Multiple Pathways Promote Dynamical Coupling between Catalytic Domains in *Escherichia coli* Prolyl-tRNA Synthetase

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SUPPLEMENTAL FIGURE LEGENDS

Figure S1. Dynamic cross-correlations between the C_α atoms of Ec ProRS obtained from the cluster analysis and PCA. A value of +1.0 was set for strongly correlated motion and is colored red, whereas -1.0 was used for strongly anti-correlated motions and is colored blue. The abbreviations used are: CD, catalytic (aminoacylation) domain; INS, insertion domain; and ACB, anticodon binding domain.

Figure S2. Conserved residues from SCA. A normalized plot of ΔG_i^{stat} vs. position (residue number). A value of 1 indicates 100% conservation over the 452 sequences examined.

Table S1. List of primers used in this study, bold letters represent the sites of mutation.

1. ProRS_D198At: 5′-GCGCCGTACAAGCC**GCC**ACCGGTTCTATCGGCGG-3′
   ProRS_D198Ab: 5′-CCGCCGATAGAACCGGTG**GCG**GCTTGTACGGCGC-3′
2. ProRS_E234At: 5′-GCAGCGAACATT**GCA**CTGGCAGAAGC-3′
   ProRS_E234Ab: 5′-GCTTCTGCCAG**TGC**AATGTTCGCTGC-3′
3. ProRS_H302At: 5′-GCGCGGTGAT**GCC**GAGCTGAACG-3′
   ProRS_H302Ab: 5′-CGTTCAGCTC**GGC**ATCACCGCGC-3′
4. ProRS_N305At: 5′-CGAGCTG**GCC**GAAGTTAAAGC -3′
   ProRS_N305Ab: 5′-GCTTTAACTTC**GGC**CAGCTCG- 3′
5. ProRS_G412At: 5′-CGTGGTATCGAAGTT**GCT**CACATCTTCCAGCTGGG-3′
   ProRS_G412Ab: 5′- CCCAGCTGGAAGATGTG**AGC**AACTTCGATACCACG-3′
6. ProRS_F415At: 5′-GGTCACATC**GCC**CAGCTGGG-3′
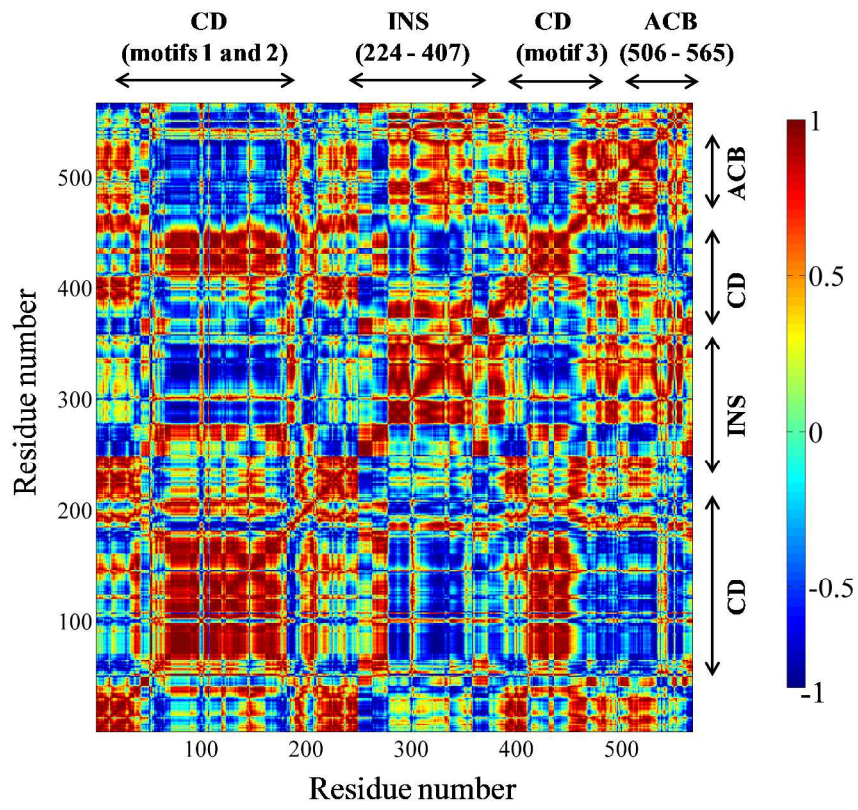   ProRS_F415Ab: 5′-CCCAGCTG**GGC**GATGTGACC-3′

Fig. S1

Fig. S2