

1. TOC – TIC translokon

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Molecule of the Month

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Grid List

2025 2024 2023 2022 2021 2020 2019 2018 2017 2016 2015 2014 2013 2012 2011

2010 2009 2008 2007 2006 2005 2004 2003 2002 2001 2000

May 2025
TOC-TIC Translocon

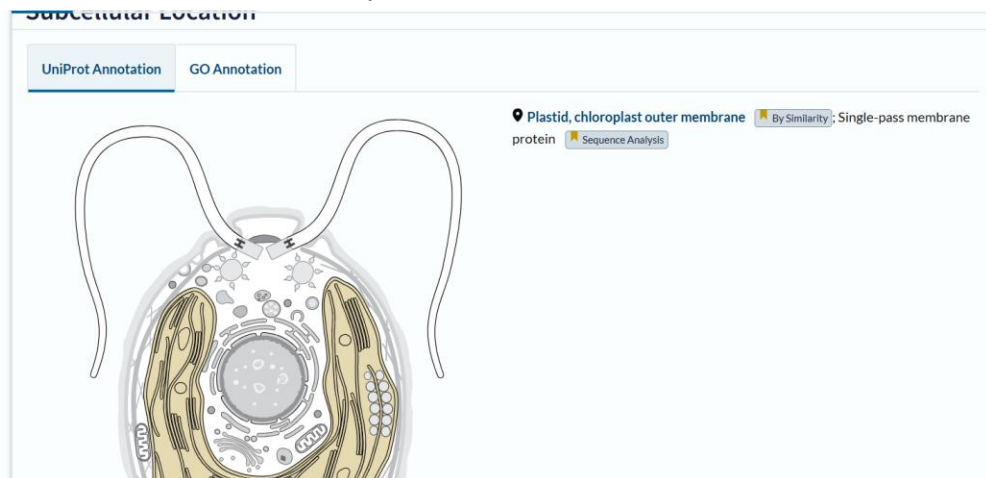
April 2025
Apolipoprotein B-100 and LDL
Receptor

March 2025
Enoyl-CoA
Carboxylases/Reductases

February 2025
H5 Hemagglutinin

January 2025
Assembly Line Polyketide
Synthases

2. Na/med membranah kloroplastov



3. Prenašanje proteinov v in iz kloroplastov

Peptide search ID mapping SPARQL UniProtKB

Advanced | List Search

A8HYJ1 · TOC34_CHLRE

Proteinⁱ Translocase of chloroplast 34 homolog, chloroplastic
 Geneⁱ TOC34
 Statusⁱ UniProtKB reviewed (Swiss-Prot)
 Organismⁱ Chlamydomonas reinhardtii (Chlamydomonas smithii)

Amino acids 397 (go to sequence)
 Protein existenceⁱ Evidence at protein level
 Annotation scoreⁱ (4/5)

Entry Variant viewer Feature viewer Genomic coordinates Publications External links History

Tools Download Add Add a publication Entry feedback

Functionⁱ

GTPase involved in protein precursor import into chloroplasts. Seems to recognize chloroplast-destined precursor proteins and regulate their presentation to the translocation channel through GTP hydrolysis (By similarity).
 Functions as an essential component of the outer chloroplast membrane translocon (TOC) complex, which, in turn, catalyzes the import of nucleus-encoded precursor polypeptides from the cytoplasm to the chloroplast (PubMed:23167510). [By Similarity](#) [1 Publication](#)

Cofactorⁱ

Mg²⁺ (UniProtKB | Rhea [↗](#) | ChEBI:18420 [↗](#)) [By Similarity](#)
 Note: Binds 1 Mg²⁺ ion by subunit. [By Similarity](#)

4. EM, ker je velik kompleks in membranski protein.
5. TIM, TOM kompleksa
6. Mg²⁺, na mesto 106, serin

Cofactorⁱ

Mg²⁺ (UniProtKB | Rhea [↗](#) | ChEBI:18420 [↗](#)) [By Similarity](#)
 Note: Binds 1 Mg²⁺ ion by subunit. [By Similarity](#)

Features

Showing features for binding siteⁱ.



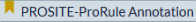



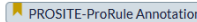







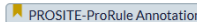





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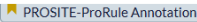





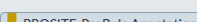



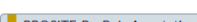



97 50 100 150 200 250 300 350 126

L L G K S S V G K S S L I N S L L G E A V V R V Q A F K L Q

±	TYPE	ID	POSITION(S)	DESCRIPTION	
+	Binding site		102-107	GTP (UniProtKB ChEBI ↗)	By Similarity Tools Add
+	Binding site		106	Mg ²⁺ (UniProtKB ChEBI ↗)	By Similarity
+	Binding site		121-126	GTP (UniProtKB ChEBI ↗)	By Similarity Tools Add

7. GTP vezavne domene: AIG1-type G, G1 do G5

 	All	ID	POSITION(S)	DESCRIPTION	
+	Domain		90-321	AIG1-type G 	 Tools   Add
+	Region		99-106	G1 	 Tools   Add
+	Region		121-124	Homodimerization 	 Tools   Add
+	Region		126-130	G2 	 Tools   Add
					 Tools 


 	TYPE	ID	POSITION(S)	DESCRIPTION	
+	Region		155-158	G3 	 Add
+	Region		193-198	Homodimerization 	 Tools   Add
+	Region		227-230	G4 	 Tools   Add
+	Region		271-273	G5 	 Tools   Add

8. AKR2A-binding sequence/motiv, vezava z AKR2A (Ankyrin repeat-containing protein 2A).

-




Motif

350-358

AKR2A-binding sequence (ABS) required for chloroplast outer envelope membrane targeting 

Manual assertion inferred from sequence similarityⁱ

UniProtKB: Q38906

 Tools 
 Add

Sequence: DDNQRRVER

9. A) Uporabi Blast
 B) V blastu jih razvrsti po Per. Ident in izberi tisti protein z največjim % ujemanja, izbereš en protein na organizem.

<input type="checkbox"/> select all	7 sequences selected	GenPept	Graphics	Distance tree of results	Multiple alignment	MSA Viewer			
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input type="checkbox"/>	uncharacterized protein CHLRE_06g252200v5 [Chlamydomonas reinhardtii]	Chlamydomonas reinhardtii	797	797	100%	0.0	100.00%	397	XP_001696644.1
<input type="checkbox"/>	TOC34m [Chlamydomonas reinhardtii]	Chlamydomonas reinhardtii	783	783	100%	0.0	97.23%	397	ADF43174.1
<input type="checkbox"/>	hypothetical protein HXX76_011027 [Chlamydomonas incerta]	Chlamydomonas incerta	639	639	100%	0.0	86.93%	398	KAG2429258.1
<input type="checkbox"/>	hypothetical protein HYH02_011261 [Chlamydomonas schloesseri]	Chlamydomonas schloesseri	663	663	100%	0.0	85.71%	395	KAG2437622.1
<input checked="" type="checkbox"/>	Translocase of chloroplast 33, chloroplastic [Tetrahena socialis]	Tetrahena socialis	164	164	25%	8e-45	83.67%	189	PNH07472.1
<input type="checkbox"/>	hypothetical protein HYH03_009068 [Edaphochlamys debaryana]	Edaphochlamys debaryana	511	511	84%	1e-177	72.75%	394	KAG2492652.1
<input checked="" type="checkbox"/>	hypothetical protein Vafri_9118 [Volvox africanus]	Volvox africanus	520	520	88%	0.0	72.24%	378	GIL53542.1
<input type="checkbox"/>	Translocase of chloroplast [Pleodorina starnii]	Pleodorina starnii	499	499	84%	2e-173	71.51%	385	GLC41020.1
<input type="checkbox"/>	translocon at the outer envelope membrane of chloroplasts 34 [Volvox africanus]	Volvox africanus	516	516	88%	1e-179	71.10%	378	GLI67129.1
<input type="checkbox"/>	hypothetical protein Agub_g4168 [Astrophomena gubernaculifera]	Astrophomena gubernaculifera	476	476	90%	3e-164	70.67%	378	GFR43145.1
<input type="checkbox"/>	translocon at the outer envelope membrane of chloroplasts 34 [Volvox reticuliferus]	Volvox reticuliferus	490	490	84%	1e-169	70.06%	378	BCL66247.1
<input type="checkbox"/>	translocon at the outer envelope membrane of chloroplasts 34 [Volvox reticuliferus]	Volvox reticuliferus	496	496	94%	2e-170	65.87%	469	BCL66170.1
<input checked="" type="checkbox"/>	AlG1-type G domain-containing protein, partial [Haematococcus lacustris]	Haematococcus lacustris	192	192	36%	3e-56	65.49%	142	GFH16887.1
<input type="checkbox"/>	TOC34f [Volvox carteri f. nagariensis]	Volvox carteri f. nagariensis	484	484	92%	2e-167	63.73%	381	ADI46839.1
<input type="checkbox"/>	uncharacterized protein VOLCADRAFT_121696 [Volvox carteri f. nagariensis]	Volvox carteri f. nagariensis	485	485	92%	3e-166	63.73%	465	XP_002958289.1
<input type="checkbox"/>	TOC34m [Volvox carteri f. nagariensis]	Volvox carteri f. nagariensis	474	474	95%	3e-163	62.70%	378	ADI46934.1
<input type="checkbox"/>	hypothetical protein VaNZ11_011202, partial [Volvox africanus]	Volvox africanus	171	171	32%	5e-48	61.24%	149	GLI67028.1
<input type="checkbox"/>	chloroplast outer envelope protein [Gonium pectorale]	Gonium pectorale	415	415	88%	1e-140	59.71%	353	BAU61571.1
<input type="checkbox"/>	chloroplast outer envelope protein [Gonium pectorale]	Gonium pectorale	416	416	88%	1e-140	58.86%	353	BAU61608.1

10. Prenesi FASTA datoteke izbranih proteinov in jih vstavi v Clustal Omega. Izvedi poravnavo in odpri »result files«, tam poišči »Percent Identity Matrix«.

Najmanj podobna: XP_020105011.1 s PNH07472.1 (24,86 %)

Najbolj podobna: XP_020105011.1 z XP_064946005.1 (83,01 %)

```
#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
```

1:	KAL2622096.1	100.00	64.60	62.78	65.05	27.91	44.53	36.22	33.95
2:	XP_020272270.1	64.60	100.00	79.59	80.61	26.38	47.66	36.14	35.19
3:	XP_020105011.1	62.78	79.59	100.00	83.01	24.86	48.44	35.76	34.87
4:	XP_064946005.1	65.05	80.61	83.01	100.00	26.01	44.53	34.77	34.87
5:	PNH07472.1	27.91	26.38	24.86	26.01	100.00	43.75	53.85	55.43
6:	GFH16887.1	44.53	47.66	48.44	44.53	43.75	100.00	65.96	66.67
7:	SP A8HYJ1 TOC34_CHLRE	36.22	36.14	35.76	34.77	53.85	65.96	100.00	68.88
8:	GIL53542.1	33.95	35.19	34.87	34.87	55.43	66.67	68.88	100.00

11. Struktura ni eksperimentalno določena.

12. GTP vezavne domene: AlG1-type G, G1 do G5

13. AKR2A-binding sequence/motiv, vezava z AKR2A (Ankyrin repeat-containing protein 2A).

14. Ne.