Table 4. Hot-spot [*] residues of selected robust modes of *E. coli* GroEL chaperonin

Mode # [†]	Residue numbers
1	**83**[‡], 141, 144, 161, 164, 165, 166, 167, 168, 169, 170, 171, 172, **173**, **174**, 175, **176**, 177, 187, 188, **189**, **190**, **191**, 192, 193, **194**, 195, 288, 291, 295, **331**, 332, 333, 346, 347, 349, 352, 353, **359**, **360**, **361**, 363, 364, 365, **366**, 367, 368, 369, 370, **371**, 372, 373, 374, **375**, 376, 377, **378**, 379, 397, 400, 404

[*] The hot-spot residues that introduce most significant site-specific perturbation have high-$\delta\omega$ values. The details of the calculations are given in ref. 1.

[†] These modes describe allosteric transitions and are also robust to sequence variations.

[‡] Residues in bold have already been experimentally identified to be significant.

1**.** Zheng, W., Brooks, B. R., Doniach, S. & Thirumalai, D. (2005) *Structure (London)* **13**, 565-577.