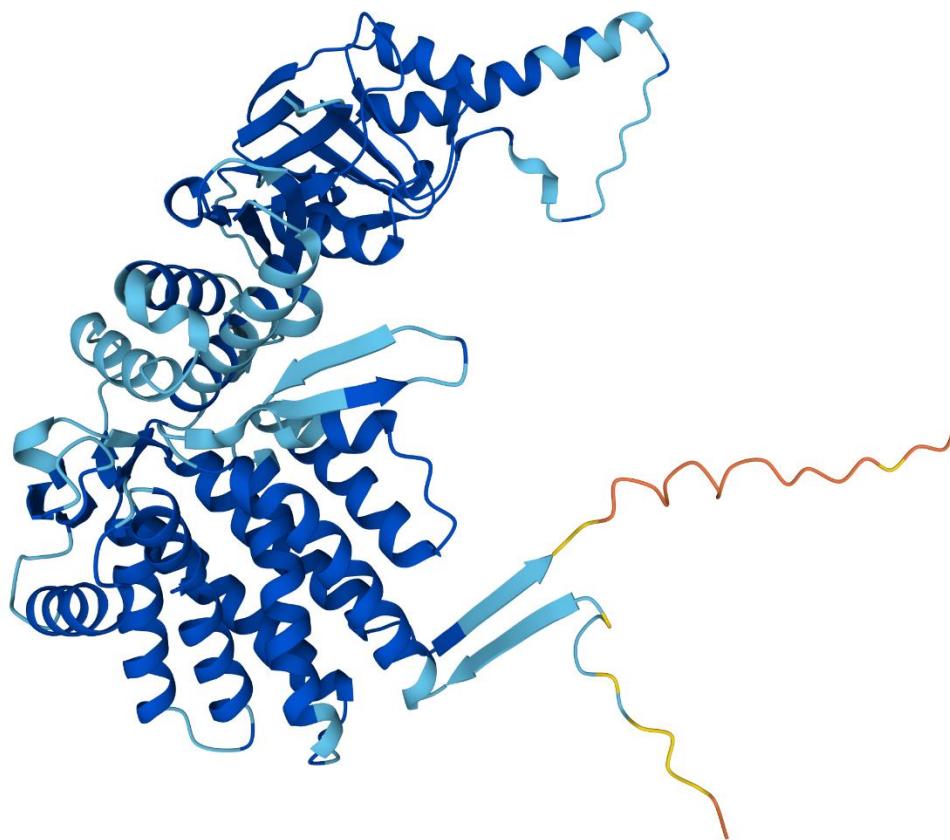
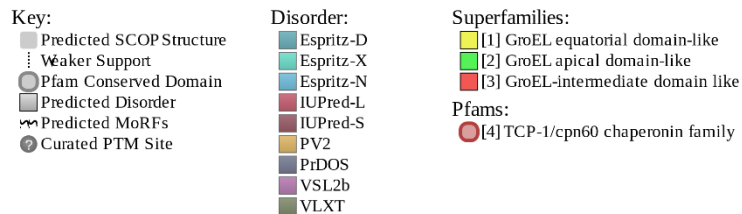
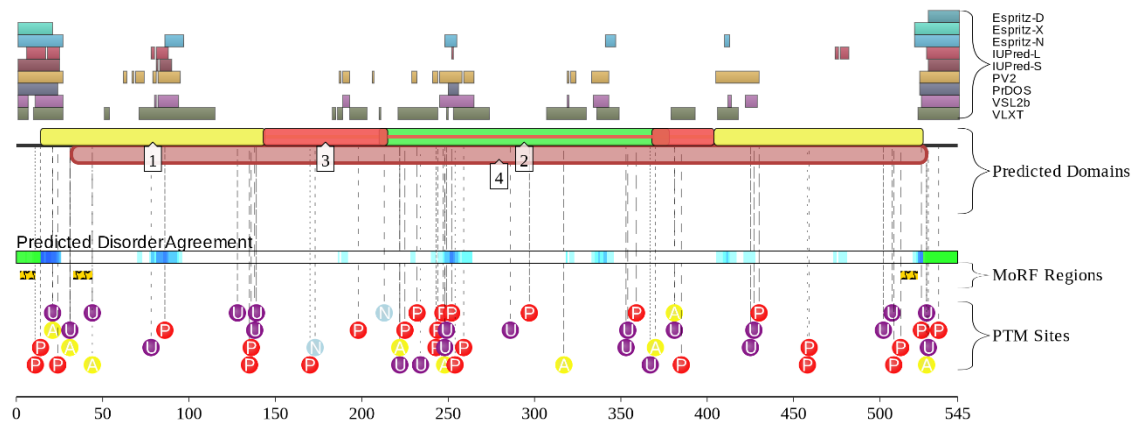


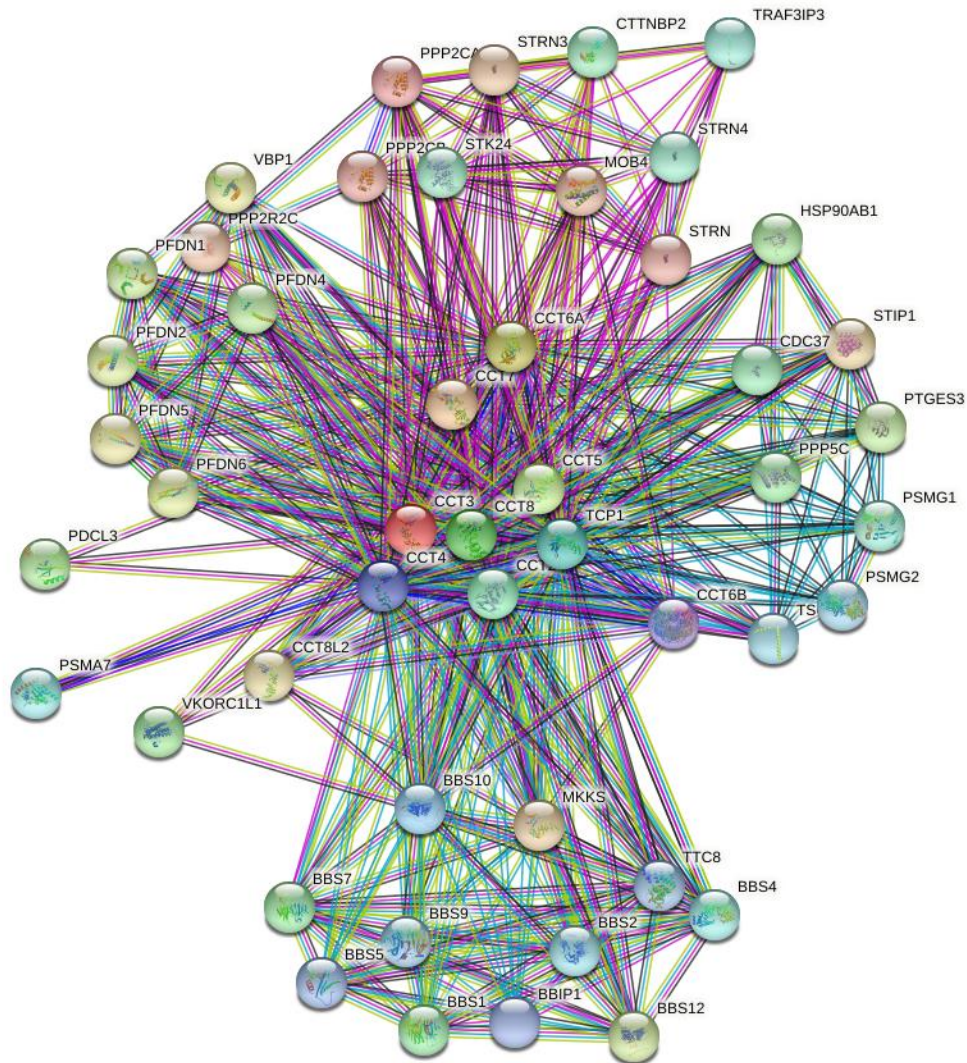
CCT γ (UniProt ID: P49368)

>sp|P49368|TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens OX=9606
GN=CCT3 PE=1 SV=4

MMGHRPVLVLSQNTKRESGRKVQSGNINAAKTIADIIRTCLGPKSMMKMLLDPMGGIV
MTNDGNAILREIQVQHPAAKSMIEISRTQDEEVGDGTTSVILAGEMLSVAEHFLEQQMH
PTVVISAYRKALDDMISTLKKISIPVDISDSMMLNIINSSITTKAISRWSSLACNIALDAV
KMQFEENGRKEIDIKKYARVEKIPGGIIEDSCVLRGVMINKDVTHTPRMRRYIKNPRIVL
LDSSLEYKKGESQTDIEITREEDFTRILQMEEYIQQLCEDIIQLKPDVVITEKGISDLAQH
YLMRANITAIRRVRKTDNNRIARACGARIVSRPEELREDDVGTGAGLLEIKKIGDEYFTFI
TDCKDPKACTILLRGASKEILSEVERNLDAMQVCRNVLLDPQLVPGGGASEMAVAHA
LTEKSKAMTGVEQWPYRAVAQALEVIPRTLQNCGASTIRLLTSLRAKHTQENCETWGV
NGETGTLVDMKELGIWEPLAVKLQTYKTAVETAVLLLRIDDIVSGHKKKGDDQSRQGG
APDAGQE







minimum required interaction score: highest confidence (0.900)

number of nodes: 48

number of edges: 443

average node degree: 18.5

avg. local clustering coefficient: 0.872

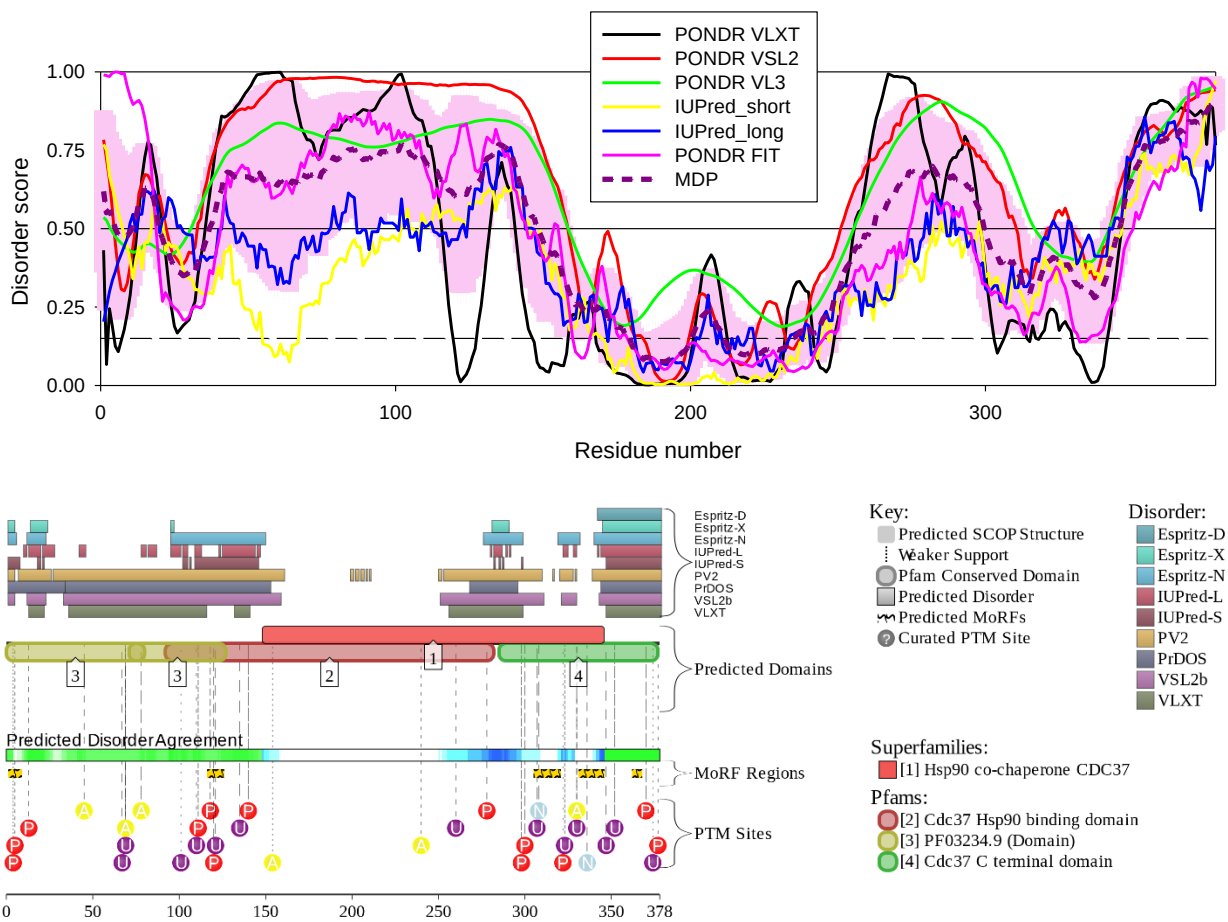
expected number of edges: 53

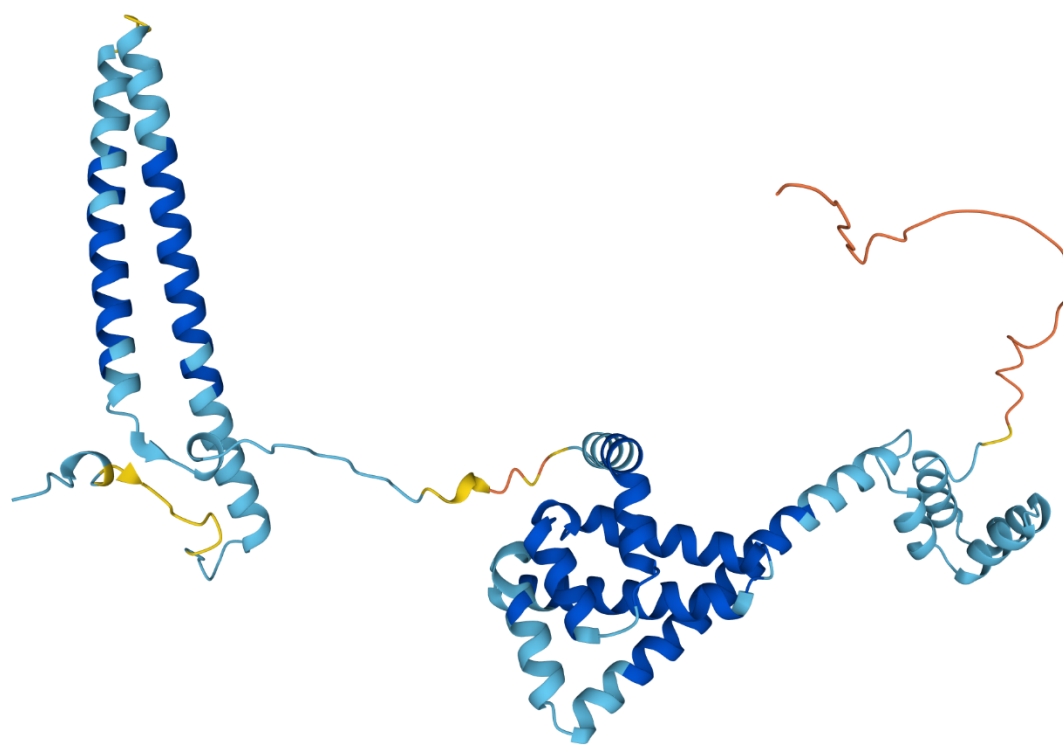
PPI enrichment p-value: $< 1.0e-16$

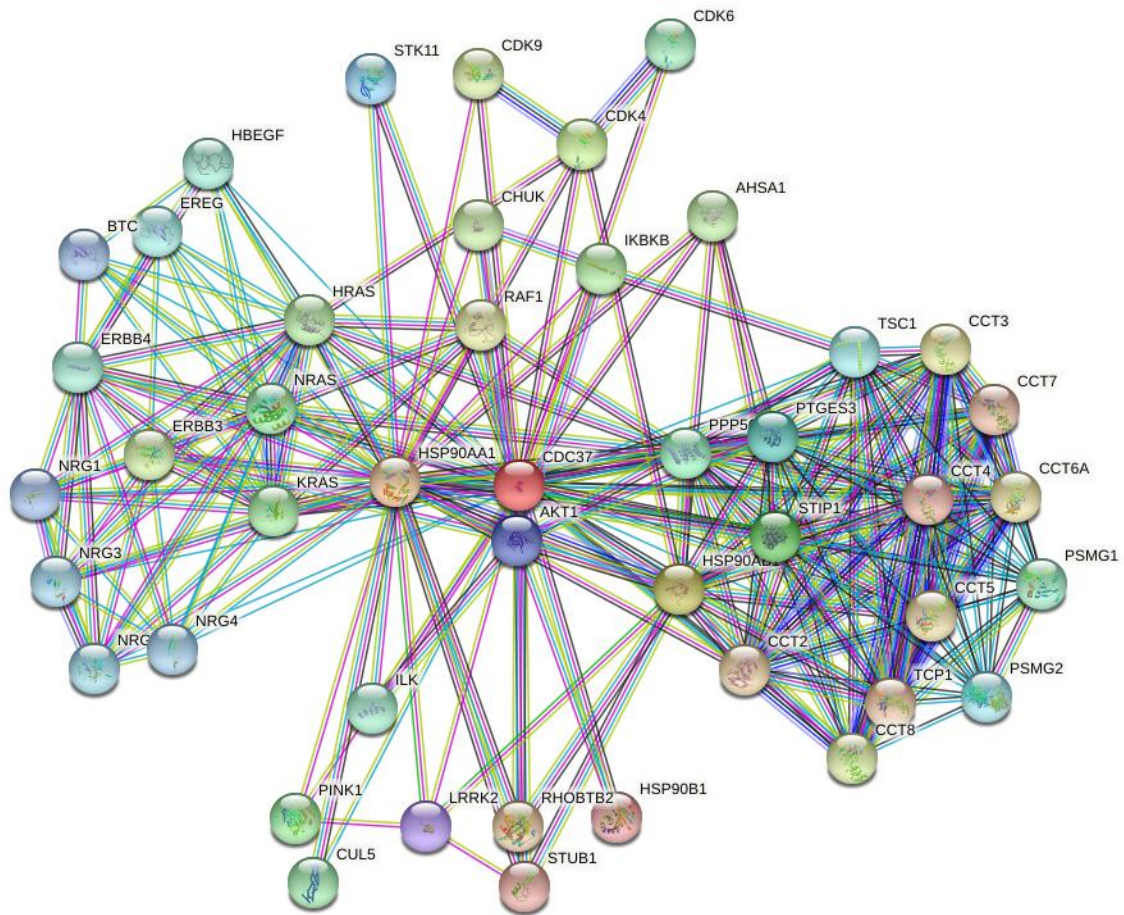
CDC37 (UniProt ID: Q16543)

>sp|Q16543|CDC37_HUMAN Hsp90 co-chaperone Cdc37 OS=Homo sapiens OX=9606
GN=CDC37 PE=1 SV=1

MVDYSVWDHIEVSDDEDETHPNIDTASLFRWRHQA RVERMEQFQKEKEELDRGCRECK
RKVAECQRKLKELEVAEGGKAELERLQAEAQQLRKEERSWEQKLEEMRKKEKSMPWN
VDTLSKDGFSKSMVNTKPEKTEEDSEEVREQKHKTFVEKYEKQIKHFGMLRRWDDSQK
YLSDNVHLVCEETANYLVIWCIDLEVEEKCALMEQVAHQ TIVMQFILELAKSLKVDPRA
CFRQFFTKIKTADRQYMEGFNDELEAFKERVGRAKLRIEKAMKEYEEEEERKKRLGPG
GLDPVEVYESLPEELQKCFDVKD VQMLQDAISKMDPTDAKYHMQRCIDSGLWVPNSK
ASEAKEGEEAGPGDPLLEAVPKTGDEKDVSV







minimum required interaction score: highest confidence (0.900)

number of nodes: 45

number of edges: 257

average node degree: 11.4

avg. local clustering coefficient: 0.856

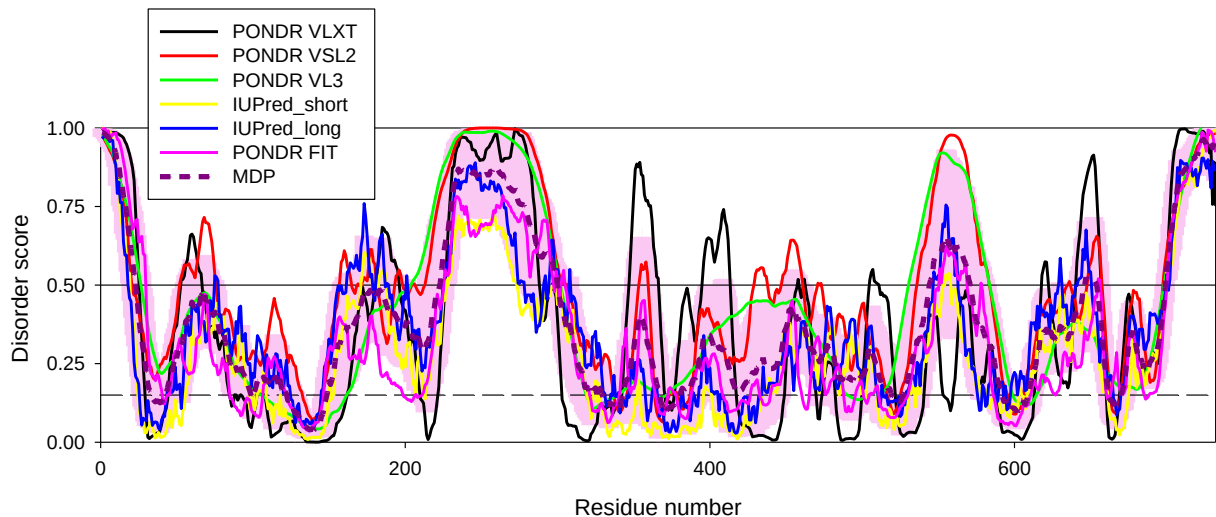
expected number of edges: 65

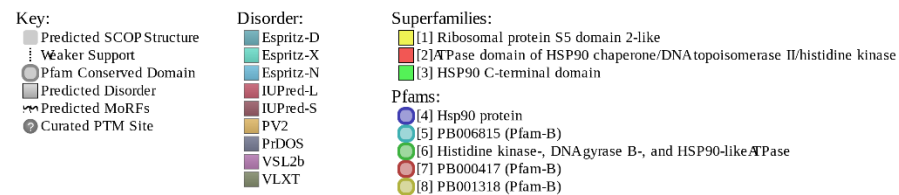
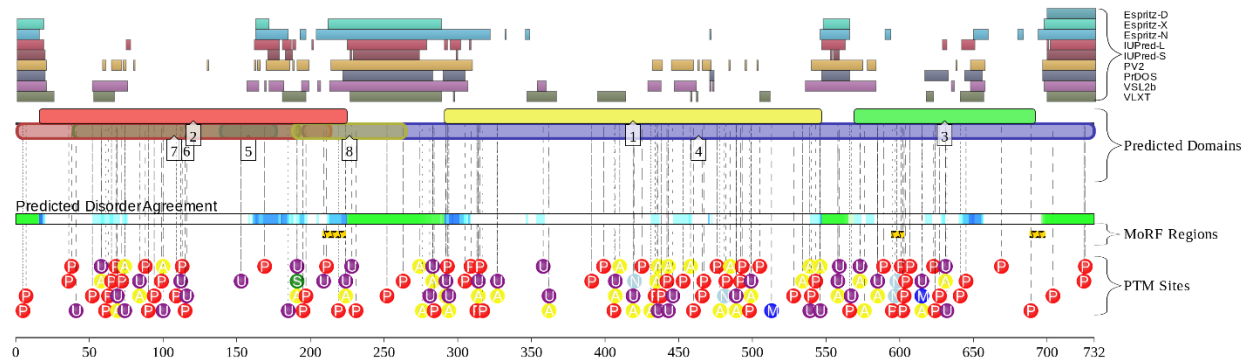
PPI enrichment p-value: $< 1.0e-16$

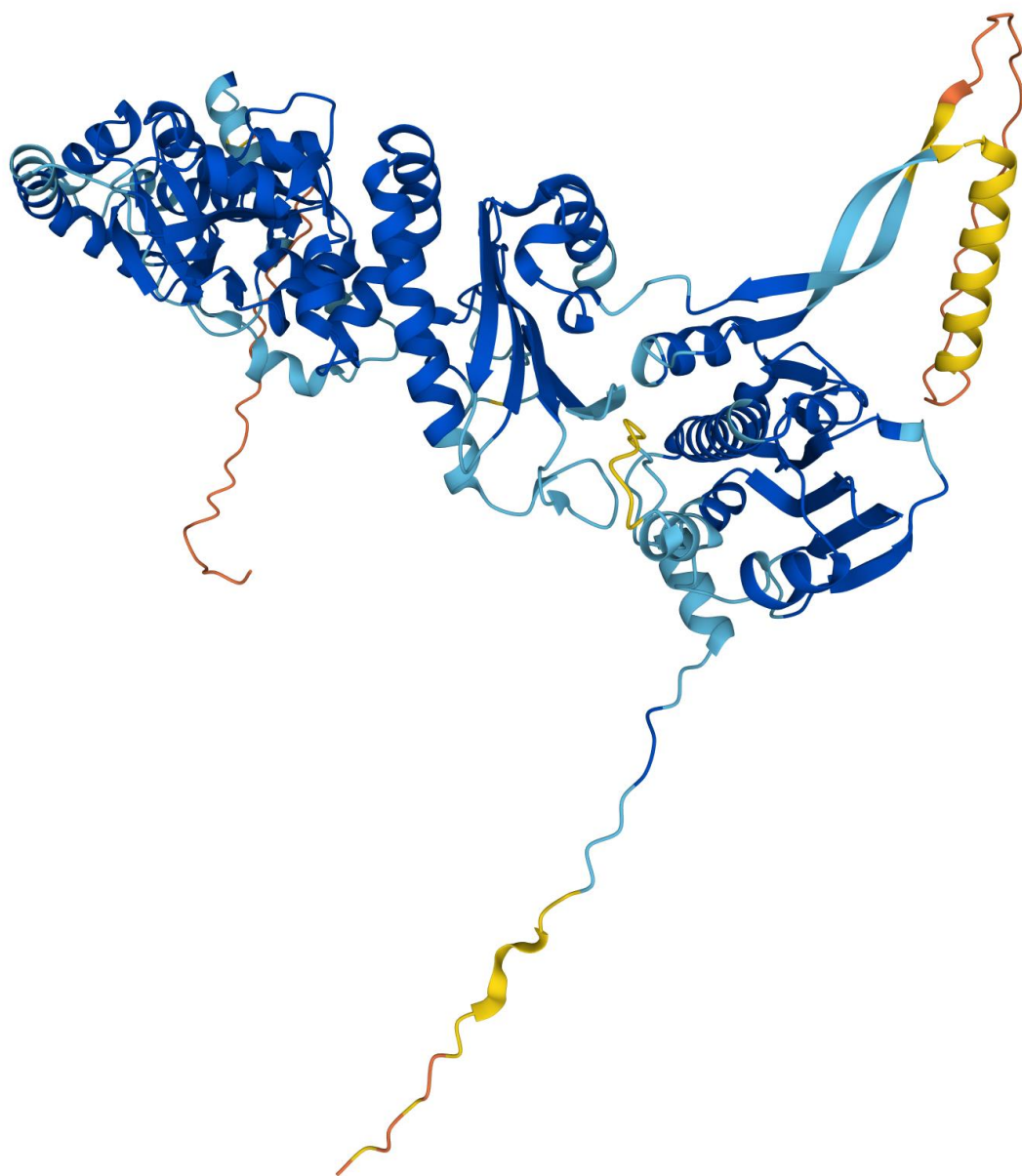
Hsp90AA1 (UniProt ID: P07900)

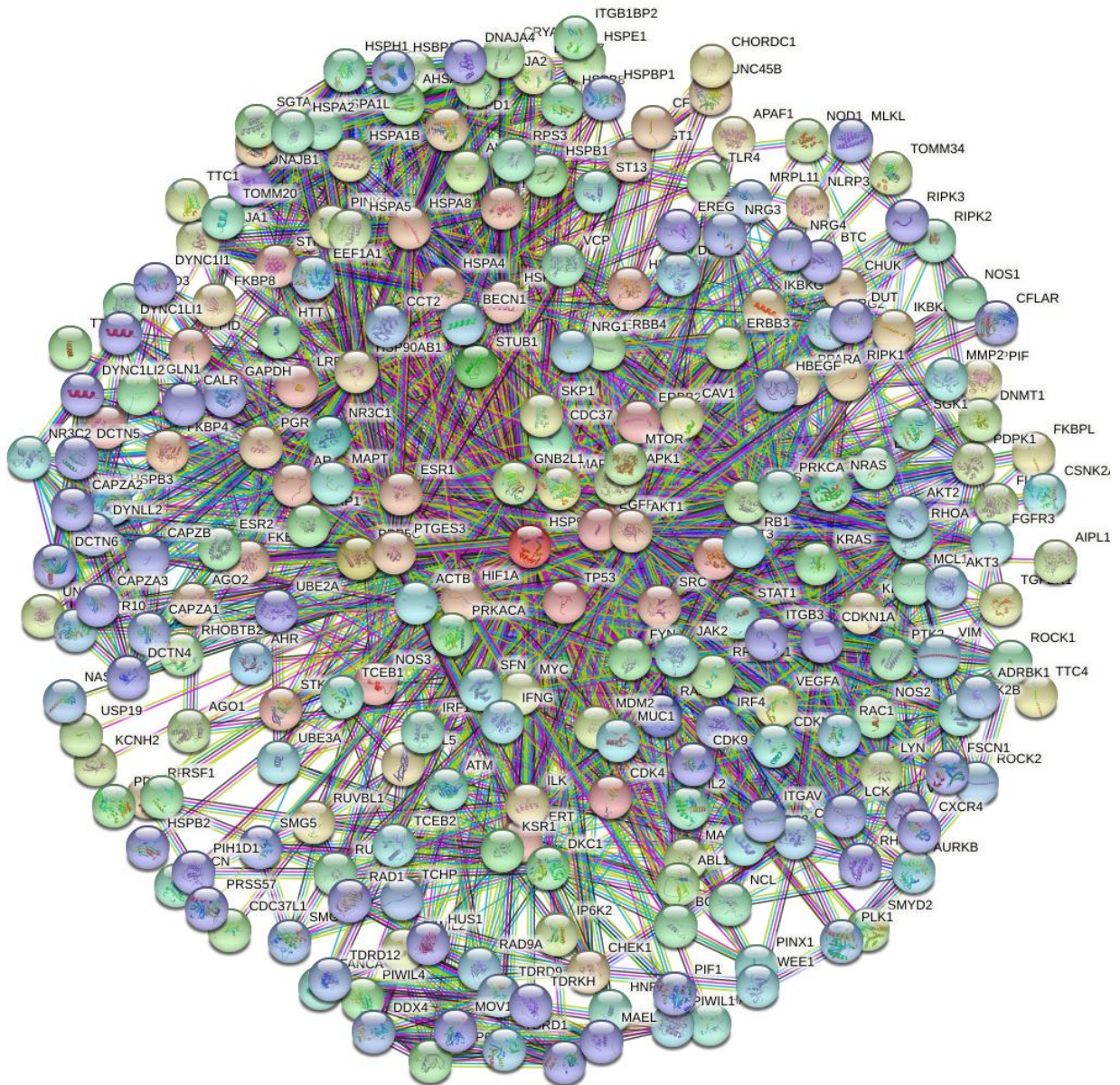
>sp|P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606
GN=HSP90AA1 PE=1 SV=5

MPEETQTQDQPMEEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIRYE
SLTDPSKLDSGKELHINLIPNKQDRTLTIIVDTGIGMTKADLINNLGTIAKSGTKAFMEALQ
AGADISMIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGGSFTVRTDTGEPMG
RGTKVILHLKEDQTEYLEERRIKEIVKKHSQFIGYPITLFVEKERDKEVSDDEAEKEDKE
EEKEKEEKESEDKPEIEDVGSDEEEEEKKDGDKKKKKKKIKEKYIDQEELNKTPIWTRNPD
DITNEEYGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFVPRRAPFDLFENRKKKNNI
KLYVRRVFIMDNCEELIPEYLNFIIRGVVDSEDLPLNISREMLQQSKILKVRKNLVKKCLE
LFTELAEDKENYKKFYEQFSKNIKLGIHEDSQNRKKLSELLRYYTASGDENVSLKDYC
TRMKENQKHIYYITGETKDQVANSFAFVERLRKHGLEVIYMIEPIDEYCVQQLKEFEGKT
LVSVTKEGLELPEDEEEKKKQEEKKTKFENLCKIMKDILEKKVEKVVVSNRLVTSPCCIV
TSTYGWTANMERIMKAQALRDNSTMGYMAAKKHLEINPDHSIETLRQKAADKNDKS
VKDLVILLYETALLSSGFSLEDPQTHANRIYRMIKLGLGIDEDDPTADDTSAAVTEEMPP
LEGDDDTSRMEEVD









minimum required interaction score: highest confidence (0.900)

number of nodes: 245

number of edges: 1782

average node degree: 14.5

avg. local clustering coefficient: 0.63

expected number of edges: 798

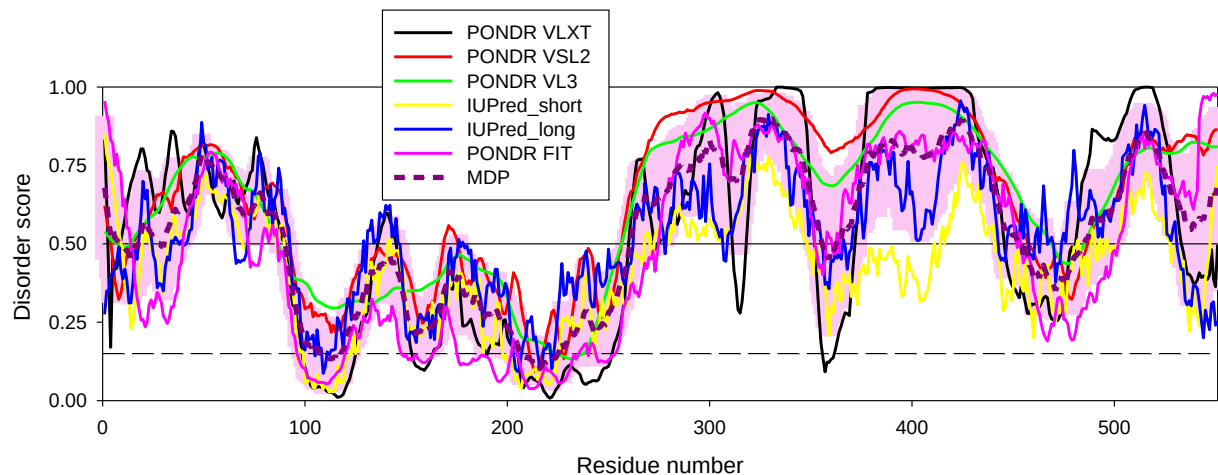
PPI enrichment p-value: $< 1.0e-16$

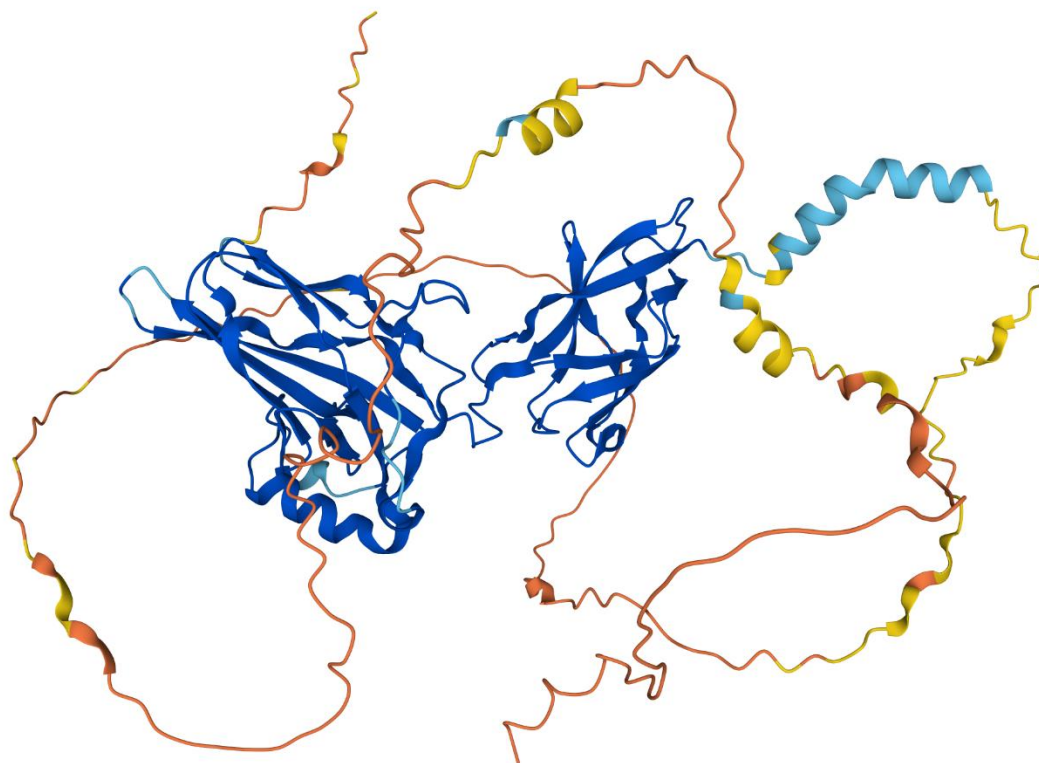
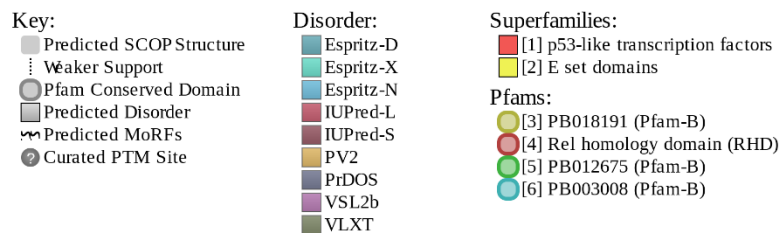
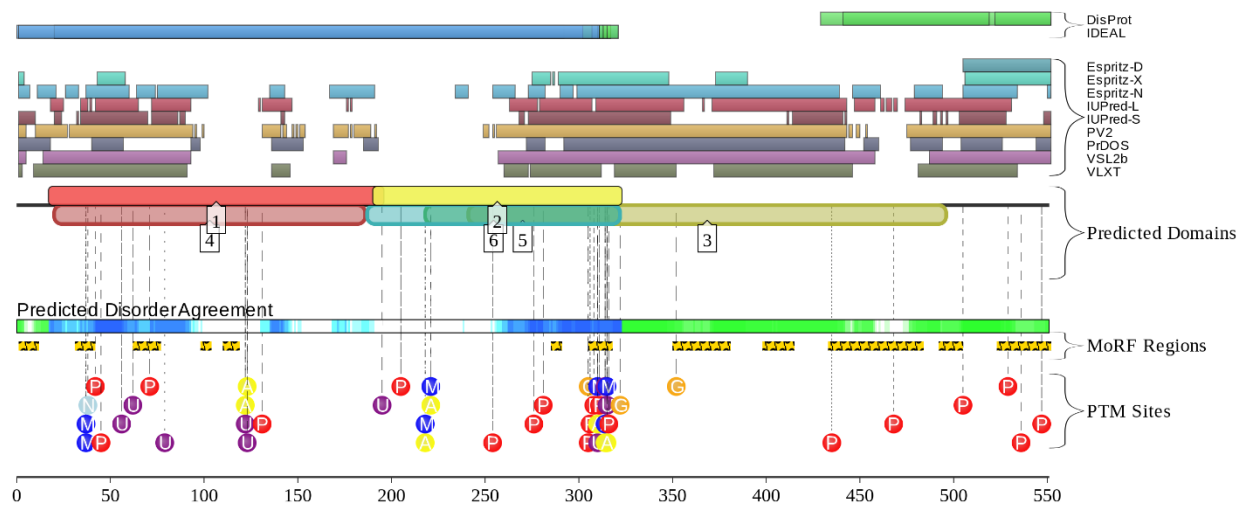
Supplementary Figure S2. Functional disorder in human proteins interacting with the RABV M-protein. For each protein, an amino acid sequence in FASTA format is shown followed by the disorder profile generated by RIDAO, D²P²-generated functional disorder profile, modeled 3D structure generated by AlphaFold, and STRING-based protein-protein interaction network.

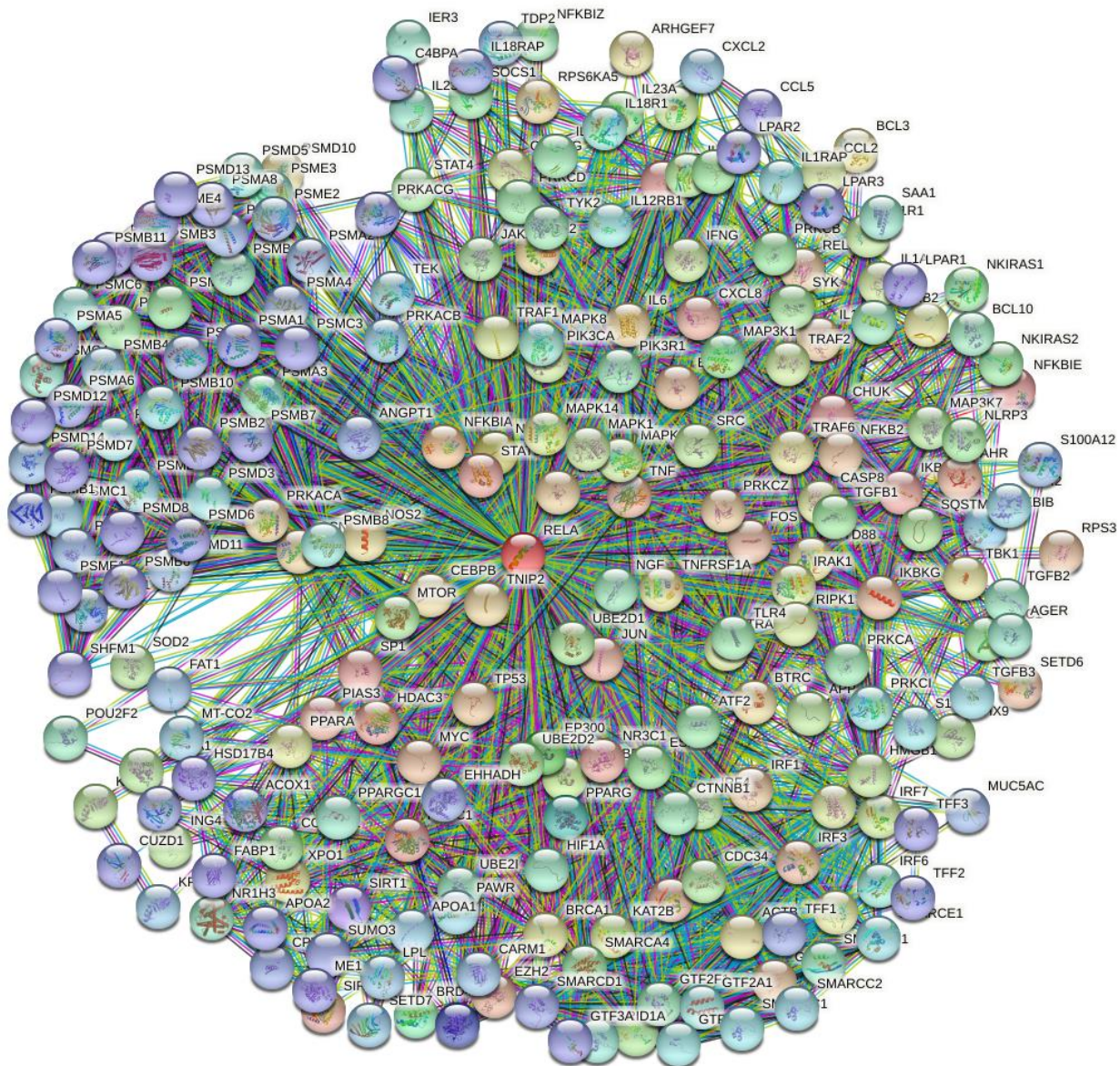
RelAp43 (UniProt ID: Q04206)

>sp|Q04206|TF65_HUMAN Transcription factor p65 OS=Homo sapiens OX=9606 GN=RELA PE=1 SV=2

MDELFLIFPAEPAQASGPYVEIIEQPKQRGMRFYKCEGRSAGSIPGERSTDTTKTHPTI
KINGYTGPGTVRISLVTKDPPHRPHPELVGKDCRDGFYEAELCPDRCIHSFQNLGIQCV
KKRDLEQAISQRIQTNNNPFQVPIEEQRGDYDLNAVRLCFQVTVRDPSPGRPLRLPPVLSH
PIFDNRAPNTAELKICRVNRNSGSLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFQ
ADVHRQVAIVFRTPPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPDTDDRHRIEE
KRKRTYETFKSIMKKSPFSGPTDPRPPPRRIAVPSRSSASVPKPAPQPYPFTSSLSTINYDEF
PTMVFPSPGQISQASALAPAPPQVLPQAPAPAPAPAMVSALAQAPAPVPVLAPGPPQAVA
PPAPKPTQAGEGTLSEALLQLQFDDEDLGALLGNSTDPVFTDLASVDNSEFQQLLNQGI
PVAPHTTEPMLMEYPEAITRLVTGAQRPPDPAPAPLGAPGLPNGLLSGDEDFSSIADMDF
SALLSQISS







minimum required interaction score: highest confidence (0.900)

number of nodes: 236

number of edges: 3109

average node degree: 26.3

avg. local clustering coefficient: 0.727

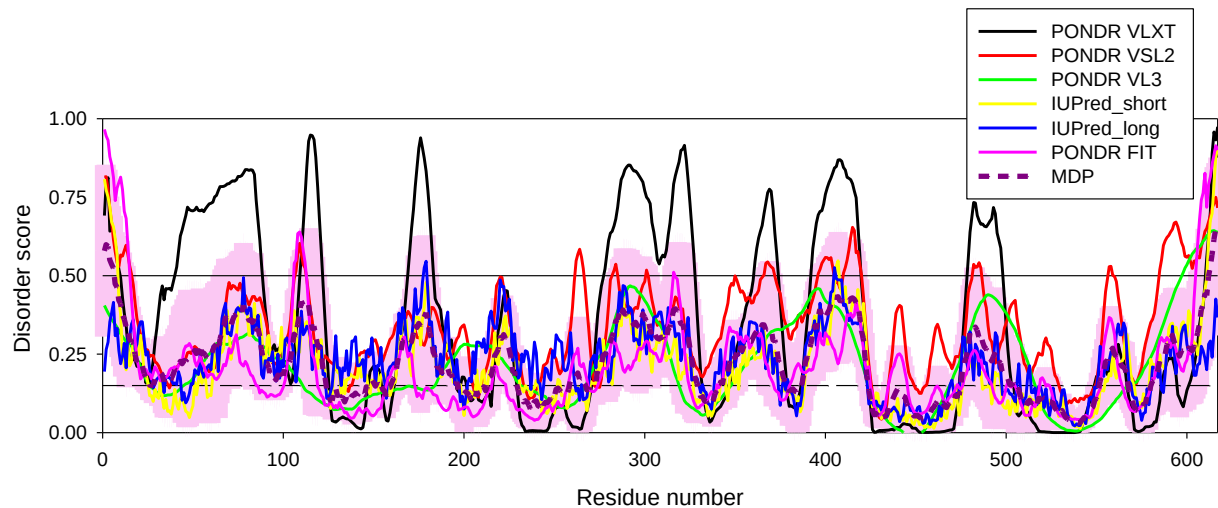
expected number of edges: 1044

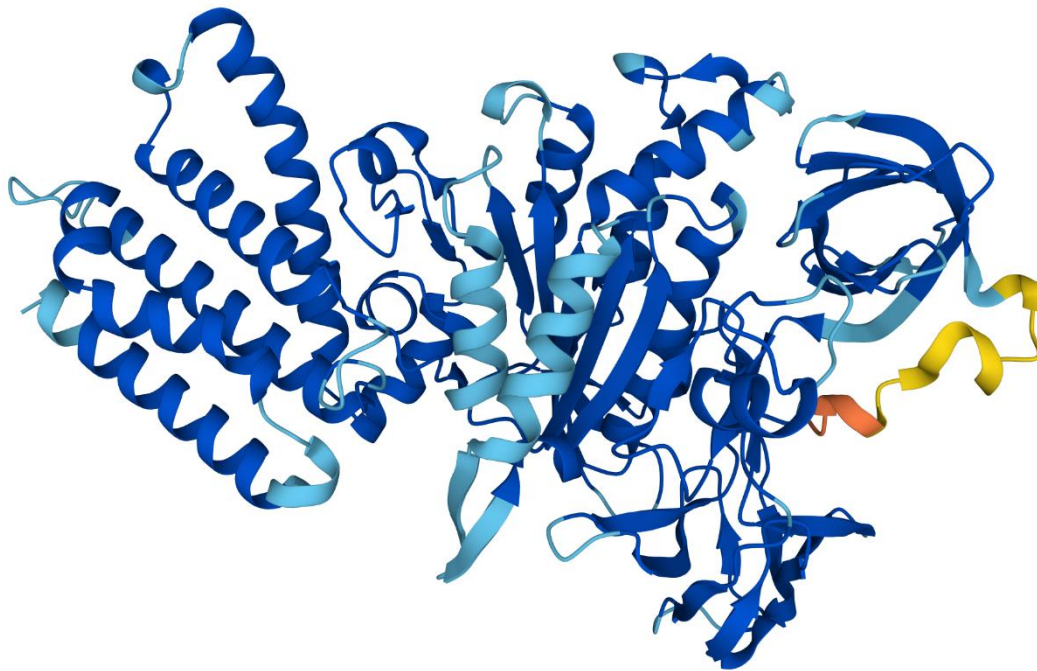
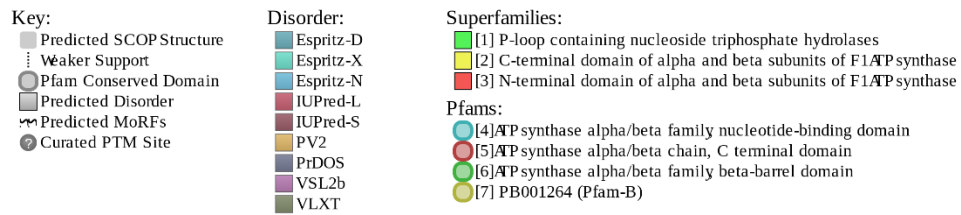
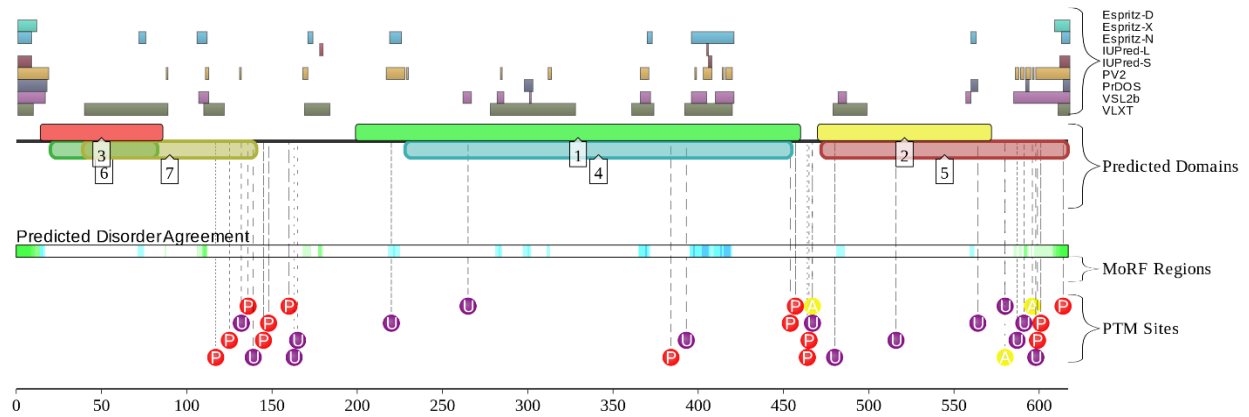
PPI enrichment p-value: $< 1.0e-16$

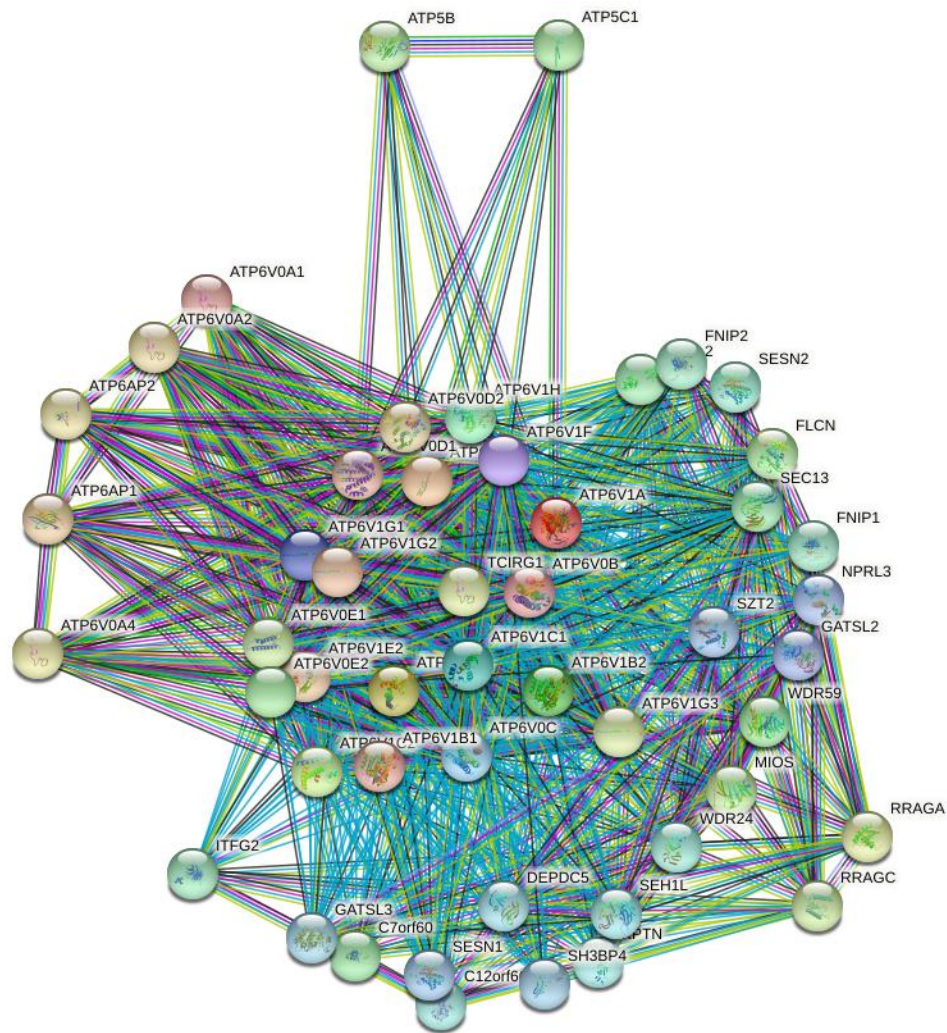
ATP6V1A (UniProt ID: P38606)

>sp|P38606|VATA_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens
OX=9606 GN=ATP6V1A PE=1 SV=2

MDFSKLPKILDEDKESTFGYVHGVSGPVVTACDMAGAAMYELVRVGHSELVGEIIRLE
GDMATIQVYEETSGVSVGDPVLRRTGKPLSVELGPGIMGAIFDGIQRPLSDISSQTQSIYIPR
GVNVSALSRLDIKWDFTPCKNLRVGSHTGGDIYGIVSENSLIHKIMLPPRNRGTVTYIAP
PGNYDTSDVVLELEFEGVKEKFTMVQVWPVRQVRPVTEKLPANHPLL TGQRVLDALFP
CVQGGTTAIPGAFGCGKTVISQSLSKYSNSDVIIYVGCGERGNEMSEVLRDFPELTMEVD
GKVESIMKRTALVANTSNNMPVAAREASIYTGITLSEYFRDMGYHVSMMADSTSRWAEA
LREISGRLAEMPADSGYPAYLGARLASFYERAGRVKCLGNPEREGSVSIVGAVSPPGGD
FSDPVT SATLGIVQVFWGLDKKLAQRKHFP SVNWLISYSKYMRLDEYYDKHFTFVPL
RTKAKEILQEEEDLAEIVQLVGKASLAETDKITLEVAKLIKDDFLQQNGYTPYDRFCPFY
KTVGMLSNMIAFYDMARRAVETTAQSDNKITWSIIREHMGDILYKLSSMKFKDPLKDG
EAKIKSDYAQLLEDQMNAFRSLED







minimum required interaction score: highest confidence (0.900)

number of nodes: 50

number of edges: 828

average node degree: 33.1

avg. local clustering coefficient: 0.801

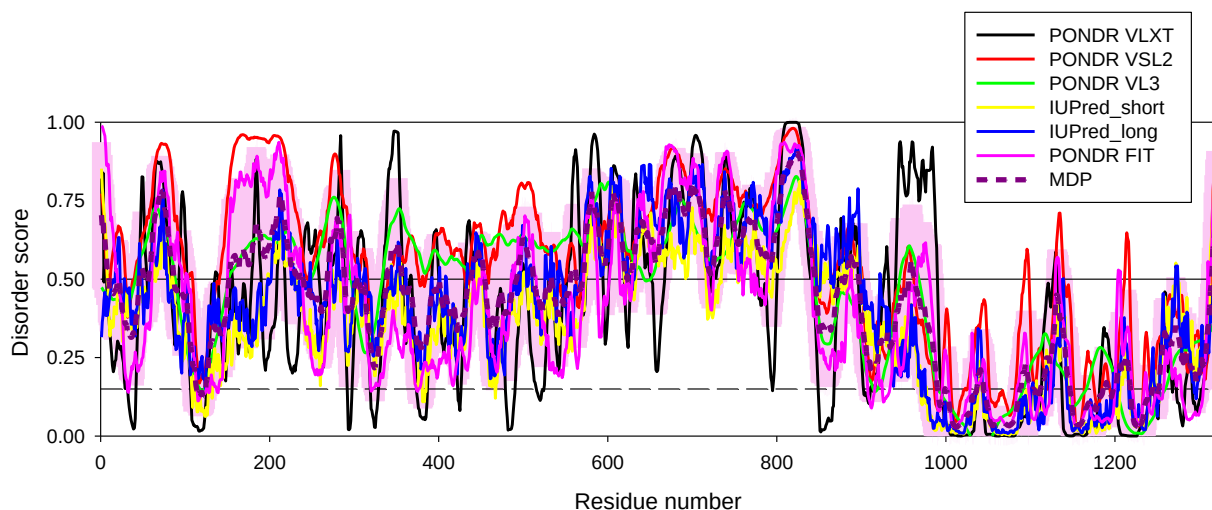
expected number of edges: 60

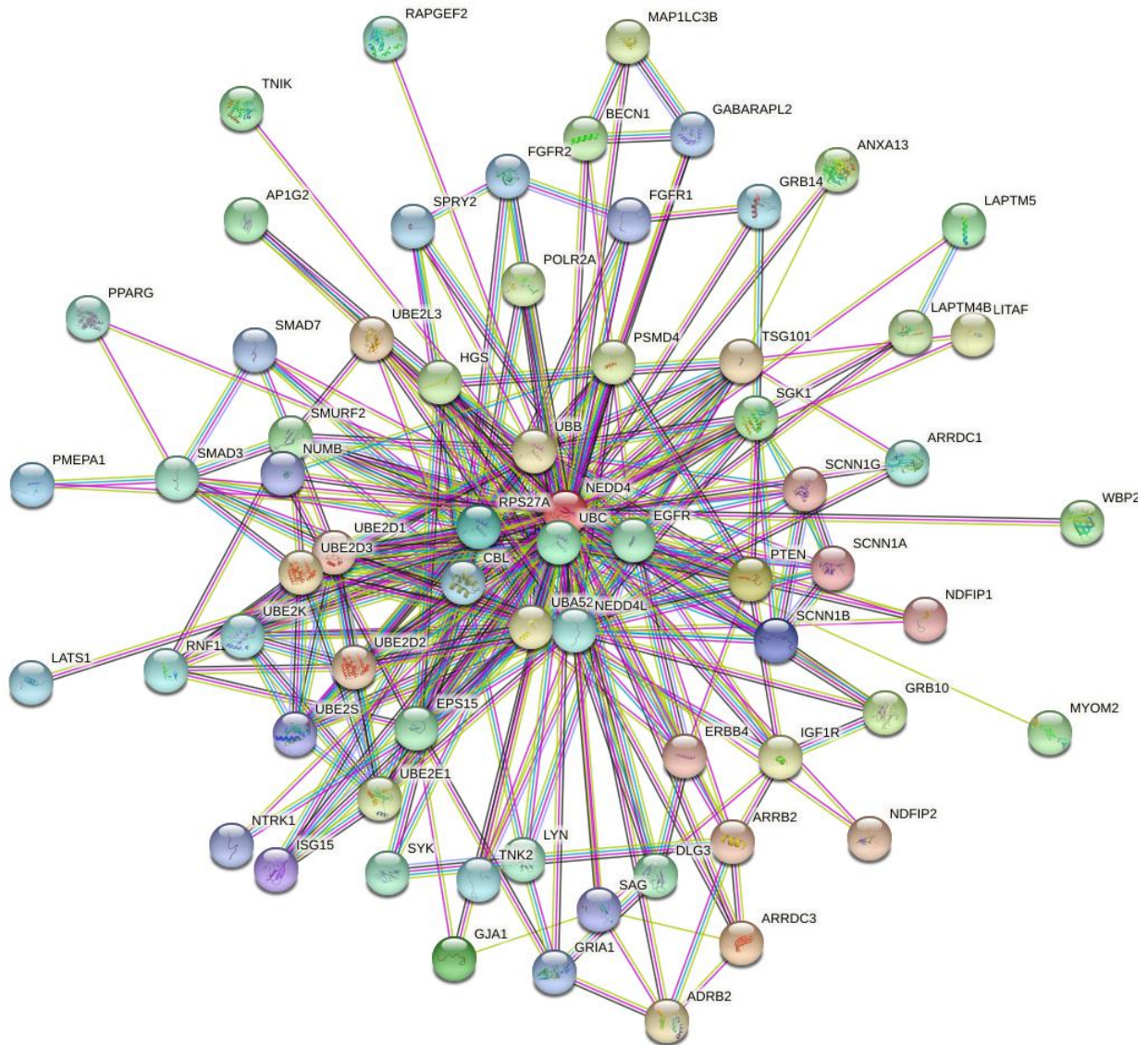
PPI enrichment p-value: $< 1.0e-16$

NEDD4 (UniProt ID: P46934)

>sp|P46934|NEDD4_HUMAN E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens
OX=9606 GN=NEDD4 PE=1 SV=4

MAQSLRLHFAARRSNTYPLSETSGDDLDSHVHMCFKRPTRISTSNVVQMKLTPRQTALA
PLIKENVQSQERSSVPSSENVNKKSSCLQISLQPTRYSGYLQSSNVLADSDDASFTCILKD
GIYSSAVVDNELNAVNDGHLVSSPAICSGSLSNFSTSDNGSYSSNGSDFGSCASITSGGSY
TNSVISDSSSYTFPPSDDTFLGGNLPSDSTSNRSVPNRNTTPCEIFSRSTSTDPPFVQDDLEH
GLEIMKLPVSRNTKIPLKRYSSLVIFPRSPSTTRPTSPTSLCTLLSKGSYQTSHQFIISPSEIA
HNEDGTSAKGFLSTAVNGLRLSKTICTPGEVRDIRPLHRKGSQKKIVLSNNTPRQTVCE
KSSEGYSVCVSVHFTQRKAATLDCETTNGDCKPEMSEIKLNSDSEYIKLMHRTSACLPSQ
NVDCQININGELERPHSQMNKNHGILRRSISLGGAYPNISCLSSLKHNCSSKGGPSQLLIK
ASGNEGKVDNLSRDSNRDCTNELSNSCKTRDDFLGQVDVPLYPLPTENPRLERPYTFKD
FVLHPRSHKSRVKGYLRLKMTYLPKTSGEDDNAEQAELEPGWVVLDQPDAAACHLQ
QQQEPSPLPPGWEERQDILGRYYVNHESTRRTQWKRPTPDNLDAENGNIQLQAQRA
FTTRRQISEETESVDNRESSENWEIREDATMYSNQAFPPSSNLDVPTHLAEELNAR
LTIFGNSAVSQPASSNHSSRRGSLQAYTFEEQPTLPVLLPTSSGLPPGWEEKQDERGRSY
YVDHNSRTTTWTKPTVQATVETSQLTSSQSSAGPQSQASTSDSGQQVTQPSEIEQGFLPK
GWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPAHLRGKTSLDTSNDLGPLPPGWEERTH
TDGRIFYINHNIKRTQWEDPRLNVAITGPAVPYSRDYKRKYEFFRRKLKKQNDIPNKF
MKLRRATVLEDSYRRIMGVKRAFLKARLWIEFDGEKGLDYGGVAREWFFLISKEMFN
PYYGLFEYSATDNYTLQINPNSGLCNEDHLSYFKFIGRVAGMAVYHGKLLDGFFIRPFY
KMMLHKPITLHDMESVDSEYYNSLRWILENDPTELDLRFIIDEELFGQTHQHELKNGGSE
IVVTNKNKKEYIYLVIQWRFVNRIQKQMAAFKEGFFELIPQDLIKIFDENELELLMCGLG
DVDVNDWREHTKYKNGYSANHQVIQWFWKAVLMMDSEKRIRLLQFVTGTSRVPMNG
FAELYGSNGPQSFTVEQWGTPEKL PRAHTCFNRLDLPPYESFEELWDKLQMAIENTQGF
DGVD





minimum required interaction score: high confidence (0.700)

number of nodes: 67

number of edges: 287

average node degree: 8.57

avg. local clustering coefficient: 0.72

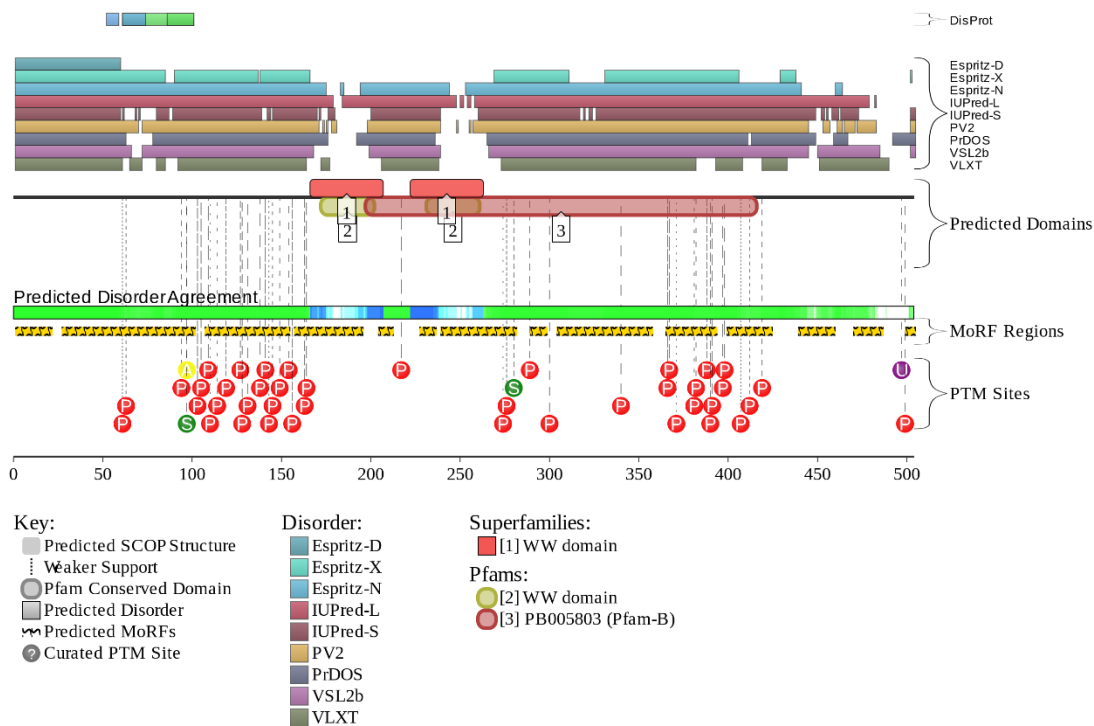
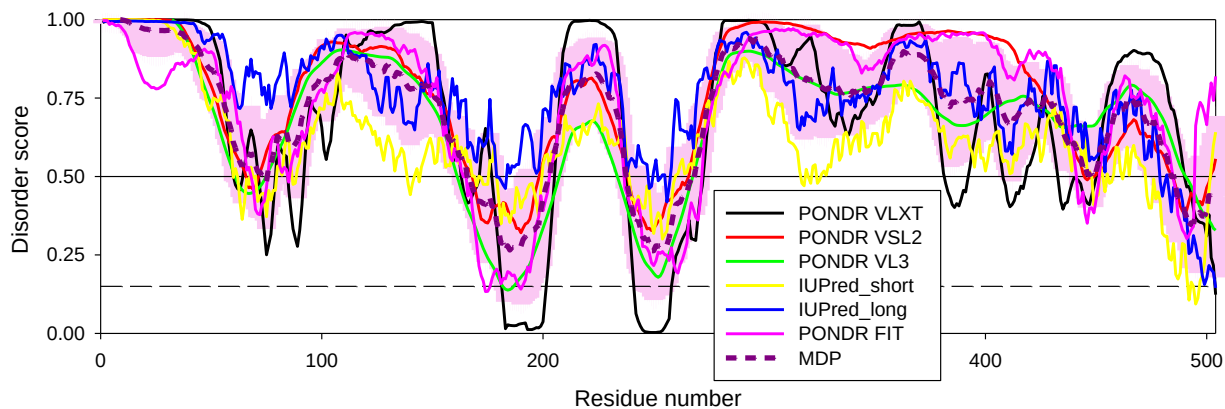
expected number of edges: 132

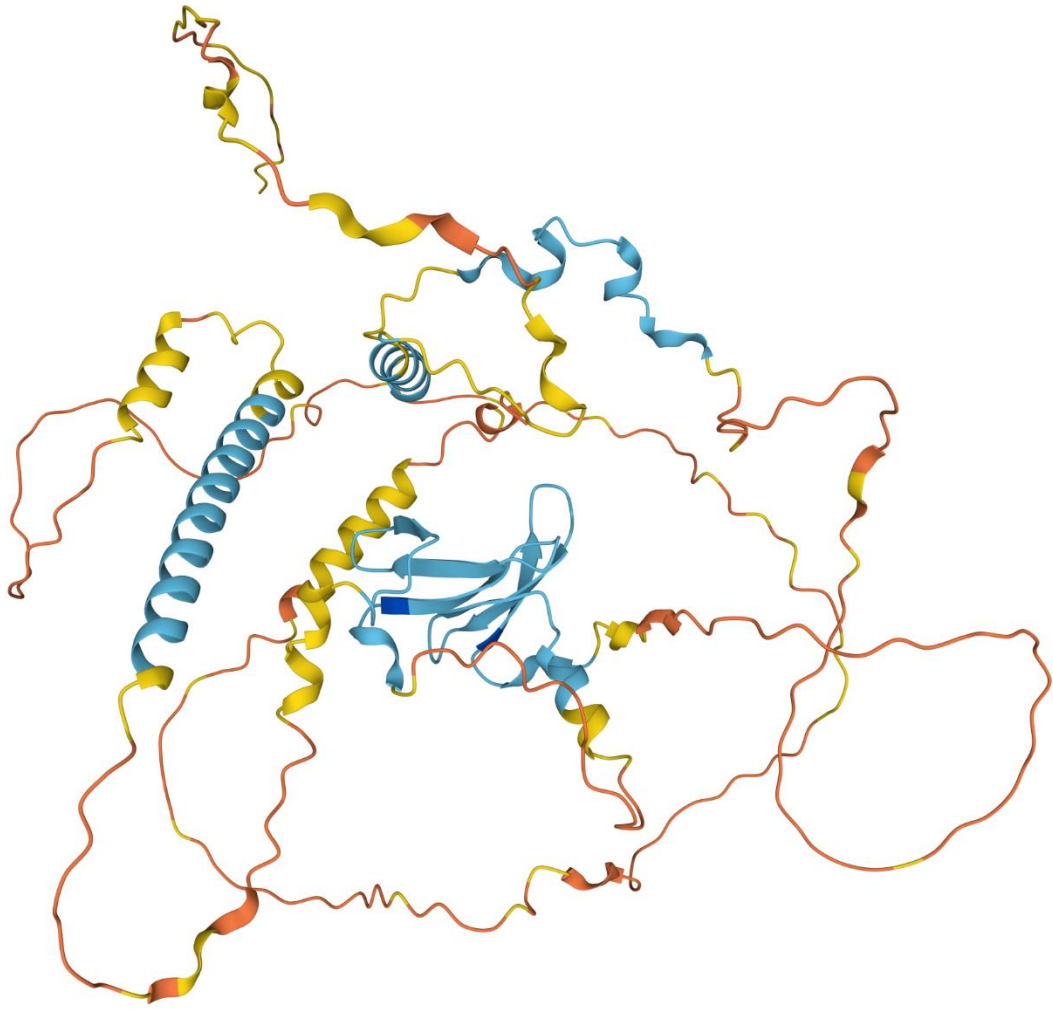
PPI enrichment p-value: $< 1.0e-16$

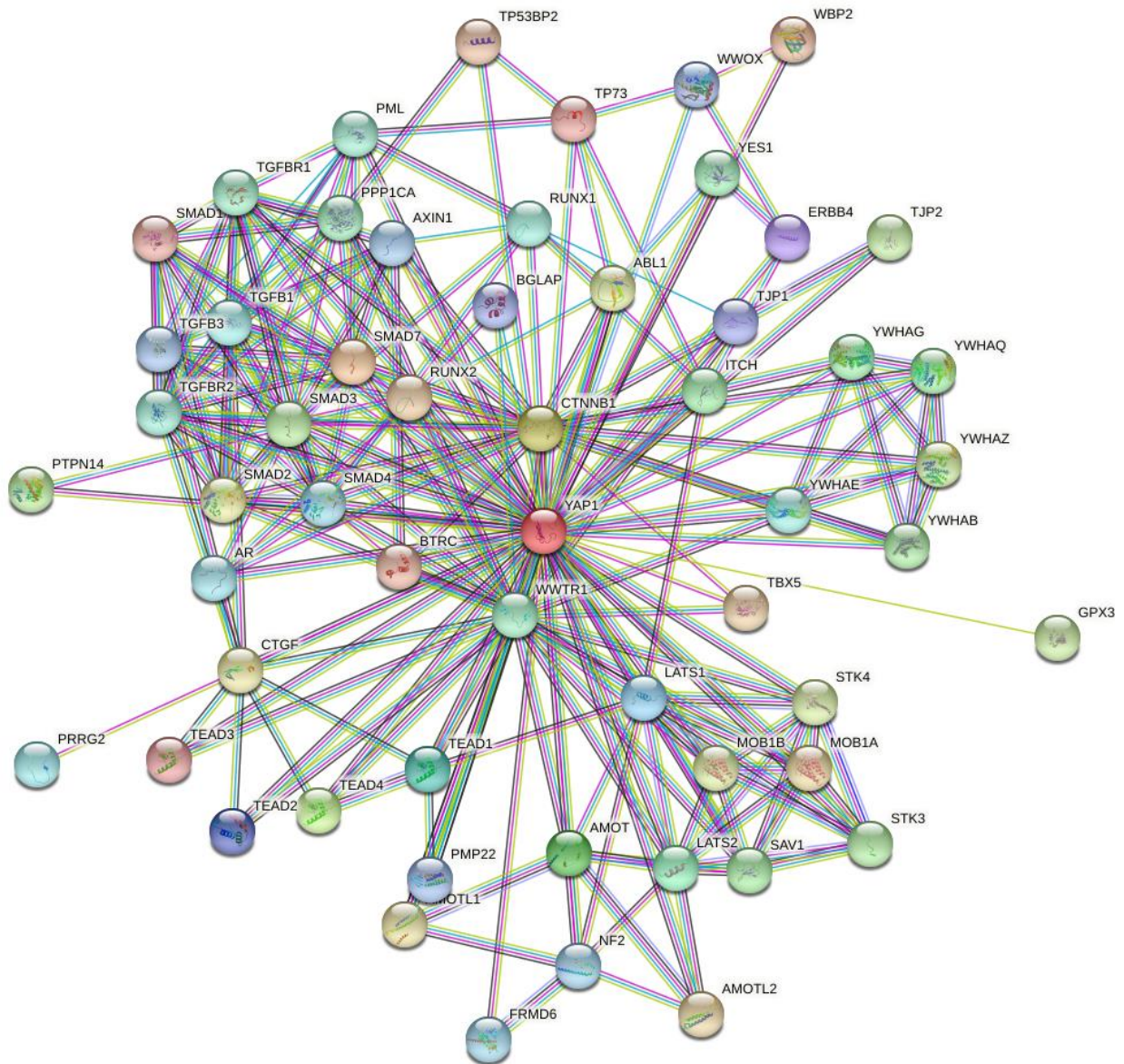
YAP1 (UniProt ID: P46937)

>sp|P46937|YAP1_HUMAN Transcriptional coactivator YAP1 OS=Homo sapiens OX=9606
GN=YAP1 PE=1 SV=2

MDPGQQPPPQPAPQGQGPPSQPPQGQGPPSGPGQPAPAATQAAPQAPPAGHQIVHVRG
DSETDLEALFNAV MNPKTANVPQTVPMRLRKL PDSFFKPPPEPKSHSRQASTDAGTAGAL
TPQHVRAHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQHLRQSSFEIPDDVPLPAGWE
MAKTSSGQRYFLNHIDQTTTWQDPRKAMLSQMNV TAPTSPPVQQNMMNSASGPLPDG
WEQAMTQDGEIYYINHKNKTTSWLDPRLDPRFAMNQ RISQSAPVKQPPPLAPQSPQGG
VMGGSNSNQQQMRLQQLQMEKERLRLKQQELLRQAMRNINPSTANSPKCQELALRS
QLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSRDESTDSGLSMSSYSVP
RTPDDFLNSVDEMDTGDTINQSTLPSQQNRFPDYLEAIPGTNVLDLGTLEGDGMNIEGEEL
MPSLQEALSSDILNDMESVLAATKLDKESFLTWL







minimum required interaction score: highest confidence (0.900)

number of nodes: 57

number of edges: 241

average node degree: 8.46

avg. local clustering coefficient: 0.754

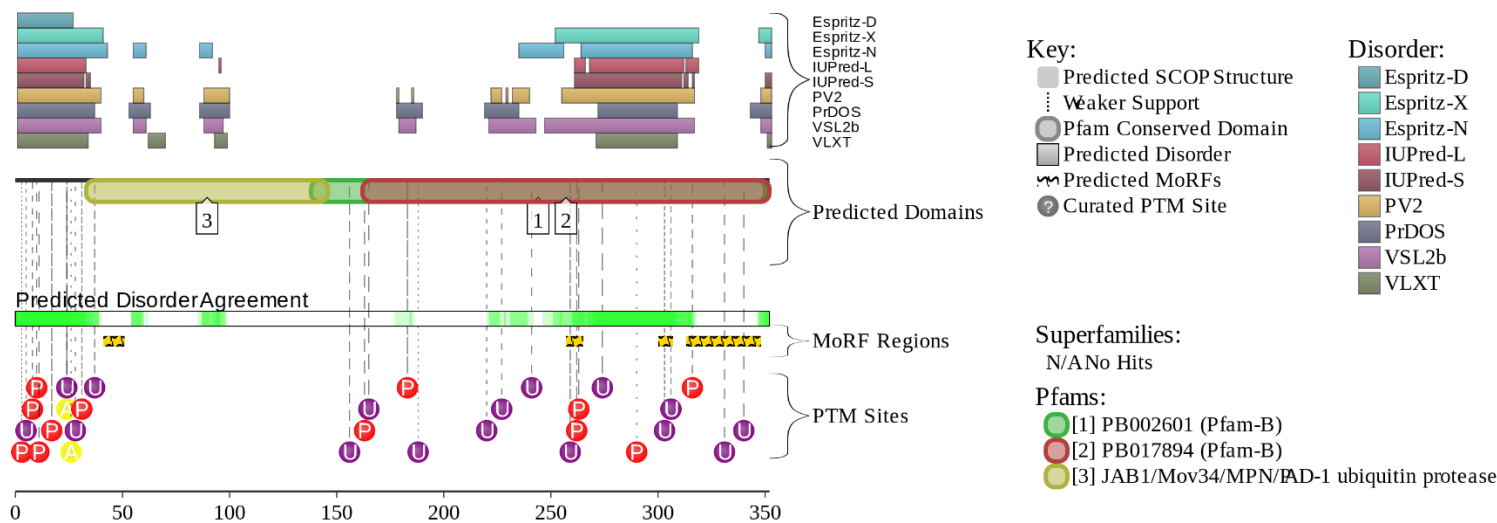
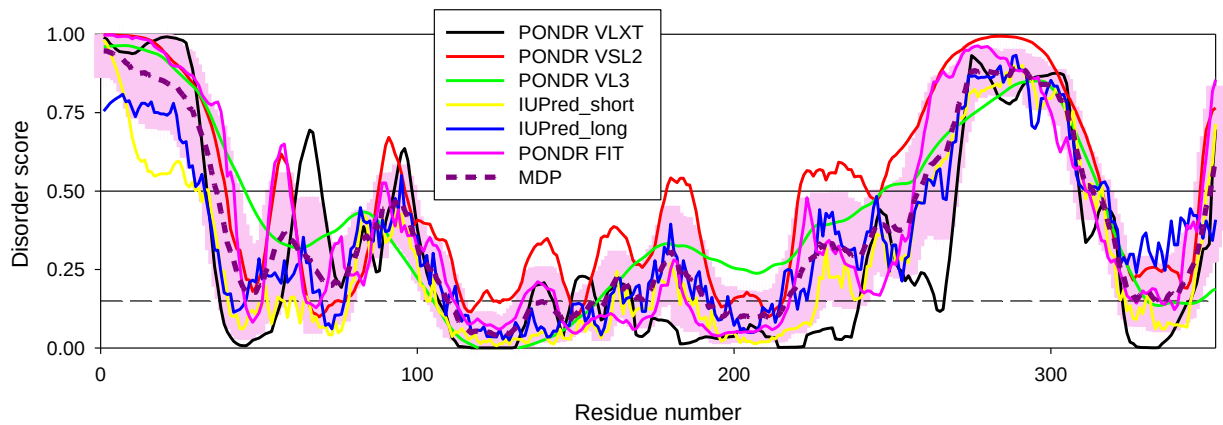
expected number of edges: 76

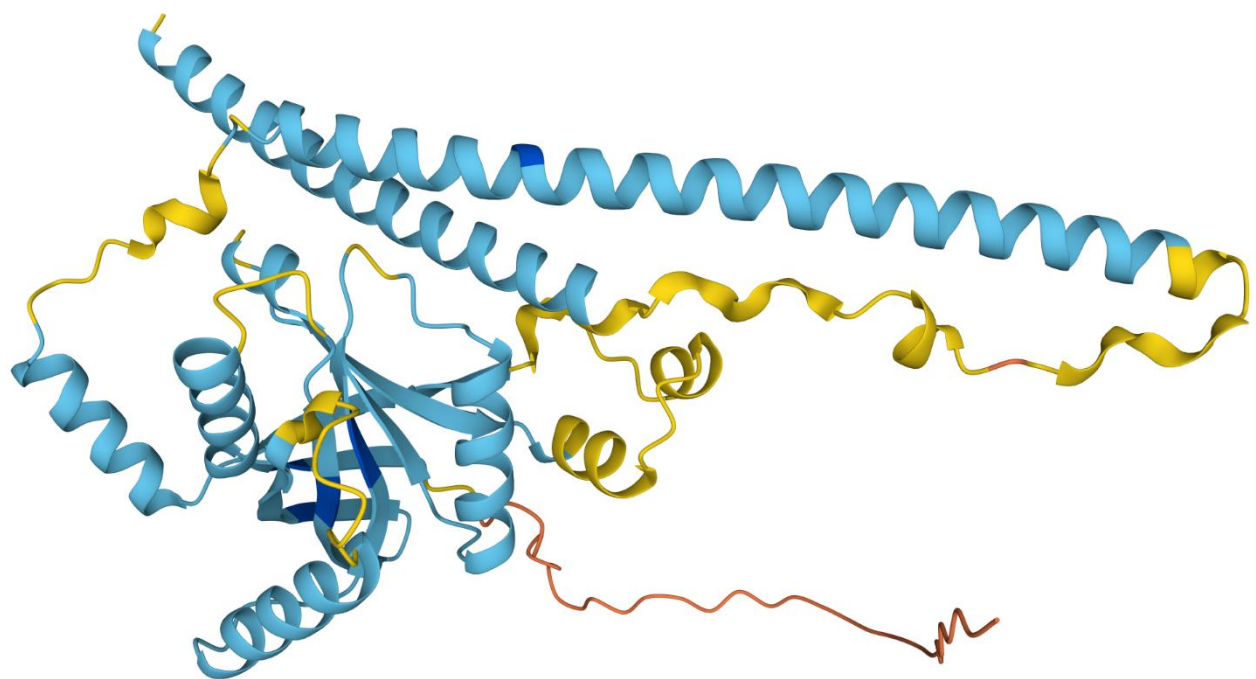
PPI enrichment p-value: $< 1.0e-16$

EIF3H (UniProt ID: O15372)

>sp|O15372|EIF3H_HUMAN Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens OX=9606 GN=EIF3H PE=1 SV=1

MASRKEGTGSTATSSSSTAGAAGKGKGKGGSGDSAVKQVQIDGLVVLKIIKHYYQEEGQ
GTEVVQGVLLGLVVEDRLEITNCFPPQHTEDDADFDEVQYQMEMMRSRLRHVNIDHLH
VGWYQSTYYGSFVTRALLDSQFSYQHAIEESVVLIIYDPIKTAQGSLSLKAYRLTPKLME
VCKEKDFSPEALKKANITFEYMFEEVPIVIKNSHLINVLWWELEKKS AVADKHELLSLAS
SNHLGKNLQLLMDRVDEMSQDIVKYNTYMRNTSKQQQKHKYQQRRQQENMQRQSR
GEPPLPEEDLSKLFKPPQPPARMDSLLIAGQINTYCNIKEFTAQNLGKLFMAQALQEYN
N

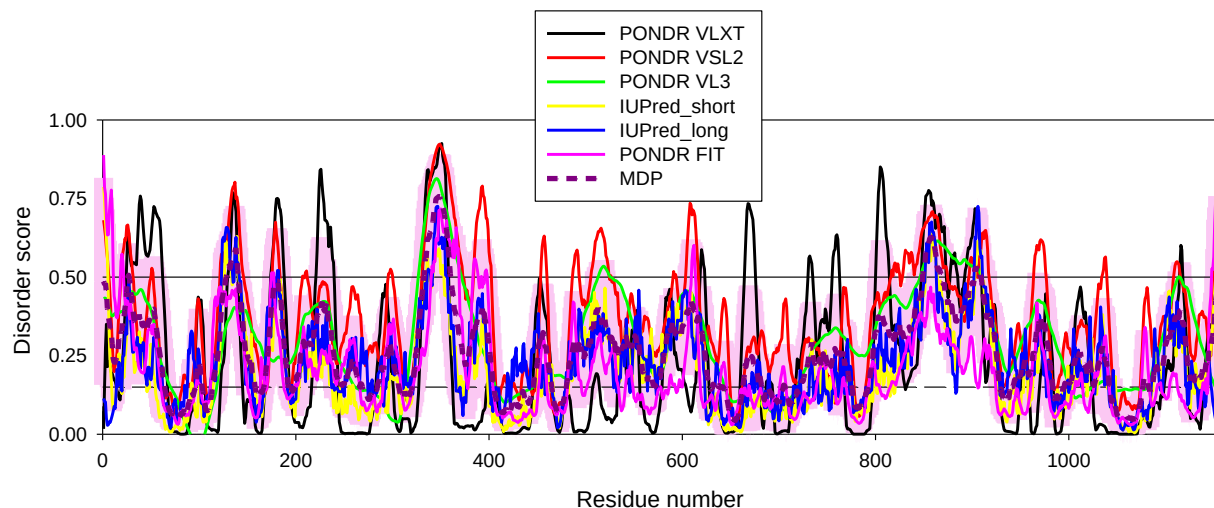


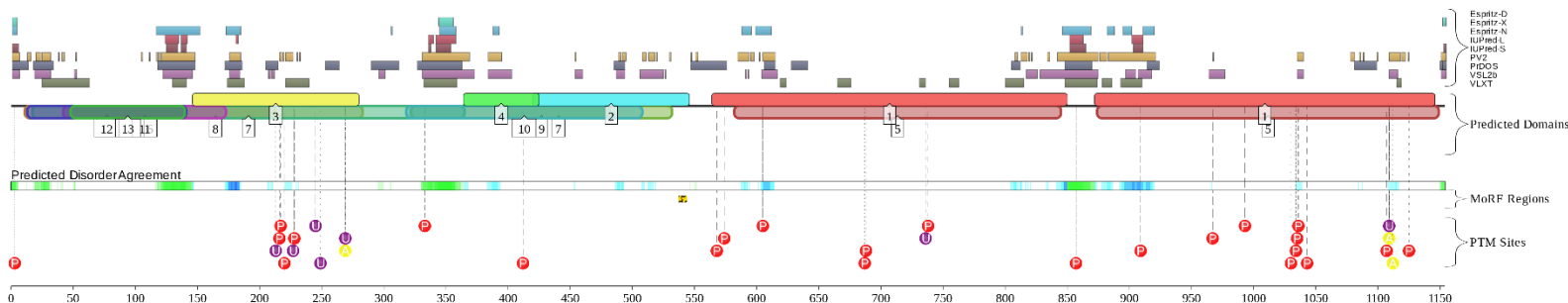


JAK1 (UniProt ID: P23458)

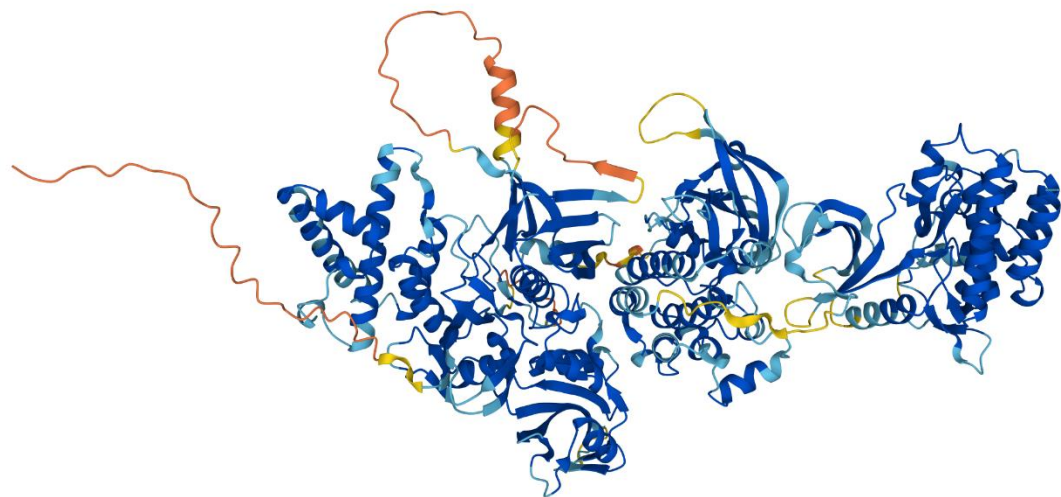
>sp|P23458|JAK1_HUMAN Tyrosine-protein kinase JAK1 OS=Homo sapiens OX=9606
GN=JAK1 PE=1 SV=2

MQYLNIEDCNAMAFCAKMRSSKKTEVNLEAPEPGVEVIFYLSDREPLRLGSGEYTAAE
LCIRAAQACRISPLCHNLFALYDENTKLWYAPNRTITVDDKMSLRLHYRMRFYFTNWH
GTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQGQYDLVKCLAPIRD
PKTEQDGHDIENECLGMAVLAISHYAMMKKMQLPELPKDISYKRYIPETLNKSIRQRNL
LTRMRINNFKDFLKEFNNTICDSSVSTHDLKVLYLATLETTLTKHYGAEIFETSMLLISS
ENEMNWFHSNDGGNVLYYEVMVTGNLGIQWRHKPNVVSVEKEKNKLKRKKLENKHK
KDEEKNKIREEWN NFSYFPEITHIVIKESVVSINKQDNKKMELKLSSHEEALS FVSLVDG
YFRLTADAHHYLCTDVAPPLIVHNIQNGCHGPICTEYAINKLRQEGSEEGMYVLRWSCT
DFDNILMTVTCTFEKSEQVQGAQKQFKNFQIEVQKGRYSLHGSDRSFPSLGLMSHLKKQ
ILRTDNISFMLKRCCQPKPREISNLLVATKKAQEWQPVYPMSQLSFDRILKKDLVQGEHL
GRGTRTHIYSGTLM DYKDD EGTSEEKKIKVILKVLDPSHRDISLAFFEAASMMRQVSHK
HIVLYLGVCVRDVENIMVEEFVEGGPLDLFMHRKSDVLTTPWKFKVAKQLASALSYLE
DKDLVHGNVCTKNLLLAREGIDSECGPFIKLSDPGIPITVLSRQECIERIPWIAPECVEDSK
NLSVAADKWSFGTTLWEICYNGEIPLKDKTLIEKERFYESRCRPVTPSCKELADLMTRC
MNYDPNQRPFFRAIMRDINKLEEQNPDIVSEKKPATEVDP THFEKRFLKRIRDLGEGHFG
KVELCRYDPEGDNTGEQVAVKSLKPESGGNHIADLKKEIEILRNLYHENIVKYKGICTED
GGNGIKLIMEFLPSGSLKEYLPKNKNKINLKQQLKYAVQICKGMDYLGSRQYVHRDLA
ARNVLVESEHQVKIGDFGLTKAIETDKEYYTVKDDRDSPVFWYAPECLMQSKFYIASDV
WSFGVTLLHELLTYCSDSDSPMALFLKMIGPTHGQMTVTRLVNTLKEGKRLPCPPNCPDE
VYQLMRKCWEFQPSNRTSFQNLIEGFEALLK





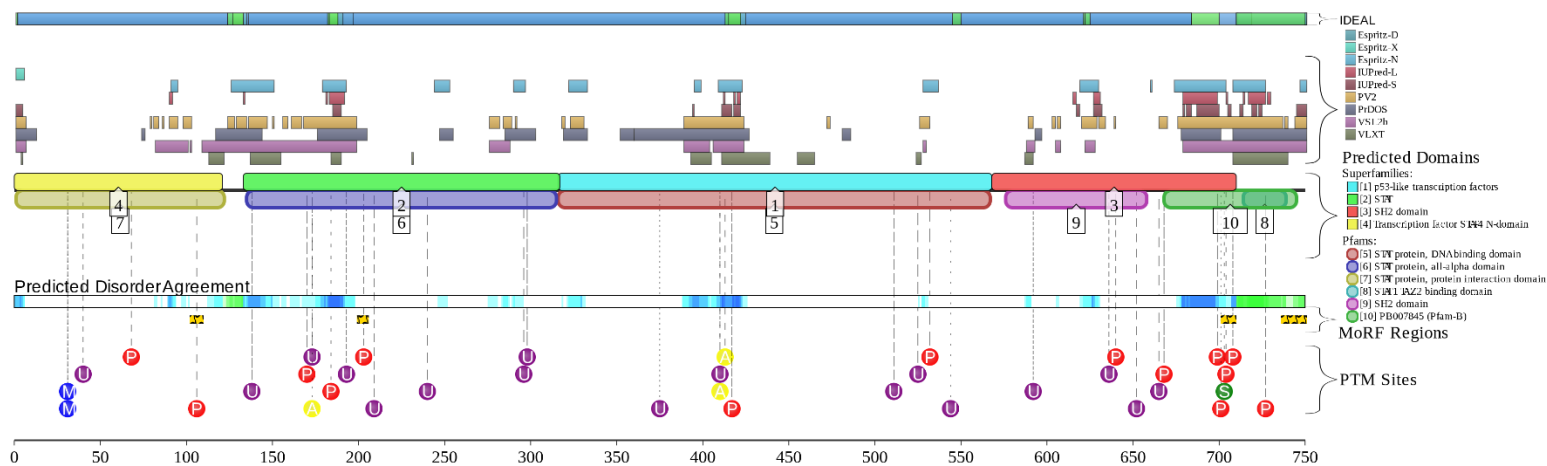
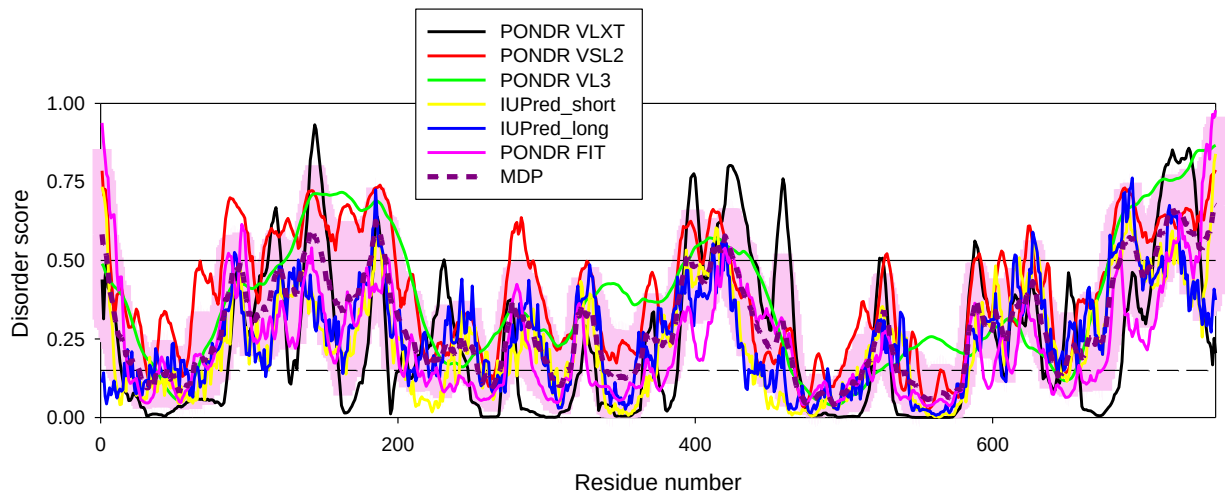
- Key:**
- Predicted SCOP Structure
 - Weak Support
 - Pfam Conserved Domain
 - Predicted Disorder
 - Predicted MoRFs
 - Curated PTM Site
- Disorder:**
- Espritz-D
 - Espritz-X
 - Espritz-N
 - IUPred-L
 - IUPred-S
 - PV2
 - PrDOS
 - VSL2b
 - VLXT
- Superfamilies:**
- [1] Protein kinase-like (PK-like)
 - [2] SH2 domain
 - [3] Second domain of FERM
 - [4] PH domain-like
- Pfams:**
- [5] Protein tyrosine kinase
 - [6] PB012686 (Pfam-B)
 - [7] PB004056 (Pfam-B)
 - [8] PB004639 (Pfam-B)
 - [9] PB000991 (Pfam-B)
 - [10] PB001288 (Pfam-B)
 - [11] PB015196 (Pfam-B)
 - [12] PB002501 (Pfam-B)
 - [13] PB005821 (Pfam-B)

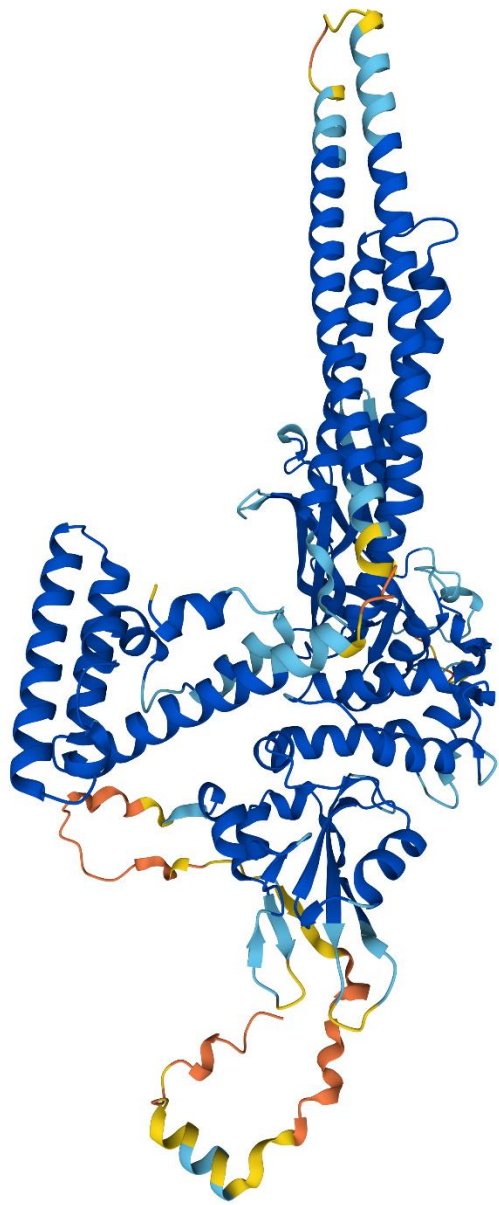


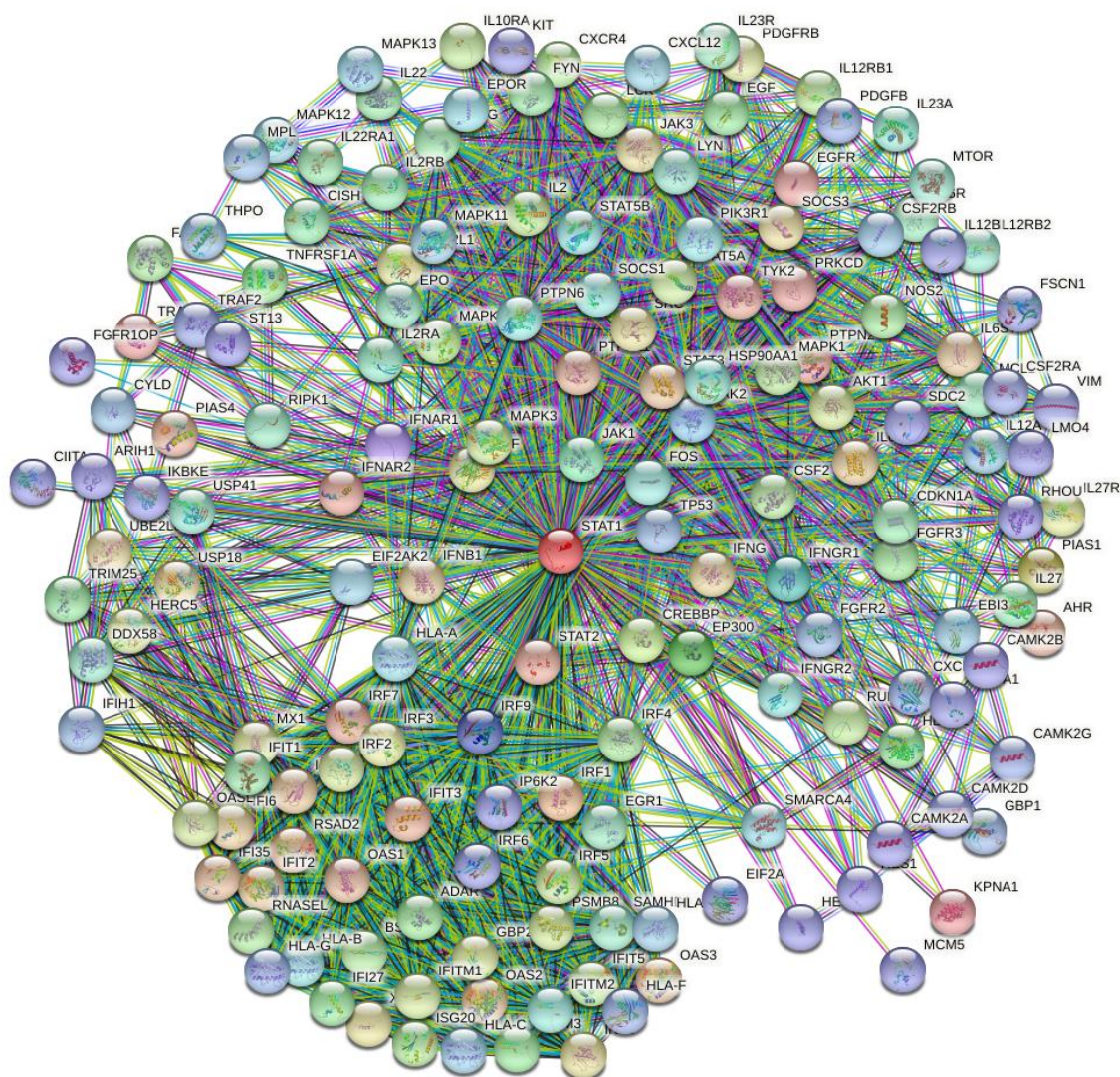
STAT1 (UniProt ID: P42224)

>sp|P42224|STAT1_HUMAN Signal transducer and activator of transcription 1-alpha/beta
OS=Homo sapiens OX=9606 GN=STAT1 PE=1 SV=2

MSQWYELQQLDSKFLEQVHQLYDDSFPMERQYLAQWLEKQDWEHAANDVSFATIRF
HDLLSQLDDQYSRFSLENNFLLQHNIRKSKRNLQDNFQEDPIQMSMIIYSCLKEERKILEN
AQRFNQAQSGNIQSTVMLDKQKELDSKVRNVKDKVMCIEHEIKSLEDLQDEYDFKCKT
LQNREHETNGVAKSDQKQEQLLLKKMYLMLDNKRKEVVHKIIELLNVTELTQNALIND
ELVEWKRRQQSACIGGPPNACLDQLQNWFTIVAESLQQVRQQLKKLEELEQKYTYEHD
PITKNKQVLWDRTFSLFQQLIQSSFVVERQPCMPHTHPQRPLVLKTGVQFTVKLRLLVKL
QELNYNLKVKVLFDKDVNERNTVKGFRKFNILGHTTKVMNMEESTNGSLAAEFRHLQL
KEQKNAGTRTNEGPLIVTEELHSLSFETQLCQPGLVIDLETTSLPVVISNVSQLP SGWAS
ILWYNMLVAEPRNLSFFLTPPCARWAQLSEVLSWQFSSVTKRGLNVDQLNMLGEKLLG
PNASPDGLIPWTRFCKENINDKNFPFWLWIESILELIKHLPLWNDGCIMGFISKERERA
LLKDQQPGTFLLRFSESSREGAITFTWVERSQNGGEPDFHAVEPYTKKELSAVTFPDIIRN
YKVMAAENIPENPLKYLYPNIDKDHAFGKYYSRPKEAPEPMELDGPKGTYIKTELISVS
EVHPSRLQTTDNLLPMSPEEFDEVSRIVGSVEFDSMMNTV







minimum required interaction score: highest confidence (0.900)

number of nodes: 43

number of edges: 257

average node degree: 12

avg. local clustering coefficient: 0.847

expected number of edges: 50

PPI enrichment p-value: $< 1.0e-16$

number of nodes: 164

number of edges: 2126

average node degree: 25.9

avg. local clustering coefficient: 0.733

expected number of edges: 507

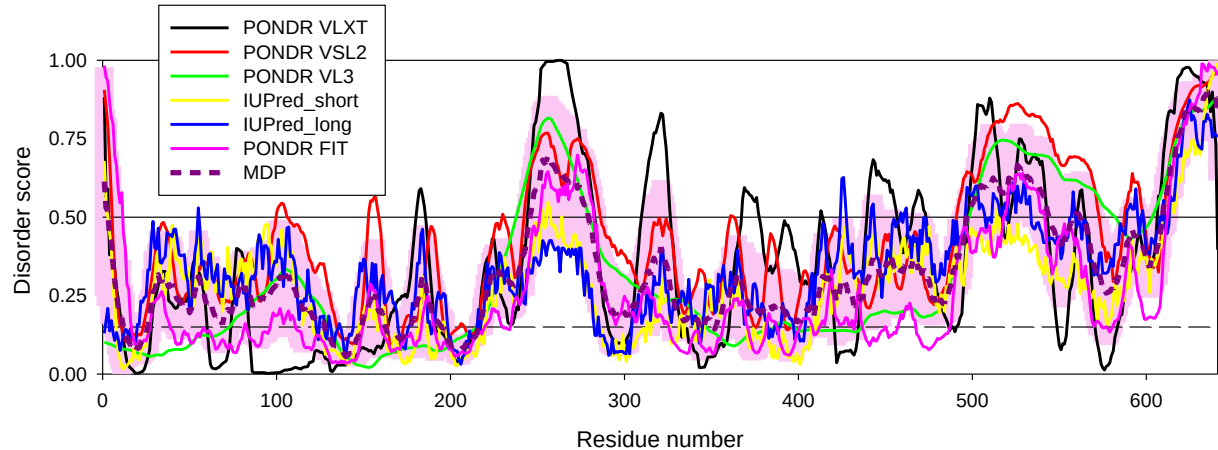
PPI enrichment p-value: $< 1.0e-16$

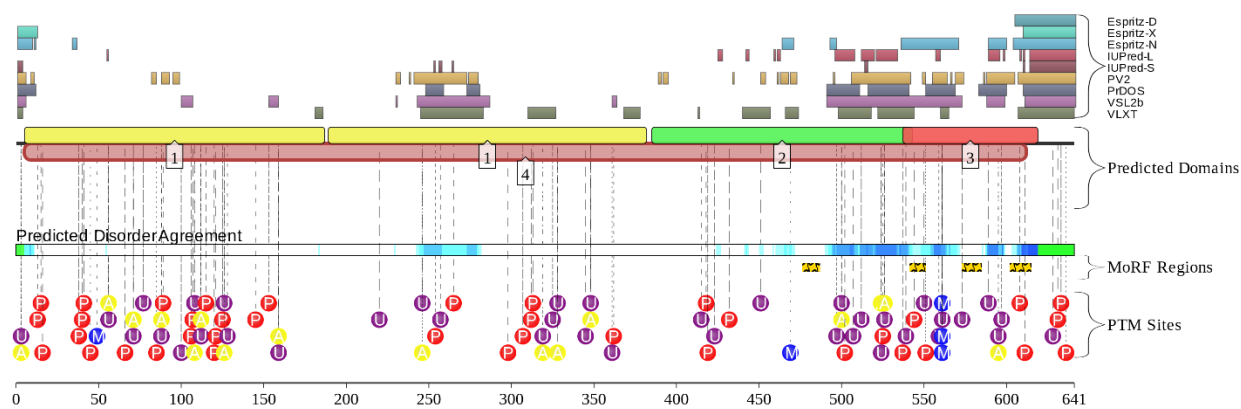
Supplementary Figure S3. Functional disorder in human proteins interacting with the RABV N-protein. For each protein, an amino acid sequence in FASTA format is shown followed by the disorder profile generated by RIDAO, D²P²-generated functional disorder profile, modeled 3D structure generated by AlphaFold, and STRING-based protein-protein interaction network.

HSPA1A (UniProt ID: P0DMV8)

>sp|P0DMV8|HS71A_HUMAN Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606
GN=HSPA1A PE=1 SV=1

MAKAAAIGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFTDTERLIGDAAKNQV
ALNPQNTVFDKRLIGRKFGDPVVQSDMKHWPVQVINDGDKPKVQVSYKGETKAFYPE
EISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRINEPT
AAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRL
VNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSIT
RARFEELCSDLFRSTLEPVEKALRDAKLDAQIHDLVLVGGSTRIPKVQKLLQDFFNGR
DLNKSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLTAGGVM TALIK
RNSTIPTKQTQIFTTYS DNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEV
TFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAKEYKAEDDEVQRER
VSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKQCQEVISWLDANTLAEKDEFE
HKRKELEQVCNPIISGLYQGAGGPGPGGFGAQQGPKGGSGSGPTIEEVD





Key:

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

Disorder:

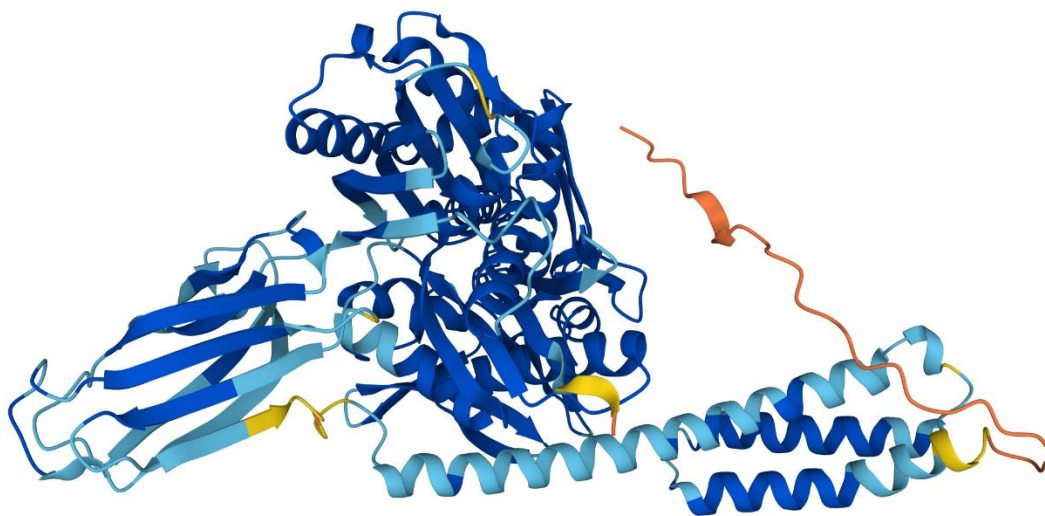
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

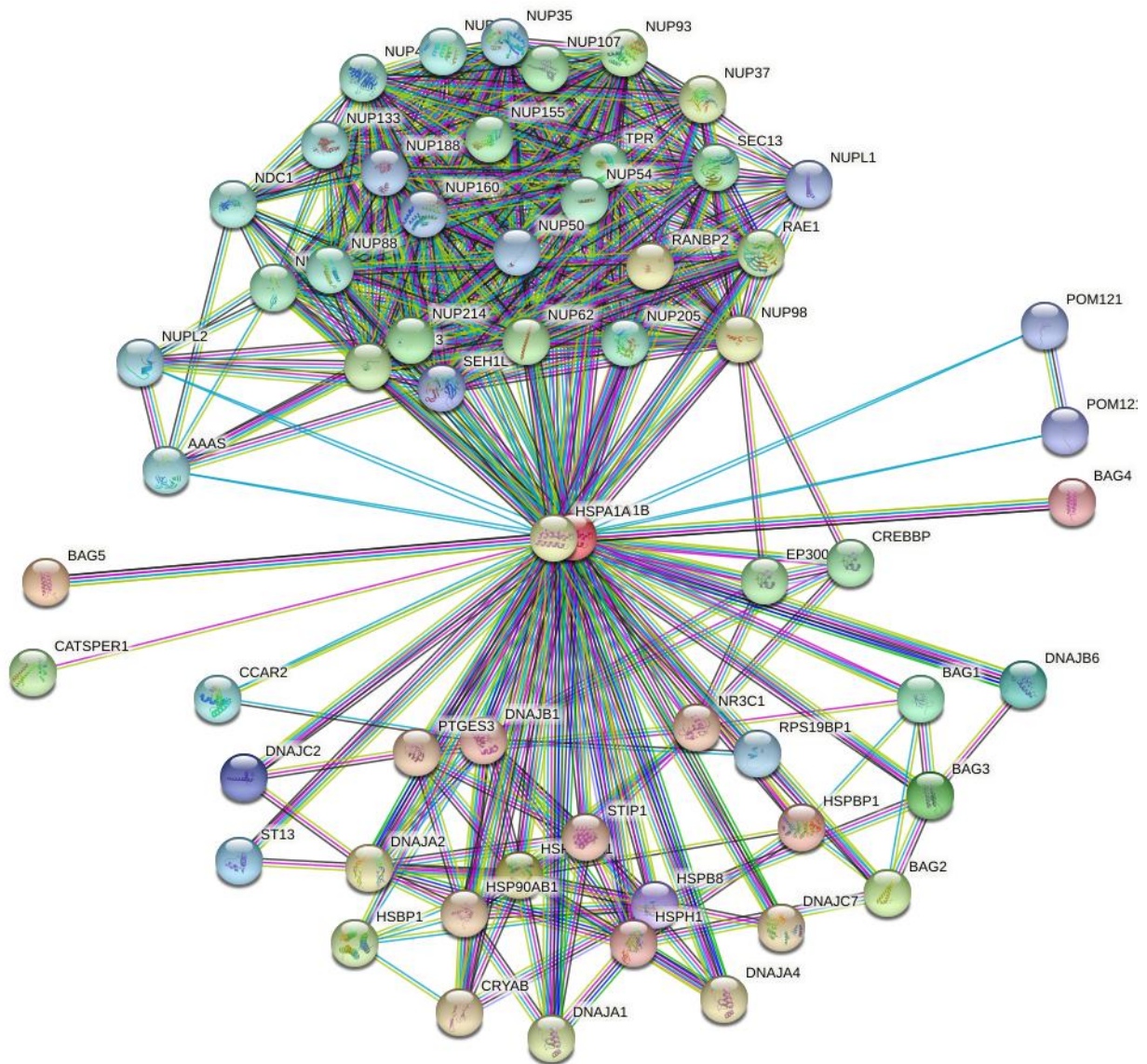
Superfamilies:

- [1] Actin-like ATPase domain
- [2] Heat shock protein 70kD (HSP70), peptide-binding domain
- [3] Heat shock protein 70kD (HSP70), C-terminal subdomain

Pfams:

- [4] Hsp70 protein





minimum required interaction score: highest confidence (0.900)

number of nodes: 60

number of edges: 459

average node degree: 15.3

avg. local clustering coefficient: 0.849

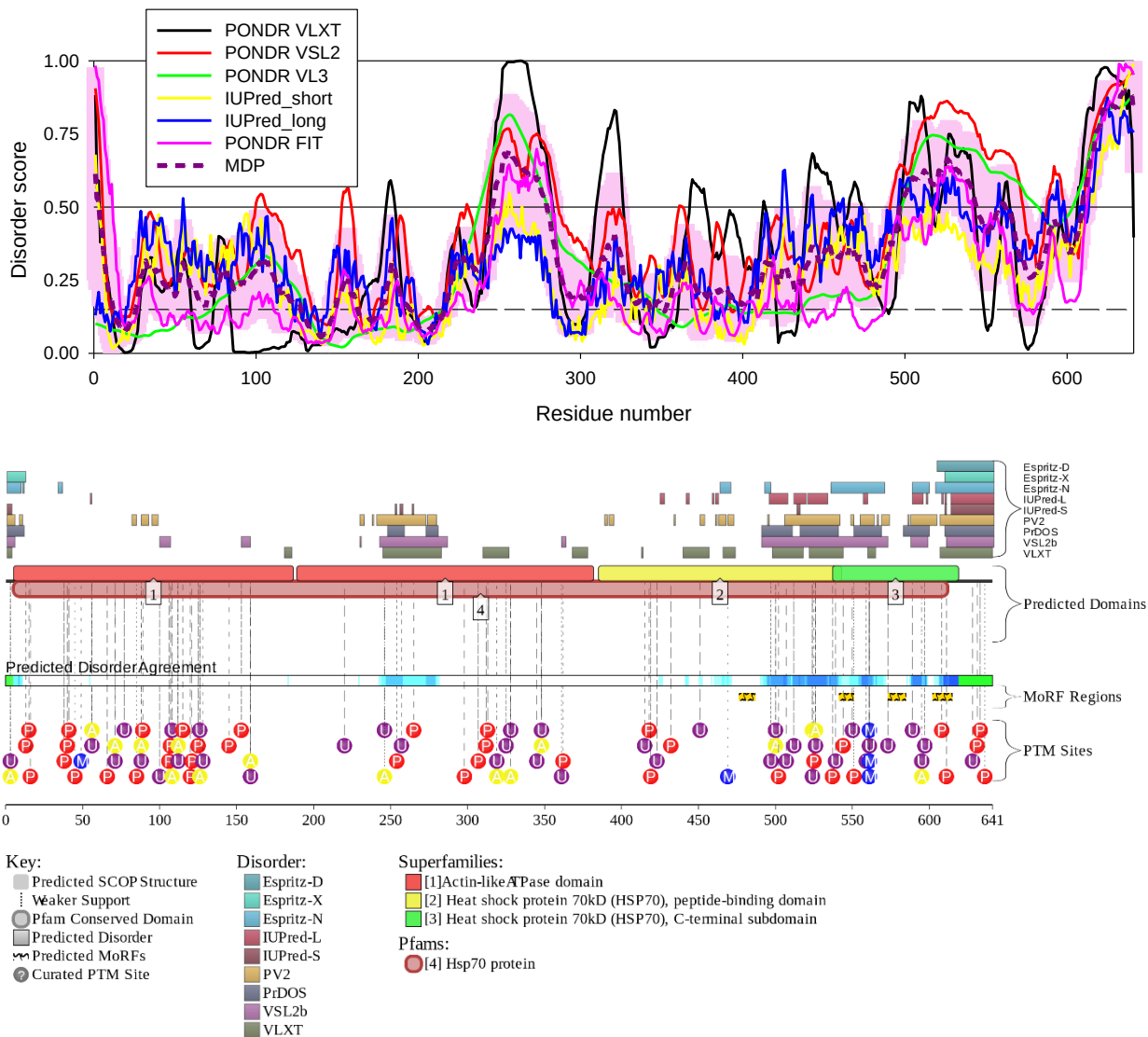
expected number of edges: 97

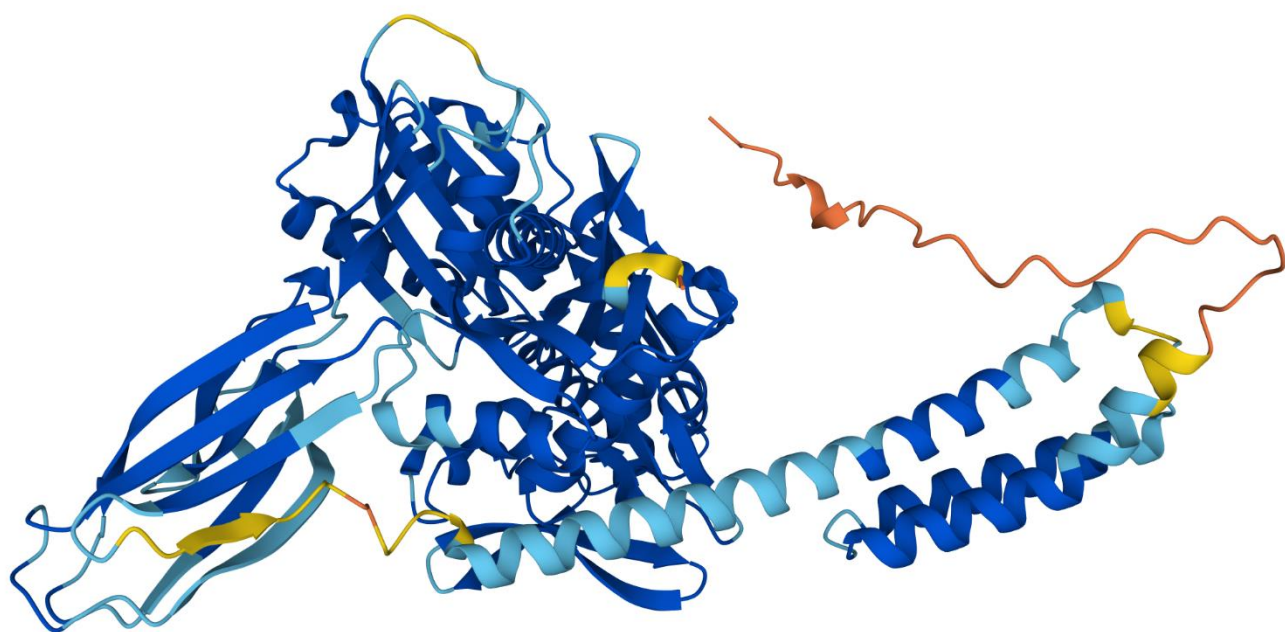
PPI enrichment p-value: $< 1.0e-16$

HSPA1B (UniProt ID: P0DMV9)

>sp|P0DMV9|HS71B_HUMAN Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606
GN=HSPA1B PE=1 SV=1

MAKAAAIGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFTDTERLIGDAAKNQV
ALNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPVQVINDGDKPKVQVQSYKGETKAFYPE
EISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRINEPT
AAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRL
VNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSIT
RARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGR
DLNKSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLTAGGVMTALIK
RNSTIPTKQTQIFTTYSNQPGLVIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVQPQIEV
TFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAKEYKAEDDEVQRER
VSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFE
HKRKELEQVCNPIISGLYQGAGGPGPGGFGAQQGPKGGSGSGPTIEEVD



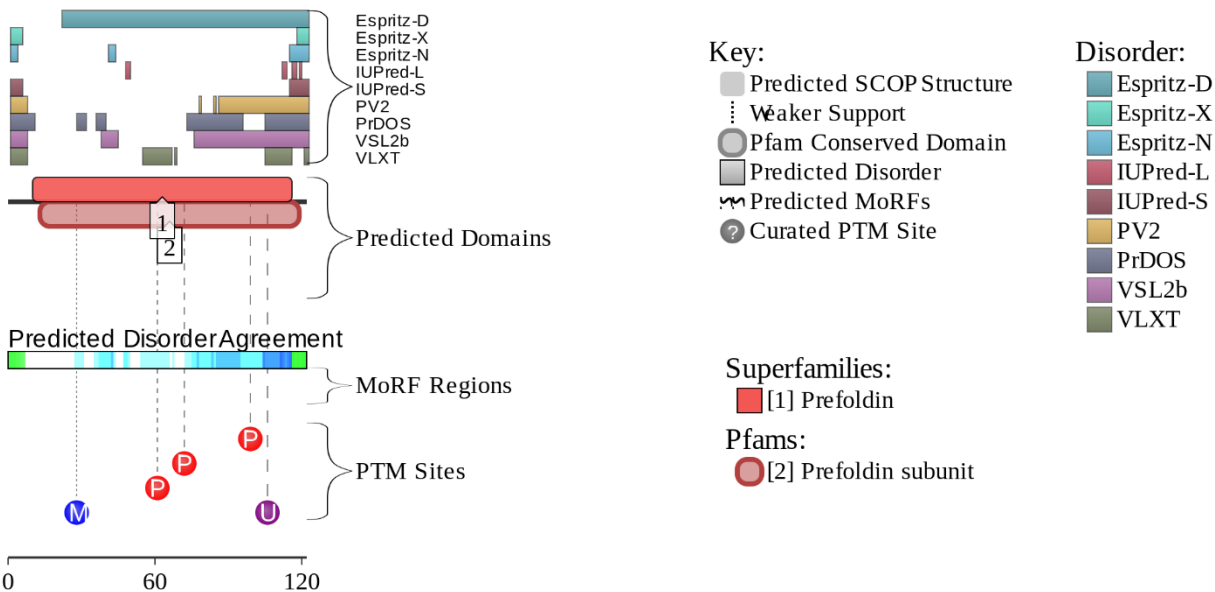
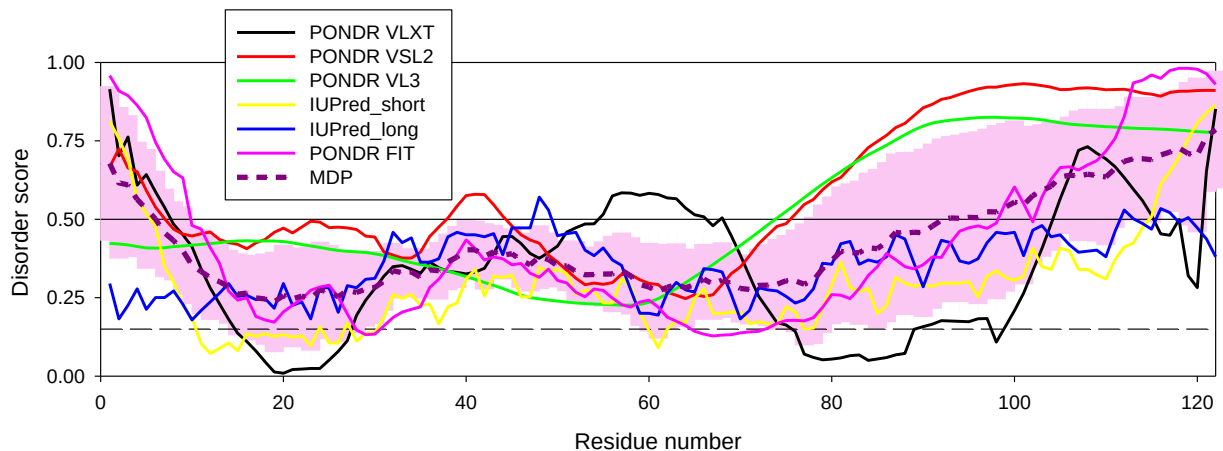


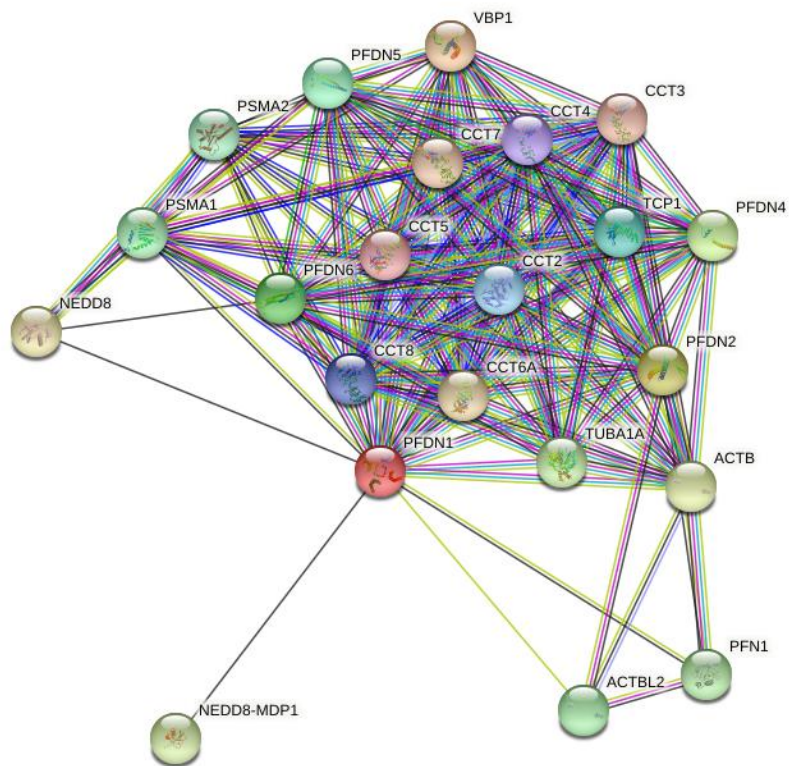
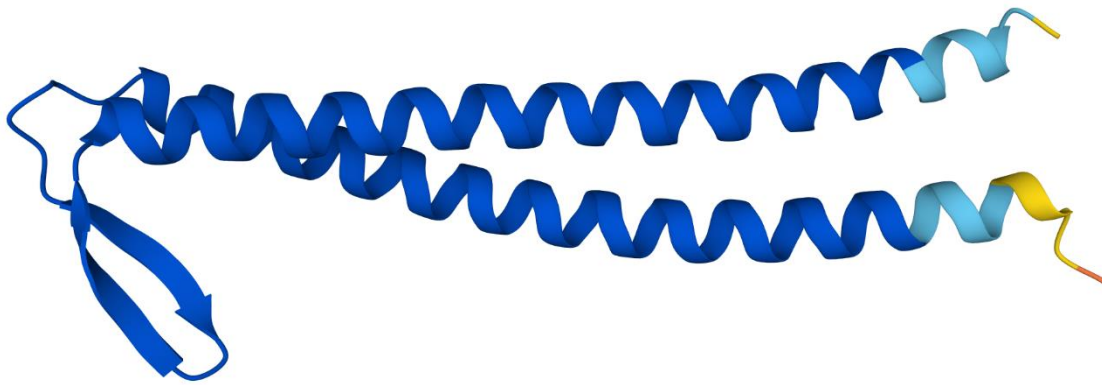
PPI enrichment p-value: $< 1.0\text{e-}16$

Prefoldin 1 (PFDN1, UniProt ID: O60925)

>sp|O60925|PFD1_HUMAN Prefoldin subunit 1 OS=Homo sapiens OX=9606 GN=PFDN1
PE=1 SV=2

MAAPVDLELKKAFTTELQAKVIDTQQKVKLADIQIEQLNRTKKHAHLTDTEIMTLVDET
NMYEGVGRMFILQSKEAIHSQELLEKQKIAEEKIKELEQKKSYLERSVKEAEDNIREMLMA
RRAQ





minimum required interaction score: high confidence (0.700)

number of nodes: 22

number of edges: 151

average node degree: 13.7

avg. local clustering coefficient: 0.895

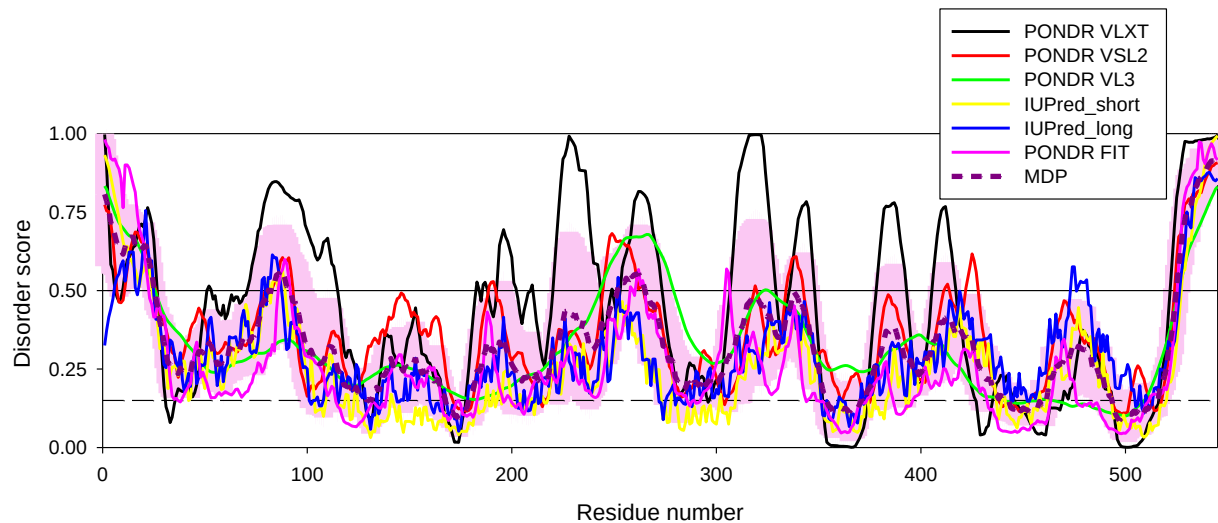
expected number of edges: 26

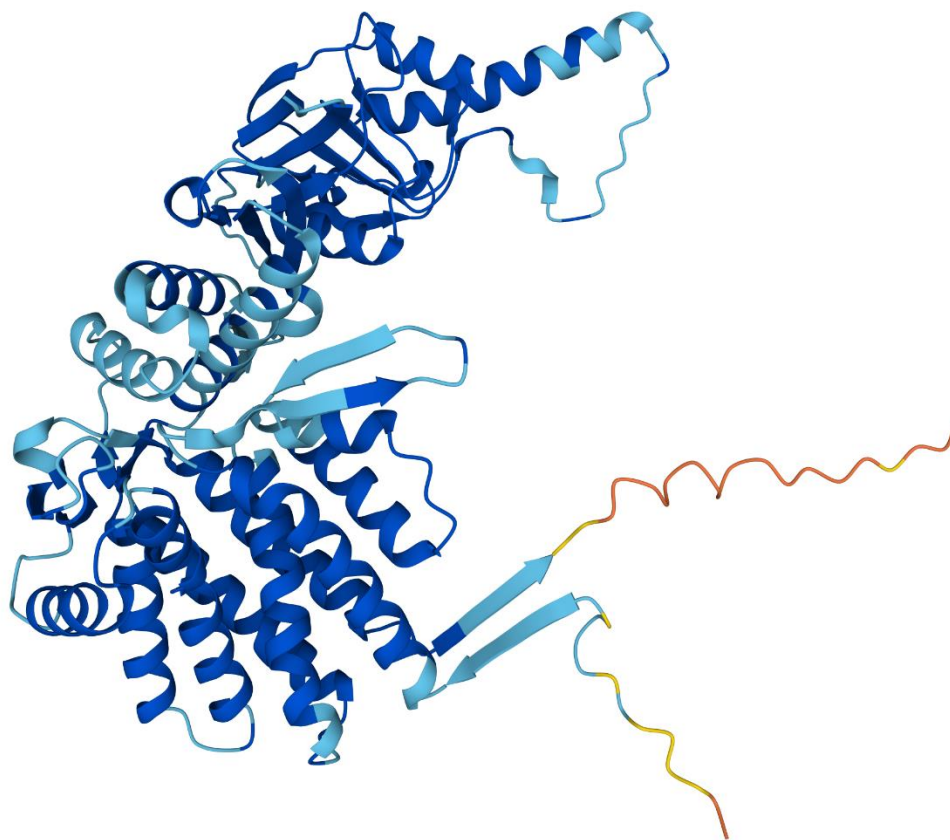
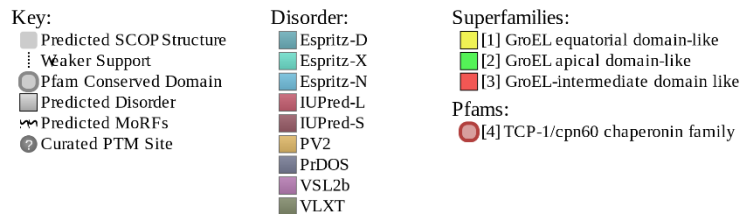
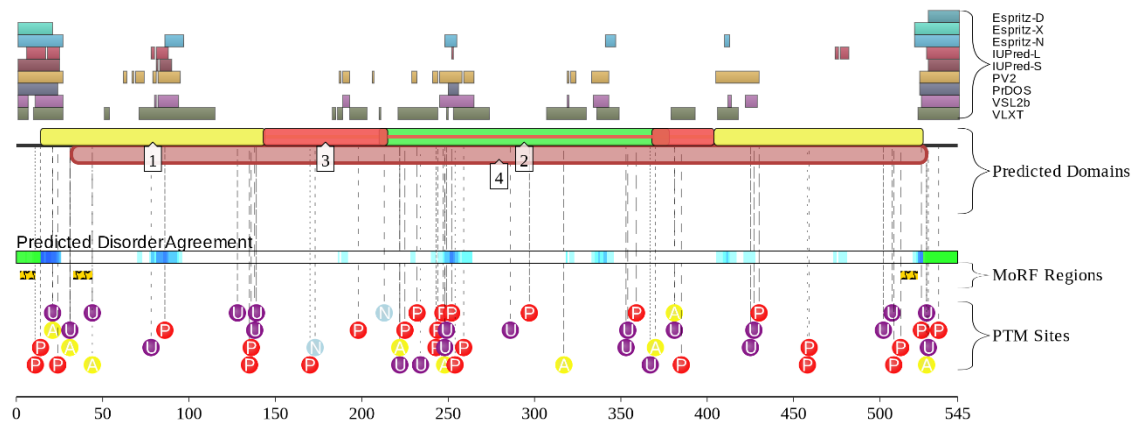
PPI enrichment p-value: $< 1.0e-16$

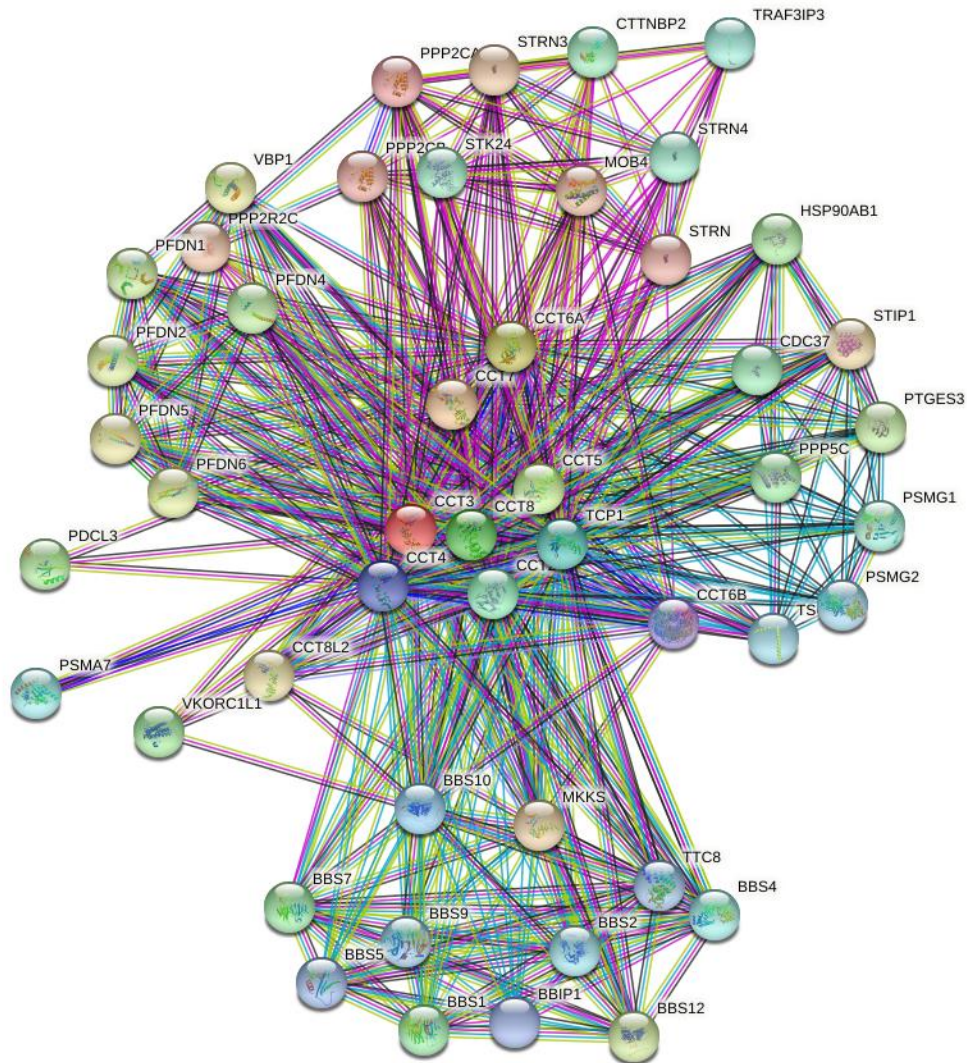
CCT γ (UniProt ID: P49368)

>sp|P49368|TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens OX=9606
GN=CCT3 PE=1 SV=4

MMGHRPVLVLSQNTKRESGRKVQSGNINAAKTIADIIRTCLGPKSMMKMLLDPMGGIV
MTNDGNAILREIQVQHPAAKSMIEISRTQDEEVGDGTTSVILAGEMLSVAEHFLEQQMH
PTVVISAYRKALDDMISTLKKISIPVDISDSMMLNIINSSITTKAISRWSSLACNIALDAV
KMQFEENGRKEIDIKKYARVEKIPGGIIEDSCVLRGVMINKDVTHTPRMRRYIKNPRIVL
LDSSLEYKKGESQTDIEITREEDFTRILQMEEYIQQLCEDIIQLKPDVVITEKGISDLAQH
YLMRANITAIRRVRKTDNNRIARACGARIVSRPEELREDDVGTGAGLLEIKKIGDEYFTFI
TDCKDPKACTILLRGASKEILSEVERNLDAMQVCRNVLLDPQLVPGGGASEMAVAHA
LTEKSKAMTGVEQWPYRAVAQALEVIPRTLQNCGASTIRLLTSLRAKHTQENCETWGV
NGETGTLVDMKELGIWEPLAVKLQTYKTAVETAVLLLRIDDIVSGHKKKGDDQSRQGG
APDAGQE







minimum required interaction score: highest confidence (0.900)

number of nodes: 48

number of edges: 443

average node degree: 18.5

avg. local clustering coefficient: 0.872

expected number of edges: 53

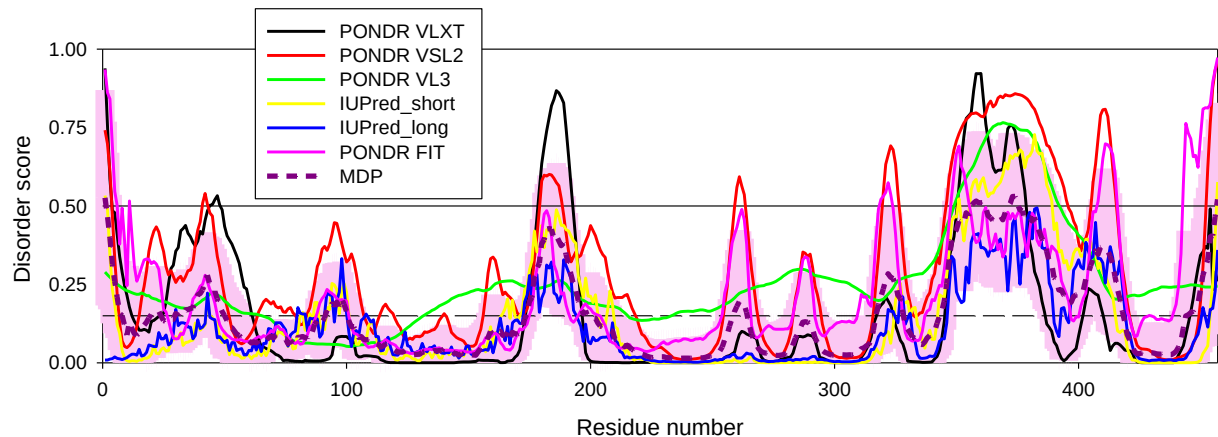
PPI enrichment p-value: $< 1.0e-16$

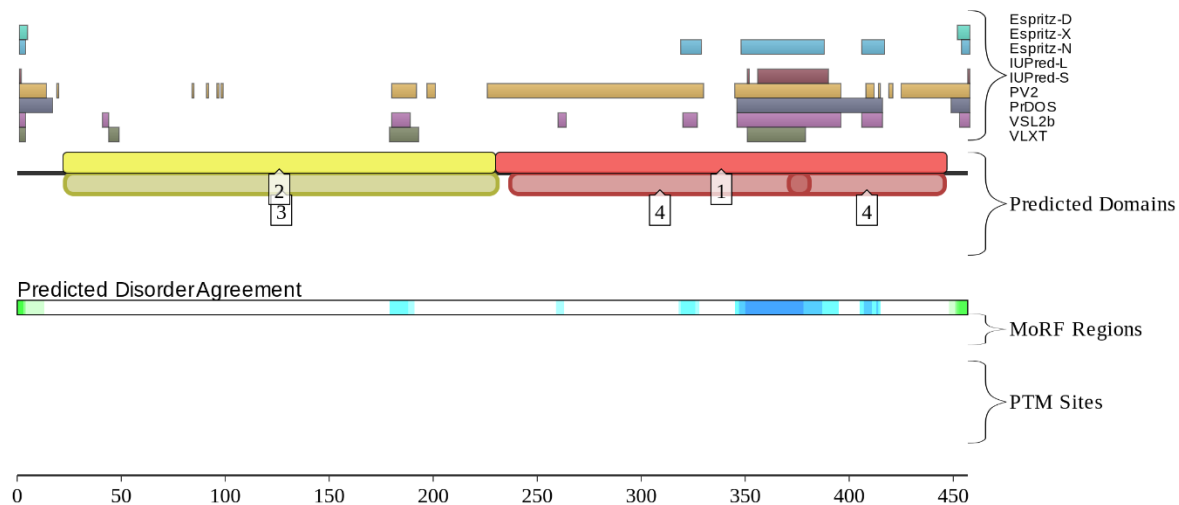
Supplementary Figure S4. Functional disorder in human proteins interacting with the RABV G-protein. For each protein, an amino acid sequence in FASTA format is shown followed by the disorder profile generated by RIDAO, D²P²-generated functional disorder profile, modeled 3D structure generated by AlphaFold, and STRING-based protein-protein interaction network.

nAChR α 1 (CHRNA1; UniProt ID: P02708)

>sp|P02708|ACHA_HUMAN Acetylcholine receptor subunit alpha OS=Homo sapiens
OX=9606 GN=CHRNA1 PE=1 SV=3

MEPWPLLLLFSLC SAGLVLGSEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTVGLQLIQ
LINVDEVNQIVTTNVRLKQQWVDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNAD
GDFAIVKFTKVLLQYTGHTWTPPAIFKSYCEIIVTHFPFDEQNC SMKLG TWTYDGSVVA
INPESDQPDLSNFMESGEWVIKESRGWKHSVTYSCCPDTPYLDITYHFVMQRLPLYFIVN
VIIPCLLFSFLTGLVFYLP TDSGEKMTLSISVLLSLTVFLLVIVELIPSTSSAVPLIGKYMLFT
MVFVIAIIITVIVINTHHRSPSTHVMPNWVRKVFIDTIPNIMFFSTMKRPSREKQDKKIFT
EDIDISDISGKPGPPPMGFHSPLIKHPEVKSAIEGIKYIAETMKSDQESNNAAEWKYVA
MVMDHILLGVFMLVCIIGTLAVFAGR LIELNQQG





Key:

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

Disorder:

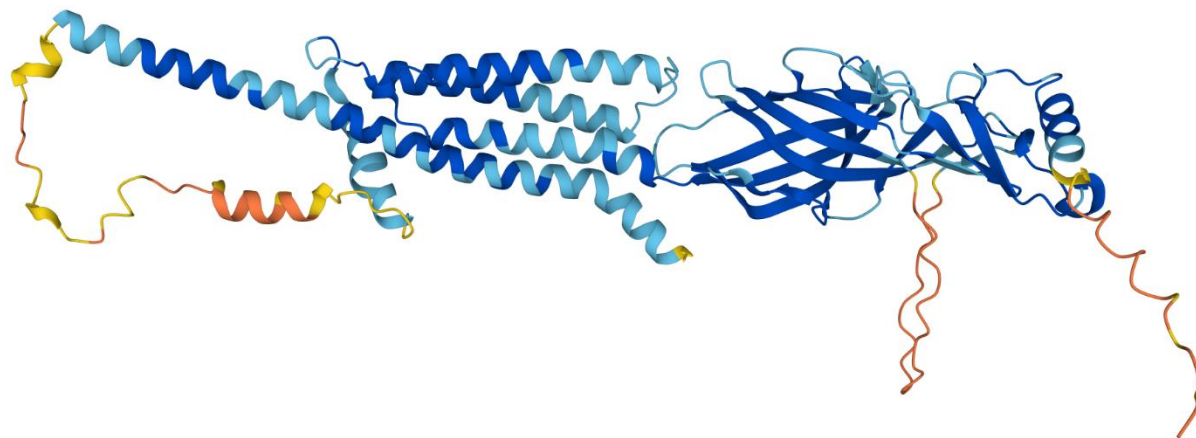
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

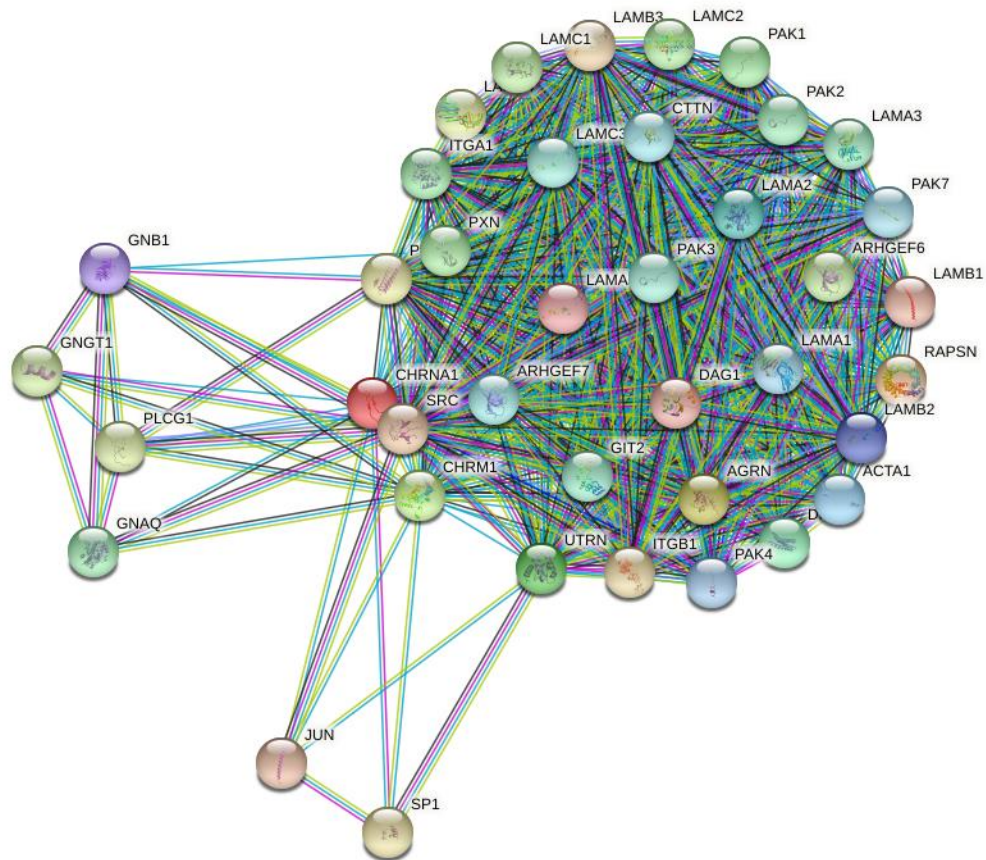
Superfamilies:

- [1] Neurotransmitter-gated ion-channel transmembrane pore
- [2] Nicotinic receptor ligand binding domain-like

Pfams:

- [3] Neurotransmitter-gated ion-channel ligand binding domain
- [4] Neurotransmitter-gated ion-channel transmembrane region





minimum required interaction score: highest confidence (0.900)

number of nodes: 39

number of edges: 558

average node degree: 28.6

avg. local clustering coefficient: 0.961

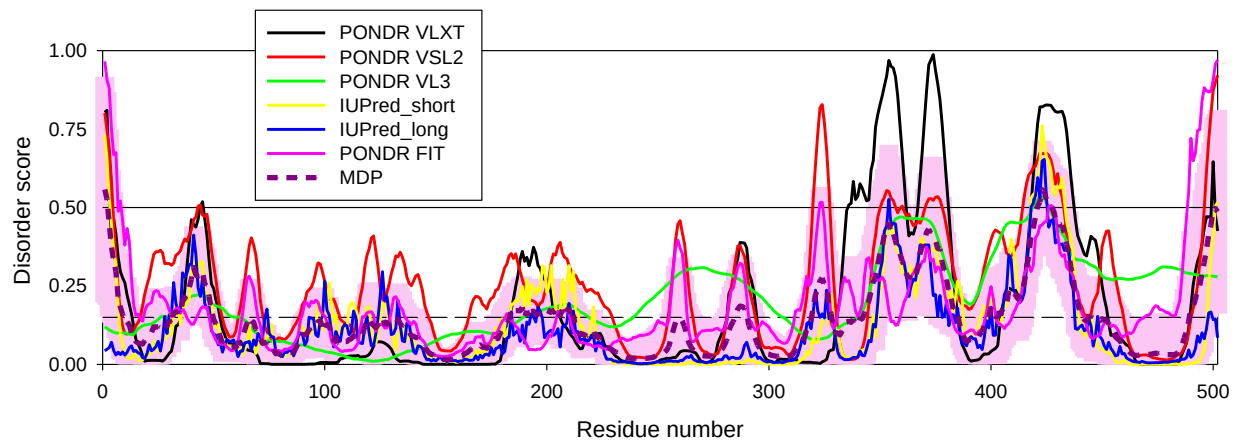
expected number of edges: 62

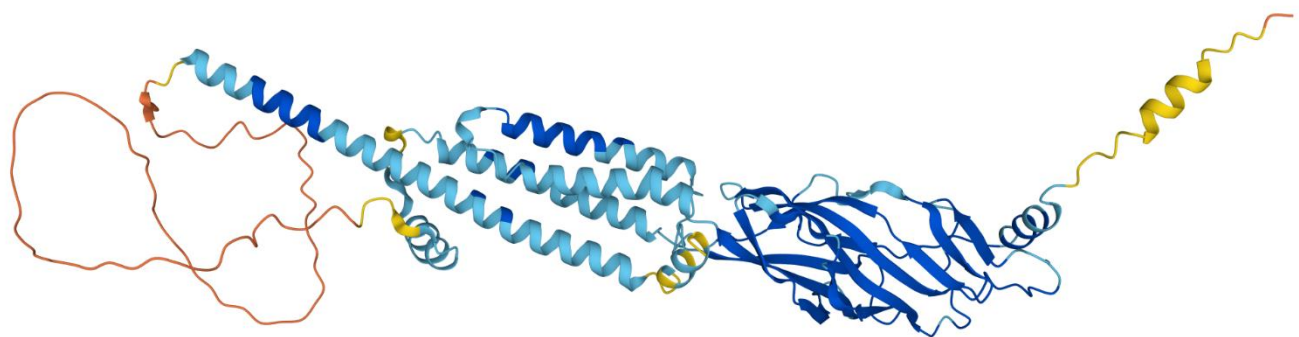
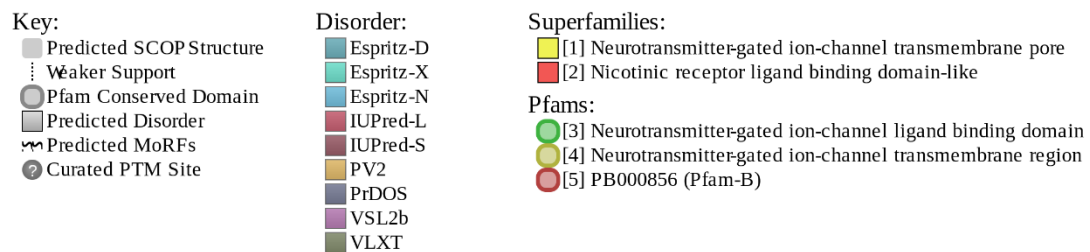
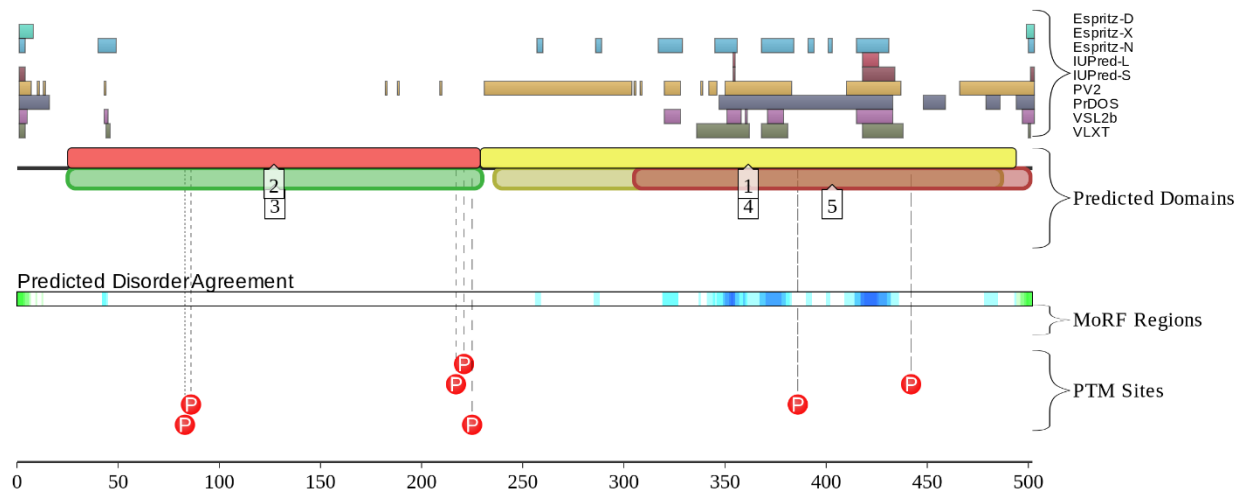
PPI enrichment p-value: $< 1.0e-16$

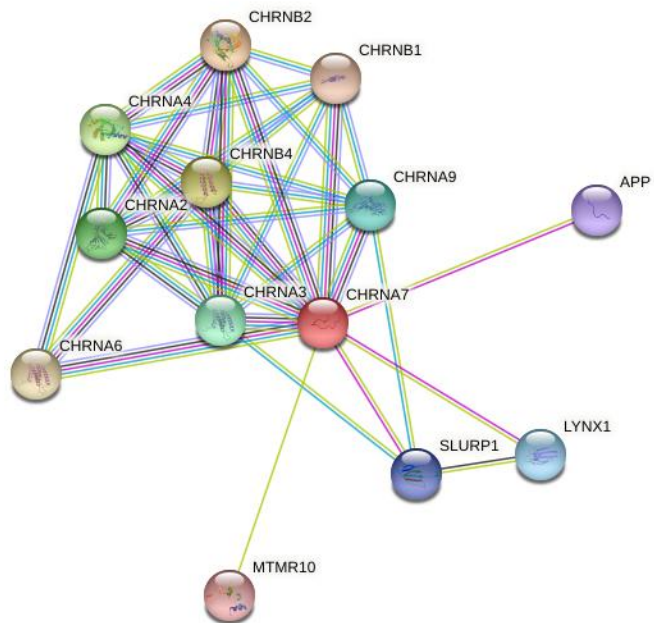
nAChr $\alpha 7$ (CHRNA7, UniProt ID: P36544)

>sp|P36544|ACHA7_HUMAN Neuronal acetylcholine receptor subunit alpha-7 OS=Homo sapiens OX=9606 GN=CHRNA7 PE=1 SV=5

MRCSPGGVWLALAASLLHVS LQGEFQRKLYKELVKNYNPLERP VANDSQPLTVYFSL S
LLQIMDVDEKNQVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDGGQIWKPDILLY
NSADERFDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYG
GWSLDLQMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTMRRRTLYY
GLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQ
YFASTMIIVGLSVVVTIVVLQYHHHDPDGGKMPKWTRVILLNWCWFLRMKRPGEDK
VRPACQHKQRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPD SGVVCGRM
ACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRQCDESEAVCSEWKFAACVVDR
LCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA







minimum required interaction score: high confidence (0.700)

number of nodes: 13

number of edges: 38

average node degree: 5.85

avg. local clustering coefficient: 0.873

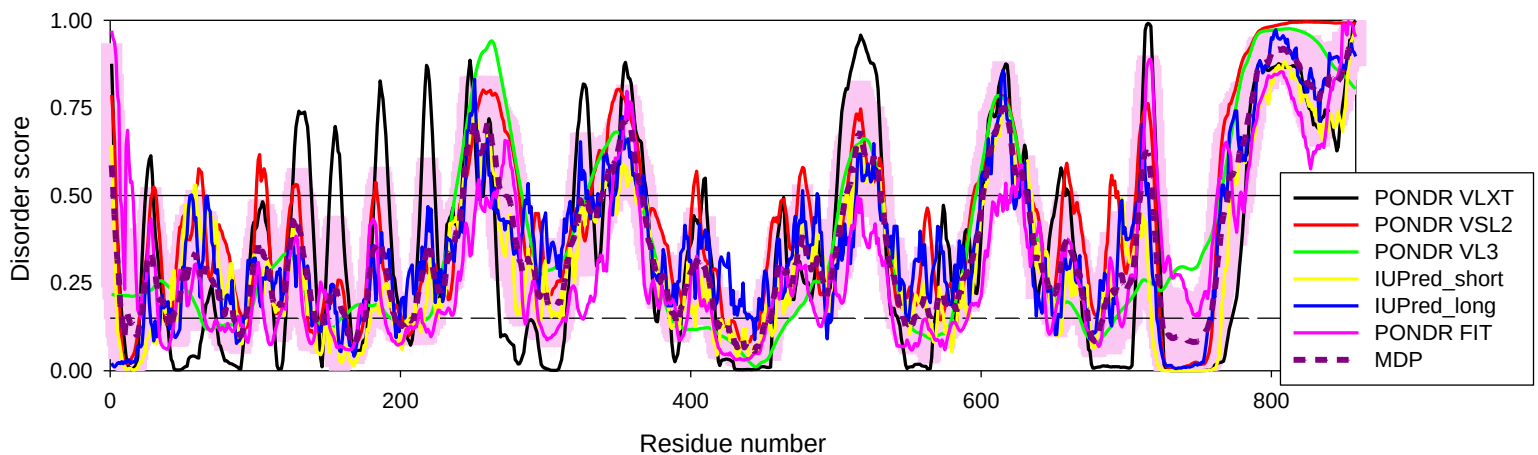
expected number of edges: 12

PPI enrichment p-value: 2.01e-09

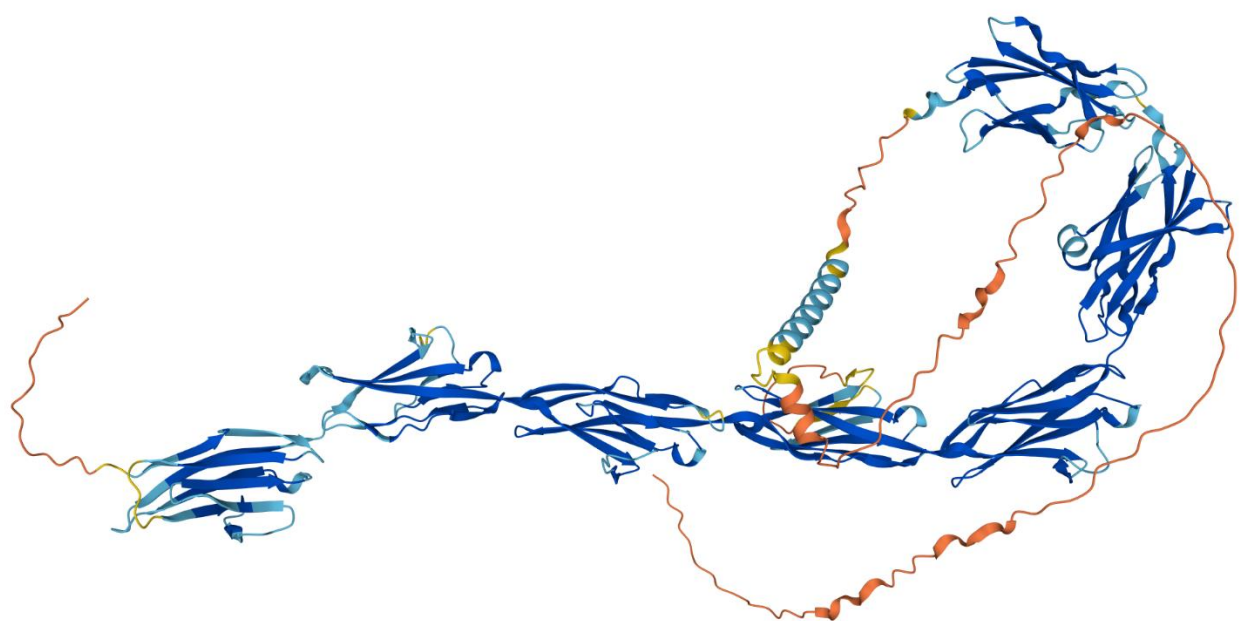
NCAM1 (UniProt ID: P13591)

>sp|P13591|NCAM1_HUMAN Neural cell adhesion molecule 1 OS=Homo sapiens OX=9606
GN=NCAM1 PE=1 SV=3

MLQTKDLIWTLFFLGTA VSLQVDIVPSQGEISVGESKFFLCQVAGDAKDKDISWFSPNGE
KLTPNQQRISVVWNDDSSSTLTIYNANIDDA GIYKCVVTGEDGSESEATVNVKIFQKLMF
KNAPTPQEFREGEDAVIVCDVVSLLPPTIIWKHKGRDVILKKDVRFIVLSNNYLQIRGIKK
TDEGTYRCEGRILARGEINFKDIQVIVNVPPTIQARQNIVNATANLGQSVTLVCDAEGFPE
PTMSWTKDGEQIEQEEDDEKYIFSDDSSQLTIKKVDKNDEAEYICIAENKAGEQDATIHL
KVFAKPKITYVENQTAMELEEQVTLTCEASGDPIPSITWRTSTRNISSEEKASWTRPEKQE
TLDGHMVVRSHARVSSLTLKSIQYTDAGEYICTASNTIGQDSQSMYLEVQYAPKLQGPV
AVYTWEQNQVNITCEVFAYPSATISWFRDQLLPSSNYSNIKIYNTPSASYLEVTPDSEN
DFGNYNCTAVNRIGQESLEFILVQADTPSSPSIDQVEPYSSAQVQFDEPEATGGVPILKY
KAEWRAVGEEVWHSKWYDAKEASMEGIVTIVGLKPETTYAVRLAALNGKGLGEISAA
SEFKTQPVQGEPSAPKLEGQMGEDGNSIKVNLIKQDDGGSPIRHYL VRYRALSSEWKPEI
RLPSGSDHVMLKSLDWNAEYEVYVVAENQQGKSAAHFVFRTSAQPTAIPANGSPTSG
LSTGAIVGILIVIFVLLL VVVDITCYFLNKCGLFMCIAVNLCGKAGPGAKGKDMEEGKAA
FSKDESKEPIVEVRTEEERTPNHDGGGKHTEPNETTPLTEPEKGPVEAKPECQETETKPAPA
EVKTVPN DATQT KENESKA



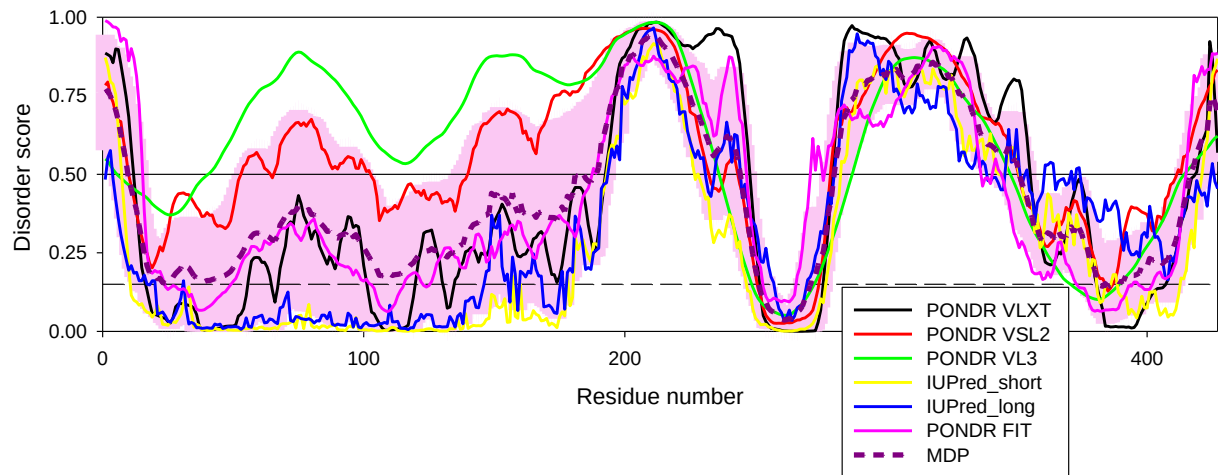
Note: D²P² profile for human NCAM1 is not available.

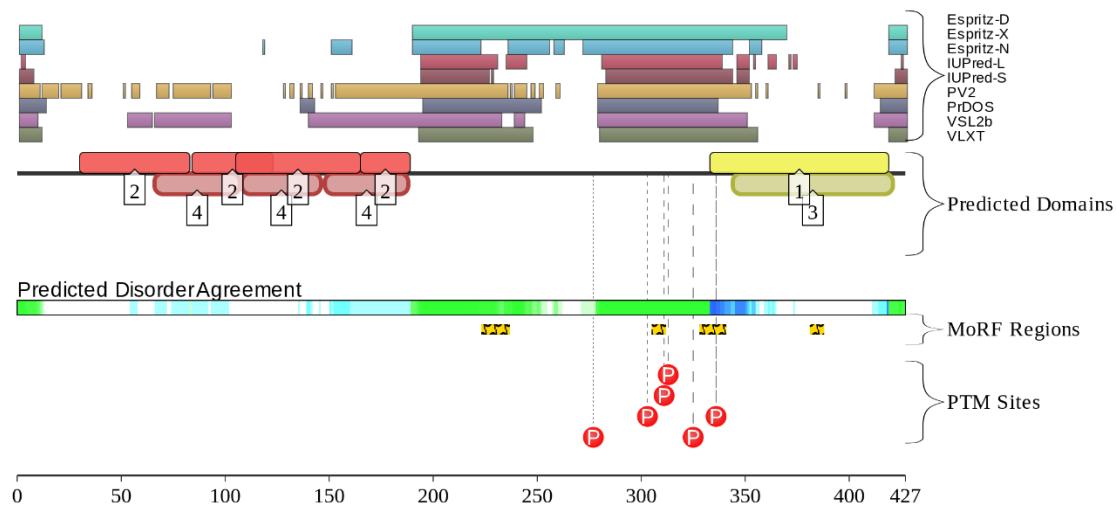


p75NTR (UniProt ID: P08138)

>sp|P08138|TNR16_HUMAN Tumor necrosis factor receptor superfamily member 16
OS=Homo sapiens OX=9606 GN=NGFR PE=1 SV=1

MGAGATGRAMDGPRLLLLLLLGVSLLGGAKEACPTGLYTHSGECCKACNLGEGVAQPC
GANQTVCEPCLDSVTFSDVVSATEPCKPCTECVGLQSMSAPCVEADDAVCRCAYGYYQ
DETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVCEDT
ERQLRECTRWADAEECEIPGRWITRSTPPEGSDSTAPSTQEPEAPPEQDLIASTVAGVVT
VMGSSQPVVTRGTTDNLIPVYCSILAAVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQ
TPPPEGEKLSHSDSGISVDSQSLHDQQPHTQTASGQALKGDGGLYSSLPPAKREEVEKLLN
GSAGDTWRHLAGELGYQPEHIDSFTHEACPVRALLASWATQDSATLDALLAALRRIQR
ADLVESLCSESTATSPV





Key:

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

Disorder:

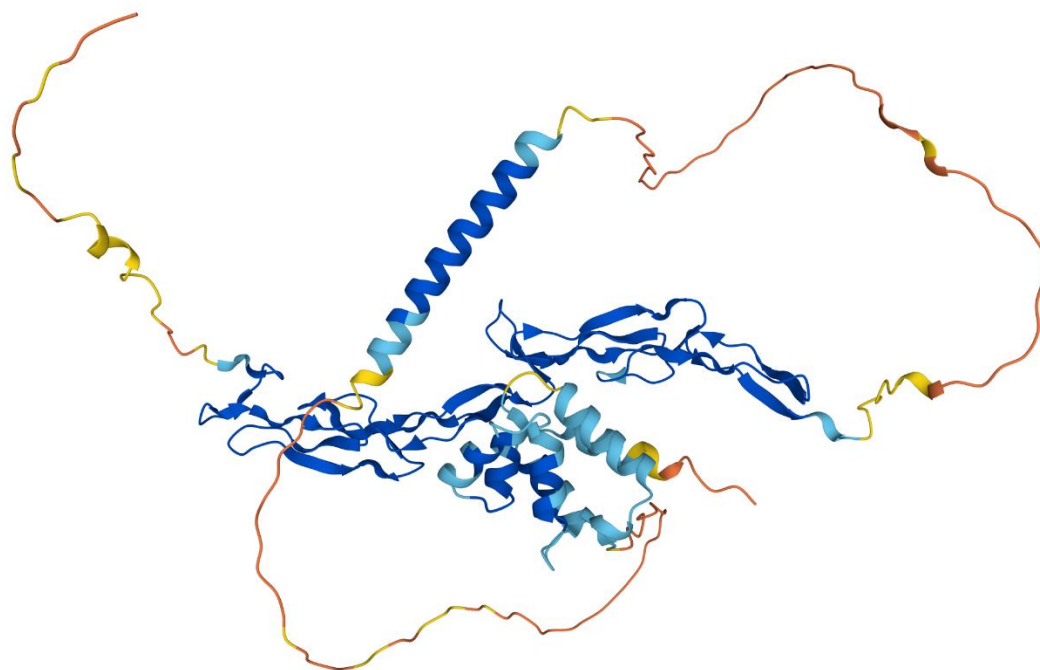
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

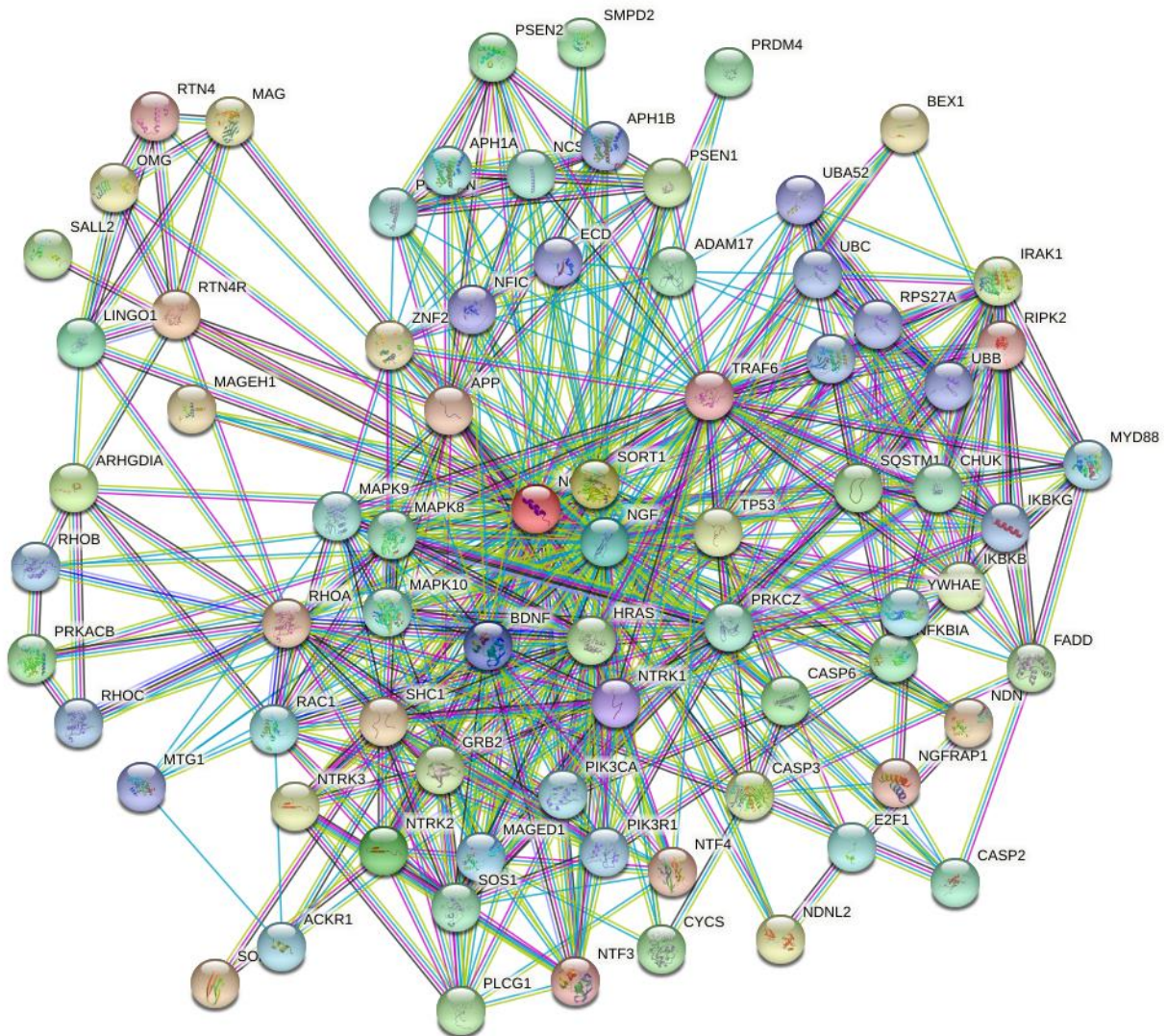
Superfamilies:

- [1] DEATH domain
- [2] TNF receptor-like

Pfams:

- [3] Death domain
- [4] TNFR/NGFR cysteine-rich region





minimum required interaction score: highest confidence (0.900)

number of nodes: 76

number of edges: 498

average node degree: 13.1

avg. local clustering coefficient: 0.731

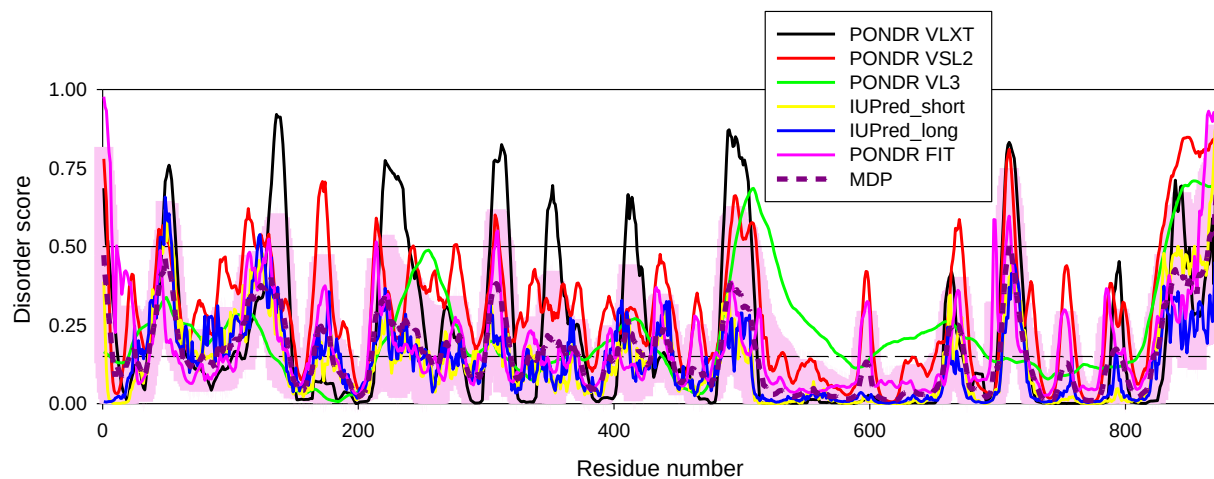
expected number of edges: 188

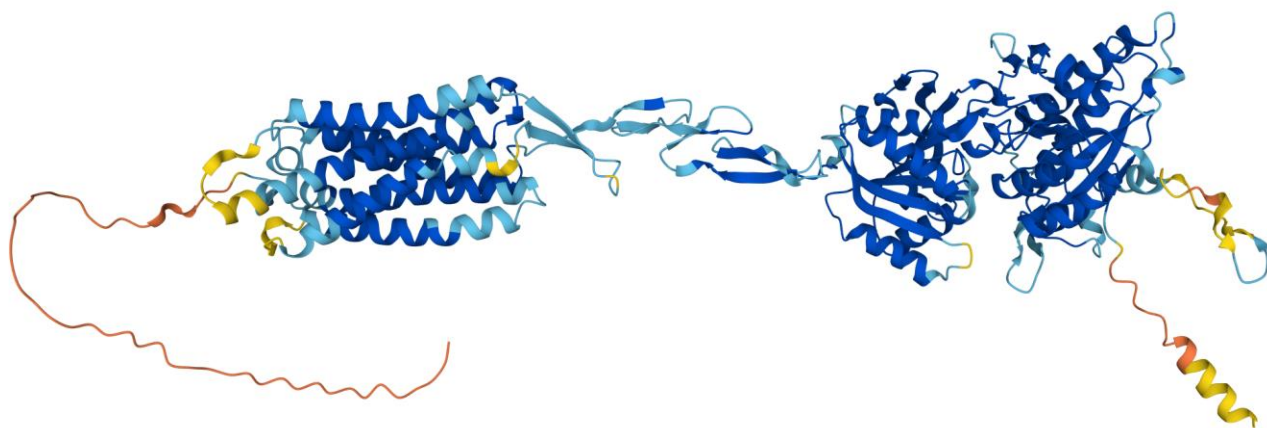
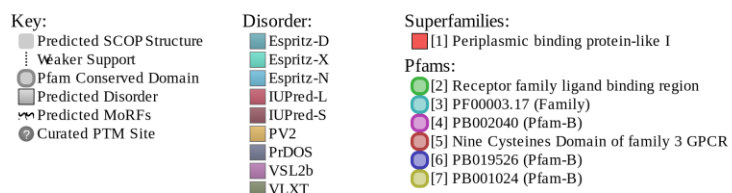
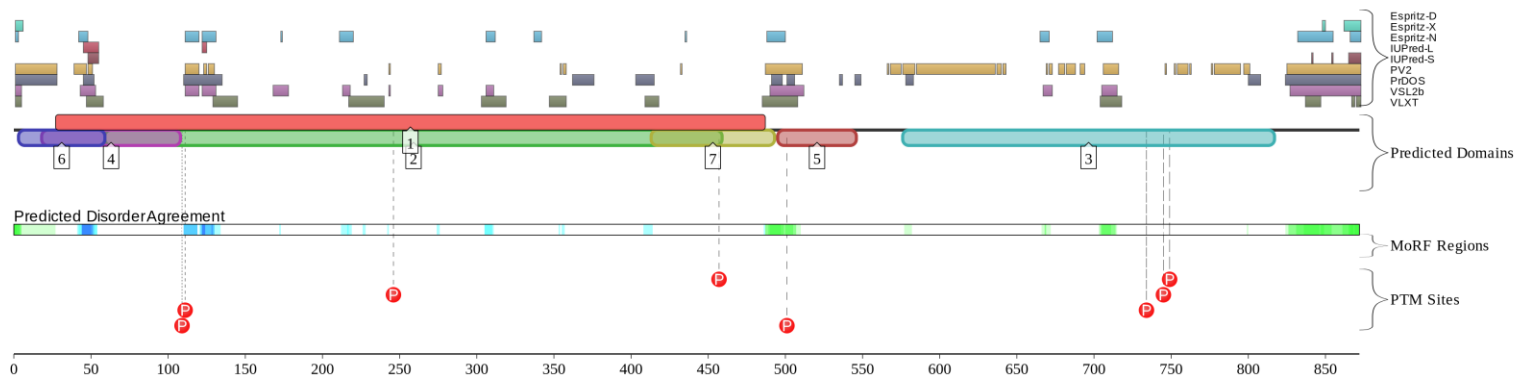
PPI enrichment p-value: $< 1.0e-16$

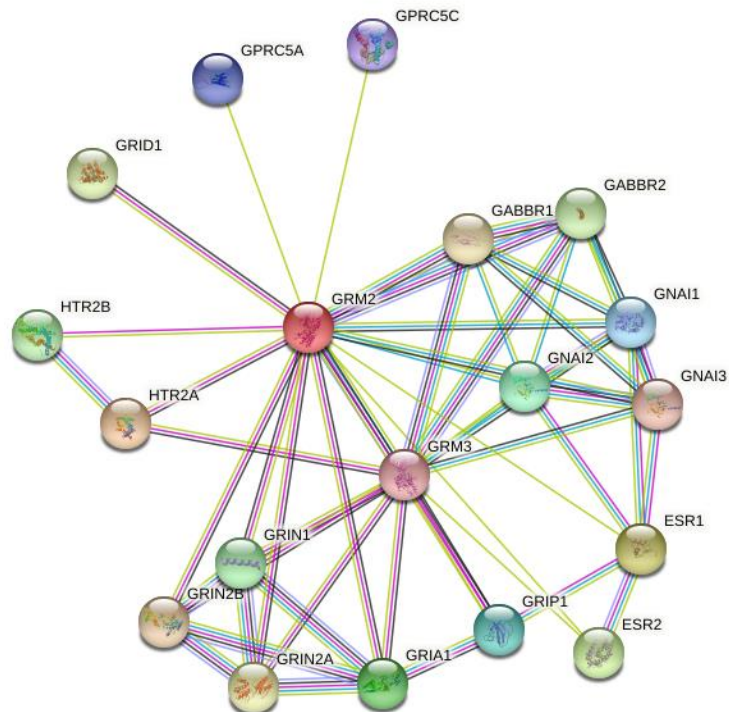
mGluR2 (UniProt ID: Q14416)

>sp|Q14416|GRM2_HUMAN Metabotropic glutamate receptor 2 OS=Homo sapiens OX=9606
GN=GRM2 PE=1 SV=2

MGSLLALLALLLLWGAVAEGPAKKVLTLEGDLVLGGLFPVHQKGGPAEDCGPVNEHR
GIQRLEAMLFALDRINRDPHLLPGVRLGAHILDSCSKDTHALEQALDFVRASLSRGADG
SRHICPDGSYATHGDAPTAITGVIGGSYSVSIQVANLLRLFQIPQISYASTSAKLSDKSR
YDYFARTVPPDFFQAKAMAEILRFFNWTYVSTVASEGDYGETGIEAFELEARARNICVA
TSEKVGRAMSRAAFEGVVRALLQKPSARVAVLFTRSEDARELLAASQRLNASFTWVAS
DGWGALESVVAGSEGAAEGAITIELASYPISDFASYFQSLDPWNNSRNPWFREFWEQRF
RCSFRQRDCAAHSLRAVPFEQESKIMFVVNAVYAMAHALHNMHRALCPNTTRLCDAM
RPVNGRRLYKDFVLNVKFDAPFRPADTHNEVRFDRFGDGIGRYNIFTYLRAGSGRYRYQ
KVGYWAEGLTLDTSIPWASPSAGPLPASRCSEPCNQNEVKSVPGEVCCWLCIPCQPY
EYRLDEFTCADCGLGYWPNASLTGCFELPQEYIRWGDAAVAVGPVTIACLGALATLFLVL
GVFVRHNATPVVKASGRELCYILLGGVFLCYCMTFIFIAPSTAVCTLRRLGLGTAFSVC
YSALLTKTNRIARIFGGAREGAQRPRFISPASQVAICLALISGQLLIVVAWLVEAPGTGK
ETAPERREVVTLRCNHRDASMLGSLAYNVLLIALCTLYAFKTRKCPENFNEAKFIGFTM
YTTCIWLAFLPIFYVTSSDYRVQTTTMCVSVSLSGSVVLGCLFAPKLHIILFQPQKNVVS
HRAPTSRFGSAAARASSSLGQSGSQFVPTVCNGREVVDSTTSSL







minimum required interaction score: high confidence (0.700)

number of nodes: 19

number of edges: 53

average node degree: 5.58

avg. local clustering coefficient: 0.816

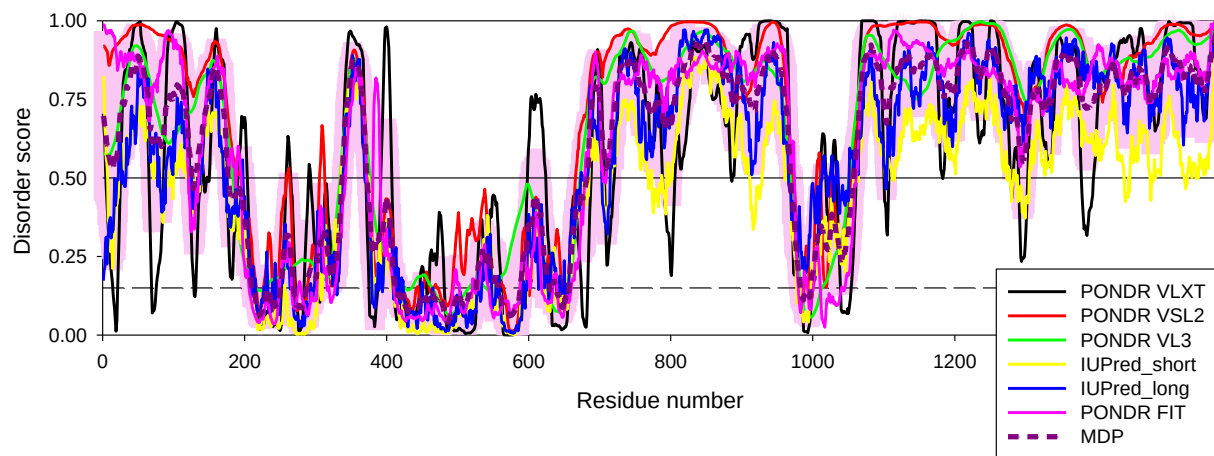
expected number of edges: 20

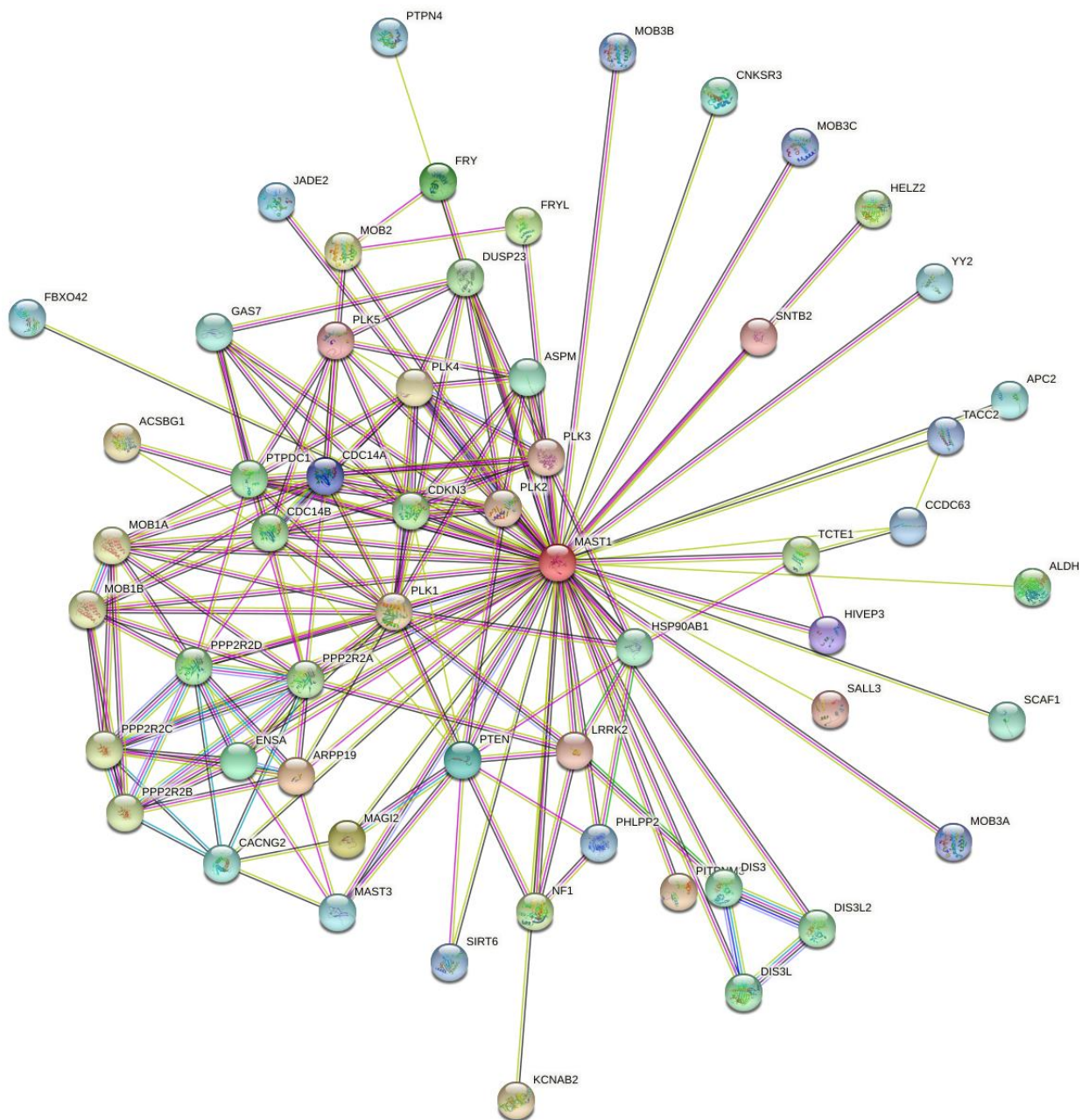
PPI enrichment p-value: 8.77e-10

MAST1 (UniProt ID: Q9Y2H9)

>sp|Q9Y2H9|MAST1_HUMAN Microtubule-associated serine/threonine-protein kinase 1
OS=Homo sapiens OX=9606 GN=MAST1 PE=1 SV=2

MSDSLWTALSNFSMPSPFPGGSMFRRTKSCRTSNRKSLILTSTSPTLPRPHSPLPGHLGSSP
LDSPRNFSPNTPAHFSFASSRRADGRRWSLASLPSSGYGTNTPSSTVSSSCSSQERLHQLP
YQPTVDELHFLSKHFGSTESITDEDGGRRSPAVRPRSRSLSPGRSPSSYDNEIVMMNHVY
KERFPKATAQMEEKLRDFTRAYEPDSVLPLADGVLSFIHHQIHELARDCLTKSRDGLITTV
YFYELQENLEKLLQDAYERSESLVAFVTQLVKKLLIISRPARLLECLEFNPEEFYHLL
AAEGHAKGHLVKTDIPRYIIRQLGLTRDPFPDVVHLEEQDSGGSNTPAQDDLSEGRSSK
AKKPPGENDFDTIKLISNGAYGAVYLVRHRDTRQRFAMKKINKQNLILRNQIQQAFVER
DILTFAENPFVVGMFCSFETRRLCMVMEYVEGGDCATLLKNIGALPVMARMYFAET
VLALAYLHNYGIVHRDLKPDNLLITSMGHIKLTDFGLSKMGLMSLTNLYEGHIEKDAR
EFLDKQVCGTPEYIAPEVILRQGYGKPVDDWWAMGIILYEFLVGCVPFFGDTPEELFGQVI
SDDILWPEGDEALPTEAQLLISSLLQTNPVRLGAGGAFEVKQHSFFRDLDWTGLLRQK
AEFIPHLESEDDTSYFDTRSDRYHHVNSYDEDDTTEEEPVEIRQFSSCSPRFSKVYSSMEQ
LSQHEPKTPVAAAGSSKREPSTKGPEEKVAGKREGLGGLTLREKTWRGGSPEIKRFSASE
ASFLEGEASPPLGARRRFSALLEPSRFSAPQEDEDEARLRRPPRPSSDPAGSLDARAPKEE
TQGEGTSSAGDSEATDRPRPGDLCPPSKGDASGPRATNDLVLRARHQQMMSGDVAVE
KRPSRTGGKVIKSASATALSVMIPAVDPHGGSSPLASPMSPRSLSSNPSSRDSSPSRDYSPA
VSGLRSPITIQRSGKKYGFTLRAIRVYMGDTDVYSVHHIVWHVEEGGPAQEAGLCAGDL
ITHVNGEPVHGMVHPEVVVELILKSGNKVAVTTTPFENTSIRIGPARRSSYKAKMARRNK
RPSAKEGQESKKRSSLFRKITKQSNLLHTSRSLSSLNRSLSSSDSLPGSPHGLPARSPH
YRSTPDSAYLGASSQSSSPASSTPNPASSASHHIRPSTLHGLSPKLHRQYRSARCKSAGN
IPLSPLAHTPSPTQASPPPLPGHTVGSSTTQSFPAKLHSSPPVVRPRPKSAEPPRSPLLKR
VQSAEKLGLASLSADKKGALRKHSLEVGHDPFRKDFHGLALHSLAESDGETPPVEGLG
APRQVAVRRLGRQESPLSLGADPLLPEGASRPVSSKEKESPGGAEACTPPRATTPGGRT
LERDVGCTRHQSVQTEDGTGGMARAVAKAALSPVQEHETGRRSSSGEAGTPLVPIVVE
PARPGAKAVVPQPLGADSKGLQEPAPLAPSVPEAPRGRERWVLEVVEERTTSLGPRSKP
ASPKLSPEPQTPSLAPAKCSAPSSAVTPVPPASLLGSGTKPQVGLTSRCPAEAVPPAGLTK
KGVSSPAPPGP





minimum required interaction score: medium confidence (0.400)

number of nodes: 57

number of edges: 178

average node degree: 6.25

avg. local clustering coefficient: 0.751

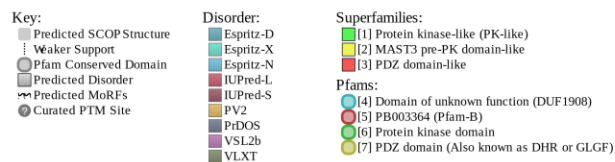
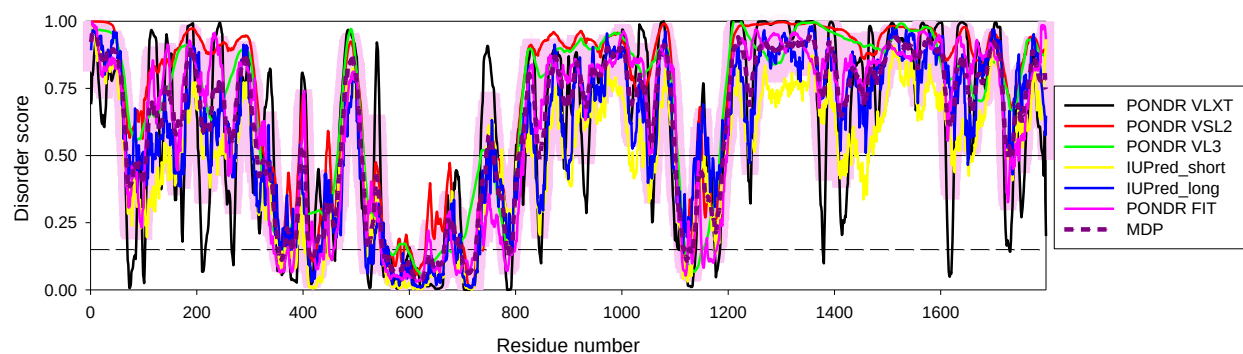
expected number of edges: 77

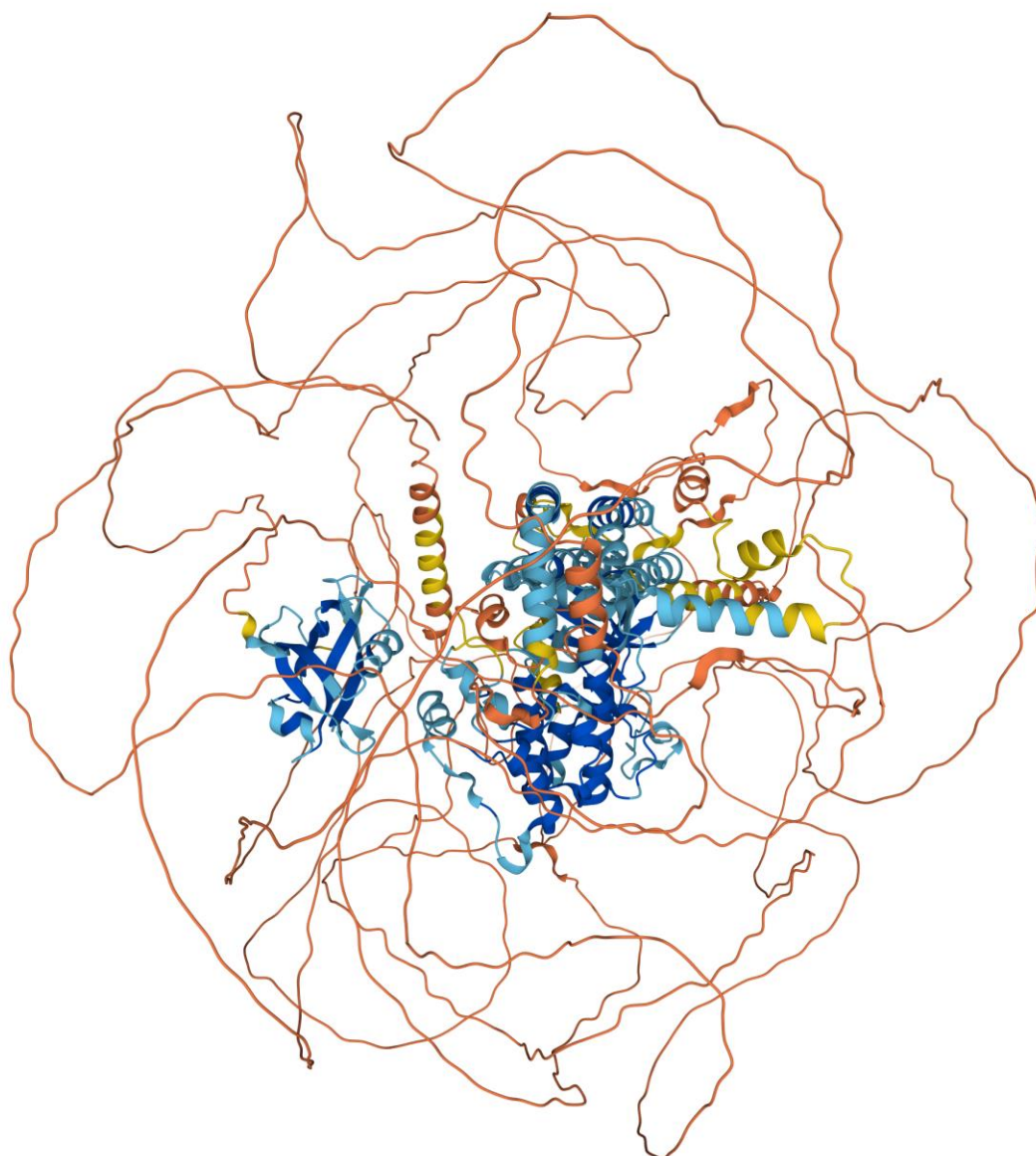
PPI enrichment p-value: $< 1.0e-16$

MAST2 (UniProt ID: Q6P0Q8)

>sp|Q6P0Q8|MAST2_HUMAN Microtubule-associated serine/threonine-protein kinase 2
OS=Homo sapiens OX=9606 GN=MAST2 PE=1 SV=2

MKRSRCRDRPQPPPPDRREDGVQRAAELSQSLPPRRRAPPGRQRLEERTGPAGPEGKEQ
DVVTGVSPLLFRKLSNPDISSSTGKVKLQRQLSQDDCKLWRGNLASSLSGKQLLPLSSSV
HSSVGQVTWQSSGEASNLVRMRNQLSGQSAPSLTAGLKELSLPRRGSFCRTSNRKSLIV
TSSTSPTLPRPHSPLHGHTGNSPLDSPRNFSNAPAHFSFVPARRTDGRRWSLASLPSSGY
GTNTPSSTVSSSCSSQEKLHQLPFQPTADELHFLTKHFSTESVPDEEGRQSPAMRPRSRSL
SPGRSPVSFDSEIIMMNHVYKERFPKATAQMEERLAEFISSNTPDSVLPLADGALSFIHHQ
VIEMARDCLDKSRSLITSQYFYELQDNLEKLLQDAHERSESSEVAFVMQLVKKLMIHA
RPARLLECLEFDPEEFYHLLAAEGHAKGQGIKCDIPRYIVSQLGLTRDPLEEMAQLSS
CDSPDTPETDDSIIEGHGASLPSKKTPSEEDFETIKLISNGAYGAVFLVRHKSTRQRFAMK
KINKQNLILRNQIQQAFVERDILTFANPFVVSVMFCSFDTKRHLCEMVMEYVEGGDCATL
LKNIGALPVDMMVRLYFAETVLALAYLHNYGIVHRDLKPDNLLITSMGHIKLTDFGLSKIG
LMSLTNNLYEGHIEKDAREFLDKQVCGTPEYIAPEVILRQGYGKPVDDWWAMGIILYEFL
VGCVPFFGDTPEELFGQVISDEIVWPEGDEALPPDAQDLTSKLLHQNPRLRGTGSAYEV
KQHPFFTGLDWTGLLRQKAEFIPQLESEDDTSYFDTRSERYYHMDSEDEEEVSEDGCLEI
RQFSSCSPRFNKVYSSMERLSLLEERTPPPTKRSLSEEKEDHSDGLAGLKGRDRSWVIG
SPEILRKRLSVSESSHTESDSSPPMTVRRRCSGLLDAPRFPEGPEEASSTLRRQPQEGIWVL
TPPSGEGVSGPVTEHSGEQRPKLDEEAVGRSSGSSPAMETRGRGTSQLAEGATAKAISDL
AVRRARHRLLSGDSTEKRTARPVNKKVKSASATALSLLIPSEHHTCSPLASPMSPHSQSSN
PSSRDSSPSRDFLPALGSMRPPIIIHRAGKKYGFTLRAIRVYMGDSDVYTVHHMVWHVE
DGGPASEAGLRQGD LITHVNGEPVHGLVHTEVVELILKSGNKVAISTTPLENTSIKVGPA
RKGSYKAKMARRSKRSRGKDGQESRKRSSLFRKITKQASLLHTSRSLSSLNRSLSSGESG
PGSPTHSHSLSPRSPTQGYRVTPDAVHSVGGNSSQSSSPSSVPSSPAGSGHTRPSSLHGL
APKLQRQYRSPRRKSAGSIPLSPLAHTPSPPPPTASPQRSPSPLSGHVAQAFPTKLHLSPL
GRQLSRPKSAEPPRSPLLKRVSQAEKLAAALAAASEKKLATSRKHSDDLPHSELKKELPPR
EVSPLEVVGARSVLSGKGALPGKGVLPAPSRALGTLRQDRAERRESLQKQEAIREVDS
SEDDTEEGPENSQGAQELSLAPHPEVSQSVAPKGAGESGEEDPFPSRDPRSLGPMVPSLL
TGITLGPPRMESPSGPHRRLGSPQAIEEAASSSSAGPNLGQSGATDPIPEGCWKAQHLHT
QALTALSPSTSGLTPTSSCSPPSSTSGKLSMWSWKSLEIGPDRAPSRKATMAGGLANLQ
DLENTTPAQPKNLSPREQGKTQPPSAPRLAHPSYEDPSQGWLWESECAQAVKEDPALSI
TQVPDASGDRRQDVPCRGCLTQKSEPSLRRGQEPGGHQKHRDLALVPDELLKQT



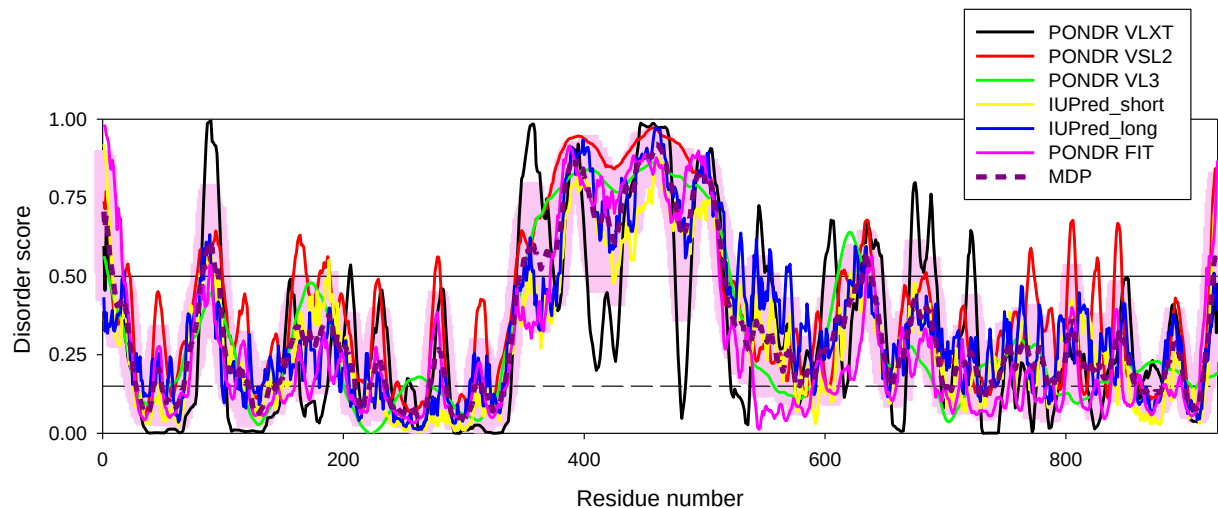


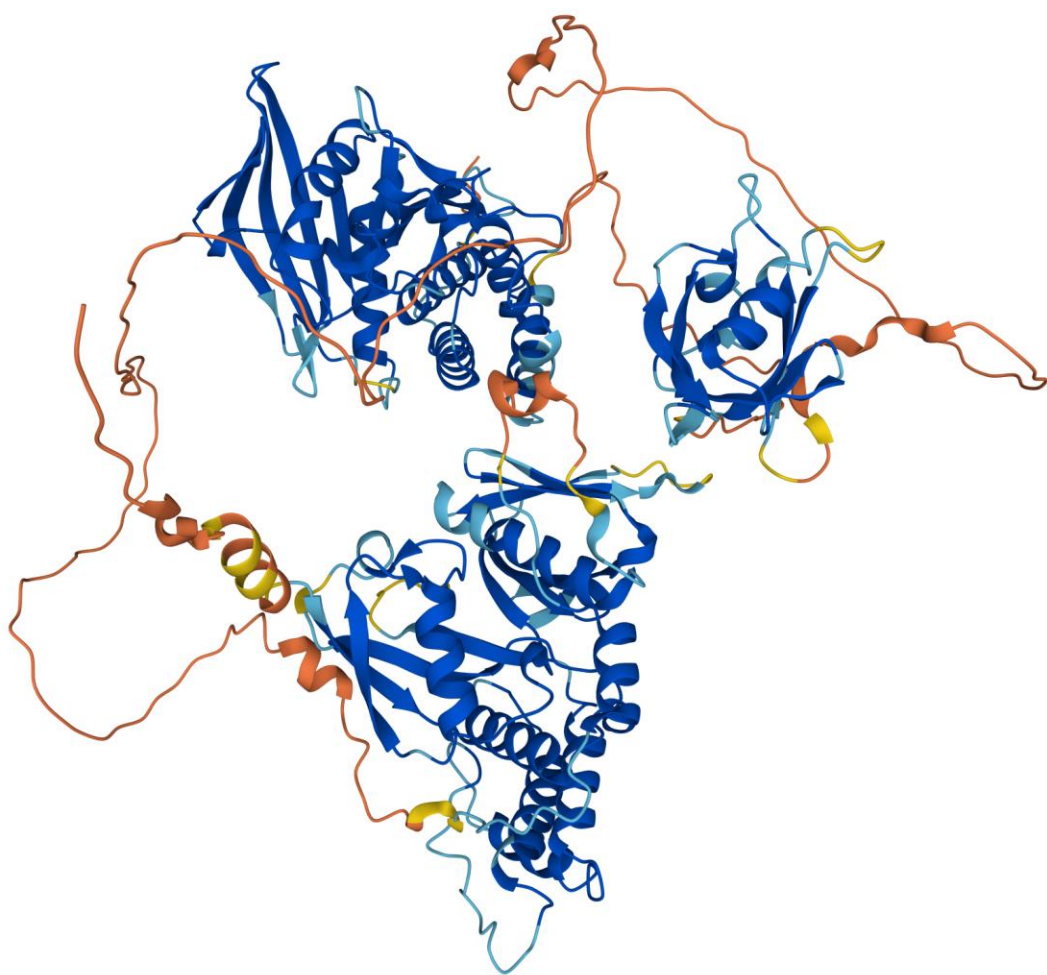
PPI enrichment p-value: 3.95e-08

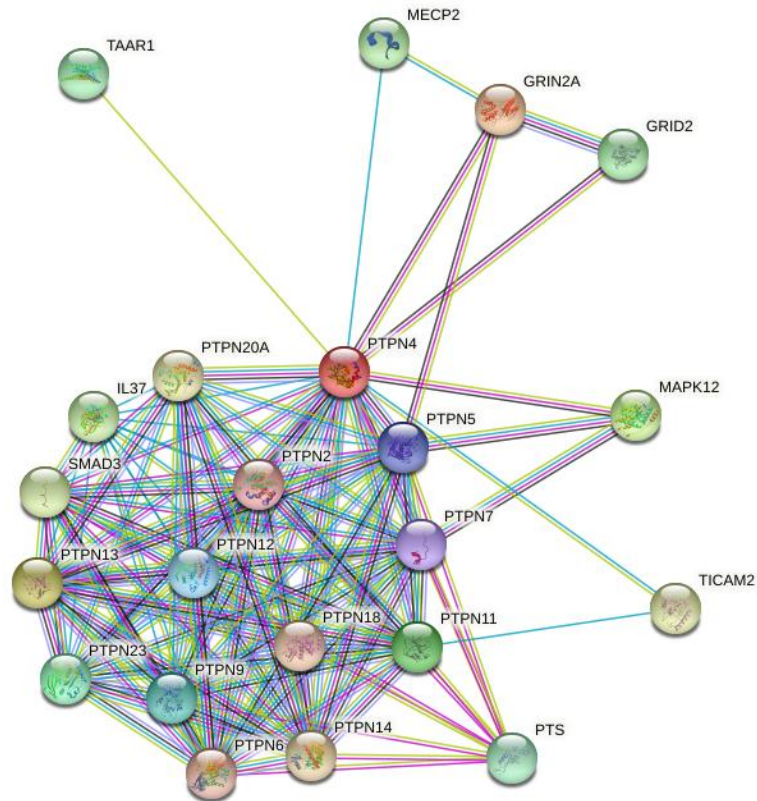
PTPN4 (UniProt ID: P29074)

>sp|P29074|PTN4_HUMAN Tyrosine-protein phosphatase non-receptor type 4 OS=Homo sapiens OX=9606 GN=PTPN4 PE=1 SV=1

MTSRFRLPAGRTYNVRASELARDRQHTEVVCNILLLDNTVQAFKVNKHDQGQVLLDVV
FKHLDLTEQDYFGLQLADDSTDNPRWLDPNKPIRKQLKRGSPYSLNFRVKFFVSDPNKL
QEEYTRYQYFLQIKQDILTGRLPCPSNTAALLASFAVQSELGDYDQSENLSGYLSDYSFIP
NQPQDFEKEIAKLHQHIGLSPAEAEFNYLNTARTLELYGVEFHYARDQSNNEIMIGVM
SGGILYKNRVRMNTFPWLKIVKISFKCKQFFIQLRKELHESRETLGFMVNYRACKNL
WKACVEHHTFFRLDRPLPPQKNFFAHYFTLGSKFRYCGRTEVQSVQYGKEKANKDRVF
ARSPSKPLARKLMDWEVVSRSISDDRLETQSLPSRSPPGTPNHRNSTFTQEGTRLRPSS
VGHLVDHMHVHTSPSEVFVNQRSPSSTQANSIVLESSPSQETPGDGKPPALPPKQSKKNSW
NQIHYSHSQDLESHINETFDIPSSPEKPTPNGGIPHDNLVLIRMKPDENGRFGFNVKGGY
DQKMPVIVSRVAPGTPADLCVPRLNEGDQVVLINGRDIAEHTHDQVVLFIKASCERHSG
ELMLLVRPNAVYDVVEEKLENEPDFQYIPEKAPLDSVHQDDHSLRESMIQLAEGITGT
VLTQFDQLYRKKPGMTMSCAKLPQNISKNNRYRDISPYDATRVILKGNEDYINANYINME
IPSSSIINQYIACQGPLPHTCTDFWQMTWEQGSSMVVMLTTQVERGRVKCHQYWPEPTG
SSSYGCYQVTCHSEEGNTAYIFRKMTLFNQEKNESRPLTQIQYIAWPDHGVDDSSDFLD
FVCHVRNKRAGKEEPVVVHCSAGIGRTGVLITMETAMCLIECNQPVYPLDIVRTMRDQR
AMMIQTPSQYRFVCEAILKVYEEGFVKPLTTSTNK







minimum required interaction score: high confidence (0.700)

number of nodes: 22

number of edges: 127

average node degree: 11.5

avg. local clustering coefficient: 0.917

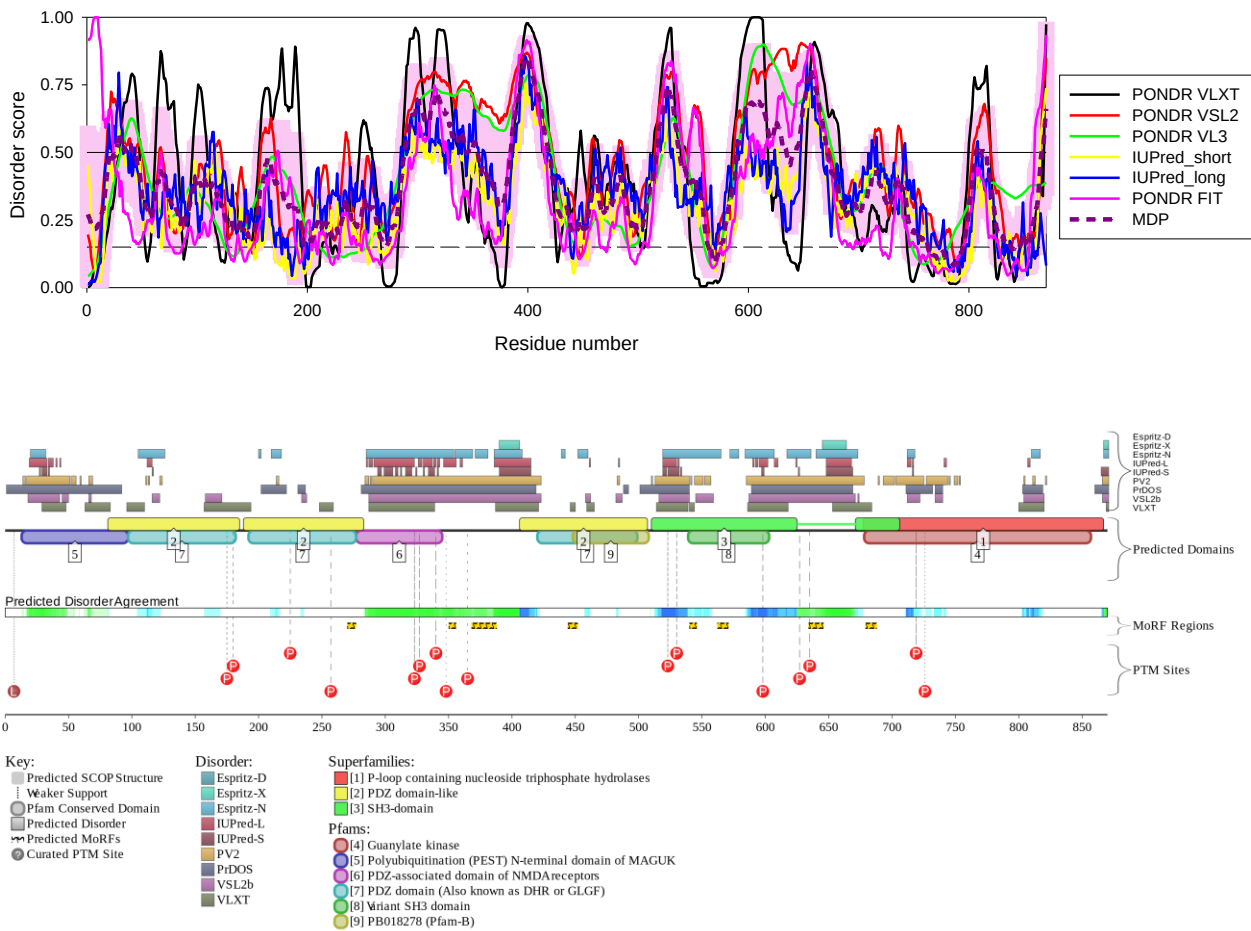
expected number of edges: 23

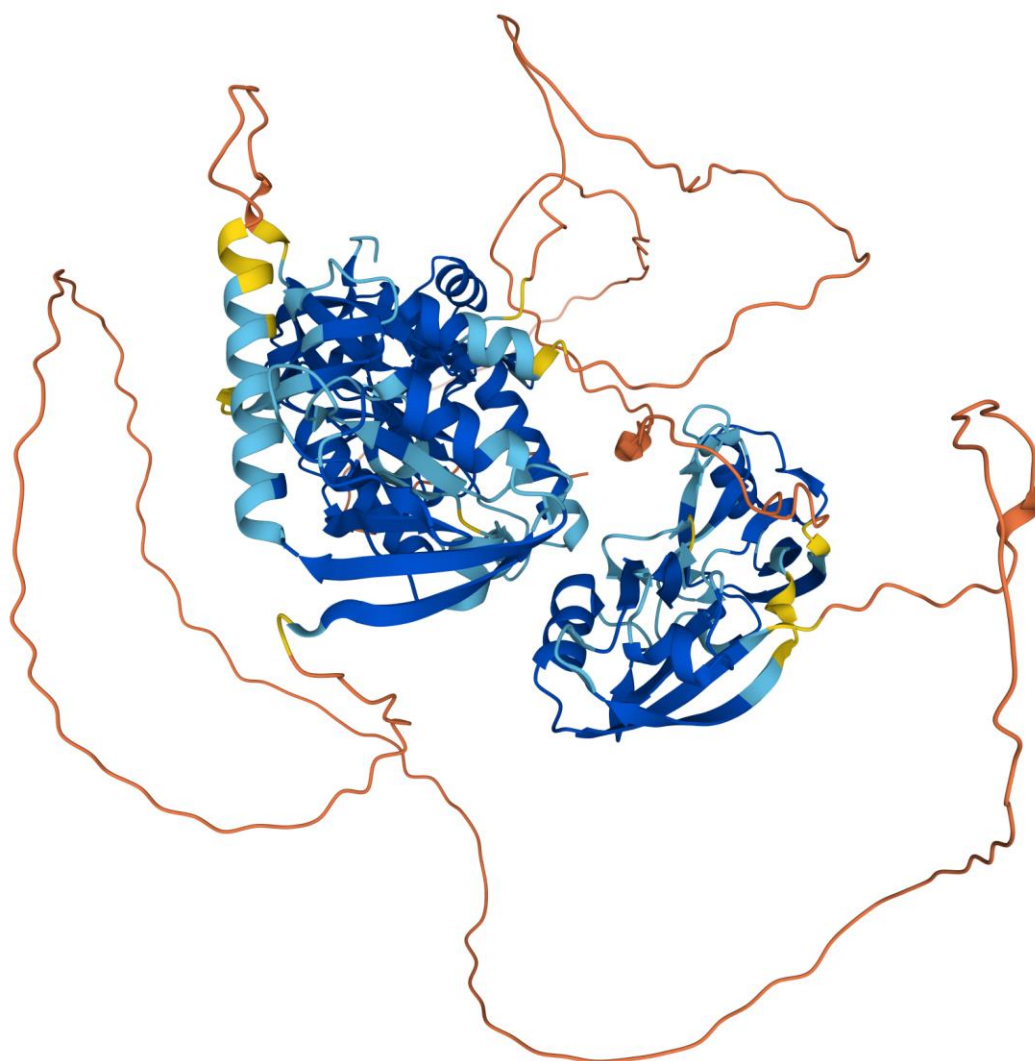
PPI enrichment p-value: $< 1.0e-16$

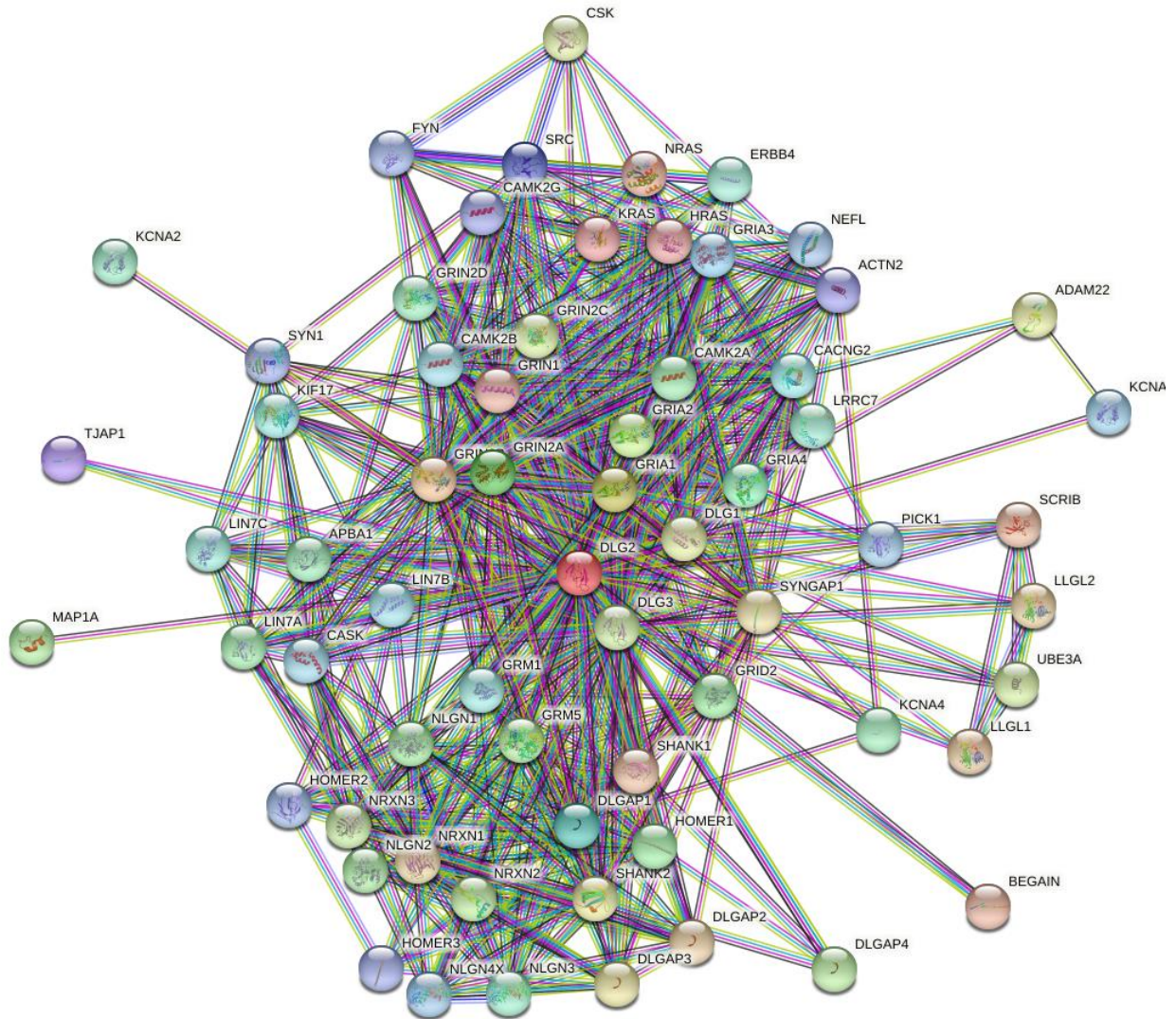
DLG2 (UniProt ID: Q15700)

>sp|Q15700|DLG2_HUMAN Disks large homolog 2 OS=Homo sapiens OX=9606 GN=DLG2 PE=1 SV=3

MFFACYCALRTNVKKYRYQDEDA PHDHS L PRLTHEVRGP ELVHVSEKNLSQIENVHGY
VLQSHISPLKASPAPIIVNTDTLDTIPYVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNPHI
GDDPGIFITKIIPGGA AEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIVRLYV
RRRRPILETVVEIKL FKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGR LQVG
DRLLMVNNYSLEEVTHEEAVAILKNTSEVVYLKVGKPTTIYMTDPYGP PDITHSYSPPM
ENHLLSGNNGTLEYKTS LPPISPG RYSPIPKHMLVDDDYTRPPEPVYSTVNKLCDKPASP
RHYS PVECDKSFLLSAPYSHYHLGLLPDSEMTSHSQHSTATRQPSMTLQRAVSLEGEPR
KVV LHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDL RGASH
EQAAAALKGAGQTVTIIAQYQPEDYARFEAKI HDLREQMMNHSMSSGSGSLRTNQKRS
LYVRAMFDYDKSKDSGLPSQGLSFKYGDILHVINASDDEWWQARRVMLEGDSEEMGV
IPSKRRVERKERARLKT VKFNAKPGVIDSKGSFNDKRKKS FIFSRKF PFYKNKEQSEQETS
DPERGQEDLILSYEPVTRQEINYTRPV IILGPMKDRINDDLISEFPDKFGSCVPHTTRPKRD
YEVDGRDYHFVISREQMEKDIQE HKFIEAGQYNDNL YGTSVQSVRFVAERGKHCILDVS
GNAIKRLQVAQLYPIAIFIKPRSLEPLMEMNKRLTEEQA K KTYDRAIKLEQEFGEYFTAIV
QGDTLEDIYNQCKLVIEEQSGPFIWIPSKEKL







minimum required interaction score: high confidence (0.700)

number of nodes: 65

number of edges: 565

average node degree: 17.4

avg. local clustering coefficient: 0.737

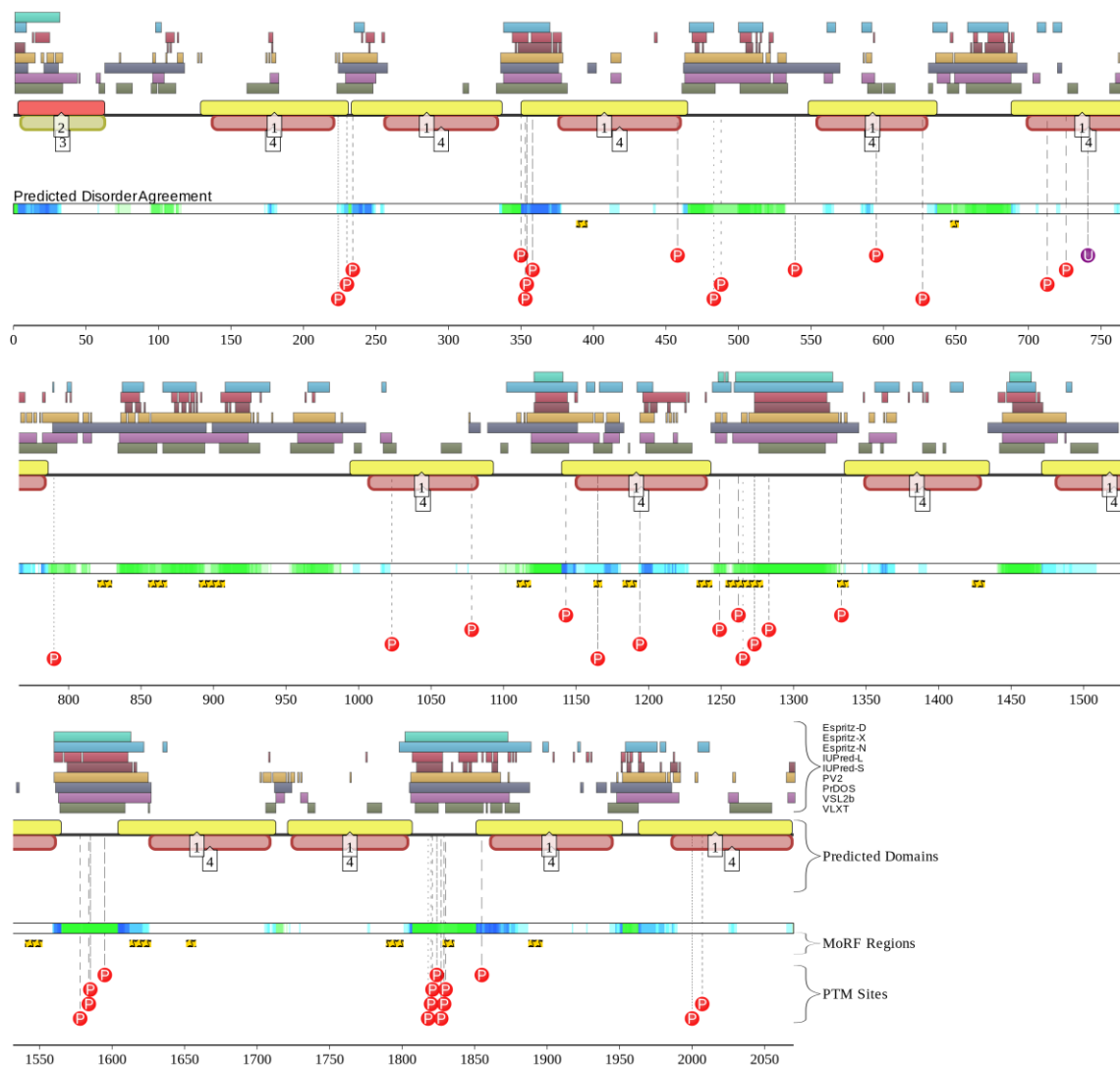
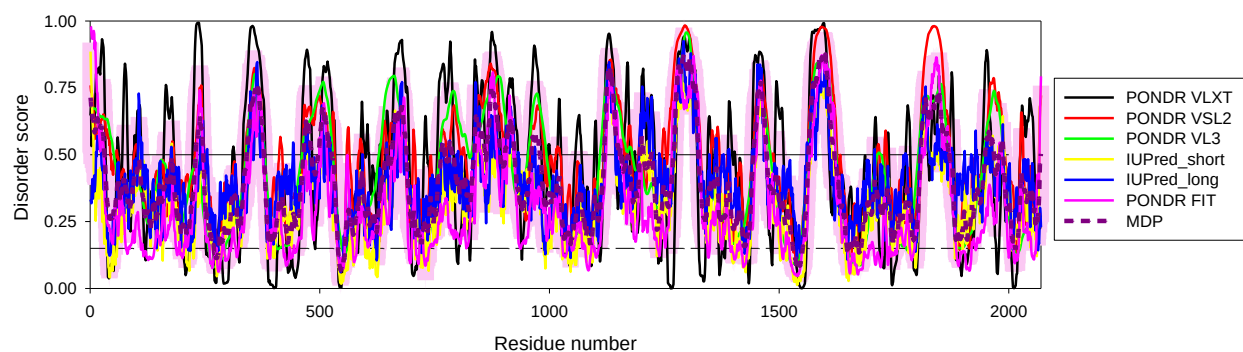
expected number of edges: 87

PPI enrichment p-value: $< 1.0e-16$

MPDZ (UniProt ID: O75970)

>sp|O75970|MPDZ_HUMAN Multiple PDZ domain protein OS=Homo sapiens OX=9606
GN=MPDZ PE=1 SV=2

MLEAIDKNRALHAAERLQTKLRERGDVANEDKLSLLKSVLQSPLFSQILSLQTSVQQLK
DQVNIATSATSNIEYAHVPHLSPAVIPTLQNESFLLSPNNGNLEALTGPGIPHINGKPACD
EFDQLIKNMAQGRHVEVFELLKPPSGGLGFSVVGLRSENREGELGIFVQEIQEGSVAHRD
GRLKETDQILAINGQALDQTITHQQAISILQKAKDTVQLVIARGSLPQLVSPIVSRSPSAAS
TISAHSNPVHWQHMETIELVNDGSGLGFGIIGGKATGVIVKTILPGGVADQHGRLCSGDH
ILKIGDTDLAGMSSEQVAQVLRQCGNRVKLMIARGAIEERTAPTALGITLSSSPTSTPELR
VDASTQKGEESETFDVELTKNVQGLGITIAGYIGDKKLEPSGIFVKSITKSSAVEHDGRIQI
GDQIIAVDGTNLQGFTNQQA VEVL RHTGQT VLLTLMRRGMKQEAELMSREDVTKDAD
LSPVNASIIKENYEKDEDFLSSTRNTNILPTEEEGYPLLSAEIEEIEDAQKQEAALLTKWQR
IMGINYEIVVAHVSKFSENSGLGISLEATVGHFFIRSVLPEGPVGHSGKLFSGDELLEVNG
ITLLGENHQDVVNILKELPIEVTMVCCRRTVPPTTQSELDSLDLCDIELTEKPHVDLGEFI
GSSETEDPVLAMTDAGQSTEEVQAPLAMWEAGIQHIELEKGSKGLGFSILDYQDPIDPAS
TVIIIRSLVPGGIAEKDGRLLPGDRLMFVNDVNLNSSLEEAVEALKGAPSGTVRIGVAKP
LPLSPEEGYVSAKEDSFLYPPHSCEEAGLADKPLFRADLALVGTNDADLVDESTFESPYS
PENDSIYSTQASILSLHGSSCGDGLNYGSSLPSSPPKDVIENTSCDPVLDLHMSLEELYTQN
LLQRQDENTPSVDISMGPASGFTINDYTPANAIEQQYECENTIVWTESHLPSEVISSAELP
SVLPDSAGKGSEYLLEQSSLACNAECVMLQNVSKESFERTINIAKGNSSLGMTVSANKD
GLGMIVRSIIHGGAISRDGRIAIGDCILSINEESTISVTNAQARAMLRRHSLIGPDIKITYVP
AEHLEEFKISLGQQSGRVMALDIFSSYTGRDIPELPEREEGEGEESELQNTAYSNNWNQPR
RVELWREPSKSLGISIVGGRGMGSRLSNGEVMRGIFIKHVLEDSPAGKNGTLKPGDRIVE
VDGMDLRDASHEQAVEAIRKAGNPVFMVQSIINRPRKSPLPSLLHNLYPKYNFSSTNPF
ADSLQINADKAPSQSESEPEKAPLCSVPPPPPSAFAEMGSDHTQSSASKISQDVKDEDFG
YSWKNIRERYGTLTGELHMIELEKGHSGGLGLSLAGNKDRSRMSVFIVGIDPNGAAGKDG
RLQIADELLEINGQILYGRSHQNASSIIKCAPSKVKIIFIRNKDAVNQMAVCPGNAVEPLP
SNSENLQNKETEPTVTTSDAAVDLSSFKNVQHLELPKDQGGGLGIAISEEDTLSGVIIKSLT
EHGVAATDGRLKVG DQILAVDDEIVVGYPIEKFISLLKTAKMTVKLTIHAENPDSQAVPS
AAGAASGEKKNSSQSLMVPQSGSPEPESIRNTSRSSSTPAIFASDPATCPIIPGCETTIEISKG
RTGLGLSIVGGSDTLLGAIHHEVYEEGAACKDGRLWAGDQILEVNGIDLRKATHDEAIN
VLRQTPQQRVRLTLYRDEAPYKEEEVCDTLTIELQKKPGKGLGLSIVGKRNDTG VFVSDIV
KGGIADADGRLMQGDQILMVNGEDVRNATQEAVAALLKCSLGTVTLEVGRKAGPFHS
ERRPSQSSQVSEGLSSFTFPLSGSSTSESLESSSKKNALASEIQGLRTVEMKKGPTDSLGI
SIAGGVGSPLGDVPIFIAMMHPTGVAAQTQKLRVGDRIVTICGTSTEGMTHTQAVNLLK
NASGSIEMQVVAGGDVSVVTGHQQEPASSLSFTGLTSSSIFQDDLGPQCKSITLERGPD
GLGFSIVGGYGSPHGDLPYVKT VFAKGAASEDGRLKRGDQIIAVNGQSLEGVTHEEAV
AILKRTKGTVTLMVLS



Key:

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

Disorder:

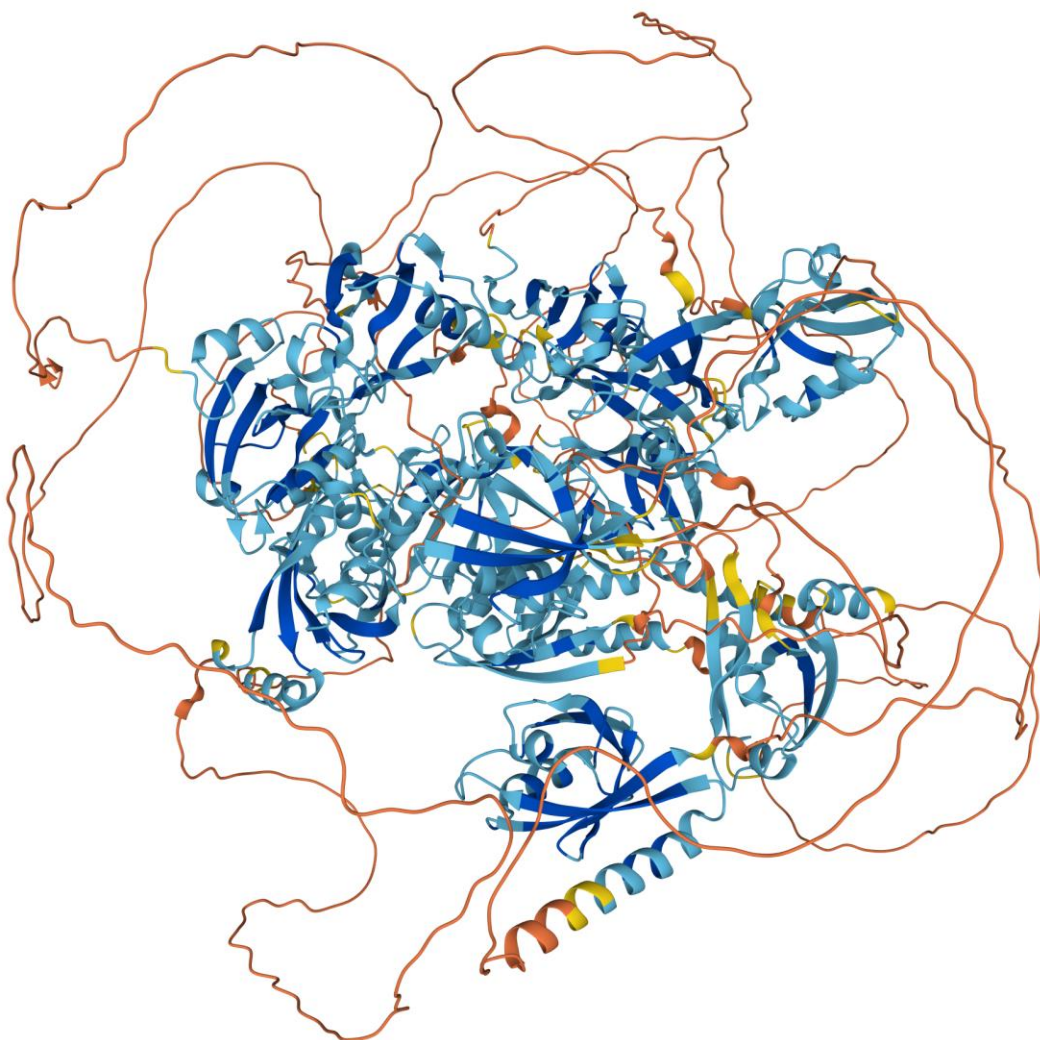
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

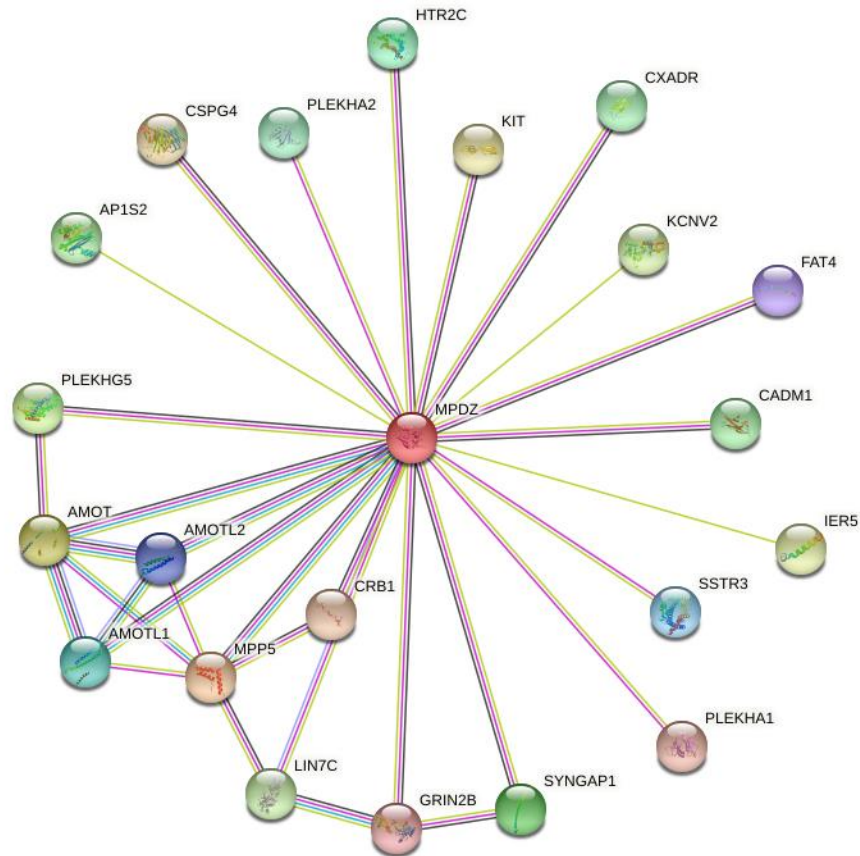
Superfamilies:

- [1] PDZ domain-like
- [2] L27 domain

Pfams:

- [3] L27_2
- [4] PDZ domain (Also known as DHR or GLGF)





minimum required interaction score: high confidence (0.700)

number of nodes: 22

number of edges: 32

average node degree: 2.91

avg. local clustering coefficient: 0.892

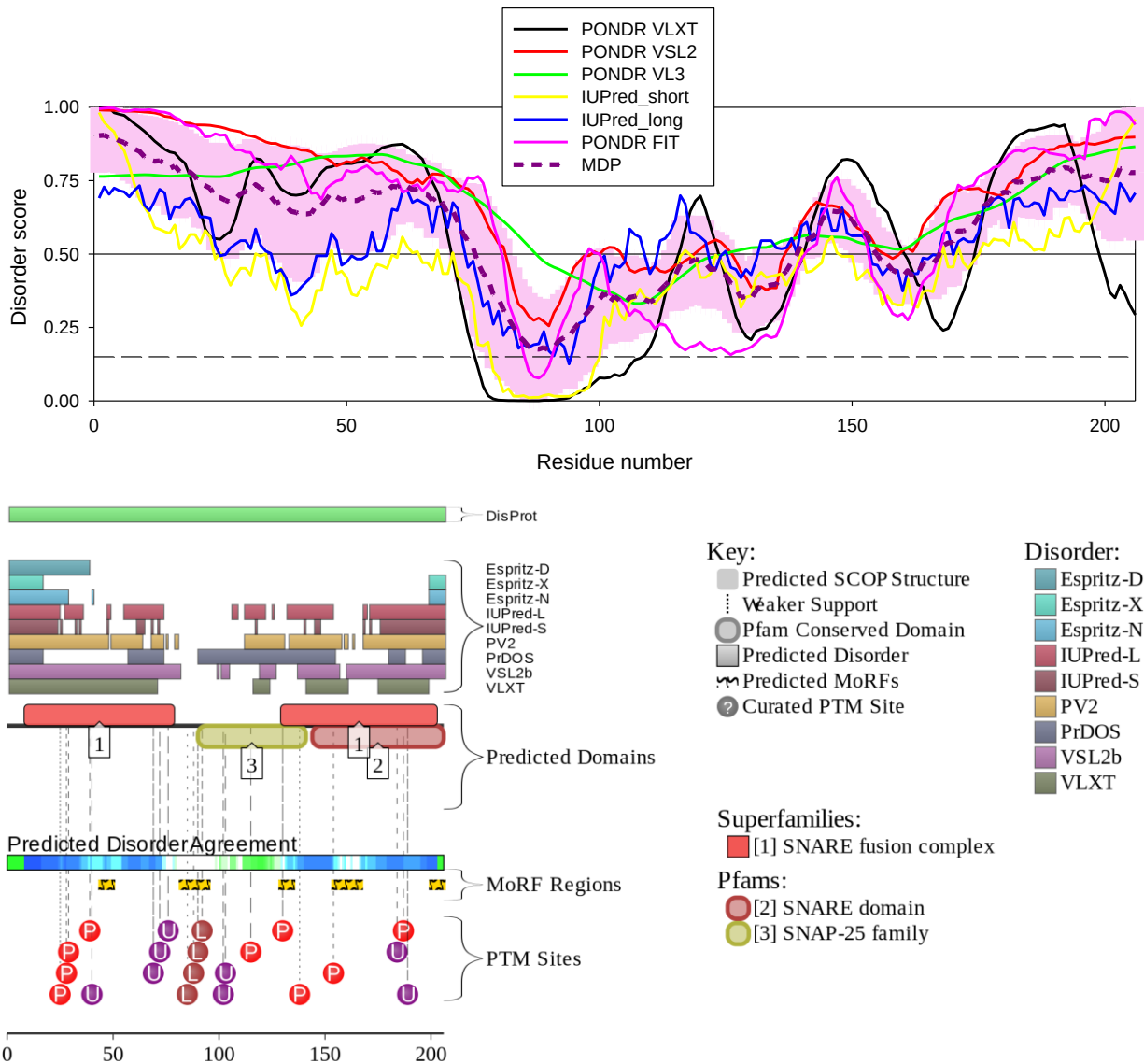
expected number of edges: 21

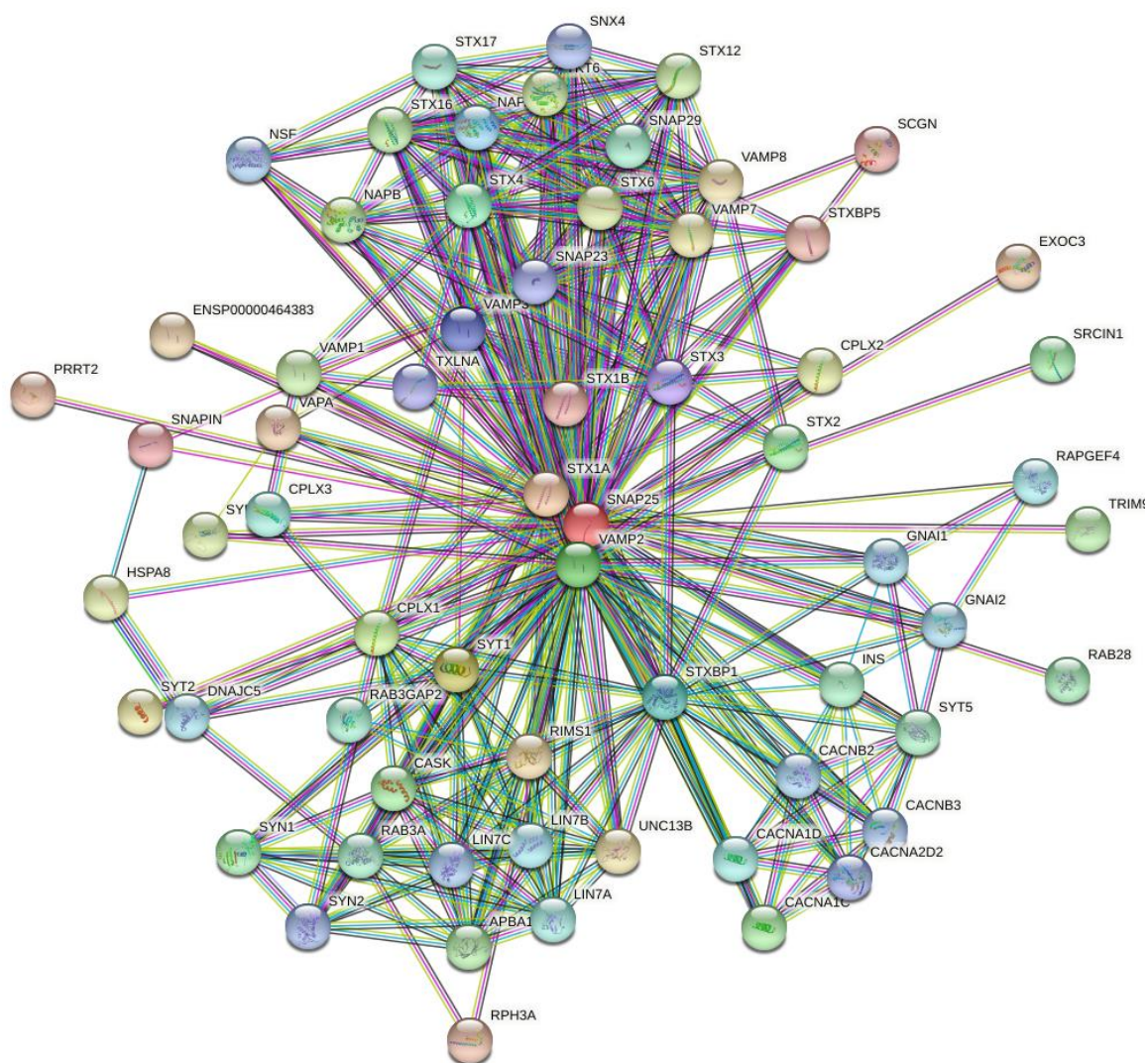
PPI enrichment p-value: 0.019

SNAP25 (UniProt ID: P60880)

>sp|P60880|SNP25_HUMAN Synaptosomal-associated protein 25 OS=Homo sapiens OX=9606 GN=SNAP25 PE=1 SV=1

MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQL
ERIEEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKA WGNNQDGVVA
SQPARVVDEREQMAISGGFIRRV TNDARENEMDENLEQVSGIIGNLRH MALDMGNEIDT
QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG





PPI enrichment p-value: $< 1.0\text{e-}16$



PPI enrichment p-value: $< 1.0e-16$