

Supporting Information

Model construction

In this study we used the substrate-binding domain from Ssa1p (392-507) in complex with the peptide NRLLLTG, which was constructed based upon the DnaK (PDB code: 1Q5L) (1), Hsc70 of *Bos taurus* (PDB code: 3C7N) (2) and Hsc70 of *Rattus norvegicus* (PDB code: 7HSC) (3) substrate-binding domain structures using Modeller 9v8 (4). Stereochemistry of the models was evaluated by Procheck. The best model was selected on the basis of DOPE score, GA341 score and Procheck. Appropriate models representing mutants of L483 residue mutations were constructed based upon the wild-type Ssa1p substrate-binding domain structure using Swiss-Pdb Viewer (5) and subjected to Procheck analysis.

References

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