



Figure S1. The siponimod bound S1PR-Gi-scFv16 complex purification, cryo-EM data collection, structure determination, and cryo-EM map quality.

(a) Comparison of siponimod induced Gi signaling potency between wild-type (WT) S1PR1 and T4L-S1PR1(1-337 aa).

(b) Comparison of siponimod induced Gi signaling potency between wild-type (WT) S1PR5 and S1PR5 (1-344 aa).

(c) Representative size-exclusion chromatography elution profile of the purified Siponimod-T4L-S1PR1(1-337 aa)-Gi-scFv16 complex using Superdex 200 10/300 Increase column.

(d) Representative size-exclusion chromatography elution profile of the purified Siponimod-S1PR5(1-344 aa)-Gi-scFv16 complex using Superdex 200 10/300 Increase column.

(e-f) SDS-PAGE analysis of siponimod bound S1PR1 (e) and S1PR5 (f) in complex with Gi and scFv16.

(g) Flow chart of cryo-EM single particle reconstruction of siponimod bound S1PR1-Gi complex. Single particle pipeline yields the final cryo-EM reconstruction with the FSC curve, corresponding angular distribution and local resolution map. FSC curve shows a 2.98 Å resolution according to the 0.143 cut-off. Particles (ptcls).

(h) Representative cryo-EM density map (contoured at 0.206) and models for TM1-7, Helix-8 of S1PR1, α 5-helix of G α i in S1PR1-Gi complex, as well as ECL1-3 and N-terminus of S1PR1-ozanimod (contoured at 0.3) and S1PR5-siponimod (contoured at 0.011).