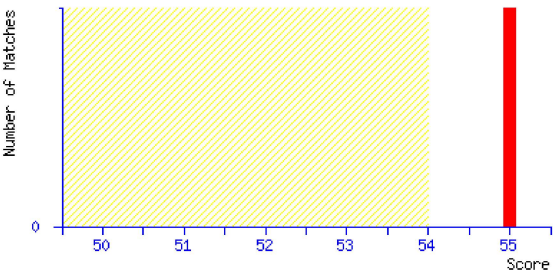


User : Lily-mascot  
E-mail : l.r.adair@pgr.reading.ac.uk  
Search title : S\_cerevisiae\_3500  
MS data file : S\_cerevisiae\_3500\_Da\_merged.txt  
Databases : 1: contaminants 20160129 (247 sequences; 128,130 residues)  
2: Swissprot\_22\_05\_2024 22\_05\_2024\_2024\_02 (571,282 sequences; 206,678,396 residues)  
Timestamp : 27 May 2025 at 07:48:38 GMT

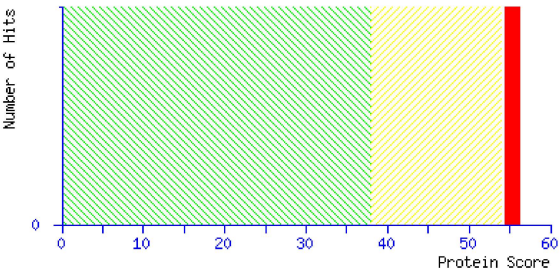
▼Search parameters

Type of search : MS/MS Ion Search  
Enzyme : None  
Variable modifications : **Acetyl (Protein N-term)**  
Mass values : Monoisotopic  
Protein mass : Unrestricted  
Peptide mass tolerance : ± 50 ppm  
Fragment mass tolerance : ± 0.2 Da  
Max missed cleavages : 0  
Instrument type : MALDI-QIT-TOF  
Number of queries : 1

▼Score distribution



**Peptide score distribution.** Ions score is  $-10\log(P)$ , where  $P$  is the probability that the observed match is a random event. There is **1** peptide match above identity threshold and **1** match above homology threshold for **1** queries. On average, individual ions scores **> 38** (beyond yellow shading) indicate **significant homology**, while individual ions scores **> 54** (beyond green shading) indicate **identity or extensive homology** ( $p<0.05$ ).



**[Deprecated]** Protein score distribution. Score distribution for family members in the first 50 proteins. Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein families.

▼Legend

Peptide columns and rows

Dupes	...	Expect	Rank	U	1	2	Peptide	
		0.037	▶	2			GAYSLSLR	significant
		9	▶	1			GFFLFVEGGR	top ranking
		6.4e-05	▶	1			GSSIFGLAPGK	significant and top ranking
		1.3e-06	▶	1	■		SSGTSYPDVLK	peptide is found in all proteins in family member 1
		6.2e-07	▶	1	■		VCNYVSWIK	peptide is found in some but not all proteins in family member 2
		6.4e-05	▶	1	U		GSSIFGLAPGK	unique
▶	2	5.7e-05	▶	1			LNTLETEEWFFK	peptide has two duplicates
		0.18	▶	1			LNTLETEEWFFK	duplicate peptide

Right-facing triangle (▶) in the Dupes or Rank column indicates content that can be expanded by clicking on it. Down-facing triangle (▼) indicates the content is expanded and can be collapsed. For more details about particular columns, see [results format help](#).

Protein quantitation ratios

	Score	...	114/113	115/113
CFAH_HUMAN	37559		0.962	1.129
FHR2_HUMAN	1330		0.859	1.128

When quantitation method is Reporter (e.g. iTRAQ) or Multiplex (e.g. IPTL), protein ratios are displayed when a family is expanded. Ratios in *italic* indicate that the peptide log-ratios do not appear to come from a normal distribution. **Bold** indicates that if you can assume peptide ratios are normally distributed, the protein ratio is significantly different from 1.0 (at significance level 0.05).

Note that lack of bold or italic can also mean that significance or normality testing has not been performed (for example, if protein ratio type does not support it).

Protein Family Summary

Significance threshold p<  Max. number of families

Target FDR (overrides sig. threshold)  FDR type

Display non-sig. matches ☐ Min. number of sig. unique sequences

Dendrograms cut at

Preferred taxonomy

▼Sensitivity and FDR (random protein sequences)

	Target	Decoy	FDR	
Protein family members	1	0	0.00%	Not enough decoy protein hits for a meaningful FDR calculation.
Sequences above homology	1	0	0.00%	Not enough decoy matches above significance threshold for a meaningful FDR calculation.

Decoy results are available in [the decoy report](#).

Protein family 1 (out of 1)

per page 1

▼1 2::G3P3\_YEAST 55 Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevis...

	Score	Mass	Matches	Sequences
1.1 2::G3P3_YEAST	55	35724	1 (1)	1 (1)
Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH3 PE=1 SV=3				

▼1 peptide matches (1 non-duplicate, 0 duplicate).

Query Dupes	Observed	Mr (expt)	Mr (calc)	ppm	M	Score	Expect	Rank	U	Peptide
1	3505.0990	3504.0917	3503.9987	26.5	0	55	0.00097	▶1	U	M.VRVAINGFGRIGRLVMRIALSRPNVEVVALND.P

per page 1

Mascot: <http://www.matrixscience.com/>

Protein View: G3P3\_YEAST

Glyceraldehyde-3-phosphate dehydrogenase 3 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)  
OX=559292 GN=TDH3 PE=1 SV=3

Detailed information about this protein hit is shown below. [\(help\)](#)

Database:	Swissprot_22_05_2024
Score:	55
Monoisotopic mass (M <sub>r</sub> ):	35724
Calculated pI:	6.46
Taxonomy:	<a href="#">Saccharomyces cerevisiae S288C</a>

Sequence similarity is available as [an NCBI BLAST search of G3P3\\_YEAST against nr](#).

Search parameters

MS data file:	S_cerevisiae_3500_Da_merged.txt
Enzyme:	No enzyme cleavage specificity.
Variable modifications:	<a href="#">Acetyl (Protein N-term)</a>

Protein sequence coverage: 9%

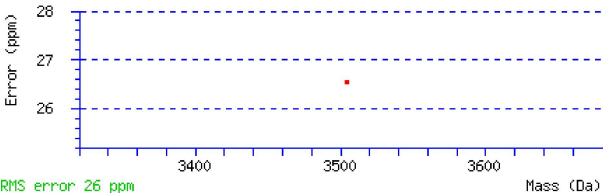
Matched peptides shown in **bold red**.

1	MVRVAINGFG	RIGRLVMRIA	LSRPNVEVVA	LND	PFITNDY	AAYMFKYDST
51	HGRYAGEVSH	DDKHIIVDGK	KIATYQERDP	ANLPWGSSNV	DI AIDSTGVF	
101	KELDTAQKHI	DAGAKKVIT	APSSSTAPMFV	MGVNEEKYTS	DLKIVSNASC	
151	TTNCLAPLAK	VINDAFGIEE	GLMTTVHSLT	ATQKTVDGPS	HKDWRGGRTA	
201	SGNIIPSSTG	AAKAVGKVL	ELQGKLTGMA	FRVPTVDVSV	VDLTVKLNKE	
251	TTYDEIKKVV	KAAAEGKLKG	VLGYTEDAVV	SSDFLGDSHS	SIFDASAGIQ	
301	LSPKFVKLVS	WYDNEYGYST	RVVDLVEHVA	KA		

Unformatted sequence string: **332 residues** (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass

Query	Start – End	Observed	Mr (expt)	Mr (calc)	ppm	M	Score	Expect	Rank	U	Peptide
<a href="#">1</a>	2 – 33	3505.0990	3504.0917	3503.9987	26.5	0	55	0.00097	1	U	M.VRVAINGFGRIGRLVMRIALSRPNVEVVALND.P



ID G3P3\_YEAST Reviewed; 332 AA.  
AC P00359; D6VUX4; Q6Q5P9;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 23-JAN-2007, sequence version 3.  
DT 27-MAR-2024, entry version 230.  
DE RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase 3 {ECO:0000303|PubMed:2999100};  
DE Short=GAPDH 3 {ECO:0000303|PubMed:2999100};  
DE EC=1.2.1.12 {ECO:0000269|PubMed:3905788};  
DE AltName: Full=Triose-phosphate dehydrogenase 1 {ECO:0000303|PubMed:2999100};  
GN Name=TDH3 {ECO:0000303|PubMed:2999100}; Synonyms=GPD3;  
GN OrderedLocusNames=YGR192C; ORFNames=G7576;  
OS *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) (Baker's yeast).  
OC Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=559292;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX PubMed=385592; DOI=10.1016/s0021-9258(19)83593-7;  
RA Holland J.P., Holland M.J.;  
RT "The primary structure of a glyceraldehyde-3-phosphate dehydrogenase gene  
RT from *Saccharomyces cerevisiae*.";  
RL J. Biol. Chem. 254:9839-9845(1979).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=ATCC 204508 / S288c;  
RX PubMed=7645350; DOI=10.1002/yea.320110609;  
RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez M., Nombela C.;  
RT "The complete sequence of a 9037 bp DNA fragment of the right arm of  
RT *Saccharomyces cerevisiae* chromosome VII.";

RL Yeast 11:587-591(1995).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 204508 / S288c;  
 RX PubMed=9169869;  
 RA Tettelin H., Agostoni-Carbone M.L., Albermann K., Albers M., Arroyo J.,  
 RA Backes U., Barreiros T., Bertani I., Bjourson A.J., Brueckner M.,  
 RA Bruschi C.V., Carignani G., Castagnoli L., Cerdan E., Clemente M.L.,  
 RA Coblenz A., Cogliervina M., Coissac E., Defoor E., Del Bino S., Delius H.,  
 RA Delneri D., de Wergifosse P., Dujon B., Durand P., Entian K.-D., Eraso P.,  
 RA Escribano V., Fabiani L., Fartmann B., Feroli F., Feuermann M.,  
 RA Frontali L., Garcia-Gonzalez M., Garcia-Saez M.I., Goffeau A.,  
 RA Guerreiro P., Hani J., Hansen M., Hebling U., Hernandez K., Heumann K.,  
 RA Hilger F., Hofmann B., Indge K.J., James C.M., Klima R., Koetter P.,  
 RA Kramer B., Kramer W., Lauquin G., Leuther H., Louis E.J., Maillier E.,  
 RA Marconi A., Martegani E., Mazon M.J., Mazzoni C., McReynolds A.D.K.,  
 RA Melchiorretto P., Mewes H.-W., Minenkova O., Mueller-Auer S., Nawrocki A.,  
 RA Netter P., Neu R., Nombela C., Oliver S.G., Panzeri L., Paoluzi S.,  
 RA Plevani P., Portetelle D., Portillo F., Potier S., Purnelle B., Rieger M.,  
 RA Riles L., Rinaldi T., Robben J., Rodrigues-Pousada C.,  
 RA Rodriguez-Belmonte E., Rodriguez-Torres A.M., Rose M., Ruzzi M.,  
 RA Salicola M., Sanchez-Perez M., Schaefer B., Schaefer M., Scharfe M.,  
 RA Schmidheini T., Schreer A., Skala J., Souciet J.-L., Steensma H.Y.,  
 RA Talla E., Thierry A., Vandenbol M., van der Aart Q.J.M., Van Dyck L.,  
 RA Vanoni M., Verhasselt P., Voet M., Volckaert G., Wambutt R., Watson M.D.,  
 RA Weber N., Wedler E., Wedler H., Wipfli P., Wolf K., Wright L.F.,  
 RA Zaccaria P., Zimmermann M., Zollner A., Kleine K.;  
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome VII.";  
 RL Nature 387:81-84(1997).  
 RN [4]  
 RP GENOME REANNOTATION.  
 RC STRAIN=ATCC 204508 / S288c;  
 RX PubMed=24374639; DOI=10.1534/g3.113.008995;  
 RA Engel S.R., Dietrich F.S., Fisk D.G., Binkley G., Balakrishnan R.,  
 RA Costanzo M.C., Dwight S.S., Hitz B.C., Karra K., Nash R.S., Weng S.,  
 RA Wong E.D., Lloyd P., Skrzypek M.S., Miyasato S.R., Simison M., Cherry J.M.;  
 RT "The reference genome sequence of *Saccharomyces cerevisiae*: Then and now.";  
 RL G3 (Bethesda) 4:389-398(2014).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=ATCC 204508 / S288c;  
 RX PubMed=17322287; DOI=10.1101/gr.6037607;  
 RA Hu Y., Rolfs A., Bhullar B., Murthy T.V.S., Zhu C., Berger M.F.,  
 RA Camargo A.A., Kelley F., McCarron S., Jepson D., Richardson A., Raphael J.,  
 RA Moreira D., Taycher E., Zuo D., Mohr S., Kane M.F., Williamson J.,  
 RA Simpson A.J.G., Bulik M.L., Harlow E., Marsischky G., Kolodner R.D.,  
 RA LaBaer J.;  
 RT "Approaching a complete repository of sequence-verified protein-encoding  
 RT clones for *Saccharomyces cerevisiae*.";  
 RL Genome Res. 17:536-543(2007).  
 RN [6]  
 RP PARTIAL PROTEIN SEQUENCE OF 2-332, AND CLEAVAGE OF INITIATOR METHIONINE.  
 RX PubMed=11946592; DOI=10.1016/0014-5793(72)80040-1;  
 RA Jones G.M., Harris J.I.;  
 RT "Glyceraldehyde 3-phosphate dehydrogenase: Amino acid sequence of enzyme  
 RT from baker's yeast.";  
 RL FEBS Lett. 22:185-189(1972).  
 RN [7]  
 RP PROTEIN SEQUENCE OF 47-58.  
 RC STRAIN=ATCC 204508 / S288c;  
 RX PubMed=7895733; DOI=10.1002/elps.11501501210;  
 RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RA Volpe T., Warner J.R., McLaughlin C.S.;  
 RT "Protein identifications for a *Saccharomyces cerevisiae* protein database.";  
 RL Electrophoresis 15:1466-1486(1994).  
 RN [8]  
 RP PARTIAL PROTEIN SEQUENCE.  
 RC STRAIN=ATCC 38531 / Y41, and ATCC 44827 / SKQ2N;  
 RX PubMed=7737086; DOI=10.1002/elps.1150160124;  
 RA Norbeck J., Blomberg A.;  
 RT "Gene linkage of two-dimensional polyacrylamide gel electrophoresis  
 RT resolved proteins from isogene families in *Saccharomyces cerevisiae* by  
 RT microsequencing of in-gel trypsin generated peptides.";  
 RL Electrophoresis 16:149-156(1995).  
 RN [9]  
 RP FUNCTION, AND CATALYTIC ACTIVITY.  
 RX PubMed=13174589; DOI=10.1016/s0021-9258(18)65605-4;  
 RA Rafter G.W., Chaykin S., Krebs E.G.;  
 RT "The action of glyceraldehyde-3-phosphate dehydrogenase on reduced  
 RT diphosphopyridine nucleotide.";  
 RL J. Biol. Chem. 208:799-811(1954).  
 RN [10]  
 RP FUNCTION, AND CATALYTIC ACTIVITY.  
 RX PubMed=4371815; DOI=10.1021/bi00720a002;  
 RA Oppenheimer N.J., Kaplan N.O.;  
 RT "Glyceraldehyde-3-phosphate dehydrogenase catalyzed hydration of the 5-6  
 RT double bond of reduced beta-nicotinamide adenine dinucleotide (betaNADH).  
 RT Formation of beta-6-hydroxy-1,4,5,6-tetrahydronicotinamide adenine  
 RT dinucleotide.";  
 RL Biochemistry 13:4685-4694(1974).  
 RN [11]  
 RP FUNCTION, AND DISRUPTION PHENOTYPE.  
 RX PubMed=2999100; DOI=10.1016/s0021-9258(18)95695-4;

RA McAlister L., Holland M.J.;  
 RT "Isolation and characterization of yeast strains carrying mutations in the  
 glycerinaldehyde-3-phosphate dehydrogenase genes.";  
 RL J. Biol. Chem. 260:15013-15018(1985).  
 RN [12]  
 RP FUNCTION, SUBUNIT, CATALYTIC ACTIVITY, AND BIOPHYSICOCHEMICAL PROPERTIES.  
 RX PubMed=3905788; DOI=10.1016/s0021-9258(18)95696-6;  
 RA McAlister L., Holland M.J.;  
 RT "Differential expression of the three yeast glycerinaldehyde-3-phosphate  
 dehydrogenase genes.";  
 RL J. Biol. Chem. 260:15019-15027(1985).  
 RN [13]  
 RP INDUCTION.  
 RX PubMed=7875559; DOI=10.1111/j.1574-6968.1995.tb07348.x;  
 RA Boucherie H., Bataille N., Fitch I.T., Perrot M., Tuite M.F.;  
 RT "Differential synthesis of glycerinaldehyde-3-phosphate dehydrogenase  
 polypeptides in stressed yeast cells.";  
 RL FEMS Microbiol. Lett. 125:127-133(1995).  
 RN [14]  
 RP SUBCELLULAR LOCATION.  
 RX PubMed=11502169; DOI=10.1021/bi010277r;  
 RA Grandier-Vazeille X., Bathany K., Chaignepain S., Camougrand N., Manon S.,  
 RA Schmitter J.-M.;  
 RT "Yeast mitochondrial dehydrogenases are associated in a supramolecular  
 complex.";  
 RL Biochemistry 40:9758-9769(2001).  
 RN [15]  
 RP LEVEL OF PROTEIN EXPRESSION [LARGE SCALE ANALYSIS].  
 RX PubMed=14562106; DOI=10.1038/nature02046;  
 RA Ghaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A., Dephoure N.,  
 RA O'Shea E.K., Weissman J.S.;  
 RT "Global analysis of protein expression in yeast.";  
 RL Nature 425:737-741(2003).  
 RN [16]  
 RP SUBCELLULAR LOCATION [LARGE SCALE ANALYSIS], AND IDENTIFICATION BY MASS  
 SPECTROMETRY.  
 RX PubMed=16823961; DOI=10.1021/pr050477f;  
 RA Reinders J., Zahedi R.P., Pfanner N., Meisinger C., Sickmann A.;  
 RT "Toward the complete yeast mitochondrial proteome: multidimensional  
 separation techniques for mitochondrial proteomics.";  
 RL J. Proteome Res. 5:1543-1554(2006).  
 RN [17]  
 RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].  
 RX PubMed=17287358; DOI=10.1073/pnas.0607084104;  
 RA Chi A., Huttenhower C., Geer L.Y., Coon J.J., Syka J.E.P., Bai D.L.,  
 RA Shabanowitz J., Burke D.J., Troyanskaya O.G., Hunt D.F.;  
 RT "Analysis of phosphorylation sites on proteins from *Saccharomyces*  
*cerevisiae* by electron transfer dissociation (ETD) mass spectrometry.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 104:2193-2198(2007).  
 RN [18]  
 RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-302, AND IDENTIFICATION BY  
 MASS SPECTROMETRY [LARGE SCALE ANALYSIS].  
 RX PubMed=18407956; DOI=10.1074/mcp.m700468-mcp200;  
 RA Albuquerque C.P., Smolka M.B., Payne S.H., Bafna V., Eng J., Zhou H.;  
 RT "A multidimensional chromatography technology for in-depth phosphoproteome  
 analysis.";  
 RL Mol. Cell. Proteomics 7:1389-1396(2008).  
 RN [19]  
 RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].  
 RX PubMed=19779198; DOI=10.1126/science.1172867;  
 RA Holt L.J., Tuch B.B., Villen J., Johnson A.D., Gygi S.P., Morgan D.O.;  
 RT "Global analysis of Cdk1 substrate phosphorylation sites provides insights  
 into evolution.";  
 RL Science 325:1682-1686(2009).  
 RN [20]  
 RP UBIQUITINATION [LARGE SCALE ANALYSIS] AT LYS-46 AND LYS-63, AND  
 IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].  
 RX PubMed=22106047; DOI=10.1002/pmic.201100166;  
 RA Starita L.M., Lo R.S., Eng J.K., von Haller P.D., Fields S.;  
 RT "Sites of ubiquitin attachment in *Saccharomyces cerevisiae*.";  
 RL Proteomics 12:236-240(2012).  
 RN [21] {ECO:0007744|PDB:3PYM}  
 RP X-RAY CRYSTALLOGRAPHY (2.00 ANGSTROMS) IN COMPLEX WITH NAD(+).  
 RA Garcia-Saez I., Kozielski F., Job D., Boscheron C.;  
 RT "Structure of GAPDH 3 from *S.cerevisiae* at 2.0 A resolution.";  
 RL Submitted (DEC-2010) to the PDB data bank.  
 RN [22] {ECO:0007744|PDB:4IQ8}  
 RP X-RAY CRYSTALLOGRAPHY (2.49 ANGSTROMS), AND SUBUNIT.  
 RX PubMed=22869137; DOI=10.1107/s1744309112028989;  
 RA Liu Q., Wang H., Liu H., Teng M., Li X.;  
 RT "Preliminary crystallographic analysis of glycerinaldehyde-3-phosphate  
 dehydrogenase 3 from *Saccharomyces cerevisiae*.";  
 RL Acta Crystallogr. F 68:978-980(2012).  
 CC -!- FUNCTION: Glycerinaldehyde-3-phosphate dehydrogenase (GAPDH) involved in  
 glycolysis and gluconeogenesis (PubMed:2999100). Catalyzes the reaction  
 of glycerinaldehyde-3-phosphate to 1,3 bis-phosphoglycerate  
 (PubMed:3905788). The contribution of the TDH1, TDH2, and TDH3 to the  
 total glycerinaldehyde-3-phosphate dehydrogenase activity is 10-15, 25-  
 30, and 50-60%, respectively (PubMed:3905788).  
 {ECO:0000269|PubMed:2999100, ECO:0000269|PubMed:3905788}.  
 CC -!- FUNCTION: As a side activity, catalyzes the hydration of the  
 nicotinamide ring of NADH or NADPH at the C6 position to give the  
 corresponding hydrates, NADHX and NADPHX, which exist as R and S

epimers, that cannot act as electron donors or acceptors and inhibit several dehydrogenases, making them toxic.  
{ECO:0000269|PubMed:13174589, ECO:0000269|PubMed:4371815}.

CC CATALYTIC ACTIVITY:  
Reaction=D-glyceraldehyde 3-phosphate + NAD(+) + phosphate = (2R)-3-phospho-glyceroyl phosphate + H(+) + NADH; Xref=Rhea:RHEA:10300, ChEBI:CHEBI:15378, ChEBI:CHEBI:43474, ChEBI:CHEBI:57540, ChEBI:CHEBI:57604, ChEBI:CHEBI:57945, ChEBI:CHEBI:59776; EC=1.2.1.12; Evidence={ECO:0000269|PubMed:3905788}; PhysiologicalDirection=left-to-right; Xref=Rhea:RHEA:10301; Evidence={ECO:0000269|PubMed:3905788};

CC CATALYTIC ACTIVITY:  
Reaction=H2O + NADH = (6R)-NADHX; Xref=Rhea:RHEA:57360, ChEBI:CHEBI:15377, ChEBI:CHEBI:57945, ChEBI:CHEBI:64075; Evidence={ECO:0000269|PubMed:13174589, ECO:0000269|PubMed:4371815}; PhysiologicalDirection=left-to-right; Xref=Rhea:RHEA:57361; Evidence={ECO:0000269|PubMed:13174589, ECO:0000269|PubMed:4371815};

CC CATALYTIC ACTIVITY:  
Reaction=H2O + NADH = (6S)-NADHX; Xref=Rhea:RHEA:57364, ChEBI:CHEBI:15377, ChEBI:CHEBI:57945, ChEBI:CHEBI:64074; Evidence={ECO:0000269|PubMed:13174589, ECO:0000269|PubMed:4371815}; PhysiologicalDirection=left-to-right; Xref=Rhea:RHEA:57365; Evidence={ECO:0000269|PubMed:13174589, ECO:0000269|PubMed:4371815};

CC CATALYTIC ACTIVITY:  
Reaction=H2O + NADPH = (6R)-NADPHX; Xref=Rhea:RHEA:57368, ChEBI:CHEBI:15377, ChEBI:CHEBI:57783, ChEBI:CHEBI:64077; Evidence={ECO:0000269|PubMed:13174589, ECO:0000269|PubMed:4371815}; PhysiologicalDirection=left-to-right; Xref=Rhea:RHEA:57369; Evidence={ECO:0000269|PubMed:13174589, ECO:0000269|PubMed:4371815};

CC CATALYTIC ACTIVITY:  
Reaction=H2O + NADPH = (6S)-NADPHX; Xref=Rhea:RHEA:57372, ChEBI:CHEBI:15377, ChEBI:CHEBI:57783, ChEBI:CHEBI:64076; Evidence={ECO:0000269|PubMed:13174589, ECO:0000269|PubMed:4371815}; PhysiologicalDirection=left-to-right; Xref=Rhea:RHEA:57373; Evidence={ECO:0000269|PubMed:13174589, ECO:0000269|PubMed:4371815};

CC BIOPHYSICOCHEMICAL PROPERTIES:  
Kinetic parameters:  
KM=0.32 uM for NAD(+) {ECO:0000303|PubMed:3905788};

CC PATHWAY: Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 1/5. {ECO:0000269|PubMed:3905788}.

CC SUBUNIT: Homotetramer. {ECO:0000269|PubMed:22869137, ECO:0000269|PubMed:3905788}.

CC SUBCELLULAR LOCATION: Cytoplasm {ECO:0000269|PubMed:11502169}. Mitochondrion {ECO:0000269|PubMed:16823961}.

CC INDUCTION: Expression is not affected by a heat shock. {ECO:0000269|PubMed:7875559}.

CC DISRUPTION PHENOTYPE: Does not affect growth when ethanol is used as carbon source but reduces growth when glucose is used as carbon source. {ECO:0000269|PubMed:2999100}.

CC MISCELLANEOUS: Present with 169000 molecules/cell in log phase SD medium. {ECO:0000269|PubMed:14562106}.

CC SIMILARITY: Belongs to the glyceraldehyde-3-phosphate dehydrogenase family. {ECO:0000305}.

-----

CC Copyrighted by the UniProt Consortium, see <https://www.uniprot.org/terms>  
Distributed under the Creative Commons Attribution (CC BY 4.0) License  
-----

DR EMBL; V01300; CAA24607.1; -; Genomic\_DNA.  
DR EMBL; J01324; AAA88714.1; -; Genomic\_DNA.  
DR EMBL; X82408; CAA57803.1; -; Genomic\_DNA.  
DR EMBL; Z72977; CAA97218.1; -; Genomic\_DNA.  
DR EMBL; AY557831; AAS56157.1; -; Genomic\_DNA.  
DR EMBL; BK006941; DAA08285.1; -; Genomic\_DNA.  
DR PIR; S55870; DEBYG2.  
DR RefSeq; NP\_011708.3; NM\_001181321.3.  
DR PDB; 3PYM; X-ray; 2.00 A; A/B=1-332.  
DR PDB; 4IQ8; X-ray; 2.49 A; A=1-332.  
DR PDBsum; 3PYM; -.  
DR PDBsum; 4IQ8; -.  
DR AlphaFoldDB; P00359; -.  
DR SMR; P00359; -.  
DR BioGRID; 33445; 326.  
DR DIP; DIP-4309N; -.  
DR IntAct; P00359; 102.  
DR MINT; P00359; -.  
DR STRING; 4932.YGR192C; -.  
DR MoonDB; P00359; Curated.  
DR MoonProt; P00359; -.  
DR CarbonylDB; P00359; -.  
DR iPTMnet; P00359; -.  
DR COMPLEYEST-2DPAGE; P00359; -.  
DR SWISS-2DPAGE; P00359; -.  
DR MaxQB; P00359; -.  
DR PaxDb; 4932-YGR192C; -.  
DR PeptideAtlas; P00359; -.  
DR TopDownProteomics; P00359; -.  
DR EnsemblFungi; YGR192C\_mRNA; YGR192C; YGR192C.  
DR GeneID; 853106; -.  
DR KEGG; sce:YGR192C; -.  
DR AGR; SGD:S000003424; -.  
DR SGD; S000003424; TDH3.  
DR VEuPathDB; FungiDB:YGR192C; -.  
DR eggNOG; KOG0657; Eukaryota.

DR GeneTree; ENSGT00940000153298; -.  
 DR HOGENOM; CLU\_030140\_0\_3\_1; -.  
 DR InParanoid; P00359; -.  
 DR OMA; YGYTCNM; -.  
 DR OrthoDB; 275384at2759; -.  
 DR BioCyc; YEAST:YGR192C-MONOMER; -.  
 DR BRENDA; 1.2.1.12; 984.  
 DR Reactome; R-SCE-70171; Glycolysis.  
 DR Reactome; R-SCE-70263; Gluconeogenesis.  
 DR SABIO-RK; P00359; -.  
 DR UniPathway; UPA00109; UER00184.  
 DR BioGRID-ORCS; 853106; 2 hits in 10 CRISPR screens.  
 DR PRO; PR:P00359; -.  
 DR Proteomes; UP000002311; Chromosome VII.  
 DR RNAct; P00359; Protein.  
 DR GO; GO:0005737; C:cytoplasm; HDA:SGD.  
 DR GO; GO:0005829; C:cytosol; IDA:SGD.  
 DR GO; GO:0009277; C:fungal-type cell wall; IDA:SGD.  
 DR GO; GO:0005811; C:lipid droplet; IDA:SGD.  
 DR GO; GO:0005739; C:mitochondrion; IDA:SGD.  
 DR GO; GO:0005634; C:nucleus; HDA:SGD.  
 DR GO; GO:0005886; C:plasma membrane; HDA:SGD.  
 DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity; IDA:SGD.  
 DR GO; GO:1904408; F:melatonin binding; IDA:SGD.  
 DR GO; GO:0051287; F:NAD binding; IEA:InterPro.  
 DR GO; GO:0050661; F:NADP binding; IEA:InterPro.  
 DR GO; GO:0003723; F:RNA binding; IDA:SGD.  
 DR GO; GO:0006915; P:apoptotic process; IMP:SGD.  
 DR GO; GO:0006094; P:gluconeogenesis; IEP:SGD.  
 DR GO; GO:0006096; P:glycolytic process; IEP:SGD.  
 DR GO; GO:0015886; P:heme transport; IMP:SGD.  
 DR GO; GO:0072593; P:reactive oxygen species metabolic process; IMP:SGD.  
 DR Gene3D; 3.40.50.720; NAD(P)-binding Rossmann-like Domain; 1.  
 DR InterPro; IPR020831; GlycerAld/Erythrose\_P\_DH.  
 DR InterPro; IPR020830; GlycerAld\_3-P\_DH\_AS.  
 DR InterPro; IPR020829; GlycerAld\_3-P\_DH\_cat.  
 DR InterPro; IPR020828; GlycerAld\_3-P\_DH\_NAD(P)-bd.  
 DR InterPro; IPR006424; Glyceraldehyde-3-P\_DH\_1.  
 DR InterPro; IPR036291; NAD(P)-bd\_dom\_sf.  
 DR NCBIfam; TIGR01534; GAPDH-I; 1.  
 DR PANTHER; PTHR10836; GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE; 1.  
 DR PANTHER; PTHR10836:SF76; GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE-RELATED; 1.  
 DR Pfam; PF02800; Gp\_dh\_C; 1.  
 DR Pfam; PF00044; Gp\_dh\_N; 1.  
 DR PIRSF; PIRSF000149; GAP\_DH; 1.  
 DR PRINTS; PR00078; G3PDHDRGNASE.  
 DR SMART; SM00846; Gp\_dh\_N; 1.  
 DR SUPFAM; SSF55347; Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain; 1.  
 DR SUPFAM; SSF51735; NAD(P)-binding Rossmann-fold domains; 1.  
 DR PROSITE; PS00071; GAPDH; 1.  
 PE 1: Evidence at protein level;  
 KW 3D-structure; Cytoplasm; Direct protein sequencing; Glycolysis;  
 KW Isopeptide bond; Mitochondrion; NAD; Oxidoreductase; Phosphoprotein;  
 KW Reference proteome; Ubl conjugation.  
 FT INIT\_MET 1  
 FT /note="Removed"  
 FT /evidence="ECO:0000269|PubMed:11946592"  
 FT CHAIN 2..332  
 FT /note="Glyceraldehyde-3-phosphate dehydrogenase 3"  
 FT /id="PRO\_0000145591"  
 FT ACT\_SITE 150  
 FT /note="Nucleophile"  
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU10009"  
 FT BINDING 11  
 FT /ligand="NAD(+)"  
 FT /ligand\_id="ChEBI:CHEBI:57540"  
 FT /evidence="ECO:0007744|PDB:3PYM"  
 FT BINDING 12  
 FT /ligand="NAD(+)"  
 FT /ligand\_id="ChEBI:CHEBI:57540"  
 FT /evidence="ECO:0007744|PDB:3PYM"  
 FT BINDING 33  
 FT /ligand="NAD(+)"  
 FT /ligand\_id="ChEBI:CHEBI:57540"  
 FT /evidence="ECO:0007744|PDB:3PYM"  
 FT BINDING 120  
 FT /ligand="NAD(+)"  
 FT /ligand\_id="ChEBI:CHEBI:57540"  
 FT /evidence="ECO:0007744|PDB:3PYM"  
 FT BINDING 149..151  
 FT /ligand="D-glyceraldehyde 3-phosphate"  
 FT /ligand\_id="ChEBI:CHEBI:59776"  
 FT /evidence="ECO:0000250|UniProtKB:P22513"  
 FT BINDING 180  
 FT /ligand="D-glyceraldehyde 3-phosphate"  
 FT /ligand\_id="ChEBI:CHEBI:59776"  
 FT /evidence="ECO:0000250|UniProtKB:P22513"  
 FT BINDING 209..210  
 FT /ligand="D-glyceraldehyde 3-phosphate"  
 FT /ligand\_id="ChEBI:CHEBI:59776"  
 FT /evidence="ECO:0000250|UniProtKB:P22513"  
 FT BINDING 232  
 FT /ligand="D-glyceraldehyde 3-phosphate"

FT		/ligand_id="ChEBI:CHEBI:59776"
FT		/evidence="ECO:0000250 UniProtKB:P22513"
FT	BINDING	314
FT		/ligand="NAD(+)"
FT		/ligand_id="ChEBI:CHEBI:57540"
FT		/evidence="ECO:0007744 PDB:3PYM"
FT	BINDING	318
FT		/ligand="NAD(+)"
FT		/ligand_id="ChEBI:CHEBI:57540"
FT		/evidence="ECO:0007744 PDB:3PYM"
FT	SITE	177
FT		/note="Activates thiol group during catalysis"
FT		/evidence="ECO:0000250 UniProtKB:P04406"
FT	MOD_RES	302
FT		/note="Phosphoserine"
FT		/evidence="ECO:0007744 PubMed:18407956"
FT	CROSSLNK	46
FT		/note="Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)"
FT		/evidence="ECO:0007744 PubMed:22106047"
FT	CROSSLNK	63
FT		/note="Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)"
FT		/evidence="ECO:0007744 PubMed:22106047"
FT	CONFLICT	136
FT		/note="E -> V (in Ref. 1; CAA24607/AAA88714)"
FT		/evidence="ECO:0000305"
FT	CONFLICT	248
FT		/note="N -> D (in Ref. 1; CAA24607/AAA88714)"
FT		/evidence="ECO:0000305"
FT	CONFLICT	287
FT		/note="D -> G (in Ref. 5; AAS56157)"
FT		/evidence="ECO:0000305"
FT	CONFLICT	329
FT		/note="V -> I (in Ref. 1; CAA24607/AAA88714)"
FT		/evidence="ECO:0000305"
FT	STRAND	3..7
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	11..22
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	27..32
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	38..46
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	TURN	49..51
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	58..60
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	62..67
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	70..75
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	80..82
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	TURN	85..89
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	91..95
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	97..100
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	103..111
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	115..121
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	124..126
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	TURN	131..133
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	135..137
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	144..146
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	150..166
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	168..178
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	183..187
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	195..197
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	200..202
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	205..208
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	211..218
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	220..222
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	225..234
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	STRAND	239..249
FT		/evidence="ECO:0007829 PDB:3PYM"
FT	HELIX	253..265



```

FT          /evidence="ECO:0007829|PDB:3PYM"
FT  TURN   266..271
FT          /evidence="ECO:0007829|PDB:3PYM"
FT  STRAND  272..275
FT          /evidence="ECO:0007829|PDB:3PYM"
FT  HELIX   281..284
FT          /evidence="ECO:0007829|PDB:3PYM"
FT  STRAND  290..294
FT          /evidence="ECO:0007829|PDB:3PYM"
FT  HELIX   295..297
FT          /evidence="ECO:0007829|PDB:3PYM"
FT  STRAND  299..302
FT          /evidence="ECO:0007829|PDB:3PYM"
FT  STRAND  305..312
FT          /evidence="ECO:0007829|PDB:3PYM"
FT  HELIX   316..331
FT          /evidence="ECO:0007829|PDB:3PYM"
SQ  SEQUENCE  332 AA;  35747 MW;  6CFFFE7061BC36F CRC64;
MVRVAINGFG RIGRLVMRIA LSRPNVEVVA LNDPFITNDY AAYMFKYDST HGRYAGEVSH
DDKHIIVDGK KIATYQERDP ANLPWGSSNV DIAIDSTGVF KELDTAQKHI DAGAKKVIT
APSSTAPMFV MGVNEEKYTS DLKIVSNASC TTNCLAPLAK VINDAFGIEE GLMTTVHSLT
ATQKTVDGFS HKDWRGGRTA SGNIIPSSTG AAKAVGKVLV ELQGKLTGMA FRVPTVDVSV
VDLTVKLNKE TTYDEIKKVV KAAAEGLKLG VLGYTEDAVV SSDFLGDSHS SIFDASAGIQ
LSPKFVKLVS WYDNEYGYST RVVDLVEHVA KA

```

**Mascot:** <http://www.matrixscience.com/>

# MASCOT Search Results

## Peptide View

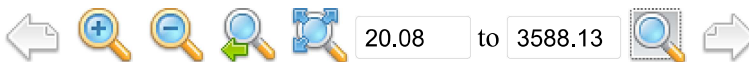
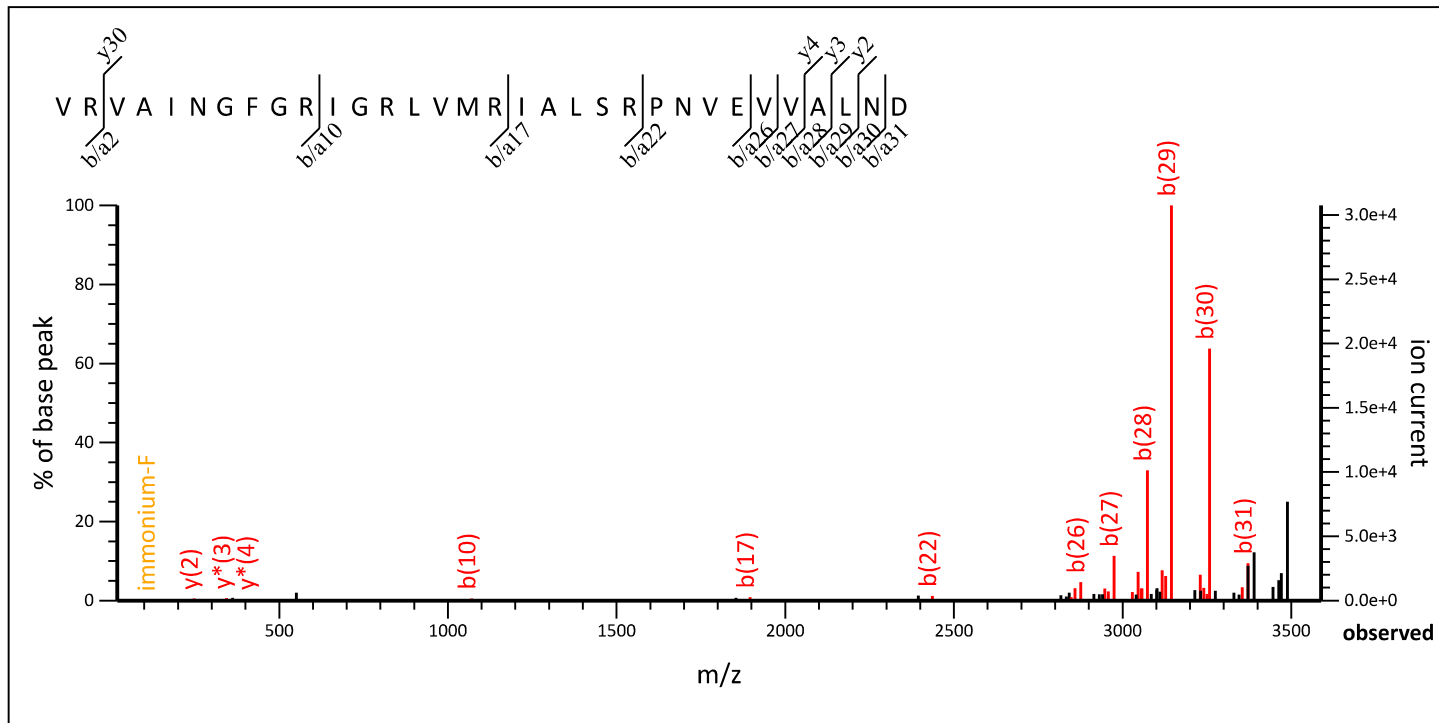
MS/MS Fragmentation of **VRVAINGFGRIGRLVMRIALSRPNVEVVVALND**

Found in **G3P3\_YEAST** in **Swissprot\_22\_05\_2024**, Glyceraldehyde-3-phosphate dehydrogenase 3 OS=*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) OX=559292 GN=TDH3 PE=1 SV=3

Match to Query 1: 3504.091724 from(3505.099000,1+) intensity(113753.4242) index(0)

Title: Reading Top-Down experiment

Data file S\_cerevisiae\_3500\_Da\_merged.txt



Monoisotopic mass of neutral peptide Mr(calc): 3503.9987

Ions Score: 55 Expect: 0.00097

Peak matches: 27/542 fragment ions using 36 most intense peaks

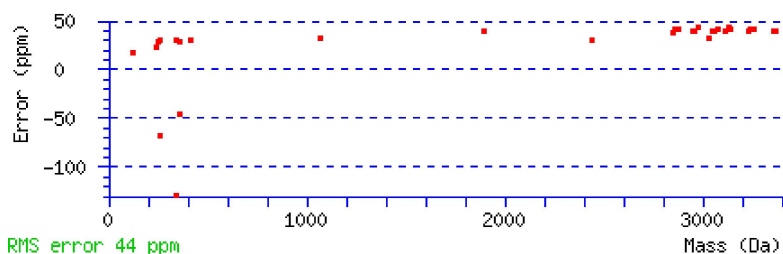
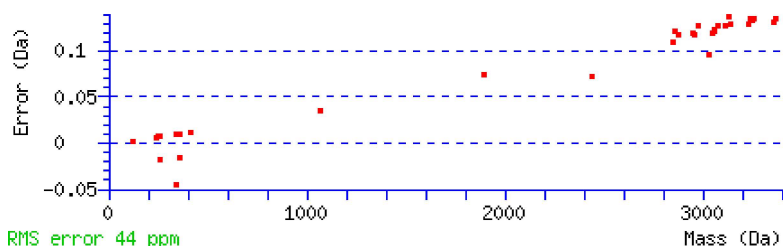
Annotated fragments: 35/542 ([help](#))

#	Immon.	a	a*	a <sup>0</sup>	b	b*	b <sup>0</sup>	Seq.	y	y*	y <sup>0</sup>	#
1	72.0808	72.0808			100.0757			V				32
2	129.1135	228.1819	211.1553		256.1768	239.1503		R	3405.9376	3388.9110	3387.9270	31
3	72.0808	327.2503	310.2238		355.2452	338.2187		V	3249.8365	3232.8099	3231.8259	30
4	44.0495	398.2874	381.2609		426.2823	409.2558		A	3150.7681	3133.7415	3132.7575	29
5	86.0964	511.3715	494.3449		539.3664	522.3398		I	3079.7310	3062.7044	3061.7204	28
6	87.0553	625.4144	608.3879		653.4093	636.3828		N	2966.6469	2949.6203	2948.6363	27
7	30.0338	682.4359	665.4093		710.4308	693.4042		G	2852.6040	2835.5774	2834.5934	26
8	120.0808	829.5043	812.4777		857.4992	840.4726		F	2795.5825	2778.5559	2777.5719	25
9	30.0338	886.5257	869.4992		914.5207	897.4941		G	2648.5141	2631.4875	2630.5035	24
10	129.1135	1042.6269	1025.6003		1070.6218	1053.5952		R	2591.4926	2574.4661	2573.4821	23

11	86.0964	1155.7109	1138.6844		1183.7058	1166.6793		I	2435.3915	2418.3650	2417.3809	22
12	30.0338	1212.7324	1195.7058		1240.7273	1223.7008		G	2322.3074	2305.2809	2304.2969	21
13	129.1135	1368.8335	1351.8069		1396.8284	1379.8019		R	2265.2860	2248.2594	2247.2754	20
14	86.0964	1481.9176	1464.8910		1509.9125	1492.8859		L	2109.1849	2092.1583	2091.1743	19
15	72.0808	1580.9860	1563.9594		1608.9809	1591.9543		V	1996.1008	1979.0743	1978.0902	18
16	104.0528	1712.0265	1694.9999		1740.0214	1722.9948		M	1897.0324	1880.0058	1879.0218	17
17	129.1135	1868.1276	1851.1010		1896.1225	1879.0959		R	1765.9919	1748.9654	1747.9813	16
18	86.0964	1981.2116	1964.1851		2009.2066	1992.1800		I	1609.8908	1592.8642	1591.8802	15
19	44.0495	2052.2487	2035.2222		2080.2437	2063.2171		A	1496.8067	1479.7802	1478.7962	14
20	86.0964	2165.3328	2148.3063		2193.3277	2176.3012		L	1425.7696	1408.7431	1407.7591	13
21	60.0444	2252.3648	2235.3383	2234.3543	2280.3598	2263.3332	2262.3492	S	1312.6856	1295.6590	1294.6750	12
22	129.1135	2408.4660	2391.4394	2390.4554	2436.4609	2419.4343	2418.4503	R	1225.6535	1208.6270	1207.6430	11
23	70.0651	2505.5187	2488.4922	2487.5082	2533.5136	2516.4871	2515.5031	P	1069.5524	1052.5259	1051.5419	10
24	87.0553	2619.5616	2602.5351	2601.5511	2647.5566	2630.5300	2629.5460	N	972.4997	955.4731	954.4891	9
25	72.0808	2718.6301	2701.6035	2700.6195	2746.6250	2729.5984	2728.6144	V	858.4567	841.4302	840.4462	8
26	102.0550	2847.6727	2830.6461	2829.6621	2875.6676	2858.6410	2857.6570	E	759.3883	742.3618	741.3777	7
27	72.0808	2946.7411	2929.7145	2928.7305	2974.7360	2957.7094	2956.7254	V	630.3457	613.3192	612.3352	6
28	72.0808	3045.8095	3028.7829	3027.7989	3073.8044	3056.7778	3055.7938	V	531.2773	514.2508	513.2667	5
29	44.0495	3116.8466	3099.8200	3098.8360	3144.8415	3127.8150	3126.8309	A	432.2089	415.1823	414.1983	4
30	86.0964	3229.9307	3212.9041	3211.9201	3257.9256	3240.8990	3239.9150	L	361.1718	344.1452	343.1612	3
31	87.0553	3343.9736	3326.9470	3325.9630	3371.9685	3354.9419	3353.9579	N	248.0877	231.0612	230.0771	2
32	88.0393							D	134.0448		116.0342	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RV	228.1819	256.1768	RVA	299.2190	327.2139	RVAI	412.3031	440.2980
RVAIN	526.3460	554.3409	RVAING	583.3675	611.3624	VA	143.1179	171.1128
VAI	256.2020	284.1969	VAIN	370.2449	398.2398	VAING	427.2663	455.2613
VAINGF	574.3348	602.3297	VAINGFG	631.3562	659.3511	AI	157.1335	185.1285
AIN	271.1765	299.1714	AING	328.1979	356.1928	AINGF	475.2663	503.2613
AINGFG	532.2878	560.2827	AINGFR	688.3889		IN	200.1394	228.1343
ING	257.1608	285.1557	INGF	404.2292	432.2241	INGFG	461.2507	489.2456
INGFR	617.3518	645.3467	NG	144.0768	172.0717	NGF	291.1452	319.1401
NGFG	348.1666	376.1615	NGFR	504.2677	532.2627	NGFRIG	617.3518	645.3467
NGFRIG	674.3733		GF	177.1022	205.0972	GFG	234.1237	262.1186
GFR	390.2248	418.2197	GFRIG	503.3089	531.3038	GFRIG	560.3303	588.3253
FG	177.1022	205.0972	FGR	333.2034	361.1983	FRIG	446.2874	474.2823
FRIG	503.3089	531.3038	FRIGR	659.4100	687.4049	GR	186.1349	214.1299
GRI	299.2190	327.2139	GRIG	356.2405	384.2354	GRIGR	512.3416	540.3365
GRIGRL	625.4256	653.4206	RI	242.1975	270.1925	RIG	299.2190	327.2139
RIGR	455.3201	483.3150	RIGRL	568.4042	596.3991	RIGRLV	667.4726	695.4675
IG	143.1179	171.1128	IGR	299.2190	327.2139	IGRL	412.3031	440.2980
IGRLV	511.3715	539.3664	IGRLVM	642.4120	670.4069	GRL	299.2190	327.2139
GRLV	398.2874	426.2823	GRLVM	529.3279	557.3228	GRLVMR	685.4290	
RL	242.1975	270.1925	RLV	341.2660	369.2609	RLVM	472.3064	500.3014
RLVMR	628.4075	656.4025	LV	185.1648	213.1598	LVM	316.2053	344.2002

<b>LVMR</b>	472.3064	500.3014	<b>LVMRI</b>	585.3905	613.3854	<b>LVMRIA</b>	656.4276	684.4225
<b>VM</b>	203.1213	231.1162	<b>VMR</b>	359.2224	387.2173	<b>VMRI</b>	472.3064	500.3014
<b>VMRIA</b>	543.3435	571.3385	<b>VMRIAL</b>	656.4276	684.4225	<b>MR</b>	260.1540	288.1489
<b>MRI</b>	373.2380	401.2329	<b>MRIA</b>	444.2751	472.2701	<b>MRIAL</b>	557.3592	585.3541
<b>MRIALS</b>	644.3912	672.3861	<b>RIA</b>	313.2347	341.2296	<b>RIAL</b>	426.3187	454.3136
<b>RIALS</b>	513.3507	541.3457	<b>RIALSR</b>	669.4519	697.4468	<b>IA</b>	157.1335	185.1285
<b>IAL</b>	270.2176	298.2125	<b>IALS</b>	357.2496	385.2445	<b>IALSR</b>	513.3507	541.3457
<b>IALSRP</b>	610.4035	638.3984	<b>AL</b>	157.1335	185.1285	<b>ALS</b>	244.1656	272.1605
<b>ALSR</b>	400.2667	428.2616	<b>ALSRP</b>	497.3194	525.3144	<b>ALSRPN</b>	611.3624	639.3573
<b>LS</b>	173.1285	201.1234	<b>LSR</b>	329.2296	357.2245	<b>LSRP</b>	426.2823	454.2772
<b>LSRPN</b>	540.3253	568.3202	<b>LSRPNV</b>	639.3937	667.3886	<b>SR</b>	216.1455	244.1404
<b>SRP</b>	313.1983	341.1932	<b>SRPN</b>	427.2412	455.2361	<b>SRPNV</b>	526.3096	554.3045
<b>SRPNVE</b>	655.3522	683.3471	<b>RP</b>	226.1662	254.1612	<b>RPN</b>	340.2092	368.2041
<b>RPNV</b>	439.2776	467.2725	<b>RPNVE</b>	568.3202	596.3151	<b>RPNVEV</b>	667.3886	695.3835
<b>PN</b>	184.1081	212.1030	<b>PNV</b>	283.1765	311.1714	<b>PNVE</b>	412.2191	440.2140
<b>PNVEV</b>	511.2875	539.2824	<b>PNVEVV</b>	610.3559	638.3508	<b>PNVEVVA</b>	681.3930	
<b>NV</b>	186.1237	214.1186	<b>NVE</b>	315.1663	343.1612	<b>NVEV</b>	414.2347	442.2296
<b>NVEVV</b>	513.3031	541.2980	<b>NVEVVA</b>	584.3402	612.3352	<b>NVEVVAL</b>	697.4243	
<b>VE</b>	201.1234	229.1183	<b>VEV</b>	300.1918	328.1867	<b>VEVV</b>	399.2602	427.2551
<b>VEVVA</b>	470.2973	498.2922	<b>VEVVAL</b>	583.3814	611.3763	<b>VEVVALN</b>	697.4243	
<b>EV</b>	201.1234	229.1183	<b>EVV</b>	300.1918	328.1867	<b>EVVA</b>	371.2289	399.2238
<b>EVVAL</b>	484.3130	512.3079	<b>EVVALN</b>	598.3559	626.3508	<b>VV</b>	171.1492	199.1441
<b>VVA</b>	242.1863	270.1812	<b>VVAL</b>	355.2704	383.2653	<b>VVALN</b>	469.3133	497.3082
<b>VAL</b>	256.2020	284.1969	<b>VALN</b>	370.2449	398.2398	<b>ALN</b>	271.1765	299.1714
<b>LN</b>	200.1394	228.1343						



NCBI **BLAST** search of [VRVAINGFGRIGRLVMRIALSRPNVEVVALND](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence

55.4	3503.9987	0.0930	<a href="#">VRVAINGFGRIGRLVMRIALSRPNVEVVALND</a>
22.3	3504.0603	0.0315	<a href="#">FPLVTVRDMVRAQARLLDLLGVRRL LAVIGGS</a>
22.2	3504.0416	0.0501	<a href="#">VSIANGFGRIGRLVLRALERKNIDVVAIND</a>
22.0	3504.0052	0.0865	<a href="#">KPKVGINGFGRIGRLALRAAVEKDTVQVVAIND</a>
17.7	3503.9576	0.1341	<a href="#">ENLHKQFSSKQLAKTKIVGNPVRKEIVALND</a>
15.3	3503.9562	0.1355	<a href="#">DDKDLARALEKKAKEKGVQLLLPSDVVLADN</a>
14.4	3503.9552	0.1365	<a href="#">FKDKLKAKKFFSKFIRCNP IYLMLLALDN</a>
14.2	3503.9688	0.1229	<a href="#">DALDVTFHAKLGTQGARVARIRALAKELAAITGA</a>
13.9	3503.9861	0.1056	<a href="#">RLVQALVACAEAVQLENLSLADALVKRVGLLAAS</a>
13.8	3504.0484	0.0434	<a href="#">TASTVVLPTLRKIFPFIVGTVP AIKPAAALSQT</a>

**Mascot:** <http://www.matrixscience.com/>