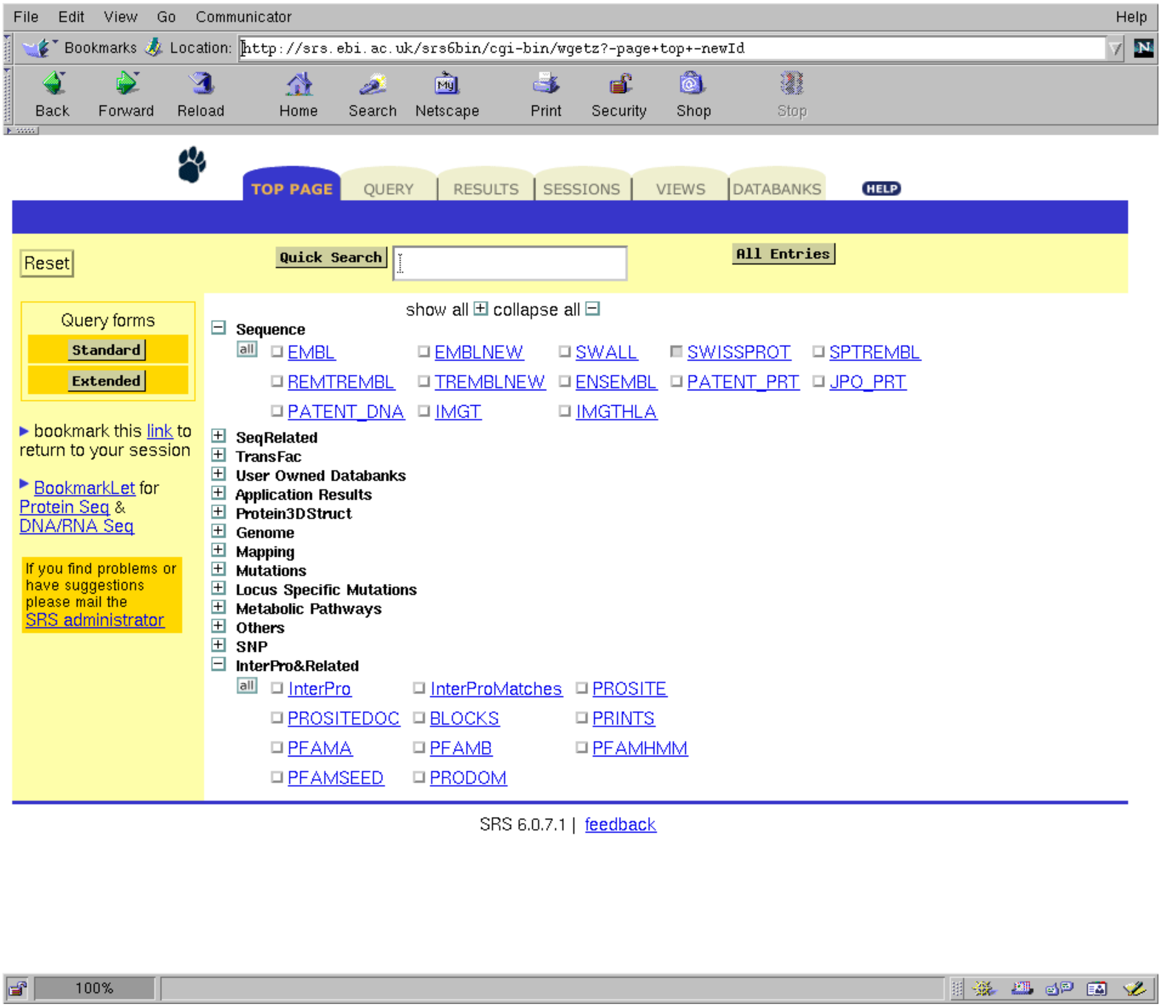


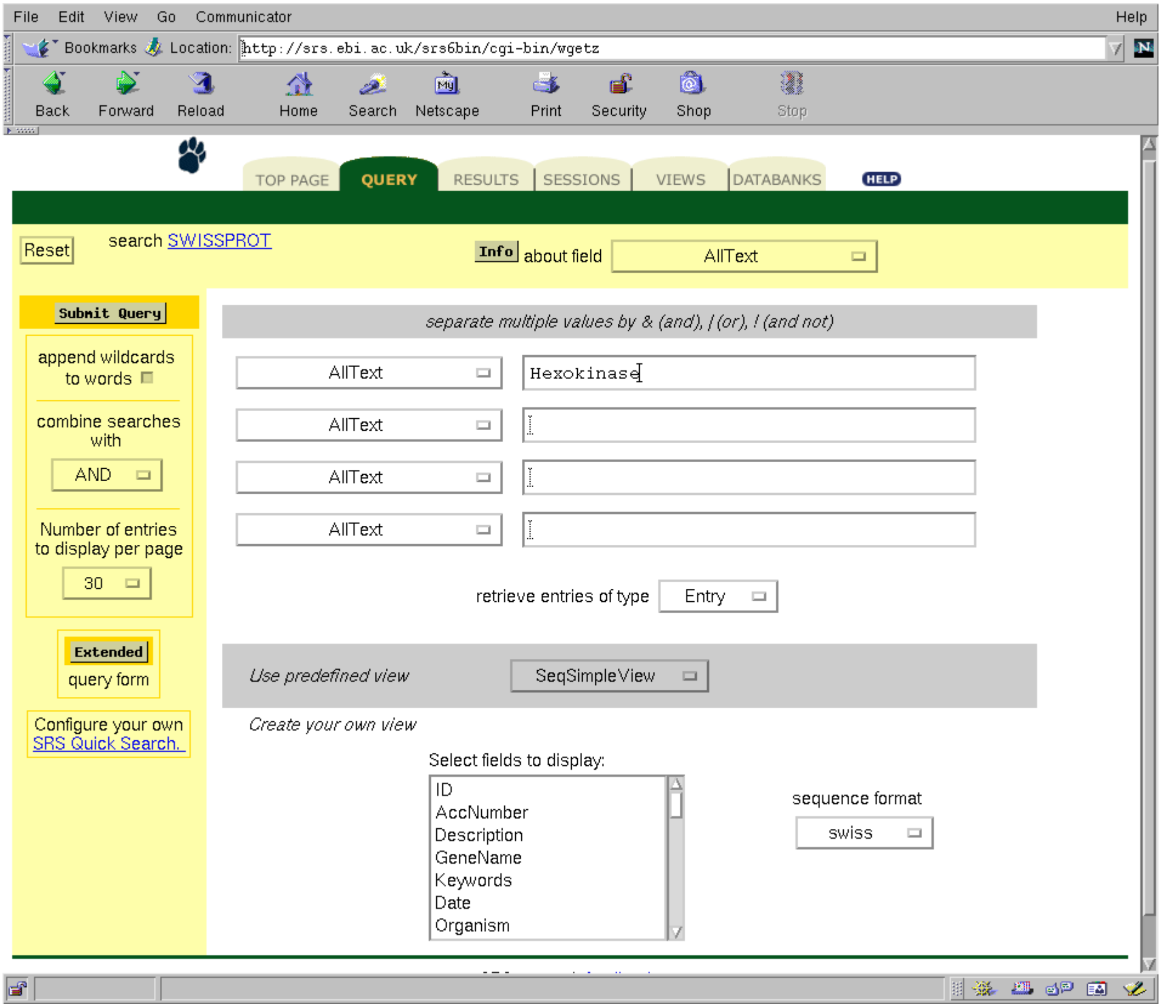
Location: `http://srs.ebi.ac.uk/srs6bin/cgi-bin/wgetz?-page+top+-newId`

▸ bookmark this link to return to your session

▸ BookmarkLet for Protein Seq & DNA/RNA Seq

If you find problems or have suggestions please mail the SRS administrator

SRS 6.0.7.1 | feedback



Location: http://srs.ebi.ac.uk/srs6bin/cgi-bin/wgetz

search SWISSPROT

Info about field: AllText

separate multiple values by & (and), | (or), ! (and not)

AllText: Hexokinase

AllText:

AllText:

AllText:

append wildcards to words ☐

combine searches with: AND

Number of entries to display per page: 30

retrieve entries of type: Entry

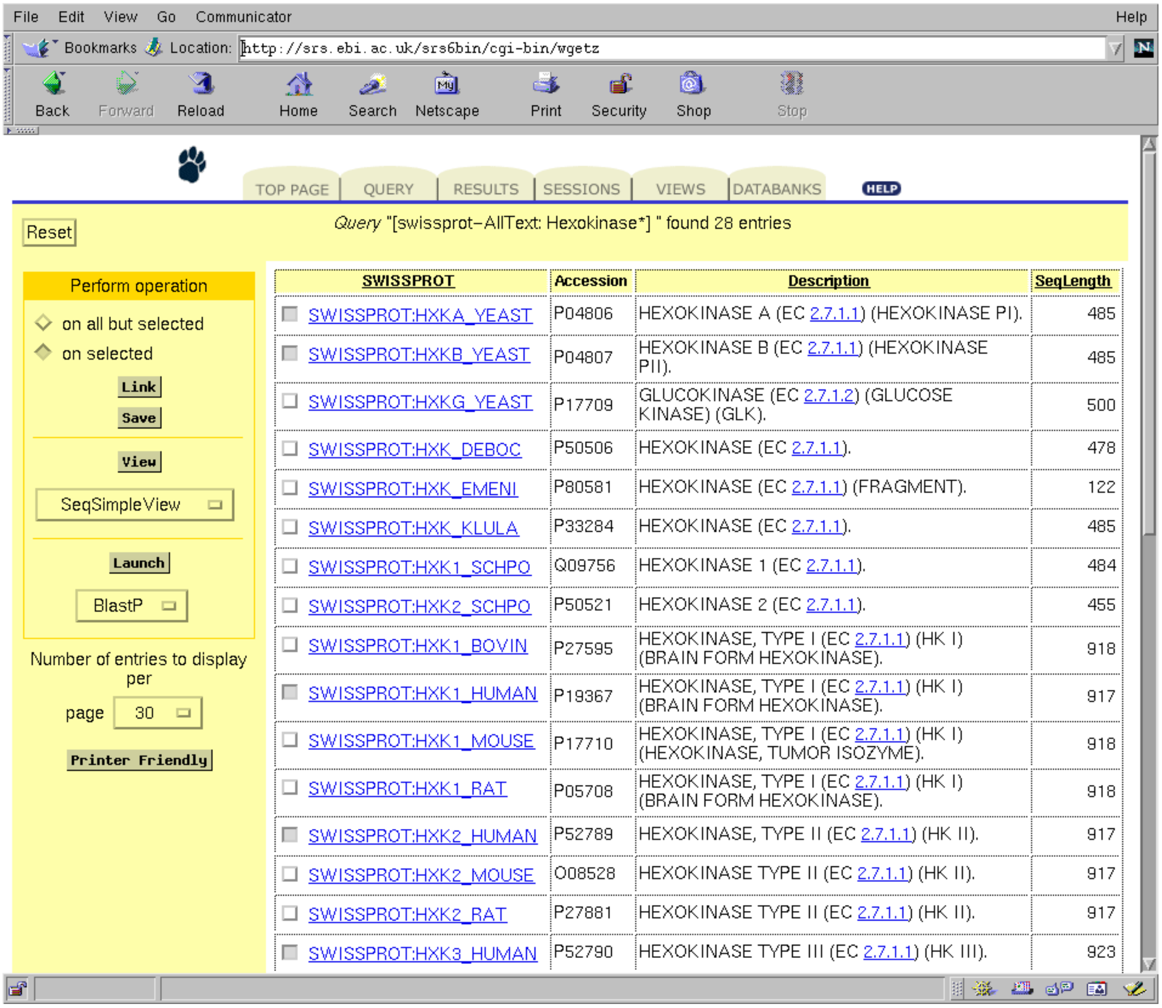
Use predefined view: SeqSimpleView

Create your own view

Select fields to display:

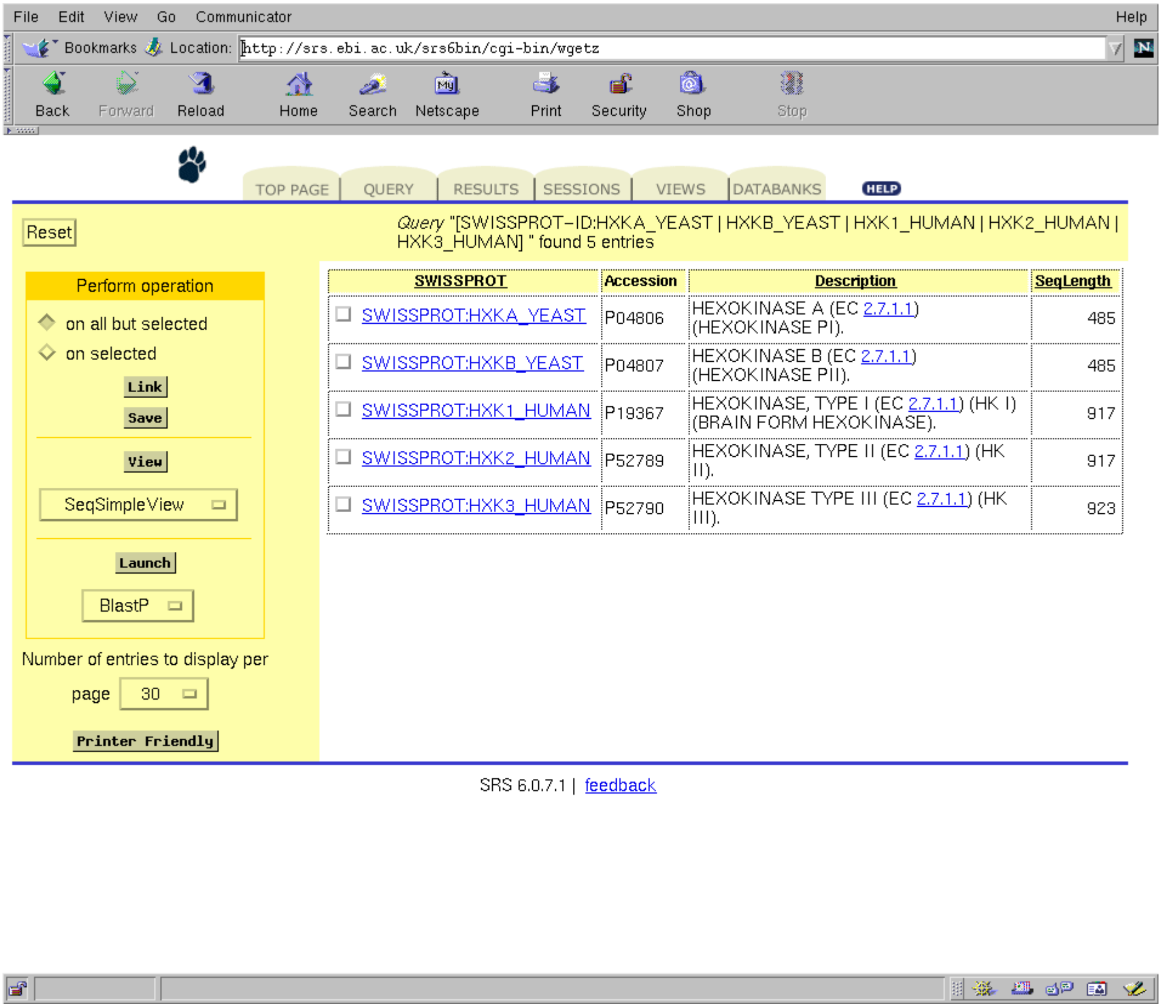
- ID
- AccNumber
- Description
- GeneName
- Keywords
- Date
- Organism

sequence format: swiss



Query "[swissprot-AllText: Hexokinase*] " found 28 entries

SWISSPROT	Accession	Description	SeqLength
☐ SWISSPROT:HXKA_YEAST	P04806	HEXOKINASE A (EC 2.7.1.1) (HEXOKINASE PI).	485
☐ SWISSPROT:HXKB_YEAST	P04807	HEXOKINASE B (EC 2.7.1.1) (HEXOKINASE PII).	485
☐ SWISSPROT:HXKG_YEAST	P17709	GLUCOKINASE (EC 2.7.1.2) (GLUCOSE KINASE) (GLK).	500
☐ SWISSPROT:HXK_DEBOC	P50506	HEXOKINASE (EC 2.7.1.1).	478
☐ SWISSPROT:HXK_EMENI	P80581	HEXOKINASE (EC 2.7.1.1) (FRAGMENT).	122
☐ SWISSPROT:HXK_KLULA	P33284	HEXOKINASE (EC 2.7.1.1).	485
☐ SWISSPROT:HXK1_SCHPO	Q09756	HEXOKINASE 1 (EC 2.7.1.1).	484
☐ SWISSPROT:HXK2_SCHPO	P50521	HEXOKINASE 2 (EC 2.7.1.1).	455
☐ SWISSPROT:HXK1_BOVIN	P27595	HEXOKINASE, TYPE I (EC 2.7.1.1) (HK I) (BRAIN FORM HEXOKINASE).	918
☐ SWISSPROT:HXK1_HUMAN	P19367	HEXOKINASE, TYPE I (EC 2.7.1.1) (HK I) (BRAIN FORM HEXOKINASE).	917
☐ SWISSPROT:HXK1_MOUSE	P17710	HEXOKINASE, TYPE I (EC 2.7.1.1) (HK I) (HEXOKINASE, TUMOR ISOZYME).	918
☐ SWISSPROT:HXK1_RAT	P05708	HEXOKINASE, TYPE I (EC 2.7.1.1) (HK I) (BRAIN FORM HEXOKINASE).	918
☐ SWISSPROT:HXK2_HUMAN	P52789	HEXOKINASE, TYPE II (EC 2.7.1.1) (HK II).	917
☐ SWISSPROT:HXK2_MOUSE	O08528	HEXOKINASE TYPE II (EC 2.7.1.1) (HK II).	917
☐ SWISSPROT:HXK2_RAT	P27881	HEXOKINASE TYPE II (EC 2.7.1.1) (HK II).	917
☐ SWISSPROT:HXK3_HUMAN	P52790	HEXOKINASE TYPE III (EC 2.7.1.1) (HK III).	923



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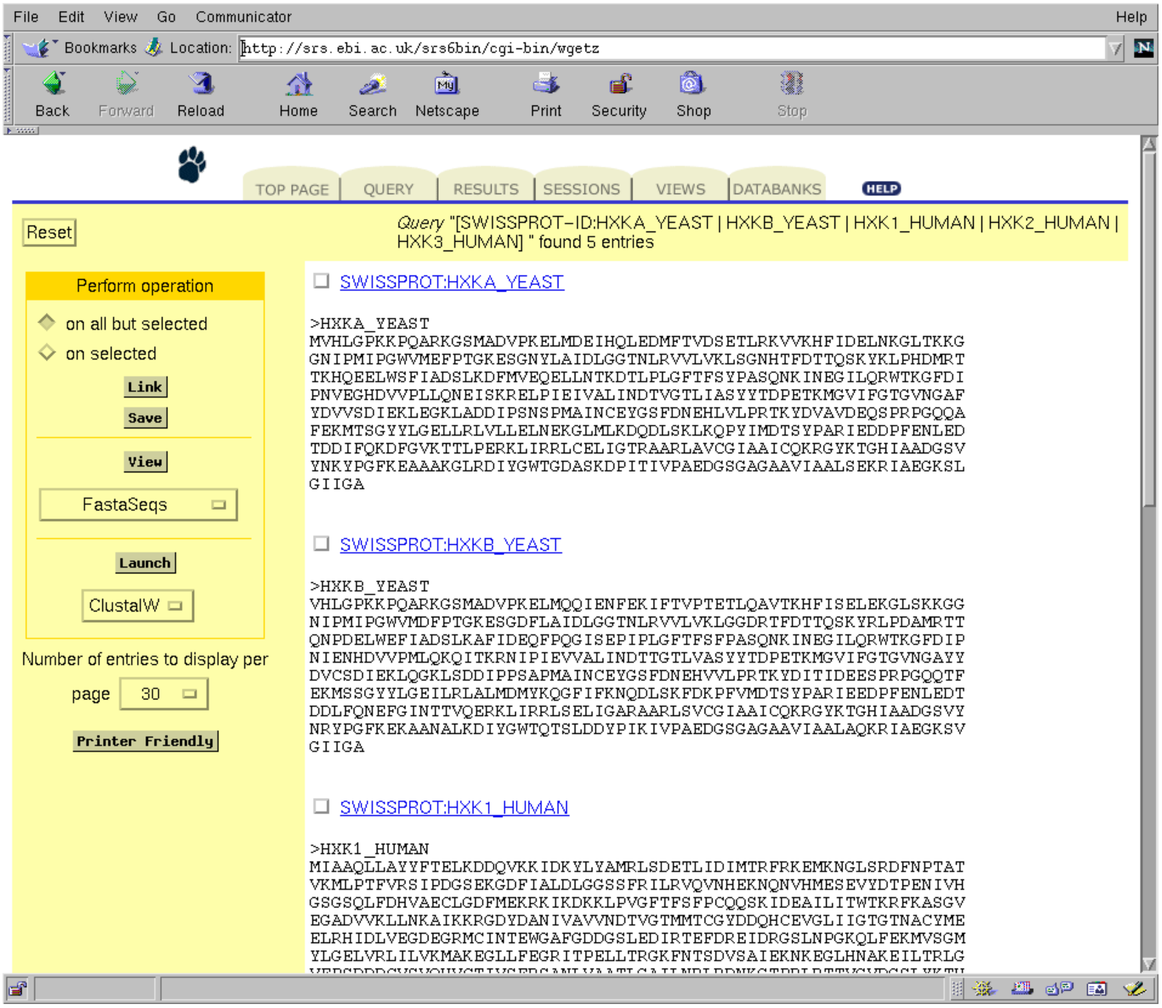
	SWISSPROT	Accession	Description	SeqLength
☐	SWISSPROT:HXKA_YEAST	P04806	HEXOKINASE A (EC 2.7.1.1) (HEXOKINASE PI).	485
☐	SWISSPROT:HXKB_YEAST	P04807	HEXOKINASE B (EC 2.7.1.1) (HEXOKINASE PII).	485
☐	SWISSPROT:HXK1_HUMAN	P19367	HEXOKINASE, TYPE I (EC 2.7.1.1) (HK I) (BRAIN FORM HEXOKINASE).	917
☐	SWISSPROT:HXK2_HUMAN	P52789	HEXOKINASE, TYPE II (EC 2.7.1.1) (HK II).	917
☐	SWISSPROT:HXK3_HUMAN	P52790	HEXOKINASE TYPE III (EC 2.7.1.1) (HK III).	923

SRS 6.0.7.1 | feedback



Query "[SWISSPROT-ID:HXKA_YEAST | HXKB_YEAST | HXK1_HUMAN | HXK2_HUMAN | HXK3_HUMAN] " found 5 entries

☐ SWISSPROT:HXKA_YEAST

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MVHLGPKKPQARKGSMADVPKELMDEIHQLEDMFTVDSETLRKVVKHFIDELNKGLTKKG
GNIPMIPGWVMEFPTGKESGNYLAIDLGGTNLRVVLVKLSGNHTFDTTQSKYKLPHDMRT
TKHQEELWSFIADSLKDFMVEQELLNTKDTLPLGFTFSYPASQNKINEGILQRWTKGFDI
PNVEGHDVVPLLQNEISKRELPIEIVALINDTVGTLIASYYTDPETKMGVIFGTGVNGAF
YDVVSDIEKLEGKLADDIPSNSPMAINCEYGSFDNEHLVLPRTKYDVAVDEQSPRPGQQA
FEKMTSGYYLGELLRLVLLELNEKGLMLKDQDLSKLKQPYIMDTSYPARIEDDPFENLED
TDDIFQKDFGVKTTLPERKLIRRLCELIGTRAARLAVCGIAAICQKRGYKTGHIAADGSV
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GIIGA
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☐ SWISSPROT:HXKB_YEAST

```
>HXKB_YEAST
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QNPDELWEFIADSLKAFIDEQFPQGISEPIPLGFTFSFPASQNKINEGILQRWTKGFDIP
NIENHDVVPMLQKQITKRNIPIEVVALINDTTGTLVASYYTDPETKMGVIFGTGVNGAYY
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DDLFQNEFGINTTVQERKLIRRLSELIGARAARLSVCGIAAICQKRGYKTGHIAADGSVY
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GIIGA
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☐ SWISSPROT:HXK1_HUMAN

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GSGSQLFDHVAECLGDFMEKRKIKDKKLPVGFTFSFPCQQSKIDEAILITWTKRFKASGV
EGADVVKLLNKAIKKRGDYDANIVAVVNDTVGTMMTCGYDDQHCEVGLIIGTGTNACYME
ELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDREIDRGSLNPGKQLFEKMVSGM
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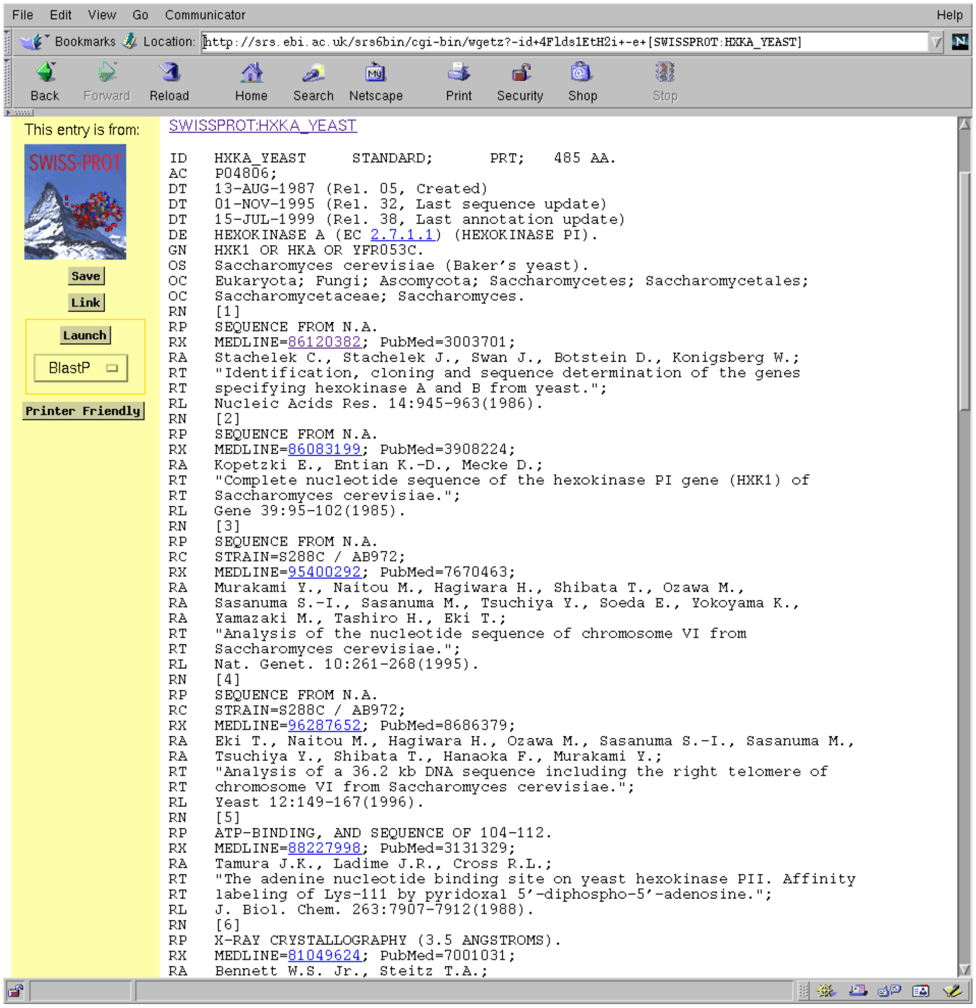

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SWISSPROT:HXKA_YEAST

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AC   P04806;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   HEXOKINASE A (EC 2.7.1.1) (HEXOKINASE PI).
GN   HXK1 OR HKA OR YFR053C.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC   Saccharomycetaceae; Saccharomyces.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86120382; PubMed=3003701;
RA   Stachelek C., Stachelek J., Swan J., Botstein D., Konigsberg W.;
RT   "Identification, cloning and sequence determination of the genes
RT   specifying hexokinase A and B from yeast.";
RL   Nucleic Acids Res. 14:945-963(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86083199; PubMed=3908224;
RA   Kopetzki E., Entian K.-D., Mecke D.;
RT   "Complete nucleotide sequence of the hexokinase PI gene (HXK1) of
RT   Saccharomyces cerevisiae.";
RL   Gene 39:95-102(1985).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RX   MEDLINE=95400292; PubMed=7670463;
RA   Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA   Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA   Yamazaki M., Tashiro H., Eki T.;
RT   "Analysis of the nucleotide sequence of chromosome VI from
RT   Saccharomyces cerevisiae.";
RL   Nat. Genet. 10:261-268(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RX   MEDLINE=96287652; PubMed=8686379;
RA   Eki T., Naitou M., Hagiwara H., Ozawa M., Sasanuma S.-I., Sasanuma M.,
RA   Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.;
RT   "Analysis of a 36.2 kb DNA sequence including the right telomere of
RT   chromosome VI from Saccharomyces cerevisiae.";
RL   Yeast 12:149-167(1996).
RN   [5]
RP   ATP-BINDING, AND SEQUENCE OF 104-112.
RX   MEDLINE=88227998; PubMed=3131329;
RA   Tamura J.K., Ladime J.R., Cross R.L.;
RT   "The adenine nucleotide binding site on yeast hexokinase PII. Affinity
RT   labeling of Lys-111 by pyridoxal 5'-diphospho-5'-adenosine.";
RL   J. Biol. Chem. 263:7907-7912(1988).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX   MEDLINE=81049624; PubMed=7001031;
RA   Bennett W.S. Jr., Steitz T.A.;
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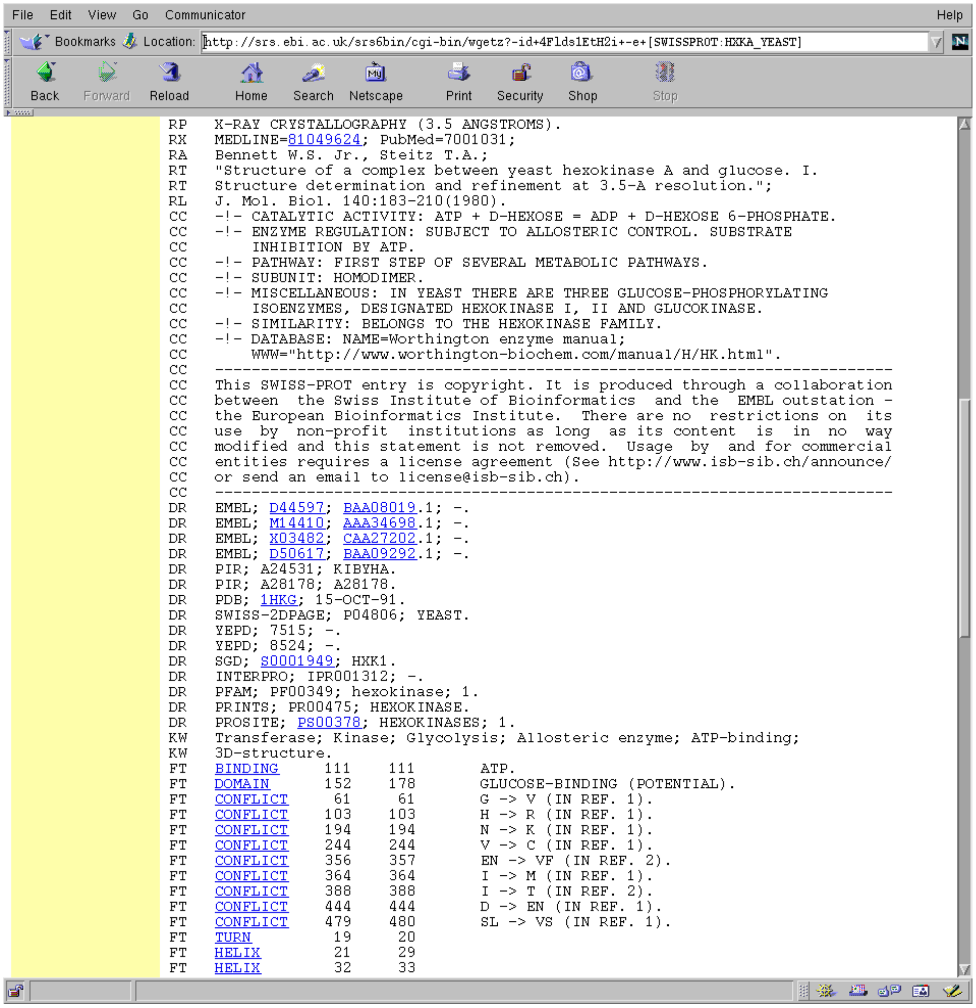

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RP   X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX   MEDLINE=81049624; PubMed=7001031;
RA   Bennett W.S. Jr., Steitz T.A.;
RT   "Structure of a complex between yeast hexokinase A and glucose. I.
RT   Structure determination and refinement at 3.5-A resolution.";
RL   J. Mol. Biol. 140:183-210(1980).
CC   -!- CATALYTIC ACTIVITY: ATP + D-HEXOSE = ADP + D-HEXOSE 6-PHOSPHATE.
CC   -!- ENZYME REGULATION: SUBJECT TO ALLOSTERIC CONTROL. SUBSTRATE
CC       INHIBITION BY ATP.
CC   -!- PATHWAY: FIRST STEP OF SEVERAL METABOLIC PATHWAYS.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- MISCELLANEOUS: IN YEAST THERE ARE THREE GLUCOSE-PHOSPHORYLATING
CC       ISOENZYMES, DESIGNATED HEXOKINASE I, II AND GLUCOKINASE.
CC   -!- SIMILARITY: BELONGS TO THE HEXOKINASE FAMILY.
CC   -!- DATABASE: NAME=Worthington enzyme manual;
CC       WWW="http://www.worthington-biochem.com/manual/H/HK.html".
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D44597; BAA08019.1; -.
DR   EMBL; M14410; AAA34698.1; -.
DR   EMBL; X03482; CAA27202.1; -.
DR   EMBL; D50617; BAA09292.1; -.
DR   PIR; A24531; KIBYHA.
DR   PIR; A28178; A28178.
DR   PDB; 1HKG; 15-OCT-91.
DR   SWISS-2DPAGE; P04806; YEAST.
DR   YEPD; 7515; -.
DR   YEPD; 8524; -.
DR   SGD; S0001949; HXK1.
DR   INTERPRO; IPR001312; -.
DR   PFAM; PF00349; hexokinase; 1.
DR   PRINTS; PR00475; HEXOKINASE.
DR   PROSITE; PS00378; HEXOKINASES; 1.
KW   Transferase; Kinase; Glycolysis; Allosteric enzyme; ATP-binding;
KW   3D-structure.
FT   BINDING     111    111       ATP.
FT   DOMAIN      152    178       GLUCOSE-BINDING (POTENTIAL).
FT   CONFLICT     61     61       G -> V (IN REF. 1).
FT   CONFLICT    103    103       H -> R (IN REF. 1).
FT   CONFLICT    194    194       N -> K (IN REF. 1).
FT   CONFLICT    244    244       V -> C (IN REF. 1).
FT   CONFLICT    356    357       EN -> VF (IN REF. 2).
FT   CONFLICT    364    364       I -> M (IN REF. 1).
FT   CONFLICT    388    388       I -> T (IN REF. 2).
FT   CONFLICT    444    444       D -> EN (IN REF. 1).
FT   CONFLICT    479    480       SL -> VS (IN REF. 1).
FT   TURN         19     20
FT   HELIX        21     29
FT   HELIX        32     33
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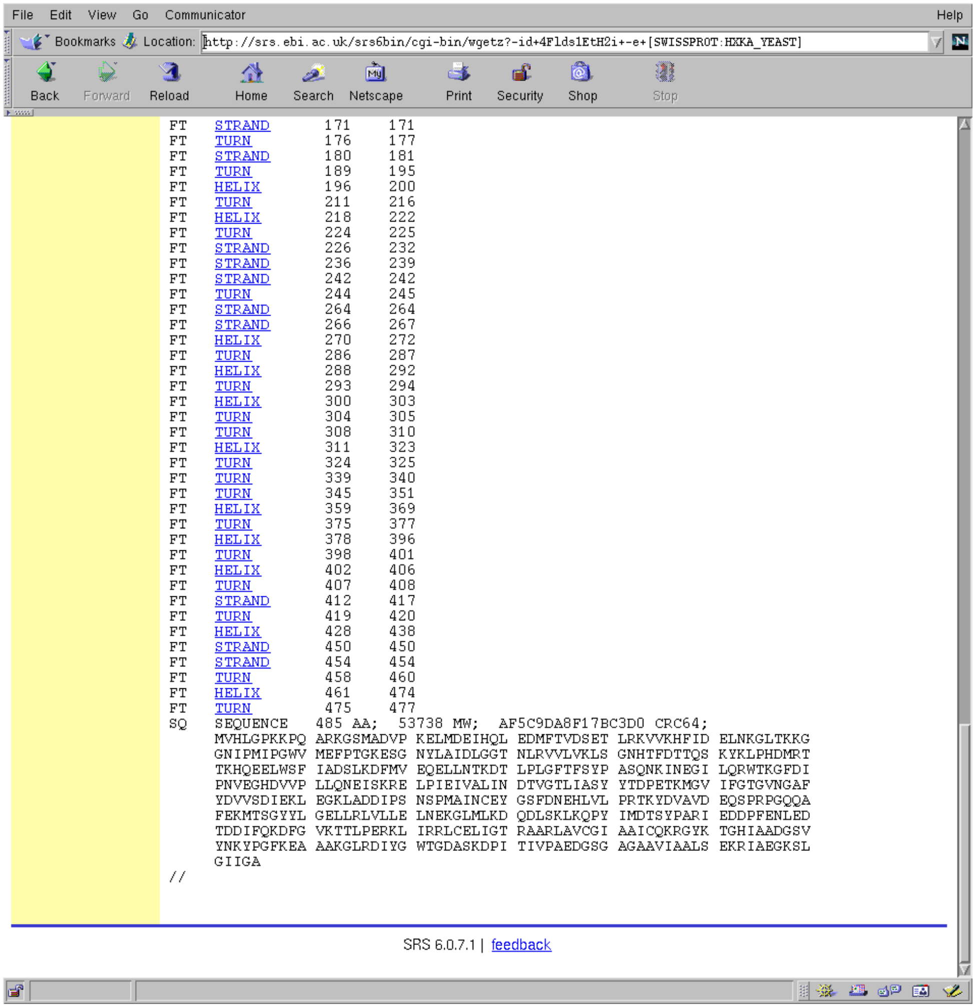

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FT   TURN        176    177
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FT   HELIX       196    200
FT   TURN        211    216
FT   HELIX       218    222
FT   TURN        224    225
FT   STRAND      226    232
FT   STRAND      236    239
FT   STRAND      242    242
FT   TURN        244    245
FT   STRAND      264    264
FT   STRAND      266    267
FT   HELIX       270    272
FT   TURN        286    287
FT   HELIX       288    292
FT   TURN        293    294
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FT   TURN        304    305
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FT   TURN        475    477
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     PNVEGHDVVP LLQNEISKRE LPIEIVALIN DTVGTLIASY YTDPETKMGV IFGTGVNGAF
     YDVVSDIEKL EGKLADDIPS NSPMAINCEY GSFDNEHLVL PRTKYDVAVD EQSPRPGQQA
     FEKMTSGYYL GELLRLVLLE LNEKGLMLKD QDLSKLKQPY IMDTSYPARI EDDPFENLED
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//
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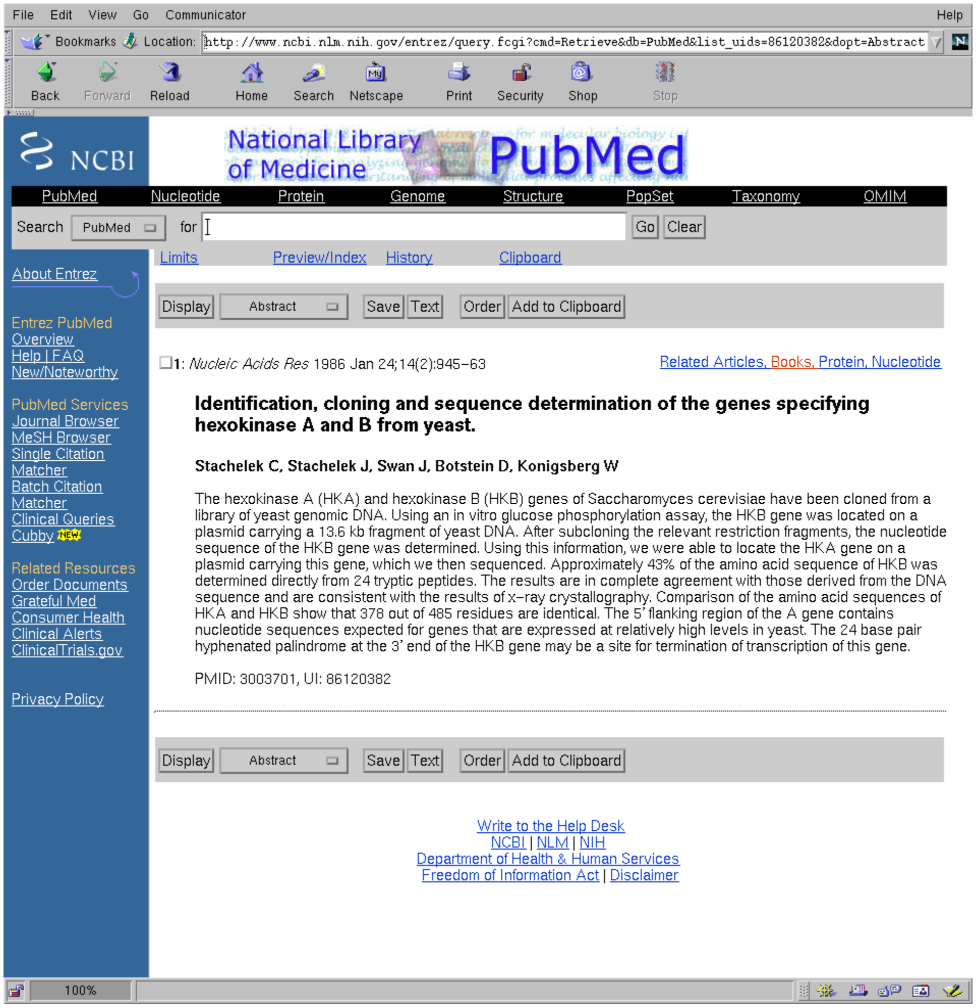
SRS 6.0.7.1 | feedback



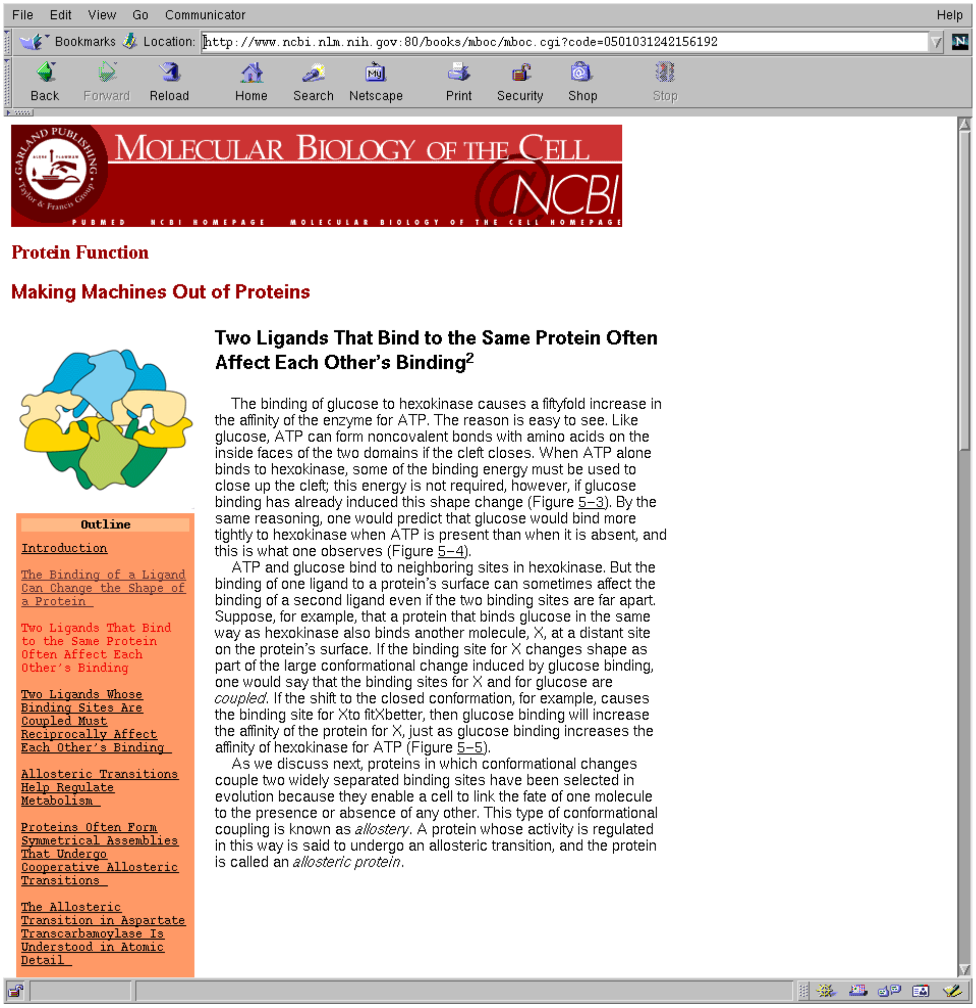
☐1: *Nucleic Acids Res* 1986 Jan 24;14(2):945–63

Identification, cloning and sequence determination of the genes specifying hexokinase A and B from yeast.

Stachelek C, Stachelek J, Swan J, Botstein D, Konigsberg W

The hexokinase A (HKA) and hexokinase B (HKB) genes of Saccharomyces cerevisiae have been cloned from a library of yeast genomic DNA. Using an in vitro glucose phosphorylation assay, the HKB gene was located on a plasmid carrying a 13.6 kb fragment of yeast DNA. After subcloning the relevant restriction fragments, the nucleotide sequence of the HKB gene was determined. Using this information, we were able to locate the HKA gene on a plasmid carrying this gene, which we then sequenced. Approximately 43% of the amino acid sequence of HKB was determined directly from 24 tryptic peptides. The results are in complete agreement with those derived from the DNA sequence and are consistent with the results of x–ray crystallography. Comparison of the amino acid sequences of HKA and HKB show that 378 out of 485 residues are identical. The 5’ flanking region of the A gene contains nucleotide sequences expected for genes that are expressed at relatively high levels in yeast. The 24 base pair hyphenated palindrome at the 3’ end of the HKB gene may be a site for termination of transcription of this gene.

PMID: 3003701, UI: 86120382



Protein Function

Making Machines Out of Proteins

Outline

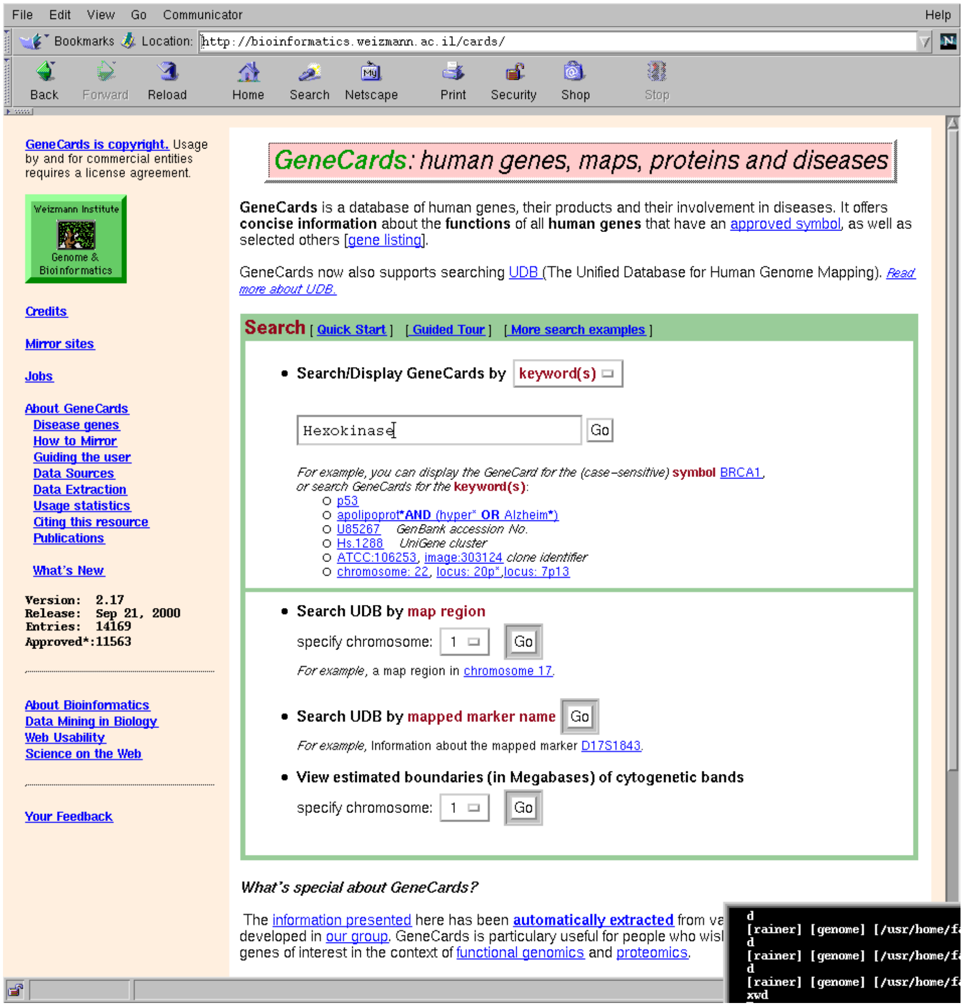
- Introduction
- The Binding of a Ligand Can Change the Shape of a Protein
- Two Ligands That Bind to the Same Protein Often Affect Each Other's Binding
- Two Ligands Whose Binding Sites Are Coupled Must Reciprocally Affect Each Other's Binding
- Allosteric Transitions Help Regulate Metabolism
- Proteins Often Form Symmetrical Assemblies That Undergo Cooperative Allosteric Transitions
- The Allosteric Transition in Aspartate Transcarbamoylase Is Understood in Atomic Detail

Two Ligands That Bind to the Same Protein Often Affect Each Other's Binding[2]

The binding of glucose to hexokinase causes a fiftyfold increase in the affinity of the enzyme for ATP. The reason is easy to see. Like glucose, ATP can form noncovalent bonds with amino acids on the inside faces of the two domains if the cleft closes. When ATP alone binds to hexokinase, some of the binding energy must be used to close up the cleft; this energy is not required, however, if glucose binding has already induced this shape change (Figure 5–3). By the same reasoning, one would predict that glucose would bind more tightly to hexokinase when ATP is present than when it is absent, and this is what one observes (Figure 5–4).

ATP and glucose bind to neighboring sites in hexokinase. But the binding of one ligand to a protein's surface can sometimes affect the binding of a second ligand even if the two binding sites are far apart. Suppose, for example, that a protein that binds glucose in the same way as hexokinase also binds another molecule, X, at a distant site on the protein's surface. If the binding site for X changes shape as part of the large conformational change induced by glucose binding, one would say that the binding sites for X and for glucose are *coupled*. If the shift to the closed conformation, for example, causes the binding site for Xto fitXbetter, then glucose binding will increase the affinity of the protein for X, just as glucose binding increases the affinity of hexokinase for ATP (Figure 5–5).

As we discuss next, proteins in which conformational changes couple two widely separated binding sites have been selected in evolution because they enable a cell to link the fate of one molecule to the presence or absence of any other. This type of conformational coupling is known as *allostery*. A protein whose activity is regulated in this way is said to undergo an allosteric transition, and the protein is called an *allosteric protein*.



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  Data Sources
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  Usage statistics
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What's New

```
Version:  2.17
Release:  Sep 21, 2000
Entries:  14169
Approved*:11563
```

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GeneCards: human genes, maps, proteins and diseases

GeneCards is a database of human genes, their products and their involvement in diseases. It offers **concise information** about the **functions** of all **human genes** that have an approved symbol, as well as selected others [gene listing].

GeneCards now also supports searching UDB (The Unified Database for Human Genome Mapping). *Read more about UDB.*

Search [**Quick Start**] [**Guided Tour**] [**More search examples**]

- **Search/Display GeneCards by** **keyword(s)**

  Hexokinase Go

  For example, you can display the GeneCard for the (case-sensitive) **symbol** BRCA1, *or search GeneCards for the* **keyword(s)**:
  - ○ p53
  - ○ apolipoprot***AND** (hyper* **OR** Alzheim*)
  - ○ U85267 *GenBank accession No.*
  - ○ Hs.1288 *UniGene cluster*
  - ○ ATCC:106253, image:303124 *clone identifier*
  - ○ chromosome: 22, locus: 20p*,locus: 7p13

- **Search UDB by map region**

  specify chromosome: 1 Go

  For example, a map region in chromosome 17.

- **Search UDB by mapped marker name** Go

  For example, Information about the mapped marker D17S1843.

- **View estimated boundaries (in Megabases) of cytogenetic bands**

  specify chromosome: 1 Go

What's special about GeneCards?

The information presented here has been **automatically extracted** from va
developed in our group. GeneCards is particulary useful for people who wisl
genes of interest in the context of functional genomics and proteomics.

```
d
[rainer] [genome] [/usr/home/fa
d
[rainer] [genome] [/usr/home/fa
d
[rainer] [genome] [/usr/home/fa
xwd
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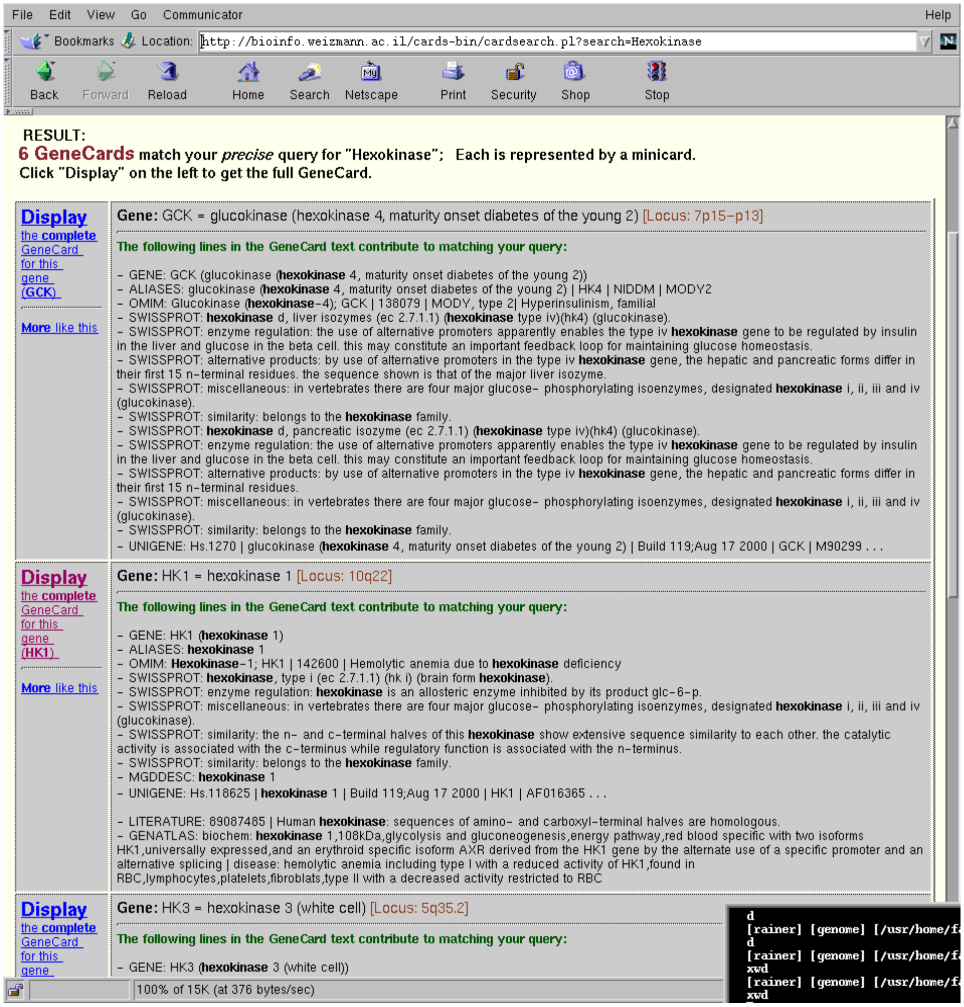


RESULT:
6 GeneCards match your *precise* query for "Hexokinase"; Each is represented by a minicard.
Click "Display" on the left to get the full GeneCard.

Gene: GCK = glucokinase (hexokinase 4, maturity onset diabetes of the young 2) [Locus: 7p15–p13]

The following lines in the GeneCard text contribute to matching your query:

– GENE: GCK (glucokinase (**hexokinase** 4, maturity onset diabetes of the young 2))
– ALIASES: glucokinase (**hexokinase** 4, maturity onset diabetes of the young 2) | HK4 | NIDDM | MODY2
– OMIM: Glucokinase (**hexokinase**–4); GCK | 138079 | MODY, type 2| Hyperinsulinism, familial
– SWISSPROT: **hexokinase** d, liver isozymes (ec 2.7.1.1) (**hexokinase** type iv)(hk4) (glucokinase).
– SWISSPROT: enzyme regulation: the use of alternative promoters apparently enables the type iv **hexokinase** gene to be regulated by insulin in the liver and glucose in the beta cell. this may constitute an important feedback loop for maintaining glucose homeostasis.
– SWISSPROT: alternative products: by use of alternative promoters in the type iv **hexokinase** gene, the hepatic and pancreatic forms differ in their first 15 n–terminal residues. the sequence shown is that of the major liver isozyme.
– SWISSPROT: miscellaneous: in vertebrates there are four major glucose– phosphorylating isoenzymes, designated **hexokinase** i, ii, iii and iv (glucokinase).
– SWISSPROT: similarity: belongs to the **hexokinase** family.
– SWISSPROT: **hexokinase** d, pancreatic isozyme (ec 2.7.1.1) (**hexokinase** type iv)(hk4) (glucokinase).
– SWISSPROT: enzyme regulation: the use of alternative promoters apparently enables the type iv **hexokinase** gene to be regulated by insulin in the liver and glucose in the beta cell. this may constitute an important feedback loop for maintaining glucose homeostasis.
– SWISSPROT: alternative products: by use of alternative promoters in the type iv **hexokinase** gene, the hepatic and pancreatic forms differ in their first 15 n–terminal residues.
– SWISSPROT: miscellaneous: in vertebrates there are four major glucose– phosphorylating isoenzymes, designated **hexokinase** i, ii, iii and iv (glucokinase).
– SWISSPROT: similarity: belongs to the **hexokinase** family.
– UNIGENE: Hs.1270 | glucokinase (**hexokinase** 4, maturity onset diabetes of the young 2) | Build 119;Aug 17 2000 | GCK | M90299 . . .

Gene: HK1 = hexokinase 1 [Locus: 10q22]

The following lines in the GeneCard text contribute to matching your query:

– GENE: HK1 (**hexokinase** 1)
– ALIASES: **hexokinase** 1
– OMIM: **Hexokinase**–1; HK1 | 142600 | Hemolytic anemia due to **hexokinase** deficiency
– SWISSPROT: **hexokinase**, type i (ec 2.7.1.1) (hk i) (brain form **hexokinase**).
– SWISSPROT: enzyme regulation: **hexokinase** is an allosteric enzyme inhibited by its product glc–6–p.
– SWISSPROT: miscellaneous: in vertebrates there are four major glucose– phosphorylating isoenzymes, designated **hexokinase** i, ii, iii and iv (glucokinase).
– SWISSPROT: similarity: the n– and c–terminal halves of this **hexokinase** show extensive sequence similarity to each other. the catalytic activity is associated with the c–terminus while regulatory function is associated with the n–terminus.
– SWISSPROT: similarity: belongs to the **hexokinase** family.
– MGDDESC: **hexokinase** 1
– UNIGENE: Hs.118625 | **hexokinase** 1 | Build 119;Aug 17 2000 | HK1 | AF016365 . . .

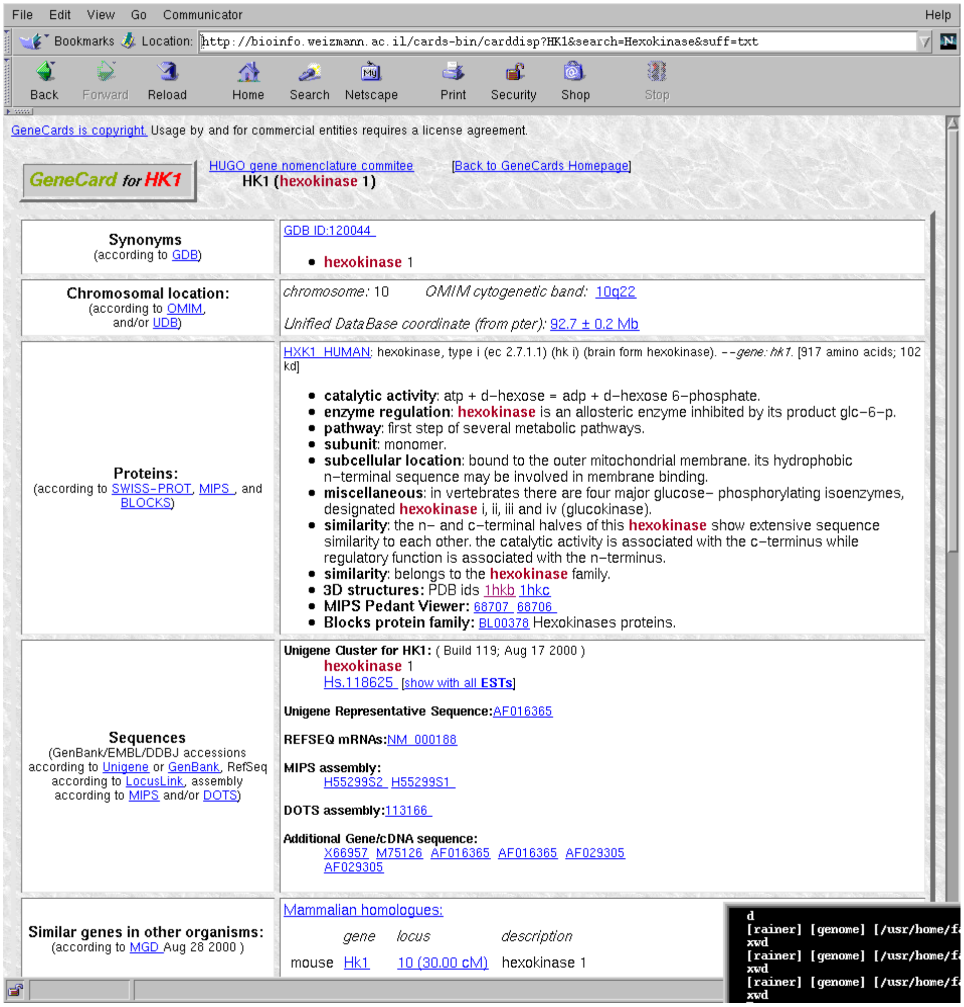
– LITERATURE: 89087485 | Human **hexokinase**: sequences of amino– and carboxyl–terminal halves are homologous.
– GENATLAS: biochem: **hexokinase** 1,108kDa,glycolysis and gluconeogenesis,energy pathway,red blood specific with two isoforms HK1,universally expressed,and an erythroid specific isoform AXR derived from the HK1 gene by the alternate use of a specific promoter and an alternative splicing | disease: hemolytic anemia including type I with a reduced activity of HK1,found in RBC,lymphocytes,platelets,fibroblats,type II with a decreased activity restricted to RBC

Gene: HK3 = hexokinase 3 (white cell) [Locus: 5q35.2]

The following lines in the GeneCard text contribute to matching your query:

– GENE: HK3 (**hexokinase** 3 (white cell))

```
d
[rainer] [genome] [/usr/home/fa
d
[rainer] [genome] [/usr/home/fa
xwd
[rainer] [genome] [/usr/home/fa
xwd
```



http://bioinfo.weizmann.ac.il/cards-bin/carddisp?HK1&search=Hexokinase&suff=txt

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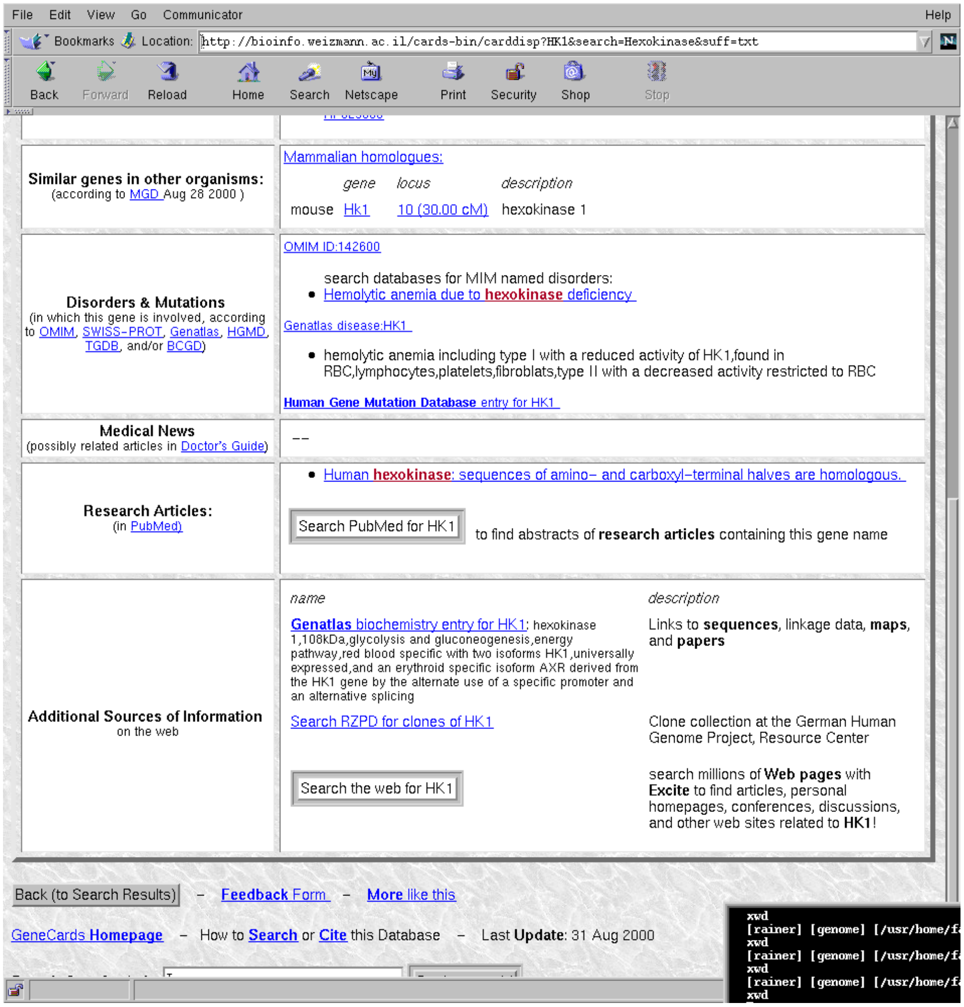
GeneCard for HK1

HUGO gene nomenclature commitee [Back to GeneCards Homepage]

HK1 (hexokinase 1)

Synonyms (according to GDB)	GDB ID:120044 • **hexokinase** 1
Chromosomal location: (according to OMIM, and/or UDB)	*chromosome:* 10 *OMIM cytogenetic band:* 10q22 *Unified DataBase coordinate (from pter):* 92.7 ± 0.2 Mb
Proteins: (according to SWISS-PROT, MIPS , and BLOCKS)	HXK1_HUMAN: hexokinase, type i (ec 2.7.1.1) (hk i) (brain form hexokinase). --*gene: hk1*. [917 amino acids; 102 kd] • **catalytic activity**: atp + d−hexose = adp + d−hexose 6−phosphate. • **enzyme regulation**: **hexokinase** is an allosteric enzyme inhibited by its product glc−6−p. • **pathway**: first step of several metabolic pathways. • **subunit**: monomer. • **subcellular location**: bound to the outer mitochondrial membrane. its hydrophobic n−terminal sequence may be involved in membrane binding. • **miscellaneous**: in vertebrates there are four major glucose− phosphorylating isoenzymes, designated **hexokinase** i, ii, iii and iv (glucokinase). • **similarity**: the n− and c−terminal halves of this **hexokinase** show extensive sequence similarity to each other. the catalytic activity is associated with the c−terminus while regulatory function is associated with the n−terminus. • **similarity**: belongs to the **hexokinase** family. • **3D structures:** PDB ids 1hkb 1hkc • **MIPS Pedant Viewer:** 68707 68706 • **Blocks protein family:** BL00378 Hexokinases proteins.
Sequences (GenBank/EMBL/DDBJ accessions according to Unigene or GenBank, RefSeq according to LocusLink, assembly according to MIPS and/or DOTS)	**Unigene Cluster for HK1:** (Build 119; Aug 17 2000) **hexokinase** 1 Hs.118625 [show with all **ESTs**] **Unigene Representative Sequence:**AF016365 **REFSEQ mRNAs:**NM_000188 **MIPS assembly:** H55299S2 H55299S1 **DOTS assembly:**113166 **Additional Gene/cDNA sequence:** X66957 M75126 AF016365 AF016365 AF029305 AF029305
Similar genes in other organisms: (according to MGD Aug 28 2000)	Mammalian homologues: *gene* *locus* *description* mouse Hk1 10 (30.00 cM) hexokinase 1

```
d
[rainer] [genome] [/usr/home/f
xwd
[rainer] [genome] [/usr/home/f
xwd
[rainer] [genome] [/usr/home/f
xwd
```



http://bioinfo.weizmann.ac.il/cards-bin/carddisp?HK1&search=Hexokinase&suff=txt

Similar genes in other organisms: (according to MGD Aug 28 2000)	Mammalian homologues: *gene* *locus* *description* mouse Hk1 10 (30.00 cM) hexokinase 1
Disorders & Mutations (in which this gene is involved, according to OMIM, SWISS-PROT, Genatlas, HGMD, TGDB, and/or BCGD)	OMIM ID:142600 search databases for MIM named disorders: • Hemolytic anemia due to **hexokinase** deficiency Genatlas disease:HK1 • hemolytic anemia including type I with a reduced activity of HK1,found in RBC,lymphocytes,platelets,fibroblats,type II with a decreased activity restricted to RBC **Human Gene Mutation Database** entry for HK1
Medical News (possibly related articles in Doctor's Guide)	--
Research Articles: (in PubMed)	• Human **hexokinase**: sequences of amino- and carboxyl-terminal halves are homologous. Search PubMed for HK1 to find abstracts of **research articles** containing this gene name
Additional Sources of Information on the web	*name* / *description* **Genatlas** biochemistry entry for HK1: hexokinase 1,108kDa,glycolysis and gluconeogenesis,energy pathway,red blood specific with two isoforms HK1,universally expressed,and an erythroid specific isoform AXR derived from the HK1 gene by the alternate use of a specific promoter and an alternative splicing / Links to **sequences**, linkage data, **maps**, and **papers** Search RZPD for clones of HK1 / Clone collection at the German Human Genome Project, Resource Center Search the web for HK1 / search millions of **Web pages** with **Excite** to find articles, personal homepages, conferences, discussions, and other web sites related to **HK1**!

Back (to Search Results) – **Feedback** Form – **More** like this

GeneCards **Homepage** – How to **Search** or **Cite** this Database – Last **Update**: 31 Aug 2000

```
xwd
[rainer] [genome] [/usr/home/fa
xwd
[rainer] [genome] [/usr/home/fa
xwd
[rainer] [genome] [/usr/home/fa
xwd
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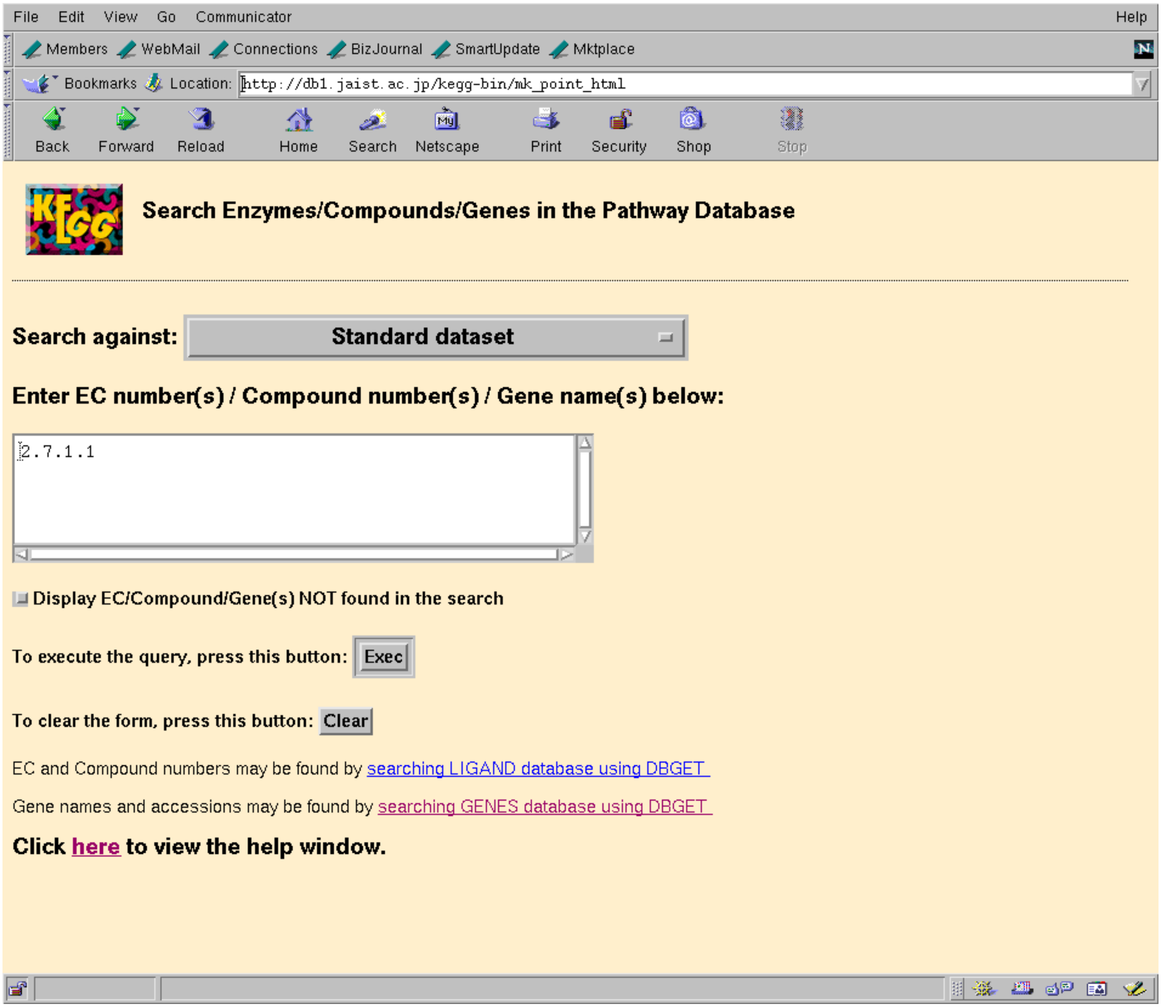


Location: http://db1.jaist.ac.jp/kegg-bin/mk_point_html

Search Enzymes/Compounds/Genes in the Pathway Database

Search against: Standard dataset

Enter EC number(s) / Compound number(s) / Gene name(s) below:

2.7.1.1

☐ Display EC/Compound/Gene(s) NOT found in the search

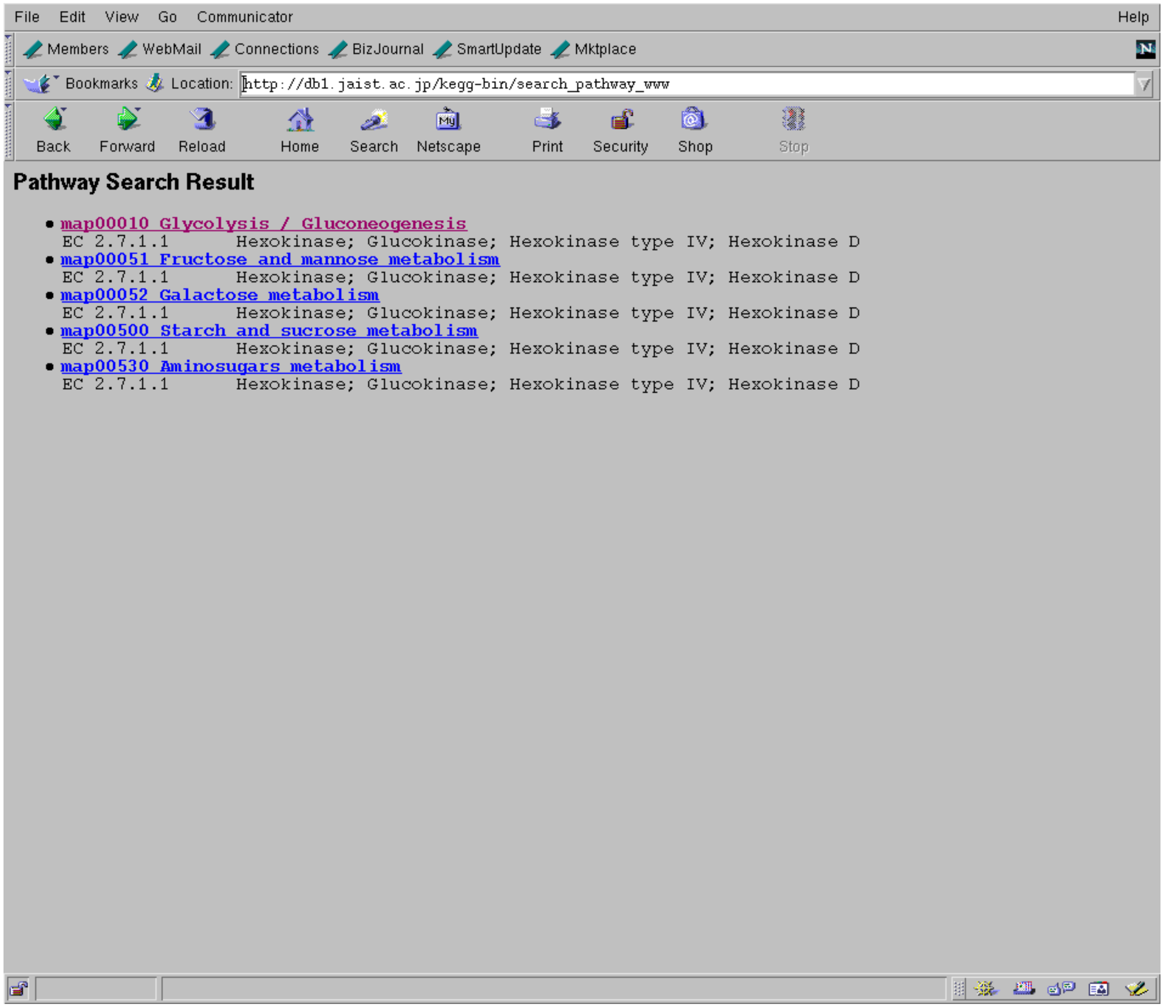
To execute the query, press this button: Exec

To clear the form, press this button: Clear

EC and Compound numbers may be found by searching LIGAND database using DBGET

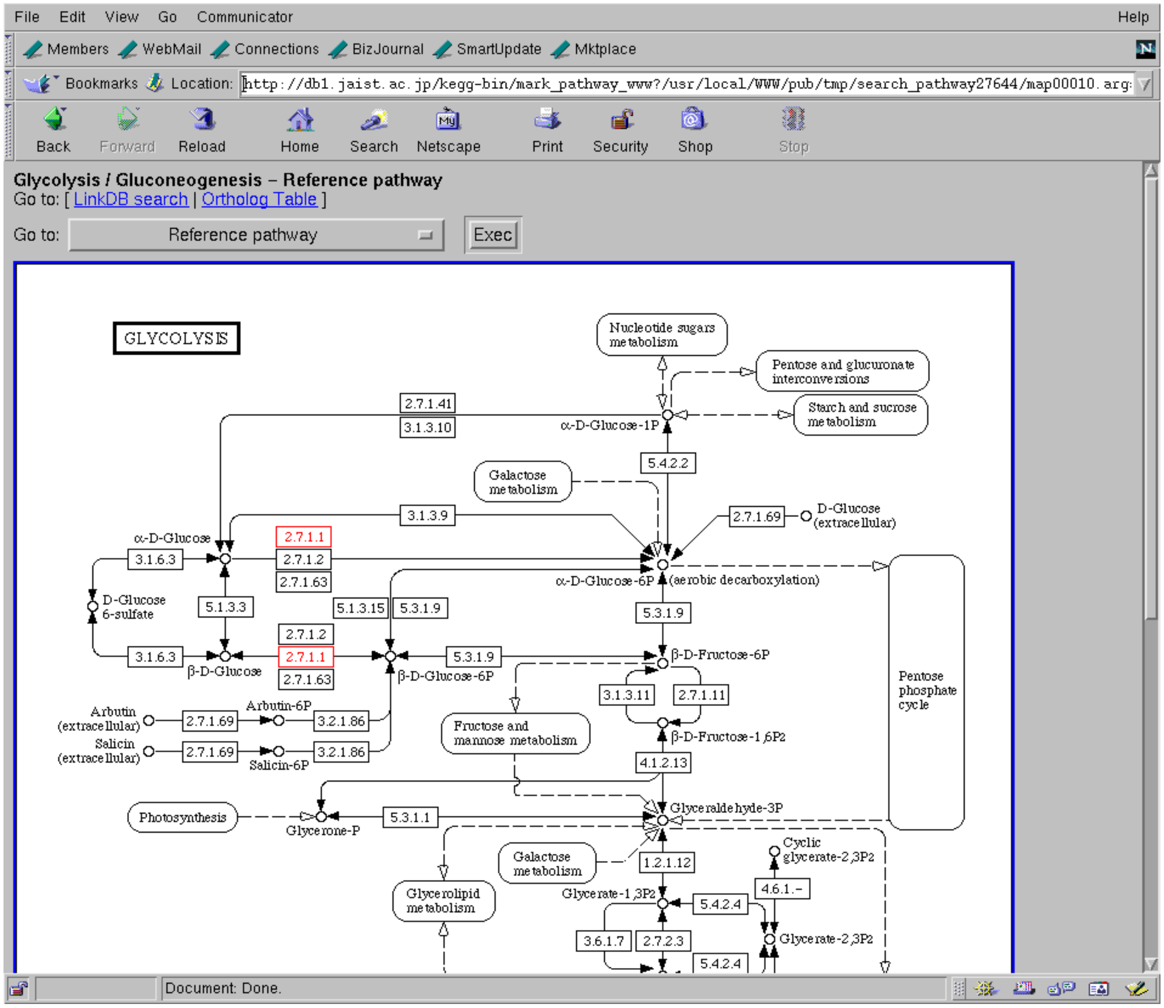
Gene names and accessions may be found by searching GENES database using DBGET

Click here to view the help window.



Pathway Search Result

- map00010 Glycolysis / Gluconeogenesis
  EC 2.7.1.1 Hexokinase; Glucokinase; Hexokinase type IV; Hexokinase D
- map00051 Fructose and mannose metabolism
  EC 2.7.1.1 Hexokinase; Glucokinase; Hexokinase type IV; Hexokinase D
- map00052 Galactose metabolism
  EC 2.7.1.1 Hexokinase; Glucokinase; Hexokinase type IV; Hexokinase D
- map00500 Starch and sucrose metabolism
  EC 2.7.1.1 Hexokinase; Glucokinase; Hexokinase type IV; Hexokinase D
- map00530 Aminosugars metabolism
  EC 2.7.1.1 Hexokinase; Glucokinase; Hexokinase type IV; Hexokinase D



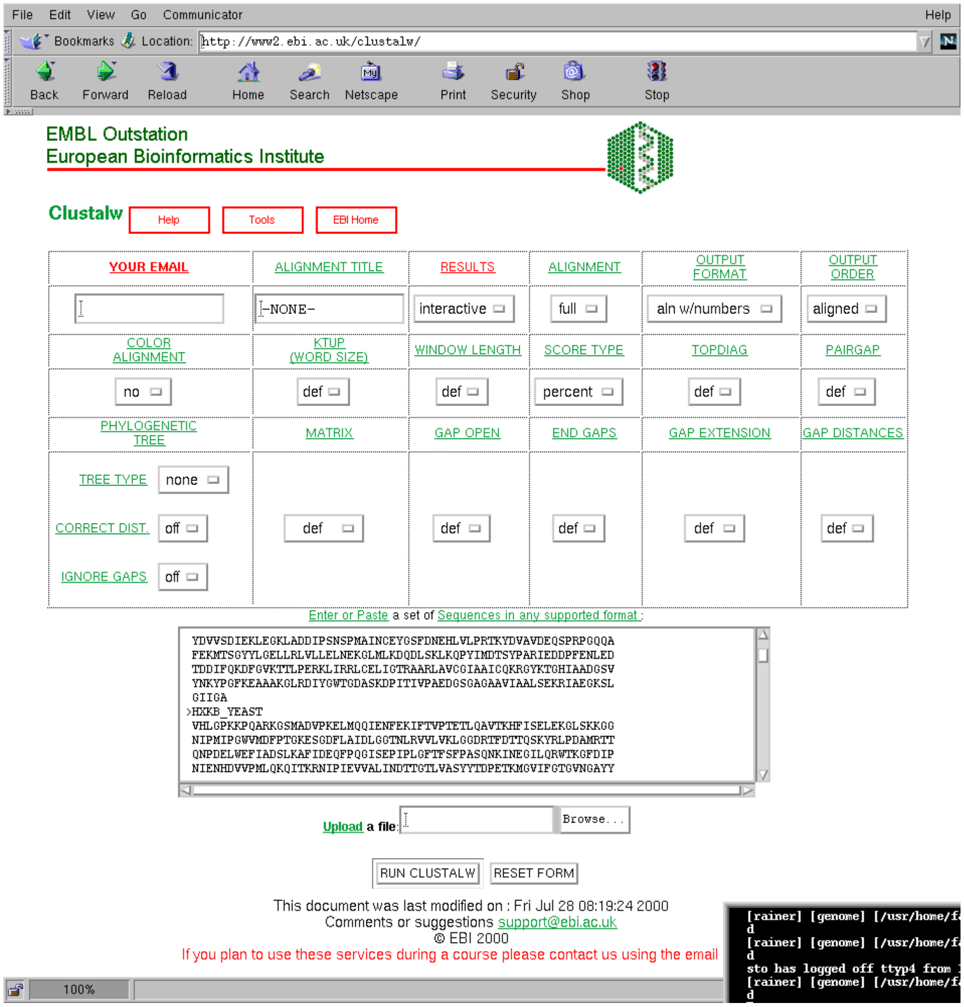
Location: http://db1.jaist.ac.jp/kegg-bin/mark_pathway_www?/usr/local/WWW/pub/tmp/search_pathway27644/map00010.arg

Glycolysis / Gluconeogenesis – Reference pathway

Go to: [LinkDB search | Ortholog Table]

Go to: Reference pathway Exec

Document: Done.



http://www2.ebi.ac.uk/clustalw/

EMBL Outstation
European Bioinformatics Institute

Clustalw

YOUR EMAIL	ALIGNMENT TITLE	RESULTS	ALIGNMENT	OUTPUT FORMAT	OUTPUT ORDER
	-NONE-	interactive	full	aln w/numbers	aligned
COLOR ALIGNMENT	KTUP (WORD SIZE)	WINDOW LENGTH	SCORE TYPE	TOPDIAG	PAIRGAP
no	def	def	percent	def	def
PHYLOGENETIC TREE	MATRIX	GAP OPEN	END GAPS	GAP EXTENSION	GAP DISTANCES
TREE TYPE none CORRECT DIST. off IGNORE GAPS off	def	def	def	def	def

Enter or Paste a set of Sequences in any supported format :

```
YDVVSDIEKLEGKLADDIPSNSPMAINCEYGSFDNEHLVLPRTKYDVAVDEQSPRPGQQA
FEKMTSGYYLGELLRLVLLELNEKGLMLKDQDLSKLKQPYIMDTSYPARIEDDPFENLED
TDDIFQKDFGVKTTLPERKLIRRLCELIGTRAARLAVCGIAAICQKRGYKTGHIAADGSV
YNKYPGFKEAAAKGLRDIYGWTGDASKDPITIVPAEDGSGAGAAVIAALSEKRIAEGKSL
GIIGA
>HXKB_YEAST
VHLGPKKPQARKGSMADVPKELMQQIENFEKIFTVPTETLQAVTKHFISELEKGLSKKGG
NIPMIPGWVMDFPTGKESGDFLAIDLGGTNLRVVLVKLGGDRTFDTTQSKYRLPDAMRTT
QNPDELWEFIADSLKAFIDEQFPQGISEPIPLGFTFSFPASQNKINEGILQRWTKGFDIP
NIENHDVVPMLQKQITKRNIPIEVVALINDTTGTLVASYYTDPETKMGVIFGTGVNGAYY
```

Upload a file:

This document was last modified on : Fri Jul 28 08:19:24 2000
Comments or suggestions support@ebi.ac.uk
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If you plan to use these services during a course please contact us using the email

```
[rainer] [genome] [/usr/home/f
d
[rainer] [genome] [/usr/home/f
d
sto has logged off ttyp4 from
[rainer] [genome] [/usr/home/f
d
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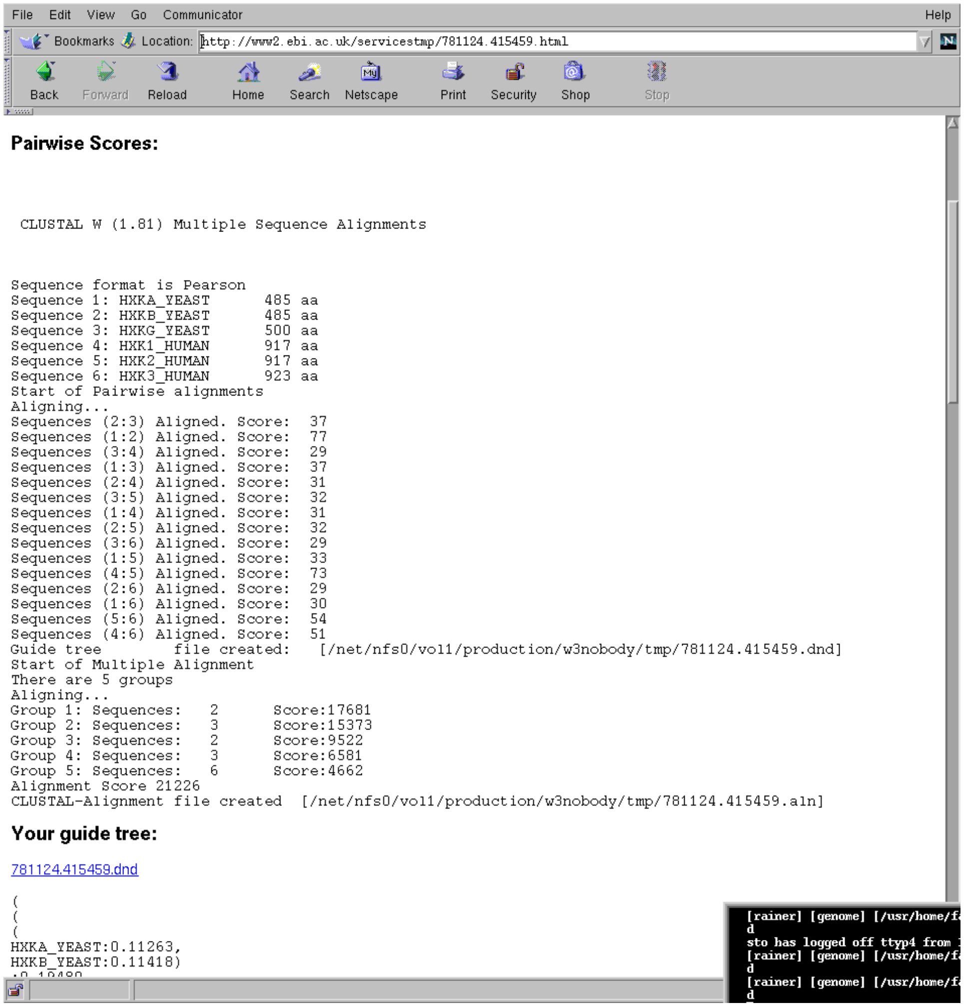

Pairwise Scores:

```
 CLUSTAL W (1.81) Multiple Sequence Alignments


Sequence format is Pearson
Sequence 1: HXKA_YEAST      485 aa
Sequence 2: HXKB_YEAST      485 aa
Sequence 3: HXKG_YEAST      500 aa
Sequence 4: HXK1_HUMAN      917 aa
Sequence 5: HXK2_HUMAN      917 aa
Sequence 6: HXK3_HUMAN      923 aa
Start of Pairwise alignments
Aligning...
Sequences (2:3) Aligned. Score:  37
Sequences (1:2) Aligned. Score:  77
Sequences (3:4) Aligned. Score:  29
Sequences (1:3) Aligned. Score:  37
Sequences (2:4) Aligned. Score:  31
Sequences (3:5) Aligned. Score:  32
Sequences (1:4) Aligned. Score:  31
Sequences (2:5) Aligned. Score:  32
Sequences (3:6) Aligned. Score:  29
Sequences (1:5) Aligned. Score:  33
Sequences (4:5) Aligned. Score:  73
Sequences (2:6) Aligned. Score:  29
Sequences (1:6) Aligned. Score:  30
Sequences (5:6) Aligned. Score:  54
Sequences (4:6) Aligned. Score:  51
Guide tree        file created:   [/net/nfs0/vol1/production/w3nobody/tmp/781124.415459.dnd]
Start of Multiple Alignment
There are 5 groups
Aligning...
Group 1: Sequences:   2      Score:17681
Group 2: Sequences:   3      Score:15373
Group 3: Sequences:   2      Score:9522
Group 4: Sequences:   3      Score:6581
Group 5: Sequences:   6      Score:4662
Alignment Score 21226
CLUSTAL-Alignment file created  [/net/nfs0/vol1/production/w3nobody/tmp/781124.415459.aln]
```

Your guide tree:

781124.415459.dnd

```
(
(
(
HXKA_YEAST:0.11263,
HXKB_YEAST:0.11418)
```

```
[rainer] [genome] [/usr/home/fa
d
sto has logged off ttyp4 from 
[rainer] [genome] [/usr/home/fa
d
[rainer] [genome] [/usr/home/fa
d
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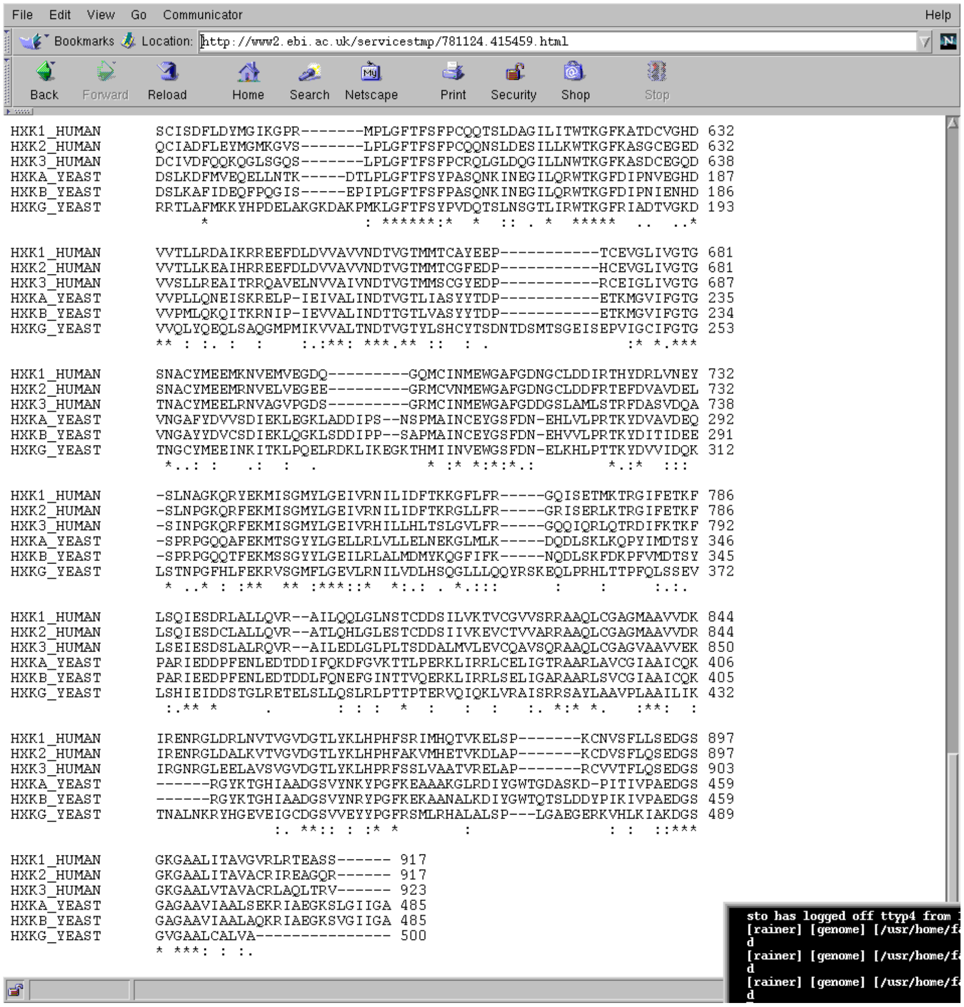

http://www2.ebi.ac.uk/servicestmp/781124.415459.html

```
HXK1_HUMAN      SCISDFLDYMGIKGPR-------MPLGFTFSFPCQQTSLDAGILITWTKGFKATDCVGHD 632
HXK2_HUMAN      QCIADFLEYMGMKGVS-------LPLGFTFSFPCQQNSLDESILLKWTKGFKASGCEGED 632
HXK3_HUMAN      DCIVDFQQKQGLSGQS-------LPLGFTFSFPCRQLGLDQGILLNWTKGFKASDCEGQD 638
HXKA_YEAST      DSLKDFMVEQELLNTK-----DTLPLGFTFSYPASQNKINEGILQRWTKGFDIPNVEGHD 187
HXKB_YEAST      DSLKAFIDEQFPQGIS-----EPIPLGFTFSFPASQNKINEGILQRWTKGFDIPNIENHD 186
HXKG_YEAST      RRTLAFMKKYHPDELAKGKDAKPMKLGFTFSYPVDQTSLNSGTLIRWTKGFRIADTVGKD 193
                     *                 : ******:*  *  :: . *  *****  ..  ..*

HXK1_HUMAN      VVTLLRDAIKRREEFDLDVVAVVNDTVGTMMTCAYEEP-----------TCEVGLIVGTG 681
HXK2_HUMAN      VVTLLKEAIHRREEFDLDVVAVVNDTVGTMMTCGFEDP-----------HCEVGLIVGTG 681
HXK3_HUMAN      VVSLLREAITRRQAVELNVVAIVNDTVGTMMSCGYEDP-----------RCEIGLIVGTG 687
HXKA_YEAST      VVPLLQNEISKRELP-IEIVALINDTVGTLIASYYTDP-----------ETKMGVIFGTG 235
HXKB_YEAST      VVPMLQKQITKRNIP-IEVVALINDTTGTLVASYYTDP-----------ETKMGVIFGTG 234
HXKG_YEAST      VVQLYQEQLSAQGMPMIKVVALTNDTVGTYLSHCYTSDNTDSMTSGEISEPVIGCIFGTG 253
                ** : :. :  :    :.:**: ***.** ::  : .               :* *.***

HXK1_HUMAN      SNACYMEEMKNVEMVEGDQ---------GQMCINMEWGAFGDNGCLDDIRTHYDRLVNEY 732
HXK2_HUMAN      SNACYMEEMRNVELVEGEE---------GRMCVNMEWGAFGDNGCLDDFRTEFDVAVDEL 732
HXK3_HUMAN      TNACYMEELRNVAGVPGDS---------GRMCINMEWGAFGDDGSLAMLSTRFDASVDQA 738
HXKA_YEAST      VNGAFYDVVSDIEKLEGKLADDIPS--NSPMAINCEYGSFDN-EHLVLPRTKYDVAVDEQ 292
HXKB_YEAST      VNGAYYDVCSDIEKLQGKLSDDIPP--SAPMAINCEYGSFDN-EHVVLPRTKYDITIDEE 291
HXKG_YEAST      TNGCYMEEINKITKLPQELRDKLIKEGKTHMIINVEWGSFDN-ELKHLPTTKYDVVIDQK 312
                 *..: :   .:  :  .            * :* *:*:*.:        *.:*  :::

HXK1_HUMAN      -SLNAGKQRYEKMISGMYLGEIVRNILIDFTKKGFLFR-----GQISETMKTRGIFETKF 786
HXK2_HUMAN      -SLNPGKQRFEKMISGMYLGEIVRNILIDFTKRGLLFR-----GRISERLKTRGIFETKF 786
HXK3_HUMAN      -SINPGKQRFEKMISGMYLGEIVRHILLHLTSLGVLFR-----GQQIQRLQTRDIFKTKF 792
HXKA_YEAST      -SPRPGQQAFEKMTSGYYLGELLRLVLLELNEKGLMLK-----DQDLSKLKQPYIMDTSY 346
HXKB_YEAST      -SPRPGQQTFEKMSSGYYLGEILRLALMDMYKQGFIFK-----NQDLSKFDKPFVMDTSY 345
HXKG_YEAST      LSTNPGFHLFEKRVSGMFLGEVLRNILVDLHSQGLLLQQYRSKEQLPRHLTTPFQLSSEV 372
                 *  ..* : :**  ** :***::*  *:.: . *.:::      :    :     :.:.

HXK1_HUMAN      LSQIESDRLALLQVR--AILQQLGLNSTCDDSILVKTVCGVVSRRAAQLCGAGMAAVVDK 844
HXK2_HUMAN      LSQIESDCLALLQVR--ATLQHLGLESTCDDSIIVKEVCTVVARRAAQLCGAGMAAVVDR 844
HXK3_HUMAN      LSEIESDSLALRQVR--AILEDLGLPLTSDDALMVLEVCQAVSQRAAQLCGAGVAAVVEK 850
HXKA_YEAST      PARIEDDPFENLEDTDDIFQKDFGVKTTLPERKLIRRLCELIGTRAARLAVCGIAAICQK 406
HXKB_YEAST      PARIEEDPFENLEDTDDLFQNEFGINTTVQERKLIRRLSELIGARAARLSVCGIAAICQK 405
HXKG_YEAST      LSHIEIDDSTGLRETELSLLQSLRLPTTPTERVQIQKLVRAISRRSAYLAAVPLAAILIK 432
                 :.** *     .       : : :  *  :   :  :   :. *:* *.   :**:  :

HXK1_HUMAN      IRENRGLDRLNVTVGVDGTLYKLHPHFSRIMHQTVKELSP-------KCNVSFLLSEDGS 897
HXK2_HUMAN      IRENRGLDALKVTVGVDGTLYKLHPHFAKVMHETVKDLAP-------KCDVSFLQSEDGS 897
HXK3_HUMAN      IRGNRGLEELAVSVGVDGTLYKLHPRFSSLVAATVRELAP-------RCVVTFLQSEDGS 903
HXKA_YEAST      ------RGYKTGHIAADGSVYNKYPGFKEAAAKGLRDIYGWTGDASKD-PITIVPAEDGS 459
HXKB_YEAST      ------RGYKTGHIAADGSVYNRYPGFKEKAANALKDIYGWTQTSLDDYPIKIVPAEDGS 459
HXKG_YEAST      TNALNKRYHGEVEIGCDGSVVEYYPGFRSMLRHALALSP---LGAEGERKVHLKIAKDGS 489
                             :. **:: : :* *       :               : :  ::***

HXK1_HUMAN      GKGAALITAVGVRLRTEASS------ 917
HXK2_HUMAN      GKGAALITAVACRIREAGQR------ 917
HXK3_HUMAN      GKGAALVTAVACRLAQLTRV------ 923
HXKA_YEAST      GAGAAVIAALSEKRIAEGKSLGIIGA 485
HXKB_YEAST      GAGAAVIAALAQKRIAEGKSVGIIGA 485
HXKG_YEAST      GVGAALCALVA--------------- 500
                * ***: : :.
```

```
sto has logged off ttyp4 from
[rainer] [genome] [/usr/home/fa
d
[rainer] [genome] [/usr/home/fa
d
[rainer] [genome] [/usr/home/fa
d
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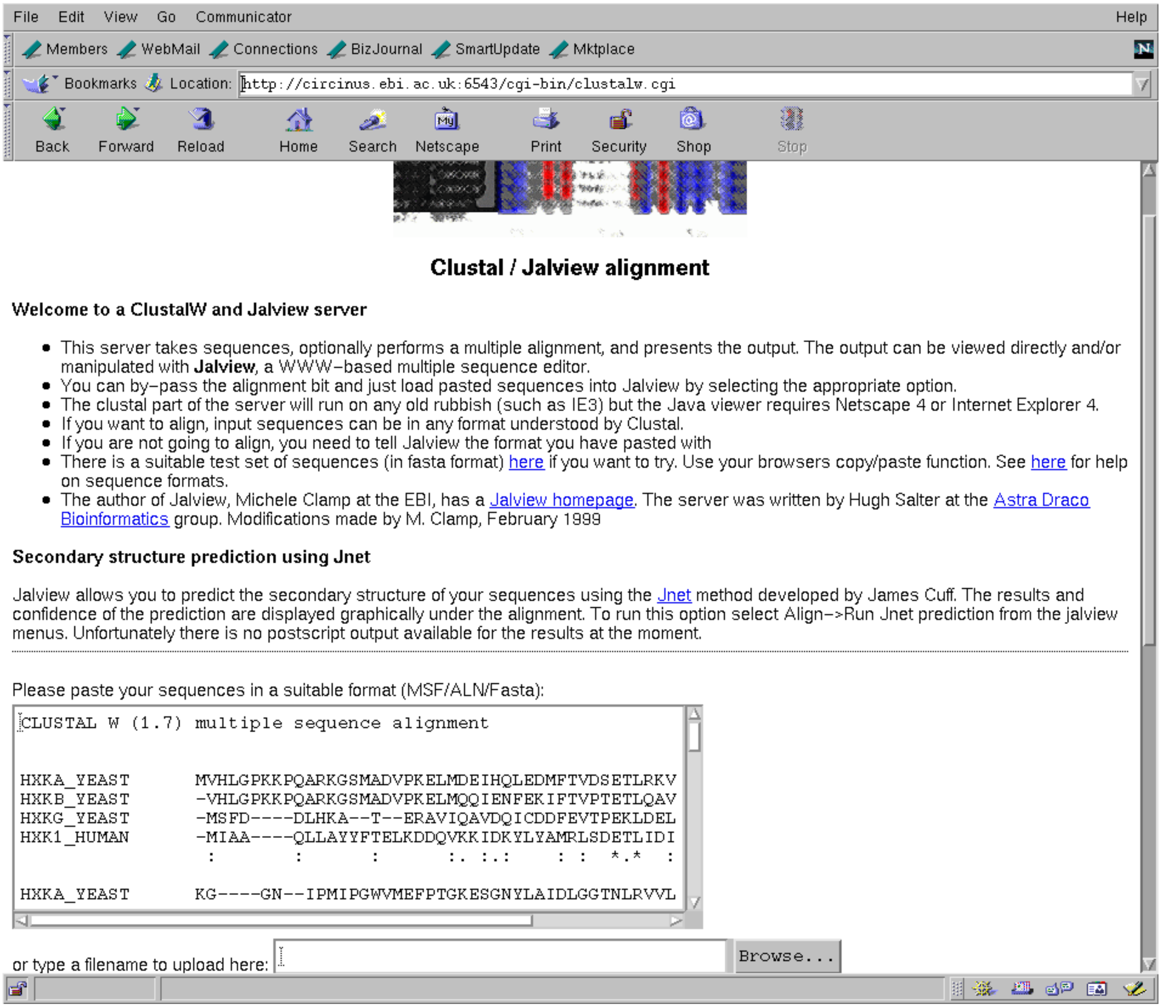


Clustal / Jalview alignment

Welcome to a ClustalW and Jalview server

- This server takes sequences, optionally performs a multiple alignment, and presents the output. The output can be viewed directly and/or manipulated with **Jalview**, a WWW-based multiple sequence editor.
- You can by-pass the alignment bit and just load pasted sequences into Jalview by selecting the appropriate option.
- The clustal part of the server will run on any old rubbish (such as IE3) but the Java viewer requires Netscape 4 or Internet Explorer 4.
- If you want to align, input sequences can be in any format understood by Clustal.
- If you are not going to align, you need to tell Jalview the format you have pasted with
- There is a suitable test set of sequences (in fasta format) here if you want to try. Use your browsers copy/paste function. See here for help on sequence formats.
- The author of Jalview, Michele Clamp at the EBI, has a Jalview homepage. The server was written by Hugh Salter at the Astra Draco Bioinformatics group. Modifications made by M. Clamp, February 1999

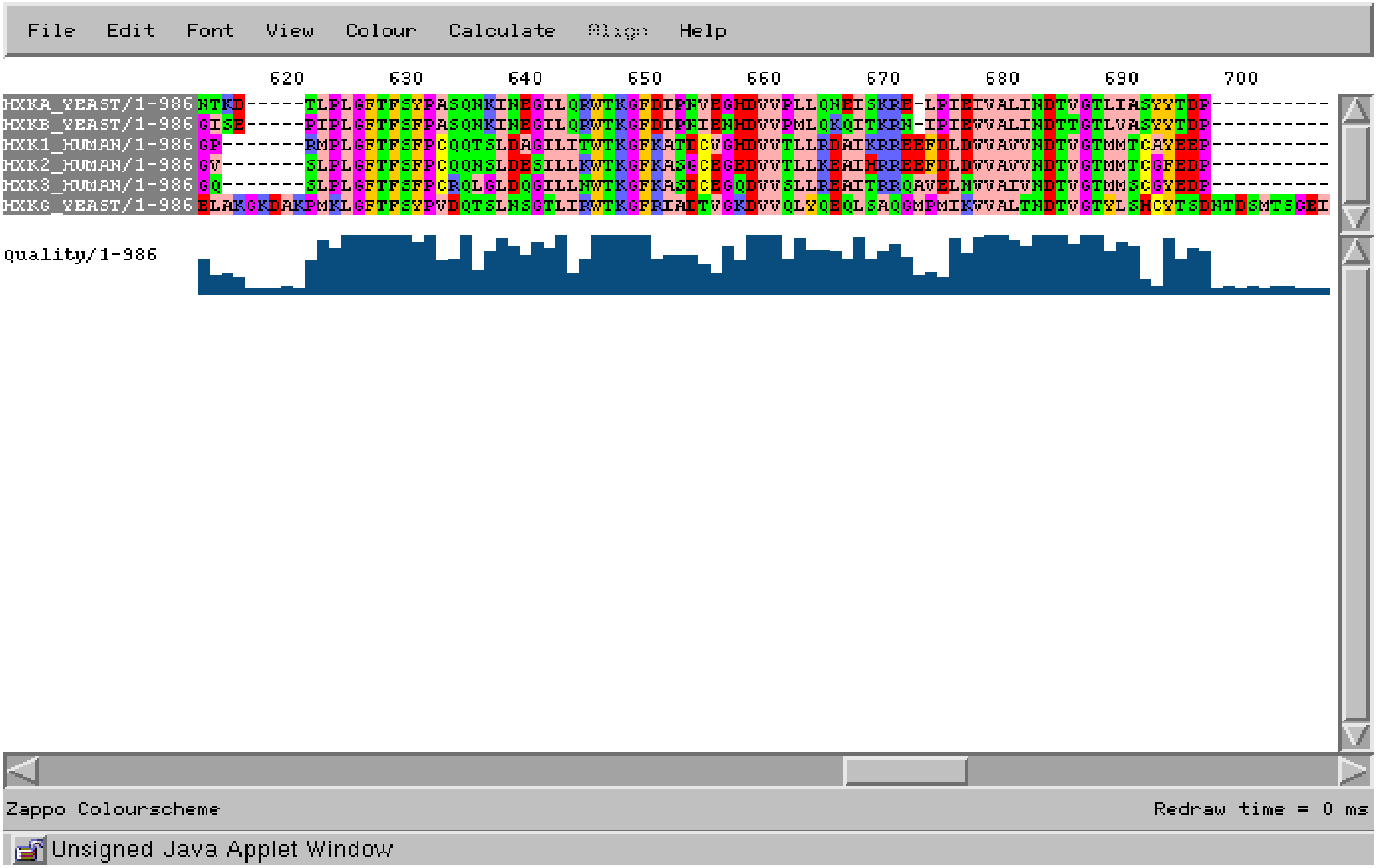
Secondary structure prediction using Jnet

Jalview allows you to predict the secondary structure of your sequences using the Jnet method developed by James Cuff. The results and confidence of the prediction are displayed graphically under the alignment. To run this option select Align->Run Jnet prediction from the jalview menus. Unfortunately there is no postscript output available for the results at the moment.

Please paste your sequences in a suitable format (MSF/ALN/Fasta):

```
CLUSTAL W (1.7) multiple sequence alignment


HXKA_YEAST      MVHLGPKKPQARKGSMADVPKELMDEIHQLEDMFTVDSETLRKV
HXKB_YEAST      -VHLGPKKPQARKGSMADVPKELMQQIENFEKIFTVPTETLQAV
HXKG_YEAST      -MSFD----DLHKA--T--ERAVIQAVDQICDDFEVTPEKLDEL
HXK1_HUMAN      -MIAA----QLLAYYFTELKDDQVKKIDKYLYAMRLSDETLIDI
                 :       :      :      :. :.:    : :  *.*  :

HXKA_YEAST      KG----GN--IPMIPGWVMEFPTGKESGNYLAIDLGGTNLRVVL
```

or type a filename to upload here:

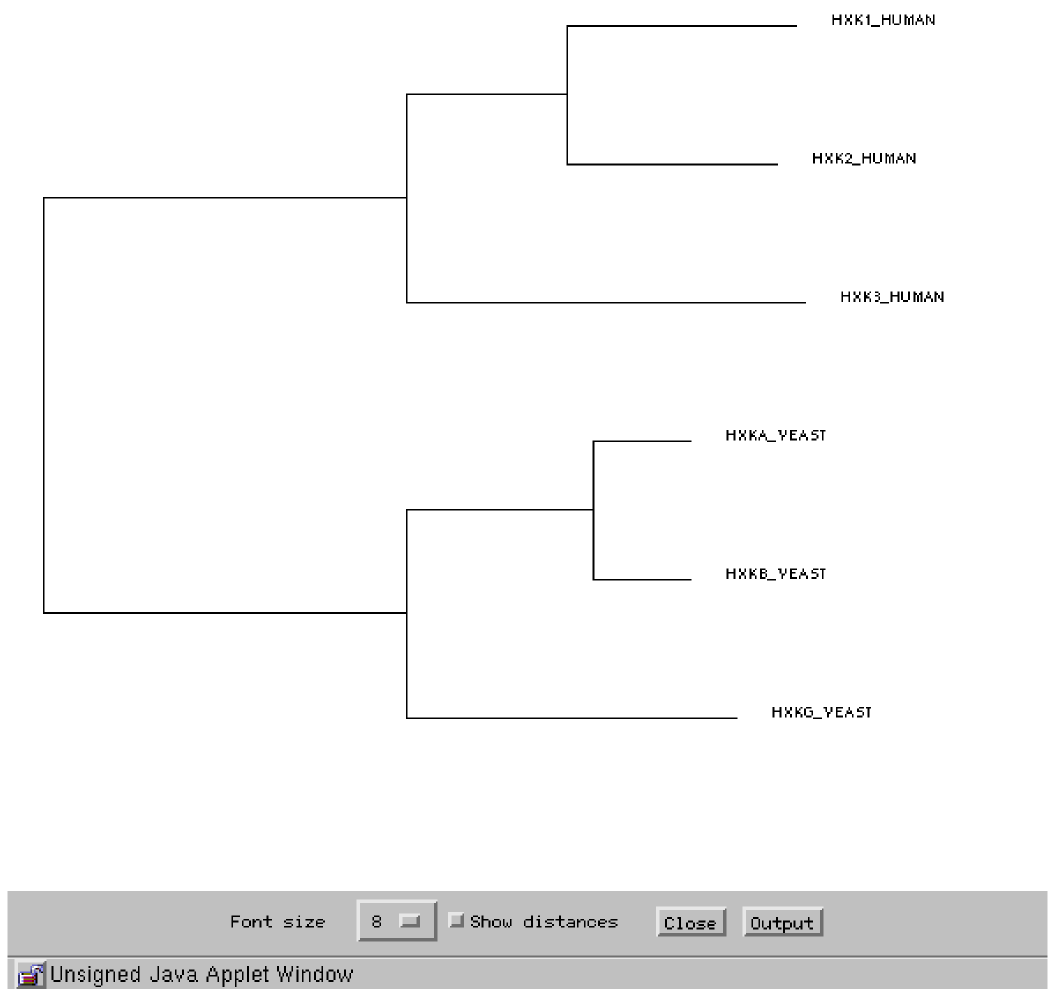


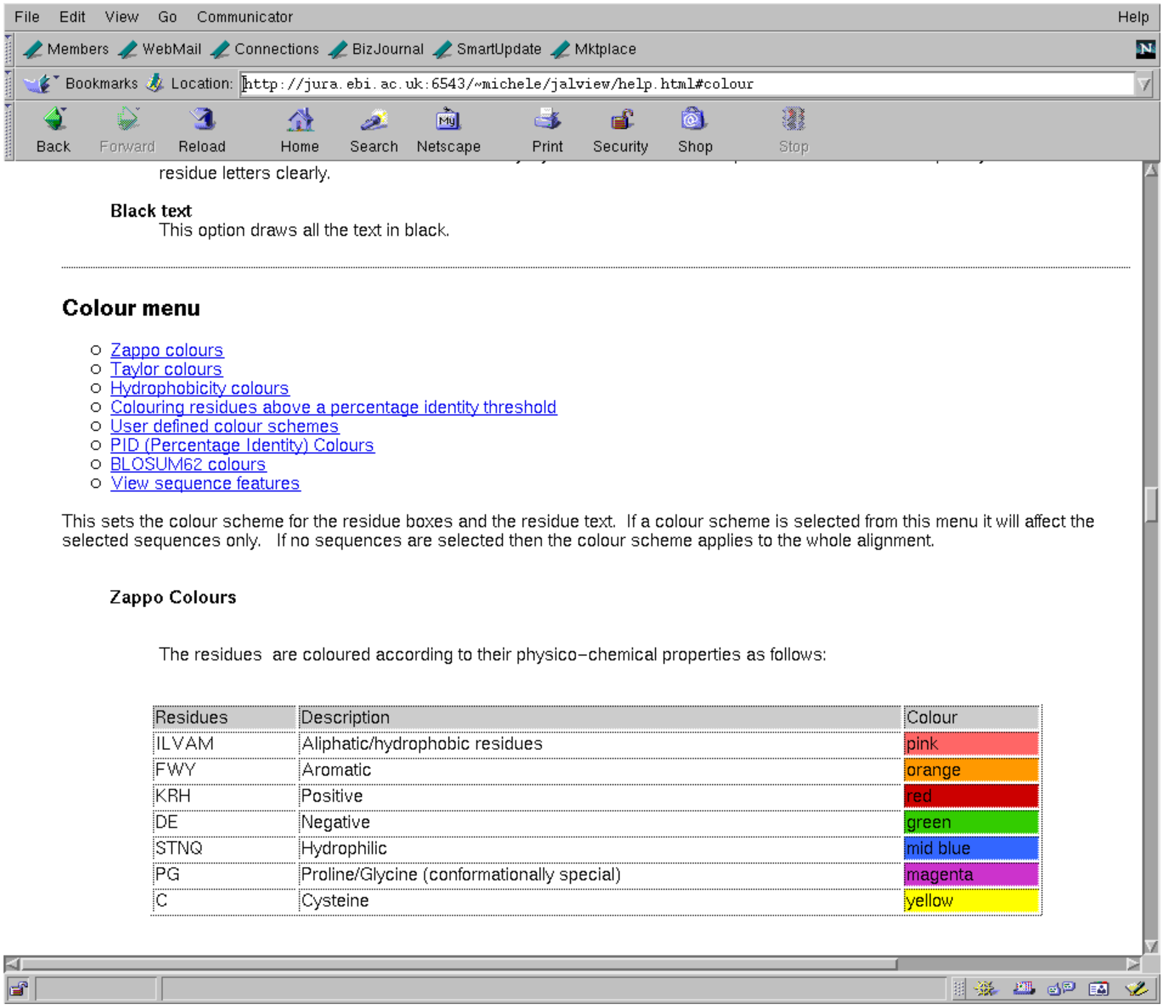
```
                       620       630       640       650       660       670       680       690       700
HXKA_YEAST/1-986 NTKD-----TLPLGFTFSYPASQNKINEGILQRWTKGFDIPNVEGHDVVPLLQNEISKRE-LPIEIVALINDTVGTLIASYYTDP----------
HXKB_YEAST/1-986 GISE-----PIPLGFTFSFPASQNKINEGILQRWTKGFDIPNIENHDVVPMLQKQITKRN-IPIEVVALINDTTGTLVASYYTDP----------
HXK1_HUMAN/1-986 GP-------RMPLGFTFSFPCQQTSLDAGILITWTKGFKATDCVGHDVVTLLRDAIKRREEFDLDVVAVVNDTVGTMMTCAYEEP----------
HXK2_HUMAN/1-986 GV-------SLPLGFTFSFPCQQHSLDESILLKWTKGFKASGCEGEDVVTLLKEAIHRREEFDLDVVAVVNDTVGTMMTCGFEDP----------
HXK3_HUMAN/1-986 GQ-------SLPLGFTFSFPCRQLGLDQGILLNWTKGFKASDCEGQDVVSLLREAITRRQAVELNVVAIVNDTVGTMMSCGYEDP----------
HXKG_YEAST/1-986 ELAKGKDAKPMKLGFTFSYPVDQTSLNSGTLIRWTKGFRIADTVGKDVVQLYQEQLSAQGMPMIKVVALTNDTVGTYLSHCYTSDNTDSMTSGEI

Quality/1-986
```

Zappo Colourscheme

Redraw time = 0 ms

Unsigned Java Applet Window


HXK1_HUMAN
HXK2_HUMAN
HXK3_HUMAN
HXKA_YEAST
HXKB_YEAST
HXKG_YEAST
Font size
8
☐ Show distances
Close
Output
Unsigned Java Applet Window



Location: http://jura.ebi.ac.uk:6543/~michele/jalview/help.html#colour

residue letters clearly.

Black text
This option draws all the text in black.

Colour menu

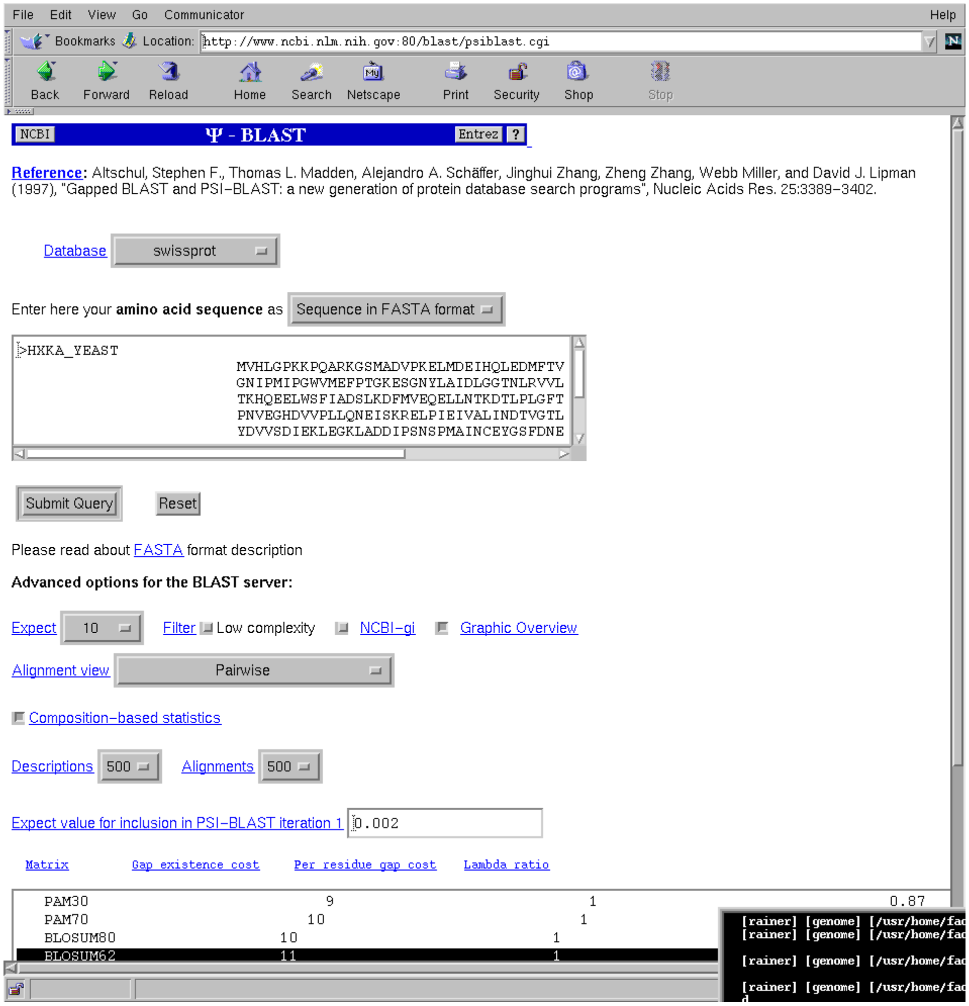
- Zappo colours
- Taylor colours
- Hydrophobicity colours
- Colouring residues above a percentage identity threshold
- User defined colour schemes
- PID (Percentage Identity) Colours
- BLOSUM62 colours
- View sequence features

This sets the colour scheme for the residue boxes and the residue text. If a colour scheme is selected from this menu it will affect the selected sequences only. If no sequences are selected then the colour scheme applies to the whole alignment.

Zappo Colours

The residues are coloured according to their physico-chemical properties as follows:

Residues	Description	Colour
ILVAM	Aliphatic/hydrophobic residues	pink
FWY	Aromatic	orange
KRH	Positive	red
DE	Negative	green
STNQ	Hydrophilic	mid blue
PG	Proline/Glycine (conformationally special)	magenta
C	Cysteine	yellow



Location: `http://www.ncbi.nlm.nih.gov:80/blast/psiblast.cgi`

Ψ - BLAST

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI–BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389–3402.

Database: swissprot

Enter here your **amino acid sequence** as Sequence in FASTA format

```
>HXKA_YEAST
                              MVHLGPKKPQARKGSMADVPKELMDEIHQLEDMFTV
                              GNIPMIPGWVMEFPTGKESGNYLAIDLGGTNLRVVL
                              TKHQEELWSFIADSLKDFMVEQELLNTKDTLPLGFT
                              PNVEGHDVVPLLQNEISKRELPIEIVALINDTVGTL
                              YDVVSDIEKLEGKLADDIPSNSPMAINCEYGSFDNE
```

Please read about FASTA format description

Advanced options for the BLAST server:

Expect 10 Filter ☐ Low complexity ☐ NCBI–gi ☑ Graphic Overview

Alignment view: Pairwise

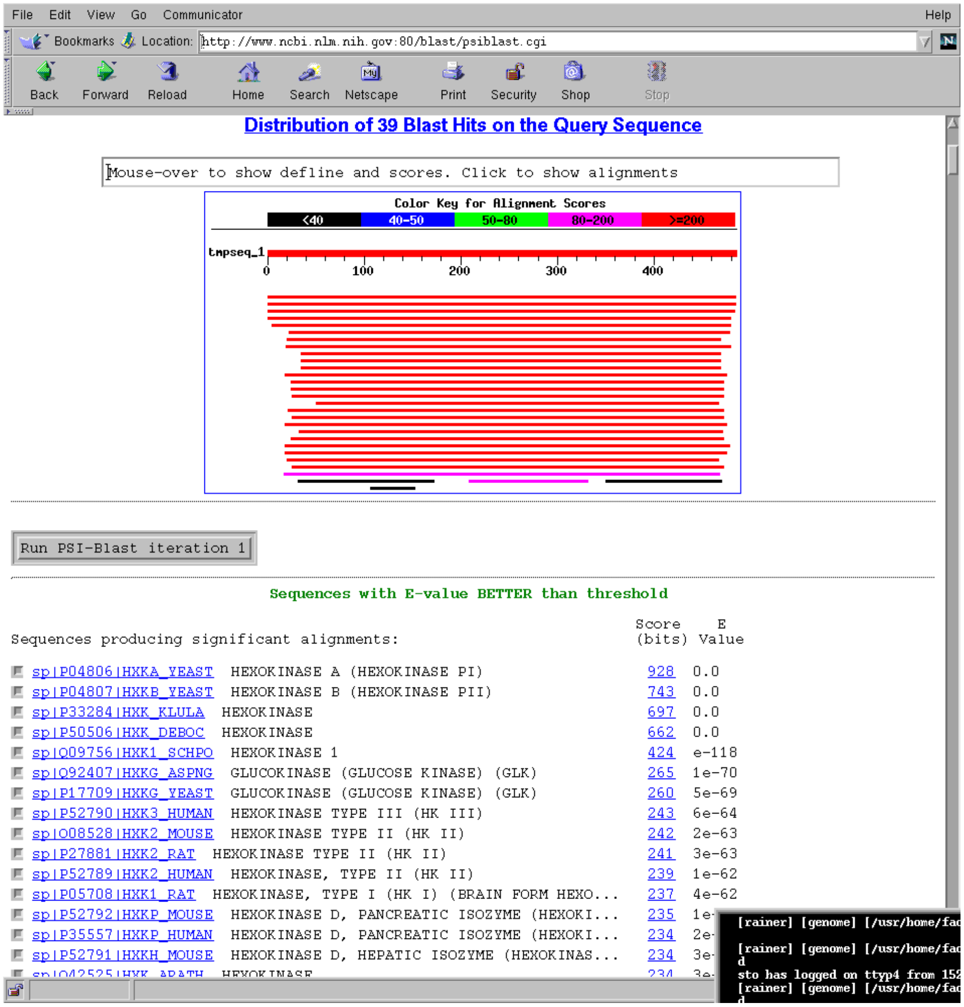
☑ Composition–based statistics

Descriptions 500 Alignments 500

Expect value for inclusion in PSI–BLAST iteration 1: 0.002

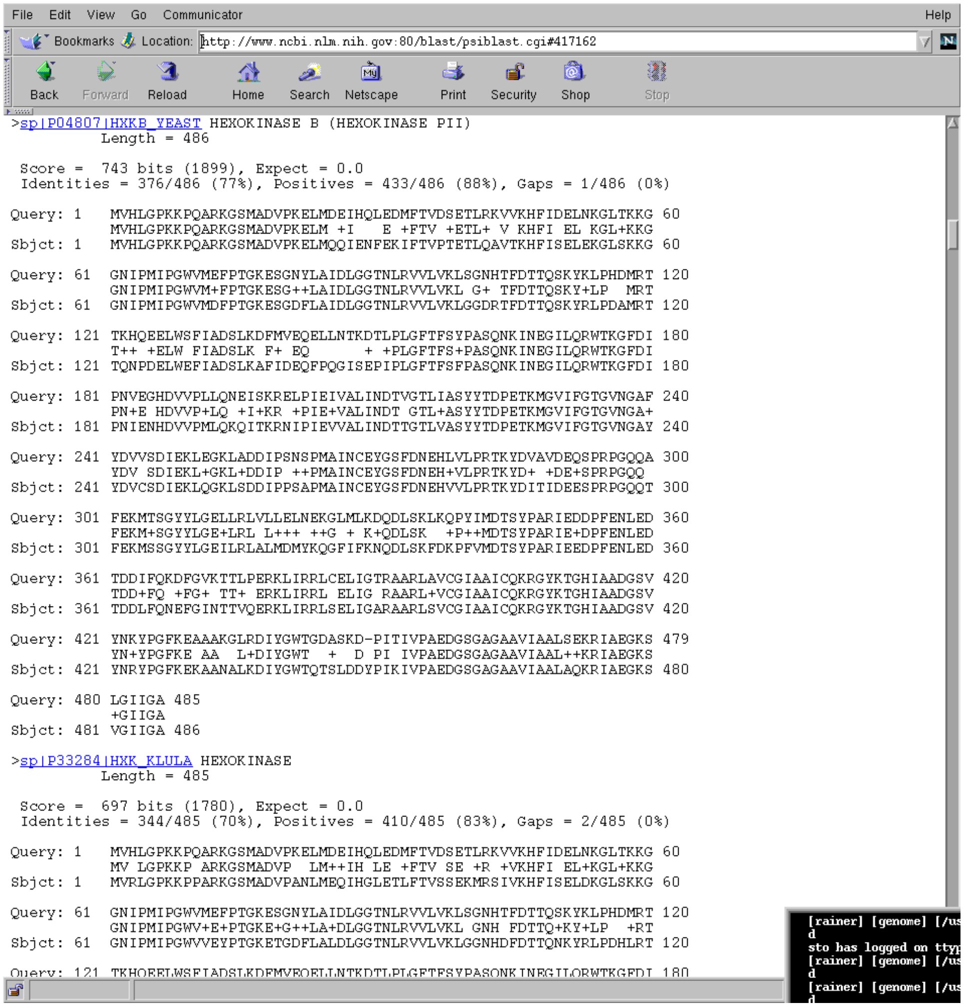
Matrix	Gap existence cost	Per residue gap cost	Lambda ratio
PAM30	9	1	0.87
PAM70	10	1	
BLOSUM80	10	1	
BLOSUM62	11	1	

```
[rainer] [genome] [/usr/home/fac
[rainer] [genome] [/usr/home/fac

[rainer] [genome] [/usr/home/fac

[rainer] [genome] [/usr/home/fac
d
```



```
                                                              Score    E
Sequences producing significant alignments:                   (bits) Value

sp|P04806|HXKA_YEAST  HEXOKINASE A (HEXOKINASE PI)             928   0.0
sp|P04807|HXKB_YEAST  HEXOKINASE B (HEXOKINASE PII)            743   0.0
sp|P33284|HXK_KLULA  HEXOKINASE                                697   0.0
sp|P50506|HXK_DEBOC  HEXOKINASE                                662   0.0
sp|Q09756|HXK1_SCHPO  HEXOKINASE 1                             424   e-118
sp|Q92407|HXKG_ASPNG  GLUCOKINASE (GLUCOSE KINASE) (GLK)       265   1e-70
sp|P17709|HXKG_YEAST  GLUCOKINASE (GLUCOSE KINASE) (GLK)       260   5e-69
sp|P52790|HXK3_HUMAN  HEXOKINASE TYPE III (HK III)             243   6e-64
sp|O08528|HXK2_MOUSE  HEXOKINASE TYPE II (HK II)               242   2e-63
sp|P27881|HXK2_RAT  HEXOKINASE TYPE II (HK II)                 241   3e-63
sp|P52789|HXK2_HUMAN  HEXOKINASE, TYPE II (HK II)              239   1e-62
sp|P05708|HXK1_RAT  HEXOKINASE, TYPE I (HK I) (BRAIN FORM HEXO...  237   4e-62
sp|P52792|HXKP_MOUSE  HEXOKINASE D, PANCREATIC ISOZYME (HEXOKI...  235   1e-
sp|P35557|HXKP_HUMAN  HEXOKINASE D, PANCREATIC ISOZYME (HEXOKI...  234   2e-
sp|P52791|HXKH_MOUSE  HEXOKINASE D, HEPATIC ISOZYME (HEXOKINAS...  234   3e-
sp|Q42525|HXK_ARATH  HEXOKINASE                                234   3e-
```

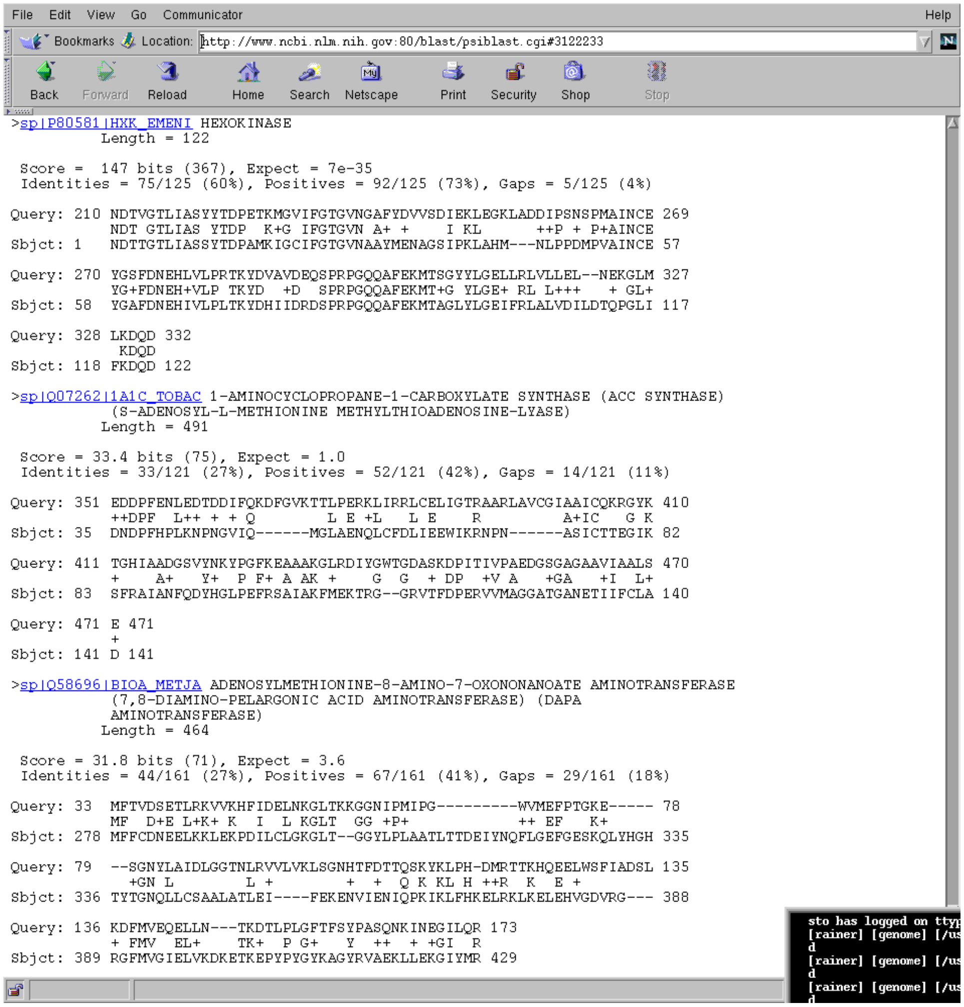
```
[rainer] [genome] [/usr/home/fac

[rainer] [genome] [/usr/home/fac
d
sto has logged on ttyp4 from 152
[rainer] [genome] [/usr/home/fac
d
```



Location: http://www.ncbi.nlm.nih.gov:80/blast/psiblast.cgi#417162

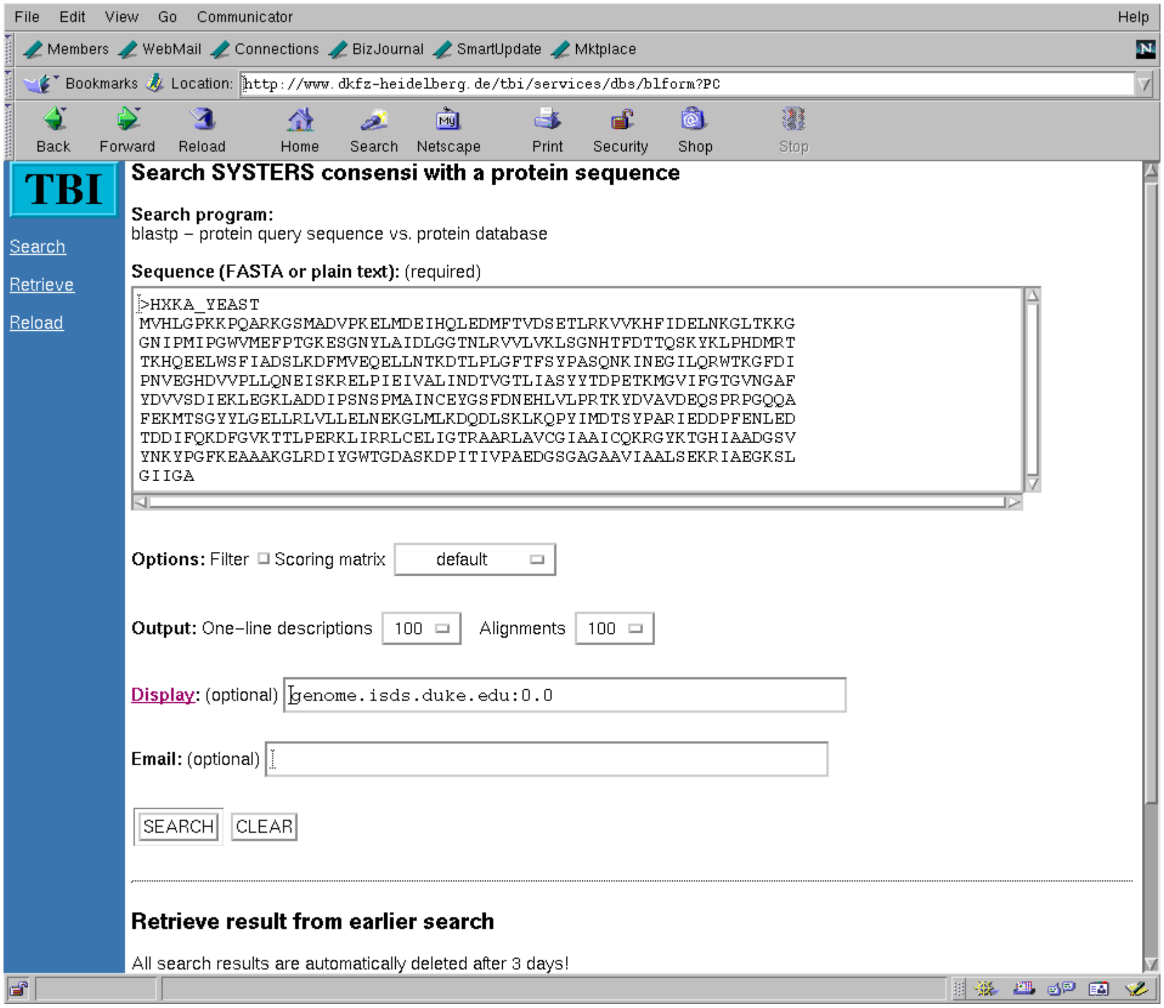
```
>sp|P04807|HXKB_YEAST HEXOKINASE B (HEXOKINASE PII)
          Length = 486

 Score =  743 bits (1899), Expect = 0.0
 Identities = 376/486 (77%), Positives = 433/486 (88%), Gaps = 1/486 (0%)

Query: 1   MVHLGPKKPQARKGSMADVPKELMDEIHQLEDMFTVDSETLRKVVKHFIDELNKGLTKKG 60
           MVHLGPKKPQARKGSMADVPKELM +I   E +FTV +ETL+ V KHFI EL KGL+KKG
Sbjct: 1   MVHLGPKKPQARKGSMADVPKELMQQIENFEKIFTVPTETLQAVTKHFISELEKGLSKKG 60

Query: 61  GNIPMIPGWVMEFPTGKESGNYLAIDLGGTNLRVVLVKLSGNHTFDTTQSKYKLPHDMRT 120
           GNIPMIPGWVM+FPTGKESG++LAIDLGGTNLRVVLVKL G+ TFDTTQSKY+LP  MRT
Sbjct: 61  GNIPMIPGWVMDFPTGKESGDFLAIDLGGTNLRVVLVKLGGDRTFDTTQSKYRLPDAMRT 120

Query: 121 TKHQEELWSFIADSLKDFMVEQELLNTKDTLPLGFTFSYPASQNKINEGILQRWTKGFDI 180
           T++ +ELW FIADSLK F+ EQ      + +PLGFTFS+PASQNKINEGILQRWTKGFDI
Sbjct: 121 TQNPDELWEFIADSLKAFIDEQFPQGISEPIPLGFTFSFPASQNKINEGILQRWTKGFDI 180

Query: 181 PNVEGHDVVPLLQNEISKRELPIEIVALINDTVGTLIASYYTDPETKMGVIFGTGVNGAF 240
           PN+E HDVVP+LQ +I+KR +PIE+VALINDT GTL+ASYYTDPETKMGVIFGTGVNGA+
Sbjct: 181 PNIENHDVVPMLQKQITKRNIPIEVVALINDTTGTLVASYYTDPETKMGVIFGTGVNGAY 240

Query: 241 YDVVSDIEKLEGKLADDIPSNSPMAINCEYGSFDNEHLVLPRTKYDVAVDEQSPRPGQQA 300
           YDV SDIEKL+GKL+DDIP ++PMAINCEYGSFDNEH+VLPRTKYD+ +DE+SPRPGQQ
Sbjct: 241 YDVCSDIEKLQGKLSDDIPPSAPMAINCEYGSFDNEHVVLPRTKYDITIDEESPRPGQQT 300

Query: 301 FEKMTSGYYLGELLRLVLLELNEKGLMLKDQDLSKLKQPYIMDTSYPARIEDDPFENLED 360
           FEKM+SGYYLGE+LRL L+++ ++G + K+QDLSK  +P++MDTSYPARIE+DPFENLED
Sbjct: 301 FEKMSSGYYLGEILRLALMDMYKQGFIFKNQDLSKFDKPFVMDTSYPARIEEDPFENLED 360

Query: 361 TDDIFQKDFGVKTTLPERKLIRRLCELIGTRAARLAVCGIAAICQKRGYKTGHIAADGSV 420
           TDD+FQ +FG+ TT+ ERKLIRRL ELIG RAARL+VCGIAAICQKRGYKTGHIAADGSV
Sbjct: 361 TDDLFQNEFGINTTVQERKLIRRLSELIGARAARLSVCGIAAICQKRGYKTGHIAADGSV 420

Query: 421 YNKYPGFKEAAAKGLRDIYGWTGDASKD-PITIVPAEDGSGAGAAVIAALSEKRIAEGKS 479
           YN+YPGFKE AA  L+DIYGWT  +  D PI IVPAEDGSGAGAAVIAAL++KRIAEGKS
Sbjct: 421 YNRYPGFKEKAANALKDIYGWTQTSLDDYPIKIVPAEDGSGAGAAVIAALAQKRIAEGKS 480

Query: 480 LGIIGA 485
           +GIIGA
Sbjct: 481 VGIIGA 486

>sp|P33284|HXK_KLULA HEXOKINASE
          Length = 485

 Score =  697 bits (1780), Expect = 0.0
 Identities = 344/485 (70%), Positives = 410/485 (83%), Gaps = 2/485 (0%)

Query: 1   MVHLGPKKPQARKGSMADVPKELMDEIHQLEDMFTVDSETLRKVVKHFIDELNKGLTKKG 60
           MV LGPKKP ARKGSMADVP  LM++IH LE +FTV SE +R +VKHFI EL+KGL+KKG
Sbjct: 1   MVRLGPKKPPARKGSMADVPANLMEQIHGLETLFTVSSEKMRSIVKHFISELDKGLSKKG 60

Query: 61  GNIPMIPGWVMEFPTGKESGNYLAIDLGGTNLRVVLVKLSGNHTFDTTQSKYKLPHDMRT 120
           GNIPMIPGWV+E+PTGKE+G++LA+DLGGTNLRVVLVKL GNH FDTTQ+KY+LP  +RT
Sbjct: 61  GNIPMIPGWVVEYPTGKETGDFLALDLGGTNLRVVLVKLGGNHDFDTTQNKYRLPDHLRT 120

Query: 121 TKHQEELWSFIADSLKDFMVEQELLNTKDTLPLGFTFSYPASQNKINEGILQRWTKGFDI 180
```

```
[rainer] [genome] [/us
d
sto has logged on ttyp
[rainer] [genome] [/us
d
[rainer] [genome] [/us
d
```



```
>sp|P80581|HXK_EMENI HEXOKINASE
          Length = 122

 Score =  147 bits (367), Expect = 7e-35
 Identities = 75/125 (60%), Positives = 92/125 (73%), Gaps = 5/125 (4%)

Query: 210 NDTVGTLIASYYTDPETKMGVIFGTGVNGAFYDVVSDIEKLEGKLADDIPSNSPMAINCE 269
           NDT GTLIAS YTDP  K+G IFGTGVN A+ +    I KL      ++P + P+AINCE
Sbjct: 1   NDTTGTLIASSYTDPAMKIGCIFGTGVNAAYMENAGSIPKLAHM---NLPPDMPVAINCE 57

Query: 270 YGSFDNEHLVLPRTKYDVAVDEQSPRPGQQAFEKMTSGYYLGELLRLVLLEL--NEKGLM 327
           YG+FDNEH+VLP TKYD  +D  SPRPGQQAFEKMT+G YLGE+ RL L+++   + GL+
Sbjct: 58  YGAFDNEHIVLPLTKYDHIIDRDSPRPGQQAFEKMTAGLYLGEIFRLALVDILDTQPGLI 117

Query: 328 LKDQD 332
            KDQD
Sbjct: 118 FKDQD 122

>sp|Q07262|1A1C_TOBAC 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE (ACC SYNTHASE)
           (S-ADENOSYL-L-METHIONINE METHYLTHIOADENOSINE-LYASE)
          Length = 491

 Score = 33.4 bits (75), Expect = 1.0
 Identities = 33/121 (27%), Positives = 52/121 (42%), Gaps = 14/121 (11%)

Query: 351 EDDPFENLEDTDDIFQKDFGVKTTLPERKLIRRLCELIGTRAARLAVCGIAAICQKRGYK 410
           ++DPF  L++ + + Q        L E +L   L E    R         A+IC   G K
Sbjct: 35  DNDPFHPLKNPNGVIQ------MGLAENQLCFDLIEEWIKRNPN------ASICTTEGIK 82

Query: 411 TGHIAADGSVYNKYPGFKEAAAKGLRDIYGWTGDASKDPITIVPAEDGSGAGAAVIAALS 470
           +    A+   Y+  P F+ A AK +    G  G  + DP  +V A   +GA   +I  L+
Sbjct: 83  SFRAIANFQDYHGLPEFRSAIAKFMEKTRG--GRVTFDPERVVMAGGATGANETIIFCLA 140

Query: 471 E 471
           +
Sbjct: 141 D 141

>sp|Q58696|BIOA_METJA ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
           (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA
           AMINOTRANSFERASE)
          Length = 464

 Score = 31.8 bits (71), Expect = 3.6
 Identities = 44/161 (27%), Positives = 67/161 (41%), Gaps = 29/161 (18%)

Query: 33  MFTVDSETLRKVVKHFIDELNKGLTKKGGNIPMIPG---------WVMEFPTGKE----- 78
           MF  D+E L+K+ K  I  L KGLT  GG +P+            ++ EF   K+
Sbjct: 278 MFFCDNEELKKLEKPDILCLGKGLT--GGYLPLAATLTTDEIYNQFLGEFGESKQLYHGH 335

Query: 79  --SGNYLAIDLGGTNLRVVLVKLSGNHTFDTTQSKYKLPH-DMRTTKHQEELWSFIADSL 135
             +GN L        L +        +  +  Q K KL H ++R  K  E +
Sbjct: 336 TYTGNQLLCSAALATLEI----FEKENVIENIQPKIKLFHKELRKLKELEHVGDVRG--- 388

Query: 136 KDFMVEQELLN---TKDTLPLGFTFSYPASQNKINEGILQR 173
           + FMV  EL+    TK+  P G+   Y  ++  + +GI  R
Sbjct: 389 RGFMVGIELVKDKETKEPYPYGYKAGYRVAEKLLEKGIYMR 429
```

```
sto has logged on ttyp
[rainer] [genome] [/us
d
[rainer] [genome] [/us
d
[rainer] [genome] [/us
d
```



Search SYSTERS consensi with a protein sequence

Search program:
blastp – protein query sequence vs. protein database

Sequence (FASTA or plain text): (required)

```
>HXKA_YEAST
MVHLGPKKPQARKGSMADVPKELMDEIHQLEDMFTVDSETLRKVVKHFIDELNKGLTKKG
GNIPMIPGWVMEFPTGKESGNYLAIDLGGTNLRVVLVKLSGNHTFDTTQSKYKLPHDMRT
TKHQEELWSFIADSLKDFMVEQELLNTKDTLPLGFTFSYPASQNKINEGILQRWTKGFDI
PNVEGHDVVPLLQNEISKRELPIEIVALINDTVGTLIASYYTDPETKMGVIFGTGVNGAF
YDVVSDIEKLEGKLADDIPSNSPMAINCEYGSFDNEHLVLPRTKYDVAVDEQSPRPGQQA
FEKMTSGYYLGELLRLVLLELNEKGLMLKDQDLSKLKQPYIMDTSYPARIEDDPFENLED
TDDIFQKDFGVKTTLPERKLIRRLCELIGTRAARLAVCGIAAICQKRGYKTGHIAADGSV
YNKYPGFKEAAAKGLRDIYGWTGDASKDPITIVPAEDGSGAGAAVIAALSEKRIAEGKSL
GIIGA
```

Options: Filter ☐ Scoring matrix default

Output: One–line descriptions 100 Alignments 100

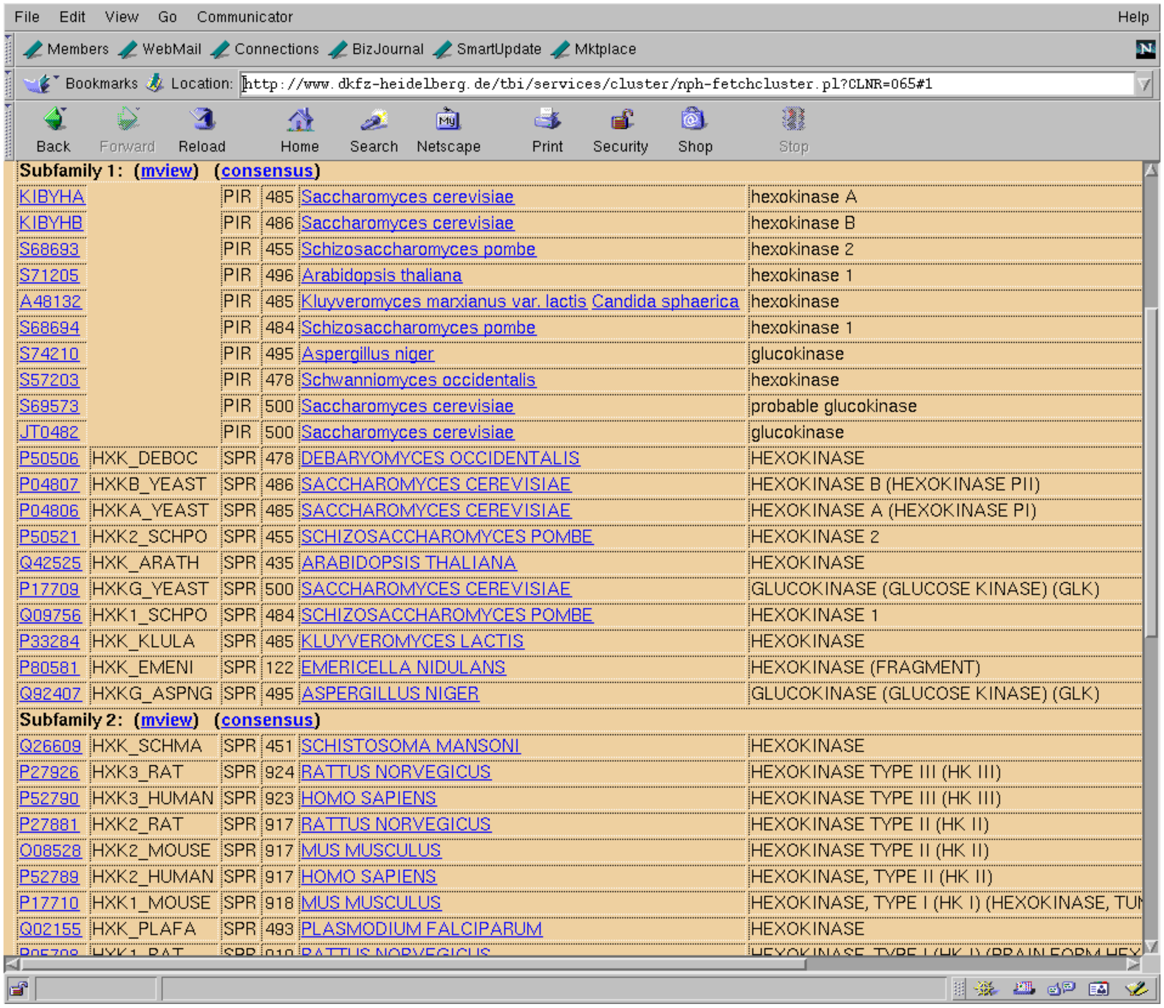
Display: (optional) genome.isds.duke.edu:0.0

Email: (optional)

SEARCH CLEAR

Retrieve result from earlier search

All search results are automatically deleted after 3 days!



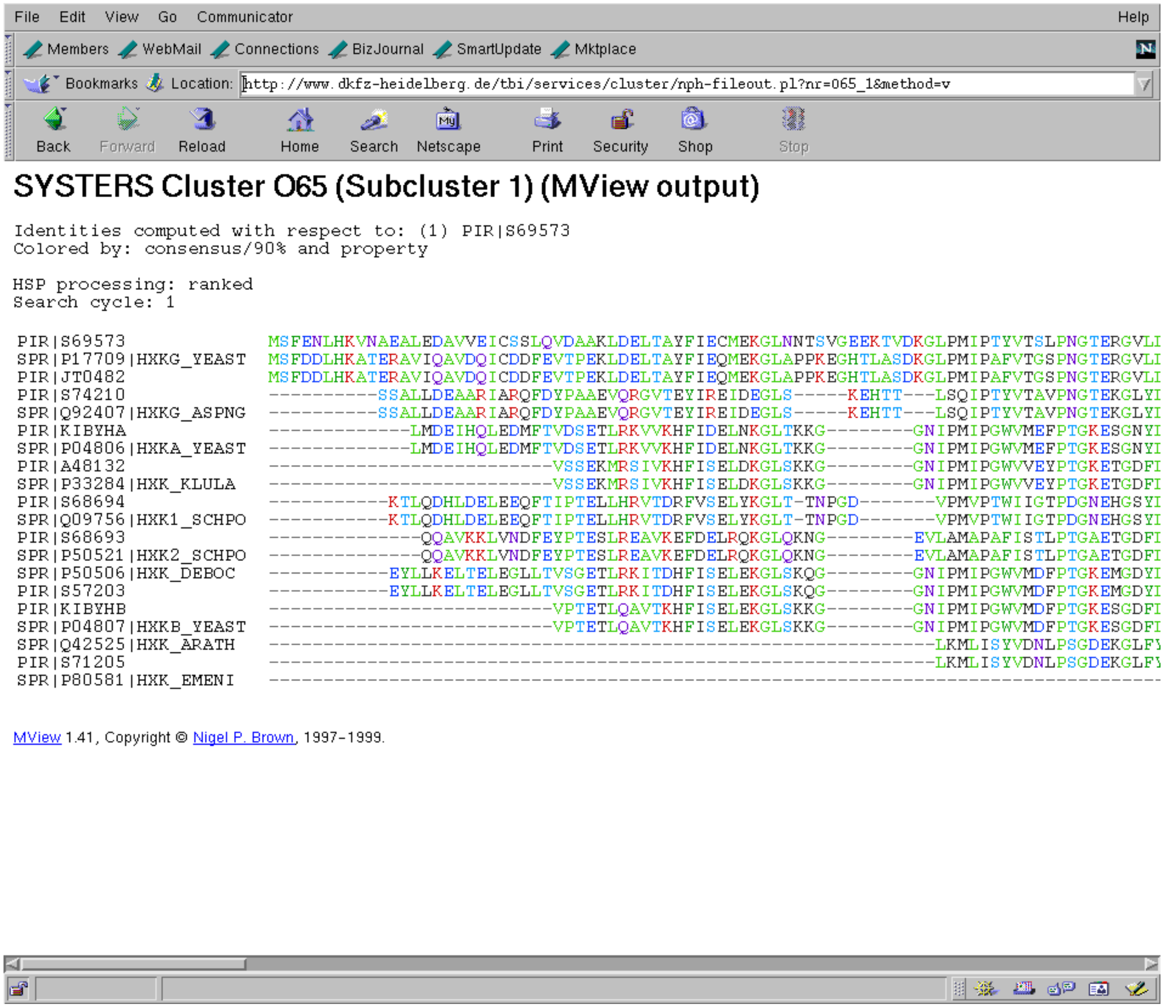
Location: http://www.dkfz-heidelberg.de/tbi/services/cluster/nph-fetchcluster.pl?CLNR=065#1

Subfamily 1: (**mview**) (**consensus**)

KIBYHA		PIR	485	Saccharomyces cerevisiae	hexokinase A
KIBYHB		PIR	486	Saccharomyces cerevisiae	hexokinase B
S68693		PIR	455	Schizosaccharomyces pombe	hexokinase 2
S71205		PIR	496	Arabidopsis thaliana	hexokinase 1
A48132		PIR	485	Kluyveromyces marxianus var. lactis Candida sphaerica	hexokinase
S68694		PIR	484	Schizosaccharomyces pombe	hexokinase 1
S74210		PIR	495	Aspergillus niger	glucokinase
S57203		PIR	478	Schwanniomyces occidentalis	hexokinase
S69573		PIR	500	Saccharomyces cerevisiae	probable glucokinase
JT0482		PIR	500	Saccharomyces cerevisiae	glucokinase
P50506	HXK_DEBOC	SPR	478	DEBARYOMYCES OCCIDENTALIS	HEXOKINASE
P04807	HXKB_YEAST	SPR	486	SACCHAROMYCES CEREVISIAE	HEXOKINASE B (HEXOKINASE PII)
P04806	HXKA_YEAST	SPR	485	SACCHAROMYCES CEREVISIAE	HEXOKINASE A (HEXOKINASE PI)
P50521	HXK2_SCHPO	SPR	455	SCHIZOSACCHAROMYCES POMBE	HEXOKINASE 2
Q42525	HXK_ARATH	SPR	435	ARABIDOPSIS THALIANA	HEXOKINASE
P17709	HXKG_YEAST	SPR	500	SACCHAROMYCES CEREVISIAE	GLUCOKINASE (GLUCOSE KINASE) (GLK)
Q09756	HXK1_SCHPO	SPR	484	SCHIZOSACCHAROMYCES POMBE	HEXOKINASE 1
P33284	HXK_KLULA	SPR	485	KLUYVEROMYCES LACTIS	HEXOKINASE
P80581	HXK_EMENI	SPR	122	EMERICELLA NIDULANS	HEXOKINASE (FRAGMENT)
Q92407	HXKG_ASPNG	SPR	495	ASPERGILLUS NIGER	GLUCOKINASE (GLUCOSE KINASE) (GLK)

Subfamily 2: (**mview**) (**consensus**)

Q26609	HXK_SCHMA	SPR	451	SCHISTOSOMA MANSONI	HEXOKINASE
P27926	HXK3_RAT	SPR	924	RATTUS NORVEGICUS	HEXOKINASE TYPE III (HK III)
P52790	HXK3_HUMAN	SPR	923	HOMO SAPIENS	HEXOKINASE TYPE III (HK III)
P27881	HXK2_RAT	SPR	917	RATTUS NORVEGICUS	HEXOKINASE TYPE II (HK II)
O08528	HXK2_MOUSE	SPR	917	MUS MUSCULUS	HEXOKINASE TYPE II (HK II)
P52789	HXK2_HUMAN	SPR	917	HOMO SAPIENS	HEXOKINASE, TYPE II (HK II)
P17710	HXK1_MOUSE	SPR	918	MUS MUSCULUS	HEXOKINASE, TYPE I (HK I) (HEXOKINASE, TU
Q02155	HXK_PLAFA	SPR	493	PLASMODIUM FALCIPARUM	HEXOKINASE
P05708	HXK1_RAT	SPR	918	RATTUS NORVEGICUS	HEXOKINASE, TYPE I (HK I) (BRAIN FORM HEX

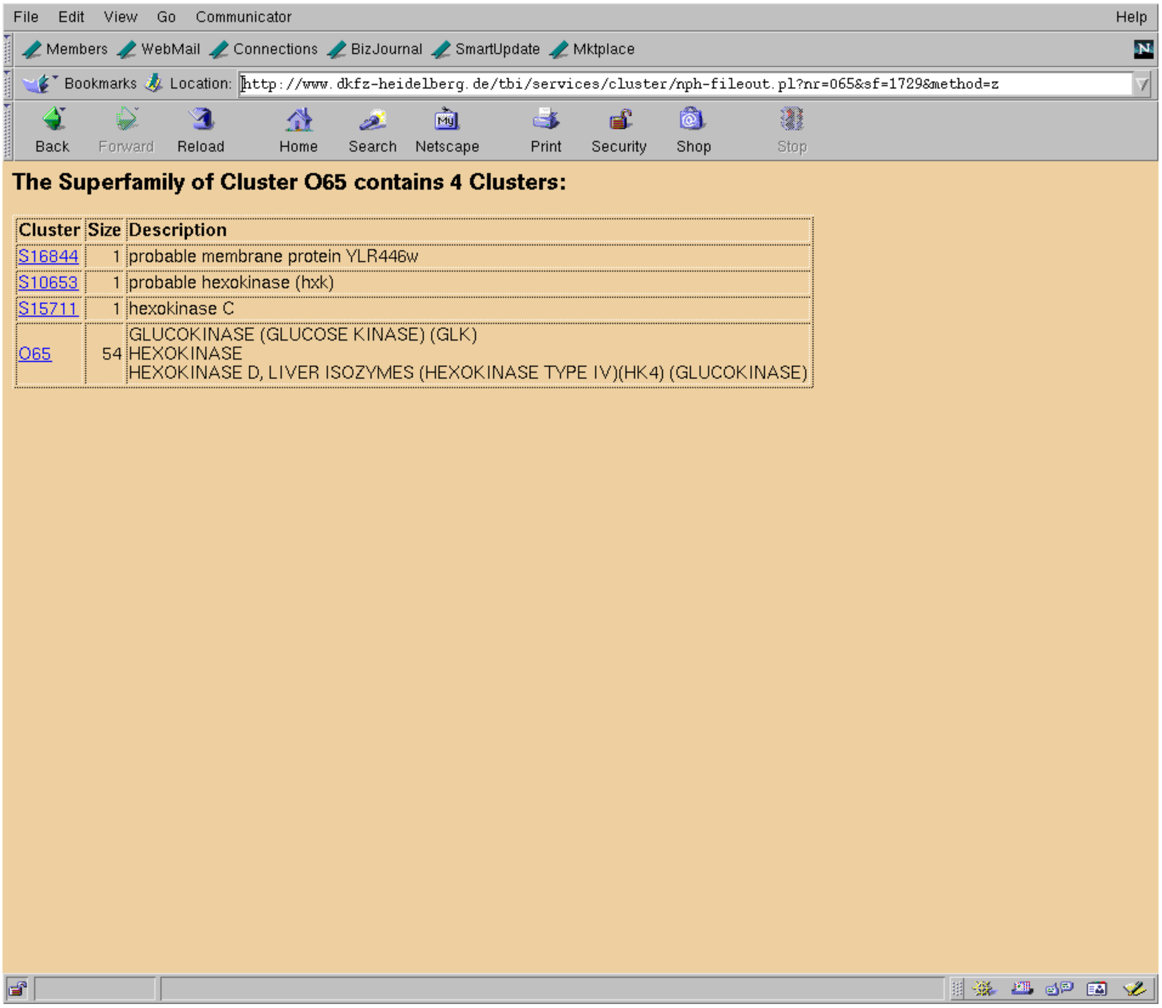


http://www.dkfz-heidelberg.de/tbi/services/cluster/nph-fileout.pl?nr=065_1&method=v

SYSTERS Cluster 065 (Subcluster 1) (MView output)

```
Identities computed with respect to: (1) PIR|S69573
Colored by: consensus/90% and property

HSP processing: ranked
Search cycle: 1

PIR|S69573             MSFENLHKVNAEALEDAVVEICSSLQVDAAKLDELTAYFIECMEKGLNNTSVGEEKTVDKGLPMIPTYVTSLPNGTERGVLI
SPR|P17709|HXKG_YEAST  MSFDDLHKATERAVIQAVDQICDDFEVTPEKLDELTAYFIEQMEKGLAPPKEGHTLASDKGLPMIPAFVTGSPNGTERGVLI
PIR|JT0482             MSFDDLHKATERAVIQAVDQICDDFEVTPEKLDELTAYFIEQMEKGLAPPKEGHTLASDKGLPMIPAFVTGSPNGTERGVLI
PIR|S74210             ----------SSALLDEAARIARQFDYPAAEVQRGVTEYIREIDEGLS-----KEHTT---LSQIPTYVTAVPNGTEKGLYI
SPR|Q92407|HXKG_ASPNG  ----------SSALLDEAARIARQFDYPAAEVQRGVTEYIREIDEGLS-----KEHTT---LSQIPTYVTAVPNGTEKGLYI
PIR|KIBYHA             -------------LMDEIHQLEDMFTVDSETLRKVVKHFIDELNKGLTKKG--------GNIPMIPGWVMEFPTGKESGNYI
SPR|P04806|HXKA_YEAST  -------------LMDEIHQLEDMFTVDSETLRKVVKHFIDELNKGLTKKG--------GNIPMIPGWVMEFPTGKESGNYI
PIR|A48132             --------------------------VSSEKMRSIVKHFISELDKGLSKKG--------GNIPMIPGWVVEYPTGKETGDFI
SPR|P33284|HXK_KLULA   --------------------------VSSEKMRSIVKHFISELDKGLSKKG--------GNIPMIPGWVVEYPTGKETGDFI
PIR|S68694             -----------KTLQDHLDELEEQFTIPTELLHRVTDRFVSELYKGLT-TNPGD-------VPMVPTWIIGTPDGNEHGSYI
SPR|Q09756|HXK1_SCHPO  -----------KTLQDHLDELEEQFTIPTELLHRVTDRFVSELYKGLT-TNPGD-------VPMVPTWIIGTPDGNEHGSYI
PIR|S68693             --------------QQAVKKLVNDFEYPTESLREAVKEFDELRQKGLQKNG--------EVLAMAPAFISTLPTGAETGDFI
SPR|P50521|HXK2_SCHPO  --------------QQAVKKLVNDFEYPTESLREAVKEFDELRQKGLQKNG--------EVLAMAPAFISTLPTGAETGDFI
SPR|P50506|HXK_DEBOC   -----------EYLLKELTELEGLLTVSGETLRKITDHFISELEKGLSKQG--------GNIPMIPGWVMDFPTGKEMGDYI
PIR|S57203             -----------EYLLKELTELEGLLTVSGETLRKITDHFISELEKGLSKQG--------GNIPMIPGWVMDFPTGKEMGDYI
PIR|KIBYHB             --------------------------VPTETLQAVTKHFISELEKGLSKKG--------GNIPMIPGWVMDFPTGKESGDFI
SPR|P04807|HXKB_YEAST  --------------------------VPTETLQAVTKHFISELEKGLSKKG--------GNIPMIPGWVMDFPTGKESGDFI
SPR|Q42525|HXK_ARATH   -------------------------------------------------------------LKMLISYVDNLPSGDEKGLF
PIR|S71205             -------------------------------------------------------------LKMLISYVDNLPSGDEKGLF
SPR|P80581|HXK_EMENI   ----------------------------------------------------------------------------------
```

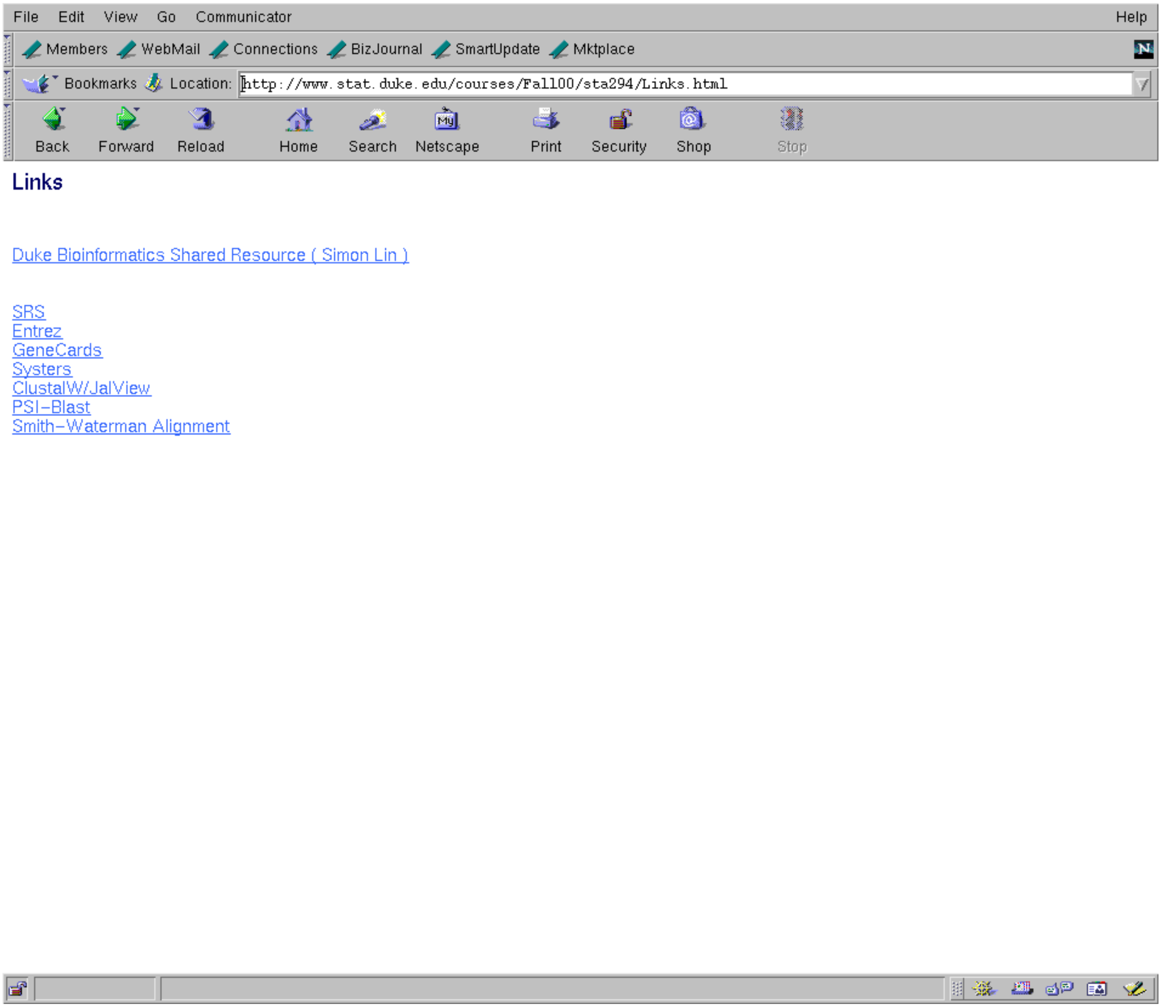
MView 1.41, Copyright © Nigel P. Brown, 1997-1999.



http://www.dkfz-heidelberg.de/tbi/services/cluster/nph-fileout.pl?nr=O65&sf=1729&method=z

The Superfamily of Cluster O65 contains 4 Clusters:

Cluster	Size	Description
S16844	1	probable membrane protein YLR446w
S10653	1	probable hexokinase (hxk)
S15711	1	hexokinase C
O65	54	GLUCOKINASE (GLUCOSE KINASE) (GLK) HEXOKINASE HEXOKINASE D, LIVER ISOZYMES (HEXOKINASE TYPE IV)(HK4) (GLUCOKINASE)



http://www.stat.duke.edu/courses/Fall00/sta294/Links.html

Links

Duke Bioinformatics Shared Resource (Simon Lin)

SRS
Entrez
GeneCards
Systers
ClustalW/JalView
PSI–Blast
Smith–Waterman Alignment