

**SUPPLEMENTARY MATERIALS (SM)**

## SUPPLEMENTARY METHODS

### **Human brain (Superior Temporal Gyrus=STG) *NTNG* transcriptome reconstruction of SCZ patients and healthy subjects**

All calculations were performed on two servers (HP ProLiant ML350 and DELL Precision 670) running FreeBSD operating system (v9.2) by using freely available software manually compiled from its source code.

#### RNA-seq data analysis of the dataset E-MTAB-1030.

Raw reads (2 groups, 9 samples in each group, 13.1 ~ 39.2 million 76 base pairs single end reads per sample, FASTQ file format) were downloaded from ArrayExpress [1] and aligned to a human reference genome by using TopHat v.2.0.8b [2] which calls BowTie v.2.1.0 [3]. Reference genome sequence, genome indexes and GTF-file containing genes annotations (version hg19 of UCSC build) adapted for using with TopHat/Cufflinks software suite were downloaded from “iGenomes” project's web site [4]. Each sample was processed by TopHat individually, using following command line options:

```
--library-type fr-unstranded --microexon-search --no-coverage-search -G genes.gtf
```

TopHat's output was passed then to Cufflinks v.2.1.1 [5] using the following command line:

```
$ cufflinks --library-type fr-unstranded -g genes.gtf C01_accepted_hits.bam
```

and so on.

Transcript models generated during the first stage of Cufflinks processing (“transcripts.gtf” files from each sample) were combined into a single GTF file by using Cuffcompare software – a part of Cufflinks software suite, using default command line options. Resulting single file was used then as a reference file during the second stage of Cufflinks processing, when Cufflinks runs in quantification-only mode, without discovering novel isoforms. Output files generated by the Cufflinks (3 files per each run, containing RPKM values of genes, isoforms and transcripts expression) were processed by custom Python script. The script combines Cufflinks results from all samples into one file with sample labels added and limiting of output information to following genome *loci* known to contain *NTNG1* and *NTNG2*:

```
chr1:107500000-108100000
```

```
chr9:135000000-135200000
```

```
chr7:127600000-127700000
```

```
chr11:400000000-415000000
```

The resulted file was then inspected and analyzed manually in order to check for the presence of multiple either non-annotated transcripts, transcripts with varying boundaries or transcripts retained after the splicing upstream or downstream introns.

### SNPs detection

Single nucleotide polymorphism detection was done by using two different approaches.

Approach 1 (per-sample SNP detection).

1. Remove duplicated reads from each alignment file generated by TopHat:

```
$ samtools rmdup -s C01_accepted_hits.bam C01_accepted_hits_rmdup.bam
```

2. Detect SNPs using 'multi pileup' pipeline provided by "SAMtools" software package, version 0.1.19-44428cd [6], processing each sample individually:

```
$ samtools mpileup -E -u -f genome.fa -b C01_accepted_hits_rmdup.bam | bcftools view -bvcg - > C01_variants.raw.bcf  
$ bcftools view C01_variants.raw.bcf | vcftutils.pl varFilter -D100 > C01_variants.flt.vcf
```

Files containing filtered SNPs obtained from different samples were combined into one file, by using custom Python script while keeping each sample's label.

Approach 2 (per-group SNP detection).

1. Merge C\*\_accepted\_hits.bam files (all controls samples) into one file, sorted by chromosome name by using 'samtools merge' routine:

```
$ samtools merge -l 1 -@ 4 accepted_hits_ctrl.bam [list of input bam files]
```

2. Do the same for samples obtained from all SCZ patients:

```
$ samtools merge -l 1 -@ 4 accepted_hits_schz.bam [list of input bam files]
```

3. Remove duplicated reads from each file:

```
$ samtools rmdup -s accepted_hits_ctrl.bam accepted_hits_ctrl_rmdup.bam
```

```
$ samtools rmdup -s accepted_hits_schz.bam accepted_hits_schz_rmdup.bam
```

4. Detect SNPs on per-group basis using 'multi pileup' pipeline:

```
$ samtools mpileup -E -u -f genome.fa -b accepted_hits_ctrl_rmdup.bam | bcftools view -bvcg - > variants_ctrl.raw.bcf  
$ bcftools view variants_ctrl.raw.bcf | vcftutils.pl varFilter -D100 > variants_ctrl.flt.vcf
```

```
$ samtools mpileup -E -u -f genome.fa -b accepted_hits_schz_rmdup.bam | bcftools view -bvcg - > variants_schz.raw.bcf  
$ bcftools view variants_schz.raw.bcf | vcftutils.pl varFilter -D100 > variants_schz.flt.vcf
```

## Supplementary References

- [1] E-MTAB-1030 dataset: <https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1030/>
- [2] Trapnell C, Pachter L, Salzberg SL. TopHat: discovering splice junctions with RNA-Seq. *Bioinformatics*. 2009;25(9):1105-1111. doi:10.1093/bioinformatics/btp120.
- [3] Langmead B, Trapnell C, Pop M, Salzberg SL. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biology*. 2009;10(3):R25. doi:10.1186/gb-2009-10-3-r25.
- [4] “iGenomes” project: [http://support.illumina.com/sequencing/sequencing\\_software/igenome.html](http://support.illumina.com/sequencing/sequencing_software/igenome.html)
- [5] Trapnell C, Hendrickson DG, Sauvageau M, Goff L, Rinn JL, Pachter L. Differential analysis of gene regulation at transcript resolution with RNA-seq. *Nature biotechnology*. 2013;31(1):10.1038/nbt.2450. doi:10.1038/nbt.2450.
- [6] Li H, Handsaker B, Wysoker A, et al. The Sequence Alignment/Map format and SAMtools. *Bioinformatics*. 2009;25(16):2078-2079. doi:10.1093/bioinformatics/btp352.

**Supplementary Table 1a (ST1a)**

Dataset Name	Link to the dataset	File name(s) used
E-MTAB-1030** (SCZ patients, (12))	<a href="https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1030/files/bam/?ref=E-MTAB-1030">https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1030/files/bam/?ref=E-MTAB-1030</a>	E-MTAB-1030.BAM.ERR103421.bam E-MTAB-1030.BAM.ERR103422.bam E-MTAB-1030.BAM.ERR103423.bam E-MTAB-1030.BAM.ERR103424.bam E-MTAB-1030.BAM.ERR103425.bam E-MTAB-1030.BAM.ERR103426.bam E-MTAB-1030.BAM.ERR103427.bam E-MTAB-1030.BAM.ERR103428.bam E-MTAB-1030.BAM.ERR103429.bam E-MTAB-1030.BAM.ERR103430.bam E-MTAB-1030.BAM.ERR103431.bam E-MTAB-1030.BAM.ERR103432.bam E-MTAB-1030.BAM.ERR103433.bam E-MTAB-1030.BAM.ERR103434.bam E-MTAB-1030.BAM.ERR103435.bam E-MTAB-1030.BAM.ERR103436.bam E-MTAB-1030.BAM.ERR103437.bam E-MTAB-1030.BAM.ERR103438.bam

\*\*aligned against hg19 (iGenome by Illumina): [http://support.illumina.com/sequencing/sequencing\\_software/igenome.html](http://support.illumina.com/sequencing/sequencing_software/igenome.html)

**Supplementary Table 1b (ST1b).** Quality control of the RNA-seq reads (E-MTAB-1030) as determined by the FastQC software. Two out of 18 analysed samples are double negative (in red) on “per base sequence quality” and displaying a non-detectable expression level of a coding *NTNG1a* isoform (typically present at a high level of the expression) and non-coding transcript *NTNG1int(9-10)*. These two samples (C02 and S05, one healthy control and one SCZ) were excluded from the comparison analysis. Related to **Figure 1B** in the main text.

	C01	C02	C04	C05	C06	C10	C23	C25	C26	S01	S02	S04	S05	S06	S10	S23	S25	S26
Basic Statistics	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS
Per base sequence quality	PASS	FAIL	PASS	PASS	FAIL	PASS	PASS	PASS	PASS	FAIL	PASS	FAIL	FAIL	FAIL	PASS	PASS	PASS	PASS
Per sequence quality scores	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS
Per base sequence content	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL
Per base GC content	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	WARN	FAIL	FAIL	FAIL	FAIL	FAIL	FAIL	WARN	FAIL	FAIL
Per sequence GC content	WARN	PASS	PASS	WARN	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	WARN	PASS	WARN	PASS	PASS	WARN
Per base N content	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS
Sequence Length Distribution	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS
Sequence Duplication Levels	FAIL	WARN	FAIL	FAIL	WARN	FAIL	FAIL	FAIL	WARN	WARN	FAIL	WARN	FAIL	WARN	FAIL	PASS	FAIL	FAIL
Overrepresented sequences	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS	PASS
Kmer Content	FAIL	WARN	FAIL	WARN	WARN	WARN	WARN	FAIL	FAIL	WARN	WARN	WARN	WARN	WARN	FAIL	FAIL	WARN	FAIL

Expression zero

NTNG1a  
NTNG1int(9-10)

yes  
yes

yes  
yes

Prosselkov P (2016) Cognitive domains function complementation by NTNG gene paralogs  
**Supplementary Table 1c (ST1c).** SNPs calling from the RNA-seq reads (E-MTAB-1030) using SAMtools. All samples except one (S23) contain rs2149171 among the group of 16 human subjects tested. Related to **Figure 1B** in the main text.

per group SNP calling										
Group	dbSNP_ref_ID	#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT
SCZ	rs2218404	chr1	107952605	.	T	G	46.8	.	DP=2;VDB=7.520000eO02;AF1=1;AC1=2;DP4=0,0,1,1;MQ=50;FQ=O33	GT:PL:GQ 1/1:78,6,0:10
SCZ	rs7851893	chr9	135040036	.	G	T	36	.	DP=3;VDB=4.480000eO02;RPB=8.745357eO01;AF1=0.5002;AC1=1;DP4=1,0,1,1;MQ=50;FQ=5.46;PV4=1,0.33,1,0.33	GT:PL:GQ 0/1:66,0,31:34
SCZ	rs3824574	chr9	135073877	.	C	T	225	.	DP=83;VDB=2.687766eO01;RPB=3.278316eO01;AF1=0.5;AC1=1;DP4=29,23,19,9;MQ=50;FQ=225;PV4=0.34,0.11,1,0.37	GT:PL:GQ 0/1:255,0,255:99
SCZ	rs2149171	chr9	135102254	.	C	T	225	.	DP=95;VDB=2.950173eO01;RPB=6.821234eO01;AF1=0.5;AC1=1;DP4=21,17,27,25;MQ=50;FQ=225;PV4=0.83,1,1,1	GT:PL:GQ 0/1:255,0,255:99
CTL	rs2218404	chr1	107952605	.	T	G	27.8	.	DP=2;VDB=6.240000eO02;AF1=1;AC1=2;DP4=0,0,2,0;MQ=50;FQ=O33	GT:PL:GQ 1/1:59,6,0:10
CTL	rs3824574	chr9	135073877	.	C	T	225	.	DP=90;VDB=2.599002eO01;RPB=9.523965eO02;AF1=0.5;AC1=1;DP4=32,21,21,11;MQ=50;FQ=225;PV4=0.65,0.3,1,0.18	GT:PL:GQ 0/1:255,0,255:99
CTL	rs2149171	chr9	135102254	.	C	T	225	.	DP=93;VDB=1.238512eO01;RPB=1.426915e+00;AF1=0.5;AC1=1;DP4=14,14,32,29;MQ=50;FQ=225;PV4=1,1,1,1	GT:PL:GQ 0/1:255,0,255:99

per sample SNP calling										
Sample	dbSNP_ref_ID	#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT
C01	rs3824574	chr9	135073877	.	C	T	179	.	DP=29;VDB=1.513890eO01;RPB=0.6429306eO01;AF1=0.5;AC1=1;DP4=9,5,9,3;MQ=50;FQ=182;PV4=0.68,0.17,1,0.18	GT:PL:GQ 0/1:209,0,255:99
C01	rs2149171	chr9	135102254	.	C	T	225	.	DP=38;VDB=1.350007eO01;RPB=1.162004e+00;AF1=0.5;AC1=1;DP4=4,12,9,11;MQ=50;FQ=211;PV4=0.3,1,1,0.072	GT:PL:GQ 0/1:255,0,238:99
C04	rs2149171	chr9	135102254	.	C	T	193	.	DP=30;VDB=1.122397eO01;RPB=0.3949202eO01;AF1=0.5;AC1=1;DP4=9,7,10,4;MQ=50;FQ=196;PV4=0.47,0.27,1,0.33	GT:PL:GQ 0/1:223,0,255:99
C05	rs3824574	chr9	135073877	.	C	T	222	.	DP=21;VDB=1.215496eO01;AF1=1;AC1=2;DP4=0,0,14,5;MQ=50;FQ=O84	GT:PL:GQ 1/1:255,57,0:99
C05	rs2149171	chr9	135102254	.	C	T	147	.	DP=22;VDB=8.058553eO02;RPB=1.991569e+00;AF1=0.5;AC1=1;DP4=5,8,3,5;MQ=50;FQ=150;PV4=1,1,1,1	GT:PL:GQ 0/1:177,0,248:99
C06	rs2149171	chr9	135102254	.	C	T	18.1	.	DP=5;VDB=3.200000eO02;RPB=0.111223e+00;AF1=0.5;AC1=1;DP4=1,1,1,1;MQ=50;FQ=19.9;PV4=1,0.077,1,1	GT:PL:GQ 0/1:48,0,53:50
C10	rs2149171	chr9	135102254	.	C	T	222	.	DP=18;VDB=1.071739eO01;AF1=1;AC1=2;DP4=0,0,7,9;MQ=50;FQ=O75	GT:PL:GQ 1/1:255,48,0:93
C23	rs3824574	chr9	135073877	.	C	T	225	.	DP=31;VDB=3.823388eO02;RPB=0.9341987eO01;AF1=0.5;AC1=1;DP4=7,4,8,7;MQ=50;FQ=199;PV4=0.7,0.055,1,1	GT:PL:GQ 0/1:255,0,226:99
C23	rs2149171	chr9	135102254	.	C	T	225	.	DP=37;VDB=1.748441eO01;RPB=1.151082e+00;AF1=0.5;AC1=1;DP4=8,5,8,11;MQ=50;FQ=210;PV4=0.47,0.27,1,1	GT:PL:GQ 0/1:255,0,237:99
C25	rs4915045	chr1	108023589	.	A	C	191	.	DP=17;VDB=1.280591eO01;RPB=1.463850eO01;AF1=0.5;AC1=1;DP4=5,2,6,4;MQ=50;FQ=137;PV4=1,0.18,1,1	GT:PL:GQ 0/1:221,0,164:99
C25	rs2149171	chr9	135102254	.	C	T	225	.	DP=30;VDB=1.577762eO01;RPB=0.1079507e+00;AF1=0.5;AC1=1;DP4=7,3,6,11;MQ=50;FQ=143;PV4=0.12,1,1,1	GT:PL:GQ 0/1:255,0,170:99
C26	rs3824574	chr9	135073877	.	C	T	175	.	DP=31;VDB=1.109656eO01;RPB=3.659625eO01;AF1=0.5;AC1=1;DP4=10,5,7,5;MQ=50;FQ=178;PV4=0.71,0.15,1,1	GT:PL:GQ 0/1:205,0,252:99
C26	rs2149171	chr9	135102254	.	C	T	222	.	DP=30;VDB=5.630463eO02;AF1=1;AC1=2;DP4=0,0,15,12;MQ=50;FQ=O108	GT:PL:GQ 1/1:255,81,0:99
S01	rs2149171	chr9	135102254	.	C	T	156	.	DP=11;VDB=4.899777eO02;AF1=1;AC1=2;DP4=0,0,8,2;MQ=50;FQ=O57	GT:PL:GQ 1/1:189,30,0:57
S02	rs3824574	chr9	135073877	.	C	T	152	.	DP=37;VDB=1.024512eO01;RPB=1.198958e+00;AF1=0.5;AC1=1;DP4=16,7,7,5;MQ=50;FQ=155;PV4=0.71,0.00015,1,0.37	GT:PL:GQ 0/1:182,0,255:99
S02	rs2149171	chr9	135102254	.	C	T	225	.	DP=34;VDB=1.847060eO01;RPB=4.087119eO01;AF1=0.5;AC1=1;DP4=6,6,9,11;MQ=50;FQ=187;PV4=1,1,1,1	GT:PL:GQ 0/1:255,0,214:99
S05	rs2149171	chr9	135102254	.	C	T	20	.	DP=15;VDB=7.269818eO02;RPB=2.245397e+00;AF1=0.5;AC1=1;DP4=4,3,4,0;MQ=50;FQ=23;PV4=0.24,0.045,1,0.1	GT:PL:GQ 0/1:50,0,139:53
S06	rs2149171	chr9	135102254	.	C	T	59	.	DP=10;VDB=4.566715eO02;RPB=0.4748531eO01;AF1=0.5;AC1=1;DP4=3,2,3,1;MQ=50;FQ=61.9;PV4=1,1,1,0.13	GT:PL:GQ 0/1:89,0,104:92
S10	rs2149171	chr9	135102254	.	C	T	204	.	DP=23;VDB=1.647063eO01;RPB=0.3464674eO01;AF1=0.5;AC1=1;DP4=5,4,3,11;MQ=50;FQ=151;PV4=0.18,1,1,1	GT:PL:GQ 0/1:234,0,178:99
S23	rs3824574	chr9	135073877	.	C	T	195	.	DP=48;VDB=1.676466eO01;RPB=0.6685032eO01;AF1=0.5;AC1=1;DP4=16,13,9,6;MQ=50;FQ=198;PV4=1,0.29,1,1	GT:PL:GQ 0/1:225,0,255:99
S25	rs4915045	chr1	108023589	.	A	C	222	.	DP=12;VDB=1.354519eO01;AF1=1;AC1=2;DP4=0,0,5,6;MQ=50;FQ=O60	GT:PL:GQ 1/1:255,33,0:63
S25	rs3824574	chr9	135073877	.	C	T	164	.	DP=30;VDB=1.565452eO01;RPB=5.440727eO01;AF1=0.5;AC1=1;DP4=9,8,10,3;MQ=50;FQ=167;PV4=0.26,0.2,1,1	GT:PL:GQ 0/1:194,0,255:99
S25	rs2149171	chr9	135102254	.	C	T	225	.	DP=26;VDB=1.440805eO01;RPB=0.3175537eO01;AF1=0.5;AC1=1;DP4=4,3,10,7;MQ=50;FQ=115;PV4=1,0.31,1,1	GT:PL:GQ 0/1:255,0,142:99
S26	rs2149171	chr9	135102254	.	C	T	222	.	DP=30;VDB=1.760676eO01;AF1=1;AC1=2;DP4=0,0,12,15;MQ=50;FQ=O108	GT:PL:GQ 1/1:255,81,0:99















# NetPhos 2.0 Server - prediction results

## Technical University of Denmark

### 587 Sequence

```

MLHLLALFLHCLPLASGDYDICKSWVTTDEGPTWEFYACQPKVMRLKDYVKVKEPSGITCGDPPERFCSHENPYLCSNE      80
CDASNPDLAHPRLMFDKEEEGLATYWQSITWSRYPSPLEANITLSWNKTVELTDDVVMTFEYGRPTVMVLEKSLDNGRT      160
WQPYQFYAEDCMEAFGMSARRARDMSSSSAHRVLCTEEYSRWAGSKKEKHVRFEVRDRFAIFAGPDLRNMDNLYTRLESA      240
KGLKEFFTLTDLRMRLLRPALGGTYVQRENLYKYFYAISNIEVIGRCKCNLHANLCSMREGSLQCECEHNTTGPDCGKCK      320
KNFRTRSWRAGSYLPLPHGSPNACATAGSFGKWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLPKPKSPQ      400
VMPIEEFQDCECYGHSNRCSYIDFLNVVTCVSCKHNRGQHCQHCRLLGYRNGSAELDDENVCIECNQIGSVHDCNE      480
TGFCECREGAAGPKCDDCLPTHYWRQGCYPNVCDDDLLCQNGGTCLQNQRACPRGYTGVRCEQPRCDPADDGGLDCD      560
RAPGAAPRPATLLGCLLLLGLAARLGR      640
.....Y.....T.....Y.....S.....Y.....      80
...S.....S.....S.....S.....T.....S.....      160
.....S.....SS.S.....Y.....S.....Y.....S.....      240
.....Y.....Y.....S.....S.....T.....      320
.....S.....S.....S.....S.....T.....S.....      400
.....Y.....SY.....Y.....S.....      480
.....Y.....T.....      560
.....      640
    
```

Phosphorylation sites predicted: Ser: 20 Thr: 5 Tyr: 11

### Serine predictions

Name	Pos	Context	Score	Pred
Sequence	16	LPLASGDYD	0.005	.
Sequence	24	DICKSWVTT	0.480	.
Sequence	57	KVEPSGITC	0.015	.
Sequence	70	ERFCSHENP	0.970	*S*
Sequence	78	PYLCSNECD	0.003	.
Sequence	84	ECDASNPDL	0.526	*S*
Sequence	109	TYWQSITWS	0.011	.
Sequence	113	SITWSRYPS	0.080	.
Sequence	117	SRYPSPLEA	0.980	*S*
Sequence	126	NITLSWNKT	0.645	*S*
Sequence	154	VLEKSLDNG	0.896	*S*
Sequence	178	AFGMSARRA	0.947	*S*
Sequence	186	ARDMSSSSA	0.992	*S*
Sequence	187	RDMSSSSAH	0.884	*S*
Sequence	188	DMSSSSAHR	0.066	.
Sequence	189	MSSSSAHRV	0.695	*S*
Sequence	200	TEEYSRWAG	0.016	.
Sequence	205	RWAGSKKEK	0.993	*S*
Sequence	239	TRLESAKGL	0.994	*S*
Sequence	279	FYAISNIEV	0.006	.
Sequence	297	ANLCSMREG	0.195	.
Sequence	302	MREGSLQCE	0.651	*S*
Sequence	327	FRTRSWRAG	0.984	*S*
Sequence	332	WRAGSYLPL	0.694	*S*
Sequence	340	LPHGSPNAC	0.012	.

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Sequence	349	ATAGSFGKW	0.009	.
Sequence	357	WTRPSTAAP	0.755	*S*
Sequence	363	AAPLSSRWS	0.961	*S*
Sequence	364	APLSSRWSQ	0.051	.
Sequence	367	SSRWSQVAS	0.983	*S*
Sequence	371	SQVASRAEA	0.286	.
Sequence	398	LKPKSPQVM	0.748	*S*
Sequence	416	CYGHSNRCS	0.080	.
Sequence	420	SNRCSYIDF	0.967	*S*
Sequence	432	VTCVSCKHN	0.097	.
Sequence	454	YRNGSAELD	0.978	*S*
Sequence	473	NQIGSVHDR	0.459	.

Threonine predictions

Name	Pos	Context	Score	Pred
Sequence	27	KSWVTTDEG	0.620	*T*
Sequence	28	SWVTTDEGP	0.497	.
Sequence	33	DEGPTWEFY	0.034	.
Sequence	60	PSGITCGDP	0.166	.
Sequence	105	EGLATYWQS	0.053	.
Sequence	111	WQSITWSRY	0.026	.
Sequence	124	EANITLSWN	0.028	.
Sequence	130	SWNKTVELT	0.163	.
Sequence	134	TVELTDDVV	0.378	.
Sequence	140	DVVMTFEYG	0.035	.
Sequence	147	YGRPTVMVL	0.895	*T*
Sequence	160	DNGRTWQPY	0.035	.
Sequence	196	RVLCTEEYS	0.018	.
Sequence	235	DNLYTRLES	0.047	.
Sequence	248	KEFFTLTDL	0.169	.
Sequence	250	FFTLTDLRM	0.017	.
Sequence	264	ALGGTYVQR	0.043	.
Sequence	311	CEHNTTGPD	0.582	*T*
Sequence	312	EHNTTGPDC	0.057	.
Sequence	325	KNFRTRSWR	0.025	.
Sequence	346	NACATAGSF	0.102	.
Sequence	354	FGKWTRPST	0.073	.
Sequence	358	TRPSTAAPL	0.363	.
Sequence	378	EAVGTPAAA	0.875	*T*
Sequence	429	LNVVTCVSC	0.014	.
Sequence	437	CKHNTRGQH	0.044	.
Sequence	481	RCNETGFCE	0.057	.
Sequence	501	DCLPTHYWR	0.107	.
Sequence	525	QNGGTCLQN	0.009	.
Sequence	539	PRGYTGVRT	0.525	*T*
Sequence	571	PRPATLLGC	0.388	.

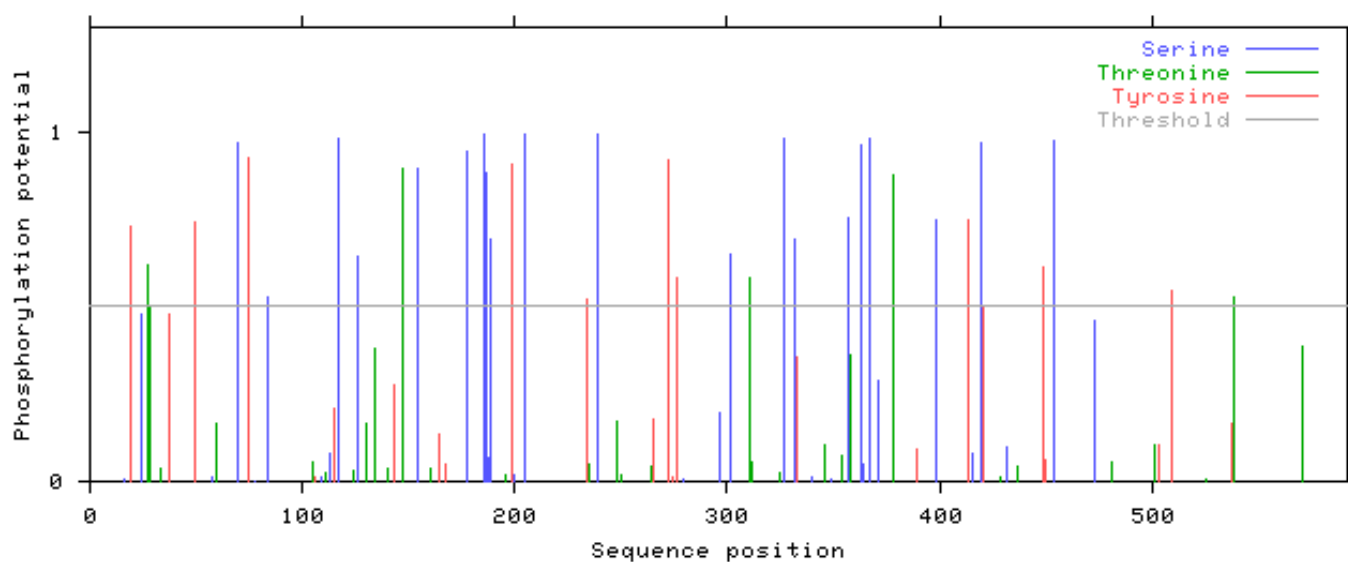
Tyrosine predictions

Name	Pos	Context	Score	Pred
Sequence	19	ASGDYDICK	0.728	*Y*
Sequence	37	TWEFYACQP	0.480	.
Sequence	49	RLKDYVKVK	0.743	*Y*
Sequence	75	HENPYLCSN	0.925	*Y*
Sequence	106	GLATYWQSI	0.014	.
Sequence	115	TWSRYPSPL	0.208	.

## Prosselkov P (2016) Cognitive domains function complementation by NTNG gene paralogs

Sequence	143	MTFEYGRPT	0.277	.
Sequence	164	TWQPYQFYA	0.134	.
Sequence	167	PYQFYAEDC	0.050	.
Sequence	199	CTEEYSRWA	0.905	*Y*
Sequence	234	MDNLYTRLE	0.522	*Y*
Sequence	265	LGGTYVQRE	0.178	.
Sequence	272	RENLYKYFY	0.921	*Y*
Sequence	274	NLYKYFYAI	0.013	.
Sequence	276	YKYFYAISN	0.583	*Y*
Sequence	333	RAGSYLPLP	0.356	.
Sequence	389	PAKGYKLFQ	0.093	.
Sequence	413	DCECYGHSN	0.749	*Y*
Sequence	421	NRCSYIDFL	0.505	*Y*
Sequence	449	CRLGYRNG	0.613	*Y*
Sequence	450	RLGYRNGS	0.062	.
Sequence	503	LPTHYWRQG	0.104	.
Sequence	509	RQGCYPNVC	0.545	*Y*
Sequence	538	CPRGYTGVR	0.163	.

NetPhos 2.0: predicted phosphorylation sites in Sequence



[Explain](#) the output. Go [back](#).





# NetOGlyc 4.0 Server - prediction results

Technical University of Denmark

```
##gff-version 2
##source-version NetOGlyc 4.0.0.13
##date 15-7-7
##Type Protein
#seqname      source  feature start      end      score  strand  frame  comment
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 16        16        0.0729462  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 24        24        0.432032   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 27        27        0.220753   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 28        28        0.622469   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 33        33        0.458255   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 57        57        0.192782   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 60        60        0.301557   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 70        70        0.572912   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 78        78        0.0297324  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 84        84        0.21773    .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 105       105       0.0989147  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 109       109       0.118147   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 111       111       0.122897   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 113       113       0.472415   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 117       117       0.155152   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 124       124       0.0368794  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 126       126       0.0751737  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 130       130       0.0125535  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 134       134       0.0249031  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 140       140       0.0382634  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 147       147       0.0233299  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 154       154       0.0755535  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 160       160       0.0708638  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 178       178       0.404214   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 186       186       0.670195   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 187       187       0.708075   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 188       188       0.799656   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 189       189       0.7729     .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 196       196       0.222735   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 200       200       0.170734   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 205       205       0.208466   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 235       235       0.125492   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 239       239       0.0423625  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 248       248       0.0403628  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 250       250       0.0358524  .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 264       264       0.243968   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 279       279       0.200806   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 297       297       0.394831   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 302       302       0.240648   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 311       311       0.653987   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 312       312       0.5         .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 325       325       0.695198   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 327       327       0.829706   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 332       332       0.873542   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 340       340       0.582599   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 346       346       0.72552    .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 349       349       0.718927   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 354       354       0.889758   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 357       357       0.933237   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 358       358       0.862541   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 363       363       0.746449   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 364       364       0.900792   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 367       367       0.828877   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 371       371       0.861973   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 378       378       0.798043   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 398       398       0.395922   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 416       416       0.116411   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 420       420       0.453928   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 429       429       0.269396   .      .
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 432       432       0.565064   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 437       437       0.556535   .      .      #POSITIVE
SEQUENCE      netOGlyc-4.0.0.13  CARBOHYD 454       454       0.149277   .      .
```

## Prosselkov P (2016) Cognitive domains function complementation by NTNG gene paralogs

SEQUENCE	netOGlyc-4.0.0.13	CARBOHYD	473	473	0.229053	.	.	
SEQUENCE	netOGlyc-4.0.0.13	CARBOHYD	481	481	0.06726	.	.	
SEQUENCE	netOGlyc-4.0.0.13	CARBOHYD	501	501	0.34238	.	.	
SEQUENCE	netOGlyc-4.0.0.13	CARBOHYD	525	525	0.226517	.	.	
SEQUENCE	netOGlyc-4.0.0.13	CARBOHYD	539	539	0.533323	.	.	#POSITIVE
SEQUENCE	netOGlyc-4.0.0.13	CARBOHYD	571	571	0.420087	.	.	

[Explain](#) the output. Go [back](#).

Prosselkov P (2016) Cognitive domains function complementation by NTNG gene paralogs

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# EMBOSS Stretcher

---

[Tools](#) > [Pairwise Sequence Alignment](#) > EMBOSS Stretcher

Results for job emboss\_stretcher-l20141117-082914-0427-41977542-pg

Prosselkov P (2016) Cognitive domains function complementation by NTNG gene paralogs

```
#####
# Program: stretcher
# Rundate: Mon 17 Nov 2014 08:29:15
# Commandline: stretcher
# -auto
# -stdout
# -asequence emboss_stretcher-I20141117-082914-0427-41977542-pg.asequence
# -bsequence emboss_stretcher-I20141117-082914-0427-41977542-pg.bsequence
# -datafile EBLOSUM62
# -gapopen 12
# -gapextend 2
# -aformat3 pair
# -sprotein1
# -sprotein2
# Align_format: pair
# Report_file: stdout
#####
```

```
#=====
#
# Aligned sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 12
# Extend_penalty: 2
#
# Length: 57
# Identity:      10/57 (17.5%)
# Similarity:   15/57 (26.3%)
# Gaps:         15/57 (26.3%)
# Score: -40
#
#
#=====
```

```
EMBOSS_001      1 NPPK-----FNRIWPNISS-LEVSNPKQVAP-----KLALSTVSSVQV      37
      ...:      .:.|...:| .|.....||      ||.....|.||
EMBOSS_001      1 KWTRPSTAAPLSSRWSQVASRAEAVGTPAAAPAPAKGYKLFQLKPKSPQV      50

EMBOSS_001      38 A--NHKR      42
      .   ...:
EMBOSS_001      51 MPIEEFQ      57
```

```
#-----
#-----
```

Prosselkov P (2016) Cognitive domains function complementation by NTNG gene paralogs



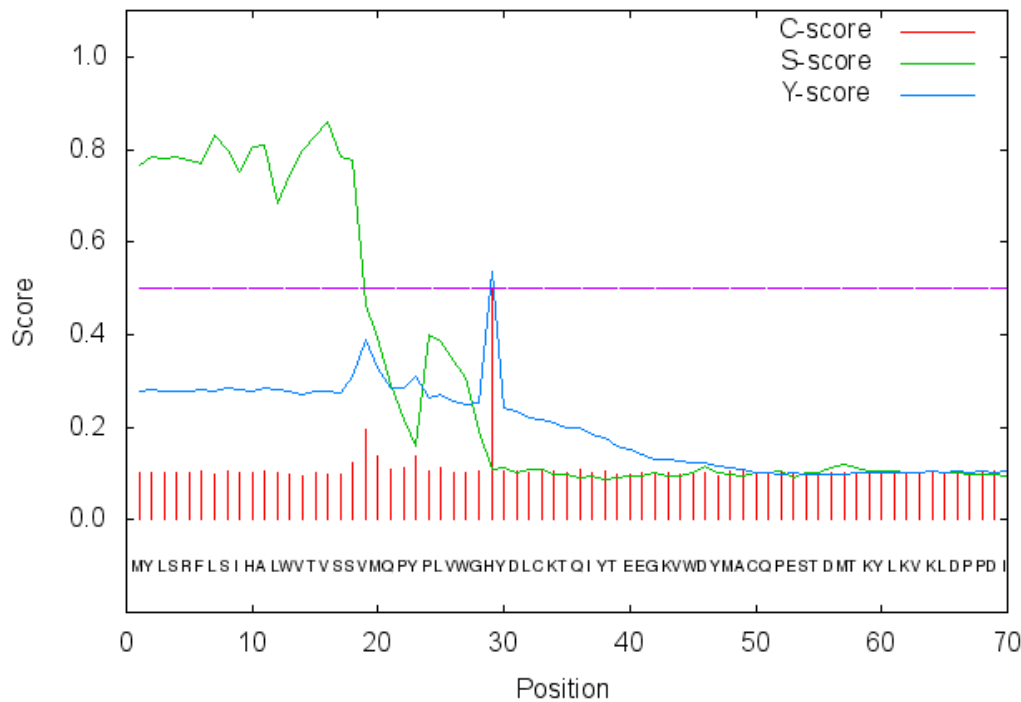
## SignalP 4.1 Server - prediction results

Technical University of Denmark

# SignalP-4.1 euk predictions

>Sequence

SignalP-4.1 prediction (euk networks): Sequence



# Measure	Position	Value	Cutoff	signal peptide?
max. C	29	0.500		
max. Y	29	0.535		
max. S	16	0.858		
mean S	1-28	0.617		
D	1-28	0.580	0.450	YES

Name=Sequence SP='YES' Cleavage site between pos. 28 and 29: VWG-HY D=0.580 D-cutoff=0.450 Networks=SignalP-noTM

# [data](#)  
# [gnuplot script](#)

Signal peptides: 1

# [processed fasta entries](#)  
# [gff file of processed entries](#)

Please cite:

SignalP 4.0: discriminating signal peptides from transmembrane regions  
Petersen TN., Brunak S., von Heijne G. & Nielsen H.  
Nature Methods, 8:785-786, 2011

[Explain](#) the output. Go [back](#).

Prosselkov P (2016) Cognitive domains function complementation by NTNG gene paralogs



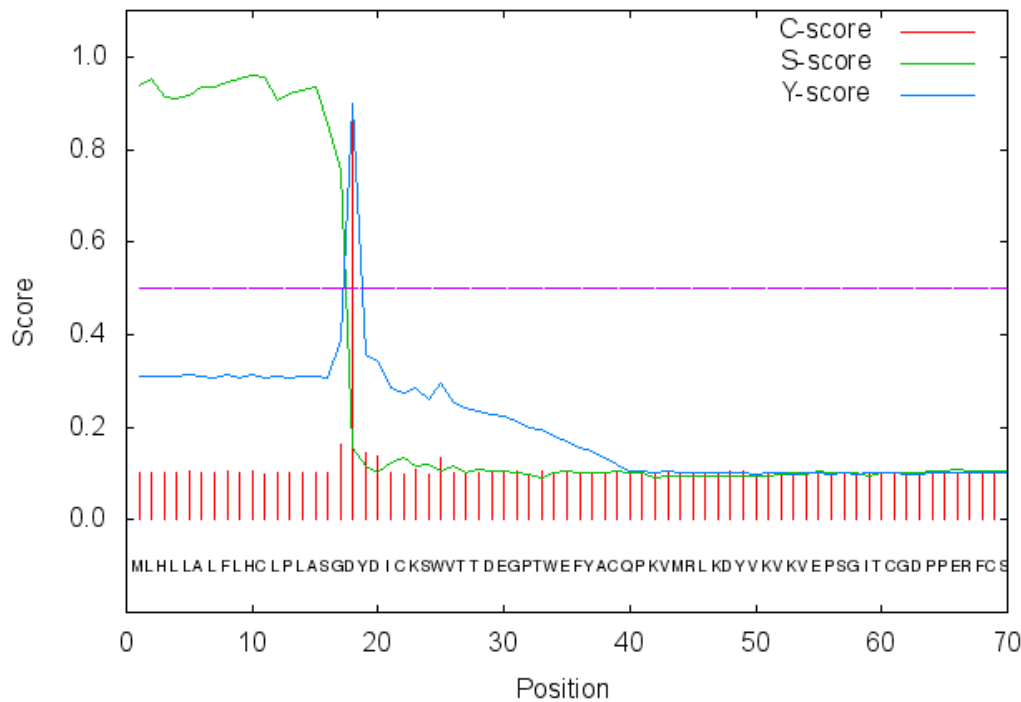
## SignalP 4.1 Server - prediction results

Technical University of Denmark

# SignalP-4.1 euk predictions

>Sequence

SignalP-4.1 prediction (euk networks): Sequence



# Measure	Position	Value	Cutoff	signal peptide?
max. C	18	0.875		
max. Y	18	0.899		
max. S	10	0.959		
mean S	1-17	0.918		
D	1-17	0.909	0.450	YES

Name=Sequence SP='YES' Cleavage site between pos. 17 and 18: ASG-DY D=0.909 D-cutoff=0.450 Networks=SignalP-noTM

# [data](#)  
# [gnuplot script](#)

Signal peptides: 1

# [processed fasta entries](#)  
# [gff file of processed entries](#)

Please cite:

SignalP 4.0: discriminating signal peptides from transmembrane regions  
Petersen TN., Brunak S., von Heijne G. & Nielsen H.  
Nature Methods, 8:785-786, 2011

[Explain](#) the output. Go [back](#).



GPI Lipid Anchor Project



# big-PI Predictor The GPI Prediction Server

Version 3.0, June 2005

## Please, refer to ...

1. Eisenhaber B., Bork P., Eisenhaber F.  
"Sequence properties of GPI-anchored proteins near the omega-site: constraints for the polypeptide binding site of the putative transamidase"  
Protein Engineering (1998) 11, No.12, 1155-1161
2. Sunyaev S.R., Eisenhaber F., Rodchenkov I.V., Eisenhaber B., Tumanyan V.G., and Kuznetsov E.N.  
"Prediction of potential GPI-modification sites in proprotein sequences"  
Protein Engineering (1999) 12, No.5, 387-394
3. Eisenhaber B., Bork P., Eisenhaber F.  
"Prediction of potential GPI-modification sites in proprotein sequences"  
JMB (1999) 292 (3), 741-758
4. Eisenhaber B., Bork P., Yuan Y., Loeffler G., Eisenhaber F.  
"Automated annotation of GPI anchor sites: case study *C.elegans*"  
TIBS (2000) 25 (7), 340-341

## Output of the prediction tool:

```

~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~
Query sequence Query (length 581 amino acids):
MYLSRFLSIH ALWVTVSSVM QPYPLVWGHY DLCKTQIYTE EGKVDYMAC QPESTDMTKY
LKVKLDPPDI TCGDPPETF C AMGNPYMCNN ECDASTPELA HPELMFDFE GRHPSTFWQS
ATWKEYPKPL QVNITLSWSK TIELTDNIVI TFESGRPDQM ILEKSLDYGR TWQPYQYYAT
DCLDAFHMDP KSVKDL SQHT VLEIICTE EY STGYTTNSKI IHFEIKDRFA FFAGPRLRNM
ASLYGQLD TT KKL R DFFTVT DL R I R L L R P A V G E I F V D E L H L A R Y F Y A I S D I K V R G R C K C N
LHATVCVYDN SKLTCECEHN TTGPDCGKCK KNYQGRPWSP GSYLPIPKGT ANTCIPSISS
IGNPPKFNRI WPNISSLEVS NPKQVAPKLA LSTVSSVQVA NHKRDCECFG HSNRCSYIDL
LNTVICVSK HNTRGQHCEL CRLGYFRNAS AQLDDENVCI ECYCNPLGSI HDRCNGSGFC
ECKTGTGTPK CDECLPGNSW HYGCQPNVCD NELLHCQNGG TCHNNVRCLC PAAYTGILCE
KLRCEEAGSC GSDSGQGAPP HGSPALLLLT TLLGTASPLV F

```

## Prossellkov P (2016) Cognitive domains function complementation by NTNG gene paralogs

Best predicted site is shown in red. Alternative site (second best) is shown in orange.

~~~~~  
 Prediction of potential C-terminal GPI-Modification Sites  
 ~~~~~

Use of the prediction function for METAZOA

Potential GPI-modification site was found.

Quality of the site ..... : P

Sequence position of the omega-site :

**555**  
 Score of the best site ..... : **7.07** (PValue = 4.524022e-04)

Potential alternative GPI-modification site was found (second best site).

Quality of the site ..... : P

Sequence position of the omega-site : **552**

Score of the site ..... : **3.13** (PValue = 9.713128e-04)



	Best Site	Alternative Site
<b>Total Score.....</b>	<b>7.07</b>	<b>3.13</b>
Components of the Score Function:		
Profile Score.....	7.36	3.45
Term 0 Contents and Windows of DE in Region [-11..1].....	0.00	0.00
Term 1 Hydrophilicity of N-terminal Region [-11..1].....	0.00	0.00
Term 2 Penalty for low Profile Score in Region [0..2].....	0.00	0.00
Term 3 Volume Limitation [-1..+2].....	0.00	0.00
Term 4 Volume Compensation (-1, 1, 2).....	0.00	0.00
Term 5 Volume Compensation (-1, 2).....	0.00	0.00
Term 6 Backbone Flexibility [-1..2].....	0.00	0.00
Term 7 Propeptide Length.....	0.00	0.00
Term 8 Hydrophilicity of Spacer Region [3..8].....	0.00	0.00
Term 9 Volume Limitation [3..8].....	0.00	0.00
Term 10 Penalty for charged AAs in Spacer Region [3..10]....	0.00	0.00
Term 11 Backbone Flexibility [3..8]....	0.00	0.00
Term 12 Penalty for low Profile Score in Region [10..end]..	0.00	0.00
Term 13 Hydrophobicity of Tail [10..end].....	0.00	-0.02
Term 14 Hydrophobicity of Tail [26..end].....	-0.29	-0.29
Term 15 Even Distribution of Hydrophobicity [9..end].....	0.00	0.00
Term 16 Penalty for polar Windows in Region [10..end].....	0.00	0.00
Term 17 Penalty for SGC-Windows in Region [10..end].....	0.00	0.00
Term 18 LVI Contents [10..end].....	0.00	0.00
Term 19 Penalty for FYHW - Sections in Region [10..end]....	0.00	0.00
Term 20 Penalty for Windows with small Volume [10..end]....	0.00	0.00
Profile independent Score.....	-0.29	-0.31

*Last modified 17th June, 2005*





GPI Lipid Anchor Project



# big-PI Predictor

## The GPI Prediction Server

Version 3.0, June 2005

### Please, refer to ...

1. Eisenhaber B., Bork P., Eisenhaber F.  
"Sequence properties of GPI-anchored proteins near the omega-site: constraints for the polypeptide binding site of the putative transamidase"  
Protein Engineering (1998) 11, No.12, 1155-1161
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"Prediction of potential GPI-modification sites in proprotein sequences"  
Protein Engineering (1999) 12, No.5, 387-394
3. Eisenhaber B., Bork P., Eisenhaber F.  
"Prediction of potential GPI-modification sites in proprotein sequences"  
JMB (1999) 292 (3), 741-758
4. Eisenhaber B., Bork P., Yuan Y., Loeffler G., Eisenhaber F.  
"Automated annotation of GPI anchor sites: case study *C.elegans*"  
TIBS (2000) 25 (7), 340-341

### Output of the prediction tool:

```

~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~
Query sequence Query (length 587 amino acids):
MLHLLALFLH CLPLASGDYD ICKSWVTTDE GPTWEFYACQ PKVMRLKDYV KVKVEPSGIT
CGDPPERFCS HENPYLCSNE CDASNPDLAH PPRLMFDKEE EGLATYWQSI TWSRYPSPLE
ANITLSWNKT VELTDDVMT FEYGRPTVMV LEKSLDNGRT WQPYQFYAED CMEAFGMSAR
RARDMSSSSA HRVLCTEEYS RWAGSKKEKH VRFEVDRDFA IFAGPDLRNM DNLYTRLESA
KGLKEFFTLT DLRMRLRPA LGGTYYVQREN LYKYFYAISN IEVIGRCKCN LHANLCSMRE
GSLQCECEHN TTGPDCGKCK KNFRTSWRA GSYLPLPHGS PNACATAGSF GKWTRPSTAA
PLSSRWSQVA SRAEAVGTPA AAPAPAKGYK LFQLKPKSPQ VMPIEEFQDC ECGHNSRCS
YIDFLNVVTC VSCKHNTRGQ HCQHCR LGYY RNSAELDDE NVCIECNCNQ IGSVHDCNE
TGFCECREGA AGPKCDDCLP THYWRQGCYP NVCDDDQLLC QNGGTCLQNO RCACPRGYTG
VRCEQPRCDP ADDDGGLDCD RAPGAAPRPA TLLGCLLLLG LAARLGR

```

## Prossellkov P (2016) Cognitive domains function complementation by NTNG gene paralogs

Best predicted site is shown in red. Alternative site (second best) is shown in orange.

~~~~~  
 Prediction of potential C-terminal GPI-Modification Sites  
 ~~~~~

Use of the prediction function for METAZOA

Potential GPI-modification site was found.

Quality of the site ..... : P

Sequence position of the omega-site :

**564**  
 Score of the best site ..... : **7.58** (PValue = 4.070180e-04)

Potential alternative GPI-modification site was found (second best site).

Quality of the site ..... : S

Sequence position of the omega-site : **560**

Score of the site ..... : **-4.00** (PValue = 3.106230e-03)



	Best Site	Alternative Site
<b>Total Score</b> .....	<b>7.58</b>	<b>-4.00</b>
Components of the Score Function:		
Profile Score.....	7.71	-1.35
Term 0 Contents and Windows of DE in Region [-11..1].....	0.00	0.00
Term 1 Hydrophilicity of N-terminal Region [-11..1].....	0.00	0.00
Term 2 Penalty for low Profile Score in Region [0..2].....	0.00	0.00
Term 3 Volume Limitation [-1..+2].....	0.00	-1.42
Term 4 Volume Compensation (-1, 1, 2).....	0.00	-1.16
Term 5 Volume Compensation (-1, 2).....	0.00	0.00
Term 6 Backbone Flexibility [-1..2].....	0.00	0.00
Term 7 Propeptide Length.....	0.00	0.00
Term 8 Hydrophilicity of Spacer Region [3..8].....	0.00	0.00
Term 9 Volume Limitation [3..8].....	-0.06	0.00
Term 10 Penalty for charged AAs in Spacer Region [3..10]....	0.00	0.00
Term 11 Backbone Flexibility [3..8]....	0.00	0.00
Term 12 Penalty for low Profile Score in Region [10..end]..	0.00	0.00
Term 13 Hydrophobicity of Tail [10..end].....	0.00	0.00
Term 14 Hydrophobicity of Tail [26..end].....	-0.07	-0.07
Term 15 Even Distribution of Hydrophobicity [9..end].....	0.00	0.00
Term 16 Penalty for polar Windows in Region [10..end].....	0.00	0.00
Term 17 Penalty for SGC-Windows in Region [10..end].....	0.00	0.00
Term 18 LVI Contents [10..end].....	0.00	0.00
Term 19 Penalty for FYHW - Sections in Region [10..end]....	0.00	0.00
Term 20 Penalty for Windows with small Volume [10..end]....	0.00	0.00
Profile independent Score.....	-0.14	-2.65

*Last modified 17th June, 2005*