

# SUPPLEMENTARY MATERIALS

## **Metalloprotein-specific or critical amino acid residues: Perspectives on plant-precise detoxification and recognition mechanisms under cadmium stress**

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Table S1: Functional protein sequence involved in Cd absorption, transport and detoxification.

Figure S1: Specific residues and transmembrane structural features of NRAMP proteins involved in Cd influx.

Figure S2: Specific residues and transmembrane structural features of ZIP proteins involved in Cd influx.

Figure S3: Specific residues and transmembrane structural features of MT proteins involved in Cd chelation.

Figure S4: Specific residues and transmembrane structural features of PDF proteins involved in Cd chelation.

Figure S5: The specific residues and transmembrane structural features of the vacuolar proteins in CAX, MTP family members.

Figure S6: The specific residues and transmembrane structural features of the vacuolar proteins in ABCC family members.

Figure S7: Specific residues and transmembrane structural features in the OPT family of long-distance transport proteins.

Figure S8: Specific residues and transmembrane structural features in the HMA family of long-distance transport proteins.

Figure S9: Specific residues and transmembrane structural features of members in PCR the family of efflux proteins.

Figure S10: Specific residues and transmembrane structural features of members in the ABCG family of efflux proteins.



**>AtNRAMP1**

[illegible]

## >OsNRAMP1

MGVTKAEAVAGDGGKVVDIEALADLRKEPAWKRFLSHIGPGFMVCLAYLDPGNMETDLQAGANHKEYELLWVILIGLIFALIIQSLSANLGVVTRGRHLAELCKTEYPVWVKTC  
LWLLAEALAVIASDIPEVIGTGFAFNLLFHIPVWTGVLIIAGSSTLLLLGLQRYGVRKLEVVVALLVFVMAGCFFVEMSIKPPVNEVLQGLFIPRLSGPGATGDSIALLGALVMPHNL  
FLHSLQLSRNTPASAKGMKDVCRRFFLFSGAGLIVALLVNIASISVGTVCNATNLSPEDAVKCSDDLTDSSSFLLRNVLGKSSATVYGVALLASGQSSTITGTAYAGQYVMQGFL  
DIKMKVLRNLMRTSIAIVPSLIVIGSSGAGRLIVIASMLSEFLPFALPLLKFSSSSNKMGENKNSIYVGFSSVVLGFVIIGINIYFLSTKLVGWILHNALPTFANVLIGIVLFPLM  
LLYVVAVIYLTFRKDTVKFVSRRELQAGDDTEKAQVATCVADEHSKEPPV

## >OsNRAMP5

MEIERESSERGSISWRASAAHDQDAKKLDDADDQLLMKEPAWKRFALHAVGPGFMVSLAYLDPGNLETDLQAGANHRYELLWVILIGLIFALIIQSLAANLGVVTRGRHIAEICKSEY  
PKFVKIFLWLLAELAVIAADPEIVGTAFAFNILFHIPVWVGVLITGTSTLLLLGLQKYGVKLEFLISMLVFMMAACFFGELSIVKPPAKEVMMKGLFIPRLNGDGATADAIALLGAL  
VMPHNLFLSHALVLSRKTPASVRGIGDKGCRFLYESGFALFVALLINIAVSVSGTACSSANLSQEDADKCANLSDTSSFLKNVLGKSSAIVYGVALLASGQSSTITGTYAGQYI  
MQGFLDIRMRKVLNMLNTRTIAIAPSLVISIIGSSRGAGRLIIIASMFLFPAIPLLLKFSKKSMGPKHNSIYIIVFSWFLGLLIIGINMYFLSTSFVGWLIHNDLPKYANVLVGA  
AVFPFMLVYIVAVVYLTIKDKSVVTFVADSSLAAVVDAEKADAGDLAVDDDEPLPYRDDDLADIPLR

**>AtIRT1**

MASNSALLMKTIFLVLIVFVSAISPATSTAPEECGESANPCVNAKAKALPLKVIAIFVILIASMIGVGAPLFSRNVSLFQPDGNIFTIHKCFASGIILGTGFMHVLPSDFEMLSSICLEENP  
WHKFPPSGFLAMLGLITLAIDSMATSLYTSKNAVGINPHGHGHGHPANDVTLPIKEDDSSNAQLRVRVIAMVLELGIIVHSVVLGSLGATSDCTIKGLIAALCFHQMFEGM  
GLGGCILQAEYTNMKKFVMAFFAVTTPFGIALGIALSTVYQDNSPKALITVGLLNACSGAGLLIYMALVDLLAAEFMGPKLQSGIKMQFKCLIAALLGCGGMSIAKWA

**>OsIRT1**

MATPRTLVPILPPVAALLLLLVAASSIPILAAQPADACGGAPDQAAADGACHDVPRALRLKLIAPTILVSSVGVCLPLLSRSVPALRPDGGGLFAVVKAFAASGVILATGYMHVLP  
DAFNNTSPCLPRKPWSEFPFAAFVAMLAAVSTLMADSLMLTYYNRSKPRPSSGGDVAADVADHGESPQDQHRHGHGHGHGHGMVAKPDDVEATQVQLRRNRVVVQVLEIG  
IVVHSVVIGLGMGASQNVCTIRPLVAMCFHQMFEFGMLGGCILQAEYGRRMRSVLVFFFSTTTPFGIALGLALTRVYRDNSPTALIVVGLLNAASAGLLHYMALVELLAADF  
GPKLQGNVRLQLAAFLAVLLGAGGMSVMAKWA

**>OsIRT2**

MMSSSQTPVRIAFVFLVILAATDAHSDHRTPPACGGAAVGGECHSVARALRLKLIAPILAAASVAGVCLPLFARSVPALRPDGGFLFAVVKAFASGVILGTGYMHVLPDSFND  
LTPCLPRKPWFSEFFAAFAVLAHVFTLMVDLSMLTFHTRGSKGRASSAVAHGHGDHGHCHAHALGQADVAALSTTEAADQGSQDVEAGNTTKAQLLRNRVIVQVLEMGIVV  
HSVIGLGMGASQNVCTIRPLVAALCFHQMFEQMGGLGGCILQAGYGGRTSALVFFSTTTPFGIALGLALTRVYSDSSPTALVVVGLLNAASAGLLHYMALVELLAADFMGPK  
LQGNVRLQLAASLAILLGAGGMSVMAKWA

## >OsZIP1

MARTIMRVSLLVAVVLLAALSFQACSGHGGINDDGGQVDAPATPASSSGVRSKGLIAVKVWCLVILLVFIFAGGVSPLYFYRWNESFLLGLTQFAAGVFLGTALMHFLADST  
STFKGLTTNQYPFSFMLTCVGFLLTMLSDLVIAAVARRSAAAGVSDNQVSEQQQRQQAEGAVMSRKEEAAAAVAHPAMLVRTSSFEHAVLLIVALCFHSVFEGIAIGVSASKSE  
AWRNLTWITGLHKIFAAMGIALLRMPKRPFLMTVVYSLAFVSSPVGVGIGIAIDATSSQGRAADWTYAISMGLATGVFIYVAINHIAKGYRPHHPTAADKPLFKFLAVLLGV  
ADWATGATGTHK

## >OsZIP3

MGAKKHHTLQVLPWLLFAQHTAASACDCANTTDGADRQGA M K L K L I A I A S I L A A G A G V L P V I G R S M A A L R P D G D I F A V K A F A A G V I L A T G M V H I L P A A F D A L T S P C L K R G  
V G D R N P F P F A G L V S M S A A V S T M V V D S L A G Y Y H R S Q F R K A R P V D N I N V H K H A G D E R A E H A Q H I N A H T H G G H T H S H G D I V V C G S P E E G S V A E S I R H K V V S Q V L E L G I L V H S V I G  
V L S G A S R P S T I R L P V G A L S F H Q F F E G V G L G G C I V Q A N F K V R A T V I M A I F F S L T A P V G I V L G I A I S S S Y N V H S S T A F V V E G V F N S A S A G I L Y M S L V D L L A T D F N N P K L Q I N T K L Q L M  
A Y L A L F L G A G L M S M L A I W A

**>AtMT2a**

MSCCGGNCGCGSGCKCGNGCGGCKMYPDLGFSGETTTTETFVLGVAPAMKNQYEASGESNNAENDACKCGSDCKCDPCTCK

## >AtMT3

MSSNCGSCDCADKTQCVKKGTSYTFDIVETQESYKEAMIMDVGAENNANCKCKCGSSCSCVNCTCCPN

## >OsMTI-1b

MSCSCGSSCGCGSNCTCGKMYPDLEEKSSSAQATVVLGVAPEKAHFEAAAESGETAHGCGCGSSCKCNPUNC

**>OsMTI-2b**

MSCCGGNCGCGSSCQCGNGCGGCRYSEVEPTTTTFLADATNKGSGAASGGSEMGAENGSCGCNTCRCGTSCGCSCCNCN

## >OsMFile

MSCSCUSSCSCUSNCSCUKKTFDLEEKSSSTKATVVLGVAFERKAQQFEAAAESUEIAHUCSCUSSCRCNFCNC

**OSM1-3a**

MSDRKGNEDCAIRKSGQVRKSTSTSTGVVVEAKRSHHLEEVHAGEELNGGKERESTTSCSTDERGRK

## MAKETEXT

YRSCFCFFSC

**>AtPDF2.5**

MENKFFAAFFLLLVLFSSQEIIIGGEGRTICQSKSHHFKYMCISNHNCAIVCRNEGFSGGRCHGFHRCYCTRLC

>AtPDF2.6

MKLSRLISALLMSVMLLFATIGMGFVEARTCESPSNKFQGVCLNSQSCAKACPSEGFSGGRCSSLRCYCSKAC

**>AtCAX2**

MSICKVVPVLEIAQVEMVSANELNENKSLFRQEDATQIKASLMEOQGSLSIFPQHTPKAPKNSVLSNKIVIPCNKENLLLPGLFLAIVHYMIDSKGWVFLEITLVGHTPLAERLGY  
ATEQLACYTGPTVGGLLNATFGNVLTEILISIALKNGMIRVVDQLTLGSLSNMLLVLGCAFFCGGLVYFYQKDDQKGIATVNSGSLGLLMAYMGILFPAVLHYTHSEVHAGSSLSA  
LSRFSSSCIMLIAAYALFFQKLKFSQNSYSPLDEESNQNEETSAEDEDPEISKWEAIWLSILTAWVSVLLSGYLVDIAEGASVSVNSNPIAFISTILLPIVGNAAEHAGAIMFAMKDKLDLS  
LGVAIGSSIQISMFAVPFCVVGWMMGQMDLNFQLFETAMLFITVIVVAFFLQEGSSNYFKGLMLILCYLIVAAFFVHEDPHQDGI

## >AtCAX4

MSSISTESSNLSLLENGGGGSDKPTAETSSRRVRRITVSASSLIRKRSDLKLISRVRWEFMRRILTNLQEVLLGTLFILFPAVPLAVVAHRYDCPRAWVFALSLLGLTPLAERISFLT  
 EQIAHFVTPTVGGMLMATCGNATEMIIAILAVGQRKHVVKLSDLSILSNLLFVLGTSLFLGGISNLRKHQSFDRQGDMSMLLYLALLCQTLPLMIMRFTMEAEEDGSDVVV  
 LRSASSFVGLIAYLAFILFHLFSHLSPPPPPLQREDVHRDDVSDKDEEGAIVGMWSAIFWLIIMTLVALDLSYLTQDAASDWGLSVGFIGILLPIVGNAAEHAGAVIFAFRN  
 KLDITLGIALGSAQTQIALFVVPVTVLVAWMTGMEIMDLNFNLLACFALSILVTSVLQDGTSNYMKGLVLLLCYVVAACFFVNSPSTETNTNTNHTITKR

**>OsCAX1a**

MEAAAAEAGRKLAARHPHGRSRTAHNMSSSSLRKKSDAALVRKVPVAPLRPLLANLQEVFLATKLAVLFPAVPLAIAAQCFRFDQVWVFALSLLGLIPLAERSVFLTEQIALY  
TGPTVGGLLNATCGNATELIIALLKKGIEVVKCSLLGSVLSNLLLVLGTSLFCGGVVNLGARQPYDRNQSDVSTALLFLAVLCHSAPLLRLRYAVAAGEHSVSATSAAASLDL  
SRACSFVMLASYVAYLFFQLKTHRQLFEPQEVDDGGDAGDDDEEPALGFASALFWLALMTAVISVLSEYVVGTEIPTSQSWGLSVSFISIILLPIVGNAAEHAGAIIFALKNKLDITLG  
VALGSATQISMFVPLSVLVAWIMGVQMDLDFKLLLETGSLFMAVLVTAFTLQDGTSHYLYGILLCCYIVIGACFFVARQPAGHANSNGALLDVPTGMSMSVQA



>OsCAX1c

MAPPESHHHLLLESGLLEVSKAPSAAVAEEEEKEAAAWTPSSSSSMTGRKIKSEASPLLRLLGGPAAQLQEVLLGTKLYPLFSAVPLAVA AESLRLGRVWVFAFSLIGLAPLA  
ERVVSFLSEHIANTVGPTAGGIMNATCGNVPELIHALFALHKNKMEILKWSLLGSILSNLLLVLGSSLLFGGIVNIGKERPLDKRQADVSIGLLLLGLVLCHIATLVSKYTSSTGDSINSS  
SVMQLSRSCAIVMLIAFYFGSLMFQLKTHRQIFEELEDSSDSSSEDDATDKSVIGFASAMVWLIGMAVVTAMLSSYVVTITIEEASESMGIPVRFISILLPIVGNAAEHAGAIIFAFKN  
KIDISLGITLGSATQISMLVVPVILIVSWVNAIPMDLDFNLLETGSLAMAVITTAFTLQDDKWHYLKGLNLVFSYIVIAVCFVFMKALPTLKEDD

>AtABCC1

MGFEPLDWYCKPVPNGVWTKTVDYAFGAYTPCAIDSFVLGISHLVLLILCLYRLWLITKDHKVDKFCFLRSKWFSYFLALLAAYATAEPLFRLVMRISVLDLDGAGFPYPYEAFML  
VLEAFAGWSALVMTVVETKTYIHRLWYVRFAYIALVGDMLVLLNLVLSVKEYYGSFKLYLYISEVAVQVAFGTLLFVYFPNLDPPYPGYTPVGTENSEDEYEEELPGGENICPE  
RHANLDFSIFSWLNPLMTLGSKRPLTEKDVWHLDTWDKTETLMRSFQKSWDKLELEKPKPWLLRALNNSLGGRFWWGGFWKIGNDCSQFVGPLLLNELLKSMQLNEPAWIGY  
IY AISIFVGVLGVLCEAQYFQNMVRGVYRLRSALIAAVFRKSLRLTNEGRKKFQTGKITNLMTTDAESLQQICQSLHTMWSAPFRIIVALVLLYQQLGVASIIGALFLVLMFPIQT  
VIISKTKQLTKEGLQRTDKRIGLMNEVLAAMDTVCKYAWENSFQSKVQTVRDDLESWFRKAQLLSAFNMFILNSIPVLTVVSFGVFSLLGGDLTPARAFTSLSLFSVLRFPFLM  
LPNIITQMVNANVSLNRLEEVLSTEERVLLPNPIEPGQPAISRNGYFSWDSKADRP TLSNINLDIPLGSLVAVVGSTGEGKTS LISAMLGELPARSDATVTLRGSVAYVPQVSWIF  
NATVRDNLFGAPDFQEKYERVIDVTALQHDLELLPGGDLTEIGERG VNISGGQKQRVSMARAVYSNSDV CILDDPLSALDAHVGQQVFEKCIKRELGQTTRVLVTNQLHFLSQV  
DKILLVHEGTVKEEGTYEELCHSGPLFQRLMENAGKVEDYSEENGEAEVDQTSVKPVENGANNLQKDGIETKNSKEGNSVLVKREERETGVVSWKVLERYQNALGGAWVV  
MMLVICYVLTQVFRVSSSTWLSWTDSGTPKTHGFLFYNIYVALLSFGQVSVTLINSYWLIMSSLYAAKKMHDAMLGSLRAPMVFFQTNPLGRIINRF AKDMGDI DRTVAVFV  
NMFMSGIAQLLSTVILIGIVSTLSLWAIMPLL VVFYGAYLYYQNTSREIKRMDSTTRSPVYAQFGEALNGLSSIRAYKAYDRMAEINGRSMDNNIRFTLVNMAANRWLGIRLEVL  
GGLMVWLTASLAVMQNGKAAANQAYASTMGLLLSYALSITSSLTAVLRLASLAENSLNSVERVGNIEIPSEAPLVIENNRPPPGWPSSGSIKFEDVVLRYRPELPPVLHGVSF LIS  
PMDKVGI VGRGTGAGKSSLLNALFRIVELEKGRILIDECDIGRFGLMDLRKVLGIIPQAPVLFSGTVRFNLDPFSEHNDADLWESLER AHLKDTIRRNPGLDAEVTEAGENFSVGQR  
QLLSLARALLRRSKILVLDEATAAVDVRTDVLQKTIREEFKSC TMLIIAHRNLNTIIDCDKVLVLD SGKVQEFSSPENLLSNGESSFSKMVQSTGTANA EYLR SITLENKRTREANGD  
DSQPLEGQRKWQASSRWAAAAQFALAVSLTSSHNDLQSL EIEDDNSILKKTDAVVTLRSVLEGKHDK EIEDSLNQSDISRERWWPSLYK MVEGLAVMSRLARNRMQHPDYNL  
EGKSFWDWNVEM

>AtABCC2

MCRKQDQNI STYLMFWWGGFWKIGNDCSQFVGPLLLNQLLKSMQEDAPAWMGYIYAFSIFVGVVFGVLCEAQYFQNMVRGVYRLRSALIAAVFRKSLRLTNEGRKKFQTGKI  
TNLMTTDAESLQQICQSLHTMWSAPFRIIHALILLYQQLGVASLIGALLLVLMFPLQTVIISKMQKL TKEGLQRTDKRIGLMNEVLAAMDTVCKYAWENSFQSKVQTVRDDLESW  
FRKSQLLGALNMFILNSIPVLTVISFGVFTLLGGDLTPARAFTSLSLFAVLRFPFLM LPNIITQVVNANVSLKRLEEVLATEERILLPNPIEPGEP AISIRNGYFSWDSKGDRPTLSNI  
NLDVPLGSLVAVVGSTGEGKTS LISAILGELPATSDAIVTLRGSVAYVPQVSWIFNATVRDNLFGSPFDREKYERAIDVTS LKHDELLPGGDLTEIGERG VNISGGQKQRVSMAR  
AVYSNSDVYIFDDPLSALDAHVGQQVFEKCIKRELGQKTRVLVTNQLHFLSQVDRIVLVHEGTVKEEGTYEELSSNGPLFQRLMENAGKVEEYSEENGEAEADQTAEQPVANGN  
TNGLQMDGSDDKKSKEGNNKKGGKSVLIKQEERETGVVSWRVLKRYQDALGGAWVVMMLLLCYVLTEVFRVTSSTWLSWTDAGTPKSHGFLFYNL IYALLSFGQVLVTLTN  
SYWLIMSSLYAAKKLHDNMLHSILRAPMSFFHTNPLGRIINRF AKDLGDI DRTVAVFVNMF MGQVSQLLSTVVLIGIVSTLSLWAIMPLL VLFYGAYLYYQNTAREVKRMDSISR  
SPVYAQFGEALNGLSTIRAYKAYDRMADINGRSMDNNIRFTLVNMGANRWLGIRLETGLGLMIWLTASF AVMQNGRAENQQAFASTMGLLLSYALNITSLLTGVLRLASLAEN  
SLNAVERVGNIEIPPEAPPVIENNRPPPGWPSSGSIKFEDVVLRYRQPLPPVLHGVSSFFIHP TDKVGIVGRTGAGKSSLLNALFRIVEVEKGRILIDCDV GKFG LMDLRKVLGIIPQ  
SPVLFSGTVRFNLDPFGEHNDADLWESLER AHLKDTIRRNPGLDAEVSEAGENFSVGQRQLLSLRALLRRSKILVLDEATAAVDVRTDALIQKTIREEFKSC TMLIIAHRNLNTIID  
CDKILVLD SGGRVQEFSSPENLLSNGESSFSKMVQSTGAANA EYLRSLVLDNKRAKDDSHHLQGQRKWLA SSRWAAAAQFALAASLTSSHNDLQSL EIEDDSSILKRTNDAVVTL  
RSVLEGKHDK EIAESLEEHNISREGWLSSLYRMVEGLAVMSRLARNRMQQPDYNFEGNTFDWDNVEM

>AtABCC3

MDFLGSTTSGT LAMLSFSESILPLDSRFLKLPLFRWLSGFLHSVLLLVLFFSWVRKKIRGDSGVTESLKDRRDFGFKSALFCSLALSLLNLVLMSLSGFYWYESGWL DNEQL  
VSSLGFLGMVSWGVL SICLHRCRDCEHKKAPFLRLWL VFYL VVSCYSLVVDVFMYERRETVPVHLLVFDIVAFIAAVFLGYVAVLKKDRSNSNGVLEEPLLNGGDSRVGGD  
DSVELNKTNGSGEATPYSRAGILSLLTFSWMSPLIDIGNKKTLDLEDVPQLHDTDSVVG LAPKFRSMLESPDGGERSGVTTFFKLIKALYFTAQWEILVTAFFAFIYTVASYVGPALI  
DTFVQYLNGRRRQYNHEGYVLVITFFAAKIVECLSQRHWFFRLQKV GIRMRSALVAMIYEKGLT LSCQSKQRTSGEINFMTVDAERIGNFSWYMHDPWMVLLQVGLALWILY  
RNLGLASIAALVATHIIVMLINFPFGRMQERFQEK LMEAKDSRMKSTSEILRNMRLKLQGWEMKFLSKIFDLRKSEEGWLKKYVYNASAVISFVFWGAPTLVSVSTFGACILLGIPLE  
SGKILSALATFRILQEPIYNLPDTISMIVQTKVSLDRLASYLCLDNLQPDIVERLPKGSSDVAVEVINSTLSWDVSSSNPTLKDINFKVFPGMKVAVCGTVGSGKSSLLSSLLGEVPK  
VSGSLKVCGTKAYVAQSPWIQSGKIEDNILFGKPMERERYDKVLEACSLSKDLEILSFGDQTVIGERGINLSGGQKQRIQIARALYQDADIYLFDDPFSAVDAHTGSHLFKEVLLGL  
LCSKSVIYVTHQVEFLPAADLILVMKDGRISQAGKYNDILNSGTDFMELIGAHQEALAVDSDVDANSVSEKSALGQENVIVKDAIAVDEKLESQDLKNDKLESVEPQRQIIQEEER  
EKGSV ALDVYWKYITLAYGGALVPFILLGQVLFQLLQIGSNYWMAWATPVSEDVQAPVKLSTLMIVYVALAFGSSL CILLRATLLVTAGYKTATEL FHKMHHCIFRSPMSFFDS  
TPSGRIMSRASTDQSAVDLELPYQFGSVAITVIQLIGIIGVMSQVSWLVLFVIPVVAASIWYQRYYIAAARELSRLVGVCAPLIQHFS ETISGATTIRSFQSQEFRFRSDNMRLSDGY  
SRPKFYTAGAMEWLCFRLDMLSSLTFVFSVLVFSIPTGVIDPSLAGLAVTYGLSLNTLQAWLIWTL CNLENKIIISVERILQYASVPSEPLVIESNRPEQSWPSRGEVEIRDLQVRY  
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SSVSENGDNWSMGQRQLVCLGRVLLKRSKILVLDEATASVDTATDNLIQKTLEHFSDCTVITIAHRISVIDSDMVLLLSNGIIEEYDTPVRLLEDKSSSF SKLV AEYTSRSSSSFD

>OsABCC9

MLGLAHL SVMYIGPSLVDRFVNFRRGGELTEGLQLVVVLLAGKAAEALASHHYEFQGQKLG MRIHAALLAAVYRKSLRLSTGARRAHGAGAIVNYMEVDAAEEVANVTHELH  
NLWLMPLEIAVALTLLYTHLGPAVLTAVAAIAVVTVVVALANRRNLEYQFKFLGKRDERMKAITELLYNMRVIKLQGWEE TFGGKIHELREAE LGWLAKSMYFMCANTVVLW  
SGPLAMTVLVFGTCVLTGVTLDAGKVFTATAFFHMLDGPMSQSFPEAIAVSVTQATVSLGRLD RYLLDVELDDTTVERVDDAGINPDGVVVEVRDGVFAWDVRGKKENEEGDDN  
EDDEEGEEEEEEKDVEETPVLETVLKGINIEVRRGELAAVVGTVGSGKSSLLSCIMGEMDKVSGKVRICGSTAYVAQTAWIQNGTIQENILFGQPMDAERYKEVLRSCSLEKDLE  
MMEFGDQTEIGERGINLSGGQKQRIQLARAVYQNCDIYLLDDVFSAVDAHTGSSIFKECLRGMLKGKTILLVTHQVDFLHNVDNIFVMRDGMIVQSGKYDELLDAGSDFLALVA  
AHDSSMELVDQSRQVVKTEYSQPKAVARIPSLRSRIGKGEKVLVAPDIEAATSKIREEERESGQVSWRVYKLYMTEAWGWVG VGM LAFIAVWQVTEMASDYWLSYETSG  
SIPFNPLSFIGVYVAIAAVSIILQVIKSLLETILGLQTAQIFFKMFDSILHAPMSFFDTTPSGRILSRASSDQTIDIVLSFFVGLTISMYISVLSTIHTVCQVAWPSVIAVIPLVLLNIWYR  
NRYLATSRELTRLEGVTKAPVIDHFSETVLGATTIRCFKKDKEFFQENLDRINSSLRMYFHNAAANEWLGRLELIGTLVLAITAF LMISLPSNFIKKEFVGMSLSYGLSLNSLVYFA  
ISISCMLENDMVAVERVNQFSTLPSEAVWKIEDHLPSPNWPTHGDIDIDDLKVRYRPNTPLILKGITVSISSGGEKIGVVGRTGSGKSTLIQALFRLVEPVQGTMIIDGIDICTLGLHDL  
RSRFGIHPQEPVLFEGTIRSNIDPIGQYSDAEIWRALEGCQLKD VVASKPQKLDALVADSGENSVSGQRQLLCLGRVILKRTRILFMDEATASVDSQTDATIQTITRQEFSSCTII SIA  
HRIPTVMDCDRVLLVDAGLVKEFDSPSRLIEQPSLFGAMVEEYANRSSNL

>OsMTP1

MDSHNSAPPQIAEVRMDISSSTSVAAGNKVCRGAACDFSDSSNSSKDARERMASLRKLIIVILCIIFMAVEVVGGIKANS LAILTDAAHLLSDVA AFAISLFSLWAAGWEATPQQS  
YGFFRIEILGALVSIQLIWLLAGILVYEAIVRLINESGEVQGSLMFAVSAFGLFVNII MAVLLGHDDHGHGHGHGHSHDHDHGGSDHDH HHHHEDQEHHGVHHHHEDHGHNSIT  
VNLHHHPGTQHHDHAEPELKSADGCDSTQSGAKDKAKARNNISIHSAYLHVLDGSIQVWIGGAIHWYKPEWKIIDLICTLIFSIVILFTTIKMLRNILEVLMESTPREIDATSL  
ENGLRDMDGVVAVHELHIWAITVGKVLLACHVTITQDADADQM LDKVIGYIKSEYNISHVTIQIERE

>AtOPT4

MATADEFSDEDTSPIEEVRLTVTNTDDPTLPVWTFRMWFLGLISCSLLSFLNQFFSYRTEPLVITQITVQVATLPIGHFLAKVLPKTRFGLPGCGSARFSLNP GPFPNMKEHVLISIFAN  
AGSAFGSGSAYAVGIITIAKFYGRSISFIAGWLLIITTQVLGYGWAGLLRKYVVEPAHMWWPSTLVQVSLFRALHEKDDQRMTRAKFFVIALVCSFGWYIVPGYLF TTLSISWV  
CWAFPRSVTAQQIGSGMRGLGLGAFTLDWTAVASFLFSP LISPFFAIANVFIGYVLLIYFVPLAYWGFDSYNATRFPIFSSHLFTSVGN TYDIPAIVNDNFELDLAKYEQQGRINLS  
MFFALTYGLGFATIASTLTHVALFYGKEISERFRVSYKGKEDIHTRLMKRYKDIPSWWFYSMLAATLLISLALCVFLNDEVQMPWWGLVFASAMAFVFTLPISIITATTNQTPGLN  
IITEYAMGLIYPGRPIANVCFKYVYGMSMAQAVSFLNDFKLGHYMKPIPRSMFLVQFIGITLAGTINITVAWQLNSIKNICQEELPPNSPWTCPGDRVFFDASVWGLVGPKRIF  
GSGQNYAAMNWFGLLGGALGPVIVWSLHKAPFKRSWIPLVNLVPLLGATAMMPATAVNYNSWILVG TIFNLFVFRYKRSWWQRYNYVLSAAMDAGVAFMAVLLYFSVGMEE  
KSLDWWGTRGEHCDLAKCPTARGVIVDGC PVK

>AtOPT6



MGEIATEFTPVMDDDDDRCVVPLEVELVTPKTDSTLPVLTFRMWVLGIGACIVLSFINQFFWYRTMPLSITGISAQIAVVPPLGHLMARVLPTRKFLEGRFQFTLNPAGAFNVKEHV  
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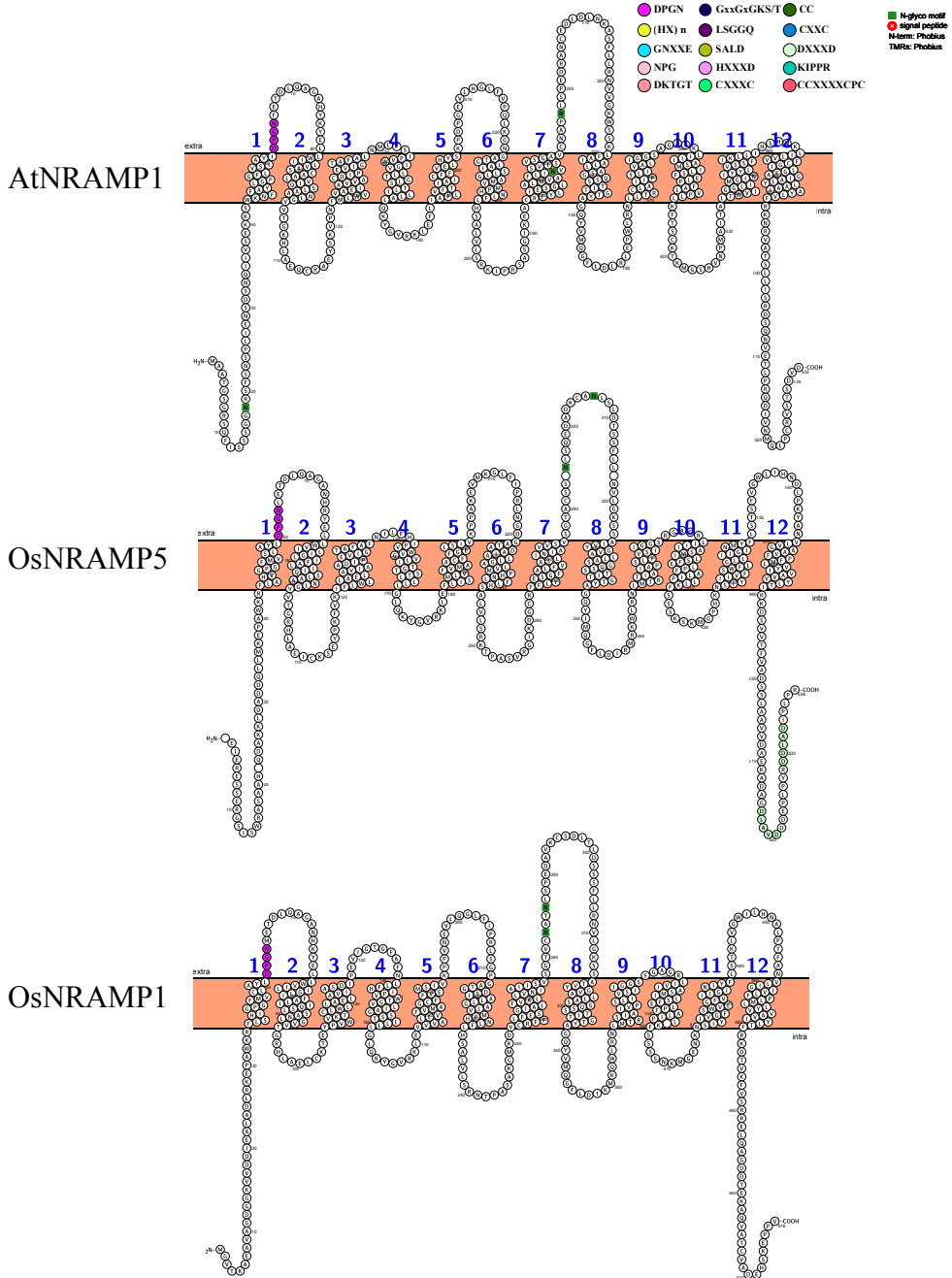


Figure S1: Specific motifs and transmembrane structural features of NRAMP proteins involved in Cd absorption, Different residues are indicated by different colors. The DPGN is near to TMD1.



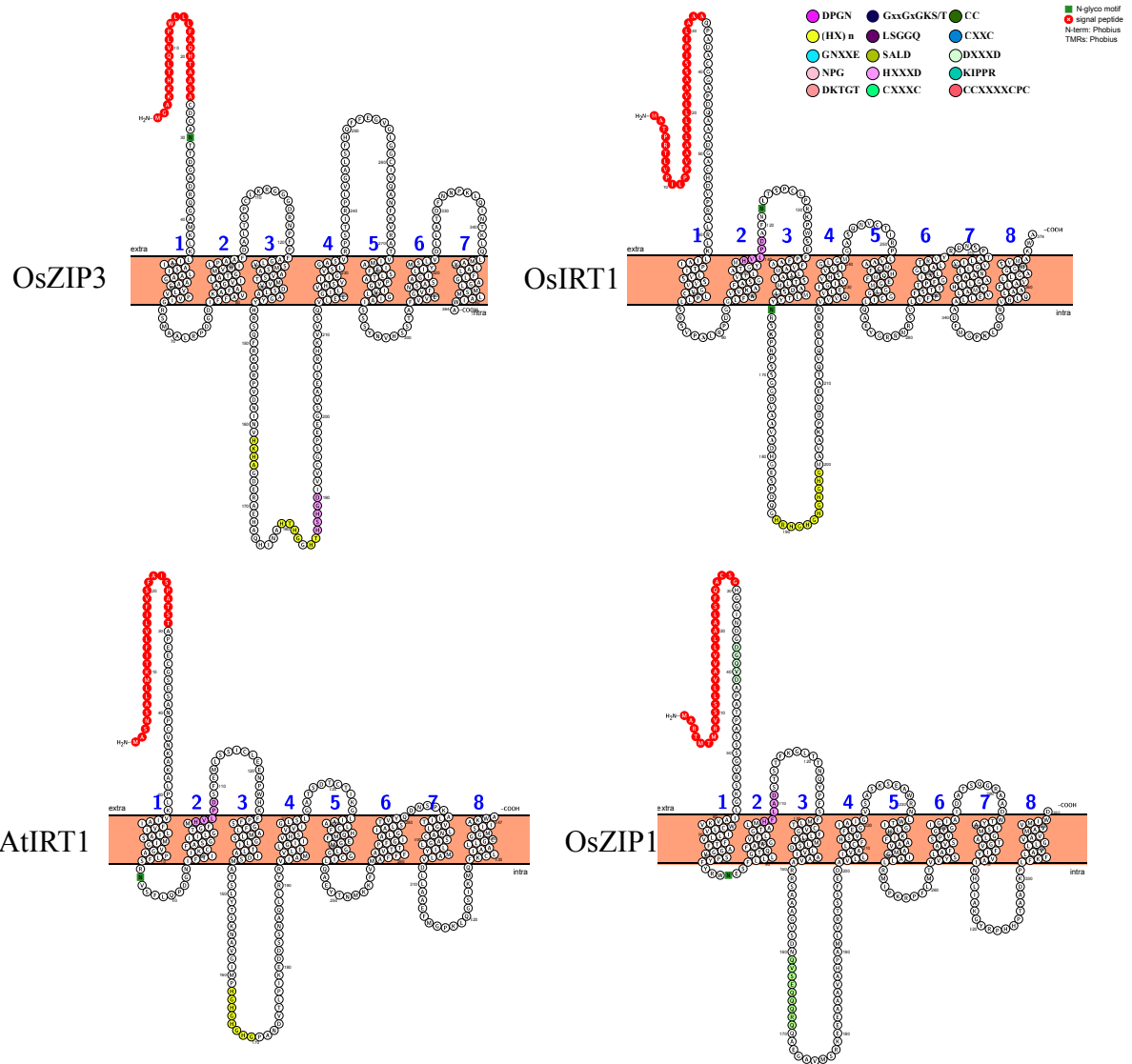


Figure S2: Specific motifs and transmembrane structural features of ZIP proteins involved in Cd absorption. Different residues are indicated by different colors. 8 transmembrane domains, with signal peptide and DXXXD residues at the N-terminus; The (HX)<sub>n</sub> residues between TMD3-TMD4.



DPGN GxxGxGKS/T CC  
 (HX) n LSGGQ CXXC  
 GNXXE SALD DXXXD  
 NPG HXXXD KIPPR  
 DKTGT CXXXC CCXXXXCPC

N-glyco motif  
 N-term: Phobius  
 TMRs: Phobius

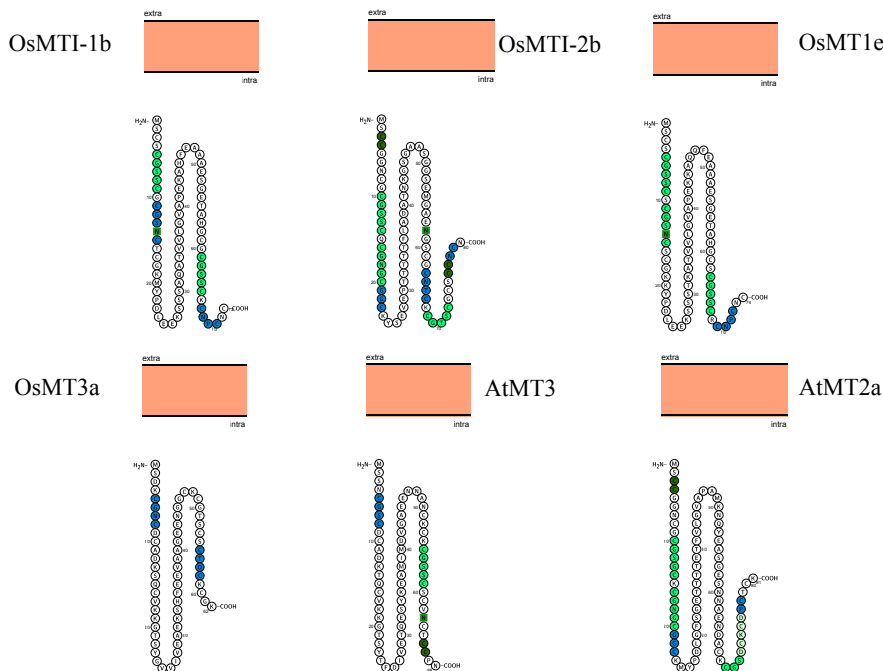
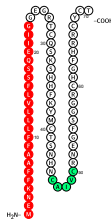


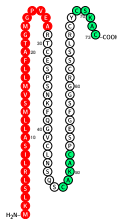
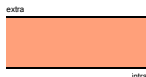
Figure S3: Specific motifs and transmembrane structural features of MT protein involved in Cd chelation. Different residues are indicated by different colors. They have no transmembrane domain, but contain cysteine residues.





- |        |            |          |                 |
|--------|------------|----------|-----------------|
| DPGN   | GxxGxGKS/T | CC       | N-glyco motif   |
| (HX) n | LSGGQ      | CXXC     | signal peptide  |
| GNXXE  | SALD       | DXXXD    | N-term: Phobius |
| NPG    | HXXXD      | KIPPR    | TMRs: Phobius   |
| DKTGT  | CXXXC      | CCXXXXPC |                 |

AtPDF2.5



AtPDF2.6



AtPDF1.5



Figure S4: Specific motifs and transmembrane structural features of PDF protein involved in Cd chelation. Different residues are indicated by different colors. They have no transmembrane domain, but contain cysteine residues.



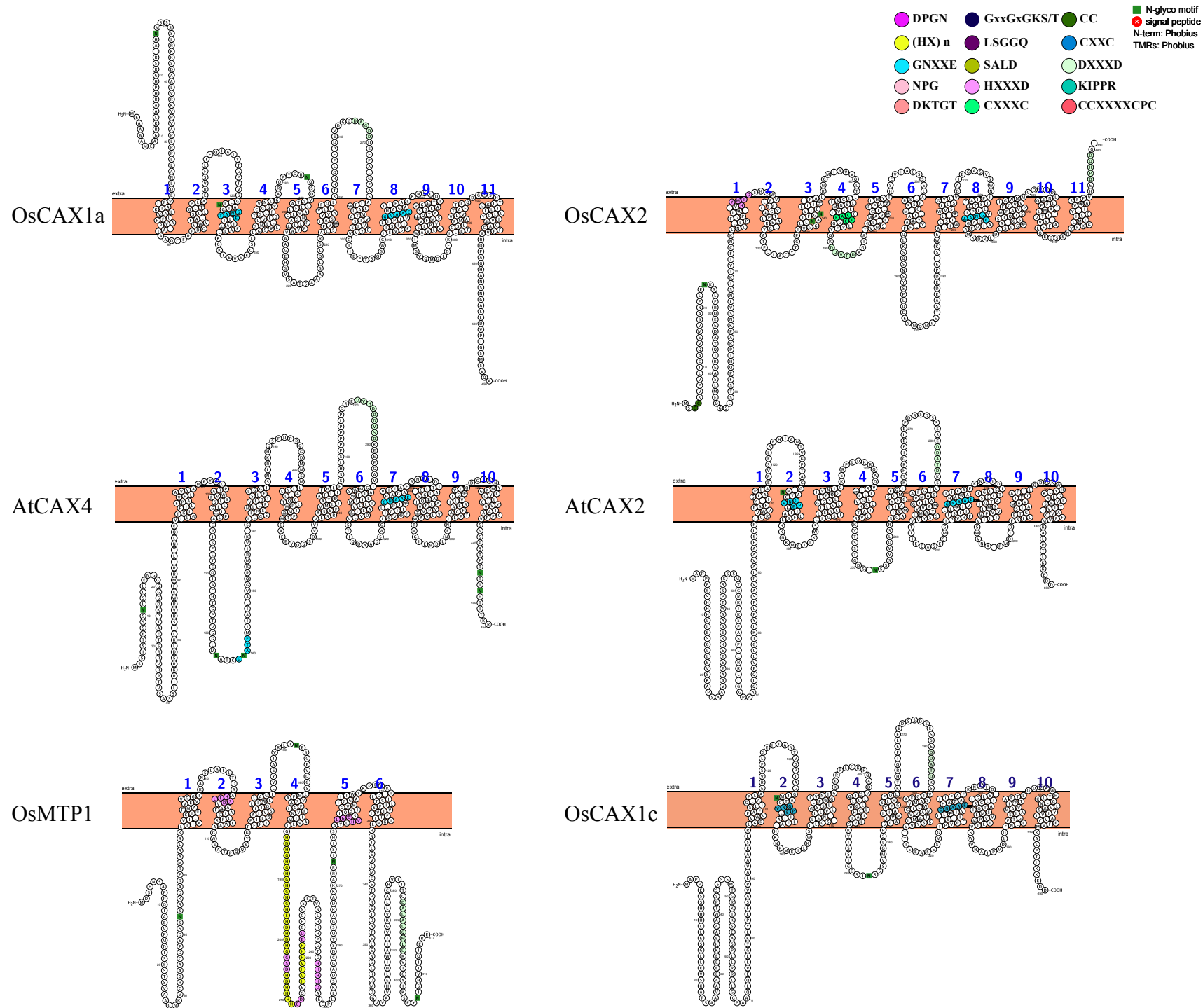


Figure S5: The specific motifs and transmembrane structural features of the vacuolar protein CAX, MTP family members. Different residues are indicated by different colors. CAX family members contain GNXXE residues, and H/DXXXD residues are widely distributed in these two family members.



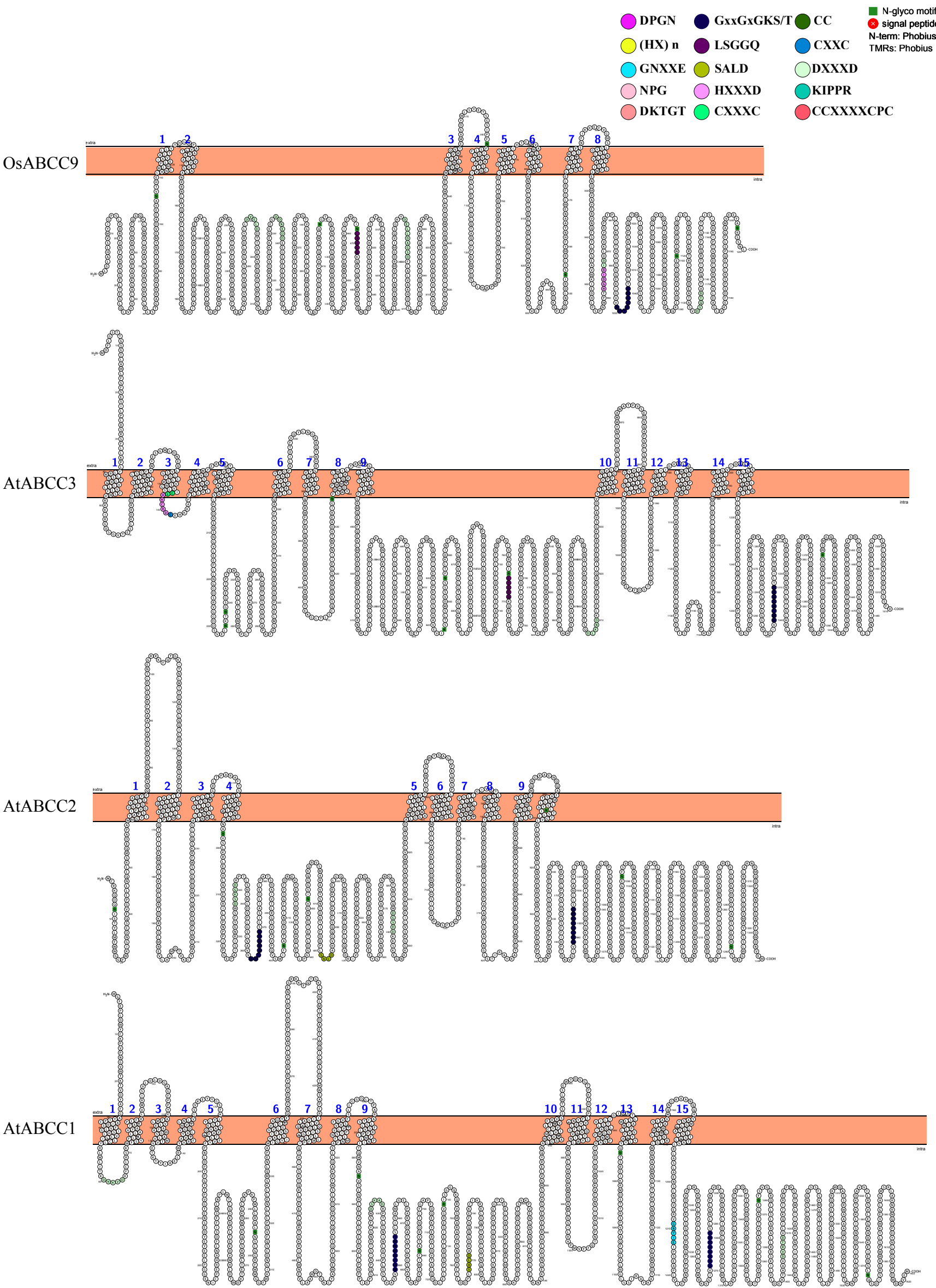
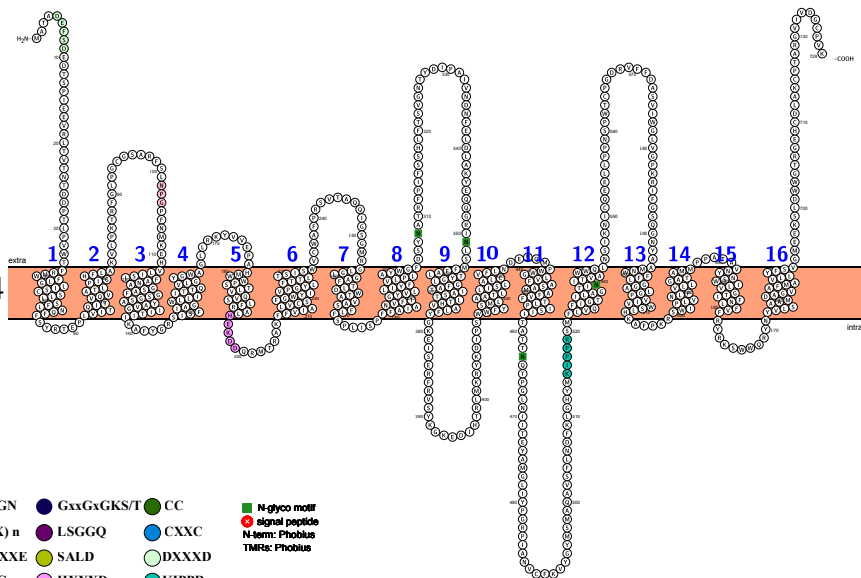


Figure S6: The specific motifs and transmembrane structural features of the vacuolar protein ABCC family members. Different residues are indicated by different colors. With cysteine-rich loop, Q-loop, Walker B motif, H/DXXXD residues.



AtOPT4



AtOPT6

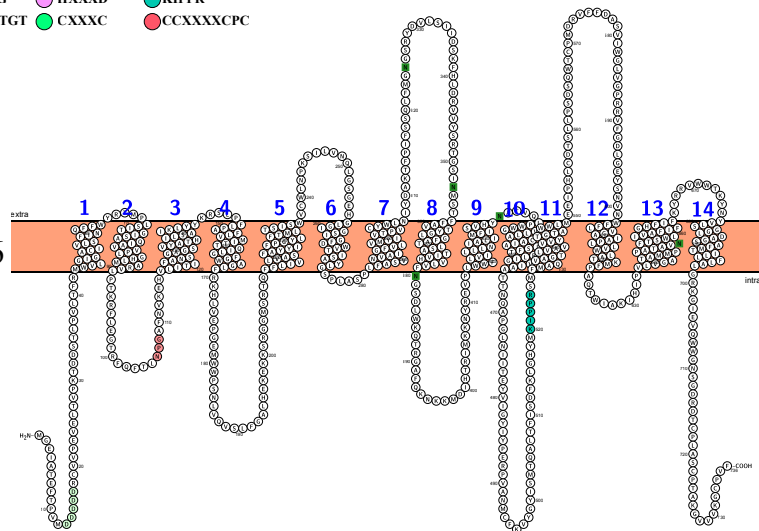


Figure S7: Specific motifs and transmembrane structural features of members of the OPT family of long-distance transport proteins. Different residues are indicated by different colors. They contain KIPPR residues unique to this family.



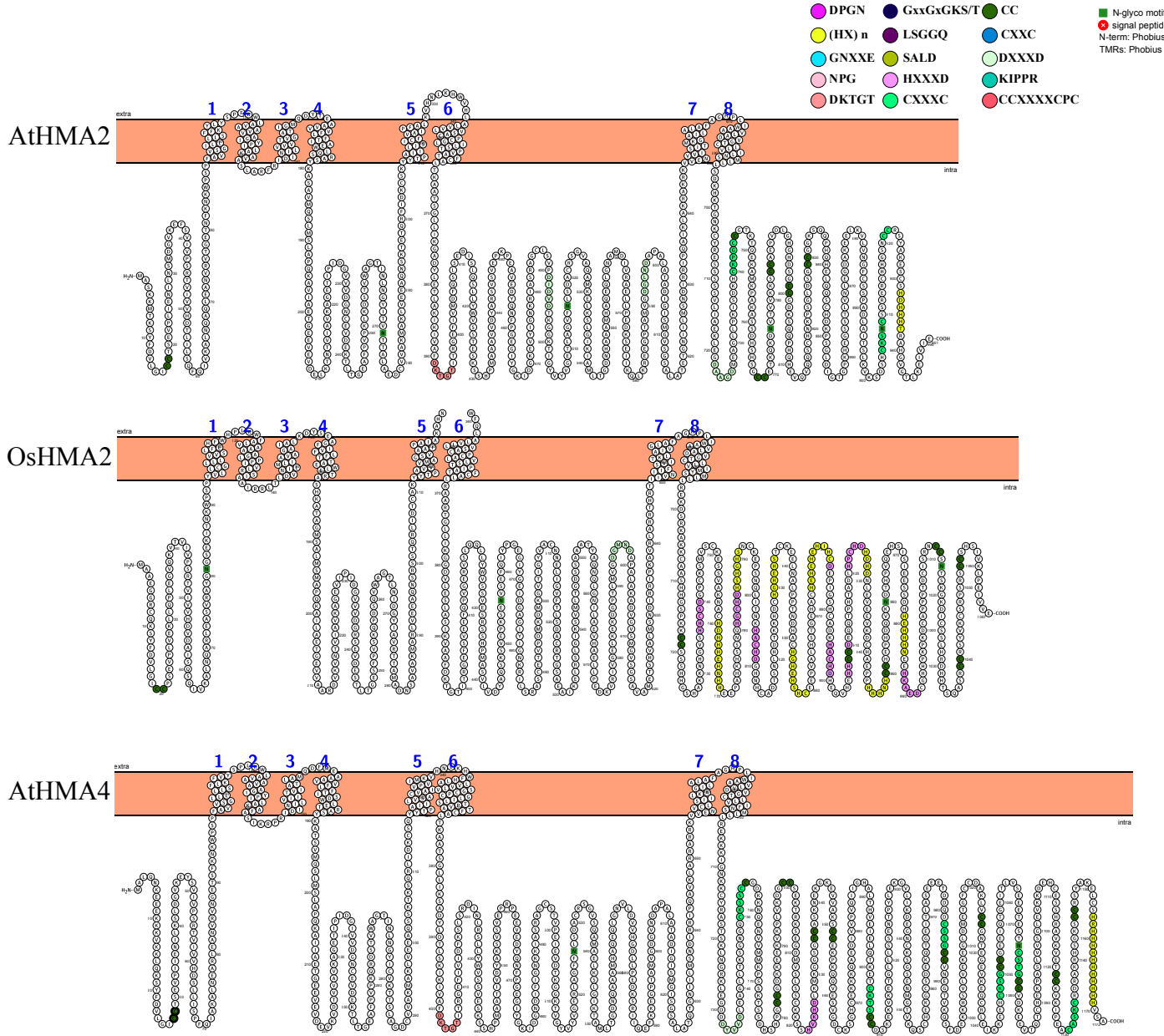
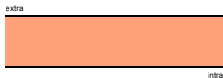


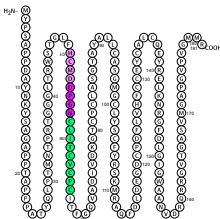
Figure S8: Specific motifs and transmembrane structural features of members of the HMA family of long-distance transport proteins. Different residues are indicated by different colors. They have (HX) $n$  and cysteine related residues.



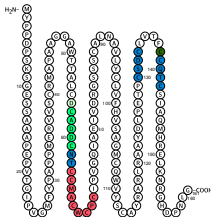
# OsPCR3



- DPGN    GxxGxGKS/T    CC
- (HX) n    LSGGQ    CXXC
- GNNXE    SALD    DXXXD
- NPG    HXXXD    KIPPR
- DKTGT    CXXXC    CCXXXXCPC
- N-glyco motif
- signal peptide
- N-term: Phobius
- TMRs: Phobius



# OsPCR1



# AtPCR1

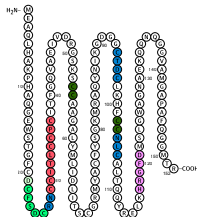
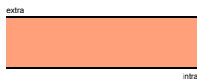


Figure S9: Specific motifs and transmembrane structural features of members of the PCR family of efflux proteins. Different residues are indicated by different colors. They have CCXXXXCPC and cysteine related residues.



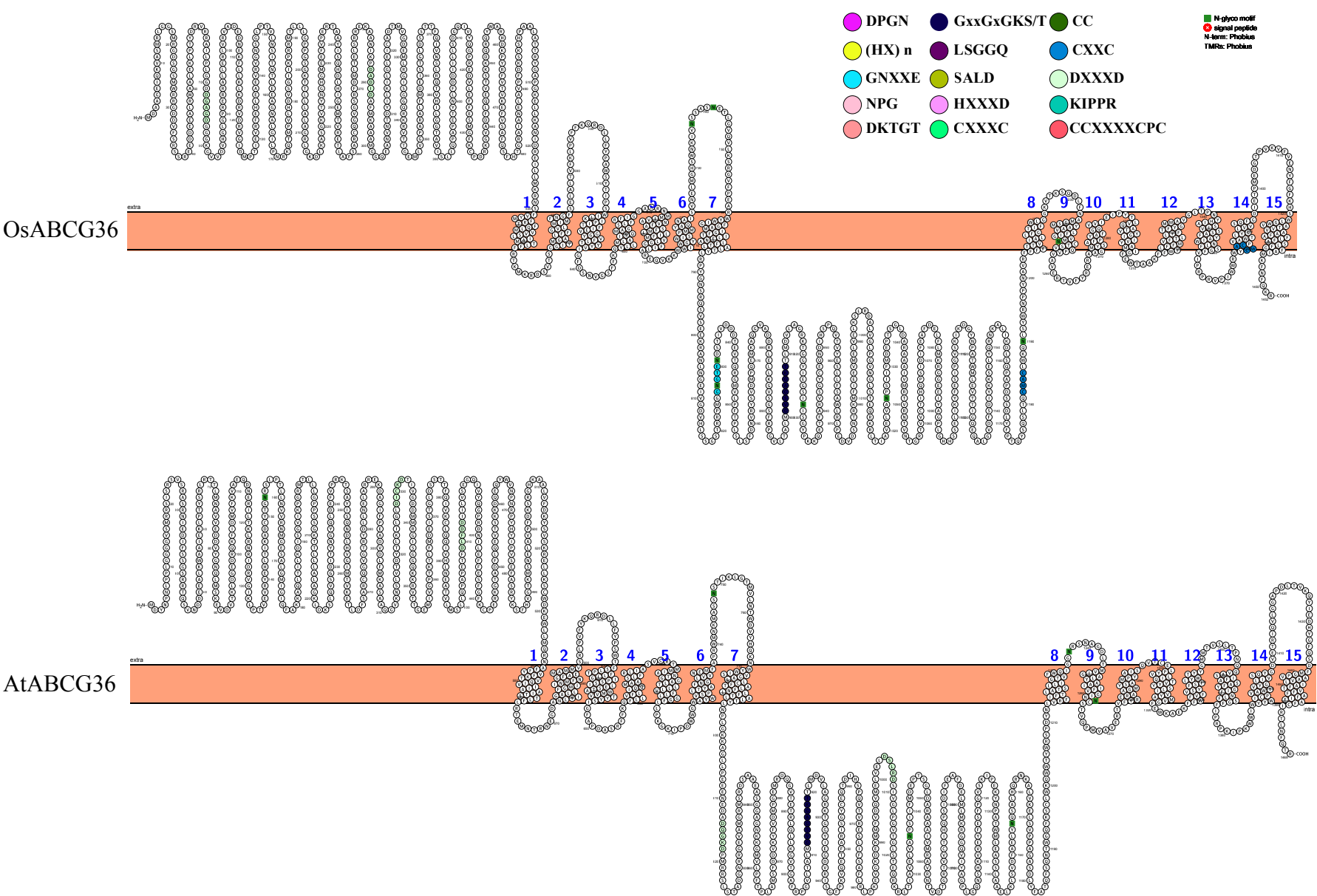


Figure S10: Specific motifs and transmembrane structural features of members of the ABCG family of efflux proteins. Different residues are indicated by different colors. They have 15 transmembrane domains and GxxGxGKS/T residues.