

Protein View: VDAC1_YEAST

Mitochondrial outer membrane protein porin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POR1 PE=1 SV=4

Database: SwissProt
 Score: 74
 Expect: 0.00033
 Monoisotopic mass (M_r): 30524
 Calculated pI: 7.70
 Taxonomy: Saccharomyces cerevisiae S288C

Sequence similarity is available as [an NCBI BLAST search of VDAC1_YEAST against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
 Fixed modifications: Carbamidomethyl (C)
 Variable modifications: Oxidation (M)
 Mass values searched: 38
 Mass values matched: 8

Protein sequence coverage: 44%

Matched peptides shown in **bold red**.

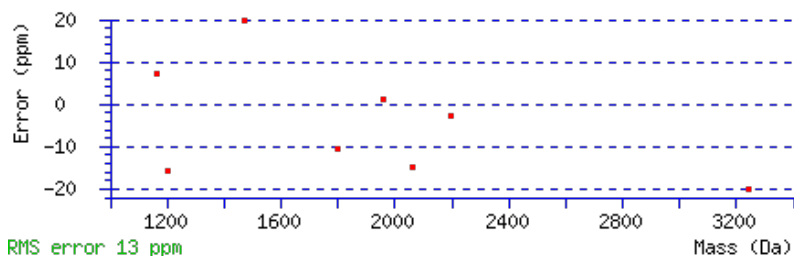
1 MSPPVYSDIS RNINDLLNKD FYHATPAAFD VQTTTANGIK FSLKAKQPVK
 51 DGPLSTNVEA KLNDK**QTGLG** **LTQGSNTNN** **LQTKLEFANL** **TPGLKNELIT**
 101 SLTPGVAK**SA** **VLNTTFTQPF** **FTARGAFDLC** **LKSPTFVGDL** **TMAHEGIVGG**
 151 **Aefgydisag** **SISRYAMALS** **YFAKDYSLGA** TLNNEQITTV DFFQNVNAFL
 201 QVGAK**ATMNC** **KLPSNVNIE** **FATRYLPDAS** SQVKAKVSDS GIVTLAYK**QL**
 251 **LRPGVTLGVG** **SSFDALKLSE** PVHKLGWLSL FDA

Unformatted sequence string: **283 residues** (for pasting into other applications).

Sort by residue number increasing mass decreasing mass
 Show matched peptides only predicted peptides also

Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Peptide
66 – 84	2061.0050	2059.9977	2060.0287	-15.0	0	K.QTGLGLTQGSNTNNLQTK.L
85 – 95	1202.6590	1201.6517	1201.6707	-15.8	0	K.LEFANLTPGLK.N
109 – 124	1800.9090	1799.9017	1799.9207	-10.5	0	K.SAVLNTTFTQPFFAR.G
133 – 164	3241.4820	3240.4747	3240.5398	-20.1	0	K.SPTFVGDLTMAHEGIVGGAefgydisagsISR.Y
165 – 174	1164.5840	1163.5767	1163.5685	7.08	0	R.YAMALSYFAK.D
206 – 224	2196.0480	2195.0407	2195.0463	-2.54	1	K.ATMNCKLPNSNVNIEFATR.Y + Oxidation (M)
212 – 224	1474.7940	1473.7867	1473.7576	19.8	0	K.LPNSNVNIEFATR.Y
249 – 267	1958.1090	1957.1017	1957.0997	1.05	0	K.QLLRPGVTLGVGSSFDALK.L

No match to: 804.3070, 806.3130, 826.2770, 833.0800, 842.2670, 855.0700, 871.0370, 877.0420, 893.0620, 1093.5430, 1109.5110, 1224.7160, 1240.6910, 1378.7250, 1727.7770, 1764.7510, 1822.9080, 1838.8760, 1884.8380, 1941.0750, 2043.9810, 2083.0020, 2098.9870, 2267.0400, 2269.0510, 2291.0440, 2307.0180, 2324.1260, 2864.3240, 3084.4220



ID VDAC1_YEAST Reviewed; 283 AA.
AC P04840; D6W1C3;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT 23-JAN-2007, sequence version 4.
DT 29-SEP-2021, entry version 196.
DE RecName: Full=Mitochondrial outer membrane protein porin 1;
DE AltName: Full=Voltage-dependent anion-selective channel protein 1;
DE Short=VDAC-1;
GN Name=POR1; Synonyms=OMP2, VDAC1; OrderedLocusNames=YNL055C;
GN ORFNames=N2441, YNL2441C;
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 [MRNA].
RX PubMed=2408884; DOI=10.1002/j.1460-2075.1985.tb03695.x;
RA Mihara K., Sato R.;
RT "Molecular cloning and sequencing of cDNA for yeast porin, an outer
RT mitochondrial membrane protein: a search for targeting signal in the
RT primary structure.";
RL EMBO J. 4:769-774(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed=2442148; DOI=10.1007/bf00768537;
RA Forte M.A., Guy H.R., Mannella C.A.;
RT "Molecular genetics of the VDAC ion channel: structural model and sequence
RT analysis.";
RL J. Bioenerg. Biomembr. 19:341-350(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=S288c / FY1676;
RX PubMed=8533472; DOI=10.1002/yea.320111008;
RA Bergez P., Doignon F., Crouzet M.;
RT "The sequence of a 44 420 bp fragment located on the left arm of chromosome
RT XIV from Saccharomyces cerevisiae.";
RL Yeast 11:967-974(1995).
RN [4]
RP ERRATUM OF PUBMED:8533472.
RX PubMed=8904343;
RX DOI=10.1002/(sici)1097-0061(19960315)12:3<297::aid-yea940>3.0.co;2-d;
RA Bergez P., Doignon F., Crouzet M.;
RL Yeast 12:297-297(1996).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 204508 / S288c;
RX PubMed=9169873;
RA Philippsen P., Kleine K., Pohlmann R., Duesterhoeft A., Hamberg K.,
RA Hegemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K.,
RA Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,
RA Beinhauer J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F.,
RA Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F., Doignon F.,
RA Domzey H., Dubois E., Fiedler T.A., Fleig U., Floeth M., Fritz C.,
RA Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N., Goffeau A.,
RA Geldener U., Herbert C.J., Heumann K., Heuss-Neitzel D., Hilbert H.,
RA Hinni K., Iraqui Houssaini I., Jacquet M., Jimenez A., Jonniaux J.-L.,
RA Karpfinger-Hartl L., Lanfranchi G., Lepingle A., Levesque H., Lyck R.,
RA Maftahi M., Mallet L., Maurer C.T.C., Messenguy F., Mewes H.-W., Moestl D.,
RA Nasr F., Nicaud J.-M., Niedenthal R.K., Pandolfo D., Pierard A.,
RA Piravandi E., Planta R.J., Pohl T.M., Purnelle B., Rebischung C.,
RA Remacha M.A., Revuelta J.L., Rinke M., Saiz J.E., Sartorello F.,
RA Scherens B., Sen-Gupta M., Soler-Mira A., Urbanus J.H.M., Valle G.,
RA Van Dyck L., Verhasselt P., Vierendeels F., Vissers S., Voet M.,
RA Volckaert G., Wach A., Wambutt R., Wedler H., Zollner A., Hani J.;

RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XIV and its
RT evolutionary implications.";
RL Nature 387:93-98(1997).
RN [6]
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 [7]
RP PROTEIN SEQUENCE OF 2-40; 45-108; 125-132; 165-174; 206-234 AND 237-274,
RP CLEAVAGE OF INITIATOR METHIONINE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RA Bienvenut W.V., Peters C.;
RL Submitted (MAY-2005) to UniProtKB.
RN [8]
RP MUTAGENESIS OF LYS-61.
RX PubMed=2478533; DOI=10.1007/bf00762519;
RA Blachly-Dyson E., Peng S.Z., Colombini M., Forte M.A.;
RT "Probing the structure of the mitochondrial channel, VDAC, by site-directed
RT mutagenesis: a progress report.";
RL J. Bioenerg. Biomembr. 21:471-483(1989).
RN [9]
RP MUTAGENESIS OF LYS-19 AND ASP-51.
RA Thomas L., Blachly-Dyson E., Colombini M., Forte M.A.;
RT "Probing for the voltage sensor of the VDAC ion channel by site-directed
RT mutagenesis.";
RL Biophys. J. 59:215A-215A(1991).
RN [10]
RP FUNCTION.
RX PubMed=9435273; DOI=10.1007/s002329900324;
RA Lee A.C., Xu X., Blachly-Dyson E., Forte M.A., Colombini M.;
RT "The role of yeast VDAC genes on the permeability of the mitochondrial
RT outer membrane.";
RL J. Membr. Biol. 161:173-181(1998).
RN [11]
RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-109, AND IDENTIFICATION BY
RP MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RC STRAIN=ATCC 76625 / YPH499;
RX PubMed=17761666; DOI=10.1074/mcp.m700098-mcp200;
RA Reinders J., Wagner K., Zahedi R.P., Stojanovski D., Eyrich B.,
RA van der Laan M., Rehling P., Sickmann A., Pfanner N., Meisinger C.;
RT "Profiling phosphoproteins of yeast mitochondria reveals a role of
RT phosphorylation in assembly of the ATP synthase.";
RL Mol. Cell. Proteomics 6:1896-1906(2007).
RN [12]
RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT THR-117, AND IDENTIFICATION BY
RP 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
RT analysis.";
RL Mol. Cell. Proteomics 7:1389-1396(2008).
RN [13]
RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-109, AND IDENTIFICATION BY
RP 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
RT into evolution.";
RL Science 325:1682-1686(2009).
RN [14]
RP INTERACTION WITH AIM5; FCJ1 AND MOS1.
RX PubMed=21987634; DOI=10.1083/jcb.201107053;
RA Hoppins S., Collins S.R., Cassidy-Stone A., Hummel E., Devay R.M.,
RA Lackner L.L., Westermann B., Schuldiner M., Weissman J.S., Nunnari J.;
RT "A mitochondrial-focused genetic interaction map reveals a scaffold-like
RT complex required for inner membrane organization in mitochondria.";
RL J. Cell Biol. 195:323-340(2011).
RN [15]
RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RX PubMed=22814378; DOI=10.1073/pnas.1210303109;
RA Van Damme P., Lasa M., Polevoda B., Gazquez C., Elosegui-Artola A.,
RA Kim D.S., De Juan-Pardo E., Demeyer K., Hole K., Larrea E., Timmerman E.,

RA Prieto J., Arnesen T., Sherman F., Gevaert K., Aldabe R.;
 RT "N-terminal acetylome analyses and functional insights of the N-terminal
 RT acetyltransferase NatB.";
 RL Proc. Natl. Acad. Sci. U.S.A. 109:12449-12454(2012).
 CC -!- FUNCTION: Forms a channel through the cell membrane that allows
 CC diffusion of small hydrophilic molecules. The channel adopts an open
 CC conformation at low or zero membrane potential and a closed
 CC conformation at potentials above 30-40 mV. The open state has a weak
 CC anion selectivity whereas the closed state is cation-selective. Is the
 CC major permeability factor of the mitochondrial outer membrane.
 CC {ECO:0000269|PubMed:9435273}.
 CC -!- SUBUNIT: Interacts with AIM5, FCJ1 and MOS1.
 CC {ECO:0000269|PubMed:21987634}.
 CC -!- SUBCELLULAR LOCATION: Mitochondrion outer membrane.
 CC -!- DOMAIN: Consists mainly of membrane-spanning sided beta-sheets. 19
 CC strands distributed along the entire VDAC protein, have the potential
 CC to adopt transmembrane beta pleated sheet structures, which rolled
 CC together may form a 'beta-barrel' type structure, possessing pore
 CC dimensions.
 CC -!- SIMILARITY: Belongs to the eukaryotic mitochondrial porin family.
 CC {ECO:0000305}.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <https://www.uniprot.org/terms>
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 CC -----
 DR EMBL; X02324; CAA26184.1; -; mRNA.
 DR EMBL; M34907; AAA35208.1; -; mRNA.
 DR EMBL; U12141; AAA99656.1; -; Genomic_DNA.
 DR EMBL; Z71331; CAA95926.1; -; Genomic_DNA.
 DR EMBL; BK006947; DAA10489.1; -; Genomic_DNA.
 DR PIR; S58721; MMBYP.
 DR RefSeq; NP_014343.1; NM_001182894.1.
 DR SMR; P04840; -.
 DR BioGRID; 35766; 450.
 DR DIP; DIP-6453N; -.
 DR IntAct; P04840; 91.
 DR MINT; P04840; -.
 DR STRING; 4932.YNL055C; -.
 DR TCDB; 1.B.8.1.1; the mitochondrial and plastid porin (mpp) family.
 DR iPTMnet; P04840; -.
 DR UCD-2DPAGE; P04840; -.
 DR MaxQB; P04840; -.
 DR PaxDb; P04840; -.
 DR PRIDE; P04840; -.
 DR DNASU; 855669; -.
 DR EnsemblFungi; YNL055C_mRNA; YNL055C; YNL055C.
 DR GeneID; 855669; -.
 DR KEGG; sce:YNL055C; -.
 DR SGD; S000005000; POR1.
 DR VEuPathDB; FungiDB:YNL055C; -.
 DR eggNOG; KOG3126; Eukaryota.
 DR GeneTree; ENSGT00950000182869; -.
 DR HOGENOM; CLU_044399_0_1_1; -.
 DR InParanoid; P04840; -.
 DR OMA; GYTTPPLY; -.
 DR Reactome; R-SCE-70268; Pyruvate metabolism.
 DR PRO; PR:P04840; -.
 DR Proteomes; UP000002311; Chromosome XIV.
 DR RNaAct; P04840; protein.
 DR GO; GO:0005737; C:cytoplasm; HDA:SGD.
 DR GO; GO:0031307; C:integral component of mitochondrial outer membrane; IDA:SGD.
 DR GO; GO:0005758; C:mitochondrial intermembrane space; TAS:Reactome.
 DR GO; GO:0005741; C:mitochondrial outer membrane; IDA:SGD.
 DR GO; GO:0005739; C:mitochondrion; IPI:SGD.
 DR GO; GO:0046930; C:pore complex; IEA:UniProtKB-KW.
 DR GO; GO:0015288; F:porin activity; IEA:UniProtKB-KW.
 DR GO; GO:0048039; F:ubiquinone binding; IDA:SGD.
 DR GO; GO:0008308; F:voltage-gated anion channel activity; IDA:SGD.
 DR GO; GO:0006915; P:apoptotic process; IMP:SGD.
 DR GO; GO:0045454; P:cell redox homeostasis; IMP:SGD.
 DR GO; GO:0051027; P:DNA transport; IMP:SGD.
 DR GO; GO:0006811; P:ion transport; IDA:SGD.
 DR GO; GO:0007005; P:mitochondrion organization; IMP:SGD.
 DR GO; GO:0042307; P:positive regulation of protein import into nucleus; IMP:SGD.
 DR GO; GO:0071902; P:positive regulation of protein serine/threonine kinase activity; IGI:SGD.
 DR CDD; cd07306; Porin3_VDAC; 1.

DR Gene3D; 2.40.160.10; -; 1.
DR InterPro; IPR023614; Porin_dom_sf.
DR InterPro; IPR001925; Porin_Euk.
DR InterPro; IPR027246; Porin_Euk/Tom40.
DR PANTHER; PTHR11743; PTHR11743; 1.
DR Pfam; PF01459; Porin_3; 1.
DR PRINTS; PR00185; EUKARYTPORIN.
DR PROSITE; PS00558; EUKARYOTIC_PORIN; 1.
PE 1: Evidence at protein level;
KW Direct protein sequencing; Ion transport; Membrane; Mitochondrion;
KW Mitochondrion outer membrane; Phosphoprotein; Porin; Reference proteome;
KW Transmembrane; Transmembrane beta strand; Transport.
FT INIT_MET 1
FT /note="Removed"
FT /evidence="ECO:0000269|Ref.7"
FT CHAIN 2..283
FT /note="Mitochondrial outer membrane protein porin 1"
FT /id="PRO_000050524"
FT MOD_RES 109
FT /note="Phosphoserine"
FT /evidence="ECO:0007744|PubMed:17761666,
FT ECO:0007744|PubMed:19779198"
FT MOD_RES 117
FT /note="Phosphothreonine"
FT /evidence="ECO:0007744|PubMed:18407956"
FT MUTAGEN 19
FT /note="K->E: 2.5-fold reduction in steepness of voltage
FT dependence."
FT /evidence="ECO:0000269|Ref.9"
FT MUTAGEN 51
FT /note="D->K: 2-fold increase in steepness of voltage
FT dependence."
FT /evidence="ECO:0000269|Ref.9"
FT MUTAGEN 61
FT /note="K->E: Alters the selectivity of VDAC."
FT /evidence="ECO:0000269|PubMed:2478533"
FT CONFLICT 118
FT /note="Q -> E (in Ref. 1; CAA26184 and 2; AAA35208)"
FT /evidence="ECO:0000305"
FT CONFLICT 203..207
FT /note="GAKAT -> AKATM (in Ref. 2; AAA35208)"
FT /evidence="ECO:0000305"
SQ SEQUENCE 283 AA; 30428 MW; C99D03711AF9B54D CRC64;
MSPPVYSDIS RNINDLLNKD FYHATPAAFD VQTTTANGIK FSLKAKQPVK DGPLSTNVEA
KLNDKQTGLG LTQGSNTNN LQTKLEFANL TPGLKNELIT SLTPGVAKSA VLNTTFTQPF
FTARGAFDLC LKSPTFVGD L TMAHEGIVGG AEFYDISAG SISRYAMALS YFAKDYSLGA
TLNNEQITTV DFFQNVNAFL QVGAKATMNC KLPNSNVNIE FATRYLPDAS SQVKAKVSDS
GIVTLAYKQL LRPGVTLGVG SSSFDALKLSE PVHKLGWLSL FDA

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