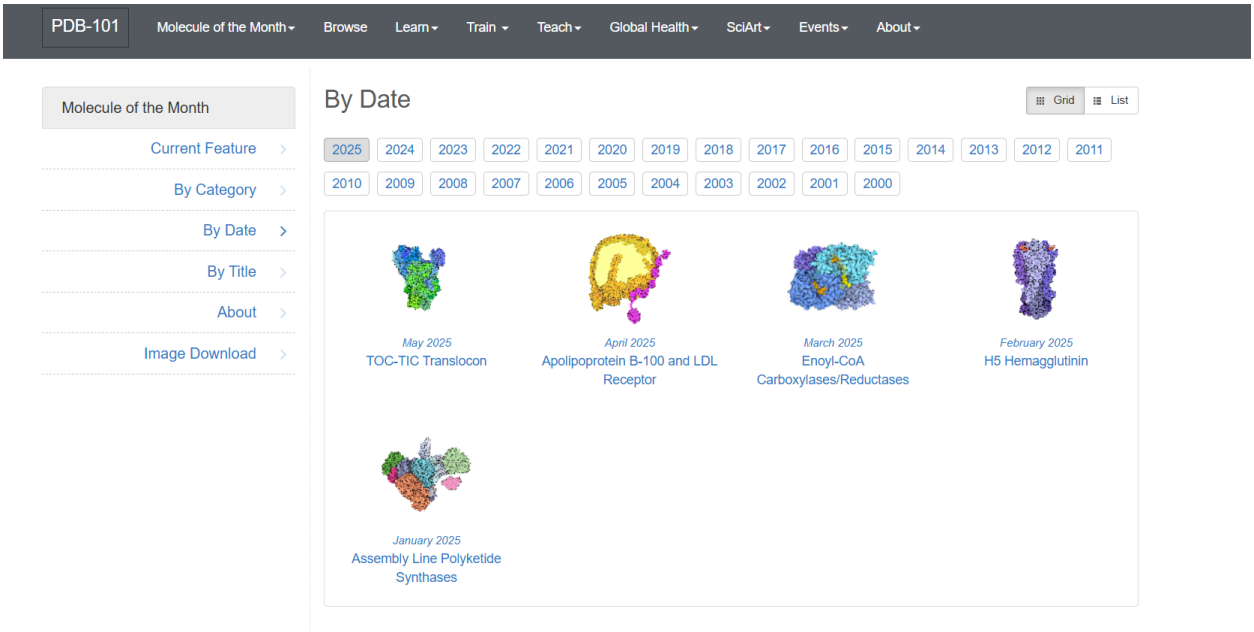
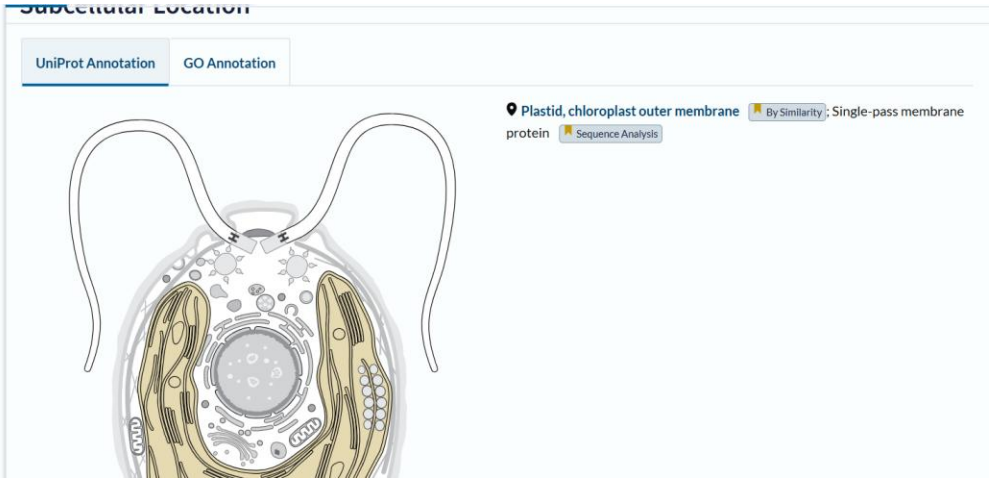
1. TOC – TIC translokon

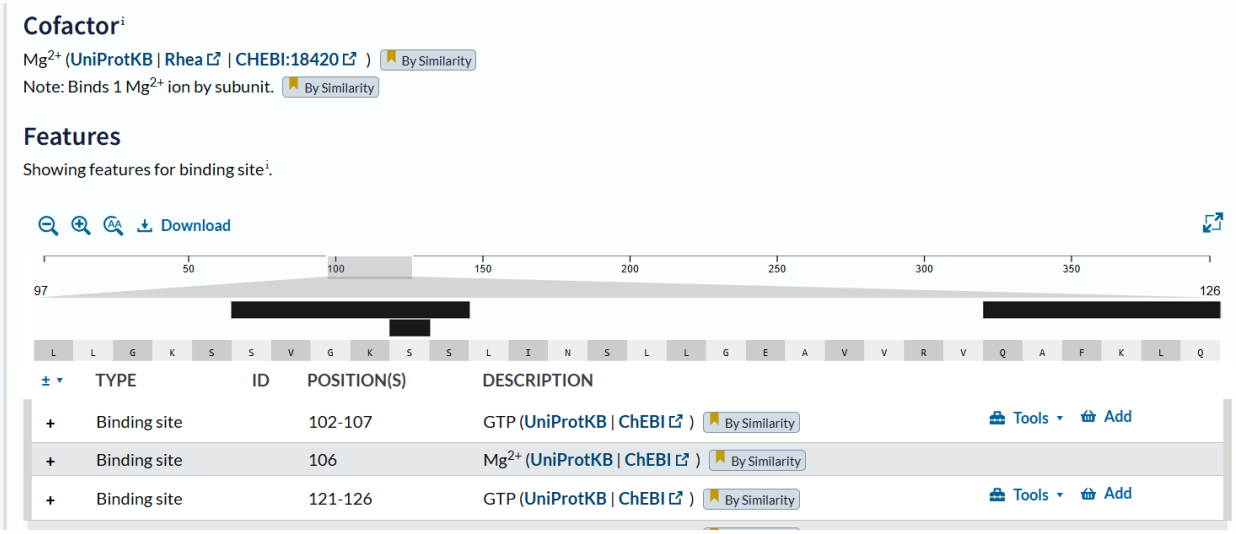


2. Na/med membranah kloroplastov

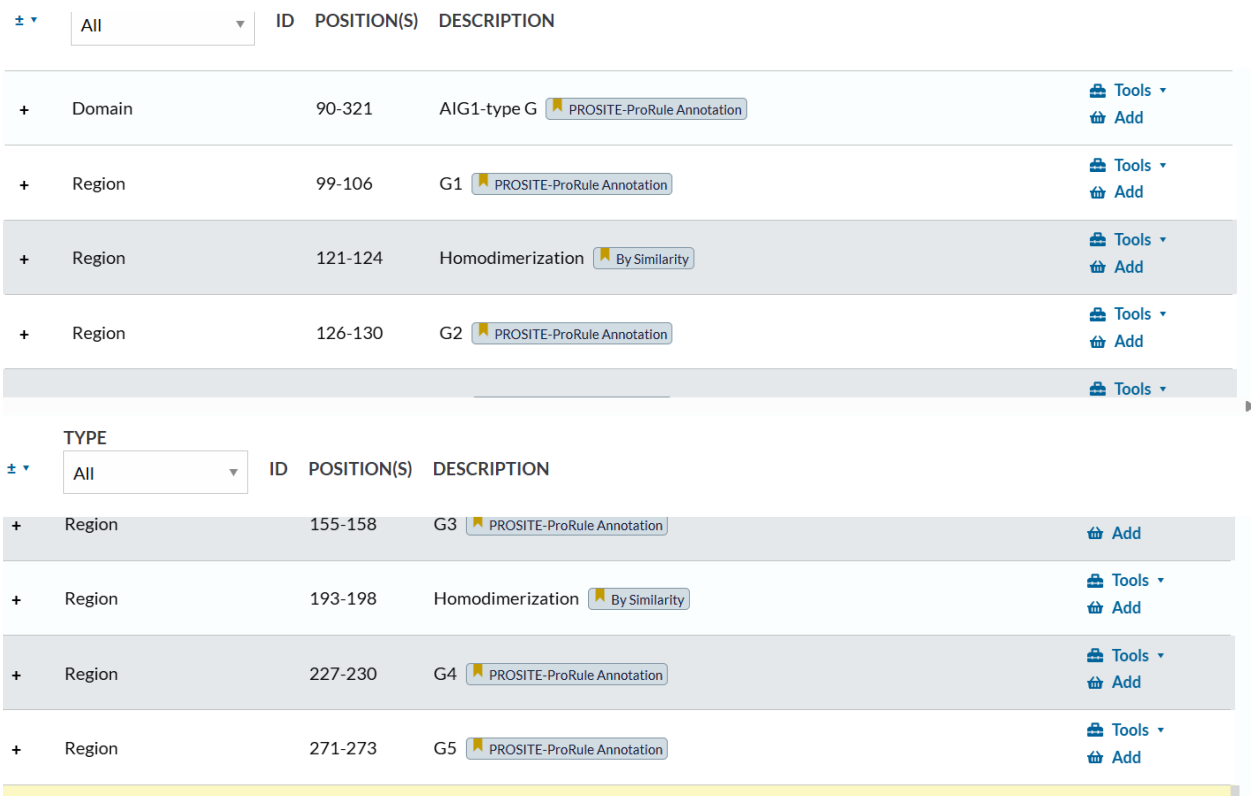


3. Prenašanje proteinov v in iz kloroplasotov

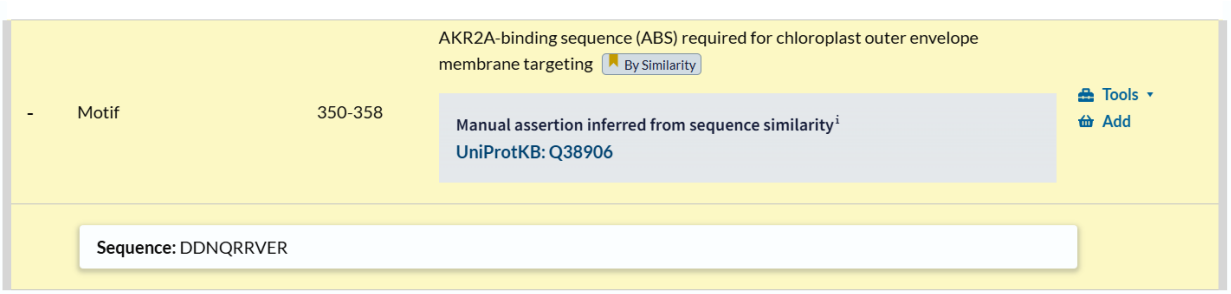
4. EM, ker je velik kompleks in membranski protein.
5. TIM, TOM kompleksa
6. Mg^{2+} , na mesto 106, serin



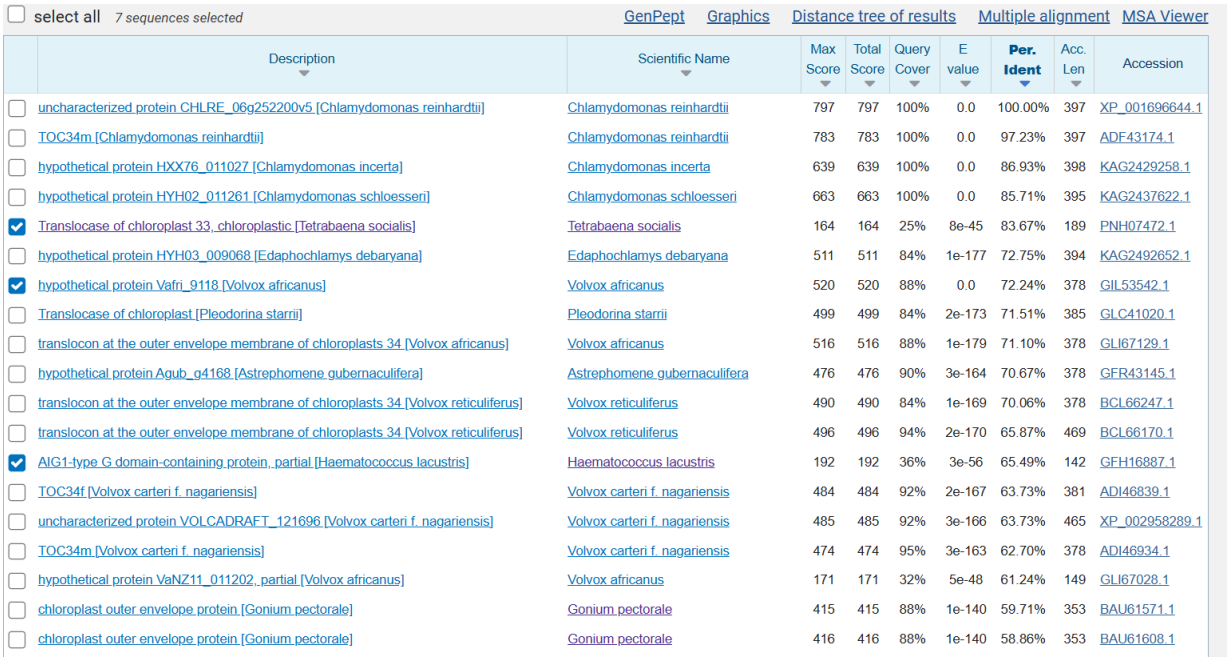
7. GTP vezavne domene: AIG1-type G, G1 do G5



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



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



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
☐	uncharacterized protein CHLRE_06g252200v5 [Chlamydomonas reinhardtii]	Chlamydomonas reinhardtii	797	797	100%	0.0	100.00%	397	XP_001696644.1
☐	TOC34m [Chlamydomonas reinhardtii]	Chlamydomonas reinhardtii	783	783	100%	0.0	97.23%	397	ADF43174.1
☐	hypothetical protein HXX76_011027 [Chlamydomonas incerta]	Chlamydomonas incerta	639	639	100%	0.0	86.93%	398	KAG2429258.1
☐	hypothetical protein HYH02_011261 [Chlamydomonas schloesseri]	Chlamydomonas schloesseri	663	663	100%	0.0	85.71%	395	KAG2437622.1
☑	Translocase of chloroplast 33, chloroplastic [Tetrabaena socialis]	Tetrabaena socialis	164	164	25%	8e-45	83.67%	189	PNH07472.1
☐	hypothetical protein HYH03_009068 [Edaphochlamys debaryana]	Edaphochlamys debaryana	511	511	84%	1e-177	72.75%	394	KAG2492652.1
☑	hypothetical protein Vafri_9118 [Volvox africanus]	Volvox africanus	520	520	88%	0.0	72.24%	378	GIL53542.1
☐	Translocase of chloroplast [Pleodorina starrii]	Pleodorina starrii	499	499	84%	2e-173	71.51%	385	GLC41020.1
☐	translocon at the outer envelope membrane of chloroplasts 34 [Volvox africanus]	Volvox africanus	516	516	88%	1e-179	71.10%	378	GLI67129.1
☐	hypothetical protein Agub_g4168 [Astrephomene gubernaculifera]	Astrephomene gubernaculifera	476	476	90%	3e-164	70.67%	378	GFR43145.1
☐	translocon at the outer envelope membrane of chloroplasts 34 [Volvox reticuliferus]	Volvox reticuliferus	490	490	84%	1e-169	70.06%	378	BCL66247.1
☐	translocon at the outer envelope membrane of chloroplasts 34 [Volvox reticuliferus]	Volvox reticuliferus	496	496	94%	2e-170	65.87%	469	BCL66170.1
☑	AIG1-type G domain-containing protein, partial [Haematococcus lacustris]	Haematococcus lacustris	192	192	36%	3e-56	65.49%	142	GFH16887.1
☐	TOC34f [Volvox carteri f. nagariensis]	Volvox carteri f. nagariensis	484	484	92%	2e-167	63.73%	381	ADI46839.1
☐	uncharacterized protein VOLCADRAFT_121696 [Volvox carteri f. nagariensis]	Volvox carteri f. nagariensis	485	485	92%	3e-166	63.73%	465	XP_002958289.1
☐	TOC34m [Volvox carteri f. nagariensis]	Volvox carteri f. nagariensis	474	474	95%	3e-163	62.70%	378	ADI46934.1
☐	hypothetical protein VaNZ11_011202, partial [Volvox africanus]	Volvox africanus	171	171	32%	5e-48	61.24%	149	GLI67028.1
☐	chloroplast outer envelope protein [Gonium pectorale]	Gonium pectorale	415	415	88%	1e-140	59.71%	353	BAU61571.1
☐	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: AIG1-type G, G1 do G5
13. AKR2A-binding sequence/motiv, vezava z AKR2A (Ankyrin repeat-containing protein 2A).
14. Ne.