

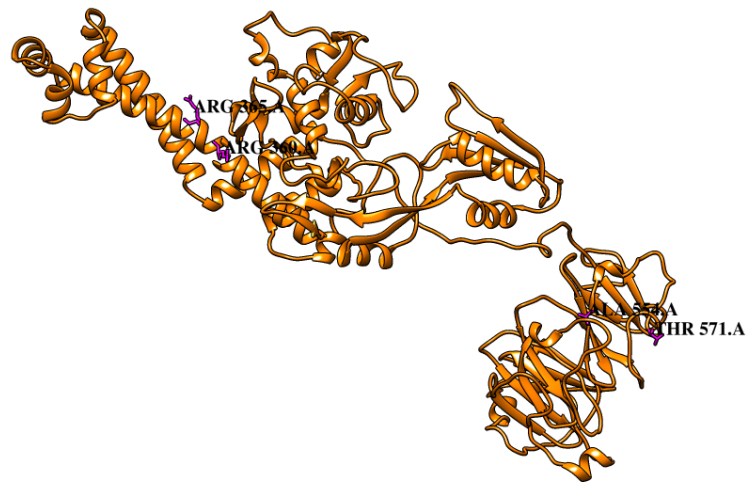
Supplementary material S1. Model quality validation: The 3D structures were generated using SWISS-MODEL and evaluated using Ramachandram plot.

Analysis of structure proteins with to new and known variants on AMR genes

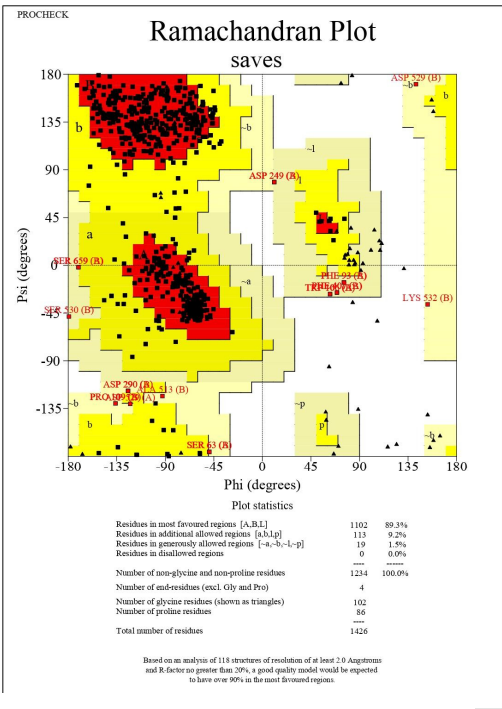
parC

Swiss Model template- PDB: 1zvu.1.A, identity is 71%.

Selected model: 1, chain A



Ramachandran Plot result:



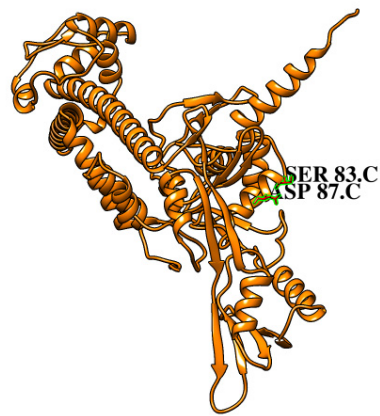
gyrA

Swiss Model template-PDB:
67%,

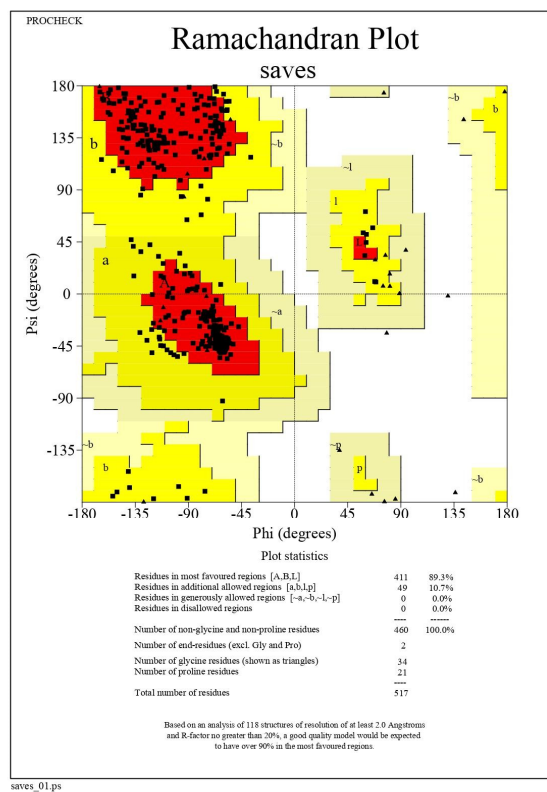
Selected model no: 2,

6rkv.1.C, identity is

chain B



Ramachandran Plot result:



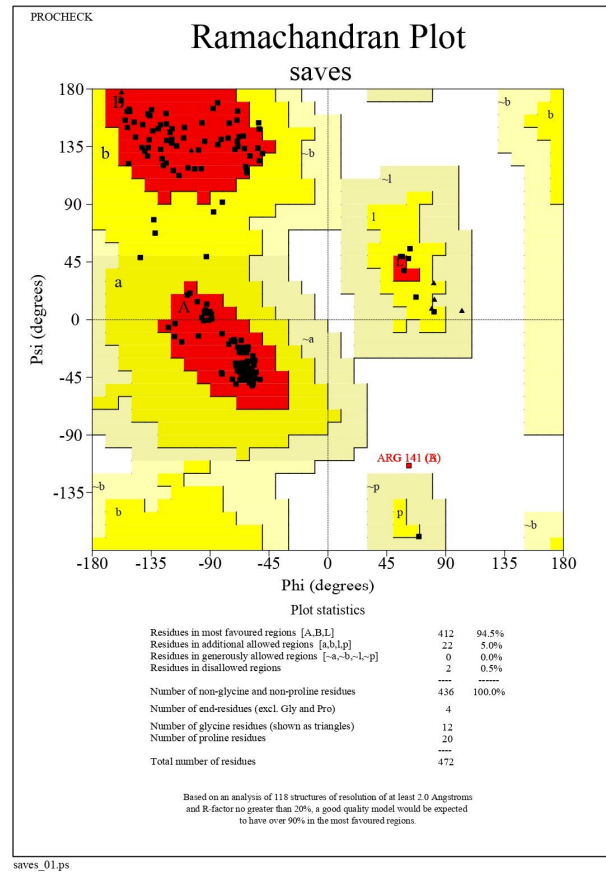
sdiA

Swiss Model template- PDB: 4y15.2.A, identity is 82%.

Selected model no: 1, chain A



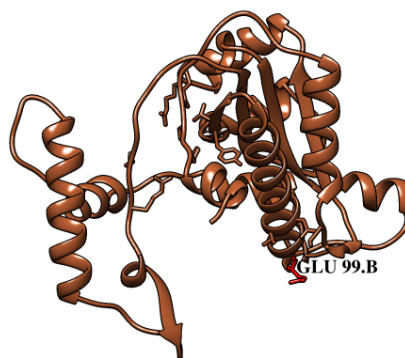
Ramachandran Plot result:



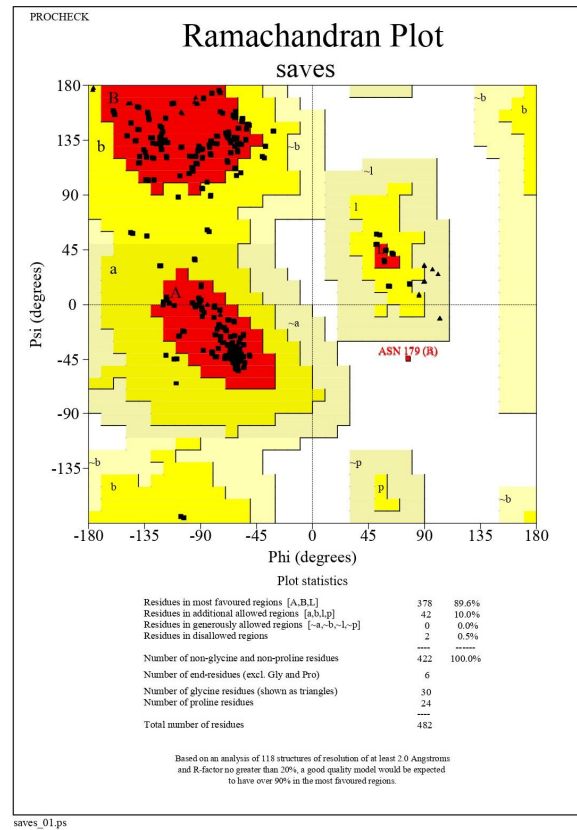
nfsa

Swiss Model template-PDB: 1f5v.1.A, identity is 92%.

Selected model no: 1



Ramachandran Plot result:

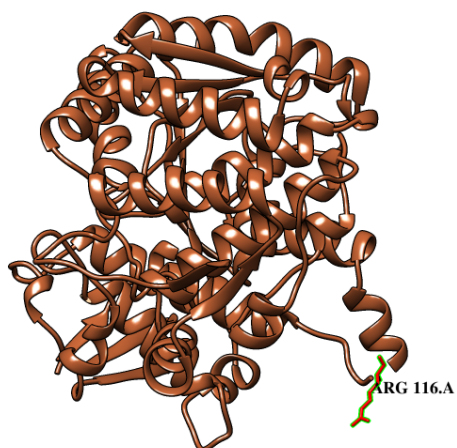


Analysis of structure proteins with GWAS-based new variants.

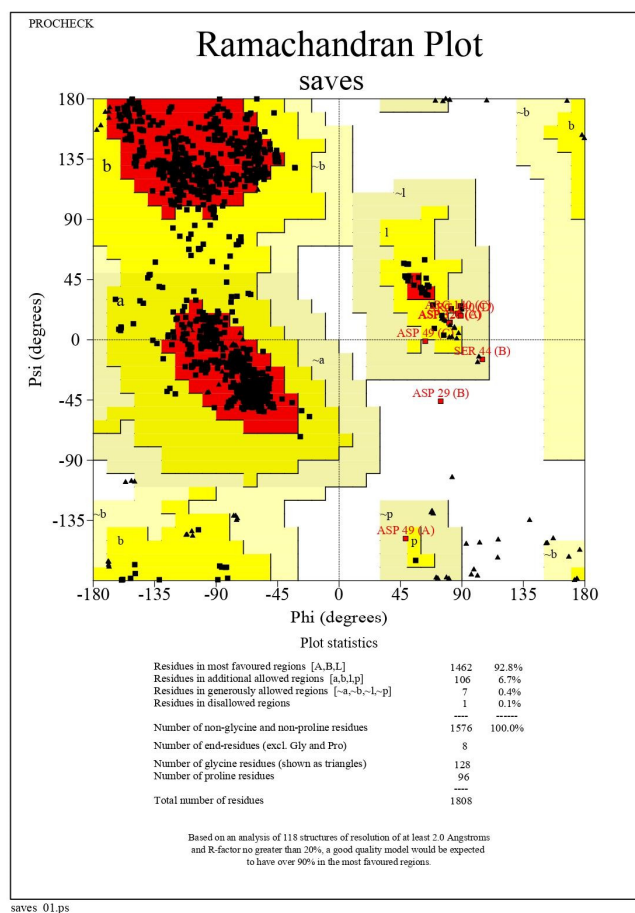
ppnn

Swiss Model template- PDB:2pmb.1.B, identity is 68%.

Selected model no: 1, chain A



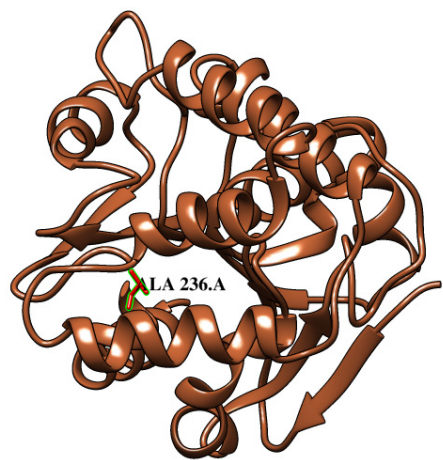
Ramachandran Plot result:



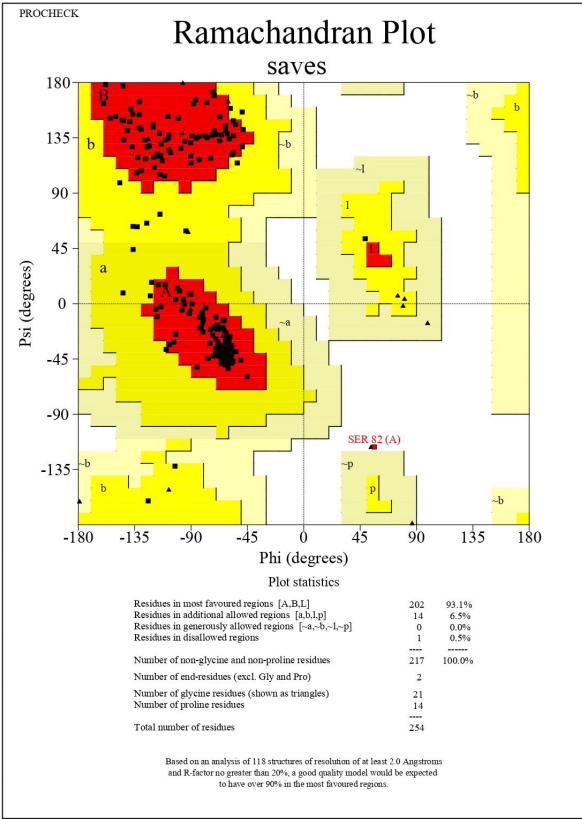
bioH

Swiss Model template-PDB:4nmw.1.A, identity is 100%

Selected model no: 1, chain A



Ramachandran Plot result:

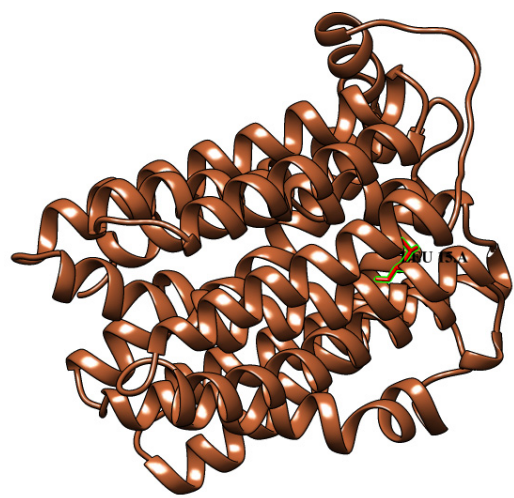


mdtH

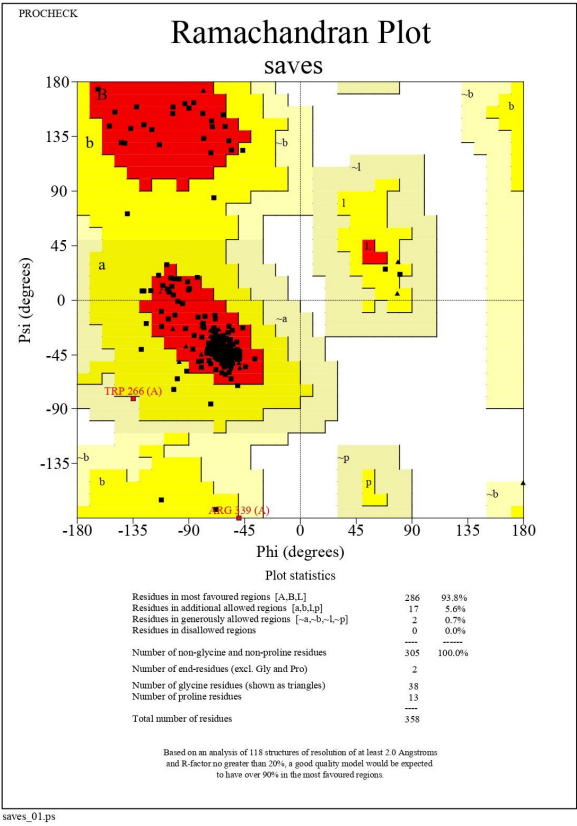
Swiss-model- PDB:
20.06%.

3wdo.1.A, identity is

Selected model no: 1



Ramachandran Plot result:



qseC

Template-
71.43%.

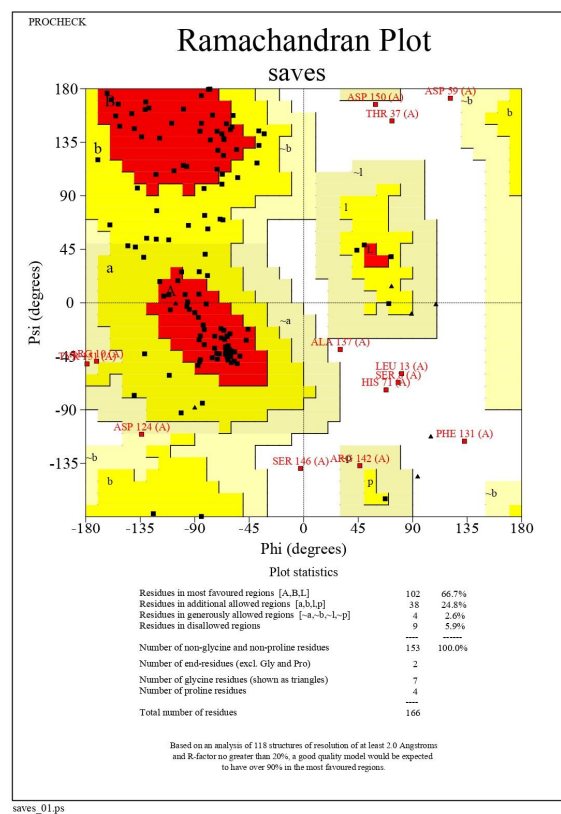
PDB:

2kse.1.A, identity is

Selected model no: 3



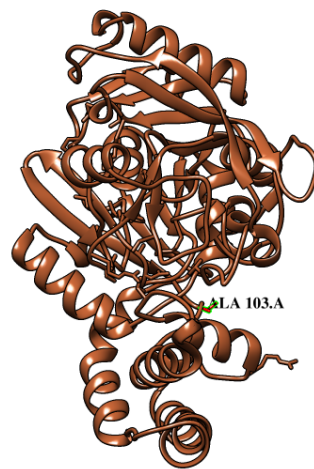
Ramachandran Plot result:



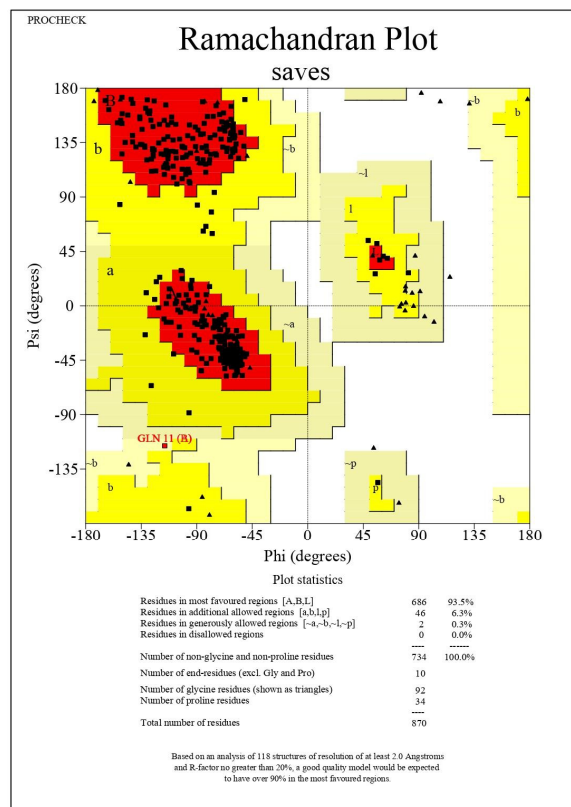
purA

Template- PDB: 2gcq.1.A , identity is 100%.

Selected model no: 1



Ramachandran Plot result:

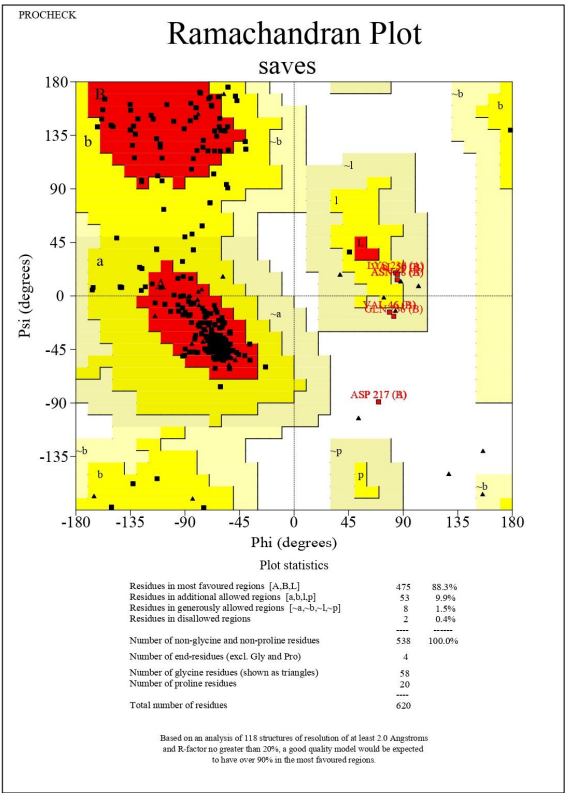
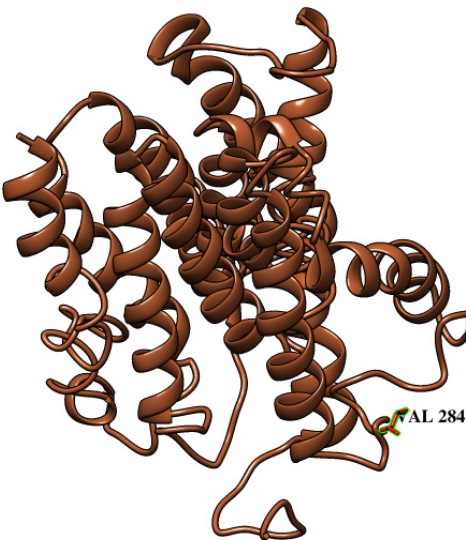


wecA

Template-identity is 33%

Selected model no: 1

PDB:5jmq.1.A,



saves_01.ps