2YPI

Μπέτα Νίκη (8348), Σαμαρά Γεωργία (8417)

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fasta

>sp|P00942|TPIS_YEAST Triosephosphate isomerase OS=Saccharomyces
cerevisiae (strain ATCC 204508 / S288c) GN=TPI1 PE=1 SV=2
MARTFFVGGNFKLNGSKQSIKEIVERLNTASIPENVEVVICPPATYLDYSVSLVKKPQVT
VGAQNAYLKASGAFTGENSVDQIKDVGAKWVILGHSERRSYFHEDDKFIADKTKFALGQG
VGVILCIGETLEEKKAGKTLDVVERQLNAVLEEVKDWTNVVVAYEPVWAIGTGLAATPED
AQDIHASIRKFLASKLGDKAASELRILYGGSANGSNAVTFKDKADVDGFLVGGASLKPEF
VDIINSRN
```

prodom

Home Form Contact Site map

Release2012.1

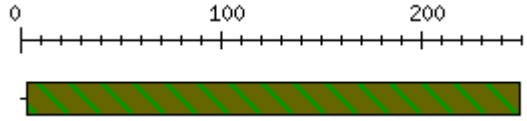
Your ncbi-blastp Query : "unkwown"

database: multiple alignments
Program: ncbi-blastp
Matrix: BLOSUM62
Expect: 0.01
Filter: seg

Graphical results and forms to other applications

The following is the graphical representation of the HSP found by BLAST.
Please note that HSPs are sorted from highest to lowest scores, so that lower scoring HSPs may be

hidden.



Align subsequence with ProDom domains, using Multalin

Domain ID	BEGIN	END
PD001005		

Domain 3D modelling using Swiss-Model

Domain ID	BEGIN	END
PD001005		

Domain 3D modelling using Geno3D

Domain ID	BEGIN	END
PD001005		

Top

HSP Results

Warning: Original output has been filtered to yield non-redundant similarities

```
blastp 2.2.26 [Sep-21-2011]


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

Query: unkwown
         (248 letters)

Database: prodom2010.1 multiple alignments
         45,292,438 sequences; 2,147,483,647 total letters



ProDom domains producing High-scoring Segment Pairs:
```

Position	ProDom domain	Score	E value
3-248	#PD001005	1287	3e-178

>**PD001005** (Closest domain: C7GTA0_YEAS2 3-248)
Number of domains in family: 3072
Commentary (automatic):
ISOMERASE FULL=TRIOSEPHOSPHATE EC=5.3.1.1 RECNAME: GLYCOLYSIS
GLUCONEOGENESIS PENTOSE SHUNT FULL=TRIOSE-PHOSPHATE SHORT=TIM
Length = 246
Score = 1287 (500.4 bits), Expect = 3e-178
Identities = 246/246 (100%), Positives = 246/246 (100%)

```
 Query:      3
RTFFVGGNFKLNGSKQSIKEIVERLNTASIPENVEVVICPPATYLDYSVSLVKKPQVTVG 62

RTFFVGGNFKLNGSKQSIKEIVERLNTASIPENVEVVICPPATYLDYSVSLVKKPQVTVG
 Sbjct:      3
RTFFVGGNFKLNGSKQSIKEIVERLNTASIPENVEVVICPPATYLDYSVSLVKKPQVTVG 62

 Query:     63
AQNAYLKASGAFTGENSVDQIKDVGAKWVILGHSERRSYFHEDDKFIADKTKFALGQGVG 122

AQNAYLKASGAFTGENSVDQIKDVGAKWVILGHSERRSYFHEDDKFIADKTKFALGQGVG
 Sbjct:     63
AQNAYLKASGAFTGENSVDQIKDVGAKWVILGHSERRSYFHEDDKFIADKTKFALGQGVG 122

 Query:    123
VILCIGETLEEKKAGKTLDVVERQLNAVLEEVKDWTNVVVAYEPVWAIGTGLAATPEDAQ 182

VILCIGETLEEKKAGKTLDVVERQLNAVLEEVKDWTNVVVAYEPVWAIGTGLAATPEDAQ
 Sbjct:    123
VILCIGETLEEKKAGKTLDVVERQLNAVLEEVKDWTNVVVAYEPVWAIGTGLAATPEDAQ 182

 Query:    183
DIHASIRKFLASKLGDKAASELRILYGGSANGSNAVTFKDKADVDGFLVGGASLKPEFVD 242

DIHASIRKFLASKLGDKAASELRILYGGSANGSNAVTFKDKADVDGFLVGGASLKPEFVD
 Sbjct:    183
DIHASIRKFLASKLGDKAASELRILYGGSANGSNAVTFKDKADVDGFLVGGASLKPEFVD 242

 Query:    243 IINSRN 248
               IINSRN
 Sbjct:    243 IINSRN 248
```

Top

ProtParam

ProtParam

User-provided sequence:

```
        10         20         30         40         50         60
MARTFFVGGN FKLNGSKQSI KEIVERLNTA SIPENVEVVI CPPATYLDYS VSLVKKPQVT

        70         80         90        100        110        120
VGAQNAYLKA SGAFTGENSV DQIKDVGAKW VILGHSERRS YFHEDDKFIA DKTKFALGQG

       130        140        150        160        170        180
VGVILCIGET LEEKKAGKTL DVVERQLNAV LEEVKDWTNV VVAYEPVWAI GTGLAATPED

       190        200        210        220        230        240
AQDIHASIRK FLASKLGDKA ASELRILYGG SANGSNAVTF KDKADVDGFL VGGASLKPEF


VDIINSRN
```

References and documentation are available.

Number of amino acids: 248

Molecular weight: 26795.4

Theoretical pI: 5.74

Amino acid composition:

Ala (A)	25	10.1%
Arg (R)	8	3.2%
Asn (N)	12	4.8%
Asp (D)	15	6.0%
Cys (C)	2	0.8%
Gln (Q)	7	2.8%
Glu (E)	17	6.9%
Gly (G)	22	8.9%
His (H)	3	1.2%
Ile (I)	15	6.0%
Leu (L)	19	7.7%
Lys (K)	21	8.5%
Met (M)	1	0.4%
Phe (F)	11	4.4%
Pro (P)	7	2.8%
Ser (S)	16	6.5%
Thr (T)	12	4.8%
Trp (W)	3	1.2%
Tyr (Y)	6	2.4%
Val (V)	26	10.5%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%

(B)	0	0.0%
(Z)	0	0.0%
(X)	0	0.0%

Total number of negatively charged residues (Asp + Glu): 32
Total number of positively charged residues (Arg + Lys): 29

Atomic composition:

Carbon	C	1201
Hydrogen	H	1907
Nitrogen	N	321
Oxygen	O	366
Sulfur	S	3

Formula: $C_{1201}H_{1907}N_{321}O_{366}S_3$
Total number of atoms: 3798

Extinction coefficients:

Extinction coefficients are in units of M^{-1} cm^{-1}, at 280 nm measured in water.

Ext. coefficient 25565
Abs 0.1% (=1 g/l) 0.954, assuming all pairs of Cys residues form cystines

Ext. coefficient 25440
Abs 0.1% (=1 g/l) 0.949, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

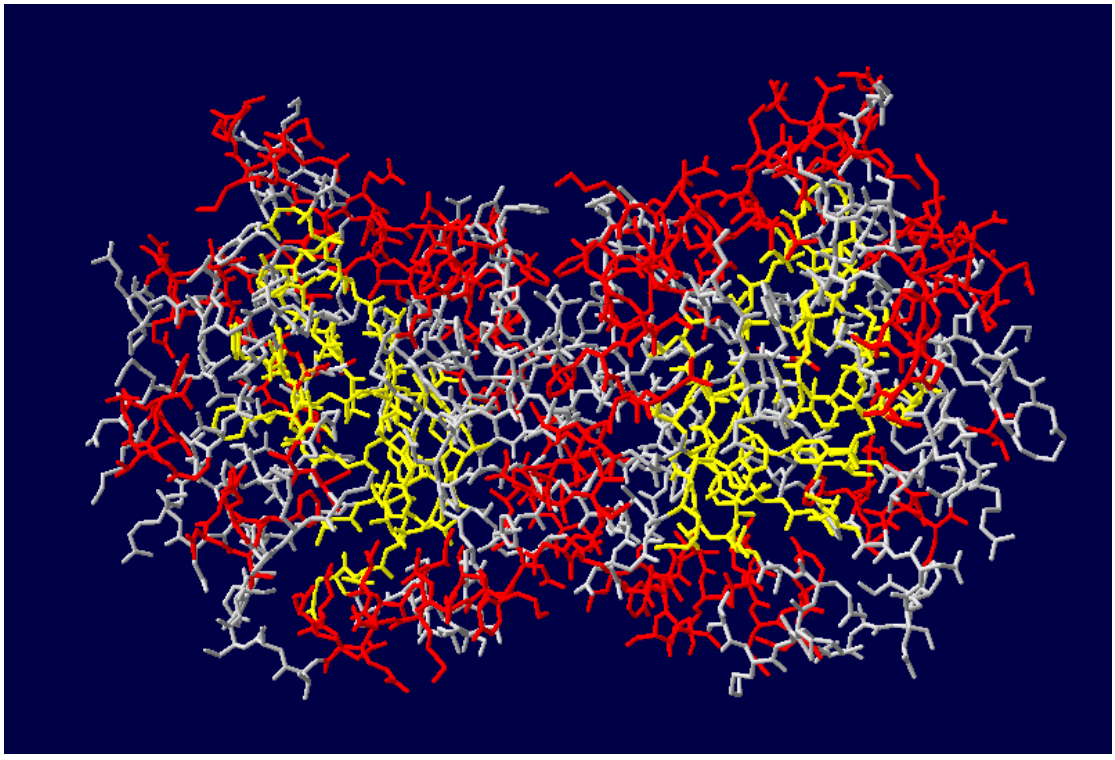
The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
>20 hours (yeast, in vivo).
>10 hours (Escherichia coli, in vivo).

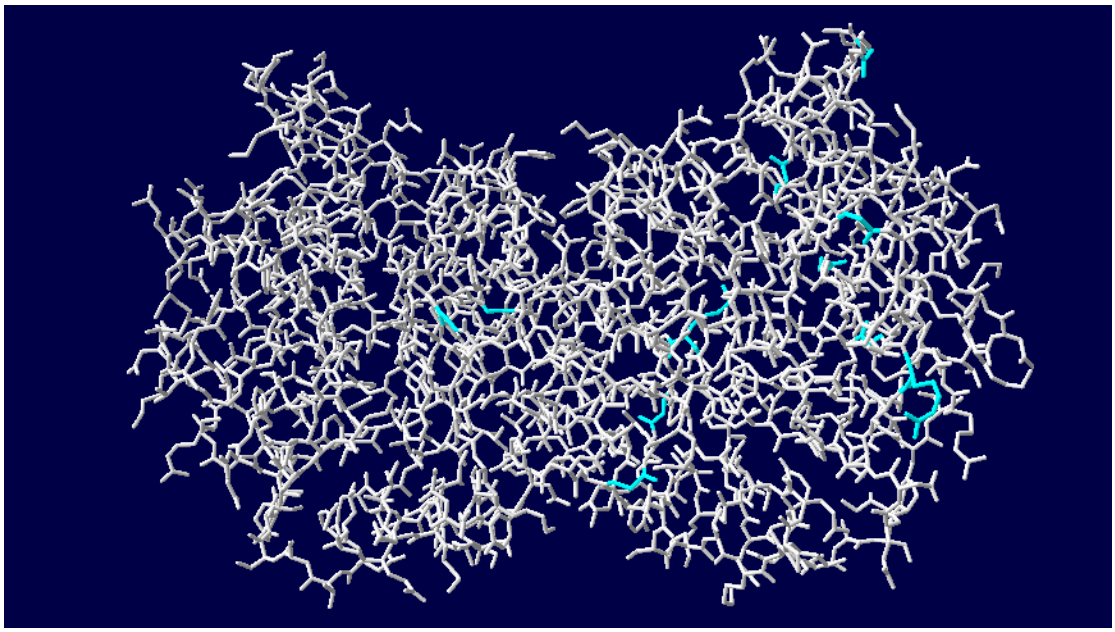
Instability index:

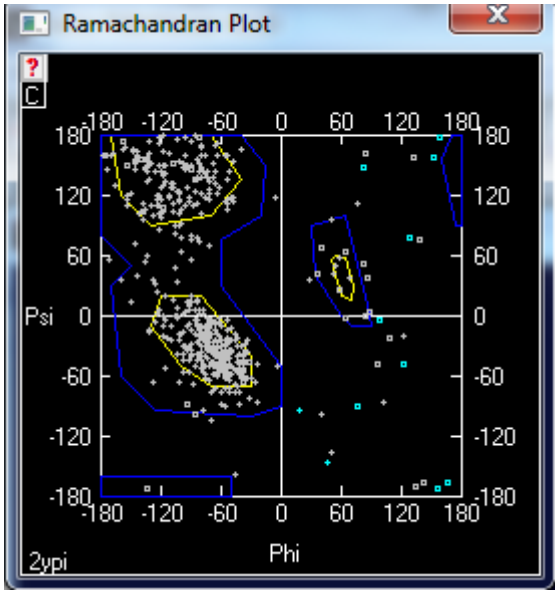
The instability index (II) is computed to be 19.66
This classifies the protein as stable.

Aliphatic index: 93.95

Grand average of hydropathicity (GRAVY): -0.105







Αμινοξέα που εμφανίζονται εκτός των επιτρεπτών στερεοτακτικών δομών:

Arg 3
Lys 12
Gly 15
Gly 72
Gly 76
Gly 87
Gly 128
Gly 137
Gly 197
Gly 210
Gly 228