

**Supplementary file 3.** Some examples of PAC domain-related proteins containing predicted functional domains suggesting intracellular functions.

The sequences were retrieved from <https://db.cngb.org/onekp/>. They were analyzed using the InterproScan software (<http://www.ebi.ac.uk/interpro/search/sequence-search>).

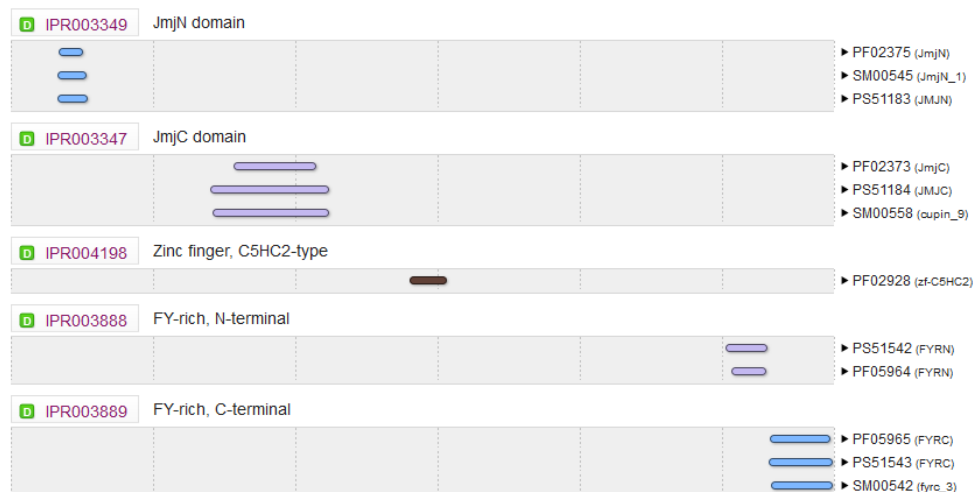
Originally, the accession numbers were of the following type: #onekp:YFGP\_scaffold\_2007785 Pallavicinia\_lyellii. They have been simplified for more convenience, as follows:

>YFGP\_2007785\_Pallavicinia\_lyellii

*Marchantiophyta*

>YFGP\_2007785\_Pallavicinia\_lyellii

KRSFPKYKEADSSSESESDFTRPARDTAMKPTGLPIGVVRGCPKCSDCQAVLARWRPEEGCKPVVDAAPVFYPT  
 EEEFKDTLKYIAKIRSAAPFGICRVVPPPGWQPPCPLREDTAKLHVMKFPTRVQEIHLQVRQPVKKCSQARQRL  
 GGRRRGGGFRGRMGRPCRRTPNLSTTKSVQPDSEFGFEPGSYFSLSKFEKYAQQFKEQYFFRADADELQSKS  
 EIGSDSTSSMSPSVDAIEAEYWRIVEKPTEQIEVLYGADVETGSFGSGFPKGKANATEPYEKSGWNLNNIARLPGS  
 MLAFEEDISGLVLPWLYVGMCFSSFCWHVEDHHFYSLNYLHWGAPKVWYGVAGHAAHDMEAVMKEHLPELF  
 DEQPDLLHKLVTQLSPSILRREGVPVYRLVQQAGEFVITFPRAYHSGFNCGFNCAEAVNLAPVDWLPHGQGAVEL  
 YREQRRKTSVSHDKLLAAAREAAKVLVHSRNQPLQKLPQMVKQEFIEEEEKKGVSSEGADADVLAWQTFCGQ  
 DGVLARALKARVELECSRQTSLTGDVLMKKMDCWYDATDERECAECHYDLHLSAVGCCCECKEKFVCLAHASLLC  
 VCHWGRKFVLYRSLAELELLVALEEQPGAMSTWLEQEQRSSSLSPFLHQDTGLAQTLPCEFNSTVFPCNR  
 NVFKAQDVESRLESQTQYMASRSNPGTSDNPLSHQSGRGVNTQSTVSLQHSSKAILSNTAQNLPESHTAASGL  
 DERKINSVGVQTRGQLAMYSEKRLTNSMKTAKQIGETSIVKSRQEVIVLSDDEEANLKTNMIVSSITKSHEGS  
 NAVLHAINSKTAFLDTARSSASCKQSTSFTAEALSGTCLERQLVVPDGLASVVPQLKLNLPKSAQLPDT  
 STPMVRAQVHHHVATEESPVSPPYVLRGRSIGNLKQARAASSTQHLGSLRTYSRADHAQRLQIGPEASASEI  
 CGHIPVPDSFTPAVNAVQSRTPARLDRPVGPRVAKVVRKKVCREVELLNVGSLVLRREGWHDKHCIFPAGFKSRTS  
 FCDVLNISQNCFYVSEIVEYGSSGPQFKVSVEGNSLAEFVNTSIDLCWRTVQEKINEEIIIRCRGIGETNLPPLQPPQ  
 SLHGLDMFGLLSPMIVQAIEALDPQHLCCEYWTAK

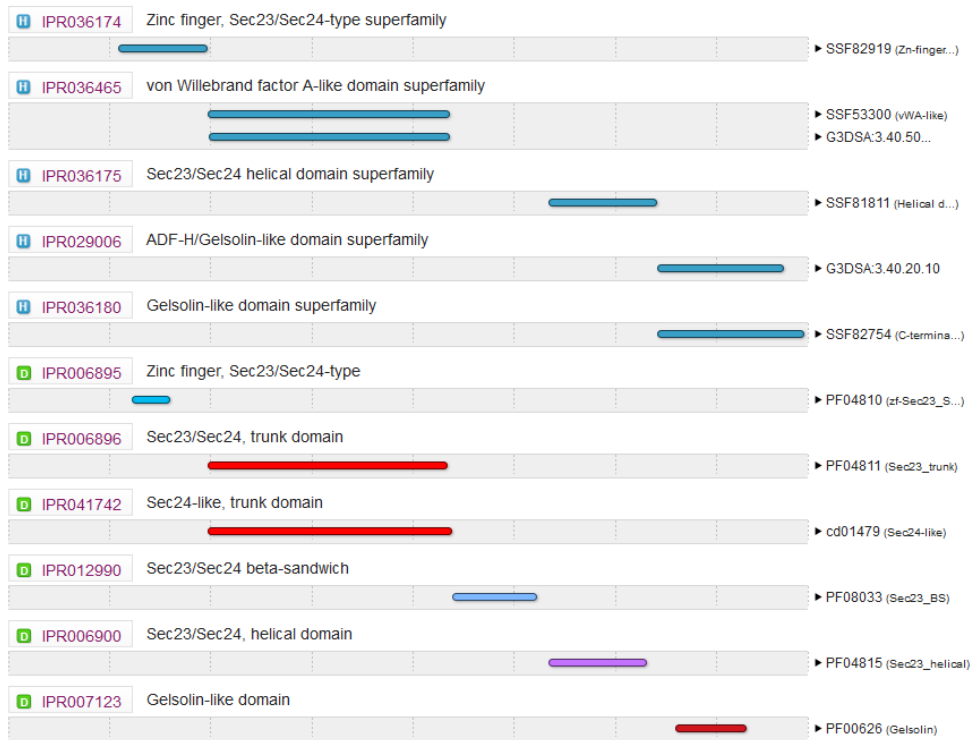


The JmjN and JmjC domains are two non-adjacent domains which have been identified in the jumoni family of transcription factors. Although it was originally suggested that the JmjN and JmjC domains always co-occur and might form a single functional unit within the folded protein, the JmjC domain was later found without the JmjN domain in organisms from bacteria to human [PMID: 10838566, PMID: 11165500]. (<http://www.ebi.ac.uk/interpro/entry/IPR003349>)

>ILBQ\_2007285\_Conocephalum\_conicum

PGVSQPGSPAASGGPPPSHPSRPTSNIDPNQIPRPQPSASHVIFETRVNGQANLPPSATTAFVVRDTGNCSPLRM  
 RSTLNQIPCSGDLNTSGMPLAVMVQPFALPHPSEEIQVVDGETGPVRCRCKAYINPFMKFIDQGRFTCNL  
 CGFTNETPRDYHCNLGPDGRRRDADQRPESLRTVEFVASAEYLRPPMPAVFFFLIDVSMNAVQTGAVAAACS  
 AINRALSDLPEGPNTLVGIATFDSTIHYYSLNRNLQQPAMLVVPDIQDPYTPLQTDLIVPLSEGKDHLEQILESIPSMF  
 QNNRVAESAFAAGAIKAYLAMKSTGGKLMVFQSVLPVGLGALPPRESEGRVSGEKEALKLLQPADKLLKTMATIE  
 FAEFQVCVDLFMTAQMYVDIASLSVVPRTTGGQLYFYQPFYAGADSALYNDLRWNVTRPQGFEAVMRVRCSSQ  
 GLQVQEYYGNFCKHIPTDVLPAIDSDKTIMVTFKHDDKFQDGSSECCFQCALLYTTVTGQRRIRVITLSLSCCTTVLS  
 NLFGRGADLDAQFTYFLKHSQAQEIPTLTQVRDQMTAQCVNILFTYRRYCATASSAGQLILPEALKLLPLYTLALTCSI

GLRADTRVDARFDDRSYWCTRVASLAGSLSIPLVYPRMFAIHNLPKESLADGDLPPVPLSSENLDPDGVFLET  
GEDAFlyVGKQAPVEVLEQLFGVHTVDEVVPGQFMLQEYDNPASKRLNAIINEIRRQRCSYLRLRLRRGDPLEFL  
FFSYLVEDKSSSGLSYVEFLVYVHKQIQKRM

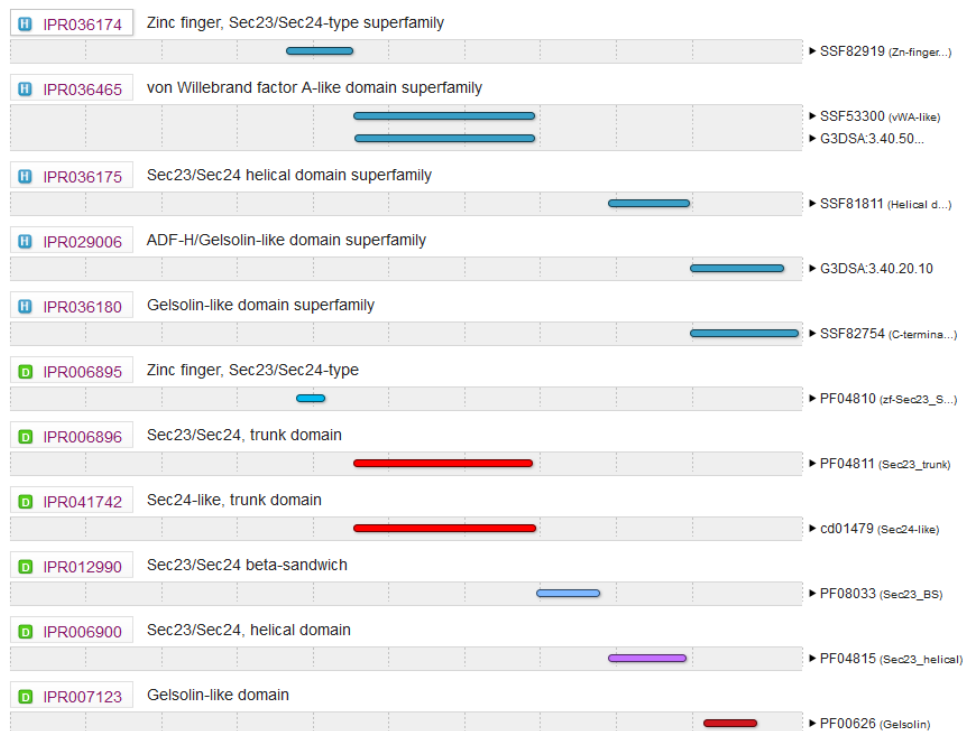


Gelsolin is a cytoplasmic, calcium-regulated, actin-modulating protein that binds to the barbed ends of actin filaments, preventing monomer exchange (end-blocking or capping) [PMID: 3023087]. It can promote nucleation (the assembly of monomers into filaments), as well as sever existing filaments. In addition, this protein binds with high affinity to fibronectin. Plasma gelsolin and cytoplasmic gelsolin are derived from a single gene by alternate initiation sites and differential splicing. (<http://www.ebi.ac.uk/interpro/entry/IPR036180>).

COPII (coat protein complex II)-coated vesicles carry proteins from the endoplasmic reticulum (ER) to the Golgi complex [PMID: 11535824]. COPII-coated vesicles form on the ER by the stepwise recruitment of three cytosolic components: Sar1-GTP to initiate coat formation, Sec23/24 heterodimer to select SNARE and cargo molecules, and Sec13/31 to induce coat polymerisation and membrane deformation [PMID: 12239560]. (<http://www.ebi.ac.uk/interpro/entry/IPR012990>).

>WJLO\_2007937\_Riccia\_berychiana

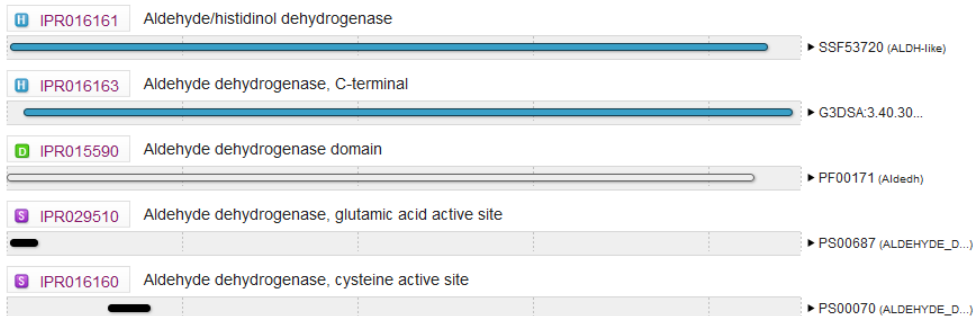
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AAQPGGPFSPSSAPMPYPYQPPQAPTQMQNLSLQNGGIPGGAPPRSFAPPTQGGVQTSAPTSWQAPPRRVY  
PDFGPPTGTGTGQAFSQIPSHLPPNVGHVTGVSDKYGSTVPGMPQPGSPATSAAQPPSHPSRPTSNIQIPR  
PQPTASHVIFETRNVGQANLPPSATSFAFVVRDTGNCSPRLMRCTLNQIPCSGDLNLTSGMPLAVMVQPFALPHPS  
EEPIQVDFGESGPVRCRCKAYINPFMKFIDQGRFTCNLCGFTNETPRDYHCNLGPDGRRRDADQRPESLRG  
TVEFVASPEYLVPRPMPAVFFFLIDVSMNAVQTGAVAAACSAINRALSDDLPEGPNTLVGIATFDSTIHYYSLNKNLQ  
QPAMLVVPDIQDPYTPLQTDLIVPLSEGKDHLEQILESIPSMFQNNRVPESSFGAAIKGAFLAMKSTGGRLMVFS  
VLPSVGLGALTPRENEGRVSGEKEALKLLQPADKVLKTMATIEFAEFQVCVDLFLTAQMYVDIASLSVVPRTTGGQV  
YFYQPFYAGADSACKLYNDLRWNVTRPQGFEAVMRVRCSSQLQVQEYYGNFCKRIPTDVLPAIDSDKTIMVTFK  
HDDKFQDGSECCFQCALLYTTVTGQRRIRVITLSLSCTTVLSNLFRGADLDAQFTYFLKHSAAQIPNVPLTQVRDQ  
MTAQCVNILYTYRKYCATASSAGQLLPEALKLLPLYTLALTKSIGLRADTRVDARFDDRSYWCTRVASLAASLSIPL  
VYPRMFAIHNLPDSQAEGELPPVPLSSENLDPDGVFLETGEDAFlyVGKQAPVELLEQLFGVHSVDEVVSGQ  
FILQEFDNPASKRLNAIVNEIRRQRCSYLRLRLRRGDPLEFLFFSYLVEDKSSSGLSYVEFLVYVHKQIQKRM



## Bryophyta

>HVBQ\_2004216\_Tetraphis\_pellucida

QMELGGKDVCIICEDADLDLAAKNIIKGGFSYSGQRCTAVKLILVVESVADKLVDMSKAVDGLSVGKPEDNCTITP  
VISKSSADFI EGLVKDCEEKGAKLLQKYRREGNLIWPLLIDHVT PFGPVVPVVRVKTVEEAVDHCNANNLALQGCV  
FSRDIDQAIRVSDAMETGTVQVNGAPARGPDHFPFQGF RDSIGSGQGIKNSLAMMVKTKTTVLNLRQPTYTMG



Aldehyde dehydrogenases (EC:1.2.1.3 and EC:1.2.1.5) are enzymes that oxidize a wide variety of aliphatic and aromatic aldehydes using NADP as a cofactor. In mammals at least four different forms of the enzyme are known [PMID: 2713359]: class-1 (or Ald C) a tetrameric cytosolic enzyme, class-2 (or Ald M) a tetrameric mitochondrial enzyme, class-3 (or Ald D) a dimeric cytosolic enzyme, and class IV a microsomal enzyme. Aldehyde dehydrogenases have also been sequenced from fungal and bacterial species. A number of enzymes are known to be evolutionary related to aldehyde dehydrogenases. (<http://www.ebi.ac.uk/interpro/entry/IPR015590>).

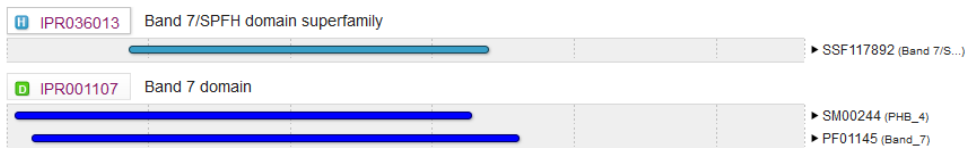
>WSPM\_2007928\_Rhytidadelphus\_loreus

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YPNEEEFQHPLRYIASIRAKAEPYGI CRVVPQSWKPP CPLRGDSATVQSMQFPTRVQQVHKLQVRQPTAMECS  
PTKQASKKRRGRAPMGRMGGA EVYAPSPVNVQPEYFGFWPGEPFPLGDFEKYANDFKNSASLSDKELAQEW  
EPTVEQIEGEYWRIVEQATDQIEVLYGADVETGKFGSGFPRADPRSEATSIYENSGWNLNNIARYPGSMLSFEEG



>ZTHV\_2082727\_Atrichum\_angustatum

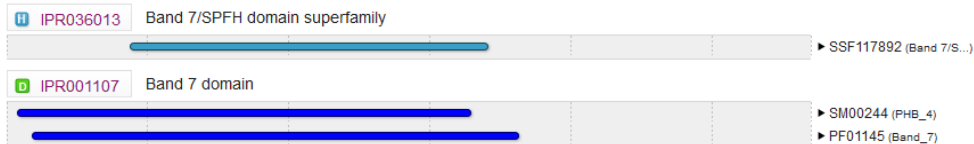
MGAFG**CLIC**VAQSTVGVEQWGRFSQIAQPGLH**CL**NPFAGEWLVTLSLRVQSLDVRCDTKTKDNVFTTV**CSI**  
 QYRVVRQNADDAFYELQNPREQIQAYVFDVVRAC**CV**PKMILDDVFEQKDDIAKAVSEELEKVMGAYGYSIEQTLIVD  
 VEPDATVRRAMNEINAAQRMMAAMDKAEEKILQVKRAEGEAEAKYLSGSGIARQRQAITEGLRESVLTFSSNNV  
 PGTSKDVMDLVLLTQYFDTMKEIGNSSKNTTIFLPHGPGHVGDITEQIRNGMMQGS



The band-7 protein family comprises a diverse set of membrane-bound proteins characterised by the presence of a conserved domain, the band-7 domain, also known as SPFH or PHB domain [PMID: 10542406]. The exact function of the band-7 domain is not known, but examples from animal and bacterial stomatin-type proteins demonstrate binding to lipids and the ability to assemble into membrane-bound oligomers that form putative scaffolds [PMID: 24782879]. A variety of proteins belong to this family. These include the prohibitins, cytoplasmic anti-proliferative proteins and stomatin, an erythrocyte membrane protein. Bacterial HflC protein also belongs to this family. (<http://www.ebi.ac.uk/interpro/entry/IPR001107>).

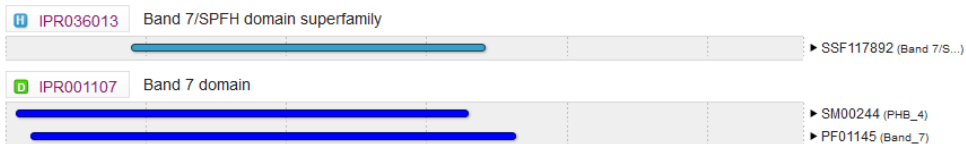
>WNGH\_2001339\_Aulacomnium\_heterostichum

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 RVVRQNADDAFYELQNPREQIQSYVFDVVRAC**CV**PRMILDDVFEQKNDIAKAVSEELEKVMGAYGYSIEQTLIVDVE  
 PDATVRRAMNEINAAQRMVAALDKAEAEKILQVKRAEGEAEAKFLSGHGIARQRQAITEGLRESVLLFSNNVPGT  
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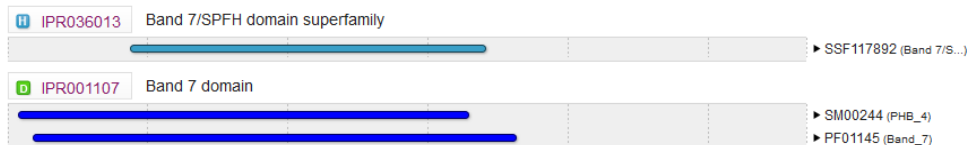
>YWNF\_2049992\_Hedwigia\_ciliata

MGGLG**CLVCI**GQSTVGVEKWGKFSGIAQPGLH**CL**NPLAGEWLAGRLSLRVQSLDVR**CD**TKTKDNVFSV**CSI**Q  
 YRVVRQNADDAFYELQNPREQIQSFVFDVVRAC**CV**PRMLLDEVFEQKNDIAKAVSEELEKVMGAYGYSIEQTLIVDV  
 EPDATVRRAMNEINAAQRMVAALDKAEAEKILQVKRAEGEAEAKYLSGHGIARQRQAITEGLRESVLLFSNNVP  
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>TAVP\_2009233\_Calliargon\_cordifolium

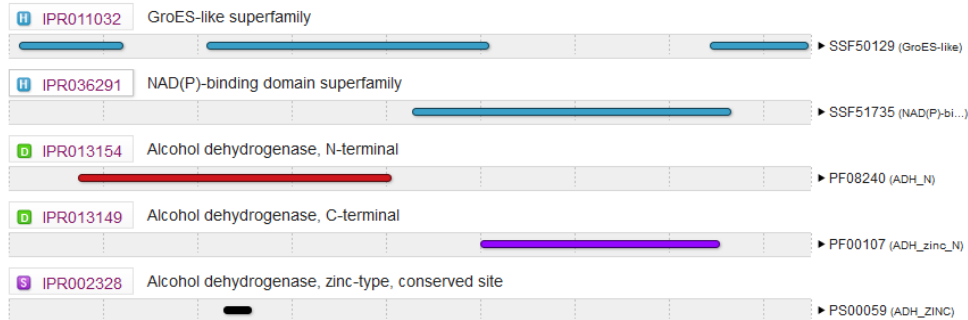
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 YRVVRQNADDAFYELQNPREQIQSYVFDVVRAC**CV**PKMILDDVFEQKNDVAKAVSEELEKVMGAYGYSIEQTLIVD  
 VEPDPTVRRAMNEINAAQRMVATLDKAEAEKILQVKRAEGEAEAKFLSGHGIARQRQAITEGLRESVLLFSNNVP  
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## Psilotales

>ALVQ\_2020591\_Tmesipteris\_parva

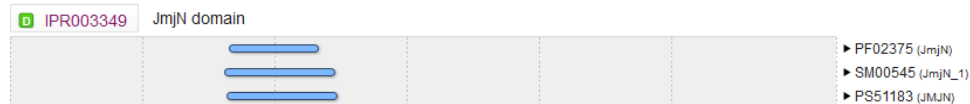
YTSSSTAGQVITCRAAVAWKPKQPLVIEYVQVDPQAGEVRIKITHSSLCHTDVIFYWEAEVGETSPND AEHLIKNCGPKSNMTQELQELNLSMNFKICLFKFHHAHLSMFPRIFGHEAAGIVESIGEGVTDIREGDHVIPLFTGECGNCKYCKSDKTNLCSKLRVNPGRVVMRLDQKTRFSFKGQPIYHFLNTSSFSEYTVVDYGCVVTVNFKAPLERICLFACCIPTGGAVWNTAKMEVGSAIGIFGLGAVGLAVALGARISGASRIIGVDINPKKFPRAKAFGVTDVFNPNDFENPIEEVLRELSNGGLDYCFECVGNVDVMRAAFQSCCHDGGWGTILVGIEASNKQLVFNPMQFFDGREIKGCTFGDFKGRTQIPNLVDTCLTKPDQLDLNAFVTHELPFSRINESFQMLKEGQSLRCVLRM



This is the catalytic domain of alcohol dehydrogenases (EC:1.1.1.1). Many of them contain an inserted zinc binding domain. This domain has a GroES-like structure; a name derived from the superfamily of proteins with a GroES fold. Proteins with a GroES fold structure have a highly conserved hydrophobic core and a glycyl-aspartate dipeptide which is thought to maintain the fold [PMID: 10556240, PMID: 8804825]. (<http://www.ebi.ac.uk/interpro/entry/IPR013154>).

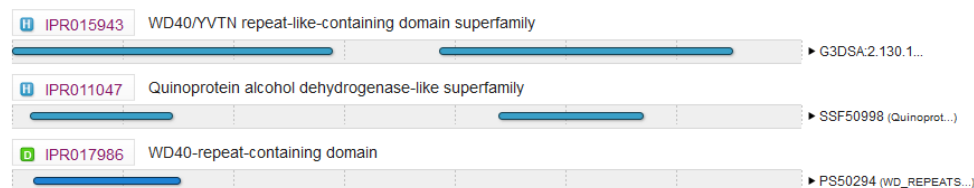
>ALVQ\_2017464\_Tmesipteris\_parva

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>QVMR\_2011678\_Psilotum\_nudum

GCIRLYTVCDDKDGMIYSHSFPVCVQGRILSVAWSVDATKLFSGGSDGCIRCWDVGRIQEVYRITAGLGGHSGSGSDMCVWSLLTLRDGTLVSGDSTGSTQFWDGKCGTLLQAYSCHGADVLALATSPSHHYVFAAGADGQVIQFQLVPES SRLADRVSSSAEEVAVVLGDKWVFCGKKRMHTHDVRALAVAFPIGEGETINKATRKKNKRIKISWMEQDMWKWA HPGVPM LISGGND AKLFTYPANAFLAFHPHDVCFAPQQTQVKLAFEPDICNGVMLMAQYENCLDVWEVPTGGGH SSQVKLGKGIVKSREGGDISVSKRKREAFESRNNKGKHCISNCNGVQETGMRLCELPNGTKKNCCNSNIVKQMG KVKCPPPELLARIKCKSPNHISCSGLSGSGHLIAFSDQIKPRLCELEQQHTSDVSNRRGWSVRKRRRLPRNLPPAH NIAFSADSSRLLLACPHNSIFVVDIENVVDVLRHFEVVGSELLEHADIASPIRMCTSDAGQWLAVSNVLGDATIFNLE TLRQHWISIPRLDGGPITSMMFHPRNSCILVVATRANQLHVLDVEARQFGEWSRKNASSLPQRLLEFPGGIQLLSM SPCKMSSIIAYSSRAMCLIDFQKPVPEKTKMTVPFTSKDKVAGSHLDLSNGSNCNLQNGGTVQSDKNFIVVPFK DPVFLQLHLSDTSVLVIEKPWLDVLHQLPPPYYRHVYGT



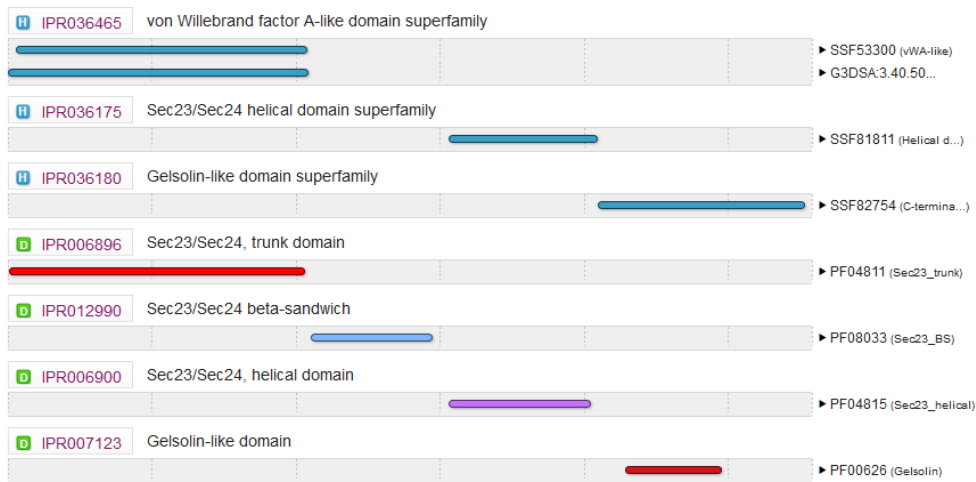
Quinoprotein alcohol dehydrogenases are a family of proteins found in methylotrophic or autotrophic bacteria. These quinoproteins use pyrroloquinoline quinone as their prosthetic group. There are three types of alcohol dehydrogenases: type I includes methanol dehydrogenase and ethanol dehydrogenase, type II includes soluble quinohaemoprotein with a C-terminal

containing haem C, and type III includes quinoprotein alcohol dehydrogenase with a C-terminal cytochrome C domain [PMID: 11761326]. (<http://www.ebi.ac.uk/interpro/entry/IPR011047>)

## Equisetales

>JVSZ\_2014214\_Equisetum\_hymale

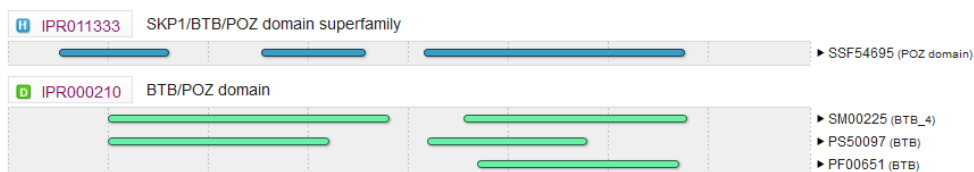
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YQVCVDLFLTTQSYVDVASLADVPRTTGGQIIYYYPFSATADSAKLYNDLRWNVSRPQGLEAVMRVRCSSQGVQV  
QDYFGNFCRRIPTDVLPAVDCDKTFMVTCLKHDDKFTEGSECFCQCALLYTTMYNERRIRVMTLSLPCCTAILNSVF  
RSADLDSQFTYFLKQAAQIPNTPLPQVKEQVVTSCVNILYAYRKYCAAASSSGQLIPETLKILPLYTLAFTKSMSL  
RPDVRIDDRCYWLARVASLSSSLVAAYVPRMFAIHDELEDLSNGSLPPFLYLSSENLGNIGIFMLENGEDVFFY  
AGKSVPPDTLYQLFGVHSVNEMASNQFILQEFDNDSSRKLNALVNEIRQRSSYLRLMRWCKQGDPLEFFFLSML  
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## Lycopodiales

>ENQF\_2016454\_Lycopodium\_annotinum

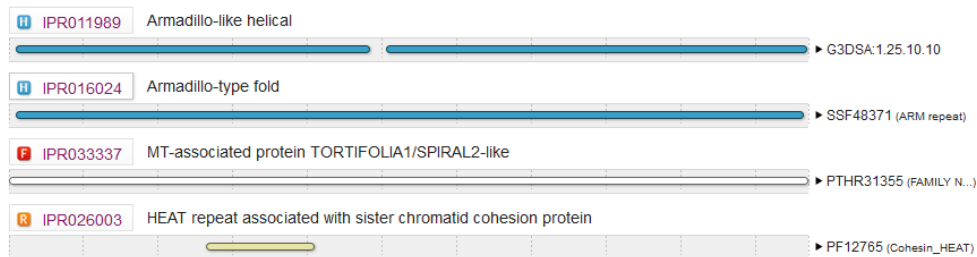
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FIYAGIVQLNAKNL TEVKLLAKRCRLKTL SGLNGESPTWGAAIPQFSLPSLLGDLGHHFVDIVLQADTCISEQGAD  
KCKLCKLTS DHVHAHRLVLSSQCEFFQALFRSGMRDSAEQAIRVHRRKNVLYLYCYGELLILSEVEGDCAWSHLG  
TQRQLTYLRQLVELAEAEWLLDLQQQCFEIIMHYVRLNVLYCPEVMSHAATSGQGLIVEELAEIAPMYTQM  
NSGAFDSLEEDLRETVRTAHVRI



The BTB (for BR-C, ttk and bab) [PMID: 7938017] or POZ (for Pox virus and Zinc finger) [PMID: 7958847, PMID: 17384421] domain is a versatile protein-protein interaction motif involved in many cellular functions, including transcriptional regulation, cytoskeleton dynamics, ion channel assembly and gating, and targeting proteins for ubiquitination [PMID: 16207353]. (<http://www.ebi.ac.uk/interpro/entry/IPR011333>).

>ULKT\_2018407\_Lycopodiella\_apressa

EDLERIAESLSPEGIPLCLGCLYDTNSEQKSLARRECIRLFGTLALLHGFLAPYLSKIISCIIIRRLKDPDTIVRDACVD  
AVGAIALNVISPEDEDPSADYGNDGSFSPSVFEVFFKPLVEALNEQNKHLQVGAAMCLARLIDSSSHPRSSSVQRLY  
PRIIKLLKASNFLAKAALLSVVGSLSLTKADEVEADQFLASIVPHVQASLESSDWAIRRA



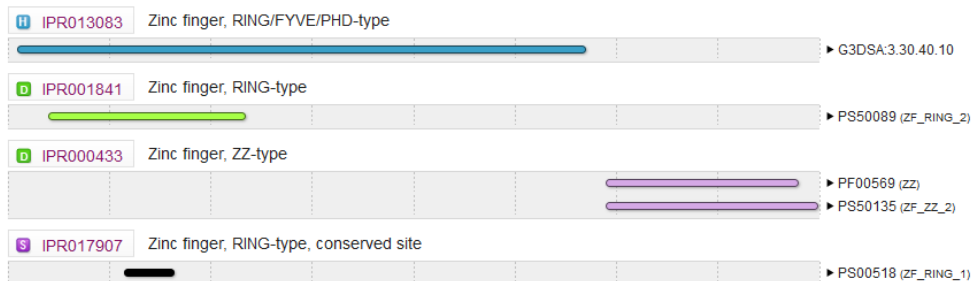
This entry includes a group of plant microtubule-associated proteins, including TORTIFOLIA1/SPIRAL2 and SPIRAL2-like (SP2L) from Arabidopsis. They regulate the orientation of cortical microtubules and the direction of organ growth [PMID: 18577573]. (<http://www.ebi.ac.uk/interpro/entry/IPR033337>).

This HEAT repeat is found most frequently in sister chromatid cohesion proteins such as Nipped-B [PMID: 15060134]. HEAT repeats are found tandemly repeated in many proteins, and they appear to serve as flexible scaffolding on which other components can assemble. (<http://www.ebi.ac.uk/interpro/entry/IPR026003>).

## Araucariales

>IZGN\_2001467\_Dacrydium\_balansae.nd

KLTVNDALCCDCRELIYLPVLNCGHAFCTCVSISEDGTLK**CQV**CQSVHPGDRPH**C**LELNHFLELMFPLEYAER  
KKSILVNKQT**C**KQSKEEST**S**CKKKAENTSAEVPANSSEQAIIHPGV**G**CDYCGIIPIMGKRYKCLDCPESIGFDLCG  
KCYEIGSNLPGRFNQKHTAEHSFEV



Zinc finger (Znf) domains are relatively small protein motifs which contain multiple finger-like protrusions that make tandem contacts with their target molecule. Some of these domains bind zinc, but many do not; instead binding other metals such as iron, or no metal at all. For example, some family members form salt bridges to stabilise the finger-like folds. They were first identified as a DNA-binding motif in transcription factor TFIIIA from *Xenopus laevis* (African clawed frog), however they are now recognised to bind DNA, RNA, protein and/or lipid substrates [PMID: 10529348, PMID: 15963892, PMID: 15718139, PMID: 17210253, PMID: 12665246]. (<http://www.ebi.ac.uk/interpro/entry/IPR013083>).