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# SignalP-5.0

## Summary of 1 predicted sequences from Eukarya

Predictions list. Use the help page for more detailed description of the output page.

### Predicted proteins

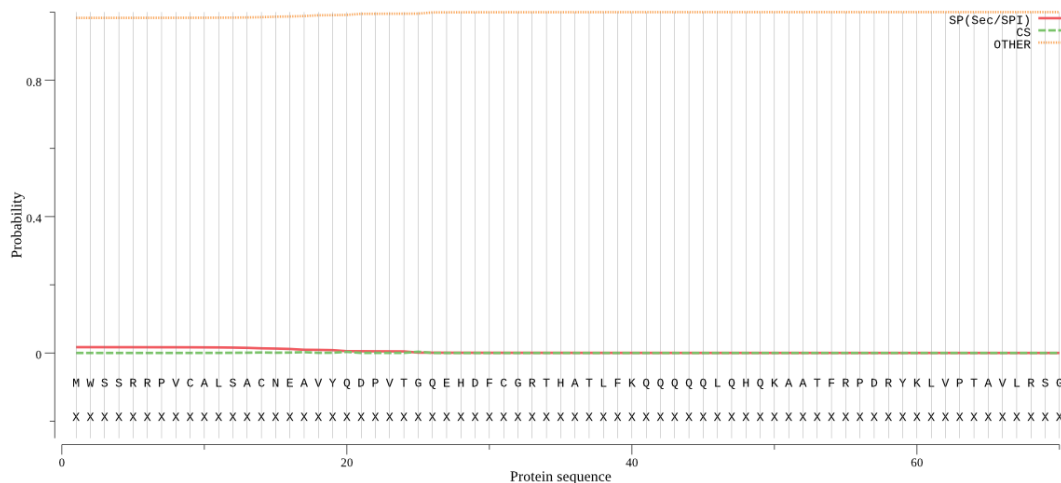
#### Sequence

Prediction: Other

Protein type	Signal Peptide (Sec/SPI)	Other
Likelihood	0.0167	0.9833

**Download:** PNG (/services/SignalP-5.0/tmp/5FDED0D00000654D26D5E92E/output\_Sequence\_plot.png) / EPS (/services/SignalP-5.0/tmp/5FDED0D00000654D26D5E92E/output\_Sequence\_plot.eps) / Tabular (/services/SignalP-5.0/tmp/5FDED0D00000654D26D5E92E/output\_Sequence\_pred.txt)

SignalP-5.0 prediction (Eukarya): Sequence



Scientific problems: Henrik Nielsen (mailto:henni@dtu.dk)

Technical problems: Support (mailto:webmaster@cbs.dtu.dk)



(/)

CBS (/index.html) >> CBS Prediction Servers (/services/) >> TargetP-2.0 (/services/TargetP-2.0/) >> Results

# TargetP-2.0

## Summary of 1 predicted sequences from Plant

Predictions list. Use the help page for more detailed description of the output page.

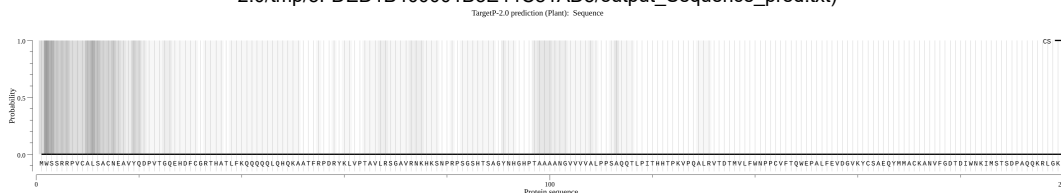
### Predicted proteins

#### Sequence

Prediction: Other

Protein type	Other	Signal peptide	Mitochondrial transfer peptide	Chloroplast transfer peptide	Thylakoid luminal transfer peptide
Likelihood	0.9807	0.0017	0.0095	0.0058	0.0024

Download: PNG (/services/TargetP-2.0/tmp/5FDED1B400001B3E44C81AD5/output\_Sequence\_plot.png) / EPS (/services/TargetP-2.0/tmp/5FDED1B400001B3E44C81AD5/output\_Sequence\_plot.eps) / Tabular (/services/TargetP-2.0/tmp/5FDED1B400001B3E44C81AD5/output\_Sequence\_pred.txt)



Scientific problems: Henrik Nielsen (mailto:hnielsen@cbs.dtu.dk)

Technical problems: Support (mailto:webmaster@cbs.dtu.dk)

# PSORT: Protein Subcellular Localization Prediction Tool

QUERY (391 aa)

```
MWSSRRPVCA LSACNEAVYQ DPVTGQEHDF CGRTHATLFK QQQQQQLQHOK AATFRPDTRYK
LVPTAVLRSG AVRNRKHSNP RPSGSHTSAG YNHGHPTAAA ANGVVVVALP PSAQQTLPTIT
HHTPKVPQAL RVTDTMVLFW NPPCVFTQWE PALFEVDGVK YCSAEQYMMMA CKANVFGDTD
IWNKIMSTSD PAQQKRLGKE VANYDHGIWN LCKVQFVLTG NYSKFTQNPG MCDQLLATGD
KMLAEASQHD KVGWIGMDAF DPNVERHECW RGQNLLGKIL MYVRNKIRWE RPDLASRRQV
QEAAAAMEAE HRLIPSNGRF VSAAGPAMTA DSLGALNMTA LQTQLHCPDM GLRAPVTAPP
TLGEPAPEVF IAAVAVQQNK ADTDAKTPSK N
```

## Results of Subprograms

PSG: a new signal peptide prediction method

N-region: length 6; pos.chg 2; neg.chg 0  
H-region: length 9; peak value 6.81  
PSG score: 2.41

GvH: von Heijne's method for signal seq. recognition

GvH score (threshold: -2.1): -5.85  
possible cleavage site: between 20 and 21

>>> Seems to have no N-terminal signal peptide

ALOM: Klein et al's method for TM region allocation

Init position for calculation: 1  
Tentative number of TMS(s) for the threshold 0.5: 0  
number of TMS(s) .. fixed  
PERIPHERAL Likelihood = 2.17 (at 97)  
ALOM score: 2.17 (number of TMSs: 0)

MTOP: Prediction of membrane topology (Hartmann et al.)

Center position for calculation: 6  
Charge difference: -6.5 C(-3.5) - N( 3.0)  
N >= C: N-terminal side will be inside

MITDISC: discrimination of mitochondrial targeting seq

R content:	2	Hyd Moment(75):	10.51
Hyd Moment(95):	8.53	G content:	0
D/E content:	1	S/T content:	3
Score:	-1.37		

Gavel: prediction of cleavage sites for mitochondrial preseq

R-2 motif at 16 RRP|VC

NUCDISC: discrimination of nuclear localization signals

pat4: none  
pat7: none  
bipartite: none  
content of basic residues: 10.2%  
NLS Score: -0.47

KDEL: ER retention motif in the C-terminus: none

#### ER Membrane Retention Signals:

XXRR-like motif in the N-terminus: WSSR

KKXX-like motif in the C-terminus: TPSK

SKL: peroxisomal targeting signal in the C-terminus: none

SKL2: 2nd peroxisomal targeting signal: none

VAC: possible vacuolar targeting motif: found  
TLPI at 116

RNA-binding motif: none

#### Actinin-type actin-binding motif:

type 1: none

type 2: none

NMYR: N-myristoylation pattern : none

Prenylation motif: none

memYQRL: transport motif from cell surface to Golgi: none

Tyrosines in the tail: none

Dileucine motif in the tail: none

checking 63 PROSITE DNA binding motifs: none

checking 71 PROSITE ribosomal protein motifs: none

checking 33 PROSITE prokaryotic DNA binding motifs: none

#### NNCN: Reinhardt's method for Cytoplasmic/Nuclear discrimination

Prediction: cytoplasmic

Reliability: 55.5

#### COIL: Lupas's algorithm to detect coiled-coil regions

total: 0 residues

## Results of the *k*-NN Prediction

*k* = 9/23

47.8 %: mitochondrial  
13.0 %: nuclear  
13.0 %: cytoplasmic  
8.7 %: endoplasmic reticulum  
8.7 %: Golgi  
4.3 %: extracellular, including cell wall  
4.3 %: vacuolar

>> prediction for 160843903028872 is mit (k=23)

## iPSORT Prediction

Predicted as: *not having any of signal, mitochondrial targeting, or chloroplast transit peptides*

Sequence (Type: plant)

**1** MWSSR RPVCA LSACN EAVYQ DPVTG QEHD F CGRTH ATLFK QQQQ LQH QK  
**51** AATFR PDRYK LVPTA VLRSG AVRNK HKS NP RPSGS HTSAG YN HGH PTAAA  
**101** ANGVV VVALP PSAQQ TLPIT HHTPK VPQAL RVTDT MVLFW NPPCV FTQWE  
**151** PALFE VDGVK YCSAE QYMM A CKANV FGDTD IWNKI MSTSD PAQQK RL GKE  
**201** VANYD HGIWN LCKVQ FVL TG NYSKF TQ NPG MCDQL LATGD KMLAE ASQHD  
**251** KVMGI GMDAF DPNVE RHECW RGQNL LGKIL MYVRN KIRWE RPD LA SRRQV  
**301** QEAAA AMEAE HRLIP SNGRF VSAAG PAMTA DSLGA LNMTA LQTQL HCPDM  
**351** GLRAP VTAPP TLGEP APEVF IAVAA VQQNK ADTDA KTPSK N

Values used for reasoning

Node	Answer	View	Substring	Value(s)	Plot
1. Signal peptide?	No	Average Hydropathy (KYTJ820101)	[6,25]	0.095 ( >= 0.9225? No)	<a href="#">show</a>
2. Mitochondrial or chloroplast ?	No	Average Negative Charge (FAUJ880112)	[1,30]	0.133333 ( < 0.083? No)	<a href="#">show</a>
		Indexing: A11 Pattern: 22121222 (ins/del <= 2)	[1,30]	MWSSR-RPVCALSACNEAVYQDPVTGQEHD F 22221-12222222002222022020002 22121222	--
3. Mitochondrial?	No	Average Isoelectric Point (ZIMJ680104)	[1,15]	6.396 ( >= 6.21? Yes)	<a href="#">show</a>
		Indexing: A12 Pattern: 100100110 (ins/del <= 3)	[1,15]	-MW-SSRR-PVCALSACN -00-0011-200000000 100100110	--

\* This color means "not used".

Name	Alphabet Indexing		
	0	1	2
A11	DEGHKN	IR	ACFLMPQSTVWY
A12	ACDEFGHLMNQSTVWY	KR	IP

[Return to iPSORT Home](#)

### PSORT features and traditional PSORTII prediction

id	site	distance	identity	comments
ODPA_SOLTU	mito	259.787	<a href="#">11.75%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Mitochondrial matrix.
GTH_SILCU	cyto	273.776	<a href="#">12.532%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Cytoplasmic.
GLN2_CHLRE	chlo	282.603	<a href="#">12.4365%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Chloroplast.
At2g30970.1	mito	285.134	<a href="#">12.761%</a>	<a href="#">[Arath]</a>
RBS1_CHLRE	chlo	287.271	<a href="#">12.0205%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Chloroplast.
PODK_MAIZE	chlo	291.348	<a href="#">11.0876%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Chloroplast.
ADH1_PETHY	cyto	291.367	<a href="#">8.39695%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Cytoplasmic.
RBS5_ACEME	chlo	294.509	<a href="#">10.9974%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Chloroplast.
FDH_SOLTU	mito	295.108	<a href="#">11.1959%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Mitochondrial.
ADH3_SOLTU	cyto	302.578	<a href="#">11.2245%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Cytoplasmic.
GLYM_FLAPR	mito	303.126	<a href="#">10.8317%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Mitochondrial.
ADH2_LYCES	cyto	304.536	<a href="#">11.9898%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Cytoplasmic.
RBS3_ACECL	chlo	304.855	<a href="#">10.9974%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Chloroplast.
CB48_MAIZE	chlo	307.547	<a href="#">15.601%</a>	<a href="#">[Uniprot]</a> SWISS-PROT45:Chloroplast thylakoid membrane.

id	site	iPSORT							PSORT Features											Amino Acid Content										Misc.
		MxHy1_30	Mx-1_20	dna	cr1	mlb	m3a	mNt	mip	mit	nuc	pox	psg	rib	mp	tms	yqr	A	C	Q	H	I	L	S	V	length				
160843885328766	chlo?	71	71	47	50	48	47	49	48	78	30	49	38	49	50	39	44	90	85	96	92	5	25	8	56	60				
ODPA_SOLTU	mito	79	71	47	50	48	47	49	64	85	30	49	38	49	50	39	44	86	68	19	82	51	25	20	15	60				
GTH_SILCU	cyto	49	71	47	50	48	47	49	55	71	30	49	38	49	50	39	44	75	13	84	97	12	95	4	56	26				
GLN2_CHLRE	chlo	55	87	47	50	48	47	49	68	84	30	49	38	49	50	39	44	68	70	14	78	43	18	9	37	57				
At2g30970.1	mito	66	87	47	50	48	47	49	66	78	30	49	38	49	50	39	44	58	54	72	89	35	48	56	26	65				
RBS1_CHLRE	chlo	85	71	47	50	48	47	49	62	83	30	49	38	49	50	39	44	98	78	91	1	19	5	21	95	21				
PODK_MAIZE	chlo	69	87	47	50	48	47	49	49	74	96	49	38	49	50	39	44	79	66	78	53	24	61	13	69	94				
ADH1_PETHY	cyto	62	71	47	50	48	47	49	52	60	30	49	38	49	50	39	44	31	93	33	88	54	14	15	92	57				
RBS5_ACEME	chlo	76	87	47	50	48	47	49	78	69	30	49	38	49	50	39	44	81	92	94	6	12	14	32	49	20				
FDH_SOLTU	mito	52	71	47	50	48	47	49	63	88	30	49	38	49	50	39	44	82	49	42	88	66	63	4	37	57				
ADH3_SOLTU	cyto	67	71	47	50	48	47	49	51	53	30	49	38	49	50	39	44	54	91	10	84	61	24	15	96	57				
GLYM_FLAPR	mito	53	71	47	50	48	47	49	59	69	30	49	38	49	50	39	44	80	11	54	75	35	53	33	55	76				
ADH2_LYCES	cyto	67	71	47	50	48	47	49	51	53	30	49	38	49	50	39	44	58	93	6	84	55	32	15	96	57				
RBS3_ACECL	chlo	64	71	47	50	48	47	49	78	74	30	49	38	49	50	39	44	69	92	94	6	20	9	32	37	20				
CB48_MAIZE	chlo	77	71	47	50	48	47	49	52	56	30	49	38	49	50	39	44	86	42	10	53	19	53	12	60	36				

id	site	iPSORT	PSORT Features																Amino Acid Content												Misc.
		<a href="#">MxHyI_30</a>	<a href="#">Mx-I_20</a>	<a href="#">dna</a>	<a href="#">erl</a>	<a href="#">mlb</a>	<a href="#">m3a</a>	<a href="#">mNr</a>	<a href="#">mip</a>	<a href="#">mit</a>	<a href="#">nuc</a>	<a href="#">pox</a>	<a href="#">psg</a>	<a href="#">rib</a>	<a href="#">rnp</a>	<a href="#">rms</a>	<a href="#">yqr</a>	<a href="#">A</a>	<a href="#">C</a>	<a href="#">Q</a>	<a href="#">H</a>	<a href="#">I</a>	<a href="#">L</a>	<a href="#">S</a>	<a href="#">V</a>	<a href="#">length</a>					
160843885328766	chlo?	13.50	2.00	0	0	0	0	0	16	-1.37	-0.47	0	-4	0	0	0	0	0.118	0.026	0.069	0.036	0.023	0.069	0.049	0.074	391					
ODPA_SOLTU	mito	15.30	2.00	0	0	0	0	0	35	-0.07	-0.47	0	-4	0	0	0	0	0.110	0.018	0.020	0.028	0.054	0.069	0.059	0.054	391					
GTH_SILCU	cyto	9.00	2.00	0	0	0	0	0	25	-2.61	-0.47	0	-4	0	0	0	0	0.097	0.005	0.046	0.051	0.032	0.120	0.042	0.074	216					
GLN2_CHLRE	chlo	10.40	3.00	0	0	0	0	0	39	-0.30	-0.47	0	-4	0	0	0	0	0.092	0.018	0.018	0.026	0.050	0.063	0.050	0.066	380					
At2g30970.1	mito	12.40	3.00	0	0	0	0	0	37	-1.50	-0.47	0	-4	0	0	0	0	0.084	0.014	0.040	0.033	0.047	0.084	0.079	0.060	430					
RBS1_CHLRE	chlo	18.00	2.00	0	0	0	0	0	33	-0.39	-0.47	0	-4	0	0	0	0	0.157	0.022	0.054	0.000	0.038	0.049	0.059	0.103	185					
PODK_MAIZE	chlo	13.10	3.00	0	0	0	0	0	17	-2.06	1.41	0	-4	0	0	0	0	0.101	0.017	0.042	0.019	0.041	0.091	0.054	0.080	947					
ADH1_PETHY	cyto	11.80	2.00	0	0	0	0	0	21	-3.66	-0.47	0	-4	0	0	0	0	0.068	0.034	0.026	0.031	0.055	0.060	0.055	0.097	382					
RBS5_ACEME	chlo	14.70	3.00	0	0	0	0	0	52	-2.89	-0.47	0	-4	0	0	0	0	0.104	0.033	0.060	0.005	0.033	0.060	0.066	0.071	183					
FDH_SOLTU	mito	9.70	2.00	0	0	0	0	0	34	0.63	-0.47	0	-4	0	0	0	0	0.105	0.013	0.029	0.031	0.060	0.092	0.042	0.066	381					
ADH3_SOLTU	cyto	12.70	2.00	0	0	0	0	0	20	-4.24	-0.47	0	-4	0	0	0	0	0.082	0.032	0.016	0.029	0.058	0.068	0.055	0.105	380					
GLYM_FLAPR	mito	10.00	2.00	0	0	0	0	0	30	-2.87	-0.47	0	-4	0	0	0	0	0.103	0.004	0.033	0.025	0.046	0.087	0.066	0.074	517					
ADH2_LYCES	cyto	12.70	2.00	0	0	0	0	0	20	-4.24	-0.47	0	-4	0	0	0	0	0.084	0.034	0.013	0.029	0.055	0.074	0.055	0.105	380					

RBS3_ACECL	chlo	12.10	2.00	0	0	0	0	0	52	-2.06	-0.47	0	-4	0	0	0	0	0.093	0.033	0.060	0.005	0.038	0.055	0.066	0.066	183
CB48_MAIZE	chlo	14.90	2.00	0	0	0	0	0	21	-4.05	-0.47	0	-4	0	0	0	0	0.110	0.011	0.015	0.019	0.038	0.087	0.053	0.076	264



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CBS (/index.html) >> CBS Prediction Servers (/services/) >> DeepLoc-1.0 (/services/DeepLoc-1.0/) >> Results

# DeepLoc-1.0

## Summary of 1 predicted sequences

Table of predicted subcellular localizations. Use the help page for more detailed description of the output page.

### Predicted proteins

#### Sequence

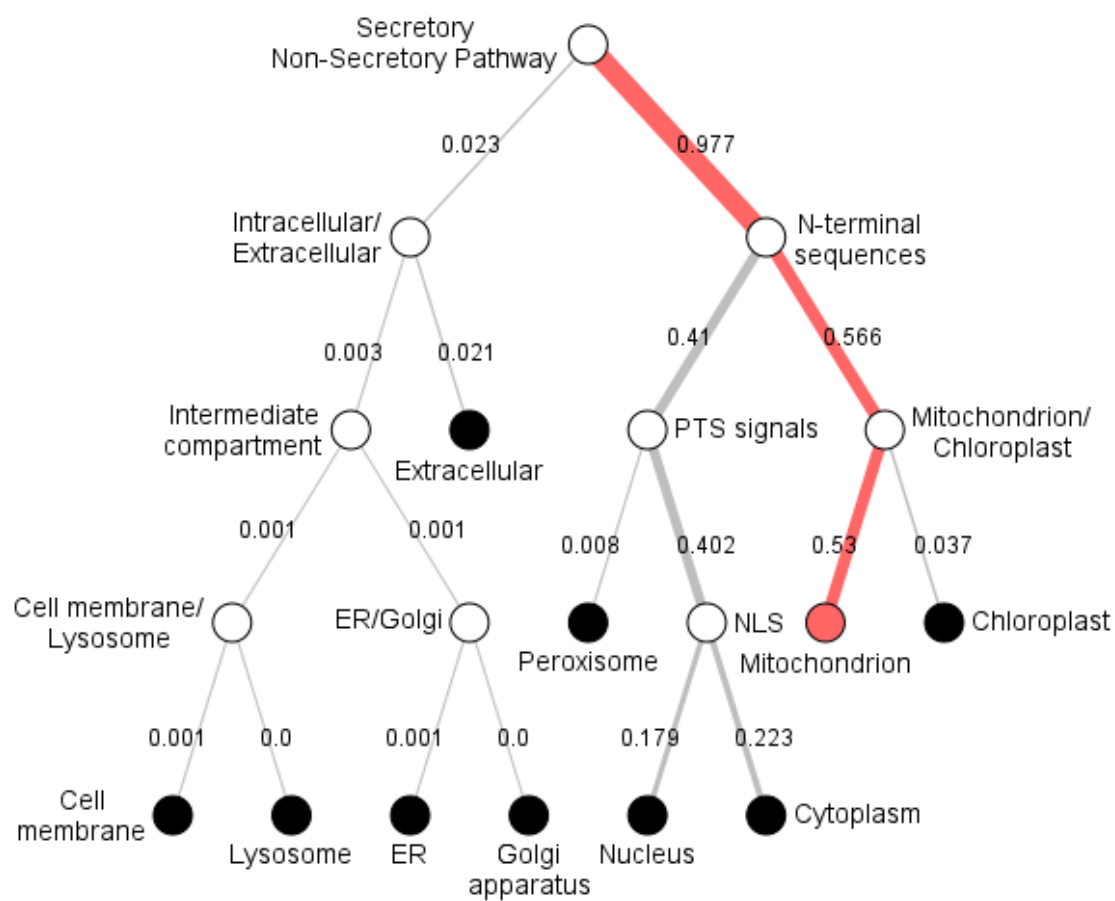
Prediction: Mitochondrion, Soluble

Localization	Mitochondrion	Cytoplasm	Extracellular	Nucleus	Plastid	Peroxisome	Lysosome/Vacuole	Cell membrane	Endoplasmic reticulum
Likelihood	0.5139	0.2099	0.145	0.0637	0.036	0.0232	0.0027	0.0024	0.0024

Type	Soluble	Membrane
Likelihood	0.8906	0.1094

**Hierarchical Tree. Download:** PNG (/services/DeepLoc-1.0/tmp/5FDED13C00000345334C3C54/tree\_1.png) / EPS (/services/DeepLoc-1.0/tmp/5FDED13C00000345334C3C54/tree\_1.eps)





**Position Importance. Download:** PNG (/services/DeepLoc-1.0/tmp/5FDED13C00000345334C3C54/alpha\_1.png) / EPS (/services/DeepLoc-1.0/tmp/5FDED13C00000345334C3C54/alpha\_1.eps) / CSV (/services/DeepLoc-1.0/tmp/5FDED13C00000345334C3C54/alpha\_1.csv)

