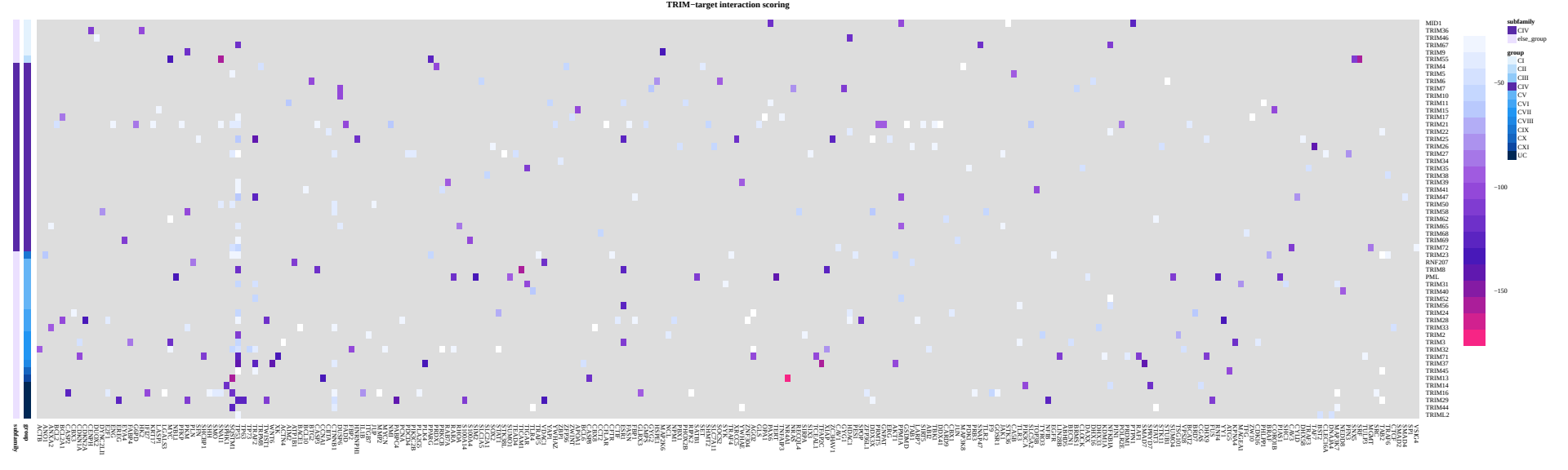
TRIM−target interaction scoring
MID1
TRIM36
TRIM46
TRIM67
TRIM9
TRIM55
TRIM4
TRIM5
TRIM6
TRIM7
TRIM10
TRIM11
TRIM15
TRIM17
TRIM21
TRIM22
TRIM25
TRIM26
TRIM27
TRIM34
TRIM35
TRIM38
TRIM39
TRIM41
TRIM47
TRIM50
TRIM58
TRIM62
TRIM65
TRIM68
TRIM69
TRIM72
TRIM23
RNF207
TRIM8
PML
TRIM31
TRIM40
TRIM52
TRIM56
TRIM24
TRIM28
TRIM33
TRIM2
TRIM3
TRIM32
TRIM71
TRIM37
TRIM45
TRIM13
TRIM14
TRIM16
TRIM29
TRIM44
TRIML2
subfamily
CIV
else_group
group
CI
CII
CIII
CIV
CV
CVI
CVII
CVIII
CIX
CX
CXI
UC
−50
−100
−150
group
subfamily

To further evaluate the docking pipeline's reliability, we sampled several reported TRIMCIV interactions and visualized complexes at varying score thresholds (**Figure S2**). Although we could not examine every predicted complex due to the scale of reported interactions, the sampled structures consistently showed that interacting proteins docked near the PRYSPRY domain of TRIMCIV, aligning with established findings that this domain is the primary interaction site. This supports the pipeline's accuracy in predicting biologically plausible binding poses.

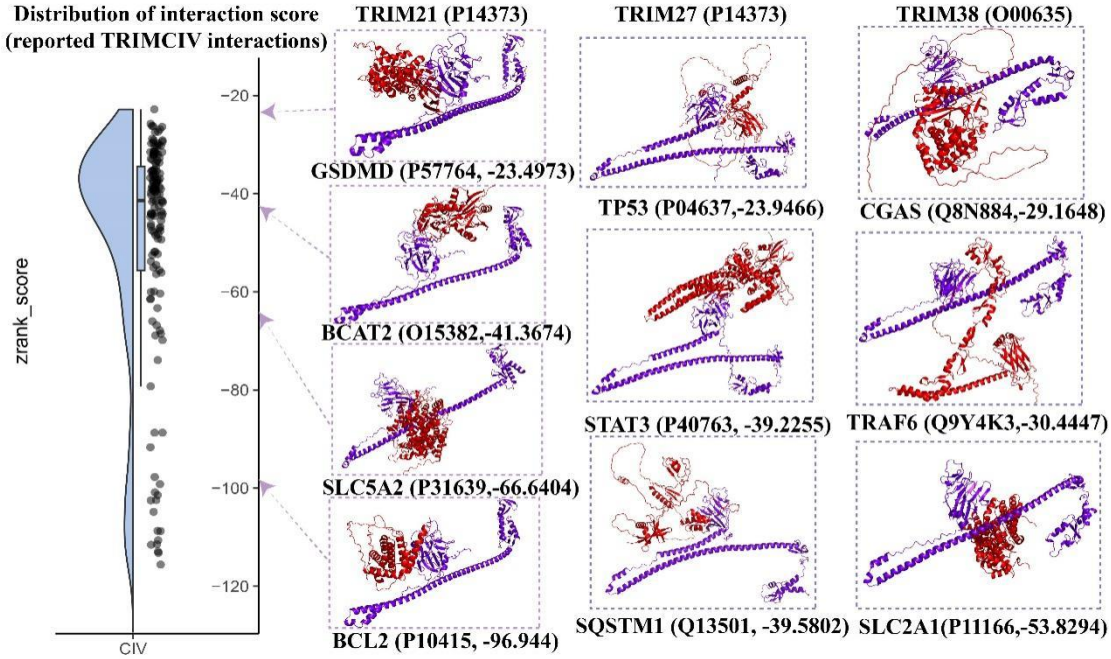

Figure S2. Examples of TRIMCIV-target pair at different scores