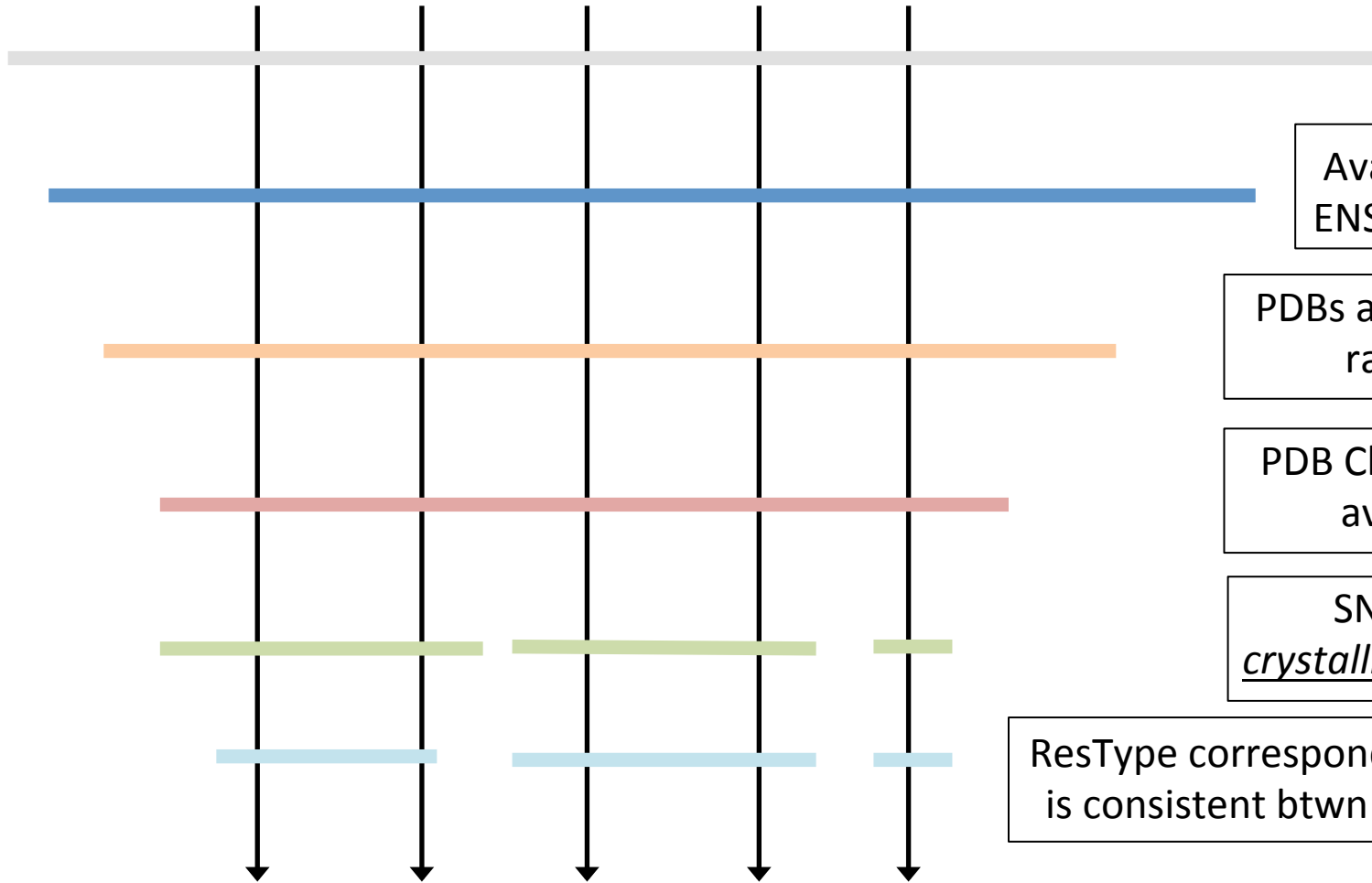


At least one SNV from

Subj. Z Subj. S na12878 1KG HGMD



Avail PDB IDs (given ENSTs) from BioMart

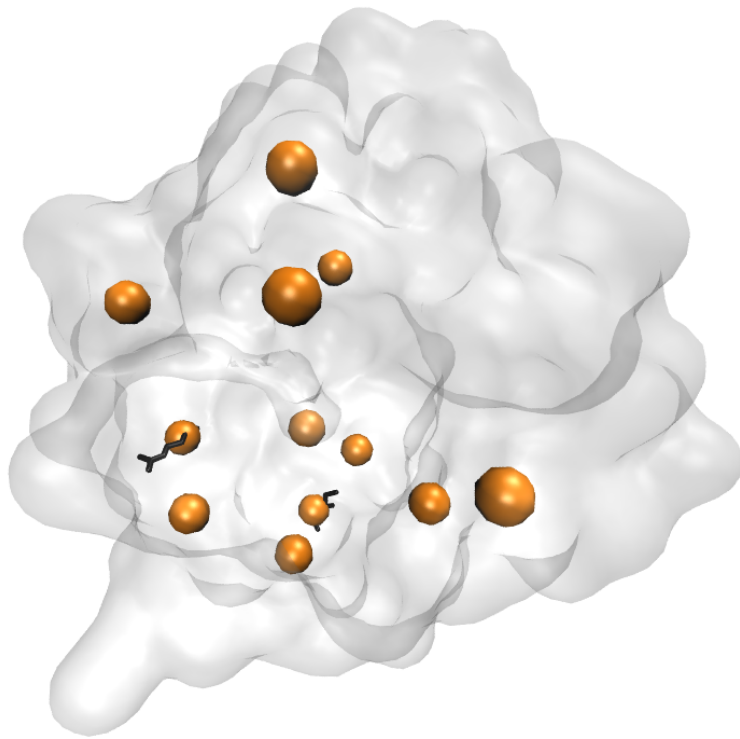
PDBs are high-quality X-ray structures

PDB Chains are known/avail (UniProt)

SNVs hit within crystallized region of PDB

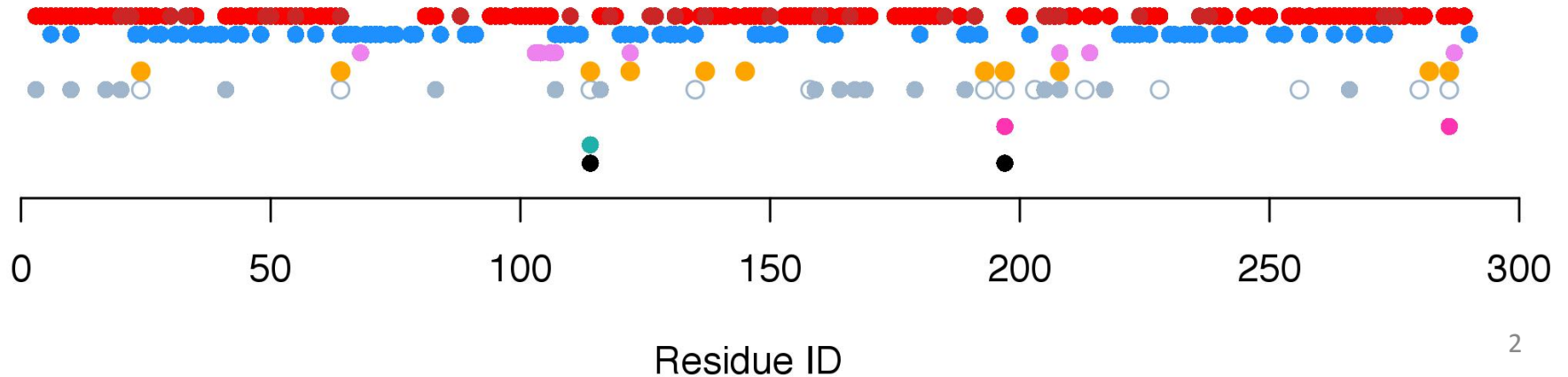
ResType corresponding to wt residue is consistent btwn VAT file and PDB

(remove redundant proteins)

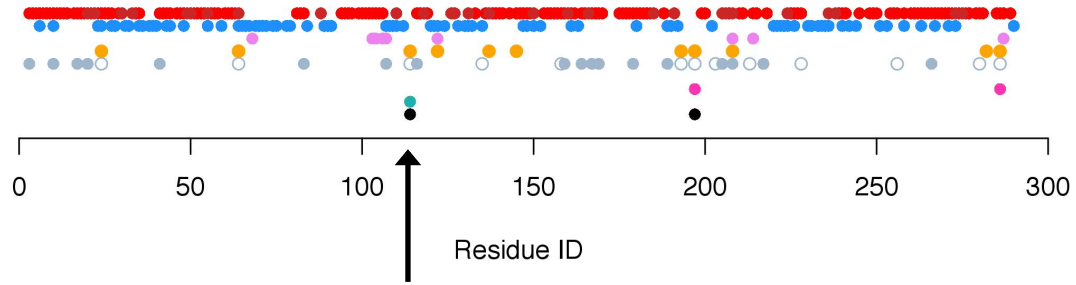


- Predicted allosteric (surface | interior)
- Buried residues
- Protein-protein interaction site
- Post-translational modifications
- ▲ ● HGMD (prem. stop | non-synon)
- ○ 1000 Genomes (rare | common)
- ▲ ● Snyder (prem. stop | non-synon)
- ▲ ● na12878 (prem. stop | non-synon)
- ▲ ● Subj. Z (prem. stop | non-synon)

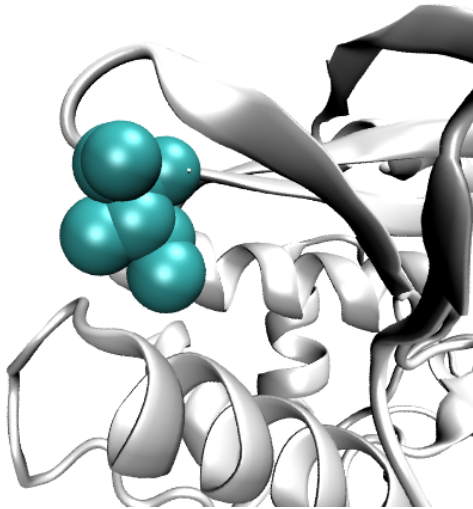
Arylamine N-acetyltransferase 2 (2PFR_A: gene = NAT2)



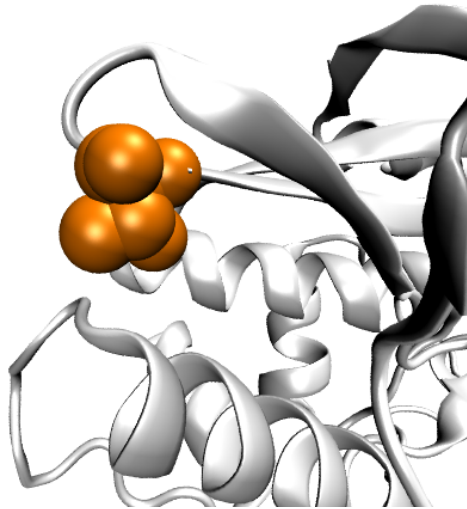
Arylamine N-acetyltransferase 2 (2PFR_A: gene = NAT2)



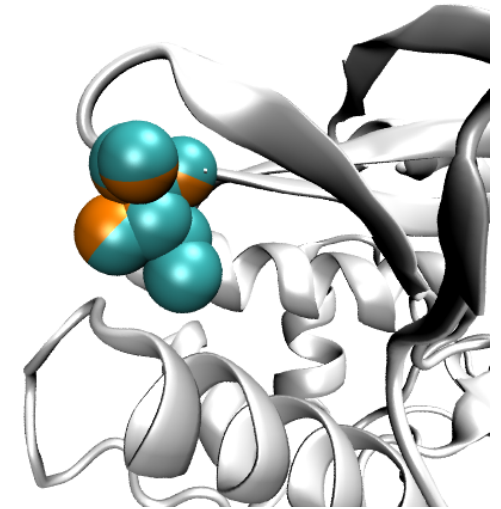
114: I->T



Wild-type

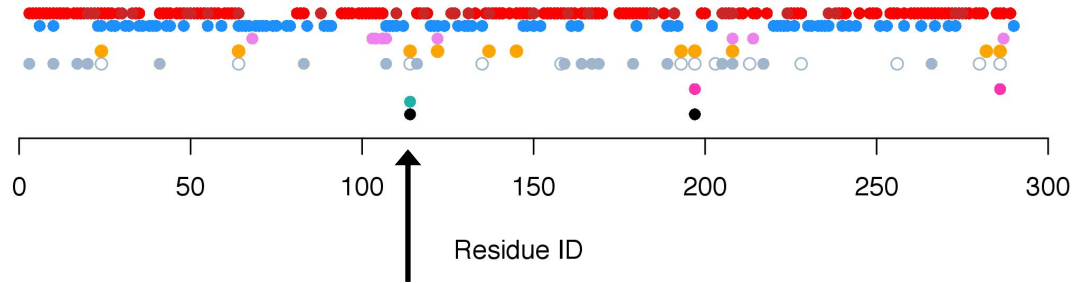


Mutated

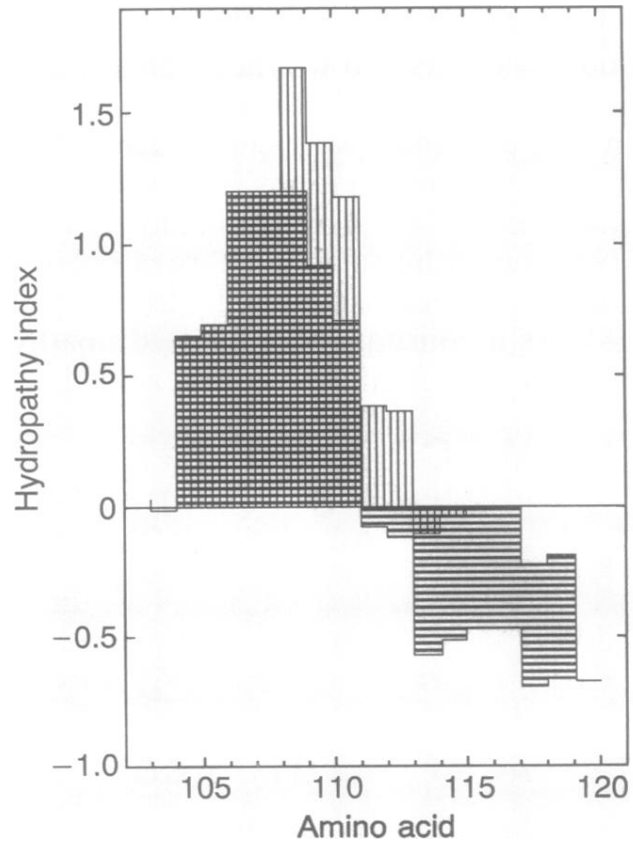


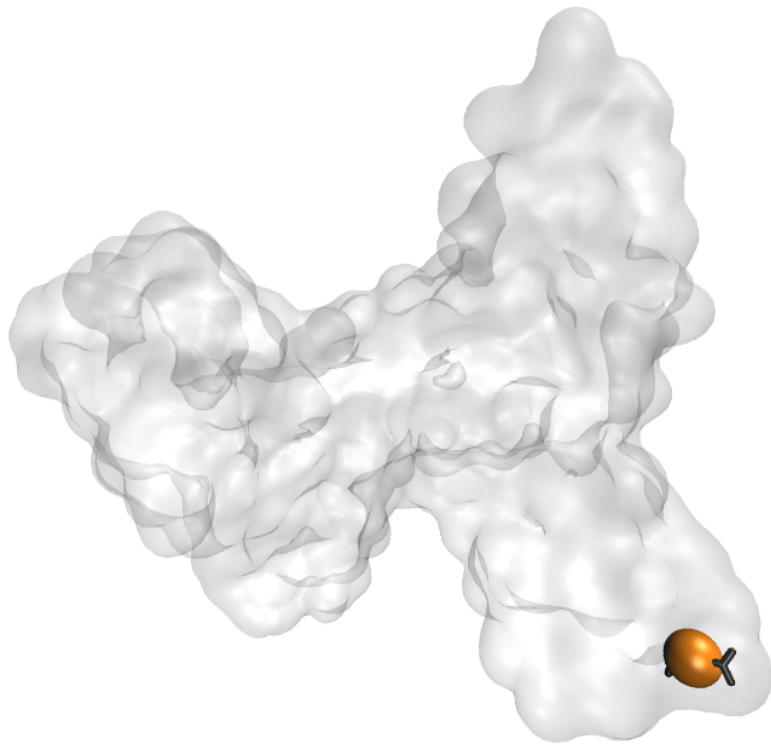
(superimposed)

Arylamine N-acetyltransferase 2 (2PFR_A: gene = NAT2)



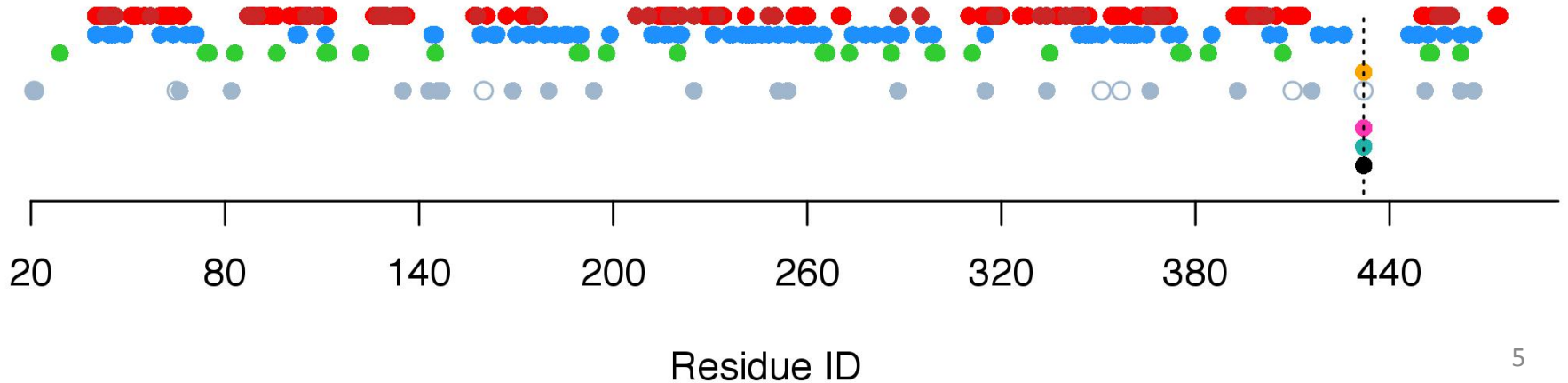
114: I->T



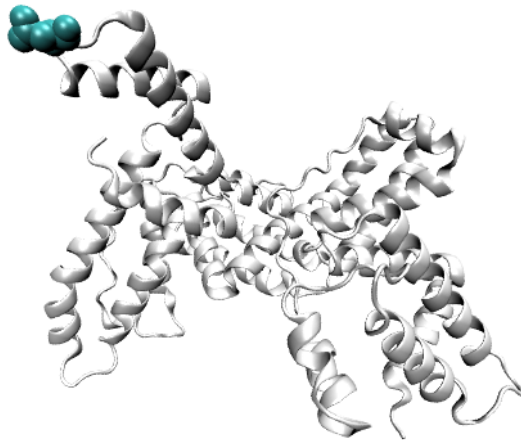
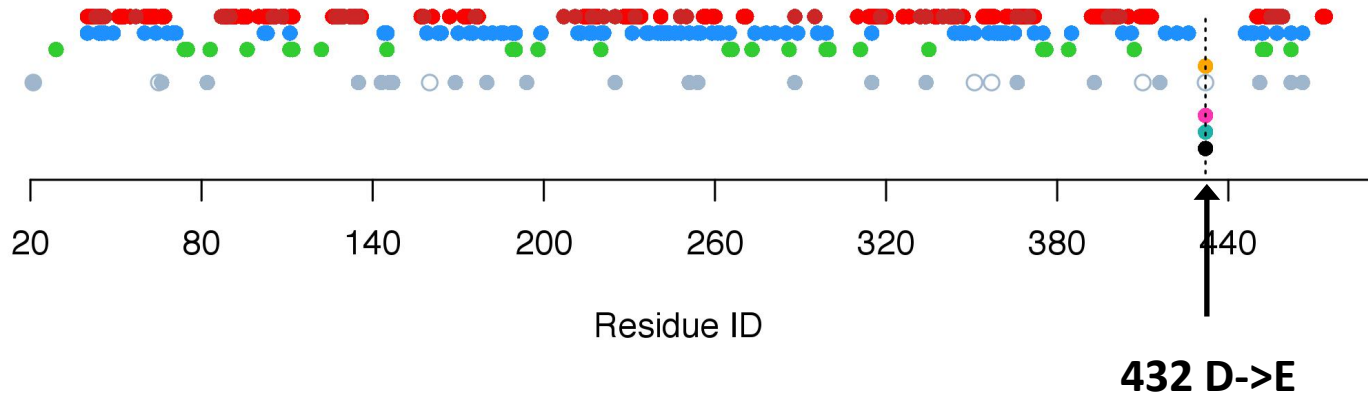


- ● Predicted allosteric (surface | interior)
- Buried residues
- Protein-protein interaction site
- Post-translational modifications
- ▲ ● HGMD (prem. stop | non-synon)
- ○ 1000 Genomes (rare | common)
- ▲ ● Snyder (prem. stop | non-synon)
- ▲ ● na12878 (prem. stop | non-synon)
- ▲ ● Subj. Z (prem. stop | non-synon)

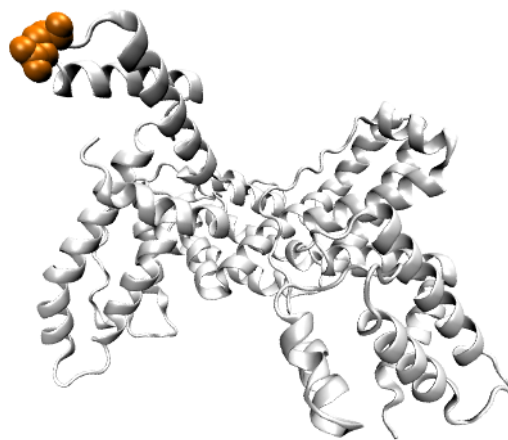
Vitamin D-binding protein (1KW2_A: gene = GC)



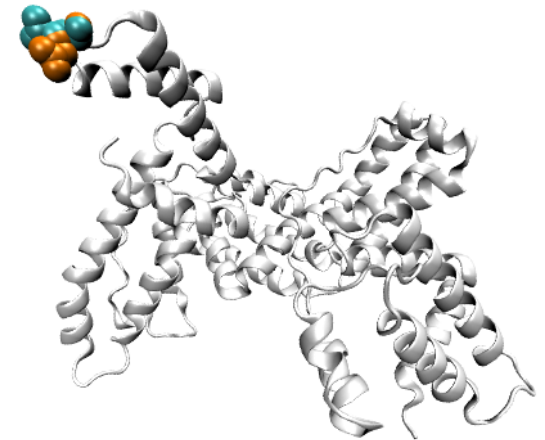
Vitamin D-binding protein (1KW2_A: gene = GC)



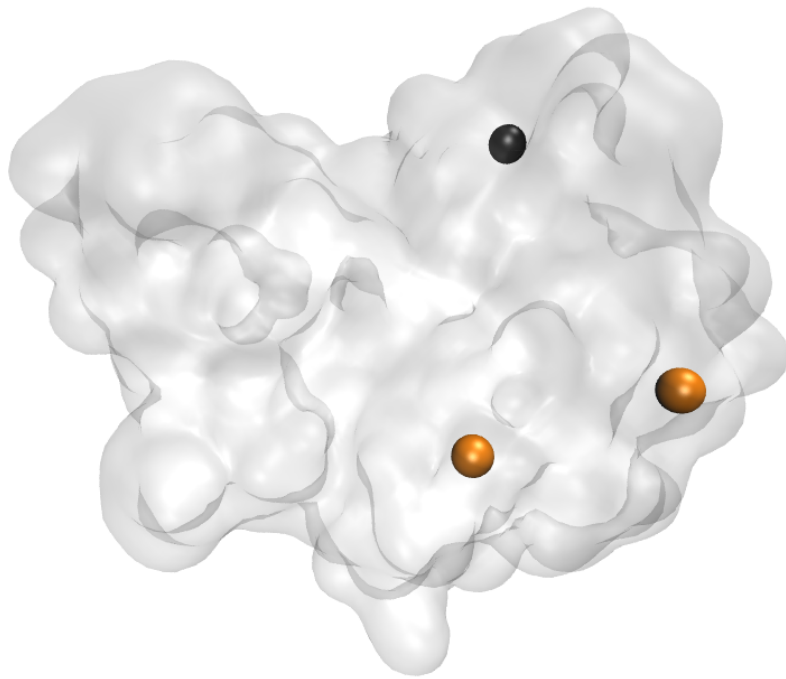
Wild-type



Mutated

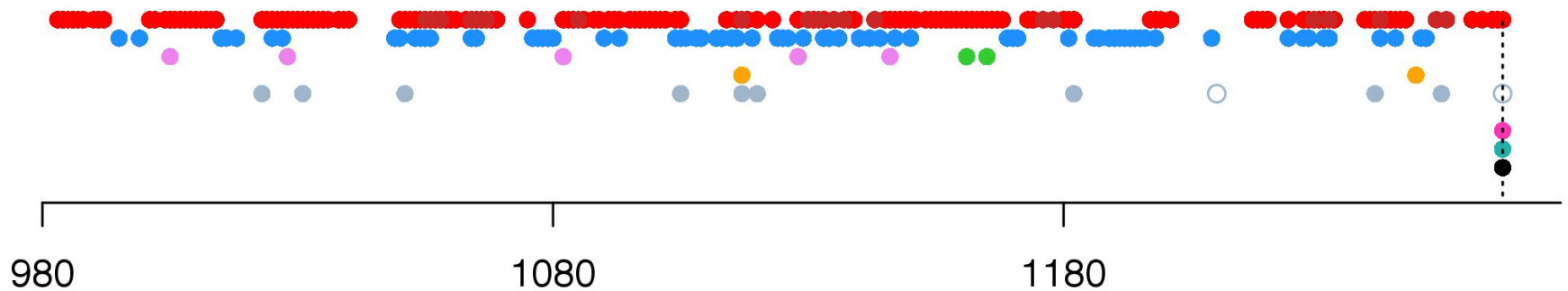


(superimposed)

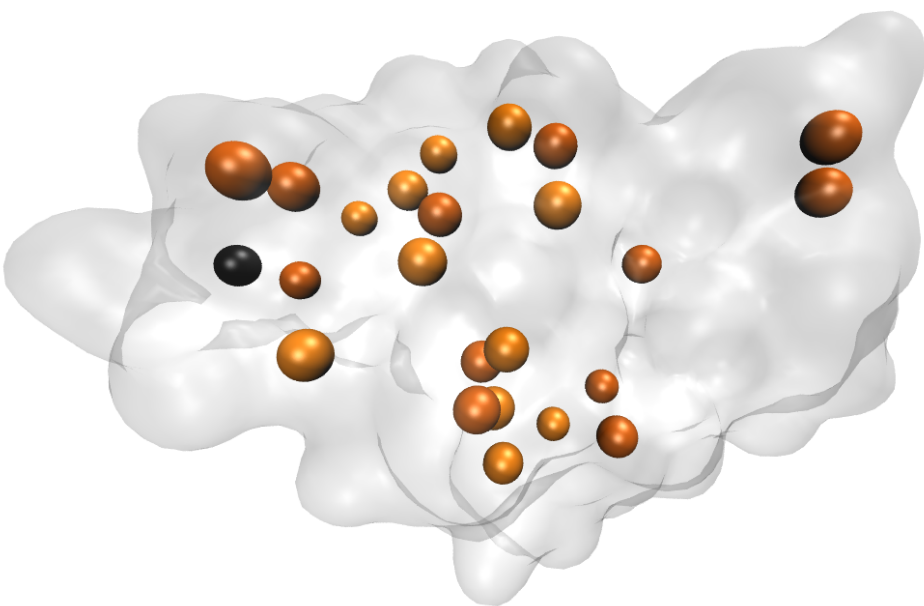


- ● Predicted allosteric (surface | interior)
- Buried residues
- Protein-protein interaction site
- Post-translational modifications
- ▲ ● HGMD (prem. stop | non-synon)
- ○ 1000 Genomes (rare | common)
- ▲ ● Snyder (prem. stop | non-synon)
- ▲ ● na12878 (prem. stop | non-synon)
- ▲ ● Subj. Z (prem. stop | non-synon)

**PAS domain-containing
serine/threonine-protein
kinase (3DLS_A: gene = PASK)**



Residue ID



- Predicted allosteric (surface | interior)
- Buried residues
- Protein-protein interaction site
- Post-translational modifications
- ▲ HGMD (prem. stop | non-synon)
- 1000 Genomes (rare | common)
- ▲ Snyder (prem. stop | non-synon)
- ▲ na12878 (prem. stop | non-synon)
- ▲ Subj. Z (prem. stop | non-synon)

Tpr Domain of Aip (4APO_A: gene = AIP)

