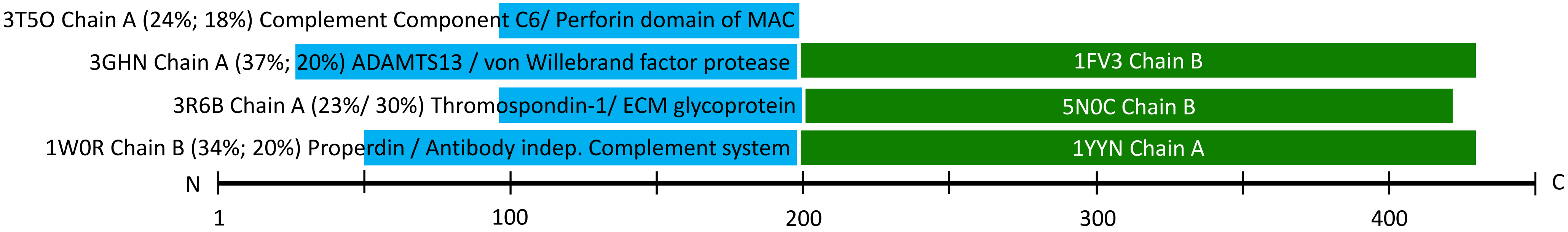
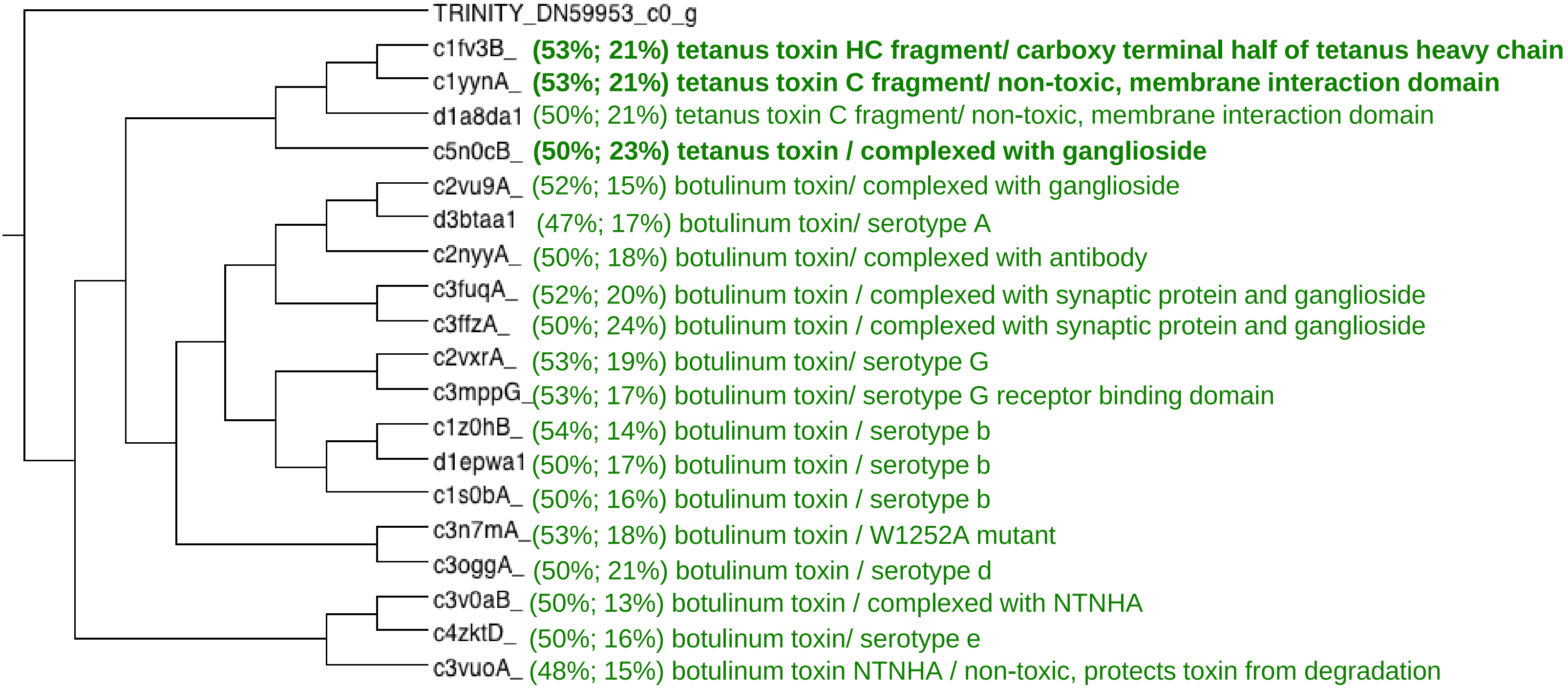
SeqID: TRINITY_DN59953_c0_g1_i1
Annotation: uncharacterized protein
Identified by seq analysis: N

Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

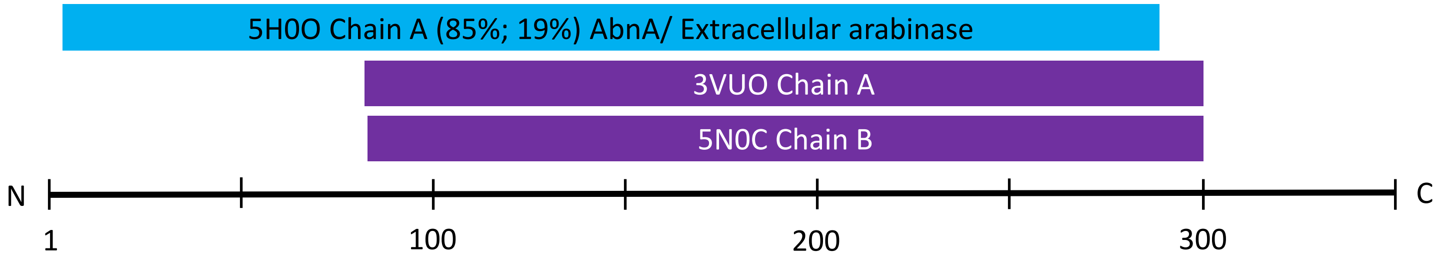
3T5O Chain A (Alignment coverage%; identity%) Complement Component C6/ Perforin domain of MAC

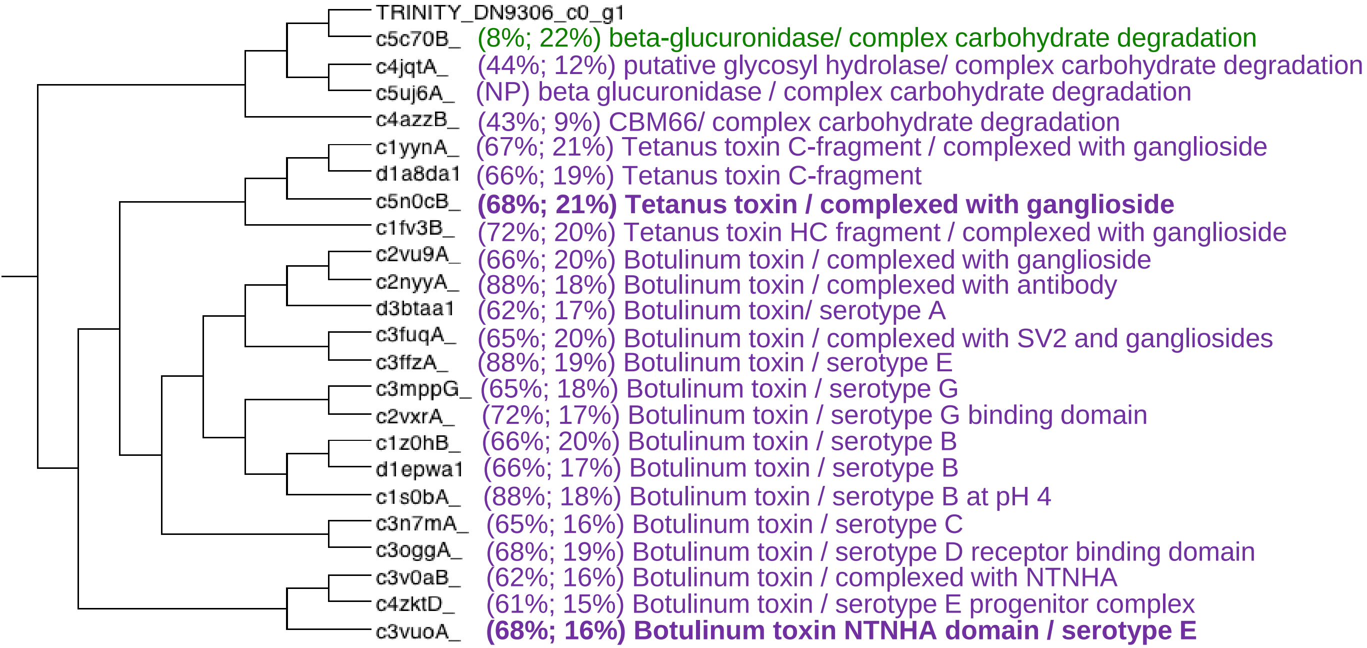




SeqID: TRINITY_DN9306_c0_g1_i1
Annotation: Nematobalst-specific nb012a
Identified by seq analysis: N

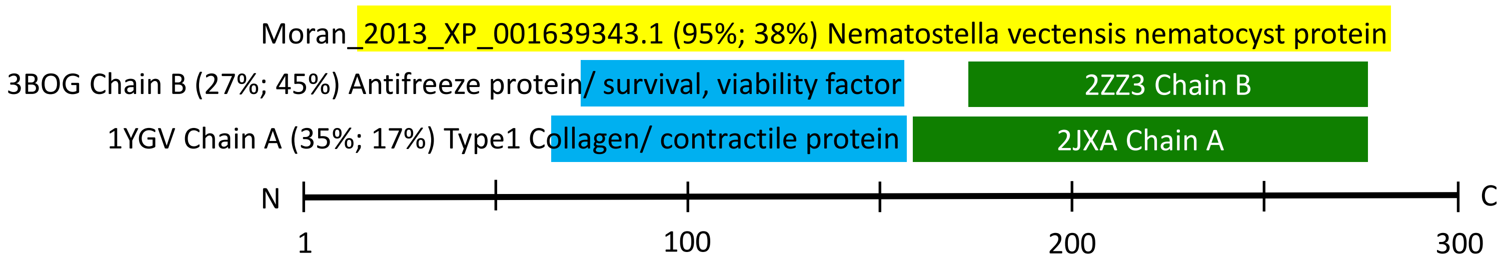
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree





SeqID: TRINITY_DN60481_c0_g1_i1
Annotation: Nematogalectin C
Identified by seq analysis: Y

Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor;
Red = Non-valid entry; Blue = Not in tree

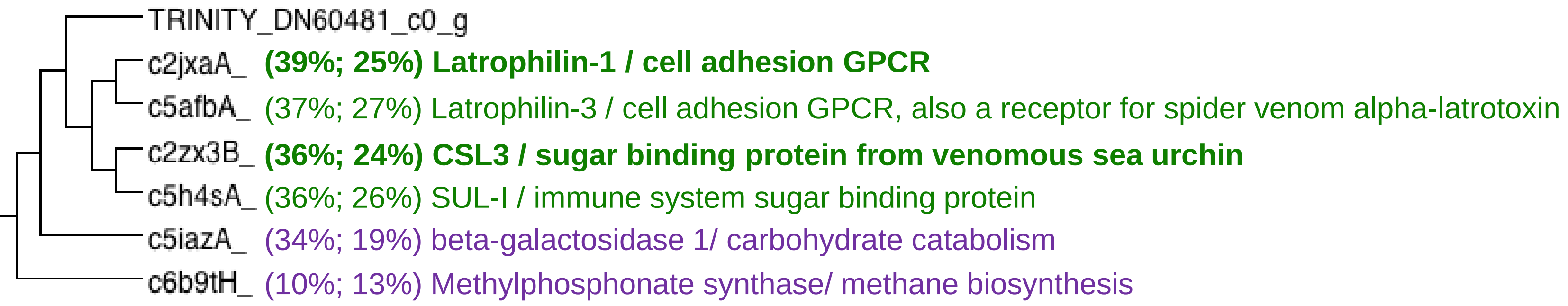

Moran_2013_XP_001639343.1 (95%; 38%) Nematostella vectensis nematocyst protein

3BOG Chain B (27%; 45%) Antifreeze protein/ survival, viability factor

2ZZ3 Chain B

1YGV Chain A (35%; 17%) Type1 Collagen/ contractile protein

2JXA Chain A


TRINITY_DN60481_c0_g

c2jxaA_ **(39%; 25%) Latrophilin-1 / cell adhesion GPCR**

c5afbA_ (37%; 27%) Latrophilin-3 / cell adhesion GPCR, also a receptor for spider venom alpha-latrotoxin

c2zx3B_ **(36%; 24%) CSL3 / sugar binding protein from venomous sea urchin**

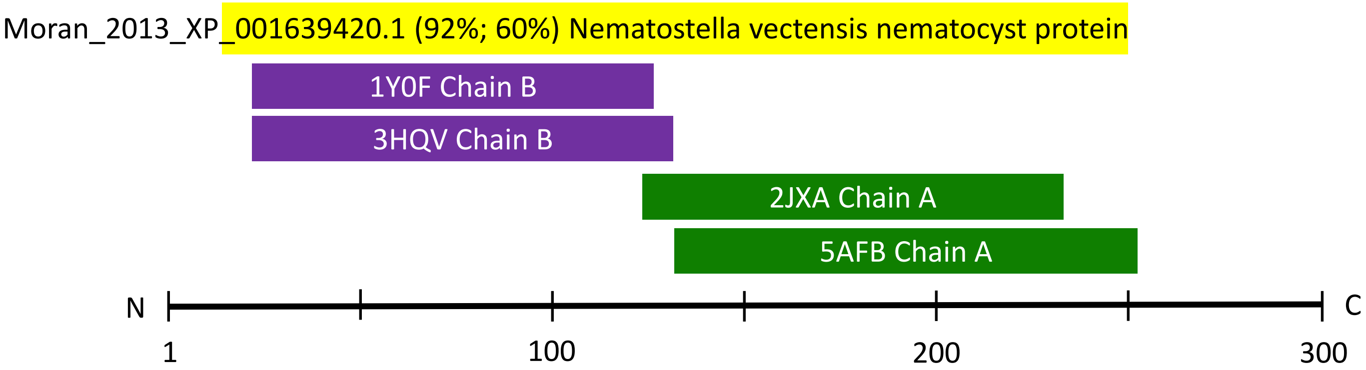
c5h4sA_ (36%; 26%) SUL-I / immune system sugar binding protein

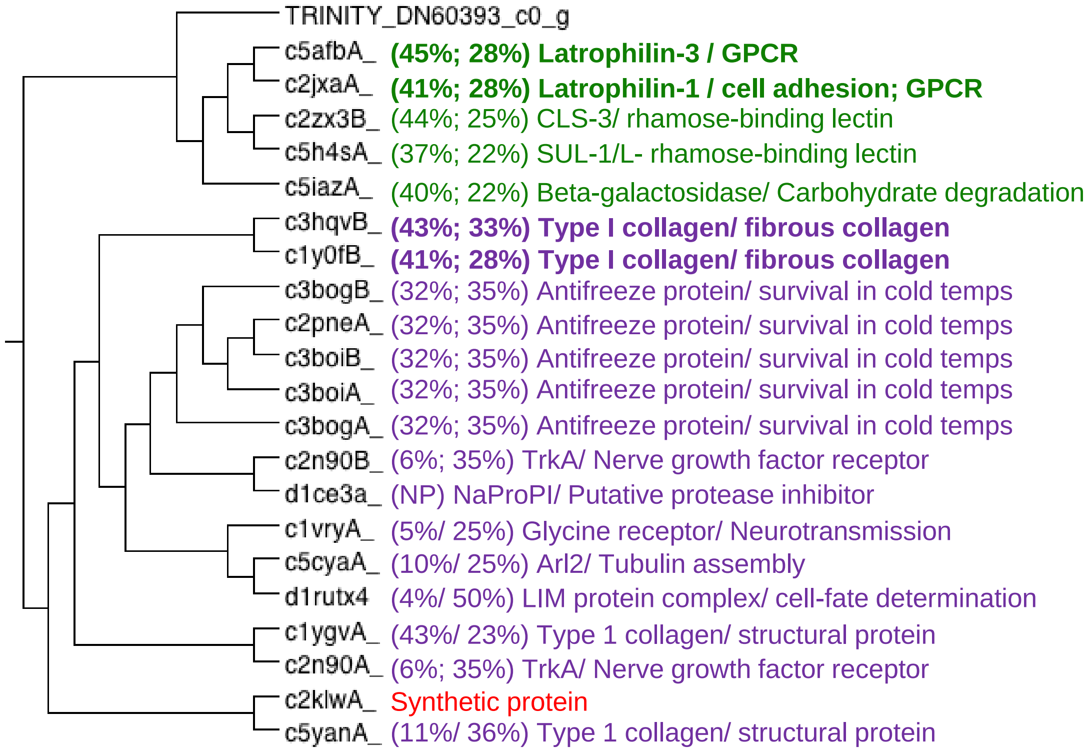
c5iazA_ (34%; 19%) beta-galactosidase 1/ carbohydrate catabolism

c6b9tH_ (10%; 13%) Methylphosphonate synthase/ methane biosynthesis

SeqID: TRINITY_DN60393_c0_g1_i1
Annotation: Nematogalectin-related
Identified by seq analysis: Y

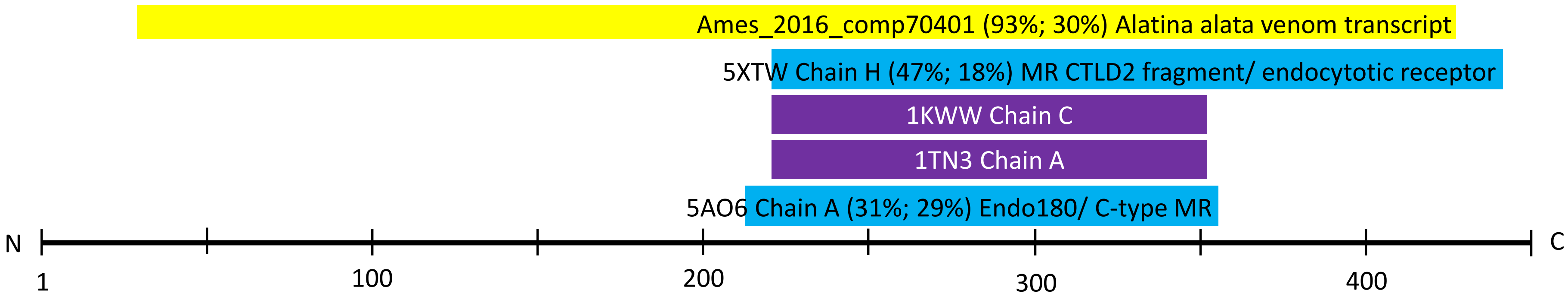
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

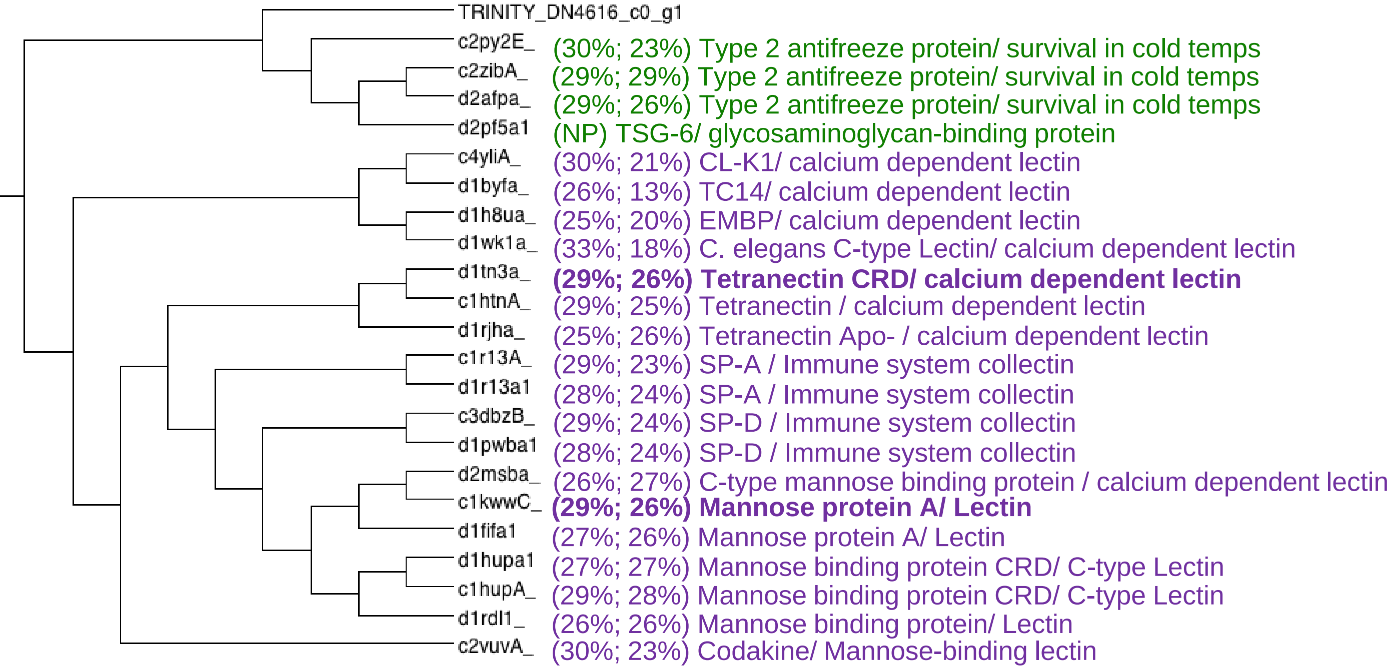




SeqID: TRINITY_DN4616_c0_g1_i1
Annotation: Macrophage mannose receptor 1-like
Identified by seq analysis: Y

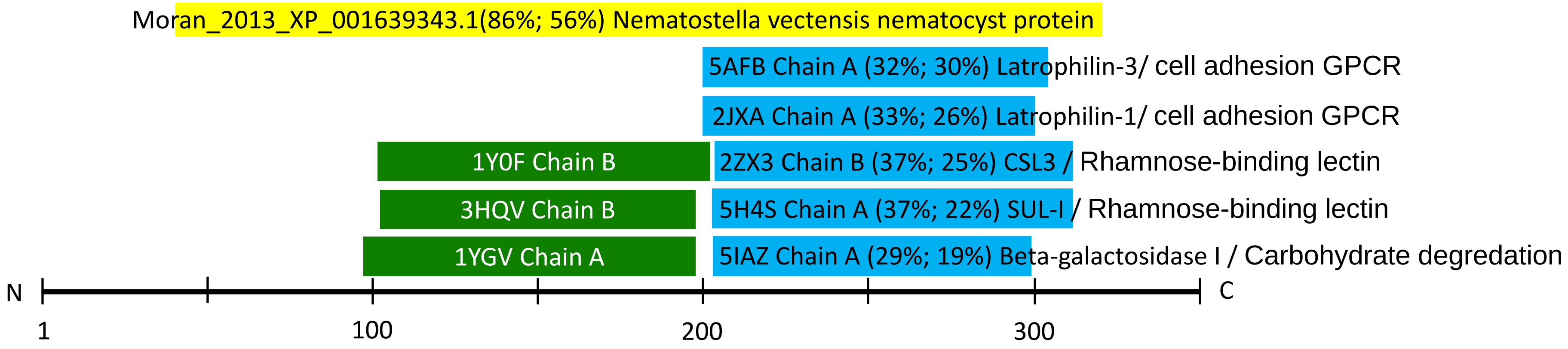
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database ; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

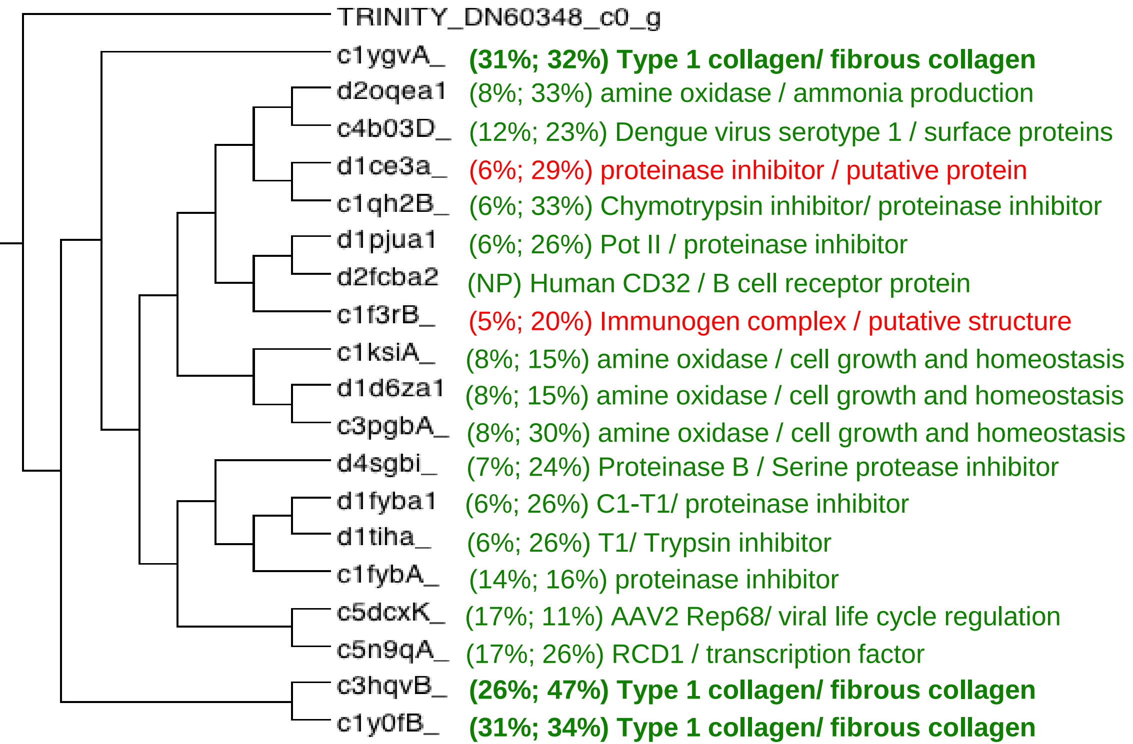




SeqID: TRINITY_DN60348_c0_g1_i1
Annotation: Nematogalectin A
Identified by seq analysis: Y

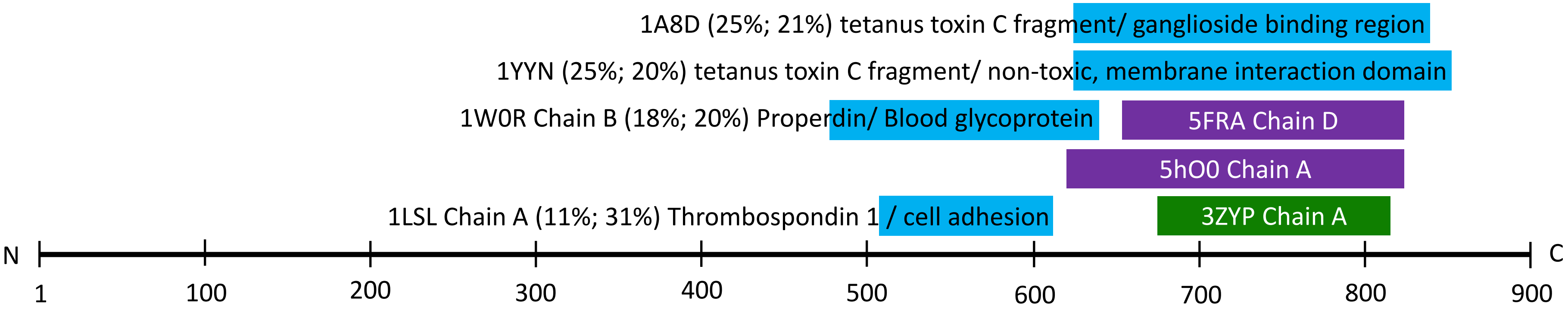
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database ; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

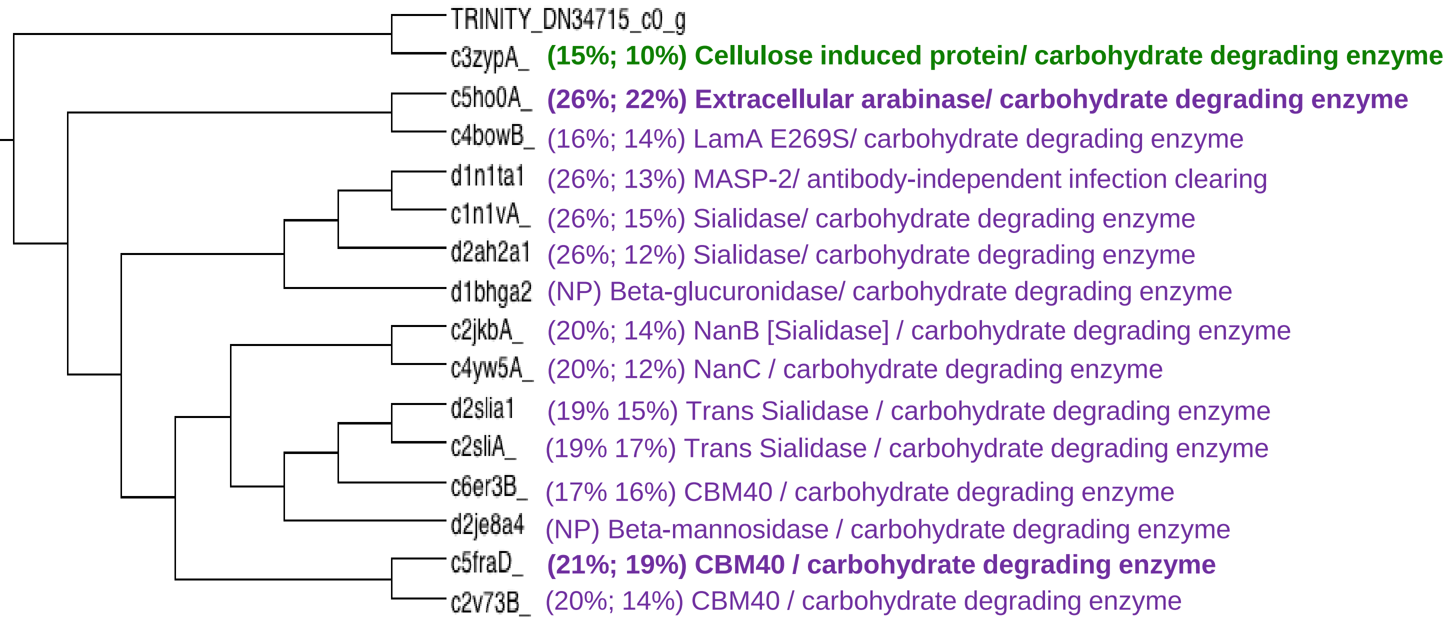

Moran_2013_XP_001639343.1(86%; 56%) Nematostella vectensis nematocyst protein
5AFB Chain A (32%; 30%) Latrophilin-3/ cell adhesion GPCR
2JXA Chain A (33%; 26%) Latrophilin-1/ cell adhesion GPCR
1Y0F Chain B
2ZX3 Chain B (37%; 25%) CSL3 / Rhamnose-binding lectin
3HQV Chain B
5H4S Chain A (37%; 22%) SUL-I / Rhamnose-binding lectin
1YGV Chain A
5IAZ Chain A (29%; 19%) Beta-galactosidase I / Carbohydrate degradation



SeqID: TRINITY_DN34715_c0_g1_i1
Annotation: Adhesion G-coupled receptor B3-like
Identified by seq analysis: N

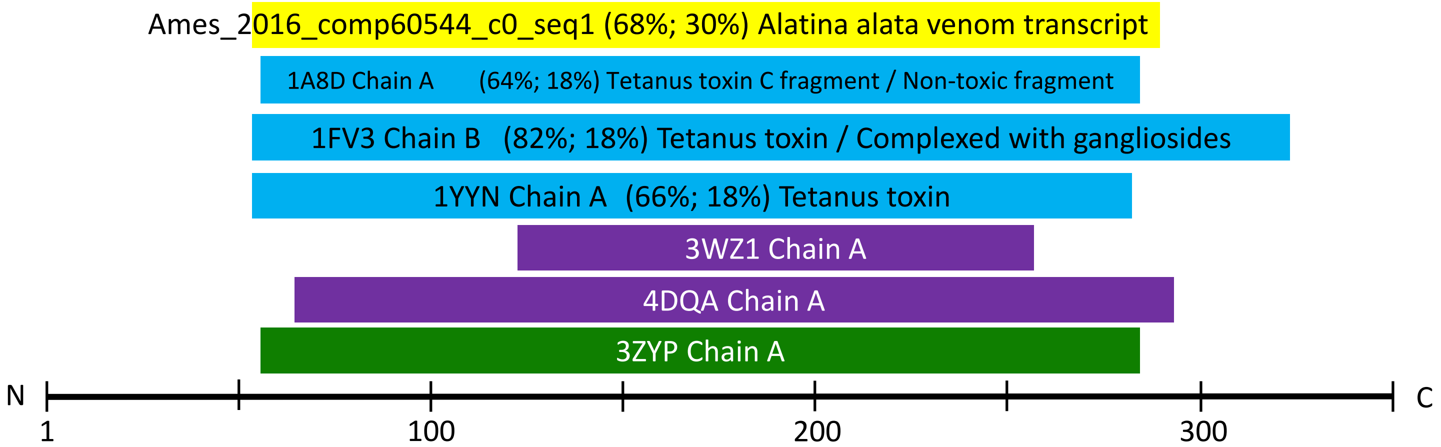
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree





SeqID: TRINITY_DN6224_c0_g2_i1
Annotation: nematoblast-specific nb012a
Identified by seq analysis: Y

Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database ; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree


Ames_2016_comp60544_c0_seq1 (68%; 30%) Alatina alata venom transcript

1A8D Chain A (64%; 18%) Tetanus toxin C fragment / Non-toxic fragment

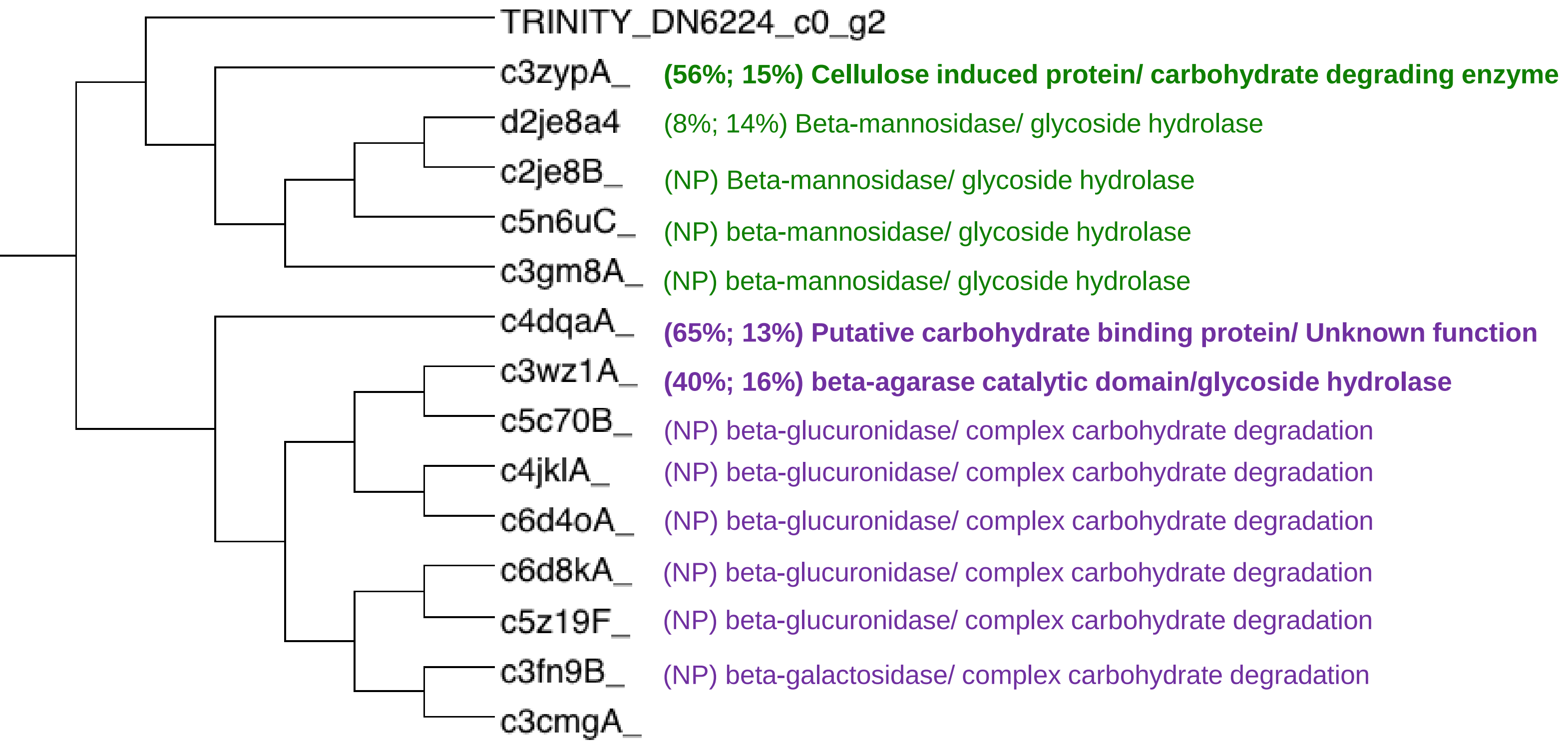
1FV3 Chain B (82%; 18%) Tetanus toxin / Complexed with gangliosides

1YYN Chain A (66%; 18%) Tetanus toxin

3WZ1 Chain A

4DQA Chain A

3ZYP Chain A



c3zypA_ **(56%; 15%) Cellulose induced protein/ carbohydrate degrading enzyme**

d2je8a4 (8%; 14%) Beta-mannosidase/ glycoside hydrolase

c2je8B_ (NP) Beta-mannosidase/ glycoside hydrolase

c5n6uC_ (NP) beta-mannosidase/ glycoside hydrolase

c3gm8A_ (NP) beta-mannosidase/ glycoside hydrolase

c4dqaA_ **(65%; 13%) Putative carbohydrate binding protein/ Unknown function**

c3wz1A_ **(40%; 16%) beta-agarase catalytic domain/glycoside hydrolase**

c5c70B_ (NP) beta-glucuronidase/ complex carbohydrate degradation

c4jklA_ (NP) beta-glucuronidase/ complex carbohydrate degradation

c6d4oA_ (NP) beta-glucuronidase/ complex carbohydrate degradation

c6d8kA_ (NP) beta-glucuronidase/ complex carbohydrate degradation

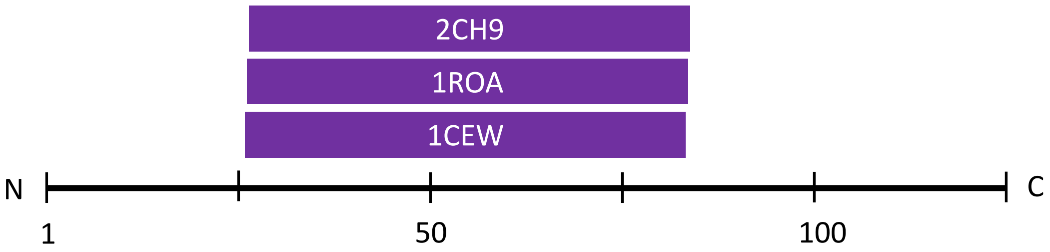
c5z19F_ (NP) beta-glucuronidase/ complex carbohydrate degradation

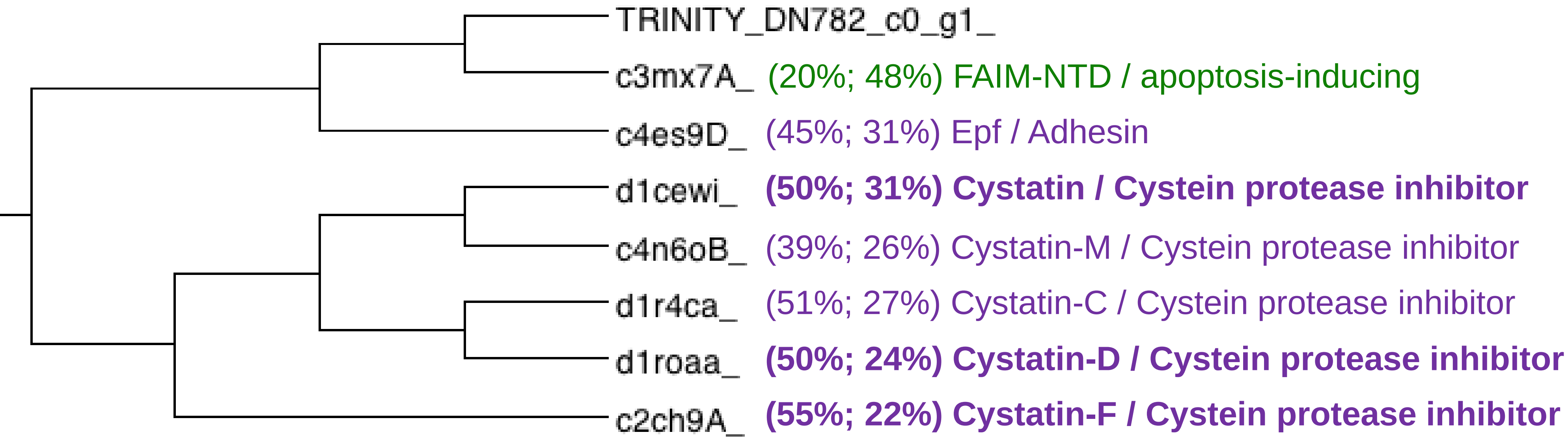
c3fn9B_ (NP) beta-galactosidase/ complex carbohydrate degradation

c3cmgA_

SeqID: TRINITY_DN782_c0_g1_i1
Annotation: Stefin 2
Identified by seq analysis: N

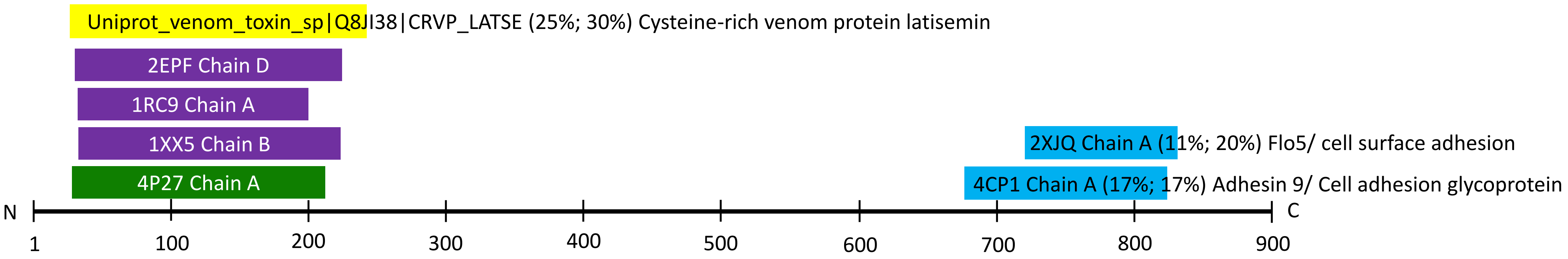
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

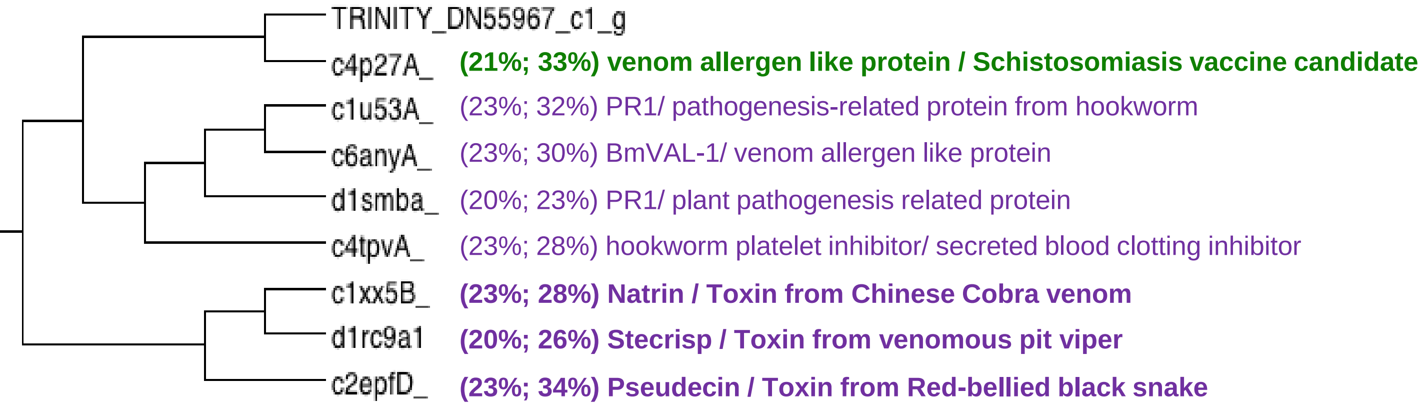




SeqID: TRINITY_DN55967_c1_g1_i2
Annotation: Peptidase inhibitor 16-like
Identified by seq analysis: Y

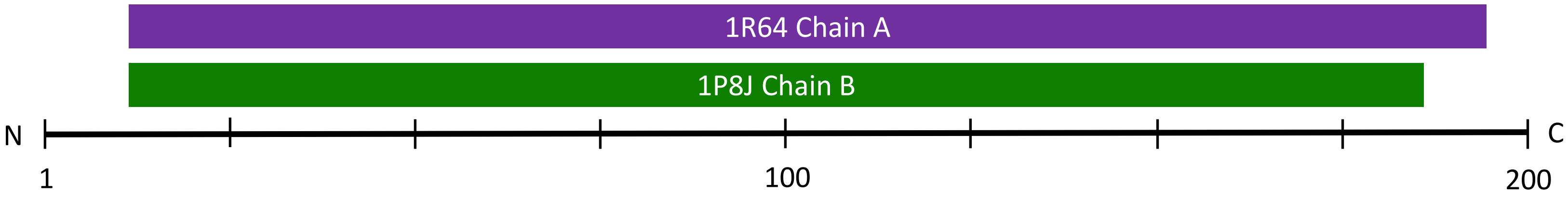
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

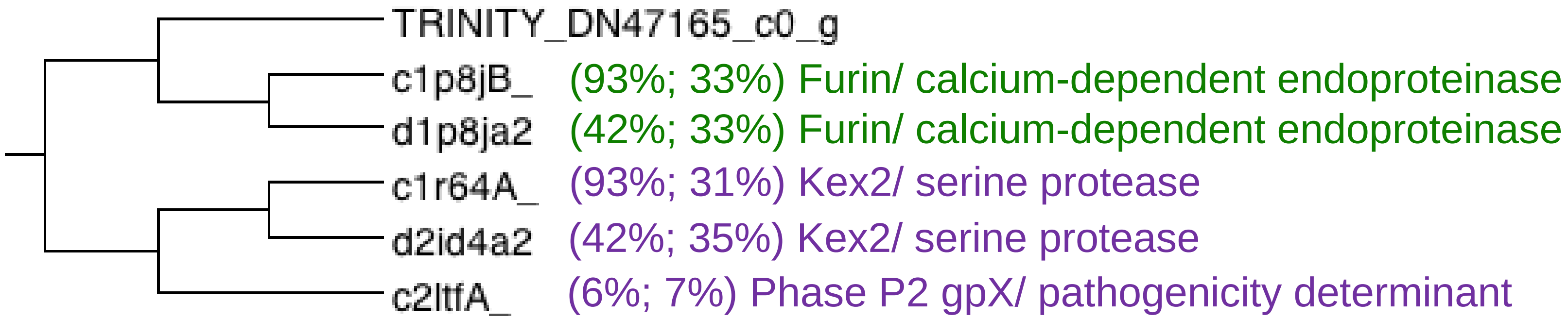




SeqID: TRINITY_DN47165_c0_g1_i4
Annotation: PC3-like endoprotease variant B
Identified by seq analysis: N

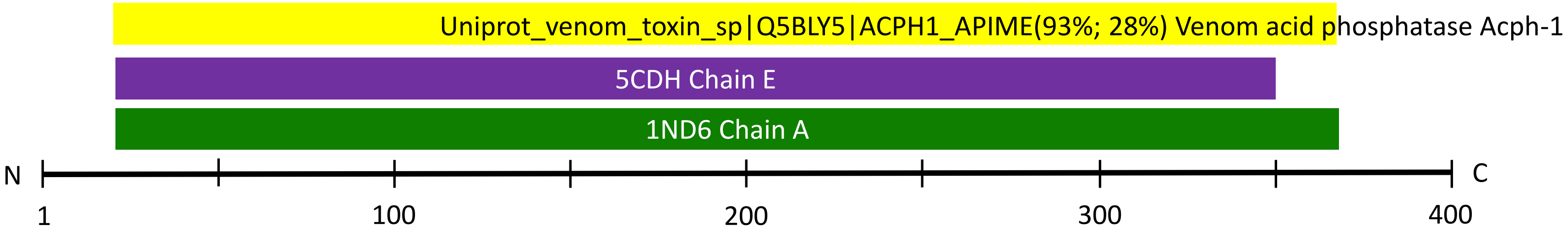
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

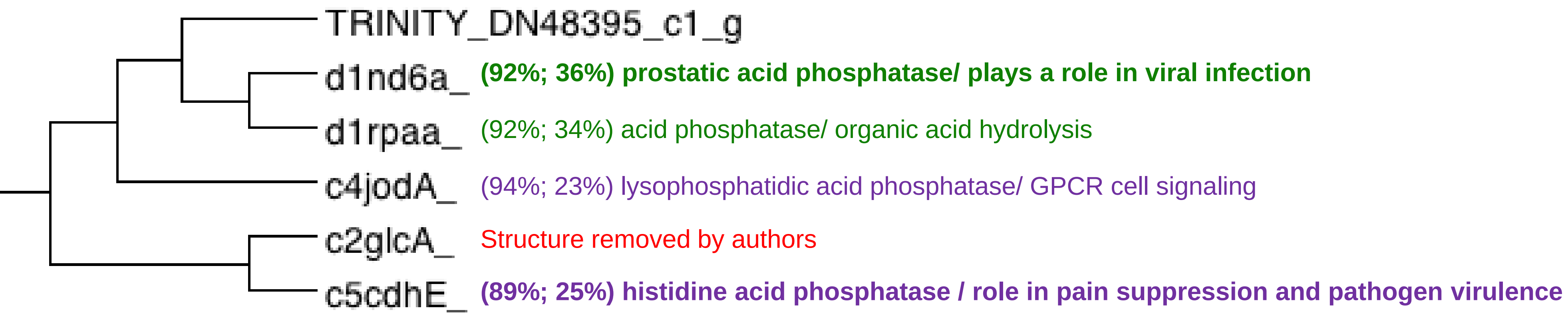




SeqID: TRINITY_DN48395_c1_g1_i1
Annotation: prostatic acid phosphatase isoform X2
Identified by seq analysis: Y

Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree




TRINITY_DN48395_c1_g

d1nd6a_ **(92%; 36%) prostatic acid phosphatase/ plays a role in viral infection**

d1rpaa_ (92%; 34%) acid phosphatase/ organic acid hydrolysis

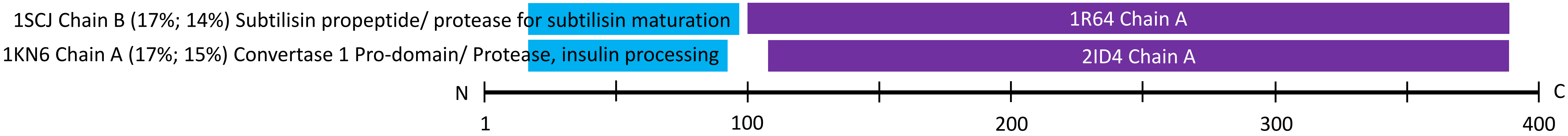
c4jodA_ (94%; 23%) lysophosphatidic acid phosphatase/ GPCR cell signaling

c2glcA_ Structure removed by authors

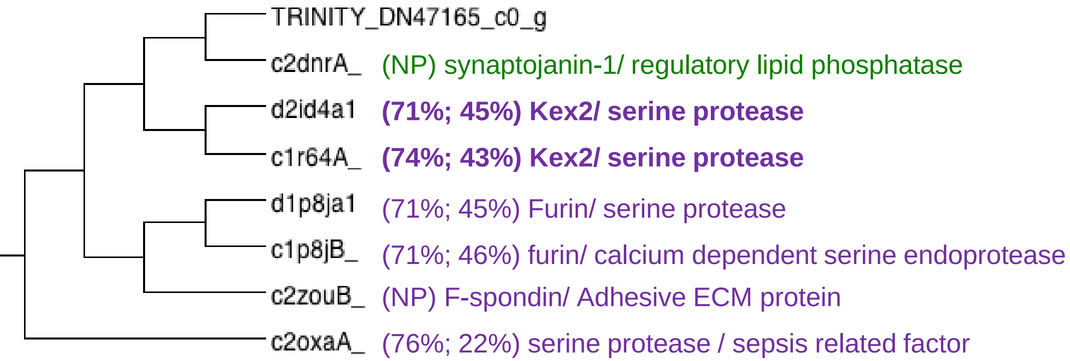
c5cdhE_ **(89%; 25%) histidine acid phosphatase / role in pain suppression and pathogen virulence**

SeqID: TRINITY_DN47165_c0_g1_i5
Annotation: PC3-like endoprotease variant B
Identified by seq analysis: N

Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree


1SCJ Chain B (17%; 14%) Subtilisin propeptide/ protease for subtilisin maturation

1KN6 Chain A (17%; 15%) Convertase 1 Pro-domain/ Protease, insulin processing


TRINITY_DN47165_c0_g

c2dnrA_ (NP) synaptojanin-1/ regulatory lipid phosphatase

d2id4a1 **(71%; 45%) Kex2/ serine protease**

c1r64A_ **(74%; 43%) Kex2/ serine protease**

d1p8ja1 (71%; 45%) Furin/ serine protease

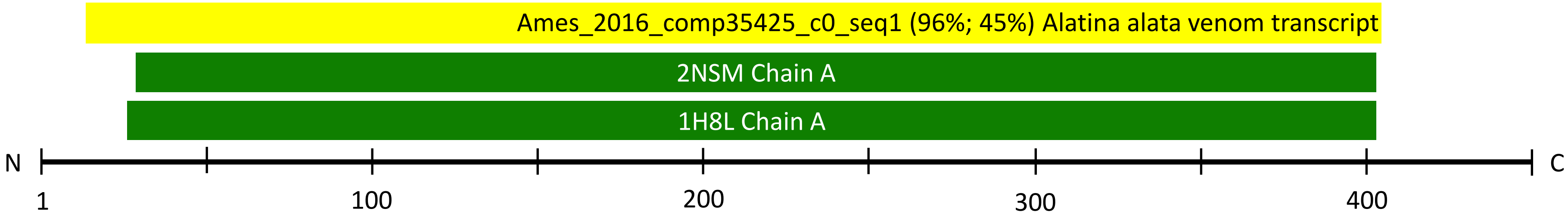
c1p8jB_ (71%; 46%) furin/ calcium dependent serine endoprotease

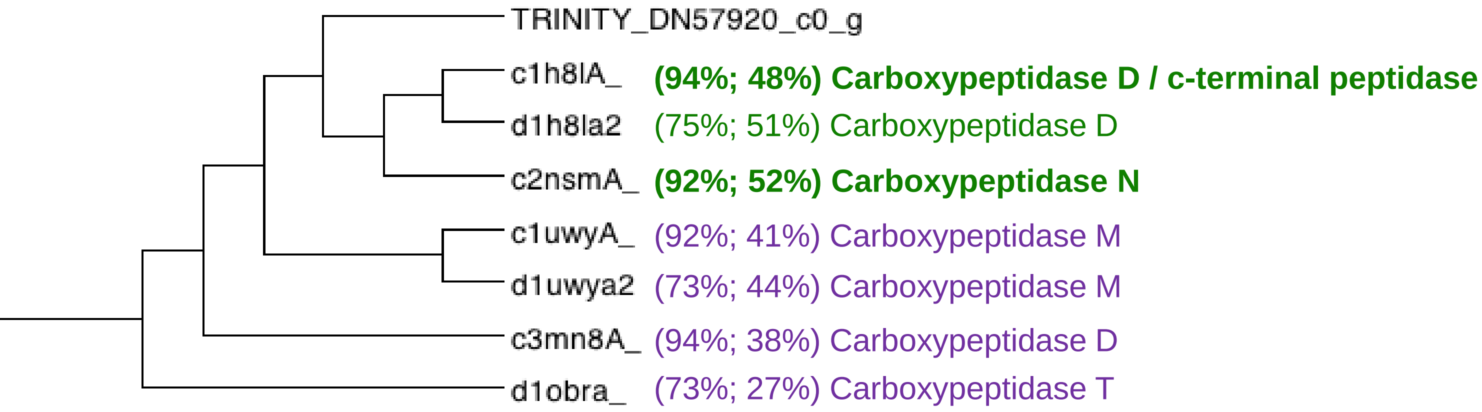
c2zouB_ (NP) F-spondin/ Adhesive ECM protein

c2oxaA_ (76%; 22%) serine protease / sepsis related factor

SeqID: TRINITY_DN57920_c0_g1_i1
Annotation: Carboxypeptidase N catalytic chain
Identified by seq analysis: Y

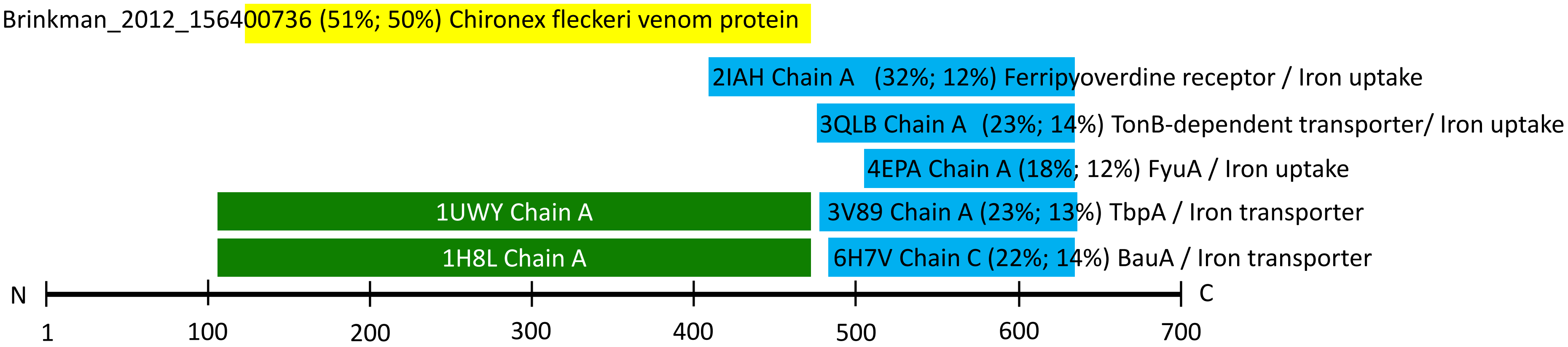
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

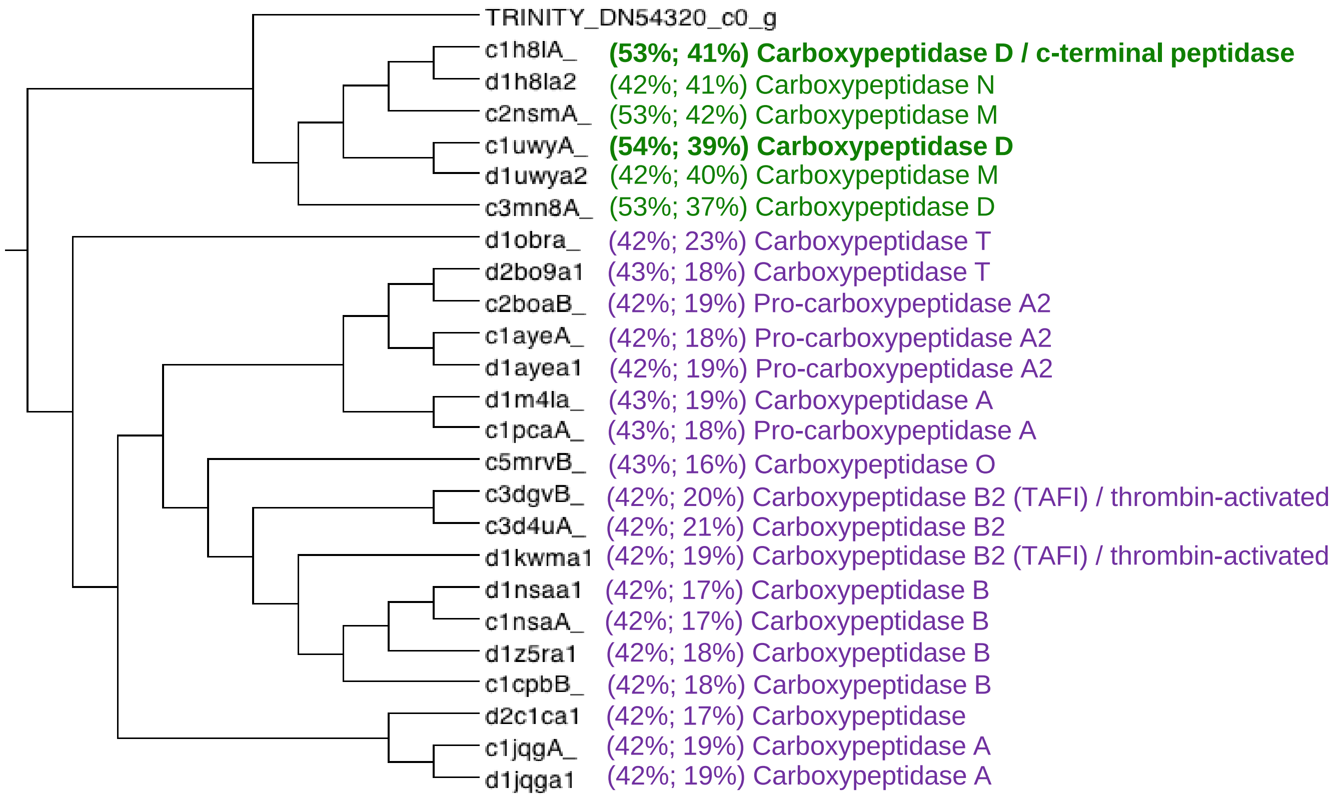




SeqID: TRINITY_DN54320_c0_g1_i1
Annotation: Carboxypeptidase_D
Identified by seq analysis: Y

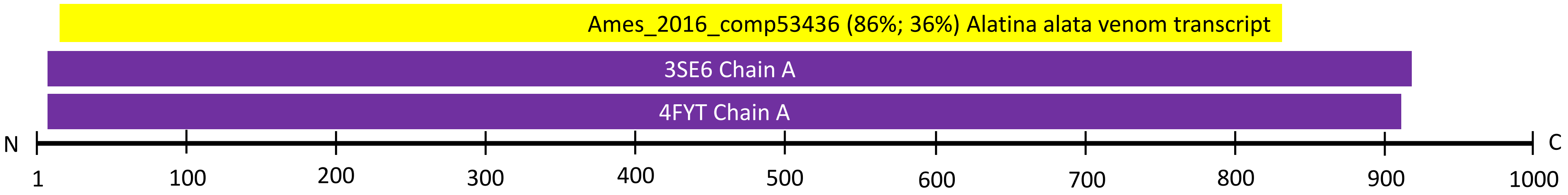
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

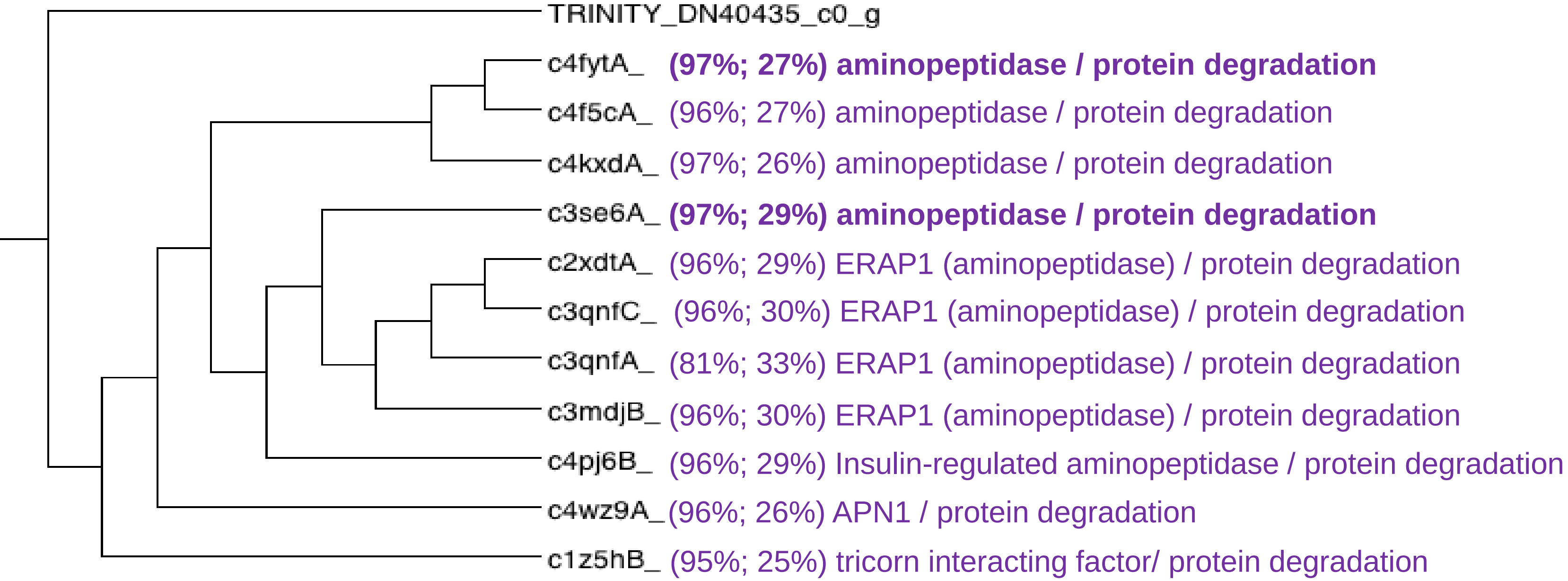




SeqID: TRINITY_DN40435_c0_g1_i1
Annotation: endoplasmic reticulum aminopeptidase 1-like
Identified by seq analysis: Y

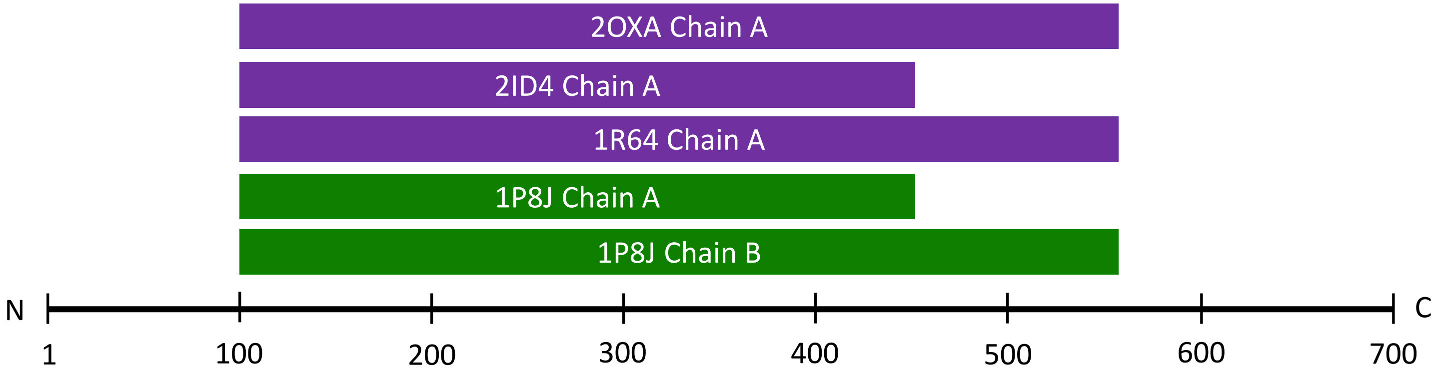
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

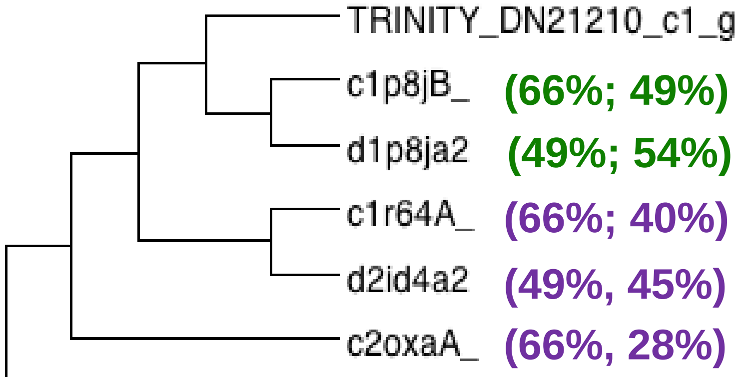




SeqID: TRINITY_DN21210_c1_g1_i1
Annotation: PC3-like endoprotease variant B
Identified by seq analysis: N

Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree





(66%; 49%) Furin/ calcium dependent serine endoprotease

(49%; 54%) Furin/ calcium dependent serine endoprotease

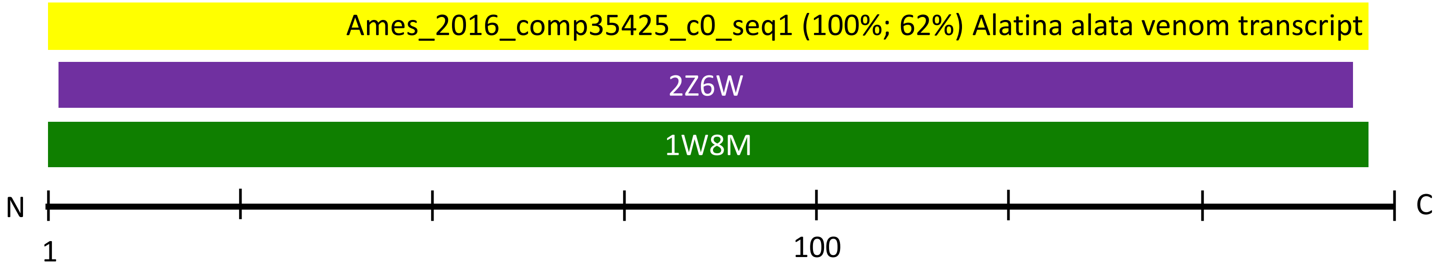
(66%; 40%) Kex2/ serine protease

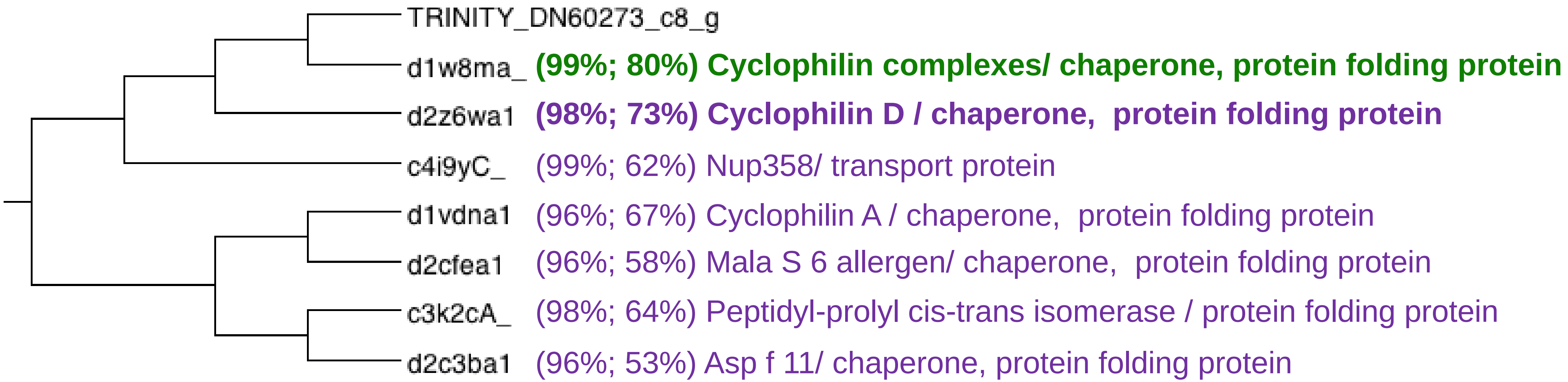
(49%, 45%) Kex2/ serine protease

(66%, 28%) serine protease/shown to induce vascular leakage

SeqID: TRINITY_DN60273_c8_g1_i1
Annotation: peptidyl-prolyl cis-trans isomerase A
Identified by seq analysis: Y

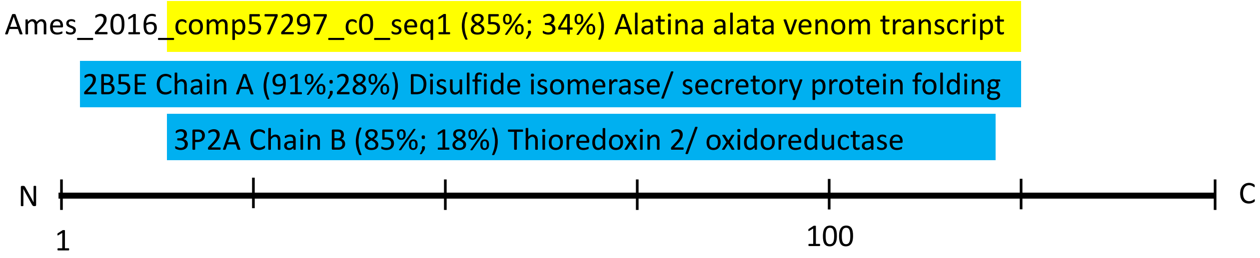
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree





SeqID: TRINITY_DN6523_c1_g1_i1
Annotation: disulfide-isomerase A3
Identified by seq analysis: Y

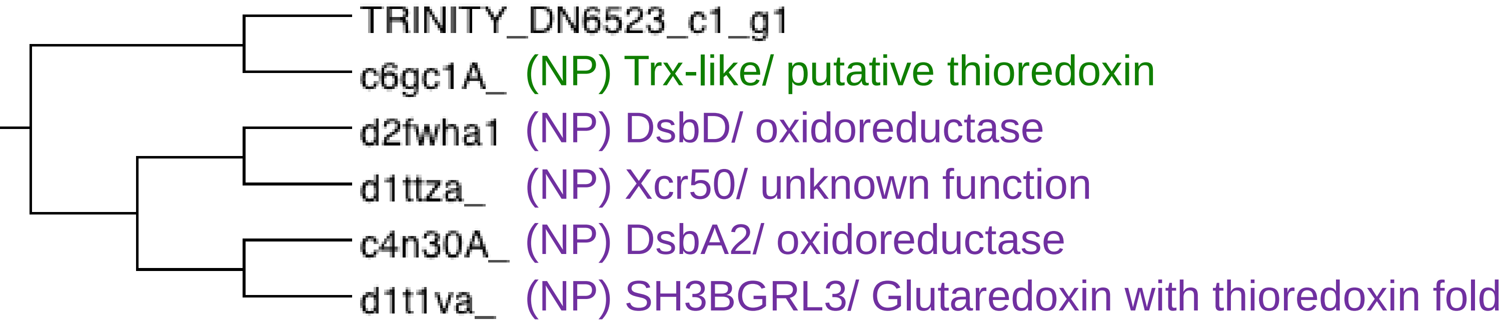
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree



Ames_2016_comp57297_c0_seq1 (85%; 34%) Alatina alata venom transcript

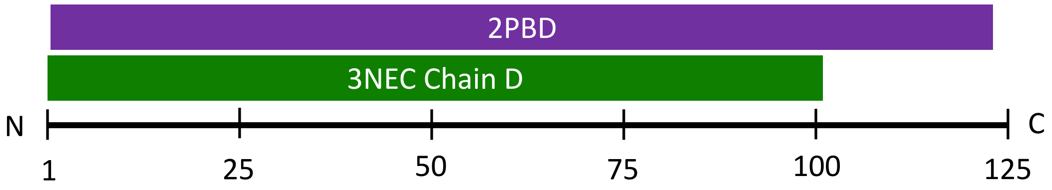
2B5E Chain A (91%;28%) Disulfide isomerase/ secretory protein folding

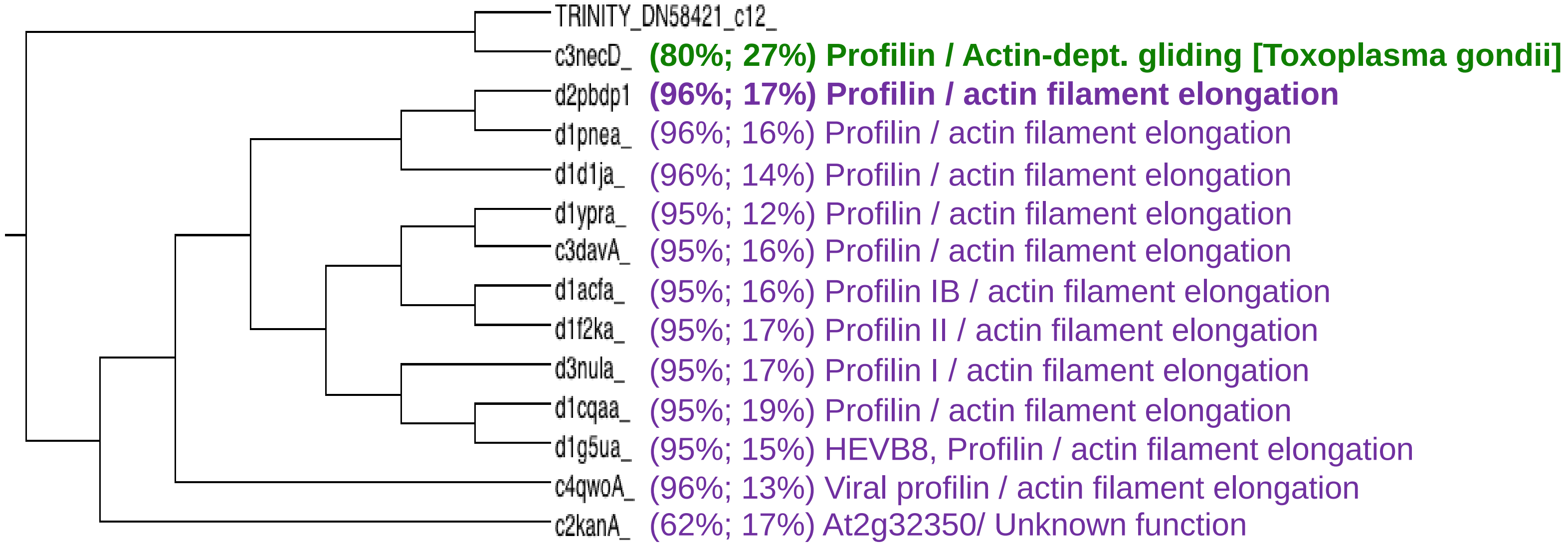
3P2A Chain B (85%; 18%) Thioredoxin 2/ oxidoreductase



SeqID: TRINITY_DN58421_c12_g1_i1
Annotation: NA
Identified by seq analysis: N

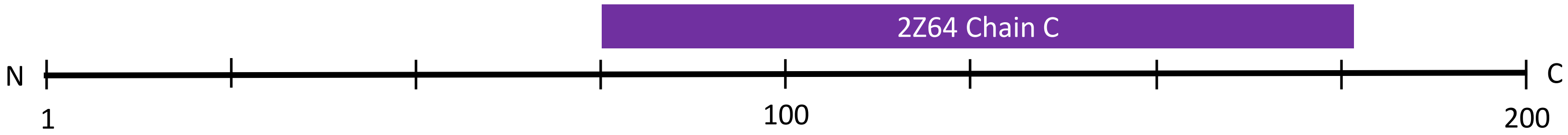
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

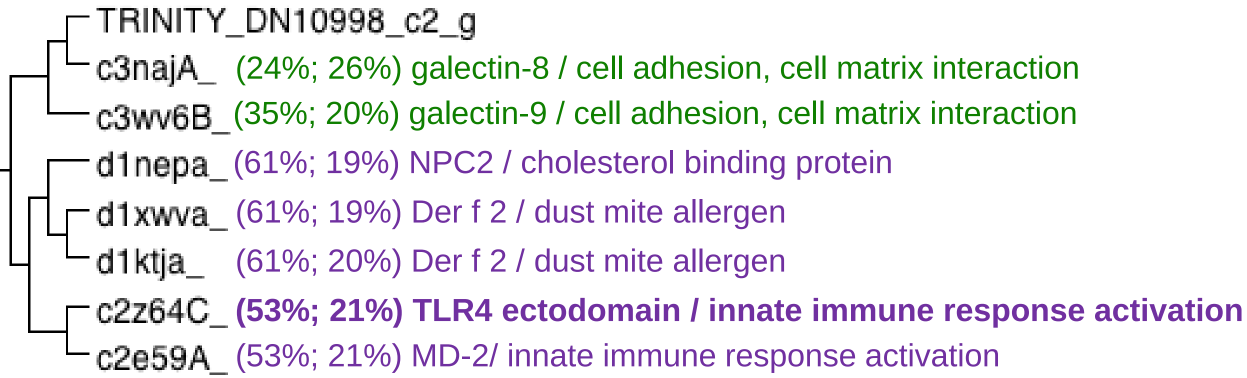




SeqID: TRINITY_DN10998_c2_g1_i1
Annotation: NA
Identified by seq analysis: N

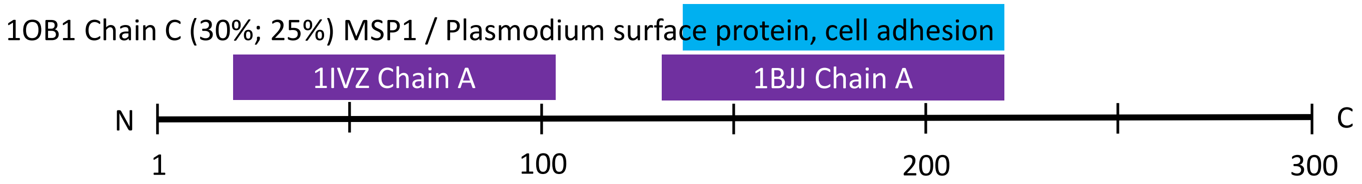
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree




TRINITY_DN10998_c2_g
c3najA_ (24%; 26%) galectin-8 / cell adhesion, cell matrix interaction
c3wv6B_ (35%; 20%) galectin-9 / cell adhesion, cell matrix interaction
d1nepa_ (61%; 19%) NPC2 / cholesterol binding protein
d1xwva_ (61%; 19%) Der f 2 / dust mite allergen
d1ktja_ (61%; 20%) Der f 2 / dust mite allergen
c2z64C_ (53%; 21%) TLR4 ectodomain / innate immune response activation
c2e59A_ (53%; 21%) MD-2/ innate immune response activation

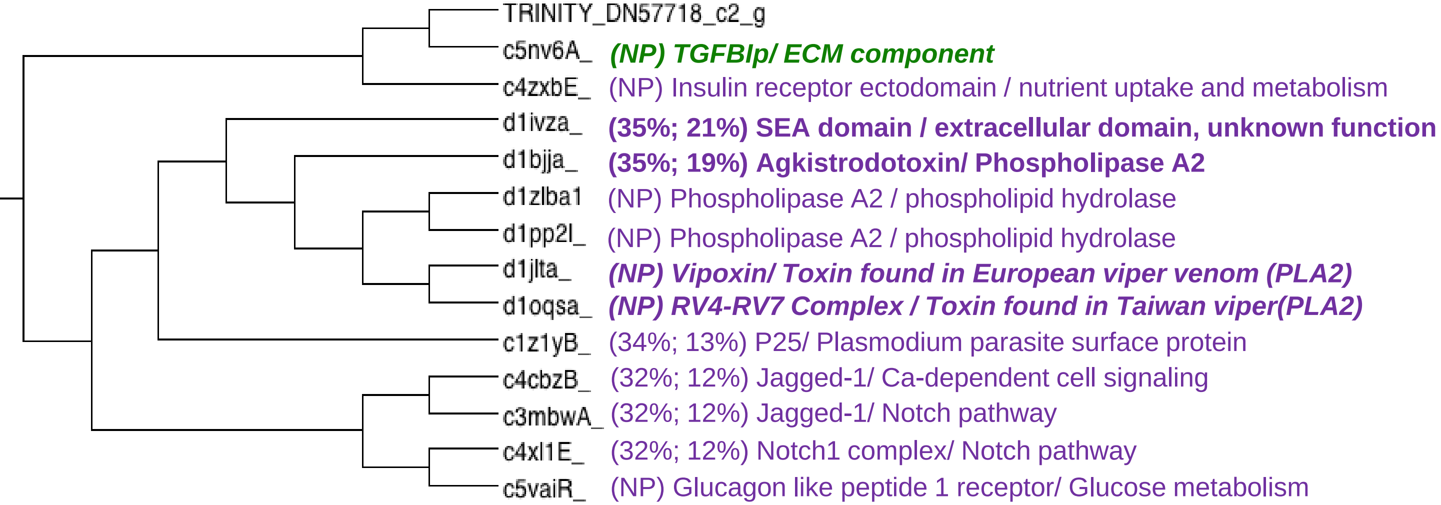
SeqID: TRINITY_DN57718_c2_g1_i1
Annotation: TKL Kinase
Identified by seq analysis: N

Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree


1OB1 Chain C (30%; 25%) MSP1 / Plasmodium surface protein, cell adhesion

1IVZ Chain A

1BJJ Chain A


TRINITY_DN57718_c2_g

c5nv6A_ ***(NP) TGFBIp/ ECM component***

c4zxbE_ (NP) Insulin receptor ectodomain / nutrient uptake and metabolism

d1ivza_ **(35%; 21%) SEA domain / extracellular domain, unknown function**

d1bjja_ **(35%; 19%) Agkistrodotoxin/ Phospholipase A2**

d1zlba1 (NP) Phospholipase A2 / phospholipid hydrolase

d1pp2l_ (NP) Phospholipase A2 / phospholipid hydrolase

d1jlta_ ***(NP) Vipoxin/ Toxin found in European viper venom (PLA2)***

d1oqsa_ ***(NP) RV4-RV7 Complex / Toxin found in Taiwan viper(PLA2)***

c1z1yB_ (34%; 13%) P25/ Plasmodium parasite surface protein

c4cbzB_ (32%; 12%) Jagged-1/ Ca-dependent cell signaling

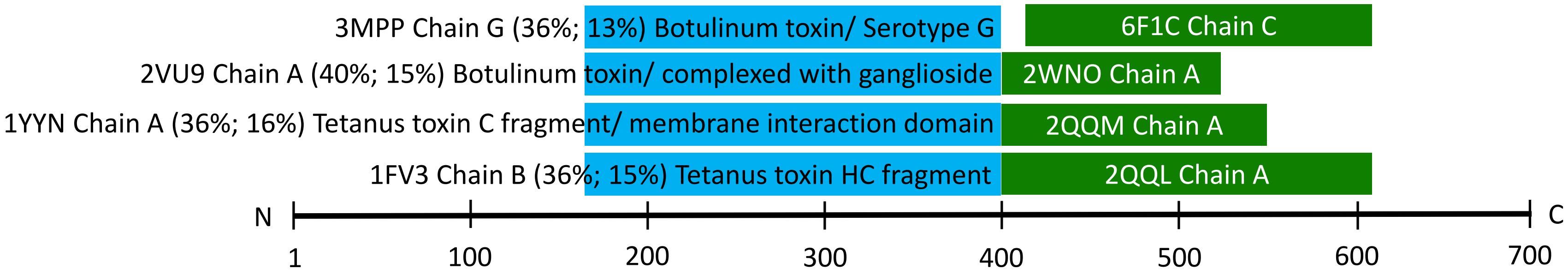
c3mbwA_ (32%; 12%) Jagged-1/ Notch pathway

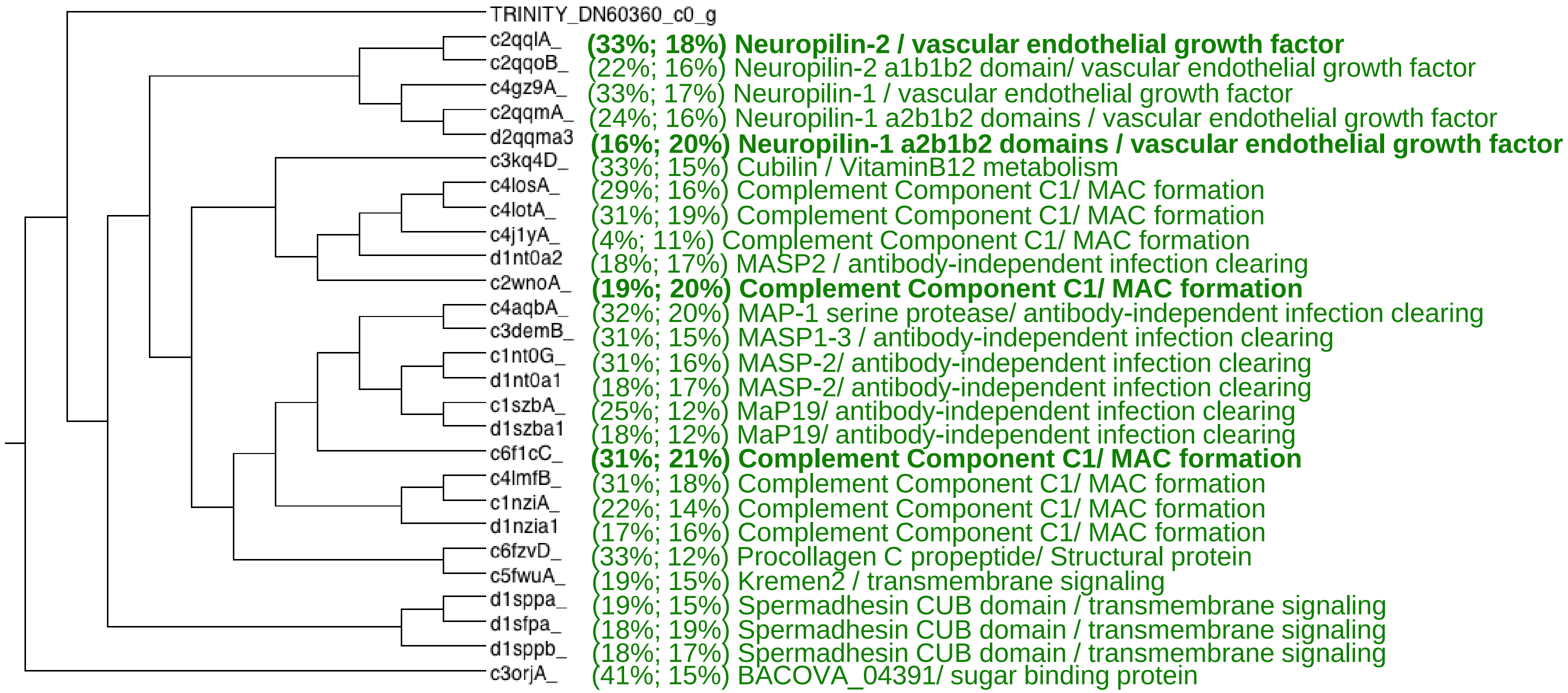
c4xl1E_ (32%; 12%) Notch1 complex/ Notch pathway

c5vaiR_ (NP) Glucagon like peptide 1 receptor/ Glucose metabolism

SeqID: TRINITY_DN60360_c0_g1_i1
Annotation: Nematoblast-specific nb012a
Identified by seq analysis: N

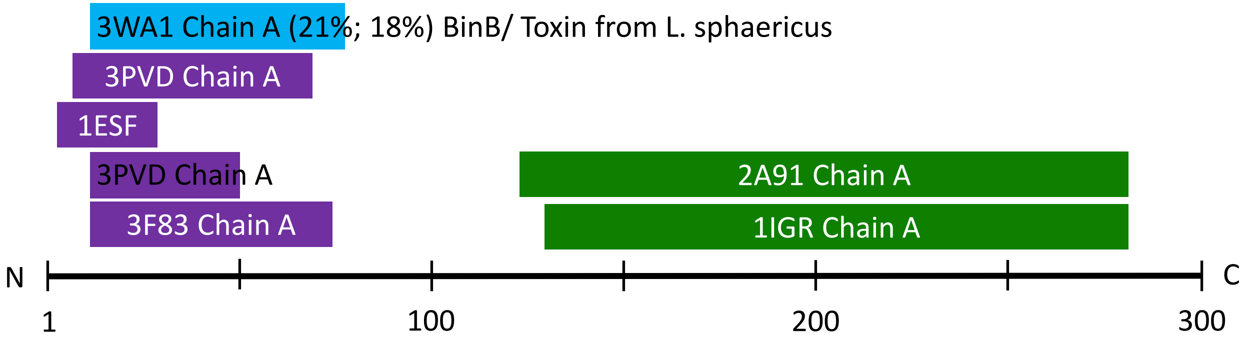
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

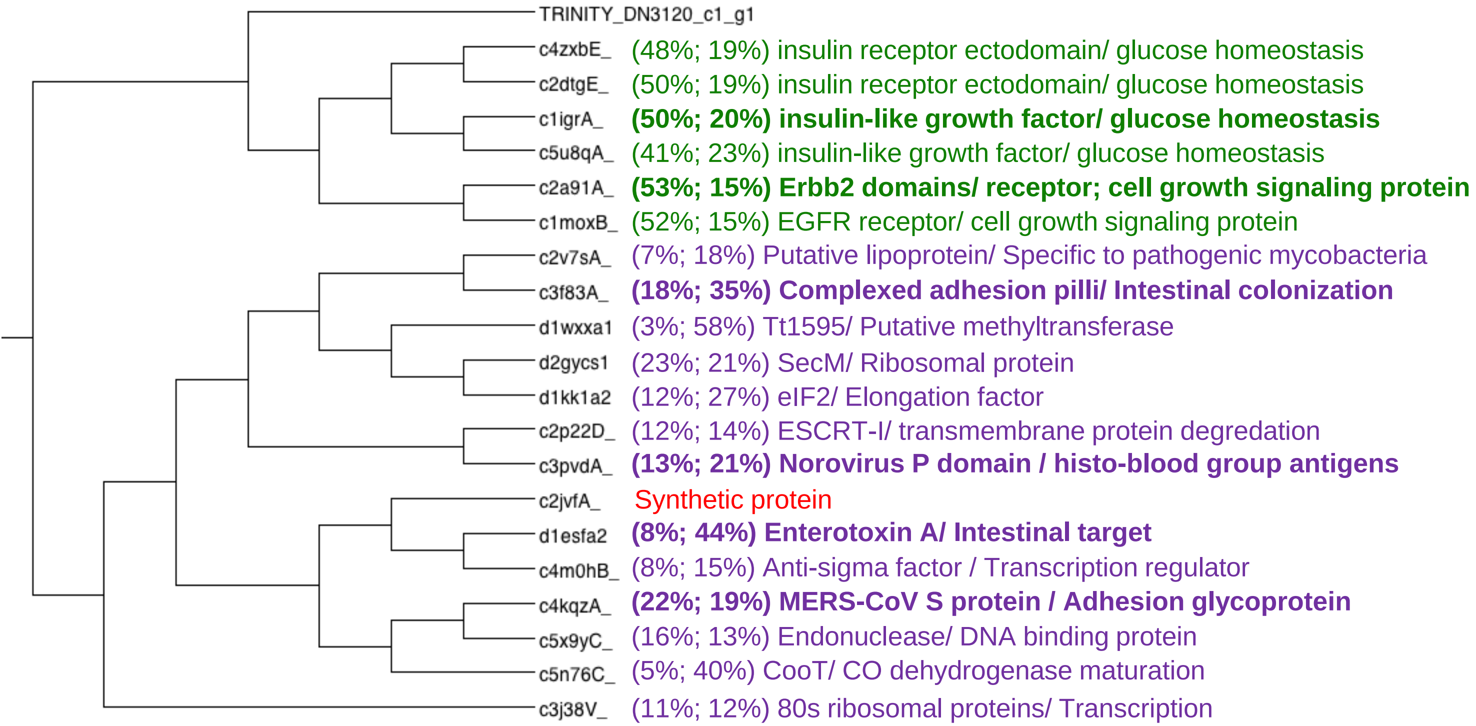

3MPP Chain G (36%; 13%) Botulinum toxin/ Serotype G
6F1C Chain C
2VU9 Chain A (40%; 15%) Botulinum toxin/ complexed with ganglioside
2WNO Chain A
1YYN Chain A (36%; 16%) Tetanus toxin C fragment/ membrane interaction domain
2QQM Chain A
1FV3 Chain B (36%; 15%) Tetanus toxin HC fragment
2QQL Chain A


TRINITY_DN60360_c0_g
c2qqlA_ **(33%; 18%) Neuropilin-2 / vascular endothelial growth factor**
c2qqoB_ (22%; 16%) Neuropilin-2 a1b1b2 domain/ vascular endothelial growth factor
c4gz9A_ (33%; 17%) Neuropilin-1 / vascular endothelial growth factor
c2qqmA_ (24%; 16%) Neuropilin-1 a2b1b2 domains / vascular endothelial growth factor
d2qqma3 **(16%; 20%) Neuropilin-1 a2b1b2 domains / vascular endothelial growth factor**
c3kq4D_ (33%; 15%) Cubilin / VitaminB12 metabolism
c4losA_ (29%; 16%) Complement Component C1/ MAC formation
c4lotA_ (31%; 19%) Complement Component C1/ MAC formation
c4j1yA_ (4%; 11%) Complement Component C1/ MAC formation
d1nt0a2 (18%; 17%) MASP2 / antibody-independent infection clearing
c2wnoA_ **(19%; 20%) Complement Component C1/ MAC formation**
c4aqbA_ (32%; 20%) MAP-1 serine protease/ antibody-independent infection clearing
c3demB_ (31%; 15%) MASP1-3 / antibody-independent infection clearing
c1nt0G_ (31%; 16%) MASP-2/ antibody-independent infection clearing
d1nt0a1 (18%; 17%) MASP-2/ antibody-independent infection clearing
c1szbA_ (25%; 12%) MaP19/ antibody-independent infection clearing
d1szba1 (18%; 12%) MaP19/ antibody-independent infection clearing
c6f1cC_ **(31%; 21%) Complement Component C1/ MAC formation**
c4lmfB_ (31%; 18%) Complement Component C1/ MAC formation
c1nziA_ (22%; 14%) Complement Component C1/ MAC formation
d1nzia1 (17%; 16%) Complement Component C1/ MAC formation
c6fzvD_ (33%; 12%) Procollagen C propeptide/ Structural protein
c5fwuA_ (19%; 15%) Kremen2 / transmembrane signaling
d1sppa_ (19%; 15%) Spermadhesin CUB domain / transmembrane signaling
d1sfpa_ (18%; 19%) Spermadhesin CUB domain / transmembrane signaling
d1sppb_ (18%; 17%) Spermadhesin CUB domain / transmembrane signaling
c3orjA_ (41%; 15%) BACOVA_04391/ sugar binding protein

SeqID: TRINITY_DN3120_c1_g1_i1
Annotation: NA
Identified by seq analysis: N

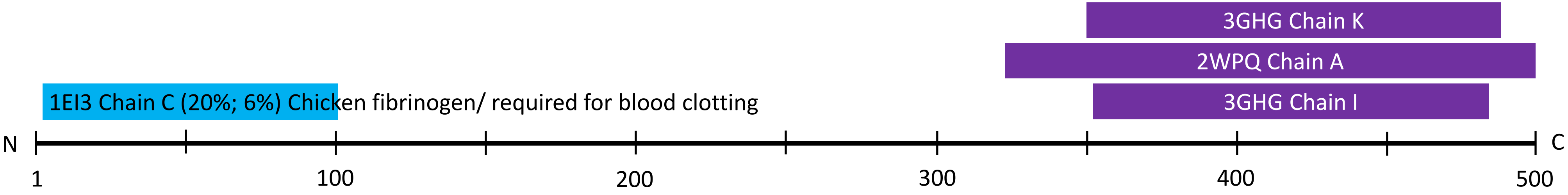
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

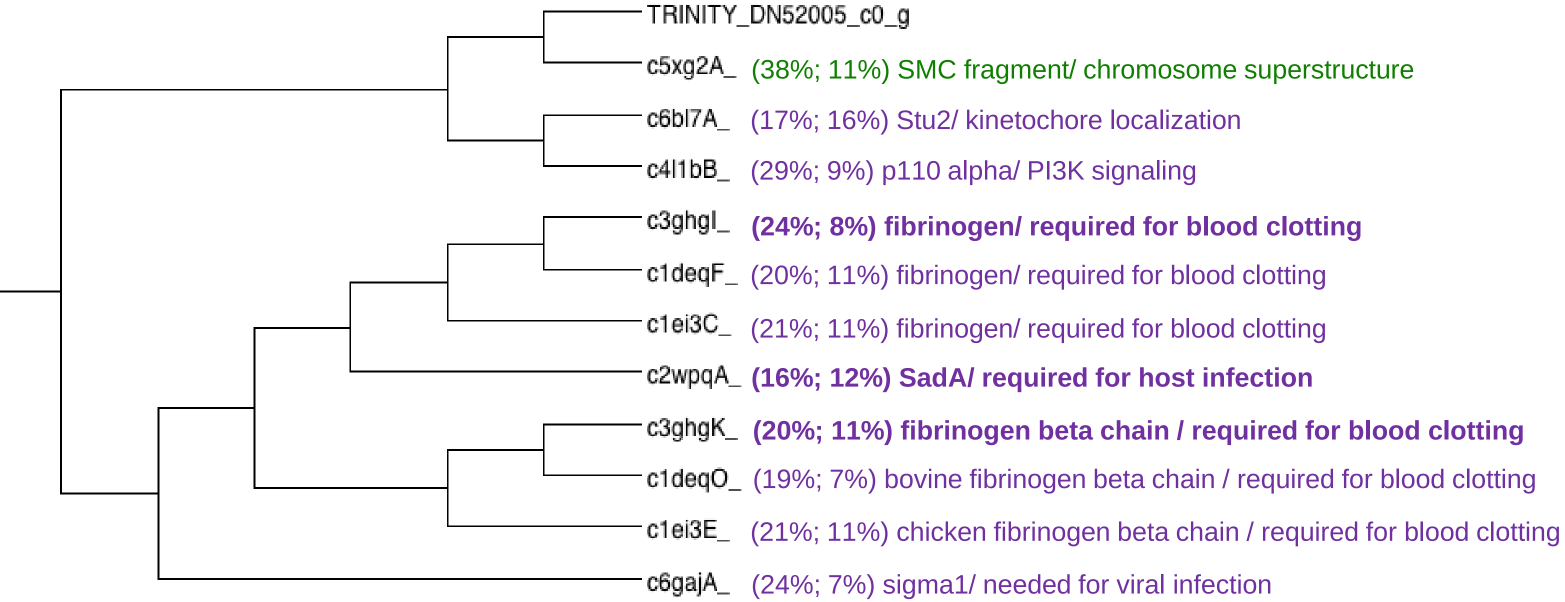



TRINITY_DN3120_c1_g1
c4zxbE_ (48%; 19%) insulin receptor ectodomain/ glucose homeostasis
c2dtgE_ (50%; 19%) insulin receptor ectodomain/ glucose homeostasis
c1igrA_ **(50%; 20%) insulin-like growth factor/ glucose homeostasis**
c5u8qA_ (41%; 23%) insulin-like growth factor/ glucose homeostasis
c2a91A_ **(53%; 15%) Erbb2 domains/ receptor; cell growth signaling protein**
c1moxB_ (52%; 15%) EGFR receptor/ cell growth signaling protein
c2v7sA_ (7%; 18%) Putative lipoprotein/ Specific to pathogenic mycobacteria
c3f83A_ **(18%; 35%) Complexed adhesion pilli/ Intestinal colonization**
d1wxxa1 (3%; 58%) Tt1595/ Putative methyltransferase
d2gycs1 (23%; 21%) SecM/ Ribosomal protein
d1kk1a2 (12%; 27%) eIF2/ Elongation factor
c2p22D_ (12%; 14%) ESCRT-I/ transmembrane protein degredation
c3pvdA_ **(13%; 21%) Norovirus P domain / histo-blood group antigens**
c2jvfA_ Synthetic protein
d1esfa2 **(8%; 44%) Enterotoxin A/ Intestinal target**
c4m0hB_ (8%; 15%) Anti-sigma factor / Transcription regulator
c4kqzA_ **(22%; 19%) MERS-CoV S protein / Adhesion glycoprotein**
c5x9yC_ (16%; 13%) Endonuclease/ DNA binding protein
c5n76C_ (5%; 40%) CooT/ CO dehydrogenase maturation
c3j38V_ (11%; 12%) 80s ribosomal proteins/ Transcription

SeqID: TRINITY_DN52005_c0_g3_i2
Annotation: NA
Identified by seq analysis: N

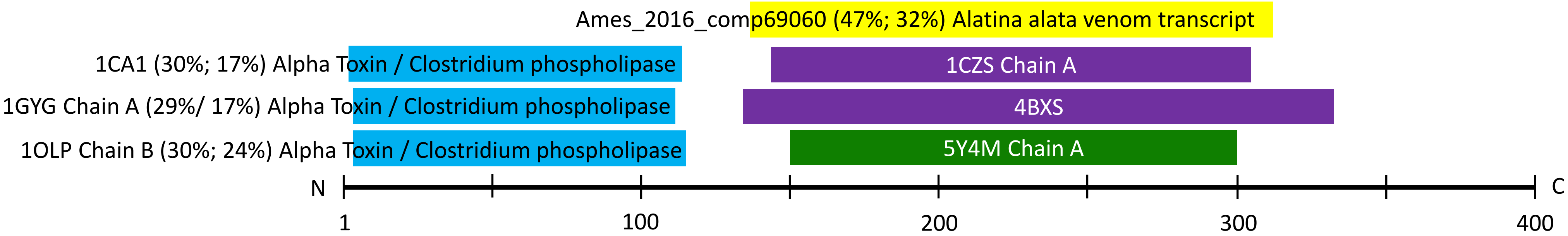
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

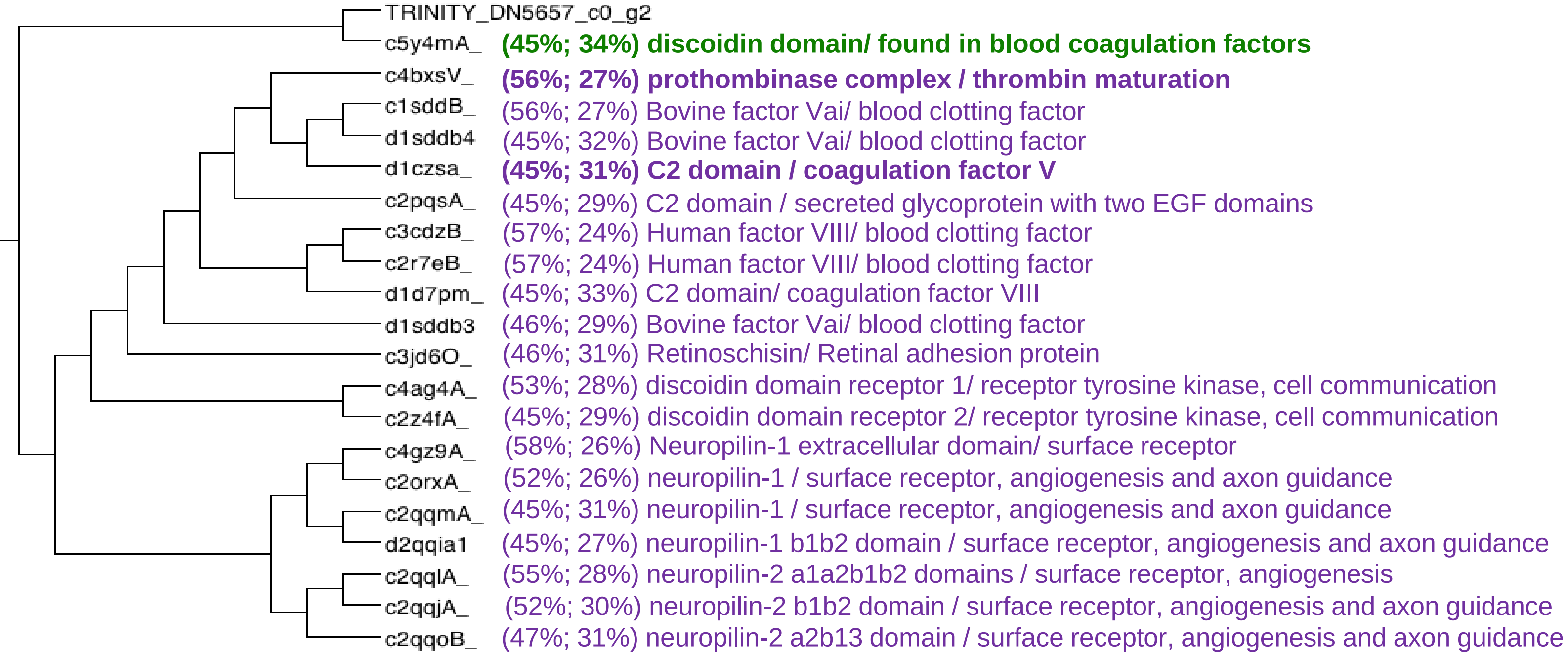

3GHG Chain K
2WPQ Chain A
1EI3 Chain C (20%; 6%) Chicken fibrinogen/ required for blood clotting
3GHG Chain I


TRINITY_DN52005_c0_g
c5xg2A_ (38%; 11%) SMC fragment/ chromosome superstructure
c6bl7A_ (17%; 16%) Stu2/ kinetochore localization
c4l1bB_ (29%; 9%) p110 alpha/ PI3K signaling
c3ghgI_ **(24%; 8%) fibrinogen/ required for blood clotting**
c1deqF_ (20%; 11%) fibrinogen/ required for blood clotting
c1ei3C_ (21%; 11%) fibrinogen/ required for blood clotting
c2wpqA_ **(16%; 12%) SadA/ required for host infection**
c3ghgK_ **(20%; 11%) fibrinogen beta chain / required for blood clotting**
c1deqO_ (19%; 7%) bovine fibrinogen beta chain / required for blood clotting
c1ei3E_ (21%; 11%) chicken fibrinogen beta chain / required for blood clotting
c6gajA_ (24%; 7%) sigma1/ needed for viral infection

SeqID: TRINITY_DN3183_c1_g2_i1
Annotation: EGF-like repeat and discoidin I-like domain-containing 3
Identified by seq analysis: Y

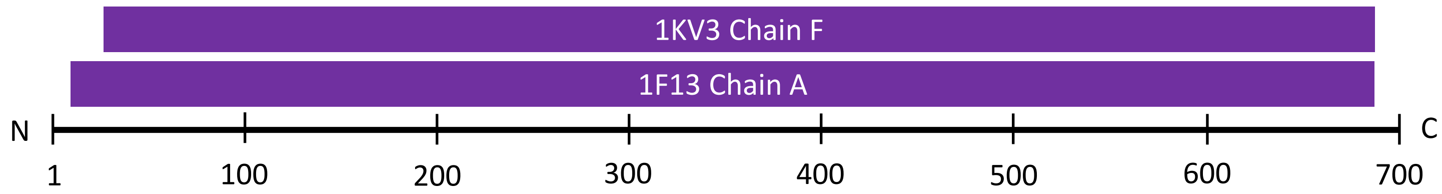
Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree

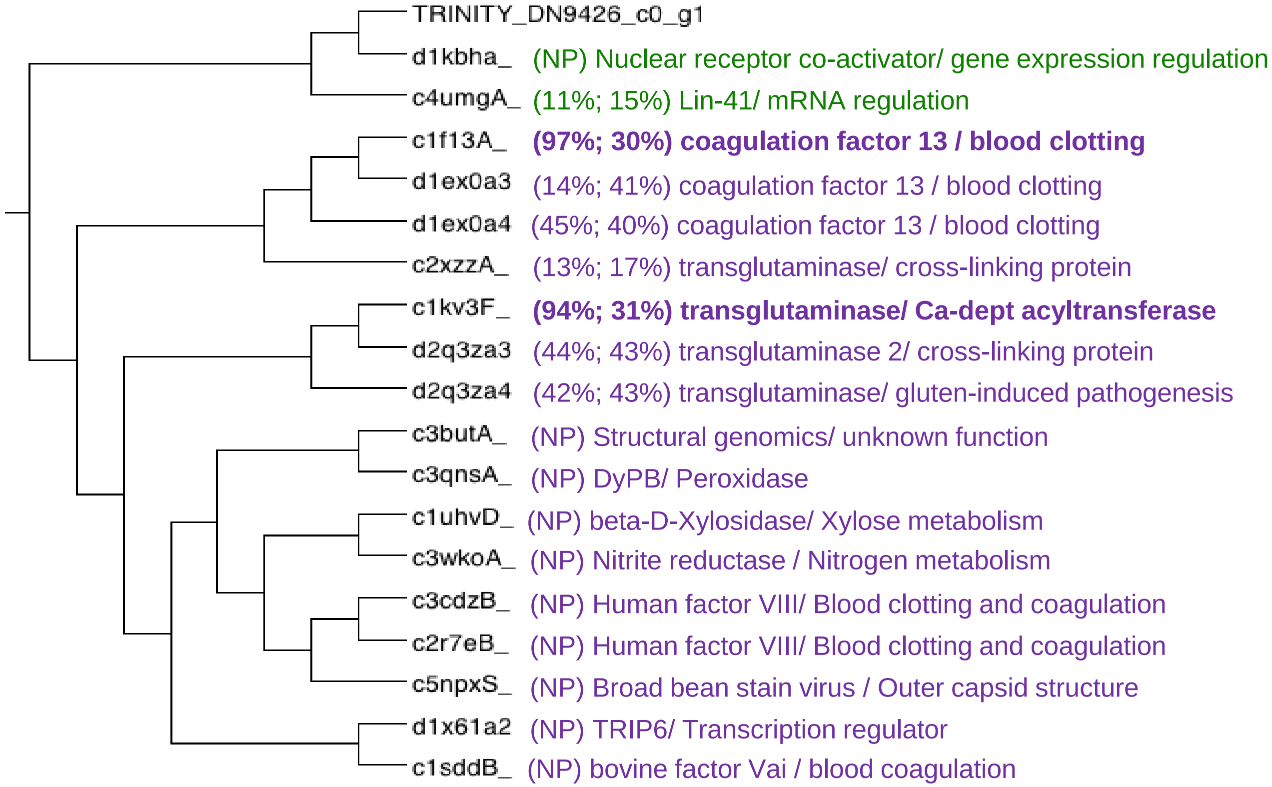




SeqID: TRINITY_DN9426_c0_g1_i2
Annotation: glutamine gamma-glutamyltransferase
Identified by seq analysis: N

Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree





SeqID: TRINITY_DN3183_c0_g2_i1
Annotation: coagulation factor V-like
Identified by seq analysis: Y

Key: (X%; Y%) A / B X = Alignment coverage Y= %ID between query and temple A = Molecule name B = Molecule description
NP= Alignment & %ID not provided by Phyre2;
Yellow = Sequence from database; Green = same clade; Purple = Earlier common ancestor; Red = Non-valid entry; Blue = Not in tree