**Supplementary File 1**

Table S1 Transposable element repeat class analysis of the *Thermobia domestica* genome assembly

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Repeat element family** | **Total number elements per family in genome** | **cumulative length [bp]** | **% of genome assembly** | **% of cumulative element length** | **% of element number** |
| **Class I - Retrotransposons** | **2,189,237** | **611,713,341** | **10.97** | **20.7** | **21.9** |
| SINEs | 1,216,723 | 206,323,846 | 3.7 | 7.0 | 12.2 |
| ALUs | 0 | 0 | 0 | 0.0 | 0.0 |
| MIRs | 0 | 0 | 0 | 0.0 | 0.0 |
| LINEs | 560,608 | 289,478,914 | 5.19 | 9.8 | 5.6 |
| LINE1 | 0 | 0 | 0 | 0.0 | 0.0 |
| LINE2 | 33,935 | 15,264,789 | 0.27 | 0.5 | 0.3 |
| L3/CR1 | 50,233 | 24,178,122 | 0.43 | 0.8 | 0.5 |
| LTRs | 411,906 | 115,910,581 | 2.08 | 3.9 | 4.1 |
| ERVL | 0 | 0 | 0 | 0.0 | 0.0 |
| ERVL-MaLRs | 0 | 0 | 0 | 0.0 | 0.0 |
| ERV\_classI | 0 | 0 | 0 | 0.0 | 0.0 |
| ERV\_classII | 0 | 0 | 0 | 0.0 | 0.0 |
|  |  |  |  |  |  |
| **Class II - DNA Transposons** | **2,140,882** | **813,267,020** | **14.58** | **27.6** | **21.4** |
| hAT-Charlie | 97,473 | 25,645,988 | 0.46 | 0.9 | 1.0 |
| TcMar-Tigger | 30,684 | 9,434,429 | 0.17 | 0.3 | 0.3 |
| **Total Classified Transposons** | **4,330,119** | **1,424,980,361** | **25.55** | **48.3** | **43.4** |
| **Unclassified** | **5,656,688** | **1,524,050,197** | **27.32** | **51.7** | **56.6** |
| Total Repeat Families | 9,986,807 | 2,949,030,558 | 52.87 | 100 | 100 |

Table S2 Details of the *Thermobia domestica* OR family genes and proteins. Columns are: Gene – the gene and protein name we are assigning (suffixes, which are not part of the name but indicate features of the gene model, are C – C-terminus missing, F – assembly was repaired, J – gene model spans scaffolds, \* - one or more join across scaffolds made on the basis of comparison with an ortholog in *Ctenolepisma longicaudata* or a close intact relative in *Thermobia*); Scaffold – the v1 genome assembly scaffold ID; Coordinates – the nucleotide range from the first position of the start codon to the last position of the stop codon in the contig/scaffold; Strand – + is forward and - is reverse; RNA – number of independent pairs of reads from Missbach et al. (2014) and 1Kite (Misof et al. 2014); Introns – phases of introns (bold indicates those supported by Missbach et al. cDNAs, or their raw RNAseq reads, or those from 1Kite); % - percent identity for most apparent 1-1 orthologs with *Ctenolepisma longicaudata*; AAs – number of encoded amino acids in the protein; Comments – comments on the gene model. Note that Orco is Orco2, Or1 is Orco1, and Or9 is Orco3 of Missbach et al. (2014).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Scaffold** | **Coordinates** | **Strand** | **RNA** | **Introns** | **AAs** | **%** | **Comments** |
| OrcoFJ | 306089 | 32493->32712 | + | 7 | **0-2-0-0-0** | 484 | 88 | Join across 7 scaffolds |
|  | 252574 | <1->6187 | + |  |  |  |  | Exon1 split across scaffolds |
|  | 166573 | <1->9235 | + |  |  |  |  | Assembly repaired |
|  | 470722 | <1->6248 | + |  |  |  |  |  |
|  | 543310 | <1->8541 | - |  |  |  |  |  |
|  | 55767 | <1->9362 | + |  |  |  |  |  |
|  | 116122 | <1-15328 | + |  |  |  |  |  |
| Or1J | 230086 | 11865->19068 | + | 6 | **0-2-0-0-0** | 478 | 82 | Join across 4 scaffolds |
|  | 33241 | <1->4012 | + |  |  |  |  |  |
|  | 277514 | <1->12364 | - |  |  |  |  |  |
|  | 78038 | 47065->47792 | - |  |  |  |  |  |
| Or2 | 305721 | 36346-52500 | + | 0 | 0-2-0-0-0 | 471 | 53 | Within one scaffold |
| Or3 | 147262 | 7163-30763 | - | 3 | 0-**2**-0-0-0 | 470 | 50 | Within one scaffold |
| Or4 | 251839 | 15006-35080 | + | 4 | **0**-2-**0**-**0**-0 | 452 | 77 | Within one scaffold |
| Or5J\* | 306089 | <1-13109 | - | 5 | **0**-2-**0**-**0**-0 | 454 | - | Join across 2 scaffolds |
|  | 395000 | 11040->32100 | - |  |  |  |  |  |
| Or6J\* | 287065 | 48->7995 | + | 4 | 0-2-0-**0**-0 | 462 | - | Join across 3 scaffolds |
|  | 315037 | <1->10435 | - |  |  |  |  |  |
|  | 459954 | <1-7255 | + |  |  |  |  |  |
| Or7JC\* | 27200 | 7160->15500 | + | 3 | 0-2-0-**0**-0 | 455 | - | Join across 3 scaffolds |
|  | 86519 | <1->11660 | + |  |  |  |  | Final exon unidentified |
|  | 127360 | <1->11085 | - |  |  |  |  |  |
| Or8J\* | 453422 | 7683->20014 | + | 2 | 0-**2**-0-0-**0** | 462 | - | Join across 2 scaffolds |
|  | 11168 | <1-3494 | + |  |  |  |  |  |
| Or9J | 580933 | 6878->16065 | + | 4 | **2-0-0-0** | 485 | 72 | Join across 3 scaffolds |
|  | 571356 | <1->10291 | + |  |  |  |  |  |
|  | 308436 | 20515->38961 | - |  |  |  |  |  |
| Or10J\* | 522795 | 673->1573 | + | 2 | 2-0-0-**0** | 456 | 68 | Join across 4 scaffolds |
|  | 121300 | <1->8137 | - |  |  |  |  | Exon1 split across scaffolds |
|  | 249181 | <1->3864 | + |  |  |  |  |  |
|  | 253685 | 6187->11780 | - |  |  |  |  |  |
| Or11J\* | 544642 | <1-24846 | - | 3 | 2-0-0-**0** | 468 | 67 | Join across 2 scaffolds |
|  | 606400 | 15713->21228 | - |  |  |  |  |  |
| Or12J\* | 455811 | 8829->21699 | + | 3 | 2-0-0-0 | 446 | 67 | Join across 2 scaffolds |
|  | 80727 | 2968->18501 | - |  |  |  |  |  |
| Or13J\* | 432607 | <1-6113 | - | 0 | 2-0-0-0 | 474 | - | Join across 2 scaffolds |
|  | 396309 | <1-1631 | + |  |  |  |  |  |
| Or14J\* | 432607 | 15872->19919 | + | 2 | 2-0-0-0 | 461 | - | Join across 4 scaffolds |
|  | 451874 | <1-6796> | + |  |  |  |  |  |
|  | 122756 | <1-4034> | - |  |  |  |  |  |
|  | 150848 | 955->7401 | - |  |  |  |  |  |
| Or15aJ | 76671 | 1168->38506 | + | 0 | 2-**0**-**0**-**0** | 470 | - | Alternatively spliced |
| Or15bJ | 76671 | 10470->38506 | + | 0 | 2-**0**-**0**-**0** | 470 | - | Alternatively spliced |
| Or15cJP | 76671 | 24385->38506 | + | 1 | 2-**0**-**0**-**0** | 456 | - | Pseudogenic first exon |
|  | 615227 | <1->6840 | + | 1 |  |  |  | Join across 4 scaffolds |
|  | 72518 | <1->5809 | + | 1 |  |  |  |  |
|  | 489799 | <1-4081 |  |  |  |  |  |  |
| Or16JC\* | 229400 | <1-6927 | - | 0 | 2-0-0-0 | 448 | 63 | Join across 3 scaffold |
|  | 238675 | <1->4045 | - |  |  |  |  | Final exon unidentified |
|  | 52482 | <1->12620 | - |  |  |  |  |  |
| Or17J\* | 162524 | <1-14232 | - | 0 | 2-0-0-0 | 476 | 62 | Join across 4 scaffolds |
|  | 154846 | <1->4087 | - |  |  |  |  |  |
|  | 52482 | <1->12620 | - |  |  |  |  |  |
|  | 366562 | <1-8024 | + |  |  |  |  |  |
| Or18 | 369759 | 3969-17958 | + | 2 | 2-0-0-**0** | 490 | 50 | Within one scaffold |
| Or19 | 192862 | 1877-45187 | + | 2 | **2**-0-0-0 | 464 | - | Within one scaffold |
| Or20J\* | 616889 | <1-13166 | - | 1 | 2-0-**0**-0 | 464 | - | Join across 2 scaffolds |
|  | 47847 | <1-4266 | + |  |  |  |  |  |
| Or21 | 317857 | 40091-63654 | - | 2 | 2-**0**-0-0 | 464 | - | Within one scaffold |
| Or22J\* | 544642 | 32803->39175 | + | 0 | 2-0-0-0 | 468 | - | Join across 2 scaffolds |
|  | 231032 | <1-19933 | + |  |  |  |  |  |
| Or23 | 47847 | 7399-41943 | + | 1 | 2-**0**-**0**-0 | 473 | - | Within one scaffold |
| Or24a | 317857 | 67501-101689 | - | 0 | 2-0-0-0 | 468 | - | Alternatively spliced |
| Or24bP | 317857 | 67501-96047 | - | 0 | 2-0-0-0 | 470 | - | Alt. spliced, but pseudogenic |
| Or25FJ\* | 407319 | 1414->1905 | + | 4 | 2-**0**-**0**-0 | 461 | 66 | Join across 3 scaffolds |
|  | 6820 | <1->16036 | + |  |  |  |  | Assembly repaired |
|  | 253685 | <1-4222 | + |  |  |  |  |  |
| Or26 | 214043 | 13203-26863 | - | 2 | 2-0-**0**-0 | 454 | 66 | Within one scaffold |
| Or27aJ\* | 377263 | 14874->20009 | + | 2 | **2**-0-0-0 | 438 | - | Alternatively spliced |
| Or27bJ\* | 125151 | 11497->37484 | + | 0 | 2-0-0-0 | 438 | - | Alternatively spliced |
| Or27cJ\* | 125121 | 19894->37484 | + | 0 | 2-0-0-0 | 438 | - | Alternatively spliced |
| Or27dJ\* | 63428 | 4673->17184 | + | 0 | 2-0-0-0 | 440 | - | Join across 2 scaffolds |
|  | 599414 | 6753->10940 | - |  |  |  |  |  |
| Or28J\* | 139075 | <1-21269 | - | 1 | 2-0-0-0 | 508 | 68 | Join across 5 scaffolds |
|  | 282012 | <1->24015 | - |  |  |  |  |  |
|  | 494962 | <1->34250 | - |  |  |  |  |  |
|  | 354737 | <1->12842 | + |  |  |  |  |  |
|  | 484088 | 13261-20877 | - |  |  |  |  |  |
| Or29J\* | 231873 | <1-5342 | - | 0 | 2-**0**-**0**-**0** | 463 | 56 | Join across 2 scaffolds |
|  | 211379 | <1-20094 | + |  |  |  |  |  |
| Or30FJ\* | 2208 | <1->18453 | - | 3 | 2-**0**-0-0 | 445 | 54 | Assembly repaired |
|  | 470596 | <1-1699 | + |  |  |  |  | Join across 2 scaffolds |
| Or31aJ\* | 8260 | 1152->3911 | + | 0 | 2-0-0-0 | 464 | - | Alternatively spliced |
| Or31bJ\* | 293478 | 5159->11177 | + | 0 | 2-0-0-0 | 448 | - | Alternatively spliced |
| Or31cJ\* | 293478 | 10589->11177 | + | 0 | 2-0-0-0 | 455 | - | Alternatively spliced |
|  | 474626 | <1->27135 | + | 0 | 2-0-0-0 |  |  | Merge across 2 scaffolds |
| Or31dJ\* | 474626 | 4472->27135 | + | 0 | 2-0-0-0 | 460 | - | Alternatively spliced |
| Or31eJ\* | 474626 | 8819->27135 | + | 0 | 2-0-0-0 | 449 | - | Alternatively spliced |
| Or31fJ\* | 474626 | 14213->27135 | + | 1 | 2-0-0-0 | 465 | - | Alternatively spliced |
|  | 57694 | <1->5992 | - |  |  |  |  | Joined across 3 scaffolds |
|  | 448088 | 13365->20877 | - |  |  |  |  |  |

Table S3 Details of the MhraOr family genes and proteins. Columns are: Gene – the gene and protein name we are assigning (suffixes, which are not part of the name but indicate features of the gene model, are F – assembly was repaired, J – gene model spans scaffolds, \* - one or more joins across scaffolds is based only on sequence similarity to the other proteins); Scaffold – the v1 genome assembly scaffold ID from i5k; Coordinates – the nucleotide range from the first position of the start codon to the last position of the stop codon; Strand – + is forward and - is reverse; RNA – number of independent pairs of reads from 1Kite and the i5k pilot project (single reads from Missbach et al. (2014) for the related species *Lepismachilis y-signata* are shown in parentheses); Introns – phases of introns (bold indicates those supported by RNAseq reads); AAs – number of encoded amino acids in the protein; Comments – comments on the gene model.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Scaffold** | **Coordinates** | **Strand** | **RNA** | **Introns** | **AAs** | **Comments** |
| Or1F | 8919 | 2606-19798 | + | 13 (5) | **2**-0-**0**-**0** | 491 | Exon4 from raw reads |
| Or2FJ | 72278 | <1-1364 | - | 7 (0) | **2**-**0**-0-0 | 498 | Repair ambiguous bases |
|  | 8919 | 25482->37666 | - |  |  |  | Join across 2 scaffolds |
| Or3F | 22483 | <6015->13286 | + | 10 (0) | **2**-**0**-**0**-**0** | 488 | Multiple assembly repairs |
| Or4FJ\* | 50778 | 1413->14342 | + | 4 (0) | 2-**0**-**0**-0 | 469 | Multiple assembly repairs |
|  | 22483 | <28546->35391 | - |  |  |  | First two scaffolds overlap |
|  | 151641 | 210->1386 | - |  |  |  | Join across 3 scaffolds |
| Or5FJ\* | 200277 | <1->737 | - | 4 (0) | 2-0-0-0 | 474 | Multiple assembly repairs |
|  | 47247 | <1->18550 | + |  |  |  | Join across 3 scaffolds |
|  | 27669 | <1-24594 | + |  |  |  |  |

**FASTA format proteins for the newly described ORs:** Suffixes, which are not part of the gene/protein name but indicate features of the gene model, are C – C-terminus missing, F – assembly was repaired, I – internal regions missing, J – gene model spans scaffolds, P – pseudogene. All proteins of the newly described ORs and the alignment used to reconstruct the gene tree are available on Dryad.

**4 *Ladona fulva* ORs.**

>LfulOrco

MDKADRRSKRKVFPHAWDKSPKREKKSSLATDLSIHIRMMRLAGHFLPDFNPDSDSKFSLVWAIYSFTHMALMSLQFIAMAVNMVKHFDEVSALTTNAISLLFYLHGPIKVFYFAIYRRRFYKTIRSWDSSLSDQGEGAAMNKASNGIESIDHSITECMKKAQFGAQEWAFENSNVRFRKLAVRRMRKLLVSVMSGSAAAAAFWSLRPFLGLGHYSRKLVMNEGNASLPMDGGQWYLLVDATYPWETSSNVAYALTFLYQVYWIVFCLAQINLLDLLLCSWLIFACEQILHLKDILKPLMQKSQDKNLQSADAVLFKRKGALFQNELSLKRGSTLERTSTLSILQVNPTAHNGYSALSDDESFGLNKGPEDGYFHMKDMSGRNGSNQSLEMRMYQNNNQEISVHCCIKYWVEKHKHIVRFVDCIEDSYGMALLIHMLTSTITLTLLSYEATNISSVDMHALTVITYLLYTLGQVFLFCIYGNKLIEESTSVMQAAYESPWYDCTEEAKAFIQIVCQKSQRAMSISGAKFFTVSLDLFASVLGAVVTYFMVLIQLK

>LfulOr1

MARRRIEYLRFHRDLLRFMWLFPSTQKKSWKTTVAIVSHFSMMAALLFQLAGELMDFVIHSHEIDIWTDVACMAVFSCSSIVRLVILFYKKDDLYNLMSKWEDQFVRKSPFNPARKDVERLIFKTKAYILTTTIITMLIAFHWCVYPIAVAILFPEQSRKLPLRAWYPFDMYASPIYEFIYLMQIIRGVFGTYIAVYWETTLMSFCILTYYEAKKLKEHLRSIATDFKEGEEDKIEDYLTKCILHHRTTVRFVKRIGETYSHALVVELFYLVVPMCFTALKVSSFFGNDTTKYLNWLEFFLAGLIQLFILCLGGHIVTSQLISIQGAAYEACARVSGRIRWKLAFMMLHSNLEMKITGGNFFILSMKTFKTIVGMSFSNFIVLRQLKESKYSTGLQS

>LfulOr2

MGRQKIRYLTVLGNIFNVMCLLPMDNRRLKIRSLVLLYHIAILVLLLLRLAGEFMDFVQHINHTYDWPRIASIMILTIMSILRIFLYAQRKEKNLRILQLWEKLFTKNLKLGTRIEDIQKDIRTCNMYSLAMIVATMGGTMHWALYPLVLGYFTPGKRVLPLRTWYPIDLYSSPTYEIVYAFQFIGTLLTTYNPALSATSFLTFSILVQKQVQELKKQLKAIGVTGKHIGASVEPLGERRQMIEADVLRCIKFHSGIIRFVREMQNYYSSVLVIEYLSFTLPLCFTIIEATSGSLHDSIAWAEFFVTCSLTILLYCWNGSRLTLQLLSIQDAISEALCGHLTNEMRWNLRFMMHQSNVEFTVTGGRLFITSMETFKNLIGFAVSNYLFFKELKG

>LfulOr3

MKKIILFFRLSGHWFPFQILEKCTSSKNGLVFCLIDLFNKLGHPQAAIKNVITTFYAIQTLGRVIFVAVRGTYIWQLLMSFGREITEINAKDKQRTTKKSFILMQNGENNDYFLYIFLMIVLGANLTGIIFTITPFVISYSHAYYQSTNSLPNETVIQRPLVFDAWYPFDMYNSPSYEMVLAIQALCGFVWINMMSSSDAIFLSILAKVLAEIRLLNLRTNKIQLLSNFRDIETRNKLFMKLLKDWVLHHQRIMKMCREIESTFSGFILMTFLFNGGSLSLLAYNVARFQDTISIISVSGYFCVVSFQLLVMSHYGQKVTDKSLNIKKNIYSIPWWKFSKYVRSTFLIILENTEQPITFTGMGYFNLSMEFLLSVFQAAFSYFIILIQLT

**47 *Ephemera danica* ORs**

>EdanOrcoF

MIQMIFTPLTNRITMMQMSHGGKGAHRGLAHDLRTLLMLMQLAGHFMPDYSVAKQQQQQSGRGLLRYVYSLVNIGLETLHFLCLLAQLLIQFGDTAALVSNTLTMLFFLHGVTKVTYFALKRKQFYRTMLVWESSHSHPLFVESDVKHRALGEREMLRLMRYVLVATGVTALLWAAHPFLSTDATPPSPDNATLLSTNVTVLGVDLLSSTAVTPVVLQLQGPKLMVNAWYPWDPYSSSFLYVITYLFQLYWLVFCICQVNLMDTLFCSWLIYGCEQLRHLKEGMQGLMQLSASEAALATAGDVFPDTREASEMADNASNLFLRSTSRVFPTMTGTARVRHTVTPEMLGFRNLEPPLPGQNAEQQQELLRQDMVVRSAIKYWVERHKHILRFVESIGETYGMALLLHMLTSTVTLTLLSYEATKIAGVNLYAFTVIGYLCYTLGQVFLFCVFGNRLIEESVSVMHAAYSCPWYDGSEEAKTFVQIVCQQCQRPMSVSGAKFFTVSLDLFASVLGAVVTYFMVLIQLN

>EdanOr1

MFSSYRMSSLSSYSQLYLKVLRVSGVWPWKTQHEPWQRILAHAYTTYAALAVTGSFLGTSLVFVMMHLSEWQAVLGDLWLKVSLASISLKLVLFLMHRKEINTLLNSSPKFISTSVPSHLNNYKTEAIQRSALQIALMIIIAIVAYFYFQADIFIVDIAHLLKPTKNTQGNTLYILGTLLLLAVERCALVILMLFHLGAFGFYLTYLRFIEGYLDHLKDSIIKISVEPKLQKDTLFTNYNASTTDQEVRYCVSLHQFIIGLVDRGNAAFSTQMLFKLWRSLVVLCLTAKELTNENQPFGNKLTITLIFLANIFELFNVCWLADVIQSKMRHAAVRDDMVTAQNGSEGFDEDDNWITMQAMSYRCQMPLDLRAGPYYHLSIHTFSAILGLSFTYFIFLTSVKT

>EdanOr2

MSTIYRTYYIKKKTNSIRNVSSKEKMNFIYNININDVFFKPIYFLNFIGFWNDEKSNFQKITSNLFTFVCILSTVAHSIFNFIDDEKTWLLLGFKLVNAFHHAIIAIVKFHLVNIKKESIFQLLANCLHNNISAPKILVTQIYHFDNRFKKYNKALVKIVTILVLLILYTPIYIFIYMYTEVKWDVKSILSFITQGLGTVFLINVTLSYSLIYITLMLTLCKILDHMNDVILTLRNATHRELSDCNENISKKLKYIVQTHQRAIRFADGINEIFSYNALLDMCLALALVIVSVIDFKSSNLFPYLNVHAFYVLMDFCTSVLLAIYCYFGSMVIEKSGKKIAENFNSYQRQNWNSDNQQITKIILIRVRFPIRILAGQIFTISNKTLAMLAGYAASYTIIFFQIQIKHKNTDTTIEQNSTVDAIVFK

>EdanOr3C

MMIDSPTTQRTTNYNLDIDMALAWPARILQIFGLWTENSNSRSRLICSRLLLACAMISSVITTVELIRTVQYHLLDITFVFTTTLRYLAWFYQIIIFATKRQYITKLLQECYYNIPAPIYLNRNIKKLKHNQSRILNRPLAMILITLIIITSFITSYDGDGYFSLTLLKIVVFRVLYASMHLTKLGFNLMYLAWLQTTLNVLDHINDVICTLHCKRKSLGPRKMDEKEQHQIAQTLQYAANLHQRVAKFINGFNRIYSSIMFLYIWTTHLMFAVIVLKIAKQEVLYSLTGMFVIIVSTAVSYLHTFLICLKATCIAEQSGTKIRNNLSHVAWWGWSRINLNTRNVIVTMTKHEMQIRAGSIFICSLSNFIT

>EdanOr4

MNIVLFLQQSALIWRQPMMKFSLDIDYILKWPKFLLQIFGLWNDNSSKICLFLLRSMLFFLVISTILSSFNEIFTTDHQLLMPANFVAQTIRYLSWLQKIFIYLTKRKKMSDLLASSFCNITAPTFLRSYTKQFRLHSNKIMNKSYIMRYVYIILFILIIIFLEHFDLSSLAMIVIFIISRLLFALLHIQALGYSIMYLSWLELSLCQLEHMNQVLRTLQYSRRNVLKKQKLQNSRNQIRITETLRYVIQLHQRVARFINGLNHIFSFVMLMELWSTHVIFSVTFVKLVFEGLLHDMALTIAIVISTILIYFYMGLICWKATCIVEQSSSKLQNNLCNVPWWEWNSSNLNLRNCMFSISMREMQIRAGPIYNFSLPTFATILSVSLYYFIFLYQLGDGFK

>EdanOr5

MKFSIDFERILMWPQIPLKIFGLWNANSSKFTLFLLRTALTFIVLSIILNTIVLIINADKNLISISIVANGIRFVAWIQRIIFFLTKRQAMVDLLSQYFHDISAPANFRRQIDRFRLKTSKLMSKTYVMRYFFAILLIVSITLYEELDVSSIPMIFIYFIVRLLFILLHVQILGFNLMYITWLQLTLCLLEHMNEIVRTLHCTRNGLGPQKWNSAHQARIKKTLRYTIQLHQRAAKFVCGLNQMFSNVMMMDLWSTHVVFSIAFVQIAIEGMLHNIATSLATVMSTLLIYFYMALICQTSTDIVEQSGRKLQDNLCHVPWWGWNQSNLNIRNGIYSSSMHGLQIKAGPIYNFSLATFATVLSVSFYYFMILYELNTTRI

>EdanOr6P

YNVNVIQSLLWPRRILKFFGLWSEDAIRYRILRQWSLLFVTFITLTWISATQIVHSQSSLRELTEMAVLITSHVTWVLKMHVLLTKGRDLTDLLHSCFRNIQAPSHLKRQVWNFX MKHPGKFIAFLVIMSTLLSLPISPIRELNTGFMLLNVKFFLMILAQSVFIITRVQYYTFNVLYVSLLIMVTKTLNHLNEVLSLLHDDDHDLQDRAQSNKDYQQLTKRTLNYVAQTHQRISRLTEGLNKILSNVIFMDVVSTHLVTCRLILEFFKKDELEVRNVVFFVAICILMNSYLFSICWLATDIKEKSGAKLQNNLWHSTWWEWESSNVRLSNAVVARAKRDLLMSAGPFYSLSVEFFSGMLGVSFSYSIILYQLQDYVQ

>EdanOr7

MVFLWLDNPTRLQNTCSKICHILVAFSFILTVVFVCIVSVTIVFSFIRSLTLTLKMFHTAKILNFVFFKQKCVIDSLKNSLSSISAPIFLSKHVYDFIDSIENVNKKWKMFYKSFSISLNFAAAIFYLFRVYMADFEFFHVLLLFFLGIAANFILFMHLGLHILQITWIRIICHVLDHINNVILTLHHEERKLNNETTNLVYQNRVARTLDHIGQIHQTALKLVNGFNTYFDTLLFVNIMTDIASVVLTPMQQIMRDEKQSLIRDYSVPVSLSLSFALLLIKSWFGSLIIRTGSTVALHSMSNARWQSWNIENKVEADKVVAMFQSELRLTAGPFYYLSMKTFSSVVGAAFSYTFLIKPLYSMMTPNN

>EdanOr8I

MFNMVFFWLDNPSRIQNICSKFCHILAAFSFIVTVVFFITSVTTVFSFARSLAITLKMFYAAKILNIVFFKQKCVIESLNNSFSDISAPIFLSKHVYDFIDSIENVNKKWKMFYKSFSISLNFAAAIFYLFRVYMADFEFFHVLLLFFLGIAANFILFMHLGLHILQITWIRIICKVLDHMNNVILTLHHEERKLNNETTNLVYQNRVARTLDHIGQIHQTALKLVNGFNTYFDTLLFVNIITDIVYVVLTPMLQIIQEEKQSLTRDYFVLISLSLSFASLLIKSWFGSLIIRTVVGVAFSYTLLIKSLYDDTE

>EdanOr9

MKRLKFIRIICPRLAIILLVLFVFLEMVDLVTSDQSLLHISYTIMLIPRQLCTIRKIYIFIFSSEFRRFIYDSEFLRFSGPRHLSPLIQKFQTRCYETAKLSIVLIITFLIGFIPIWNLSFFNWEGTTFINITDNAVVKPKLQFSIWHPFDFNQNKLIFNVILVLQSLIMIFAGVLITSFNIFYTSLAAMCSRLFDHLYDVLLHNQLLDNTFYNLRRCQNLNDLNISQSDIFLSHEPISFPKKEIKDESGISALNEGLHDWNSKHKYLESDDKVMETLRYAVQHHQRSVRFVHGVNKIFSGVMLLDIWTVVLIMCVLAFQVVSSEEGALRTSALAKNFILHLIFFALICWASNEVMVKSSAPIHAAANHACWLCWRTSTRNVVHCLATYSYFPLRLSAGPFYTLSLETFTALLSLTFSYFMFLYQIYESKDKT

>EdanOr10

MNWPRRFMQCINMWYHDAFPGSKKHLHRFLRFLQKLILKITYFSIVTLWLANCSYLLITDRHQPFVKNTHSFLIIIRQFFGFCKTVVVHRNKRQMERLLKESFCDITVPTCLGRQLNKYRKSFKKSHKILLINTVYIIITMIPIVLMSPLALTKFLKIENFDIKLLDWNVSTIFPLLIYVIQIFAIVPIVIMMMGSSLYYLGLLCLANGMLDHLNLVLETLHEKRSKFKRRGMTHTNNPEDSPGYQQRVGATLKYIVQHQIKVTRYLKGINNIFSNVLLFEVLSLHVVFSVSAFAIVTAGITSSLVIGMIPALLNYFFNFAFCCWAANDVNVKCSDTLHKSTTHMASWTWDRDNKLLGQCITEYSKVVLRVSAGPFYSLSLNTINTVLSASFSYLLLLYNLNGTL

>EdanOr11

MDLWPENIFPGFKRTLFDRCVWIFQKIMFVFSVTLLSFLCISNITHLLLVDRGKTFLNFTQTLMIICRQTFGLFKMYTYFKNKRELRHLLNDTFYDVPAPTCLRQQIKKYKQSCLKTPKVVSISSIIIIVALIPVLIGAPLQVTPVLKYQNSELVLLNLNVPKIIPQLIYIAQVLGIILVFNVAFGCIIIYIALLTIAHRMLDHLHEVLKTLHHGHKKIGKNKMLHDHQQRVADTLKYVVQHQFRINRFITRINDFYSNVMFLEVFSLHLVFSVATFQISQEGLTTMRYGMIPLLLIFLAIFTVCSWTANDVEVKSAAVEEISSHASWWTWNSSNRIVGQCVSEFANFKLHLNAGLFNSMSLDTFTDVLKISFSYFLFLHSLHVAQRKAD

>EdanOr12P

LYLSRFFILGINLWHEDIFAGHLRHQFLRFQKLLLTLYYATYVIMLIANIIHYLFIDWHKPFAKNVNILVLIIRQSYGIYKLYIIHTNRHTVHKLLKETFYDVAAPICLRPLINNYKQLFLKKSKVMSFTSIYLFMIFIPTVLSTILPFLNYKDIELKMFNFEIPQIIPKIMYALKPLAVYPVLVVTLGINVFYIALLTVAQRMLEHLREVLNFLHHGIGTREINVERIQNSQQEYQQRVAAMLKYVIQHQSKIFRFIEDVNDLFSNVMLLEIWTLHVLYCTFILEIVATKRLSTAQGAAMIHLAATYVLIFAICCWAGNEVKVKCNIIVQESATHVAWWTWNTENRIMGQCIIEYAGYKLRLIAGSFYSISLNTLTTVLSASFSYFLYLYSLYTSE

>EdanOr13P

MNRQNRKLDKNSHQFNLRFRFVLIINFLFGHWFYIAPLKLRGIYYVSALFFVFTINFFSISMTIIDISNLYRATPNFTLVLYFSLGVLASCRSTFQTIYVLIKRKSFEETIQRLNRILNFKELEDZQFKAIDKAMKFTYRIAIFFCIGFTACIIMFHLSWWIQTESGGAISIELLVEVCTITNVIKIGDMLRHAILYFVAFLVYAGKVIAMDIMFLSWYSLLVEQMDLLVEGIEKSLHQADVKTARRSLTSWLHFHHELRRVMQKVNRVAAPCIVLIVVVNTLQMCLLVFFVGFVNSLSAAVLLMFALFAFLQSFYYCHFGQKIRDRLIRLQDAVYTSPWLGSRREIQHAALMICNAATERAMPLPGAPFFALSLEFFASIIGAVFTYFILLFQLK

>EdanOr14

MSPFSVYSFLKYIMRGCNLSSEIQHHFRFILVLNFVFGHWFHVSPLKLRGVAYICAAIFITLVNLAVIVRATFNVHNLIHALPHFAPSLLISLGVIGAVQSVFRTTVVLLKRKEIENIFLKLKVVVDGHIFPDIQTKTIKTALKYSYISVSIYIIGFITAMIFHSFSWQMQDDFIGRNENTTTIKSIIKHNALISKSGYWEQLTYTILYYTVFLISVGKIAATDLLFFSWYSLLIAEMDLLVKGINQLLCQPKSNTMHCNLSTWLQFHQEIVRLMQRVSTVASPCAVLTIAVNTLHMCFLAYIVTKRYVDTLSMTVFMAFALLALLQSFFYCNIGQKIRNKVAELQQAAYAAPWLDSPRDTQHAMVMICSSATERAMPLPGAPFFALSLEFFASVLGAVFTYFIVLLQIN

>EdanOr15

MGGYRFTRNDVALKFRLVLSLNFIFGHIYPCKLGGIKRVIARIYIIFINFFLFVMTLLTINNLINAFSSFLVALYIFVALIGISHAAFRSAYIIIKRKNIRMIIYQFRRLVNEETFKKSQNKAIQKAFKRSYRTLFIDTIIYCLCLILHLILWIVKNIDTDEDETGLSLREVVIKYNPVSYLSGINTKRLYCILYFITFFISIGKVVTTDLLFHSWYALIIEEMDLLMEGLKVLIRQSEPRVAQRNLNQWLLFHHQFMRVMQKVTTLTSPCIVVTIIVDILFVCILVYIVVKGIVGAFGMTVLLGFAFVSLIQAFLYCRIGQEIRNRIIKLQTVAYSAPWLGSPHNTQHAALMICGAATERAMPLPGAPFFALSLEFFASTLGAIFTYFLVLLQLN

>EdanOr16P

MAYVTVATTSSKTYKSTNRIHLVLNFIFGHWFHVSPLRFRDTSYILAYIFVTAINVTTIGFSIMSIYNMILSARDIKNAVFLAAGVSSMIQSAVRSLLLITKNNNXKLTNKVSGYTRFIAIFLTIVVSIMNILGFVLIGVMYNWNKSTDAVNNEDTLDFQEVFTIFDSYVHGSSATVFILVMLCSWLVTSFILGKIVATDVLFCSWYMQIVEHYKLLVASISTDLLPSNNETAESITQWMQMQHEINRLLTKVNSITSPCIMLTMVGGTLQICFYAYLVAKNAVIAMHAGLLIVYSFLTLFQMFVYCNFGQKIRNQVARLQDAAYSAPWQRSRREVQHAALMICSAATERAMPLPGAPFFALSLEFFASILGAVFTYFIVLLQLS

>EdanOr17P

MQKLFYRAVYKNEPSIIPTWSKPVQLGYGFTIVTILGAVFGEIFPISPLQRRHLHKLLYFMIKTYTILINLILIVFAISIYYGIVKYLQSFSSIVYSASGIFSVTEGILRIYFMFINRKRIQKFVLQLKSFINIPEHRSFQSAITSRISIGIVILILFVFVAYKLALVQLLXSVNFEALKSLKDNLTMSNAASNTSNVPVELVEFYLYMDGMHRLIPEMSINVSAGLVYAFCLMGVGKVFITDVFFLACYWLIGEQLEILTCRIIPVIRDANREQLASWLDYHQQLTQILQDVNGATSYPFAVGIIFSSLQICVLTFVIIRQNLDLTNSLSLILFNTVIIWHLFSYCIFGHRIRSKISRLQAAVYAAPWLGSRRDAQHATLMICSAATERAMPLPGAPFFTLSLEFLASVLGAVVTYFIVLLQINE

>EdanOr18P

IFKETKKRSKDDVLFLFSKENDLGTGVRTISIVCTIFGFWLPIKPTFCIRRCSVSYILNRLYTTILCVCLMCVTVTSAYAVITSTHRFATTVYLFSAFFGQMEMSVRPLFLLFKESQIKKLIVTLHSFINEPLLKNLQAAVIKKLSRYIHCMLTFEVFLFIISMIASFLSTKVEIESVSLDGIVTNFTQVGLSPEIAEIRAYAEVFFSFMSQSIFEYCMYMIYMVCFCGLMIRVSTDCFFYACYWLVAKQLELLADNLENSMRPPTQLATWLRLHRDLNRTLNSLNSTSAAVIITSVVCNTMVMCCVTFAIIKQQMATPNILSMLVFSTTSLLQLFIYCLMGQKIRNKVTRLQEAAYSASWLGSRRDTQNAILMICNAATERAMPLPGAPFFTLSLEFFASIVGAIFTYFFILLQMNDTQS

>EdanOr19

MAAIRRANEIGLGIGFRVLGILSIVFGQLFNIHPINIRKRSIAYYVTHAYTFIMVFYSSFITIGGLILILKNSSNFSVVVYYSTGFLGVAKCCLRSYFLILKKRRIELFTENFRRLLNESWLKSHQRRIIFRLTRYILILYAFLMSFYVCAMITNFNALITRIKHANETNSIAVPQFFKDATNEVMNNMWLNNSNISRFFDNLIPISISMVLVYSVAFLCIGKLITSDVLFYASYWLIIKELELLISKLKGVIRRSSTEELTLWLNYHHKLEKLLLEINNITSLPVFVSVIFTAIQLCFVAVVIVKRFLQDSSDSISLLLFAITSMQQLFMFCLLGQKIREQLVELQRTAYSAPWLRSQRGMHSALMICNAATERAMPLPGAPFFALSLEFFASIMGVVVTYFIVLLQFNKE

>EdanOr20

MNTNRLSVVLSFMFGHWFYVSPLRFRGVFYIFAWFYTITVNLSCTLMTFVCIFNFFMANRDFKRIIFLATGMFGMIQTITRAIFSLFYKKQIENILELFQNLLNNSEYKYRKVKLLFKVSRYSKGIAAFLILIYLTCFLYGFIIFGVVYENGRGNTTIDIFDENITDVREEWAKVDGIIGNIPSNLFTLYLSFIYLTTNWGYGKIIASDVLFFSWYMQIVEHYKILCYNLSSILLNCNKLDTEKMKRWKRLQHELNRLLTRVNTVTSPCIVVSMVINTLQVCFVIYLVAKGVLDVILAGSYIIMAGMALFQMFTYCHHSQKIKNQISKLQGIAYSAPWHNTQHNTQHAALMICSAATERAMPLPGAPFFALSLEFFASILGAIFTYFIVLLQIN

>EdanOr21FI

MVQVASADGKKMLSYNKKNVLDTHRLPMVSNFIFGHWFHVPPLQFKGAAYMLAWSYIILIHAIFVMFCAAGIYNLISVATSGFKVSVFIITEMSNLIHSNCRAVFVLFRKHEIEEISTRLIKMRQRSNVTSNVARNISIIFTFLTLTYSLTVGLGLISFLTQYKFENITSANENEIYLKNAYSNMNSNLKDSPIYIMILIVLVAFILSNLGLGKIISTDVLFYSWYMQIEDQYKQLTMSLGMAFLHCNHGHSDSAAHWIQTHREINRTHKKIIELIIEINNLQVAEESVAYLVAKSSKLQEASYSAPWLGSRHDTQHAALMICGAATERAMPLPGAPFFALSLEFFASILGAVFTYFIVLLQMK

>EdanOr22

MVQVASADGKKLLSYNEKNILDTHRLPVVSNFVFGHWFHVPPLQFKGAAYILAFSYAIFTNAIFVMFCGAGIYNLISVATSGFKVTVFIITELSNLIHSNSRAVFVLIRKHEVEEISTQLIKMRQRSNVISNVARTISIIFTFLILMYSLIIGLGLTSFFTQYNFENVTLANENEIYLKNAYSNVNSTLKDTPNYIIILIVILTYILSFIGLGKIISTDVLFYSWYMQIEDQYKQLTMSLGVALLHCNRGNNDSTAHWIQTHREINWLLARVNSVTSPCITVSIVVNTTQICIVAYFVAKDTLALVHLAALLIFASLGLFQMFMYCNLGQKIRDQTVKLQEAVYSMPCLGSRRDTQYASLLICNAATERAMPLPGAPFFALSLEFFASILGVVFTYFIVLLQFN

>EdanOr23

MITNRLPVVSNFVFGHWFHVSPLQFKGAAYILAWFHTIFVNVISIMFCMGCVSNMISAYSFGFKVTVFIATGAFGMIHTLSRAIFVLTRKRKIEEILVRLLIIRQRSKIISNITRNISCLFIFYTVTYSFTIVLGFVAYEIEYKTRNVNDTNENIIFLQEAVSNVNAMVEGMPNYMADVLIFITMTITSVFGIGKIISTDILFYSWYMQIQDQYRQLTKSFAKVLINCDKGDMESATHWIQTHREINRLLARVNSITSPCITVSIVLSTIQICLVAYLIAKNTLITLHLAALLIFASLGLFQMFMYCNLGQKIRDQTAKLQEAVYSMPCLGSRRDTQYASLLICNAATERTIPLPGAPFFALSLEFFASILGAVFTYFIVLLQFN

>EdanOr24P

MKVHVFGALTEKRYVNSNRVPVVLNFIFGHWFNVPPLRFKGVAYILACIYTLIVNANTLLTAVGVIFNFFGGKKESFQVFIVLAMGMFAALQPICRAIIFWVKKKEIEMVLMEFQTILIVLQQPQLSFKSSRKTLHLAIFLSVSYIIAGIMSFVLFAIYYENDNSKESKDEESTKYLKDVWSSINIISRDIPTHILAICVTLVCISTIPTVGKIVATDVLLYSWYIQILDFYQKLTENLATVLMHHNDHDAVGIAHWMQMQREINRLLTRVNAIASPIFVVAIVLSTTQICFVAYLVAKNSLIILHWGSYAIFAGLGLFQMFIYCSLGQRIRDHSKFQEAAYYSATZLRSRHDTQHAALMICNAATERAMPLPGAPFFALSLEFFASILGAVFTYFIVLLQMK

>EdanOr25

MLQSEGVVPFGVRVMIWCNRISGFWLPIPASPWRRLLLLAFESLVLIANALSFLAHIVRIHTDKIDFIVYMLGIASLMKYAYIVCASTFLLLYKKQVEQIFKDAQNLLKNRQFYYYQMSVLNRTSKRLIVYLSLPILLFFVIQMFLATNSARILRLSKMPNVTSEEDKFVESILRNDGTTLDYSLIILTFTTNVLTQFKAIALDAMFLGLLSFVSEQLGVLKITLHEAILVGPSPSYKRTDLDAWLNFQYRLARLTGKINATWSFLVVVLFFCTALTLCSLSYSAVKLSPLGIVTYVIIAHGLISVLPLFLYCHAGQNLRTQGEALAEMAFRGPWLHMKPALMPGVLLLALDCSRSFVARGGPFFTLSLEFFASVVGAVLTYLVVLLQMK

>EdanOr26

MLTIDNHVFLGFRMLTLCNLITGFWLHTPSSWPRRFLVLIYEFFTICIVITSIFIHSLQISSNEDFFVLIISMTATLKLTTIFVFAVTLLVQKRSVLKIICETQNLINTYKFRFHQNTVLQRTSKIITIYFLVPFLFLIVNNFHAMFSMKMIEMLGTNESNVTSNEKKFFDALIHRDENDQNRDVNNMILFLFAFSQTFSLAKSITMSATFLGLLYFVGEELRVLRLTLHEAMLTGHVTSYKRIQLVDWLRYQYRLARLMGQINSVWSYAVAVMFACDTVSICFLCYAVVRVAQYISVIRVLISYWLLAILPIFLYCQAGHRLRTQADALVEATCRCPWLRVTPSLVPGLHLVALDCSRSFVARGGPFFTLSLEFFASVVGAVLTYLVVLLQIK

>EdanOr27

MLQGEGIVPLGVRAVVFCNRLAGFWLPIPVSPWHRLFLFVFECLVILINAATLVVQIIKLYHVQNFVIFLIWIGALLKYSYTVILSIYLLISKKNIEQIFKDAQGILKNKHFYYYQVSLLNRTSKRIVIYLTIPFLCFIALQICSITFTNSIMKISTTTNVTTDQDKFIKAMFLNNGTFFDQALIILTLISNILSQFKSIAVDAMFLGLLYFVSEQLNVLKITLRDAMTVTGKVSSFKRTDLQTWLNFQSRIARLTNKINATWSFVVVLVFICTTLITCFLSYVMVKLPQLGIVTYISLAYWLLSLLPIFLYCHAGHRLRIKGEEITEAACRGPWMQMNSALVPGVHLIALDCSRSFVARGGPFFTLSLEFFASVMGAVLTYLVVLLQVV

>EdanOr28

MDDVVPKGLRVMFFCNKISGLWLQLPTASSKRLAVFCFEISIAAMLVCDVIFNIVHLFSAKNFVLFILSTSGILGMTHTTFSSIMLIINRRNINNIIKEAQHLIKLPTFRYHRSIILRRVSTKSIAYLMLPILGFVVAQINTIYFTSYNVLNPTTNVTSAEEQFIKDAMESSADSEMNSIIKILLFMNFLIQSLASFKLIAMDMLLLTLIYFVSEVLKVLRATLHDAMIVGPVLSFKKVDLNTWLYCQRRLSGFISRINVLWAPMIVVTILCNTLTICFLSYSIVKVYEIKIFMWIVFGFTMMTMLEVFIYCEAGHQLRTQGDAITATACQGPWLNMKPSLVPGIHLVALDCSRCFVLRGGPFFTLSLEFFASLVGAVFTYLVVLLQMK

>EdanOr29P

MLTMNGVTPLGLRVVVLLNKMTGLWLQVPSSRSQRLAVSVFEWIIVVVLIFNIIFTFIRLLSIKNFVLLILSISSILLMIQSTFSSIILLINKRHITNIFKEAQYLIELSNFRHHQAILLRRVSKRSAFYLIFIFLAFVVTQINSLHFTATITINPTVNATNPEKQFIEEAIGNNGNEMNILMMISFFSQTLAIFKLISMDILLLILLYFMSEELKVLRATLHEAMLIGQAPAFGKVDLGTWLSLQCRLSRLLARINKTWAPMIVVTILSHTLSICFLSYTIVRXFKTLVWIVAGYTLLTFLDVFFYCEAGHRLRTQGEAITEAACQGPWLQMKPSLVPGMHLVTNNCSRCFVVRGGPFFTLSLEFFASLVGAVFTYIVVLLQFK

>EdanOr30

MLSMNGVVPRGLRAMILCNQISGFWLQSPTSRSKRLLVSIFEWFIVILLIYNTIYNIVRLFSIKNFVLLVLTTSAILGITHTTFSSIMLIIKKKQIISIIKEAQYIVKIPNFYYQQLALLHRVSMRTVYYLIFPFLGFVFAHSNSLYFASYIVINPTINATSPEEQFIKDAVANSDDDINIMQILVLINLFSQSFSALKLVCMDTLLFTLLYFVSEELKILRATLYEAMLIGPVPSFKRVDLTTWLHCQRRLSRLMARINKTWAPMIVVTVLCNTLAICFLSYTIVRVSEFKILVWIVIGYTLLTFLDVFLYCEAGHRLKTQGEAITDAVCQGPWLHMKSSFVPGMNLVANNCSRSFVARGGPFFTLSLEFFASLVGAVLTYLIVLLQIK

>EdanOr31P

MESVKIMKTPIGFRAVVVSNFVTGFWIPESPLKFKSTQVITRYAMKFYMALITVSLTLHVFVQAKVVLKLQLSQKIAMQLILVISQITSSIIIAYRILSIELNRRSILRVIKNIZQLINLPYFESFKNSLTNRLSNRCIVYLSLPAFGFVCFQIYVMFNFHLVQILASTDPNVSNFTNTSTSKVVKTAFSDISLNDTLQGILIFITTWIQVVVIAKNIAMDALFLGLVHFVAEELDVLRRTLHEAVLVENSAIKFSSCVHLTAWLEHQRKLARVMELINTVWSPHVVAIFLNSTFCMSLVAFAVIKALEHGISMALLVAGFLLLNMLPIFLYCQAGHHLRTKGESVAEAICRGPWLCGRCRLDLVPGLHLVALDCSRSFVARGGPFFTLSLEFFASVVGAVLTYFVVLLQIK

>EdanOr32

MVAFQLCLEDLASKMWENHEDDLKPFGIKTVHIFNLVTGLWLPLTQFNNRIVSILIHVYEGFLVVFLASYIVVEIYTLTTTIDFEDAFDLIAIYSVVGIIVFSSLCRSVYLLLFRKKLLALFQNIRKLCNQRQVIHHKHELINRVSKNFLKNTIFPAILLLILHLSSLIYYSSHLREEPFRLDGNATGETKSVFQKLRELGNKLEGTWMYYGWVFGMSSQFIANMKLIASDALLLGTVEVLGEQLSILESTLDLTLHHKDFLFKNFSFSIQGWIALQRKLIQLTEEANAFWSPIVVLTFTCNTVLLCLNAFTFVKTRSSSVSTIPIILLGYLVVNLMPTVIVCHAGHRFRRKGHAVSDAVRRCDWLRAPRALVPGLSLVAADCRDSFLLRGGPFFTVGLEFLVSVVGAVLTYLVVLLQFK

>EdanOr33

MLHAAYSKRPLGLLAIQAVNLVTGFWIPLPPFNFSSIYTPYFVAYEWILNLGLIFHLLYSQLNDIVSYTEMLSKDLISFLGIYVYTVAFIQSTIRSMLFSSNKSKLIKILESLQSLIDRRIFRQFQAKILKSSPNKPIKTIVIIFVGYCIIQTANVVNLFMNPNYTTKITHHNSSDFDARVYMLQQKTREFDFFLKTVFNTVVATISILKLLSTDVLMLTILNLVTEELILLKNSIKNAIYVNNSNKNIIRNNDNLDLGAWIDFQQTLARILGNINSFSFVYTSIMIGINASNMCLMAYICTKLVSHSSLIVAVLAGYCFLIVIQTFLYCEAGHRLKQQGEGISEAVCRIPWLRTQPYLVPGLQLLVQDCSRSFVVRIGPFFTLSMEFFSSLIGVVLTYFIVLVQFN

>EdanOr34P

MVKSVKICGSTVTKTLGFRAVLYTNLISGFWIPLPPLNFKLKFLVKCIQIFEWFIVLSLGTQLVLTTYFLSQNHIFTWNSILRIVASIQNLFHSVARSLIFANSKKQLIQIIIDAKKLTNRRMFKSLQGGVILRTSKAILRALILPLTLLAGGQFFSXLYKLIEAWLEATHLERSKWPDFVLSTFASLGYTISYIKIMSLDALFIGLFHFVAEELRVLQSTLFDAVHATSKNDNCNKKLDFVVWTNQQHALTKLVENINAMTSPIVLLTMLGNTLCLCFLTFISARHAIRNESILEVDTLTAIYCVITLVQTALYCEAGDRMKKEGLGVSDVACHGPWLRANPLIVTSLPLLARDCRRCFVVRGGQFFVLSFEFFASVIGVVITYFLVLLQMK

>EdanOr35FI

MVLKSRILKSVRICTSMGMDVFYPARALDIFGLYGKKKYSFGKVMGRGLMVSMFILQVFFQWKVMRHMEHTVITILYSFYLSFVGINTVFRFNFFVLKSVYIYVMQCIVLAVTDAFICSLMLAAAERGAFLARVAPRALLPGRDGEVTRMCRAWIRYHQHYLEILKKINKEIGPLLLQMQIFSIIRLLFNTFLGVVEGKVLILPSLSDSAPLLINLLMFSVAGQKIINASNRLARMALSQEEVSRGALESGPTRNVLQIVRARCAVRDGKITGLGLFVVSIGFFTRVLSATFSYILVLYQLHYKKT

>EdanOr36

MGLDVFYPAWALDFFGLYGKPRYNWNTILTYTVLVSVLMLHTLLLLRVQFLEYTVVMTVFSICLSLIGTNFVFRFCFFVYKHTPHNECKQFDALYSDMRAQSSRTIRRFCRTYFTYTAFCSLLLVATQFISSFFYSERYRFDADNKYFYVDQWRPLLYEIWLPWGDPHEWPYYPYVLLWQEFVYLMQSCVNAVTDAFICSLMLAAAERGAFLARVAPRALLPGRDGEVTRMCRAWIRYHQHYLGILTMINKELGPLLLEIQLFGITKVMFNVFLGIVSGEIIAILAIADAGPLLINLLTFSIAGQKIINASNQLARVTVNAAEIARGGLQLVSLRNLLQVVRARCAATADGCITGLGYFKVSIAFFARVLSAGFTYVLVLNQLKSKK

>EdanOr37F

MDVSYASNTLKSFGMYGKTKMTFSVLLTYVTLFLFFSFNTLMVVRLLLNNYTILMSTFIFYLVIIAFNVLFRFYFFALNNVTPRSVSVNFDVLETEMRIKSNQKLRKFCRMCYVFGAVCNLVFVSSPQLLSLTYDQRCRVDVEGMRLYLDQWHPLLYEIWLPGTDAHEKPLYPYIYVLQSFTIQLIIDVVTYAFLCSLMLAVSERGAFLARLAPRALRPGRKGHVTLMGRAWIRYHQHYLGIIRRINKELGPFVLLIQVYGVTKLMFNVFFGLVAGEMMIALAASDVCPLILNLLAFSVVGQKIINSSEQLARSTVSVMEITRGGLKPGPTLSALQVVRARCAMGDGKITGLRLFTVHIGFFAKVFSAAMSYILVLIQVQHHK

>EdanOr38F

MDVAYPVRVLRFFGMYGAARKNTFFTFIFVLLLSIITVLMIYRFFYFEYSMMMYIFISYISVITLNIIYRFWFLVAPPYIASQNFSELEKKMMAKSTRNIRRFCLFFYIFCALCNIVFVFVPSISSIFYKERFRKDTEGIRLYLDLWRPLIYEIWLPYFGNPHEYPVYPFVLVLEVSAFWMQAVIDVVTYAYLCSLMLAVAERGAFLARLAPRALRPGRKGHVTPMGRAWIRYHQQYLEIIRRINHELGTFVLEIETYGVIKLMFSAFFGKTSGEMIATMVASDTGPLLLNIFAFSIVGQKIIDSGNKLAKSTISVAEISRGILESGSTRNTLQVVRARCAVPDAKITGLRLFTVSIRFFVKVISAACSYVLVLLQLQSKKI

>EdanOr39

MLWNTAPVRVLHAFGFFWDRKVSLVLTFIFLISHMTTHVLLLINMRQIKVNLTDACTIALIELRAWHGIARAFHILLNRRGIFDLVDFMNNSIDPNNKNFLAMETTIRLRTSRIIRKFCRVVFSYKFFSHIFFLLGFFSGIMKPERYVKGTIYNDQWRPLVYEVWWPWGDIHEFPNYYYMLPLQLLMHFVHNGINTIMDLFLGSLMFLVAEQATFLTNTASRALRSGRRGQVTSSCRAWIRYHQYHLETIRHLNSELGQQILMTYASTACQLMLATFLFRELRHYPGTMIIHSIFVITPVLLHLLVFSMIGQRVINKEASLTSTVLNTVEVSRGELGPCPVRYTLEVLRARCAVARDYINGLGVFTVSMEFFTQTLSAAVSYFVVLIHLKT

>EdanOr40I

MELQFILEALKILGIYKDKDSSFIFRLCRYVTIIQFLILHVFVGLQFISATVYIRVNIIYYFLVAATVIGGPLYISRCGKRIRYIIDLLEGDLPGITNYGEMMREEIRMKFRSERYIRRYCIFVFSHTIVTMLIIIGSFVIFRTIATMIGFTSIITNSSQGQSTIPRFLMYVMWWPTNIRELPTYYYIIAWQSFNGVYTIAITNVMNAFTSSLLLAASSRAEMLAKTAKTCLVPLRNNPKRFSKKFRTWLCKHQRYLTFNDTTMSATIIIVMLEKILQMAIMSYAGQKVIDSSLLLSHSVVSSSQIDTGVLSASRNTSALQVLHTRTSGPISKVSGLGFFTVSMEFFASVLSASTTYLLFLLQFKAVGGPTAYEVPKE

>EdanOr41

MRESSNMLLFNKLCYEMNYASPNITCSLALDVMEVDLNLTVLRFAGFPDLRKSNSTRRTWFWINLIQFLIPHILMVIYYLPIGLNVYSGVNYFFYASNCIFTITRWFYFMRNNNDINIILNNICEKEVNGSVTMMKRKVRSRLAQRIRRYNAVSFSYLACCAIALIGGFILYKVKSPSGTSLKPPRRILLFGVWWFTDWHENELTYVMLFLWEGVVLMTSLAASIAVNALICALLLAVSARANILSYAARTTLMPNKIQRTKRTLSAFRSWICKHQRYLSTLKRINIVFGPMILLSHFEAIISIIAFSYMSIKVRDQVMSALCLAPVFGSLLHIFLLSKAGQEVIDMSVRLSGSVMSIAHLQSGATVSKRIRSILQVLTARLSVINDRASGLSYFTVSLGVFTSILNACVSYLLVLLSFRGPENEPEYFAKKPI

>EdanOr42I

MEFEFNLKALKVLGFLVPTDKRPSCLHRLWNVVTLLQLVILHALIVIDFVAGLSPTMYARVLSSFHMMLGTIVVFRSXXXXXXTIATFLRVGSYTMNKKSKGTIRFILYITWWPTNVRETPTYYFIILWQGFTATFTLAVLTITDAFTCALLLAASARAEFLSRTISRALQPNRYNKHQLSRSFRAWLMRHQRYLAMMEQLNVVAGPMVFIAHLTTLLMCIVFSYVIYKISDTIMAGMLMGLNLGALIQLAIMSYAGQHVIDTSARLNCSIMHASRVQQGLLSRGPNRSAFQVLMTRTSVLNDRCSRVSGIGFFTVSMEFFSSVLSASMSYLLFLLQFKSAGPKVIQDLNDK

>EdanOr43

MDSWLQFQINLRALKIVGIFIPIHTWEKPSKLLQTWKFLGIFLYIVLHLLVIANLLLESKTLGIFSRLMSSYNIFVCTIILLKIVYFSMNSMRIRKLITLIDEVTAGRTNGWRLRGLSLREDLYMRRKSARNCRFISMYIFLVTIGAIFVFIGTVMLFRTITIVLDWSKPVNENKQIIRKFRRVTLYHMWWPNKIMELPTYYFILLWQVFCSMISLTVSCTTDALTCALMLAASERADMLAKTAPRALVPTANRNTLAPAFRAWIRTHQRYLKMMECLMQVIGPMVFISHTMAFVTFIIISLGVFKASSNSIGDSIMVATMLTITVRGLIQLTFMSYSGQKIIDSSARLSRSVVNAAQVQRGLLSRGPNRSALQVLVTRMSVLGDRYAQVSGLGFFTVSMEFFSSVISGSLSYLLVLLQFKSIVSTI

>EdanOr44C

METDFILRTMRAVGMCVTNSVKPKFSKTGIVMLFMFVSIMEVLMIAGYLTAKSQSLYSKLMSIYHTFNFVVTIFRVVYFSTRRFHLHFIIELMEDFPVISNPCILFHRTFLIYLQSIDASIVDAANKPVKRYLISYMWWPTNIRKTPTYYFILTWQCFAALYATFIAAVSDAFTCSLMLAVSARAEMLTRTALRAIALSKPNVRLTAKFRYWLQRHQHYLKLVKMLQQINNLTSPLVFVSYLHSLVTCIIAAFIIMKDNNETLAMVAGTYALLGTIQLALLSHAGQNNARLSSCLLGTITNEVLSRGANRSSLQVLMARTSIIDDRFARISGFGFFTASLEFFSS

>EdanOr45

MDTSELMFPVETLGWVGFLAPHVKPLSRRSFTWSALTLLQYLGMNLLIFARLASVDFSLSLVISLVAHTVNLVETIFLRIYYTIRRDAISNLVQDISAVSEMNEPFASADREMRNNSRRRIKNFSSSVFLFNFAVALLTVLRYMFSSAVRGLNECMPENDCRNTEGANDHHGRLLFDIWWPGNPSVTPVYYFIMAWQLATLFTHISNVAASDAFACSLALAISERSALLTKDAGCALLPGHDNQVTPFCRGWLKYHQNYLRVVVTVNDVLGPVFFFTFCIAGLNVITLSYISAKAQDSGLLTSTVTVIAVLLVRLFALAYAGQCVHTKSEELSRNSLSAAQVAKGALKDGPARTTLLVLITRLSGGIKPEEISGLGYFAISLEFYTKILSITVSLLLILLQLQQ

>EdanOr46

MVIETIRTQLHSSEWQREHETAEVLVGAHLVISPAFMTPSNVTLTAAFVSNSLQTAMRHIYFFVRRKQIAELVENIRSSPSKESVDVGAAETAMRLTSATQVHHYSAVIALHHACAAAVSSVFIFILPTVLQSSENPPRRPLYSEMWFPYDLKDPLVHTYVLFWQALAVLLNVASAATTDAFTCSVMLVTAERSAMLARVAPKALLPSQGNLTPHFRAWVKHHQHYLGLFSRINTLMGPIIFSVHLFGIINIIVFAYLIMKVDLFSMLVALAHLASVLLQVYTFANAGQRVIDNSEELGRNTLSAAQVARGGLCEGHARSALLVLVARCSGARPEELSGMGYFTVSVPLFSAVLGASVSFLLVLVQFK

**43 *Thermobia domestica* ORs**

>TdomOrcoFJ

MKYIRQGLVADIYPIIRTMRFVGHYILRYYQDDGPMKRAFRAIYSVSNISLITLHFLLGAVSIMFKMNDIEGLVANAISTFFAFHAVTKMIYFAVRKKAFYETLDCWDVTNSHPMFAESNARFKMSAIRRTKILLLSVSGGCALFIIFWSIRPFFVAPFRTIMDGNETIVVENSPLIVDAWYPWSLKDFTFFAASYFYQLYWLIFCIFQVNSIDVLFCSFLIYACEQLKHLKEIMTPLVELSAGRDPEALRKAELWPEITAIDKSASRLDGTPPPYQTATRNRIYPETLGVDMERSLVLSDFAHLKEPMVTYSTDEANIGENVLTKKQQLYVRSAIKYWVERHKHVVRFVESVGDTYGLALLLHMLTSTITLSLLAYEATKISAFDIYAMNVIGYLLYTLLQVFLFCIFGNDLIEESLSVMKAAYECPWYNGSEEAKTFIQIVCQQCQRALSISGAKFFTVSLDLFASVLGAVVTYFMVLIQLK

>TdomOr1J

MPEPQKGLIALLQTHIKFLQFSGHFMLDFHSNDAPMMRWFRAMYSIMQILISTLHMIFCVLRILYSLSNLSKLVPVVVSTTFAIHGVIKLIYVAVRRKTFTKVLRLWDDAGTHPMFEKADEMTLQVTRYRTKRWLIISTVFYLFYTVFWTVSPFFDKDYEDIIVDNETMRVDKPRLIVGAWYPLDLTSSPGYQIAFLYQTYWAFFGPMQVHSIDILFCCMLVHASEQLKHLKKILIPLVELSSNPDGKSVTEKSKYMGVSQLSLLSEGNNYMSELPRRRQMAWSTNRIYVDEVLNRENVMNSGGGNTPMDAGGAAELIENEKARHLRSAIKYWVERHRQIMRFASDVEEMYGLALLFHILLASLTLCLLAYEASQIREMNVYSINVLGYMIQNLLHIFVFCIEGNSLIEQSSSLMRSVYDSSWYAGSEDAKVFIQIVSQQCQRPLSISGAKFFTLSFDFFGSVLGAVITYFIVLVQMK

>TdomOr2

MKLEEYKAHGVAELLSPLIYLMKYTGYLFLFEKDNKRVKRKWKTYFQVAFSLLLYVLITLHIASFITDAVLKSNDFRQFIRSFLPTMSALTGYYKLYYVAIRRQVFYKALRSWKEGLKTHPLIEDLEDRTIEYTYRMCKKLTIGGLILVYIVYVLWSLKPFFIVEKTSVQRGNTTVEVIQRHLIIDGWYPFDISSMPNFIAAYIVQLIYAWFVCGQLIAFDLLLCEMIYHLSQQIRMLKRLIAPFALLDSDQLSEEVDDLVQMIVQNKLNHNSQRLKLDSLARNLEKGEAKIQLSEYKLFIQLSKYRSELLPEMRKDLMSSLIKYWVDRHRSIIRFTDSVQETFGTALMLQMQNSVLILSLLAYEASMEKQFSMYSLAIIGYIFHCLSSVLLFCYFGDQLIQESNSMLRSLYDSAWYHTSRDFKHFITIASQQCQWPLKITGHMFFTLSYEFLASLLSVVMTYYLFLIQLN

>TdomOr3

MKLEEYKTHGLAELLWPLIYMMKYTGYLFLFDKEGVKVQRKCKTYFHIVFSLLLYILITLQTASFIAYVVLKSDDLKQFIRGILPLMNIITAYYKFYYVAIRRQVFYKTLRSWKAGLKTHPLIEDLEDRTIQYTYRICKKMAFGGVTLVYIVCIIWFLKPFFMVKKIIDQRGNTTIEIIRRPLIVDGWYPLDISYTPNYIALYISQAIYAWLICGQMIAFDLLLCQMMYHLSQQIRMLKRLVTPLALLDSDKLSEEVDEVVQMTVCNNINLNRKRFKVESLERNLKEEADIQLSVYNLLLQLSKYRSELLPQQRKDLMASLIKYWVDRHRSIIRFTDSVQDTFGISLMYQMTIAVLILTLLAYEASTEKEFSMYSLAIIGYIFHCLATVLLFCYFGDLLLQESNSMLRSLYDSAWYHTSRDFKHFISIACQQCQSPLKITGHMFFTLSYGFLASLLSLVMSYYLFLIQLN

>TdomOr4

MHTKFKSRGLVAIVWPSIRVLQISGHFILDFYNDNTFSKVLVRALHSIIQIAFNALHFIFCFVDIVLKADDFEKMVGTVATTFYAVHGMTKLFYVVFRRKLLYHTLSSWNGLKEHPLFWKSGLEACKRSYVTSKKLLYYVNGFILIDAVFWAAKTFFSYNLEEVQVGNSTVTIKTKRLIVESWYPWDIKGSGFIAAYIFQYYWINVCVIQVTTFDMLFCSMLVFAVNQIRHLKTTLKEIVELGCENNEERETKIIDQWLDTYNEVDNSNFTSIEQHNMEMIKSFRNGRNKLKKKVLIQSLIAYWVCRHRDVIRFVTAVDNTYGLPVMFHMLLATITLSLVAFEASNKQDSGIYVGNVLGYLIHNISQVYLFCAYGNKLLEESSSLLRTLYDTPWYETSKEVQTFLKIVGQQCQRPLIFSGAKFFSLSYDFFSAMMGSVLTYYLFLVQIKNER

>TdomOr5J

MGNQSDYRRYPGLPGLYWRSVRLFQLGGHFFYDFHTNYNFWVVILRIAYSVFSISVVTLHFILCIVDIFYNIVDFRKFLSTIATTTYAFQGILKGWYSAFHIKSFRDLLHSWDHVQTHPLFAPDNEICERTASRRAKRVVTIVFALIVFDANFWIIKPLFEYKLTEVDTGNETIIVKEKRLVVESWYPFNKAENFVAAYVFQTVWLYCCLLQVTSLDLVLISMTIHAIHQVIHLKHTAKKIIYLSSSLKVPEDYNHLSSDESRYNSRKDDQGRQYMFSAVADIQLDLVEGLGDLRSTRTKLVYSLIKSWVDRHREIIRFVDRMEETYGLGITLHILVSSVTLTAIAYEASREGNSGLHVGALLWHFIHSITQVFIFSYYGDELMQTHSNLIQDLYNAPWEDATRETQMFLQVVSEQCEKPLRLTGTQFFTLSFDFFGAFFGAVVSYYLFLVQFK

>TdomOr6J

MKKNTDYKTRPGLAGLYWRGIYLIQVAGHFFYDYHQNYGFWRMLYRIIYSIFSITVSSLHLIFCTVDIINKRADFRRMINAIATTTYAFQGVSKMLYLAFRPKSFQNLLHCWDHVQTHPLFAVDNESCDRTAYVRAKKIVTLVFTLIVLDATFWAIKPLLEYKEKELTEGNETIIVKEKRLIVESWYPFDPAESRINFLAAYMFQVVWIYLCVTQVTSLDMLLCCMVIHAIEQIEHLRNAARIVVNFSTKYPQQKNNFFLEELAYRYRKEFSQLQQPSNQGTQQLVSTSPASAELGLIGNSDSDERNKLVFSLIKSWVVRHTDIIRFVDIVEYTYGISLALHMLVATLTLSVLAYEASMEETLGIQVGNILGYLLHSIGQVFLFCYYGDILMQSSVNIMQDLYETSWDDANADTQMFIKIVYVQCQRPLKLTGYKFFTLSFDFLGTFMGAVMSYYIFLVQFK

>TdomOr7JC

MTQSLNIRDLKEQTGCRVQPGLAGLYWYSVRFIEISGHFFYDYNVNYSFQRRILRLLYSTITFCVTLSHFLLSTIHIVLKTKDLRQVINAITTYAYSFLGVLKVLYLISRVKGFKRLLHYWDDVQPHPLFVNENENCEKTTYIRAKNIITFSITFGLVNCLFWIIKPFLINKVQEVNIGNDTTIIEEASLIVDSGYPFDRSSLATFISVYVFQVIWLFVCFMQITSIDVFLCCVIIHAIEQMNYLRKCAEKITDLSITLSHSGQTTGFSPEYTGYANTTRVPKYGRSINEENCQFKTSSNMYEKLPIAISDPDAKSKFWSAVTKSWADRHTKIIQFVDSIEETFGIVMCFHMFTATVTVSVLAYEASREETIGVQAGNLLGYIIHTLGQVFMFCYYGNELMEVSTNLGRDLYETPWDDATEDTHMFIKIVNVQCQKPLKLTGYKFFTLSYDFFTT

>TdomOr8J

MSKNSDFHKRPGLAGLYWYSIRILELGHHFSYRTKYTFCRSVIRVVYTCFSIIITYLHFVFTTVQIINTRTNFKEMVYTIAPATYAFHSVTKTSYLALRTKTLLNLLHSWDHVKVHPLFAADYEKFEKIAYSRAKKIVLLIFTLISINGIFWALKPLVSLRERKIDTGNETIVLKEKFLSVPSWYPLDPQENDANFYAAFLFQVFWMICAMLQVTSFDLVLCCMIIHAIHQMEFLSMIVKKIVALSASVKNAKKNEDMSLEKLPYDYRNDFLLLQQPPLRDDKQSTDSLNPNSQLDIPEDLDSASRTKLVSILIKEWVDHHRDIMRFVGKIEETYGFALMMHMALATMTLSILAYEASLEESLNMQVVNLLGYIMHTLGQVFLFCYYGDELIEVSNNLGPYIYETPWEEANNEVKIFIKVVNEQCKQPLKLTGYFFFTLSFDFFGTYVGAVVSYYLFLVQFK

>TdomOr9J

MLGFQSLQVCLQFNFRLLKVAGHWITEPAQDNNNRQNAALHWSYWLLLLYRVFITLITTIHVISVVAGCLKNADKFKDQPMIGAMGLFAFQALVKLVYIILKRAKIKNVLSTWNDTYTHSSFIWSRINAIESSTKSSKTVSTCLLASYVVLAIQWCLAPTSVSKDTTEEYNITTFINVTSSSKPLPFLAWFPLDFERSPIYTFIFAFQVVASLYFALIVAAFDGLFCALLSQAVNQMDHLRDSLGFLIDVCIENEPLLKDNIKSPNRTAIDNLASEIAGGLYRRYITSSSGSRIRPIELPYDQTTNKSTNLIVKSGRNKGFTHFGGDDYWENMRTSMSYCIHHHQYLIRFTDTLEELFSASMLIQFLYSTGLLCVLAFEATLIRGFDMKTFTLVVFLLVSVIQLFAICSYGNKILSESTRVTEEAYSKAWHKGSEDVRNVLQLIFQRSQRALVLSGANIFTVDLETFANVLAASFTYFMVLIQLG

>TdomOr10J

MVAKDNTVISFANFLAFHIKFMSISGHWLRLEPHNKWFTKKKVWFTLYRCFIRVFSDIHSITCFIEFLLNITDIEAATGNIVIVLYNTNAFVKMVYYSFRRRQFEELIENFNQEIEELHRLNDIRDAKRKTIATAHKHSKIIGSAIVTSSLLLVGKWCFFPLTVTQPPPDWKPDIAPNSTEEVVFRVLPANAWYPFDTLKTPVYEILAFFQTIGAVYSAFQLATYESHFVAILIYIVALMQHLRWSLGRLVEVSKVDEDIKTEDHSENTDNVRNSLYRDDPRVNVRANEIFTGPRSNNNSNKDVDDVLSYCVQQHQLILRFEKQINILFGPMVFMQFGISILTFCTLAFQATTIRGYGLKIMNLIEYLVVASVQLLTFSIFGNRLITESVSMVDDAYAKEWQKTTAKVKSTLKLIFLNSRKPLSMTGLGLYTLSLETFSSITTASFSYFMVLMQLR

>TdomOr11J

MQIKTDLRSFMRLTDRFMWYSGHFMNVSSTGKCFPLRMMLRAIYVLLARFFIDMHAITCTVEFLRNITDIDQATSVVVVIIFSFNTWFKTYYYTYRRNAFNEMFGLWSDTIDIPSSLREARASSIEAGRKHAKRISFLMMFSLVGMTGKWCLFPLTVAAPPSESIWSNGTLVTSEVRRPLPANAWFPFDPYVTPAYELVTTFQAVGAMYTAAQLASYDAFFVTLMIYAVAQMKHLKYSLGYLVDIDIQLSSQTKRNQKQTTQPAYLDNKRLNMSSFSEARGIDKTTGSEISVKSRDVQNRNENTMNNLEPSLEEHINVLDYCVRLHQLILEFCVELNRLFGVIVLEQFLVSTLTLCTLAFQASTITGYGLKVLNIVEYIICAVIQLLIMSTYGNRILVESVSLTNDVYAKDWHYCSPEVKSCLKLIFLNSKRRLQISGAGVYTLSLESFASIVTASFSYFMVLMQLRK

>TdomOr12J

MEDIKLHPMDHYTSAQIRLFKLLGLWPLDPSKVYGWRLVLHRLHTLYILSIAFLHSLCYLAKFLIYIHDIEQVAKNGVVMLYVLLGVMKQWYMLYKRRQIQSILRMWDNVMEDKRFVKDRVDVTTAMAAKCKKLTYSMWIFGLAMVVHWHLYPLFMNESAEQDIINNGNSSEVVRPYKYLPIEAVYPFDEQISPNYEIAYMLQNMMGPTILTTNVTFDNFFIVLLMLVSVQFDHVVNTLKSVSLRNSNSIFSNDRSRNRMIHSQLHGEDDGVDDSHDEFASGVVIKNEEDEAIYSLVMYCVKVHRESIRVANELEKLYSPFMLVFYLFFLIIMCLLAFDGSNMNDFGVKMFAMIEYLLLLVGELFVISYCGNELITKSTAVKNAVFESPWYGCSDKVKYAVRMMMIRSESAMKITGKGMFIVQMDAFSNVMGAAVSYYMVLMSFKE

>TdomOr13J

MLENTDERYFTDLEFCLNFILAFLRYVGLMPFTDETSSFIKKVGAYILMTLLSLPVIIQAITSSVQMFLSFEDLGKLATNAVLTLYVDIILIKNFYLYFNRERVLFLFQMWKNCRRSDVFDPLRLESIKKSTRFARNMWLLLWIPSFLMAAQWLFFPATVKTPPPDWDSANGTRIFRVLPASAWFPFDWSRSPAYELCYLQQAIVGILCVSQAGGFDSLFVSMIILNVAQLRHISECLSKFPSLVFPRQSTVSFHLNNDQGKRQMPRNSLEKIDSVGSFSLPYDGKEQSYKINISARGTYNLSHEDETKVTLAAKYIVHNHIMSIRFVEEVERFFTPVMLAQFVVTTLCLCLVTFEASTIQGYGSKIVSLVEYFAVTSLQMFILCYFGNQMITASSSVKEAAYASQWYSYGKKFKFCVRMIVLRAQIPLILTGGGIFTLSLETFKSIMAAAASYYLVLKQVKEDSSGLPIETPF

>TdomOr14J

MKISGENRKSFLTNLQLALDFNLKFLRYVGLIPHTNKTSSLVKKFLAYCVMILLALPITIQGIIGTVQLCYSFRDLGELATTAVVTFYIDTVFIKVYYMFFNRRKALRLFEMWNLCVKHEIFDDLRLESVEKSIRTSKIACLLLWLPPLFTGCQWLFLPLGQSAPTDWDSSNGTRPFRKLPAQAWYPFDYSISPAYEICYLQQAFSAFIPVCQAGAFDALFASMIIVNVAQFKHLSKCLSEFPSLVFPNSRQNNLKALPNTLLTVKDADRSTEQNPDLRDFVWRSKSIQNLPTEDEEKVASAAKYIIQNHALFLRFVEEVESFYSPIMLAQFVITTLSLCLVTFEASTIQEFSLKIITLVEYFTALSLQLFILCLFGDQMISASKSVKDAAYASTWYSYGKKFHYCVRMIVLRSQMPLRLTGGNIFTLSLETFNSIMTASVSYFLVLKQLREDSEGATTDN

>TdomOr15aJ

MYFTGNNFYTFVKSLFARKEVSAEVNNYVVKLLSAVGYWLEDLPCYSSSKISWFSFIYFLSSTSLLCLAFILNVLDLLLSEVPFILKTENIINALHLFKAMISAVVITLKRKELKSLPTVIINDNFVLFSHSENTPCCAYSMKLVIRIMSVMVFVVSLTGMSSWIYVSLNRTVCSAPSLVYNTSDNNCNTSAEPAVIRMWLPFDASASPAFEYVATFQIVCLCCYVLKNIGSTITIFIFLMKAGRSLEFLHRFLEILLSNGALGTLLRSSSSLVKNKSIINMASRPRSKFRYIANNNKLWNLSRSCISSQSVISTRLMNNNGINLWIKIHQNVIRFMESIESIFSLIIFVNVATDTGSLCLLAYTAANVHNQGGTAGAMLGFFFINTFEIFILCYLGSRIKNHHSSIISSIYRSAWMQNPVARQSDLQMIVLQCQQPLTISGAGFFTLSLELFLSIFGIVTSYFLVLVQL

>TdomOr15bJ

MFFIGNTFYTFLKSLFTKLKVNTKETNHVVNLLSVSGYWLENMPSYNSSKFSWFLFAYFLSTAFLVSCSLILNILALFLAKVQFVEKAEYIVNTLNLFKAMFTTVLITLKRKEIRSLSTMVIHDNFVRLPHTGKSSCLVYSMESAIRFIAVLAFVVPSGGMLFWIYTALNRDACPLSSLPYNISVNNCNNSFVPSIIMMWYPFDASSSPVYEYVAIFQIICLCCYALKIIGSDVTIFIFLFKTGRYLEILQKSMEELLSNRPLATSFRSTSTSIENNSVYNVTPRPRSKFGYVANKGKLWILSRSSVTSQSIIRKESINSSGLNLWITNHQNIIRFMESIESIFSLIIFVNVATDTGSLCLLAYTAANVHNQGGTAGAMLGFFFINTFEIFILCYLGSRIKNHHSSIISSIYRSAWMQNPVARQSDLQMIVLQCQQPLTISGAGFFTLSLELFLSIFGIVTSYFLVLVQL

>TdomOr15cJP

MYDTRNTFYTFLKSSFTKREVSSKVNNHVVKLLSATGYWLDDFPCCSSSILSWILFVYFVSTTILTCFSSIPTILGLFFSKVPLLQEADIIVHTINILKAMIATVVITLNRKEIRTLLTMIIKDNFVPLSHSGETCVYNIKSTNRFIASVMFGIPLFGMAFWIYVSLSQTVCPTSSLSYNMSVNSCIAVVEPFVLRMYPFDASVSPVYEYVATFQVACYYSYGMKIIGSDIILFISLFKIVRDLEFLQKSMEVLLSNISLSTTIFNLTPETRSKFGYNANKSKLQIFSTSIKVNSQSVISTQFVNSNGIHLWIKNHQKLIRFMESIESIFSLIIFVNVATDTGSLCLLAYTAANVHNQGGTAGAMLGFFFINTFEIFILCYLGSRIKNHHSSIISSIYRSAWMQNPVARQSDLQMIVLQCQQPLTISGAGFFTLSLELFLSIFGIVTSYFLVLVQL

>TdomOr16JC

MPFTKIVNINLVIVAFSTLFSPKCVFEDKASVLYWFRNTLVGILGSITVYHTSLSIIAIFMNIHDFTSVIFICMTLLYAFQALFRFFFVIINQKRIVKLMDVCSSLPQTCPEFNYSLKQAFECIKKESKKLFLMMFLGSEIVGLGYIGLPILRASILSNVTAHNEELPFKSGIAAKRPLITTCWYPYDVFVTPVYETEFFMEAIGTLWVIAVTSSCDSFLCSFIIYPIEMMEHLSRTILLITSDNLPTTHVRNNPFFSSSESISAIGYTMPSNCIRRGRNHDISQVNFIDIEEDIDNDQDSEGRSSAAKIIYQRRLLKAWIQQHQTITRTVDEIEAVFSPLILYTFLQGGIALCFLAYVAVRIRDLVPIVLITGYFFIIVLQLYTLSMHGERLMKVTSSPTNIMYDAPWWKCPRSIRQDIKMIYFRCQKPLKLTGMGYFTLSFEFFGS

>TdomOr17J

MQKMKLKEWRNSKMTSSGVIPFTSVAKPLIFMMLISAHWYPELTLRKKSIWYWIRAVYATVAISIPIYHVALATIDIFLNIKEFMNIIFVTMTLLYVVQGVFRVFFVILKKKSITKLVGMCSQMPAMCQDFEDSMTTASRNTGAKSLKLFLIMYIYIQMIAFAYIGLPFINAARLTNATMEENSPLKRGIAAPRPLIVTCWFPYDVFQTPVYETEVLLQAIGTLWTVGMVTTCDTLFCTFVIYVIEVIEHLGRMSIHITDETTRNTVHNCETFEKSESTINLSVSHKDIKGTFCENKGDTVAVKINPNIGKSNLIKWGQPYLTSKKKLLEVWVQQHQHILKTVDEIEAVFSPLILYTFLQGGIALCFLAYVAVRIRDLVPIVLITGYFFIIVLQLYTLSMHGERLMKVTSSPTNIMYDAPWWKCPRSIRQDIKMIYFRCQKPLKLTGMGYFTLSFEFFGSMLGAALSYFIVLMQLQ

>TdomOr18

MDVGEYTFEKLNKYTIRLLYISGLWFPDWPKQDPRWLMLPLRVLYFIFSAGFQSIHCVIGILDLMFQVSSFRDIIVNLVTTLYLFQAVFKTLFIFYNKGNLKRLVEMCNNVTTRQTKYITFQNSMAELHKGIEKDSKIMSHSIVDISLIVGSSFGLIPFVQSIFFQPTESDDMLYLNNTGGSTEFLTVSPLEIHHNESEIVTHPVARALVFRAYYPFDLAVDWIYGIVAFVQSYETVICVVVNTSCDALFFSFAVLIKHYLRHLQRISKMMRFASDFYGLPQDETIYNIKYQTHKVVVKNRKERSNTNKTNVTFTNDFFKLNDRSEGIMGYLQDSRNTRDEVVLWIVDHQTMLSLLDEINSIFAPLILFTSLQCMLTLCLLAYVAAMVDEAFFRFCISGYLIVVLTQTWTYSINGQGVINESVNLCKEIYGTGWYGYSDSEKNAMKIVCEVCKRELFFAGMGFFRLSTEFFTNTVGAAFTYFMVLIQFKD

>TdomOr19

MEQNKNKLEKLFSYNLKVFTVCGTSFPEWPVKNPKWWFYIIRIFYFMITAAIPLLQIPFTIMDLMYQVTVFQEAIMNMVVTLVLFLQLFRECFLFYNRKRMKRLFNAANILIENCGKVPKFRVSLEECLKETGKQSKIFTHLLVDILAIAGLLYAFLPLAQSFFFPSKFGNFSVDSNDSSIAAPTKRPLAFRAYYPVDLENEVIYGIIGFLQNMTGIIAVSIIGAGDSLFMSFVVFVRQLLRHLERMCQQIFLHPNTNIPLEEKPARSTMLPVDDSTTQEEIDVRVSGDDLNQQHNINGLTDKLSYEDSIKLRRDLIIWIQQHQSIISLYHEIEDIFSPLVLQTFLVTMMELCLSAYYAAMIDDYYDLLPLAGYQVAVFLQIFLYSFNGQRVINESENLERVVYESEWYCFNHVEEQAVKIIREICSKELSFTGMGYFHLTQVFFTNTVGAAVTYFMVLIQFKD

>TdomOr20J

MEKDKNKLEKLFAYTLKVAKICGNSFPEWQVKNPKWWFYVVRVMHFMMTAAVPMLHIPFTLVDLFYKVSSFQEVIINMVMTLVLIQTVVRELFYLYNKKRLKRLFDTSNILIENCGKFPGFRASLEESLSETAKHSSMFTHLLVDSLAIDAVLYISLPLATNIFFPTKVASFSVDSNETVDLVAVSGNRPLAFRAYYPFDLQSNWLYGIVAYFQYVSTIVSVSVLGDSDALFLFFSVFVRELLRHLQRISQQYFLYPNNKAFPRTKSQSHTRHPVDDSIFNKELDDRERGNILNNKDYENSENLSYEHSKNLRKELILWIQQHQSIISLYYDIEAVFSPLVLWAFLVCMMELCMSAYFAAVVDDYYDLLPEAGYLVAVLLEIFLYAIHGQRVINESVNLAKLIYESEWYSLNPVEEQAMKIIKEIFIKEVSFTGMEYFHPTQVFFTSIVTAAISYFLVLIQFKD

>TdomOr21

MGGDICSINKLFGYTIKLLKISGTLSRERRKESSKCIFYITRFVHYIITAGMPWLHACLGIVDLCLEVSTISTAIVNMQMSLFFLQATFRVLFMLYNTKAMKHLFEATDTLISCSKKDLKFQKSFETCLRITAKHSKIVTHFFVDFCSVIAVMYGFLPLSRSIFYPPASDDLSAQDNETERIVETTRPLPIRVYYPFDLQSNWIYGGVIFVQTWTIVMGVFVVGAGDALIFSFAILVRQLLCHLERLCVQLLIDTNNDKGSRITLCNAIAGDPDCLTPVEIRLCKKIKSQKTTQNNKNERSHTDLIEVSDCFKIELILWIEEHQRILSLFYEIEEIFQPVVLQIFVIAILELCLSAYLLATESDYFFLFCVTGYMFAALFQICLYAVHGQLVINQNARLVNIICEIDWTTFNLKEQQAVKLITKMCNKDLHFTGMSFFHLSLNFFTNTVAAAVTYFMVLIHFQD

>TdomOr22J

MEHDKPSIRKLFVYDVKLINLSGIIELPEEPIGRFKCKHFITRSVYFIITVGLLLLHAALAVLDLFLQVSAFQTAIENIITTLAFVQYVIRVGFLLSKKKQLVRLFEKTDKFFRKSSQHPEFQNSLEVCIEEIAKQSKKLTHMFVDTWIVTAFLYSLFTASATIIQLSIGNNIRHGEMNETDTVVHYERPLVFRAYYPFDLLSNWVYGIIVLFQTYVAVMVILSISSCDCLFLSYIIFIRQFVCHLERLCVQLFLATNLKNSALDFSMASRSNSPHLRKEVPDFYKRHETEIVRKNTIEDVGTILTNNHIKSSSGLRIELILWIKDHQRVLKLFYEVEDVFSPLVLQVFLIVISELCLTAYLIATVDEYFFLLSMGVYAFAILFQIWLYASIGQLVINESENLSRVFYKSNWYFFNAAEKEAVKLITNMSNRIIYFTGMGFFRLSQEFFTNVVSAAISYFMVLITFKE

>TdomOr23

MLHSEIEFMGKRFYEQIFGYNMKLLKLCGIINFAARPVDRVKCIPYITRTVHFIITVGIILLHTHLAILGLFLEVSSFQTAFENIIATLVYLQYMFHLCFILYRKKQLEILFNKSISFISNPSRYSEFQNSFEICIQETTSQTRKFTHMFVDTCIVFAFLYCLNSLSANIIFLPSIENNLFTELNETTAVVDDRKPPIFGAYYPFALQSNWVYGIVAIFQIYTTVLTVVTIASCDCLFINYTIFIRQLLRYLGRLYAQIGRENNPVNSRVTSAKVSSRVNLHAVPSEVALSKEVENNKTRIENTNFQNFTCINKIRDSAKLRTELAVWIQEHQSILSLFHEVETIFSPFVLHIFLLTIVQLCLAAYLVTRVGDKFILICLGSYLFIILLQVWLYAIFGQLVTNESVNLSKAIYENEWYTFNNSEKQVVKIISLISAKELFFTGMGFFQLTQEFFTNIVAAAISYFLILIQLKD

>TdomOr24a

MERENFPINKLFSYTIKLLNVCGILLVHFPQHQIGRHNWKFYIIRVSYSIFTLGLPLLHVLLSILDLFLQVSTFETAVENIMVTMGFFEFLFRISFMLYKQRQMKHLFKSTNTLIVSLSKRSEFQNSFESCFQKTIKESRKLTHVVVDSITILGFVYCFLPLSVNLFPESGNLSEGINVTECSIEVSRPLIFRAYYPFALQSNWVYIVVLLIQTYVTIMITVTVCTCDCLFFSYTIFIRHLLRHLERLCVQLLFDQKLKTFPGTQINVTTSDPLSPDQDTYFNKVIENGSINQDEITNDKIKQFLYYKEAQNSNERKITLISWIEEHRSVLRLFDEVEAVFSPFVLQIFLITIIELCLTAYLTTKVDNYFFFFCLGSYFGVVLFQIWLYAIFGQLVTNESVNLSRIIYESDWYNFNNSETQVLKVISRMAARDLSFSGMKFFRLSQVFFTNILTAAITYFMVLIQLKD

>TdomOr24bP

MEREKYSIEKLFDYVIKVFSISGLIFRQPHFDTLNTKHYIVLVGYSTITVGLIVVHALLSILDLFIQVSTFEEAVENIIITIIFLQYVFRVCFIIYKKQQLRILFEKANTLIYNSLRHRKFQNSFQICLQETAKQSKKLTHMFVDTCIIVALLYSILSVASEAIQFTSRDNSTSFERNETITIVCSRRQLVFRAYYPFDLQSNLIYIFVVIFQICIAVMMVLGIGSCDCLYLSCTVFIZQLLCHLLRLCELLFILNIHCKSEISSKEDVRNVPVNGILRKAMLCTELEYSNTTNMTYKPNSNEKECYSENTNEDSSEVRKYITIWIKEHQSILRLFDEVEAVFSPFVLQIFLITIIELCLTAYLTTKVDNYFFFFCLGSYFGVVLFQIWLYAIFGQLVTNESVNLSRIIYESDWYNFNNSETQVLKVISRMAARDLSFSGMKFFRLSQVFFTNILTAAITYFMVLIQLKD

>TdomOr25FJ

MEPFGDSFEDSSKYVTNLIRYSGHWVPYLRDPNTKIPKFVFVIITIFSFSMQAYHATTVTIRLIVTPQNFAKMIFNFAVFLYIWQVAFRVAVVAFKEKNLWNIFHRKTLQDVYNEDCRKSWKIVMTETHKKSVNMFIILTVFAIVAVSGKMYNVEETSDKKAAGDSDEKVANETETEEVPEITLIYDSWYPFEVNTPTRYWIVFGMQMYSLVHLAMLNFPVDAVYSSVLIRALEEIRHLQRMSDILGNTISKVIGDKQSSLTENMGDLELTDSGDVNRDVSAIVSSSQWDSMKFNVENRKKTNEPIPPEIMEILEQWILTHQSVQRLLADIEKTFSPVAFIILLVDEFVLCLIAYGAAKYDDKSAVTFFVAFMTFLIPELFIVCYYGQKICDESDLLPASIETIPWYNCPDSFKSTVNIILVRCKMLPKLTALGFFNVNVETFGNVLTVAVSYFMVLNSLS

>TdomOr26

MSANEDRALTLLWKIFPFIGFWFPSYRSSKSRRLYWFCYIYQVISLIICGWHTIMIPATSFIEYKALEPFLADLSLSLSVFQMGFRVFWISLKFGTFCTIYDLHRKIVNLRNEMSPKVQESWDIVHQESFRKAKVNFVLFGIPPILSTISRLLAPMADPKNDEDGVILNITAEADEGLRPLVANCIYPFDYSEDFAYAIAMVIQVFGCFTLVNSMVVTDLFQIFALIRLTEECHHLQRMADIMGSTVISVGNSKIGTPLAHKTTDPSSETTEDEVSAIVTRRKFVRDLKLSLDPDAYAMSQLDVDLRMWLTLHRLLIRFLEQLREITSPFILVTFLTNQCSLFLSAYTAVTITDPVFLTFHLCFNLFVFTQIGLPSYWGSKLTEEGVEISRSMYAVPWWNCSKSIQLTFKIILTILERPLTLTGMGFFTLSVEMFGSALGVAFSYFMVLRNLER

>TdomOr27aJ

MNSPCEDKILKFLKKVLPFLGFWTPTESRNFRTTGVHILLYIYYSVASFLMTWTSLGMIIGTLLDSDFNSILINSSLTIYATQNTIRYLLASYLSRTLPGIFKVFEEAPNVKNKFSSRIEESWNLLLTNSNKKTLKCVIIEFCSLFIAGGSRMILPMLLSSEDGSNSRKLSLNSWYPFDYKPSPVYELVQSVQMIYIIIAMMTICPTDLITYYLTVRFTEELKHLERISVLMREVTLKMGSESIVRGRRGQNESDISDQGRQGSTMNNSSHLDIDNTHETDVSQLLSFWIERHKLLIRLFDDIHRVVSPFIFFIFFTDQCVLFLVAYALVKVHDPVYVVFFFSFIVMVIAQLGIVSYLGNQVKKESRRTLRCLYNIEWWHCNKEIRQCIRIVQTRCKVPFMITGLGFFQLSVENFRKVLGVAMSYFLVLIQLEETGMV

>TdomOr27bJ

MNSPSEDKILKFLKKVLPFCGFWTPTESRNFSIMGIHILFYIYYFLFSLMMLWSWLSMVVGTVLDTDLNSILINSSLTFYATQNTCRYLHVSYIARRLPGIFKILEEIPNVKNKFSSSILESRNLLLSSCTRKTLKCVVIDLCSLFIAGGCRMILPMLLSSEDQGDTRKLSLQSWYPFDYQSSPVYELVQFSQMLYITFAMMIISPTDLITYYLTVRFTEELKHLERIAGLMRGITLEMGSESIVHCRAVKNVSDISFQDHEEKAMDISSISDLNNTHEADVSQLLSFWIEHHKLLDRLFDDIHRVVSPFIFFIFFTDQCVLFLVAYALVKVHDPVYVVFFFSFIVMVIAQLGIVSYLGNQVKKESRRTLRCLYNIEWWHCNKEIRQCIRIVQTRCKVPFMITGLGFFQLSVENFRKVLGVAMSYFLVLIQLEETGMV

>TdomOr27cJ

MDSPCEDKILKFLKIILPFCGFWTPSNMRKYSVGGIHIFFSIYYTVASFFMIWSWVSMVIAAFFEFDFISILTSASLVIYGIQNTMRYLLVSYKSRKLPEIFRTLGETPNVKNKFSSTIRESRYLLFKSCTRKTVRFITIIFCSLSIAAGTRMILPIFISSEDQSGSRKLSLNSWYPFDYQPSPIYELVQCSQLIYILFAMATILPTDLIIYYLLIRFTEELKHLERLSKLMREVTLAMDFTSDFSSLKGEGQLVINNDCREETIIDSPDLVINNSHQEDDFSDLLMCWTKHHLILVRLFDDIHRVVSPFIFFIFFTDQCVLFLVAYALVKVHDPVYVVFFFSFIVMVIAQLGIVSYLGNQVKKESRRTLRCLYNIEWWHCNKEIRQCIRIVQTRCKVPFMITGLGFFQLSVENFRKVLGVAMSYFLVLIQLEETGMV

>TdomOr27dJ

MLNLLRKCIFLFGVFTATNVKKKSQVLSLLLYSYKFTISVLMFGHTIGTILRSMLETHFETLLINLSLTIYITQILLRYIIVNASSERSLNILNRFKTTSNFSNMLSSDVKLSYDRMIARCNRNILSITIILMTAYIPTVLSRFISPSLATTDSSENKTVGSDLSQSRKLLIECWYPFDYHPSPMYEITLCFQTVVSLFATFIVITTDLIINYLLVRLIEEYKHVQRLLPMLIKMADIGQELTEKKVLFQKDDIISIISIDSTDDTDTIYRNKISGQCAEDVIFGEHVKIWIKYHLSLTRLFDDIHRVVSPFIFFIFFTDQCVLFLVAYALVKVHDPVYVVFFFSFIVMVIAQLGIVSYLGNQVKKESRRTLRCLYNIEWWHCNKEIRQCIRIVQTRCKVPFMITGLGFFQLSVENFRKVLGVAMSYFLVLIQLEETGMV

>TdomOr28J

MDFGLEAALRPIMILLHLSGHWLITWPNHSRDWPKILKVIHSVLVTIMMTLLVLGNIVDFLSTIYDIRCLVVNGLMVAFFVQGFVYLISIMLHRTSFLKLINLCKEFENCLFFRKSRRCVRKRMVFRSRKTLIVSSILSCTCASLWVYPLLTYKPLVVNGVRYQNSNFSNFSWVFHLSYWYPLENVSSPLYELVLIFEVGSLYVAFLVVLACENLFVTLVLYPLEEVRHMRKIFQAVLNFCDQHLISYNYAEDNDEFSDNIETFKQCKNKSLHTRGDKTRSTMHVSMPQDRNASEYKECWKILFPQLINSNVNNEEDITSEIERDAWKLVESYPNGVEEAVKKCIIHHQTIIRLTSAVEARLADILVTVILSSGCILCMMSYIVFATAKAYPNLVLALLISFIVTFHRTYLACRYGTELIEESREIFFTAYNSPWYEATGNVRFYLEIICQRTQTPLSITGGKFFTVSLGLFGKIMGVILTYFVVLVQLNYNNTTSCVNNQNETDNKT

>TdomOr29J

MSRMSNANQLIGRILSPLLFMCELSGYWISWTHDNRKYTGSYSKRIIKNTLKLIYFIIVNCFGVAIALAAVADLWTKIEHFQEAVYNLISTIYVLLSAVRSLFFALKRRQIIKLISYCNTKVPSCILKDLEREKYRRFACRFKNISIIYSTITILSICTWNVVPFVTSSIEIKEENGRNVSHIRIMGLSTWYPFDTRYSPSYELSIGFQLLGSILINLRCVTCDILWLGIFLFIAEELSVLSYCIENTMLSAYYGVKKNFQAWSSVGALEYSHNRPNADRRYCDKLHNIPSNILLYRDVCPKFGSPPNALENILPEWIILHQNLRRYVYEVNETISPFLLTMFLFSSVNLCLQAYLASRVRGNIAMAISVITYGVLLLLQMYLYCKYGSDIRQRSLGFGSTLYDTPWYQHSSSEVSYYIQVIMLTTQTPMSLNGAGFFSLSLELYASILGAIFTYFLVLLQLT

>TdomOr30FJ

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>TdomOr31aJ

MSGTTFLRENSWAIQNMKGFFHVGRFVGLWVPSQELEKNIFKKYAGYIYNFIMCINTFVLLTFAAIDWSLKSPAFVPVAYNSLSSLIIIQTFVKIVHSLFRRRFLFEVLKKCDYISNTSTFFVPLQKLSFEKGERFYRNTFFILPITFVACGSFWCSLPFILKNSSELSHNETYYRSQILASWYPFDYSTSPGYEISVAYQIIEALSCSVIIVVSDGYFIAFYTYIVAQSHFLGESLKQILVEFDSGIFRGVQRRGPTLKHRRFLTLVVESSVVPDNQQIYSSGFDCTTALTLKETRRYLHEWISYHQSTIRLCDEINSITSPVVVLIFLVDGLILCLLAFMATRVNDVVSVCSLLVYFVLILAQVYLYCLCGDKVKTQSESLADVVYNARWMDLDPDTIQILQMISQRCQKPLTINGGSFFTLSREFFLAMMGSVLTYFIVLTQLPDRQDHENK

>TdomOr31bJ

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>TdomOr31cJ

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>TdomOr31dJ

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>TdomOr31eJ

MHTWSMNSILRSVKHIGIFAGLHIPCDLTEQSKVCSNLQKCYSIFHICDSGIFLLLSIIDLFLKFNNILDLIFSIISTLHVIQTLLKPLYFLLLTKAFRKVFMKLNQIANQSSLELVQKQVLLALSNKCFIVIYVYFLFHLLSLFGWIVAPFYGASEKSSMEKFRCHQVRSSWYPFDYSSSPGYEISVSYQIFQSIKGSLVRCSTDACMFVLVLFVESQLSLMRDALAEILRSNELEQCRSDSKCSSPVEDRHDSLHCPTCGCNQRYWIQSNEAKSLKSKQFTKLREWLEAHQSLIRLCDEINSITSPVVVLIFLVDGLILCLLAFMATRVNDVVSVCSLLVYFVLILAQVYLYCLCGDKVKTQSESLADVVYNARWMDLDPDTIQILQMISQRCQKPLTINGGSFFTLSREFFLAMMGSVLTYFIVLTQLPDRQDHENK

>TdomOr31fJ

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**5 *Machilis hrabei* ORs**

>MhraOr1F

MREKTVFETVGKKWRVRNKVKQLRQNNEFQDVQNFTRRIGTLMVASGYPLFMFSNSVRCRFKCKLHIFYSGAIISIVALHLLSCCVDLCFSKNASEAIFNILTTSYILQCFLYYVFVIIKRRHFENLIDCIFVKEIPTIYVESNTFQAKSVLERSKVRIFALVMLSLFGWFVWSIFPFVITLVKPYSLASTNDNITIPLRISASWYPFDITTSPVKEIIATLEATILLWSMSAITSIDMLFCISMVTLVEYLKCLGRNLKFLSQHSVHRISQTLNQTRHTTCSPIKSSTEHAIQFTYLESLKMKNLASVNSKDTENEPGKRSTESIHSFHCKHDSTLEQLGLWIDSQVHICSIVQEVQSAYSFIFVNAFLLNGLEVCIITYILAAVSMPTSRVVGMVLYMVCVLFRTFLLCHLGTELTDQGLNVCCAGHSSTWLNAPDQIRSTLQIILTRSQMPLSITGAGLFTVNLPFLASMVSAIVTYFIVLLQVNKSS

>MhraOr2FJ

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>MhraOr3F

MFYIFFQSWSNPHQDYYLHTINKTMNEIFGKANVVYLEYTTNNRVLRKWVERLVKLMKISGHWPLRMPGEIRSPLQNKFQVIYCSIVITLALTYCICYCTALFTSRSSQLALNNISITSFIIQCCICYIVFVVHKRKLETLLNYIFENDMPECPRRYKALSVKMLLSRCKFLILSLGIIDSIGWLIWTLFPFAVSSANSNRTSLRFAEAWYPFDSMTSPVNEIISVYEAVIMLLIITATTTCDMLFCVVMTFVSEHLKCIGKALDCRVDGISHDVSRHHYLQAEKLLVSELERKVVTIDTGLIHVPIMLHTDKGNYKCHQLSASQIVTRCDSVERLGATIDSHVKIFRILETVQSVYSFYLLTLFLTIGLALCIMAYILASADNSLTRIAGMVCYMTCAFVRIFLLCLAATDVTEQGQNLSRAGYSSKLALVSDGVRSTIQATATRAHIPLCITGGRFFTVNLSFLASMTSVIFTYFIVLLQVNGKQH

>MhraOr4FJ

MNYNYRSTKVASFNKTNSNTDIQKWIKRMRILMSISGLWPLSLPNENEGTFQKIRHIIYSCCILTLGCMFCVTYCIALYLSRNAQHVLNNIIMTSYVFQGCVCYIVRIVKRKNFEALLNYISENSIPECPKTHRFVASKTILTRCKSTILSLGIVTLPAWLGWTLLPLILLAVDPGVSSSNHTELRFAEAWYPFDAKVSPTNEIITIYESILLLLFIWSIASSDMMFCLVMTLVVEHLKCLGKNVECVVDGITQHAPKLQYLGEERFPKESNKLDNFVVRKHVSGPSTHFHPSRDRSFTLKCSNSSDISRNRVEFESLTSTVDSHVKVCRIMEVVQSTYSSYFTIMFFSSGLGFCVMTYFLAVGTNSTSRIVAMIIYMAAVFRRIFFLCVLATDVAEQGLNLCKAGYSSKLISAPDHIRSALKILTSQAQIPLCITGARFFTVNLTFFVSFAGVIFTYFILLIQLNGRQ

>MhraOr5FJ

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