

Homo sapiens Nup98

500 residues (443 without GLEBS domain)

MFNKSFGTPFGGTGFGTTSTFGQNTGFGTTSGGAFGTSAFGSSNNTGLFGNSQTKPGLFGTSSFSQP
 ATSTSTGFGFGTSTGTANTLFGTASTGTSLFSSQNNAFAQNKPTGFGNFGTSSGLFGTTNTSNPFGS
 TSGSLFGPSSFTAAptgttikfnpptgtdtmvkagvstnistkhqcitamkeyesksleerledyqanrk
 GPQNQVGAGTTTGLFGSPATSSATGLFSSTTNSGFAYGQNKTAFGTSTTGFGTNPGLFGQQNQTTSL
FSKPFGQATTTQNTGFSFGNTSTIGQPSTNTMGSFGVTQASQPGLFGTATNTSTGTAFGTGLFGQTNT
GFGAVGSTLFGNNKLTTFGSGTSAPSFGTTSGLFGFGTNTSGNSIFGSKPAPGTLGTGLGAGFGTALGA
 GQASLFGNNQPKIGGPLGTGAFGAPGFNTTTATLGFGAPQAPVALTDPNASAAQQAVLQQHINSLTYSPFG
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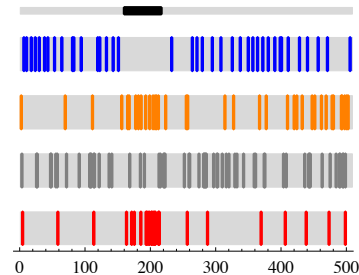
Localization of GLEBS domain:

Distribution of all 39 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:



Branchiostoma floridae Nup98

479 residues (427 without GLEBS domain)

MFGQQKTPFGGTTGFGTGAFGTSSFGATQTPATGLFGGTATNTGTGLFGGTSFGTPSTSTSTFGGFGTS
 TQTGGGLFGTSTSTAGTGLFATPQQQTAPFGAANKTGFGGFGTQTSTAATGTGLFGATQQTPSLFGGGQT
 STGLFGAVGGIAAGTNGTTvkfnpvsgsdtmmkngvsqnirtahqcitamkeyetksleervedyanrk
 GGSTGTTAMFGATATPQTGGGLFGNTATTTSTTGFTFGKAAFGTGQTQAKGATGFGTTSTGTGLFGQTQT
 QAGGLFASPFGGTATTTTPSTGFSFGQNTGTGLFGQTQQKTGLFGQPTTQTTGLFGTPSTTTTTGFGTT
 GTGTFGTQNQAGGLFGANKAPTFGATTTTSTTGLFGNTATNTGLFGQNKPGLTLGLGTGFGTGAFGTT
 TSTGTSLFGPKPTNTFGAGLTGLGAGLTLGTGSIFGNTGLGAGIGTGTTG

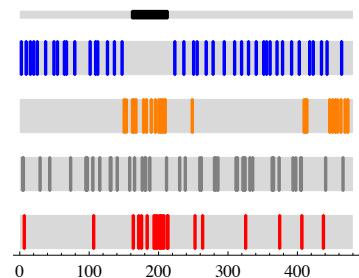
Localization of GLEBS domain:

Distribution of all 40 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:



Drosophila melongaster Nup98

581 residues (528 without GLEBS domain)

MFGGAKPSFGATPAATSFGGFSGTTTTTPFGQSAFGKPAAPAFGNTSTFAAQPAQQSLFGAATPAQPAGG
LFGANTSTGFGSTATAQPTAFGAFSQPQOTSNIFGSTQTAASTSLFGQSTLPAFGAAKPTMTAFGQTAAAQ
PTGSLFGQPAAATSTTGFGGFGTSAPTTTNVFGSGTASAFAQPQATAVGASGVNTGTAvakyqptigtdtl
mksggansvntkqhcitamkefegksleerledymcgrkGPQAGNAPGAFGFGAQVTQPAQPASGGLFGS
TAQPSTGLFGQTVTENKSMFGTTAFGQQPATNNAFGAATQQNNFLQKPFGATTTTPFAAPADASNPFGAK
PAFGQGGSLFGQAPATSAAPAFGQTNTGFGGFGTTAGATQQSTLFGATPAADPNKSAFGLGTAASAATTGF
GFGAPATSTAGGLFGNKPATSFAAPTFGATSTASTPFSNFLNTSTAATGGLFNSGLNKPATSGFGGFG
ATSAAPLNFNAGNTGGSLFGNTAKPGGGLFGGGTTLGGTGAAPTGLFGGGTTSFGVGGSLGGGGFGMG
TNNSLTGGIMGA

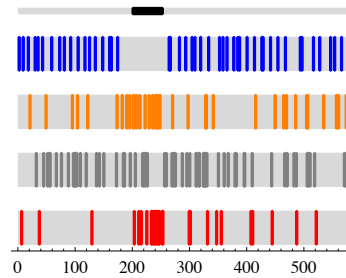
Localization of GLEBS domain:

Distribution of all 46 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:



Caenorhabditis elegans Nup98

494 residues (442 without GLEBS domain)

MFGQNKSFGSSFGGSSGSLFGQNNQNNQNKGLFGQPANNSGTTGLFGAQNKPAGSIFGAASNTSSIF
GSPQQPQNNQSSLFGGGQNNANRSIFGSTSSAPASSSLFGNNANNTGTSSIFGSNNNAPSGGLFGASTV
SGTTvkfeppissdtmmrngttqtistkhmcisamskydgksielrvedyianrkAPGTGTTSTGGLFG
ASNTTNQAGSSLFGSSNAQQKTSLFGASTSSPFGNTSTANTGSSLFGNNNANTSAASGSLFGAKPAGS
SLFGSTATTGASTFGQTTGSSLFGNQQPQTNTGGSLFGNTQNQNQSGSLFGNTGTTGLFGQAQQPQQ
SSGFSFGGAPAATNAFGQPAAANTGGSLFGNTSTANTGSSLFGAKPATSTGFTFGATQPTTTNAFGSTNTG
GLFGNNAKPGLFGNTTNTGTGGLFGSQPQASSGLFGSNTQATQPLNTGFGNLAQPQIVMQQQ

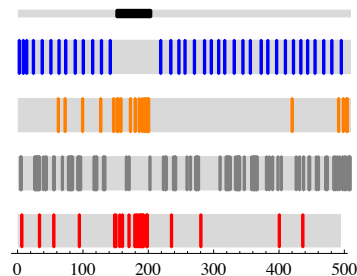
Localization of GLEBS domain:

Distribution of all 36 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:



Saccharomyces cerevisiae Nup100

578 residues (578 without GLEBS domain)

MFGNNRPMFGGSNL~~S~~FGSNTSSFGGQOSQOPN~~S~~LFNGSNNNNNSTSNNAQS~~G~~FGGFTSAAGSNSN~~S~~LFGNN
 NTQNN~~G~~AFGQSMGATQNS~~P~~FGSLNSSNASNGN~~T~~FGSSSMG~~S~~FGGNTNNAFNNNSNSTNS~~P~~FGFN~~K~~PNTGG
 TLFGSQNNNSAGTSS~~S~~LFGGQSTSTTG~~T~~FGNTGSS~~S~~FGTGLNGNSN~~I~~FGAGNNSQSN~~T~~TG~~S~~LFGNQOSS~~A~~FG
 TNNQOG~~S~~LFGQOSQNTNN~~A~~FGNQNLGGSS~~S~~FGSKPVGSG~~S~~LFGQSNNTLGN~~T~~TNNR~~G~~LFQMNSSNQSS
 NS~~G~~LFQNSMNSSTQ~~G~~VFGQNNNQMQINGNNNN~~S~~LF~~G~~KANTFSNSASG~~G~~LFQNNQOQGS~~G~~LFQNSQTS
 SS~~G~~LFQNNQKQPN~~T~~FTQSN~~T~~G~~I~~LFQNNNQOQOST~~G~~LF~~G~~AKPAGTTG~~S~~LFGGNSSTQPN~~S~~LF~~G~~TTNVPT
 SNTQSQQGN~~S~~LF~~G~~AT~~K~~LTN~~M~~PFGNPTANQSGSGN~~S~~LF~~G~~T~~K~~PASTTG~~S~~LFGNNTASTTV~~P~~STN~~G~~LF~~G~~NNAN
 NSTSTNT~~T~~LF~~G~~AKP~~D~~SQ~~K~~PALGG~~S~~LF~~G~~NSNSNSTIGQNK~~P~~VFGTTQNT~~G~~LF~~G~~ATGTNSSAVGSTG~~K~~Q
 NNN~~T~~LN~~V~~GT

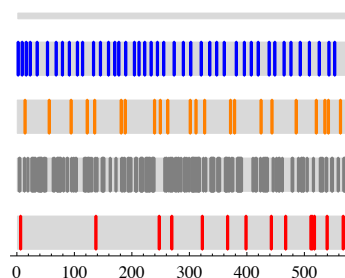
Localization of GLEBS domain:

Distribution of all 43 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:



Saccharomyces cerevisiae Nup116

737 residues (680 without GLEBS domain)

MFGVSRGAFPSATTQ~~P~~FGSTGS~~T~~FGGQOQOQOPVANTS~~A~~FGLSQQTNTTQ~~A~~PAFGNFGNQTSSNS~~P~~FGMSG
 TTANGT~~P~~FGQSQLTNNNASGS~~I~~FGGMGNNTALSAGSASvvpnstagtsikpfttfeekdpttgvinvfqsi
 tcmpeyrnfsfeelrfqdyqagr~~K~~FGTSQNGTGTTFNNPQGTNT~~T~~GFGIMGNNSSTTSATTG~~G~~LFQ~~K~~PAT
 GMFGTGTGSGG~~G~~FGSGATNST~~G~~LFGSSTNLSGNS~~A~~FGANKPATSG~~G~~LFQNTNNPTNGTNN~~T~~LF~~G~~QONS
 TNG~~G~~LFQOQN~~S~~FGANNVSNGG~~A~~FGQVNRGAFPOQQTQOGSGG~~I~~FGQSNANANGG~~A~~FGQOQGTGAL~~F~~GAKP
 ASG~~G~~LFQQSAGS~~K~~AFGMNTNP~~T~~GTTG~~G~~LFQQTNQOQSGG~~G~~LFQOQNSNAG~~G~~LFQNNQSQNQ~~S~~LF~~G~~QON
 SSN~~A~~FGQPQOQ~~G~~LF~~G~~SKPAG~~G~~LFQOQOQASTFASGNAQNN~~S~~IFGQNNQOQOST~~G~~LF~~G~~QNNQSQSQ~~P~~GG
 LFGQTNQNNNQ~~P~~FGQNGLQOPQOQNN~~S~~LF~~G~~AKPT~~G~~FGNTSLFSNSTTNQSNGISGNNLQOQSGGLFQNKQOP
 ASG~~G~~LF~~G~~SKPSNTVGG~~G~~LF~~G~~NNQVANQNNPASTSG~~G~~LF~~G~~SKPATG~~S~~LFGGTNSTAPNASSGG~~I~~FGSNNASN
 TAATTNST~~G~~LF~~G~~NKPVGAGASTSAG~~G~~LF~~G~~NNNNSSLNNSNGST~~G~~LF~~G~~SNNTSQSTNAG~~G~~LFQNN~~T~~STNTSG
 GGLFSQPSQSMASQSNALQOQOQOQR

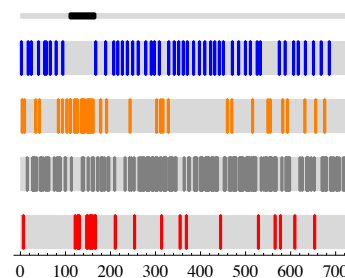
Localization of GLEBS domain:

Distribution of all 47 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:



Dictyostelium discoideum Nup220

719 residues (669 without GLEBS domain)

MFGGQFGSFGAKPAATASPFGAPSAAPTTS~~SLFG~~STAPSSGFGGFGSTAQTTPTTGFGGFGGGFGGATTTO
QPAASPFGGGGTGGSGLFGSSAQTTPPGASPFGGGFGTTTTTTTQPGASPFGGTGGGLFGSSAQTTPQ
QOGASPFGGFGGATTTPSLLSGATGGFGGFGSTTSQTQLGGGGGATSGAFGGSSSPFGSGGATTSSPF
GGGGGSGFATTQkqygtpipyqqtiegnfvsisampqyndrsfeelrfedithrkdivykTGGSGGGN
SLFGSTPTTPSSPFGAQTTPQTGGGLFGGQTTS~~PFG~~GOTSATPGSSSLFGSTOPTQOOTSGLFGSVOPT
QOQAGGGLFGSMPTGGSSSLFGSTOPTQOQTGGAOPTQSLFGGQTTPPFGSQTSTPFGQPQONTGSG
LFGAQQTQONTGGGLFGAOPTQTSGGGLFGTQPTSGTGLFGTSPTAGGTGLFGTTQPTSQGTGLFGTTQ
PTTQGTGLFGTSPTSGTGLFGSTPTSGTGLFGSTPTSGTGLFGSAOPPQOQSOTSLFGNTGTGATNTGTG
LFGSAQPSNPGGGLFGSAQPTTTGGLFGSNQPTAQPTTSLFGNTTGSVGLGATPNIISGLFGSNPAQT
GGLFGSTOPTTQTS~~SLFG~~NTGSTGLGAQNGGGLFGNLSOPTATAGQLSGGLFGNLSOPTATAGQLSSGG
LFGNTLLG

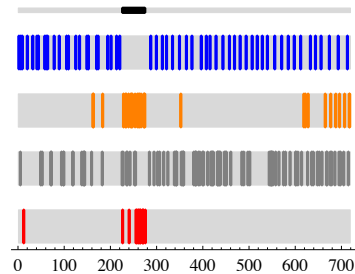
Localization of GLEBS domain:

Distribution of all 56 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:



Arabidopsis thaliana Nup98B

668 residues (620 without GLEBS domain)

MFGSSNNNPFQSSISSPFGTQTHSLFGQTNNNASNNPFATKPFGTSTPFGAQTGSSMFGTSTGVFGAPQ
TSSPFGASPPAFGSSTQAFGASSTPSFGSSNSPFGGTSTFGKSFGLSTPSSPFGSTTQOSQPAFGNSTF
GSSTPFGASTTAPFGASSTPAFGVSNSTSGFGATNTPGFGATNTTGFGSSTPGFGASSTPAFGSTNTPAFG
ASSTPLFGSSSSPAFGASPPAFGSSGNAFGNNTFSSGGAFGSSSTPTFGASNTSAFGASSSPSFNFGSSP
AFGQSTSAFGSSSFGSTQSSLGSTPSPFGAQAQASTSTFGGQSTIGGQGGsrvipyaptttdasgtesk
serlqsisampahkgknmeelrwydqrgdkGGQRSTGQSPFAGFGVTNSQPSIFSTSPAFSQTTPVNPTN
PFSQTTPTSNNTNFSPFSQPTTPSFGQPTTPSFRTSVSNSTTSVFGSSSLTTNTSQPLGSSIFGSTPAHGS
TPGFSIGGFNNSQSSPLFGSNPSFAQNTTPAFSQTSPPLFGQNTTPALGQSSSVFGQNTNPALVQSNFTSTP
STGFGNTFSSSSSLTTSISPFGQITPAVTPFQSAOPTQPLGAFGFNFGQTQIANTTDIAGAMGTFSGQNF
KQOPALGNSAVMQPTPVTNPFGTLPALPQ

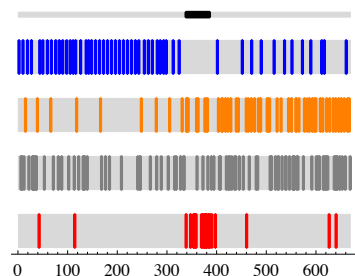
Localization of GLEBS domain:

Distribution of all 52 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:



Tetrahymena thermophila macronuclear Nup98A

666 residues (633 without GLEBS domain)

MFGNTGGGGLFGNTQTQQTGGGLFGQPQQTQFGQTGATGGGLFGGATNTFGGGGGGLFGGNNNQTNPTA
 GGGIFGQGTTLGGAPAQTTGGGLFGAPQNNQGGGLFGGGTTTGGGMFGNQANTQTGGGGLFGGPSQPTTQP
 PAFSLNNPTTGGGGLFGQPANTMGGNNGGLFGGQTNSTFGANNMLGNNNRPOGAGIFGGATTTAPTGTNTGM
 FGGIGANNNGGGLFGMNNNTNTNPTGGFGATNPTAGGGGLFGGGATTTGGGGLFGGGNTQGGGLLTANTTA
 GGLLGGGFNMNNNTGGILGQTNNOFGLGSFGTNNNAAAAPFQPKASANGvltkpnecnlyaisngtdfci
 felaltqrklvkAGQLKPGAQQAGGMFGQPAQGGNGLFGGGGAATTTTFFGAQNGNLFGGQNTQAQGGGLF
 GAPVNNAATGAGGGLFGAKPAATTTGGGLFGQMPAQTTGGFLGNATQAPAGGGLFGGATTTQAPGGGGGGGL
 FGGNTTAATTGGGLFGGNTQTGGATGGLFGGQPPNNQGGFLNTGNANNANTGGGLFGGATTTTPATGGGLF
 GGSTNTQPLATGGGLFGNNQGASQPAQGGGLFGGAAPQONSLFGGATAGGQTTGLFGGATGATQQQGGGL
 FGQTASNPTQGGGLFGAANPLGGAAA

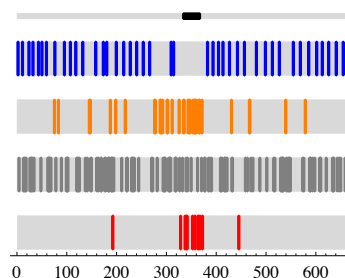
Localization of GLEBS domain:

Distribution of all 42 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:



Trypanosoma brucei Nup158

565 residues (565 without GLEBS domain)

MSAGFGGGFGQPAATGFGQPTGFGQAPQGGAFGQVAPAAATGFGQPSQSAVTGFGQTNTGFGQPAATG
 FGQPAQGAVTGFGQTNTGFGQPAATGFGQPAQSAVTGFGQTNTGFGQPAQGGFGQTAAAANAFGQAG
 PSGFGQTNTGFGQQSNSTGFGQAGRGATAGFGQPGTGGFGQPATGGFGQATSASPFQAAAAGRGVGGFGGT
 AAGTVGGFGQPAATGFGQTATTGFGQPAQAAAAGFGQPATGGFGQATSASPFQAAAAGRGVGGFGGTAA
 AGTVGGFGQPAAPGGFGQTATAGFGQPARGAAAGFGQPATGGFGQATSASPFQAAAAGRGVGGFGGTAA
 GTVGGFGQPAATGFGQTATTGFGQPAQGANTFGQGTTPSAGFGQAGRGVTGFGQTGVTGFGQTATTG
 GFGQPAQGAATGFGQAGRGAAADGFGRPAQAAAAGFGQPATGGFGQATSASPFQAAAAGRGVGGFGGTAA
 GTVGGFGQPAAPGGFGQTATTGFGQPPRGAAAGFGQPATGGLLAGGSGFGAAAAGAGFGQOSTAS

Localization of GLEBS domain:

Distribution of all 58 FG dipeptides:

Distribution of remaining hydrophobic residues:

Distribution of NQ residues:

Distribution of charged residues:

