

In Silico Design and Evaluation of a Novel Chimeric Vaccine Candidate Based on SAG1, GRA1, and MIC4 Antigens of *Toxoplasma gondii*



Ebrahim Nayeri¹, Tooran Nayeri^{2,*} and Mahdi Fasihi-Ramandi³

¹Taleghani Hospital, Kermanshah University of Medical Sciences, Kermanshah, Iran

²Infectious and Tropical Diseases Research Center, Dezful University of Medical Sciences, Dezful, Iran

³Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

© 2026 The Author(s). Published by Bentham Open.

This is an open access article distributed under the terms of the Creative Commons Attribution 4.0 International Public License (CC-BY 4.0), a copy of which is available at: <https://creativecommons.org/licenses/by/4.0/legalcode>. This license permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.



*Address correspondence to this author at the Infectious and Tropical Diseases Research Center, Dezful University of Medical Sciences, Dezful, PC 6461643993, Iran; Tel: 06142429731; E-mail: tooran.nayeri@gmail.com

Published: May 12, 2026

Cite as: Nayeri E, Nayeri T, Fasihi-Ramandi M. In Silico Design and Evaluation of a Novel Chimeric Vaccine Candidate Based on SAG1, GRA1, and MIC4 Antigens of *Toxoplasma gondii*. Open Microbiol J, 2026; 20: e18742858468656. <http://dx.doi.org/10.2174/0118742858468656260430102334>



Send Orders for Reprints to reprints@benthamscience.net

```
# tr|C7E5T3|C7E5T3_TOXGO Length: 336
# tr|C7E5T3|C7E5T3_TOXGO Number of predicted TMHs: 0
# tr|C7E5T3|C7E5T3_TOXGO Exp number of AAs in TMHs: 16.85296
# tr|C7E5T3|C7E5T3_TOXGO Exp number, first 60 AAs: 1.16787
# tr|C7E5T3|C7E5T3_TOXGO Total prob of N-in: 0.03995
tr|C7E5T3|C7E5T3_TOXGO TMHMM2.0 outside 1 336
```

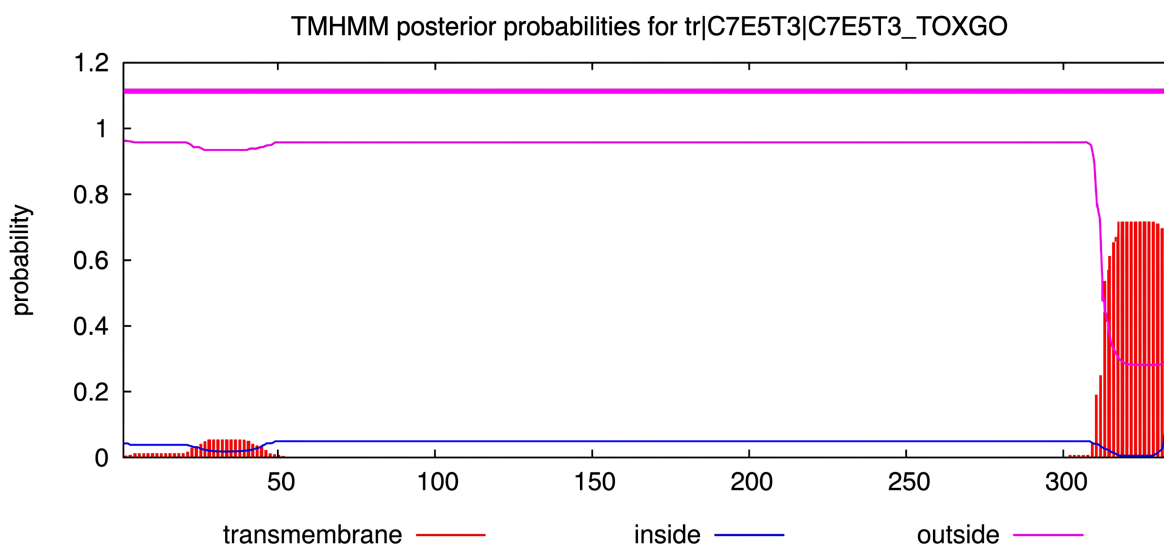


Fig. (S1). Prediction of transmembrane helices in the SAG1 protein using the TMHMM Server v2.0. The plot shows the probability of amino acid residues being located in transmembrane regions, inside, or outside the membrane. Proteins with an expected number of amino acids in transmembrane helices (Exp number of AAs in TMHs) greater than 18 are considered likely transmembrane proteins.

```
# WEBSEQUENCE Length: 190
# WEBSEQUENCE Number of predicted TMHs: 0
# WEBSEQUENCE Exp number of AAs in TMHs: 17.50476
# WEBSEQUENCE Exp number, first 60 AAs: 17.45996
# WEBSEQUENCE Total prob of N-in: 0.64287
# WEBSEQUENCE POSSIBLE N-term signal sequence
WEBSEQUENCE TMHMM2.0 outside 1 190
```

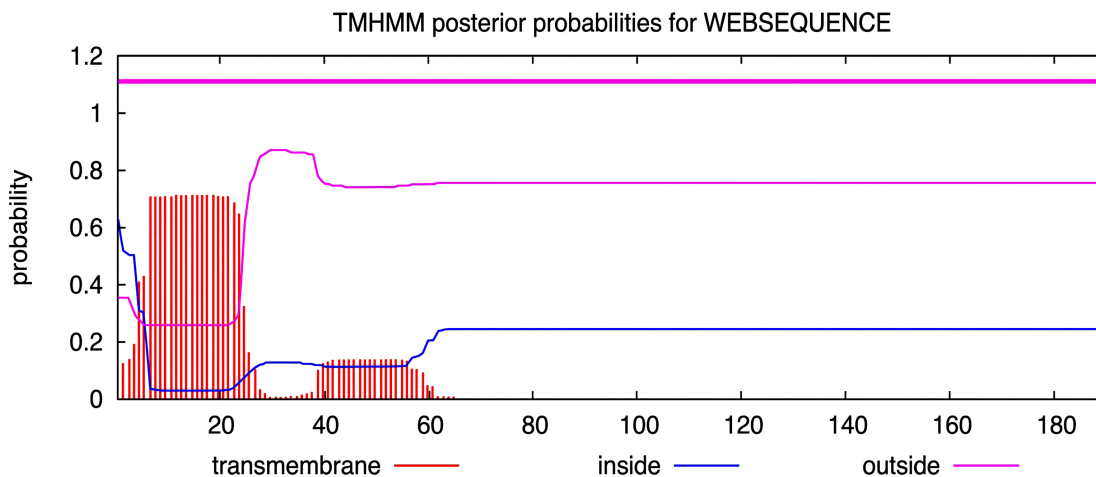


Fig. (S2). Prediction of transmembrane helices in the GRA1 protein using the TMHMM Server v2.0.

```
# tr|D8L550|D8L550_TOXGO Length: 580
# tr|D8L550|D8L550_TOXGO Number of predicted TMHs: 0
# tr|D8L550|D8L550_TOXGO Exp number of AAs in TMHs: 1.25429
# tr|D8L550|D8L550_TOXGO Exp number, first 60 AAs: 1.24804
# tr|D8L550|D8L550_TOXGO Total prob of N-in: 0.06330
tr|D8L550|D8L550_TOXGO THHMM2.0 outside 1 580
```

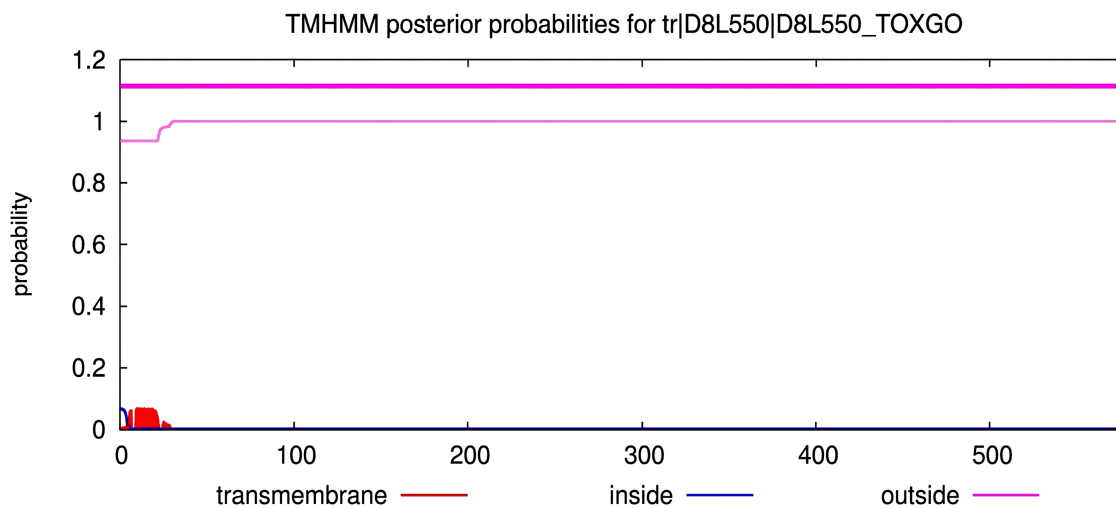


Fig. (S3). Prediction of transmembrane helices in the MIC4 protein using the TMHMM Server v2.0.

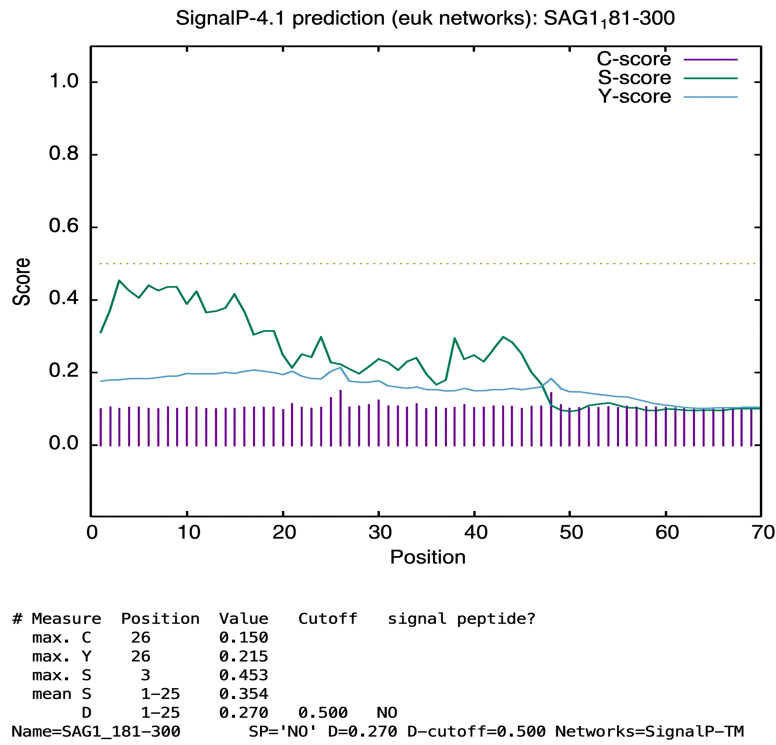


Fig. (S4). Signal peptide prediction of the SAG1 protein using SignalP 4.1. The analysis shows the predicted N-terminal signal peptide and cleavage site probability.

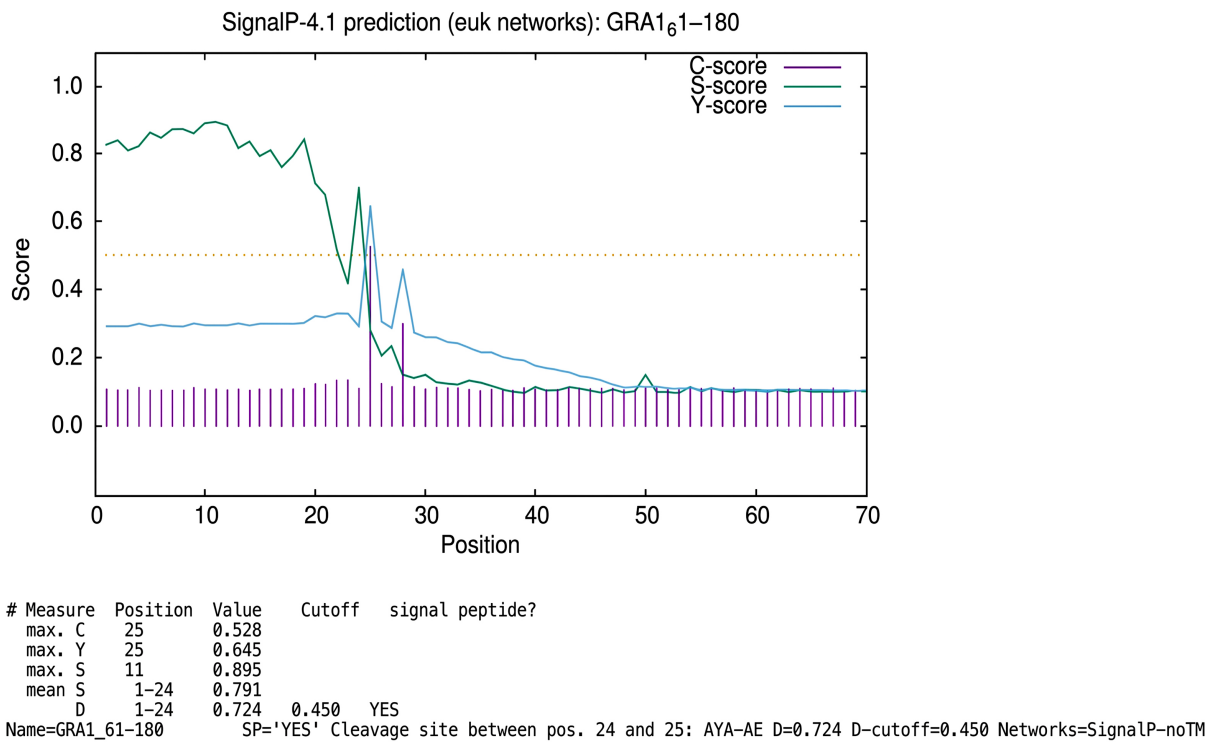


Fig. (S5). Signal peptide prediction of the GRA1 protein using SignalP 4.1. The analysis shows the predicted N-terminal signal peptide and cleavage site probability.

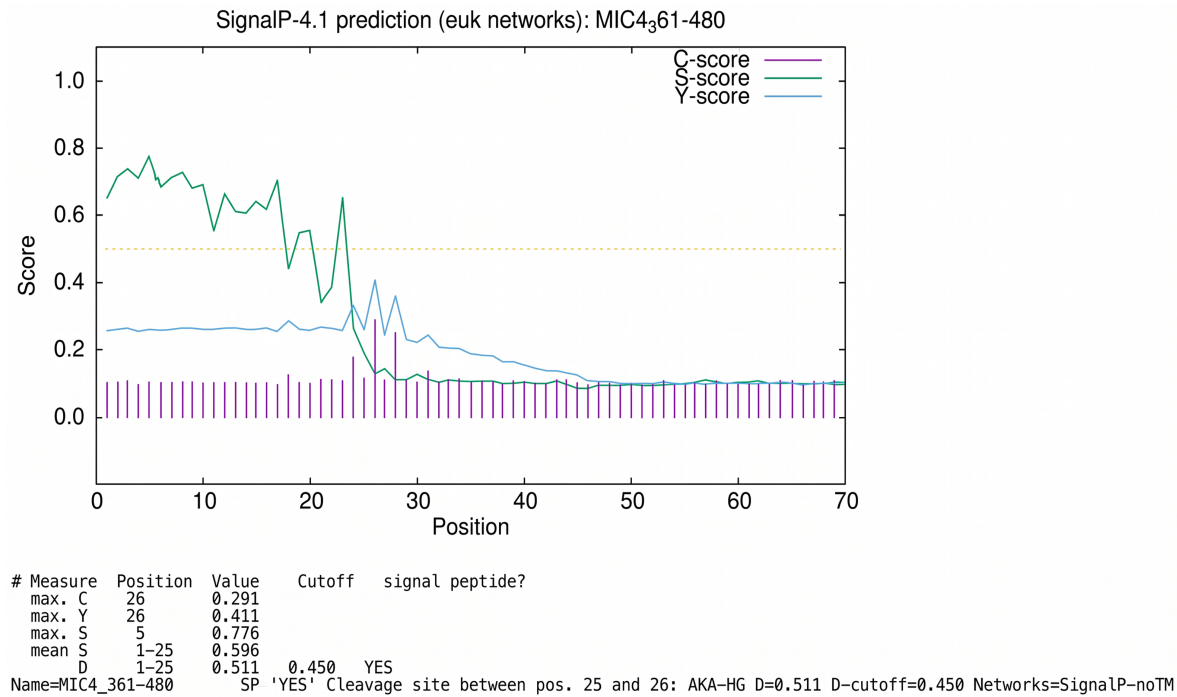


Fig. (S6). Signal peptide prediction of the MIC4 protein using SignalP 4.1. The analysis shows the predicted N-terminal signal peptide and cleavage site probability.