

# REŠITVE SEMINARJA S1-07

## Naloga 1

### 1. Katerima organizmoma pripadata zaporedji?

#### Zaporedje 1:

<input checked="" type="checkbox"/> select all 100 sequences selected <span style="float: right;"> <a href="#">GenBank</a> <a href="#">Graphics</a> <a href="#">Distance tree of results</a> <a href="#">MSA Viewer</a> </span>									
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	
<input checked="" type="checkbox"/> <a href="#">Rhodobacter sphaeroides gene for cytochrome oxidase subunit 1</a>	<a href="#">Cereibacter sphaeroi...</a>	3068	3068	100%	0.0	100.00%	2177	<a href="#">X62645.2</a>	
<input checked="" type="checkbox"/> <a href="#">Cereibacter sphaeroides strain MBTLJ-13 chromosome 1 complete sequence</a>	<a href="#">Cereibacter sphaeroi...</a>	3064	3064	100%	0.0	99.94%	3188543	<a href="#">CP015210.1</a>	
<input checked="" type="checkbox"/> <a href="#">Cereibacter sphaeroides strain 2.4.1 substr. H2 chromosome 1 complete sequence</a>	<a href="#">Cereibacter sphaeroi...</a>	3064	3064	100%	0.0	99.94%	3188565	<a href="#">CP186567.1</a>	
<input checked="" type="checkbox"/> <a href="#">Cereibacter sphaeroides 2.4.1 chromosome 1 complete sequence</a>	<a href="#">Cereibacter sphaeroi...</a>	3064	3064	100%	0.0	99.94%	3188530	<a href="#">CP030271.1</a>	
<input checked="" type="checkbox"/> <a href="#">Cereibacter sphaeroides strain DSM 158 chromosome 1 complete sequence</a>	<a href="#">Cereibacter sphaeroi...</a>	3064	3064	100%	0.0	99.94%	3190321	<a href="#">CP047031.1</a>	

#### Rhodobacter sphaeroides gene for cytochrome oxidase subunit 1

GenBank: X62645.2

[FASTA](#) [Graphics](#)

[Go to:](#)

LOCUS X62645 2177 bp DNA linear BCT 24-JUL-2002  
 DEFINITION Rhodobacter sphaeroides gene for cytochrome oxidase subunit 1.  
 ACCESSION X62645  
 VERSION X62645.2  
 KEYWORDS cytochrome oxidase subunit 1.  
 SOURCE Cereibacter sphaeroides GA  
 ORGANISM [Cereibacter sphaeroides GA](#)  
 Bacteria; Pseudomonadati; Pseudomonadota; Alphaproteobacteria;  
 Rhodobacterales; Paracoccaceae; Cereibacter.  
 REFERENCE 1 (bases 1 to 2166)  
 AUTHORS Shapleigh,J.P. and Gennis,R.B.  
 TITLE Cloning, sequencing and deletion from the chromosome of the gene  
 encoding subunit I of the aa3-type cytochrome c oxidase of  
 Rhodobacter sphaeroides  
 JOURNAL Mol. Microbiol. 6 (5), 635-642 (1992)  
 PUBMED [1313140](#)  
 REFERENCE 2 (bases 1 to 2177)  
 AUTHORS Shapleigh,J.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-OCT-1991) J.P. Shapleigh, University of Illinois,  
 Dept of Biochemistry, 595 S Mathews, Urbana IL 61801, USA  
 COMMENT On Jul 25, 2002 this sequence version replaced [X62645.1](#).  
 FEATURES  
 Location/Qualifiers  
 source 1..2177  
 /organism="Cereibacter sphaeroides GA"  
 /mol\_type="genomic DNA"  
 /strain="GA"  
 /db\_xref="taxon:633146"  
 protein\_bind 86..99  
 /bound\_moiety="transcriptional activator protein FnrL"  
 CDS 211..1911  
 /codon\_start=1  
 /transl\_table=11  
 /product="cytochrome oxidase subunit 1"  
 /protein\_id="CAA44514.2"  
 /db\_xref="GDA:P33512"  
 /db\_xref="InterPro:IPR008883"  
 /db\_xref="InterPro:IPR014241"  
 /db\_xref="PDB:1M56"  
 /db\_xref="PDB:1M57"  
 /db\_xref="PDB:2G5H"  
 /db\_xref="PDB:3DUU"  
 /db\_xref="PDB:3FJE"  
 /db\_xref="PDB:3FV1"  
 /db\_xref="UniProtKB/Swiss-Prot:P33512"

#### Zaporedje 2:

<input checked="" type="checkbox"/> select all 100 sequences selected <span style="float: right;"> <a href="#">GenBank</a> <a href="#">Graphics</a> <a href="#">Distance tree of results</a> <a href="#">MSA Viewer</a> </span>									
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	
<input checked="" type="checkbox"/> <a href="#">Bos taurus thrombospondin 1 (THBS1) mRNA</a>	<a href="#">Bos taurus</a>	6336	6517	100%	0.0	100.00%	5269	<a href="#">NM_174196.1</a>	
<input checked="" type="checkbox"/> <a href="#">PREDICTED: Bos taurus thrombospondin 1 (THBS1) transcript variant X1 mRNA</a>	<a href="#">Bos taurus</a>	6299	6480	100%	0.0	99.74%	5801	<a href="#">XM_024997243.2</a>	
<input checked="" type="checkbox"/> <a href="#">PREDICTED: Bos indicus thrombospondin 1 (THBS1) transcript variant X2 mRNA</a>	<a href="#">Bos indicus</a>	6295	6477	100%	0.0	99.74%	5806	<a href="#">XM_019968496.2</a>	
<input checked="" type="checkbox"/> <a href="#">PREDICTED: Bos indicus x Bos taurus thrombospondin 1 (THBS1) transcript variant X2 mRNA</a>	<a href="#">Bos indicus x Bos taurus</a>	6291	6472	100%	0.0	99.72%	5801	<a href="#">XM_027553498.1</a>	
<input checked="" type="checkbox"/> <a href="#">PREDICTED: Bos indicus thrombospondin 1 (THBS1) transcript variant X1 mRNA</a>	<a href="#">Bos indicus</a>	6286	6467	100%	0.0	99.66%	5809	<a href="#">XM_070797250.1</a>	
<input checked="" type="checkbox"/> <a href="#">PREDICTED: Bos indicus x Bos taurus thrombospondin 1 (THBS1) transcript variant X1 mRNA</a>	<a href="#">Bos indicus x Bos taurus</a>	6281	6462	100%	0.0	99.63%	5804	<a href="#">XM_027553497.1</a>	
<input checked="" type="checkbox"/> <a href="#">PREDICTED: Bison bison bison thrombospondin 1 (THBS1) transcript variant X1 mRNA</a>	<a href="#">Bison bison bison</a>	6268	6450	100%	0.0	99.57%	5809	<a href="#">XM_010847929.1</a>	
<input checked="" type="checkbox"/> <a href="#">PREDICTED: Bos mutus thrombospondin 1 (THBS1) transcript variant X2 mRNA</a>	<a href="#">Bos mutus</a>	6264	6450	100%	0.0	99.54%	5797	<a href="#">XM_014482984.2</a>	
<input checked="" type="checkbox"/> <a href="#">PREDICTED: Bos javanicus thrombospondin 1 (THBS1) transcript variant X2 mRNA</a>	<a href="#">Bos javanicus</a>	6255	6440	100%	0.0	99.49%	5796	<a href="#">XM_061430722.1</a>	

## Bos taurus thrombospondin 1 (THBS1), mRNA

NCBI Reference Sequence: NM\_174196.1

[FASTA](#) [Graphics](#)

[Go to:](#)

LOCUS NM\_174196 5269 bp mRNA linear MAM 23-JUN-2025  
DEFINITION Bos taurus thrombospondin 1 (THBS1), mRNA.  
ACCESSION NM\_174196  
VERSION NM\_174196.1  
KEYWORDS RefSeq.  
SOURCE Bos taurus (domestic cattle)  
ORGANISM Bos\_taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Artiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 5269)  
AUTHORS Farberov,S. and Meidan,R.  
TITLE Fibroblast growth factor-2 and transforming growth factor-beta1  
oppositely regulate miR-221 that targets thrombospondin-1 in bovine  
luteal endothelial cells  
JOURNAL Biol Reprod 98 (3), 366-375 (2018)  
PUBMED 29283113  
REMARK GeneREF: These data support the contention that FGF2 and TGFBI  
modulate THBS1 via miR-221.  
REFERENCE 2 (bases 1 to 5269)  
AUTHORS Berisha,B., Schams,D., Rodler,D., Sinowatz,F. and Pfaffl,M.W.  
TITLE Expression and localization of members of the thrombospondin family  
during final follicle maturation and corpus luteum formation and  
function in the bovine ovary  
JOURNAL J Reprod Dev 62 (5), 501-510 (2016)  
PUBMED 27396384

Zaporedje 1 in 2 identificiramo z blast-om. Prvo zaporedje zapisuje citokrom c oksidazno podenoto 1 pri Rhodobacter sphaeroides in drugo zaporedje kravji trombospodin 1 (Bos taurus).

2. Kje v celici najdemo protein 1 in kakšno maso ima (Da)?

Protein 1 poiščemo v UniProt.

### P33517 · COX1\_CERSP

Protein<sup>i</sup> | Cytochrome c oxidase subunit 1

Gene<sup>1</sup> | ctaD

Status<sup>1</sup> | UniProtKB reviewed (Swiss-Prot)

Organism<sup>1</sup> | Cereibacter sphaeroides (Rhodobacter sphaeroides)

Amino acids | 566 (go to sequence)

Protein existence<sup>1</sup> | Evidence at protein level

Annotation score<sup>1</sup> |

[Entry](#) [Variant viewer](#) [Feature viewer](#) [Genomic coordinates](#) [Publications](#) [External links](#) [History](#)

[Tools](#) [Download](#) [Add](#) [Add a publication](#) [Entry feedback](#)

#### Function<sup>i</sup>

Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-3 form the functional core of the enzyme complex. Co I is the catalytic subunit of the enzyme. Electrons originating in cytochrome c are transferred via the copper A center of subunit 2 and heme a of subunit 1 to the bimetallic center formed by heme a<sub>3</sub> and copper B. This cytochrome c oxidase shows proton pump activity across the membrane in addition to the electron transfer.

#### Catalytic activity<sup>1</sup>

Rhea:11436

4 Fe(II)-[cytochrome c] + O<sub>2</sub> + 8 H<sup>+</sup>(in) = 4 Fe(III)-[cytochrome c] + 2 H<sub>2</sub>O + 4 H<sup>+</sup>(out)

EC:7.1.1.9 (UniProtKB | ENZYME | Rhea )

[Hide reaction details](#)

[Reaction](#) [Atom map](#)

#### Subcellular Location

[UniProt Annotation](#) [GO Annotation](#)

Cell membrane - Membrane protein



#### Sequence<sup>i</sup>

Sequence status<sup>1</sup> | Complete

See also sequence in UniParc or sequence clusters in UniRef

[Tools](#) [Download](#) [Add](#) [Highlight](#) [Copy sequence](#)

Length 566

Mass (Da) 63.147

Last updated 2003-01-17 v2

MD5 Checksum<sup>1</sup> 99B214973139B7D8

229B1BC9A72DD480

Protein 1 je transmembranski protein – najdemo ga v celični membrani. Maso najdemo pod Sequence - masa je 63 147 Da.

### 3. Kako dolg je signalni peptid zaporedja 2?

Dolžina signalnega peptida v zaporedju 2 je  $201 - 147 = 54$  nukleotidov (oziroma 18 aminokislinskih ostankov – UniProt). Podatke najdemo v GenBank.

```
sig_peptide 148..201
/gene="THBS1"
/gene_synonym="THBS"
/note="evidence=ECO:0000250; propagated from
UniProtKB/Swiss-Prot (Q28178.2)"
```

### 4. Kakšne posttranslacijske modifikacije so prisotne pri proteinu 2?

Protein 2 poiščemo v UniProt.

**Q28178 · TSP1\_BOVIN**

Protein<sup>1</sup> | Thrombospondin-1 | Amino acids | 1170 (go to sequence)

Gene<sup>1</sup> | THBS1 | Protein existence<sup>1</sup> | Evidence at transcript level

Status<sup>1</sup> | UniProtKB reviewed (Swiss-Prot) | Annotation score<sup>1</sup> | 59

Organism<sup>1</sup> | Bos taurus (Bovine)

Entry | Variant viewer | Feature viewer | Genomic coordinates | Publications | External links | History

Tools | Download | Add | Add a publication | Entry feedback

#### Function<sup>1</sup>

Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Multifunctional, involved in inflammation, angiogenesis, wound healing, reactive oxygen species (ROS) signaling, nitrous oxide (NO) signaling, apoptosis, senescence, aging, cellular self-renewal, stemness, and cardiovascular and metabolic homeostasis. Negatively modulates dendritic cell activation and cytokine release, as part of an autocrine feedback loop, contributing to the resolution of inflammation and immune homeostasis. Ligand for receptor CD47 (By similarity). Modulates nitrous oxide (NO) signaling via CD47, hence playing a role as a pressor agent, supporting blood pressure (By similarity). Plays a role in endothelial cell senescence, acting via CD47, by increasing the abundance and activation of NADPH oxidase NOX1, and so generating excess ROS (By similarity). Inhibits stem cell self-renewal, acting via CD47 signaling, probably by regulation of the stem cell transcription factors POU5F1/OCT4, SOX2, MYC/c-Myc and KLF4. Negatively modulates wound healing, acting via CD47 (By similarity). Ligand for receptor CD36 (By similarity). Involved in inducing apoptosis in podocytes in response to elevated free fatty acids, acting via CD36 (By similarity). Plays a role in suppressing angiogenesis, acting, depending on context, via CD36 or CD47. Promotes cellular senescence in a TP53-CDKN1A-RB1 signaling-dependent manner. Ligand for immunoglobulin-like cell surface receptor SIRPA. Involved in ROS signaling in non-phagocytic cells, stimulating NADPH oxidase-derived ROS production, acting via interaction with SIRPA (By similarity). Plays a role in metabolic dysfunction in diet-induced obesity, perhaps acting by exacerbating adipose inflammatory activity, its effects may be mediated, at least in part, through enhanced adipocyte proliferation. Plays a role in ER stress response, via its interaction with the activating transcription factor 6 alpha (ATF6) which produces adaptive ER stress response factors (By similarity). May be involved in age-related conditions, including metabolic dysregulation, during normal aging (By similarity). [By Similarity](#)

Posttranslacijske modifikacije najdemo pod PMT/Processing - disulfidne vezi in glikozilacija.

### 5. Napiši max score in Uniprot kodo za homolog proteina 1 v organizmu 2. Zapiši na katerih mestih v zapisu proteina je transmembranska regija 6.

Homolog poiščemo z blastp:

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> cytochrome c oxidase subunit I [Bos taurus]	Bos taurus	527	527	95%	0.0	50.46%	514	<a href="#">UFG26479.1</a>
<input checked="" type="checkbox"/> cytochrome c oxidase subunit I [Bos taurus]	Bos taurus	523	523	95%	0.0	50.46%	514	<a href="#">UFG26830.1</a>
<input checked="" type="checkbox"/> cytochrome c oxidase subunit I [Bos taurus]	Bos taurus	522	522	95%	0.0	50.46%	514	<a href="#">AGU00420.1</a>
<input checked="" type="checkbox"/> cytochrome c oxidase subunit I [Bos taurus]	Bos taurus	522	522	95%	0.0	50.46%	514	<a href="#">ALM02894.1</a>
<input checked="" type="checkbox"/> Chain N_Cytochrome c oxidase subunit 1 [Bos taurus]	Bos taurus	522	522	95%	0.0	50.46%	513	<a href="#">8D4T_N</a>

Max score je 527.

Protein nato najdemo še v UniProt – UniProt koda je P00396.

**P00396 · COX1\_BOVIN**

Protein<sup>1</sup> | Cytochrome c oxidase subunit 1 | Amino acids | 514 (go to sequence)

Gene<sup>1</sup> | MT-CO1 | Protein existence<sup>1</sup> | Evidence at protein level

Status<sup>1</sup> | UniProtKB reviewed (Swiss-Prot) | Annotation score<sup>1</sup> | 59

Organism<sup>1</sup> | Bos taurus (Bovine)

Transmembranske regije najdemo v UniProt pod razdelkom Features. Vidimo lahko, da protein vsebuje 12 transmembranskih regij. Regija 6 je na pozicijah 228 – 261.

TYPE	ID	POSITION(S)	DESCRIPTION
Transmembrane			
+ Transmembrane		12-40	Helical; Name=I <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		51-86	Helical; Name=II <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		95-117	Helical; Name=III <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		141-170	Helical; Name=IV <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		183-212	Helical; Name=V <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		228-261	Helical; Name=VI <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		270-286	Helical; Name=VII <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		299-327	Helical; Name=VIII <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		336-357	Helical; Name=IX <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		371-400	Helical; Name=X <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		407-433	Helical; Name=XI <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>
+ Transmembrane		447-478	Helical; Name=XII <a href="#">1 Publication</a> <a href="#">Tools</a> <a href="#">Add</a>

6. Koliko znanstvenih člankov, ki v naslovu vsebujejo znanstveno ime organizma 2, je bilo objavljenih med letoma 2020 in 2022 (vključno s tema dvema letoma)?

Odgovor poiščemo v PubMed – 166 člankov.

PubMed search results for the query: (Bos taurus[Title]) AND (("2020"[Date - Publication] : "2022"[Date - Publication]).

166 results

RESULTS BY YEAR

2019 2026

MY CUSTOM FILTERS

1 **Bos taurus** haplotypes segregating in Nelore (*Bos indicus*) cattle.

1 Utsunomiya YT, Fortunato AAAD, Milanesi M, Trigo BB, Alves NF, Sonstegard TS, Garcia JF. Anim Genet. 2022 Feb;53(1):58-67. doi: 10.1111/age.13164. Epub 2021 Dec 17. PMID: 34921423

2 Human-Animal Interactions with **Bos taurus** Cattle and Their Impacts on On-Farm Safety: A Systematic Review.

2 Titterington FM, Knox R, Buijs S, Lowe DE, Morrison SJ, Lively FO, Shirali M. Animals (Basel). 2022 Mar 19;12(6):776. doi: 10.3390/ani12060776. PMID: 35327173 [Free PMC article](#). Review.

## NALOGA 2

1. Napiši aminokislinski ostanek, ki se pojavlja v vezavnem mestu. Kateri ion se veže na to mesto?

Spondin 1 poiščemo v UniProt. Aminokislinski ostanek v vezavnem mestu za  $\text{Ca}^{2+}$  je D – asparaginska kislina.

**Features**  
Showing features for binding site<sup>1</sup>.

TYPE	ID	POSITION(S)	DESCRIPTION
- Binding site		325	$\text{Ca}^{2+}$ (UniProtKB   ChEBI) <a href="#">By Similarity</a>
Sequence: D			
- Binding site		354	$\text{Ca}^{2+}$ (UniProtKB   ChEBI) <a href="#">By Similarity</a>
Sequence: D			
- Binding site		358	$\text{Ca}^{2+}$ (UniProtKB   ChEBI) <a href="#">By Similarity</a>
Sequence: D			

2. Je ta protein podoben kateremu od zgornjih proteinov? Če ja, koliko mest je identičnih?

Na UniProt preverimo, kakšne domene vsebujeta proteina 1 in 2. Človeški spondin 1 in trombospondin 1 (protein 2) imata ponovitve TSP tip-1 domene. Naredimo lokalno poravnavo – najdemo 104 identičnih mest. Domene lahko prav tako primerjamo z Interpro.

Za primerjavo:

lokalna poravnava


```
#=====
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 453
# Identity: 104/453 (23.0%)
# Similarity: 148/453 (32.7%)
# Gaps: 162/453 (35.8%)
# Score: 284.0
#
#
#=====
```

globalna poravnava

```
#=====
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 20.0
# Extend_penalty: 0.5
#
# Length: 1572
# Identity: 104/1572 ( 6.6%)
# Similarity: 162/1572 (10.3%)
# Gaps: 1167/1572 (74.2%)
# Score: 41.5
#
#
#=====
```

3. V kakšnem ekspresijskem sistemu je bila izražena struktura spondina 1 z resolucijo 2.00 Å?

Pod zavihkom Structure v UniProtu so napisane PDB kode. Potrebno je izbrati tretjo (2.00 Å resolucija) ter jo poiskati v PDB – 3COO. Ekspresijski sistem je *Drosophila melanogaster*.

 3COO | pdb\_00003coo 


The crystal structure of Reelin-N domain of F-spondin

PDB DOI: <https://doi.org/10.2210/pdb3COO/pdb>

Classification: CELL ADHESION

Organism(s): [Homo sapiens](#)

Expression System: [Drosophila melanogaster](#)

Mutation(s): No 

4. Kakšna je izoelektrična točka spondina 1?

Za iskanje uporabimo ProtParam. Izelektrična točka je pri pH 5.85.

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Number of amino acids: 807

Theoretical pI: 5.85

Molecular weight: 90973.48