

**SI Table 1.** A consolidated list of dynamically stable<sup>a</sup> k=3 clique/communities<sup>x</sup> in five different systems A, B, C, D, and E<sup>y</sup> for Imin=3%.

| MetRS           | MetRS+ Met(L1)  | MetRS+ ATP(L2)  | MetRS+ MetAMP(L3) | tRNA +MetAMP EI (0.5-5.5ns) | tRNA +MetAMP EI (5.5-10.0ns) |
|-----------------|-----------------|-----------------|-------------------|-----------------------------|------------------------------|
| :118F 197F 311G | :118F 197F 311G | :118F 197F 311G | :118F 197F 311G   | :118F 197F 311G             | :118F 197F 311G              |
| :120K 193D 228Q | :120K 193D 228Q | :120K 193D 228Q | :120K193D228Q     | :122R 191F 228Q             | :122R 191F 228Q              |
| :122R 191F 228Q | :122R 191F 228Q | :122R191F 228Q  | :454Y 458Q 476I   | :417L 454Y 479M             | :417L 454Y 479M              |
| :417L 454Y 479M | :417L454Y 479M  | :417L 454Y 479M | :417L454Y479M     | :414D                       |                              |
| 483L            |                 |                 |                   |                             |                              |
| :266N 270K 93N  | :101E 266N 95H  | :101E 266N 95H  | :101E 266N 95H    | :101E 266N 95H              | :266N 270K 93N               |
|                 | :266N 270K 93N  | :266N 270K 93N  | :266N 270K 93N    | :266N 270K 93N              |                              |
| :412L418Y 482N  | :412L418Y482N   | :412L 418Y 482N | :412L 418Y 482N   | :412L 418Y 482N             | :412L 418Y 482N              |
|                 | 517Q            |                 | 517Q              | 517Q                        | 517Q                         |
| :428I 444I 490Y | :428I 444I 490Y | :428I 444I 490Y | :428I 444I 490Y   | :418Y 422T 486V             | :418Y 422T 486V              |
| :486V 490Y 515I | :486V 490Y 515I | :486V 490Y 515I | :486V 490Y 515I   | :515I                       | :486V 490Y 515I              |
| :292F 321F 435R | :290Y 292F 321F | :290Y 292F 321F | :292F 321F 34W    | :428I 432W 444I             |                              |
|                 | 34W             | 34W 435R        | 290Y              | 490Y                        |                              |
| :33V 360T 437F  |                 |                 |                   |                             |                              |
| :295K 325Y 369D | :295K325Y369D   | :33V 360T 437F  | :295K325Y369D     | :295K 324G 325Y             |                              |
| 324G            | 324G            |                 | 324G              | 369D                        |                              |
| :205T 218M 222F | :205T 218M 222F |                 | :205T 218M 222F   |                             | :357Y 384D 445M              |
| 210L 302S       | 210L 302S       |                 |                   |                             |                              |
| :357Y 380R 384D | :357Y 384D 445M | :357Y 384D 388K |                   |                             |                              |
| :358Y 376D 380R | 380R            | 445M            |                   |                             |                              |
| :129D 136L 175S | :129D 136L 175S | :129D 132K 136L | :129D 132K 136L   | :129D 136L 175S             | :129D 132K 136L              |
| 178S            | 178S            | 175S 178S       | 175S 178S         | 178S                        | 178S                         |
| :136L 140F 56T  |                 | :136L 140F 56T  | :136L 140F 60L    |                             |                              |
| :22L 346W 355L  | :22L 346W 355L  |                 |                   |                             |                              |
| :346W 50F 542L  |                 | :358Y362K376D   |                   |                             |                              |
| :189H 234D 248K | :189H 230D 233R | :189H 234D 248K | :189H234D248K     |                             |                              |
| 187S            |                 |                 |                   |                             |                              |
|                 | :128Y 135F 185R | :128Y 135F 185R |                   |                             | :128Y 135F 185R              |
|                 | :187S 234D 248K | :126Q 135F 230D |                   |                             | :126Q 135F 187S              |
|                 | 135F            | 233R            |                   |                             |                              |

**SI Table 1** (continued)

| MetRS  | MetRS+ Met(LI)   | MetRS+ ATP(LI)                                    | MetRS+ MetAMP(L3)  | tRNA +MetAMP EI (0.5-5.5ns)                                       | tRNA+MetAMP EII (5.5-10ns)  |
|--|--|---|--|---|---|
| :110Y242I 250F<br>119I 190F 232S                   | :110Y 242I 250F<br>119I 190F 232S                                  | :110Y 244N 250F<br>114K 119I 190F<br>232S 242I    | :110Y 242I 250F<br>119I 190F 232S<br>202N 106S 240F<br>250F 255D 258I<br>54H | :110Y 114K 119I<br>:110Y 242I 250F                                | :110Y 242I 250F   |
| :253W 300F 304F<br>229W                            | :264F 280Y 8L<br>277F 281W 289L<br>46N                             | :253W 300F 304F<br>229W                           | :221W299Y303L<br>:229W 253W 299Y   |   |   |
| :264F 46N 280Y<br>277F 281W 289L<br>8L             | :214V 293I 298V<br>322V  | :264F 277F 280Y<br>281W 289 L46N<br>8L            | :264F 280Y 281W<br>289L 46N 8L   | :264F 280Y 281W<br>289L 46N 8L                                    | :264F 280Y 281W<br>46N 8L   |
| :293I 297I 301H<br>:293I 298V 322V                 | :293I (#297I 301H<br>253W L1) 13L<br>(#260Y 291H<br>305W 301H) 10T | :105L 265K 277F                                   | :293I 297I 301H<br>:291H301H305W<br>L3 13L 10T<br>(#260Y 291H<br>301H 305W)  | #253W 293I 297I<br>301H L3  | #253W 293I 297I<br>301H L3  |
| :10T 260Y 291H<br>204W 305W316K<br>:200M 310E 316K | :256A 52D L1<br>:204W305W316K<br>:200M310E316K                     | :10T 260Y 291H<br>:204W305W316K<br>:200M 310E316K | :27E 323H 294G<br>L3   | :293I 298V 322V<br>:52D 256A L3<br>:13L 260Y L3<br>:10T 260Y 291H | :293I 298V 322V<br>:52D 256A L3<br>:13L 260Y L3<br>:10T 260Y 291H |
| :354S 377F 381V<br>534I                            | :145C 148C153Q<br>158C 165Y169E                                    | :27E 323H 294G<br>L2                              | :21H 333M L3<br>:204W 305 W316K  | :350F 534I 538Q<br>:346W 350F 377F<br>542L                        |   |
| :397A 505F 527F                                    | :23G 326V 333M<br>:26L 326V 359Y                                   | :23D 326V L2<br>: 15Y 139R L2<br>: 325Y 332K L2   | :204W 305 W316K  | :346W 350F 377F<br>381V   |   |
| :353D 495L 498L                                    | :102N 240F 255D  |   | :351D 354S 531Y<br>381V  | :346W 355L 87F  | :346W 355L 87F  |
| :508T 519L 522H                                    | :30Q 363L437F<br>323H  | :346W350F 377F<br>355L 542L                       | :346W 350F377F<br>381V 534I 538Q<br>542L                                     | :200M 310E 316K   | :200M 310E 316K   |
|  | :27E 294G 323H   | :354S 381V 385I<br>531Y 534I                      | :341I 542L 546S<br>:346W 355L 87F  | :205T 218M 222F   |   |
|  | :341I 542L 546S  | :397A 505F 527F                                   | :356R 36R 495L   | :508T 519L 522H   | :353D 495L 498L   |
|  | :37Y432W 512W  | :356R 36R 495L                                    | :37Y 432W 512W   |   | :508T 519L 522H   |
|  |  | :102N 106S 240F                                   | :145C148C165Y<br>153Q  |   | :378V 536M 539V   |
|  |  | :194L 226L 303L                                   | :214V 322V 367I  |   | :26L 326V 359Y  |
|  |  | :27E 294G 323H                                    | :105L 265K 277F  |   | :30Q 363L 435R  |
|  |  | :347L 352A 87F                                    | :391N 395R 452N  |   | :399F 473L 477C   |
|  |  | :392K 499T 503E                                   | :492K499T 503E   |   |   |
|  |  |   | :396N 455V 459A  |   |   |
|  |  |   | :30Q 323H435R  |   |   |

**L1**, **L2** and **L3** are the ligands Met, ATP and MetAMP respectively.

<sup>a</sup> : 50% of snapshots in which the listed residues appear as cliques.

<sup>x</sup> : The list of residues in a clique/community begins with the symbol “:” and each clique /community is separated by a blank space.

<sup>y</sup> : The analysis of system E (presented in this Table and in Table 2) is carried out in two parts

(EI and EII), which exhibited different RMSD values in Figure 1b.

The list beginning with the symbol “#” are the cliques/communities with k=4 (clique of residues 260Y, 301H, 305W, 291H is present in systems B and D and of residues Met/MetAMP, 253W, 301H and 297I is present in system B and E). More than 3 residues representing communities, which share 2 residues in common are highlighted. The cliques/communities connected by a single residue are also highlighted and have been written one below the other without a blank space. The three largest communities in system D and their variants in other systems are highlighted in blue, magenta and red color boxes.



<sup>x</sup> : 50% of snapshots in which the listed residues appear as hubs.

<sup>y</sup> : All those residues which appear as hubs in at least one of the simulations are listed. A (✓) in the 1<sup>st</sup> column of a given system (e.g. A or B) represents that the residue is a hub in that simulation. A (✓) in the 2<sup>nd</sup> column indicates that the residue is part of a clique.

\* : A: MetRS; B: MetRS+Met; C: MetRS+ATP; D: MetRS+MetAMP;

E: MetRS+MetAMP+ tRNA<sub>f</sub><sup>Met</sup>

**SI Table 3.** Composition of residues in top three communities in systems D and E.

| Community  | Res  | D* | E* | CP <sup>a</sup> | Conserved <sup>b</sup> |
|------------|------|----|----|-----------------|------------------------|
| <b>I</b>   | 8L   | ✓  |    |                 |                        |
|            | 10T  | X  | X  |                 | ✓                      |
|            | 13L  | ✓  | X  |                 | ✓                      |
|            | 21H  | X  |    |                 | ✓                      |
|            | 27E  | X  |    |                 |                        |
|            | 46N  | X  |    |                 |                        |
|            | 52D  | X  | X  |                 | ✓                      |
|            | 200M | X  |    |                 |                        |
|            | 204W | ✓  |    |                 |                        |
|            | 256A | X  | X  |                 | ✓                      |
|            | 260Y | ✓  | X  |                 | ✓                      |
|            | 261M | X  |    |                 | ✓                      |
|            | 264F | ✓  |    |                 |                        |
|            | 280Y | ✓  |    |                 | ✓                      |
|            | 281W | ✓° |    |                 | ✓                      |
|            | 289L | X  |    |                 |                        |
|            | 291H | ✓  | ✓° |                 | ✓                      |
|            | 293I | ✓  | ✓° |                 | ✓                      |
|            | 294G | X  |    |                 | ✓                      |
|            | 297I | X  | X  |                 |                        |
|            | 301H | ✓  | ✓  |                 | ✓                      |
|            | 305W | ✓° | ✓  |                 | ✓                      |
|            | 310E | X  |    |                 |                        |
|            | 316K | ✓° |    |                 |                        |
|            | 323H | ✓  |    |                 |                        |
|            | 333M | X  |    |                 |                        |
| <b>II</b>  | 87F  | ✓  | ✓  | ✓               |                        |
|            | 341I | X  |    |                 |                        |
|            | 346W | ✓° | ✓° | ✓               | ✓                      |
|            | 350F | ✓  | ✓° | ✓               |                        |
|            | 351D | X  |    |                 |                        |
|            | 354S | X  |    |                 |                        |
|            | 355L | X  | X  | ✓               |                        |
|            | 377F | ✓  | ✓  | ✓               | ✓                      |
|            | 381V | ✓° |    | ✓               |                        |
|            | 531Y | X  |    | ✓               | ✓                      |
|            | 534I | ✓  | X  | ✓               |                        |
|            | 538Q | X  | X  | ✓               |                        |
|            | 546S | X  |    |                 |                        |
|            | 542L | ✓° | X  |                 |                        |
| <b>III</b> | 54H  | ✓  |    |                 | ✓                      |
|            | 102N | X  |    |                 | ✓                      |
|            | 106S | X  |    |                 |                        |
|            | 110Y | ✓  | ✓° |                 | ✓                      |
|            | 119I | X  | X  |                 |                        |
|            | 190F | X  |    |                 |                        |
|            | 232S | X  |    |                 | ✓                      |
|            | 240F | ✓  | ✓  |                 | ✓                      |
|            | 242I | X  |    |                 |                        |
|            | 250F | ✓° | X  |                 |                        |
|            | 255D | X  |    |                 | ✓                      |
|            | 258I | ✓  |    |                 | ✓                      |

<sup>\*</sup> : The presence of residue in the community is shown by one of the symbols (X), ( $\checkmark$ ) or ( $\checkmark^o$ ) where (X) represents a member of the clique, ( $\checkmark$ ) represents that the clique member is a hub residue and ( $\checkmark^o$ ) indicates that the clique member is a hub and also connects two cliques.

<sup>a</sup> : A ( $\checkmark$ ) represents the conservation of the residue along different species of MetRS.

<sup>b</sup> : A ( $\checkmark$ ) represents the participation of the residue in communication paths (CP).

SI Figure 4. Sequence alignment of MetRSs. Abbreviations are as follows: T.ther, *T. thermophilus*; B.su, *Bacillus subtilis*; M.ge, *Mycoplasma genitalium*; M.p, *Mycoplasma pneumoniae*; A.aeol, *A. aeolicus*; H.i, *Haemophilus influenzae*; M.t, *Methanobacterium thermoautotrophicum*; B.b, *Borrelia burgdorferi*; T.p, *Treponema pallidum*; B.st, *Bacillus stearothermophilus*; S.ce, *S. cerevisiae* nuclear; HUMAN, *Homo Sapiens*. The symbols '\*' , ':' and '!' below the alignment correspond respectively to completely conserved, partially conserved and mutationally conserved residues. Residues conserved along different families of MetRS and participating in communication paths and the three largest communities are highlighted in different colors. The markings  $\alpha$ ,  $\varepsilon$ ,  $\pi$  on top of the alignment indicate the residues involved in top three communities, communication path and in both, respectively.

