Supplementary File 1

Protein IDs		
	Presenilin Protien	
	Species	**Protein Id**
	Homo sapiens	NP_000012.1
		NP_000438.2
	Pan troglodytes	XP_016781825.1
		XP_001142009.2
	Bos taurus	NP_777146.1
		NP_776865.2
	Mus musculus	NP_032969.1
		NP_035313.2
	Xenopustropicalis	NP_001027027.1
		NP_001017181.1
	Anolis carolinensis	XP_008102150.1
		XP_003216113.1
	Daniorerio	NP_571099.1
		NP_571589.2
	Takifugurubripes	XP_003978532.1
		XP_003972298.1
	Latimeria chalumnae	XP_006000568.2
		XP_014342519.1
	Callorhinchus milii	XP_007891435.1
		XP_007891888.1
	Lethenteron japonicum	XP_006000568.2
		XP_014342519.1
	Branchiostoma floridae	XP_002597164.1
	Saccoglossus kowalevskii	XP_002738746.1
	Strongylocentrotus purpuratus	XP_001178715.1
	Caenorhabditis elegans	NP_508175.1
		NP_491328.1
		NP_492095.1
	Drosophila melanogaster	NP_524184.1
	Hydra vulgaris	XP_012561939.1
		XP_012562740.1
	Amphimedon queenslandica	XP_019849527.1
	Monosiga brevicollis	XP_001750030.1
	Chlamydomonas reinhardtii	XP_001701664.1
	Populus trichocarpa	XP_006374407.1
	Chondrus crispus	XP_005715796.1
	Trypanosoma brucei	XP_803800
	Trichomonas vaginalis	XP_001326572.1
		XP_001312406.1
		XP_001299078.1
	Rozella allomycis	EPZ36881

	Fonticula alba	XP_009493699.1
		XP_009496662.1
	Batrachochytrium salamandrivorans	XP_006677768.1
	Capsaspora owczarzaki	XP_004349389.2
	Neospora caninum Liverpool	XP_003882351.1
	Toxoplasma gondii	XP_018637326.1
	Hammondia hammondi	XP_008884684.1
	Blastocystis hominis	XP_012899044.1
	Aphanomyces invadans	XP_008862967.1
		XP_008860947.1
		XP_008864272.1
		XP_008864273.1
	Saprolegnia diclina	XP_008615248.1
		XP_008610558.1
		XP_008610969.1
	Thalassiosira pseudonana	XP_002288037.1
		XP_002290889.1
	Phaeodactylum tricornutum	XP_002176847.1
	Ectocarpus siliculosus	CBN74004.1
	Aureococcus anophagefferens	XP_009040959
	Nannochloropsis gaditana	EWM27520.1
	Bigelowiella natans	aug1.9_g4262 (JGI Genome portal: http://genome.jgi.doe.gov/pages/blast-query.jsf?db=rhizaria)
	Reticulomyxa filose	ETO23872 (ENSEMBL)
	Entamoeba histolytica	XP_653696.1
	Polysphondylium pallidum	XP_020436456.1
	Dictyostelium discoideum	XP_635158.1
		XP_629693.1
	Guillardia theta	XP_005841632.1
	Emiliania huxleyi	XP_005788433
	Chrysochromulina	KOO22168

Nicastrin Proteins

Species	Protein ID
Homo sapiens	NP_001277113.1
Homo sapiens	NP_056146.1
Pan troglodytes	XP_513923.2
Mus musculus	NP_067620.3
Bos taurus	NP_001029647.1
Anolis carolinensis	XP_008121550.1
Xenopus tropicalis	NP_001123711.2
Danio rerio	NP_001009556.1
Takifugu rubripes	XP_003978286.1
Saccoglossus kowalevskii	NP_001161608.1
Strongylocentrotus purpuratus	XP_788243.4
Hydra vulgaris	XP_012561598.1
Drosophila melanogaster	NP_001262932.1
Amphimedon queenslandica	XP_019855736.1
Monosiga brevicollis	XP_001748010.1
Populus trichocarpa	XP_002305230.2
Dictyostelium discoideum	XP_637065.2
Chlamydomonas reinhardtii	XP_001701591.1
Capsaspora owczarzaki	XP_004342890.1
Batrachochytrium salamandrivora	OON03627.1
Polysphondylium pallidum	XP_020431244.1
Dictyostelium discoideum	XP_637065.2
Batrachochytrium salamandrivora	OON03628.1
Chrysochromulina	KOO29656.1
Guillardia theta	XP_005827562.1
Ectocarpus siliculosus	CBJ31078.1
Nannochloropsis gaditana	EWM23993.1
Aphanomyces invadans	XP_008876423.1
Trichomonas vaginalis	XP_001312893.1
Thalassiosira pseudonana	XP_002290995.1
Reticulomyxa filosa	ETO25807.1
Fonticula alba	XP_009496472.1
Saprolegnia diclina	XP_008618124.1

	APH Proteins	
	Species	**Protein ID**
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	Mus musculus	NP_666246.1
		NP_080950.1
		NP_808251.1
	Bos taurus	NP_001029842.1
		NP_001178332.1
	Anolis carolinensis	XP_003228723.1
		XP_008123904.1
	Xenopus tropicalis	NP_001015843.1
	Pan troglodytes	
		XP_009428545.1
	Takifugu rubripes	XP_003969662.1
		XP_003969662.1
	Danio rerio	NP_956409.1
		NP_001025300.1
	Lethenteron japonicum (Japanese Lamprey genome) (	JL4297
		JL380
		JL381
	Latimeria chalumnae	XP_014349599.1
	Callorhinchus milii	XP_007910223.1
	Branchiostoma floridae	XP_002607668.1
	Saccoglossus kowalevskii	XP_002736656.1
	Strongylocentrotus purpura	XP_783542.1
	Caenorhabditis elegans	NP_492469.1
	Drosophila melanogaster	NP_608710.1
	Hydra vulgaris	XP_002167184.1
	Amphimedonqueenslandic	XP_003382482.1
	DictyosteliumdiscoideumA	XP_647460.1
	Chlamydomonasreinhardti	XP_001693775.1
	Capsasporaowczarzaki	XP_004365170.1
	Aphanomycesinvadans	XP_008879360.1
	Fonticulaalba	XP_009492849.1
	Batrachochytriumsalaman	OON06716.1
	Ectocarpussiliculosus	CBN76993.1
	Guillardia theta	XP_005832892.1
	Phaeodactylumtricornutum	XP_002181033.1
	Polysphondyliumpallidum	XP_020437801.1
	Rozellaallomycis	EPZ35700.1
	Entamoebahistolytica	EMS12153.1
	Emilianiahuxleyi	XP_005772054.1

Supplementary file 1

PEN-2 Proteins

	Species	Protein ID
	Homo sapiens	NP_758844.1
	Musmusculus	NP_079774.1
	Bostaurus	NP_001008669.1
	Anoliscarolinensis	XP_003225015.1
	Daniorerio	NP_991139.1
	Takifugurubripes	XP_003966057.1
	Xenopustropicalis	NP_001016336.1
	Drosophila melanogaste	NP_788401.2
	Branchiostomafloridae	XP_002610690.1
	Strongylocentrotuspurpu	XP_791533.1
	Saccoglossuskowalevsk	XP_791533.1
	Hydra vulgaris	XP_002166668.1
	Amphimedonqueenslan	XP_011407614.1
	Populustrichocarpa	XP_002306247.2
	Dictyosteliumdiscoideu	XP_629118.1
	Chlamydomonasreinhar	XP_001700868.1
	Capsasporaowczarzaki	XP_004364102.2
	Batrachochytriumsalama	OON04588.1
	Polysphondyliumpallidu	XP_020434406.1
	Aureococcusanophagef	XP_009038719.1
	Saprolegniadiclina	XP_008614431.1
	Aphanomycesinvadans	XP_008879623.1
	Chrysochromulina	KOO31300.1
	Entamoebahistolytica	GAT91830.1
	Hammondiahammondi	XP_008886995.1
	Toxoplasma gondiiFOU	KFG49711.1
	Toxoplasma gondiiGAB	KFG34828.1
	Toxoplasma gondiiME4	XP_018638436.1
	Toxoplasma gondii ARI	KYF41243.1
	Toxoplasma gondii RUB	KFG60490.1
	Toxoplasma gondiip89	KFG29220.1
	Toxoplasma gondiiGT1	EPR57907.1
	Fonticulaalba	XP_009496614.1
	Toxoplasma gondiiVA	KFH05526.1
	Toxoplasma gondii V	ESS29517.1
	Toxoplasma gondii V	CEL71754.1
	Neosporacaninum Liv	XP_003879933.1

Supplementary File 2

Protein Sequences

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>NP_000012.1 presenilin-1 isoform I-467 [Homo sapiens]
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EELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTEDTETVGQRALHSILNAAIMI
SVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYITVALLIWNFGVVGM
ISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNE
TLFPALIYSSTMVWLVNMAEGDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGP
HRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL
TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI

>XP_016781825.1 PREDICTED: presenilin-1 isoform X1 [Pan troglodytes]
MTTTVRVLGRGLGQAAPGSAVSHRKQNSGWSGRNLSYEPRRQRGGGEAYNDNRERQEHNDRRSLGHPEPL
SNGRPQGNSRQVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE
DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYN
VAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVA
VLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGDPEAQRRVSKNSKYNAESTERESQDTVAE
NDDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATA
SGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI

>NP_032969.1 presenilin-1 [Mus musculus]
MTEIPAPLSYFQNAQMSEDSHSSSAIRSQNDSQERQQQHDRQRLDNPEPISNGRPQSNSRQVVEQDEEED
EELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTEDTETVGQRALHSILNAAIMI
SVIVIMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYNVAVDYVTVALLIWNFGVVGM
IAIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNE
TLFPALIYSSTMVWLVNMAEGDPEAQRRVPKNPKYNTQRAERETQDSGSGNDDGGFSEEWEAQRDSHLGP
HRSTPESRAAVQELSGSILTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL
TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI

>NP_777146.1 presenilin-1 [Bostaurus]
MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDSRERHEHGNERRRRGNTESVSNGRAPSSSQQVVEQEEEE
DEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTEDTETVAQRALHSILNAVIM
ISVIVIMTILLVVLYKYRCYKVIHAWLIVSSLLLLFFFSFIYLGEVFKTYNVAMDYISVALLIWNFGVVG
MIAIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERN
ETLFPALIYSSTMVWLVNMAEGDPEAQRKVSKNSNYNAQRPANSPVTTTGTESESQDPVTESDDGGFSEE
WEAQRDSRLGPHHSTAESRSAVQDLSSSILASEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIA
CFVAILIGLCLTLLLLAIFKKALPALPVSITFGLIFYFATDYLVQPFMDQLAFHQFYI

>XP_008102150.1 PREDICTED: presenilin-1 isoform X1 [Anoliscarolinensis]
MAELSAHLSQVQRGQLKETSPDNHLTNTNDNIERRRQEGSSQRRTDNPDAASNGQPQNSTRQVVEQDDDD
EEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTEDTETVGQRALNSVLNAAIM
ISVIIVMTILLVVLYKYRCYKVIHGWLIVSSLFLLFFFSFIYLGEVFKTYNVAMDYITVALMIWNFGVVG
MICIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLIAVLCPKGPLRMLVETAQERN
ETLFPALIYSSTMIWLVNMAEEDPEAQKRAPKSSTYDKQVTANQNQNAGAETDDGGFSQEWEQQRDNRIG
PLESTPETRAVVQAMPADSVGSEDPDERGVKLGLGDFIFYSVLVGKASATASGDWNTTLACFVAILIGLC
LTLLLLAIFKKALPALPISITFGLVFYFATDNLVQPFMDQLAYHQFYI

>NP_001027027.1 presenilin-1 [Xenopustropicalis]
MNDTNERRSNEHSESQSNGQTQSSSQQVLEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVS
FYTRYDGQLIYTPFTEDTDSVGQRALNSILNTAIMISVIIVMTILLVVLYKYRCYKVIHGWLIISSLLLL
FFFSYIYLGEVFKTYNVAMDYITLALMIWNFGVVGMICIHWKGPLLLQQAYLIMISALMALVFIKYLPEW
TTWLILAVISVYDLIAVLSPKGPLRMLVETAQERNETLFPALIYSSTMIWLVKMADGDPGFKQSASKKTY
NAQAPVAQPRSDSAASDDNGGFDTAWEEQRNEQIGQINSTPESRAAVQALPSNNPPSEDPEERGVKLGLG
DFIFYSVLVGKASATASGDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDYLVQ
PFMDQLAFHQFYI
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>NP_571099.1 presenilin-1 [Danio rerio]
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IMLFIPVTLCMVVVVATIKSVSFYTQKDGQQLIYTPFREDTETVGQRALHSMLNAIIMISVIVVMTLVLV
VLYKYRCYKVIQAWLFFSNLLLLFFFSLIYLGEVFKTYNVAMDYFTLALIIWNFGVVGMICIHWKGPLRL
QQAYLIMISALMALVFIKYLPEWTAWLILAAISVYDLLAVLCPKGPLRILVETAQERNEAIFPALIYSST
MVWLFNMADSAETRNNSSHPVPQQENQVVAMAPTAQAEDDGGFTPAWVDHQQHQLGPMQSTEESRRQIQE
MPSARPPPPADDDEERGVKLGLGDFIFYSMLVGKASATASGDWNTTLACFVAILIGLCLTLLLLAIFKKA
LPALPISITFGLVFYFATDNLVRPFMDQLAVHQFYI

>XP_003978532.1 PREDICTED: presenilin-1 [Takifugurubripes]
MANNAEDIENNMNQEPSVVNHEPAVQPQEVSVTRSRSRGGGGHGEGGPEQNGQPPATHAAHVVETEEDED
EELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVTYYTQNDGQRLIYTPFPEDTDTVAQRALNSILNATIM
ITVIIIMTLVLVVLYKYRCYKVIQGWLFLSSLLLLFFFSYIYLQEVFKTYNLAMDYFTVAIIIWNFGVVG
MMCIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVISVYDLLAVLCPKGPLRILVETAQERN
EPIFPALIYSSTMVWLVNMADTDRPKRSSTDAAPPQQETQEAVASPTPSSLSQDDGGFTPSWVSQQEHQL
GTLQSTEQSRQEIQEMPSARPAAEDDDEERGVKLGLGDFIFYSMLVGKASATASGDWNTTLACFVAILIG
LCLTLLLLAIFKKALPALPISIFFGLVFYFATDNLVQPFMDKLALHQFYI

>XP_007891435.1 PREDICTED: presenilin-1 isoform X1 [Callorhinchusmilii]
MSGLSAQAVPVFQGGQLGESPSEIHQNSLGWFKMDSADENEENVPLLIVREDVSEEDVRHNQNDVNRIAA
DDGVPVSNGQSENNTRPIREQTDDGDEEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVTFYTQNDGQL
LYTPFTEDTDTVGQRAVNSILNAMIMISVIIVMTLLLVLLYKYRCYKVIHGWLIISSLLLLFFFSFIYLG
EVFKTYNVAMDYFTLALVIWNFGIVGMICIHWKGPLRLQQAYLIMISALMALVFIKYLPEWTAWLILAVI
SVYDLVAVLCPKGPLRILVETAQERNEPIFPALIYSSTMVWLVGMADQEARASSPADEHLTSANISLNNT
CVDETAEGPTNAGETNTDDGGFDTRWRCNRDETLGNVESTPESRAVVQAMPSPPTLDDDPEERGVKLGLG
DFIFYSVLVGKASAAASGDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATDNLVR
PFMDQLAFHQFYI


>XP_006000568.2 PREDICTED: presenilin-1 [Latimeriachalumnae]
MTELSASLPVYQQGQLTEDFPDSRQTNSNESGERRPNESRNAESNGEPQAASQRVVVSDEEEDEELTLKY
GAKHVIMLFVPVTLCMVVVVATIKSVSFYTKKNGQLIYTPFSEDTDTVGQRALNSILNAAIMISVIIVMT
LLLVLLYKCRCYKVIHGWLIISSLLLLFFFSFIYLGEVFKTYNVAMDYITVALIIWNFGVVGMICIHWKG
PLRLQQAYLIMISALMALVFIKYLPEWTGWLILVVISVYDLIAVLCPKGPLRMLVETAQERNEPIFPALI
YSSTMVWLVGMADPDPEARRKEPEDSRREAEASTNHTASATPADDGGFTQDWVQQQNETLGDMHSTMETR
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RPFMDQLAFHQFYI

>JL2681 len=427 1-427- Presenilin [Lethenteronjaponicum]
MCCVACVQPQVTTTTTTRQRGERREDGDGSGRERSHSEPHTDEESEEEELSLKYGAKHVIM
LFVPVTLCMLVVVATIKSVTFYTEKNGQLIYTPFTEDTDTVGQRVLNSILNTIILISVIV
VLTIFLVLLYKYRCYKFIHGWLIMSSLMLLFLFTYLYLGEVFKTYNVAMDYPTLILIMWN
FGVVGMICIHWKGPLLLQQAYLIMISALMALVFIKYLPEWSAWVILGAISIYDLIAVLSP
KGPLRMLVETAQERNEPIFPALIYSSTMVWMVGMADTNSTEQQSTRPSPEPNNDAQGDPQ
PSEPDVPRTTHEARELARERARANPPMPPEESEEERGGIKLGLGDFIFYSVLVGKASAAA
SGDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLIFYFATDNLVRPFMDSL
AFHQYYI
>XP_002738746.1 PREDICTED: presenilin-1-like [Saccoglossuskowalevskii]
MSLSNEEEEDCSERSQLMETVPNVRYSGTGGSVNFSDPPDTEDGGIRTHMYGGFDRTRPTGVREQNVESD
SDEACNRRIQQESSTRRTVQQHDDEDDEELTLKYGAKHVIMLFAPVSLCMLVVVATVGAVTFYTDDSGGA
YLIYTPFHEDKGGAGTKAWNAFANAAIMIGVILVMTIFLVILYKKRCYKFIHGWLIVSSLMLLFLFTYIY
LQELLSTYNVPMDYITLTIFMWNFGVVGMMCIHWKGPLHLQQAYLIIISALMALVFIKYLPEWTTWVILG
AISIYDLVAVLCPRGPLRVLVETAQERNEPIFPALIYSSTMVWLVGMADNNPEQRPKRKKKKSNKKTELE
QPIREPGKRHDDALNEDLDEGGFTDWSNRQPIQTPTDPRTQSVESVDARAAASALRRSASNERPRDTTAT
LDLEEEEEERGVKLGLGDFIFYSVLVGKASSYGDWTTTLACFVAILIGLCLTLLLLAIFKKALPALPISIT
FGLIFYFTTRYLVSPFTDTLASQQVYI
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>XP_001178715.1 PREDICTED: presenilin-1 isoform X2
[Strongylocentrotuspurpuratus]
MGVWDQDEDNSTENTRLMLDTEEEEQAPTETMSAEILAPTSDGASNARRPIQVEGSNNPSYGTSVNAEVR
GTSVQRRANAGNRPANQERRRERDPPPMEEEEEDEMLKYGAKHVIMLFVPVSLCMLVVVATISTVSFYTE
SGDVYLIYTPFHEKSDQAGTKAWNALANALIIIGIVLIMTIFLVVLYKYRCYKVIHGWLVLSSLLLLFFF
TFFYLQELLVTYNIPMDYFTIAVIMWNFGMVGMVSIHWKGPLRLQQLYLIVISALMALIFIKYLPEWTLW
TILAAIAVYDLFAVLCPKGPLRMLVETAQERDEQIFPALIYSSTMVWLVGMADIDSPPPKSKAKQEPPVE
EHTAEENATGGQEDQTVSSDQEVNGGFDTVFTERRERDLERSANSSVTSEDRRAAVRALRQNNGPSNRQP
PVDEEEEEEERGVKLGLGDFIFYSVLVGKASASGDWTTTIACFVAILIGLCLTLILLAIFKKALPALPISI
AFGLVFYFCTSNLVFPFTDELASQQVYI

>NP_508175.1 Presenilin sel-12 [Caenorhabditiselegans]
MPSTRRQQEGGGADAETHTVYGTNLITNRNSQEDENVVEEAELKYGASHVIHLFVPVSLCMALVVFTMNT
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LLLFLFTTIYVQEVLKSFDVSPSALLVLFGLGNYGVLGMMCIHWKGPLRLQQFYLITMSALMALVFIKYL
PEWTVWFVLFVISVWDLVAVLTPKGPLRYLVETAQERNEPIFPALIYSSGVIYPYVLVTAVENTTDPREP
TSSDSNTSTAFPGEASCSSETPKRPKVKRIPQKVQIESNTTASTTQNSGVRVERELAAERPTVQDANFHR
HEEEERGVKLGLGDFIFYSVLLGKASSYFDWNTTIACYVAILIGLCFTLVLLAVFKRALPALPISIFSGL
IFYFCTRWIITPFVTQVSQKCLLY

>NP_491328.1 Presenilin hop-1 [Caenorhabditiselegans]
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TTSLGVFCYQMKFYKAIKVYVLANSIGILLVYSVFHFQRIAEAQSIPVSVPTFFFLILQFGGLGITCLHW
KSHRRLHQFYLIMLAGLTAIFILNILPDWTVWMALTAISFWDIVAVLTPCGPLKMLVETANRRGDDKFPA
ILYNSSSYVNEVDSPDTTRSNSTPLTEFNNSSSSRLLESDSLLRPPVIPRQIREVREVEGTIRLGMGDFV
FYSLMLGNTVQTCPLPTVVACFVSNLVGLTITLPIVTLSQTALPALPFPLAIAAIFYFSSHIALTPFTDL
CTSQLILI

>NP_492095.1 Presenilin spe-4 [Caenorhabditiselegans]
MDTLRSISSELVRSSQLRWTLFSVIANMSLTLSIWIGVYNMEVNSELSKTYFLDPSFEQTTGNLLLDGFI
NGVGTILVLGCVSFIMLAFVLFDFRRIVKAWLTLSCLLILFGVSAQTLHDMFSQVFDQDDNNQYYMTIVL
IVVPTVVYGFGGIYAFFSNSSLILHQIFVVTNCSLISVFYLRVFPSKTTWFVLWIVLFWDLFAVLAPMGP
LKKVQEKASDYSKCVLNLIMFSANEKRLTAGSNQEETNEGEESTIRRTVKQTIEYYTKREAQDDEFYQKI
RQRRAAINPDSVPTEHSPLVEAEPSPIELKEKNSTEELSDDESDTSETSSGSSNLSSSDSSTTVSTSDIS
TAEECDQKEWDDLVSNSLPNNDKRPATAADALNDGEVLRLGFGDFVFYSLLIGQAAASGCPFAVISAALG
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>XP_012561939.1 PREDICTED: presenilin-1-like [Hydra vulgaris]
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SVLMLIIPVSICLLVVVATISSVTYYTQNAGTYLVYTPFHEEGNISHAEKFGQALANSLIVIGVILVMTI
ILVILYKCRCYRIIEAWLILSSLMLLFFFSTIYLQELLRVYNVAMDYITVVLLIWNFGVVGMICIHWKGP
LLLQQAYLIIISALMALVFIKYLPDWTLWFILAAVSIYDLFAVLCPKGPLRILVQTAQERNEQLFPSLIY
SSTFMYPTVVNQVQEATSSQAKLTENTDDNHEDEPNNIQQQTAPILNEQNVEATATTPPTQSEGPEERGV
KLGLGDFIFYSVLVGKASSYKDWNTTLACFVAILIGLCLTLLLLAIYRKALPALPISITFGLIFNFATSY
FVKPFTDHLAGEQAFI

>XP_002597164.1 hypothetical protein BRAFLDRAFT_118108
[Branchiostomafloridae]
MSQYNSGSDSEHCNERTSLMEVQVDVRSGVGEAVTTQRVSRSSGRRSQQIQENVPDGADRREAGDGGEDH
GIRHREDEEEEDTEMTLKYGAKHVIMLFAPVSLCMAVVVATISSITFYTEKNGYLIYTPFHEEGASTASK
VGDSLANAAIMVGVILVMTVFLVILYKYRCYKFIHGWLILSSLMLLFLFAYIYLGEVLQAYNIPCDYITL
AIVMWNFGAVGMVCIHWKGPLLLQQAYLIVISALMALVFIKYLPDWTTWFILGAISLYDLVAVLCPKGPL
KVLVETAQERNEPIFPALIYSSTMMWFVGMADSDPEAKKKKKKKKKRRGDGDAQGAAPAGAVGGEEEGGF
GQDWNESRGFQPTRRPNRGGNASDASVNSEDARQAAQNLSNGRLSPSGNQQQQQQQQMEEDEDEEERGV
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KLGLGDFIFYSVLVGKASSNGDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLIFNFATAN
LVTPFTDALASQQVYV

>NP_524184.1 presenilin, isoform A [Drosophila melanogaster]
MAAVNLQASCSSGLASEDDANVGSQIGAAERLERPPRRQQQRNNYGSSNQDQPDAAILAVPNVVMREPCG
SRPSRLTGGGGGSGGPPTNEMEEEQGLKYGAQHVIKLFVPVSLCMLVVVATINSISFYNSTDVYLLYTPF
HEQSPEPSVKFWSALANSLILMSVVVVMTFLLIVLYKKRCYRIIHGWLILSSFMLLFIFTYLYLEELLRA
YNIPMDYPTALLIMWNFGVVGMMSIHWQGPLRLQQGYLIFVAALMALVFIKYLPEWTAWAVLAAISIWDL
IAVLSPRGPLRILVETAQERNEQIFPALIYSSTVVYALVNTVTPQQSQATASSSPSSSNSTTTTRATQNS
LASPEAAAASGQRTGNSHPRQNQRDDGSVLATEGMPLVTFKSNLRGNAEAAGFTQEWSANLSERVARRQI
EVQSTQSGNAQRSNEYRTVTAPDQNHPDGQEERGIKLGLGDFIFYSVLVGKASSYGDWTTTIACFVAILI
GLCLTLLLLAIWRKALPALPISITFGLIFCFATSAVVKPFMEDLSAKQVFI

>XP_001750030.1 hypothetical protein [Monosigabrevicollis MX1]
MMMMNCLSLSLSLSSLSLSLSLSIHSLSLSLLLLSTLLFTSLFSNQFISLLSLSLSSLCFLTGVVNTMIR
NENKRILHTQREREREREKRQRWLASLSLSLSLSLSHSESALLRRDRSIMAGDGSEAPEVASTNSGDPLI
EHDRRTTQDDGRRATRPLDANVHERLLSAGRENSVNYTAEEREARIRARQEEAARRELELDLKYDAESVL
ALIKPVSACMIVVIATIRSITYFSQNDTQFAYTPFESNGGAGESSGERFGGAVLNALIVVGIVIVMTFIL
VMLYIYEYYKIIYGWLALSALLLLYFFSYQYIECVMCTRRQVLIAHNASIDWITMAFIIWNFGTVGFIAI
FWRSPLAVQQVYLVIVSALMALVLIKNLPDWTTWVLLAAIAIYDLFAVLSPCGPLKCLVEVAQERNQPLF
PSLIYSSTMMWTVTMADVGDSSSNSATIESQPRVADGGASTRGTEMTSMSSQPRARQGSRADSEADDGAR
DISTFAAPRGETRSTNQAAPASQPSFQPDDEDDSGVKLGLGDFIFYSVLVGKAATAHEWTTILACYVAIL
IGLACTLLLLSIFKKALPALPISIFFGLCFFFLTSEVLDPLIDRLNERQIFL

>XP_019849527.1 PREDICTED: presenilin-1-like isoform X1
[Amphimedonqueenslandica]
MSTNSETASLLSGEARETEYGSDNDEGMEEQEEDGITVSPPLQGTREEEEETEQKDDEQSCGMKYVFKKI
LNVLPSFGDDGDDPTSEANEEALRFGAQQMILLIFPVFICMALVVAIQLSVEKNVTSSGTLIYTPFDEDT
ASNDGFVLLFALANVAIVITLVVVMTIILVCLYKYRCYKIIYGWLVVASALLLFVFSSFFFVEVLQVHYL
FIDWPSFLVLIWNFGGMGVLVIHWKGPLRLQQAYLIFCSALTANIFVKYLPNWTAWILLAAISLYDLIAV
LCPKGPLRVLVETARERNETIFPSLIYSTTMVWLVGMADRPTNKKKDKKNTDDTSGSSDGSHEEEEEEEG
GGEREGRRDNDDGDDDTDGIEMRSIRAAADTNRERRRERQQQQQEEEEEEEEEQEERQGFKLGLGDFIFY
SILVGKAAHDSTGDWVVISSCFVAILIGLCMTIIILGIVRRALPALPISIFCGLIFYFSSQYVIAPFAQV
LATTQTFI

>XP_635158.1 presenilin family protein [Dictyosteliumdiscoideum AX4]
MKENEDEINKTDEKYKIKNPSNNGNNKNKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGNSNLENIEGLN
KYNIYKKKKGKNESNTSLNNIYISSPNLSERSDNSIGSYCTNKTMKSENSIINIETLFRDSVSEQNSDEC
GSKVDKDLDEDDDDDDDETEVPELVDYSEMIVSILYPVCITMVIVVLAIRAISSSTSKNSQIVEISNDNS
GGNGDSSSGADKMVFDSVVNSLIFLAVIILSTTIMVVLYKFKLMKALYAWLMGTSILLLGVFGGFLFLIL
LAYLNLGLDYVTFVIVVWNFSVGGIVCIFWYSPKLLNQGYLISISVLMALFFSRLPDWTTWGILSIVSIY
DIFAVLCPGGPLRILIETAQKRNENIPAMIYNASIYIGMIYNEDNLENNNNNNNNNNIELNINEVDIENN
NNNEDENKNNTEDGNNNNNKNKNNNNNNNNRIENENGAENSSENGSITPPPTIPNFIKDEKEINRSSGSN
GFPNFKKCANDNILIGDAETNDEIVSNAESSIDSTISESYVKPKQSIRLGLGDFVFYSVLIGKAASYQIT
TVFTVFIAIITGLFLTLILLAVFRRALPALPMSIIFGIIVFFLTFKILIQYIYFLGENQIFV

>XP_629693.1 presenilin family protein [Dictyosteliumdiscoideum AX4]
MSSDNNNDPFDLNEDGHDYFNRVSTTTSPNRQSINSSPKQSSPKSTNNNDDKNNIILDLNDNNNDNNNTN
NYNDEDIDVDNKNKFENKDNTYNSNGGSNNKNKNKKKDNKSNNSSDNEEADENTSLISDSEPLLNKKEKD
DEQIEIENLDGEDYDDEVSLQDFSSMIVSIIIPVSITMMAVVFFVKYLNNQTLYASTLSYTIAGGSSGGG
SGADSITGNSFVDSLIVAGIVLGMIIVTTVAFVLLYKYRCLKILYGWLFLSVGMMLGSFGTTFFQAMLSA
ANLPLDYITFAFLIFNFTVCGIIGVFWYAHQYVNQLYLVIISVLMAISLTRLPQWTIFTLLVIVAIYDLF
AVLCPRGPLKVLVELSQERNENIPALVYETGKGSDSNLKLGLGDFIFYSLLISRAALVHMSCVFSTFIAI
LTGLFLTLLCLAIFKKALPALPISIFLGILFYYLSNNFLTPFIEALTLSQIFV

>XP_001701664.1 presenilin protease [Chlamydomonasreinhardtii]
MRDCSSIIVLPSAVNAAGNLCFAWAFCQPVPVRVPASAMATPSLLDDLGEEVTGIVAPVSLCMAVTVLLV
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RLLNPEGVSSSNTVLIASIAYQEQASDSSGKKFGGALLNALIFVAVVAGMTVVLFLLFKYKCYKFIFAYM
GFAVFNIFFFITGALFIQVMQVIDLHIDAFSLAYGLFNFSIVGTLGLLFMPIPLLSKQVYLIWVGIIVAY
IFTFIPEWTAWVILCFMALYDIVAVLVPGGPLKALVELAIERQQELPALIYEARPAGGRPYVRGWGNRGQ
RGEGEEGGPEGPAGPDGPGGPAANGAVPAAPPNVVPSPHANGRGPRPVAEASSPAASLEMRQPTTRASCG
ARAAAPAQGRGRSRRGGSRASGSRCRRHPRTLTAPRAPAAAAALATAAPGRRGARCAACSRAPARRQARG
RWTHTCAAPVAAAARNTLDGELPASEPPPQLAGAPPPDGHHPHHRGHGHHHDGGADGGGEGGGDLPDLPD
SIKLGLGDFIFYSMLVGRAAMYDFMTVFAAYLAIIAGLGLTLLCLAVFQKALPALPFSIALGVAFYFLTR
LTLEPFLIPLATNLAFF

>EMT04448.1 Presenilin-like protein [Aegilopstauschii]
MAVYDLGAVLIPGGPLRVLLELAIERNEEIPALVYEARPVDPRHGQNWRLWRERARQPGGDLDPSSTVEV
IGEVLGRNPLLNSAGNSPNSTTQAGEQTNLTGAVSNSRLRESPVPDLSSGSANAQAREALALPETRLHIA
ELRVPLIQPQPDRTSDDDDDDDDEDGIGLGSSGAIKLGLGDFIFYSVLVGRAAMYDYMTVYACYLAIIAG
LGITLLLLAFYRKALPALPVSITLGVLFYVLTRTLLESFVMQCSTNFLMF

>XP_012562740.1 PREDICTED: presenilin-1-like [Hydra vulgaris]
MTKSKELYQIKKEMYRFYLLARFRNVRTNNEGRSTVQPPQPLEQRSMNVVESEDDDHEEMLQYGAKSVLM
LIIPVSICLLVVVATISSVTYYTQNAGTYLVYTPFHEEGNISHAEKFGQALANSLIVIGVILVMTIILVI
LYKCRCYRVFSYMVFSYSRLGQKGVRFHGFI

>NP_000438.2 presenilin-2 isoform 1 [Homo sapiens]
MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVPG
RPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLLNSVL
NTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWN
FGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVET
AQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGE
ELEEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISI
TFGLIFYFSTDNLVRPFMDTLASHQLYI

>XP_001142009.2 PREDICTED: presenilin-2 isoform X1 [Pan troglodytes]
MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDGEEDPDRYVCSGVPG
RPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTASVGQRLLNSVL
NTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWN
FGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVET
AQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGE
ELEEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISI
TFGLIFYFSTDNLVRPFMDTLASHQLYI

>NP_776865.2 presenilin-2 [Bostaurus]
MLTFMASDSEEEVCDERTSLMSAESPTPRSCQDGRQGLEDGESAAQWRSQESEEDHEEEDPDRYVCSGVP
GRPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFSEDTPSVGQRLLNSV
LNTLIMISVIVTMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLFLTVW
NFGAVGMVCIHWKGPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVE
TAQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPDVFEPPLPGYPG
EELEEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPIS
ITFGLIFYFSTDNLVRPFMDTLASHQLYI

>NP_035313.2 presenilin-2 [Mus musculus]
MLAFMASDSEEEVCDERTSLMSAESPTSRSCQEGRPGPEDGESTAQWRTQESEEDCEEDPDRYACSGAPG
RPSGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLLNSVL
NTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLFLAVWN
FGAVGMVCIHWKGPLVLQQAYLIVISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVET
AQERNEPIFPALIYSSAMVWTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEAFEAPLPGYPGE
ELEEEEERGVKLGLGDFIFYSVLVGKAAATGNGDWNTTLACFIAILIGLCLTLLLLAVFKKALPALPISI
TFGLIFYFSTDNLVRPFMDTLASHQLYI

>NP_001017181.1 presenilin-2 [Xenopustropicalis]
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MITFANSSDSEDDECNERTSLITSQSPPLPSYQDGLQASGGSESSDPMKTQTDTQVIEDVPNGRTSGADA
YNSDAAMENEEEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTEKDGQLIYTPFSEDTTSVGQRL
LNSVLNTLIMISVIIVMTIFLVLLYKYRCYKFIHGWLILSSLMLLFMFTYIYLSEVFKTYNIAMDYPTLF
MVIWNFGAVGMICIHWKGPLQLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLLAVLCPKGPLR
MLVETAQERNEPIFPALIYSSAMVWTVGMADSATADGRMNQQVQRTDRNAPNHTNSSQEDAAETSVQTQS
NVSSEDPDEERGVKLGLGDFIFYSVLVGKAAATASGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALP
ISITFGLIFYFSTDNIVRPFMDTLASHQMYI

>XP_003216113.1 PREDICTED: presenilin-2 [Anoliscarolinensis]
MITFMNNSDSEEESCNERTSLMSAESPLLPPYHDVSQAPAATETQTHRKRRTGSSGSNKTADGNVPESDG
ATRGSVALDNVEEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVRFYTEKNGQLIYTPFSEDTPYVGQR
LLSSVLNTLIMISVILVMTIFLVVLYKYRCYKFIHGWLILSSLMLLFLFTYIYLGEVLKTYNVAMDYPTL
FFVIWNFGAVGMICIHWKGPLQLQQAYLIMISALMALVFIKYLPEWSAWVILGGISIYDLVAVLCPKGPL
RMLVETAQERNEPIFPALIYSSAMIWTVGMAKPDSGRRGSSEETWDLAEGAENHQNSSYTDPEISERRHL
TDGQAGQRVEQTDRQLGQMGHNLEEMEEEERGVKLGLGDFIFYSVLVGKAAATASGDWNTTLACFVAILI
GLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVQPFMDTLAAHQLYI

>NP_571589.2 presenilin-2 [Danio rerio]
MNTSDSEEDSYNERSALVQSESPTVPSYNQDNAMSLPQDTDSKRSGAVRSRSASGSGDAGPVDRERADTP
DGEEEELTLKYGAKHVIMLFIPVTLCMVVVVATIKSVSFYTEKSGQRLIYTPFEEDPNSVGQRLLNSVLN
TLVMISVIVFMTIILVLLYKYRCYKFIHGWLILSSLMLLFWFSFMYLGEVFKTYNVAMDYPTLVMIIWNF
GVVGMICIHWKGPLRLQQAYLIVISALMALIFIKYLPEWSAWVILGAISIYDLIAVLCPKGPLRMLVETA
QERNEPIFPALIYSSAMVWMVGMADSNNPDSAGERRRSGGGVRTQEGVESEDDAPQAGRRQYSAEEDLEE
DRGVKLGLGDFIFYSVLVGKAAATGGDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFY
FSTDNLVRPFMDSLAAHQYYI

>XP_003972298.1 PREDICTED: presenilin-2 [Takifugurubripes]
MNSSDSDDDSYNERSALVPSQNPAVPSYRPTVDPRSPIAQPCKQMAGNRREGPPDSGGSDQDIDMDDEEL
TLKYGAKHVIMLFIPVTLCMVVVVTTIKSVSFYSEKSDQQLIYTPFTENTSSVGRRLLNSVLNTIIMISV
IVVMTIFLVVLYKYRCYKFIHGWLILSSLMLLFWFSFMYLGEVFKTYNVAMDYPTVGLLIWNFGAVGMIC
IHWKGPLQLQQIYLILISALMALVFIKYLPEWSAWVILGAISVYDLVAVLSPKGPLRMLVETAQERNEPI
FPALIYSSAMMWAVGMAKPVDAPHSGRETDEEVMQSCTEQLSPHSPAETEPETDRGVKLGLGDFIFYSVL
VGKAAATGGDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLIFYFSTDFLVQPFMDNLAAH
QFYI

>XP_001326572.1 Clan AD, family A22, presenilin-like aspartic peptidase
[Trichomonas vaginalis G3]
MGKKVGIHTFLEFYARKVAKIAVPVVLTLILDAVCIRFIERTHGSAELNRNFVDTMSRNDSGISVTASIW
SAVGIIFMIIVVTAILLTLYYFGCMKIIFGWLILAVSLLLSMYFLVGFGTYPSIVNIPVDYLSLAVFLLN
LVVVGNMSIFWRAPQRITQAFLVLISILTSIVFRYLPDWTVWILLVLLIIYDACVVLCPNGLLILLLKKS
EERGDAIPALLYSAAAWEEADPEKGNQNNEEGDGNEGNQEDPAEQADNQDNNEEEEEEEEAENNQPQENA
NGEAQNGNQNNNKKKKNMSKRDNEGIKLGLGDFVFYGILVSRAARIGWDITILCIFAVILGLSLTLVCLA
VWERPLPALPFSLALGIVFFIIGAMTFRQFCEHMRWGLVAF

>XP_006677768.1 hypothetical protein BATDEDRAFT_10859
[Batrachochytriumdendrobatidis JAM81]
MLGTTLLFVAALPLDYISFAFFLWNLVAVGLAVIFWKGPLFIQQGYLILMSSMMAFSLSQLPDLVTWILL
GLLAIWDLIAVLCPFGPLRLLLESAQTQDQQLPAALLYTDLSSRGIELETMGDIRQNHPGINTSNHDNYE
IPPVVDDTDDDEDSGLKLGLGDFVFYSVLLTNPTLPLCRLALFDWITTMSTIVAVTAGLSMTIFFLAVYR
KPLPALPFSIAFGILFYFLSAITLTPFLDHFVIRPPIIIPPTVGSSLWVGKSVGGGMIYL

>XP_009493699.1 hypothetical protein H696_01527 [Fonticulaalba]
MASSLFRAAPLMADTFTQAQPPVAPGTEQSAMPAQSAPPAHPTSMPQTPGTPPPALVDPFFSGRGPTGQE
ADLLGEGLVTHEAHDDGAGAFDDGRLDARPEDLGADGDDDDDDDDDDDDDDLAMTPRVAAQFYLPQIYGL
FASLFATFFLVIWWAPTIFLSVPFNYTGVVLSTGTNTLSTGSQLLVAVASAAILLVIILVNTVILLALFY
YGYIRVIYGWLIVATGLILSFIGGIVFYRLLETYNLPVDWVTFCFLLFNFSVVGLLAVFGKLTLRMQQVY
LVIVSALVATNLSGLPSWTAWAVLIVVSIYDLFAVLCPQGPLNLLINLSQTRQQSIPALLYSAGMARLAS
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SNDDSVPILAFTAGTSDDSGDEQPEDADTQVGQALLSSGHLESVLLGEAMPSAASDLDSAAVPAIDSTTG
NPILDAETGPKDVSDEQDDGDDDDGEDGDEPPGRGPVQLGLGDYIFYSLLVARGALTSDGSDGGASAAIA
VISCVLSTLVGLGLTLSLLALFRKPLPALPISIGLGILAYVFSAFLSTPMVVEMTRQVVFV

>XP_009496662.1 hypothetical protein H696_04506 [Fonticulaalba]
MADPPGAGDPLAGRRPVHPTGQGEVLYDDLSFEGIGAAINNSRLGPGPPADPRVVPLSEYTASEDPLSGP
MPGAAESADMQQPSPTDSSGQDPGYGGTVDSTDQLFVAPLVLDDEEDPGQTQPGEEPGADGGDGGGGGGM
TVEDVRHYVRQIDHIFRPVLICMCLVIWWVKVEAVMRADTDGMRLFGFSTVETGDNIGGFIIDAIIIISA
VIIMTIILAVMFWFGLFKIIFGYLIFSTGVLLGGMGALFAISQSLALNIPMDYITIVFAAVNFAVGGLVL
VFYCSHLRLQQAYLTVMSALLAWSLTRINEITTWVLLGLLVIWDIIAVLTPCGPLKLLIAASRRHQKDIP
ALLYSVTMVWFMAHDPEHGILGGGKSSDASPVDSSDEVLAPVRTGGRHGGNGGGRRRQSTPPRGALLTDE
GVELHDLTGPVPASPEHAPASEGDLRSGTEAEAADVDPHLADADPDAADTGAQEDEDAPPAEAKARDGLK
LGLGDFVFYSVLLGRAALSDWTTTVTCLVAVSAGLMSTIFLLAFFRRALPALPISLVLGIIFFFVTRAVI
TPFVLEHVSGVVGL

>XP_001312406.1 Clan AD, family A22, presenilin-like aspartic peptidase
[Trichomonas vaginalis G3]
MKIAIPVVITLLLDVFLTRLKEQSFLNTTIDRTITVFTRTSSSSSGISTKWAIILAVILVAGIFLVTIVL
LLLYYYGCTKCIIVWMVIAVTLLLSYYVYLAVGEIPSLENWPIDWITVVFFLLNIVIVGNMAVFWRAPKI
VTQIILILISVMTCCVFLFLPDWTVWLLLGMLVIYDICVVLCPRGPLQLLIKKSQERGDAIPALIYSSAA
YTWKDGPEEEEESHEIQIDRSTEQEENNQSNEPSTHESNEQTNQETNEQEDKKPLEKDPENGHHKKHKKR
RPKKFPLGSKKIHPAEPKELNSEQSTESSSSSSSSSSSEDDSEALELESKEGIKLGLGDFVFYGILISRA
ARKGWDTSVVCIEAVLLGLSITLIFLAILERPLPALPFSLVLGIIFYFIMPYTLKPFALNLRKLLLVY

>XP_001299078.1 Clan AD, family A22, presenilin-like aspartic peptidase
[Trichomonas vaginalis G3]
MPIKVTKHEFLEIYSKRIYKIAVPVILTLVIDVWLTRTLEEKFDNTALSTSFASVVSQSSGGVSTAVAIY
IAIGFIVAIALVTGLLLLLYWFNCVKCIYVWMVVAVSLLLSYYVYLAVGKIPSLYNIPIDYIAVVIFLLN
GVVVGGMSIFWRAPPIVTQAFMIWISVMTACVFLTLPDWTVWILLVLLIIWDCCVVLCPNGLLHLLIKKS
QERGDAIPALVYSSAAFFWKEADDGEEQNEEGEDHENLDNYDEEYDSASEDESTDPDSSASSDDALPINP
DEFVGLSNNPEDQPPPQPKPEQQPESELAQPAGEPTKPKKKRPNQDNQHGDPENPDKRKKKSGSAKSTPT
SEGVKLGLGDFIFYGILVTRAARVGWDIAILDILAVMDGLALTLICLAYFERPLPALPFSLALGIIFYLI
GAYTFRGFSTNLRKLVLVF


>XP_004349389.2 Presenilin2 [Capsasporaowczarzaki ATCC 30864]
MSSGGKLARSDSTDSTDSVTADTPLLTPSSPTSAPAPSYSTTTTTTGTPSNPASSSSSDQQRRRTASAAL
GSSPYSSSSFSSSAAAAPLNAEMASRGNFDTQSVSSVSSTDQLLLSPTQPQRSQQLLEDAQERRRQQSAA
ATQNSQPGAAAAPQPPRRAVAPQGNANSLNGNERTDAAGSPNAGANAAGDAAEGEEEDEDEELKYGAKEV
MALIVPVTLCMAIVVASIQSITYYAQDSGDYLAYIAFKEDSDSGAENFGGAIINALIIVGVILVMTCVLV
LLYKYRCYKAIWMWLFLSTVMLLFLFTYIYLELVFDRYNVAMDWVTFAFVIWNFGCVGVVAVHWKAPLLL
QQAYLITTSALLALTLIKHLPEWTTWVLLAAIAVYDLFAVLCPRGPLKVLVETAQERNEPIFPALIYSST
MAWIAVAAVDKPVPSEDAEEVPQLQAARNDPEAAPVSTAQPTAPAAARQRRTGTNAGAAADEDEATNATA
AAEQSQDSTAPAEDDEEHGVKLGLGDFIFYSVLVGKASVSNNWSTILSCFFAILVGLCLTLVLLAIYRRA
LPALPISIAFGLLFYYVSNEVLVPFNNQLSAVQVFV
>XP_003882351.1 conserved hypothetical protein [Neosporacaninum Liverpool]
MRELRGFPSGLGAESEGTGPAPRVPLVSDSSPSDRAPPRNFDRDGIHPGASRIQRLEVIHGQLVAALRKE
AKQVATLLVTGLLRPVIICMLTATLLSFVLTSSSFALFPRPVSPLTAPSLLSPSSSSDPHSSEGDAARLP
SFPSSSSLRQTRSLVRDFSRGLGAVCHIFSSFCGIFFSTVFDLSLDVLIYVAVLTFCLALAVRRGWHRFL
YYVMASSASFSLAAGCGGAIYLFTCRYLQPEEGGFTANASFSSDTLLADKNHGVPPETDAANRDVIGSED
RKRLCFFLSHLIGLLAKIPEHVSTVSFLPQPDTVLVLVALWNLSLGGAFVLLWLAPIGIRSQLLVAISVA
SAFTLHVLLLHFGVNYSPESPSTPTTVLLLCMAAWDLFAVLSPWGPLRWILQGTSAADARPMPLLAYEAS
VARPLLSGESVRSAPMAPEPTGPGVSSVWERPSGMRTPGALRLQAEPRLQLEQGETATVIGYTGSEARVR
VRLLEPDSIRNYLVKQNMRLEPLEAGFIIQDERARVHAETRRRQQASYASAAPGDSQPSSREERSSPSEA
RRKQPCPAETQSRGSGETLRGVHELPVAAFGQLSVRTLRGAARGGAEPRVIRNAEREGEGRHRTEACLAT
TGRELKETIRDGEKQEGGAHRKFSTHTGPPRNGVTNREERGGETVEGQPAAGLAGHSGEGEAAEERERTL
EIEIAVAKRQLHRLRRGNGRAMLGLGDFVFYSLLACNLTSWSFEAGLAASVAVWAGLVITSLGTTFGSRP
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FLPALPLSIILGLGVGAGIFYFVEPQADFLISVDAFF
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>XP_018637326.1 hypothetical protein TGME49_204040 [Toxoplasma gondii ME49]
MREVRGVPQTEGERSDGHQRLPPTPRSSRPALAPESAFETDGRGRTLERLQRLERMHCQLVSAIRREANQ
VATLLVTGLLRPVVICMLTATLMSLLLTSPSPPSLPTAPPPCFPSPDSPPSCVSSSSTADAPSEGGSVSL
SSSPASSLRRSRSFVRDVSRAVCTVRRLFSLVHGEFVSHFFELGLDALLYVAVLTFGLALAIRWGWHRLL
YYLMASSAAFSLVAGCGGAVYLFACRYLQPKAGAVTQNVAFPAGKAPVFRQETNGDDGGVLVATEQNSLL
AFVSHSVFSTSHLKDGVSSLSVAPQLDTVLVLIALWNLCVGGAFALLWLAPLRIRSQFLVATSSAAAFTL
QLLLLHFGAKYSPESPSTPTTFLLLCLAAWDIFAVLSPWGPLRWILQGLRSTDARPMPLLAYEASLARPV
LPHAGVRSARMASEPAGPGAPSARDTPSGVWTPGSLWSVAEPGSPLQRGEAGETRTGVNGREVRIRMRLP
EYGSRRSCLAEEQNLQLEPLAAGFLIQDERSRFDAEVRRRHISEAAAAGGDSQASRSRGRSRGQPVLEET
ERRGNGGSLTGVQGMAVTGVGQLGVYTPREVGRGGAEQRAPEDAECDGEGRESSKARLSFAGGEQETMRG
GEEEVEDVNGRVRSRGESERHRPNTQEGRGAATREGWPTGDPLGRSNETETAEEREKILEMEIATIKQQL
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>XP_008884684.1 hypothetical protein HHA_204040 [Hammondiahammondi]
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VSTLLVTGLLRPVVICMLIATLLSLLLTSPSLPSLPSVPPPHFPSPASPSRVSSSSTADAPSDGGGVSLP
SSAASSLRRSRSFVRDVSRAVCTVRCLFSLVQREFVSHLFQLSLDALLYVAVLTFGLALAIRWGWHRLLY
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FLSHSVFFTNHLKDGVSSLSDVPQLDTVLVLIALWNLCVGGAFALLWLAPLRIRSQFLVATSSAAAFTLQ
LLLLHFGAKYSPESPSTPTTVLLLCLAAWDIFAVLSPWGPLRWILQGLRSADARPMPLLAYEVSLARPVL
SHASDRSARVAPEPAGPGAPSAWDTPSGVWTPGPLRSVAEPGSLLQRGEAGETRTGVNGREVRIRMRLPE
SGSRRSCLAEEQNLRLEPLAAGFLIQDERARFEAEVWRRHISEAAAASGDSHASGSRGRSRRQPVLEETE
RRGNGGPPTGVQGMAVTAVGQLGVYTPREAGRGGAEQRASEDAECDREGRQSSKVCLSFAGREQETMRGG
EEEVEDVNGKVRTRGESERHRPNKQEGRGAATREGWPAGDWLGRRNETETAEEREKTLEMEIAAIKQQLH
RLGRGSGRAMLGLGDFVFYSLLACNLTSWSFAAGLAGSVAVWVGLIITAAGTTFGPCPFLPALPLSIALG
LGVGAGVFYFVEPQAEYLISVDAFF

>XP_012899044.1 uncharacterized protein [Blastocystishominis]
MSQEDANISPSSAKEEKNLLNDSTYVIWYGVNHLASIVIPVGLTMLFSAILVNVVRPASFTSALEQGLTV
YMVYKQEADNTWDSIWQAVINSLVIVLFIGLMTFIMVILYKYNCIKVLYGLLYFSTFMAIGYTGWVIFYM
AAMQYQFSCDLFSSAFIFFNLGVVSVISIFGTYAPPLVKKAFLIFISCLVCYLLSFFPDWTTWILLIAMA
LYDICAVLTPCGPLKLLINISQNRDDAIPGLLYETTLDHSDGPLPIDETPDEGVIPAGEGVITDGDYVAD
SEIEMEEGGKINRIFEKESVSLGLGDFIFYSLMVSKASLASSVPFVFVFVIILTGLLLTMAFLSVLEMAL
PALPFSMILGVVTYALTYFVVTAMTNQFALNGVLF

>XP_008862967.1 hypothetical protein H310_01595 [Aphanomycesinvadans]
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RLAEVALENLSVPVDVWSYWFIMYNFAVVGVLSIFYQKGVNMSLTQSYLVAVSIIMAWQLSKFPEWTTWA
LVVVLAFYDLCAVLTPCGPLKCLVNLIQQEGRPLPGLLYEAEVQRTFHSDAHSPSYYQRGGPPCPEQATG
TQTTCTFTRRRSRPDDSHEPLLAAASSTDTSEMTTTAKLPLRDRLVAFYNEYNPSAIERVDQVLAIYEGR
ERDLWNDLAAKYGPHDDDEDDNTIKLGLGDFVFYSVLVSRAAMFDVMAMIACLVSILMGLGSTLFLLSVY
KKALPALPISILLGVAIYLWVRFVLVDFMDSTVVMQ

>XP_008860947.1 hypothetical protein H310_00092 [Aphanomycesinvadans]
MATEAFKTTFDEPLLAPHHHPPPKDSPSSSFSLGYGLSLGTVVTQLNSFLAVLWPVQVTMVLASIVAVSM
RDPDAERSMSRYLYYKDIDESIESTSTKVMEALTNALVIIFFIAIVTFAVVLMYKVNCMGGLQGYLMASS
ATLLGLVGSVLAEKIVCERLLWHVDAISMTFVMYNFAIVGTLSIFYQKGVSPDVGRAYLVVTSVIMSWQL
CQLPSWSTWAILCGLAFWDLFAVLTPCGPLRCLVNLIHSEGRPMPGLLYEAEIKATHKNSPNYTNGSFYT
AHNLQAAHGAGVYKAPLYTSQTAPIVYAIPVAGASTNLARQQVVFENQLLEFCRDYNSPHSDHVATVAKQ
YLHKQQECWQLLYTKYNVSYIRSNRSYPSYAEVFDGTPMPDLDTQEKETIKLGLGDFIFYSVLVARAAMT
SFGAFIACFLCVIVGLAITMYLLGHFNALPALPISILLGVSAFFWMAQMANDYLAFLVFRGVC

>XP_008864272.1 hypothetical protein H310_02517 [Aphanomycesinvadans]
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MRGTATDVATVATDKTLQERDGLIRNGSMPISNGVPPSAPKYEQVMTPSEGIVPASSDHPGDAPTSAPHV
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GHSLVNALVVIGFVTGLTFFMALLYKFNCMRILVGYIMFSSSAILGFVGGQLVDTVNDTYLHWPIDWVSF
LFIMVNFSFVGVVAIFYQKGVAKWIQNTYLVLVSVILAWQFSMWPEWTTWIFCIMFACYDLCAVLTPCGP
LKVLINLIQEKQAPMPGLLYEAEVRDGVGNAAAHNSSATAPAPRRPPTSSSGPSSAARPPREPRQIDPPP
TAVPPSLDGVDLTAPFDVHDCATEDEFKALLFAFYARYSPDDTWKVDQVAARFFANQPRMWPSLFHKYMV
CSCGTDGVPCSVQIAIDLRNQQQRRDHDDDDDKTIKLGLGDFIFYSVLVGRAAIFDFTTCVICFVCILMG
LGGTLFLLSVLHKALPALPISIFLATAFYFWARYTLTAFCTFVTSVPSAL

>XP_008864273.1 hypothetical protein, variant [Aphanomycesinvadans]
MCGLDGFFNVGRRAAVPVWCVLLSSRCGGAMPMNARLTRQFPWRRASRRRHGQPSSGGEWFGWLARCFRA
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PFDVHDCATEDEFKALLFAFYARYSPDDTWKVDQVAARFFANQPRMWPSLFHKYMVCSCGTDGVPCSVQI
AIDLRNQQQRRDHDDDDDKTIKLGLGDFIFYSVLVGRAAIFDFTTCVICFVCILMGLGGTLFLLSVLHKA
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>XP_008615248.1 hypothetical protein SDRG_11008 [Saprolegniadiclina VS20]
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YLVYLPEDGESDGSLLGHAIVNALAIVGVFVIATFVIVFCYKFQFTNFLVGYMFFSSAVLLGILGGHLAT
VLLERLDVAVDILSWSIVMYNFAIVGVLSIFYQKGLPMSVTQSYLVAVSVIMAWQLSKFPEWTTWALVVV
LAFYDLCAVLTPCGPLKCLVNLIQSEGRPLPGLLYEAEVQTRFDHSEPNYYQHGGPLPAITTTTTASDVC
SFARRRSKPQDEDEESLEKEAQTEPLLPPQPVAKKPKPSVRDRLVAFYTAYNPDALSRIDNILAMYEGRE
GDLWRDLERKYGLDTDDEEDNTIKLGLGDFVFYSVLVSRAALYDVAAMWACAVAILVGLGGTLFLLGIHK
QALPALPISILLGVAVYVWMRCVLFEFMNVTLALGIEM

>XP_008610558.1 hypothetical protein SDRG_06555 [Saprolegniadiclina VS20]
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MNQYLYYKDIDASSATAGTKTIEALTNALVVIFFIAIVTFVVVLLYKVNCMIGLTGYLMLSSSTLLGLVG
SALVQKIFCGLFHWRLEVYTTSLIMYNFAIVGTVSIFYQKGVSPNIGRMYLILTSVIMAWQLCQLPEWST
WAILFALAFWDLFAVLTPCGPLRCLVNLIQSEGRPMPGLLYEAEIHDGHVRKHKSGSTRALPMAPAASSD
MEMVQRRSDDAFLTFESQLRDFCVDVGSPNGHHVRAVALQYVDRQKDCWRMLYTKYNITFVAAHKSYPDV
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>XP_008610969.1 hypothetical protein SDRG_06936 [Saprolegniadiclina VS20]
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GVNSFWAVLWPVCVTMVIASVAVVNFRSAALQASMSTYLVYNEVQGAKTGTVVGHSLVNALVVIGFVTVL
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LLYEAQIRDGVGNRRQQQHQQEDEQQQQQQQQRQQPQPQQRPPQPPAPVKSTPAPPAARQPAAEPSTASY
TIELSTSHADHVVDDTPFESYPCETEAEFEALLGAFYQRYSPNDVWKVEQVAAKFFLKQDRMWPSMFHKY
LVCSCGTASTPCDVQMAIDIRNARREERAAEAEDDNTIKLGLGDFIFYSVLVGRAAMYDFSTFVVCFLCI
LMGLGGTLFLLSVLHKALPALPISIFLSVAFYFWSRATFVDFCNFVTVLPSAL

>XP_002288037.1 presenilin, partial [Thalassiosirapseudonana CCMP1335]
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IDWFTFVFSMFNFAVVGVTSIFYAKGIPPYITQTYLICSSVIIAWQLSHFDTISTWTLLIMLALYDLCAV
LTPVGPLRLLVNLMSDEDSPEMPGLLYEAQIPEGLKRPVMGGRNKDDNGDEGEHDDSSQSPPASMSAERY
QQPSIKENGVPGRTSSDVSASQGDDSAPGVEMSSAVNRTRNDSYDSVTLDQSENNATTTPDLAPAHASSS
AKTAMIPFAIAELFSNTIKLGLGDFIFYSVLVAKSAQYSFACFVSSFLVVLAGLGGTLVLLAVFKHALPA
LPISIFLAVTFYVFTRFIIEPW

>XP_002290889.1 presenilin [Thalassiosirapseudonana CCMP1335]
MILSSLSVIYINTPSTKAAGEAALSSTYQVFTISDDQSKAASLGLSLVNGLVIVSVIGLMTFLIVILYKF
RCMKFLLGYMILATTVLLGFLGSQMFTVAINKYQLPIDKLSFYLTMYNFAIVGTLAVFYQKGVPTIVNQG
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AVRPGRGRRRKWRHQRYSAKTKSRKKRQNTQQSTTSSNNEDEMTQSDNQEQPVIQMMEEVPKECEDDEKG
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TIYCMEPWIQDMWQVPYYF

>XP_002176847.1 predicted protein [Phaeodactylumtricornutum CCAP 1055/1]
MANALIMVSFICALTFVIVLLYHLRFMKCLIGYMIISSGTLLGVLGGNMMQVAVAIYEIPVDKLTFYGFI
YNFCVVGVLAIFFGRGIPKSVTQGYLIATSVILAWHLSYFDDWTTWTLLMMLALYDLCAVLTPCGPLKAL
VNLMSQDDSPDMPGLLFEAELPPEAKRPGGKKSRPDNSAETNSQVTSHQEGSGLVKSTEQQDQAGNDGHN
SIRLGLGDFIFYSVLVAKAAQYSFATFAACLLVILAGLGGTLVLLSVYHSALPALPISIFLGVIFYILTR
WSVEPWIEAILTRPYYV

>XP_002176848.1 predicted protein, partial [Phaeodactylumtricornutum CCAP
1055/1]
DSLLNGIIIVCVVCALTFFIVILYKYRCMKILLGYMILSSMLLLGFLCSIMFEVAIDRYELNVDVLSFYF
FLYNFSVVGTVAIFFGKGIPPFVTQGYLIATSVIVAWQLAFFDAWTAWVLLVLLALYDLFAVLTPCGPLK
ALVNLMQQEDAPDMPGLLYEASGRNSIKLGLGDFIFYSILVSKAAIYSFATFAASSLAILAGLGLTLLLL
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>CBN74004.1 conserved unknown protein [Ectocarpussiliculosus]
MASTAEPIEDSDAGVGAAEEARAPLLEEGHGTLQPPHRRRTAQQGNPDENGQDDGALDQADVAYSANSFM
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FVIVWMYWMRCMRCLVGYMAMSSAVLLGVMGGAVWAAALEVYQLPCDAFTYYGVLWNFAVVGVVAIFYQK
GIPTVVTQAYLVATSIIMAWQLSRFEEWTGWCLLVVLALYDLCAVLTPCGPLKALVNLMQEYEEPMPGLL
YEAELPAGPPRRRRPENDRRAPSQQQARREQPGATGGPQEGDVSSSPRAPVGTATMGGGGLADLAGGGDE
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ASADGSGTRSGREQGKRRLATVRRGIRGGGCLDPEPPGWRTVQAEKKLELFSPVPTSSRAAAAAENDEDE
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>XP_009040959.1 hypothetical protein AURANDRAFT_67233
[Aureococcusanophagefferens]
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LDDGDEEALTFGNEQLTLSGEGNAFGDSTVADVADDYRFPISYVADAILGFGIPPPIRDDARIADILDAD
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FGFAAYAPDPLDKVYEDFGFKPLDETAEPLDPEARKMPEYVQDADRPTYQDGAPETYCDMRSCAGFPGQL
TNSLRPRLRVPLRCASMRARSSVTKAAVASRAPPPKRHGFDAGDASYALASFGAVVRPVSATMLVASFFV
VTVRVETGSLVVYDDDPADSGLERVGKGAANAGVVVCALLAATLAVLALYKFRCTRILRGYMMLSSGLLL
GLLGGVLVLASLEELGLEFADLASFGLCAYNGAVLGVLAIYEPAYLRFPKAATQAALVVVAVVMAWQLSH
YPPVTSWCLLVALAAYDAFAVLAPCGPLRWLVQLMGETGEPLPGLLYEADLDGDGDGAGAGAGAPSSVKL
GLGDFVFYSVLVSNAFSSHAASGAACFVATLLGLGVTFLLLALHRAPLPALPVSIAAGVASYVLVEYAVL
PLAGALRAARAVA

>EWM27520.1 presenilin-like protein [Nannochloropsisgaditana]
MSRTSPSLPDSLPASHVRREPTSTSYEGRSPQLPLADASRAEGLDIEDVLYSANSFWAVLKPVALTMFLA
SLVVVNVAFATEDQGVSVYAIDDGDADGNGGDSNSVKLGKSLVNALTIVGVICGATFVVVLLYKFRCMKC
LFGYMALSSTMLLGLMGGLLWYTALIRWDLPCDYFTFVIVLYNFAFVGVVAIFYQKGIPTWVTQGYLVMI
SVIMAWQLSRFEEWTGWALLVVLALYDLCAVLTPCGPLRYLVGLMQEYNEPMPGLLYEAELPGHARHHHR
IPPSTALRGSERATGALASAGSLDGGCEGDDVRLQAPVGDDGAFSPAMALGSQAHTVHSTSPPSPLDPLL
DGTQSSPGGTHLGQHHPPHPSRSLRRVSRSQGGETLLEDGMGSPVEGGNEHGGESERGERGESGRGHGPS
EGLSSSSHHQGGTPEQERSIKLGLGDFVFYSVLVGKAALYGFATCAACFLVIIAGLGATLVLLSVFRKAL
PALPISIGLGVLFYLLTRVAIIPYIDALVSTPIYV
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>jgi-gw1.9.112.1|Bigelowiella natans|24448|

FPLDIITYFLVIVNFTIGGLVSMSMRTLRRTIFNRAYLVCLCLSLVWPFAEFPEWTVWCTLGLITLYDLLAVLAPCGPLRFIM
ERELSTASSLPGLMYPGEFFRIGLGDFVFYGVLIARSMFVDSNTTIACSIAVVVGLIVTIIITRSIRSLRAIPALPVSVVLGFVF
YAATPLVINP

>ETO23872 peptide: ETO23872 pep:ANNOTATED_protein_coding- Reticulomyxa filose

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YALAAFLAVIVIICIGYRCQRQCQRVFRFCLMADIFLILLIGALILGFILCYNYNWTTDL

ISYLILTWNFGVIGTVTFYCPVPGVVHRMFSVFLNTVMSIIIASTSGWYVIFFVFLMVAI

DVVAMVRAGFGAVFTPFLFPTDVLFVNTTPRIFYEVYGLRVRASDFMFYGLMTGAVQLQL

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ASP

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>XP_653696.1 presenilin 1 peptidase [Entamoebahistolytica HM-1:IMSS]
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AVITPVAITLLLTVIIVKLLERSNDLYSQATSYIFSEGIESSTTIPIWLIAIIVSVIFIIMIVIVTFVFV
LLFYYRCMKLIVGWLLFSVILLLMLFGGSIMKSLLSVFNWPVDWISFAFLLFNFGVLGVISIFYISPMKL
NQFYMIIISVFMASFFTNLPEWTTWTLLIGMACYDLVAVLCPKGPLRILVNLAQERKEPIPALVYSTAVW
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>XP_020435220.1 presenilin family protein [Polysphondylium pallidum PN500]
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EPPCIIDYSDQMVSIAIPVFFTMVVVTAVIRAISVPDNQSSPPPANRIDIPAGFKYDTDPNIQQVFLNTL
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ARKRGESIPALIYNASVFIGMAESESIEMNTTTTATQQQLLQNNTNNSQKPSPFPTPTSIPINLPSQSEM
IEPKSSPNSESMSTGVSTSELSESTDSVTLEKGRGIKLGLGDFVFYSVLVGRAAYKEIILVFICFVAILT
GLFITLLLLAVYKRALPALPIKMKFNKLLLVSILLIVHLFHKTNAFTITRISERLGYTDGGNLFRIESPD
FPVLLPTLKVINGNKEAVFAYRGLVATNIYEWVVPAKPMDLTILKKRGRDNNDQQVRLHIILANTPNPLY
QYDFNYVTPVIDDFKPKSNYLHQAGTSVTISGNYFKLHDYDTDPEVRFDGVQAVVTSASGFKIICVAPTA
VAVNDLVLKVRLATGKEIKADFLFQNIMPIVDDVSPNKAVSQVSKNIKIYGKEDSIIPEADQPATTIAIG
GQPCTNVRFLQKGVISCDTPLLTVAAGLSTPFDITIQIRATVFTHVPKFIVYTPVISNFLPKFSLAAGGT
RVVVSGRHLNDIDAIRIGDSNCVVDYNSYNKDANTEVESISCTAASCDMGGLSEKVNNFNVIVDGQIFNA
GLNPTFTYYVPAIKSIEPESITEAIRKSIVIRANYVNSVTKVTIGGVDHIPSSVLHNNMIIVEINAASYQ
PGSYDVTVVAENILTNKLNLDIGPPDIIDLNIKKGFINSYTPVTFRVRSFPVVPLEDMDTVIAFKIGTQF
CEYLERTSNTEYTCSVPPKGIVSTDLISLVINGVEKITGFGFSYAIPTVTGQTQSSNIPMGGGNLVIDGL
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>XP_020436456.1 presenilin family protein [Polysphondylium pallidum PN500]
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MLVYNESSDDSTGQKIWGSLLNGLVFLVVIVLTTVAFVLLYKYRCLKAIYAWLFLSVGILLASMGSYVFM
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>XP_005841632.1 hypothetical protein GUITHDRAFT_159148 [Guillardia theta
CCMP2712]
MAILVFTVIFFFLYKYRCMKILYGWLGLSVAMLLGFSGGALSYSLIISLSKTQAGWFPSIDVYSFMFLQT
NFAAMGVLVVFWKSPLIVKQVYLIIASCIMAWVLSRYFPDWTTWALLFGLSVYDIFAVLSPCGPLKALVE
LSQDRGDAIPGLVYEAAPPEKRAGRSRQERVKLGLGDFVFYSVLIGRAAIFDFTTVVTCFLAILTGLILT
LFCLAVFRKALPALPFSIFLGIATFLVSKAVLIPFLQPLQMQQVLL

>XP_005788433.1 hypothetical protein EMIHUDRAFT_467266 [Emilianiahuxleyi
CCMP1516]
MQNIELGESSVDVERAAPSQQPASSSADSRALSSQPLSDVAGSSGGGAGSSGGAGAGGECDGGDGDGEYE
LDPAAQVASLLAPVCATMAIVVYLLKTVDAAEQPASGFSEIMVYQEHSSDDAATIAGGVALNALAMVALL
FVAIIAYNLTKLPEWTTWGVLGAVALWDIVAVLTPRGPLKVLVETAEQRNEPIPGLVYEGHGIKLGLGDF
VFYSLLVGRACLSSITAFAACAIAVLAGLCATLALLPVLERVLPALPISVAVGILFYFISSSLIEPLAAF
AADQSLFL

>XP_005790756.1 hypothetical protein EMIHUDRAFT_454700 [Emilianiahuxleyi
CCMP1516]
MAGKASAAVFHFTGPIPLGSFTWASPGTRFPNRVCPSNTPYATLGCGASAARVASLLAPVCATMAIVVYL
LKTVDAAEQPASGFSEIMVYQEHSSDDAATIAGGVALNALAMVALLFVVTSGRVAIIAYNLTKLPEWTTW
GVLGAVALWDIVAVLTPRGPLKVLVETAEQRDEPIPGLVYEGHGIKLGLGDFVFYSLLVGRACLSSITAF
AACAIAVLAGLCATLALLPVLERVLPALPISVAVGILFYFISSSLIEPLAAFAADQSLFL

>KOO22168.1 presenilin family protein [Chrysochromulina sp. CCMP291]
MTADATAEAASQPPDPYKQRPTEVEEFGDPGAQVLSLLKPVSITMALVVFLVHEMSAASQGIAGGFSELM
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VYQESATDSPGTILGGVVLNALVVVFTLFLVTSGLLLLYKCHCYRIIYAWLFFSVSTLLFIFGGYVLREL
LFMHDVPMDSPTFFVCMYNFAAVGTLLVFWTEYGCGPTPPLQLQQAYLIIISALLAWSATRLPEWSTWGL
LGAVALWDLYAVLAPRGPLKMLVEEAERRGDPIPGLVYQGNDIKLGLGDFVFYSVLVGRASMHSSAALLA
CAVAIIAGLCATLALLPILQKVLPALPISIAGGIGVYFLTSATLAPMASEAALSHVFL
>NP_001071096.1 gamma-secretase subunit APH-1A isoform 1 [Homo sapiens]
MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYG
LLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILAD
ALGPGVVGIHGDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWY
EASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCRRQEDSRVMVYSALRIPPED

>NP_666246.1 gamma-secretase subunit APH-1A isoform 2 [Mus musculus]
MGAAVFFGCTFVAFGPAFSLFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYG
LLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILAD
ALGPGVVGIHGDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWY
EASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLSCRRQEDSRVMVYSALRIPPED

>NP_001029842.1 gamma-secretase subunit APH-1A [Bos taurus]
MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYG
LLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILAD
ALGPGVVGIHGDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWY
EASLLPIYAVTISMGLWAFITAGGSFRSIQRSLSCKD

>XP_003228723.1 PREDICTED: gamma-secretase subunit APH-1A [Anolis
carolinensis]
MGAAVFFGCTFIAFGPALALCLLTVAGDPLRVIILVAGAFFWLVSLLLASLIWFISVHLSDREDGRLQHG
LLMFGAAISVLLQEAFRFAYFKLLKKADEGLVTISEDGRSPISIKQMAYVSGLSFGIISGVFSVINILAD
SIGPGTVGIHGDSPHYFITSAFLTMAIVLLHTFWGTIFFDACEKRCYWKLALVVASHLMTSGLTFLNPCY
EASLIPIFMITLSTGVWAFFTAGGSFRRILSCLSCRRKEENHVMVYSALQLPSEN


>NP_001089056.1 aph-1 homolog A, gamma secretase subunit L homeolog [Xenopus
laevis]
MALAVFFGCTFVAFGPALSLFILTIAADPLKVIILVAGSFFWLVSVLLSSLIWFISVQISNKNDANLQYG
LLIFGAAVSVLLQETFRYAYYRLLKKADEGLATISEDGRSPISIQQMAYVSGFSFGIISGVFSVINILAD
AIGPGTVGVHGDSQYYFLTSAFLTMAIVFLHTFWGIVFFAACEKRRPLHIVGVVLSHLVTSGLTFLNPMY
EASLIPIYIITLGMALWAFVAAGGNYRNIRKCLACAR

>XP_018086940.1 PREDICTED: gamma-secretase subunit APH-1A-like isoform X1
[Xenopus laevis]
MALAVFFGCTFVAFGPALSLFILTIAVDPLKVIILVAGSFFWLVSVLLSSLIWFISVQISNKNDANLQYG
LLIFGAAISVLLQETFRYAYYRLLKKADEGLATISEDGRSPISIQQMAYVSGFSFGIISGVFSVINILAD
AIGPGIVGVHGDSQYYFLTSAFLTMAIVFLHTFWGIVFFAACEKRKPLHIVGVVLSHLVTSGLTFLNPMY
EASLIPIYIITLGMALWAFVAAGGNYRNIRKCLACRRQESNQVMVYSALQVPAED



>XP_009428545.1 PREDICTED: gamma-secretase subunit APH-1A isoform X2 [Pan
troglodytes]
MIATTFPHKVTKGNSDGSATEPWNWCLDWSIPGPPPLTGSSHSQDEVKASEGDYNSQQEVFRFAYYKLLK
KADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIHGDSPYYFLTSAFLTA
AIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGS
LRSIQRSLLCRRQEDSRVMVYSALRIPPED

>XP_003969662.1 PREDICTED: gamma-secretase subunit Aph-1b [Takifugu rubripes]
MTAAVFFGCTFIAFGPAISLFVFTIAREPLRVIFLIAGAFFWLVSLLLSSLVWFISVQISNKESASQQKG
LLIFGVVLSVVLQETFRFGYYKLLKKANEGLLTLSQEETMPISIRQLAYVSGLGFGFMSGAFSVVNILAD
SVGPGTVGIHGDSQYYFLSSAFMTMAIILLHMFWGVVFFDACEKQRWWAVAAVVISHLAVSCLTFQNPAY
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VNSLVPTYVILLVMGIWAFYTAGGSLRNLKLCITCKDKDFLLANHRSR

>NP_001025300.1 gamma-secretase subunit APH-1A [Danio rerio]
MTLAVFFGCAFIAFGPAFALFVFTVAKDPLRVIILIAGAFFWLLSLLLSSLVWFIAVKASNSQDPSLPRG
LLIFGVFFSVLLQEVFRFAYYRLLRKATEGLAAISDDASSAISVRQMAYVAGLGFGVMRGAFSMINILSD
SLGPGTVGIFGDSQYYFITAALMTLALTLLHTFWGVLFFEGCEKSSWWVIAVVVSLHLLVAGLSLLNPLY
EGSLPPVYCITLLMGIWAFFSSGGSLQNLSALCTRRKVEAESS

>XP_014349599.1 PREDICTED: gamma-secretase subunit APH-1A [Latimeria
chalumnae]
MGAAVFFGCTFIAFGPAFSLFVITVAGDPLRVIILVAGAFFWLVSLLLSSLIWFISVQLSNPENSSLQYG
LLIFGAAVSVLLQEAFRFAYYRLLKKADEGLAAISEDGKSPISIQQMAYVSGLSFGIISGAFSLINILAD
SIGPGTVGIHGDSPHYFITSAFLTMALVFLHIFWGVIVFNACETQRYWALGTVVVSHMITSGLTFLNPWY
AGSLIPISMLTVSTGIWAFFTAGGSLQNLHRCATCKADMDSQVLVYSALQTPADD

>XP_005987783.1 PREDICTED: gamma-secretase subunit APH-1B [Latimeria
chalumnae]
MTAAVFFGCTFIAFGPALSLFIFTIAKDPLKVIFLIAGAFFWLVSLLLSSLVWFIAVQISDQSNVSVQRG
LLIFGVVFSVLLQEAFRFAYYKLLKKANEGLMTLSQEDTMLISIQQLAYVSGLGFGIMSGAFSVVNILAD
SAGPGTVGIHGDSPYYFLSSAFMTLAVILLHMFWGIVFFDACEKKKWWALTAVVLSHLVVSGLTFLNPQY
EGSLVPAYIIMFVMGTWAFFTVGGSFRNLKLCLMCRDKDFLLANHRPR

>XP_006002709.2 PREDICTED: gamma-secretase subunit Aph-1b-like [Latimeria
chalumnae]
MLYDDAAGYRKSLARWLRDRGVEGAAGRAGREDPGPPGELRLQARAEFGPRVTVALLRPERESPGLSGGP
GAAGSPRVPFGFLPSRPRLRRSRDGFVALVAWGVNDRQAAMTLAVFFGCMCIAFGPAAALFVFTVARDPL
RVILFIAAAFFWLLSLLLSSLVWFIAVKASDARDQRLQKGLLIFGVVFSVLLQELFRLAYYKLLRKAMDG
LVALSEEGQSPVSIRQMAYVTGLGFGIISGTFSMINILADSLGPGTVGIHGDSQYYFITSAFMTLVVILL
NTFWGVVFFHGCERQQWWDVLTVVATHLLVSGLTFLNPLYEGSLIPAYLIMLLMGTWAYFLSGGSVRNLQ
RFLRCKKSERSPTESS



>XP_002607668.1 hypothetical protein BRAFLDRAFT_123275 [Branchiostoma
floridae]
MTVKEFFGCTFIAYGPAFALFIFTIAREPLRIIILIAGCFFWLLSLLFSSVLWNIVWPLKDQLAFGVVFS
VLFQEIFRFFIYKLLRKADEGLQTFSDEPPTASDKHTIAYVAGLGFGLMSGAFSLVNVLAMATGPGTVGI
HGDTPYFFLTSALMTSCFILLHTFWNVIFFWGCDKRNFPAVGFVVGFHMLISCLTLIRPLQPATIIPAYC
ILLVTMAIAYKLVGGSVNNLMAFLTCKRAGYASN

>XP_002736656.1 PREDICTED: gamma-secretase subunit Aph-1b-like [Saccoglossus
kowalevskii]
MTTMSLFGATFIAFGPLIAMFIFTIVKDPLKVIIMIAGSFFWLLSLLLSSLLWVIVSPLQDELAFAVIFS
VIFQELFRLAYYKLLRKADDGMQQFTDVDQDVISKNQTGYVAGVGFALMSSTMSTVNILADHSGPGTVGI
NGDDELFLLTSAFFTCCFTLLHTFWGVIFFYGMDKKKYLMVLGVVVSHLAVSCLTLLNQYDPPMYMASLI
PSYVIMVLMGTWAYYVAGGSFQNVLAFFTCKHGGYDFD

>XP_783542.1 PREDICTED: gamma-secretase subunit Aph-1-like
[Strongylocentrotus purpuratus]
MTLLQLFGSMFIAYGPAFSLFLFTISREPLRIIVMMAGMFFWLCSLLTSSVLWFAVWPLKGQISFGLTFS
ILFQELFRFIYYKILRKAEDGLQQFNQTTPEQAQQQAQNSNGDSTSDKTRHGYAYVAGLGFGTMSGIFSF
INVLADSKGPGTVGIHGDPHDFLITSAFLTSCFILLHIMWNVIFYWGFETRRYWAVLIVVASHFLVSELT
LLNKSQLYSITLPVAYVTLAVMTLFAFFIAGGSSRGIKQAFSLNRSRYAL

>NP_492469.1 Gamma-secretase subunit aph-1 [Caenorhabditis elegans]
MGYLLTIACYIASFSPSIALFCSFIAHDPVRIILFFLGSFFWLVSLLFSSLAWLGLSTVLPDTFLLSLTV
CIIAQELSRVAYFMLLKKAQRGLNKITRQGQISVAPGVSDLHNARHMLALVCGLGMGVISALFYTMNAFA
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IFSGPGTIGLPNALKTGEIDTNRAGKYLPLCYTLSAILLTLFHVTWTIMVWDSCHKIGRIPSAFVPGAAA
VVSHLLVTFLSSLNSRGFHVLVFAVQFLILLICIAYCNVIMGGTISSFVNGIGQSITDAVTLKQVRTLIE
ERKLRTQRQSVPDEPMTERAGTSNTVNA

>NP_608710.1 anterior pharynx defective 1, isoform A [Drosophila
melanogaster]
MTLPEFFGCTFIAFGPPFALFVFTIANDPVRIIILIAAAFFWLLSLLISSLWYALIPLKEFLAFGVVFSV
CFQEAFRYIIYRILRSTEQGLHAVAEDTRVTDNKHILAYVSGLGFGIISGMFALVNVLADMSGPGTMGLK
GGTELFFVTSAAQALSIILLHTFWSVIFFNAFDTNNYIHIGYVVFSHLFVSLITLLNANELYTTTLLINY
LVTILTGVLAFRVAGGTSRSFRKFITCQ

>XP_002167184.1 PREDICTED: gamma-secretase subunit Aph-1-like [Hydra
vulgaris]
MTLESFFGCAFVAFGPALSMFAITVFNDAQQVLVLISSAFFWLLSLLVSAMWWQLFNFTILKNYLVFSMI
FSVIFQEMFRLFLWMVLRRAEEGLIVMNGSYTPLRKIRFHYVSGLGYGLMSGLFAMVNILADITGPGTVG
LFGDNNHFVIVSAFLTNCFVLLHTCWGILFFDAMDAKKWKTVLFVCTSHLAISLLTLLNKHYTYWPSLIT
GYILLVVMGIWSFRVVGGSSNNLTQLFKKKDSS

>XP_003382482.1 PREDICTED: gamma-secretase subunit Aph-1b-like [Amphimedon
queenslandica]
MTVLTAFAYGIYTFGPPVALFFVTVARHPHEIITMILGAFFWLLALLFASLVWIIVIPLKDTPAFTLPIS
VILQEVFRWLYFKLLKKADHLLEIVSEDKSDLRKHKIAYVGGLGFGLIAGIVMFANVLSVASGPGTVRSN
QYFVTVSAFSTQVMIILHICWGVIFFAGLESKNWLYIFAVPISHMFISCLSLLINLANTPAYFLSFGYFL
CVVFVALAFFAAGARPKTLVDFFKR

>XP_647460.1 gamma-secretase subunit Aph-1 [Dictyostelium discoideum AX4]
MTQVLFYGCLFITFSPILAFFFMVIAKNSQLVILTIGGSFFWLVSILIAAIWWYIIPPMREHWWFIISFS
VLFQEIFRYIFFRLYSYGFNDRPSLNQIKETQHQMALDSMRKRKQAQQQKQQPPTNEIESINNEIIDTTN
NNTNNNNNNNNNINDDDNKEITEEEKEKRKIEKQKQREIEINARLETLSARPNHTLSSAAIGVGSGVAYG
FIMFGSILWESTGPGTLFSPACPSVNLFMLSSIITLFMTLLHVVYNVLAFQGYRSKKYHLVAFVIITHFV
TTYLTLLNLPTKTTSCVGSILPIGIITVFSVGFCIFSLLKSDSITKIH

>XP_001693775.1 gamma-secretase accessory subunit [Chlamydomonas reinhardtii]
MPIDFFGLFFLGLGPGIAFFIVLIARKSFLVLLALFSAFLWLVVLLFISAIFRAFVPLSPTIGPYTGMLA
ASVFIEEAVRYGTWWLHRVTLNTLDGMARASGHRFGLLDKLYMAVAWGYGHGACHAVFFFLSLLPLTTGD
GTLYVAECPQMSVFLVGALYSLAFGMILTSLTVIAFDGYMNKNYLVVAAVALLHWGAAFLTLLNFQRDGC
VVSMPVLVALGLLLTGYTVALCWKKGQVAR

>XP_004365170.1 hypothetical protein CAOG_00299 [Capsaspora owczarzaki ATCC
30864]
MSFMVLLGIALIAFSPVLVLVLLTVAQSAELVVLLVCSAFFWLLSILVTSILWFIISPIRDAYVWAIFLA
VALQEVGRWATYRVLKRAEPGLLKVADFANSRLVHHRLAYVSGLGFGIMSALIQFNPVLSVATGPGMLPS
PGCTGNSYYLVSAFTICCFSLLHVFWHVVFSHGMNTNSKVLVAIVPIAHLAASLLTLINESGESCAGALV
PLYIELALFGFICWRIISKRPSREF

>XP_008879360.1 hypothetical protein H310_13585 [Aphanomyces invadans]
MVQWALFWGCMLTGFAPVSFLFLTVVAQRAQLVILSITAAFFYLLGLLVAATLWSVIPPLHDSIHATIPV
AILVQELFRYAFFVVYIRCEQAVKRVTTKQNQLPLNDLTSSFASGVGFALMRALMLYGTVLASSMAGEGA
AFTATCPQIPLVFASALSTLALTLMDIALMILAFEGYRKRSATHIVAVVLLHLGSGLSNMLNLNEVGCTA
SIPLTYVAALLAIFAATVSVKRSSPSFAS

>XP_009492849.1 hypothetical protein H696_00694 [Fonticula alba]
MGAMTFVGCLLTAYSAPAYLTWRHILPQSLRVILMMTGMFIYLLGVFLASLFWFAVVPLRQNLWFSIPFS
VGFQFLARYAYYRLYMRIGNGINAISDNPANKWNGLDYAFVGGHGFGLMSALVMNAAALAESLGPAFVPC
ASCPSLSSFFVYAILALYFWYIHILMMPLCMNAFSRQPPRRAIFRVATLYLTQTGASYATNLFHNAPGLV
AGVGNGGPCSIAFLVMIAIAVGLSFEAWRVLDRATMR
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>OON06716.1 hypothetical protein BSLG_03664 [Batrachochytrium
salamandrivorans]
MTLLSFFGNLFTAYGPALMVMLLYLGPSARLMMMSLSSGFIWLLSILIIAIIAHFLPDLSSNSPQMVVMS
SVIQELGRVAIFYMFKFADPVLVSIASDPTTKFNRVHHAVAAGFGIGMMSGIVSYITPLTESASPGIMNC
NSCPGADVFFIGAITTSLFIFLHISWTVVAFDGWFKGNWFQFVWVLASHIGASMATLWIPSSTSGGCVYS
ILVSLAILASNGGYSFWVVQSKIKTKQS

>CBN76993.1 conserved unknown protein [Ectocarpus siliculosus]
MGLVLVAGCSLIAFGPSIMLWVVVVGKRPALVIIGLVGAFFWLASMAAASVLWTIVPAAQDAWLLSMITG
VVLHGFGRLALAKVYVKTEAVINEAAAHAAPASNAHGSSGRYGGALGAEGSGGVGEGRGERKTGDVPDQP
EESSGLLRLNGVSSSIAAGVGWGLIHAVIMVGTALSKHMGPGAAFSPSCPHVPSVIVSALSAQAFVVLDL
LLMAAAFAAARSGDAGLMSFSFGLHFAAALTTGFNFIEGGCTASLPLLYGVVALAAIALTRYRPLKSAMI
RLRR

>XP_005832892.1 hypothetical protein GUITHDRAFT_152603 [Guillardia theta
CCMP2712]
MKAVMIAACAAAMGLVVAVSMIWMSQSSSAVALEVNMPEENHPPLFDHTFWGVGNEDRIERRANWALRAI
GKMNGTLIEAMIANGTIASESEAIDPALIAEIHQAQHEQDMESDINAPAPERFPFEQDTPAAEEGTEAEG
SEEGAEGEEGATEEGAEGASEGAEGEEGATEETTTEEGGESAAVGPDTEEESAQ

>XP_002181033.1 predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
MTEVSLTIGSALLAFGPFLSLFGLLVYQKAQLVIVVTTAAFFFLLAAVTASLAWTIFHAIGLGGPLAALV
PGVFFQFAFRCGFVALYHNVEQVIQNSMEKSDQRRRDVAHPEQGINSTDAPNARIEQNITQESDQWTEAT
KLRLQLNDASCGVAAGVGFGGMHVIMLYGTLWASQVGDSEGVLYQDACPQVPSLALSAVYAFLFSILDVF
WMLFTFFGMRRRRMFHRGAQGEDEYVSVGAWFGNSRTGGNFALLLCLVTHSFAAVFTTADYFNHGCLISI
PLTSGMVFVTAYLFWAGVGRIYMPPSQIAMVHGEAPAVSFHED

>XP_020437801.1 gamma-secretase subunit Aph-1 [Polysphondylium pallidum
PN500]
MTALLFYGCLFVAFSPSIVFFTMVISRNSQLVIMAIAIGTGSGITYGFVMYGTILWEAQGPGNLFSPACP
TVSLFILSAIYALCFSLLHIAWNITAFQGYRTKNYFNVGVVLLSHFAASYFIEAAMVPTVIGYTFRTMIK
GDSITKIT

>EPZ35700.1 hypothetical protein O9G_004357 [Rozella allomycis CSF55]
MRSKSSTASTLVVSKPLFMDYNKQKLEAVEQKIEALLDDHKLLELKKKKKKRQLDEDGEAELEQLLEKVA
ELKDSAKRWFELVKITTKKDAKMEEETITFGDATAEQIQAVTGVKFPIQDLDEFPSYEDVVPSDDFMAQY
FKNRQVWCINSEASQRTYIDLFLRDVVARLEFQQRLKIFCELSMGVSNEQGSKKIKLSGRCDYTIGHTRP
TALDFGSHPNDIHLLTVEAKEAWINKDCLQCIAEMATVYKSRKDAGKENCTVWGIWTNAYSWQFFLIDND
GQVYRTVMYVLQKDDDIKKIYRFVYHCVKQAYNASPTESCAPTPVIV

>EMS12153.1 hypothetical protein KM1_238650 [Entamoeba histolytica HM-3:IMSS]
MLFCLASIFVASGVSLIFLIYFAMKNSQQLIASIAGSISWLIALSIISLVWLVLPFSHQHYVLIIYSFII
TEVIRFTTLIGIHYFTKKFDEIKLVGFGLGVGAAVCQVLIHNVPYLLLSTGDADLYLLNPIIGNFTVVAF
NGFCYSVYLICSYTSLSLLLHRNKKDIIYSIIFVSLHGAILVAGIMNYYVSVYLGITLMLLIDIITVIMT
FIILYHYRH

>XP_005772054.1 hypothetical protein EMIHUDRAFT_436113 [Emiliania huxleyi
CCMP1516]
MPALLAAAVWAAAFSPAAVLFATVVARRPVLVVLVFLSAFAWLLSISLAAALAAALRAAVPAAGTSVAVV
AAAAALCQEGSRYGMYSAYVLFLRSLRQLGVAVDTGPPAAHLLSAAVANGVGIWAAYTLVLYGDVLWRSS
LPGSLYSDQCEGLSTFAVDAMSACGIGLVNVLLSCIGWVAAYPRRSPALAATTVGLHVAATAATALNAGP
RGLAKDGCSASLPALGGAVLLSAAVAAFSTRDGGAAAARDLGLCSGVVRFKEKDEPLLSSQSRAHRSSAP
LDEPPPEETTRQRLNRPSAAASGD

>NP_112591.2 gamma-secretase subunit APH-1B isoform 1 [Homo sapiens]
MTAAVFFGCAFIAFGPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDGPTQKY
LLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDS
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LGPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKWGILLIVLLTHLLVSAQTFISSYYG
INLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKNFLLYNQRSR

>NP_808251.1 gamma-secretase subunit APH-1B [Mus musculus]
MTAAVFFGCAFIAFGPALALYVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVITDNRDGPVQNY
LLIFGVLLSVCIQELFRLAYYKLLKKASEGLKSINPEETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSNS
LGPGTVGIHGDSPQFFLNSAFMTLVVIMLHVFWGVVFFDGCEKNKWYTLLTVLLTHLVVSTQTFLSPYYE
VNLVTAYIIMVLMGIWAFYVAGGSCRSLKLCLLCQDKDFLLYNQRSR

>NP_080950.1 putative gamma-secretase subunit APH-1C [Mus musculus]
MTLPVFFGCAFIAFGPAFALYLFTIATDPLRVIFLIAGAFFWLVSLLLSSMFWFLVRVITNNRDESVQNY
LLIFGALLSVCIQELFRLAYYKLLKKASEGLKSINPEEDIAPSMRLLAYVSGLGFGIMSGVFSFVNTLSN
SLGPGTVGIHGDSPQFFLNSAFMTLVVIMLHVFWGVVFFDGCEKNKWYTLLTVLLTHLVVSTQTFLSPYY
EVNLVTAYIIMVLMGIWAFYVAGGSCRSLKFCLLCQDKDFLLYNQRSR


>NP_001178332.1 gamma-secretase subunit APH-1B [Bos taurus]
MTAAVFFGCAFIAFGPALALYIFTIVTEPLRIIFLIIGAFFWLVSLLFSSLIWFTTATLIGNKDEPREKY
LLIFGVLISVLIQEMFRFAYYKLLKKASEGLKTINPYEKAPSMRLLAYAFMTLVITLLHVFWGIVFFDGC
EKKKWYTLLVVLLSHLLVSALTLISPHYGLNLVLAYIIMVLMGVWAFFVSGGSCRSLKLCLLCQDKDFLL
FNQRAR

>NP_956409.1 gamma-secretase subunit Aph-1b [Danio rerio]
MTVAVFFGCTFIAFGPAIALFMFTIARDPLRVIFLIAGAFFWLVSLLLSSLVWFITVQISNKNSATQQRG
LLIFGVVLSVLLQEAFRYGYYRLLKKANEGLLALSQEDTMPISMRQLAYVSGLGFGFMSGAFSVVNILSD
SLGPGTVGIHGESQHYFISSAFMTLAIILLHMFWGVVFFEACERQRWWALGAVVASHLVVSCLTFVNPHY
QGSLIPTYIILSVMAVWAYLCAGGSLRNLKLCLTCKDKDFLLANHRPR

>NP_001029842.1 gamma-secretase subunit APH-1A [Bos taurus]
MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYG
LLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILAD
ALGPGVVGIHGDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWY
EASLLPIYAVTISMGLWAFITAGGSFRSIQRSLSCKD

>XP_008123904.1 PREDICTED: gamma-secretase subunit Aph-1b-like [Anolis
carolinensis]
MMHGLVLDPPSQCFCPAVAGLGFGLMSGAFSMINLLADSLGPGTVGIYGDSQLYFLTSAFMTLVLILLHT
FWGIIFFHGCETRRWWEVAAVVISHLIVSCLVSCHEHRTRWSLPLL

>NP_112591.2 gamma-secretase subunit APH-1B isoform 1 [Homo sapiens]
MTAAVFFGCAFIAFGPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDGPTQKY
LLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDS
LGPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKWGILLIVLLTHLLVSAQTFISSYYG
INLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKNFLLYNQRSR

>NP_808251.1 gamma-secretase subunit APH-1B [Mus musculus]
MTAAVFFGCAFIAFGPALALYVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVITDNRDGPVQNY
LLIFGVLLSVCIQELFRLAYYKLLKKASEGLKSINPEETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSNS
LGPGTVGIHGDSPQFFLNSAFMTLVVIMLHVFWGVVFFDGCEKNKWYTLLTVLLTHLVVSTQTFLSPYYE
VNLVTAYIIMVLMGIWAFYVAGGSCRSLKLCLLCQDKDFLLYNQRSR

>NP_080950.1 putative gamma-secretase subunit APH-1C [Mus musculus]
MTLPVFFGCAFIAFGPAFALYLFTIATDPLRVIFLIAGAFFWLVSLLLSSMFWFLVRVITNNRDESVQNY
LLIFGALLSVCIQELFRLAYYKLLKKASEGLKSINPEEDIAPSMRLLAYVSGLGFGIMSGVFSFVNTLSN
SLGPGTVGIHGDSPQFFLNSAFMTLVVIMLHVFWGVVFFDGCEKNKWYTLLTVLLTHLVVSTQTFLSPYY
EVNLVTAYIIMVLMGIWAFYVAGGSCRSLKFCLLCQDKDFLLYNQRSR
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>XP_003969662.1 PREDICTED: gamma-secretase subunit Aph-1b [Takifugu rubripes]
MTAAVFFGCTFIAFGPAISLFVFTIAREPLRVIFLIAGAFFWLVSLLLSSLVWFISVQISNKESASQQKG
LLIFGVVLSVVLQETFRFGYYKLLKKANEGLLTLSQEETMPISIRQLAYVSGLGFGFMSGAFSVVNILAD
SVGPGTVGIHGDSQYYFLSSAFMTMAIILLHMFWGVVFFDACEKQRWWAVAAVVISHLAVSCLTFQNPAY
VNSLVPTYVILLVMGIWAFYTAGGSLRNLKLCITCKDKDFLLANHRSR

>NP_001178332.1 gamma-secretase subunit APH-1B [Bos taurus]
MTAAVFFGCAFIAFGPALALYIFTIVTEPLRIIFLIIGAFFWLVSLLFSSLIWFTTATLIGNKDEPREKY
LLIFGVLISVLIQEMFRFAYYKLLKKASEGLKTINPYEKAPSMRLLAYAFMTLVITLLHVFWGIVFFDGC
EKKKWYTLLVVLLSHLLVSALTLISPHYGLNLVLAYIIMVLMGVWAFFVSGGSCRSLKLCLLCQDKDFLL
FNQRAR

>NP_956409.1 gamma-secretase subunit Aph-1b [Danio rerio]
MTVAVFFGCTFIAFGPAIALFMFTIARDPLRVIFLIAGAFFWLVSLLLSSLVWFITVQISNKNSATQQRG
LLIFGVVLSVLLQEAFRYGYYRLLKKANEGLLALSQEDTMPISMRQLAYVSGLGFGFMSGAFSVVNILSD
SLGPGTVGIHGESQHYFISSAFMTLAIILLHMFWGVVFFEACERQRWWALGAVVASHLVVSCLTFVNPHY
QGSLIPTYIILSVMAVWAYLCAGGSLRNLKLCLTCKDKDFLLANHRPR

>NP_001029842.1 gamma-secretase subunit APH-1A [Bos taurus]
MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYG
LLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILAD
ALGPGVVGIHGDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWY
EASLLPIYAVTISMGLWAFITAGGSFRSIQRSLSCKD

>XP_008123904.1 PREDICTED: gamma-secretase subunit Aph-1b-like [Anolis
carolinensis]
MMHGLVLDPPSQCFCPAVAGLGFGLMSGAFSMINLLADSLGPGTVGIYGDSQLYFLTSAFMTLVLILLHT
FWGIIFFHGCETRRWWEVAAVVISHLIVSCLVSCHEHRTRWSLPLL

>NP_001277113.1 nicastrin isoform 2 [Homo sapiens]
MDFNLILESLCRGNSVERKIYIPLNKTAPCVRLLNATHQIGCQSSISGDTGVIHVVEKEEDLQWVLTDGP
NPPYMVLLESKHFTRDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCR
EIQWNSLGNGLAYEDFSFPIFLLEDENETKVIKQCYQDHNLSQNGSAPTFPLCAMQLFSHMHAVISTATC
MRRSSIQSTFSINPEIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVAATRLDSRSFFWNVAPGAESAVA
SFVTQLAAAEALQKAPDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVAL
RTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQSQPLPPSSLQRFLRARNISGVV
LADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFVTDTAKALADVATVLGRALYELAGGTNFSDT
VQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYIAVSSPTNTTYVVQYALANLTGTVVN
LTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARALSPAFELSQWSSTEYSTWTE
SRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGAVSY

>NP_056146.1 nicastrin isoform 1 precursor [Homo sapiens]
MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQIGCQSSISGDT
GVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFTRDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQC
PNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVIKQCYQDHNLSQNGSAPTF
PLCAMQLFSHMHAVISTATCMRRSSIQSTFSINPEIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVAAT
RLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKAPDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKG
KFPVQLENVDSFVELGQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQSQ
PLPPSSLQRFLRARNISGVVLADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFVTDTAKALADV
ATVLGRALYELAGGTNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYIAVSSP
TNTTYVVQYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARA
LSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAKADVLFIA
PREPGAVSY

>XP_513923.2 PREDICTED: nicastrin [Pan troglodytes]
MATAGGGSVADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQIGCQSSISGDT
GVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFTRDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQC
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PNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVIKQCYQDHNLSQNGSAPTF
PLCAMQLFSHMHAVISTATCMRRSSIQSTFSINPEIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVAAT
RLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKAPDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKG
KFPVQLENVDSFVELGQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRTNQSQ
PLPPSSLQRFLRARNISGVVLADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFVTDTAKALADV
ATVLGRALYELAGGTNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYIAVSSP
TNTTYVVQYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARA
LSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAKADVLFIA
PREPGAVSY

>NP_067620.3 nicastrin precursor [Mus musculus]
MATTRGGSGPDPGSRGLLLLSFSVVLAGLCGGNSVERKIYIPLNKTAPCVRLLNATHQIGCQSSISGDTG
VIHVVEKEEDLKWVLTDGPNPPYMVLLEGKLFTRDVMEKLKGTTSRIAGLAVTLAKPNSTSSFSPSVQCP
NDGFGIYSNSYGPEFAHCKKTLWNELGNGLAYEDFSFPIFLLEDENETKVIKQCYQDHNLGQNGSAPSFP
LCAMQLFSHMHAVISTATCMRRSFIQSTFSINPEIVCDPLSDYNVWSMLKPINTSVGLEPDVRVVVAATR
LDSRSFFWNVAPGAESAVASFVTQLAAAEALHKAPDVTTLSRNVMFVFFQGETFDYIGSSRMVYDMENGK
FPVRLENIDSFVELGQVALRTSLDLWMHTDPMSQKNESVKNQVEDLLATLEKSGAGVPEVVLRRLAQSQA
LPPSSLQRFLRARNISGVVLADHSGSFHNRYYQSIYDTAENINVTYPEWQSPEEDLNFVTDTAKALANVA
TVLARALYELAGGTNFSSSIQADPQTVTRLLYGFLVRANNSWFQSILKHDLRSYLDDRPLQHYIAVSSPT
NTTYVVQYALANLTGKATNLTREQCQDPSKVPNESKDLYEYSWVQGPWNSNRTERLPQCVRSTVRLARAL
SPAFELSQWSSTEYSTWAESRWKDIQARIFLIASKELEFITLIVGFSTLVFSLIVTYCINAKADVLFVAP
REPGAVSY

>NP_001029647.1 nicastrin precursor [Bos taurus]
MATAGGGCVADPGSRSLLRLLSFCVLLAGLCEGNSVERKIYIPLNKTAPCVRLLNATHQIGCQSSISGDT
GVIHVVEKEEDLQWVLTDGPNPPYVVLLEGTLFTRDVMEKLKGRSGRIAGLAVSLAKPSPASGFSPSVQC
PNDGFGVYSNSYGSQFAHCRAFQWNKVGDGLAYEDFSFPIFLLEDENETNVIKQCYRDHNLSPNGSAPAF
PLCAMQLFSHMHAVVSTVTCMRRSLIQSSFSISPEIVCDPLSDYNVWSLLKPINTSGTLEPDDRVVVAAT
RLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKAPDAATLPRNVMFVFFQGETFDYIGSSRMVYDMENG
KFPVQLENIDSFVELGQVALRNSLELWMHTDPMSQKNETVLNQVEVLLSTLEQSGAGVPTVVLRRLNQSQ
PLPPSSLQRFLRARNVSGVVLADHSDSFHNLYYQSIYDTAENINVTYPAGQSPEEDLNFVTDTAKALAGV
ATVLARALYRLAGGASFNDTIQADPHTVTRLLYGFLVRANNSWFQSILRPDLRSYLGDGPLQHYIAVSSP
TNATYVVQYALANLTGKVIDLTREQCQDPSQVPTENKDLYEYTWVQGPLNANETDRLPRCVRSTARLARA
LSPAFELKQWGSTEYSTWTESRWKDIRARIFLIASKELEAEFGSMAELLDVAGKGLNQLSVEANLQEWRL
KPAFSPHCWPRACLQRA

>XP_008121550.1 PREDICTED: nicastrin [Anolis carolinensis]
MAAVEEEGGSAGFLLKGLLLFAVAGGSVRCNSVERKIYIPLNRTATCVRLLNATHQIGCQSSLNGDTGII
HVVEDEEVDLKWVLEEGPHAPYVLLLDGELFTGELMQRLKGSSRISGLAVAIAKPSPSRGFSPGLKCPND
GFGVYNGSYGPEFAHCNVTAWNLLGNGLSYQDFGFPIFLLQDQNETEVIKQCFQTYNRPRGGSAPQYPLC
AMQLSSHMHAVTSTVTCMRRSAIQSTFSLNPEVVCDPLTDFNVWSAVKPINESDKPPPDSIVMAAARIDS
HSFFWNVAPGAESAVGSFVTLLAAAEAIHKAPRAQALPRNILFAFFQGETFDYIGSSRMVYDMQNGKFPI
KLDNIHSFLEISQVALRNGSDLWMHTDPVSQRNQSLQGSIQTMLGALKNMSVGTPLSLREIGLTQPLPPS
SFQRFLRARPIPGVVLADHQTTFHNRYFQSIYDTAENIRLQYPEGLTPEEELNHVTDVAKSLAEVSTVVA
RSLFLLAGGSNADALAMQADPETVTRLLYGFLVKANNSWFQAIVKPEVQAYLGDEPLQYYIAVSSPVNTT
LVVQAVLANLTGTRMNESVTKEQCQNLGRGPNADLYEYYWAQGPLWPSNGSSSGKRSPWCVRSAVRLSVA
SSPAFELQDWASQEFSTWTESRWKELHARIFLVASRQLEMVTLSMGLLILLLSFGATYFINAKADLLFGD
AGGVAY

>NP_001123711.2 nicastrin [Xenopus tropicalis]
MAVRTACCVRMMGEAYRGWRGLGLVVALLAVVCGGNSVERKIYIPLNSTAPCVRLLNATHQVGCQSSKNG
DTGVIHVVEQEDDLQWVLESGPHPPYMVVLEASLLRRDTMQKLKGSTRVSGIAVTFSQTGPAAGFSPDPQ
CPNDGFGLYTSDHGPQFAHCNHTTWNPLGSGISYEDFQFPIFLLREENETEVIKQCYREHNMPQNGSAPQ
YPLCAMQLSSFMYGVTNTVTCMRRNSLQSSFSLSAGVCDTIIVHNVWSSLKPINTTGTVPPEEQIVVAAA
RADSHSFFWNLAPGADSTVSGFVTLLAAAEALHKRNDTQDLPRNIMFVLFQGEVYDYIGSSRMVYDMEKG
RFPVSLGNIHSFVELNQVALRNDSFLWVHTDPISRTNETVNATVQEVVDSLVAASQGSNVTIQEVDRSQP
LPPASLQRFLRVRNIPGVVLTDHRTAYSNRYYHSVYDTADNIHMRYPEGLTKDEELKYVTDTARSLAGVA
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TVLANSLYRLAGGKSTEEIKADPNTVTQMLYGFLKMSNNSWFQSIIRDEWRNVLEATQPQYYMTGTIKST
SREPNSPARLLLAVFANLTGAVVNLTKEECQNPDKIDDPNKELYSYTWVQGPLDGNSTSRLPFCVRSATH
SHVAESPAFELDQWDSTEYSTWTESRWKEIKARIFLVPSHELEVITLVVGIAVLLVSLLTTYFINAKADI
LFTNTQDSDVAY

>NP_001009556.1 nicastrin precursor [Danio rerio]
MENLISINCVQLLITALFYTCISCSSVEQKIYVELNKTAPCVRLLNATHQIGCQSSISGDTGVVHVLESE
SDLDWILSAGPHPPYMVIMETAFFNRSVMLSMKNSSRVAGVAVIISKAGLAEHFSPHTTCPNQNTGVYSA
GSEFANCNGTVWNPLGNGLSYEDFTFPVFALKDENQTQVIRKCYEDHNLRVNGSAPQYPLCAMQLFSHMH
AVTDTVTCMRRTDLQNKFSINPEILCDPLSDYNVWTSIRPLNNSARGHAENESVVIAAVRLDGRSFFWEE
APAAEGTVSAIVTLLAAIHALYPVIQEAPPLRNIFFTFFQGEAFDYIGSSRMVFDMERNQFVMDLDNVHS
MLEIGQVGLRGGRDVWIHSDPVSRRNSSMEKQVSEMIKDVNSSAAGLNINLQEPSVSQPLPPSSFQRFLR
VRPIPGLVLTDHEKAFNNRYYESMYDDAENLNVSYPPNLTPDEQLVYPTDAAKSLAEVATLVARSLYTQA
GGEQNNLSNITADATMVSQLLYGFLVQKNNSWFRSLLPPEITKKGGSSILSSGPPQFYIGLGPRLQSPVH
SVTLFVQYILANLTGNVTNLTESQCQNPKELSGENKDLYSYFWVSGPSSGNSSADPLCVRASVRLSKAVS
PAFELLQYGSSDYSTWTESRWKSIRARIFLVASRELEMLTLGVGVAVLLLSLLVTYFISSKAELLFSSAR
ETPTTTY

>XP_003978286.1 PREDICTED: nicastrin [Takifugu rubripes]
MGGWSNKWAIILVVGCVSIGISSNSVEKKIYVNLNYTIPCVRLLNATHQIGCQSSLSGNVGVLHVLDSED
NLEWVLNSGPNPPYLVILDYLLFTRAVMMKLKNGSNRVAGVAVVAPTINPSTGFSPHTTCPNENTGVYVE
DYDPAFAHCNVTVWNPLGNGLSYEQFNFPIFSLKDDNETQLIRQCYINHNLAVNNNAPQYPLCAMQMYSH
MSAVTDTSTCMRRSDKNSFSISPEMVCDPLGDFNVWAATRPLNVTSKGHKMWESVVIAAARLDSRSFFFD
IAPGGESGVSGFVTLLAAAHALRNITQENHPNRTILYTLFQGETFDYIGSSRMVYDMQNDEFAVDLDNVH
SVLEIGQVGFWSDSKLWLHSDPVSRKNGSINDEVRKLINNVELAANQSAIPVEEPGFSQPLPPSSFQRFL
RAHPIPGVVIEDHRSAFTNRFYESMYDNAEYLKVSYPSNMTQEEQLDFLTDTAKSLTEVATMVARTLYLQ
AGGAETQLGNINADPQIVTRMLYGFLVQSNNSWFQQIIPSEWISHLANKPTNFYVGVTGQSSEATFLVQY
LLANLTGSIVNITQENCQNQREDQDDKESKHIYTYMWVQGTLPLNSTERHGFCVRSTVHLSKAVSPAFHL
QEYNSKDYSTWTESRWKSIKGRIFLVASHDLEMLTLGVGFGVLLTSLLLTYIVSSKADILFGSEREPSNA
TY
>XP_014347416.1 PREDICTED: nicastrin [Latimeria chalumnae]
MATLGMKLPQTGSLISFLGFSYIFLLIGLSSSNSVERKIYIPLNYTAPCVRLLNATHQIGCQSSINGDTG
VIHVVEKEEDLQWVLKDGPNPPYMVLLEGDLFTREVMLKLKDTRRVSGMAVVISKPNPAGGYSPDLRCPN
DGFGAYSPTHSPELAHCNGTVWNPFGNGLSYEDFKFPIFLLKDENETQVIKQCYLEHNIPVNGSAPKFPL
CAMQLFSHMLAVTDTVTCMRRNSIQARFNLNPEMLCDALGDYNVWSVVKPINNSGTAEPEEKFILAATRL
DSRSFFWDIVPAAESTVSGFVTLLAAAQTIQKLPDVQSLKKNIMFVFFQGETFDYIGSSRMVYDMEQGKF
VLNLDNIDSFLELSQVGFSSNFSLWAHSDPVSRRNATINQQVMDLVSVVQNSSAGTNITVAEPPNSQALP
PSSFQRFLRARNIPGVVLTDHKSSFSNRYYQSVYDTAENLLLKYPRELSPEEALNHVTDVAESLTEVATT
VARTLYLLAGGTQRPSMIKADPLTFSGNTPLWYYVSVSSPATPTRLVQYVLANLTGTATDLTKDQCQNPT
KDAGAEKDLYDYIWVQGSSSENSSEPTPFCVETTVRLSKALSPAFELKEWGSTEYSTWTESRWKEIRARI
FLIASKELEIITLIVGLVILVVSLVGIYFINAKVDVLFTSAREPSTVAY

>NP_001161608.1 nicastrin-like protein [Saccoglossus kowalevskii]
MIYVGINYFSPCIRRLNATHQIGCTSAIHGNTGVLHYIDNDASLNWLVNKGPHGPYIPLMTADMFTFKNL
QMLQKSGKINGIMVIHLADQAPPSGGFSPDYQCPNQEYGLYPDSDCSQFPWNPLGSGMMYVDYEYPIFAM
TDENEVRHLIQYYYKENNPVNDTIPEYPLCAVQLSDRMHAAKDTETCMRRSSRYTNMEQFVYCDPLGNQN
VFGFLKPTNKSEPLQNNSLIIAASKLDSDTLFYNMSPVAGAENDVTGFVTLLSVIEALGRLSQETKDNMS
NIMFTFFQGESWDYIGSSRMVYDMQRDSFPNVLVEDLDQPALVSLSHISHFLELRQLGLLNASKLWVHSD
PRSQQVDPRVGPENKKIYDALHAAGVQNDIDVNRIINTALPPASLQQFLKRGNISGVVVTDHEHKFANRF
YQSRFDLPGLLNADYDNQTEEYISPLAEQLNNVSSVIAQALYTLAYPNGTDVMKTDLTVTNQLLYCFMYR
PNCTLLRTVLSSDNARKLANRAYSRYVGVYRADVKNQNSFLVSHLLHYYLGEAIPNVTNKEHCHDLDMKD
AVYAYGYISGVDGNGSCVRSMSYESPALSPAFLLEDWTSTEYSTWTESRWTGYSARAFYVSSKAQQTIIL
SIGVIILLVSLVTVYFIDKKSDILFSQERESSY

>XP_788243.4 PREDICTED: nicastrin isoform X1 [Strongylocentrotus purpuratus]
MTTKLTTSLSKMATIMALETHIRSLIFTLLVVLSVVDHIHGAQQTTSRKTHNMIYYDIKNFGPCVRRFNA
THQIGCTSEFNGNNGVLHLIEKVADLDWLLKNGTYSPYIAVMSPQMFTLDNVQRLLDSKKVNGIMVDHSD
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PMSMINQTTPFSPDKSCPNDNYGMYAGNPEYSNCKKVTWNSVGNGMTFMDLGIPIFALIDPEDVQTVKDC
YEEHNHRDAEDKEQPFPQCAGEMYDFMFGAKDTPTCMWRTQRMTNLESSVYCDPLGDWNVWATLLPTNKS
TPPPDKSMIIAAAQLDIADLFYQALPTQGAENTVSGFVALLAAAQAIGALPLTTKQAMTNIMFTFFQGES
YDYIGSSRMVYDMNKGIFPYKLDDTKTQPSKVNLSTVAAVLEVRQLALSEGDHFYMHIDPLSQSDSTTQQ
GTERLMQLLRSSAVNVTMNNVSLDQPLPPASFQQFLRNGTDIPGVVITDHEREYANKYYNSRLDIAEVWG
INYTQYNSTEFLPIFPVAQTLANLATTIARGLYLYARPGATDADNITADVNLVNDLLYCFNQRPNCSRVR
EAVSPEEWKSISNSTYNYYVGVDSQQSQVTILVGKLLAYYLELDSEPMTQDTAKENCIGEKDDQIFSYDF
MAGADYNGTHGLCVKSSRHLTPAISPAFDSETPDWGSTVYSTWTESQWSSYRIRAFLKPSRSQEVVAFSV
GMIVILISLCGAFFLSKRSDDLFP

>XP_012561598.1 PREDICTED: nicastrin-like [Hydra vulgaris]
MAASSMVLVLLICLNNYVSSSKIEFKIYKSIKSYSPCILLTNATHQVGCTSNMGGNRGILHVVESDDDVD
WLIDKGTNQPYIPLLNSSFFNENVMNKLMNSKKISGVLVVHKSTTVLPTSFSPDSKCPLDQFGAYSNDKE
NGNCQKIKWNPTGNDMSKKYYGIPIFALADGEEINELVKCYQKHNKPKEAEATPSFPLCAIEMKDFMFAS
KDTPTCRRKTEMPNPIQSTYCDPLGDNNIYGSLFPMVDKIENDEVIMAATRLDSTAFFHDFAPAADNGVT
GIVTLLAAAHALGDYKRYIISENITEKLKPIVFTFFNGEVWDYIGSSKMVYDMERDSFPYSLKKSNTIKN
SSKPDDGAWTSKFNLKNIAYFMEITQVGLSDKIYAHTDPVSLKDNVTMNKVEEMLKYTKESFENAFMPFD
VVNQSLKQPLPPASFQRFLRSYKKIAGVVLADHDKEFINKYYNSRFDNLDNVGLYVKSINNVSYLKIHGP
LVKRLTNLSEAVANSLYLLASGGIPPKQRIVVPANLTANLLYCLMISANCPSYKEVLGKKSNPLPNVPMS
RYVSVLQIDNPITQVIHRLLSYYTGEWLEETQCENKAKTSLPYAFSYFAVTGRGSMVCVRSTTYMTPAVS
PAFELQDYHSSEYSTWAESMWNSDIGMQMYLVASPASETGVLFTGIVIFAISFALVYLINRNAEVLFTPT
PSM

>NP_001262932.1 nicastrin, isoform E [Drosophila melanogaster]
MEMRLNAASIWLLILSYGATIAQGERTRDKMYEPIGGASCFRRLNGTHQTGCSSTYSGSVGVLHLINVEA
DLEFLLSSPPSPPYAPMIPPHLFTRNNLMRLKEAGPKNISVVLLINRTNQMKQFSHELNCPNQYSGLNST
SETCDASNPAKNWNPWGTGLLHEDFPFPIYYIADLDQVTKLEKCFQDFNNHNYETHALRSLCAVEVKSFM
SAAVNTEVCMRRTNFINNLGGSKYCDPLEGRNVYATLYPRKPAIENNLETVHTNEKFILVTCRLDTTTMF
DGVGLGAMDSLMGFAVFTHVAYLLKQLLPPQSKDLHNVLFVTFNGESYDYIGSQRFVYDMEKLQFPTEST
GTPPIAFDNIDFMLDIGTLDDISNIKLHALNGTTLAQQILERLNNYAKSPRYGFNLNIQSEMSAHLPPTS
AQSFLRRDPNFNALILNARPTNKYYHSIYDDADNVDFTYANTSKDFTQLTEVNDFKSLNPDSLQMKVRNV
SSIVAMALYQTITGKEYTGTKVANPLMADEFLYCFLQSADCPLFKAASYPGSQLTNLPPMRYISVLGGSQ
ESSGYTYRLLGYLLSQLQPDIHRDNCTDLPLHYFAGFNNIGECRLTTQNYSHALSPAFLIDGYDWSSGMY
STWTESTWSQFSARIFLRPSNVHQVTTLSVGIVVLIISFCLVYIISSRSEVLFEDLPASNAASPRPTAC

>XP_019855736.1 PREDICTED: nicastrin-like [Amphimedon queenslandica]
MRLSFPLTFSLLFLVSLTAGLETVYQKIYTEISGIVPCFRLTNATSQIGCSATPRNVSGRVWFIDTQSSL
DYLISSYHYYKPYIVVLEPELFTSSNVLQLYNSDVVNGIIIRYIQENATIPSDILNFSPAKPCPNNGFGS
SQCRNWNNGTSLNFVNFDKFAIFAITSNESYNSLYECYRDNNLPLNGAPFYENNRADYPLCTAELMADMQ
SVGSTPECFQRGRIWTNLGTAPCDPLGDMNVWGTLFELRQEQNVIMIATKLDSSAFFPYLAYGANNEMAG
IVTLLTIAKLLGDMKRNGSLINTTDSIMFTFFQGESYDYIGSSRMVYDMINNEFPYSYDSSKQQPPRFGL
PKIKAFIELSQVGIQTERETTSPVYYLHHNDQQSLVSALQNGADQYNVSFQSSSSSLPLPPASAQMFLRE
NQSVPVVIVTDFDQQYNNKFFGSRYDILDNLIGPDGILDSSHPLVLQLANLAGSIARAALTLSGPNPLTA
SLPEPDTELIVQLLHCFLQNSDCDFFKGLFSSNVEDVLLPKPMYRYVTVNTVTNTETYVAYQLLSNFTGE
SIPYTGCGSNCTTPDNIETYYLLNQSNCACTKAYTHMHTATSPAFIDGNYSSDYYSTWAESRWTSTAMRI
YIVNSYFVEMWILIAGILLTGILTAVSFQCYRKAKNIFAISASSLNGKTIHPVN

>XP_001748010.1 hypothetical protein [Monosiga brevicollis MX1]
MSANTSLDVGLHLDLCQEIWLRCRAAISAMDLFTALSACHTVHATVALASLLSIWPHEASCRLGSLLVAL
TQCRQPVDALSPLWQAWAVHVSQAQWEQLLTTAEPLVPSGEVAMLILALSRALFEAQRYDLCEVLCALIQ
RPDWRTVLTDPAISLHPHLTRVFAPPVYACSTPQLKSVFVAQPLPEPLWPQLSREHPQHVGMLTPPASLT
ATPAAVDETNSLLPSCHAASTLAGASIYLASPSMPSVEALDLPLSPISRPVHVDIDVLCAHLDVEAAERP
ALPAMAPNQPVVPPSPPSPLPPAVLALDSDSAILAAFIDEPLLPDATLSDARTQLLQNLPQLPVETPPLT
AIGGELFSRGQRQLNRAAPADITARHWRQYLIEEPEINGTLGHTAAWQHRCRWLQNLGVTYRGGALRVLS
SLSWNPVLVLQTMHQSVVAPSSTLPADLMHDSACLLYLPSARLPTVNHEPVLPTLLNVVPSPILVSDESD
QGVVTGEARLTNSQLQGGLELHAGNSDLGGQEIWLPCRQGLSDALVFALETKQITCVMCAEEQFPLDVVV
DEQVGIVLLPDLSPDGRTLSARVLRAAALCTRIVVIVVNREWCVKVTCSDLIERELALAARESPYTQDAW

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CKRDWLAECHESPQWQWLMASGCFNPMAAGTLLLALTLRQLLEAVAVKDFEGVLQSAPGVPLASLKMMRV
LSLVAVLALWATTLRDKVYTKLSGNEGVNSCTRLINVTHEIGCTSPEDGAVGIFFKIESADELDDFRSAT
ESAYIVLLEQNMFAQSAVLRELGRMDKVKGAFVYKGASLPMSGQTNWNPYGGGFAMDSLADSGTIGSHWV
DFGSKAIYYLSDSDRDDVLARYAALNVAGKGKKPNYPVWGARLKNFMYGVRDTDLCLRRKHCDPLSGQNV
WGSTRLVESDSEVILATAQMDAFSFFHDLSYGANSDASAVVSLIGAARLLGLEENYDVVANLQRNIIFNL
FNGESFGYIGSSRLGFDLSRAPHWPSVDQSLSFENIKGYLELSQVLEGDSLHAHSYKSNADTANIVAKLQ
AAAAGSSTTVVDDTASELPPASLRGFLNEWRDTTKQDAFPGVVVTAYDSTGFANKYHGSHLDDGIATSST
SDETRARLCDTAVLTAKTLVAMANNTDVASVSLPVDSADSAFCDFLQEMFDCVARNQTCELARKAIGQSG
ATADMPLSRYIGVTRSSTVLNRGVYFFFNMLSEALAKDKNVSLGVNATCAPNNKVNEFQTVDWTDGRCMN
TTAYVSYIMSPAFESYYKLKSEGSNLTIHRDPRWSTWTESVWGAISADMFLMEDPAVQRTHRLPTGATTT
MPSAENMFSELQHHPRATQHAGPPPAADVPHNGPQIMERMAMAARDYNAAEPQGRDLLRFLNSSFLPMPT
SGGFNTALLKLDMQAGPGLSAPIELPPGSMVTVATQTDYRESETQTDPYTPDYVVRPGSAPEVLTLATLA
HGVGLPAGLAEVEMIERARARRAWEATLPPVEDASRAIERSRAIEARELEELKFREEEIQRVQDERLQVL
EQLIVELESNKQQDREDKLNRHYQQRQIERNRMLARSERQAVKDIRKLTKARQNIEGNLKRRDIVEQYSN
PASEEFAPTRTLGGGVHDQHANRYRVDSKHVSSYQGLLDLEASLPKSVTTPRARAAKGTNTSATGRRGGM
ASASRRRMQDTLRQLDETMSMARTGTLPILPPIRCVERIEKAKSILRGRAMQNEMYEQKEQRRDLIEELR
STHALQAAQQAVKEKEREQLQARREADARETRRQATITAAVNATQSAHLGNTLDFLSKELVRLQEEHRIH
AFAVMAERERRMREAEEAGQRQAEEHRRAQGDEIFRQMMQVHNGTVDSYLESILLAAQEDVADEQAREFV
REQARRIDAAAAEAHASGYDETDLGAQAIASELVTSFLLPEVEREALRGSLQREQRKLLQGAHEAVFAKT
QEVEGQRRWTGSRAATASGSRPRTASAQTQSRPHTTPAIAEHTGLEEDNN

>XP_002305230.2 nicastrin-related family protein [Populus trichocarpa]
MATDLPCLLPFLLFLFISHFPLSFSGSVNSMESVPDLTKSMYVDFDGYPCVRLLNLTGEIGCSNPGRDKV
VAPVVRYKNVNEVSKPSAVLVSLDEFLELIGRISNDSSFAKNIGGVLVEQGMDSQIKLKGFSPDQKFPGA
EYAPYKSINYEWNPIGSGMMWKAYSFPVFLLTEGGAQLVQEVAMNNEKKRNDYTADVVEFDSVMQTTKSG
THDSESCLQEQTCFPLGGYSVWSSLPPINNSSTNHSKPIILTVASMDSASFFRDKNLGAESPISGLIALL
AAVDSLSHVNGLDDLGKQLVFSVFTGEAWGYLGSRRFLFELDLQSEAVNGLNSSLIETVIEIGSVGKGFS
QGNSTFFAHTAAVSLATNETLNALKHARDSLENITVSSASTLNPGIPPSSLMAFLKKNPSTSGMVLEDFD
TSFSDKFYHSHLDDMSNINSSAIVAAASLVARTLYILASDDKSLSSTALDAINVNASLVEELMSCLLDCE
PGLSCELVKSYIVPTNQCPNHYVGVILGEPSSNPYLGYVDDVSRFMWNFLADRTSSSMEDASSDCSKECS
NKGGVCIKAEVDGKGVCAISTTRYVPAYSTRLNYESGTWRVLPSDSSDPMGMVDPVWTESNWDTIRLRVY
TVQDAAFDRLVLLAGITITVMAYLAIVLTRAYIAKALKRD

>XP_637065.2 hypothetical protein DDB_G0287801 [Dictyostelium discoideum AX4]
MKIKNYFIIVFIIIVLSTDVISSQSSIEDKMYTSLNSYPCTRIMTLNGQIGCSSSHGGDSGILYLIDSDE
SYHNYFSYNQQKDIIVVFDSNYFNKTLVLEMYSKKKMNGALVLTDIGKTYPYSPEDQYPIKQFGLYPDSN
LNWNPNGDGFTYMNFPFPMFALELKTSIIIRNLSTINRDGKYPAYGAELDSFMQGAINAETCLRRGFCEP
VGGQSIWSSFSEVIDQSKPIILVMLPIDATAFFRDLATGTDQSGYALTVLLSMLNTLQGVDKTKWDKEVI
FAMWNSERWGYVGSTNFVNDLLNFNCTSLDSNNQNSCSSPPMLDLTFEQIKFENIYAIIEFNQIGRPVNS
GKKTPNKLDIYNLVFHPNGGAGANQLMDVFSQSTQSYENSTIQFQKTTQNELPPCSSMSFIKEINKKSAP
NFIGTLVITDHDYQYNNPYFGDEQDNSGNINTTTSTLFDMVQVFSKSIDLLAGGNGTVKVDDLFIREINV
CLTQSITCNWVTKLMSTFPYNPIPNFYSGVYGVSPVNHITPIETRFIFRMATYLTQHRTNATNCTSDNDC
DTSSSICVNKVCLYSNTHYHNAISLAFSFDNSKSSWTIVNTSYPVFVESNWDYTTVRLFQVGSYANEIWF
LVSGLIELLLSVGIIFYIKKYLSKRYKLL

>XP_001701591.1 nicastrin [Chlamydomonas reinhardtii]
MRLALKLLAGALLVAVLSRSCNANSEARGWSQLSEVKAAMYEDMKYTRACVKLLNNSGPQGCEAADMKLI
TGPLVHYSDLTHLAGQKVVLVPAEDASKLFTQFLRDSSLRKDVIGILVDPTTGRPPGDSAAPPFPGAEFA
PYSARDYVWNPYGAGLTQQWFGIPIYMLTETLANETGWRADYNAQNDLKGGKHVARMQLPMQAVGNSSQC
ISDQHCLPVGGYGVWSAVPVLPDPLYVNVSARPITLVTASMDSNSLFHDLTKGANTAMSGLIAGLVAMSL
LVRANHTATYARQLAFAALPGEAFGYMGSKRLLYEMQLNSTFVRGLSLDLIDQVIDVNQVGAAFNASTNT
SSFYLHTQLAGGFGDASKLVGAAQSAATAEEPLVQAAAASPSNPGIPPSPLMSFLRVKPGTAGMVLADFD
SRFNSPYYQSEYDDGFNITVQALVDASVLLARTLHSLAGSPETPALEVNRTATRFLVAELAVCLILEDPG
MRCPLASLLMSPADCGRDPSSNADVDVYYDGSTSAAVKGYPGVLRWVDVDPRASRSKPNLARFVYNYLGN
LTAAPLPADRSNSSWEGAPCDTTVNICPAPLACIGWRYGTKDPAGMGRCRNTTTLYFPAYSTRLWYGNRQ
GSWRWWVDDAAAVWERNYSWPTDPMWTESDWPARTPTLTIFQEEAEAVRFWEGDEGRGGEEPLTSSGAVR
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PVADEVIASASLQ


>XP_004342890.1 hypothetical protein CAOG_07817 [Capsaspora owczarzaki ATCC
30864]
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GEVGCASSLSGNVGVLYSIQSDADLSFFIHSAERSPYSVVTTPAYFNLSIIEQLEATGKMNGLIILSDAT
RPTQSSHAPKCPNCKHGLYANTDAANYAWNPEGSGLTHRRFQYPIYWLGSTSAETIRNRALSNAPKSGVE
PDYPLWAVEMNSFMYAGGDSNICLRRGSTWCEPLGSQSIWGSTRPIRSGDTYVLATAAIDALSLFHKQSF
GAEADAAAVVALLAAADALAKEPTTITLPHNIMFMLLNGEKFDYTGSSAIANQIATGNFPSASKAFGFDD
IKAVLDVEQIGLLDSATGPIYLHIDSNSTDPVAVANVASIVNAQVTATAGFAANIINNTATGLPPASLQA
FLKESRGIPGVVVTDHGLTFNNKLYGTPFDDATLVNASDAATVNNICNVALAIANSLYALASDNSGSVPA
MTVNCTFVQSLLTCLTVNEKCALFQQTGNNLPSNLPSRYVSVFRTNTIFAFIYALRDVLAVAVASDSQPS
LSQKACNNAKLTYIAPGLCLNTTVAFIDALSPGFDFDNFAIKNQRWNLWAESVWGSDPSMNLFLRASYSS
EVVIIVVGFIILGISIAVVWPVRQLIHKKYE

>OON03627.1 hypothetical protein BSLG_06104 [Batrachochytrium
salamandrivorans]
MTIVMDIAGRREPGHPLEETHAPIGISDHCLSGLLSMLWPTTTTTATTTYTQLSVLGSKSLSLVKRASMP
LLELLKLLKLLPQLLLQSFIMNTQSRLIETIMYAVLLTAACTFPVVYAQTSANRQNYFLESSMYQGFSSA
ACTRLHTAQGTIGCSALKLVSGTLYRVSSVSDVQAFAANAPSGVMYVVVMPGSLMTIDVINTLRGSGKLT
GIFTITDSIHPPGYSPEMSCPNCAYGLYANQPTRYLWNPSGNSLVNSDFDFPIFGIYPGDPTSIQTINAI
NEVLDFNAARKYINYPLYAMELDSRMSSAIDSSTCLRRKRCQPLGGYSVWSTFSSGISANDQKPIVFVAS
KIDSTALLHDYGFGAGSRSGVVAMLAVVETLSRVQGGMASLPKTVVFSAFEAESWAFAGSQRMVQDMSQP
LVCKDTSGKPTSGCPVIGAQCNSPCLISTDFTKLNIDLIESFIEFDSIGDIHHPAGATSPHYLHVDTLNP
QTSALVDSFKSAASPAPSTPRTSQPINVTIDVAATASNTNNRLPPSSAMAFLARRGDIPAMVVTDYLSQF
SNPYYHSQFDDGSTWTADHVAAICGVVGTMSRGIYARAGGQTTNAASIIPNCTLVGQLMECFTRNVSCPL
FQQLKVDSQSAQFSGYSSVYIPTSISPMTMLSNLLMINWTASEVVGNCSDTRCTKLPSDYRCSGNRCMLS
MTRLHRAFGTGLEASDSGIYTVVDPKRGTWTESSWDTTRLRVFKVSSLAYQGMQLGVGLALTIGTGILTW
YLRSKFRMHIKKDRS

>XP_020431244.1 nicastrin [Polysphondylium pallidum PN500]
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PCSRLLDVNGQFGCTSKEFGNSGLVHLVDSDASLADLPSHAIAVLDANFFNGTIVNRIISKVEGIVVLTD
TKQNYRYSPDLPVPNAPYGLYPKPTFSFNSAGDSLSYQSFDKPFFVLDKNNSAIARSYGNWNRDGNLPQY
GCHLESFMHAAINAQTCLRRSFCVPVGGKSSWSTFSPEFDQSSTIIMVSVPLDATAFFHDLAYGSQTSAY
GQTVLLGIVEALSRVANQTSTWKYTVIFAAYDGERWGYLGSTKLVDDIINTECKKYTSDGYGCLDPRILD
VTFMNISFTKIKFIVELNQIGNPLKVDGSGHYVYALNSLKSNANNPDQQLLYQTFADVAKELAGKVKIST
QPVDQDEVPEIPPSSSMAYLKQNPNIPTIIVTDHFGVYTNNYFSSHNDDYTNINANIIVDAVTYFATVID
RLAGGNNTIVQNSLFVEDMLDCLTKNFTCKYAQQFAGSSQPVPSFYTSVYGYGPDNQYLTIQSLFVHSVM
AYFAASNRTGIMCDESNSCPESAQACIGGTCVITNSHFHDAISLGFTFDEPSYSWVIGNTSYPTYVESNW
NSIVINFYQQDSHTTEALFLVFGIIEMFVVIAIIFVSKRYLSKRYKLLMGGFENN

>XP_637065.2 hypothetical protein DDB_G0287801 [Dictyostelium discoideum AX4]
MKIKNYFIIVFIIIVLSTDVISSQSSIEDKMYTSLNSYPCTRIMTLNGQIGCSSSHGGDSGILYLIDSDE
SYHNYFSYNQQKDIIVVFDSNYFNKTLVLEMYSKKKMNGALVLTDIGKTYPYSPEDQYPIKQFGLYPDSN
LNWNPNGDGFTYMNFPFPMFALELKTSIIIRNLSTINRDGKYPAYGAELDSFMQGAINAETCLRRGFCEP
VGGQSIWSSFSEVIDQSKPIILVMLPIDATAFFRDLATGTDQSGYALTVLLSMLNTLQGVDKTKWDKEVI
FAMWNSERWGYVGSTNFVNDLLNFNCTSLDSNNQNSCSSPPMLDLTFEQIKFENIYAIIEFNQIGRPVNS
GKKTPNKLDIYNLVFHPNGGAGANQLMDVFSQSTQSYENSTIQFQKTTQNELPPCSSMSFIKEINKKSAP
NFIGTLVITDHDYQYNNPYFGDEQDNSGNINTTTSTLFDMVQVFSKSIDLLAGGNGTVKVDDLFIREINV
CLTQSITCNWVTKLMSTFPYNPIPNFYSGVYGVSPVNHITPIETRFIFRMATYLTQHRTNATNCTSDNDC
DTSSSICVNKVCLYSNTHYHNAISLAFSFDNSKSSWTIVNTSYPVFVESNWDYTTVRLFQVGSYANEIWF
LVSGLIELLLSVGIIFYIKKYLSKRYKLL

>OON03628.1 hypothetical protein, variant [Batrachochytrium salamandrivorans]
MTIVMDIAGRREPGHPLEETHAPIGISDHCLSGLLSMLWPTTTTTATTTYTQLSVLGSKSLSLVKRASMP
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LLELLKLLKLLPQLLLQSFIMNTQSRLIETIMYAVLLTAACTFPVVYAQTSANRQNYFLESSMYQGFSSA
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GIFTITDSIHPPGYSPEMSCPNCAYGLYANQPTRYLWNPSGNSLVNSDFDFPIFGIYPGDPTSIQTINAI
NEVLDFNAARKYINYPLYAMELDSRMSSAIDSSTCLRRKRCQPLGGYSVWSTFSSGISANDQKPIVFVAS
KIDSTALLHDYGFGAGSRSGVVAMLAVVETLSRVQGGMASLPKTVVFSAFEAESWAFAGSQRMVQDMSQP
LVCKDTSGKPTSGCPVIGAQCNSPCLISTDFTKLNIDLIESFIEFDSIGDIHHPAGATSPHYLHVDTLNP
QTSALVDSFKSAASPAPSTPRTSQPINVTIDVAATASNTNNRLPPSSAMAFLARRGDIPAMVVTDYLSQF
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GCYLC

>KOO29656.1 nicastrin [Chrysochromulina sp. CCMP291]
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GTGFSHERFPFAIVLLGLVESAAVLMHGVHAGTSVGSGNRPLVELRYPMSARGDAPSCLASETCLPLGGQ
SVWGSLEPRTAPDTELLRLGKPAVALTASLDATGFFHETAPGANAAVASLVAVLAAVDAIVSDPALASQL
GSLPNTALFFLFTGEAWGELGSRRLLTDAPFKRDLRFLELRERRLTTLVHVGPIGAREAGEELFIHTSAA
ATNGATNGAAEALRAAASAAPVLSAPSLQVRDATGARGLPPGAARSFVDPKLQLPNSALPSVATLADFED
AYHGGGRYGSHFDTIDGLNVSLVCAAATVAGPGIERDPSTGRWRVTDPDEPLWTESNWPNEMYAFLYPHG
APSTVEGLALLGVGALGALLTYVATHVSRYQYKNAYKRL

>XP_005827562.1 hypothetical protein GUITHDRAFT_113369 [Guillardia theta
CCMP2712]
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LKKSSRCSGILLARSDDLPTSGVFSPANPMRYCKCEEQKAPSGCSGKWNVPGNSLSEQSFNFPIIAVNSS
RTAQLKGLIAQVKPWMPALVVRMNFYMDVFQGFRLEQESWWELQQVDSCCPNCRPNCAGSCCDFGFECTS
SKTHPVSWAQPTCARQKEPTSYDCIGKQTCLPLGGYNIWSVDSPSFPPPPSQGIIVAAAAMDSSAFFHDL
AEGASSQGSAVVALIAAADALKDVRRKMQELAGTPIVFALLQGEQWDHIGSRKLLSDIANFSCRKIKTSP
SNGLPNDVCVDPPMLSPEIVQLRDNPIDFVLEVDQLTSAGGELGESQGLFFHTGCSPSDSSVKARELVLK
QASVPGVAGVASPDEGLPFPPSTIVGSVLEEATGQQEARKLAKAPKGRALLAGYSSHFTNPFYQSRFDKI
QSGGAELRAEGLCRAASRLSMVLYSLSTGAEAPALHANCTLVRELAGKIMWKHSEQEAPSSSYTSVYQPP
TLRGPSERERFLFEQLAMATSAPGEVNETSKEASACDCCDPSGSCQPVKHFRCLQGKCVRSFAFFQDALP
LGVAWDVNQSQFVLSQGDRNMSHVVWTESNWQLNLGAMVYLEEETTVEQAVFACGLVLCACTFLLVSSMS
KYYERRFKHN

>CBJ31078.1 conserved unknown protein [Ectocarpus siliculosus]
MLAAVSWCWTASAGPRRRKPVAAAGGPAAGKNPSSAAALLLACIALLSTRSEAWTGGFSPGLGHAPCVRL
FHASGDVGCRTRGREGVAGPLFLVDSERALQDIEARGLSSFRKDAQREEEGLLPQEGSAEAMEGMGDGLM
AVLPDAFFNRTILHRLSATGLLGGVLVLESAGGGRAAASPAHSLAQGNVVRSNPDVKTPQLTCSAFKELS
CKAGRLSFFERTEEGDSTPSAAFDVDASYPWNSGGDGLLMESFDFPMVLVAGGSSDDVRARAVSNGNVGG
PSWRYPLHKARMAFYFGGSAMDLNSQECLGWTDINGDRSPQCKPLGGQSSWASVGGAGLGGRQTVLAVSG
MDSTSMFHDRAPGANSAVSGLVALLSAAESLGTAGRSGSVDFSALPRQIVFVAFQGEAYGFTGSRRFVQD
WRGEGISCLNRVDPTVSPTGQEACLDPLYPSLEFQKLGKPAHVVSVDQVGCLPESTLWVHPSPGASSVDT
GVVSELSPGGGIVLTNSTRTELPPSPLTAFVKADPEQSGFVLCGYDETFSCPHYHDHADARDTVDAGSVA
AAAKVLAKATLVLAGGTESSAEALQVNGTLVETLLDCLLEDWSCDTVKEYVVGELANNAERLGFRVSVEA
PFPPTLYTGPLEFHYGGGMATVRHTKGDGSWRLHPSWTEPFDPEHDKIQLVPNLLETFCRAFLSEQAGAA
HAGRYGEAECQVSGDCPLEQCQESPSTSADNNHDDDANKSRDGLEGGRVRPGKGSEERSGNVLRSASSSS
SSSSSVTTSSSSAVQRPECVRGRCGCPAGFHHIALDVGLEREEELDQYRVVDGAVGQGAPLWTEPNWRGI
GAEVYLDPGVTAGKVALGVGAAVTVAAGVGSWVLLRSLDKRKLL

>EWM23993.1 nicastrin [Nannochloropsis gaditana]
MLPRARQASIALTLLVGVIIPFSALTEYDGIHLGKGLLKEVTQAPCVRLFSSQGTVGCRTRSREGATAPL
YYLSGFGEDDQHEYMNLEEGVAVVMPASMLNSTVLEFLKAQSPARTRGVIVLEESKDMAADFERDSVSPD
VSTPQGDGTPSAAFTVGPDHAWNPRGSGLLNQKHDFPVVLASVDGDSTGVGAAQVKAWAQHNGGLRRAGP
LPRYKAKFDFYFGPDSPSTRAESDLTSADCLSWRDVAGNPAPQCLPIGGQSVWGTFGGRTGLQTKPSVLL
TTAMDGLSFFHERTPAANEAVASILTLLAATSALKNASRAGALDLDAAPYNLAVAFFQADEWGFAGSRRF
ARDISPGGVDCPATVPDNSSRDGSGACVGSDGVYPSMAFKDLAEKGFVHVLAVDQVGVLGTGGQAGSLPL
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RYHSHEDTAAVLDPTALSSVAALVARAFWKLAAGPGEGAASAAELEAIGVEPAFVSDLLDCLTRDWDCPA
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VFPVGAHDKAYVVPKPLEAFLRAWLGHTLGQGGEDAPVACQGPSDCSDLTCDAGLSTRECVLDACVCRTA
AFYHTALDPGLAPLPEPGLFAVSDPAAPNWAEPNWEDIGLAVFPDAGSRMEATALGVGVGVAALSVVGAL
VLQRSLIKHHYFD

>XP_008876423.1 hypothetical protein H310_11498 [Aphanomyces invadans]
MKLCGVPTLPVSVVMVTMLGLLETSRGVNAGAVTSGAPQNPVVPGGECVRMFHSKGNVGCFSLDKDGSRA
RLVSVSTASALNRDTLKENSIVLLPDSLFTSENVAKLNGEFIKGLLVYPTPTSPFNYDSTHPQGKGTVDG
VLNPVFGDYEWNPLGRDIMSSSLPYPVLEVESEAKAKEFLDLARKNEHAPAEATFGVVYRGAMDYYFGPA
KMDSITCLNFRNIYGDRSPKCLPVGGQSAWGVKGDLSSPRPAIVAMASMDTTSFSHVYAPGANAGASGLV
ALLAAADALKTIPSSALKKNIVFSAFQGESYGFVGSRRFLADLKQAKASPHGVCASPITTPTPFGSSHCA
SPVRSSLAFTSLSLDSIDLAVHVDQVAQGNAWFVHPNPNAASKAVMDALTNAPSAKSRVQVSTATAALPP
GPLVSFLNDQEFGNASLASAVLSGYDTAFSSTYHSRRDTNTSNADAAENIATAAQVLAEALFASSAAVAG
SELLASIQVNATLVRALWTCITTQWNCPLMQAMSKPAVASMNEYLAFTATSSPSFVEPVRLYTSVYSDNR
MPTVVVNKSYVVADLRDMKWDNAFKLHLYPNAYETFTRAFLASALRDVDPHAPACASNKDCNMDGGDECV
YPGVCSRRRAYFHDALSPGLKREPTVGHYTVVNASMPLWTEPNWMTLGTFVYPDPGTTIGYVALGTGAVS
IVVGYVVARRFVAHFRKQKLL

>XP_001312893.1 hypothetical protein [Trichomonas vaginalis G3]
MFIFACLYLTKEYSLSFPNEFNFRMPTTDGWMGPKTRWQGNNGYLVKITTAEELTNHIANKHYYSETLLL
PTSLVTDEILTNLENNFKPIKYLRAIIMYPTGDANVSSAPRYPNQKYSYHKEDYDWNPYGSGSDRKQHSF
DIYQITSEEYLAAFLALMNAFPEESGVYINNRQYSRGNFKKSYTTKKSGNPLADPVSGVNIYGSFDANFT
GPAVWAIASIDSFGLTPYNHVGADRSMSGFIGLLAALRALQNLTWSEATKPLRYIFFDTEEFAYSGSERF
LYDIANFKCQTPDSDNSDACSIPYRAYMGFKNITLDDFDTVIELQSIGLYNDSSKLFAHSEKEVNAEFLS
NVTSVNYSGVSISQADSDLPGVPPSSMNSFLKYKNRTFNHVVLTGFNRQYVNKNIGMPDDSYNNIDIDYM
TKAATNTARLLAKLCFPDLPEANLSSIVADKDMINQTLYGFAVNPNASSIFLHFWPLSEKRPQLSTVPGS
IYTGVSIGYSYRTKHQFIKMFMDETKAAKYVDVDCSDSEKVNCSKIDPELKCGWNNRCVKSNVEFSPALY
PGLEFDYDDYKYNVSTWDNPYFAETRWNNQMLYYVTLGQAYIGRYAIFVGVLLWLILAIGGAKLWSWNLT
KLSK

>XP_002290995.1 predicted protein [Thalassiosira pseudonana CCMP1335]
MVGRILHWSSVVENANNDDDAAENNGNRRLANPEMAPYVTILNESEYTSNTIAQLVLYSSSYVASDAYGS
VEVGGPLRGILVLADGDGSSSSDGNVNNGNNNSNGYTSPESPTPQGDNTPMSSLSIGSSYEWNVNGNGLT
MTDMYGIPTVYVYDAATAEYLREVGTEQSASLQSSSNSNNEDDTTNAVYPSILSEFNYYMGPQVTESGET
VTSKECLEWKNVDGTWSPKCLPLGGNSVWSVAGSPVSLDYSGGEGNNNSKNKPVVMLSTNIDTTSAFHDI
SPGANTAASNILTLLLSAQLVGSITDEVLDQLPGKIAFGFFQGESYGYLGSRRFLEDVVQGFNCQNGNEG
VASVYKRKDEKGIARACLHPLRADLTFQNINNLRGMIAVDQVGNLGGGKTLYVHGGEKSATNAQDGFAGF
LAEVMVELSTDDYSVQASSVGEQDGVNPLPPTPLTSLVQVSEGALGGIVLTGYDNAFVDNSLYHSHLDSV
SKLQMIDSDAIASAATVLARSAVAAAYQNENEEVDAATAAAYALELLPNAASSSSDTFQSLYNCLFQDGN
CETLLTYGNVERNNDAKRTGIDLGLGQPLKTPPNYYVSIYDGDNGQAFVRASEVIYGSLVAEESGENANI
KPYGQDAGDVFLLRPSLLEMSIAGLLNAFLGRGSFAPGDDGNTASPNLLKCESTADCSSVSYCSTSSSSL
AVPTCAGGMCVCGSRSHYHPALDEAIAPATNKRTSYFTVQDDDGGISALYTEPFWSSSVGVRVYNDAGNT
PGVWASSIGSVFAVICLTFVFRLKTKLIKEKVY

>ETO25807.1 hypothetical protein RFI_11329, partial [Reticulomyxa filosa]
KFPYRYVEFTYEMFAKNTSLDCLQDDTCLPVGGYSVWTSFEKVSKKNPNQTSGENAKKGYVFGITSMDTT
AMFHQNVCRGSDANQSGLVALLAALSALSGVKEIIYKLSKQIMIGVFQGEAYDFVGSRKFVHDITHPFNC
TKWMTSYSDGCWQPFVSSSDFTNIEFNNIGTVIELQQIGIKADSKPRQLFAHYERNVSSTTNLTTQALIA
NISRIAAQVANESNQQFVVSPANDPSLPGTPPSSFWSFLQANTNITGVVLTDFQTNYSNQWFHSVFDSIY
QIDADQVCMTATLFARTLLTAADTDGLLNDSFLQKNVNADCILVETLINCLMEDMTCNLVASIAPSATDP
TPSHYTSVYQIVEDQSIIGTPQFVFRYLANLTRIGGLHGSCSEQNDCFGQHQVCAGTYDGSFCVNSSTYY
HAAVDPQLTFNYDSQLFEVPNISNFTGLLWTESTWPSKIGTRFYVKESDDAVTTMIVCGSVAFVLSLAVT
WKLQSYCQTRFKKPSTTVLCFVASFALLIIGTQSYLKWFAHQLFFRLFLFKNTTLLLRFATTKKKIVVSV
LTWDFVNMFGSIQIKINQVCPFFHAYFQKVLPSNLLLFQVKKNCKKRDWTYGLLYAIKITLLHLKK

>XP_009496472.1 hypothetical protein H696_04320 [Fonticula alba]
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>NP_788401.2 presenilin enhancer, isoform A [Drosophila melanogaster]
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Supplementary File 3

Presenilin mRNAs for Selection analysis

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>NM_131024.1:62-1432 Danio rerio presenilin 1 (psen1), mRNA
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>NM_011183.3:91-1437 Mus musculus presenilin 2 (Psen2), transcript variant 1,
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>NM_174440.4:267-1616 Bos taurus presenilin 2 (PSEN2), mRNA
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>NM_131514.2:115-1440 Danio rerio presenilin 2 (psen2), mRNA
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Supplementary File 4

Paralogs of Gamma Secretase proteins

		No of paralogs			
Group	**Species**	**Presenilin**	**APH**	**Nicastrin**	**PEN-2**
Mammals	Homo sapiens	2	2	1	1
	Mus musculus	2	3	1	1
Birds	Galus galus	2	2	1	0
Reptiles	Anolis lizard	2	2	1	1
Amphibians	Xenopus	2	1	2	2
Fish	Danio rerio	2	2	1	1
	Latimeria chalumnae	2	3	1	1
	Lethenteron japonicum	1	2	1	0
Non-vertebrate chordates	Caenorhabditis elegans	3	1	1	1
	Branchiostoma floridae	1	1	1	1
	Saccoglossus kowalevskii	1	1	1	1
Invertebrates	Strongylocentrotus purpuratus	1	1	1	1
	Drosophila melanogaster	1	1	1	1
	Hydra vulgaris	2	1	1	1
	Amphimedon queenslandica	1	1	1	1
	Monosiga brevicollis	1	1	1	
	Dictyostelium discoideum	2	1	1	1
	Chondrus crispus	1	0	0	0
	Trypanosoma brucei	1	0	0	1
	Naegleria gruberi	0	0	0	0
	Trichomonas vaginalis	3	0	1	0
	Rozella allomycis	1	0	1	0
	Fonticula alba	2	1	1	1
	Batrachochytrium salamandrivorans	1	1	1	1
	Capsaspora owczarzaki	1	1	1	1
	Neospora caninum Liverpool	1	0	0	1
	Toxoplasma gondii	1	0	0	1
	Hammondia hammondi	1	0	0	1
	Blastocystis hominis	1	0	0	1
	Aphanomyces invadans	4	1	1	1
	Saprolegnia diclina	3	0	1	1

Protists	Thalassiosira pseudonana	2	0	1	0
	Phaeodactylum tricornutum	2	0	0	1
	Ectocarpus siliculosus	1	1	1	0
	Aureococcus anophagefferens	1	0	0	1
	Nannochloropsis gaditana	1	0	1	0
	Bigelowiella natans	1	0	0	0
	Reticulomyxa filose	1	0	1	0
	Entamoeba histolytica	1	1	0	1
	Polysphondylium pallidum	2	1	1	1
	Guillardia theta	1	1	1	0
	Emiliania huxleyi	2	1	0	0
	Chrysochromulina	1	0	1	1

Supplementary File 5

SLAC Method for sliding window analysis of selection

PSN1

Codon	Observed S Changes	Observed NS Changes	E[S Sites]	E[NS Sites]	Observed S. Prop.	P{S}	dS	dN	dN-dS	P{NS >= observed }	P{NS <= observed }	Normalized dN-dS
1	0	0	0	0.77	0	0	0	0	0	0	0	0
2	0	1	0.9	1.86	0	0.33	0	0.54	0.54	0.67	0.33	0.41
3	2	2	1	2.24	0.5	0.31	2	0.89	-1.11	0.91	0.36	-0.85
4	1	3	0.7	3.82	0.25	0.15	1.43	0.79	-0.65	0.88	0.49	-0.5
5	2	3	0.46	3.95	0.4	0.1	4.39	0.76	-3.63	0.99	0.09	-2.79
6	0	5	1.46	3.05	0	0.32	0	1.64	1.64	0.14	0.86	1.26
7	0	0	0	0	0	0	0	0	0	0	0	0
8	2	0	1.51	2.61	1	0.37	1.33	0	-1.33	1	0.13	-1.02
9	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
10	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
11	1	1	0.8	3.37	0.5	0.19	1.24	0.3	-0.95	0.96	0.35	-0.73
12	1	2	0.8	3.39	0.33	0.19	1.25	0.59	-0.66	0.91	0.47	-0.51
13	2	1	0.81	3.43	0.67	0.19	2.47	0.29	-2.17	0.99	0.1	-1.67
14	1.33	4.67	1.47	3.03	0.22	0.33	0.91	1.54	0.63	0.47	0.82	0.49
15	2	1	0.8	3.3	0.67	0.2	2.49	0.3	-2.18	0.99	0.1	-1.68
16	1	1	0.8	3.71	0.5	0.18	1.24	0.27	-0.97	0.97	0.32	-0.75
17	1	0	0.78	3.37	1	0.19	1.28	0	-1.28	1	0.19	-0.99
18	2	0	1.41	3.03	1	0.32	1.42	0	-1.42	1	0.1	-1.09
19	3	1	1.51	2.88	0.75	0.34	1.99	0.35	-1.64	0.99	0.12	-1.27
20	3	1	1.51	3.01	0.75	0.33	1.99	0.33	-1.66	0.99	0.11	-1.28
21	3	0	2.21	2.26	1	0.49	1.36	0	-1.36	1	0.12	-1.04
22	2	2	0.42	4.1	0.5	0.09	4.78	0.49	-4.29	1	0.05	-3.3
23	2	3	1.47	2.53	0.4	0.37	1.36	1.19	-0.17	0.74	0.6	-0.13
24	4	2	1.51	2.66	0.67	0.36	2.66	0.75	-1.9	0.97	0.13	-1.47
25	1	1	0.78	3.35	0.5	0.19	1.28	0.3	-0.98	0.96	0.34	-0.76
26	1	1	0.8	3.71	0.5	0.18	1.24	0.27	-0.97	0.97	0.32	-0.75
27	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
28	4	3	1.52	3	0.57	0.34	2.63	1	-1.63	0.95	0.18	-1.26
29	4	3	1.82	2.65	0.57	0.41	2.2	1.13	-1.07	0.9	0.3	-0.82
30	4	1	1.51	3.01	0.8	0.33	2.66	0.33	-2.32	1	0.05	-1.79

31	3	1	1.51	2.94	0.75	0.34	1.99	0.34	-1.65	0.99	0.12	-1.27
32	1	1	0.8	3.16	0.5	0.2	1.24	0.32	-0.93	0.96	0.37	-0.71
33	1	3	0.71	2.76	0.25	0.21	1.4	1.09	-0.31	0.81	0.6	-0.24
34	1	4	0.73	3.33	0.2	0.18	1.37	1.2	-0.16	0.78	0.63	-0.13
35	1	3	1.33	2.78	0.25	0.32	0.75	1.08	0.32	0.61	0.79	0.25
36	1.83	6.17	1.2	3.3	0.23	0.27	1.53	1.87	0.34	0.58	0.71	0.26
37	3	3	1.03	2.94	0.5	0.26	2.9	1.02	-1.88	0.96	0.19	-1.45
38	0.5	3.5	1.45	3.07	0.12	0.32	0.35	1.14	0.79	0.41	0.79	0.61
39	4	5	1.51	2.98	0.44	0.34	2.64	1.68	-0.96	0.85	0.36	-0.74
40	2	4	0.87	3.39	0.33	0.2	2.29	1.18	-1.11	0.9	0.36	-0.86
41	4.5	3.5	1.24	3.26	0.56	0.28	3.62	1.07	-2.55	0.98	0.1	-1.96
42	2.5	5.5	1.32	3.03	0.31	0.3	1.9	1.81	-0.08	0.67	0.6	-0.06
43	1	3	0.83	3.35	0.25	0.2	1.2	0.9	-0.3	0.82	0.59	-0.23
44	3	4	1.24	3.28	0.43	0.27	2.41	1.22	-1.19	0.9	0.3	-0.92
45	3.5	7.5	1.4	3.09	0.32	0.31	2.49	2.43	-0.07	0.65	0.59	-0.05
46	2	5	1.44	3.05	0.29	0.32	1.38	1.64	0.26	0.6	0.71	0.2
47	2	2	0.79	3.15	0.5	0.2	2.54	0.63	-1.91	0.97	0.18	-1.47
48	2	2	0.95	2.97	0.5	0.24	2.1	0.67	-1.42	0.95	0.25	-1.09
49	1	3	0.96	2.9	0.25	0.25	1.04	1.04	0	0.74	0.68	0
50	2	3	0.87	3.16	0.4	0.22	2.3	0.95	-1.35	0.93	0.3	-1.04
51	1.5	3.5	0.79	2.69	0.3	0.23	1.9	1.3	-0.6	0.8	0.52	-0.46
52	2	4	1.1	2.88	0.33	0.28	1.82	1.39	-0.43	0.79	0.53	-0.33
53	3	5	1.07	3.02	0.38	0.26	2.8	1.65	-1.15	0.87	0.35	-0.89
54	2.5	4.5	0.9	3.04	0.36	0.23	2.78	1.48	-1.29	0.87	0.35	-1
55	2	5	0.91	3.06	0.29	0.23	2.19	1.63	-0.56	0.8	0.5	-0.43
56	1	5	0.8	3.26	0.17	0.2	1.25	1.53	0.29	0.66	0.73	0.22
57	1	1	0.32	1.48	0.5	0.18	3.12	0.68	-2.45	0.97	0.32	-1.88
58	1.5	4.5	0.75	2.66	0.25	0.22	2.01	1.69	-0.32	0.74	0.58	-0.25
59	2	1	0.62	2.69	0.67	0.19	3.21	0.37	-2.84	0.99	0.09	-2.18
60	0	2	0.62	2.69	0	0.19	0	0.74	0.74	0.66	0.34	0.57
61	0.5	1.5	0.53	2.25	0.25	0.19	0.94	0.67	-0.27	0.81	0.35	-0.21
62	2.67	4.33	1.48	3.04	0.38	0.33	1.81	1.42	-0.38	0.75	0.52	-0.29
63	3	3	0.97	3.54	0.5	0.22	3.09	0.85	-2.24	0.98	0.12	-1.72
64	1.33	4.67	1.46	3.03	0.22	0.32	0.92	1.54	0.63	0.48	0.81	0.48
65	4	6	0.89	3.34	0.4	0.21	4.5	1.8	-2.7	0.96	0.14	-2.08
66	3	4	1.49	2.94	0.43	0.34	2.01	1.36	-0.65	0.82	0.44	-0.5

67	2.5	6.5	0.96	3.32	0.28	0.23	2.59	1.96	-0.64	0.77	0.48	-0.49
68	2.5	3.5	1.21	3.28	0.42	0.27	2.07	1.07	-1	0.87	0.36	-0.77
69	2.33	3.67	1.46	3.03	0.39	0.33	1.6	1.21	-0.39	0.77	0.52	-0.3
70	3	4	1.47	3.05	0.43	0.33	2.04	1.31	-0.73	0.84	0.41	-0.56
71	3	3	1.51	3.01	0.5	0.33	1.98	1	-0.98	0.9	0.32	-0.76
72	0	0	0	0	0	0	0	0	0	0	0	0
73	0	0	0	0	0	0	0	0	0	0	0	0
74	0	0	0	0	0	0	0	0	0	0	0	0
75	3	3	1.42	3.1	0.5	0.31	2.11	0.97	-1.14	0.92	0.28	-0.88
76	2	5	1.45	2.73	0.29	0.35	1.38	1.83	0.45	0.54	0.76	0.35
77	0	0	0	0	0	0	0	0	0	0	0	0
78	0	0	0	0	0	0	0	0	0	0	0	0
79	0	0	0	0	0	0	0	0	0	0	0	0
80	0	0	0	0	0	0	0	0	0	0	0	0
81	0	0	0	0	0	0	0	0	0	0	0	0
82	4	5	1.44	3.06	0.44	0.32	2.78	1.63	-1.15	0.88	0.32	-0.88
83	0	0	0	0	0	0	0	0	0	0	0	0
84	0	0	0	0	0	0	0	0	0	0	0	0
85	0	0	0	0	0	0	0	0	0	0	0	0
86	0	0	0	0	0	0	0	0	0	0	0	0
87	0	0	0	0	0	0	0	0	0	0	0	0
88	0	0	0	0	0	0	0	0	0	0	0	0
89	2.5	7.5	1.1	3.33	0.25	0.25	2.26	2.25	-0.01	0.65	0.61	-0.01
90	2.5	4.5	1.34	3.15	0.36	0.3	1.86	1.43	-0.43	0.76	0.51	-0.33
91	0.5	3.5	1.72	2.78	0.12	0.38	0.29	1.26	0.97	0.32	0.86	0.75
92	0	0	0	0	0	0	0	0	0	0	0	0
93	0	0	0	0	0	0	0	0	0	0	0	0
94	0	0	0	0	0	0	0	0	0	0	0	0
95	2	1	0.78	3.39	0.67	0.19	2.55	0.3	-2.25	0.99	0.09	-1.73
96	3	0	0.81	3.34	1	0.19	3.7	0	-3.7	1	0.01	-2.85
97	1	0	0.78	3.37	1	0.19	1.28	0	-1.28	1	0.19	-0.99
98	3	0	2.19	2.31	1	0.49	1.37	0	-1.37	1	0.12	-1.05
99	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
100	3	0	1.55	2.97	1	0.34	1.94	0	-1.94	1	0.04	-1.49
101	2	0	0.82	3.38	1	0.19	2.45	0	-2.45	1	0.04	-1.89
102	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91

103	4	0	1.51	2.82	1	0.35	2.66	0	-2.66	1	0.01	-2.04
104	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
105	1	1	0.82	3.37	0.5	0.2	1.21	0.3	-0.92	0.96	0.35	-0.7
106	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
107	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
108	1	0	1.13	3.39	1	0.25	0.89	0	-0.89	1	0.25	-0.68
109	0	0	0	4.52	0	0	0	0	0	0	0	0
110	3	0	1.8	2.71	1	0.4	1.67	0	-1.67	1	0.06	-1.28
111	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
112	3	1	1.42	3.1	0.75	0.31	2.12	0.32	-1.8	0.99	0.09	-1.38
113	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
114	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
115	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
116	2	0	2.12	2.4	1	0.47	0.94	0	-0.94	1	0.22	-0.73
117	2	0	0.8	3.39	1	0.19	2.49	0	-2.49	1	0.04	-1.91
118	0	0	0	4.52	0	0	0	0	0	0	0	0
119	2.5	1.5	1.35	3.17	0.62	0.3	1.86	0.47	-1.38	0.95	0.21	-1.06
120	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
121	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
122	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
123	1	1	1.51	3.01	0.5	0.33	0.66	0.33	-0.33	0.89	0.56	-0.26
124	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
125	1	0	1.01	3.5	1	0.22	0.99	0	-0.99	1	0.22	-0.76
126	1	0	0.79	3.41	1	0.19	1.27	0	-1.27	1	0.19	-0.97
127	5	0	1.51	2.95	1	0.34	3.32	0	-3.32	1	0	-2.55
128	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
129	3	2	1.12	3.4	0.6	0.25	2.68	0.59	-2.09	0.98	0.1	-1.61
130	0	0	0.8	3.71	0	0.18	0	0	0	0	0	0
131	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
132	3	1	1.51	2.98	0.75	0.34	1.99	0.34	-1.66	0.99	0.11	-1.27
133	0	0	0.78	3.38	0	0.19	0	0	0	0	0	0
134	1	0	0.78	3.41	1	0.19	1.28	0	-1.28	1	0.19	-0.98
135	2	2	0.8	3.71	0.5	0.18	2.49	0.54	-1.95	0.98	0.15	-1.5
136	2.5	1.5	1.47	2.74	0.62	0.35	1.7	0.55	-1.15	0.93	0.28	-0.88
137	1	0	0.78	2.93	1	0.21	1.28	0	-1.28	1	0.21	-0.99
138	0	0	0	0	0	0	0	0	0	0	0	0

139	3	0	1.63	2.89	1	0.36	1.85	0	-1.85	1	0.05	-1.42
140	1	0	1.13	3.39	1	0.25	0.89	0	-0.89	1	0.25	-0.68
141	3	0	0.8	3.01	1	0.21	3.73	0	-3.73	1	0.01	-2.87
142	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
143	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
144	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
145	3.5	5.5	1.44	3.07	0.39	0.32	2.44	1.79	-0.65	0.78	0.45	-0.5
146	2	0	0.8	3.35	1	0.19	2.49	0	-2.49	1	0.04	-1.92
147	1	1	0.8	3.71	0.5	0.18	1.24	0.27	-0.97	0.97	0.32	-0.75
148	4	1	1.51	3.01	0.8	0.33	2.66	0.33	-2.32	1	0.05	-1.79
149	3	5	1.47	3.03	0.38	0.33	2.04	1.65	-0.39	0.75	0.52	-0.3
150	5	1	1.48	2.71	0.83	0.35	3.37	0.37	-3	1	0.02	-2.31
151	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
152	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
153	0.5	2.5	0.82	2.97	0.17	0.22	0.61	0.84	0.23	0.68	0.52	0.18
154	5	0	1.74	2.75	1	0.39	2.87	0	-2.87	1	0.01	-2.21
155	1	0	1.55	2.97	1	0.34	0.65	0	-0.65	1	0.34	-0.5
156	4	0	1.79	2.63	1	0.41	2.23	0	-2.23	1	0.03	-1.72
157	1	1	0.8	3.71	0.5	0.18	1.24	0.27	-0.97	0.97	0.32	-0.75
158	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
159	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
160	5	0	1.83	2.69	1	0.41	2.73	0	-2.73	1	0.01	-2.1
161	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
162	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
163	3	1	1.54	2.98	0.75	0.34	1.95	0.34	-1.62	0.99	0.12	-1.24
164	1	1	1.12	3.4	0.5	0.25	0.89	0.29	-0.6	0.94	0.43	-0.46
165	0	0	0	4.52	0	0	0	0	0	0	0	0
166	0	0	1.13	3.39	0	0.25	0	0	0	0	0	0
167	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
168	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
169	3	0	1.01	3.5	1	0.22	2.96	0	-2.96	1	0.01	-2.27
170	5	1	1.67	2.85	0.83	0.37	3	0.35	-2.65	1	0.03	-2.04
171	3	3	1.47	3.05	0.5	0.33	2.04	0.98	-1.06	0.91	0.3	-0.82
172	0	0	0	4.52	0	0	0	0	0	0	0	0
173	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
174	2	0	1.1	3.42	1	0.24	1.82	0	-1.82	1	0.06	-1.4

175	0	1	0.82	3.7	0	0.18	0	0.27	0.27	0.82	0.18	0.21
176	5	0	2.19	2.3	1	0.49	2.28	0	-2.28	1	0.03	-1.76
177	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
178	3	2	1.56	2.96	0.6	0.35	1.92	0.68	-1.24	0.95	0.23	-0.96
179	2	1	1.51	2.98	0.67	0.34	1.32	0.34	-0.99	0.96	0.26	-0.76
180	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
181	3	0	0.8	3.39	1	0.19	3.73	0	-3.73	1	0.01	-2.87
182	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
183	1	0	1.51	3	1	0.33	0.66	0	-0.66	1	0.33	-0.51
184	2	0	0.8	3.39	1	0.19	2.49	0	-2.49	1	0.04	-1.91
185	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
186	1	0	0.78	3.41	1	0.19	1.28	0	-1.28	1	0.19	-0.98
187	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
188	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
189	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
190	4	0	1.51	2.99	1	0.33	2.66	0	-2.66	1	0.01	-2.04
191	0	0	0	2.96	0	0	0	0	0	0	0	0
192	3	0	2.2	2.29	1	0.49	1.36	0	-1.36	1	0.12	-1.05
193	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
194	2	1	1.24	3.28	0.67	0.27	1.61	0.31	-1.31	0.98	0.18	-1.01
195	2	0	1.51	2.84	1	0.35	1.33	0	-1.33	1	0.12	-1.02
196	3	0	1.51	2.9	1	0.34	1.99	0	-1.99	1	0.04	-1.53
197	3	0	2.24	2.25	1	0.5	1.34	0	-1.34	1	0.12	-1.03
198	0	0	0	4.52	0	0	0	0	0	0	0	0
199	3	0	2.2	2.32	1	0.49	1.37	0	-1.37	1	0.12	-1.05
200	3	0	1.59	2.93	1	0.35	1.89	0	-1.89	1	0.04	-1.46
201	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
202	2	4	1.11	2.89	0.33	0.28	1.81	1.38	-0.42	0.79	0.53	-0.33
203	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
204	1	1	1.34	3.18	0.5	0.3	0.75	0.31	-0.43	0.91	0.5	-0.33
205	2	1	0.8	3.18	0.67	0.2	2.49	0.31	-2.17	0.99	0.11	-1.67
206	1	1	0.83	3.68	0.5	0.18	1.2	0.27	-0.93	0.97	0.34	-0.71
207	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
208	3	0	1.59	2.93	1	0.35	1.89	0	-1.89	1	0.04	-1.45
209	2	1	1.47	3.03	0.67	0.33	1.36	0.33	-1.03	0.97	0.25	-0.79
210	1	0	0.81	3.34	1	0.2	1.23	0	-1.23	1	0.2	-0.95

211	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
212	2	3	1.14	3.37	0.4	0.25	1.76	0.89	-0.87	0.89	0.37	-0.67
213	1	0	0.78	3.41	1	0.19	1.28	0	-1.28	1	0.19	-0.99
214	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
215	1	0	0.8	3.01	1	0.21	1.24	0	-1.24	1	0.21	-0.96
216	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
217	0.5	1.5	1.45	3.07	0.25	0.32	0.34	0.49	0.14	0.68	0.54	0.11
218	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
219	0	0	0	4.52	0	0	0	0	0	0	0	0
220	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
221	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
222	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
223	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
224	3	1	2.19	2.31	0.75	0.49	1.37	0.43	-0.94	0.94	0.29	-0.72
225	0.5	3.5	1.02	3.48	0.12	0.23	0.49	1.01	0.52	0.57	0.64	0.4
226	1	3	1.65	2.72	0.25	0.38	0.61	1.1	0.5	0.51	0.85	0.38
227	3	4	1.51	3.01	0.43	0.33	1.99	1.33	-0.66	0.83	0.43	-0.5
228	2	1	1.24	3.27	0.67	0.28	1.61	0.31	-1.3	0.98	0.19	-1
229	0	0	0	2.96	0	0	0	0	0	0	0	0
230	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
231	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
232	2	0	1.51	2.99	1	0.33	1.33	0	-1.33	1	0.11	-1.02
233	3	1	1.51	3.01	0.75	0.33	1.99	0.33	-1.66	0.99	0.11	-1.28
234	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
235	3	0	1.51	2.82	1	0.35	1.99	0	-1.99	1	0.04	-1.53
236	0	0	0	4.52	0	0	0	0	0	0	0	0
237	2.5	1.5	1.23	3.29	0.62	0.27	2.03	0.46	-1.58	0.97	0.18	-1.21
238	0	0	0.8	3.39	0	0.19	0	0	0	0	0	0
239	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
240	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
241	0	0	0	2.96	0	0	0	0	0	0	0	0
242	1	0	0.78	3.41	1	0.19	1.28	0	-1.28	1	0.19	-0.99
243	4	0	1.51	2.99	1	0.33	2.66	0	-2.66	1	0.01	-2.04
244	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
245	2	0	2.27	2.25	1	0.5	0.88	0	-0.88	1	0.25	-0.68
246	1	3	1.12	2.94	0.25	0.28	0.89	1.02	0.13	0.69	0.72	0.1

247	3	0	1.84	2.68	1	0.41	1.63	0	-1.63	1	0.07	-1.26
248	0	0	0.78	2.93	0	0.21	0	0	0	0	0	0
249	1	0	0.79	2.92	1	0.21	1.27	0	-1.27	1	0.21	-0.97
250	3	2	1.49	3.02	0.6	0.33	2.01	0.66	-1.35	0.96	0.21	-1.04
251	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
252	2	0	1.54	2.98	1	0.34	1.3	0	-1.3	1	0.12	-1
253	1	0	1.13	3.39	1	0.25	0.89	0	-0.89	1	0.25	-0.68
254	0.5	3.5	0.5	4.02	0.12	0.11	1.01	0.87	-0.13	0.78	0.37	-0.1
255	1	0	1.1	3.42	1	0.24	0.91	0	-0.91	1	0.24	-0.7
256	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
257	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
258	2	1	1.51	3	0.67	0.34	1.32	0.33	-0.99	0.96	0.26	-0.76
259	0	0	0	4.52	0	0	0	0	0	0	0	0
260	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
261	5	0	2.03	2.47	1	0.45	2.46	0	-2.46	1	0.02	-1.89
262	2	1	1.49	3.03	0.67	0.33	1.35	0.33	-1.02	0.96	0.25	-0.78
263	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
264	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
265	2	0	0.78	3.41	1	0.19	2.55	0	-2.55	1	0.03	-1.96
266	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
267	1	0	2.18	2.34	1	0.48	0.46	0	-0.46	1	0.48	-0.35
268	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
269	1	0	0.78	3.37	1	0.19	1.28	0	-1.28	1	0.19	-0.98
270	0	0	0	2.96	0	0	0	0	0	0	0	0
271	3	0	1.51	2.82	1	0.35	1.99	0	-1.99	1	0.04	-1.53
272	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
273	0	0	0	2.96	0	0	0	0	0	0	0	0
274	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
275	3	0	1.1	3.42	1	0.24	2.72	0	-2.72	1	0.01	-2.09
276	2	0	2.21	2.28	1	0.49	0.91	0	-0.91	1	0.24	-0.7
277	3	0	1.51	2.79	1	0.35	1.99	0	-1.99	1	0.04	-1.53
278	0	1	1.51	3.01	0	0.33	0	0.33	0.33	0.67	0.33	0.26
279	1	0	1.13	3.39	1	0.25	0.89	0	-0.89	1	0.25	-0.68
280	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
281	2	2	1.45	3.07	0.5	0.32	1.38	0.65	-0.72	0.9	0.39	-0.56
282	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91

283	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
284	2	0	2.01	2.51	1	0.44	1	0	-1	1	0.2	-0.77
285	1.5	2.5	1.51	3.01	0.38	0.33	0.99	0.83	-0.16	0.74	0.61	-0.12
286	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
287	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
288	4	0	2.2	2.28	1	0.49	1.82	0	-1.82	1	0.06	-1.4
289	2.5	1.5	0.82	3.36	0.62	0.2	3.03	0.45	-2.59	0.99	0.1	-1.99
290	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
291	1	0	0.81	3.39	1	0.19	1.23	0	-1.23	1	0.19	-0.95
292	3	0	1.51	2.99	1	0.33	1.99	0	-1.99	1	0.04	-1.53
293	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
294	4	0	2.16	2.33	1	0.48	1.85	0	-1.85	1	0.05	-1.43
295	4	0	1.21	3.26	1	0.27	3.31	0	-3.31	1	0.01	-2.55
296	0	0	0	4.52	0	0	0	0	0	0	0	0
297	4	0	2.19	2.3	1	0.49	1.83	0	-1.83	1	0.06	-1.41
298	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
299	2	0	0.82	3.34	1	0.2	2.45	0	-2.45	1	0.04	-1.88
300	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
301	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
302	2	0	0.8	2.91	1	0.22	2.49	0	-2.49	1	0.05	-1.92
303	3	0	0.8	3.35	1	0.19	3.73	0	-3.73	1	0.01	-2.87
304	2	0	1.21	2.99	1	0.29	1.65	0	-1.65	1	0.08	-1.27
305	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
306	1	0	0.78	3.37	1	0.19	1.28	0	-1.28	1	0.19	-0.99
307	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
308	2	0	0.73	3.79	1	0.16	2.75	0	-2.75	1	0.03	-2.11
309	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
310	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
311	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
312	3	0	1.55	2.97	1	0.34	1.93	0	-1.93	1	0.04	-1.49
313	2	0	0.73	3.79	1	0.16	2.75	0	-2.75	1	0.03	-2.12
314	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
315	2	0	1.51	2.71	1	0.36	1.33	0	-1.33	1	0.13	-1.02
316	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
317	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
318	0	0	0	4.52	0	0	0	0	0	0	0	0

319	0.5	3.5	0.7	3.82	0.12	0.15	0.72	0.92	0.2	0.7	0.49	0.15
320	0	0	0	2.96	0	0	0	0	0	0	0	0
321	3	2	1.43	3.09	0.6	0.32	2.1	0.65	-1.45	0.96	0.19	-1.12
322	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
323	2	0	1.51	2.8	1	0.35	1.33	0	-1.33	1	0.12	-1.02
324	0	0	0	4.52	0	0	0	0	0	0	0	0
325	5	0	1.51	3.01	1	0.33	3.32	0	-3.32	1	0	-2.55
326	1	4	0.8	3.42	0.2	0.19	1.24	1.17	-0.08	0.76	0.65	-0.06
327	0	0	0	0	0	0	0	0	0	0	0	0
328	1.33	4.67	1.78	2.25	0.22	0.44	0.75	2.07	1.32	0.27	0.92	1.02
329	1	3	0.84	3.66	0.25	0.19	1.19	0.82	-0.37	0.84	0.56	-0.28
330	3	4	1.48	3.04	0.43	0.33	2.02	1.32	-0.71	0.83	0.42	-0.54
331	2.5	5.5	1.47	3.03	0.31	0.33	1.7	1.82	0.12	0.62	0.66	0.09
332	2	5	1.49	2.96	0.29	0.33	1.34	1.69	0.35	0.57	0.74	0.27
333	1.17	6.83	0.98	3.22	0.15	0.23	1.19	2.12	0.93	0.46	0.83	0.72
334	2	0	1.51	2.69	1	0.36	1.33	0	-1.33	1	0.13	-1.02
335	3	4	1.32	2.74	0.43	0.33	2.27	1.46	-0.81	0.84	0.41	-0.62
336	3.5	2.5	1.18	1.99	0.58	0.37	2.97	1.26	-1.71	0.91	0.27	-1.32
337	1	3	0.56	2.27	0.25	0.2	1.78	1.32	-0.46	0.82	0.59	-0.35
338	1.5	2.5	0.85	2.15	0.38	0.28	1.77	1.16	-0.61	0.81	0.53	-0.47
339	2	2	1.04	2.15	0.5	0.33	1.92	0.93	-0.99	0.9	0.39	-0.76
340	1	4	0.48	2.18	0.2	0.18	2.07	1.84	-0.23	0.77	0.63	-0.18
341	0	0	0	0	0	0	0	0	0	0	0	0
342	0	0	0	0	0	0	0	0	0	0	0	0
343	0	0	0	0	0	0	0	0	0	0	0	0
344	0	0	0	0	0	0	0	0	0	0	0	0
345	0	0	0	0	0	0	0	0	0	0	0	0
346	0	0	0	0	0	0	0	0	0	0	0	0
347	0	0	0	0	0	0	0	0	0	0	0	0
348	0	0	0	0	0	0	0	0	0	0	0	0
349	0	0	0	0	0	0	0	0	0	0	0	0
350	0	0	0	0	0	0	0	0	0	0	0	0
351	0	0	0	0	0	0	0	0	0	0	0	0
352	0	0	0	0	0	0	0	0	0	0	0	0
353	0	0	0	0	0	0	0	0	0	0	0	0
354	0	0	0	0	0	0	0	0	0	0	0	0

355	0	0	0	0	0	0	0	0	0	0	0	0
356	2.17	2.83	0.75	3.35	0.43	0.18	2.88	0.84	-2.03	0.96	0.2	-1.57
357	6	2	1.64	2.54	0.75	0.39	3.67	0.79	-2.88	0.99	0.05	-2.21
358	1.5	4.5	0.84	3.34	0.25	0.2	1.78	1.35	-0.44	0.78	0.54	-0.34
359	2	4	0.89	3.62	0.33	0.2	2.24	1.11	-1.13	0.9	0.34	-0.87
360	1.5	5.5	1.02	3.35	0.21	0.23	1.47	1.64	0.17	0.64	0.68	0.13
361	2.5	1.5	0.85	3.32	0.62	0.2	2.93	0.45	-2.48	0.98	0.11	-1.91
362	2.5	3.5	1.19	3.14	0.42	0.28	2.09	1.12	-0.98	0.87	0.37	-0.75
363	3	4	1.49	3.02	0.43	0.33	2.01	1.32	-0.68	0.83	0.42	-0.53
364	2	5	0.78	3.43	0.29	0.19	2.56	1.46	-1.1	0.88	0.38	-0.84
365	1.25	7.75	0.86	3.55	0.14	0.19	1.45	2.18	0.73	0.53	0.78	0.56
366	1.83	4.17	1	3.49	0.31	0.22	1.83	1.2	-0.63	0.82	0.47	-0.49
367	2.5	5.5	1.14	3.34	0.31	0.25	2.19	1.64	-0.55	0.77	0.49	-0.42
368	3	3	1.46	3.03	0.5	0.33	2.05	0.99	-1.06	0.91	0.3	-0.82
369	1	3	0.82	3.35	0.25	0.2	1.22	0.9	-0.32	0.82	0.58	-0.25
370	3	3	1.33	3.02	0.5	0.31	2.25	0.99	-1.26	0.92	0.27	-0.97
371	3	3	1.51	2.5	0.5	0.38	1.99	1.2	-0.79	0.85	0.41	-0.6
372	1.17	5.83	0.81	3.24	0.17	0.2	1.45	1.8	0.35	0.62	0.73	0.27
373	4	4	1.48	3.01	0.5	0.33	2.7	1.33	-1.37	0.92	0.25	-1.06
374	0.17	5.83	0.79	3.18	0.03	0.2	0.21	1.83	1.62	0.33	0.74	1.25
375	2.5	4.5	1.32	2.78	0.36	0.32	1.89	1.62	-0.27	0.72	0.56	-0.21
376	1.5	3.5	0.95	2.98	0.3	0.24	1.58	1.18	-0.41	0.78	0.55	-0.31
377	3	3	0.9	2.96	0.5	0.23	3.35	1.01	-2.34	0.97	0.14	-1.8
378	3	2	1.17	2.45	0.6	0.32	2.55	0.81	-1.74	0.96	0.2	-1.34
379	3	2	1.33	2.26	0.6	0.37	2.26	0.88	-1.38	0.93	0.27	-1.06
380	2.5	3.5	1.28	2.43	0.42	0.34	1.96	1.44	-0.52	0.77	0.51	-0.4
381	1	5	1.31	2.8	0.17	0.32	0.76	1.79	1.03	0.38	0.9	0.79
382	1.5	4.5	1.29	2.8	0.25	0.31	1.17	1.61	0.44	0.55	0.75	0.34
383	1	4	0.84	3.34	0.2	0.2	1.19	1.2	0.01	0.73	0.68	0.01
384	2.67	3.33	1.46	2.7	0.44	0.35	1.82	1.24	-0.59	0.8	0.47	-0.45
385	3	4	1.51	2.98	0.43	0.34	1.99	1.34	-0.65	0.82	0.44	-0.5
386	2	3	0.82	3.36	0.4	0.2	2.43	0.89	-1.54	0.94	0.26	-1.19
387	1	2	0.79	3.46	0.33	0.18	1.27	0.58	-0.7	0.91	0.46	-0.53
388	2	6	1.81	2.71	0.25	0.4	1.11	2.21	1.1	0.32	0.89	0.85
389	1	3	0.85	3.34	0.25	0.2	1.18	0.9	-0.28	0.82	0.6	-0.22
390	0	0	0	0	0	0	0	0	0	0	0	0

391	0	0	0	0	0	0	0	0	0	0	0	0
392	1	2	0.65	2.64	0.33	0.2	1.53	0.76	-0.77	0.9	0.49	-0.59
393	0	0	0.7	3.01	0	0.19	0	0	0	0	0	0
394	2	2	0.83	3.34	0.5	0.2	2.4	0.6	-1.8	0.97	0.18	-1.38
395	0	1	0.82	3.42	0	0.19	0	0.29	0.29	0.81	0.19	0.22
396	2	0	1.32	2.88	1	0.31	1.51	0	-1.51	1	0.1	-1.17
397	4	0	1.51	2.97	1	0.34	2.66	0	-2.66	1	0.01	-2.04
398	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
399	0	0	0.78	3.42	0	0.19	0	0	0	0	0	0
400	5	1	1.55	2.96	0.83	0.34	3.22	0.34	-2.88	1	0.02	-2.22
401	4	0	1.51	2.99	1	0.33	2.66	0	-2.66	1	0.01	-2.04
402	3	0	1.61	2.91	1	0.36	1.86	0	-1.86	1	0.05	-1.43
403	1	0	1.51	2.67	1	0.36	0.66	0	-0.66	1	0.36	-0.51
404	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
405	0	0	0.8	3.71	0	0.18	0	0	0	0	0	0
406	1	0	1.1	3.42	1	0.24	0.91	0	-0.91	1	0.24	-0.7
407	0	0	0.8	3.71	0	0.18	0	0	0	0	0	0
408	0	0	0.8	3.01	0	0.21	0	0	0	0	0	0
409	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
410	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
411	2	0	2.27	2.25	1	0.5	0.88	0	-0.88	1	0.25	-0.68
412	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
413	3	0	1.51	2.98	1	0.34	1.99	0	-1.99	1	0.04	-1.53
414	1	0	0.81	3.39	1	0.19	1.24	0	-1.24	1	0.19	-0.96
415	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
416	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
417	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
418	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
419	3	1	1.51	2.99	0.75	0.33	1.99	0.33	-1.66	0.99	0.11	-1.28
420	2	1	0.58	2.66	0.67	0.18	3.47	0.38	-3.09	0.99	0.08	-2.38
421	1	0	1.51	2.71	1	0.36	0.66	0	-0.66	1	0.36	-0.51
422	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
423	0	0	0	2.96	0	0	0	0	0	0	0	0
424	2	1	0.8	3.71	0.67	0.18	2.49	0.27	-2.22	0.99	0.08	-1.71
425	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
426	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53

427	1	0	2.13	2.31	1	0.48	0.47	0	-0.47	1	0.48	-0.36
428	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
429	2	0	0.8	3.39	1	0.19	2.49	0	-2.49	1	0.04	-1.91
430	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
431	2.5	1.5	1.46	3.06	0.62	0.32	1.71	0.49	-1.22	0.94	0.25	-0.94
432	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
433	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
434	2	1	1.55	2.95	0.67	0.34	1.29	0.34	-0.95	0.96	0.27	-0.73
435	2	0	1.01	3.5	1	0.22	1.97	0	-1.97	1	0.05	-1.52
436	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
437	4	0	1.96	2.41	1	0.45	2.04	0	-2.04	1	0.04	-1.57
438	0	0	0.8	3.39	0	0.19	0	0	0	0	0	0
439	3	0	2.21	2.28	1	0.49	1.36	0	-1.36	1	0.12	-1.04
440	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
441	3	0	1.59	2.93	1	0.35	1.89	0	-1.89	1	0.04	-1.46
442	3	0	2.09	2.33	1	0.47	1.44	0	-1.44	1	0.11	-1.11
443	2	0	1.89	2.44	1	0.44	1.06	0	-1.06	1	0.19	-0.81
444	4	0	1.98	2.53	1	0.44	2.02	0	-2.02	1	0.04	-1.56
445	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
446	3	1	1.42	3.1	0.75	0.31	2.12	0.32	-1.8	0.99	0.09	-1.38
447	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
448	0	0	0.78	3.42	0	0.19	0	0	0	0	0	0
449	1	0	0.79	3.41	1	0.19	1.27	0	-1.27	1	0.19	-0.97
450	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
451	4	0	2.19	2.31	1	0.49	1.83	0	-1.83	1	0.06	-1.41
452	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
453	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
454	3	0	1.97	2.55	1	0.44	1.52	0	-1.52	1	0.08	-1.17
455	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
456	1	0	1.13	3.39	1	0.25	0.89	0	-0.89	1	0.25	-0.68
457	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
458	0	0	1.13	3.39	0	0.25	0	0	0	0	0	0
459	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
460	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
461	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
462	2	0	1.83	2.61	1	0.41	1.1	0	-1.1	1	0.17	-0.84

463	0	1	1.15	3.37	0	0.25	0	0.3	0.3	0.75	0.25	0.23
464	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
465	0	0	0.8	3.01	0	0.21	0	0	0	0	0	0
466	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
467	3	0	1.51	2.98	1	0.34	1.99	0	-1.99	1	0.04	-1.53
468	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
469	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
470	2	2	0.81	3.7	0.5	0.18	2.47	0.54	-1.93	0.98	0.15	-1.49
471	2.5	1.5	2.14	2.38	0.62	0.47	1.17	0.63	-0.54	0.84	0.46	-0.42
472	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
473	5	2	1.69	2.41	0.71	0.41	2.96	0.83	-2.13	0.98	0.11	-1.64
474	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
475	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
476	0	0	0	4.52	0	0	0	0	0	0	0	0
477	0	0	0.8	3.71	0	0.18	0	0	0	0	0	0
478	3	2	1.34	3.18	0.6	0.3	2.24	0.63	-1.61	0.97	0.16	-1.24
479	2	0	2.26	2.25	1	0.5	0.88	0	-0.88	1	0.25	-0.68
480	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
481	3	2	1.51	3.01	0.6	0.33	1.99	0.66	-1.33	0.95	0.21	-1.02
482	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
483	1	0	0.78	2.93	1	0.21	1.28	0	-1.28	1	0.21	-0.98
484	3	3	1.42	3.06	0.5	0.32	2.12	0.98	-1.14	0.92	0.29	-0.87
485	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
486	1	0	1.01	3.05	1	0.25	0.99	0	-0.99	1	0.25	-0.76
487	0	0	0	0	0	0	0	0	0	0	0	0

PSN2

Codon	Observed S Changes	Observed NS Changes	E[S Sites]	E[NS Sites]	Observed S. Prop.	P{S}	dS	dN	dN-dS	P{NS >= observed }	P{NS <= observed }	Normalized dN-dS
1	0	0	0	0.77	0	0	0	0	0	0	0	0
2	0	1	0.9	1.86	0	0.33	0	0.54	0.54	0.67	0.33	0.41
3	2	2	1	2.24	0.5	0.31	2	0.89	-1.11	0.91	0.36	-0.85
4	1	3	0.7	3.82	0.25	0.15	1.43	0.79	-0.65	0.88	0.49	-0.5

5	2	3	0.46	3.95	0.4	0.1	4.39	0.76	-3.63	0.99	0.09	-2.79
6	0	5	1.46	3.05	0	0.32	0	1.64	1.64	0.14	0.86	1.26
7	0	0	0	0	0	0	0	0	0	0	0	0
8	2	0	1.51	2.61	1	0.37	1.33	0	-1.33	1	0.13	-1.02
9	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
10	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
11	1	1	0.8	3.37	0.5	0.19	1.24	0.3	-0.95	0.96	0.35	-0.73
12	1	2	0.8	3.39	0.33	0.19	1.25	0.59	-0.66	0.91	0.47	-0.51
13	2	1	0.81	3.43	0.67	0.19	2.47	0.29	-2.17	0.99	0.1	-1.67
14	1.33	4.67	1.47	3.03	0.22	0.33	0.91	1.54	0.63	0.47	0.82	0.49
15	2	1	0.8	3.3	0.67	0.2	2.49	0.3	-2.18	0.99	0.1	-1.68
16	1	1	0.8	3.71	0.5	0.18	1.24	0.27	-0.97	0.97	0.32	-0.75
17	1	0	0.78	3.37	1	0.19	1.28	0	-1.28	1	0.19	-0.99
18	2	0	1.41	3.03	1	0.32	1.42	0	-1.42	1	0.1	-1.09
19	3	1	1.51	2.88	0.75	0.34	1.99	0.35	-1.64	0.99	0.12	-1.27
20	3	1	1.51	3.01	0.75	0.33	1.99	0.33	-1.66	0.99	0.11	-1.28
21	3	0	2.21	2.26	1	0.49	1.36	0	-1.36	1	0.12	-1.04
22	2	2	0.42	4.1	0.5	0.09	4.78	0.49	-4.29	1	0.05	-3.3
23	2	3	1.47	2.53	0.4	0.37	1.36	1.19	-0.17	0.74	0.6	-0.13
24	4	2	1.51	2.66	0.67	0.36	2.66	0.75	-1.9	0.97	0.13	-1.47
25	1	1	0.78	3.35	0.5	0.19	1.28	0.3	-0.98	0.96	0.34	-0.76
26	1	1	0.8	3.71	0.5	0.18	1.24	0.27	-0.97	0.97	0.32	-0.75
27	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
28	4	3	1.51	3.01	0.57	0.33	2.66	1	-1.66	0.95	0.17	-1.28
29	4	3	1.82	2.68	0.57	0.4	2.2	1.12	-1.08	0.9	0.3	-0.83
30	4	1	1.51	3.01	0.8	0.33	2.66	0.33	-2.32	1	0.05	-1.79
31	3	1	1.51	2.94	0.75	0.34	1.99	0.34	-1.65	0.99	0.12	-1.27
32	1	1	0.8	3.16	0.5	0.2	1.24	0.32	-0.93	0.96	0.37	-0.71
33	1	3	0.71	2.76	0.25	0.21	1.4	1.09	-0.31	0.81	0.6	-0.24
34	1	4	0.73	3.33	0.2	0.18	1.37	1.2	-0.16	0.78	0.63	-0.13
35	1	3	1.33	2.78	0.25	0.32	0.75	1.08	0.32	0.61	0.79	0.25
36	1.83	6.17	1.2	3.3	0.23	0.27	1.53	1.87	0.34	0.58	0.71	0.26
37	3	3	1.03	2.94	0.5	0.26	2.9	1.02	-1.88	0.96	0.19	-1.45
38	0.5	3.5	1.45	3.07	0.12	0.32	0.35	1.14	0.79	0.41	0.79	0.61
39	4	5	1.51	2.98	0.44	0.34	2.64	1.68	-0.96	0.85	0.36	-0.74
40	2	4	0.87	3.39	0.33	0.2	2.29	1.18	-1.11	0.9	0.36	-0.86

41	4.5	3.5	1.24	3.26	0.56	0.28	3.62	1.07	-2.55	0.98	0.1	-1.96
42	2.5	5.5	1.32	3.03	0.31	0.3	1.9	1.81	-0.08	0.67	0.6	-0.06
43	1	3	0.83	3.35	0.25	0.2	1.2	0.9	-0.3	0.82	0.59	-0.23
44	4	4	1.24	3.28	0.5	0.27	3.22	1.22	-2	0.96	0.15	-1.54
45	3.5	7.5	1.4	3.09	0.32	0.31	2.49	2.43	-0.07	0.65	0.59	-0.05
46	2	5	1.44	3.05	0.29	0.32	1.38	1.64	0.26	0.6	0.71	0.2
47	2	2	0.79	3.15	0.5	0.2	2.54	0.63	-1.91	0.97	0.18	-1.47
48	2	2	0.95	2.97	0.5	0.24	2.1	0.67	-1.42	0.95	0.25	-1.09
49	1	3	0.96	2.9	0.25	0.25	1.04	1.04	0	0.74	0.68	0
50	2	3	0.87	3.16	0.4	0.22	2.3	0.95	-1.35	0.93	0.3	-1.04
51	1.5	3.5	0.79	2.69	0.3	0.23	1.9	1.3	-0.6	0.8	0.52	-0.46
52	2	4	1.1	2.88	0.33	0.28	1.82	1.39	-0.43	0.79	0.53	-0.33
53	3	5	0.91	3.19	0.38	0.22	3.31	1.57	-1.74	0.92	0.25	-1.34
54	2.5	4.5	0.9	3.04	0.36	0.23	2.78	1.48	-1.29	0.87	0.35	-1
55	2	5	0.91	3.06	0.29	0.23	2.19	1.63	-0.56	0.8	0.5	-0.43
56	1	5	0.8	3.26	0.17	0.2	1.25	1.53	0.29	0.66	0.73	0.22
57	1	1	0.32	1.48	0.5	0.18	3.12	0.68	-2.45	0.97	0.32	-1.88
58	1.5	4.5	0.75	2.66	0.25	0.22	2.01	1.69	-0.32	0.74	0.58	-0.25
59	2	1	0.62	2.69	0.67	0.19	3.21	0.37	-2.84	0.99	0.09	-2.18
60	0	2	0.62	2.69	0	0.19	0	0.74	0.74	0.66	0.34	0.57
61	0.5	1.5	0.53	2.25	0.25	0.19	0.94	0.67	-0.27	0.81	0.35	-0.21
62	2.67	4.33	1.48	3.04	0.38	0.33	1.81	1.42	-0.38	0.75	0.52	-0.29
63	3	3	0.97	3.54	0.5	0.22	3.09	0.85	-2.24	0.98	0.12	-1.72
64	1.33	4.67	1.46	3.03	0.22	0.32	0.92	1.54	0.63	0.48	0.81	0.48
65	4	6	0.89	3.34	0.4	0.21	4.5	1.8	-2.7	0.96	0.14	-2.08
66	3	4	1.49	2.94	0.43	0.34	2.01	1.36	-0.65	0.82	0.44	-0.5
67	2.5	6.5	0.96	3.32	0.28	0.23	2.59	1.96	-0.64	0.77	0.48	-0.49
68	2.5	3.5	1.21	3.28	0.42	0.27	2.07	1.07	-1	0.87	0.36	-0.77
69	2.33	3.67	1.46	3.03	0.39	0.33	1.6	1.21	-0.39	0.77	0.52	-0.3
70	3	4	1.47	3.05	0.43	0.33	2.04	1.31	-0.73	0.84	0.41	-0.56
71	3	3	1.51	3.01	0.5	0.33	1.98	1	-0.98	0.9	0.32	-0.76
72	0	0	0	0	0	0	0	0	0	0	0	0
73	0	0	0	0	0	0	0	0	0	0	0	0
74	0	0	0	0	0	0	0	0	0	0	0	0
75	3	3	1.42	3.1	0.5	0.31	2.11	0.97	-1.14	0.92	0.28	-0.88
76	2	5	1.45	2.73	0.29	0.35	1.38	1.83	0.45	0.54	0.76	0.35

77	0	0	0	0	0	0	0	0	0	0	0	0
78	0	0	0	0	0	0	0	0	0	0	0	0
79	0	0	0	0	0	0	0	0	0	0	0	0
80	0	0	0	0	0	0	0	0	0	0	0	0
81	0	0	0	0	0	0	0	0	0	0	0	0
82	4	5	1.44	3.06	0.44	0.32	2.78	1.63	-1.15	0.88	0.32	-0.88
83	0	0	0	0	0	0	0	0	0	0	0	0
84	0	0	0	0	0	0	0	0	0	0	0	0
85	0	0	0	0	0	0	0	0	0	0	0	0
86	0	0	0	0	0	0	0	0	0	0	0	0
87	0	0	0	0	0	0	0	0	0	0	0	0
88	0	0	0	0	0	0	0	0	0	0	0	0
89	2.5	7.5	1.1	3.33	0.25	0.25	2.26	2.25	-0.01	0.65	0.61	-0.01
90	2.5	4.5	1.34	3.15	0.36	0.3	1.86	1.43	-0.43	0.76	0.51	-0.33
91	0.5	3.5	1.72	2.78	0.12	0.38	0.29	1.26	0.97	0.32	0.86	0.75
92	0	0	0	0	0	0	0	0	0	0	0	0
93	0	0	0	0	0	0	0	0	0	0	0	0
94	0	0	0	0	0	0	0	0	0	0	0	0
95	2	1	0.78	3.39	0.67	0.19	2.55	0.3	-2.25	0.99	0.09	-1.73
96	3	0	0.81	3.34	1	0.19	3.7	0	-3.7	1	0.01	-2.85
97	1	0	0.78	3.37	1	0.19	1.28	0	-1.28	1	0.19	-0.99
98	3	0	2.19	2.31	1	0.49	1.37	0	-1.37	1	0.12	-1.05
99	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
100	3	0	1.55	2.97	1	0.34	1.94	0	-1.94	1	0.04	-1.49
101	2	0	0.82	3.38	1	0.19	2.45	0	-2.45	1	0.04	-1.89
102	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
103	4	0	1.51	2.82	1	0.35	2.66	0	-2.66	1	0.01	-2.04
104	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
105	1	1	0.82	3.37	0.5	0.2	1.21	0.3	-0.92	0.96	0.35	-0.7
106	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
107	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
108	1	0	1.13	3.39	1	0.25	0.89	0	-0.89	1	0.25	-0.68
109	0	0	0	4.52	0	0	0	0	0	0	0	0
110	3	0	1.8	2.71	1	0.4	1.67	0	-1.67	1	0.06	-1.28
111	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
112	3	1	1.42	3.1	0.75	0.31	2.12	0.32	-1.8	0.99	0.09	-1.38

113	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
114	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
115	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
116	2	0	2.12	2.4	1	0.47	0.94	0	-0.94	1	0.22	-0.73
117	2	0	0.8	3.39	1	0.19	2.49	0	-2.49	1	0.04	-1.91
118	0	0	0	4.52	0	0	0	0	0	0	0	0
119	2.5	1.5	1.35	3.17	0.62	0.3	1.86	0.47	-1.38	0.95	0.21	-1.06
120	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
121	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
122	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
123	1	1	1.51	3.01	0.5	0.33	0.66	0.33	-0.33	0.89	0.56	-0.26
124	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
125	1	0	1.01	3.5	1	0.22	0.99	0	-0.99	1	0.22	-0.76
126	1	0	0.79	3.41	1	0.19	1.27	0	-1.27	1	0.19	-0.97
127	5	0	1.51	2.95	1	0.34	3.32	0	-3.32	1	0	-2.55
128	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
129	3	2	1.12	3.4	0.6	0.25	2.68	0.59	-2.09	0.98	0.1	-1.61
130	0	0	0.8	3.71	0	0.18	0	0	0	0	0	0
131	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
132	3	1	1.51	2.98	0.75	0.34	1.99	0.34	-1.66	0.99	0.11	-1.27
133	0	0	0.78	3.38	0	0.19	0	0	0	0	0	0
134	1	0	0.78	3.41	1	0.19	1.28	0	-1.28	1	0.19	-0.98
135	2	2	0.8	3.71	0.5	0.18	2.49	0.54	-1.95	0.98	0.15	-1.5
136	2.5	1.5	1.47	2.74	0.62	0.35	1.7	0.55	-1.15	0.93	0.28	-0.88
137	1	0	0.78	2.93	1	0.21	1.28	0	-1.28	1	0.21	-0.99
138	0	0	0	0	0	0	0	0	0	0	0	0
139	3	0	1.63	2.89	1	0.36	1.85	0	-1.85	1	0.05	-1.42
140	1	0	1.13	3.39	1	0.25	0.89	0	-0.89	1	0.25	-0.68
141	3	0	0.8	3.01	1	0.21	3.73	0	-3.73	1	0.01	-2.87
142	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
143	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
144	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
145	3.5	5.5	1.44	3.07	0.39	0.32	2.44	1.79	-0.65	0.78	0.45	-0.5
146	2	0	0.8	3.35	1	0.19	2.49	0	-2.49	1	0.04	-1.92
147	1	1	0.8	3.71	0.5	0.18	1.24	0.27	-0.97	0.97	0.32	-0.75
148	4	1	1.51	3.01	0.8	0.33	2.66	0.33	-2.32	1	0.05	-1.79

149	3	5	1.47	3.03	0.38	0.33	2.04	1.65	-0.39	0.75	0.52	-0.3
150	5	1	1.48	2.71	0.83	0.35	3.37	0.37	-3	1	0.02	-2.31
151	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
152	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
153	0.5	2.5	0.82	2.97	0.17	0.22	0.61	0.84	0.23	0.68	0.52	0.18
154	5	0	1.74	2.75	1	0.39	2.87	0	-2.87	1	0.01	-2.21
155	1	0	1.55	2.97	1	0.34	0.65	0	-0.65	1	0.34	-0.5
156	4	0	1.79	2.63	1	0.41	2.23	0	-2.23	1	0.03	-1.72
157	1	1	0.8	3.71	0.5	0.18	1.24	0.27	-0.97	0.97	0.32	-0.75
158	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
159	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
160	5	0	1.83	2.69	1	0.41	2.73	0	-2.73	1	0.01	-2.1
161	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
162	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
163	3	1	1.54	2.98	0.75	0.34	1.95	0.34	-1.62	0.99	0.12	-1.24
164	1	1	1.12	3.4	0.5	0.25	0.89	0.29	-0.6	0.94	0.43	-0.46
165	0	0	0	4.52	0	0	0	0	0	0	0	0
166	0	0	1.13	3.39	0	0.25	0	0	0	0	0	0
167	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
168	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
169	3	0	1.01	3.5	1	0.22	2.96	0	-2.96	1	0.01	-2.27
170	5	1	1.67	2.85	0.83	0.37	3	0.35	-2.65	1	0.03	-2.04
171	3	3	1.47	3.05	0.5	0.33	2.04	0.98	-1.06	0.91	0.3	-0.82
172	0	0	0	4.52	0	0	0	0	0	0	0	0
173	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
174	2	0	1.1	3.42	1	0.24	1.82	0	-1.82	1	0.06	-1.4
175	0	1	0.82	3.7	0	0.18	0	0.27	0.27	0.82	0.18	0.21
176	5	0	2.19	2.3	1	0.49	2.28	0	-2.28	1	0.03	-1.76
177	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
178	3	2	1.56	2.96	0.6	0.35	1.92	0.68	-1.24	0.95	0.23	-0.96
179	2	1	1.51	2.98	0.67	0.34	1.32	0.34	-0.99	0.96	0.26	-0.76
180	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
181	3	0	0.8	3.39	1	0.19	3.73	0	-3.73	1	0.01	-2.87
182	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
183	1	0	1.51	3	1	0.33	0.66	0	-0.66	1	0.33	-0.51
184	2	0	0.8	3.39	1	0.19	2.49	0	-2.49	1	0.04	-1.91

185	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
186	1	0	0.78	3.41	1	0.19	1.28	0	-1.28	1	0.19	-0.98
187	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
188	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
189	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
190	4	0	1.51	2.99	1	0.33	2.66	0	-2.66	1	0.01	-2.04
191	0	0	0	2.96	0	0	0	0	0	0	0	0
192	3	0	2.2	2.29	1	0.49	1.36	0	-1.36	1	0.12	-1.05
193	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
194	2	1	1.24	3.28	0.67	0.27	1.61	0.31	-1.31	0.98	0.18	-1.01
195	2	0	1.51	2.84	1	0.35	1.33	0	-1.33	1	0.12	-1.02
196	3	0	1.51	2.9	1	0.34	1.99	0	-1.99	1	0.04	-1.53
197	3	0	2.24	2.25	1	0.5	1.34	0	-1.34	1	0.12	-1.03
198	0	0	0	4.52	0	0	0	0	0	0	0	0
199	3	0	2.2	2.32	1	0.49	1.37	0	-1.37	1	0.12	-1.05
200	3	0	1.59	2.93	1	0.35	1.89	0	-1.89	1	0.04	-1.46
201	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
202	2	4	1.11	2.89	0.33	0.28	1.81	1.38	-0.42	0.79	0.53	-0.33
203	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
204	1	1	1.34	3.18	0.5	0.3	0.75	0.31	-0.43	0.91	0.5	-0.33
205	2	1	0.8	3.18	0.67	0.2	2.49	0.31	-2.17	0.99	0.11	-1.67
206	1	1	0.83	3.68	0.5	0.18	1.2	0.27	-0.93	0.97	0.34	-0.71
207	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
208	3	0	1.59	2.93	1	0.35	1.89	0	-1.89	1	0.04	-1.45
209	2	1	1.47	3.03	0.67	0.33	1.36	0.33	-1.03	0.97	0.25	-0.79
210	1	0	0.81	3.34	1	0.2	1.23	0	-1.23	1	0.2	-0.95
211	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
212	2	3	1.14	3.37	0.4	0.25	1.76	0.89	-0.87	0.89	0.37	-0.67
213	1	0	0.78	3.41	1	0.19	1.28	0	-1.28	1	0.19	-0.99
214	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
215	1	0	0.8	3.01	1	0.21	1.24	0	-1.24	1	0.21	-0.96
216	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
217	0.5	1.5	1.45	3.07	0.25	0.32	0.34	0.49	0.14	0.68	0.54	0.11
218	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
219	0	0	0	4.52	0	0	0	0	0	0	0	0
220	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91

221	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
222	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
223	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
224	3	1	2.19	2.31	0.75	0.49	1.37	0.43	-0.94	0.94	0.29	-0.72
225	2	3	1.01	3.49	0.4	0.22	1.98	0.86	-1.12	0.92	0.31	-0.86
226	1	3	1.65	2.72	0.25	0.38	0.61	1.1	0.5	0.51	0.85	0.38
227	3	4	1.51	3.01	0.43	0.33	1.99	1.33	-0.66	0.83	0.43	-0.5
228	2	1	1.24	3.27	0.67	0.28	1.61	0.31	-1.3	0.98	0.19	-1
229	0	0	0	2.96	0	0	0	0	0	0	0	0
230	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
231	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
232	2	0	1.51	2.99	1	0.33	1.33	0	-1.33	1	0.11	-1.02
233	3	1	1.51	3.01	0.75	0.33	1.99	0.33	-1.66	0.99	0.11	-1.28
234	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
235	3	0	1.51	2.82	1	0.35	1.99	0	-1.99	1	0.04	-1.53
236	0	0	0	4.52	0	0	0	0	0	0	0	0
237	2.5	1.5	1.23	3.29	0.62	0.27	2.03	0.46	-1.58	0.97	0.18	-1.21
238	0	0	0.8	3.39	0	0.19	0	0	0	0	0	0
239	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
240	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
241	0	0	0	2.96	0	0	0	0	0	0	0	0
242	1	0	0.78	3.41	1	0.19	1.28	0	-1.28	1	0.19	-0.99
243	4	0	1.51	2.99	1	0.33	2.66	0	-2.66	1	0.01	-2.04
244	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
245	2	0	2.27	2.25	1	0.5	0.88	0	-0.88	1	0.25	-0.68
246	1	3	1.12	2.94	0.25	0.28	0.89	1.02	0.13	0.69	0.72	0.1
247	3	0	1.84	2.68	1	0.41	1.63	0	-1.63	1	0.07	-1.26
248	0	0	0.78	2.93	0	0.21	0	0	0	0	0	0
249	1	0	0.79	2.92	1	0.21	1.27	0	-1.27	1	0.21	-0.97
250	3	2	1.49	3.02	0.6	0.33	2.01	0.66	-1.35	0.96	0.21	-1.04
251	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
252	2	0	1.54	2.98	1	0.34	1.3	0	-1.3	1	0.12	-1
253	1	0	1.13	3.39	1	0.25	0.89	0	-0.89	1	0.25	-0.68
254	1	4	0.32	4.2	0.2	0.07	3.17	0.95	-2.22	0.96	0.3	-1.7
255	1	0	1.1	3.42	1	0.24	0.91	0	-0.91	1	0.24	-0.7
256	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87

257	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
258	2	1	1.51	3	0.67	0.34	1.32	0.33	-0.99	0.96	0.26	-0.76
259	0	0	0	4.52	0	0	0	0	0	0	0	0
260	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
261	5	0	2.03	2.47	1	0.45	2.46	0	-2.46	1	0.02	-1.89
262	2	1	1.49	3.03	0.67	0.33	1.35	0.33	-1.02	0.96	0.25	-0.78
263	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
264	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
265	2	0	0.78	3.41	1	0.19	2.55	0	-2.55	1	0.03	-1.96
266	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
267	1	0	2.18	2.34	1	0.48	0.46	0	-0.46	1	0.48	-0.35
268	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
269	1	0	0.78	3.37	1	0.19	1.28	0	-1.28	1	0.19	-0.98
270	0	0	0	2.96	0	0	0	0	0	0	0	0
271	3	0	1.51	2.82	1	0.35	1.99	0	-1.99	1	0.04	-1.53
272	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
273	0	0	0	2.96	0	0	0	0	0	0	0	0
274	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
275	3	0	1.1	3.42	1	0.24	2.72	0	-2.72	1	0.01	-2.09
276	2	0	2.21	2.28	1	0.49	0.91	0	-0.91	1	0.24	-0.7
277	3	0	1.51	2.79	1	0.35	1.99	0	-1.99	1	0.04	-1.53
278	0	1	1.51	3.01	0	0.33	0	0.33	0.33	0.67	0.33	0.26
279	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
280	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
281	2	2	1.45	3.07	0.5	0.32	1.38	0.65	-0.72	0.9	0.39	-0.56
282	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
283	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
284	2	0	2.01	2.51	1	0.44	1	0	-1	1	0.2	-0.77
285	2.5	2.5	1.51	3.01	0.5	0.33	1.66	0.83	-0.82	0.87	0.38	-0.63
286	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
287	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
288	4	0	2.2	2.28	1	0.49	1.82	0	-1.82	1	0.06	-1.4
289	2.5	1.5	0.82	3.36	0.62	0.2	3.03	0.45	-2.59	0.99	0.1	-1.99
290	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
291	1	0	0.81	3.39	1	0.19	1.23	0	-1.23	1	0.19	-0.95
292	3	0	1.51	2.99	1	0.33	1.99	0	-1.99	1	0.04	-1.53

293	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
294	4	0	2.16	2.33	1	0.48	1.85	0	-1.85	1	0.05	-1.43
295	4	0	1.21	3.26	1	0.27	3.31	0	-3.31	1	0.01	-2.55
296	0	0	0	4.52	0	0	0	0	0	0	0	0
297	4	0	2.19	2.3	1	0.49	1.83	0	-1.83	1	0.06	-1.41
298	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
299	2	0	0.82	3.34	1	0.2	2.45	0	-2.45	1	0.04	-1.88
300	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
301	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
302	2	0	0.8	2.91	1	0.22	2.49	0	-2.49	1	0.05	-1.92
303	3	0	0.8	3.35	1	0.19	3.73	0	-3.73	1	0.01	-2.87
304	2	0	1.21	2.99	1	0.29	1.65	0	-1.65	1	0.08	-1.27
305	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
306	1	0	0.78	3.37	1	0.19	1.28	0	-1.28	1	0.19	-0.99
307	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
308	2	0	0.73	3.79	1	0.16	2.75	0	-2.75	1	0.03	-2.11
309	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
310	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
311	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
312	3	0	1.55	2.97	1	0.34	1.93	0	-1.93	1	0.04	-1.49
313	2	0	0.73	3.79	1	0.16	2.75	0	-2.75	1	0.03	-2.12
314	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
315	2	0	1.51	2.71	1	0.36	1.33	0	-1.33	1	0.13	-1.02
316	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
317	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
318	0	0	0	4.52	0	0	0	0	0	0	0	0
319	0.5	3.5	0.7	3.82	0.12	0.15	0.72	0.92	0.2	0.7	0.49	0.15
320	0	0	0	2.96	0	0	0	0	0	0	0	0
321	3	2	1.43	3.09	0.6	0.32	2.1	0.65	-1.45	0.96	0.19	-1.12
322	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
323	2	0	1.51	2.8	1	0.35	1.33	0	-1.33	1	0.12	-1.02
324	0	0	0	4.52	0	0	0	0	0	0	0	0
325	5	0	1.51	3.01	1	0.33	3.32	0	-3.32	1	0	-2.55
326	1	4	0.8	3.42	0.2	0.19	1.24	1.17	-0.08	0.76	0.65	-0.06
327	0	0	0	0	0	0	0	0	0	0	0	0
328	1.33	4.67	1.78	2.25	0.22	0.44	0.75	2.07	1.32	0.27	0.92	1.02

329	1	3	0.84	3.66	0.25	0.19	1.19	0.82	-0.37	0.84	0.56	-0.28
330	3	4	1.48	3.04	0.43	0.33	2.02	1.32	-0.71	0.83	0.42	-0.54
331	2.5	5.5	1.47	3.03	0.31	0.33	1.7	1.82	0.12	0.62	0.66	0.09
332	2	5	1.49	2.96	0.29	0.33	1.34	1.69	0.35	0.57	0.74	0.27
333	4	6	0.98	3.12	0.4	0.24	4.08	1.92	-2.16	0.93	0.2	-1.66
334	2	0	1.51	2.69	1	0.36	1.33	0	-1.33	1	0.13	-1.02
335	3	4	1.32	2.74	0.43	0.33	2.27	1.46	-0.81	0.84	0.41	-0.62
336	3.5	2.5	1.18	1.99	0.58	0.37	2.97	1.26	-1.71	0.91	0.27	-1.32
337	1	3	0.56	2.27	0.25	0.2	1.78	1.32	-0.46	0.82	0.59	-0.35
338	1.5	2.5	0.85	2.15	0.38	0.28	1.77	1.16	-0.61	0.81	0.53	-0.47
339	2	2	1.04	2.15	0.5	0.33	1.92	0.93	-0.99	0.9	0.39	-0.76
340	1	4	0.48	2.18	0.2	0.18	2.07	1.84	-0.23	0.77	0.63	-0.18
341	0	0	0	0	0	0	0	0	0	0	0	0
342	0	0	0	0	0	0	0	0	0	0	0	0
343	0	0	0	0	0	0	0	0	0	0	0	0
344	0	0	0	0	0	0	0	0	0	0	0	0
345	0	0	0	0	0	0	0	0	0	0	0	0
346	0	0	0	0	0	0	0	0	0	0	0	0
347	0	0	0	0	0	0	0	0	0	0	0	0
348	0	0	0	0	0	0	0	0	0	0	0	0
349	0	0	0	0	0	0	0	0	0	0	0	0
350	0	0	0	0	0	0	0	0	0	0	0	0
351	0	0	0	0	0	0	0	0	0	0	0	0
352	0	0	0	0	0	0	0	0	0	0	0	0
353	0	0	0	0	0	0	0	0	0	0	0	0
354	0	0	0	0	0	0	0	0	0	0	0	0
355	0	0	0	0	0	0	0	0	0	0	0	0
356	2.17	2.83	0.75	3.35	0.43	0.18	2.88	0.84	-2.03	0.96	0.2	-1.57
357	6	2	1.64	2.54	0.75	0.39	3.67	0.79	-2.88	0.99	0.05	-2.21
358	1.5	4.5	0.84	3.34	0.25	0.2	1.78	1.35	-0.44	0.78	0.54	-0.34
359	3	4	0.87	3.65	0.43	0.19	3.44	1.1	-2.34	0.97	0.14	-1.8
360	3	5	1.02	3.26	0.38	0.24	2.95	1.53	-1.42	0.9	0.29	-1.09
361	2.5	1.5	0.85	3.32	0.62	0.2	2.93	0.45	-2.48	0.98	0.11	-1.91
362	2.5	3.5	1.19	3.14	0.42	0.28	2.09	1.12	-0.98	0.87	0.37	-0.75
363	3	4	1.49	3.02	0.43	0.33	2.01	1.32	-0.68	0.83	0.42	-0.53
364	2	5	0.78	3.43	0.29	0.19	2.56	1.46	-1.1	0.88	0.38	-0.84

365	1.25	7.75	0.86	3.55	0.14	0.19	1.45	2.18	0.73	0.53	0.78	0.56
366	3.33	3.67	1	3.5	0.48	0.22	3.34	1.05	-2.29	0.97	0.14	-1.76
367	2.5	5.5	1.14	3.34	0.31	0.25	2.19	1.64	-0.55	0.77	0.49	-0.42
368	3	3	1.46	3.03	0.5	0.33	2.05	0.99	-1.06	0.91	0.3	-0.82
369	1	3	0.82	3.35	0.25	0.2	1.22	0.9	-0.32	0.82	0.58	-0.25
370	3	3	1.33	3.02	0.5	0.31	2.25	0.99	-1.26	0.92	0.27	-0.97
371	3	3	1.51	2.5	0.5	0.38	1.99	1.2	-0.79	0.85	0.41	-0.6
372	1.17	5.83	0.81	3.24	0.17	0.2	1.45	1.8	0.35	0.62	0.73	0.27
373	4	4	1.48	3.01	0.5	0.33	2.7	1.33	-1.37	0.92	0.25	-1.06
374	1.5	5.5	0.79	3.06	0.21	0.2	1.9	1.8	-0.11	0.7	0.62	-0.08
375	2.5	4.5	1.32	2.78	0.36	0.32	1.89	1.62	-0.27	0.72	0.56	-0.21
376	1.5	3.5	0.95	2.98	0.3	0.24	1.58	1.18	-0.41	0.78	0.55	-0.31
377	3	3	0.9	2.96	0.5	0.23	3.35	1.01	-2.34	0.97	0.14	-1.8
378	3	2	1.17	2.45	0.6	0.32	2.55	0.81	-1.74	0.96	0.2	-1.34
379	3	2	1.23	2.36	0.6	0.34	2.44	0.85	-1.59	0.95	0.22	-1.22
380	2.5	3.5	1.28	2.43	0.42	0.34	1.96	1.44	-0.52	0.77	0.51	-0.4
381	1	5	1.31	2.8	0.17	0.32	0.76	1.79	1.03	0.38	0.9	0.79
382	1.5	4.5	1.29	2.8	0.25	0.31	1.17	1.61	0.44	0.55	0.75	0.34
383	1	4	0.84	3.34	0.2	0.2	1.19	1.2	0.01	0.73	0.68	0.01
384	2.67	3.33	1.46	2.7	0.44	0.35	1.82	1.24	-0.59	0.8	0.47	-0.45
385	3	4	1.51	2.98	0.43	0.34	1.99	1.34	-0.65	0.82	0.44	-0.5
386	2	3	0.82	3.36	0.4	0.2	2.43	0.89	-1.54	0.94	0.26	-1.19
387	1	2	0.79	3.46	0.33	0.18	1.27	0.58	-0.7	0.91	0.46	-0.53
388	2	6	1.81	2.71	0.25	0.4	1.11	2.21	1.1	0.32	0.89	0.85
389	1	3	0.85	3.34	0.25	0.2	1.18	0.9	-0.28	0.82	0.6	-0.22
390	0	0	0	0	0	0	0	0	0	0	0	0
391	0	0	0	0	0	0	0	0	0	0	0	0
392	1	2	0.65	2.64	0.33	0.2	1.53	0.76	-0.77	0.9	0.49	-0.59
393	0	0	0.7	3.01	0	0.19	0	0	0	0	0	0
394	2	2	0.83	3.34	0.5	0.2	2.4	0.6	-1.8	0.97	0.18	-1.38
395	0	1	0.82	3.42	0	0.19	0	0.29	0.29	0.81	0.19	0.22
396	2	0	1.32	2.88	1	0.31	1.51	0	-1.51	1	0.1	-1.17
397	4	0	1.51	2.97	1	0.34	2.66	0	-2.66	1	0.01	-2.04
398	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
399	0	0	0.78	3.42	0	0.19	0	0	0	0	0	0
400	5	1	1.55	2.96	0.83	0.34	3.22	0.34	-2.88	1	0.02	-2.22

401	4	0	1.51	2.99	1	0.33	2.66	0	-2.66	1	0.01	-2.04
402	3	0	1.61	2.91	1	0.36	1.86	0	-1.86	1	0.05	-1.43
403	1	0	1.51	2.67	1	0.36	0.66	0	-0.66	1	0.36	-0.51
404	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
405	0	0	0.8	3.71	0	0.18	0	0	0	0	0	0
406	1	0	1.1	3.42	1	0.24	0.91	0	-0.91	1	0.24	-0.7
407	0	0	0.8	3.71	0	0.18	0	0	0	0	0	0
408	0	0	0.8	3.01	0	0.21	0	0	0	0	0	0
409	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
410	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
411	2	0	2.27	2.25	1	0.5	0.88	0	-0.88	1	0.25	-0.68
412	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
413	3	0	1.51	2.98	1	0.34	1.99	0	-1.99	1	0.04	-1.53
414	1	0	0.81	3.39	1	0.19	1.24	0	-1.24	1	0.19	-0.96
415	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
416	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
417	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
418	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
419	3	1	1.51	2.99	0.75	0.33	1.99	0.33	-1.66	0.99	0.11	-1.28
420	2	1	0.58	2.66	0.67	0.18	3.47	0.38	-3.09	0.99	0.08	-2.38
421	1	0	1.51	2.71	1	0.36	0.66	0	-0.66	1	0.36	-0.51
422	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
423	0	0	0	2.96	0	0	0	0	0	0	0	0
424	3	1	0.8	3.71	0.75	0.18	3.73	0.27	-3.46	1	0.02	-2.66
425	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
426	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
427	1	0	2.13	2.31	1	0.48	0.47	0	-0.47	1	0.48	-0.36
428	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
429	3	0	0.8	3.39	1	0.19	3.73	0	-3.73	1	0.01	-2.87
430	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
431	2.5	1.5	1.46	3.06	0.62	0.32	1.71	0.49	-1.22	0.94	0.25	-0.94
432	0	0	1.51	3.01	0	0.33	0	0	0	0	0	0
433	2	0	1.13	3.39	1	0.25	1.78	0	-1.78	1	0.06	-1.37
434	2	1	1.55	2.95	0.67	0.34	1.29	0.34	-0.95	0.96	0.27	-0.73
435	2	0	1.01	3.5	1	0.22	1.97	0	-1.97	1	0.05	-1.52
436	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53

437	4	0	1.96	2.41	1	0.45	2.04	0	-2.04	1	0.04	-1.57
438	0	0	0.8	3.39	0	0.19	0	0	0	0	0	0
439	3	0	2.21	2.28	1	0.49	1.36	0	-1.36	1	0.12	-1.04
440	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
441	3	0	1.59	2.93	1	0.35	1.89	0	-1.89	1	0.04	-1.46
442	3	0	2.09	2.33	1	0.47	1.44	0	-1.44	1	0.11	-1.11
443	2	0	1.89	2.44	1	0.44	1.06	0	-1.06	1	0.19	-0.81
444	4	0	1.98	2.53	1	0.44	2.02	0	-2.02	1	0.04	-1.56
445	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
446	3	1	1.42	3.1	0.75	0.31	2.12	0.32	-1.8	0.99	0.09	-1.38
447	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
448	0	0	0.78	3.42	0	0.19	0	0	0	0	0	0
449	1	0	0.79	3.41	1	0.19	1.27	0	-1.27	1	0.19	-0.97
450	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
451	4	0	2.19	2.31	1	0.49	1.83	0	-1.83	1	0.06	-1.41
452	4	0	1.51	3.01	1	0.33	2.66	0	-2.66	1	0.01	-2.04
453	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
454	4	0	1.63	2.89	1	0.36	2.46	0	-2.46	1	0.02	-1.89
455	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
456	1	0	1.13	3.39	1	0.25	0.89	0	-0.89	1	0.25	-0.68
457	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
458	0	0	1.13	3.39	0	0.25	0	0	0	0	0	0
459	1	0	1.51	3.01	1	0.33	0.66	0	-0.66	1	0.33	-0.51
460	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
461	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53
462	2	0	1.83	2.61	1	0.41	1.1	0	-1.1	1	0.17	-0.84
463	0	1	1.15	3.37	0	0.25	0	0.3	0.3	0.75	0.25	0.23
464	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
465	0	0	0.8	3.01	0	0.21	0	0	0	0	0	0
466	1	0	0.8	3.71	1	0.18	1.24	0	-1.24	1	0.18	-0.96
467	3	0	1.51	2.98	1	0.34	1.99	0	-1.99	1	0.04	-1.53
468	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
469	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
470	2	2	0.81	3.7	0.5	0.18	2.47	0.54	-1.93	0.98	0.15	-1.49
471	3	1	1.83	2.69	0.75	0.4	1.64	0.37	-1.27	0.97	0.18	-0.98
472	3	0	1.51	3.01	1	0.33	1.99	0	-1.99	1	0.04	-1.53

473	5	2	1.69	2.73	0.71	0.38	2.96	0.73	-2.23	0.99	0.08	-1.72
474	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
475	2	0	0.8	3.71	1	0.18	2.49	0	-2.49	1	0.03	-1.91
476	0	0	0	4.52	0	0	0	0	0	0	0	0
477	0	0	0.8	3.71	0	0.18	0	0	0	0	0	0
478	3	2	1.34	3.18	0.6	0.3	2.24	0.63	-1.61	0.97	0.16	-1.24
479	2	0	2.26	2.25	1	0.5	0.88	0	-0.88	1	0.25	-0.68
480	2	0	1.51	3.01	1	0.33	1.33	0	-1.33	1	0.11	-1.02
481	3	2	1.51	3.01	0.6	0.33	1.99	0.66	-1.33	0.95	0.21	-1.02
482	3	0	0.8	3.71	1	0.18	3.73	0	-3.73	1	0.01	-2.87
483	1	0	0.78	2.93	1	0.21	1.28	0	-1.28	1	0.21	-0.98
484	3	3	1.42	3.06	0.5	0.32	2.12	0.98	-1.14	0.92	0.29	-0.87
485	2	0	0.8	3.01	1	0.21	2.49	0	-2.49	1	0.04	-1.91
486	1	0	1.01	3.05	1	0.25	0.99	0	-0.99	1	0.25	-0.76
487	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary File 6

Lineage specific dn/ds values Kindlins.

Branch Name	Mean	Std.Dev.	2.50%	Median	97.50%	Prob{dN>dS}†
PSN_1_HS	0.08382	0.13	0.04124	0.04521	0.78095	0
PSN_1_PT	0.78069	0.0174	0.78036	0.78174	0.78483	0
Node6	0.1163	0.03054	0.04577	0.12884	0.13269	0
PSN_1_BT	0.13873	0.0201	0.12635	0.12948	0.18787	0
Node5	0.14722	0.02813	0.12588	0.13023	0.19449	0
PSN_RN	0.13124	0.01591	0.12315	0.12931	0.18401	0
PSN_1_MM	0.04582	0.00712	0.04149	0.04518	0.04877	0
Node10	0.04514	0.00217	0.04124	0.04517	0.04749	0
Node4	0.18221	0.01879	0.13166	0.18748	0.19719	0
PSN_1_AC	0.13067	0.00721	0.12588	0.12933	0.15825	0
Node3	0.133	0.01344	0.12588	0.12933	0.18577	0
PSN_1_XL	0.04591	0.00226	0.04396	0.04524	0.05381	0
Node2	0.04493	0.00142	0.0404	0.04514	0.04665	0
PSN_1_TR	0.12931	0.0031	0.12539	0.12926	0.13474	0
PSN_1_DR	0.12975	0.00437	0.1251	0.12928	0.13597	0
Node15	0.18603	0.01442	0.13351	0.18899	0.19906	0
Node1	0.18869	0.00912	0.16987	0.1912	0.19948	0
PSN_2_HS	0.05053	0.02951	0.03999	0.04517	0.13162	0
PSN_2_PT	0.07069	0.05304	0.04217	0.0455	0.18982	0
Node21	0.04418	0.00421	0.02545	0.04508	0.04698	0
PSN_2_BT	0.04522	0.00223	0.0415	0.04517	0.04758	0
Node20	0.04593	0.00804	0.0415	0.04518	0.04918	0
PSN_2_MM	0.04497	0.00255	0.04009	0.04515	0.04747	0
PSN_2_RN	0.04786	0.01216	0.04265	0.04524	0.06715	0
Node25	0.04608	0.00683	0.04263	0.0452	0.05428	0
Node19	0.14343	0.02271	0.12669	0.13041	0.18699	0
PSN_2_AC	0.12952	0.00321	0.12519	0.12927	0.13512	0
PSN_2_XL	0.1313	0.00837	0.1264	0.12935	0.17136	0
Node28	0.04506	0.00142	0.04124	0.04515	0.04751	0
Node18	0.18632	0.01813	0.1299	0.19012	0.20126	0
PSN_2_DR	0.1318	0.00951	0.12631	0.12937	0.17406	0
PSN_2_TF	0.12924	0.00349	0.12446	0.12924	0.13501	0
Node31	0.18493	0.02053	0.13107	0.18838	0.19918	0

† Note: not a p-value!

Supplementary File 6

RESIDUE RANKS

Alignment	Residue#	Amino aci	Variation	Rank
109	1	M	SE.NMQR	7
110	2	T	ES.LTA	6
111	3	E	TA.QRDES	8
112	4	L	AL.IP	5
113	5	P	SL.MPG	6
117	6	A	GRM.EAS	7
118	7	P	ESPL.HAVT	9
119	8	L	AIS.ELVQ	8
120	9	S	RMTS.EVP	8
121	10	Y	EAR.QYHDN	9
122	11	F	TGRDMAVF	8
123	12	Q	EDQPKR	6
124	13	N	YGQAHTNR	9
125	14	A	GSENA	5
126	15	Q	SEGVDTAQ	8
127	16	M	DAGEM.LVT	9
128	17	S	NPGSV.KW	8
129	18	E	DEAQ.SG	7
133	19	D	ETASNDGF	8
134	20	N	ENHPSRQ	7
135	21	H	QSTRVHND	8
136	22	L	EGVL.SP	7
137	23	S	ED.TSP	6
138	24	N	DP.RGNSY	8
139	25	T	GL.PATE	7
140	26	V	I.PSVE	6
141	27	R	TE.RND	6
142	28	S	VH.RASG	7
143	29	Q	.DQRG	5
151	30	N	SG.EN	5
152	31	D	PR.SNDF	7
153	32	N	PR.NGSD	7
154	33	R	LA.QVPMIR	9
155	34	E	QT.DSE	6
157	35	R	TPGFSR	6
158	36	Q	RLTDNHQS	8
159	37	E	EDNALSHQ	9
160	38	H	EALVTHQR	8
162	39	N	EVTLRASN	9
163	40	D	EHNAFTSD	9
164	41	R	TERVAQN	7
165	42	R	ERNPAQIV	8
166	43	S	QLSNVGPR	9
167	44	L	KLQVRTPES	9
168	45	G	DSEVTGN	7
169	46	H	DAMNVRHS	8

170	47	P	EGRNQPTD	8
171	48	E	QRNED	5
172	49	P	SEVPGRA	7
173	50	L	CNVRAEIL	8
174	51	S	GSENLD	6
175	52	N	MV.STANR	8
176	53	G	KN.RVG	6
177	54	R	Y.PQNREI	8
181	55	P	KT.SPRAQ	8
182	56	Q	IA.RPQG	7
183	57	G	LE.QATNSG	10
184	58	N	NE.TPASG	8
185	59	S	VR.GLQPTS	9
188	60	R	SR.GQH	6
189	61	Q	FI.GSRVQT	9
190	62	V	GR.SMEVI	8
191	63	V	DA.GNRTVC	9
192	64	E	DR.GVEHQ	8
193	65	Q	GQ.PVSRH	8
194	66	D	DE.P	4
195	67	E	DE.TSP	6
196	68	E	PA.NEMD	7
197	69	E	TA.ED	5
198	70	D	SR.MDE	6
199	71	E	ER.D	4
202	72	E	ED	2
203	73	L	ELAQM	5
204	74	T	ADEGMT	6
205	75	L	L	1
206	76	K	RKQ	3
207	77	Y	FY	2
208	78	G	GD	2
209	79	A	A	1
210	80	K	QESK	4
211	81	H	QSH	3
212	82	V	MV	2
213	83	I	IL	2
214	84	M	LAHKM	5
215	85	L	L	1
216	86	F	IF	2
217	87	V	FKVIA	5
218	88	P	P	1
219	89	V	V	1
220	90	T	FST	3
221	91	L	IAL	3
222	92	C	C	1
223	93	M	ML	2
224	94	V	AILV	4
225	95	V	LV	2

226	96	V	V	1
227	97	V	VI	2
228	98	A	AF	2
229	99	T	IT	2
230	100	I	QIMV	4
231	101	K	LRNSKG	6
232	102	S	STA	3
233	103	V	VI	2
234	104	S	ETS	3
235	105	F	KYF	3
236	106	Y	NFY	3
237	107	T	VSNT	4
238	108	R	TQSERD	6
239	109	K	SNT.KD	6
240	110	D	SDNA	4
241	111	G	GTV	3
244	112	Q	TQHY	4
245	113	L	LF	2
246	114	I	IALV	4
247	115	Y	Y	1
248	116	T	T	1
249	117	P	P	1
250	118	F	F	1
251	119	T	DEVHRT	6
252	120	E	ESR	3
253	121	D	DNEQK	5
254	122	T	TGSK	4
255	123	E	AGDPNE	6
259	124	T	NSEQTG	6
260	125	V	DSIPHAVT	8
261	126	G	GVSA	4
262	127	Q	FEVTQS	6
263	128	R	VRK	3
264	129	A	LFGAV	5
265	130	L	LGW	3
266	131	H	FGMSQNHD	8
267	132	S	AS	2
268	133	I	LVMIF	5
269	134	L	ALG	3
270	135	N	N	1
271	136	A	VAS	3
272	137	A	ALIV	4
273	138	I	IV	2
274	139	M	VMLI	4
275	140	I	IVLM	4
276	141	S	TGCS	4
277	142	V	LIV	3
278	143	I	VI	2
279	144	V	VIL	3

280	145	V	VLI	3
281	146	M	M	1
282	147	T	T	1
283	148	I	IFVL	4
284	149	L	ILFV	4
285	150	L	L	1
286	151	V	VI	2
287	152	V	CMVI	4
288	153	L	LF	2
289	154	Y	Y	1
290	155	K	KI	2
291	156	Y	YKC	3
292	157	R	REK	3
293	158	C	CYF	3
294	159	Y	Y	1
295	160	K	KR	2
296	161	V	ILVF	4
297	162	I	I	1
298	163	H	YHEQ	4
299	164	A	GA	2
300	165	W	W	1
301	166	L	L	1
302	167	I	VAIF	4
303	168	I	VLFI	4
304	169	S	AS	2
305	170	S	SAN	3
306	171	L	ALF	3
307	172	L	LMF	3
308	173	L	L	1
309	174	L	L	1
310	175	F	FY	2
311	176	F	VFLI	4
312	177	F	F	1
313	178	S	STA	3
314	179	F	SYTFL	5
315	180	I	FQIL	4
316	181	Y	FY	2
317	182	L	FIVL	4
318	183	G	VEQG	4
326	184	E	EQ	2
327	185	V	VL	2
328	186	F	LF	2
329	187	K	QIKRVS	6
330	188	T	VAST	4
331	189	Y	HFY	3
332	190	N	YND	3
333	191	V	LAVI	4
334	192	A	FSPA	4
335	193	V	IPMVC	5

336	194	D	DS	2
337	195	Y	WAY	3
338	196	I	PILFV	5
339	197	T	STL	3
340	198	V	FMVAIL	6
341	199	A	LAVT	4
342	200	L	VFLI	4
343	201	L	LIGMVF	6
344	202	I	ILM	3
345	203	W	WG	2
346	204	N	N	1
347	205	F	FY	2
348	206	G	G	1
349	207	V	GTVMA	5
350	208	V	MVL	3
351	209	G	G	1
352	210	M	VFM	3
353	211	I	LIMV	4
354	212	S	VACS	4
355	213	I	I	1
356	214	H	HF	2
357	215	W	W	1
358	216	K	KRQ	3
359	217	G	GS	2
360	218	P	P	1
361	219	L	L	1
362	220	R	RALH	4
363	221	L	LV	2
364	222	Q	Q	1
365	223	Q	Q	1
366	224	A	AVFGL	5
367	225	Y	Y	1
368	226	L	L	1
369	227	I	IV	2
370	228	M	FITVM	5
371	229	I	CVMI	4
372	230	S	SA	2
373	231	A	A	1
374	232	L	L	1
375	233	M	TM	2
376	234	A	A	1
377	235	L	NL	2
378	236	V	IV	2
379	237	F	FL	2
380	238	I	VI	2
381	239	K	K	1
382	240	Y	YN	2
383	241	L	L	1
384	242	P	P	1

385	243	E	NDE	3
386	244	W	W	1
387	245	T	T	1
388	246	A	ATVL	4
389	247	W	W	1
390	248	L	IVFATL	6
391	249	I	LVI	3
392	250	L	L	1
393	251	A	AFG	3
394	252	V	AV	2
395	253	I	IV	2
396	254	S	SA	2
397	255	V	LIV	3
398	256	Y	YW	2
399	257	D	D	1
400	258	L	L	1
401	259	V	IFVL	4
402	260	A	A	1
403	261	V	V	1
404	262	L	L	1
405	263	C	CST	3
406	264	P	P	1
407	265	K	KCR	3
408	266	G	G	1
409	267	P	P	1
410	268	L	L	1
411	269	R	RK	2
412	270	M	VCYIM	5
413	271	L	L	1
414	272	V	V	1
415	273	E	EQ	2
416	274	T	TV	2
417	275	A	A	1
418	276	Q	RQ	2
419	277	E	E	1
420	278	R	R	1
421	279	N	ND	2
422	280	E	EQ	2
423	281	T	TPQA	4
424	282	L	IL	2
425	283	F	F	1
426	284	P	P	1
427	285	A	SA	2
428	286	L	L	1
429	287	I	I	1
430	288	Y	Y	1
431	289	S	S	1
432	290	S	TS	2
433	291	T	TG	2

434	292	M	MVF	3
435	293	V	VMI	3
436	294	W	WY	2
437	295	L	LTPAF	5
438	296	V	VYLTF	5
439	297	N	GTVN	4
450	298	M	MLTV	4
451	299	A	AVN	3
452	300	E	DTSQE	5
453	301	G	RVASIEGN	8
454	302	D	PGVSQDAN	8
455	303	P	TDEPS	5
456	304	E	NSAPTE	6
457	305	A	KSTPRAQ	7
458	306	Q	KSTPNQR	7
459	307	R	KNDSRP	6
460	308	R	DSPQRK	6
461	309	V	KARTSV	6
462	310	S	KTEAHPS	7
463	311	K	NIPTLK	6
464	312	N	TEQVSNK	7
465	313	S	DSREPK	6
466	314	K	DQSANPTK	8
467	315	Y	TPDQYRN	7
468	316	N	SRQDVENK	8
469	317	A	GVNDEKAT	8
470	318	E	SATNEQD	7
471	319	S	SDLHVRGE	8
482	320	T	ETSQ.ADL	8
483	321	E	GSERDA.	7
484	322	R	GMTEVNSR	9
485	323	E	GSPEAQ	6
486	324	S	ESKNMTAI	8
487	325	Q	RQSNA	5
488	326	D	EPHITND	7
489	327	T	GRKP.TAS	8
490	328	V	RAV.G	5
491	329	A	RKQ.ATS	7
492	330	E	DQRN.EAG	9
493	331	N	NGIQ.DETS	10
494	332	D	DSPR.QG	7
495	333	D	DRQ.TE	6
504	334	G	G.	2
522	335	G	.G	2
523	336	F	.F	2
524	337	S	.TDSG	5
525	338	E	.QTPE	5
526	339	E	.EVAD	5
527	340	W	.WF	3

528	341 E	.STVEN	6
529	342 A	.AEDQN	6
530	343 Q	.NRHQS	6
531	344 R	.LRQ	4
534	345 D	DAKRQ	5
535	346 S	DVQLHNSP	8
536	347 H	DSQAERHT	9
537	348 L	TEIRLQ	6
538	349 G	DAERSGT	7
539	350 P	GDSQPA	6
540	351 H	IDNMLHT	7
541	352 R	EGTLSQHR	9
551	353 S	TPVQNSE	7
552	354 T	NREST	5
553	355 P	RGVSQEPA	8
554	356 E	END	3
555	357 S	RTEVSA	6
556	358 R	REY	3
557	359 A	RSLAQ	5
558	360 A	ETAQV	5
559	361 V	RNAVI	5
560	362 Q	QET.RS	6
561	363 E	QAR.EDN	7
562	364 L	QAP.LM	6
563	365 S	QPTD.RS	7
564	366 S	QAV.SGNR	8
579	367 S	QS.TRAD	7
582	368 I	ESN.PIMT	8
583	369 L	EFNTVPL	7
584	370 A	EQHDPGAT	8
585	371 G	EPRSAGDL	8
586	372 E	EDH	3
587	373 D	EDG	3
588	374 P	QEPD	4
589	375 E	ED	2
590	376 E	ED	2
591	377 R	RS	2
593	378 G	G	1
594	379 V	FVI	3
595	380 K	K	1
596	381 L	L	1
597	382 G	G	1
598	383 L	L	1
599	384 G	G	1
600	385 D	D	1
601	386 F	F	1
602	387 I	I	1
603	388 F	F	1
604	389 Y	Y	1

605	390	S	S	1
606	391	V	IVM	3
607	392	L	L	1
608	393	V	VL	2
609	394	G	G	1
610	395	K	K	1
611	396	A	A	1
612	397	S	AS	2
613	398	A	HTSA	4
614	399	T	D.T	3
615	400	A	S.A	3
616	401	S	TAYSN	5
617	402	G	GHFK	4
618	403	D	DE	2
619	404	W	W	1
620	405	N	VTN	3
621	406	T	VT	2
622	407	T	IT	2
623	408	I	SLI	3
624	409	A	SA	2
625	410	C	C	1
626	411	F	FY	2
627	412	V	V	1
628	413	A	A	1
629	414	I	I	1
630	415	L	L	1
631	416	I	I	1
632	417	G	G	1
633	418	L	L	1
634	419	C	CA	2
635	420	L	MCFL	4
636	421	T	T	1
637	422	L	IL	2
638	423	L	ILV	3
639	424	L	IL	2
640	425	L	L	1
641	426	A	GSA	3
642	427	I	IV	2
643	428	F	VFWY	4
644	429	K	RK	2
645	430	K	RK	2
646	431	A	A	1
647	432	L	L	1
648	433	P	P	1
649	434	A	A	1
650	435	L	L	1
651	436	P	P	1
652	437	I	IV	2
653	438	S	S	1

654	439	I	I	1
655	440	T	FTA	3
656	441	F	CFS	3
657	442	G	G	1
658	443	L	L	1
659	444	V	ICV	3
660	445	F	F	1
661	446	Y	YFCN	4
662	447	F	F	1
663	448	A	SLCAT	5
664	449	T	ST	2
665	450	D	QSRDA	5
666	451	Y	YEWAN	5
667	452	L	VIFL	4
668	453	V	ILV	3
669	454	Q	ADTKFRQS	8
670	455	P	P	1
671	456	F	FL	2
672	457	M	AIVMT	5
673	458	D	QDTE	4
674	459	Q	VRQDHEAT	8
675	460	L	LV	2
676	461	A	ANS	3
677	462	F	TEQAGSVY	9
678	463	H	TRKEQH	6
679	464	Q	QC	2
680	465	F	TILVAF	6
681	466	Y	FLY	3
682	467	I	ILYV	4