

Fig. S4 (1 of 4)

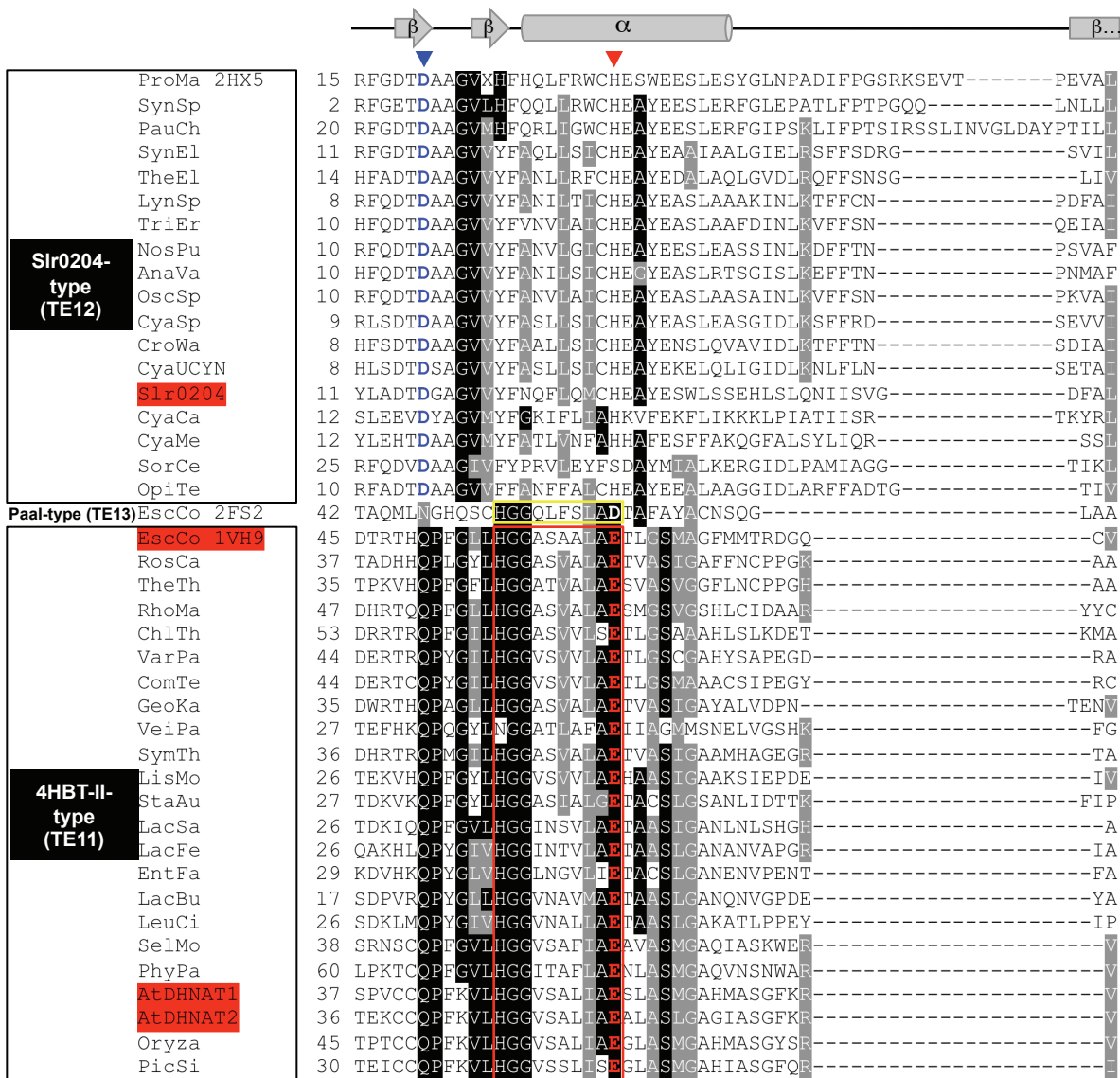
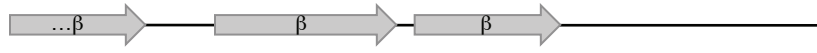


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	ProMa 2HX5	68	PIIHCQADFRRPHTHTGDAIAXELRPERLNPNNSFQVHFEFRC-----EEQI
	SynSp	52	PITHCSADFLAPLICGDPALATALTPQWLDPFAFEVAYSFSS-----AGRP
	PauCh	80	PITHCSADYIMPVVCGDSLLINLTKALDLESFEIKYTFDC-----KNLH
	SynEl	58	PIVHAEIDYQRPITYCGDREIELEQATALGRDRFRVDYRISH-----NHQP
	TheEl	60	PITEAQIRFLKPTFYCGDRVRVTIDPQRLDTRFQLTYTELYN-----EGGDR
	LynSp	54	PIVHTSVDFDFQPLFCGDRVVIHLMFQQITENTFEINYNIILL-----HDSEKW
	TriEr	56	PIIHANVDFRRPMFCGDELTIELMPKTWGDDEFEISYQVFLK-----EVGKKW
Slr0204-type (TE12)	NosPu	56	PIVHASVDFLRPMFVGDKLLISLTPQKIGVEKFEITYEYTV-----AEVV
	AnaVa	56	PIVHASVDFLRPLFCGDOVVIISLVPQKIGAEKFEINYETYL-----ADVL
	OscSp	56	PIVHASVDFYRPMFCGNEIADLTPQQLANDEFEITYQIFSN-----EVADRC
	CyaSp	55	PIVHAEIDFFRPLYSGDRIITLTLTQLKDEFEITYQVGLV-----APQSSL
	CroWa	54	PIIYAEIDFYQPLFCGDRVQINLTPVQINEFEFEINYQVFHE-----SNLEKL
	CyaUCYN	54	PITHAEIDFYQPLFCGYNRLDTSINHYSNTEFSVIYYIFSE-----SIPSRY
	Slr0204	57	PLVHASIDFFAPAHCGDRLVNLTIQASAHRFCCDYETISQA-----ESAQL
	CyaCa	58	PIVQARADYVRPPIHLSDKLIDILYIEKTEISFCLQYRFFVN-----QKQL
	CyaMe	56	PLVHHAEEYSTCYLGDHLKITLTYLQKTKHTLHFHYRTCK-----HHQL
	SorCe	71	PLVHAEADYLLPFRFGDAIEVEVLAPKLGDSFTVGYRVTT-----AGRV
OpTe	56	PIAKSEAEYLRPLRPGERVRVTLSEPERLGENSFAIRYEVFRA-----GPPEKL	
Paal-type (TE13)	EscCo 2FS2	77	VASACTIDFLRPGFAGDTTATATAQVRHQGKQTGVYDIEIVNQ-----QQK
EscCo 1VH9	83	VGTEINATHHRPVSEG-KVGRVCOPLHIGRQNSWEIVVFD-----EQGR	
RosCa	75	FGLEINANHIRPKREG-VVTAIGAPLHVGKSTQVWEVRIVD-----EQER	
TheTh	73	FGLEINCNHHRKREG-TTRAVGRPLHVGRITQVWEVKVYD-----EEGR	
RhoMa	86	VGLEINANHTRAVRSG-QVKGVARPLHIGRRTQVWDIRTYD-----EQER	
ChlTh	92	VGLEINANHVRRPKDG-YVYGKTEPLHIGKTTQVWQTKIMD-----EQNR	
VarPa	82	VGLDINANHTRSATSG-WVTGTARPVHRGRTQVWQIDMTN-----DAGE	
ComTe	82	VGLGV TANHV RAGRKGSWITATARPTHIGRTHVWAVEIRD-----EEGK	
GeoKa	74	VGLEINANHVRAVRRG-TVTATGTVLRGRITMVVDVRI TD-----EQGE	
VeiPa	65	VGQSV TANH LRPVKCEGSLTALGTL LVKGTSHVWRFD MID-----DAQR	
SymTh	74	VGMEINANHIRPKREG-TVRAEATPVHVGRSSVWEIRITD-----EDGR	
4HBT-II-type (TE11)	LisMo	64	FGLEINANHLASKQEG-LVTATAEATHLGKSTQVWEIKITD-----ETEK
	StaAu	66	LGLEMNANHIHSAKDG-RVTATAEILHRGKSTHVVDIKIKN-----DKEQ
	LacSa	63	VGVNISTNHLSVTSG-KITVEATPLRIGKIQVWQANTFD-----DKNN
	LacFe	64	VGVNVTQHIRATREG-EITFVVATPDHVGRITLQVWQAKILV-----SN-R
	EntFa	67	VGIDLQVNHLSVHDG-SITVVIATPEHSGKTLQVWEAKIYN-----ADHQ
	LacBu	55	VGVNINTQHLLPVTSG-LIATATPLQLGHRITRQVTTITN-----YDHL
	LeuCi	64	VGVDIQTHHLKTVSAG-HLIATAEPIHIGHSIQVWSVTIHE-----QTAN
	SelMo	75	AGIEININHTRAVPLGHRVTVDALPLLVGRIQVWEVKLWAPPASSSS-----SSSDSSSD
	PhyPa	97	AGLDLVNHNHLLSASIGETVYVVRATPLRVGKRVQVVDVKFSKPVQSGS-----LATTEMA
	AtDHNAT1	74	AGIQLSINHLKSA DLGDLVFAEATPVSTGKTIQVWEVKLWKTTQK-----DKANKI
AtDHNAT2	73	AGIHLSIHHLRPAALGEIVFAESFPMVSGKNIQVWEVRLWKAKKT-----ETPDNKI	
Oryza	82	AGVQLSINHFRSAALGDTVLRRAAPLHVGRITQVWAVKLVKLDPS-----TKEKGA	
PicSi	67	AGIEININHRAAALGEHVYAQAKPI TVGRVQVWEVKLWKISASLFSSQIDPSNLPEKS	

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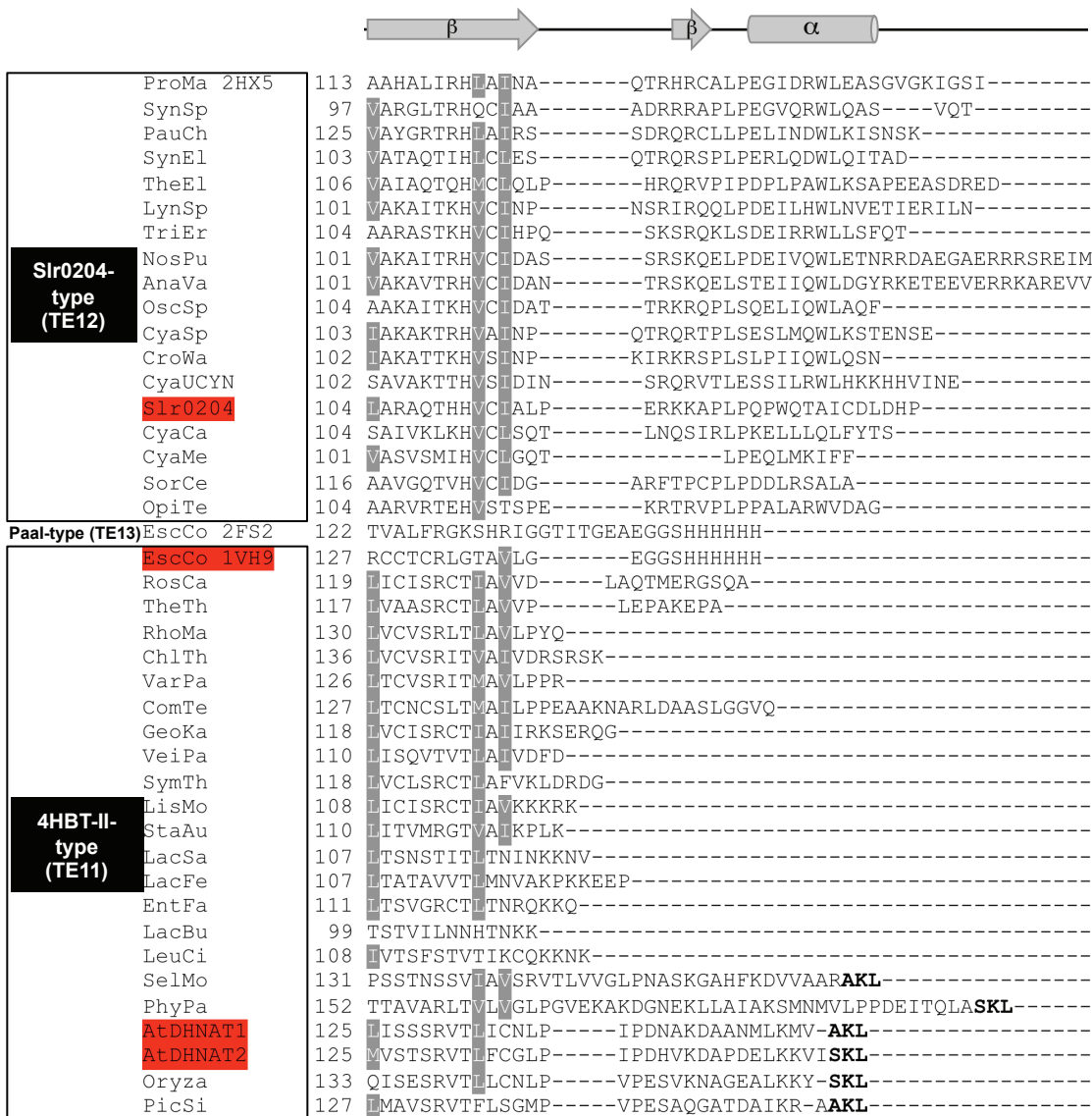


Figure S4. Sequence alignment of prokaryotic and eukaryotic DHNA-CoA thioesterases and related proteins. Proteins highlighted in red have been shown to bear DHNA-CoA thioesterase activity *in vitro* and *in vivo* (Slr0204; DHNAT1-2) or *in vitro* (EscCo 1VH9). 2HX5, 2FS2, and 1VH9 indicate PDB numbers of reference tri-dimensional structures used to adjust the alignment. Corresponding secondary structures are shown on top. Identical residues are shaded in black, similar ones in grey. The TE (Thioester-active Enzymes) nomenclature and classification is from (Cantu *et al.*, 2010). The blue and red arrows point to the conserved catalytic residue in the Slr0204-type (TE12) and 4HBT-II (TE11) subfamilies, respectively. The red and yellow boxes indicate the 4HBT-II and Paal motifs, respectively, as defined in (Dillon and Bateman, 2004). Full names and taxonomic origin of species, and protein accession numbers are listed in Table S2.