

Evolutionary connections in human and yeast aging: Mechanism and therapeutic targeting

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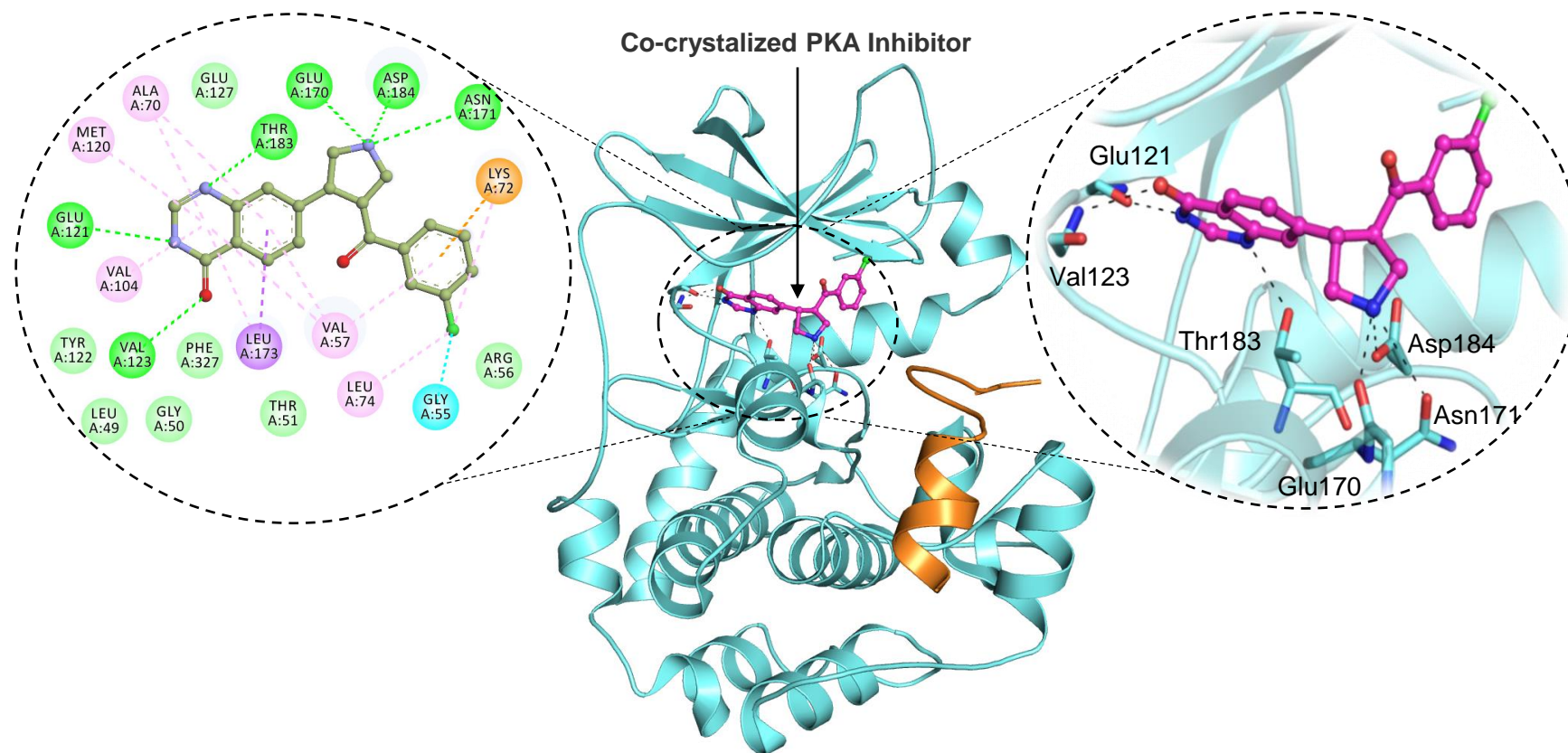


Figure S1: Structural representation of PKA-inhibitor complex (PDB ID: 4UJ1). Left panel showing 2D representation of inhibitor 7-[(3S,4R)-4-(3-chlorophenyl)carbonylpyrrolidin-3-yl]-3H-quinazolin-4-one and its interactions to PKA binding-pocket residues (Dark green is showing conventional hydrogen bond, and other residues are participating in different significant interactions). Right panel showing 3D representation of inhibitor and its interactions to PKA binding-pocket residues.

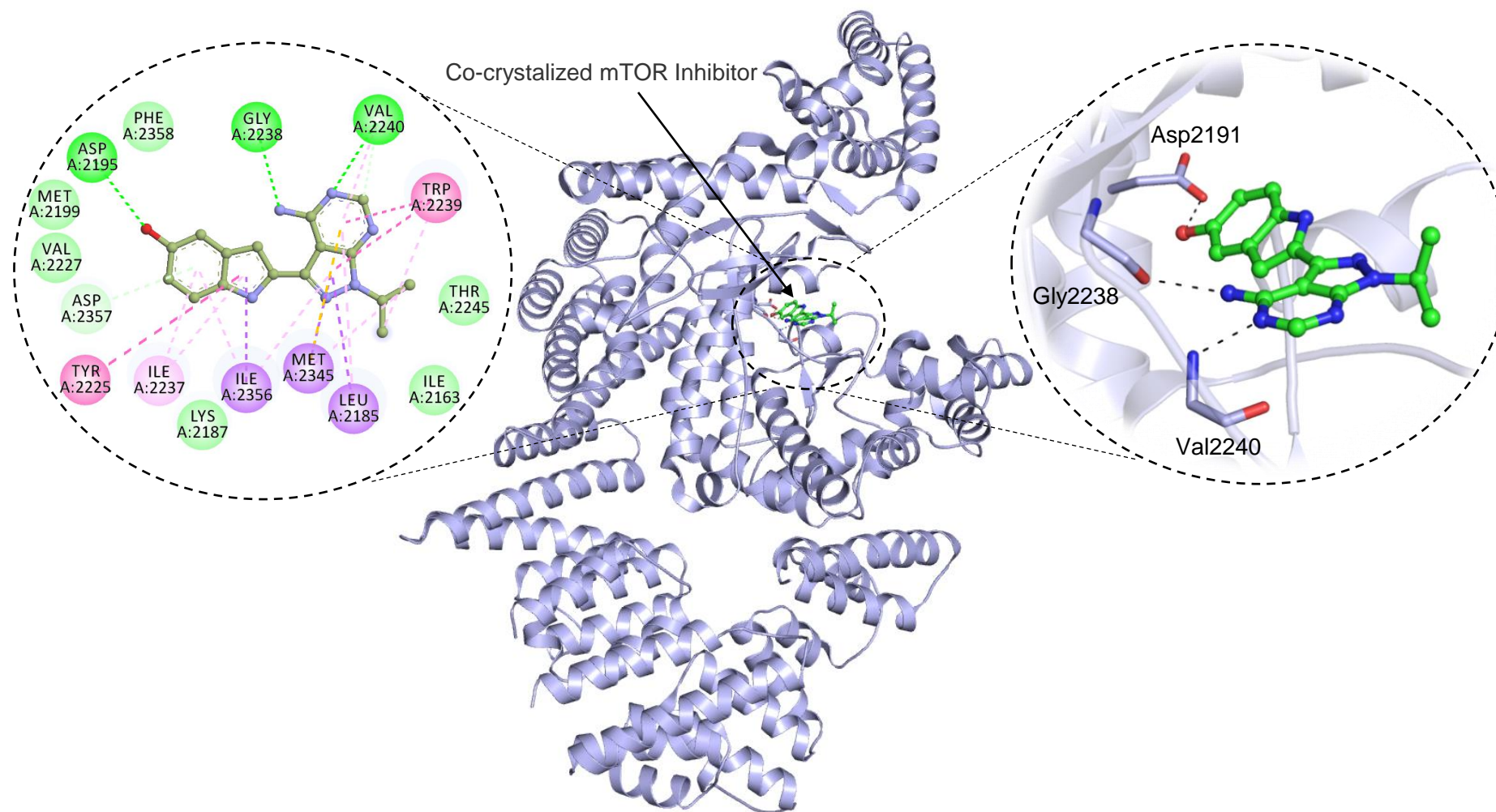


Figure S2: Structural representation of mTOR-inhibitor complex (PDB ID: 4JT5). Left panel showing 2D representation of inhibitor 2-[4-amino-1-(propan-2-yl)-1H-pyrazolo[3,4-d]pyrimidin-3-yl]-1H-indol-5-ol and its interactions to mTOR binding-pocket residues (Dark green is showing conventional hydrogen bond, and other residues are participating in different significant interactions). Right panel showing 3D representation of inhibitor and its interactions within PKA binding-pocket.

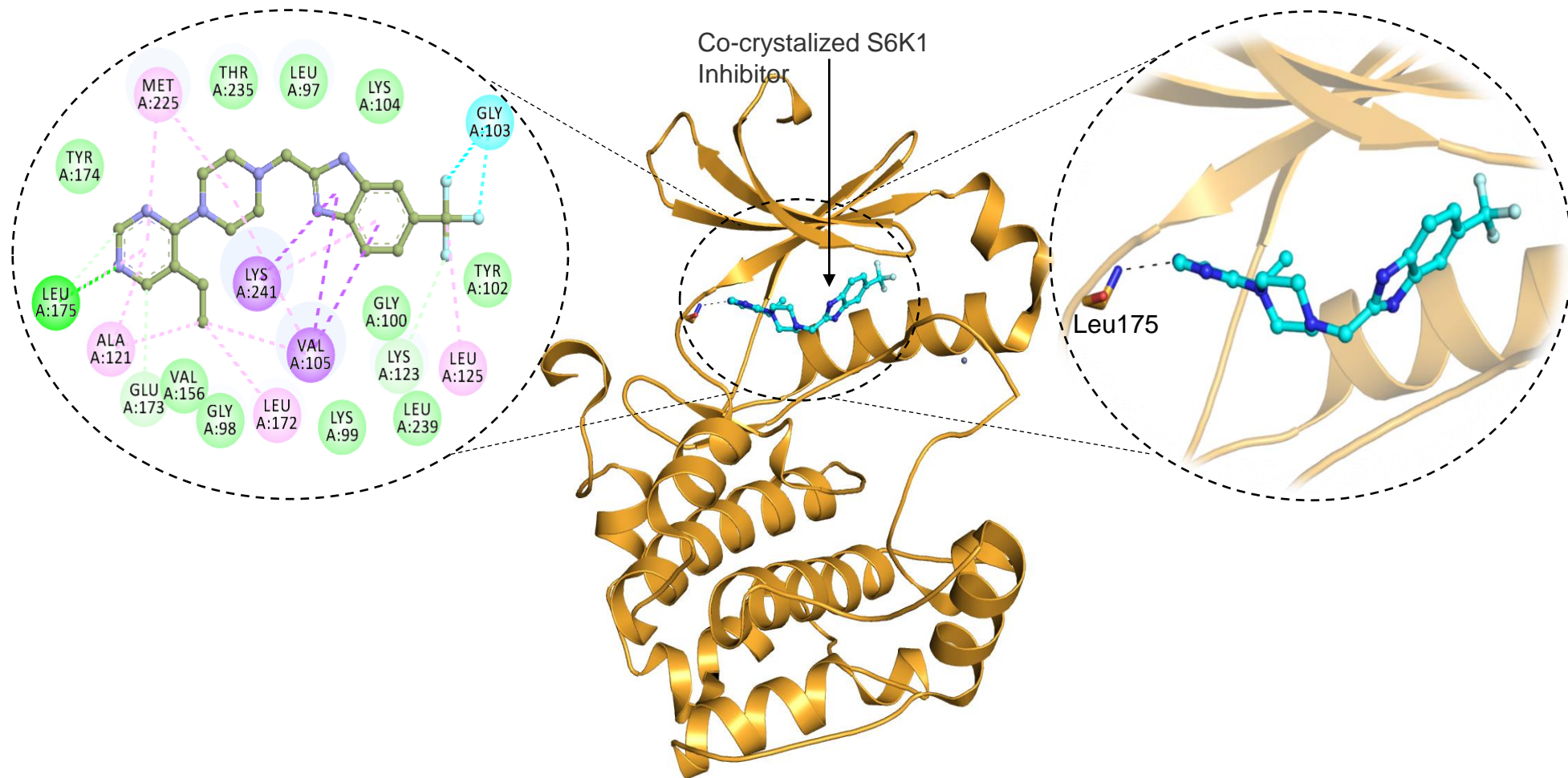


Figure S3: Structural representation of S6K1-inhibitor complex (PDB ID: 3WE4). Left panel showing 2D representation of inhibitor 2- $\{[4-(5\text{-ethylpyrimidin-4-yl})\text{ piperazin-1-yl}] \text{ methyl}\}$ -5-(trifluoromethyl)-1H-benzimidazole and its interactions to S6K1 binding-pocket residues (Dark green is showing conventional hydrogen bond, and other residues are participating in different significant interactions). Right panel showing 3D representation of inhibitor and its interactions to PKA binding-pocket residues.