Supplementary Information

Prediction of Functional Loss of Human Angiogenin Mutants Associated with ALS by Molecular Dynamics Simulations

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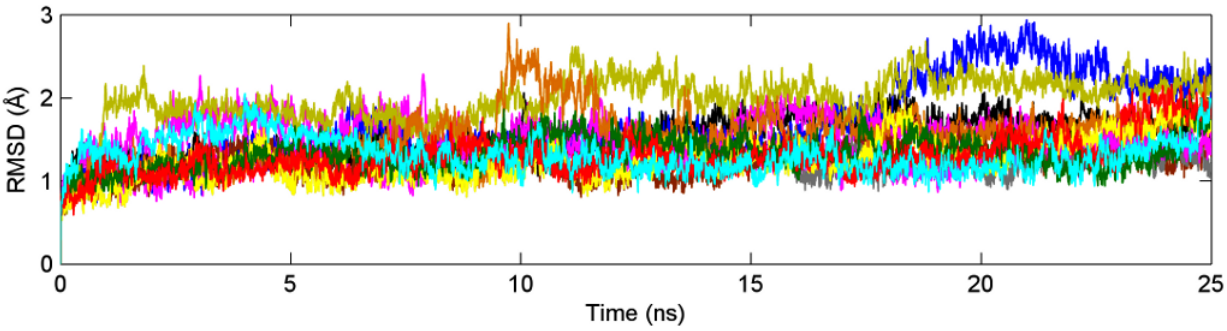

Supplementary Figure S1. Computed RMSD profiles of ALS associated ANG mutants. Computed RMSD values for all the ANG mutants representing their stability during the simulation run are plotted. The root mean square deviation (RMSD) values of the backbone atoms were computed from the equilibrated conformation. RMSD values for angiogenin mutants are represented in the following colour lines (WT-ANG: black, I46V: blue, K17E: light pink, R31K: brown, D22G: gray, N49S: magenta, T80S: light green, V103I: orange, K54E: yellow, F100I: green, R121C: red and R121H: cyan).

Supplementary Table S1. Computed hydrogen bonding occupancy between Thr44-Thr80 and Asp116-Ser118 from MD simulations for the ANG mutants.

ANG	H-bonding occupancy (%)	
	Thr44 ─ Thr80	Asp116 ─ Ser118
WT-ANG	50.11	57.61
I46V	81.45	80.78
K17E	76.71	71.23
R31K	48.60	46.27
D22G	89.59	90.12
N49S	52.50	63.23
T80S	82.89	87.22
V103I	41.55	48.72
K54E	46.60	54.05
F100I	48.50	47.94
R121C	55.52	51.06
R121H	53.59	44.14

Supplementary Table S2. Computed binding free energy scores for ANG mutants and NCI-65828 complexes using ParDOCK.

	ParDOCK binding energy scores	
ANG	**Native His114 conformation**	**Altered His114 conformation**
WT-ANG*	-4.96 kcal/mol	
I46V	-3.99 kcal/mol	-2.94 kcal/mol
K17E	-3.58 kcal/mol	-2.61 kcal/mol
R31K	-3.10 kcal/mol	-1.86 kcal/mol
D22G	-3.36 kcal/mol	-2.47 kcal/mol
N49S	-3.98 kcal/mol	-2.05 kcal/mol
T80S	-4.15 kcal/mol	-1.93 kcal/mol
V103I*	-4.01 kcal/mol	
K54E*	-3.91 kcal/mol	
F100I*	-4.11 kcal/mol	
R121C*	-4.00 kcal/mol	
R121H*	-3.89 kcal/mol	

*ANG mutants which do not exhibit characteristic conformational change of the catalytic residue His114.