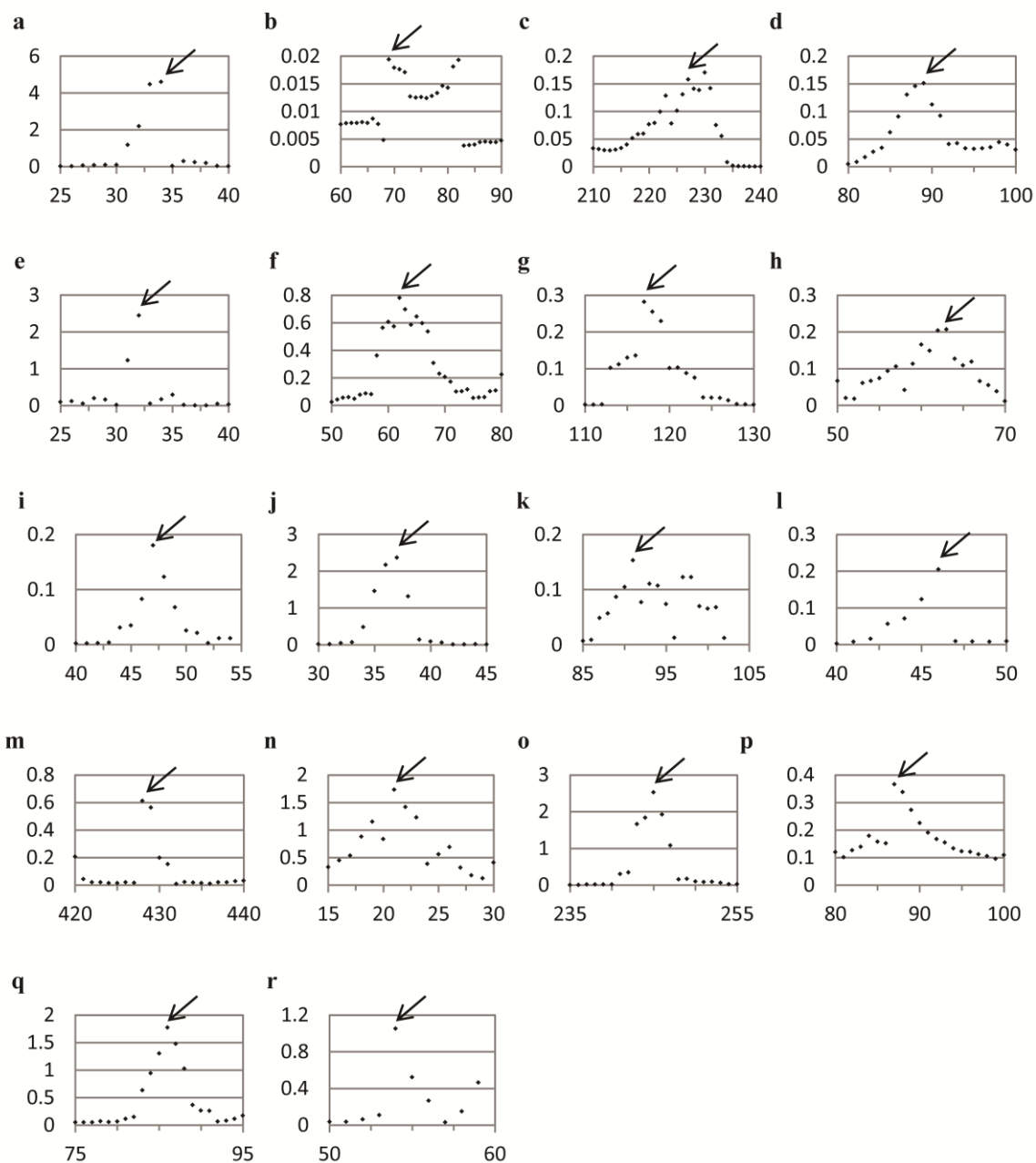


The enigma of the near-symmetry of proteins: Domain swapping

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Supporting Information



S2 Fig. Additional running ruler symmetry analyses (see also Fig. 5). The neighborhood of the hinge region is shown. Black arrows - the hinge region. **(a)** scaffold protein IscA (1X0G), **(b)** sulerythrin (PDB code: 1J30), **(c)** Soluble epoxide hydrolase (PDB code: 1CQZ), **(d)** Cyclin-dependent kinase (PDB code: 1QB3), **(e)** Designed helical bundle (PDB code: 1G6U), **(f)** Endonuclease VII (PDB code: 1EN7), **(g)** Guanine deaminase (PDB code: 1WKQ), **(h)** T-SNARE (PDB code: 2C5J), **(i)** Hemophore HasA (PDB code: 2CN4), **(j)** Dynactin-1 (PDB code: 2HKN), **(k)** Caspase-recruitment domain CARD (PDB code: 2NZ7), **(l)** Cystatin B (PDB code: 2OCT), **(m)** Macrophage receptor MARCO (PDB code: 2OYA), **(n)** Saposin C Dimer (PDB code: 2QYP), **(o)** Survival protein E (PDB code: 1L5X), **(p)** Endonuclease VII (PDB code: 1E7D), **(q)** Suc1 (PDB code: 1SCE), **(r)** Cro repressor protein (PDB code: 5CRO). See Table 1 for more information. For data sources see ref.'s 60–77.