**Supplementary data**

**Table S1.** The classification and number among different species used in OBPs, CSPs and GRs in the phylogenetic trees. OBPs and CSPs in non-coleoptera species were not used in the phylogenetic analyses. The number of GR in non-coleoptera species of annotated proteins in those genomes were marked in green, in the transcriptome data was marked in bule. The italic numbers were used to structure the GR tree.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Order | Family | Species | OBPs | CSPs | GRs |
| Coleoptera | Chrysomelidae | *Plagiodera versicolora* | 29 | 6 | *13* |
|  | Chrysomelidae | *Colaphellus bowringi* | 26 | 12 | *10* |
|  | Cerambycidae | *Monochamus alternatus* | 29 | 12 | - |
|  | Chrysomelidae | *Ophraella communa* | 25 | 11 | *17* |
|  | Colydiidae | *Dastarcus helophoroides* | - | 7 | - |
| Lepidoptera | Plutellidae | *Plutella xylostella* | - | - | 69 (*2*) |
|  | Noctuidae | *Helicoverpa armigera* | - | - | 213 (*5*) |
|  | Bombycidae | *Bombyx mori* | - | - | 69 (*3*) |
| Diptera | Culicidae | *Anopheles gambiae* | - | - | 59 (*3*) |
|  | Culicidae | *Aedes aegypti* | - | - | 91 (*3*) |
|  | Culicidae | *Anopheles coluzzii* | - | - | 23 (*3*) |
|  | Drosophilidae | *Drosophila melanogaster* | - | - | *60* |

**Table S2.** Primers for qRT-PCR of chemosensory genes in *P. versicolora*.

|  |  |  |  |
| --- | --- | --- | --- |
| OBP31-F | TGTACCTCAGGCTCGGTATAA | GR22-F | TGGAGAAACTGCGTGCTAAA |
| OBP31-R | ACCTATGAACCGCCCTACT | GR22-R | GTTTGACAGATCGCACCAAATAC |
| OBP33-F | AGTTCTGAAAGAGGGCAAAGG | GR24-F | CTTCTCCTTCGGCTTTCTAGTC |
| OBP33-R | CACTGCTTCATAGCCCAGAAT | GR24-R | CCAAAGGCTTCCTTGTTTCTTC |
| OBP34-F | CTCCCAAGGCAACGAAAGA | CSP12-F | CTCCTGACGGCGAAGTATTG |
| OBP34-R | CAGGAGCGAATTTGACAAACG | CSP12-R | TACCCACTTTGCGTACTGATTT |
| OBP36-F | CTCAAGTCAGTTGCTCCAGAA | CSP13-F | TGAAGCTCTGCCGGAAATC |
| OBP36-R | CAATCTCCAAAGCTCCCATACA | CSP13-R | CTGGACCAAAGCATTCCAAAC |
| OBP37-F | ATCGGTATCGGTTCTTGTTTGT | IR12-F | CCTTAAGCACTGAAGATTTCTTTGA |
| OBP37-R | CCTTGTCCATCAGGTCTTCTTC | IR12-R | GCCTACTTGATGGAGCCTTT |
| OBP38-F | CAGTGTGTGTACAAGGAGACAG | IR14-F | GACTAGTTACCAGCATGGAAGG |
| OBP38-R | ATCCGGGTAGAACTGGGATAA | IR14-R | GATACAAATGGCGGTTGATGTG |
| OBP39-F | ACCGTTGGTCTCAAGAACTG | OR41-F | CTATGGGAGCTGTGCAGAAA |
| OBP39-R | GCACACAGAATGCTGCAATAG | OR41-R | CAGAGTAGCATGGGCTAAGATG |
| OBP40-F | ATTGTTGACGAGTGTGGAGAG | OR42-F | CATGTCCTACAACTTGCTGAAAC |
| OBP40-R | GCAGGACGGTGTTTCCTATAA | OR42-R | GTGTTCATTGCAGCCCAATAC |
| q18S-F | CTTCCTCGTCGGAGCATTCT | q18S-R | GTTCGCCTTAACTGCCATCAA |

**Table S3**. The Blastx match of *P. versicolora* candidate CSP and OBP genes. The new genes compared to previous reports were marked with bule color.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Name | ORF  (aa) | Signal peptide | complete | Blast best hit  ACC. NO. Gene Species | Evalue | Identity  (%) |
| **CSP** | | | | | | |
| CSP3 | 128 | 1-17 | Y | QFO46789.1| chemosensory protein [Cylas formicarius] | 5e-56 | 68.8 |
| CSP5 | 134 | 1-16 | Y | ALR72526.1| chemosensory protein 12 [Colaphellus bowringi] | 1e-68 | 80.7 |
| CSP9 | 131 | 1-18 | Y | ALR72517.1| chemosensory protein 3 [Colaphellus bowringi] | 5e-48 | 64.9 |
| CSP11 | 122 | 1-19 | Y | AUF73000.1| chemosensory protein [Anoplophora chinensis] | 8e-48 | 65.4 |
| CSP12 | 137 | 1-19 | Y | ALR72516.1| chemosensory protein 2 [Colaphellus bowringi] | 3e-51 | 63.5 |
| CSP13 | 79 | N | N | ALR72522.1| chemosensory protein 8 [Colaphellus bowringi] | 1e-19 | 77.5 |
| **OBP** | | | | | | |
| OBP1 | 131 | 1-19 | Y | AIX97052.1| odorant-binding protein 6 [Dastarcus helophoroides] | 4e-25 | 40.3 |
| OBP4 | 132 | 1-17 | Y | ALR72508.1| odorant binding protein 20 [Colaphellus bowringi] | 9e-56 | 60.6 |
| OBP6 | 61 | N | N | AWK23450.1| odorant-binding protein 13 [Chrysomela populi] | 5e-27 | 90.9 |
| OBP7 | 131 | 1-17 | Y | AXO78397.1| odorant binding protein 19 [Xylotrechus quadripes] | 3e-21 | 43.6 |
| OBP10 | 155 | 1-20 | Y | ALR72497.1| odorant binding protein 9 [Colaphellus bowringi] | 2e-39 | 65 |
| OBP12 | 136 | 1-18 | Y | ALR72505.1| odorant binding protein 17 [Colaphellus bowringi] | 8e-70 | 75 |
| OBP13 | 183 | 1-23 | Y | AUF72969.1| odorant-binding protein [Anoplophora chinensis] | 3e-84 | 70 |
| OBP14 | 241 | 1-18 | Y | ALR72500.1| odorant binding protein 12 [Colaphellus bowringi] | 1e-61 | 47.2 |
| OBP15 | 129 | 1-19 | Y | AQY18986.1| odorant-binding protein [Galeruca daurica] | 5e-26 | 40.6 |
| OBP16 | 134 | 1-17 | Y | AXO78395.1| odorant binding protein 17 [Xylotrechus quadripes] | 2e-41 | 47.7 |
| OBP17 | 143 | 1-27 | Y | ALR72503.1| odorant binding protein 15 [Colaphellus bowringi] | 2e-16 | 40.4 |
| OBP19 | 135 | 1-19 | Y | ALR72494.1| odorant binding protein [Colaphellus bowringi] | 4e-46 | 65.2 |
| OBP21 | 138 | 1-19 | Y | AQY18990.1| odorant-binding protein [Galeruca daurica] | 1e-21 | 40.8 |
| OBP22 | 133 | 1-19 | Y | ALR72503.1| odorant binding protein 15 [Colaphellus bowringi] | 3e-25 | 55.2 |
| OBP24 | 148 | 1-16 | Y | AWT23276.1| OBP5 [Hycleus cichorii] | 9e-30 | 37.6 |
| OBP26 | 92 | N | N | ALR72494.1| odorant binding protein [Colaphellus bowringi] | 5e-35 | 70.4 |
| OBP28 | 134 | 1-23 | Y | ALR72503.1| odorant binding protein 15 [Colaphellus bowringi] | 6e-24 | 40.91 |
| OBP29 | 105 | N | N | ALR72513.1| odorant binding protein 25 [Colaphellus bowringi] | 3e-35 | 69.1 |
| OBP30 | 93 | N | N | ALR72513.1| odorant binding protein 25 [Colaphellus bowringi] | 3e-30 | 70.2 |
| OBP31 | 146 | 1-20 | Y | AIX97023.1| odorant-binding protein 8 [Monochamus alternatus] | 6e-12 | 31.3 |
| OBP32 | 63 | N | N | ALR72495.1| odorant binding protein 7 [Colaphellus bowringi] | 2e-23 | 77.8 |
| OBP33 | 145 | 1-17 | Y | APC94284.1| odorant-binding protein 30 [Pyrrhalta aenescens] | 8e-10 | 32.7 |
| OBP34 | 123 | 1-25 | Y | ARH65468.1| odorant binding protein 13 [Anoplophora glabripennis] | 7e-10 | 38.3 |
| OBP35 | 107 | N | N | AQY18990.1| odorant-binding protein [Galeruca daurica] | 8e-16 | 39.2 |
| OBP36 | 142 | 1-20 | Y | ALR72489.1| odorant binding protein 1 [Colaphellus bowringi] | 3e-61 | 62.7 |
| OBP37 | 132 | 1-19 | Y | AUF72972.1| odorant-binding protein [Anoplophora chinensis] | 1e-15 | 36.6 |
| OBP38 | 259 | 1-20 | Y | QKV34985.1| Odorant binding protein 4 [Dendroctonus adjunctus] | 1e-18 | 28.3 |
| OBP39 | 171 | N | N | ALR72504.1| odorant binding protein 16 [Colaphellus bowringi] | 3e-24 | 36.0 |
| OBP40 | 160 | 1-23 | Y | APC94279.1| odorant-binding protein 4 [Pyrrhalta aenescens] | 1e-21 | 42.6 |

**Table S4.** The Blastx match of *P. versicolora* candidate GR, IR, OR and SNMP genes. The new genes compared to previous reports were marked with bule color.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Name | ORF  (aa) | TMD | complete | Blast best hit  ACC. NO. Gene Species | Evalue | Identity  (%) |
| **GR** | | | | | | |
| GR3 | 86 | – | N | AUF73052.1| gustatory receptor [Anoplophora chinensis] | 3e-19 | 50.0 |
| GR7 | 101 | – | N | APC94333.1| gustatory receptor 3 [Pyrrhalta aenescens] | 2e-28 | 28.7 |
| GR9 | 111 | – | N | AVN97874.1| gustatory receptor 9 [Anoplophora chinensis] | 4e-80 | 38.2 |
| GR11 | 131 | – | N | AWK23449.1| gustatory receptor 1 [Chrysomela populi] | 3e-67 | 79.4 |
| GR12 | 289 | – | N | AVN97874.1| gustatory receptor 9 [Anoplophora chinensis] | 4e-70 | 41.8 |
| GR15 | 345 | 7 | Y | RZC42344.1| gustatory and odorant receptor 24  [Asbolus verrucosus] | 9e-153 | 65.5 |
| GR18 | 130 | – | N | RZC41799.1| gustatory receptor 2 [Asbolus verrucosus] | 5e-53 | 70.9 |
| GR19 | 147 | – | N | APC94332.1| gustatory receptor 2 [Pyrrhalta aenescens] | 2e-28 | 40.0 |
| GR20 | 126 | – | N | AVN97870.1| gustatory receptor 5 [Anoplophora chinensis] | 4e-18 | 44.3 |
| GR21 | 215 | – | N | AUF73059.1| gustatory receptor [Anoplophora chinensis] | 3e-30 | 54.5 |
| GR22 | 102 | – | N | AUF73051.1| gustatory receptor [Anoplophora chinensis] | 2e-09 | 44.2 |
| GR23 | 302 | – | N | KYB27621.1| Gustatory receptor for sugar taste 64f-like Protein [Tribolium castaneum] | 5e-106 | 51.8 |
| GR24 | 67 | – | N | AVN97870.1| gustatory receptor 5 [Anoplophora chinensis] | 3e-21 | 55.2 |
| **IR** | | | | | | |
| IR2 | 639 | 3 | Y | AKC58589.1| ionotropic receptor 75q [Anomala corpulenta] | 2e-95 | 33.8 |
| IR5 | 926 | 3 | Y | ALR72535.1| ionotropic receptor IR6 [Colaphellus bowringi] | 0.0 | 83.5 |
| IR9 | 917 | 4 | Y | ANQ46493.1| ionotropic receptor 1 [Phyllotreta striolata] | 0.0 | 66.9 |
| IR10 | 81 | – | N | AJO62241.1| chemosensory ionotropic receptor IR3  [Tenebrio molitor] | 5e-42 | 89.6 |
| IR11 | 74 | – | N | AIX97122.1| ionotropic receptor 6 [Rhyzopertha dominica] | 6e-34 | 77.0 |
| IR12 | 126 | – | N | AUF73071.1| ionotropic receptor [Anoplophora chinensis] | 1e-38 | 65.1 |
| IR13 | 64 | – | N | QBB73021.1| ionotropic receptor [Protaetia brevitarsis] | 1e-18 | 60.0 |
| IR14 | 322 | – | N | APC94262.1| ionotropic receptor 4 [Pyrrhalta maculicollis] | 1e-88 | 50.7 |
| **OR** | | | | | | |
| OR3 | 45 | – | N | AUF73019.1| odorant receptor [Anoplophora chinensis] | 2e-15 | 71.1 |
| OR9 | 143 | – | N | ALR72565.1| odorant receptor OR20 [Colaphellus bowringi] | 5e-18 | 45.8 |
| OR26 | 69 | – | N | ALR72583.1| odorant receptor OR40 [Colaphellus bowringi] | 1e-31 | 82.6 |
| OR27 | 188 | – | N | AUF73039.1| odorant receptor [Anoplophora chinensis] | 3e-21 | 34.8 |
| OR36 | 200 | – | N | QXE93269.1| odorant receptor 43 [Eucryptorrhynchus brandti] | 4e-36 | 34.3 |
| OR38 | 48 | – | N | QXE93221.1| odorant receptor 41 [Eucryptorrhynchus scrobiculatus] | 1e-73 | 31.3 |
| OR39 | 49 | – | N | AVN97831.1| odorant receptor 19 [Anoplophora chinensis] | 4e-07 | 55.5 |
| Orco | 289 | – | N | QEE83332.1| odorant co-receptor [Ophraella communa] | 4e-179 | 94.4 |
| OR40 | 220 | – | N | AVN97822.1| odorant receptor 10 [Anoplophora chinensis] | 8e-76 | 52.7 |
| OR41 | 316 | – | N | ALR72556.1| odorant receptor OR11 [Colaphellus bowringi] | 1e-173 | 73.4 |
| OR42 | 239 | – | N | ALR72564.1| odorant receptor OR19 [Colaphellus bowringi] | 3e-67 | 44.8 |
| OR43 | 86 | – | N | EEZ99426.1| odorant receptor 322 [Tribolium castaneum] | 0.03 | 32.2 |
| OR44 | 92 | – | N | ALR72565.1| odorant receptor OR20 [Colaphellus bowringi] | 5e-18 | 45.8 |
| OR45 | 45 | – | N | AVN97859.1| odorant receptor 47 [Anoplophora chinensis] | 6e-13 | 72.7 |
| **SNMP** | | | | | | |
| SNMP1a | 482 |  | Y | ALR72542.1| sensory neuron membrane protein SNMP1a [Colaphellus bowringi] | 0 | 66.0 |
| SNMP1b | 522 |  | Y | ALR72543.1| sensory neuron membrane protein SNMP1b [Colaphellus bowringi] | 0 | 54.9 |
| SNMP2a | 515 |  | Y | ALR72544.1| sensory neuron membrane protein SNMP2 [Colaphellus bowringi] | 0 | 57.4 |
| SNMP2b | 506 |  | Y | ALR72545.1| sensory neuron membrane protein SNMP3 [Colaphellus bowringi] | 0 | 63.6 |

**Fig. S1.** Distribution of unigene size of transcriptome assembly from third instar larvae head in *P. versicolora*.



**Fig. S2.** Gene ontology (GO) classification of transcriptome unigenesfrom third instar larvae head in *P. versicolora*.



**Figure S3.** Phylogenetic analysis of the IRs. The *P. versicolora* genes are shown in blue. The values at the branch nodes represent bootstrap values based on 1000 replicates. 

**Figure S4.** TheVenn diagrams of chemosensory genes in *P. versicolora* from the transcriptome of antennae, forelegs and larvae.

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**Figure S5**. Phylogenetic analysis of the ORs. The *P. versicolora* genes are shown in blue. Pver, *P. versicolora*; Harm, *Helicoverpa armigera*; Cbow, *Colaphellus bowringi*. The values at the branch nodes represent bootstrap values based on 1000 replicates.

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**File S1.** The amino acid sequences of *Plagiodera versicolora* putative chemosensory genes.

**OBP**

>PverOBP1

MKIIVLVCFAFAFFENGKCFSDEEKTMIMNIHTECVGMSGITDAMIEQARTGDFPPDSEFKEYLLCFAKKAGVMNESGELQTGKITKMVQMHIADAAKADKMVETCLVNKETPQDTIFETAKCMFEVYRFF

>PverOBP4

MFSFIVVGLCIICSISAFTEEEQQMMEALHAECVSQTGCPEDLISRASSGDFPEDEKLKCYMKCIFNELGVIDDDGKIDSSGLVAMFPEDIQAIAKPIFAKCGTVAGTDLCDSIYQTNKCYYGENPGAYFLP

>PverOBP6

MQSSGITPELLAKTKKGEFPDNQKLKEHMYCFAKKAELMDAQGKIKKDVLLAKVSAIESFE

>PverOBP7

MGKVLFALFLVFTVAFCKPLSDEVKAEILKIHEECAVTSGVNPREILDKVFGEGGDEDQIKTHVFCIGQKLKVIDDDNKIDRETLKTHLSEIITEDGEVEEIVTKCAVEKDDAKETAYYLTKCIHESMQKE

>PverOBP10

MKSTYFTLLLATSLFSATLGARRGRTGLLDPSNHKKVLNDCRTQSGATNSDMEAIKMKKLPDTKTGRCLVQCIFNNAKIMDEGKFNKNGMVIAFTPALKGDLTKLGKLKQLSEVCDKEIGPAVSKDCEGPKKIVECIAKHGSAYGFSYDNTNVNL

>PverOBP12

MTLKSFLYFTVLLGLGSCIELPPELQEFVEDLHKICVSKSGITESDYAAYDVKGNPHDTKLQCYMKCLMMEAKWMNSAGAIQYDFIIDTAHPTIKDLLEPAINKCRKIDEGANLCEKASNFNFCMYEADPENWYLI

>PverOBP13

MSTVRHCLLYGVCFLVFNVRIEAAEIHKNYTNKCDIPPTAPKKIEAVINQCQDEIKLAILSEALESLNVNEHTHSRAKRAAFSDDERRIAGCLLQCVYKKMNAINDKGFPTADGLVSLYTDGISQKDYILATVDAVKYCLSFAQKKFRVTPNSIEVHGMSCDIAYDVFDCVSDEIANYCGQSP

>PverOBP14

MRGLILIFVSCYVVHSKAIECGIDKSNRDEIKQALAMCVKNNATLNKIWEMTSSAQTTPSSTEEGTDSMEENDKSVPSIPTRNIAKNQRSGKSGRIKRAKSMKSFNTQKFSTTTMRSSDDSNGMKNSDEEEKNESNDVSEDNENSRQDSTDKCIIHCVLEKMSLTDDNGLPDHSKILEELLKNTPKRELKNFLQDSTDECFQEVDEANESDSCEYSNKLIFCLAEKGRSNCADWPAGSLPF

>PverOBP15

MKPIALVAFILVLVAMIAAEDIHSRMKNIHEECQADPATKIDHGVMEKFFEGEKVDQDQFARHSLCMNKKIGLQKENGDVDKDALRKIFEHNDKLDEAVEECGQGKGTAEETALALLKCIKKYRPSRTP

>PverOBP16

MNSVLVLVICLISIVKAGMLTDEQKEKILKYGQECLKESNVDFDVVMDAAKGKYADDPNLKKQILCFNKKIGVQDSDGKLVMDTVKARLMGITNDPKKTEDIIKECVIEKSTPEDTAFETAKCLHRLAPDEKIV

>PverOBP17

MFSIRTMKIFLVTICVVSFVVMALVSGKDLRIKTYFHECQSDPKTYVDEELLQKGLKGELADETPVGPHAFCMNLKRGFQVPNGDVDVVALRTYLEQSESRNDTLIDRAIKECGQRNGSTAQQAALALLDCIHRIIPHKDENH

>PverOBP19

MKSTLVVFSCIVVAVLANSLPESERLKLARVHAECQANPKTRCDENLLRNLGANANNAQVGIHMLCMSVKEGLQRPNGDLDRNFIKSKIDLVSDDKSKVDHYLQTCAVKKQTPEKTAVDLVLCFVQNGIPYYYRL

>PverOBP21

MKSIALIVFILAFTAMIDADDIQDEREKARKVHGECQADPATKIDADAMDRFFRDEAVNEAQLAKHSLCMNKKMGLQNENGDIDKDLMRKLIRHDSNVDEIVAECGQRKGSAEETTLALLKCMKKYRHREDEHHHHGH

>PverOBP22

MKSIALIAFILALGAMIAADDIQERVEKMKKIHGECQADPATKVDEEDMEKFFRSETIDEAQFAKHTLCMNKKLGLQKENGDVDKDNLRKSAERSDKVDEIVEECGQRKGTAEETALAVLKCIRKYLPKQEHH

>PverOBP24

MQRLIVFAALTIAVQSVDQSFINEFKEKATEIGIKCVEQTGASNDDIASIMDQKVPSSKEGKCMISCFHKAVGVQNDDGSLNPNGMKVFMEKLKSNDEDMYNKFRQLLDECLIPGNVLPDHCDTSAKVATCAIEVAKKVGLSSSFMKL

>PverOBP26

MRMISQSIIIGNSILDKTKHQINSSFLRSLLFHSACLQIMVYFRLIVRYQVDFALDEVSVQVSVGSLQTLFHRHAEHVNSNLSVVGVGSEVS

>PverOBP28

MNTMGNITVIACILAFMTLSVSCRNDRLRRFHTECQLDPAYRVEEGLIRKAMRGETVDESVVGPHVLCINIKAGIQNQNGNVIEKGLRTILKERIKDDSVVEDVMSRCGHKNGGTPHEAAVALTRCLHKHARNH

>PverOBP29

MTNAFRKPPIITHKHILSELFHFLTVEWIKWTSMVFIWSSLRFVLACYLLETSSLYVFVVIIWLPEQFFATAQRFSSSRATFILFRSGFFSTYSRMIESVSVDVF

>PverOBP30

MHSENLLSLLTSISFLNCSTFSQLNGSNGPPWCLSGLPSGLSLPVISLKQALFMSLSSSFGFLNSSSPQHRGFPLLGRHLSSSEVVSSLRTLG

>PverOBP31

MKACTVFFCIVSALITLVNTQSNLFGPFLDAHEACQENPETRIVGNLMDMAAAGQPVDEVSFGNHMLCMYLRLGIMSRDGRVNASRTIDLLTDVLNDRPVVSRAVHRCCGPRRPFQTPQQVASELFKCVTRNLPGLSTVKPPASEP

>PverOBP32

MILNHTHISCFMLITFVCQPCILTRGGTFDCTTFSYYRCTFGSIFFWENSDSSFFIYNAIIIN

>PverOBP33

MMFSILLIIIASASIQGHMDESEYGCAFSRLVKFLRPYCINKFPITDEDWDIVKEGNFGEHNEKLKKYYECCMTESGLVDGSFEVNEILLKTFMPKVLKEGKGGELIPKCAAKAKAMSDSIPSEDRFWAMKQCIYHGDPENVIIL

>PverOBP34

MKRNMMLNFAGIMFVLSTGLPIILADMNSINEECLKSSGADPKDFEQMPPKATKEVLCYMKCVMDKDKILDGNGNIDVDSFVKFAPDDVNVTILKEVKQCVSKVGKISKCEDIGKIMACLPKK

>PverOBP35

MHLLKATASSSGLPGDLFPHACAKVANRSSSGSETNSFTRSWKSGGVFPSWSWRPIPICMHSRWLPRDGSWTSSPWSNLESSAGSMWVEGLAWHEWWILTNFWLGVS

>PverOBP36

MMKWLIVLINILVIAHYGYSEMSEKQLKATQKLVRNTCQNKVKASSDELDAMRAGNFEQGKTAQCYMLCIMNTYKLFSKEGSFDWQTGVQTLKSVAPEKIAGPGVVSIQNCKDAKKATDKCMGALEIAKCIYNDNPQNYFLP

>PverOBP37

MNSALVFLSVSVLVCLSTAQKNLTGEFRKAHEFCQIRPETRIEEDLMDKAAAGQSVDEYKLGNHLFCMYIKMGIMSRDGKIKKDVLKQQLVEPVKDEAVINRIVRNCATERGTSQETAAELFRCVRRNLTTV

>PverOBP38

MNFFLAVVTTLLVAIHEIPANPVSPNEVRVPLFSHSDCREKSGVDEYHILNPHKALQSEDLKFKEYLLCFLQKSGYVNELGEFQHEPIRKQLNDLYEDQSVVEVVLKECVVKENIPLEAALGFYKCYHRYYPQEGFLYKNSFTDNEKEKLSQIHAKCREESSFEDSLMEQFKAGNFDHPLGKKHLQCVYKETGLFDESGNFNQEKIREKLSQFYPDTNLVQQYLNKCLIKKDSSEETTYYLQSCLYENTPHKFNVFSVL

>PverOBP39

MIGKSQSHRLGIHYVQNMIKSSELILYIHFSISYIFSTKGVTPSTSFQQSDIILGILSFRAGGQSFITISILIIPLVSRTVDSCHKHVIYSLISLFSMKFPCLMLSIAAFCVPVLLIHVLCREVIRSTKSFPKSSIFHVDECPVKDMIKTMYNNFLLFIIYNSLMQFLRNI

>PverOBP40

MSEIMKPIILISSILALVAVVTAKPNAVIPEIEQYRSIQDECRADPATRVDNETIEKFFEGESIDEVKFGKFILCMNIKVRVQNENGDIDKEALKKEMKKVAGENNEMVQEIVDECGEKKGNTALEAALALAKCYRKHRPAFIHEIEHKHGQEQHHQIEK

**CSP**

>PverCSP3

MGVCTIFLICLVGLVLAKPDEKKYTTKYDNLDIDTILKSERLLKNYVHCLLDKGKCTPDGAELKEHLPDALLTDCSKCSEFQKKNSKKIIRYLIDNKPDWYKELEVKYDPEGTYKAKYDEEIKDKAAE

>PverCSP5

MFSLFILSCFVIGSLSTVTEKTKYTTKYDNINVEDIVKNDRLLKNYVDCLLDRGKCTPDGLELKKNMPDAIETDCSKCSEKQKEGSEFMMRYLIDNKPAYWDPLQEKYDPSGSYKKRYLDAKKTEVNIQPIVKS

>PverCSP9

MKSIIVFCFVVVLASVIARPDDSKYTSKYDNVDLDAIIHNDRLLRNYVDCLLGKKKCTKDGEELKRILPDALKTKCAKCSEFQKNNAKKVINHLIKNQRAWWDELEAVYDSEGIYRKEYEAEAKKEGIDLN

>PverCSP11

MFRLSFLFCVLVVVSLVEGQKYQSKYDNIDVDSILTNRRVLKSYLRCILDEGPCPPPAREFRTHIPDAISNNCARCTDAQVNIIKKTSKFIMRNNPEDWEKISKKFDPQRKYRASFTKFLNA

>PverCSP12

MKRLLSASVLFVVLAVVLATDRKDRSKVAGYTTKYDNVDLDAILRNERILRNYVDCCLGKKKCTPDGEVLKGHIKDAIENECDKCSDVQKKSVRKVGKTIYQKHPTWWKELCDHFDPEAKYQKRYEKFIQDALKEVE

>PverCSP13

MVALLGITQENMNIRIQYLYLRFRYISKDHEALPEIIGNNCRSCDNRQLSNARRIAVLVQSKYPDVWNALVQKYSSQSS

**OR**

>PverOR3

MIITMTRMQRPVYLTIGKFTPLTLTALITVFRGSFSYFTVFKSIQ

>PverOR9

MSIKQWILMRNWNAEEKFLLIAGWFPVDLTKHFNLAYFHQISVVFNLTLYSLALDSLIISLVNFAAVRLVILGYKFEHLGSDVGSRTQPVYDSLRDIVMEHKRVIRYVENLNLSLKWYFFGDFVSRSYHLSLTIMNVIRHRSQ

>PverOR26

MVLVEIITALLCMNMYVLSLPNTTVVDYIRCGTMVCAFTTEFLFLYGVPAQKLMDEAEQVANSAFYHCD

>PverOR27

MTENHPIYDSFKYNVLIMKLCAIYPPDSWSNSLYKIYAYSSYITITVLFPILAAIYLFSAEIVDVHQTCWNIILTIETGALIVKVFVFVIKPQQVKKSREDLGKDIFILYAPSQEWIIKDTIQEYYTVFIAITIFSVFSFLAHIFLTAVSLERKFPVNIWLPFDGLTDTKIYVMVFIYITFGKLIVSI

>PverOR36

MIAATTCNNVTQTFFVTMMNFMIGRLIVLQQHFRNFDSYRFDGATITDEKAVLGALKELIKDHLGIIGLVENFDNSMRLLMLLEFLTNSLQIASLLVQFLMNDDTLVILHVITYIGIVTSQLFLLAWNANEIKEQSSALSVALYESRWYEHGISVRKCILLMMMRSQKPLTMQIGPFYPMTADTAISTMKAAYSYVTIMR

>PverOR38

MMVFFLARIQNPPTITLYKWVNVDMVFYLNVVRMASSFYMLISNVNTK

>PverOR39

MAVLTIMANQKPAKISAGSFVDINLETSLATIKTMVSYCMFLRTMSIDE

>PverOrco

MSGMTYYISLIFQIYYVLFSLTHANLLDSLFCSWLIFACEQLQHLKEIMKPLMELSATLDTYVPKSADLFRAPSANFQDNLIENDYNTKNEELNLKGVYSTRQELGANFRSGALQTFGQGGGGVGPNGLSKKQELMVRSAIKYWVERHKHVVRLVTAIGDAYGVALLLHMLTSTVLLTLLAYQATQINGVNTYAASVIGYLVYSLAQVFHFCIFGNRLIEESSSVMEAAYSCHWYDGSEEAKTFVQIVCQQCQKAMSISGAKFFTISLDLFASVLGAVVTYFMVLVQLK

>PverOR40

MVIKAIPLSAWYPYDEQKHYLPSFCWNVLDGSIGASFLAYSDILSFSLIIFPLGQIHILKHIVANFDDYVKKIENQIGVSQKEASFITIRECILNHNEIIRYIRDLNDAMRNVMLLDFLQSSIQLASLVLQLFEDLILPNIVLFGQFLCSMLIRLLLYYWYSNEITYQSSDIAVAIWNSKWYEQSPKVKNIMLIMMMRCSQKLYLEIGLFSTMSLGTFIY

>PverOR41

MSTLESPHFHYGSCAERNFFPGTTSQRFKKVGITYTMLFYILAHATLISSYLPPLIAAIQHDKNDPEKPLPKRLPYYSWMPFEFNTATLYLIALGYQAIPMFSYAYSIVGMDTLFMNIMNCIVMNLEIVQGAFRTVRERACENTIGPLLTPDELYNTEELGIAMKREMKKINKHLRIIYEMCENLENVYTFLTLSQILATLIILCSCLYLVSTTPTSSKQFAEIIYMIAMGFQLSLYCWFGNEVTLKADRIPFYIWECDWISADTEFKKSMIFTMVRAKRPLHLTAGKFVPLTLSTFIGIIRASYSAYAVIKNTSR

>PverOR42

MFFTRTIIRGMLLRQQDVETSEDLLVMFGSLGATVVCVFFTRSRERWHDFLQCLIDFKPYTSSFEFEEKISERNILGLFYGAYYLMGLIIYGIAAYTDNSTCHRIKEEKNINLFCDTYFPIWIPFDITSRAIHWVIFFVQFFLSTCSFFPAAMICFLAWEATKVICIHINLLKEHFKYIIDNNCRTRPDGLAFWVEYHNHVLQLAETLRVLVKETVGSVALCSAVVLGCNEHSIMRVGI

>PverOR43

MMLLYGDYATLALTFAGIHIFLCVAAFMIFNVHPQSNWRISMSLVPAVIFALNICSNGQRTKDESERVYYNALECGWYNWNIKNRR

>PverOR44

MTNSSILFVEVASLYIQANDVSLESQNLGTNIYESNWYERSPEIKKSLHIMMLRTQQPLKLESGGIVVLGNTLFLKIIKAAYTYILFSNKLN

>PverOR45

MYPMRDQRIFQLLLSWVFLLSPSMSARFSLIFDHSYTICSCRWQY

**GR**

>PverGR3

MIFRLVLISIYAASVNEESKRFLLVLNNVPSELWHHEVERMIGQIDFGGAQLSGYGLFTIDRGLILKVCMTVLSYELILIQFGNSS

>PverGR7

MGRKILDLVQPLFHSVSLLLFTEACDAVEKSGRRIVRTCYSLHKNIQGDALLKEKVKVLARYAEERRPVFCFWNFFHLNRSSLLTFFSAIITYTVIVIQFN

>PverGR9

MLIMLSCLVHLVVTPYFLVAELIKDKSNYFFIFLQVLWIITHTCRLLIIVEPCQACSLEGQRTTMLLCDLLGLSSTDESFRKAVQSFSIYLSQNQIKFSCSGLFTIDRSVI

>PverGR11

MFTRILAMVSVSLLLTEITEGAPAVASSRQFLSGHPGFIPVYIRAGDTPLEDINPELAEAFNSYAQRHGRLTYRRSLEDKSGETGGDEEFPDFAEVGETSLEEDVKPEGDNNKISGSQEASGSHIQKIPRN

>PverGR12

MECLNQTQKTIPIKASRRYALSSIYFLAIVISAFMVLFIFDIIMWYHRGNNNSTYLKEYSTFYFLYAMVVMKEVFFWHVIFLIKIKISLLNNKLLDIKNKAISTDIHFIGLGGNLNTIDNGYKCGNSKDLVKEFIALSSSHKKIVEAVGIVNNSIEFGIHILMLSCLLHLIVTPYFLLMEILSAINDFSNITVQIFWALAHIGRVLIIVEPCQLCINEYEKTLNILCDLATFDFDEEVKKMITLFSLQHSYYKLSFSSCGYFQINRSLLTSIAGAVTTYLVILFQLNNN

>PverGR15

MLAYSIVVFLVVLTYIAYIRWDKVEMFRTAEGRFEEAVIDYLFTVYLVPIVINPIAWYEGRKQARVLTTMMSFEKIYRRVTRKNLSVSLGNTPLVITIGLPALAISAMVVTHVTMVHFKLFQVIPYCYINTTTYLIGGSWYIYCDLIGHVAQTVAADFQQALKNIGPSSRIADYRALWMMLAKLVRDVGNAFAYAVTFLCLYLFLIITLTIYGLLSRIQDGVGIKDVGLTLTAFLSGVLLFFVCDEAHYASNCVKVQFQKKLLLVELNWMNDDAQQEINMFLRATEMNPTDISLGGFFDVNRNLFKSLIATMVTYLVVLLQFQISIPGDDYSEGDASKTNATKIK

>PverGR18

MAHLYGEELHIKQITKFSRQSPRAQEIAKRATLNSADGRVIDKHDQFYRDHKLLLALFRILGVMPIQRGKIGKITFGWLSGPMLYAYVFYAAMTYQVTMVGYERMGILLNESRKFDEYIYSIIFIIFLVP

>PverGR19

MDIVKPRSRKHGPPLSGVLRQQKELLLHHGVLDRVVQVVASLDDLEAALLRRIARHYHDGQRHDHDEGFQEVEDLPAGVVVDGVGEVEEQVQHRDADAVGGDASVEFVEFFDDAVGCFAGVHHFLDWLHACLVFVSGAAQKVVQEVV

>PverGR20

MLLQTLSDELHFQFATTPMVIILDDKFQVSLFLLTEAFDGVEKSGMKIIKTCYTIHKNIQDDVQLKRRVYVLAKYAQKWRPVFSLWNFSRLNRSTSTKFLTAIVTYTVIVIQFNIMMGERTKKQSK

>PverGR21

MLQFSAAMLVLRERFRWINEELKVLIREWKKSCEMKKKDFIVGYVDLRWKSNEEAFIEVLEKLRAKYYDIHDLTIELNAIFSIPAVLTIMQCFLSSLVNILYLVRSVKRRSWYKTVLFRWFGGSILSISAIKLVTISYTSSFLFSEAKKTEAILHQIDSTSEDVNDFVQHFSYQILELKPRITACNLFTIDKSLIYEVVALLTSYLVVCVQLDLK

>PverGR22

MLSIIRSFYTMIQVLVIIFCIDLATREPYKLLKFCINLQGKMPVGSREYQRMELFKRRITELLPKFTAANFFQITRSTILSVISVITTYFIVVVQFYLTMKT

>PverGR23

MAFYLCNCLASIQLIIIARNWSKILGQWSYTEISLRGYPQEENVRRKFLLITLVFMGLGLAEHLLFILNGIFLSKQCVGYEKSHARVYFEVSFQNYFTFIQYNVWLASVIKFANTISTFTWIYTDLFITLISVALTAKFKLITRKLKANTMVHEKFWREMRQDYQKLNNLCMYIEKYLAPLVTVSFVHNIFFLCIQLYNSLSERSGVLETTYFFFSFGFLVLRLMTVSMYGAWLHEETRKPLGFLYRVNTEHYCTDISRWIQQIYVSPTGISGSGFFLVTKPFLLKMAGTIVTFELMLFQFA

>PverGR24

MSCDAVEQSGKKVIQACYDLHHKTTGDERLKSRILMLAIYAEEWRPIFSAAGFYDVNQKCLNSIFSA

**IR**

>PverIR2

MPVNSIIYKVGNTKSSRIVVEALYKFDRTSTNFLTNRIAEWSPENGFRYFRKLISTTNRTNFMGTPIRTSYVIFDNDSLNHLSDYRFIDTDKLSKINYRLIDSLKDLLNTSRVNIWTSSWGNKNLTTGEYSDGIFKDLLSNKADITGTTAFISKDRLDSFTYLVPTTYEEIKFVFRAPSLSYTKNVYTTSFSPMFYLSCLSILVLGGFLLYFLELVEYQCGAIPNRMTLMDVVATQICSITQNSVVRTPELPATRIAVFFNMIFCMLVYTAFSAYIVILLQKTTDEIKDVRSLYDSKMPIGVQNTPYNKYYFSTPNLLTNEHYRKLFYENRLGGSQSNFISPEKGMKNVQGGFYAFQVEQATAHYFIKTTFNENEKCSVKSIPTIFVGFQPYLVIPKNSSYYNHFQVGFRRLFETGLHQREYVRFFTKEHKCQGAQRNYDSVRLMDCYFPFLIFAFGFTLSIFVLMTEKIIKRIGKKGLMQEVCRTKDGYRKRITQPLDFIN

>PverIR5

MKMGLNKIWLVFLSFLLENCQGETTQNINVLFVNEENNGVAEKALDVAMTYLKKNNKLGIAVDLKKVVGNRTDSNKFLEALCSTYNSMLSTQTFPHLVLDMTMTGLGSETVKSFTQALALPTISASFGQEGDLRQWRNINESETDFLIQISPPADVIPEIIRTIVLNQNITNAAILYDSSFVMDHKYKALLQNVATRHIITPIKEVSQLAEQLTQLRKLDLVNYFVLGNLKSIKNVLDAADGLNYFNRKFAWHAITQDDGDIRCTCRNATILFAKPLPNALYQDRLGAMRRTYQLNAEPIVASAFYFDLILHALMAVNEMISDGSWKSGGGGFITCDEYDGSNTPKRGGLELRRFFSKQSSEDPTYGPFSVASNGWSHMEFQMQLTAVGVRDGASDKSVNIGAWWAGFDNNLTLLDAQAMGNLTADVVYRVVTVEQKPFVFRDESSRSGFNGYCVDLIDKIADILKFDYEIVAVDNFGVMDENGKWNGVVKELVEKRADIGLGSMSVMAERENVIDFTVPYYDLVGITILMKLPESPTSLFKFLTVLENEVWLCILAAYFFTSFLMWIFDRWSPYSYQNNREKYKDDEEKREFNLKECLWFCMTSLTPQGGGEAPKNLSGRLVAATWWLFGFIIIASYTANLAAFLTVSRLDTPIESLDDLSKQYKIQYAPLNSSSTQTYFERMANIESRFYEIWKDMSLNDSLSEVERAKLAVWDYPVSDKYTKMWQAMKEAGLPANMAEAVERVRASKSSSEGFAFLGDATDIRYLELTNCDLTRVGEEFSRKPYAIAVQQGSPLKDQFNTAILQLLNRRELERLKEKWWNKNPEKQNCDKIEDQSDGISIQNIGGVFIVIFVGIGLACVTLAFEYWWYKYRKNSKIIDIREAPNAHQDATSKTNPKMRRLFDSKSSDNPTFKNTKAVYPRSRF

>PverIR9

MKRIIQSVVLILFCFGFQMVSSSEVTIGVLLNDLTSQVQLPLNSVIYNKNVFDQNAHFSTDVSLVSNIDSFDASRTLCNMMNSSIGITAVIVEDIPNTIPVLESICTNFEIPFIMTSWRPPVVRNPDQERALLSFYPEAERFAEGLAEIVKSLQWTSFVIVYENEDGLIKMQDVLKLQEYKKNTRRNNIFVKQLGPGPDYRPLLKEIRNTTEDNMILDCKTENILPILLQAKSVNMLNLHNRILITSLNAHTVDFSVLNTTANITILRLHDPKTENFENAIHRWQLTEFENRDIHTQLDPKSIMTETLLFHDAILLLTDAVRDLSITPKIETSPISCSENQTTRDGFAIRNYMRIKTPSMTLTGPLEFNNNGDRIKFNIYAIDIIEDTVIATYFAGNKSITLARSGKESMDAAVLNLQKITVIVSSRLGPPYLMPREPTYEGEEFVGNRRYVGYSMDLIDGIAKIIGFKYEFVITSKYGKYDEEAKRWNGLIGELLEKRAHLAVCDLTITPERTEVVDFSMPFMTLGISILYKKPDKKDINMFGFLETFSKAVWIYTATLYLIISIVLFFISRMTPGDWENPHPCEDEPEELENIWDIKNCLWLTLGSIMTQGCDILPKGISSRMAVAMWWFFSLIMTSSYTANLAAFLTKANLEPEIDGAEALSKQTKIKYGFLAGGSTESFFRNSNFSVYQRMWLNMQQFKPSVFEENNADGVNRVQTTKNSLYAFLMESTQIEYEVETKCTLKQIGNWLDTKSYGIAMPMNSPYRTAINRAVLKMQEAGELGLLKKKWWKDERKEPSCDQNASDDGDSAKLALANVGGVFLVLGVGIAMACIFAILEFLWNVRNITVEEHVSYWEALKVELIFACKVWITKKRTKRLMTESSSSSEKSDRTDDRSIIHSILHSAGSFMHLNAQS

>PverIR10

MAGRETLFFDIQRFGASNFHLSEKLNTAYSAIALQLGCPYTEEINKILTAIFEAGIITKMTENEYEKLGKQKELTSDIAES

>PverIR11

MHLPHADSARILVGSWWLVVLVIATTYCGNLVAFLTFPKIDIAISTVEDLVTHKDTVSWSFREGSFLEDKLQTA

>PverIR12

MKKRFLETGKCEFTLSTEDFFEEELALILPQESPYLARINEEIKRLHQVGLIHKWLQDYLPKKDQCWKNRNIVEVKNHTVNMDDMQGIFFVLFLGFMLSLVLLLFETIWKKHFRKKQQIIIHPFTT

>PverIR13

MVLPVRRSLTIIQSVSIISRIGDGVHFHGIVDVPHEVTFERVFSPIEDINGVSAYEISVVNLLQ

>PverIR14

MTTISAEEVHHLPTMRLGAALLVTTLATLLVESHLLESNQEAKWADSFLKGTKIESTLHIVELLKYIALNYLTDCTPMILFDSSEKNDDLFIEKLLTQFPIPYFHGRISDSYEMMMGSDSAPTTCVSYILFLTDVMRCRNIIGDISHQRVVVIVRSSQWRVLDFLMHEDSRVFMNILVIVKSERIVSPQKPIFQEAPYILYTHELYADALGSSRPIVLTSYQHGRFTRLVNLFPKKMSTGFSGHRFVVAVAHQPPFVSREKFSDGDKKFVGIEVGLVEMLSRIYNFTTDYREATDDIVLGSVQISRSGFQFILCTEKTPSSL

**SNMP**

>PverSNMP1a

MLQMINLGPGTDIRDMFLKVPFPLTYRVYIFNVTNPDRIQKGDMPVVNEVGPFCYEEWKEKMNVEDMEADDTIAYDPKDTFLKKRWPGCKTGKEIITVPHPMILGLVNTVARQKPGALSLANKAIKSIYANPSSIFITTEADNILFDGVIINCGVTDFAGKAICSQLKSSGNLKLINGDQLLFSLLGPKNATLNTRMKAYRGKKHFQDVGRIVEFGGAKNLDVWPTDECNEIKGTDGTIFPPFLKKEQGLVSYSPDLCRSLRATFVKDTVYDGIPCAEFTATLGDMSKNEDEKCYCLTPDTCMKKGIMDLYKCAGVPVYASLPHFYGTDKSYLDGVNGLTPNKSKHEIKILFESTTGSPLYARKRIQLSMPLEPIQKVELFMNFTPTVIPVLWIEEGVELNRTYTGQLKSLFTMKKIVGAFKWVVLLSSLGGLAAAGYMFYKNNGKIEITPIHESKRDGISTIHSLEGQVNHGMSENSIDKF

>PverSNMP2a

MLACSRFFSNKVLAVLTTILTLIFVGVLVLAFYGIPVIINKSIHNSVHLEKGTIQWDRFVDLPVDILMKVFLYHVTNSDDVLNGAKPIVEERGPYCYKQNIHKNILSTSSSQDTVTYEQNFKIEFDQEASGNLKESDKVVIVNPVMLTLYKLTSRLERLVVFGCLDKIFPKEYIGVFIEVDVKTVMFDGFAFAQRSEDLGPACNIVRNQILDKTLPMKNVERITDDDGILELRFALLQYKIRGPDGNYTINRGIDDITKLGHIIKWNDETELPFWGRMQSINNDTCKKVRGSDSTIYPPQVDKTRSFDIFSTDICRVVEISFQRTDTYNGIDAYRFGITKNTFRSATTNPENDCYCIKQSAGIDGEPSCYLDGVLDVYPCFGAPILLSFPHFLYADESYVDAIEGIGPSDPDIHELFLLIEPNTGTPLQGMKRVQLNTVLMPMQNIPGTSKISPLVMPILWLEEGVSLPQNLIDELNSHYFQTVKLVEGIIYGLIAVVAASVLISSGFLIRRKCC

>PverSNMP2b

MVFNLKFNLSKKTLKILGCFGLFLACAGVYFGYKALPDIVTDKIWEMKVLKENTQQWDMFKKMPFPFTFKVFIFDIKNPDEIMQGAKPTIKEIGPFVYKVYKWNSDIKWESPDDISYFAYTRFEFDEEASGRFTEDYIVTILNTPYLGMLLKVADIQAAALPMVEGVLGDIFKENDGLFIKVKVKDYLFQGLKMCENEGKDGDFAAGLVCKQVIAEAATSNNLRVENNTILFANLHYKNNTHLGRFTIKAGIQNHNEIAHLALYNNQSYISIWGEEKSICNKIEGLSTTVFPVNINKDMIFESFAEDICRRMKLTYKMDETVKGLKGYKFTAANDSFSMKNENNTCYCNKKTTLMDGKLGCVKDGITDLSTCTGGPVMVSFPHLLYADKEYLNSVEGLDPDSMKHESFVVLEPMSGFPLSLAQRVQFNIFLRPIDESTILANVSRALFPLIWVEESLQLDDKFTDMLKNNLFKTLDMINILKWVVIASGSACFLFAVSMAIYNDAS

>PverSNMP1b

MQLAIKVLVSGVVITLSSVIFALVIYDPLIKYVIRDQTSLKKNNQIRDIYLKIPFPLDFRIYLFNVSNPMEVQDGAKPVLKEVGPYCYDEYEEKVDVIDNEMEDSLTYNSYDIFRFNANKSIGLSENDYVTIIHPLIVAMAYQVNRDTPALLSFLNQAIVTIFKNPKSIYLTDTVKNILFDGFEINCNVTEFAAKAVCTQIMNSNIPGLKTDPSRNNTLVFSLFGARNATLGHTMKVLRGIKRSEFVGKVLEVDGKKEMNLWTSKACNRYRGTDGWIIPPLLEPGVGVWTHSVDMCRNVEAKYIKETVLNGVNARLYEADLGDMQKNEDEKCYCPTPSTCSRKGTFDLTKCMGAPIIASLPHFLRADEIYRQQVDGMQPVHEKHIISIYLEGVTSAPLRATKRMQLNFPITTIPKLTLMTKLPEALHPLLWLEEGVEVEGEFLKLITDKLMLLNVANYGRWLAVFGGLITTGVGVYLHNKNKNSVAISTIHSGDIDREITRSTNELMDQMNRIQGNEKGHVN