

Golgin-45

Homo sapiens:

>sp|Q9H2G9|G045 HUMAN Golgin-45 OS=Homo sapiens OX=9606 GN=BLZF1 PE=1 SV=2
MTTKNLETKVTVTSSPFI**SGAGDGQW**TEEPPKSVEVTSQVSRKHHSLSQSPWKKAVPSES
GVLQLGKMLTEKAMEVKAVRILVPKAAITHDIPNKNTKVKSLGHHKGEFLGQSEGVIEPN
KELSEVKNVLEKLNKNSERRLLQDKEGLSNQLRVQTEVNRRELKLLVASVGDDLQYHFERL
AREKNQLILENEALGRNTAQLSEQLERMSIQCDVWRSKFLASRVMADEL TNSRAALQRQN
RDAHGAIQDLLSEREQFRQEMIATQKLEELLVSLQWGREQTYSPSVQPHSTAELALTNH
KLAKAVNSHLLGNVGINNQKKIPSTVEFCSTPAEKMAETVLRILDPVTCKESSPDNPFPE
SSPTTLATKKNIGRFHPYTRYENITFNCCNHCRGELIAL

Pongo abelii:

>NP_001126836.1 golgin-45 [Pongo abelii]
MTTKNLETKVTVTSSPFI**SGAGDGQW**TEEPPKSVEITSGVQSRKHHSLSQSPWKKAVPSESPGVLQLGKMLT
EKAMEVKAVRILVPKAAITHDIPNKNTKVKSLGHHKGEFLGQSEGVIEPNKELSEVKNVLEKLNKNSERRL
LQDKEGLSNQLRVQTEVNRRELKLLVASVGDDLQYHFERLAREKNQLILENEALGRNTAQLSEQLERMSI
QCDVWRSKFLASRVMADEL TNSRAVLQRQNRDAHGAIQDLLSEREQFRQEMIATQKLEELLVSLQWGRE
QTYSPSVQPHSTAELALTNHKLAKAVNSHLLGNVGINNQKKIPSTVEFCSTPAEKMAETVLRILDPVTC
ESSPDDPFFESSPTTLATKKNIGRFHPYTRYENITFNCCNHCQGELIAL

Mus musculus:

>NP_001153680.1 golgin-45 isoform b [Mus musculus]
MEKMTTKLKSSENKILTSTPI**SGAGDGQW**TEEPPKSVEVTHGVQPINQHVLPSPRKKVSSDSPGVLQLGK
ILNERTVEEAVRIFVPKAAITHDIPTKNTKVKSLGHHREELHNQAEVVDPRKELSEVKVLEKLNKSE
RRLLDQKEGLSNQLRVQTEINRELKLLVASVGDDPQYHFERLAREKNQLILENEALGRNTAQLSEQLER
MSIQCDVWRSKFLASRVMADEL TNFRVVLQRQNRDAQSAIQDLLSEREQFRQEMTSQKFLLEELLVSLQW
GREQTYSPNTPHQSTADLALTNHGLAQAIHAHLLGNVGISHQKKIPTTVEFCSTPAEKMAEKVLRILDPV
ACTESSPDNQFAESSPTTLTTLTKNIGRFHPYTRYENITFNCCNHCQGELIAL

Gallus gallus:

>XP_004938283.1 golgin-45 [Gallus gallus]
MTSLKEVDYASSPI**SGAGDGQW**TEQMGESLEVSAASATNHQVRHSPQKKAVSSLSPGVLQLGQIHADKS
VEVEAVRILVPKAAITHVVAATKNAKVAKSAGHKDAFHQSDGTADPKKEQTELKNAIEKLNSEKRLIQD
KEGLSNQLRIQTEVNRRELKLLVASVGDDLQYHFERMAREKNQLILENEVLGRNLSQLEQLERMSIQCD
VWRSKFLASRVMADEL TNTRAILQRQTRDAQTAIQDLLNERDQFRQEMIHTQKLEELMVLQWGRQQT
YPSAQPYTTTELASVNCKLAKAVSSHLLGNVGTSSPKKTSVAVEFCNTPAEKMAERVLRVLDPAARTETS
TEASFSETSPSSFLSTKKNIGRFHPYTRYEDITFNCCDHCQGELIAL

Xenopus laevis:

>NP_001088348.2 Golgin-45 [Xenopus laevis]
MAATMETLKTLATSTPI**SGAGDGQW**TEAPLKSEVNSPHTKATQSPRKKSTVSPSLSPGVLQLGKMQSDKA
VEIEAIRILIPKAAITHATTATKNSKHLESNHGSSTELAESVTDVPWKQLSPELKSITLEKLNKNSERRLLQDKE
GLANQLKVQTEVNRRELKLLVASVGDDLQYHFERMAREKNQLILENEVLNQNTAQLSEQLERMSIQCDVW
RSKFLASRVMADEL TNIRTNLQRQNRDAQSALQDLLSEREQFRHEMSETQKLTLEALLVSLQWGRQKTYAP
IPQPHTTTELIAANLKLAKSIQSHLIGNTGSDHQKPAAKPIEYCSTPAENMAETVLKALDPVSCDNDSSD
ISLSDDSPFLLAKKNIGRFHPYTRYENITFNCCNQCQRELIAV

Salmo salar:

>XP_014008079.1 PREDICTED: golgin-45-like [Salmo salar]
MSTAVADRGSVHPI**SGAGDGQW**TDEPPVAKEIGVVDTPLFVSPLLKVASPKQSPKTTHTPSPASLQHS
STPOQSFRASPRDIASAFQLPGVLHLGKVPREACVVVEAVRIVVPRAAISRSQGHMGPAEEKGEAWAGQO
MEERPSPSLPLEDLRGAMEKLQNSERRLLQDKEGLLNQLHVQTEVNRRELKLLVASVGDDLQYHFERLA
REKNQMLDNEALGRSLASTAEQLERMSIQCDVWRKFLASRVMAEELTNARVSLQHQTREAQSAITDLL
SERDEFSRDMMLTHRSLEQLLVLQWGRQQTYYPSAQPLSTGELSLANHKLAEAINSRLLGKGVPGVSSS
GAGLKKRGQASELFNSTHTPAEKMAEKVLKILDPISCSDNEEKISPLSISDSSPSAFLTNKKSIGRFHPY
TRYENITFNCCERCSGDILVL

Petromyzon marinus:

>XP_032834970.1 golgin-45 [Petromyzon marinus]
MATTLTRDGTGWPAQVS**SGFADGQW**VTADGAGGDPAKRRPAGSSSSPPLPVRVSQPAPRSSWQHRRPPAKP
APQHHLHPQPRPLSPAAAAAATPLPHRPQQQQQQQPVVPLAGGQVELTVVQIQVPKEAILHHSARSPLA
LELGVKPDLSLEAGGSAAAAAAATAALRQEVKELKVEVKRLEESERRLMDDKESVVSQLSRSQTEVNRE
LKLLVASVGDDLQFHFERAVRERGRQAQAEQELSRSLASASEQLERIGIQCDVWRSKFLASRVMSSEVA
GARVHALRFLFREQSAVHDLFSERTQLCVDLQDTHRLLLEELVLALQWGRQPTYSLGTRRAHNSLELAEAC
TTLASLLTQRLGGGSGVSKSPFPAAAGGGGAAGGAAGGGGAAGGGGAAGGGGAAGGGGAAGGAAVAAQPPAQL
CSTAERMAQQVLRMTEVRMTDFMLVDDAAGGAAGRLLTSKPSGRGFHPYTRYEHITFTCCSRCTGDIVV
V

Branchiostoma belcheri:

>XP_019628762.1 PREDICTED: golgin-45-like [Branchiostoma belcheri]
MESAFFPAVKPQAHSSQSKKTT**SLHGGGGR**DSTLNAMRRSQLSRTRSETRIFGVQGFQKPKLINDVPLSS
AKITQFKAEMEERGSSDLQYQFERMAREKAQLSVHDHNLVQQYADLSEEVERLSIQCDVWRSKFLGSRQTQV
SQLIDLRNAIYQQFGKAAIDNVMKERAPIRKEMVETYRYLLDQLVKALRWGKQPQLQQAANPRNMKELV
QANHRLVSAVSAQLLGNIKPMNSANQETVESGIGLTNAEAAATQVLNMNFDLQLLSPESAAPVGRMGRF
HPQHYYEITVNCCNKCKGEIKVV

Drosophila melanogaster:

>NP_649889.1 uncharacterized protein Dmel_CG9356, isoform A [Drosophila melanogaster]
MEANEASMPGTDKQSAQ**STGSDGQW**QPENSGAAKTESEIPASADVDNKVKRPQLSRKDSSVVQEAVMGRK
TSTSGSHSNLPLPLGLHTLYRRPENVTRSLAPVVKGELVQMRPRLVTSADSLPEHKKTAKPKFVPEPY
PGAVNPMSIPTNKKHIRDKNNLDIAVLVDQVSTLRKTQELTETTTDIKETDTASSHEVNSLKEELAKMR
DERNYFQAQYKFQTVQNSSELKSLVASVGEDLQTRVNLLTEDKLQLARALLDTANNLTHTHTEQIEFLAQ
CEVWRSKFLASSVMEELARWKADLTQKQLLNESTRQLLHATHQIREIQLDMLKQLKFLAKIRFLNLP
ADVLSLSAENLNLQRMVLHTGVCIPEETLKLSSASTSPLCEAEKYAVRALEFISQPLMATDEAIRALFD
QAQRPHYVQSPASEVTFACDNQQLDKMQ

Hydra vulgaris:

>XP_002164131.1 PREDICTED: golgin-45-like [Hydra vulgaris]
MEPSILKISRFPALNLNQDEITKEPTFGDQSVASKNVLPKDEFSNIEKIKLFSPPNFQLNQEQAIRP
HNPDEDLIKYLSSSTRPHIPDQELLESLQSKVKFLQEYNEKLIDEKLKVSHQLATQTQINNELKNLLVASI
GDDLETRYEKMILNRIQSDLELKRILNLVEEYQEEKQAYIQVDVWRSKFLASRVMNEELTQWKSALYYK
YRDSHTALQSLLEEHSKIRVLNDATRIGLIKIAELLNSKDALDSEMRLTLVDTAFINHDLVESLIEIIE
ESSWAEPKNEIKQNIFFKQFKNHLKEIYVLPSELSTAEQLAHEIVNTGTIQTEELVRMRDYLAHNRISH
FLSTNYHVTYNCCNSCKGRIIHL

Nematostella vectensis:

>XP_001635606.1 golgin-45 [Nematostella vectensis]
MNSLEPHALKMERIPKPGSDIVDYSKVPSGSDGSHSGAALEPTDTRKPHALKQKQPIHFSFGHVELML
ESDTEEKEEGTKNTENDTIRKHPKATKSTPVLNQIERTSVDSSTQGNNDTHIFIKEEPKQEIILQSSAS
TLCDKPTGSSTEELKKLQSKVEELEEQTSLTDEKTKLTIQLGIQTEVNSDLKLLVASMEEELNRMEA
LAHRNAQLRVEVEHWQTLCD EYAEESDRLAIDCDVWRKFMASRMSDQLTCWKTTLYTRYQALAAALQR
MLDERDELKHVYLVHTTRLLESLDYVVKSGGSFSDTLMDRHPIQGQSILEMATITSCLAQDVTAQVQGFI
PSGSLPTHALLLNEEKEPALDSTPAEKMALQLLTSSIELQSDDVPSVDSSVLRRMGQYIGNSYHSRLMT
NSFRVTYDCCDRCTGPVHV

Amphimedon queenslandica:

>XP_019850840.1 PREDICTED: golgin-45-like [Amphimedon queenslandica]
MESCRRRKQALKEKYLKKAQDLISKKKYEKYKVTDVSWSDPLITSTPLITRTRSTLPSSLRLSPHRDITE
LERMIEDQNKAMKELKRLLLLASVGGEMGTEIETLIRDKVTLESKLNHSITELMEMNEEIEGLTIECDVWK
CKVLASRLLI DELREWGNHYHLSVNTLQTLLDERDQLMNHKAIHQVLVNNISRKLMSTSSSTANSTASGI
KIATVTVPVLQPIHQGCNVLELAKNTSVAVQMISDKISARHEATPMPSSLSLNTSLTEGEKLAHKLLYPV
PKETTPTSRGLPHLSFSEKTLMEQRKHQQARTLPWTD DRHDGNNDIANNNSYFCNKCNGRAIMI I

XP_019850840.1[A. queenslandica] 0
 NP_649889.1[D.melanogaster] -----MEANESAMPQPTDKSQAC[SGVAKG]QPENSGAAKTESEIPASADVNDKV 1
 XP_002164131.1[H.vulgaris] -----MEPSLTKISRFALNIN--QDEITKE[SGVAKG]PQENSGAAKTESEIPASADVNDKV 1
 XP_001635606.1[N.vectensis] -----MNSLEPHALKMERIPKPGSDIVDYSKV[SGVAKG]QPENSGAAKTESEIPASADVNDKV 41
 XP_019628762.1[B.belcheri] -----MNSLEPHALKMERIPKPGSDIVDYSKV[SGVAKG]QPENSGAAKTESEIPASADVNDKV 52
 XP_032834970.1[P.marinus] -----MNTTLTRDGTGWPQAVS[SGVAKG]VTADGAGGGDPAPKAPGAGSSSS 0
 XP_014008079.1[S.salar] -----MSTAADVADRGSVHPV[SGVAKG]TDEPVPKAEI---GVVDFTPL--F 46
 NP_001088348.2[X.laewis] -----MAAMETLTKLATSTPLRGT[SGVAKG]TEAPLKSEVN--SF 37
 XP_004938283.1[G.gallus] -----MTSLKVDVYASSIP[SGVAKG]TEAPLKSEVN--SAGASAT 41
 NP_001153680.1[M.musculus] -----KMTTLKSENGKILSTSP[SGVAKG]TEEPKPSVEV---THGVPQFI 39
 Q9H2G9[H.sapiens] -----MTTNKLETKVITVTS[SGVAKG]TEEPKPSVEV---TSVGQSR 46
 NP_001126836.1[P.abelii] -----MTTNKLETKVITVTS[SGVAKG]TEEPKPSVEI---TSVGQSR 42

 XP_019850840.1[A. queenslandica] 0
 NP_649889.1[D.melanogaster] -----KRPQLSRKSDSVVQEAVMGRKSTTSSGHSS-----NLP.LPLGLHTLYRPFENQ 96
 XP_002164131.1[H.vulgaris] -----LQKQ-----KPQIHFSPGHVLEMLSDTEEEKECTKNTENDTIRGHFKK 67
 XP_001635606.1[N.vectensis] -----LQKQ-----KPQIHFSPGHVLEMLSDTEEEKECTKNTENDTIRGHFKK 95
 XP_019628762.1[B.belcheri] -----PPLPVRS--VQP-----APRS--SWQHRPPA-----KP-APQHHLHPQHPFELS 0
 XP_032834970.1[P.marinus] -----SVPLLKVAS--PKQ-----SKPT--T--HPSPA-----SLQHSHPSTFTQSPRA-S 80
 XP_014008079.1[S.salar] -----N-----N-----HQTQSPFRK 47
 NP_001088348.2[X.laewis] -----K-----K-----HQTQSPFRK 49
 XP_004938283.1[G.gallus] -----N-----N-----HQTQSPFRK 47
 NP_001153680.1[M.musculus] -----K-----K-----HQTQSPFRK 56
 Q9H2G9[H.sapiens] -----K-----K-----HQTQSPFRK 52
 NP_001126836.1[P.abelii] -----K-----K-----HQTQSPFRK 52

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 XP_002164131.1[H.vulgaris] -----LQKQ-----KPQIHFSPGHVLEMLSDTEEEKECTKNTENDTIRGHFKK 67
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 XP_019628762.1[B.belcheri] -----PPLPVRS--VQP-----APRS--SWQHRPPA-----KP-APQHHLHPQHPFELS 0
 XP_032834970.1[P.marinus] -----SVPLLKVAS--PKQ-----SKPT--T--HPSPA-----SLQHSHPSTFTQSPRA-S 80
 XP_014008079.1[S.salar] -----N-----N-----HQTQSPFRK 47
 NP_001088348.2[X.laewis] -----K-----K-----HQTQSPFRK 49
 XP_004938283.1[G.gallus] -----N-----N-----HQTQSPFRK 47
 NP_001153680.1[M.musculus] -----K-----K-----HQTQSPFRK 56
 Q9H2G9[H.sapiens] -----K-----K-----HQTQSPFRK 52
 NP_001126836.1[P.abelii] -----K-----K-----HQTQSPFRK 52

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 XP_019628762.1[B.belcheri] -----PPLPVRS--VQP-----APRS--SWQHRPPA-----KP-APQHHLHPQHPFELS 0
 XP_032834970.1[P.marinus] -----SVPLLKVAS--PKQ-----SKPT--T--HPSPA-----SLQHSHPSTFTQSPRA-S 80
 XP_014008079.1[S.salar] -----N-----N-----HQTQSPFRK 47
 NP_001088348.2[X.laewis] -----K-----K-----HQTQSPFRK 49
 XP_004938283.1[G.gallus] -----N-----N-----HQTQSPFRK 47
 NP_001153680.1[M.musculus] -----K-----K-----HQTQSPFRK 56
 Q9H2G9[H.sapiens] -----K-----K-----HQTQSPFRK 52
 NP_001126836.1[P.abelii] -----K-----K-----HQTQSPFRK 52

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 XP_032834970.1[P.marinus] -----SVPLLKVAS--PKQ-----SKPT--T--HPSPA-----SLQHSHPSTFTQSPRA-S 80
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 NP

