TASK 1

Nucleic Acids Research, 2023, Vol. 51, Database issue ***D1–D8***
https://doi.org/10.1093/nar/gkac1186

The 2023 *Nucleic Acids Research* Database Issue and the online molecular biology database collection

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ABSTRACT

The 2023 *Nucleic Acids Research* Database Issue contains 178 papers ranging across biology and related fields. There are 90 papers reporting on new databases and 82 updates from resources previously published in the Issue. Six more papers are updates from databases most recently published elsewhere. Major nucleic acid databases reporting updates include Genbank, ENA, ChIPBase, JASPAR, mirDIP and the Issue's first Breakthrough Article, NACDDB for Circular Dichroism data. Updates from BMRB and RCSB cover experimental protein structural data while AlphaFold 2 computational structure predictions feature widely. STRING and REBASE are stand-out updates in the signalling and enzymes section. Immunology-related databases include CEDAR, the second Breakthrough Article, for cancer epitopes and receptors alongside returning IPD-IMGT/HLA and the new PGG.MHC. Genomics-related resources include Ensembl, GWAS Central and UCSC Genome Browser. Major returning databases for drugs and their targets include Open Targets, DrugCentral, CTD and Pubchem. The EMPIAR image archive appears in the Issue for the first time. The entire database Issue is freely available online on the *Nucleic Acids Research* website (https://academic.oup.com/nar). The NAR online Molecular Biology Database Collection has been updated, revisiting 463 entries, adding 92 new resources and eliminating 96 discontinued URLs so bringing the current total to 1764 databases. It is available at http://www.oxfordjournals.org/nar/database/c/.

NEW AND UPDATED DATABASES

In its 30th incarnation, the *Nucleic Acids Research* Database Issue once again ranges across biology with a total of 178 papers. Table 1 lists the 90 new databases included, a recent record number, and there are 82 update papers from resources previously covered by NAR. Finally, six databases most recently published elsewhere contribute updates (Table 2). As usual, updates from the major database providers at the European Bioinformatics Institute (EBI), the U.S. National Center for Biotechnology Information (NCBI), and the National Genomics Data Center (NGDC) in China (1–3) are placed first. The usual categorisation then follows: (i) nucleic acid sequence and structure, transcriptional regulation; (ii) protein sequence and structure; (iii) metabolic and signalling pathways, enzymes and networks; (iv) genomics of viruses, bacteria, protozoa and fungi; (v) genomics of human and model organisms plus comparative genomics; (vi) human genomic variation, diseases and drugs; (vii) plants and (viii) other topics, such as proteomics databases. Many papers are not easily placed in a single category so readers are well advised to browse the full list.

The 'Nucleic acid databases' section contains the first of the Issue's Breakthrough Articles, reporting on the Nucleic Acid Circular Dichroism Database (NACCDDB; (4)). CD data can give insights into the folding, stability, dynamics and interactions of nucleic acids. NACDDB archives and disseminates the experimental spectra for the first time alongside the metadata describing the experiment and any associated structure models. At this early stage, the database is keen to receive new data and feedback directly from the community. A trio of new nucleic acid quadruplex-related databases also feature. G4Atlas (5) focuses on experimentally determined RNA G-quadruplexes (rG4s) across transcriptomes, determined by a variety of experimental methods, and accompanied by their classification into canonical and other types. QUADRAtlas (6) similarly focuses on rG4s, covering both experimental and predicted structures and including information on rG4-binding proteins, while GAIA (7) surveys predicted quadruplexes in both genomes and transcriptomes across all three kingdoms. RNA modifications are also addressed by three new databases. tModBase (8) focuses on modifications of tRNA, their dynamics and biomedical implications, and the enzymes involved. RM2Target (9), a development of the earlier m6A2Target database (10), covers writes, erasers and readers of nine RNA modifications as well as diverse annotations and biomedical implications. The third of the trio, DirectRMDB (11), collects data from direct RNA sequencing that captures quantitative RNA modifications,

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TASK 2

Database Summary Paper Categories (oxfordjournals.org)

TASK 3

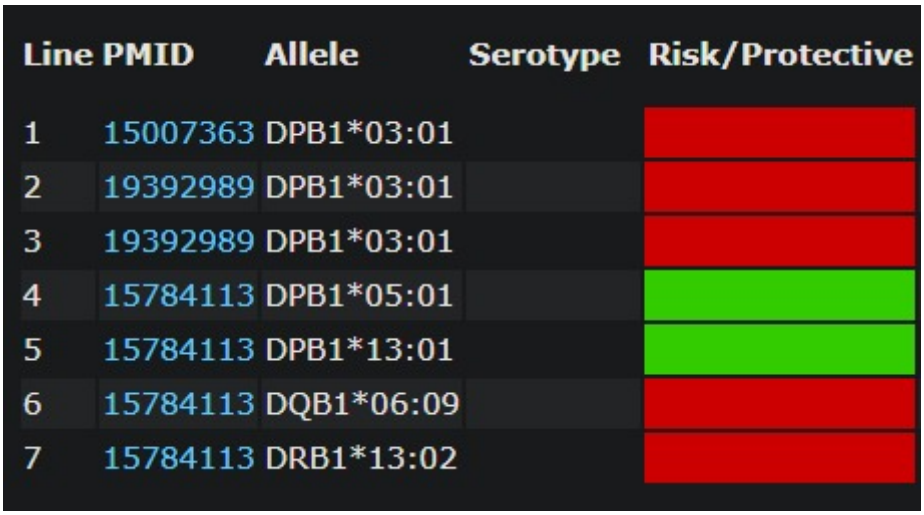
Co dwa miesiące.

TASK 4

Nazwa to "MGDB", znajduje się ona pod linkiem: http://bioinfo.ahu.edu.cn:8080/Melanoma/

TASK 5

Dla 2 z 7 alleli aspiryna podnosi ryzyko chorób autoimmunologicznych.



Line	PMID	Allele	Serotype	Risk/Protective
1	15007363	DPB1*03:01		
2	19392989	DPB1*03:01		
3	19392989	DPB1*03:01		
4	15784113	DPB1*05:01		
5	15784113	DPB1*13:01		
6	15784113	DQB1*06:09		
7	15784113	DRB1*13:02		

TASK 6

Lista wyników spokrewnionych, po wyszukaniu nukleotydów związanych z "Kuzdraliński"

- Fusarium poae (155)
- Rhizopus arrhizus (96)
- Rhizopus stolonifer (54)
- Blumeria graminis f. sp. tritici (33)
- Fusarium sp. (30)
- Puccinia triticina (26)
- Puccinia striiformis f. sp. tritici (22)
- Epicoccum nigrum (18)
- Fusarium sporotrichioides (16)
- Fusarium avenaceum (14)
- Lactobacillus helveticus (9)
- Fusarium culmorum (6)
- Pichia kudriavzevii (4)
- Fusarium graminearum (3)
- Aureobasidium pullulans (3)
- Rhizopus microsporus (3)
- Fusarium equiseti (2)

- Fusarium oxysporum (2)
- Alternaria sp. (2)
- Rhizoctonia solani (2)

TASK 7

> KJ195691.1 Pichia kudriavzevii isolate 4 26S ribosomal RNA gene, partial sequence
> GCGGCGAGTGAGCGGCAGAGCTCAGATTTGAAATCGTGCTTTGCGGCACGAGTTGTAGATTGCAGGTTG
> G
> AGTCTGTGTGGAAGGCGGTGTCCAAGTCCCTTGGAACAGGGCGCCCAGGAGGGTGAGAGCCCCGTGGG
> AT
> GCCGGCGGAAGCAGTGAGGCCCTTCTGACGAGTCGAGTTGTTTGGGAATGCAGCTCCAAGCGGGTGGT
> AA
> ATTCCATCTAAGGCTAAATACTGGCGAGAGACCGATAGCGAACAAGTACTGTGAAGGAAAGATGAAAAG
> C
> ACTTTGAAAAGAGAGTGAAACAGCACGTGAAATTGTTGAAAGGGAAGGGTATTGCGCCCGACATGGGGA
> T
> TGCGCACCGCTGCCTCTCGTGGGCGGCGCTCTGGGCTTTCCCTGGGCCAGCATCGGTTCTTGCTGCAGG
> A
> GAAGGGGTTCTGGAACGTGGCTCTTCGGAGTGTTATAGCCAGGGCCAGATGCTGCGTGCGGGGACCGA
> GG
> ACTGCGGCCGTGTAGGTCACGGATGCTGGCAGAACGGCGCAACACCGCCCGTCTTGAAAC

> KJ195690.1 Pichia kudriavzevii isolate 3 26S ribosomal RNA gene, partial sequence
> AGCGGCAAGAGCTCAGATTTGAAATCGTGCTTTGCGGCACGAGTTGTAGATTGCAGGTTGGAGTCTGTG
> T
> GGAAGGCGGTGTCCAAGTCCCTTGGAACAGGGCGCCCAGGAGGGTGAGAGCCCCGTGGGATGCCGGC
> GGA
> AGCAGTGAGGCCCTTCTGACGAGTCGAGTTGTTTGGGAATGCAGCTCCAAGCGGGTGGTAAATTCCATC
> T
> AAGGCTAAATACTGGCGAGAGACCGATAGCGAACAAGTACTGTGAAGGAAAGATGAAAAGCACTTTGAA
> A
> AGAGAGTGAAACAGCACGTGAAATTGTTGAAAGGGAAGGGTATTGCGCCCGACATGGGGATTGCGCAC
> CG
> CTGCCTCTCGTGGGCGGCGCTCTGGGCTTTCCCTGGGCCAGCATCGGTTCTTGCTGCAGGAGAAGGGGT
> T
> CTGGAACGTGGCTCTTCGGAGTGTTATAGCCAGGGCCAGATGCTGCGTGCGGGGACCGAGGACTGCGG
> CC
> GTGTAGGTCACGGATGCTGGCAGAACGGCGCAACACCGCCCGTCTTGAAC

> KJ195689.1 Pichia kudriavzevii isolate 4 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence
> CTACACTGCGTGAGCGGACGAAAACAACAACACCTAAAATGTGGAATATAGCATATAGTCGACAAGAGAA
> ATCTACGGACAAGAGAAATCTACGAAAAAACAAACAAAACTTTCAACAACGGATCTCTTGGTTCTCGCAT
> CGATGAAGAGCGCAGCGAAATGCGATACCTAGTGTGAATTGCAGCCATCGTGAATCATCGAGTTCTTGAA
> CGCACATTGCGCCCCTCGGCATTCCGGGGGGCATGCCTGTTTGAGCGTCGTTTCCATCTTGCGCGTGCGC

> AGAGTTGGGGGAGCGGAGCGGACGACGTGTAAAGAGCGTCGGAGCTGCGACTCGCCTGAAAGGGAGC
> GAA
> GCTGGCCGAGCGAACTAGACTTTTTTTCAGGGACGCTTGGCGGCCGAGAGCGAGTGTTGCGAGACAACA
> A
> AAAGCTCGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGGAT
> CATTACTGTGATTTAGTA

> KJ195688.1 Pichia kudriavzevii isolate 3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence
> AAACAACAACACCTAAAATGTGGAATATAGCATATAGTCGACAAGAGAAATCTACGAAAAACAAACAAAA
> CTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAGCGCAGCGAAATGCGATACCTAGTGTGAAT
> TGCAGCCATCGTGAATCATCGAGTTCTTGAACGCACATTGCGCCCCTCGGCATTCCGGGGGGCATGCCTG
> TTTGAGCGTCGTTTCCATCTTGCGCGTGCGCAGAGTTGGGGGAGCGGAGCGGACGACGTGTAAAGAGC
> GT
> CGGAGCTGCGACTCGCCTGAAAGGGAGCGAAGCTGGCCGAGCGAACTAGACTTTTTTTCAGGGACGCTT
> G
> GCGGCCGAGAGCGAGTGTTGCGAGACAACAATAAGCTCGACCTCAAATCAGGTAGGAATACCCGCTGAA
> C
> TTAAGCATATCAATAAGCGGAGGAAAAGGATCATTACTGTGATTTAGTA

TASK 8

JX669571

TASK 9

Zakładam, że *ostatni* autor, jest to ostatni wymieniony autor w publikacji na stronie NCBI. Jest to "Targonski,Z", więc zakładam, że jest to Zdzisław Jan Targoński w bazie Nauki Polskiej, ponieważ tylko on posiada jakiekolwiek publikacjie.

Ostatnia (najnowsza) wymieniona pubikacja to: "2014, A new insight into the physiological role of bile salt hydrolase among intestinal bacteria from the genus *Bifidobacterium, Piotr Paweł Jarocki, Paweł Robert Glibowski, Zdzisław Jan Targoński | Artykuł*".

TASK 10

Na stronie scholar.google.com, jest wiele nowszych publikacji, a najnowsza z nich (ostatnia) to: "A novel biocatalyst, Enterobacter aerogenes LU2, for efficient production of succinic acid using whey permeate as a cost-effective carbon sourceH Szczerba, E Komoń-Janczara, K Dudziak, A Waśko, Z TargońskiBiotechnology for biofuels 13 (1), 1-12" z 2020 roku.

W formacie zbliżonym do APA (ponieważ Markdown nie obsługuje regulowania wcięć, odstępów wmiędzy wierszami i kontroli akapitów):

Szczerba, H., Komoń-Janczara, E., Dudziak, K., Waśko, A., & Targoński, Z. (2020). A novel biocatalyst, Enterobacter aerogenes LU2, for efficient production of succinic acid using whey permeate as a cost-effective carbon source. Biotechnology for biofuels, 13(1), 1-12. https://doi.org/10.1186/s13068-020-01789-8

TASK 11

Ocenia się na 20,024.

TASK 12

W latach 90. XX w. szacowano, że liczba ludzkich genów wynosi ponad 100 tysięcy. Dzięki wynikom projektu HGP możliwe było dokładniejsze oszacowanie liczby genów w genomie człowieka.

Analizy z 2008 roku wskazywały, że liczba ta jest znacznie mniejsza i wynosi około 23 tysięcy.

TASK 13

50 818 468 bp

TASK 14

Chromosomy są uporządkowane po kolei od 1 do 18,, potem 20, 19, Y, 22 i 21.

TASK 15

```
1. Homo sapiens chromosome 1, GRCh38.p14 Primary Assembly
248,956,422 bp linear DNA
NC_000001.11 GI:568815597

2. Homo sapiens chromosome 2, GRCh38.p14 Primary Assembly
242,193,529 bp linear DNA
NC_000002.12 GI:568815596

3. Homo sapiens chromosome 3, GRCh38.p14 Primary Assembly
198,295,559 bp linear DNA
NC_000003.12 GI:568815595

4. Homo sapiens chromosome 4, GRCh38.p14 Primary Assembly
190,214,555 bp linear DNA
NC_000004.12 GI:568815594

5. Homo sapiens chromosome 5, GRCh38.p14 Primary Assembly
181,538,259 bp linear DNA
NC_000005.10 GI:568815593

6. Homo sapiens chromosome 6, GRCh38.p14 Primary Assembly
170,805,979 bp linear DNA
NC_000006.12 GI:568815592

7. Homo sapiens chromosome 7, GRCh38.p14 Primary Assembly
159,345,973 bp linear DNA
NC_000007.14 GI:568815591

8. Homo sapiens chromosome X, GRCh38.p14 Primary Assembly
```

```
156,040,895 bp linear DNA
NC_000023.11 GI:568815575

9. Homo sapiens chromosome 8, GRCh38.p14 Primary Assembly
145,138,636 bp linear DNA
NC_000008.11 GI:568815590

10. Homo sapiens chromosome 9, GRCh38.p14 Primary Assembly
138,394,717 bp linear DNA
NC_000009.12 GI:568815589

11. Homo sapiens chromosome 11, GRCh38.p14 Primary Assembly
135,086,622 bp linear DNA
NC_000011.10 GI:568815587

12. Homo sapiens chromosome 10, GRCh38.p14 Primary Assembly
133,797,422 bp linear DNA
NC_000010.11 GI:568815588

13. Homo sapiens chromosome 12, GRCh38.p14 Primary Assembly
133,275,309 bp linear DNA
NC_000012.12 GI:568815586

14. Homo sapiens chromosome 13, GRCh38.p14 Primary Assembly
114,364,328 bp linear DNA
NC_000013.11 GI:568815585

15. Homo sapiens chromosome 14, GRCh38.p14 Primary Assembly
107,043,718 bp linear DNA
NC_000014.9 GI:568815584

16. Homo sapiens chromosome 15, GRCh38.p14 Primary Assembly
101,991,189 bp linear DNA
NC_000015.10 GI:568815583

17. Homo sapiens chromosome 16, GRCh38.p14 Primary Assembly
90,338,345 bp linear DNA
NC_000016.10 GI:568815582

18. Homo sapiens chromosome 17, GRCh38.p14 Primary Assembly
83,257,441 bp linear DNA
NC_000017.11 GI:568815581

19. Homo sapiens chromosome 18, GRCh38.p14 Primary Assembly
80,373,285 bp linear DNA
NC_000018.10 GI:568815580

20. Homo sapiens chromosome 20, GRCh38.p14 Primary Assembly
64,444,167 bp linear DNA
NC_000020.11 GI:568815578

21. Homo sapiens chromosome 19, GRCh38.p14 Primary Assembly
```

```
58,617,616 bp linear DNA
NC_000019.10 GI:568815579

22. Homo sapiens chromosome Y, GRCh38.p14 Primary Assembly
57,227,415 bp linear DNA
NC_000024.10 GI:568815574

23. Homo sapiens chromosome 22, GRCh38.p14 Primary Assembly
50,818,468 bp linear DNA
NC_000022.11 GI:568815576

24. Homo sapiens chromosome 21, GRCh38.p14 Primary Assembly
46,709,983 bp linear DNA
NC_000021.9 GI:568815577

25. Homo sapiens mitochondrion, complete genome
16,569 bp circular DNA
NC_012920.1 GI:251831106
```

TASK 16

240,251

TASK 22

Search query: Poland[Affiliation]
Year,Count
2022,26147
2021,27901
2020,23639
2019,18676
2018,17296
2017,15962
2016,15123
2015,13743

TASK 17

Są dwie publikacje po query: `(intestinal cancer[Title]) AND (Poland[Affiliation])`:

- PMID: 14555796
- PMID: 12721399

TASK 18

Population: Total
Group: Globab
Sample Size: 74968
Ref Allele: A = 0.32646

Alt Allele: G=0.67354, T=0.0

todo *TODO: Zamienić w tabelę*

TASK 19

MAF jest to częstotliwość występowania drugiego najczęściej występującego allelu w danej populacji.

TASK 20

W populacji Afrykańskiej

TASK 21

GGKYTRRGGTTAGCTTTYRAGTTTTTTGATTTTKGATTTTTGTCTTTTTAGCTGTTATTW
RTCAAACCTTYDBGGGDRAAAGAAVTGMARTCACCACAGGRCAGAAACCBTAAGGGAAAA
YAWTAAYAYTAGCTAAGAACATAAAAGAAYAYACARTTRCTTAATCATATAADTGTCTGA
MGTTAAYTGTCCATYYAATTGTGATTTSTACCCAGAAGGRCHRAGCYTGTRYACTYTTCA
YGGYYYAGAGYSAATRTCYTGTCYMARCTTCTCCTGCYRRCYCMCHVYGBTCTCCACRTC
ASTGDGTYAYCKCAAGAAAAMGCCCCTCCAAGRRGHCTSRTYCCYYACACYTHDGGHACA
GMATTCRYGGAAWGGAAARSYRTABDGRACATRCCYRABRDTCYTCAVTYCCACAGAWAC
AGGGAGRRGCTGGGAAGCTCWTTCTACRGATGSRGWAACAGYTCAARYCAGGCCYCCYGT
GCCTRTCAGCCTTYYTCSCAGTCCARYRYTCCYGASAGAYGTTTGGYTGCCYCAGTGRHG
GGRYRCTCCTTTCTTTYYCAGGTTRSCARTTCTGKTYCAGRYAKYTRYTYAGMAAGYCCC
TATTCCTCCTGAGTSCAGCTCTTCAYGGCYATCCCTKYCCYRTCTYASTCACCYYTMTGC
TCCCATTTTCCAYRTRTTTGGCAAGCACYKGTTGAGYTAYMAATGACTGTGCAGVCTTGT
GYCASGSATCCCCTGGGGTAAAAGGCRTMCCCTGGMGYTGTGYCACAAAASAGMCCACAC
AWTRGACTTRGGCTTAACAAG

TASK 22

Jest to Fasarium poae - gatunek grzybów.

TASK 23

37,7 Mb

TASK 24

Contig N50: 62 040 b

Jest to długość sekwencji, która jest osiągana przez 50% całkowitej długości sekwencji.

TASK 25

Lipaza Q05469

TASK 26

Biorę inny: **Colipase** P04118 i jest cofactorem pancreatic lipase

Kofaktor to substancja niebiałkowa, która ściśle wiąże się z enzymem i wspomaga jego działanie. Wraz z apoenzymem, czyli białkową częścią enzymu, tworzy katalitycznie aktywny enzym, nazywany holoenzymem, dzięki niemu dochodzi do katalizowania reakcji zachodzących między różnymi związkami chemicznymi, co oznacza, że enzymy są aktywne katalitycznie.

Kofaktory można podzielić na grupy prostetyczne:

- silnie,
- kowalencyjnie związane z apoenzymami,
- koenzymy – łączą się z apoenzymem nietrwale

TASK 27

3D structure databases:

- AlphaFoldDB
  - P04118
- SMR
  - P04118
- ModBase
  - Search...

TASK 28

Enzymy o tym samym numerze EC mogą występować u różnych gatunków, ale ich sekwencje aminokwasowe są różne. Różnice te wynikają z mutacji i zmian w sekwencjach DNA w trakcie ewolucji.

TASK 29

202

TASK 30

Jest to gen kodujący receptor Dopaminy D3

TASK 31

Odmiana polimorfizmu: rs167771

Fenotyp: Individuals carrying the AA variant of the rs167771 SNP scored significantly higher on the IS-factor (resp $U = 590$, $p < .01$), indicating more rigid behavior than individuals carrying one or two copies of the minor G-allele.

TASK 32

29 903 bp

TASK 33

Grudzień 2019

TASK 34

```
MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPF
FSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQS
LLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQP
FLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIG
INITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVD
CALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFA
SVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDE
VRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPF
ERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPA
TVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQ
TLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYST
GSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYT
MSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLL
QYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKP
SKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMI
AQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFN
SAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDK
VEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCG
KGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHW
FVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHT
SPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWL
GFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT
```