

Table II: Patterns of Complementary Superfamilies and Horizontal Transfer

A/ Complementary clades between bacterial/archaeal and eukaryotic genes

B/ Complementary clades between bacterial and eukaryotic/archaeal genomes

C/ Other complementary patterns

D/ Horizontal Transfer between Archaea and Bacteria

E/ Horizontal Transfer between Eukaryotes and Bacteria

	afu	mjan	mthe	pfor	scer	cele	aaeo	syne	ecol	bsub	mtub	hirf	hpyl	ingen	mpne	bbur	tpal	ctra	cpne	lpro	Sfam	domain	SCOP Function	Swissprot	Swissprot Function		
A	3.25.1	d1fsz_1	Tubulin, GTPase domain	FTSZ_ECOLI	CELL DIVISION PROTEIN FTSZ	
	4.57.1	d1puc	Cell cycle regulatory proteins	CKS1_YEAST	CELL DIVISION CONTROL PROTEIN CKS1
B	1.22.1	d1tafb	Histone-fold	T2D5_YEAST	TRANSCRIPTION INITIATION FACTOR TFIID	
	1.63.1	d1kxu_2	Cyclin-like	TF2B_RAT	TRANSCRIPTION INITIATION FACTOR IIB
	7.35.3	d1qyp	Rubredoxin-like transcriptional factor domain	TFS2_YEAST	TRANSCRIPTION ELONGATION FACTOR S-II
	1.34.1	d1coo	C' domain of RNA polymerase alpha subunit	RPOA_TREPA	DNA-DIRECTED RNA POLYMERASE
	1.75.1	d1gln_1	Glu-tRNA synthetase AC-binding domain	SYE_BACSU	GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17)
	1.88.1	d1sig	RNA polymerase, sigma70 subunit	RPOS_ECOLI	RNA POLYMERASE SIGMA FACTOR
	4.104.1	d2def	Peptide deformylase catalytic core	DEF_HAEIN	POLYPEPTIDE DEFORMYLASE (EC 3.5.1.31)
	4.11.7	d1tif	Translation initiation factor, N' domain	IF3_BORBU	TRANSLATION INITIATION FACTOR IF-3
	4.28.1	d2reb_2	RecA protein, C-terminal domain	RECA_HAEIN	RECA PROTEIN (RECOMBINASE)
	4.36.1	d1ife	Translation initiation factor IF3	IF3_BORBU	TRANSLATION INITIATION FACTOR IF-3
.	4.88.1	d1div	Ribosomal protein L9	RL9_BACSU	50S RIBOSOMAL PROTEIN L9	
C	4.40.1	d2chsa	Chorismate mutase	CHMU_BACSU	CHORISMATE MUTASE (EC 5.4.99.5)	
	1.101.1	d5csma	Chorismate mutase II	CHMU_YEAST	CHORISMATE MUTASE (EC 5.4.99.5)	
	1.81.1	d1cem	Glycosyltransferases of the superhelical fold	GUN6_DICDI	ENDOGLUCANASE (EC 3.2.1.4)	
	2.21.1	d1yna	ConA-like lectins/glucanases	GUN1_TRIRE	ENDOGLUCANASE EG-1 (EC 3.2.1.4)
	3.1.1	d1edt	Glycosyltransferases	GUNB_NEOPA	ENDOGLUCANASE B (EC 3.2.1.4)
.	4.2.1	d153l	Lysozyme-like	CHIT_SOLTU	ENDOCHITINASE PRECURSOR (EC 3.2.1.14)	
.	2.65.2	d1hcz_2	Rudiment single hybrid motif	PYC_PICPA	PYRUVATE CARBOXYLASE (EC 6.4.1.1)	
.	2.65.3	d1f3z	Duplicated hybrid motif	PTGA_BACSU	PTS SYSTEM, GLUCOSE-SPECIFIC IIABC COMP	
D	1.86.1	d1aora1	Aldehyde FerOR C' domain	AOR_PYRFU	ALDEHYDE:FERREDOXIN OXIDOREDUCTASE	
	4.94.1	d1aora2	Aldehyde FerOR N' domain	AOR_PYRFU	ALDEHYDE:FERREDOXIN OXIDOREDUCTASE	
	3.1.10	d5ruba1	RuBisCo, C' domain	RBL_NITVU	RUBISCO LARGE SUBUNIT	
E	1.101.1	d5csma	Chorismate mutase II	CHMU_ARATH	CHORISMATE MUTASE (EC 5.4.99.5)	
	1.37.1	d1rec	EF-hand	TPC2_DROME	TROPONIN C	
	2.1.5	d1suh	Cadherin	CAD5_HUMAN	VASCULAR ENDOTHELIAL-CADHERIN	
	2.45.1	d1eal	Lipocalins	PGHD_HUMAN	PROSTAGLANDIN-H2
	3.7.1	d2bnh	Leucine-rich repeats	RINI_PIG	RIBONUCLEASE INHIBITOR
	4.70.1	d1axx	Cytochrome b5	NI1_MAIZE	NITRATE REDUCTASE (EC 1.6.6.1)
.	4.112.1	d1toh	Tyrosine hydroxylase	TY3H_HUMAN	TYROSINE 3-HYDROXYLASE (EC 1.14.16.2)	