

Novel zebrafish mono-alpha2,8-sialyltransferase (ST8Sia VIII): an evolutionary perspective of alpha2,8-sialylation.

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Supplemental figures legends

Supplemental Figure S1 : Molecular Phylogenetic analysis by Maximum Likelihood (ML) method.

Supplemental FigureS2 : Molecular Phylogenetic analysis by Minimum Evolution (ME).

Supplemental Figure S1 : Molecular Phylogenetic analysis by Maximum Likelihood (ML) method.

The evolutionary history of vertebrate oligo- and mono- α 2,8-sialyltransferases was inferred using the Maximum Likelihood method based on the JTT matrix-based model [1]. The tree with the highest log likelihood (-26151.14) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.3753)). The rate variation model allowed for some sites to be evolutionarily invariable ([+I], 4.68% sites). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 147 amino acid sialyltransferase sequences. All positions with less than 95% site coverage were eliminated. That is, fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 283 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [2].

Supplemental Figure S2 : Molecular Phylogenetic analysis by Minimum Evolution (ME).

The evolutionary history of vertebrate oligo- and mono- α 2,8-sialyltransferases was inferred using the Minimum Evolution method and the optimal tree with the sum of branch length = 21.18281333 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the JTT matrix-based method and are in the units of the number of amino acid substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1.5). The ME tree was searched using the Close-Neighbor-Interchange (CNI) algorithm at a search level of 1. The Neighbor-joining algorithm [1] was used to generate the initial tree. The analysis involved 147 amino acid of vertebrate oligo- and mono- α 2,8-sialyltransferases sequences, all positions with less than 95% site coverage were eliminated and there were a total of 283 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.0 [2].

Additional references for supplemental figure legends :

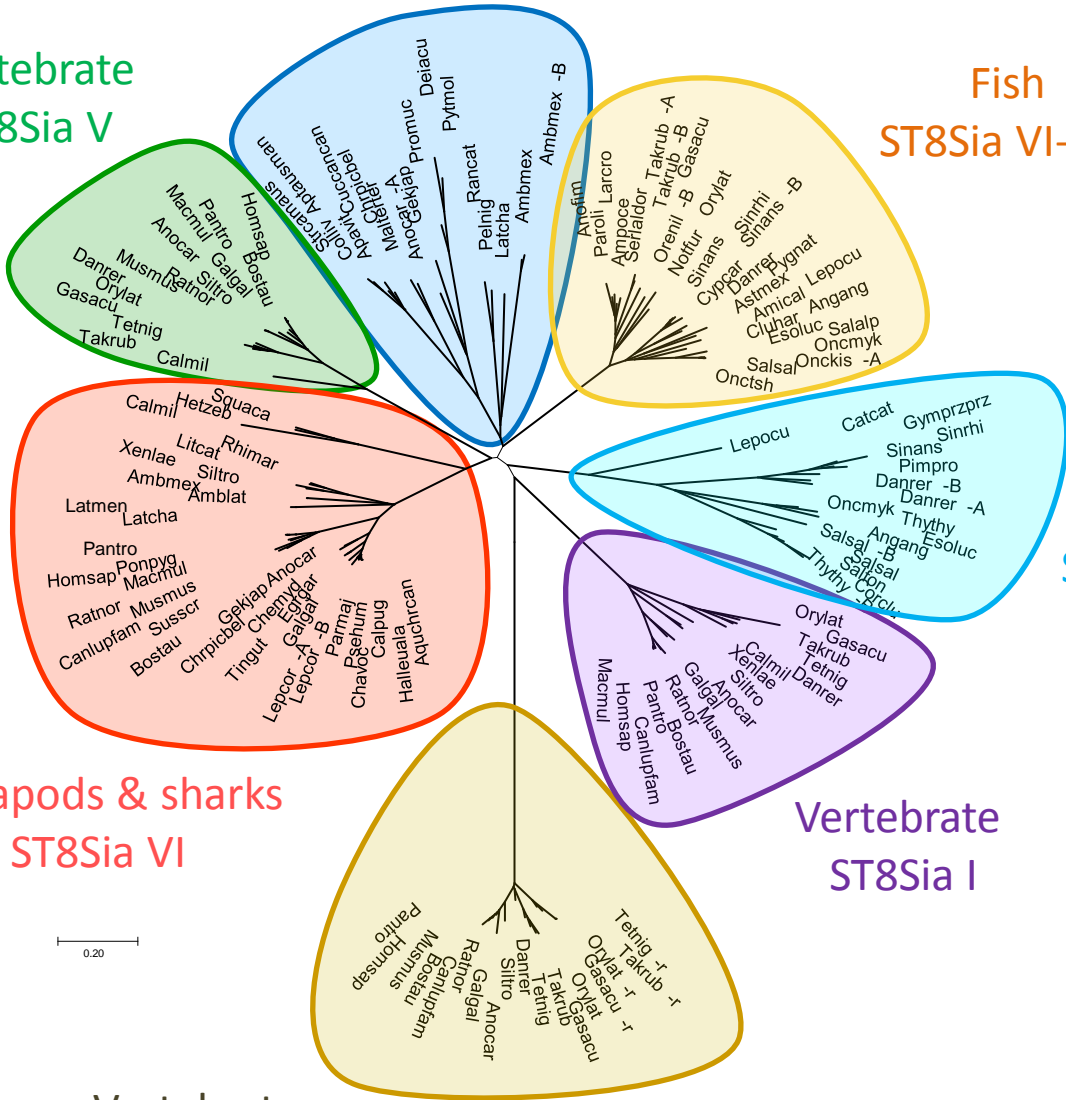
1. Saitou N, Nei M: **The neighbor-joining method: a new method for reconstructing phylogenetic trees.** *Mol Biol Evol* 1987, **4**(4):406-425.
2. Kumar S, Stecher G, Tamura K: **MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets.** *Mol Biol Evol* 2016, **33**(7):1870-1874.

ME tree

Tetrapods
ST8Sia VII

Vertebrate
ST8Sia V

Fish
ST8Sia VI-like



Fish
ST8Sia VII

Vertebrate
ST8Sia I

Tetrapods & sharks
ST8Sia VI

Vertebrate
ST8Sia III

Color Key

- ST8Sia I
- ST8Sia III
- ST8Sia V
- ST8Sia VI
- ST8Sia VI-like
- Fish
- ST8Sia VII
- ST8Sia VII
- Tetrapods
- Fish

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List of supplementary data

Supplementary data1 : Full length sequences of 147 vertebrate mono- and oligo- α 2,8-sialyltransferases.

Supplementary data2: Multiple sequence alignments of 147 vertebrate mono- and oligo- α 2,8-sialyltransferases.

1 – Supplementary data1: Full length sequences of 147 vertebrate mono- and oligo- α 2,8-sialyltransferases. Protein sequence of 147 selected vertebrate ST8Sia sequences: 129 mono- α 2,8-sialyltransferases *i.e.* 17 ST8Sia I (green), 15 ST8Sia V (blue), 63 ST8Sia VI (black and teleost fish sequences in red) and 34 ST8Sia VII (violet) and 18 oligo- α 2,8-sialyltransferases ST8Sia III (brown), which are used as an outgroup. Corresponding abbreviated names are as follows: Homsap: Homo sapiens; Pantro : Pan troglodytes; Macmul: Macaca mulatta; Musmus: Mus musculus; Ratnor: Rattus norvegicus; Bostau: Bos Taurus; Canlupfam: Canis lupus familiaris; Galgal: Gallus gallus; Siltro: Silurana tropicalis; Anocar: Anolis carolinensis; Susscr ; Sus scrofa ; Ponpyg: Pongo pygmaeus; Latcha: Latimeria chalumnae; Chemyd: Chelonia mydas; Chrcpicbel: Chrysemys picta bellii; Aquchrca: Aquila chrysaetos Canadensis; Egrgar: Egretta garzetta; Psehum: Pseudopodoces humilis; Lepcor: Lepidothrix coronata; Halleuala: Haliaeetus leucocephalus alascanus; Chavoc: Charadrius vociferous; Calpug: Calidris pugnax; Tingut : Tinamus guttatus ; Parmaj : Parus major ; Gekjap : Gekko japonicus ; Xenlae : Xenopus laevis ; Calmil : Callorhynchus milii ; Amblat : Ambystoma laterale ; Litcat: Rana catesbeiana; Hetzeb: Heterodontus zebra; Squaca: Squalus acanthias; Ambmex: Ambystoma mexicanum; Rhimar: Rhinella marina; Latmen: Latimeria menadoensis; Colliv: Columba livia; Deiacu: Deinagkistrodon acutus; Pytmol: Python molurus; Strcamaus: Struthio camelus australis; Apavit: Apaloderma vittatum; Promuc : Protobothrops mucrosquamatus ; Rancat : Rana catesbeiana ; Malterter : Malaclemys terrapin terrapin ; Gymprzprz : Gymnocypris przewalskii przewalskii ; Catcat : Catla catla ; Pimpro : Pimephales promelas ; Salfon : Salvelinus fontinalis ; Corclu : Coregonus clupeaformis ; Thythy : Thymallus thymallus ; Pelnig : Pelophylax nigromaculatus ; Aptausman : Apteryx australis mantelli ; **Lepocu : Lepisosteus oculatus ; Anofim : Anoplopoma fimbria ; Amical : Amia calva ; Sinans : Sinocyclocheilus anshuiensis ; Sinrhi : Sinocyclocheilus rhinoceros ; Cypcar : Cyprinus carpio ; Pygnat: Pygocentrus nattereri; Onckis: Oncorhynchus kisutch; Esoluc: Esox Lucius; Salsal: Salmo salar; Astmex: Astyanax mexicanus; Salalp: Salvelinus alpinus; Cluhar : Clupea harengus ; Notfur : Nothobranchius furzeri ; Serlaldor ; Seriola lalandi dorsalis ; Larcro : Larimichthys crocea ; Paroli : Paralichthys olivaceus ; Ampoce : Amphiprion ocellaris ; Gasacu : Gasterosteus aculeatus ; Tetnig : Tetraodon nigroviridis ; Takrub: Takifugu rubripes; Gasacu: Gasterosteus aculeatus; Danrer: Danio rerio; Oncmyk: Oncorhynchus mykiss; Orylat: Oryzias latipes; Angang: Anguilla Anguilla; Orenil: Oreochromis niloticus; Onctsh: Oncorhynchus tshawytscha;**

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>Deiacu_GT29_ST8Sia7

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>Pytmol_GT29_ST8Sia7

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>Strcamaus_GT29_ST8Sia7

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>Apavit_GT29_ST8Sia7

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>Gekjap_GT29_ST8Sia7

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>Promuc_GT29_ST8Sia7

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LKDIGLPHQAFFLNPHYLGALDMYWKQKGMTEIRLSTGFMTSFALEFCDHITLYGFWPF LF
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>Ambmex_GT29_ST8Sia7

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>Rancat_GT29_ST8Sia7

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>Catcat_GT29_ST8Sia7

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>Pimpro_GT29_ST8Sia7

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>Salsal_GT29_ST8Sia7

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>Salfon_GT29_ST8Sia7

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LKLHTQGV LQLHLGRC

>Corclu_GT29_ST8Sia7

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>Thythy_GT29_ST8Sia7

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>Angang_GT29_ST8Sia7

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>Ambmex_GT29_ST8Sia7-B

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>Pelnig_GT29_ST8Sia7

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>Aptausman_GT29_ST8Sia7

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>Cuccancan_GT29_ST8Sia7

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GGILRNSSCGSQIDGYQFVIRFNLP SADFPELVGRKSSIVTVNPSILHKRFHGLNGRRLPFV
EAAASYGKTWFFI PAFSYPGNSEASYRAFYALQDSESQSHVFFFHPQYLSALS KYWHDGRGFH
TYRLSSGFMLVNAALELCEHITLYGFWPFSLHPDGHALPHHYDNLVLPNQRIHIMPREFAYY
VDMHFQGV LRLHVGRC

Supplementary data2: Multiple sequence alignment of the 147 selected vertebrate ST8Sia sequences: 129 mono- α 2,8-sialyltransferases *i.e.* 17 ST8Sia I, 15 ST8Sia V, 63 ST8Sia VI and 34 ST8Sia VII and 18 oligo- α 2,8-sialyltransferases ST8Sia III, which are used as an outgroup were aligned using Clustal Omega in MEGA 7.0. Species name abbreviations are given in supplemental data1 legend.

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!Title siat8.txt;

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NK---HYSLCSVVGNSGILTGSHCGANIDQADVFVRCNFAPTE-VYSKDVGRKTNMTTFN
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KVELAWPGNIMHDVNKYWKNKNSPKRVSTGIFMYTLASAMCDEIHLYGFWPFWDPTG
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NK---HYSLCSVVGNSGILTGSHCGANIDQADVFVRCNFAPTE-VYSKDVGRKTNMTTFN
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KVELAWPGNIMHDVNKYWKNKNSPKRVSTGIFMYTLASAMCDEIHLYGFWPFWDPTG
KELPYHYDDKKGTKFTTKWQETHQLPTEFKLLYKLHREGVIRLSLTHCT-----

#Orylat_GT29_ST8Sia3-B
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NK---HYSVCAVVGNSGILTGSHCGPEIDQADVFVRCNFAPTD-VYSKDVGRKTNMTTFN
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KVELAWPGNIMHNVNKYWKTKNLSPKRSLTGILMYTLAFSMCDEIHLYGFWPFWDPTG
KDLPHYHYDDKKGTKFTTKWQETHQLPSEFKLLYKLHREGVTKLGLSHCT-----

#Gasacu_GT29_ST8Sia3-rB
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#Anocar_GT29_ST8Sia3
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NK---HYNICAVVGNSGILVGSQCGQEIDKYDFVRCNFAPTE-AFHKDVGRKTNITTFN
PSILEKYNNLLTIQDRNNFFLNKLLKLDGAILWIPAFFFHTSATITRRTLVDFFIEHRAQL
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#Siltro_GT29_ST8Sia3
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NK---RYNCAVIGNSGILTESQCGAEIDKADVFVRCNFAPTE-GFQKDVGRKTNLTTFN
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#Bostau_GT29_ST8Sia3

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NK---RYNICAVVGNISGILTGSRGCPQIDKSDVFRFCNFAPTE-AFQRDVGRKTNLTTFN
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KLQLAWPGNIMQHVNRWKNKHLSPKRLSTGILMYTLASAVCEEIHLYGFWPFPGFDPNTR
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#Galgal_GT29_ST8Sia3

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NK---HYNVCAVVGNISGILTGSCQGEIDKSDVFRFCNFAPTE-AFQKDVGRKTNLTTFN
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#Canlupfam_GT29_ST8Sia3

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#Ratnor_GT29_ST8Sia3

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#Musmus_GT29_ST8Sia3

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-----SLTKSSVRIGQLMHYDYSSHKYVFSISNNFRSLLP-----D-VSPIM
NK---RYNCAVVGNISGILTGSCQGEIDKSDVFRFCNFAPTE-AFHKDVGRKTNLTTFN
PSILEKYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFHSTATVTRTLVDFVVEHRGQL
KVQLAWPGNIMQHVNRWKNKHLSPKRLSTGILMYTLASAICEEIHLYGFWPFPGFDPNTR
EDLPYHYDDKKGTKFTTKWQESHQLPAEFQLLYRMHGEGGLTKLTLSCA-----

#Homsap_GT29_ST8Sia3

VP-----ITNSLQELQEKPSKWFNRTAFLHQRQEILQHVDVIKNF-----
-----SLTKNSVRIGQLMHYDYSSHKYVFSISNNFRSLLP-----D-VSPIM
NK---HYNICAVVGNISGILTFIQGREIDKSDVFRFCNFAPSE-AFQRDVGRKTNLTTFN
PSILEKYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFHSTATVTRTLVDFVVEHRGQL
KVQLAWPGNIMQHVNRWKNKHLSPKRLSTGILMYTLASAICEEIHLYGFWPFPGFDPNTR
EDLPYHYDDKKGTKFTTKWQESHQLPAEFQLLYRMHGEGGLTKLTLSCA-----

#Pantro_GT29_ST8Sia3

VP-----ITNSLQELQEKPSKWFNRTAFLHQRQEILQHVDVIKNF-----
-----SLTKNSVRIGQLMHYDYSSHKYVFSISNNFRSLLP-----D-VSPIM
NK---HYNICAVVGNISGILTGSCQGEIDKSDVFRFCNFAPTE-AFQRDVGRKTNLTTFN
PSILEKYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFHSTATVTRTLVDFVVEHRGQL
KVQLAWPGNIMQHVNRWKNKHLSPKRLSTGILMYTLASAICEEIHLYGFWPFPGFDPNTR
EDLPYHYDDKKGTKFTTKWQESHQLPAEFQLLYRMHGEGGLTKLTLSCA-----

#Danrer_GT29_ST8Sia3

TS-----LNTALNENLQE-SSNWRFNRSAYAEINKEIAQHIDVPHNF-----
-----TLTKNSVRVQGLMHYDYSSHKYVFSIGENLRSLLP-----D-ASPVL

NK---RYNTCAVVGNSGILTGSRGPEIDKYDFVFR CNFAPTE-VFRRDVGRRTNLTTFN
PSILEKYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFH TSATVTRTLVDFVVEHKGQL
KVQLAWPGNIMQYVNYWKTQKLSPKRLSTGILMFTLASSLCEQVHLYGFWPFWD PNTG
KELPYHYDDKKGTKFTTKWQESHQLPTEFKLLFKMHADGVLKLSLSHCA-----

#Orylat_GT29_ST8Sia3-A

TS-----LSSAINEDLKN-SSKWTYNSTAFIQLRTEISHHIDMPHNF-----
-----TLTRDAVKVQGLMHFDYSSHKYVYSIGENFRSLLP-----E-VSPIL
NR---HYNVCAVVGNSGILTGSLCGAQIEKYDFVFR CNFAPTE-IFKKDVGRRTNMTTFN
PSILEKYNNLLTVQDRNNFFLSLKKLDGAILWIPAFFFH TSATVTRTLVDFVVEHKGQL
KVQLAWPGNIMQYINNYWKTQKLSPKRLSTGILMYTLASSMCDQIHLYGFWPFWD PNTG
KELPYHYDDKKGTKFTTKWQESHQLPAEFKLLHKMHTEGLLKLTL SHCA-----

#Tetnig_GT29_ST8Sia3-A

IP-----LTSALSEDLQN-SSKWSHNGSAFTQLKKEISQYIDIPRNF-----
-----TLTRDSVRIGQLMHDYSSHKYVFSIGENFRSLLP-----E-VSPIL
QK---HYNVCAVVGNSGILTGSRGQEI DSLDFVFR CNFAPTE-LFKKDVGRRTNMTTFN
PSILEKYNNLLTVQDRNNFFLSLKR LDPAILWIPAFFFH TSATVTRTLVDFVVEPRGQL
KVQLAWPGNIMQYINNYWKTQKLSPKRLSTGILMYTLASSMCDQIHLYGFWPFWD PNTG
RELPHYHYDDKKGTKFTTKWQESHQLPTEFKLLYKMHREGVLKLSLSHCG-----

#Takrub_GT29_ST8Sia3-A

TP-----LTSSLESDLQN-ASKWSFNSSAFAQLKNEISQYIDVPRNF-----
-----TLTRDSVRIGQLMHDYSSHKYVFSIGENFRSLLP-----E-TSPIL
QK---HYNVCAVVGNSGILTGSRGQO I DRFDFVFR CNFAPTE-IFKKDVGRRTNMTTFN
PSILEKYNNLLTVQDRNNFFLSLKKLD TTILWIPAFFFH TSATVTRTLVDFVVEHKGQL
KVRLAWPGNIMQYINNYWKTQKLSPKRLSTGILMYTLASSMCDQIHLYGFWPFWD PNTG
KELPHYHYDDKKGTKFTTKWQESHQLPTEFKLLYKMHREGVLKLSLSHCA-----

#Gasacu_GT29_ST8Sia3-rA

SP-----LTNALGEDLQN-SSKWTYNSSAFLQLKNEISQYIDIPHNF-----
-----TLTRDSVRIGQLMHDYSGHKYVFSIGENFRSLLP-----E-VSPIL
NK---HYNVCAVVGNSGILTGSRGQOIEKFDFVFR CNFAPTE-IFKKDVGRRTNMTTFN
PSILEKYNNLLTVQDRNNFFLSLKKLDG VILWIPAFFFH TSATVTRTLVDFVVEHKGQL
KVRLAWPGNIMQYVNSYWKTKQKLSPKRLSTGILMYTLASTMCDQIHLYGFWPFWD PNTG
KELPHYHYDDKKGTKFTTKWQESHQLPAEFKLLYKMHTEGLLKLTL SHCA-----

#Danrer_GT29_ST8Sia7-B

-----HGCRMRLQYCCNATHSL-----
-----ILTKRNTAVDHIITYETEGKRT-YRVKADLHKMLP-----E-DSPWS
AG---ALGLCAVVGSSGILKNSSCGRQID SADFVIRFNLALVN--DS-DVGLKTDLMNIN
PSQI-RRYKTM--QDPGPLVERISVYGNSSLIIPAFAYGFCTSPSLRVLRVLPQIRPQ-
QPVVFFNPHYLRALDRFWKWRGLKEPRLSSGFILISA ALEMCEHVHVYGFWPFGTDLQE-
NPVPYHYDDQSKPSP-----YHMRMPEEFVRLQLHSQGALTLHLQPCHTHRAVFPNPVP

#Danrer_GT29_ST8Sia7-A

SVIKPAKSIKFSF---AREVSDFLSCPYSNETEQELNRIRLRFCCNATESF-----
-----VLTKRNTAISQSI PYETNSRRT-YKMNADVHKLLP-----E-DSPWS
AG---ALGLCAVVGSSGILKNSSCGRQID SADVIRFNLALIN--DS-DVGLKTNLITIN
PSQI-RGYRNLE--KKPGPLVKRVSVYGNSSLIIPAFAYVICTSPSLRVLRVLPQIRPQ-
QPVLFFSPHYLRALDRFWKGRGLKERRLSTGFMLISA ALEMCEHVHVYGFWPFGTDLQE-
NPIPHYHYDDQMSR-G-----SVHRMPEEFVRLQLHSQGALTLHLQPCDTH-----

#Pimpro_GT29_ST8Sia7

SIIKSAKSIKFRF---TQELSDYLSCPYSNQTERELNRIRLQFCCNATGSF-----
-----ILTKRNTAITQSIQYETST-KT-YKMKAE LHKMLP-----E-DIPWS
GR---RLGRCAVVGSSGILKNSSCGREIDNADFVIRFNLA EVN--DS-DVGLKTDLITIN
PSQI--RYKNLQ--NNPDPLVERVSVYGNASLIIPAFAYTFCTSVSIVLKVLPQIRPH-
QPVVFFSPSYLRSLDRFWKGRGLQEERLSTGFMLI STALELCEHVHVYGFWPFDDNDLQD-
QPIPHYHYDDLSPSS-----HRHKMPEEFVRLQLHSQGALTLHLLPCDSPETDRENNL-

#Catcat_GT29_ST8Sia7

AIIKPAKSIQLQRF---TQELSDFMSCPYKSNTTERELNRMRLQYFCNATGSL-----
-----FLTKRNTAINQTIPIYETSTVKT-YKMNAAIHGMLP-----E-DFPWS
GR---RMGRCAVVGSGGILKNSSCGREIDSADYVIRFNLASIN--DS-DVGLKTDLITIN
PSQI--QFKNLD--KNPEPLVERVSVYGNASLIMPAFAYTFCTGQSIKTLRVLHPIRPQ-
QPVVFFSPTYLRTLDRFWKGRGLKEVRLSTGFMLISTALELCEVDHVYGFWPFPGTDLHN-
NSVPYHYDQLSPHR-----YMHAMPEEFVRLQLLHSGALTLHLQPCS-----

#Gymprzprz_GT29_ST8Sia7

SIIKPAQSIKLESF---TQELSDFMNCPHKPNTTERELNRMRMQFCCNATGSL-----
-----FLTKRNTAINQTIPIYETSTIRT-YMNPNVIHSMLP-----E-DFPWT
GR---RLGRCAVVGSGGILKNSSCGREIDSADVFIRFNLAYIN--DS-DVGLKTDLVTIN
PSQI--RYKNLE--QNPDPPLVERVSVYGNASLAMAFAFAYTFCTGLSIKTLKVLHPIRPQ-
QPVVFFSPIYLRTLDRFWKGRGLKSIKTLRVLHPIRPQ-
NSVPYHYDQLSPHR-----YKHKMP-----

#Sinrhi_GT29_ST8Sia7

SIIKPAKSLNLESF---TQELSDFMSCPYKSNTTERELNRMKLOFCCNATRSL-----
-----FLTKRNTAVNQTIPYETSTIST-YTMNDTLHSMLP-----E-DFPWS
GR---RLGRCAVVGSGGILKNSSCGREIDSADVFIRFNLASIN--DS-DVGLKTDLVTIN
PSQIQREYKDL--KKNPPLVKRVSVYGNASLIMPAFAYTFCTGLSIRTLKALHPIRPQ-
QPVVFFSPYYLQTLDRFWKGRGLKSIKTLRVLHPIRPQ-
NPVPYHYDQLSPHR-----RMHKMPEEFVRLQLLHSGALTLHLQPCSSDAS-----

#Sinans_GT29_ST8Sia7

SVITSVKRLNMESEF---TEELVDLFLKCPQKPNTEQELNRMKLOFCCNATGSI-----
-----FLTKRNTAINQTIPIYETDTKHT-YRMNAAIHNMLP-----E-DFPWS
GR---RLGRCAVVGSGGILKNSSCGREIDSADVFIRFNLASIN--DS-DVGLKTDLVTIN
PSQIQREYKDL--KKNPPLVKRVSVYGNASLIMPAFAYTFCTGLSIRTLKALHPIRPQ-
QPVVFFSPYYLQTLDRFWKGRGLKSIKTLRVLHPIRPQ-
NLVPYHYDQLSPHR-----SMHKMPEEFVRLQLLHSGALTLHLQPCSSDAS-----

#Lepocu_GT29_ST8Sia7

LGMQSLKKNVSTLL---CGQVTQLMRCPWTLNLTQLEQQORTELRSLSCNATGRL-----
-----VVTQDNTPLGGTITYDAEKWT--RQVDTEIFNMLP-----Q-SPPWA
GGPGARLRRCVAVGNGGILRNSSCGAHDRAFDVIRFNLPPLN--YSRDVGVKSSLVTVN
PSQIINSYRNLN--YARRPFVQRVSTYENAHVLPFAFAF'SFCTDPCFRVYYTLQDNRP-
QRALFYHPDYLRQLATYWQEKGLRETRLSTGLMMVSAALELCEVLYGFWPF'SFDLSE-
RPLSNHYDDVPPNR-----GMHAMPEEFVRLQLLHSGALTLHLQPCSSDAS-----

#Angang_GT29_ST8Sia7

FSLT-ASKINTKSF---TEDVRLMSPHESNITQERHRVELRSCCNATGSL-----
-----FLTRQNTREGQRIKQYETNRKKN-ILVDKSIKMLP-----K-STPWR
ND--SRFQRCVAVGNGGILRNSSCGAEIDSADIVFRLNMAPIN--NSRDVGVKTSLVTVN
PSQIRVGYPDQ--KRPQPLVERVSVYGNASLIMPAFAYTTCTDISFKVHKVQKMRPN-
QKVVFFNPEYLLELFQYWKHGLEELRLTTGLMLASVAMELCDSVHLYGFWPFELDLFQ-
CPVTHHYDDVPPNR-----RMHAMPEEFVRLQLLHSGALTLHLQPCSSDAS-----

#Salsal_GT29_ST8Sia7-B

VTMTSMKKVDIALF---SQEVRELMNCPWRNLNITHRELHRTELWSSCNASDRL-----
-----MVTRQNTNQNQSLTYEVERRMK-RKVDQALWEMLP-----Q-TVPWS
KG---SLSRCVAVGSGGILQNSSCGAEIDSADYIIRFNLPVVT--NSKDVGNKTHLMTIN
PSQIR-GYRNLN--KAPQPLANRVAVYGNASLLLPAFASYQFSTGLSLDVYHALQPLRPY-
QKVVFFNPNFMLNLGRKWKQGLKEPRLSTGLMLASVAMELCEEVHLYGFWPFSLDLNH-
NPLPHHYDDVPPNR-----GFHSMPEEFVRLQLLHSGALTLHLQPCSSDAS-----

#Salsal_GT29_ST8Sia7

LTLTSAKAINMRTL---IMDVRQLMTCTHRPNITQRELYRVILRSCCNATGEM-----
-----ILTKQNTKLGQKIHYETNQKLF-KTVDKKLHSMMLP-----K-DLPWS
KG---LLSHCAVVGSGGILQNSSCGAEIDSADYIIRFNLPVVT--NSKDVGNKTHLMTIN
PSQIR-GYRNLN--KAPQPLANRVAVYGNASLLLPAFASYQFSTGLSLDVYHALQPLRPY-

QKVVFNNPMLNLGRKWKQGLKEPRLSTGLMLASVAMELCEEVHIYGFWPFSLDLNH-
NPLPHHYDNDVGPKI-----GFHSMPEEFQQLLKLHTQGALQLHLGRC-----

#Salfon_GT29_ST8Sia7

-----SINTRTL---IMDVRELMNCPHRPNITQRELYRVILRSCCNATGEM-----
-----ILTNQNTKSGQKIHYETNOKLF-KTVDKKLHSMMLP-----K-ALPWS
KG---LLGHCAVVGSGGILQNSSCGAEIDSADYIIRFNLGPVT--NSKDVGNKTHLMTIN
PSQIR-GYPNLT--KDPQPLANRVAVYGNASLLLPAFSYQFCTGLSLNAYHALQPLRPN-
QKVVFNNPMLNLGRKWKQGLKEPRLSTGLMLASVAMELCEEVHIYGFWPFSLDLNH-
NPLPHHYDNDVGPCK-----GVHSMPEEFQQLLKLHTQGVQLHLHLGRC-----

#Corclu_GT29_ST8Sia7

LTVTSAKAINPRTL---IMDIRQLMDCSHRPNITQRELYRVILRSCCNATGEM-----
-----ILTNQNTKLGQKIHYETNOKLF-KTVDKKLHSMMLP-----N-ALPWS
KG---LLGRCVAVVGSGGILQNSSCGAEIDSADYIIRFNLGPVS--NSEDVGNKTHLMTIN
PSQIRTGYRNL--KDPQPLANRVAAYGNASLLLPFSYQFCTGLSLDVYHVLRLRPN-
QKVVFNNPMLLQLSRKWKGRGLKEPRLTSGMLMLASVAMELCEEVHLYGFWPFPLDLYH-
NPLPHHYDNDVGPCK-----GVHSMPEEFLLMLQLHTQGVQLHLHLGRC-----

#Thythy_GT29_ST8Sia7-B

LNVTSAKAINPRTL---IMEVRQLMNCTYRPNITQRELYRVTLRSCCNATGEM-----
-----ILTNQNTKLGQKIHYETNOKQF-KTVDKKLHSMMLP-----K-ALPWS
QG---LLGHCAVVGSGGILQNSSCGAAIDSADYIIRFNLGPVS--NSEDVGNNTNLMITIN
PSQIRTCYRNL--KDPQPLANRVAVYGNASLLLPFSYQFSTGLSLDVYRALRPLRPN-
Q-VLFFNPNFLKLGRKWKERGLKESRLTSGMLMLASVAMELCEEVHLYGFWPFPLDLYD-
NPLPHHYDNDVGPKN-----GIHSMPEEFRLLLKLHTLGVQLHLHLGSC-----

#Esoluc_GT29_ST8Sia7

VAMTTMKKVDIVPF---SQVRELMDCPWRLNLTREHRLHRTLWACCNASDRL-----
-----IVTRQNTNHNQTLTYEAERWRK-KLVDQTLWEMFP-----K-NVPWS
KG---LLGRCVAVVGSGGILQNSSCGEEIDRAHYIIRFNLAPVN--QSRDVGLKTDLITAN
PSQIIKQYDLH--KNPGRLAEQMSVYGNARLLLPAFSFAFGTAPCFKVYHALQKALPQ-
QEVVFFHPDYLFELGQFWRRRGQKASRISTGLMLASSALEICDQVHLYGFWPFVLDLH-
NPLQHYYDNDVGPNH-----YMHAMPEEFLLLLQLHSQGALQLHVGHC-----

#Oncmyk_GT29_ST8Sia7

VTMSTIKKVDIALF---SQDVRELMDCPWRLNLTRELYRTELWSSCNASDRL-----
-----MVTRQNTNQLNQSLSYIEHRWKK-RKVDQALWEMLP-----Q-TVPWS
KG---SLSRCAVVGSGGILQNSSCGAEIDNADYVIRFNLAPIN--KSCDVGVKTDLVTAN
PSQIIKGYTDLQ--QNPGLAEVLSFYGHALLLPAFSSASGTAPCFKVYHALRKARPQ-
QEVVFFHPDYLFELGRFWRHRGQRARLSTGLMLASTALEICEQVHLYGFWPFPLDLSH-
NSLPHHYDNDVGPNR-----KMHAMPEEFLLLLQLHSQGALQLHVGPCCTLPTP-----

#Thythy_GT29_ST8Sia7

VTMTTMKKANIALF---SQEVRELMDCPWRLNLTREHRLHRTLWSSCNASDRL-----
-----MVTRQNTNQNQILTYEAEKWRK-RKVDKALWEMLP-----Q-TVPWS
KG---SLSRCAVVGSGGILQNSSCGAEIDTADYVIRFNLAPIN--KSCDVGVKTDLITAN
PSQIIKGYHNLQ--RNPGLVLRMSVYGHALLLHAFYFGTSPCFKVYHALRKARPQ-
QEVVFFHPDYLLQLDRFWRRRGQRAPRLSTGLMLASTALEICEQVHLYGFWPFHLDLSQ-
NTLPHHYDNDVGPSPR-----FMHAMPEEFLLLLQLHSQGALQLHVGPCCTL-----

#Takrub_GT29_ST8Sia6-A

-----EI---TDKVNRLYAQTLEKKEDKSKILRSELSSKCQGFKA-----
-----IITQANTVVGSKIYVDGERKSL-VQVTPPEMNTFP-----K-EHPFP
NK---TWETCAVVGNGGILSDSGCGKMIQSAQFVIRCNLPLNNGYQDHVGVKTDLVTAN
PSILVEKYGALM--GRRRPFIESLRSYGNLPTFSYRSNTPVSLRAFYSIEDFGSP-
TRAI SFNPQYLQKLDVFWRSKGLRAVRLSSGLMVASLALCNSVHLYGFWPFVSNHNPGL
RTLKNHYDDIIPPK-----KFHAMPEEFELLLKLHTEGVLRRLHLDLDCVPEVNLMGSTG

#Takrub_GT29_ST8Sia6-B

-----EI---IDKVNRLYAQTWEKKEDKYKKFRSELSSKCQGFKA-----

-----IITQANTVVGSKIVYDGERKRS-VKVSTEMFNTFP-----K-EHPFP
NK---TWETCAVVGNGGILSDSGCGKVIDSAQFVIRC�LPPLNNGYQDHVGVKTDLVTAN
PSILFEKYGALM--GRRRPFIESLRSYGNLILLIPAFSYGNNTPVSLRAFYSIEDFGSP-
TRTIFFFNPQYLQKLAVFWRSKGLRAVRLSSGLMVASLALCLSNVHLFGFWPFSNHPHGL
RTLKNHYYDDIQTKK-----KFHAMPVEFELLLQLHTEGVLRRLHLDDCVPGEVNLMSGTR

#Orylat_GT29_ST8Sia6

-----EN---IMKALELYSEPWWKQEDNYHQFRSOLNSKCHGLEKA-----
-----IITQANTPQGTKLVYDAERKRT-LVVNAEVFNTFI-----K-ENPFP
NK---TWDTCAVVGNGGILANSSCGKTIDSAQFVIRC�LPPLSNGFEKDVGIKSDIVTAN
PSIITEKYFSLM--RHRPFAMRIYGNMVLIPAFSFGHNTALSMRAFYTLEDFESS-
ARAVYFNPEYLNLANFWRSEGLKSPRLSTGIMMASIALEVCSEVHLYGFWPFVHPYSH
QGLTNHYYDDRKAKN-----KFHAMPTEFNLLQLHRKGVLRRLHLGDCTPDEK-----

#Notfur_GT29_ST8Sia6

-----ED---IKKALELYSQTWKKQEDSYQNFRSLLNRKCKCFDKA-----
-----IITQNTPLGSKLVYDGERKRT-LQVNQEIFNTFP-----K-GHPFS
NK---TLHTCAVVGNGGILANSSCGKTIDSAEFVIRC�LPPLSNGYEKHVGIKTHLVTAN
PSILMEKYAALM--ARRRPFVENLRSYGDSSMLLIPAFSYGRNTPVSLRAFYTLEDFESP-
IQSIFFFNPAYLRNLAAFWRSQLKAVRLSTGIIMTSLALEICENVHLYGFWPFVHPYSS
QDLTNHYYDDRKTKI-----KFHAMPDEFNLLNLHLSQGVLMHMLGDCEPDEKRFHRSD-

#Orenil_GT29_ST8Sia6-B

-----EI---ISKVQERYNQTWKKQEDNYLKFRTNLSVKCNGFDKA-----
-----IITKNTPVGLKLVYDGEKKRT-LQVNKDFNIFT-----K-ENPFS
NK---KWDTCSVVGNGGILSESSCGKVIDSAFVIRC�LPPLSNGYEKDVGIKTSLV TAN
PSIFTQRYGSLV--GRRLPFVESLHKGNSLILLIPAFSFGINTAVCQRVAYTIEDFKSP-
IRPVFFNPQYLDLSLAQFWRSEGLKERRLSTGLIMASMALELCENVHLYGFWPFVHPYGF
YTLTNHYYDDKPAKT-----SFHAMPAEFDRLQLHTEGVLRRLHLEDCK-----

#Gasacu_GT29_ST8Sia6

-----QF---IDKVRERYNKTWIKQVDDYLEFRSOLSRKCHGFDSA-----
-----FITQYNTPVGAKIVYDGEKTRT-LQVTPEIFSTFP-----K-EHPFS
NK---IWGTCSVVGNGGILSNSSCGKVIDSAEFVMRC�LPPLDNGYENDVGIKTDLVTAN
PSILIKKYGSLQ--QRRRPFVESLRSYGNLILLIPAFSYGFNTPLSLRAVYSIEDFKSP-
TRPVFFNPPEYLESGLFWRSRGLKAVRASTGLMMASLALHCTDVHLYGFWPFVGNHPQGL
HALTNHYYDDVQPKN-----TVHAMPVEFEFLQLHSQGVLRRLHLEDQCPGEK-----

#Anofim_GT29_ST8Sia6

-----EV---INKVIERYSKTWKKQEENYQKFRSOLSSKCHGFDKA-----
-----IITQANTPVGAKLVYDGEKKRT-LQVTPEIFSTFA-----K-EHPFQ
NK---IWDTCAVVGNGGILTNSCGKTIDSAQFVMRC�LPPLDKGYEKHVGIKTDLVTAN
PSILLEKYGALM--GRRRPFVESLRSYGNLILLIPAFSFGFNTPVCLRAVYSIEDFESP-
TRPVFFNPPEYLQKLALFLRSQGLRAPRSTGIIMASLALHCANVHLYGFWPFVSSHPHGL
HALTNHYYDDRQTKK-----KFHSMPAEFDLLQLHSQGVLRRLHLGDCPPGER-----

#Larcro_GT29_ST8Sia6

-----EV---IDKVMERYSQSWERQEDNYQKFRALNNKCHGFDKA-----
-----IITQANTPVGSKLAYDGEKKRI-LQVTPEIFSTFA-----K-ERPFP
NK---TWDTCAVVGNGGILTNSCGKVIDSAQFVIRC�LPPLSNGYEKHVGIKTDLVTAN
PSIFLEKYGGLM--GRRRPFVESLHSGNSLILLIPAFSYGHNTPVSLRVAYSLEDFKSS-
TRPIFFNPPEYLHSLALFWRSQGLRAVRLSTGIIMASLALHLCANVDLYGFWPFVSNHPHGF
HTLTNHYYDDRQTKV-----KFHAMPAEFELLLRLHLSQGVLRRLHLGDCQPSEK-----

#Ampoce_GT29_ST8Sia6

-----EV---IDKVARYSQPWKRQEDSYQKFRFQLSSKCHGFNKA-----
-----IITKTNPVGSKLVYDGEKKRT-LQVTPEIFSTFI-----K-DHPFS
NK---TWDTCAVVGNGGILTNSCGKTIDSAQFVIRC�LPPLANGYEKHVGVKTDLVTAN
PSILLEKYGALM--GRRRPFVESLRTYGDSSMLLIPAFSFGHNTPVSLRAAYTIEDFESP-
TRPVFFNPPEYLHSLALFWRSQGLKAVRLSTGLIMASLALHLCANVHLYGFWPFVSNHPHGL
QPLTNHYYDNRQTKT-----KFHAMPAEFDLLRLHLSQGVLRRLHLGDCPTSGK-----

#Serlaldor_GT29_ST8Sia6

-----EI---IDNVIERYSQTWKKQEDNYQKFRSQLNSKCRGFNKA-----
-----IITQANTPVGSKLVYDGEKRRS-LQVTPEIFSTFV-----K-EHPFS
NK---TWGTCAVVGNGGILTNSSCGQTIDSAQFVIRC�LPPLKNGYEKHVGNKTDLVTAN
PSILVEKYGALM--AHRPFVDSLHTYGNL LLLP AFSFGHNTPVSLRAAYTIEDFGSP-
IKPVFFNPEYLQRLAVFWRSQLRAVRLSTGIIMASLAL ELCADVHLYGFWPFSSTHPHGF
HPLTNHYYDDRKT KM-----KFHAMP AEFDLLRLRHSQGVLRRLHLGDCRPHEK-----

#Paroli_GT29_ST8Sia6

-----EI---IDKVIQRYSQTWKRQEDNYQKIRSQLSSKCHGFDKA-----
-----IITQANTPVGSKLVYDGEKRT-LQVTPEVFSTFI-----K-ERPFS
NK---TWDTCVAVVGNGGILTNSSCGQ MIDSAQFVIRC�LPPL ENGYEKHVGTKTDLVTAN
PSILMEKYGALM--GRRRPFVESLRIYGD SLLLI PAFSYGHNTPVSLRVVYTIEDFESP-
TRPIFFNPEYLQSLAVFWRSQLKAVRLSTGIIMASLAL ELCNVHLYGFWPFSNHPHGL
HVLNNHYYDDRKT KT-----KFHAMP AEFDLLRLRHSQ GALRLHLGDC-----

#Lepocu_GT29_ST8Sia6

-----EKAN---IDKLAQVHSQTWKRQESRLQTFRAQLNMKQCQGSRA-----
-----IITQANTLLGSKVTYDGERRKP-VEVTPKLYSTFP-----K-EHPFG
NV---SFQSCAVVGNGGILANSSCGEEIDGAQFVIRC�LPVDRKYQDDVGNKTDLVTAN
PSILLERFEGLM--ELRRPFVESLGDYGPMLALPAFSYGHNTPVSLRAVYTLQDFNSP-
VRAVFLNPEYLQNLARFWKAHGLRTVRLSTGLIVASLAL ELCASVTLYGFWPFSLHPFSK
QHLTNHYYDDQ QSK-----SFHAMP AEFEQLRLRHSQGVIRVHLGSC-----

#Amical_GT29_ST8Sia6

-----EQSV---IDRLLQTHIVDWEKQEHKFQSFRAQLNSRCDGLSKA-----
-----IISQTNTPLGSKVVYDGEKRP-IQVTPKLFSTFP-----K-EHPFG
NR---TFTSCAVVGNGGILMNSSCGGEIDEAQFVIRC�LPVDPHGYQRDVGNKTSLV TAN
PSILLDKFNGLM--ELRRPFVDSLGSYGDPLLVLP AFSYSRNPVSLRALYTLQDFDSP-
VRPVFLNPEYLNARFWKAQGLQAIRLSTGLIMASLAL ELCANVQLYGFWPFSKDPHSK
HPLTNHYYDDQ QAK-----TIHAMSTEF SHLLMLHNQGIIRVQLGKCQAGTRRATPSLH

#Angang_GT29_ST8Sia6

-----EY-T---IDKMVELYSYAWKKQANFNKFRSQLSSRCRGVSTA-----
-----IVTQNTPLDSKIYYDGEKRP-LQVTPKLYSTFA-----K-EQPFV
NV---TWKTCVAVVGNGGILVNSSCGE AIDSAHFVFR CNLPPLDKAYQKDVGNKTNLVTAN
PSILIEKFEGLM--EYRRPFVESLSDYGEALL LLLP AFSYAHNTPVSLRAFYT LRDFGGR-
ARPAFLSPAYLQSLAHFWRAQGLRTVRLSTGLIVASLAL ELCANVHLYGFWPHAQH PHDR
RPLTNHYYDDRQ GK-----KVHAMP AEFGHLLRLHRQGVVRVHLGQCEDRPR-----

#Cluhar_GT29_ST8Sia6

-----DS-V---IDKVLERYSKNWKKQENNYKRFRALLSSRCHGATKA-----
-----VVTQANTPLGSKVVYDGEKRP-LQVTSALFNVP-----K-EPPFG
NT---SWDTCVAVVGNGGILANSSCGRRIDSAQFVIRC�LPPL EHG YEEDVGNKTDLVTAN
PSILHEKFGGLM--ERRRPFVEGLRPGNSL LLLP AFSYSHNTPVSLRAVYTL EDFRSP-
ARPVFLSPDYLTSLARFWRSQLRSVRLSTGLIVASLAL ELCNTVDLYGFWPFSQHPHGH
QPLTNHYYDNRETKK-----KIHAMP AEFDHLLRLRHGQGILRVHLGQCPRSDG-----

#Esoluc_GT29_ST8Sia6

-----DTTI---IEKVVEHYSHSWKKQEDNFRKFRSLLRNTCHGLTKA-----
-----VVTQSNTPLGSKVVYDGEKRP-LQVTAELFSTFA-----K-EHPFV
NA---TWDTCVAVVGNGGILANSSCGERIDSAQFI IRC�LPPL ANGYERDVGNKTDLVTAN
PSILQEKYKGLQ--EHRLPFVKSLSYGD SFVLLP AFSYGHNTPLSLRALYTIQDFNSP-
SRPIFLNPEYLRSLARFWRSQLKTARLSTGLIVASLAL ELCANVHLYGFWPFSQHPQH
RPLTNHYYDDRQ SK-----TVHAMP AEFDQLQRLHNQGVLRRLHLGECAPAAAT-----

#Onckis_GT29_ST8Sia6-A

-----DT-V---TDKVVELYSYSHSWKKQEDKFRNFRSLLSNRCNGLTKA-----
-----MVTQANTPLGSKVVYDGEKRP-LQVTPELFSTFA-----K-ENPFV
NT---TWDTCVAVVGNGGILANSSCGEKIDSAQFVIRC�LPPL ENGYERDVGNKTDLVTAN

PSILMEKYGGLQ--ERRRPFVESLRSYGDLSMLLLPAFSYGHNTPVSLRALYTIQDFDSP-
SRPVFLNPEYLQSLARFWQGOGLRTVRLSTGLIVASLALALELCANVHLYGFWPFNEHPHRH
QPLTNHYYDDRQSKK-----TVHAMPAEFDHLLRLRHTQGVLRIRHLGECAPTARCRPSSPL

#Salalp_GT29_ST8Sia6

-----DT-V---TEKVVERYSHSWKKQEDKFRNFRSLLSNRCHGLTKA-----
-----MVTQANTPLGSKVVYDGEKRKP-LQVTPELFSTFA-----K-ENPFV
NT---TWDTCSVVGNGGILANSSCGERIDSAQFVIRC�LPLENGYERDVGNKTDLV TAN
PSILMEKYGGLQ--ERRRPFVESLRSYGDLSMLLLPAFSYGPNTPVSLRALYTIQDFDSP-
LRPVFLNPEYLQSLARFWQGOGLRTVRLSTGLIVASLALALELCANVHLYGFWPFNEHPHRH
QPLTNHYYDNRQSKK-----TVHAMPAEFDHLLRLRHSQGVLRIRHLGECAPAAR-----

#Salsal_GT29_ST8Sia6

-----DT-V---TEKVVERYSHSWKKQEDKFRNFRSLLSNRCHGLTKA-----
-----MVTQANTPLGSKVVYDGEKRKP-LQVTPELFSTFA-----K-ENPFV
NT---TWDTCSVVGNGGILANSSCGEKIDSAQFVIRC�LPLENGYERDVGNKTDLV TAN
PSILMEKYGGLQ--ERRRPFVESLRSYGDLSMLLLPAFSYGHNTPVSLRALYTIQDFDSP-
SRPVFLNPEYLQSLARFWQGOGLRTVRLSTGLIVASLALALELCANVHLYGFWPFNKHPHRH
QNLTNHYYDDRQSKK-----TVHAMPAEFDHLLRLRHTQGVLRIRHLGECTPTASPGCSS-K

#Oncmyk_GT29_ST8Sia6

-----DT-V---TDKVLELYSHSWRKQEDKFRKFRSLLSNRCHGLTKA-----
-----MVTQANTPLGSKVVYDGEKRKP-LQVTPELFSTFA-----K-ENPFV
NT---TWDTCSVVGNGGILANSSCGEKIDSAQFVIRC�LPLENGYERDVGNKTDLV TAN
PSILMEKYGGLQ--ERRRPFVESLRSYGDLSMLLLPAFSYGHNTPVSLRALYTIQDFDSP-
SRPVFLNPEYLQSLARFWQGOGLRTVRLSTGLIVASLALALELCANVHLYGFWPFNEHPHRH
QPLTNHYYDNRQSKK-----TVHAMPAEFDHLLRLRHTQGVLRIRHLGECAPTASPGCSS-K

#Onctsh_GT29_ST8Sia6

-----DT-V---TDKVVELYSHSWRKQEDKFRNFRSLLSNRCHGLTKA-----
-----MVTQANTPLGSKVVYDGEKRKP-LQVTPELFSTFA-----K-ENPFV
NT---TWDTCSVVGNGGILANSSCGEKIDSAQFVIRC�LPLENGYERDVGNKTDLV TAN
PSILMEKYGGLQ--ERRRPFVESLRSYGDLSMLLLPAFSYGHNTPVSLRALYTIQDFDSP-
SRPVFLNPEYLQSLARFWQGOGLRTVRLSTGLIVASLALALELCANVHLYGFWPFNEHPHRH
QPLTNHYYDDRQSKK-----TVHAMPAEFDHLLRLRHTQGVLRIRHLGECAPTASPGCSS-K

#Danrer_GT29_ST8Sia6

-----DSVI---IGKALGNYSNSWKKHEANYKRFRLLLNKCHAVSKA-----
-----VVTQNNTPLGSNVYDGERRKP-LQVTQALFNILA-----K-EQPF
NA---TWESCAVVGNGGVLANS SCGEEINSAQFVIRC�LPPLDDRYEKDVGNKTNLV TAN
PSILHEKYSGLM--ERRRPFVESLHSYQALLLLPAFSYGHNTPVSLRAFYTLEDFGREG
PLPIFLNPEYLRKLTKFWREQGLNSVRPSTGLIMASLALICTNVHLYGFWPFGKHPNDS
RPITNHYYDNRESKK-----NVHSMPEFEQQLLKLHKQGVVHIRHLGECQPAHR-----

#Cypcar_GT29_ST8Sia6

-----DDVL---IAKALENYS DKWKKQETNFKKFRSLLSNKCHAVSKA-----
-----VVTQNNTPLGSNVIYDGERRKP-LHVTQALFNILA-----K-EQPF
NA---TWESCAVVGNGGILANSSCGEEINSAQFVIRC�LPPLDKGYEKDVGNKTNLV TAN
PSILHEKYSGLM--ERRRPFVESLRPYQALLLLPAFSYGHNTPVSLRAFYTLEDFGSNS
PLPVFLNPDYLRRLSKFWREGLNSVRPSTGLIVASLALICSNVHLYGFWPFSKHPYDS
QAITNHYYDNRESKK-----NVHSMPTFEFYLLKLHNQGVIRIRHLGKCQPTH-----

#Sinans_GT29_ST8Sia6-B

-----DSVL---IAKALENYS DKWKKHEANLKRFRSLMSSKCHAVSKA-----
-----VVTQNNTPLGSNVIYDGERRKP-LQVTQALFNILA-----K-EQPF
NA---TWESCAVVGNGGILANSSCGEEINSAQFVIRC�LPPLDKGYEKDVGKKTNLV TAN
PSILHEKYSGLM--ERRRPFVESLRPYQALLLLPAFSYGHNTPVSLRAFYTLEDFGSNS
PLPVFLNPEYLRRLSKFWREQGLNSVRPSTGLIVASLALICSNVHLYGFWPFSKHPYDS
QPITNHYYNDRESKK-----NVHSMNEFAHLLKLHKQGVIRIRHLGECQPTH-----

#Sinans_GT29_ST8Sia6

-----DNVL---IAKALENYSHKWKKEANFKRFRSLLSSKCHAVSKA-----
-----VVTQNNTPLGSNVIYDGERRKP-LQVTQALFNILA-----K-EQPF
NA---TWESCAVVGNGGILANSSCGEEINSAQFVIRC�LPPLDNRYEKDVGNKTSLV
TANPSILHEKYSGLM--ERRRPFVESLRPYGQALLLLPAFSYGHNTPVSLRAFYTLEDFGSDS
PLPVFLNPEYLRRLSKFWRERGLNSVRPSTGLIMASLALICSNVHLYGFWPFNKHPNDS
RPITNHYYDDRESKK-----NVHSMPTFEFEHLLKLHKQGVIRIHLGECQPT-----

#Sinrhi_GT29_ST8Sia6

-----DNVL---IAKALENYSHKWKKEANFKRFRSLLSSKCHAVSKA-----
-----VVTQNNTPLGSNVIYDGERRKP-LQVTQALFNILA-----K-EQPF
NA---TWESCAVVGNGGILANSSCGEEINSAQFVIRC�LPPLDNRYEKDVGNKTSLV
TANPSILHEKYSGLM--ERRRPFVESLRPYGQALLLLPAFSYGHSTPVSLRAFYTLEDFGSDS
PLPVFLNPEYLRRLKFWRERGLNSVRPSTGLIMASLALICSNVHLYGFWPFNKHPNDS
RPITNHYYDDRESKK-----NVHSMPTFEFEHLLKLHKQGVIRIHLGECQPT-----

#Pygnat_GT29_ST8Sia6

-----ENVI---IDKALRVYSSRWRQEANFKRFRSLLSRNCHALSKA-----
-----VVTQANTPVGSKLVYDGEKTKP-LQVTSALFNFTA-----K-EQPF
NA---TWDTCAVVGNGGILANSSCGEKINSADFIIRC�LPPLGSGYEKDVGNQTSLV
TANPSILIEKFGLM--ERRRPFVESLRPYGDSLLVLPAFSYGHNTPVSLRAFYTLEDFGITS
ARPVFLNPEYLSLARFWRGQGLRSARLSTGLIVASLALICSNVHLYGFWPFQHPYGR
QPITNHYYDDRQSKK-----NVHSMPEAFDHLRLRHMQGVIQMHLGACSMNRNRTSN----

#Astmex_GT29_ST8Sia6

-----DNAI---IDRLLKSYSRWKRREANFSKFRSLLSSSCHAVSKA-----
-----VVTQSNTPVGSKLVYDGEKTKP-LQVTKALFNFTA-----K-EQPF
NA---SWDTCAVVGNGGILVNSSCAEKINSANLVIRC�LPPLGNGYEKDVGNKTSLV
TANPSILIEKFSGLM--ERRRPFVESLRPYGDSLLLLPAFSYSHNTPVSLRALYALEDFNAVG
PRPVFFNPEYLSLARFWRGRGLRARTARLSTGLIVTSLALELCTNVHLYGFWPFSLHPHGR
QTITNHYYDNRQSKK-----NVHSMPSEFEHLLRLHVSQVILHLGECSTTDLNHTEKT-

#Danrer_GT29_ST8Sia1

-----SDKEMV---EEVLR--QGQTSRNQTAVELYRKLLTDCCNPKRMF-----
-----AVTKENSPLGKVLWYDGEFYHY-HTVTNETYPIFV-----Q-DTPLQ
L----PLKRCSVVGNGGVLKHSKGCNEIDRADFIMRC�LPPLSKDYTDVVGTKTHLV
SANPSIIIEKSFQNL--WSRKSFVESMKAYGSSYIYIPAFSMKPGTDP SLRAYHALADSSN-
QTVLFANPDFLKNVGI FWKNHG VHGKRLSTGLFLVSLALGLCEEVTAYGFWPF SVGLDE-
RPVSHHYYDNILPSS-----RFHAMPEEFLQLWHLHKSGTLRMRVGSACAKERMELKREK-

#Orylat_GT29_ST8Sia1

-----RDKDIV---AEVLR--QGDVWRKNQGTGIDLRYRDLTKCCNPKKMF-----
-----AVTKENSPIGKVLWYDGEIYHS-HTVNSETYQLFI-----K-RRGAA
S----SCRRCAVVGNGGILKGSKKGKEIDHHYIFRC�LPPLSREYVEDVGTKTHLV
TANPSIIIEKRFQNLV--WSRKT FVDSMKVYGSYIYMPAFSMAPGTDP SLRAYFALTDVPSN-
LTMLFANPDFLLSVSKFWKAHG VHARRLSTGLFLVSLAMGLCEVTYGFWPF SVDLDE-
QPI SHHYYDNILPYK-----WFHAMPEEFVQLWHLHKSGILRMKVGHCSQON-----

#Gasacu_GT29_ST8Sia1

-----RDKDIV---EEVLK--QGGVWQKNQGTGIDLRYRDLTECCDPRRMF-----
-----AVTKENSPTGKVLWYDGEFYHS-HTVNNETYPLLIV-----K-DNPLR
L----PLKKCAVVGNGGILRHSQCGRIDIQADFLVRC�LPPLSKEYVDDVGTTRTHLV
TANPSIIIEKRFQNL--WSRKFVDSMKVYGSYIYMPAFSMKTGTDP SLRAYHALADSSN-
LTMLFANPEFLRTVGRFVKARGVHARRLSTGLFLVSLALGLCEEVTAYGFWPF SVGLDE-
QPVSHHYYDNILPYT-----WFHAMPEEFVQLWHLHKSGALRVRVGRCSAQGGG-----

#Takrub_GT29_ST8Sia1

-----ADKEIV---DEVLR--QGEAWQKNQGTGIDLRYRDLTECCDPRRMF-----
-----AVTKQNSPLGKVMWYDGEFYHS-HTVNNETYPLFV-----Q-ENPLQ
L----PLKKCAVVGNGGILRGSKCGKIDRADFIMRC�LPPLSKEYLEDVGTKTHLV
TANPSI IENRFQNL--WSRKHVDSMKVYGTSYIYMPAFSMSPGTNP SLRAYALADASAN-
LTMLFANPEFLRSVKGFWKARNVHAKRLSTGLFMVSLALALCKEVTYGFWPF FAIDLDE-

QPVSHHYDNLIPYK-----WFHTMPEEFVQLWHLHKSGTLRMRVGRCPPEDEGGR-----

#Tetnig_GT29_ST8Sia1

-----GDKEIV--AEVLR--QGEAWHRNQTGIDLYRRLTDCDDPPKMF-----
-----AVTKRNSPLGKVMWYDGEFYHS-HTVNNETYRLFV-----Q-DNPLQ
L----PLKKCAVVGNGGILRASKCGKIDIDQADFIMRCNLPPLSEEYLEDVGTKTHLVTAN
PSI IENRFQSL--WSRKHFVDSIKVYGTSYIYMPAFSMRPGTEPSLRAYYALADTSSN-
LTVLFANPEFLRTVVGKFWKARNVHAKRLSTGLFMVSLALALCEEVTVYGFWPFPAIDLDE-
QPVSHHYDNLIPYK-----WFHTMPEEFVQLWHLHKSGTLRMRVGRCSSQGGGR-----

#Calmil_GT29_ST8Sia1

-----DQKEIV--NDVLH---QPVWRRNQTATTAFRRLENCCETKRMF-----
-----AVTQHNSPMGKNLWFDGEFLHS-LSVNNEMFAMFP-----Q-DTPFQ
I----PLKKCSVVGNGGILKRSACGDKIDKADFVMRCNLPPLSNEYARDVGHRTQLVTAN
PSI IKKRYQNL--WSRKAFVESMKVYGRSYIYMPGFSMKAGTEPSFRYYTLDSDVNAN-
QTIIIFANPDFLRNVQKFWKGVHAKRLSTGLFLVSVALGLCEEVTLYGFWPFSTDLEE-
RTISHHYDNLVMPDT-----SYHAMPEEFVQLWHLHKSGILKIHVGKCGQIPM-----

#Xenlae_GT29_ST8Sia1

-----GHKEMI--RQVL--QFGPRWGRNRSSGDSFRKLLQDCCDPPRLF-----
-----SMTKANTALGENLWYDGEFFQS-LTIDNTRSLFP-----Q-DTPIK
L----PLKRCSVVGNGGILKNSRCGEQIDEADFVMRCNLPPLSREYTDVGTQTQLVTAN
PSI IDKRFQNL--WSRKSFVESVSVYKQSYVYMPAFSTKRGTDPVSLRVYYTLEDFGTN-
QTVLFANPNFLRVNGKFWKSGVHAKRLSTGLFMVSAALSCEEVTIYGFWPFQMDLGG-
RHISHHYDNLMLPLS-----GVHAMPEEFVQLWHLHKSGVLMQQLDQCKKDVSSKKPH--

#Siltro_GT29_ST8Sia1

-----GHKEMV--REVL--RFGPGWRKNRTEMDSFRKLLQDCCDPPHLF-----
-----SLTKVNTPLGENLWYDGEFFHS-LTIDNSTRSLFP-----Q-DTPFK
L----PLKRCSVVGNGGILKNSRCGEQIDEADFVMRCNLPPLSREYTEDVGTTRTQLVTAN
PSI IDKRYQNL--WSRKSFVENLRVYQQSYVYMPAFSTKRGTDPVSLRVYYTLADFGTN-
QTVLFANPNFLRVNGKFWKSRGIHAKRLSTGLFMVSAALSCEEVTIYGFWPFQMDLGG-
RYISHHYDNLPLS-----GVHAMPEEFVQLWHLHKSGVLMQQLDQCKKDVSSQKPH--

#Anocar_GT29_ST8Sia1

-----GEKEIM--CGMRLQKCKAWQRGHAAHAFRKLKKECCDPGQLF-----
-----AMTKENSPVGKNLWYDGEFLYS-FTIDNETFSLFP-----K-ATPFQ
L----PLKKCSVVGNGGILKKSNCGRQIDQADFVMRCNLPPLTSEYSKDVGSKTQLVTAN
PSI IKKRFQNL--WSRKAFVDSVKVYNQSYIYMPAFSMKAGTEPSLRVYYTLADV GAR-
QTVIFANPNFLRDIGKFWKSGIHKRLSTGLFLVSAALGMCEEVTIYGFWPFMSMDLHG-
NFISHHYDNLIPDS-----GFHAMPEEFVQLWFLHKSGVLRMQLEHCEDSIFHPAS---

#Galgal_GT29_ST8Sia1

-----DEKEIV--QGVLMQ--GKAWRRNHTAVAVFRKLLDCCDPGQLF-----
-----AMTKQNSPMGKNLWYDGEFLYS-FTIDNTTYSLFP-----Q-ATPLQ
L----PLKKCSVVGNGGILKKS GCGKQIDQADFVMRCNLPPLSREYSKDVGLKTQLVTAN
PSI IQRFQNL--WSRKAFVDSVKVYNHSYIYMPAFSMKTGTGPSLRVYYTLKDFGAK-
QAVLFANPNFLRDIGKFWKNGIHKRLSTGLFLVSAALGLCEEVTIYGFWPFVSDLHG-
KFISHHYDNLVLPDS-----GFHAMPEEFVQLWFLHKSGVLRMQLEQCEDPLTQSSA---

#Bostau_GT29_ST8Sia1

-----DEKEIV--QGVLMQ--GTAWRRNRTAAGIFRKQMEDCCDPAHLF-----
-----AMTKMNA PMGKSLWYDGEFLYS-FTIDNSTYSLFP-----Q-ATPFQ
L----PLKKCAVVGNGGILKKS GCGRQIDEADFVMRCNLPPLSSEYTKDVGSKSHLVTAN
PSI IRQRFQNL--WSRKT FVDHMKVYNHSYIYMPAFSMKTGTGTEPSLRVYYTLDSDVGAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFVSNMHE-
QPISHHYDNLVLPFS-----GFHAMPEEFVQLWFLHKGALRMQLDPCEDNSL-QPTS--

#Canlupfam_GT29_ST8Sia1

-----NEKEIV--QGVLMQ--GTAWRRNQTAAARVFRKQMEDCCDPAHLF-----
-----AMTKLNSPMGKSMWYDGEFLYS-FTIDNSTYSLFP-----Q-ATPFQ

L----PLKKCAVVGNGGILKKSQCGRQIDEANFVMRCNLPPLSSEYTKDVGSKSHLVTAN
PSIIRQRFQNL--WSRKTFFVNDMKIYNHSYIYMPAFSMKTGTPEPSLRVYYTLDVGVAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFVSNMHE-
QPISHHYDNLVLPFS-----GFHAMPEEFLQLWYLHKIGALRMQLDPCEDTSL-QPTS--

#Pantro_GT29_ST8Sia1

-----NEKEIV--QGVL-QQ-GTAWRRNQTAARAFRKQMEDCCDPAHLF-----
-----AMTKMNSPMGKSMWYDGEFLYS-FTIDNSTYSLFP-----Q-ATPFQ
L----PLKKCAVVGNGGILKKSQCGRQIDEANFVMRCNLPPLSSEYTKDVGSKSQLVTAN
PSIIRQRFQNL--WSRKTFFVNDMKIYNHSYIYMPAFSMKTGTPEPSLRVYYTLDVGVAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFVSNMHE-
QPISHHYDNLVLPFS-----GFHAMPEEFLQLWYLHKIGALRMQLERCEDTSL-QPTS--

#Homsap_GT29_ST8Sia1

-----NEKEIV--QGVL-QQ-GTAWRRNQTAARAFRKQMEDCCDPAHLF-----
-----AMTKMNSPMGKSMWYDGEFLYS-FTIDNSTYSLFP-----Q-ATPFQ
L----PLKKCAVVGNGGILKKSQCGRQIDEANFVMRCNLPPLSSEYTKDVGSKSQLVTAN
PSIIRQRFQNL--WSRKTFFVNDMKIYNHSYIYMPAFSMKTGTPEPSLRVYYTLDVGVAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFVSNMHE-
QPISHHYDNLVLPFS-----GFHAMPEEFLQLWYLHKIGALRMQLDPCEDTSL-QPTS--

#Macmul_GT29_ST8Sia1

-----NEKEIV--QGVL-QQ-GTAWRRNQTAARAFRKQMEDCCDPAHLF-----
-----AMTKMNSPMGKSMWYDGEFLYS-FTIDNSTYSLFP-----Q-ATPFQ
L----PLKKCAVVGNGGILKKSQCGRQIDEANFVMRCNLPPLSSEYTKDVGSKSHLVTAN
PSIIRQRFQNL--WSRKTFFVNDMKIYNHSYIYMPAFSMKTGTPEPSLRVYYTLDVGVAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFVSNMHE-
QPISHHYDNLVLPFS-----GFHAMPEEFLQLWYLHKIGALRMQLDPCEDTSL-QPTS--

#Musmus_GT29_ST8Sia1

-----NEKEIV--QGVL-AQ-STAWRTNQTSASLFRQMEDCCDPAHLF-----
-----AMTKMNSPMGKSLWYDGEFLYS-FTIDNSTYSLFP-----Q-ATPFQ
L----PLKKCAVVGNGGILKMSQCGRQIDEANFVMRCNLPPLSSEYTRDVGSKTQLVTAN
PSIIRQRFENLL--WSRKKFFVNDMKIYNHSYIYMPAFSMKTGTPEPSLRVYYTLKDVGAN-
QTVLFANPNFLRNIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVSIYGSWPFVSNMQG-
DPISHHYDNLVLPFT-----GYHAMPEEFLQLWYLHKIGALRMQLDPCEEP-SPQPTS--

#Ratnor_GT29_ST8Sia1

-----NEKEIV--QGVL-AQ-RTAWRRNQTSARLFRKQMEDCCNPAHLF-----
-----AMTKVNSPMGKSLWYDGEFLYS-LTIDTSTYSLFP-----Q-ATPFQ
L----PLKKCAVVGNGGILKMSQCGRQIDEANFVMRCNLPPLSSEYTRDVGSKTQLVTAN
PSIIRQRFENLL--WSRKKFFVNDMKIYNHSYIYMPAFSMKTGTPEPSLRVYYTLKDAGAN-
QTVLFANPNFLRNIGKFWKGRGIHAKRLSTGLFLVSAALGLCEEVSIYGFWPFVSNMQG-
EPISHHYDNLVLPFS-----GFHAMPEEFLQLWYLHKMGALRMQLDPCENPPSPQPTS--

#Calmil_GT29_ST8Sia6

ASASNQWR-SEEDV---LRNIAKIHQCKWGKQKRAVENFRWELRKCCTRSLSGS-----
-----FVTQRNTPVGTTELFYEAEPKKK-IKITPSIFAIFP-----K-DSPFR
GR---SIQRCAVVGNGGILHNSSCGAEIDQADFVFRCNLPPMGGNFTKDVGSKTHLVTAN
PKVIIERYAELH--KRRKPFANTLVIYNDALLLFPAFYHSKNTALSFRAYTLQDFKSK-
QRVIFFNPIYLLKHLAHFWLSKGMQVQNLSTGITVASMAMELCSEVWIYGFWPFVSNMTEG-
ELMSHHYFDSLLAEP-----DLHSTSNEFYQLLRMHSKGIVKLMQMGQCEAEETDEFTLKP

#Hetzeb_GT29_ST8Sia6

ASSPIQWK-TEKDV---IKSVAKLQKCQWHKQEVAAEELRSELKRCCHAAANY-----
-----LVTQKNMPVGTTELIYDAESKNK-INITPQIFSIFP-----K-NSFFS
GR---QYRRCAVIGNGGILANSSCGAEIDQADFVFRCNLPPMGGEFTRDIGTKTNLVTAN
PSIILERYAKLQ--DRRRSFFTNLAVYDEALLLPAFYSKNTDLCFRALYTLQDFQAK-
QKVVFNFVYLLKHLANFWLSKGIQVKRLSTGIMIVSVAVELCEEVWIYGFWPFVSNMVEG-
KVVSHHYFDNLLPKP-----DTHSMPLFHHLLQMHSGMIKLMQMTQCQADPK-----

#Squaca_GT29_ST8Sia6
-----EEEV---IKTVAQLQCCQWHKQELEAEKFRSELKRCCYAAAYDG-----
-----LVTQRNTPVGTETLYDAEPKKK- IKITHPIFTIFP-----K-DSAFS
SR---QYRRCAVIGNGGILANSSCGAEIDQADFVFRCLNPPVGGDFAQDVGKTNLVTAN
PSIIAERYAELH--DRRKPFFTNTLVYNEALLLPAFSYTKNTVLCFRALYTLQDFQAK-
QKVFFNPVYLKHLTEFWLSKGIQVNRSLSTGIMVVSVAIELCEEVWIYGFWPFGRNVEG-
RVMSHHYFDNLLPKP-----DVHSMPSFEHQLLQMHSKGI IKLQTAQCQADPKEMGNI--

#Calmil_GT29_ST8Sia5
TEVKVLSMVKQSEL---FERWRTLQLCKWELNKTEANT--ARLTNCCNAIQNF-----
-----TVTQVNTALGANLTYDAQPKKQ-ITITEDI FNLLP-----Q-EMPYS
RS---QFKKCAVVGNGGILKKECGKEINSADVFVFCNLPPLSNEYARDVGHRTQLVTAN
PSIIKKRFQKLD--KWRPFFVELLQVYENTSVVMPAFYNTRNTDVS LRVRYALDDFSAP-
QDLFYFHPRYLENVARFWGRQGVRAKRPSSGLMLVTAAMELCQEVHLYGFWGFPMDFPSG-
IHITHHYYDNVKKPRP-----GFHSMPEIFFTFLMHMSRGVLQVHTTPCR-----

#Danrer_GT29_ST8Sia5
TDVKVLT MVKTSSEL---FERWRNLQVCKWDQNKKEETDNFKMSLSRCCNAPSFL-----
-----FTTKRNTPSGKTLRYEVDTSGI-LHISPEIFKMF-----D-DMPFS
KS---QFKKCAVIGNGGI IKNSKCGREIDASDFVFRCLNPPVSDLYSQDVGSKTDLVTIN
PSIITERFQKLE--KWRKPFYEV LQNYENSSVVLPAFYNTRNTDVSFRVKYMLDDFESS-
RGVFFFHPQYLLNVQRFWAVQGVRAKRLSSGLMLVTAAMELCQEVHLYGFWAFPMNPSG-
IFITHHYYDNVKKPRP-----GFHAMPEIFNFIMMHARGIVHVHTGPCR-----

#Gasacu_GT29_ST8Sia5
MDVKVLT MVKTSDL---FERWRNLQVCRWEQNKKEETS NFKMSLTRCCNAPSFL-----
-----FTTKRNTPAGTKLRYEVDTSGI-LPITTEVFKMF-----D-DMPYS
KS---QYKKCAVVGNGGI IKSTKCGKEIDSADVFVFRCLNPLDNGYENDVGIKTDLVTAN
PSILVCRFQKLE--KWRPFFYEV LQKYENSSVVLPAFYNTRNTDVSFRVKYMLDDFDSQ-
RGVFFFHPQYLLNVQRFWAVQGVRAKRVSSGLMLVTAALEMCEEVHLYGFWAFPMNPSG-
IYITHHYYDNVKKPRP-----GFHAMPEIFNFIMHTRGIVNVHTGQCT-----

#Orylat_GT29_ST8Sia5
MDVKVLT MVKTSDL---FERWRNLQVCKWEQSKKEETS NFKLSLSRCCNAPSFL-----
-----FTTKRNTPAGSKLRYEVDTSGI-LPITNEVFKMF-----H-DMPYS
KS---QFKKCAVIGNGGI IKNSKCGKEIDSADVFVFRCLNPPIKEKYSTDVGSKTDLVTIN
PSIITERFQKLE--KWRPFFYDVLQNYENSSVVLPAFYNTRNTDVSFRVKYMLDDFDSQ-
RSVFFFHPQYLLNVQRFWAVQGVRAKRLSSGLMLVTAALEICEEVHLYGFWAFPMNPSG-
VYITHHYYDNVKKPRP-----GFHAMPEIFNFIMHTRGI INVHTDQCM-----

#Takrub_GT29_ST8Sia5
MDVKVLT MVKTSDL---FERWRNLQICRWEQNKKEETS NFKMSLSRCCNAPSFL-----
-----FTTKRNTPAGTKLRYEVDTSGI-LPITAEVFKMF-----D-DMPYS
KS---QFKKCAVVGNGGI IKNSKCGKEIDSADVFVFRCLNPPISEKYSADVGTKTDLVSI
PSIITERFQKLE--KWRPFFYEV LQNYENSSAVLPAFYNTRNTDVSFRVKYMLDDFDSQ-
RGVFFFHPQYLLNVQRFWAVQGVRAKRLSSGLMLVTAALEMCEEVHLYGFWAFPMNPSG-
IFITHHYYDNVKKPRP-----GFHAMPEIFNFIMHTRGIVNVHTGQCT-----

#Tetnig_GT29_ST8Sia5
MDVKVLT MVKTSDL---FERWRNLQVCKWEQNKKEETS NFKMSLSRCCNAPSFL-----
-----FTTRRNTPAGTKLRYEVDTSGI-LPITAEIFKMF-----D-DMPYA
KS---QFKKCAVVGNGGI IKNSKCGTEIDSADVFVFRCLNPPISEKYSADVGTKTDLVSI
PSIITERFQKLE--KWRPFFYEV LQNYENSSVVLPAFYNTRNTDVSFRVKYMLDDFDSQ-
RGVFFFHPQYLLNVQRFWAVQGVRAKRLSSGLMLVTAALEMCEEVHLYGFWAFPMNPSG-
IFITHHYYDNVKKPRP-----GFHAMPEIFNFIMHTRGIVNVHTGRCV-----

#Siltro_GT29_ST8Sia5
TNVKVLSMVKESDL---FDRWKS LQVCKWEMNVTEANAFKSALTRCCNAPSFL-----
-----FTTQKNTPLGKTLRYEVDTSGI-FPISSEIFNIFP-----KQDMPYY
RS---QFKKCAVVGNGGILKDSKCGKIDISTDFVFRCLNPPITPKYVEDVGMKTDVVTIN
PSIITERFNKLE--KWRPFFYEV LQGYENASLLLPAFYNTRNTDVSIRVKYVLDDEFESQ-

QAVYYFHPQYLINVSRLFWMQGVHAKRISSGLILVTAALELCEEVHLYGFWGFPMDFSG-
NFITHHYYDNVKKPRP-----GFHAMPSEIFNFIHMHSGILRVHTGTC-----

#Musmus_GT29_ST8Sia5

LEVKVLSMVKQSEL---FERWKS LQICKWAMGASEASLFKSTLSRCCNAPNFL-----
-----FTTQKNTPVETNLRYEVESSGL-YHIDQEIFKMFP-----K-EMPHY
RS---QFKKCAVVGNGGILKNSGCGKEINSADVFVRCNLPPISGIYTTDVGEKTDVVTVN
PSIIIDRFHKLKLE--KWRPFFSVLQRYENASVLLPAFYNVRNTLVSRVKYMLDDFQSR-
QPVYFFHPQYLSVSRYWLSLGVRRARISTGLSLVTAALELCEEVHLFGFWAFPMNPSG-
FFITHHYYDNVKKPKP-----GFHAMPSEIFTFLRMHSGILRVHTGTCNCC-----

#Ratnor_GT29_ST8Sia5

LEVKVLSMVKQSEL---FERWKS LQICKWAMDASEASLFKSTLSRCCNAPNFL-----
-----FTTQKNTPVETNLRYEVESSGL-YHIDQEIFKMFP-----K-EMPHY
RS---QFKKCAVVGNGGILKNSGCGKEINSADVFVRCNLPPISGIYTTDVGEKTDVVTVN
PSIIIDRFHKLKLE--KWRPFFSVLQRYENASVLLPAFYNVRNTLVSRVKYMLDDFQSG-
EPVYFFHPHYLSSVSRYWLSLGVRRARISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
FFITHHYYDNVKKPKP-----GFHAMPSEIFTFLRMHSGILRVHTGTCNCC-----

#Anocar_GT29_ST8Sia5

TDVKVLSMVKQTEL---FERWKNLQ MCKWEMNITQANIFKATLLRCCNAPAF-----
-----FTTQKNTPLGTKLKYEVDTSGI-FHVNQETFRMFP-----Q-EMPYS
RS---QFKKCAVVGNGGILKNSRCGREIDSADVFVRCNLPPISEKYIADVGVKTDIVTVN
PSIITERFHKLKLE--KWRKPFVNLQTYENASVLLPAFYNTRNTDVSIRVRYALDDFESQ-
QSVYFFHPQYLINLSRYWLNQGVRAKRISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
IYITHHYYDNVKKPRP-----GFHAMPSEIFNFLHMHSGILRVHTDACNCC-----

#Galgal_GT29_ST8Sia5

LEVKVLSMVKQTEL---FDRWKS LQ MCKWEMNVTEANILKSTLSRCCNAPAF-----
-----FTTQKNTPLGTKLKYEVDTSGI-FHINQEIFKMFP-----K-DMPYH
RS---QFKKCAVVGNGGILKNSRCGREIDSADVFVRCNLPPISEKYLTDVGVKTDVVTVN
PSIITERFHKLKLE--KWRKPFYDVLQVYENASVLLPAFYNTRNTDVSIRVKYVLDDFESQ-
QAVYYFHPQYLINVSRYWLGQVRAKRISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
IFITHHYYDNVKKPRP-----GFHAMPSEIFNFLHMHSGILRVHTGTCGCC-----

#Bostau_GT29_ST8Sia5

LEVKVLSMVKQSEL---FDRWKS LQ MCKWAMNISEANQFKSTLYRCCNAPPFL-----
-----FTTQKNTPLGTKLKYEVDTSGI-YHINQEIFRMFP-----K-DMPYH
RS---QFKKCAVVGNGGILKNSRCGREINSADVFVRCNLPPISEKYTMDVGVKTDVVTVN
PSIITERFHKLKLE--KWRPFFYRVLQVYENASVLLPAFYNTRNTDVSIRVKYVLDDFESP-
QAVYYFHPQYLVNVSRYWLSLGVRAKRISTGLILATAALELCEEVHLFGFWAFPMNPSG-
LYITHHYYDNVKKPRP-----GFHAMPSEIFNFLHLSRSGILRVHTGTCSCC-----

#Homsap_GT29_ST8Sia5

LEVKVLSMVKQSEL---FDRWKS LQ MCKWAMNISEANQFKSTLSRCCNAPAF-----
-----FTTQKNTPLGTKLKYEVDTSGI-YHINQEIFRMFP-----K-DMPYH
RS---QFKKCAVVGNGGILKNSRCGREINSADVFVRCNLPPISEKYTMDVGVKTDVVTVN
PSIITERFHKLKLE--KWRPFFYRVLQVYENASVLLPAFYNTRNTDVSIRVKYVLDDFESP-
QAVYYFHPQYLVNVSRYWLSLGVRAKRISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
LYITHHYYDNVKKPRP-----GGHAMPSEIFNFLHLSRSGILRVHTGTCSCC-----

#Pantro_GT29_ST8Sia5

LEVKVLSMVKQSEL---FDRWKS LQ MCKWAMNISEANQFKSTLSRCCNAPAF-----
-----FTTQKNTPLGTKLKYEVDTSGI-YHINQEIFRMFP-----K-DMPYH
RS---QFKKCAVVGNGGILKNSRCGREINSADVFVRCNLPPISEKYTMDVGVKTDVVTVN
PSIITERFHKLKLE--KWRPFFYRVLQVYENASVLLPAFYNTRNTDVSIRVKYVLDDFESP-
QAVYYFHPQYLVNVSRYWLSLGVRAKRISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
LYITHHYYDNVKKPRP-----GFHAMPSEIFNFLHLSRSGILRVHTGTCSCC-----

#Macmul_GT29_ST8Sia5

LEVKVLSMVKQSEL---FDRWKS LQ MCKWAMNISEANQFKSTLSRCCNAPAF-----

-----FTTQKNTPLGTKLKYEVDTSGI-YHINQEIFRMFP-----K-DMPYY
RS---QFKKCAVVGNGGILKNSRCGREINSADVFVRCNLPPISEKYTMDVGVKTDVVTVN
PSIIITERFHKLE--KWRPFPYRVLQVYENASVLLPAFYNTRNTDVSIRVKYVLDDEFESP-
QAVYYFHPQYLVNVSRYWLSLGVRAKRISTGLILATAALELCEEVHLFGFWAFPMNPSG-
LYITHHYYDNVKKPRP-----GFHAMPSEIFNFLHLHSRGILRVHTGTCCSC-----

#Ambmex_GT29_ST8Sia7

ATLSAHKKIGEKSI---MRNAELQRCPWQENREKKEFYRSEINQCCNSSHGL-----
-----IVTQENTRVGENIVYETQKSVK-INVTTIEIFNMFP-----K-ESPF
GK---AYKTCAVVGNGAILVDSCCGQQIDQAEFVFRFNLPLN--YTKDSGKKVDLVTAN
PSIMINRFQSLN--HRRKAFVDMLRAYRGALILMPTFSHTFGTQLAFKVQYTLDDFGLG-
SRMLSFHPVYLENLAKYWRKGLYVKRLSSGIMLVSAAMELCDSITLYGFWPFYSNLEG-
RTIGYHYYDKMAPNI-----QVHAMPKEFLIYSQMHAQGALKLQVGQCS-----

#Ambmex_GT29_ST8Sia7-B

ATLSANKTINERSI---MRNAVELQRCPWLENRKKKEFYRSEINQCKTSHEL-----
-----ILTQENTQVGEDIVYETQKSKK-INVTTKIFNMFP-----K-ESPF
GK---AYKTCAVVGNGAILVDSCCGQQIDQAEFVFRFNLPLN--YTRDAGRVDLVTAN
PSIMINRFQSLN--QRRKAFGNTLREYRGALILMAAFSHTRSTQVAFKVQYTLDDFGLG-
SRMLSFHPVYLENLAKYWRKGLYVKRLSSGIMLVSAAMELCDSITLYGFWPFYSNLEG-
RTIGYHYYDKMAPNI-----QVHAMPKEFLIYSQMHAQGALKLQVGQCS-----

#Latcha_GT29_ST8Sia7

TS-----QELPKETDLNKCSNLTQRL-----
-----VLTRENAPIGHEIEYEVAE-QR-VRVEEPLFKLLPRFPPPFYQ-ESPFK
KA---PYKRCAVVGNGAGILLNSGCGRRIDQADFVFRNLPPLN--YSKDVGSKTDLVTAN
PSIIIQKYHGLK--ESRRLFVERMKVYKDALILMAAFSQSFATEISLAVAYALEDFGSK-
QKAIFFFHPAYLRQLGSLWRSWVRRRLSSGLMLVSAALELCDSVALYGFWPFSTGLDG-
EAVLHHYYDNVPEP-----GVHAMSEFVHYLQMHKGVQLHVGKC-----

#Rancat_GT29_ST8Sia7

LNSVLRIFKQQAFF---FKVVKTLOGCPWKEDQTERNLLQANLGKCCNASYSM-----
-----IMTQENTVIGQTITFDAETKIK-QNITKSLYSLFP-----K-KSPFQ
K----PIRTCAVVGNGGILTNSSCGAQIDGADFVFRNLPPLN--WTDDIGAKTDLVTSN
PSILMNKFSSTL--EKRKPFIMMVQEYSSPLILLPAFSYSANTEVSLRVLYTIEDFELN-
SKVFFFNPEYLNLSAYWKSMLKFGRLSSGLMVVSIAMEVCDKVTLYGFWPFKDLNG-
VPILHHYYDNVPPKP-----GIHAMPDEFYKYLMHIQGSRLRLNLEHC-----

#Pelniq_GT29_ST8Sia7

LNSVMKIFRRKTF---FEVVKALQGPCWREDQTERNLLKAKFRKCCNASYSM-----
-----MVTQENTPIGHIHYDGDGK-GR-KNVTESLYSLFP-----E-KSPFQ
K----PIRSCAVVGNGGILNSSFCGAEIDRANFVFRNLPPLN--WTNDVGTKTDDVVTVN
PSILIDKFGSLM--ERRKPFITRMKEYGSTLIILPAFSYLLNTAVSLRALYTIISDFNLN-
SRAVFFNPDYLRNLTAYWKDMGIKSLRLSSGLMLVSAAIEMCDKVTLYGFWPFQDLDG-
VPIPHHYYDNALPTP-----KIHSMPDEFYQFLQMHQGSRLRLNLGQC-----

#Strcamaus_GT29_ST8Sia7

TESFL-KRVDEVWS---LSHLKLMQSCRWNFNASALAQYRAELGHCCNASAWL-----
-----ALTQVNTPLGSNIVYDGYRSKS-LKVSSGLLEILP-----E-ESPFQ
EP---FYKTCAVVGNGGILRNSSCGSEIDEHQFVIRFNLPSMD--FPEDVGRKSSIVTVN
PSILQKRFGHGLN--GRRLPFVKAAYIYGETWFLIIPAFSYPGQNEASYRALYALQDSGSR-
SPIFFFHPQYLSALTRYWHEHGPHPTRLSSGFMLVNAALELCQHITLYGFWPFSLHPDG-
HPLPHHYYDNQLPNP-----RMHLMPOEFACYVMNHFGVQLHVGKC-----

#Aptausman_GT29_ST8Sia7

TESFL-KRVNEVWS---LRHLKLMQSCRWNFNASALAQYRAELGHCCNASAWL-----
-----VLTRVNTPLGKTIYDGDHDSKS-LKVSSGLLEILP-----E-ESPFQ
DP---FYKTCAVVGNGGILLNSSCGSEIDGHQFVIRFNLPSMD--FPEDVGRKSSIVTVN
PSILQERFHGLT--GRRLPFVKAAYIYGETWFLIIPAFSYPGQNEASYRALYALQDSGSR-
SPVFFFHPQYLSALSRYWHERGFHTPRLSSGFMLVNAALELCQHITLYGFWPFSLHPDG-
HPLPHHYYDNQLPKP-----RVHLMPOEFAYVVMNHFGVQLHHLHGKC-----

#Cuccancan_GT29_ST8Sia7

-----QLGHYCNASAWL-----
-----AVTQENTPLGSNIVFDGYRSKS-LKVSSGLLEILP-----E-KSPFQ
DL---LYKTCAVVGNNGGILRNSSCGSQIDGYQFVIRFNLPSAD--FPEDVGRKSSIVTVN
PSILHKRFHGLN--GRRLPFVEAAAASYGKTWFFI PAFSYPGNSEASYRAFYALQDSESQ-
SHVFFFHPQYLSALSKEYWHDGRGFHTYRLSSGFMLVNAALELCEHITLYGFWPFSLHPDG-
HALPHHYYDNVLPNQ-----RIHIMPREFAYYVDMHFQGVLRRLHVGRC-----

#Colliv_GT29_ST8Sia7

TQP-----QKAELGRCCNASAWL-----
-----AVTQDNTPLGSEIVYDAYPSKR-LKVSSGLLEILP-----E-KSPFQ
ES---PYKTCAVVGNNGGILRNSSCGSKIDGHEFVIRFNLPSVD--FPEDVGKSSIVTVN
PSILHKRFHGLN--GRRLPFVAAAASYGKTWFLI PAFSYPNSSEASYRALYALQDSASQ-
SHIFFFFHPQYLSLSSKYWHDHGFHTPRLSSGFMLVNAALELCQHITLYGFWPFSLHPDG-
HSLPHHYYDNVLPNS-----RIHIMPKEFTYYVDMHFHGVQLHLGR-----

#Apavit_GT29_ST8Sia7

TQP-----HKAELGHCCNASAWL-----
-----AVTQENAPLGSEIVYDGYPSKR-LKVSSGLLEILP-----E-KSPFQ
NP---LYKTCAVVGNNGGILRNSSCGAKIDEHQFVIRFNLPSMD--FPEDVGRKSSIVTVN
PSILQKRFHGLN--GRRLPFVAAAAPYGKTWFLI PSFSFPDDTEASYRALYALQDSASE-
SHVFFFHPHYLSALSKEYWHDLGFHTYRLSSGFMLVNAALELCQHITLYGFWPFSLHPDG-
HSLPHHYYDNVLPKQ-----NIHIMPKEFSYYVDMHFHGVQLHLGR-----

#Chrpicbel_GT29_ST8Sia7

SQRVLPVRLHEAWIWR---LKLMOQSCPWAYNARALGRYREQLGHCNASADL-----
-----VLTRDNTPLGSRIVCDGQPAKK-LLVQEALLEILP-----Q-G-----
-A---PYDSCAVVGNNGGILHNSGCGPEIDRAQFVIRFNLPPMG--FAEDVGTKSSVITVN
PSILVLRFGALS--RWRPFAEAMGTYGAPLLLI PAFSFSFAAVSSQALYTLDFGSP-
ARAVFMNPEYLAGLDGHWHRRLRAKRLSSGFMLVNAALELCQHITLYGFWPFPTDPEG-
RPLPYHYYDKQTPKP-----GVHAMPDEFTRYLGMHLQGALRLHLGRQEGLAGGHAQQG

#Malterter_GT29_ST8Sia7

SPI--P-----EALVMGAEQCRGLM--QNWSA---GTL PAREQLGSSCNASANL-----
-----VLTQNTQLGSQIVYDAQRDKK-HPVKEELLEMLP-----Q-GSPFQ
GA---PYECCAVVGNNGGILRNSSCGSEIDRAQFVIRFNLPPMD--FADDVGTKSSVVTMN
PSILHARFRGLS--RWRPFAEAVGIYGAPLLLI PAFS FVQSTV SFQALYTLDFGSP-
ARAVFMNPEYLARLDGHWPRGLRAKRLSSGFMLVSAALELCQHITLYGFWPFPTDPEG-
RLLPHHYYDNQPPKP-----GIHAMPDEFTRYLGMHMQGALRLHLGRQ-----

#Promuc_GT29_ST8Sia7

-----QLMLIQECPWKPNATAVMQHRAELGQCCNASHRL-----
-----VVTKENAPLGSTIHFDGVKVKI-ITVDSKLTNMLL-----E-RFPLA
DA---QYSKCALIGNGGILQDSRCGQEIDQADFI IRFNLPPLN--RTEDVGTKTHLVTIN
PSVLTNRFKNLV--GPPMAFIDAVRAYPNALFLI PALS FHDHIELGYRALHILKDIGLP-
HQAFFLNPHYLGALDMYWKQKGMTEIRLSTGFMFTSFALEFCDHITLYGFWPFDFDLTG-
KPISSHYYDNVLPNA-----FVHSMSEEFSTRYIDMYAQGVLR IQLGKCQ-----

#Deiacu_GT29_ST8Sia7

VI-----ILLPAPLN----GVLLKSSKWTPTSANLFCSRAL--DCCVCGFHLGFSLSCF
SFEDSKTWCVLR CATGERTAGIHPPFDGVKVKI-ITVDSKLTNMLL-----E-RFPLA
DA---QYSKCALIGNGGILQDSRCGQEIDQADFI IRFNLPPLN--RTEDVGTKTHLVTIN
PSILTNRFKSLV--RSPVAFIDAVRAYPNALFLI PALS FHDHIELGYRALHILKDIGLP-
HQAFFLNPHYLGALDTYWKQKGMTEIRLSTGFMFTSFALEFCDHITLYGFWPFDFDLTG-
KPINHHYYDNVLPHP-----FVHSMSEEFSTRYIDMYAQGVLR IQLGKC-----

#Pytmol_GT29_ST8Sia7

VI-----ILLPAPLN----GVLLKSSKWTPTSANLFCSRAL--DCCVCGFHLGFSLSCF
SFEDSKTWCVLR CATGERTAGIHPPFDGVKVKI-ITVDSKLTNMLL-----E-RSPLA
GF---QYNKCALIGNGGILRHSSCGQEIDQADLI IRFNLPPMN--YTEDVGTKTSLVITIN

PSILNNKFQSLQ--GPQKPFLLDALQAYRDALFLIPSLSFSSHVLCRAVSIKDSGLT-
HRAFFLHPHYLGAIKRYWEQKGLKEIRLSTGFLFISIALEFCEHITLYGFWPFYSYDLTG-
EPLSHHYDNLIPNA-----GFHTMSEEFLLHYLNMYAQGVLRILQLGKC-----

#Anocar_GT29_ST8Sia7-A

-----TQLQCCNASFRF-----
-----VTTKENIRLGSYIIFDGNPTRK-LRVDTKLLDLLP-----E-KSPFM
DT---SYRKCAVVGNGGILLNSSCGQEIDRADLVIRFNLPPMN--FSEDIGTKTSLVTIN
PSILQNRFKLLQ--ERRKPFVEALHSYSDATFLLPVLSFVGHNILGYRVLYTLEDFGVE-
QQAFFLNPOYLSNLANFWKKRGLKTNRLSSGFMLVSMALFECQHITLYGFWPFYSYDLNN-
QSIPIHHYYDNMMPTP-----GVHAMPTTEFSYYLSMYAEGVLRRLRVGKCQ-----

#Gekjap_GT29_ST8Sia7

LQ-----KLDEEILA----HLLLTQGCWPQASARAMAQYRTELGRCCNASFWL-----
-----AITKENTPLGSDILLDGNKGGK-LPVGAELMDLLP-----E-RSPIP
GI---LYDQCAVVGNGGILQNSSCGQEIDQADLIIRFNLPPMN--YSEDVGTKTSLVITIN
PSILQTKFNKLE--AHRKPFADALRPYRSALVFIPAFSFGVHSELAYRALYTMEDFGTG-
QRAYFWNPHYLDTLGIYWKARGFYPHRLSSGFMLVNMALFECRITLYGFWPFSDHPAG-
RPIPHHYDNTWPKP-----GVHAMSQEFSHYLMHYAQGVLLQLRLGSCQ-----

#Amblat_GT29_ST8Sia6

LSATL-RKRYSEDFY--IQSFRKVQNTWTRRPEEYKFRSKLASCCNAVNNF-----
-----IVSQNNTSLGSNMSYEVDNKKK-IVISSETIFKMLP-----Q-SQPFV
ER---SYKHCAVVGNGGILQNSSCGAEIDESDFVFRCNLPPVNGDFHKDVGNKTNVVTVN
PSIIALRYGKLS--QKKTVFLQNTIKYGDAYFLLPAFSYRSNTAVCFKVFALKEAKAN-
QKAIFFHPKYLKNLGQFWRANGVRAYRLSTGLMIASAAIELCDHVKLYGFWPFSSKNTEG-
NLISSHYYDNQLPKP-----GFHAMPKEFIQYLLQLHNGKILKLQVGECEENKTKI-----

#Ambmex_GT29_ST8Sia6

LSATL-RKRYSEDFY--IQSFRKVQNTWTRRPEEYKFRSKLASCCNAVNNF-----
-----IVSQNNTSLGSNMSYEVDTKKN-IVISSETIFKMLP-----Q-SQPFV
ER---SYKHCAVVGNGGILQNSSCGAEIDESDFVFRCNLPPVNGDFHKDVGNKTNVVTVN
PSIIALRYGKLS--QKKTVFLQNTIKYGDAYFLLPAFSYRSNTAVCFKVFALKEAKAN-
QKAIFFHPKYLKNLGQFWRANGVRAYRLSTGLMIASAAIELCDHVKLYGFWPFSSKNTEG-
NLISSHYYDNQLPKP-----GFHAMPKEFIQYLLQLHNGKILKLQVGECEENKTKI-----

#Siltro_GT29_ST8Sia6

LTVSL-KKRYSEDYY--IQTVDNLQNTWHRPEERSKFRLDLSSCCNGVKNF-----
-----IVSQNNTSVGINITYEVESKKR-ILITEEIIYRMLP-----K-SQPFV
GT---PFKQCAVVGNGGILANSKCGVEIDQSDVFRCNLPPTSGNVSDVGNKTNLVTVN
PSIISQKYRKLN--KVKNVFLKYVSNYGNLSSLLLPAFSYSSNTAISFEVHRVLEKNQAK-
QKAVFFHPNYLKNLAKFWKGGVRAVRLSTGLMITSAAMELCEEVILYGFWPFSSKDLEG-
KPISSHYYDNMLPKP-----GFHAMPKEFYQVLLQLHNGKILKLQVGECEENKTKI-----

#Xenlae_GT29_ST8Sia6

LTVSL-KKRYSEDYY--IQTVDNLQNTWQKRPQEYSKFRLYLSTCCNGLKNF-----
-----IVSQNNTSLGSNITYEVESKKK-ILIAEEIYRMFP-----K-SQPFV
GA---PFKQCAVVGNGGILANSKCGAEIDQSDVFRCNLPPTWGNI SVDVGNKTNLVTVN
PSIISRKYRKLN--KVKNVFLKNSNYGYSFLLLPAFSYSSNTAISFEVHRILEKNQAK-
QKAIFFHPYYLKNLAQFWKGRGVRAVRLSTGLMITSAAMELCEEVILYGFWPFSSKNQEG-
KPISSHYYDNILPKP-----GFHAMPKEFYQVLLQLHNGKILKLQVGECEENKTKI-----

#Litcat_GT29_ST8Sia6

LSVSL-RKRYSEDYY--IQAVNDVQNTWKKKQPQEYSRFRLYLSSCCNAVNNF-----
-----IVSQNNTSLGSNITYEVESKKK-ILIAEDIYKMLP-----K-SQPFV
GI---PFKQCAVVGNGGILKNSCGAEIDQSDVFRCNLPPIWGNVSDVGNKTDLVTVN
PSIIALKYGKLN--DMKTAFLKNTNYGYSFLLLPAFSYSSNTAISFEVHLLRKYQAK-
QKAIFFHPNYLKSQAQFWKGRGVRAVRLSTGFMITSAAMELCEEVILYGFWPFSSKNLDG-
KPISSHYYDNQLPKP-----GFHAMPKEFYQVLLQLHNGKILKLQVGECEENKTKI-----

#Rhimar_GT29_ST8Sia6

LTVSL-RKRYSEDCY--IQAVNEVQNCWTQKKPQEYSRFRFYLSGCCNAVNNF-----
-----IVSQNNTSLGNSITYEVESKKN-ILIAEDIYKMLP-----K-SQPFE
GI---PFKQCAVVGNGGILTNSSCGAEIDRSDFVFRCLNPPIWGNAAVDVGKNTDLVTVN
PSIIALKYGKLN--EMKTAFLRNLTSYGGSFLLLPAFSNTAISFEVHNLKLYQAK-
QRAIFFHPNYLKSALQFWRGRGVRAYRLSTGFMITSAAIELCEDVKLYGFWPFSKNPNG-
KPISSHYYDNQLPKP-----GFHAMPKEFYQVLQLHYKGVLLKQIGECQKR-----

#Latcha_GT29_ST8Sia6

MSATTPRKRYSDDY--IQTVNELQKCSWVIRPEEHEKFRSELSVCCNAVRNF-----
-----IVSQNNTPLGTNMSYEVENGRT-FLITQRIFKMFP-----Q-SQPFA
GY---PYNQCAVVGNGGILKNSACGTEIDQADFVFRCLNPPTLGNISIDVGSKTSLVTLN
PSIITHRFGKLN--EKRKPFVETVSHYGEAFLLLPAFSFRSNTALSFKVYHTLEAFRGK-
QKTIFFFHPKYLKSLALFWRSKGIKVYRLSSGFMIANAIIELCKEVRLYGFWPFSKNNEG-
KNISHHYYDNQLPKP-----GIHSMPEFYHFLKLHNKGI IKLQFGRCDIT-----

#Latmen_GT29_ST8Sia6

MSATTPRKRYSDDY--IQTVNELQKCSWVIRPEEHEKFRSELSVCCNAVRNF-----
-----IVSQNNTPLGTNMSYEVENGRT-FLITQRIFKMFP-----Q-SQPFA
GY---PYNQCAVVGNGGILKNSACGTEIDQADFVFRCLNPPTLGNISIDVGSKTSLVTLN
PSIITHRFGKLN--EKRKPFVETVSHYGEAFLLLPAFSFRSNTALSFKVYHTLEAFRGK-
QKTIFFFHPKYLKSLALFWRSKGIKVYRLSSGFMIANAARRLCKEVRLYGFWPFSKNNEG-
KNISHHYYDNQLPKP-----GIHSMPEFYHFLKLHNKGI IKLQFGRCDIT-----

#Canlupfam_GT29_ST8Sia6

QRLYSKAKNYLES DY--LQIIRNIQNC PWKRQEEYENFRAKLASCCDAAQNF-----
-----IVSQNNTPAGTNMSYEVESKNE-ILIRENIFNMFP-----V-SQPFV
EY---PYNQCAVVGNGGILNKSLCGAEIDKSDFVFRCLNPPITGNISKDVGSKTNVTVN
PSIIRLKYGNLK--KKKEIFLEDIATYGD AFLLLPAFSFRANTIASFKVYSTLKE SNAR-
QKVIFFHPKYLRLALFWRTGVT EFR LSSGLMITSVAVELCEHVKLYGFWPFSRTVKD-
TPVSHHYYDNMLPKR-----GFHEMPKEYRQILQLHLKGI LKLFQSKCEIA-----

#Musmus_GT29_ST8Sia6

NSLSNKTRRYSEDDY--LQITITNIQRCPWNRQAEYDNFRAKLASCCDAIQDF-----
-----VVSQNNTPVGTNMSYEVESKKN-IPIRENIFHMFP-----V-SQPFV
DY---PYNQCAVVGNGGILNKSLCGAEIDKSDFVFRCLNPPITGSASKDVGSKTNLVTVN
PSIITLKYQNLK--EKKAQFLEDISTYGD AFLLLPAFSYRANTGISFKVYQTLKESKMR-
QKVLFFHPRYLRHLALFWRTKGVTAYRLSTGLMIASVAVELCENVKLYGFWPFSKTIED-
TPLSHHYYDNMLPKH-----GFHQMPKEYSQMLQLHMRGILKLFQSKCETA-----

#Ratnor_GT29_ST8Sia6

DSLANKTRRYSEDDY--LQIVTNIQRCPWNRQAEYENFRAKLASCCDAIQDF-----
-----VVSQNNTPVGSNMTYEVESKQ-IPIRENIFHMFP-----V-SQPFV
DY---PYNQCAVVGNGGILNKSLCGAEIDKSDFVFRCLNPPITGSASQDVGSKTNLVTVN
PSIITLKYKNLK--EKKARFLEDISAYGD AFLLLPAFSYRVNTGISFKVYQTLKESKVR-
QKVLFFHPRYLRHLALFWRTKGVTAYRLSTGLMIASIAVELCENVTLYGFWPF SKTVEE-
IPLSHHYYDNKLPKH-----GFHQMPKEYSQMLQLHMKGILKLFQSKCEAA-----

#Macmul_GT29_ST8Sia6

ESFSNNTKGYSENDY--LQIITDIQSCPWKRQAEYANFRAKLASCCDAVQNF-----
-----VVSQNNTPVGTNMSYEVESKKN-IPIKKNIFHMFP-----V-SQPFV
EY---PYNQCAVVGNGGILNKSLCGAEIDKSDFVFRCLNPPITGDVSKDVGSKTNLVTVN
PSIITLKYGNLK--EKRALFLEDIATYGD AFFLLPAFSFRANTGTSFKVYYTLEESKAR-
QKVLFFHPKYLKHLALFWRTKGVTAYRLSTGLMITSVAVELCENVKLYGFWPFSKTVED-
IPVSHHYYDNKLPKH-----GFHQMPKEYSQILQLHMKGILKLFQSKCEVA-----

#Ponpyg_GT29_ST8Sia6

ESFSNNTKGYSENDY--LQIITDIQSCPWKRQAEYANFRAKLASCCDAVQNF-----
-----VVSQNNTPVGTNMSYEVESKKE-IPIKKNIFHMFP-----V-SQPFV
EY---PYNQCAVVGNGGILNKSLCGTEIDKSDFVFRCLNPPITGDVSKDVGSKTNLVTVN
PSIITLKYGNLK--EKKALFLEDIATYGD AFFLLPAFSFRANTGTSFKVYYTLEESKAR-
QKVLFFHPKYLKDLALFWRTKGVTAYRLSTGLMITSVAVELCKNVKLYGFWPFSKTVED-

TPVSHHHYDNKLPKR-----GFHQMPKEYSQILQLHMKGILKLOFSKCEVA-----

#Homsap_GT29_ST8Sia6

ESFSNKTKRYSENDY--LQIITDIQSCPWKRQAEYANFRAKLASCCDAVQNF-----
-----VVSQNNTPVGTNMSYEVEESKKE-IPIKKNIFHMF-----V-SQPFV
DY---PYNQCAVVGNGGILNKSCLGTEIDKSDVFVRCNLPPTTGVDVSKDVGSKTNLVTIN
PSIITLKYGNLK--EKKALFLEDIATYGDFAFFLLPAFSFRANTGTSFKVYYTLEESKAR-
QKVLFFHPKYLKDLALFWRTKGVTAAYRLSTGLIMITSVAVELCKNVKLYGFWPFPSKTVED-
IPVSHHHYDNKLPKH-----GFHQMPKEYSQILQLHMKGILKLOFSKCEVA-----

#Pantro_GT29_ST8Sia6

ESFSNKTKGYSENDY--LQIITDIQSCPWKRQAEYANFRAKLASCCDAVQNF-----
-----VVSQNNTPVGTNMSYEVEESKKE-IPIKKNIFHMF-----V-SQPFV
DY---PYNQCAVVGNGGILNKSCLGTEIDKSDVFVRCNLPPTTGVDVSKDVGSKTNLVTIN
PSIITLKYGNLK--EKKALFLEDIATYGEAFAFFLLPAFSFRANTGTSFKVYYTLEESKAR-
QKVLFFHPKYLKDLALFWRTKGVTAAYRLSTGLIMITSVAVELCKNVKLYGFWPFPSKTVED-
IPVSHHHYDNKLPKH-----GFHQMPKEYSQILQLHMKGILKLOFSKCEVA-----

#Bostau_GT29_ST8Sia6

ETLSNRTKGYSEDEY--LQIITNIQSCPWKRQVEEYENFRAKLASCCDAVQNF-----
-----IVSQNNTPIGTNMTYEVEESKSK-IQIKENIFDMLE-----V-VQPFV
GY---SFNQCAVVGNGGILNQSLCGAEIDKADFVRCNLPPTTGNTNDVGTNLTNLVTIN
PSIIKLRYGNLK--EKKAI FLEDVAAYGDFAVLLPAFSFRANTAASFVYYTLKESKAR-
QKVLFFHPKYLKDLALFWRTKGVTEYRLSSGLIMITSVAVELCENVKLYGFWPFPSRTGEN-
MPVSHHHYDNKLPKR-----GFHEMPKEYSQILQLHVKGILKLOFSKCETA-----

#Susscr_GT29_ST8Sia6

KALSNTKRYSEDDY--LQIITNIQSCPWKRQAEAYENFRAKLASCCDAVQNF-----
-----IVSQNNTPVGTNMSYEVEESKSE-IQIRESIFDMLE-----V-FQPFV
GY---PYNQCAVVGNGGILNQSLCGAEIDKSDVFVRCNLPPTTGNISNDVGSKTNLVTIN
PSIIRLRYGNLK--EKKAVFLEDIATYGDFAVLLPAFSFRANTAASFVYYALKESNSR-
QKVLFFHPKYLKHLAVFWRTKGVTEYRLSSGLMIASVAVELCENVKLYGFWPFPSKTGEN-
TPVSHHHYDNKLPKR-----GFHEMPKEYRQILQLHVKGILKLOFSKCDTS-----

#Gekjap_GT29_ST8Sia6

WAASVKKRYAEDY--LQVVGRLQONCTWKNRPQYAKFKSELASCCDAAHNF-----
-----ITSQNNTPLGSNMSYEVDNKKT-IHITEEIFRMLP-----E-SQPL-
EQ---PFKNCAVVGNGGILKNSNCGAEIDQSDVFVRCNLPPTMGSIQDVGSKTNLVTIN
PSIISQKYNKLN--EKKATFLENIASYGDFTLLLPFAFSFRSNTAASFVHHTLKEFSKAK-
QKAIFFYPYRLNLAQFWRTKGVKAYRLSSGFMITSAALEL CENVKLYGFWPFPSKNVAG-
TPISHHHYDNQLPKP-----GFHAMPKEYNQILQLHGRGILKLOFGKCLPD-----

#Anocar_GT29_ST8Sia6

WSSSIKTKRYSEDDY--LQIVGKLQONCTWKKRPQYAKFRSELTSCCDAIHNF-----
-----ISSQNNTPLGSNMSYEVDNKKT-IHITEEIFKMLP-----E-SQPL-
DY---PFKQCAVVGNGGILKNSNCGAEIDKSDVFVRCNLPPTGSGSVQDVGNKTNLVTIN
PSIIAQKYNKLN--EKKATFLENIASYGDFAFLLLPAFSFRSNTATSFKVHHTLREFSAK-
QKAIFFYPYRLKLAQFWRTKGVKAYRLSSGFMITSAAVELCENVKLYGFWPFPSKSIAG-
NPISHHHYDNQLPKP-----GFHAMPKEYNQILQLHGRGILKLOFGKCHTE-----

#Tingut_GT29_ST8Sia6

LSSLTKKKRYSEDDF--LHLVTKLQONCTWVKRPEECTKFRSELASCCDAVHNF-----
-----VASQNNTPLGSNMSYEVEESKKT-ILITENIFRMLP-----V-SSPFS
AY---PFKNCAVVGNGGILKNSSCGAEIDRADVFVRCNLPPTTGSMKDVGNKTNLVTIN
PSIIAQKYNKLN--KKKTEFLQNI AVYGDFAFLLLPAFSYRSNTATSFKVYQTLKEFKAM-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAAIELCENVKIYGFWPFPSKSTEK-
MPISHHHYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLOFGKCESE-----

#Chemyd_GT29_ST8Sia6

WSSSIKTKRYSEDDY--LQIVTKIQONCTWKKRPEEYTKFRLELASCCDAVHNF-----
-----IASQNNTALGSNMSYEVDNKKT-LLITEDI FRMLP-----E-SPPLL

DY---PFKHCAVVGNGGILKNSSCGAEIDKSDFVFRCLNPPTTGSVSKDVGNGKTNLVTVN
PSIIAQKYNKLN--EKKVTFLENIASYGNAFLLLPAFSFKSNTAASFVKVYHTLQEFRAK-
QRAIFFHPRYLKSLAQFWRTKGVKAYRLSSGFMIASAAIELCENVKLYGFWPFPSKTTEE-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGIVKLQFGKCDSDXKGTSDSSK

#Chrpicbel_GT29_ST8Sia6

WSSSIKKKRYSEDYY--LQIVTKIQNCTWKRPEEYTKFRLELASCCDAVHNF-----
-----IASQNNTLLGSNMSYEVDNKKT-ILITEDI FRMLP-----E-SPPFL
GY---PFKHCAVVGNGGVLKNSSCGAEIDNSDFVFRCLNPPTTGSVSKDVGNGKTNLVTVN
PSIIAQKYNKLN--EKKVTFLENIASYGNAFLLLPAFSFKSNTAASFVKVYHTLQEFRAK-
QRAIFFHPRYLKSLAQFWRTKGVKAYRLSSGFMIASAAIELCENVKLYGFWPFPSKTTEE-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCDSD-----

#Galgal_GT29_ST8Sia6

LSSSFKKKRYPEDYY--LHIVKKLQNCTWVRRPEESAKFRSELASCCNAVHNF-----
-----IASQNNTPLGSNMSYEVDNKKT-ILITEDI FRMLP-----V-SSPLS
VY---PFKNCAVVGNGGILKNSSCGAEIDRSDFVFRCLNPPTMGSIKDVGNKTKLVTVN
PSIIAQKYNKLN--EKKTEFVENVAVYGD AFLLLPAFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAAVELCENVKLYGFWPFPSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGIKKLQFGKCESD-----

#Chavoc_GT29_ST8Sia6

LSSSIKKKRYSEDYY--LHIVTKLQNCTWTRRPEESTKFRSELASCCDAVHNF-----
-----IASQNNTPLGSNMSYEVDNKKT-ILITEDI FKMLP-----V-SSPLS
AY---PFKTCVAVVGNGGILKNSSCGAEIDRSDFVFRCLNPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENI AVYGD AFLLLPAFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFPSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD-----

#Egrgar_GT29_ST8Sia6

LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRRPEESMKFRSELASCCDAVHNF-----
-----IASQNNTPLGSNMSYEVDNKKT-ILITEDI FKMLP-----V-SSPLS
VY---PFKTCVAVVGNGGILKNSSCGAEIDRSDFVFRCLNPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLEDVAVYGD AFLLLPAFSFRSNTATSFKVYHTLKEFRAS-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFPSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD-----

#Calpug_GT29_ST8Sia6

LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRRPEESTKFRSELASCCDAVHNF-----
-----IASQNNTPLGSNMSYEVDNKKT-VLITEDI FKMLP-----V-SSPLS
VY---PFKTCVAVVGNGGILKNSSCGAEIDRSDFVFRCLNPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLDNIAVYGD AFLLLPAFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFPSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHSGKILKVQFGKCESD-----

#Psehum_GT29_ST8Sia6

LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRKPEESTKFRSELASCCDAVHNF-----
-----IASQNNSPLGSNMSYEVDNKKT-ILITEDI FKMLP-----V-SSPLS
VY---PFKNCAVVGNGGILKNSSCGAEIDSSDFVFRCLNPPTTGNISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENI AAYGD AFLLLPAFSFRSNTATSFKVYHTLKEFKAT-
QRAIFFHPSYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFPSKSI EK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGVLKLQFGKCESD-----

#Parmaj_GT29_ST8Sia6

LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRKPEESTKFRSELASCCDAVHNF-----
-----IASQNNSPLGSNMSYEVDNKKT-ILITEDI FKMLP-----V-SSPLS
VY---PFKNCAVVGNGGILKNSSCGAEIDSSDFVFRCLNPPTTGNISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENI AAYGD AFLLLPAFSFRSNTATSFKVYHTLKEFKAT-
QRAIFFHPAYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFPSKSI EK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD-----

#Lepcor_GT29_ST8Sia6-B

LSSSIKKKRYSEDYY--LHIVTKLQONCTWIRRPEESTKFRSELASCCDAVHNF-----
-----IASQNNNSPLGSNMSYEVDSKKT-ILITEDI FKMLP-----V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDSSDFVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENI AVYGD AFLLLP AFSFRSNTATSFKVYHTLKEFKAT-
QRAIFFHPAYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD-----

#Lepcor_GT29_ST8Sia6-A

LSSSIKKKRYSEDYY--LHIVTKLQONCTWIRRPEESTKFRSELASCCDAVHNF-----
-----IASQNNNSPLGSNMSYEVDSKKT-ILITEDI FKMLP-----V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDSSDFVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENI AVYGD AFLLLP AFSFRSNTATSFKVYHTLKEFKAT-
QRAIFFHPAYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD-----

#Aquchrcan_GT29_ST8Sia6

LSSSIKKKRYSEDYY--LHIVTKLQONCTWIRRPEESTKFRSELASCCDAVHNF-----
-----IASQNNNSPLGSNMSYEVDSKKT-ILITEDI FKMLP-----V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDHSDVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENI AVYGD AFLLLP AFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD-----

#Halleuala_GT29_ST8Sia6

LSSSIKKKRYSEDYY--LHIVTKLQONCTWIRRPEESTKFRSELASCCDAVHNF-----
-----IASQNNNSPLGSNMSYEVDSKKT-ILITEDI FKMLP-----V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDHSDVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENI AVYGD AFLLLP AFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD-----