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

Lan Yi Chang[1], Roxana Elin Teppa[2], Maxence Noel[1], Pierre-André Gilormini[1], Mathieu Decloquement[1], Christine Thisse[2], Bernard Thisse[2], Anne Marie Mir[1], Virginie Cogez[1], Philippe Delannoy[1], Kay Hooi Khoo[4], Daniel Petit[5], Yann Guérardel[1], Anne Harduin-Lepers[1‡]

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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.

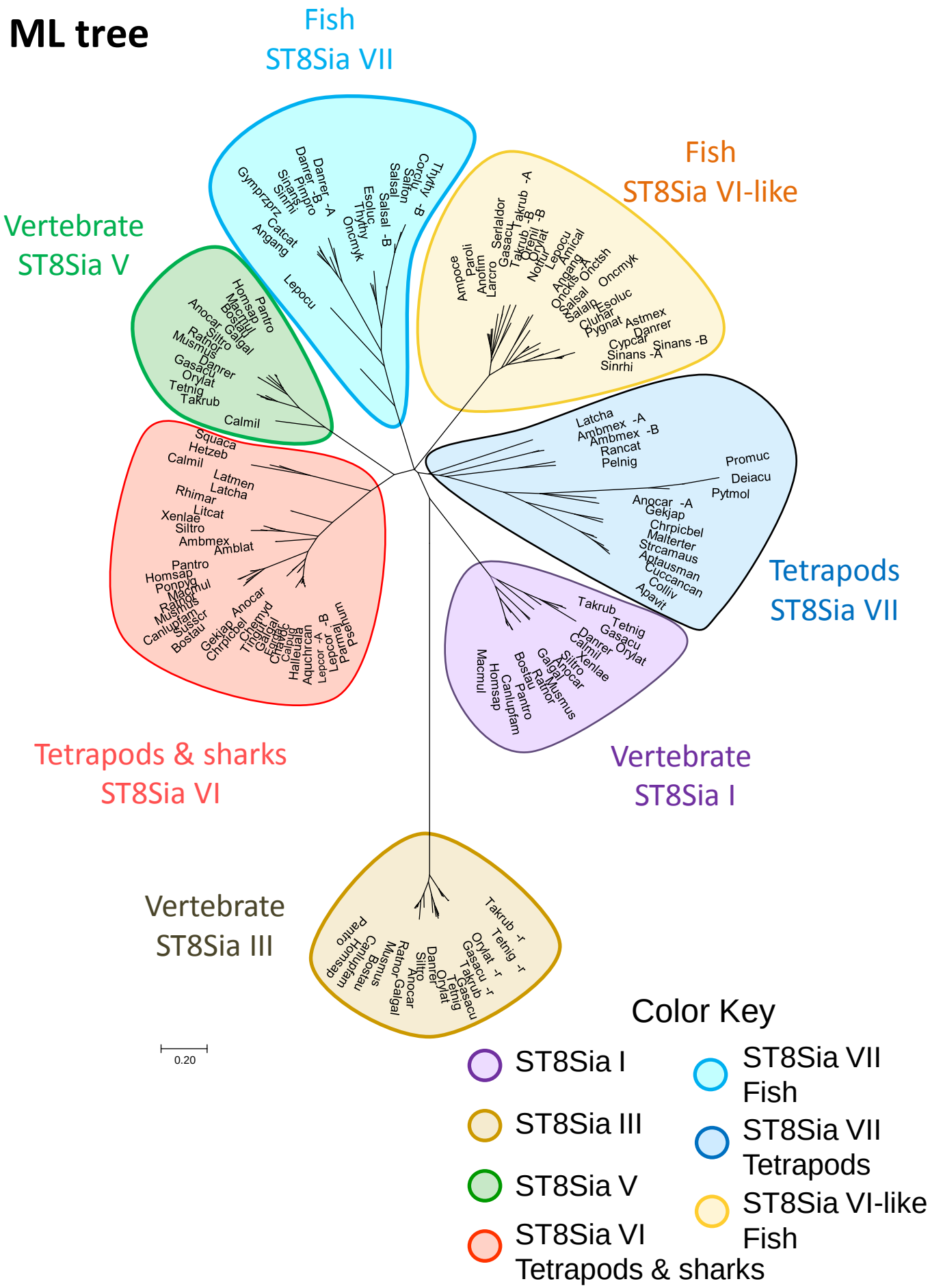
The evolutionary history of vertebrate oligo- and mono-α2,8-sialyltransferases was inferred using the Maximum Likelihood method based on the JTT matrix-based model [1]. The tree with the highest log likelihood (-26151.14) is shown. Initial tree(s) for the heuristic search were obtained automatically 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-α2,8-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-α2,8-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.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Fish
ST8Sia VI-like
Vertebrate
ST8Sia V
Tetrapods
ST8Sia VII
Tetrapods & sharks
ST8Sia VI
Vertebrate
ST8Sia I
Vertebrate
ST8Sia III
0.20
Color Key
ST8Sia I
ST8Sia III
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Tetrapods & sharks
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Tetrapods
ST8Sia VI-like
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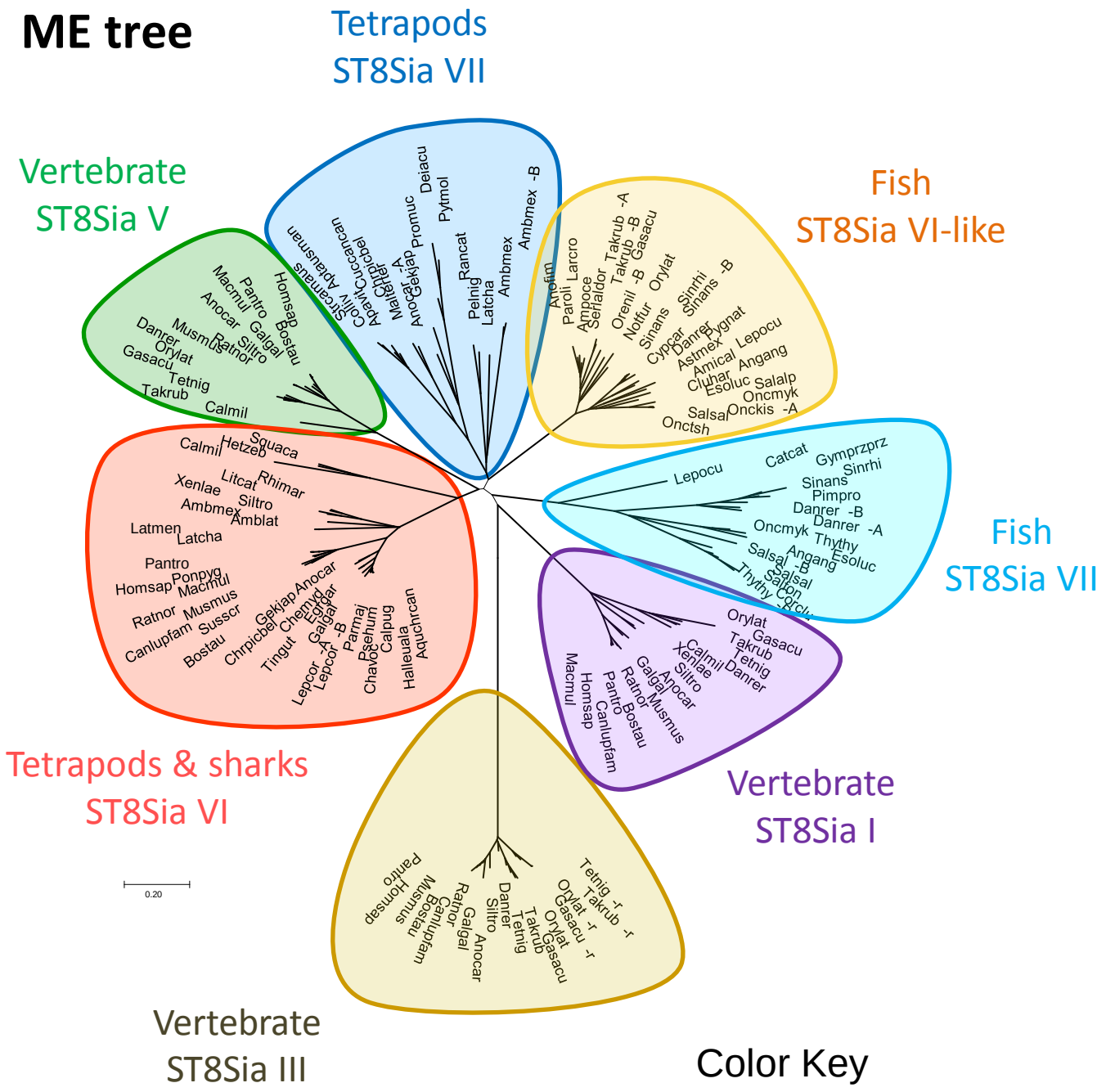
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ST8Sia VII
Vertebrate
ST8Sia V
Fish
ST8Sia VI-like
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Tetrapods & sharks
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Vertebrate
ST8Sia I
Vertebrate
ST8Sia III
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Color Key
ST8Sia I
ST8Sia III
ST8Sia V
ST8Sia VI
Tetrapods & sharks
ST8Sia VII
Fish
ST8Sia VII
Tetrapods
ST8Sia VI-like
Fish

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List of supplementary data

Supplementary data1 : Full length sequences of 147 vertebrate mono- and oligo-α2,8-sialyltransferases.

Supplementary data2: Multiple sequence alignments of 147 vertebrate mono- and oligo-α2,8-sialyltransferases.

1 – Supplementary data1: Full length sequences of 147 vertebrate mono- and oligo-α2,8-sialyltransferases. Protein sequence of 147 selected vertebrate ST8Sia sequences: 129 mono-α2,8-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-α2,8-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; Chrpicbel: Chrysemys picta bellii; Aquchrcan: 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 : Callorhinchus 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 rhinocerous ; 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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>Lepocu_GT29_ST8Sia7

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>Strcamaus_GT29_ST8Sia7

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>Apavit_GT29_ST8Sia7

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>Pelnig_GT29_ST8Sia7

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>Cuccancan_GT29_ST8Sia7

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VDMHFQGVLRLHVGRC

Supplementary data2: Multiple sequence alignment of the 147 selected vertebrate ST8Sia sequences: 129 mono- α2,8-sialyltransferases *i.e.* 17 ST8Sia I, 15 ST8Sia V, 63 ST8Sia VI and 34 ST8Sia VII and 18 oligo-α2,8-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---HYSLCSVVGNSGILTGSHCGANIDQADFVFRCNFAPTE-VYSKDVGRKTNMTTFN
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NK---RYNICAVVGNSGILTGSRCGPQIDKSDFVFRCNFAPTE-AFQRDVGRKTNLTTFN
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NK---HFNICAVVGNSGILTGSRCGQEIDKSDFVFRCNFAPTE-AFQRDVGRKTNLTTFN
PSILEKYYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFHTSATVTRTLVDFFVEHRGQL
KVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTLASAICEEIHLYGFWPFGFDPNTR
EDLPYHYYDKKGTKFTTKWQESHQLPAEFQLLYRMHGEGLTKLTLSHCA----------

#Ratnor_GT29_ST8Sia3
VP----------ITNFLTHELQEKPSKWTFNRTAFLHQRQEILQHVDVIKNF-------
----------SLTKNSVRIGQLIHYDYSSHKYVFSISNNFRSLLP-------D-VSPIL
NK---RYNICAVVGNSGILTGSQCGQEIDKSDFVFRCNFAPTE-AFHKDVGKKTNLTTFN
PSILEKYYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFHTSATVTRTLVDFFVEHRGQL
KVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGFLMYTLASAICEEIHLYGFWPFGFDPNTR
EDLPYHYYDKKGTKFTTKWQESHQLPAEFQLLYRMHGEGLTKLTLSHCA----------

#Musmus_GT29_ST8Sia3
VP----------ITNSLTHELQEKPSKWTFNRTAFLHQRQEILQHVDVIKNF-------
----------SLTKSSVRIGQLMHYDYSSHKYVFSISNNFRSLLP-------D-VSPIM
NK---RYNVCAVVGNSGILTGSQCGQEIDKSDFVSRCNFAPTE-AFHKDVGRKTNLTTFN
PSILEKYYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFHTSATVTRTLVDFFVEHRGQL
KVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTLASAICEEIHLYGFWPFGFDPNTR
EDLPYHYYDKKGTKFTTKWQESHQLPAEFQLLYRMHGEGLTKLTLSHCA----------

#Homsap_GT29_ST8Sia3
VP----------ITNSLTQELQEKPSKWKFNRTAFLHQRQEILQHVDVIKNF-------
----------SLTKNSVRIGQLMHYDYSSHKYVFSISNNFRSLLP-------D-VSPIM
NK---HYNICAVVGNSGILTFIQCGREIDKSDFVFRCNFAPSE-AFQRDVGRKTNLTTFN
PSILEKYYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFHTSATVTRTLVDFFVEHRGQL
KVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTLASAICEEIHLYGFWPFGFDPNTR
EDLPYHYYDKKGTKFTTKWQESHQLPAEFQLLYRMHGEGLTKLTLSHCA----------

#Pantro_GT29_ST8Sia3
VP----------ITNSLTQELQEKPSKWTFNRTAFLHQRQEILQHVDVIKNF-------
----------SLTKNSVRIGQLMHYDYSSHKYVFSISNNFRSLLP-------D-VSPIM
NK---HYNICAVVGNSGILTGSQCGQEIDKSDFVFRCNFAPTE-AFQRDVGRKTNLTTFN
PSILEKYYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFHTSATVTRTLVDFFVEHRGQL
KVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTLASAICEEIHLYGFWPFGFDPNTR
EDLPYHYYDKKGTKFTTKWQESHQLPAEFQLLYRMHGEGLTKLTLSHCA----------

#Danrer_GT29_ST8Sia3
TS----------LNTALNENLQE-SSNWRFNRSAYAELNKEIAQHIDVPHNF-------
----------TLTKNSVRVGQLMHYDYSSHKYVFSIGENLRSLLP-------D-ASPVL
```

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NK---RYNTCAVVGNSGILTGSRCGPEIDKYDFVFRCNFAPTE-VFRRDVGRRTNLTTFN
PSILEKYYNNLLTIQDRNNFFLSLKKLDGAILWIPAFFFHTSATVTRTLVDFFVEHKGQL
KVQLAWPGNIMQYVNKYWKTKQLSPKRLSTGILMFTLASSLCEQVHLYGFWPFGWDPNTG
KELPYHYYDKKGTKFTTKWQESHQLPTEFKLLFKMHADGVLKLSLSHCA-----------

#Orylat_GT29_ST8Sia3-A
TS-----------LSSAINEDLKN-SSKWTYNSTAFIQLRTEISHHIDMPHNF-------
-----------TLTRDAVKVGQLMHFDYSSHKYVYSIGENFRSLLP-------E-VSPIL
NR---HYNVCAVVGNSGILTGSLCGAQIEKYDFVFRCNFAPTE-IFKKDVGRRTNMTTFN
PSILEKYYNNLLTVQDRNNFFLSLKKLDGAILWIPAFFFHTSATVTRTLVDFFVEHRGQL
KVQLAWPGNIMQYINNYWKTKQLSPKRLSTGILMYTLASSMCDQIHLYGFWPFGWDPNTG
KELPYHYYDRKGTKFTTKWQESHQLPAEFKLLHKMHTEGLLKLTLSHCA-----------

#Tetnig_GT29_ST8Sia3-A
IP-----------LTSALSEDLQN-SSKWSHNGSAFTQLKKEISQYIDIPRNF-------
-----------TLTRDSVRIGQLMHYDYSSHKYVFSIGENFRSLLP-------E-VSPIR
QK---HYNVCAVVGNSGILTGSRCGQEIDSLDFVFRCNFAPTE-LFKKDVGRRTNMTTFN
PSILEKYYNNLLTVQDRNNFFLSLKRLDPAILWIPAFFFHTSATVTRTLVDFFVEPRGQL
KVQLAWPGNIMQYINNYWKTKQLSPKRLSTGILMYTLASSMCERIHLYGFWPFGWDPNTG
RELPYHYYDKKGTKFTTKWQESHQLPTEFKLLYKMHREGVLKLSLSHCG-----------

#Takrub_GT29_ST8Sia3-A
TP-----------LTSSLSEDLQN-ASKWSFNSSAFAQLKNEISQYIDVPRNF-------
-----------TLTRDSVRIGQLMHYDYSSHKYVFSIGENFRSLLP-------E-TSPIL
QK---HYNVCAVVGNSGILTGSRCGQQIDRFDFVFRCNFAPTE-IFKKDVGRRTNMTTFN
PSILEKYYNNLLTVQDRNNFFLSLKKLDTTILWIPAFFFHTSATVTRTLVDFFVEHRGQL
KVRLAWPGNIMQYINNYWKTKQLSPKRLSTGILMYTLASSMCDQIHLYGFWPFGWDPNTG
KELPYHYYDKKGTKFTTKWQESHQLPTEFKLLYKMHREGLLKLSLSHCA-----------

#Gasacu_GT29_ST8Sia3-rA
SP-----------LTNALGEDLQN-SSKWTYNSSAFLQLKNEISQYIDIPHNF-------
-----------TLTRDSVRIGQLMHYDYSGHKYVFSIGENFRSLLP-------E-VSPIL
NK---HYNVCAVVGNSGILTGSRCGPQIEKFDFVFRCNFAPTE-IFKKDVGRRTNMTTFN
PSILEKYYNNLLTVQDRNNFFLSLKKLDGVILWIPAFFFHTSATVTRTLVDFFVEHRGQL
KVRLAWPGNIMQYVNSYWKTKQLSPKRLSTGILMYTLASTMCDQIHLYGFWPFGWDPNTG
KELPYHYYDKKGTKFTTKWQESHQLPAEFKLLYKMHTQGLLKLSLSHCA-----------

#Danrer_GT29_ST8Sia7-B
-----------------------------------HGCRMRLQYCCNATHSL-------
-----------ILTKRNTAVDHIITYETEGKRT-YRVKADLHKMLP-------E-DSPWS
AG---ALGLCAVVGSSGILKNSSCGRQIDSADFVIRFNLALVN--DS-DVGLKTDLMNIN
PSQI-RRYKTME--QDPGPLVERISVYGNSSLIIPAFAYGFCTSPSLRVLRVLQPIRPQ-
QPVVFFNPHYLRALDRFWKWRGLKEPRLSSGFILISAALEMCEHVHVYGFWPFGTDLQE-
NPVPYHYYDQSKPSP-----YMHRMPEEFVRLLQLHSQGALTLHLQPCHTHRAVFPNPVP

#Danrer_GT29_ST8Sia7-A
SVIKPAKSIKFKSF---AREVSDFLSCPYKSNETEQELNRIRLRFCCNATESF-------
-----------VLTKRNTAISQSIPYETNSRRT-YKMNADVHKLLP-------E-DSPWS
AG---ALGLCAVVGSSGILKNSSCGRQIDSADYVIRFNLALIN--DS-DVGLKTNLITIN
PSQI-RGYRNLE--KKPGPLVKRVSVYGNSSLIIPAFAYVICTSPSLRVLRVLQPIRPQ-
QPVLFFSPHYLRALDRFWKGRGLKERRLSTGFMLISAALEMCEHVHVYGFWPFGTDLQE-
NPIPYHYYDQMRS-G-----SVHRMPEEFLRLLQLHSQGALTLHLQPCDTH---------

#Pimpro_GT29_ST8Sia7
SIIKSAKSINFKRF---TQELSDYLSCPYKSNQTERELNRIRLQFCCNATGSF-------
-----------ILTKRNTAITQSIQYETST-KT-YKMKAELHKMLP-------E-DIPWS
GR---RLGRCAVVGSGGILKNSSCGREIDNADFVIRFNLAEVN--DS-DVGLKTDLITIN
PSQI--RYKNLQ--NNPDPLVERVSVYGNASLIIPAFAYTFCTSVSIKVLKVLQPIRPH-
QPVVFFSPSYLRSLDRFWKGRGLQEERLSTGFMLISTALELCEHVHVYGFWPFDNDLQD-
QPIPYHYYDLSRPSS-----HRHKMPEEFVRLLQLHSQGALTLHLLPCDSPETDRENNL-
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#Catcat_GT29_ST8Sia7
AIIKPAKSIQLQRF---TQELSDFMSCPYKSNTTERELNRMRLQYFCNATGSL-------
-----------FLTKRNTAINQTIPYETSTVKT-YKMNAAIHGMLP-------E-DFPWS
GR---RMGRCAVVGSGGILKNSSCGREIDSADYVIRFNLASIN--DS-DVGLKTDLITIN
PSQI--QFKNLD--KNPEPLVERVSVYGNASLIMPAFAYTFCTGQSIKTLRVLHPIRPQ-
QPVVFFSPTYLRTLDRFWKGRGLKEVRLSTGFMLISTALELCEDVHVYGFWPFGTDLHN-
NSVPYHYYDQLSPHR-----YMHAMPEEFVRLLQLHSKGALTLHLQPCS-----------

#Gymprzprz_GT29_ST8Sia7
SIIKPAQSIKLESF---TQELSDFMNCPHKPNTTERELNRMRMQFCCNATGSL-------
-----------FLTKRNTAINQTIPYETSTIRT-YNMNPVIHSMLP-------E-DFPWT
GR---RLGRCAVVGSGGILKNSSCGREIDSADFVIRFNLAYIN--DS-DVGLKTDLVTIN
PSQI--RYKNLE--QNPDPLVERVSVYGNASLAMAAFAYTFCTGLSIKTLKVLHPIRPQ-
QPVVFFSPIYLRTLDRFWKGRGLKSIRLSSGFMLINTALELCEHVHVYGFWPFGTDLQN-
NSVPYHYYDELSPHR-----YKHKMP----------------------------------

#Sinrhi_GT29_ST8Sia7
SIIKPAKSLNLESF---TQELSDFMSCPYKSNTTERELNRMKLQFCCNATRSL-------
-----------FLTKRNTAVNQTIPYETSTIST-YTMNDTLHSMLP-------E-DFPWS
GR---RLGRCAVVGSGGILKNSSCGREIDSADFVIRFNLASIN--DS-DVGLKTDLVTIN
PSQIQREYKDLE--KKPNPLVKRVSVYGNASLIMPAFAYTFCTGLSIRTLKALHPIRPQ-
QPVVFFSPYYLQTLDRFWKGRGLKSIRLSTGFMLISAALEVCEHVHVYGFWPFDTDLQD-
NPVPYHYYDLRRPSK-----RMHKMPEEFVRLLQLHSQGALTLHLQPCSSDAS-------

#Sinans_GT29_ST8Sia7
SVITSVKRLNMESF---TEELVDFLKCPQKPNTTEQELNRMKLQFCCNATGSI-------
-----------FLTKRNTAINQTIPYETDTKHT-YRMNAAIHNMLP-------E-DFPWS
GR---RLGRCAVVGSGGILKNSSCGREIDSADFVIRFNLASIN--DS-DVGLKTDLVTIN
PSQIQREYKDLE--KKLNPLVKRVSVYGNTSLIMPAFAYTFCTGLSIKTLKALHPIRPQ-
QPVVFFSPYYLQTLDHFWKGRGLKSIRLSTGFMLISTALELCENVHVYGFWPFDTDLQD-
NLVPYHYYDLRRPSK-----SMHKMPEEFVRLLQLHSQGALTLHLQPCSSDAS-------

#Lepocu_GT29_ST8Sia7
LGMQSLKKVNSTLL---CGQVTQLMRCPWTLNLTQLEQQRTELRLSCNATGRL-------
-----------VVTQDNTPLGGTITYDAEKWT--RQVDTEIFNMLP-------Q-SPPWA
GGPGARLRRCAVVGNGGILRNSSCGAHIDRADFVIRFNLPPLN--YSRDVGVKSSLVTVN
PSQIINSYRNLN--YARRPFVQRVSTYENAHLVLPAFAFSFCTDPCFRVYYTLQDNRPH-
QRALFYHPDYLRQLATYWQEKGLRETRLSTGLMMVSAALELCDRVELYGFWPFSFDLSE-
RPLSNHYYDDVPPNR-----GMHAMPEEFLRLLRMHSQGVLRLRVGQCP-----------

#Angang_GT29_ST8Sia7
FSLT-ASKINTKSF---TEDVRALMSCPHESNITQRERHRVELRSCCNATGSL-------
-----------FLTRQNTREGQRIKYETNRKKN-ILVDKSIFKMLP-------K-STPWR
ND--SRFQRCAVVGNGGILRNSSCGAEIDSADIVFRLNMAPIN--NSRDVGVKTSLVTIN
PSQIRVGYPDLQ--KRPQPLVERVSAYGDAPLLMPAFAYTTCTDISFKVHKVVQKMRPN-
QKVVFFNPEYLLELFQYWKHRGLEELRLTTGLMLASVAMELCDSVHLYGFWPFELDLFQ-
CPVTHHYYDNVGPSR-----RMHAMPKEFLQLLKMHCQGSIHLQLTRCH-----------

#Salsal_GT29_ST8Sia7-B
VTMTSMKKVDIALF---SQEVRELMNCPWRLNITHRELHRTELWSCCNASDRL-------
-----------MVTRQNTNQNQSLTYEVERRMK-RKVDQALWEMLP-------Q-TVPWS
KG---SLSRCAVVGSGGILQNSSCGAEIDSADYIIRFNLGPVT--NSKDVGNKTHLMTIN
PSQIR-GYRNLT--KAPQPLANRVAVYGNASLLLPAFSYQFSTGLSLDVYHALQPLRPY-
QKVVFFNPNFMLNLGRKWKGQGLKEPRLSTGLMLASVAMELCEEVHIYGFWPFSLDLNH-
NPLPHHYYDNVGPKI-----GFHSMPEEFQLLLKLHTQGALQLHLGRC------------

#Salsal_GT29_ST8Sia7
LTLTSAKAINMRTL---IMDVRQLMTCTHRPNITQRELYRVILRSCCNATGEM-------
-----------ILTKQNTKLGQKIHYETNQKLF-KTVDKKLHSMLP-------K-DLPWS
KG---LLSHCAVVGSGGILQNSSCGAEIDSADYIIRFNLGPVT--NSKDVGNKTHLMTIN
PSQIR-GYRNLT--KAPQPLANRVAVYGNASLLLPAFSYQFSTGLSLDVYHALQPLRPY-
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QKVVFFNPNFMLNLGRKWKGQGLKEPRLSTGLMLASVAMELCEEVHIYGFWPFSLDLNH-
NPLPHHYYDNVGPKI-----GFHSMPEEFQLLLKLHTQGALQLHLGRC------------

#Salfon_GT29_ST8Sia7
-------SINTRTL---IMDVRELMNCPHRPNITQRELYRVILRSCCNATGEM-------
-----------ILTNQNTKSGQKIHYETNQKLF-KTVDKKLHSMLP-------K-ALPWS
KG---LLGHCAVVGSGGILQNSSCGAEIDSADYIIRFNLGPVT--NSKDVGNKTHLMTIN
PSQIR-GYPNLT--KDPQPLANRVAVYGNASLLLPAFSYQFCTGLSLNAYHALQPLRPN-
QKVVFFNPNFMLNLGRKWKGQGLKEPRLSTGLMLASVAMELCEEVHIYGFWPFSLDLNH-
NPLPHHYYDNVGPKK-----GVHSMPDEFQLLLKLHTQGVLQLHLGRC------------

#Corclu_GT29_ST8Sia7
LTVTSAKAINPRTL---IMDIRQLMDCSHRPNITQRELYRVILRSCCNATGEM-------
-----------ILTNQNTKLGQKIHYETNQKLF-KTVDKKLHSMLP-------N-ALPWS
KG---LLGRCAVVGSGGILQNSSCGAEIDSADYIIRFNLGPVS--NSEDVGNKTHLMTIN
PSQIRTGYRNLT--KDPQPLANRVAAYGNASLLLSPFSYQFCTGLSLDVYHVLRPLRPN-
QKVVFFNPNFLLQLSRKWKGRGLKEPRLTSGLMLASVAMELCEEVHLYGFWPFPLDLYH-
NPLPHHYYDNVGPKK-----GVHSMPDEFLLMLQLHTQGVLQLHLGGC------------

#Thythy_GT29_ST8Sia7-B
LNVTSAKAINTRTL---IMEVRQLMNCTYRPNITQRELYRVTLRSCCNATGEM-------
-----------ILTNQNTKLGQKIHYETNQKQF-KTVDKKLHSMLP-------K-ALPWS
QG---LLGHCAVVGSGGILQNSSCGAAIDSADYIIRFNLGPVS--NSEDVGNNTNLMTIN
PSQIRTCYRNLT--KDPRPLANRVAVYGNASLLLSPFSYQFSTGLSLDVYRALRPLRPN-
Q-VLFFNPNFLLKLGRKWKERGLKESRLTSGLMLASVAMELCEEVHLYGFWPFPLDLYD-
NPLPHHYYDNVGPNK-----GIHSMPNEFRLLLKLHTLGVLQLHLGSC------------

#Esoluc_GT29_ST8Sia7
VAMTTMKKVDIVPF---SQVVRELMDCPWRLNLTHRELHRTELWACCNASDRL-------
-----------IVTRQNTHVNQTLTYEAERWRK-KLVDQTLWEMFP-------K-NVPWS
KG---LLGRCAVVGSGGILQNSSCGEEIDRAHYIIRFNLAPVN--QSRDVGLKTDLITAN
PSQIIKQYPDLH--KNPGRLAEQMSVYGNARLLLPAFSFAFGTAPCFKVYHALQKALPQ-
QEVVFFHPDYLFELGQFWRRRGQKASRISTGLMLASSALEICDQVHLYGFWPFSVDLSH-
NPLQHHYFDNVGPNH-----YMHAMPEEFLLLLQLHSQGALQLHVGHCR-----------

#Oncmyk_GT29_ST8Sia7
VTMSTIKKVDIALF---SQDVRELMDCPWRLNLTHRELYRTELWSCCNASDRL-------
-----------MVTRQNTNLNQSLSYEIHRWKK-RKVDQALWEMLP-------Q-TVPWS
KG---SLSRCAVVGSGGILQNSSCGAEIDNADYVIRFNLAPIN--KSCDVGVKTDLVTAN
PSQIIKGYTDLQ--QNPGHLAEVLSFYGHAHLLLPAFSSASGTAPCFKVYHALRKARPQ-
QEVVFFHPDYLFELGRFWRHRGQRARRLSTGLMLASTALEICEQVHLYGFWPFPLDLSH-
NSLPHHYYDNVGPNR-----KMHAMPEEFLLLLQLHSQGALQLHVGPCTLTPTP------

#Thythy_GT29_ST8Sia7
VTMTTMKKANIALF---SQEVRELMDCPWRLNLTHRELHRTELWSCCNASDRL-------
-----------MVTRQNTNQNQILTYEAEKWRK-RKVDKALWEMLP-------Q-TVPWS
KG---SLSRCAVVGSGGILQNSSCGAEIDTADYVIRFNLAPIN--KSCDVGVKTDLITAN
PSQIIKGYHNLQ--RNPGPLVKRMSVYGHAHLLLHAFAFGFGTSPCFKVYHALRKARPQ-
QEVVFFHPDYLLQLDRFWRRRGQRAPRLSTGLMLASTALEICEQVHLYGFWPFHLDLSQ-
NTLPHHYYDNVGPSR-----FMHAMPEEFLLLLQLHSQGALQLHVGPCTL----------

#Takrub_GT29_ST8Sia6-A
------------EI---TDKVNRLYAQTLEKKEDKSKILRSELSSKCQGFEKA-------
-----------IITQANTVVGSKIVYDGERKSL-VQVTPEMFNTFP-------K-EHPFP
NK---TWETCAVVGNGGILSDSGCGKMIDSAQFVIRCNLPPLNNGYQDHVGVKTDLVTAN
PSILVEKYGALM--GRRRPFIESLRSYGNSLLLLPTFSYRSNTPVSLRAFYSIEDFGSP-
TRAISFNPQYLQKLDVFWRSKGLRAVRLSSGLMVASLALELCSNVHLYGFWPFSNHPNGL
RTLKNHYYDDIPPKK-----KFHAMPVEFELLLKLHTEGVLRLHLDDCVPGEVNLMGSTG

#Takrub_GT29_ST8Sia6-B
------------EI---IDKVNRLYAQTWEKKEDKYKKFRSELSSKCQGFEKA-------
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-----------IITQANTVVGSKIVYDGERKRS-VKVSTEMFNTFP-------K-EHPFP
NK---TWETCAVVGNGGILSDSGCGKMIDSAQFVIRCNLPPLNNGYQDHVGVKTDLVTAN
PSILFEKYGALM--GRRRPFIESLRSYGNSLLLIPAFSYGNNTPVSLRAFYSIEDFGSP-
TRTIFFNPQYLQKLAVFWRSKGLRAVRLSSGLMVASLALELCSNVHLFGFWPFSNHPHGL
RTLKNHYYDDIQTKK-----KFHAMPVEFELLLQLHTEGVLRLHLDDCVPGEVNLMGSTR

#Orylat_GT29_ST8Sia6
------------EN---IMKALELYSEPWKKQEDNYHQFRSQLNSKCHGLEKA-------
-----------IITQANTPQGTKLVYDAERKRT-LVVNAEVFNTFI-------K-ENPFP
NK---TWDTCAVVGNGGILANSSCGKTIDSAQFVIRCNLPPLSNGFEKDVGIKSDIVTAN
PSIITEKYFSLM--RHRRPFAEAMRIYGNSMVLLPAFSFGHNTALSMRAFYTLEDFESS-
ARAVYFNPEYLKNLANFWRSEGLKSPRLSTGIMMASIALEVCSEVHLYGFWPFDVHPYSH
QGLTNHYYDDRKAKN-----KFHAMPTEFNLLLQLHRKGVLRLHLGDCTPDEK-------

#Notfur_GT29_ST8Sia6
------------ED---IKKALELYSQTWKKQEDSYQNFRSLLNRKCKCFDKA-------
-----------IITQNNTPLGSKLVYDGERKRT-LQVNQEIFNTFP-------K-GHPFS
NK---TLHTCAVVGNGGILANSSCGKTIDSAEFVIRCNLPPLSNGYEKHVGIKTHLVTAN
PSILMEKYAALM--ARRRPFVENLRSYGDSMLLLPAFSYGRNTPVSLRAFYTLEDFESP-
IQSIFFNPAYLRNLAAFWRSQGLKAVRLSTGIIMTSLALEICENVHLYGFWPFGVHPYSS
QDLTNHYYDDRKTKI-----KFHAMPDEFNLLLNLHSQGVLKMHLGDCEPDEKRFHRSD-

#Orenil_GT29_ST8Sia6-B
------------EI---ISKVQERYNQTWKKQEDNYLKFRTNLSVKCNGFDKA-------
-----------IITKNNTPVGLKLVYDGEKKRT-LQVNKDFFNIFT-------K-ENPFS
NK---KWDTCSVVGNGGILSESSCGKMIDSADFVIRCNLPPLENGYEKDVGIKTSLVTAN
PSIFTQRYGSLV--GRRLPFVESLHKYGNSLLLLPAFSFGINTAVCQRVAYTIEDFKSP-
IRPVFFNPQYLDSLAQFWRSEGLKERRLSTGLIMASMALELCENVHLYGFWPFSNHPYGF
YTLTNHYYDDKPAKT-----SFHAMPAEFDRLLQLHTEGVLRLHLEDCK-----------

#Gasacu_GT29_ST8Sia6
------------QF---IDKVRERYNKTWIKQVDDYLEFRSQLSRKCHGFDSA-------
-----------FITQYNTPVGAKIVYDGEKTRT-LQVTPEIFSTFP-------K-EHPFS
NK---IWGTCSVVGNGGILSNSSCGKMIDSAEFVMRCNLPPLDNGYENDVGIKTDLVTAN
PSILIKKYGSLQ--QRRRPFVESLRSYGNSLLLLPAFSYGFNTPLSLRAVYSIEDFKSP-
TRPVFFNPEYLESLGLFWRSRGLKAVRASTGLMMASLALEHCTDVHLYGFWPFGNHPQGL
HALTNHYYDDVQPKN-----TVHAMPVEFEFLLQLHSQGVLRLHLEDCQPGEK-------

#Anofim_GT29_ST8Sia6
------------EV---INKVIERYSKTWKKQEENYQKFRSQLSSKCHGFDKA-------
-----------IITQANTPVGAKLVYDGEKKRT-LQVTPEIFSTFA-------K-EHPFQ
NK---IWDTCAVVGNGGILTNSSCGKTIDSAQFVMRCNLPPLDKGYEKHVGIKTDLVTAN
PSILLEKYGALM--GRRRPFVESLRSYGNSLLLLPAFSFGFNTPVCLRAVYSIEDFESP-
TRPVFFNPEYLQKLALFLRSQGLRAPRPSTGIIMASLALEHCANVHLYGFWPFSSHPHGL
HALTNHYYDDRQTKK-----KFHSMPAEFDLLLQLHSQGVLRLHLGDCPPGER-------

#Larcro_GT29_ST8Sia6
------------EV---IDKVMERYSQSWERQEDNYQKFRAQLNNKCHGFDKA-------
-----------IITQANTPVGSKLAYDGEKKRI-LQVTPEIFSTFA-------K-ERPFP
NK---TWDTCAVVGNGGILTNSGCGKVIDSAQFVIRCNLPPLENGYEKHVGIKTDLVTAN
PSIFLEKYGGLM--GRRRPFVESLHSYGNSLLLIPAFSYGHNTPVSLRVAYSLEDFKSS-
TRPIFFNPEYLHSLALFWRSQGLRAVRLSTGIIMASLALELCANVDLYGFWPFSNHPHGF
HTLTNHYYDDRQTKV-----KFHAMPAEFELLLRLHSQGVLRLHLGDCQPSEK-------

#Ampoce_GT29_ST8Sia6
------------EV---IDKVVARYSQPWKRQEDSYQKFRFQLSSKCHGFNKA-------
-----------IITKTNTPVGSKLVYDGEKKRT-LQVTPEIFSTFI-------K-DHPFS
NK---TWDTCAVVGNGGILTNSSCGKTIDSAQFVIRCNLPPLANGYEKHVGVKTDLVTAN
PSILLEKYGALM--GRRRPFVESLRTYGDSLLLLPAFSFGHNTPVSLRAAYTIEDFESP-
TRPVFFNPEYLHSLALFWRSQGLKAVRLSTGLIMASLAVELCSNVHLYGFWPFSNHPHGL
QPLTNHYYDNRQTKT-----KFHAMPAEFDLLLRLHSQGVLRLHLGDCPTSGK-------
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#Serlaldor_GT29_ST8Sia6
------------EI---IDNVIERYSQTWKKQEDNYQKFRSQLNSKCRGFNKA-------
-----------IITQANTPVGSKLVYDGEKRRS-LQVTPEIFSTFV-------K-EHPFS
NK---TWGTCAVVGNGGILTNSSCGQTIDSAQFVIRCNLPPLKNGYEKHVGNKTDLVTAN
PSILVEKYGALM--AHRRPFVDSLHTYGNSLLLLPAFSFGHNTPVSLRAAYTIEDFGSP-
IKPVFFNPEYLQRLAVFWRSQGLRAVRLSTGIIMASLALELCADVHLYGFWPFSTHPHGF
HPLTNHYYDDRKTKM-----KFHAMPAEFDLLLRLHSQGVLRLHLGDCRPHEK-------

#Paroli_GT29_ST8Sia6
------------EI---IDKVIQRYSQTWKRQEDNYQKIRSQLSSKCHGFDKA-------
-----------IITQANTPVGSKLVYDGEKKRT-LQVTPEVFSTFI-------K-ERPFS
NK---TWDTCAVVGNGGILTNSSCGQMIDSAQFVIRCNLPPLENGYEKHVGTKTDLVTAN
PSILMEKYGALM--GRRRPFVESLRIYGDSLLLIPAFSYGHNTPVSLRVVYTIEDFESP-
TRPIFFNPEYLQSLAVFWRSQGLKAVRLSTGIIMASLALELCSNVHLYGFWPFSNHPHGL
HVLNNHYYDDRKTKT-----KFHAMPAEFDLLLRLHSQGALRLHLGDC------------

#Lepocu_GT29_ST8Sia6
----------EKAN---IDKLAQVHSQTWRKQESRLQTFRAQLNMKCQGFSRA-------
-----------IITQANTLLGSKVTYDGERRKP-VEVTPKLYSTFP-------K-EHPFG
NV---SFQSCAVVGNGGILANSSCGEEIDGAQFVIRCNLPPVDRKYQDDVGNKTDLVTAN
PSILLERFEGLM--ELRRPFVESLGDYGQPMLALPAFSYGHNTPVSLRAVYTLQDFNSP-
VRAVFLNPEYLQNLARFWKAHGLRTVRLSTGLIVASLALELCASVTLYGFWPFSLHPFSK
QHLTNHYYDDQQSKK-----SFHAMPAEFEQLLRLHSQGVIRVHLGSC------------

#Amical_GT29_ST8Sia6
----------EQSV---IDRLLQTHIVDWEKQEHKFQSFRAQLNSRCDGLSKA-------
-----------IISQTNTPLGSKVVYDGEKRKP-IQVTPKLFSTFP-------K-EHPFG
NR---TFTSCAVVGNGGILMNSSCGGEIDEAQFVIRCNLPPVDHGYQRDVGNKTSLVTAN
PSILLDKFNGLM--ELRRPFVDSLGSYGDPLLVLPAFSYSRNTPVSLRALYTLQDFDSP-
VRPVFLNPEYLHNLARFWKAQGLQAIRLSTGLIMASLALELCANVQLYGFWPFSKDPHSK
HPLTNHYYDDQQAKK-----TIHAMSTEFSHLLMLHNQGIIRVQLGKCQAGTRRATPSLH

#Angang_GT29_ST8Sia6
----------EY-T---IDKMVELYSYAWKKQNANFNKFRSQLSSRCRGVSTA-------
-----------IVTQNNTPLDSKIYYDGEKRKP-LQVTPKLYSTFA-------K-EQPFE
NV---TWKTCAVVGNGGILVNSSCGEAIDSAHFVFRCNLPPLDKAYQKDVGNKTNLVTAN
PSILIEKFEGLM--EYRRPFVESLSDYGEALLLLPAFSYAHNTPVSLRAFYTLRDFGGR-
ARPAFLSPAYLQSLAHFWRAQGLRTVRLSTGLIVASLALELCANVHLYGFWPHAQHPHDR
RPLTNHYYDDRQGKK-----KVHAMPAEFGHLLRLHRQGVVRVHLGQCEDRPR-------

#Cluhar_GT29_ST8Sia6
----------DS-V---IDKVLERYSKNWKKQENNYKRFRALLSSRCHGATKA-------
-----------VVTQANTPLGSKVVYDGEKRKP-LQVTSALFNVFP-------K-EPPFG
NT---SWDTCSVVGNGGILANSSCGRRIDSAQFVIRCNLPPLEHGYEEDVGNKTDLVTAN
PSILHEKFGGLM--ERRRPFVEGLRPYGNSLILLPAFSYSHNTPVSLRAVYTLEDFRSP-
ARPVFLSPDYLTSLARFWRSQGLRSVRLSTGLIVASLALELCTNVDLYGFWPFSQHPHGH
QPLTNHYYDNRETKK-----KIHAMPAEFDHLLRLHGQGILRVHLGQCPRSDG-------

#Esoluc_GT29_ST8Sia6
----------DTTI---IEKVVEHYSHSWKKQEDNFRKFRSLLRNTCHGLTKA-------
-----------VVTQSNTPLGSKVVYDGEKRKP-LQVTAELFSTFA-------K-EHPFV
NA---TWDTCSVVGNGGILANSSCGERIDSAQFIIRCNLPPLANGYERDVGNKTDLVTAN
PSILQEKYKGLQ--EHRLPFVKSLHSYGDSFVLLPAFSYGHNTPLSLRALYTIQDFNSP-
SRPIFLNPEYLRSLARFWRSQGLKTARLSTGLIVASLALELCANVHLYGFWPFSQHPQHH
RPLTNHYYDDRQSKK-----TVHAMPAEFDQLQRLHNQGVLRLHLGECAPAAT-------

#Onckis_GT29_ST8Sia6-A
----------DT-V---TDKVVELYSHSWKKQEDKFRNFRSLLSNRCNGLTKA-------
-----------MVTQANTPLGSKVVYDGEKRKP-LQVTPELFSTFA-------K-ENPFV
NT---TWDTCSVVGNGGILANSSCGEKIDSAQFVIRCNLPPLENGYERDVGNKTDLVTAN
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PSILMEKYGGLQ--ERRRPFVESLRSYGDSLMLLPAFSYGHNTPVSLRALYTIQDFDSP-
SRPVFLNPEYLQSLARFWQGQGLRTVRLSTGLIVASLALELCANVHLYGFWPFNEHPHRH
QPLTNHYYDDRQSKK-----TVHAMPAEFDHLLRLHTQGVLRIHLGECAPTARCRPSSPL

#Salalp_GT29_ST8Sia6
----------DT-V---TEKVVERYSHSWKKQEDKFRNFRSLLSNRCHGLTKA-------
-----------MVTQANTPLGSKVVYDGEKRKP-LQVTPELFSTFA-------K-ENPFV
NT---TWDTCSVVGNGGILANSSCGERIDSAQFVIRCNLPPLENGYERDVGNKTDLVTAN
PSILMEKYGGLQ--ERRRPFVESLRSYGDSLMLLPAFSYGPNTPVSLRALYTIQDFDSP-
LRPVFLNPEYLQSLAHFWQGQGLRTVRLSTGLIVASLALELCANVHLYGFWPFNEHPHRH
QPLTNHYYDNRQSKK-----TVHAMPAEFDHLLRLHSQGVLRIHLGECAPAAR-------

#Salsal_GT29_ST8Sia6
----------DT-V---TEKVVERYSHSWKKQEDKFRNFRSLLSNRCHGLTKA-------
-----------MVTQANTPLGSKVVYDGEKRKP-LQVTPELFSTFA-------K-ENPFV
NT---TWDTCSVVGNGGILANSSCGEKIDSAQFVIRCNLPPLENGYERDVGNKTDLVTAN
PSILMEKYGGLQ--ERRRPFVESLRSYGDSLMLLPAFSYGHNTPVSLRALYTIQDFDSP-
SRPVFLNPEYLQSLARFWQGQGLRTVRLSTGLIVASLALELCANVHLYGFWPFNKHPHRH
QNLTNHYYDDRQSKK-----TVHAMPAEFDHLLRLHTQGVLRIHLGECTPTASPGCSS-K

#Oncmyk_GT29_ST8Sia6
----------DT-V---TDKVLELYSHSWRKQEDKFRKFRSLLSNRCHGLTKA-------
-----------MVTQANTPLGSKVVYDGEKRKP-LQVTPELFSTFA-------K-ENPFV
NT---TWDTCSVVGNGGILANSSCGEKIDSAQFVIRCNLPPLENGYERDVGNKTDLVTAN
PSILMEKYGGLQ--ERRRPFVESLRSYGDSLMLLPAFSYGHNTPVSLRALYTIQDFDSP-
SRPVFLNPEYLQSLARFWQGQGLRTVRLSTGLIVASLALELCANVHLYGFWPFNEHPHRH
QPLTNHYYDNRQSKK-----TVHAMPAEFDHLLRLHTQGVLRIHLGECAPTASPGCSS-K

#Onctsh_GT29_ST8Sia6
----------DT-V---TDKVVELYSHSWRKQEDKFRNFRSLLSNRCHGLTKA-------
-----------MVTQANTPLGSKVVYDGEKRKP-LQVTPELFSTFA-------K-ENPFV
NT---TWDTCSVVGNGGILANSSCGEKIDSAQFVIRCNLPPLENGYERDVGNKTDLVTAN
PSILMEKYGGLQ--ERRRPFVESLRSYGDSLMLLPAFSYGHNTPVSLRALYTIQDFDSP-
SRPVFLNPEYLQSLARFWQGQGLRTVRLSTGLIVASLALELCANVHLYGFWPFNEHPHRH
QPLTNHYYDDRQSKK-----TVHAMPAEFDHLLRLHTQGVLRIHLGECAPTASPGCSS-K

#Danrer_GT29_ST8Sia6
----------DSVI---IGKALGNYSNSWKKHEANYKRFRLLLNEKCHAVSKA-------
-----------VVTQNNTPLGSNVVYDGERRKP-LQVTQALYNILA-------K-EQPFG
NA---TWESCAVVGNGGVLANSSCGEEINSAQFVIRCNLPPLDDRYEKDVGNKTNLVTAN
PSILHEKYSGLM--ERRRPFVESLHSYGQALLLLPAFSYGHNTPVSLRAFYTLEDFGREG
PLPIFLNPEYLRKLTKFWREQGLNSVRPSTGLIMASLALEICTNVHLYGFWPFGKHPNDS
RPITNHYYDNRESKK-----NVHSMPSEFEQLLKLHKQGVVHIHLGECQPAHR-------

#Cypcar_GT29_ST8Sia6
----------DDVL---IAKALENYSDKWKKQETNFKKFRSLLSNKCHAVSKA-------
-----------VVTQNNTPLGSNVIYDGERRKP-LHVTQALFNILA-------K-EQPFG
NA---TWESCAVVGNGGILANSSCGEEINSAQFVIRCNLPPLDKGYEKDVGNKTNLVTAN
PSILHEKYSGLM--ERRRPFVESLRPYGQALLLLPAFSYGHNTPVSLRAFYTLEDFGSNS
PLPVFLNPDYLRRLSKFWRERGLNSVRPSTGLIVASLALEICSNVHLYGFWPFSKHPYDS
QAITNHYYDNRESKK-----NVHSMPTEFEYLLKLHNQGVIRIHLGKCQPTHS-------

#Sinans_GT29_ST8Sia6-B
----------DSVL---IAKALENYSDKWKKHEANLKRFRSLMSSKCHAVSKA-------
-----------VVTQNNTPLGSNVIYDGERRKP-LQVTQALFNILA-------K-EQPFG
NA---TWESCAVVGNGGILANSSCGEEINSAQFVIRCNLPPLDKGYEKDVGKKTNLVTAN
PSILHEKYSGLM--ERRRPFVESLRPYGQALLLLPAFSYGHNTPVSLRAFYTLEDFGSNS
PLPVFLNPEYLRRLSKFWREQGLNSVRPSTGLIVASLALEICSNVHLYGFWPFSKHPYDS
QPITNHYYNDRESKK-----NVHSMPNEFAHLLKLHKQGVIRIHLGECQPTHS-------

#Sinans_GT29_ST8Sia6
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----------DNVL---IAKALENYSHKWKKHEANFKRFRSLLSSKCHAVSKA-------
-----------VVTQNNTPLGSNVIYDGERRKP-LQVTQALFNILA-------K-EQPFG
NA---TWESCAVVGNGGILANSSCGEEINSAQFVIRCNLPPLDNRYEKDVGNKTSLVTAN
PSILHEKYSGLM--ERRRPFVESLRPYGQALLLLPAFSYGHNTPVSLRAFYTLEDFGSDS
PLPVFLNPEYLRRLSKFWRERGLNSVRPSTGLIMASLALEICSNVHLYGFWPFNKHPNDS
RPITNHYYDDRESKK-----NVHSMPTEFEHLLKLHKQGVIRIHLGECQPT---------

#Sinrhi_GT29_ST8Sia6
----------DNVL---IAKALENYSHKWKKHEANFKRFRSLLSSKCHAVSKA-------
-----------VVTQNNTPLGSNVIYDGERRKP-LQVTQALFNILA-------K-EQPFG
NA---TWESCAVVGNGGILANSSCGEEINSAQFVIRCNLPPLDNRYEKDVGNKTSLVTAN
PSILHEKYSGLM--ERRRPFVESLRPYGQALLLLPAFSYGHSTPVSLRAFYTLEDFGSDS
PLPVFLNPEYLRRLLKFWRERGLNSVRPSTGLIMASLALEICSNVHLYGFWPFNKHPNDS
RPITNHYYDDRESKK-----NVHSMPTEFEHLLKLHKQGVIRIHLGECQPT---------

#Pygnat_GT29_ST8Sia6
----------ENVI---IDKALRVYSSRWRRQEANFKRFRSLLSRNCHALSKA-------
-----------VVTQANTPVGSKLVYDGEKTKP-LQVTSALFNTFA-------K-EQPFG
NA---TWDTCAVVGNGGILANSSCGEKINSADFIIRCNLPPLGSGYEKDVGNQTSLVTAN
PSILIEKFGGLM--ERRRPFVESLRPYGDSLLVLPAFSYGHNTPVSLRAFYTLEDFGITS
ARPVFLNPEYLSSLARFWRGQGLRSARLSTGLIVASLALELCTNVHLYGFWPFSQHPYGR
QPITNHYYDDRQSKK-----NVHSMPAEFDHLLRLHMQGVIQMHLGACSMLNRTSN----

#Astmex_GT29_ST8Sia6
----------DNAI---IDRLLKSYSPRWKRREANFSKFRSLLSSSCHAVSKA-------
-----------VVTQSNTPVGSKVVYDGEKTKP-LQVTKALFSTFA-------K-EQPFG
NA---SWDTCAVVGNGGILVNSSCAEKINSANLVIRCNLPPLGNGYEKDVGNKTSLVTAN
PSILIEKFSGLM--ERRRPFVESLRPYGDSLLLLPAFSYSHNTPVSLRALYALEDFNAVG
PRPVFFNPEYLSSLARFWRGRGLRTARLSTGLIVTSLALELCTNVHLYGFWPFSLHPHGR
QTITNHYYDNRQSKK-----NVHSMPSEFEHLLRLHVSGVIQLHLGECSTTDLNHTEKT-

#Danrer_GT29_ST8Sia1
---------SDKEMV--EEVLR--QGQTWSRNQTAVELYRKLLTDCCNPKRMF-------
-----------AVTKENSPLGKVLWYDGEFYHY-HTVTNETYPIFV-------Q-DTPLQ
L----PLKRCSVVGNGGVLKHSGCGNEIDRADFIMRCNLPPLSKDYTDDVGTKTHLVSAN
PSIIEKSFQNLL--WSRKSFVESMKAYGSSYIYIPAFSMKPGTDPSLRAYHALADSSSN-
QTVLFANPDFLKNVGIFWKNHGVHGKRLSTGLFLVSLALGLCEEVTAYGFWPFSVGLDE-
RPVSHHYYDNILPSS-----RFHAMPEEFLQLWHLHKSGTLRMRVGSCAKERMELKREK-

#Orylat_GT29_ST8Sia1
---------RDKDIV--AEVLR--QGDVWRKNQTGIDLYRDLLTKCCNPKKMF-------
-----------AVTKENSPIGKVLWYDGEIYHS-HTVNSETYQLFI-------K-RRGAA
S----SCRRCAVVGNGGILKGSKKGKEIDHHHYIFRCNLPPLSREYVEDVGTKTHLVTAN
PSIIEKRFQNLV--WSRKTFVDSMKVYGSSYIYMPAFSMAPGTDPSLRAYFALTDVPSN-
LTMLFANPDFLLSVSKFWKAHGVHARRLSTGLFLVSLAMGLCDEVTTYGFWPFSVDLDE-
QPISHHYYDNILPYK-----WFHAMPEEFVQLWHLHKSGILRMKVGHCSPQN--------

#Gasacu_GT29_ST8Sia1
---------RDKDIV--EEVLK--QGGVWQKNQTGIDLYRKLLTECCDPRRMF-------
-----------AVTKENSPTGKVLWYDGEFYHS-HTVNNETYPLLV-------K-DNPLR
L----PLKKCAVVGNGGILRHSQCGRDIDQADFVLRCNLPPLSKEYVDDVGTRTHLVTAN
PSIIEKRFQNLL--WSRKVFVDSMKVYGSGYIYMPAFSMKTGTDPSLRAYHALADSSSN-
LTMLFANPEFLRTVGRFWKARGVHARRLSTGLFLVSLALGLCEEVTAYGFWPFSVGLDE-
QPVSHHYYDNILPYT-----WFHAMPEEFVQLWHLHKSGALRVRVGRCSAQGGGG-----

#Takrub_GT29_ST8Sia1
---------ADKEIV--DEVLR--QGEAWQKNQTGIDLYRKLLTECCDPPRMF-------
-----------AVTKQNSPLGKVMWYDGEFYHS-HTVNNETYPLFV-------Q-ENPLQ
L----PLKKCAVVGNGGILRGSKCGKDIDRADFIMRCNLPPLSKEYLEDVGTKTHLVTAN
PSIIENRFQNLL--WSRKHFVDSMKVYGTSYIYMPAFSMSPGTNPSLRAYYALADASAN-
LTMLFANPEFLRSVGKFWKARNVHAKRLSTGLFMVSLALALCKEVTVYGFWPFAIDLDE-
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QPVSHHYYDNILPYK-----WFHTMPEEFVQLWHLHKSGTLRMRVGRCPPEDGGR-----

#Tetnig_GT29_ST8Sia1
---------GDKEIV--AEVLR--QGEAWHRNQTGIDLYRRLLTDCCDPPKMF-------
-----------AVTKRNSPLGKVMWYDGEFYHS-HTVNNETYRLFV-------Q-DNPLQ
L----PLKKCAVVGNGGILRASKCGKDIDQADFIMRCNLPPLSEEYLEDVGTKTHLVTAN
PSIIENRFQSLL--WSRKHFVDSIKVYGTSYIYMPAFSMRPGTEPSLRAYYALADTSSN-
LTVLFANPEFLRTVGKFWKARNVHAKRLSTGLFMVSLALALCEEVTVYGFWPFAIDLDE-
QPVSHHYYDNILPYK-----WFHTMPEEFVQLWHLHKSGTLRMRVGRCSSQGGGR-----

#Calmil_GT29_ST8Sia1
---------DQKEIV--NDVLH---QPVWRRNQTATTAFRRLLENCCETKRMF-------
-----------AVTQHNSPMGKNLWFDGEFLHS-LSVNNEMFAMFP-------Q-DTPFQ
I----PLKKCSVVGNGGILKRSACGDKIDKADFVMRCNLPPLSNEYARDVGHRTQLVTAN
PSIIKKRYQNLM--WSRKAFVESMKVYGRSYIYMPGFSMKAGTEPSFRTYYTLSDVNAN-
QTIIFANPDFLRNVQKFWKGKGVHAKRLSTGLFLVSVALGLCEEVTLYGFWPFSTDLEE-
RTISHHYYDNVMPDT-----SYHAMPEEFLQLWLLHKSGILKIHVGKCGQIPM-------

#Xenlae_GT29_ST8Sia1
---------GHKEMI--RQVL--QFGPRWGRNRSSGDSFRKLLQDCCDPPRLF-------
-----------SMTKANTALGENLWYDGEFFQS-LTIDNTTRSLFP-------Q-DTPIK
L----PLKRCSVVGNGGILKNSRCGEQIDEADFVMRCNLPPLSREYTDDVGTKTQLVTVN
PSIIDKRFQNLL--WSRKSFVESVSVYKQSYVYMPAFSTKRGTDPSLRVYYTLEDFGTN-
QTVLFANPNFLRNVGKFWKSKGVHSKRLSTGLFMVSAALSLCEEVTIYGFWPFQMDLGG-
RHISHHYYDNMLPLS-----GVHAMPEEFLQLWHLHKSGVLQMQLDQCKKDVSSKKPH--

#Siltro_GT29_ST8Sia1
---------GHKEMV--REVL--RFGPGWRKNRTEMDSFRKLLQDCCDPPHLF-------
-----------SLTKVNTPLGENLWFDGEFFHS-LTIDNSTRSLFP-------Q-DTPFK
L----PLKRCSVVGNGGILKNSRCGEQIDEADFVMRCNLPPLSREYTEDVGTRTQLVTVN
PSIIDKRYQNLL--WSRKSFVENLRVYQQSYVYMPAFSTKRGTDPSLRVYYTLADFGTN-
QTVLFANPNFLRNVGKFWKSRGIHSKRLSTGLFMVSAALSLCEEVTIYGFWPFQMDLGG-
RYISHHYYDNTLPLS-----GVHAMPEEFLQLWLLHKSGVLQMQLDQCKKDVSSQKPH--

#Anocar_GT29_ST8Sia1
---------GEKEIM--CGMRLQQKCKAWQRGHHAAHAFRKLLKECCDPGQLF-------
-----------AMTKENSPVGKNLWYDGEFLYS-FTIDNETFSLFP-------K-ATPFQ
L----PLKKCSVVGNGGILKKSNCGRQIDQADFVMRCNLPPLTSEYSKDVGSKTQLVTAN
PSIIKKRFQNLL--WSRKAFVDSVKVYNQSYIYMPAFSMKAGTEPSLRVYYTLADVGAR-
QTVIFANPNFLRDIGKFWKSKGIHGKRLSTGLFLVSAALGMCEEVTIYGFWPFSMDLHG-
NFISHHYYDNILPDS-----GFHAMPEEFLQLWFLHKSGVLRMQLEHCEDSIFHPAS---

#Galgal_GT29_ST8Sia1
---------DEKEIV--QGVLMQQ-GKAWRRNHTAVAVFRKLLEDCCDPGQLF-------
-----------AMTKQNSPMGKNLWFDGEFLYS-FTIDNTTYSLFP-------Q-ATPLQ
L----PLKKCSVVGNGGILKKSGCGKQIDQADFVMRCNLPPLSREYSKDVGLKTQLVTAN
PSIIQKRFQNLL--WSRKAFVDSVKVYNHSYIYMPAFSMKTGTGPSLRVYYTLKDFGAK-
QAVLFANPNFLRDIGKFWKNKGIHAKRLSTGLFLVSAALGLCEEVTIYGFWPFSVDLHG-
KFISHHYYDNVLPDS-----GFHAMPEEFLQLWFLHKSGVLRMQLEQCEDPLTQSSA---

#Bostau_GT29_ST8Sia1
---------DEKEIV--QGVL-QQ-GTAWRRNRTAAGIFRKQMEDCCDPAHLF-------
-----------AMTKMNAPMGKSLWYDGEFLYS-FTIDNSTYSLFP-------Q-ATPFQ
L----PLKKCAVVGNGGILKKSGCGRQIDEADFVMRCNLPPLSSEYTKDVGSKSHLVTAN
PSIIRQRFQNLL--WSRKTFVDHMKVYNHSYIYMPAFSMKTGTEPSLRVYYTLSDVGAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFSVNMHE-
QPISHHYYDNVLPFS-----GFHAMPEEFLQLWYLHKIGALRMQLDPCEDNSL-QPTS--

#Canlupfam_GT29_ST8Sia1
---------NEKEIV--QGVL-QQ-GTAWRRNQTAARVFRKQMEDCCDPAHLF-------
-----------AMTKLNSPMGKSMWYDGEFLYS-FTIDNSTYSLFP-------Q-ATPFQ
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L----PLKKCAVVGNGGILKKSGCGRQIDEANFVMRCNLPPLSSEYTKDVGSKSHLVTAN
PSIIRQRFQNLL--WSRKTFVDNMKIYNHSYIYMPAFSMKTGTEPSLRVYYTLSDVGAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFSVNMHE-
QPISHHYYDNVLPFS-----GFHAMPEEFLQLWYLHKIGALRMQLDPCEDTSL-QPTS--

#Pantro_GT29_ST8Sia1
---------NEKEIV--QGVL-QQ-GTAWRRNQTAARAFRKQMEDCCDPAHLF-------
-----------AMTKMNSPMGKSMWYDGEFLYS-FTIDNSTYSLFP-------Q-ATPFQ
L----PLKKCAVVGNGGILKKSGCGRQIDEANFVMRCNLPPLSSEYTKDVGSKSQLVTAN
PSIIRQRFQNLL--WSRKTFVDNMKIYNHSYIYMPAFSMKTGTEPSLRVYYTLSDVGAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFSVNMHE-
QPISHHYYDNVLPFS-----GFHAMPEEFLQLWYLHKIGALRMQLERCEDTSL-QPTS--

#Homsap_GT29_ST8Sia1
---------NEKEIV--QGVL-QQ-GTAWRRNQTAARAFRKQMEDCCDPAHLF-------
-----------AMTKMNSPMGKSMWYDGEFLYS-FTIDNSTYSLFP-------Q-ATPFQ
L----PLKKCAVVGNGGILKKSGCGRQIDEANFVMRCNLPPLSSEYTKDVGSKSQLVTAN
PSIIRQRFQNLL--WSRKTFVDNMKIYNHSYIYMPAFSMKTGTEPSLRVYYTLSDVGAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFSVNMHE-
QPISHHYYDNVLPFS-----GFHAMPEEFLQLWYLHKIGALRMQLDPCEDTSL-QPTS--

#Macmul_GT29_ST8Sia1
---------NEKEIV--QGVL-QQ-GTAWRRNQTAARAFRKQMEDCCDPAHLF-------
-----------AMTKMNSPMGKSMWYDGEFLYS-FTIDNSTYSLFP-------Q-ATPFQ
L----PLKKCAVVGNGGILKKSGCGRQIDEANFVMRCNLPPLSSEYTKDVGSKSHLVTAN
PSIIRQRFQNLL--WSRKTFVDNMKIYNHSYIYMPAFSMKTGTEPSLRVYYTLSDVGAN-
QTVLFANPNFLRSIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVAIYGFWPFSVNMHE-
QPISHHYYDNVLPFS-----GFHAMPEEFLQLWYLHKIGALRMQLDPCEDTSL-QPTS--

#Musmus_GT29_ST8Sia1
---------NEKEIV--QGVL-AQ-STAWRTNQTSASLFRRQMEDCCDPAHLF-------
-----------AMTKMNSPMGKSLWYDGELLYS-FTIDNSTYSLFP-------Q-ATPFQ
L----PLKKCAVVGNGGILKMSGCGRQIDEANFVMRCNLPPLSSEYTRDVGSKTQLVTAN
PSIIRQRFENLL--WSRKKFVDNMKIYNHSYIYMPAFSMKTGTEPSLRVYYTLKDVGAN-
QTVLFANPNFLRNIGKFWKSRGIHAKRLSTGLFLVSAALGLCEEVSIYGSWPFSVNMQG-
DPISHHYYDNVLPFT-----GYHAMPEEFLQLWYLHKIGALRMQLDPCEEP-SPQPTS--

#Ratnor_GT29_ST8Sia1
---------NEKEIV--QGVL-AQ-RTAWRRNQTSARLFRKQMEDCCNPAHLF-------
-----------AMTKVNSPMGKSLWYDGEFLYS-LTIDTSTYSLFP-------Q-ATPFQ
L----PLKKCAVVGNGGILKMSGCGRQIDEANFVMRCNLPPLSSEYTRDVGSKTQLVTAN
PSIIRQRFENLL--WSRKKFVDNMKIYNHSYIYMPAFSMKTGTEPSLRVYYTLKDAGAN-
QTVLFANPNFLRNIGKFWKGRGIHAKRLSTGLFLVSAALGLCEEVSIYGFWPFSVNMQG-
EPISHHYYDNVLPFS-----GFHAMPEEFLQLWYLHKMGALRMQLDPCENPPSPQPTS--

#Calmil_GT29_ST8Sia6
ASASNQWR-SEEDV---LRNIAKIHQCKWGKQKRAVENFRWELRKCCRTLSGS-------
-----------FVTQRNTPVGTELFYEAEPKKK-IKITPSIFAIFP-------K-DSPFR
GR---SIQRCAVVGNAGILHNSSCGAEIDQADFVFRCNLPPMGGNFTKDVGSKTHLVTAN
PKVIIERYAELH--KRRKPFANTLVIYNDALLLFPAFYHSKNTALSFRAHYTLQDFKSK-
QRVIFFNPIYLKHLAHFWLSKGMQVQNLSTGITVASMAMELCSEVWIYGFWPFGKNTEG-
ELMSHHYFDSLLAEP-----DLHSTSNEFYQLLRMHSKGIVKLQMGQCEAEETDEFTLKP

#Hetzeb_GT29_ST8Sia6
ASSPIQWK-TEKDV---IKSVAKLQKCQWHKQEVAAEELRSELKRCCHAAYNY-------
-----------LVTQKNMPVGTELIYDAESKNK-INITPQIFSIFP-------K-NSFFS
GR---QYRRCAVIGNGGILANSSCGAEIDQADFVFRCNLPPMGGEFTRDIGTKTNLVTAN
PSIILERYAKLQ--DRRRSFFTNLAVYDEALLLLPAFSYSKNTDLCFRALYTLQDFQAK-
QKVVFFNPVYLKNLANFWLSKGIQVKRLSTGIMIVSVAVELCEEVWIYGFWPFGKNVEG-
KVVSHHYFDNLLPKP-----DTHSMPLEFHHLLQMHSKGMIKLQMTQCQADPK-------
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#Squaca_GT29_ST8Sia6
----------EEEV---IKTVAQLQQCQWHKQELEAEKFRSELKRCCYAAYDG-------
-----------LVTQRNTPVGTELTYDAEPKKK-IKITHPIFTIFP-------K-DSAFS
SR---QYRRCAVIGNGGILANSSCGAEIDQADFVFRCNLPPVGGDFAQDVGTKTNLVTAN
PSIIAERYAELH--DRRKPFFTNLTVYNEALLLLPAFSYTKNTVLCFRALYTLQDFQAK-
QKVVFFNPVYLKHLTEFWLSKGIQVNRLSTGIMVVSVAIELCEEVWIYGFWPFGRNVEG-
RVMSHHYFDNLLPKP-----DVHSMPSEFHQLLQMHSKGIIKLQTAQCQADPKEMGNI--

#Calmil_GT29_ST8Sia5
TEVKVLSMVKQSEL---FERWRTLQLCKWELNKTEANT--ARLTNCCNAIQNF-------
-----------TVTQVNTALGANLTYDAQPKKQ-ITITEDIFNLLP-------Q-EMPYS
RS---QFKKCAVVGNGGILKKSECGKEINSADFVFSCNLPPLSNEYARDVGHRTQLVTAN
PSIIKKRFQKLD--KWRRPFVELLQVYENTSVVMPAFYNTRNTDVSLRVRYALDDFSAP-
QDLFYFHPRYLENVARFWGRQGVRAKRPSSGLMLVTAAMELCQEVHLYGFWGFPMDPSG-
IHITHHYYDNVKPRP-----GFHSMPNEIFTFLHMHSRGVLQVHTTPCR-----------

#Danrer_GT29_ST8Sia5
TDVKVLTMVKTSEL---FERWRNLQVCKWDQNKEETDNFKMSLSRCCNAPSFL-------
-----------FTTKRNTPSGTKLRYEVDTSGI-LHISPEIFKMFP-------D-DMPFS
KS---QFKKCAVIGNGGIIKNSKCGREIDASDFVFRCNIPPVSDLYSQDVGSKTDLVTIN
PSIITERFQKLE--KWRKPFYEVLQNYENSSVVLPAFYNTRNTDVSFRVKYMLDDFESS-
RGVFFFHPQYLLNVQRFWAVQGVRAKRLSSGLMLVTAAMELCEEVHLYGFWAFPMNPSG-
IFITHHYYDNVKPRP-----GFHAMPYEIFNFMHMHARGIVHVHTGPCR-----------

#Gasacu_GT29_ST8Sia5
MDVKVLTMVKTSDL---FERWRNLQVCRWEQNKEETSNFKMSLTRCCNAPSFL-------
-----------FTTKKNTPAGTKLRYEVDTSGI-LPITTEVFKMFP-------D-DMPYS
KS---QYKKCAVVGNGGIIKSTKCGKEIDSADFVFRCNLPPLDNGYENDVGIKTDLVTAN
PSILVCRFQKLE--KWRRPFYEVLQKYENSSVVLPAFYNTRNTDVSFRVKYMLDDFDSQ-
RGVFFFHPQYLLNVQRFWAVQGVRAKRVSSGLMLVTAALEMCEEVHLYGFWAFPMNPSG-
IYITHHYYDNVKPRP-----GFHAMPHEIFNFIHMHTRGIVNVHTGQCT-----------

#Orylat_GT29_ST8Sia5
MDVKVLTMVKTSDL---FERWRNLQVCKWEQSKEETSNFKLSLSRCCNAPSFL-------
-----------FTTKRNTPAGSKLRYEVDTSGI-LPITNEVFKMFP-------H-DMPYS
KS---QFKKCAVIGNGGIIKNSKCGKEIDSADFVFRCNIPPIKEKYSTDVGSKTDLVTIN
PSIITERFQKLE--KWRRPFYDVLQNYENSSVVLPAFYNTRNTDVSFRVKYMLDDFDSQ-
RSVFFFHPQYLLNVQRFWAVQGVRAKRLSSGLMLVTAALEICEEVHLYGFWAFPMNPSG-
VYITHHYYDNVKPRP-----GFHAMPHEIFNFIHMHTRGIINVHTDQCM-----------

#Takrub_GT29_ST8Sia5
MDVKVLTMVKTSDL---FERWRNLQICRWEQNKEETSNFKMSLSRCCNAPSFL-------
-----------FTTKRNTPAGTKLRYEVDTSGI-LPITAEVFKMFP-------D-DMPYS
KS---QFKKCAVVGNGGIIKNSKCGKEIDSADFVFRCNIPPISEKYSADVGTKTDLVSIN
PSIITERFQKLE--KWRRPFYEVLQNYENSSAVLPAFYNTRNTDVSFRVKYMLDDFDSQ-
RGVFFFHPQYLLNVQRFWAVQGVRAKRLSSGLMLVTAALEMCEEVHLYGFWAFPMNPSG-
IFITHHYYDNVKPRP-----GFHAMPHEIFNFIHMHTRGIVNVHTGQCT-----------

#Tetnig_GT29_ST8Sia5
MDVKVLTMVKTSDL---FERWRNLQVCKWEQNKEETSNFKMSLSRCCNAPSFL-------
-----------FTTRRNTPAGTKLRYEVDTSGI-LPITAEIFKMFP-------D-DMPYA
KS---QFKKCAVVGNGGIIKNSKCGTEIDSADFVFRCNIPPISEKYSADVGTKTDLVSIN
PSIITERFQKLE--KWRRPFYEVLQNYENSSVVLPAFYNTRNTDVSFRVKYMLDDFDSQ-
RGVFFFHPQYLLNVQRFWAVQGVRAKRLSSGLMLVTAALEMCEEVHLYGFWAFPMNPSG-
IFITHHYYDNVKPRP-----GFHAMPHEIFNFIHMHTRGIVNVHTGRCV-----------

#Siltro_GT29_ST8Sia5
TNVKVLSMVKESDL---FDRWKSLQVCKWEMNVTEANAFKSALTRCCNAPSFL-------
-----------FTTQKNTPLGTKLRYEVDTSGI-FPISSEIFNIFP-------KQDMPYY
RS---QFKKCAVVGNGGILKDSKCGKDIDSTDFVFRCNLPPITPKYVEDVGMKTDVVTIN
PSIITERFNKLE--KWRRPFYEVLQGYENASLLLPAFYNTRNTDVSIRVKYVLDDFESQ-
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QAVYYFHPQYLINVSRFWLMQGVHAKRISSGLILVTAALELCEEVHLYGFWGFPMDPSG-
NFITHHYYDNVKPRP-----GFHAMPSEIFNFIHMHSKGILRVHTGTC------------

#Musmus_GT29_ST8Sia5
LEVKVLSMVKQSEL---FERWKSLQICKWAMGASEASLFKSTLSRCCNAPNFL-------
-----------FTTQKNTPVETNLRYEVESSGL-YHIDQEIFKMFP-------K-EMPYY
RS---QFKKCAVVGNGGILKNSGCGKEINSADFVFRCNLPPISGIYTTDVGEKTDVVTVN
PSIIIDRFHKLE--KWRRPFFSVLQRYENASVLLPAFYNVRNTLVSFRVKYMLDDFQSR-
QPVYFFHPQYLSSVSRYWLSLGVRARRISTGLSLVTAALELCEEVHLFGFWAFPMNPSG-
FFITHHYYDNVKPKP-----GFHAMPSEIFTFLRMHSRGILRVHTGTCNCC---------

#Ratnor_GT29_ST8Sia5
LEVKVLSMVKQSEL---FERWKSLQICKWAMDASEASLFKSTLSRCCNAPNFL-------
-----------FTTQKNTPVETNLRYEVESSGL-YHIDQEIFKMFP-------K-EMPYY
RS---QFKKCAVVGNGGILKNSGCGKEINSADFVFRCNLPPISGIYTTDVGEKTDVVTVN
PSIIIDRFHKLE--KWRRPFFSVLQRYENASVLLPAFYNVRNTLVSFRVKYMLDDFQSG-
EPVYFFHPHYLSSVSRYWLSLGVRARRISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
FFITHHYYDNVKPKP-----GFHAMPSEIFTFLRMHSRGILRVHTGTCNCC---------

#Anocar_GT29_ST8Sia5
TDVKVLSMVKQTEL---FERWKNLQMCKWEMNITQANIFKATLLRCCNAPAFL-------
-----------FTTQKNTPLGTKLKYEVDTSGI-FHVNQETFRMFP-------Q-EMPYS
RS---QFKKCAVVGNGGILKNSRCGREIDSADFVFRCNLPPISEKYIADVGVKTDIVTVN
PSIITERFHKLE--KWRKPFFNVLQTYENASVLLPAFYNTRNTDVSIRVRYALDDFESQ-
QSVYFFHPQYLINLSRYWLNQGVRAKRISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
IYITHHYYDNVKPRP-----GFHAMPSEIFNFLHMHSKGILRVHTDACNCC---------

#Galgal_GT29_ST8Sia5
LEVKVLSMVKQTEL---FDRWKSLQMCKWEMNVTEANILKSTLSRCCNAPAFL-------
-----------FTTQKNTPLGTKLKYEVDTSGI-FHINQEIFKMFP-------K-DMPYH
RS---QFKKCAVVGNGGILKNSRCGREIDSADFVFRCNLPPISEKYLTDVGVKTDVVTVN
PSIITERFHKLE--KWRKPFYDVLQVYENASVLLPAFYNTRNTDVSIRVKYVLDDFESQ-
QAVYYFHPQYLINVSRYWLGQGVRAKRISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
IFITHHYYDNVKPRP-----GFHAMPSEIFNFLHMHSKGILRVHTGTCGCC---------

#Bostau_GT29_ST8Sia5
LEVKVLSMVKQSEL---FDRWKSLQMCKWAMNISEANQFKSTLYRCCNAPPFL-------
-----------FTTQKNTPLGTKLKYEVDTSGI-YHINQEIFRMFP-------K-DMPYY
RS---QFKKCAVVGNGGILKNSRCGREINSADFVFRCNLPPISEKYTMDVGVKTDVVTVN
PSIITERFHKLE--KWRRPFYRVLQLYENASVLLPAFYNTRNTDVSIRVKYVLDDFESP-
QAVYYFHPQYLVNVSRYWLSLGVRAKRISTGLILATAALELCEEVHLFGFWAFPMNPSG-
LYITHHYYDNVKPRP-----GFHAMPSEIFNFLHLHSRGILRVHTGTCSCC---------

#Homsap_GT29_ST8Sia5
LEVKVLSMVKQSEL---FDRWKSLQMCKWAMNISEANQFKSTLSRCCNAPAFL-------
-----------FTTQKNTPLGTKLKYEVDTSGI-YHINQEIFRMFP-------K-DMPYY
RS---QFKKCAVVGNGGILKNSRCGREINSADFVFRCNLPPISEKYTMDVGVKTDVVTVN
PSIITERFHKLE--KWRRPFYRVLQVYENASVLLPAFYNTRNTDVSIRVKYVLDDFESP-
QAVYYFHPQYLVNVSRYWLSLGVRAKRISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
LYITHHYYDNVKPRP-----GGHAMPSEIFNFLHLHSRGILRVHTGTCSCC---------

#Pantro_GT29_ST8Sia5
LEVKVLSMVKQSEL---FDRWKSLQMCKWAMNISEANQFKSTLSRCCNAPAFL-------
-----------FTTQKNTPLGTKLKYEVDTSGI-YHINQEIFRMFP-------K-DMPYY
RS---QFKKCAVVGNGGILKNSRCGREINSADFVFRCNLPPISEKYTMDVGVKTDVVTVN
PSIITERFHKLE--KWRRPFYRVLQVYENASVLLPAFYNTRNTDVSIRVKYVLDDFESP-
QAVYYFHPQYLVNVSRYWLSLGVRAKRISTGLILVTAALELCEEVHLFGFWAFPMNPSG-
LYITHHYYDNVKPRP-----GFHAMPSEIFNFLHLHSRGILRVHTGTCSCC---------

#Macmul_GT29_ST8Sia5
LEVKVLSMVKQSEL---FDRWKSLQMCKWAMNISEANQFKSTLSRCCNAPAFL-------
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----------FTTQKNTPLGTKLKYEVDTSGI-YHINQEIFRMFP-------K-DMPYY
RS---QFKKCAVVGNGGILKNSRCGREINSADFVFRCNLPPISEKYTMDVGVKTDVVTVN
PSIITERFHKLE--KWRRPFYRVLQVYENASVLLPAFYNTRNTDVSIRVKYVLDDFESP-
QAVYYFHPQYLVNVSRYWLSLGVRAKRISTGLILATAALELCEEVHLFGFWAFPMNPSG-
LYITHHYYDNVKPRP-----GFHAMPSEIFNFLHLHSRGILRVHTGTCSCC---------

#Ambmex_GT29_ST8Sia7
ATLSAHKKIGEKSI---MRNAAELQRCPWQENREKKEFYRSEINQCCNSSHGL-------
----------IVTQENTRVGENIVYETQKSVK-INVTTEIFNMFP-------K-ESPFS
GK---AYKTCAVVGNGAILVDSCCGQQIDQAEFVFRFNLPPLN--YTKDSGKKVDLVTAN
PSIMINRFQSLN--HRRKAFVDMLRAYRGALILMPTFSHTFGTQLAFKVQYTLDDFGLG-
SRMLSFHPVYLENLAKYWRSKGLYVKRLSSGIMLVSAAMELCDSITLYGFWPFYSNLEG-
RTIGYHYYDKMAPNI-----QVHAMPKEFLIYSQMHAQGALKLQVGQCS----------

#Ambmex_GT29_ST8Sia7-B
ATLSANKTINERSI---MRNAVELQRCPWLENRKKKEFYRSEINQCCKTSHEL-------
----------ILTQENTQVGEDIVYETQKSKK-INVTTKIFNMFP-------K-ESPFS
GK---AYKTCAVVGNGAILVDSCCGQQIDQAEFVFRFNLPPLN--YTRDAGRRVDLVTAN
PSIMINRFQSLN--QRRKAFGNTLREYRGALILMAAFSHTRSTQVAFKVQYTLDDFGLG-
SRMLSFHPVYLENLAKYWRSKGLYVKRLSSGIMLVSAAMELCDSITLYGFWPFYSNLEG-
RTIGYHYYDKMAPNI-----QVHAMPKEFLIYSQMHAQGALKLQVGQCS----------

#Latcha_GT29_ST8Sia7
TS--------------------------------QELPKETDLNKCSNLTQRL-------
----------VLTRENAPIGHEIEYEVAE-QR-VRVEEPLFKLLPRFPPPFYQ-ESPFK
KA---PYKRCAVVGNAGILLNSGCGRRIDQADFVFRCNLPPLN--YSKDVGSKTDLVTAN
PSIIIQKYHGLK--ESRRLFVERMKVYKDALILMAAFSQSFATEISLAVAYALEDFGSK-
QKAIFFHPAYLRQLGSLWRSWGVRARRLSSGLMLVSAALELCDSVALYGFWPFSTGLDG-
EAVLHHYYDNVPPEP-----GVHAMSSEFVHYLQMHSKGVLQLHVGKC-----------

#Rancat_GT29_ST8Sia7
LNSVLRIFKQQAF----FKVVKTLQGCPWKEDQTERNLLQANLGKCCNASYSM-------
----------IMTQENTVIGQTITFDAETKIK-QNITKSLYSLFP-------K-KSPFQ
K----PIRTCAVVGNGGILTNSSCGAQIDGADFVFRLNFPPLN--WTDDIGAKTDLVTSN
PSILMNKFSSLT--EKRKPFIMMVQEYSSPLILLPAFSYSANTEVSLRVLYTIEDFELN-
SKVVFFNPEYLKNLSAYWKSMGLKFGRLSSGLMVVSIAMEVCDKVTLFGFWPFSKDLNG-
VPILHHYYDNVPPKP-----GIHAMPDEFYKYLQMHIQGSLRLNLEHC-----------

#Pelnig_GT29_ST8Sia7
LNSVMKIFRRKTF----FEVVKALQGCPWREDQTERNLLKAKFRKCCNASYSM-------
----------MVTQENTPIGHIIHYDGDK-GR-KNVTESLYSLFP-------E-KSPFQ
K----PIRSCAVVGNGGILNSSFCGAEIDRANFVFRLNLPPMN--WTNDVGTKTDVVTAN
PSILIDKFGSLM--ERRKPFITRMKEYGSTLIILPAFSYLLNTAVSLRALYTISDFNLN-
SRAVFFNPDYLRNLTAYWKDMGIKSLRLSSGLMLVSAAIEMCDKVTLYGFWPFSQDLDG-
VPIPHHYYDNALPTP-----KIHSMPDEFYQFLQMHIQGSLRLNLGQC-----------

#Strcamaus_GT29_ST8Sia7
TESFL-KRVDEVWS---LSHLKLMQSCRWNFNASALAQYRAELGHCCNASAWL-------
----------ALTQVNTPLGSNIVYDGYRSKS-LKVSSGLLEILP-------E-ESPFQ
EP---FYKTCAVVGNGGILRNSSCGSEIDEHQFVIRFNLPSMD--FPEDVGRKSSIVTVN
PSILQKRFHGLN--GRRLPFVKAAAIYGETWFLIPAFSYPGQNEASYRALYALQDSGSR-
SPIFFFHPQYLSALTRYWHEHGFHPTRLSSGFMLVNAALELCQHITLYGFWPFSLHPDG-
HPLPHHYYDNQLPNP-----RMHLMPQEFACYVNMHFQGVLQLHVGKC-----------

#Aptausman_GT29_ST8Sia7
TESFL-KRVNEVWS---LRHLKLMQSCRWNFNASALAQYRAELGHCCNASAWL-------
----------VLTRVNTPLGTKIVYDGDHSKS-LKVSSGLLEILP-------E-ESPFQ
DP---FYKTCAVVGNGGILLNSSCGSEIDGHQFVIRFNLPSTD--FPEDVGRKSSIVTVN
PSILQERFHGLT--GRRLPFVKAAAFYGETWFLIPAFSYPGQNEASYRALYALQDSGSR-
SPVFFFHPQYLSALSRYWHERGFHTPRLSSGFMLVNAALELCQHITLYGFWPFSLHPDG-
HPLPHHYYDNQLPKP-----RVHLMPQEFAYYVNMHFQGVLHLHLGKC-----------
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#Cuccancan_GT29_ST8Sia7
----------------------------------------QLGHYCNASAWL-------
-----------AVTQENTPLGSNIVFDGYRSKS-LKVSSGLLEILP-------E-KSPFQ
DL---LYKTCAVVGNGGILRNSSCGSQIDGYQFVIRFNLPSAD--FPEDVGRKSSIVTVN
PSILHKRFHGLN--GRRLPFVEAAASYGKTWFFIPAFSYPGNSEASYRAFYALQDSESQ-
SHVFFFHPQYLSALSKYWHDRGFHTYRLSSGFMLVNAALELCEHITLYGFWPFSLHPDG-
HALPHHYYDNVLPNQ-----RIHIMPREFAYYVDMHFQGVLRLHVGRC------------

#Colliv_GT29_ST8Sia7
TQP-----------------------------------QKAELGRCCNASAWL-------
-----------AVTQDNTPLGSEIVYDAYPSKR-LKVSSGLLEILP-------E-KSPFQ
ES---PYKTCAVVGNGGILRNSSCGSKIDGHEFVIRFNLPSVD--FPEDVGKKSSIVTVN
PSILHKRFHGLN--GRRLPFVKAAASYGKTWFLIPAFSYPSNSEASYRALYALQDSASQ-
SHIFFFHPQYLSSLSKYWHDHGFHTPRLSSGFMLVNAALELCQHITLYGFWPFSLHPDG-
HSLPHHYYDNVLPNS-----RIHIMPKEFTYYVDMHFHGVLQLHLGR-------------

#Apavit_GT29_ST8Sia7
TQP-----------------------------------HKAELGHCCNASAWL-------
-----------AVTQENAPLGSEIVYDGYPSKR-LKVSSGLLEILP-------E-KSPFQ
NP---LYKTCAVVGNGGILRNSSCGAKIDEHQFVIRFNLPSMD--FPEDVGRKSSIVTVN
PSILQKRFHGLN--GRRLPFVKAAAPYGKTWFLIPSFSFPDDTEASYRALYALQDSASE-
SHVFFFHPHYLSALSKYWHDLGFHTYRLSSGFMLVNAALELCQHITLYGFWPFSFHPDG-
HSLPHHYYDNVLPKQ-----NIHIMPKEFSYYVDMHFHGVLQLHLGRC------------

#Chrpicbel_GT29_ST8Sia7
SQRVLPVRLHEAWIWRR---LKLMQSCPWAYNARALGRYREQLGHCCNASADL-------
-----------VLTRDNTPLGSRIVCDGQPAKK-LLVQEALLEILP-------Q-G----
-A---PYDSCAVVGNGGILHNSGCGPEIDRAQFVIRFNLPPMG--FAEDVGTKSSVITVN
PSILVLRFGALS--RWRRPFAEAMGTYGAPLLLIPAFSFISFAAVSSQALYTLEDFGSP-
ARAVFMNPEYLAGLDGHWHRRGLRAKRLSSGFMLVNAALELCQHLTLYGFWPFPTDPEG-
RPLPYHYYDKQTPKP-----GVHAMPDEFTRYLGMHLQGALRLHLGRCQEGLAGGHAQQG

#Malterter_GT29_ST8Sia7
SPI--P----EALVMGAEQCRGLM--QNWSA---GTLPAREQLGSSCNASANL-------
-----------VLTQNNTQLGSQIVYDAQRDKK-HPVKEELLEMLP-------Q-GSPFQ
GA---PYECCAVVGNGGILRNSSCGSEIDRAQFVIRFNLPPMD--FADDVGTKSSVVTMN
PSILHARFRGLS--RWRRPFAEAVGIYGAPLLLIPAFSFVGQSTVSFQALYTLEDFGSP-
ARAVFMNPEYLARLDGHWRPRGLRAKRLSSGFMLVSAALELCQHLTLYGFWPFPTDPEG-
RLLPHHYYDNQPPKP-----GIHAMPDEFTRYLGMHMQGALRLHLGRCQ-----------

#Promuc_GT29_ST8Sia7
-------------RW----QLMLIQECPWKPNATAVMQHRAELGQCCNASHRL-------
-----------VVTKENAPLGSTIHFDGVKVKI-ITVDSKLTNMLL-------E-RFPLA
DA---QYSKCALIGNGGILQDSRCGQEIDQADFIIRFNLPPLN--RTEDVGTKTHLVTIN
PSVLTNRFKNLV--GPPMAFIDAVRAYPNALFLIPALSFHDHIELGYRALHILKDIGLP-
HQAFFLNPHYLGALDMYWKQKGMTEIRLSTGFMFTSFALEFCDHITLYGFWPFLFDLTG-
KPISHHYYDNVLPNA-----FVHSMSEEFSRYIDMYAQGVLRIQLGKCQ-----------

#Deiacu_GT29_ST8Sia7
VI-----ILLPAPLN----GVLLKKSSKWTPTSANLFCSRAL--DCCVCGFHLGFSLSCF
SFEDSKTWCVLRCATGERTAGIHPPFDGVKVKI-ITVDSKLTNMLL-------E-RFPLA
DA---QYSKCALIGNGGILQDSRCGQEIDQADFIIRFNLPPLN--RTEDVGTKTHLVTIN
PSILTNRFKSLV--RSPVAFIDAVRAYPNALFLIPALSFHDHIELGYRALHILKDIGLP-
HQAFFLNPHYLGALDTYWKQKGMTEIRLSTGFMFTSFALEFCDHITLYGFWPFLFDLTG-
KPINHHYYDNVLPHP-----FVHSMSEEFSRYIDMYAQGVLRIQLGKC------------

#Pytmol_GT29_ST8Sia7
VI-----ILLPAPLN----GVLLKKSSKWTPTSANLFCSRAL--DCCVCGFHLGFSLSCF
SFEDSKTWCVLRCATGERTAGIHPPFDGVKVKI-ITVDSKLTNMLL-------E-RSPLA
GF---QYNKCALIGNGGILRHSSCGQEIDQADLIIRFNLPPMN--YTEDVGTKTSLVTIN
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PSILNNKFQSLQ--GPQKPFLDALQAYRDALFLIPSLSFSSHHVLGCRAVSIMKDSGLT-
HRAFFLHPHYLGAIRKYWEQKGLKEIRLSTGFLFISIALEFCEHITLYGFWPFSYDLTG-
EPLSHHYYDNILPNA-----GFHTMSEEFLHYLNMYAQGVLRIQLGKC------------

#Anocar_GT29_ST8Sia7-A
----------------------------------------TQLQQCCNASFRF-------
-----------VTTKENIRLGSYIIFDGNPTRK-LRVDTKLLDLLP-------E-KSPFM
DT---SYRKCAVVGNGGILLNSSCGQEIDRADLVIRFNLPPMN--FSEDIGTKTSLVTIN
PSILQNRFKLLQ--ERRKPFVEALHSYSDATFLLPVLSFVGHNILGYRVLYTLEDFGVE-
QQAFFLNPQYLSNLANFWKKRGLKTNRLSSGFMLVSMALEFCQHITLYGFWPFSYDLNN-
QSIPHHYYDNMMPTP-----GVHAMPTEFSYYLSMYAEGVLRLRVGKCQ-----------

#Gekjap_GT29_ST8Sia7
LQ-----KLDEEILA----HLLLTQGCPWQASARAMAQYRTELGRCCNASFWL-------
-----------AITKENTPLGSDILLDGNKGKK-LPVGAELMDLLP-------E-RSPIP
GI---LYDQCAVVGNGGILQNSSCGQEIDQADLIIRFNLPPMN--YSEDVGTKTSLVTIN
PSILQTKFNKLE--AHRKPFADALRPYRSALVFIPAFSFVGHSELAYRALYTMEDFGTG-
QRAYFWNPHYLDTLGIYWKARGFYPHRLSSGFMLVNMALEFCKRITLYGFWPFSHDPAG-
RPIPHHYYDNTWPKP-----GVHAMSQEFSHYLHMYAQGVLQLRLGSCQ-----------

#Amblat_GT29_ST8Sia6
LSATL-RKRYSEDFY--IQSFRKVQNCTWTRRPEEYYKFRSKLASCCNAVNNF-------
-----------IVSQNNTSLGSNMSYEVDNKKN-IVISETIFKMLP-------Q-SQPFV
ER---SYKHCAVVGNGGILQNSSCGAEIDESDFVFRCNLPPVNGDFHKDVGNKTNVVTVN
PSIIALRYGKLS--QKKTVFLQNITKYGDAYFLLPAFSYRSNTAVCFKVFNALKEAKAN-
QKAIFFHPKYLKNLGQFWRANGVRAYRLSTGLMIASAAIELCDHVKLYGFWPFSKNTEG-
NLISHHYYDNQLPKP-----GFHAMPKEFIQYLQLHNKGILKLQVGECENKTKI------

#Ambmex_GT29_ST8Sia6
LSATL-RKRYSEDFY--IQSFRKVQNCTWTRRPEEYYKFRSKLASCCNAVNNF-------
-----------IVSQNNTSLGSNMSYEVDTKKN-IVISETIFKMLP-------Q-SQPFV
ER---SYKHCAVVGNGGILQNSSCGAEIDESDFVFRCNLPPVNGDFHKDVGNKTNVVTVN
PSIIALRYGKLS--QKKTVFLQNITKYGDAYFLLPAFSYRSNTAVCFKVFNALKEAKAN-
QKAIFFHPKYLKNLGQFWRANGVRAYRLSTGLMIASAAIELCDHVKLYGFWPFSKNTEG-
NLISHHYYDNQLPKP-----GFHAMPKEFIQYLQLHNKGILKLQVGECENKTKI------

#Siltro_GT29_ST8Sia6
LTVSL-KKRYSEDYY--IQTVNDLQNCTWHKRPEERSKFRLDLSSCCNGVKNF-------
-----------IVSQNNTSVGINITYEVESKKR-ILITEEIYRMLP-------K-SQPFD
GT---PFKQCAVVGNGGILANSGCGVEIDQSDFVFRCNLPPTSGNVSVDVGNKTNLVTVN
PSIISQKYRKLN--KVKNVFLKYVSNYGNSLLLLPAFSYSSNTAISFEVHRVLEKNQAK-
QKAVFFHPNYLKNLAKFWKGKGVRAYRLSTGLMITSAAMELCEEVILYGFWPFSKDLEG-
KPISHHYYDNMLPKP-----GFHAMPKEFYQVLQLHHKGVLRLQIGKCEKR---------

#Xenlae_GT29_ST8Sia6
LTVSL-KKRYSEDYY--IQTVNELQNCTWQKRPQEYSKFRLYLSTCCNGLKNF-------
-----------IVSQNNTSLGSNITYEVESKKK-ILIAEEIYRMFP-------K-SQPFV
GA---PFKQCAVVGNGGILANSGCGAEIDQSDFVFRCNLPPTWGNISVDVGNKTNLVTVN
PSIISRKYRKLN--KVKNVFLKNVSNYGYSFLLLPAFSYSSNTAISFEVHRILEKNQAK-
QKAIFFHPYYLKNLAQFWKGRGVRAYRLSTGLMITSAAIELCEEVKLYGFWPFSKNQEG-
KPISHHYYDNILPKP-----GFHAMPKEFYQVLQLHHKGVLRLQIGKCEKR---------

#Litcat_GT29_ST8Sia6
LSVSL-RKRYSEDYY--IQAVNDVQNCTWKKKPQEYSRFRLYLSSCCNAVNNF-------
-----------IVSQNNTSLGSNITYEVESKKN-ILIAEDIYKMLP-------K-SQPFD
GI---PFKQCAVVGNGGILKNSSCGAEIDQSDFVFRCNLPPIWGNVSIDVGNKTDLVTVN
PSIIALKYGKLN--DMKTAFLKNLTNYGYSFLLLPAFSYSSNTAISFEVHHLLRKYQAK-
QKAIFFHPNYLKSLAQFWKGRGVRAYRLSTGFMITSAAIELCQDVTLYGFWPFSKNLDG-
KPISHHYYDNQLPKP-----GFHAMPKEFYQVLQLHHKGVLKLQLGECEKR---------

#Rhimar_GT29_ST8Sia6
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LTVSL-RKRYSEDCY--IQAVNEVQNCTWQKKPQEYSRFRFYLSSCCNAVNNF-------
-----------IVSQNNTSLGSNITYEVESKKN-ILIAEDIYKMLP-------K-SQPFE
GI---PFKQCAVVGNGGILTNSSCGAEIDRSDFVFRCNLPPIWGNAAVDVGNKTDLVTVN
PSIIALKYGKLN--EMKTAFLRNLTSYGGSFLLLPAFSYSSNTAISFEVHNLLKKYQAK-
QRAIFFHPNYLKSLAQFWRGRGVRAYRLSTGFMITSAAIELCEDVKLYGFWPFSKNPNG-
KPISHHYYDNQLPKP-----GFHAMPKEFYQVLQLHYKGVLKLQIGECQKR---------

#Latcha_GT29_ST8Sia6
MSATTPRKRYSDDYY--IQTVNELQKCSWVIRPEEHEKFRSELSVCCNAVRNF-------
-----------IVSQNNTPLGTNMSYEVENGRT-FLITQRIFKMFP-------Q-SQPFA
GY---PYNQCAVVGNGGILKNSACGTEIDQADFVFRCNLPPTLGNISIDVGSKTSLVTLN
PSIITHRFGKLN--EKRKPFVETVSHYGEAFLLLPAFSFRSNTALSFKVYHTLEAFRGK-
QKTIFFHPKYLKSLALFWRSKGIKVYRLSSGFMIANAAIELCKEVRLYGFWPFSKNNEG-
KNISHHYYDNQLPKP-----GIHSMPKEFYHFLKLHNKGIIKLQFGRCDIT---------

#Latmen_GT29_ST8Sia6
MSATTPRKRYSDDYY--IQTVNELQKCSWVIRPEEHEKFRSELSVCCNAVRNF-------
-----------IVSQNNTPLGTNMSYEVENGRT-FLITQRIFKMFP-------Q-SQPFA
GY---PYNQCAVVGNGGILKNSACGTEIDQADFVFRCNLPPTLGNISIDVGSKTSLVTLN
PSIITHRFGKLN--EKRKPFVETVSHYGEAFLLLPAFSFRSNTALSFKVYHTLEAFRGK-
QKTIFFHPKYLKSLALFWRSKGIKVYRLSSGFMIANAARRLCKEVRLYGFWPFSKNNEG-
KNISHHYYDNQLPKP-----GIHSMPKEFYHFLKLHNKGIIKLQFGRCDIT---------

#Canlupfam_GT29_ST8Sia6
QRLYSKAKNYLESDY--LQIIRNIQNCPWKRQEEEYENFRAKLASCCDAAQNF-------
-----------IVSQNNTPAGTNMSYEVESKNE-ILIRENIFNMFP-------V-SQPFV
EY---PYNQCAVVGNGGILNKSLCGAEIDKSDFVFRCNLPPITGNISKDVGSKTNVVTVN
PSIIRLKYGNLK--KKKEIFLEDIATYGDAFLLLPAFSFRANTIASFKVYSTLKESNAR-
QKVIFFHPKYLRNLALFWRTEGVTEFRLSSGLMITSVAVELCEHVKLYGFWPFSRTVKD-
TPVSHHYYDNNLPKR-----GFHEMPKEYRQILQLHLKGILKLQFSKCEIA---------

#Musmus_GT29_ST8Sia6
NSLSNKTRRYSEDDY--LQTITNIQRCPWNRQAEEYDNFRAKLASCCDAIQDF-------
-----------VVSQNNTPVGTNMSYEVESKKH-IPIRENIFHMFP-------V-SQPFV
DY---PYNQCAVVGNGGILNKSLCGAEIDKSDFVFRCNLPPITGSASKDVGSKTNLVTVN
PSIITLKYQNLK--EKKAQFLEDISTYGDAFLLLPAFSYRANTGISFKVYQTLKESKMR-
QKVLFFHPRYLRHLALFWRTKGVTAYRLSTGLMIASVAVELCENVKLYGFWPFSKTIED-
TPLSHHYYDNMLPKH-----GFHQMPKEYSQMLQLHMRGILKLQFSKCETA---------

#Ratnor_GT29_ST8Sia6
DSLANKTRRYSEDDY--LQIVTNIQRCPWKRQAEEYENFRAKLASCCDAIQDF-------
-----------VVSQNNTPVGSNMTYEVESKKQ-IPIRENIFHMFP-------V-SQPFV
DY---PYNQCAVVGNGGILNKSLCGAEIDKSDFVFRCNLPPITGSASQDVGSKTNLVTVN
PSIITLKYKNLK--EKKARFLEDISAYGDAFLLLPAFSYRVNTGISFKVYQTLKESKVR-
QKVLFFHPRYLRHLALFWRTKGVTAYRLSTGLMIASIAVELCENVTLYGFWPFSKTVEE-
IPLSHHYYDNKLPKH-----GFHQMPKEYSQMLQLHMKGILKLQFSKCEAA---------

#Macmul_GT29_ST8Sia6
ESFSNNTKGYSENDY--LQIITDIQSCPWKRQAEEYANFRAKLASCCDAVQNF-------
-----------VVSQNNTPVGTNMSYEVESKKK-IPIKKNIFHMFP-------V-SQPFV
EY---PYNQCAVVGNGGILNKSLCGAEIDKSDFVFRCNLPPTTGDVSKDVGSKTNLVTIN
PSIITLKYGNLK--EKRALFLEDIATYGDAFFLLPAFSFRANTGTSFKVYYTLEESKAR-
QKVLFFHPKYLKHLALFWRTKGVTAYRLSTGLMITSVAVELCENVKLYGFWPFSKTVED-
IPVSHHYYDNKLPKR-----GFHQMPKEYSQILQLHMKGILKLQFSKCEVA---------

#Ponpyg_GT29_ST8Sia6
ESFSNKTKGYSENDY--LQIITDIQSCPWKRQAEEYANFRAKLASCCDAVQNF-------
-----------VVSQNNTPVGTNMSYEVESKKE-IPIKKNIFHMFP-------V-SQPFV
EY---PYNQCAVVGNGGILNKSLCGTEIDKSDFVFRCNLPPTTGDVSKDVGSKTNLVTIN
PSIITLKYGNLK--EKKALFLEDIATYGDAFFLLPAFSFRANTGTSFKVYYTLEESKAR-
QKVLFFHPKYLKDLALFWRTKGVTAYRLSTGLMITSVAVELCKNVKLYGFWPFSKTVED-
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TPVSHHYYDNKLPKR-----GFHQMPKEYSQILQLHMKGILKLQFSKCEVA---------

#Homsap_GT29_ST8Sia6
ESFSNKTKRYSENDY--LQIITDIQSCPWKRQAEEYANFRAKLASCCDAVQNF-------
-----------VVSQNNTPVGTNMSYEVESKKE-IPIKKNIFHMFP-------V-SQPFV
DY---PYNQCAVVGNGGILNKSLCGTEIDKSDFVFRCNLPPTTGDVSKDVGSKTNLVTIN
PSIITLKYGNLK--EKKALFLEDIATYGDAFFLLPAFSFRANTGTSFKVYYTLEESKAR-
QKVLFFHPKYLKDLALFWRTKGVTAYRLSTGLMITSVAVELCKNVKLYGFWPFSKTVED-
IPVSHHYYDNKLPKH-----GFHQMPKEYSQILQLHMKGILKLQFSKCEVA---------

#Pantro_GT29_ST8Sia6
ESFSNKTKGYSENDY--LQIITDIQSCPWKRQAEEYANFRAKLASCCDAVQNF-------
-----------VVSQNNTPVGTNMSYEVESKKE-IPIKKNIFHMFP-------V-SQPFV
DY---PYNQCAVVGNGGILNKSLCGTEIDKSDFVFRCNLPPTTGDVSKDVGSKTNLVTIN
PSIITLKYGNLK--EKKALFLEDIATYGEAFFLLPAFSFRANTGTSFKVYYTLEESKAR-
QKVLFFHPKYLKDLALFWRTKGVTAYRLSTGLMITSVAVELCKNVKLYGFWPFSKTVED-
IPVSHHYYDNKLPKH-----GFHQMPKEYSQILQLHMKGILKLQFSKCEVA---------

#Bostau_GT29_ST8Sia6
ETLSNRTKGYSEDEY--LQIITNIQSCPWKRQVEEYENFRAKLASCCDAVQNF-------
-----------IVSQNNTPIGTNMTYEVESKSK-IQIKENIFDMLP-------V-VQPFV
GY---SFNQCAVVGNGGILNQSLCGAEIDKADFVFRCNLPPTTGNVTNDVGTKTNLVTLN
PSIIKLRYGNLK--EKKAIFLEDVAAYGDAFVLLPAFSFRANTAASFKVYYTLKESKAR-
QKVLFFHPKYLKNLALFWRTKGVTEYRLSSGLMITSVAVELCENVKLYGFWPFSRTGEN-
MPVSHHYYDNKLPKR-----GFHEMPKEYSQILQLHVKGILKLQFSKCETA---------

#Susscr_GT29_ST8Sia6
KALSNKTRKYSEDDY--LQIITNIQSCPWKRQAEAYENFRAKLASCCDAVQNF-------
-----------IVSQNNTPVGTNMSYEVESKSE-IQIRESIFDMLP-------V-FQPFI
GY---PYNQCAVVGNGGILNQSLCGAEIDKSDFVFRCNLPPTTGNISNDVGSKTNLVTLN
PSIIRLRYGNLK--EKKAVFLEDIATYGDAFVLLPAFSFRANTAASFKVYYALKESNSR-
QKVLFFHPKYLKHLAVFWRTKGVTEYRLSSGLMIASVAVELCENVKLYGFWPFSKTGEN-
TPVSHHYYDNKLPKR-----GFHEMPKEYRQILQLHVKGILQLQFSKCDTS---------

#Gekjap_GT29_ST8Sia6
WAASVKRKRYAEDYY--LQVVGRLQNCTWNKRPQEYAKFKSELASCCDAAHNF-------
-----------ITSQNNTPLGSNMSYEVDNKKT-IHITEEIFRMLP-------E-SQPL-
EQ---PFKNCAVVGNGGILKNSNCGAEIDQSDFVFRCNLPPTMGSIRQDVGSKTNLVTIN
PSIISQKYNKLN--EKKATFLENIASYGDTFLLLPAFSFRSNTAASFKVHHTLKEFSAK-
QKAIFFYPRYLRNLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKNVAG-
TPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGRGILKLQFGKCLPD---------

#Anocar_GT29_ST8Sia6
WSSSIKKKRYSEDYY--LQIVGKLQNCTWKKRPQEYAKFRSELTSCCDAIHNF-------
-----------ISSQNNTPLGSNMSYEVDNKKT-IHITEEIFKMLP-------E-SQPL-
DY---PFKQCAVVGNGGILKNSNCGAEIDKSDFVFRCNLPPTEGSVSQDVGNKTNLVTVN
PSIIAQKYNKLN--EKKATFLENIASYGDAFLLLPAFSFRSNTATSFKVHHTLREFSAK-
QKAIFFYPRYLKNLAQFWRTKGVKAYRLSSGFMITSAAVELCENVKLYGFWPFSKSIAG-
NPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGRGILKLQLGKCHTE---------

#Tingut_GT29_ST8Sia6
LSSLTKKKRYSEDDF--LHLVTKLQNCTWVKRPEECTKFRSELASCCDAVHNF-------
-----------VASQNNTPLGSNMSYEVESKKT-ILITENIFRMLP-------V-SSPFS
AY---PFKNCAVVGNGGILKNSSCGAEIDRADFVFRCNLPPTTGSMSKDVGNKTNLVTVN
PSIIAQKYNKLN--KKKTEFLQNIAVYGDAFLLLPAFSYRSNTATSFKVYQTLKEFKAM-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAAIELCENVKIYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESE---------

#Chemyd_GT29_ST8Sia6
WSSSIKKKRYSEDYY--LQIVTKIQNCTWKRRPEEYTKFRLELASCCDAVHNF-------
-----------IASQNNTALGSNMSYEVDNKKT-LLITEDIFRMLP-------E-SPPLL
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DY---PFKHCAVVGNGGILKNSSCGAEIDKSDFVFRCNLPPTTGSVSKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKVTFLENIASYGNAFLLLPAFSFKSNTAASFKVYHTLQEFRAK-
QRAIFFHPRYLKSLAQFWRTKGVKAYRLSSGFMIASAAIELCENVKLYGFWPFSKTTEE-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGIVKLQFGKCDSDXKGTSDSSK

#Chrpicbel_GT29_ST8Sia6
WSSSIKKKRYSEDYY--LQIVTKIQNCTWKRRPEEYTKFRLELASCCDAVHNF-------
-----------IASQNNTLLGSNMSYEVDNKKT-ILITEDIFRMLP-------E-SPPFL
GY---PFKHCAVVGNGGVLKNSSCGAEIDNSDFVFRCNLPPTTGSVSKDVGNKTSLVTVN
PSIIAQKYNKLN--EKKVTFLENIASYGNAFLLLPAFSFKSNTAASFKVYHTLQEFRAK-
QRAIFFHPRYLKNLAQFWRTKGVKAYRLSSGFMIASAAIELCENVKLYGFWPFSKTTEE-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCDSD---------

#Galgal_GT29_ST8Sia6
LSSSFKKKRYPEDYY--LHIVKKLQNCTWVRRPEESAKFRSELASCCNAVHNF-------
-----------IASQNNTPLGSNMSYEVDSKKT-ILITEDIFRMLP-------V-SSPLS
VY---PFKNCAVVGNGGILKNSSCGAEIDRSDFVFRCNLPPTMGSISKDVGNKTKLVTVN
PSIIAQKYNKLN--EKKTEFVENVAVYGDAFLLLPAFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLKNLAQFWRTKGVKAYRLSSGFMITSAAVELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGIKKLQFGKCESD---------

#Chavoc_GT29_ST8Sia6
LSSSIKKKRYSEDYY--LHIVTKLQNCTWTRRPEESTKFRSELASCCDAVHNF-------
-----------IASQNNTPLGSNMSYEVDSKKT-ILITEDIFKMLP-------V-SSPLS
AY---PFKTCAVVGNGGILKNSSCGAEVDRSDFVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENIAVYGDAFLLLPAFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLRSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD---------

#Egrgar_GT29_ST8Sia6
LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRRPEESMKFRSELASCCDAVHNF-------
-----------IASQNNTPLGSNMSYEVDSKKT-ILITEDIFKMLP-------V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDRSDFVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLEDVAVYGDAFLLLPAFSFRSNTATSFKVYHTLKEFRAS-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD---------

#Calpug_GT29_ST8Sia6
LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRRPEESTKFRSELASCCDAVHNF-------
-----------IASQNNTPLGSNMSYEVDSKKT-VLITEDIFKMLP-------V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDRSDFVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLDNIAVYGDAFLLLPAFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHSKGILKVQFGKCESD---------

#Psehum_GT29_ST8Sia6
LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRKPEESTKFRSELASCCDAVHNF-------
-----------IASQNNSPLGSNMSYEVDSKKT-ILITEDIFKMLP-------V-SSPLS
VY---PFKNCAVVGNGGILKNSSCGAEIDSSDFVFRCNLPPTTGNISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENIAAYGDAFLLLPAFSFRSNTATSFKVYHTLKEFKAT-
QRAIFFHPSYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSIEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGVLKLQFGKCESD---------

#Parmaj_GT29_ST8Sia6
LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRKPEESTKFRSELASCCDAVHNF-------
-----------IASQNNSPLGSNMSYEVDSKKT-ILITEDIFKMLP-------V-SSPLS
VY---PFKNCAVVGNGGILKNSSCGAEIDSSDFVFRCNLPPTTGNISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENIAAYGDAFLLLPAFSFRSNTATSFKVYHTLKEFKAT-
QRAIFFHPAYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSIEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD---------
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#Lepcor_GT29_ST8Sia6-B
LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRRPEESTKFRSELASCCDAVHNF-------
-----------IASQNNSPLGSNMSYEVDSKKT-ILITEDIFKMLP-------V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDSSDFVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENIAVYGDAFLLLPAFSFRSNTATSFKVYHTLKEFKAT-
QRAIFFHPAYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD---------

#Lepcor_GT29_ST8Sia6-A
LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRRPEESTKFRSELASCCDAVHNF-------
-----------IASQNNSPLGSNMSYEVDSKKT-ILITEDIFKMLP-------V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDSSDFVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENIAVYGDAFLLLPAFSFRSNTATSFKVYHTLKEFKAT-
QRAIFFHPAYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD---------

#Aquchrcan_GT29_ST8Sia6
LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRRPEESTKFRSELASCCDAVHNF-------
-----------IASQNNSPLGSNMSYEVDSKKT-ILITEDIFKMLP-------V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDHSDFVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENIAVYGDAFLLLPAFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD---------

#Halleuala_GT29_ST8Sia6
LSSSIKKKRYSEDYY--LHIVTKLQNCTWIRRPEESTKFRSELASCCDAVHNF-------
-----------IASQNNSPLGSNMSYEVDSKKT-ILITEDIFKMLP-------V-SSPLS
VY---PFKTCAVVGNGGILKNSSCGAEIDHSDFVFRCNLPPTTGSISKDVGNKTNLVTVN
PSIIAQKYNKLN--EKKTEFLENIAVYGDAFLLLPAFSFRSNTATSFKVYHTLQEFKAT-
QRAIFFHPTYLKSLAQFWRTKGVKAYRLSSGFMITSAALELCENVKLYGFWPFSKSTEK-
MPISHHYYDNQLPKP-----GFHAMPKEYNQILQLHGKGILKLQFGKCESD---------
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