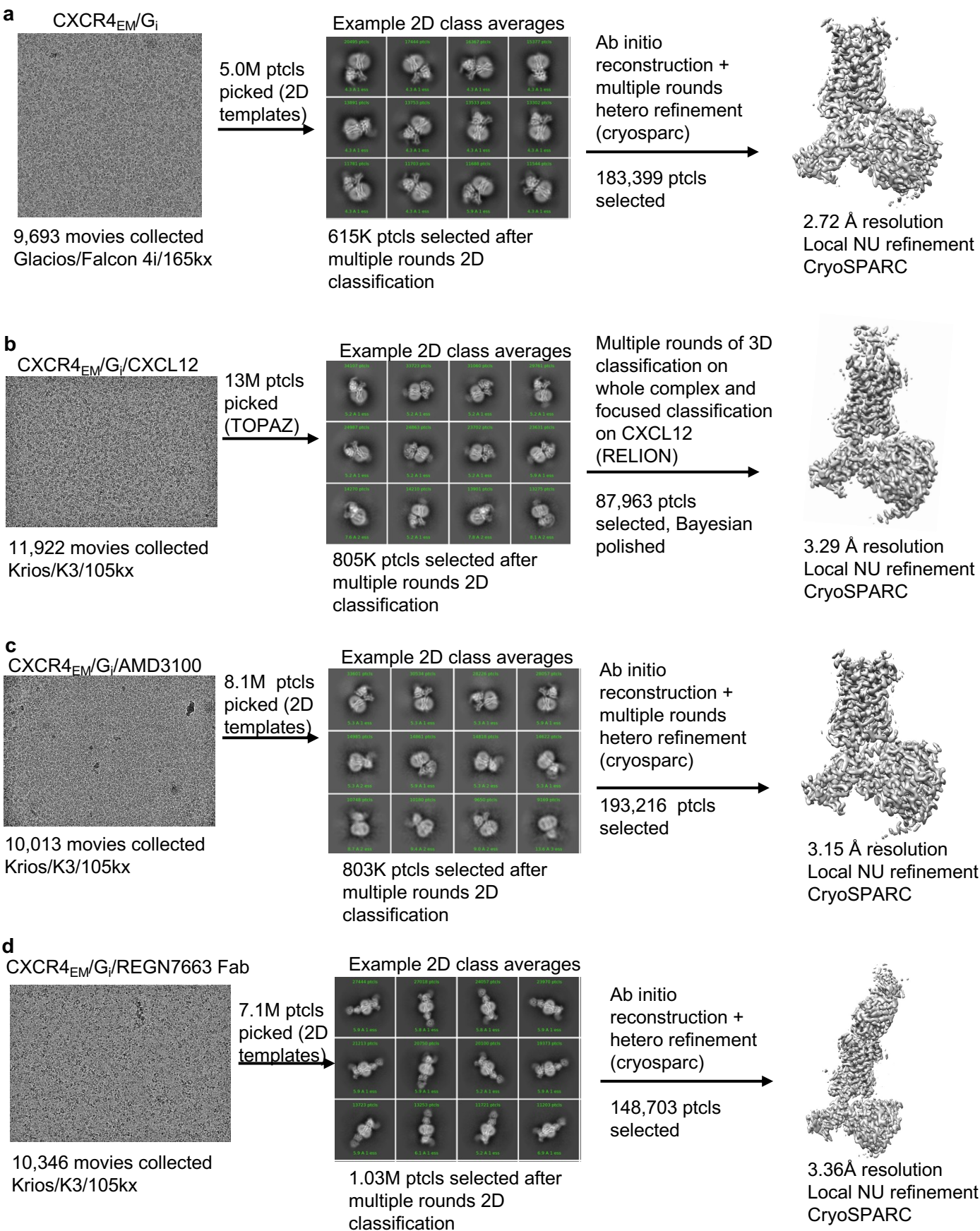




Structural insights into CXCR4 modulation and oligomerization

In the format provided by the
authors and unedited

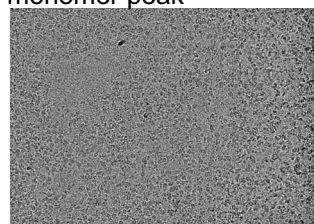
Supplementary Figure 1. CryoEM data processing workflows for CXCR4_{EM}/G_i (a), CXCR4_{EM}/G_i/CXCL12 (b), CXCR4_{EM}/G_i/AMD3100 (c), CXCR4_{EM}/G_i/REGN7663 Fab (d)



Supplementary Figure 2. CryoEM data processing workflows for CXCR4_{EM}/REGN7663 Fab monomer (a) and CXCR4_{EM}/REGN7663 Fab oligomer (b).

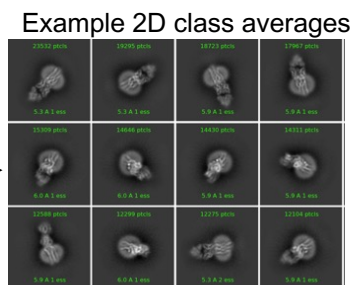
a

CXCR4_{EM}/REGN7663 Fab monomer peak



5,827 movies collected
Krios/K3/105kx

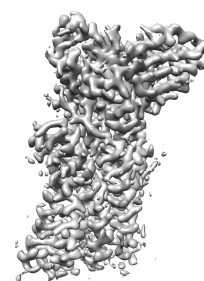
6.2M ptcls
picked
(TOPAZ)



639K particles selected after
multiple rounds 2D classification

Multiple rounds of 3D
classification
(RELION)

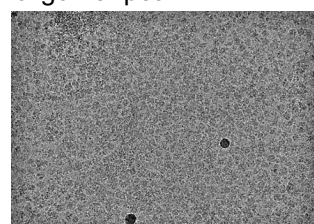
102,810 ptcls
selected, Bayesian
polished



3.10Å resolution
Local NU refinement with
Fab C region subtracted
in CryoSPARC

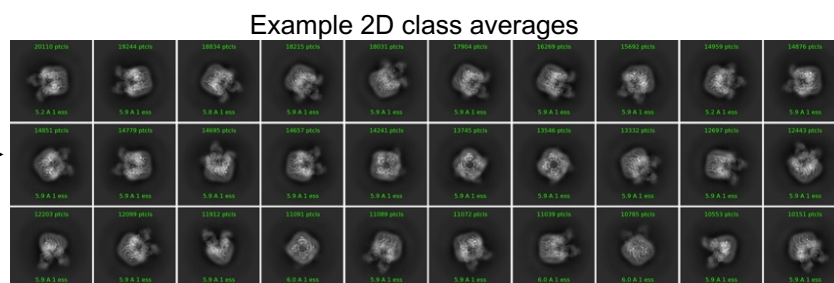
b

CXCR4_{EM}/REGN7663 Fab oligomer peak



5,329 movies collected
Krios/K3/105kx/40° stage tilt

3.0M ptcls
picked
(TOPAZ)



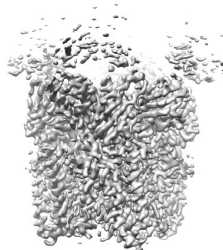
585K ptcls selected after multiple rounds 2D classification

Ab initio
reconstruction
(CryoSPARC)

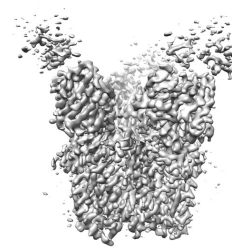
205,502
Tetrameric 4 fab class

104,863 ptcls
Trimeric 3 fab class

Additional rounds of Ab
initio reconstruction
(cryoSPARC)



31,775 particles
3.38 Å resolution
C4 symmetry
Local NU refinement
CryoSPARC



27,104 particles
3.35 Å resolution
C3 symmetry
Local NU refinement
CryoSPARC