Domain architecture	Origins	Pfam AC #	Genesis
GntR * LacI	2	PF00392, PF00532	Bac/*B. subtilis, C. acetobutylicum*
			Bac/*E. faecalis*
Beta/Gamma crystallin * Beta/Gamma crystallin * Ricin-type beta-trefoil lectin domain	3	PF00030, PF00652	Euk/*M. musculus*
			Euk/*M. musculus*
			Euk/*H. sapiens*
FKBP-type peptidyl-prolyl cis-trans isomerase * EF hand * EF hand	2	PF00254, PF00036	Euk/*H. sapiens, M. musculus*
			Euk/*D. melanogaster, A. gambiae*
Urease gamma subunit * Urease beta subunit	2	PF00547, PF00699	Bac/*D. radiodurans*
			Bac/*H. pylori*
CBS domain pair * ACT domain	2	PF00571, PF01842	Bac/*D. psychrophila*
			Bac/*S. thermophilum*
DAHP synthetase I family * Chorismate mutase type II	2	PF00793, PF01817	Bac/*S. thermophilum*
			Bac/*B. fragilis*
NeuB family * SAF domain	2	PF03102, PF08666	Euk/*D. melanogaster, M. musculus, H. sapiens*
			Bac/*M. jannaschii, C. jejuni, H. pylori, C. acetobutylicum, N. meningitidis, S. sp (WH8102), L. interrogans, B. subtilis*[1]
PTS system fructose IIA component * PTS system sorbose subfamily IIB component	2	PF03610, PF03830	Bac/*E. faecalis*
			Bac/*E. faecalis, C. acetbutylicum, E. coli*
Fumarate hydratase (Fumerase) * Fumarase C-terminus	2	PF05681, PF05683	Bac/*C. tepidum*
			Bac+Euk/*T. cruzi, P. falciparum, E. coli, B. fragilis, A. sp (ADP1), N. meningitidis, A. sp (EbN1), D. psychrophilia, B. bacteriovorus*

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[1] For the SAF domains, rooting varies widely among the bootstrap trees; roughly half display this clustering.

Response regulator receiver domain * PAS fold * PAS fold * PAS fold * His Kinase A (phosphoacceptor) domain * Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	2	PF00072, PF08448, PF08447, PF08448, PF00512, PF02518	Arch/*H. marismortui* Arch/*H. marismortui*
Phosphoribosylglycinamide synthetase, N domain * Phosphoribosylglycinamide synthetase, ATP-grasp (A) domain	2	PF02844, PF01071	Euk/*A. gambiae* Arch/*T. acidophilum*
Tetrapyrrole (Corrin/Porphyrin) Methylase * Precorrin-8X methylmutase	2	PF00590, PF02570	Bac/*C. tepidum, B. fragilis* Arch/*A. fulgidus*
S-adenosylmethionine decarboxylase * Spermine/spermidine synthase	2	PF02675, PF01564	Bac/*A. sp* Bac/*B. bacteriovorus*
CLIP, MHC2 interacting * Class II MHC-associated invariant chain trimerisation domain	2	PF09307, PF08831	Euk/*H. sapiens, M. musculus* Euk/*M. musculus*
MarR * DUF120	2	PF01047, PF01982	Arch/*P. abyssi* Arch/*T. acidophilum*
NADH pyrophosphatase-like rudimentary NUDIX domain * NUDIX domain	3	PF09296, PF00293	Euk/*M. musculus* Euk/*S. pombe* Euk/*C. elegans, C. briggsae*
RNA polymerase Rpb2, domain 6 * RNA polymerase Rpb2, domain 7	2	PF00562, PF04560	Euk/*H. sapiens* Euk/*T. cruzi*
MoaC * Probable molybdopterin binding domain	2	PF01967, PF00994	Bac/*A. sp (ADP1)* Bac/*C. tepidum*
Sodium/hydrogen exchanger * TrkA-C domain	2	PF00999, PF02080	Bac/*L. interrogans* Bac/*B. fragilis*
Response regulator receiver domain * Histidine kinase * Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	2	PF00072, PF07568, PF02518	Bac/*A. tumefaciens* Bac/*M. thermoautothrophicum*
GAF * GGDEF * EAL	2	PF01590, PF00990, PF00563	Bac/*M. bovis* Bac/*A. sp*

Glutaminyl-tRNA synthetase (non-specific RNA binding region part 2) * tRNA synthetases class I (E and Q; catalytic domain) * tRNA synthetases class I (E and Q; anti-codon binding domain)	3	PF04557, PF00749, PF03950	Euk/*H. sapiens* Euk/*M. musculus*

Table S4. Domain architectures common to the *max50* and *nolimit* datasets found to have arisen multiple times independently. The 22 domain architectures where bootstrap results for all domains agree and where the number of origins inferred are exactly the same for both datasets are presented. The domains in the domain architecture description are given in an N- to C-terminal order separated by an asterisk. For each architecture, the number of origins inferred for the domains in the architecture are given in the second column. In the third column, the Pfam accession numbers for the domains are given. Finally, the taxonomic level of each genesis and the species involved are given.