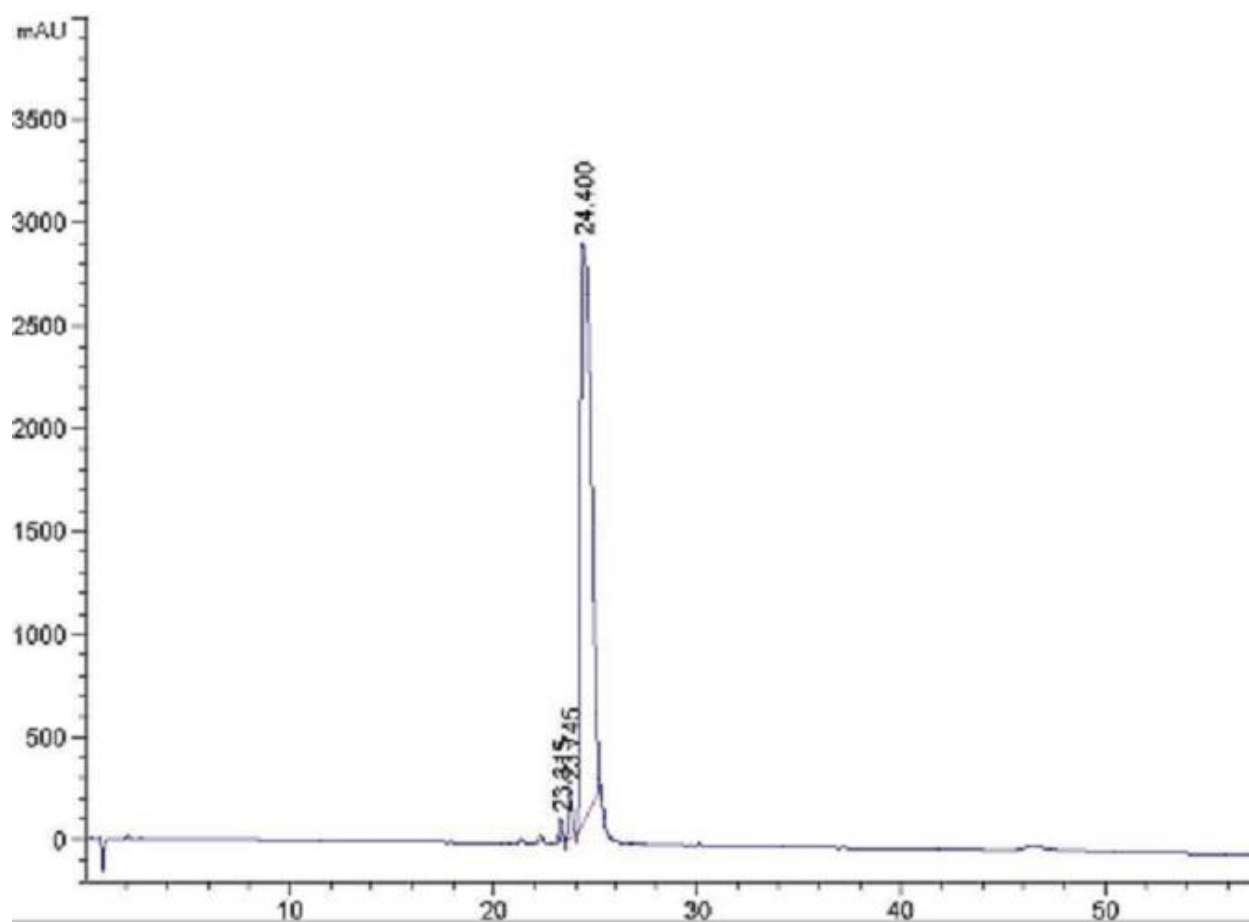


Supplementary material



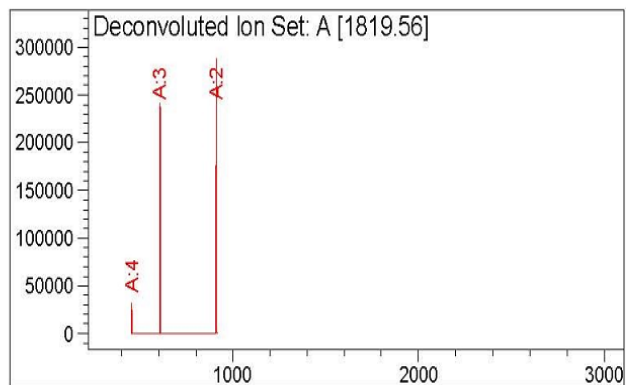
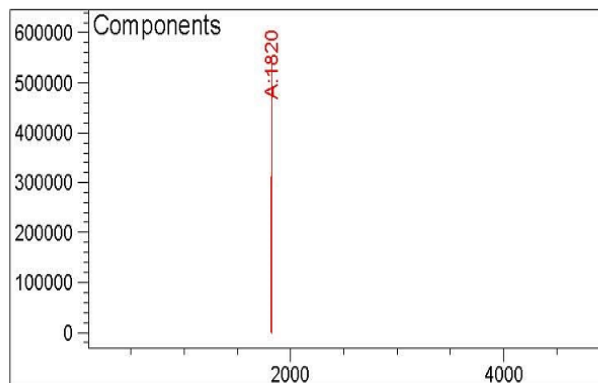
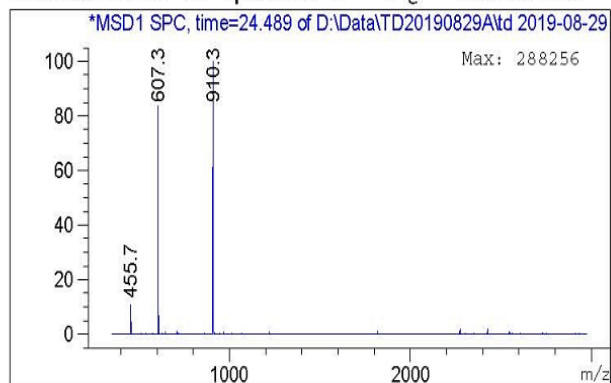
S1. Purification of TMOF-FITC by HPLC

Spectrum Deconvolution

Data File D:\Data\TD20190829A\td 2019-08-29 10-32-00\012-P1-A2-Brovosky-Pure.D

Sample Name: Brovosky-Pure

Deconvolution of Spectrum # 1 @ 24.489 min



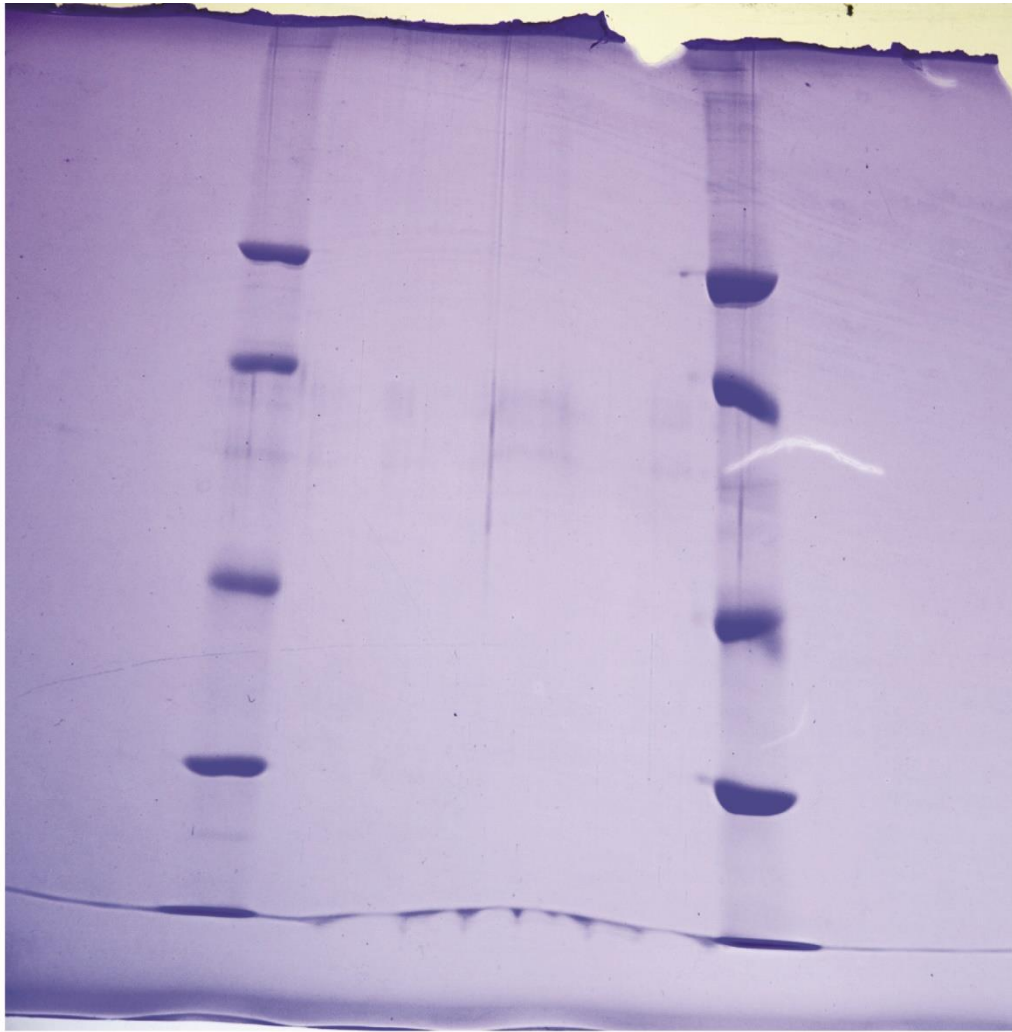
Component	Molecular Weight	Absolute Abundance	Relative Abundance
A	1819.56	550224	100.00

*** End of Report ***

S2. Mass spectrometry of purified TMOF-FITC after HPLC purification, note the distinct expected ions at 455.7, 607.3 and 910.3.

901IMLESWYTESSGLKEKQSLESAIKLAVEAISNIRTVASLGQEPYVLERYYYKEIAKVD
ACKKKSRLRGVVFALGQIMPFGYGLALFYGGKLVSEAELEYKDVIKVSEALIFGAWMLG
ALAYAPNVNSAMLSAGRLMKLLDRTPKMHNPPSSSYLSTFENHEGNIKFTDVEFRYPTRPT
PILQGLNLDIKKGNTVALVGPSGCGKSTCIQLLLRYYPDNGKVDIDGITTTDFQLGRIR
QMGLVSQEPVLFDRITIAENIAYGDNTREISMPEIIEASKMANIHEFTIVNLPKGYDTSLGT
GAQLSGGQKQRIAIARALVRNPRILLDEATSALDNQSEKIVQNALDHARKGRTCIIIAH
LTTIQNADLICVIQSGVVVECGTHDELMAQNKIYAKLYAMQQVA1304

S3. *AeaABC*-TMOF receptor sequence of the 45 kDa SDS PAGE stained band (Figure 1B) corresponding to the C-terminal end of the *AeaABC*-TMOF receptor sequence (Figure 3) is highlighted in yellow. The sequence highlighted in cyan corresponds to the α helical sequence involved in the binding of TMOF to its receptor (Figure 8 A,B). The sequence highlighted in red corresponds to MS/MS identified peptide. The ATP binding domain at the C-terminal of the receptor is underlined.



Original SDS PAGE that part was used for Figure 1B.