Examples of attribute-based protein-QA

Protein id: Q29DY1

Protein

Kinesin-like protein Klp68D: <seq>MSAKSRRPGTASSQTPNECVQVVVRCRPMSNRERSEGSPEVVNVYPNRGVVELQNVVDANKEQRKVFTYDAAYDASASQTTLYHEVVFPLVSSVLEGFNGCIFAYGQTGTGKTFTMEGVRGNDDLMGIIPRTFEQIWLHINRTENFQFLVDVSYLEIYMEELRDLLKPNSKHLEVRERGSGVYVPNLHAINCKSVDDMIRVMKVGNKNRTVGFTNMNEHSSRSHAIFMIKIEMCDTETNTIKVGKLNLIDLAGSERQSKTGASAERLKEASKINLALSSLGNVISALAESSPHVPYRDSKLTRLLQDSLGGNSKTIMIANIGPSNYNYNETLTTLRYASRAKSIQNQPIKNEDPQDAKLKEYQEEIERLKRLIAPQQQQRSEKQGTIKKQRVKKPKKEPISQELIGSALQASSADLQVDEDRDSDGDGAESESDKENEAEVAKSNEELERERVENAKLAAKLAELEGQLVRGGKNLLDTYSERQIELEKKLVEIAERKKREIEIQQQLELQEETTLEIRERNVSLEQEVELKKRKLSKCYAKYLALQQELNDCKHDHNQDLRELEMAQNELVKELKRQLLIIDNFVPIEVKQRLYTQAKYDEEQEEWKFSSFPLPLPPSGGDGRQGYRRPVSHPQRRRPTSEHALQEAKSNAPSSLRFKSENIVSYELEMPCRTTQEYRTPKVSASLQAVLAQAMQTGGDDIDIVDSHTNSLRSRLENIINANSSSNGGPGSGAGPLAANTAGSGVGSMPNVRNIKSSRGLPSAGTALDSNRRPPTGRIPAKKPASAYPKARGLVNK</seq>

Question

Analyze the provided protein amino acid sequence, accurately predict and describe its function, subcellular_location, family, key_sequence_motif.\nResponse in the following exact format:\nFUNCTION: …\nSUBCELLULAR LOCATION: …\nFAMILY: …\nKEY SEQUENCE MOTIF: …\nDetailed Analysis (≤300 words): [in one brief paragraph of ≤ 300 words, describe potential catalytic mechanisms, key domains, post-translational modifications, associations with diseases, etc.]\nKeep the tone professional yet fluent; let every word earn its place.

Answer

FUNCTION: Plus-end directed microtubule motor involved in anterograde axonal transport, potentially moving distinct cargos in fly neurons compared to other kinesin motors.\nSUBCELLULAR LOCATION: Cytoplasm, cytoskeleton (microtubule-associated)\nFAMILY: TRAFAC class myosin-kinesin ATPase superfamily, Kinesin family, Kinesin II subfamily\nKEY SEQUENCE MOTIF: ATP-binding site (106-113)\n\n**Extended Information**\n\nKlp68D is a microtubule-associated motor protein that utilizes ATP hydrolysis to drive anterograde transport along microtubules, likely facilitating cargo movement in *Drosophila* neurons. It contains a conserved kinesin motor domain (19-344) responsible for ATP binding and microtubule interaction, along with two coiled-coil regions (350-384, 432-580) that may mediate dimerization or cargo binding. The protein exhibits multiple disordered regions and compositional biases, including basic and acidic residue clusters, which may regulate its function or interactions. Klp68D belongs to the Kinesin II subfamily, suggesting specialized roles distinct from conventional kinesin heavy chains. Its localization to the cytoskeleton underscores its involvement in microtubule-based motility processes.

Protein id: Q29J90

Protein

G-protein coupled receptor moody: <seq>MSDETTGSLGDAFSPMDTPTTTIMPPPADVDESGFSHSLLTFAAVMTFLIMIVGICGNLLTVVALLKCPKVRNVAAAFIISLCIADLLFCALVLPFQGLRFVQGTWRHGEVLCRLIPFIQYGNIGVSLLCIAMITINRYVMITHYSLYNRIYKRHWIAIMIAACWLFSYGMQLPTLLGAWGRFGYDARLQTCSIMSDRHGHSSKTTLFITAFVIPCLVIIACYAKIFWVVHKSEQRLKRHATKQNSIPNNLRPLAAATSMPSGDGANPSQVPAGCRVSSDSSSNYSTDVPDTTPGGAGGGAGVKQQPSRVKDQREVRAKRNEWRITKMVLAIFLSFVICYLPITIVKVADKDVEHPSLHIFSYIMLYLSACINPIIYVIMNKQYRKAYKTVVFCQPAARLLMPFGKGNGASSAAEKWKDTGLSNNHSRTIVSQMSAGATATATATAAAGTQPQSTSTQGPVQALELTARVPDLISKSSNLPLPQPLPQIPPAGARPSLTPPPPPSVLTATHSNGSGSQRLPLKKNNHSYTNSGFNSSVISANPSSSPSPSSSGGGIYRPGIGSMGNGSASIRRITMVGDDIILEEEELPPTPTASSPPQMQAPPPPPSSSRQTTMNALNTTPKTPIYMNVDSPKRNQSYSERNIPVPAREGHDQGVKDSQGLPSKLMDKKKFPKD</seq>

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Answer

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Examples of true or false protein-QA

Protein id: O43374

Protein

<seq>MAKRSSLYIRIVEGKNLPAKDITGSSDPYCIVKVDNEPIIRTATVWKTLCPFWGEEYQVHLPPTFHAVAFYVMDEDALSRDDVIGKVCLTRDTIASHPKGFSGWAHLTEVDPDEEVQGEIHLRLEVWPGARACRLRCSVLEARDLAPKDRNGTSDPFVRVRYKGRTRETSIVKKSCYPRWNETFEFELQEGAMEALCVEAWDWDLVSRNDFLGKVVIDVQRLRVVQQEEGWFRLQPDQSKSRRHDEGNLGSLQLEVRLRDETVLPSSYYQPLVHLLCHEVKLGMQGPGQLIPLIEETTSTECRQDVATNLLKLFLGQGLAKDFLDLLFQLELSRTSETNTLFRSNSLASKSMESFLKVAGMQYLHGVLGPIINKVFEEKKYVELDPSKVEVKDVGCSGLHRPQTEAEVLEQSAQTLRAHLGALLSALSRSVRACPAVVRATFRQLFRRVRERFPGAQHENVPFIAVTSFLCLRFFSPAIMSPKLFHLRERHADARTSRTLLLLAKAVQNVGNMDTPASRAKEAWMEPLQPTVRQGVAQLKDFITKLVDIEEKDELDLQRTLSLQAPPVKEGPLFIHRTKGKGPLMSSSFKKLYFSLTTEALSFAKTPSSKKSALIKLANIRAAEKVEEKSFGGSHVMQVIYTDDAGRPQTAYLQCKCVNELNQWLSALRKVSINNTGLLGSYHPGVFRGDKWSCCHQKEKTGQGCDKTRSRVTLQEWNDPLDHDLEAQLIYRHLLGVEAMLWERHRELSGGAEAGTVPTSPGKVPEDSLARLLRVLQDLREAHSSSPAGSPPSEPNCLLELQT</seq>

Question

Determine whether this statement about the given protein is true or false: although this calcium-binding protein translocates to the plasma membrane upon intracellular calcium elevation to inactivate Ras signaling, its pleckstrin homology domain mediates this membrane association through specific phosphoinositide interactions, which is essential for its GTPase-activating function.

Answer

False. The PH domain lacks phosphoinositide binding activity due to a leucine substitution at position 592, preventing it from mediating membrane association; calcium-dependent membrane binding occurs through its C2 domains instead.

Protein id: O43390

Protein

<seq>MANQVNGNAVQLKEEEEPMDTSSVTHTEHYKTLIEAGLPQKVAERLDEIFQTGLVAYVDLDERAIDALREFNEEGALSVLQQFKESDLSHVQNKSAFLCGVMKTYRQREKQGSKVQESTKGPDEAKIKALLERTGYTLDVTTGQRKYGGPPPDSVYSGVQPGIGTEVFVGKIPRDLYEDELVPLFEKAGPIWDLRLMMDPLSGQNRGYAFITFCGKEAAQEAVKLCDSYEIRPGKHLGVCISVANNRLFVGSIPKNKTKENILEEFSKVTEGLVDVILYHQPDDKKKNRGFCFLEYEDHKSAAQARRRLMSGKVKVWGNVVTVEWADPVEEPDPEVMAKVKVLFVRNLATTVTEEILEKSFSEFGKLERVKKLKDYAFVHFEDRGAAVKAMDEMNGKEIEGEEIEIVLAKPPDKKRKERQAARQASRSTAYEDYYYHPPPRMPPPIRGRGRGGGRGGYGYPPDYYGYEDYYDDYYGYDYHDYRGGYEDPYYGYDDGYAVRGRGGGRGGRGAPPPPRGRGAPPPRGRAGYSQRGAPLGPPRGSRGGRGGPAQQQRGRGSRGSRGNRGGNVGGKRKADGYNQPDSKRRQTNNQQNWGSQPIAQQPLQQGGDYSGNYGYNNDNQEFYQDTYGQQWK</seq>

Question

Determine whether this statement about the given protein is true or false: although this protein's SUMOylation at specific lysine residues supports its role in mRNA processing complexes, and mutations causing an autosomal recessive neurodevelopmental disorder implicate its functional importance, structural studies reveal that these covalent modifications occur exclusively at lysine-359 within its third RNA recognition motif domain

Answer

False; Explanation: SUMOylation occurs at Lys-13, Lys-171, and Lys-359, not exclusively at Lys-359, and the associated neurodevelopmental disorder is autosomal dominant, not recessive.