Computer-Aided Drug Design

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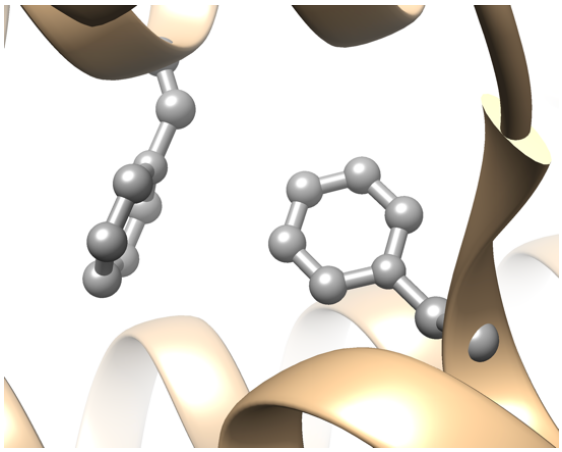
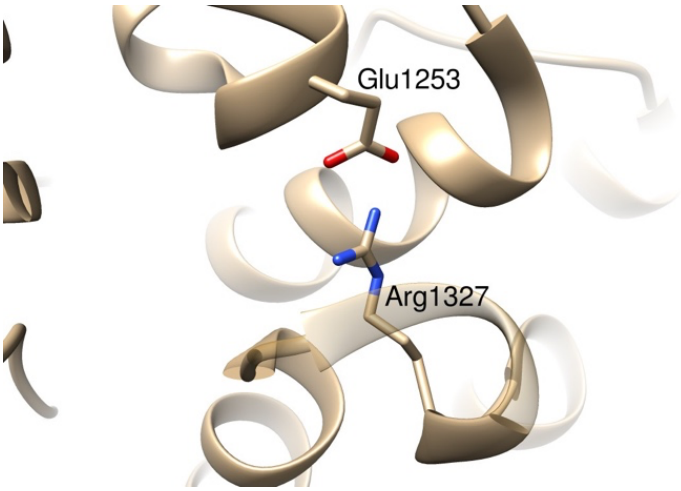
Your name:

Choose one answer or statement that matches best each of the 12 questions.
There is no penalty for bad answers.



1. In the above structure, the side chains of the two amino acids displayed in ball-and-stick representation are making:
   a. a hydrogen bond
   b. a T-shaped π-stacking aromatic interaction
   c. an ionic interaction
   d. a disulfide bridge



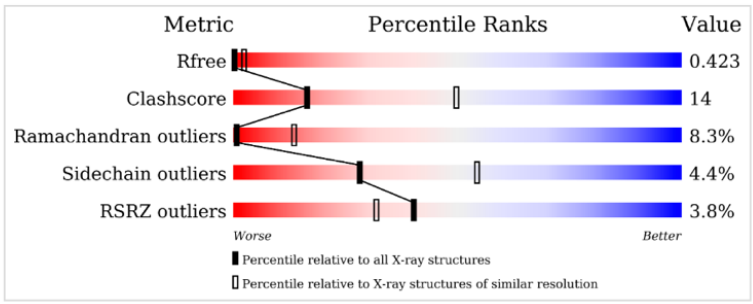
2. In the structure displayed above the arginine (Arg1237) and glutamate (a.k.a. glutamic acid; Glu1253) residues are making:
   a. an aromatic interaction
   b. an ionic interaction (a.k.a. salt bridge in this case)
   c. a disulfide bridge
   d. a covalent bond

3. The quality report on the X-ray structure below indicates that :
   a. the overall quality of the experimental structure will enable a fine analysis of the position of a large proportion of the atoms
   b. the overall quality of the experimental structure is limited and will, for example, only enable a qualitative analysis of the relative position of residues

Experimental Data Snapshot

Method: X-RAY DIFFRACTION
Resolution: 4.20 Å
R-Value Free: 0.444
R-Value Work: 0.381
R-Value Observed: 0.388

wwPDB Validation 3D Report | Full Report



4. Small-molecule docking programs are generally composed of
   a. a posing (sampling) algorithm and a scoring function
   b. a ligand and a protein
   c. a graphical interface and a force field

5. Virtual screening
   a. replaces experimental screening using in silico methods to identify all the actives and only the actives from a large library of small molecules.
   b. applies structure-based or ligand-based approaches to a large collection of molecules, to establish a short list enriched in compounds likely to be active against the target and that could be tested in priority.
   c. filters out all inactive and toxic molecules.

6. A molecule is considered druglike
   a. if it shows high similarity of molecular structure with known bioactive molecules
   b. if its physicochemical properties are within optimal ranges for oral bioavailability
   c. if it satisfies all criteria to enter clinical development

7. Which one is a database of bioactive molecules?
   a. the Protein DataBank (PDB)
   b. ChEMBL
   c. AutoDock Vina

8. Bioavailability is a measurement of
   a. how strong a small molecule binds to a protein
   b. the stability of a chemical compound
   c. the amount of unchanged active ingredient in the bloodstream

9. PAINS filter is to define if a molecule is:
   a. druglike
   b. easy to synthesize
   c. a frequent hitter (promiscuous compound)

10. What is the most probable human protein targeted by molecule_1, whose SMILES is given below?
`NC[C@H](N[C@@H](CCc1ccccc1)C(O)=O)C(=O)N1CCC[C@H]1C(O)=O`

a. SwissTargetPrediction predicts the Angiotensin-converting enzyme (ACE) with a probability of 1, thus it is not a prediction.
b. SwissTargetPrediction predicts the Angiotensin-converting enzyme (ACE) with a probability of ~0.6.
c. SwissTargetPrediction predicts the Angiotensin-converting enzyme (ACE) by homology.
d. SwissADME displays violations in some druglikeness filters, thus it is not a bioactive molecule.

11. Which drug molecule in DrugBank is most similar to molecule_1 for 3D-shape ?

a. Ligand-based screening with SwissSimilarity returned compound CHEMBL3989406 with an Electroshape score of 0.953
b. Ligand-based screening with SwissSimilarity returned Lisinopril with a ECFP4 score of 0.823
c. Ligand-based screening with SwissSimilarity returned ligand 9YK with an Electroshape score of 0.948
d. Ligand-based screening with SwissSimilarity returned Enalaprilat with an Electroshape score of 0.928

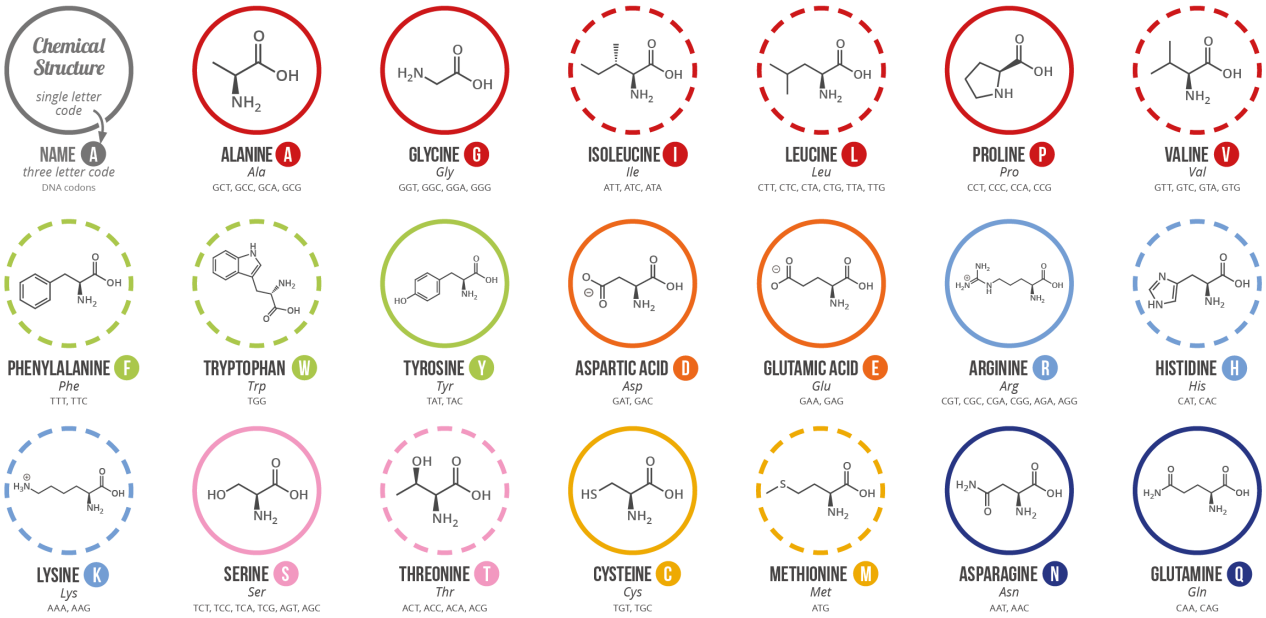
12. What prediction about the absorption and distribution of molecule_1 is given by the BOILED-Egg? This compound:

a. displays properties to be well absorbed by the gastrointestinal tract but it can't permeate through the blood-brain barrier.
b. displays properties to be well absorbed by the gastrointestinal tract but will not stay in high concentration in the brain because it is probably effluxed.
c. cannot be well absorbed by the gastrointestinal tract, because it is not druglike.
d. is too lipophilic to access the central nervous system.

A GUIDE TO THE TWENTY COMMON AMINO ACIDS

AMINO ACIDS ARE THE BUILDING BLOCKS OF PROTEINS IN LIVING ORGANISMS. THERE ARE OVER 500 AMINO ACIDS FOUND IN NATURE - HOWEVER, THE HUMAN GENETIC CODE ONLY DIRECTLY ENCODES 20. 'ESSENTIAL' AMINO ACIDS MUST BE OBTAINED FROM THE DIET, WHILST NON-ESSENTIAL AMINO ACIDS CAN BE SYNTHESISED IN THE BODY.

Chart Key: ALIPHATIC · AROMATIC · ACIDIC · BASIC · HYDROXYLIC · SULFUR-CONTAINING · AMIDIC · NON-ESSENTIAL · ESSENTIAL



Note: This chart only shows those amino acids for which the human genetic code directly codes for. Selenocysteine is often referred to as the 21st amino acid, but is encoded in a special manner. In some cases, distinguishing between asparagine/aspartic acid and glutamine/glutamic acid is difficult. In these cases, the codes asx (B) and glx (Z) are respectively used.