

Table S6. Residue types at monomer-monomer interaction positions in thermosome, CCT, BBS, and CCT8L proteins

A. Intra-ring						Conserved aa types in CCTs
Thermosome¹	CCTs²	BBS12³	BBS10³	MKKS³	CCT8L³	
19 Q	HQRST	R	S	R	S	
24 Q	LQRV	R	V	V	L	
27 N	HNS	G*	A*	T*	S	
40 T	ST	T	C*	S	P*	Hydroxyl
45 K	KNRV	L*	E*	S*	H*	
47 M	LMT	S*	R*	R*	R*	
48 D	DMN	S*	Q*	L*	Q*	
49 K	K	K	V*	K	K	Lysine
50 M	ILM	F*	L	Q*	F*	Intermediate-size hydrophobic
51 L	ILMV	I	C*	L	L	Intermediate-size hydrophobic
52 V	ILQV	I	T*	H*	V	
57 D	DGK	H*	E*	G	E*	
58 I	AILV	S*	V	V	T*	Aliphatic
60 I	ILMV	L	L	T*	C*	Intermediate-size hydrophobic
76 P	PQ	A*	P	P	P	
77 T	AIT	V*	I	I	A	
79 K	KRS	Q*	R	K	W*	
80 M	LMSTV	L	M	I*	L	
83 E	DEKM	E	D	A*	E	
87 A	ALMSTV	A	S	N*	T	
88 Q	Q	Q	H*	H*	Q	Glutamine
89 D	DE	N*	L*	V*	A*	Acidic
90 T*	ADEIKQ	N*	K	S*	E	
18 V*	ILM	V*	K*	L	L	Intermediate-size hydrophobic
119 H	HS	P*	D*	T*	P*	
120 P	PV	I*	P	P	R	
121 T	IQRST	S	L*	T	P*	
128 R	EQR	S*	K*	K*	A*	
135 R	HILRV	S*	L	I	L	
163 N*	AILQV	P*	V	P*	P*	
166 L*	EHIQRS	S	N*	M*	*	
203 N*	HKLPQV	P	N*	K	HP	
206 S	AGILRST	P*	P*	R	T	
207 V*	EGILQ	E	V*	V*	L	
208 N*	ADEMST	T	S	I*	E	
224 H	GHNSVY	N	V	Q*	G	
226 K*	DGQR	P*	-*	M*	M*	
245 I*	AGKLPTY	Y	P	G	P	
246 K	DEKMPT	R*	L*	D	A*	
247 K	AIK	H*	F*	T*	H*	
248 T	EGIMPT	L*	S*	S*	P	
249 E	DEK	G*	T*	D	N*	Charged
250 I	DILMSTV	F*	S	T	A*	
251 E*	DGKNQ	N	G	G	P*	
252 A	AGHNSTV	K*	S	E*	A	
253 K	DEGKQRT	S*	E	G	T	
254 V	FILV	A*	F	T*	A*	Hydrophobic

Table S6 (continued 1)

Thermosome ¹	CCTs ²	BBS12 ³	BBS10 ³	MKKS ³	CCT8L ³	Conserved aa types in CCTs
255 Q*	DEFLRV	N*	I*	V	C*R	
256 I	IVY	I	L*	V	L*	
257 S	DHKST	K	N*	V*	S	
259 P	AEPTVY	V	E	Y	P	
262 I*	FKLMRVY	S*	F	-*	L	
263 Q	ADEKMQT	M	Q	V*	A	
264 D*	AEKNQR	R	T*	S*	Q	
265 F	FILV	L	S*	L	F	Hydrophobic
266 L	ELQRSV	Q	Q	E	S	
268 Q*	AEGMRY	D*	W*	A	G	
269 E	E	S*	I*	V*	S*	Glutamate
270 T*	EKRSW	S	M*	L*	D*	
274 K	DEKLQY	N*	K	L	E	
275 Q	ADENQ	H*	A	N	K*	
297 V	EFLMVY	R*	L	S*	E	
300 H	DHKQ	E*	Y*	Q	T*	
301 Y	AFLSY	K*	Y	F	L	
304 K	ADEKQR	N*	V*	M*	K	
315 K	EFGKR	G	S*	V*	RW*	
319 E	EKNR	Q*	S*	E	I*	
328 K	EKMRSTV	V	S	Q*	P*	
330 V	ALQV	V	F*	I*	L	
331 T	ANPST	A	V*	G*	P	
332 D	HRST	Y*	P	S	R	
335 D	ADEHNPQ	Q	A	S*	P	
340 V	CDEKMV	C	L*	S*	R*	
354 D	DEGKS	R*	Y*	-*	D	
376 G	AGPS	P	P	R*	A	
377 T	ANST	V*	V*	N	T	
378 D	DEKQ	T*	H*	D	T*	
379 H	EFHLMNQ	A*	G*	T*	Q	
380 V	FILMTV	Q*	L	A*	G*	Hydrophobic
500 H	KNQSW	E*	Q	S	Q	
503 E	HKLST	R*	T	Q*	R*	
504 S	AFLST	R*	S	V*	A	
507 E	ENQV	D*	Q	E	E	
508 V	AIMT	L*	C*	T	V*	
510 T	CEIRTV	L*	T	N*	L*	
511 M	LMNSTV	L	K*	L	Q*	
514 R	KLRS	Q*	T*	D*	T*	
515 I	IV	T*	I	L*	V	Beta-branched aliphatic
516 D	D	D	D	S*	D	Aspartate
517 D	DENQ	S*	M*	Y*	E	
518 V	ILTV	E*	V	V	I	Intermediate-size hydrophobic
519 I	IMRV	I	I	I	V	
520 A	KMNRS	I*	T*	E*	V*	

Table S6 (continued 2)

B. Inter-ring							
Thermosome¹	CCTs²	BBS12³	BBS10³	MKKS³	CCT8L³	Conserved aa types in CCTs	
25 R*	AFKLSVY	H*	K	R*	L	Charged/hydrophilic	
29 E*	CIMNQS	Q	Q	S	A*		
108 K	DEKRS	S	R	E	E		
115 D	ADEKQRS	H*	D	.*	K		
116 Q	EIKQR	L*	R	.*	A*F*		
117 G	GKQ	G	E*	G	G		
429 R	KLMRV	W*	E*	E*	P*		
432 L	LVWY	N*	M*	L	P*		
439 K	DEKQR	S*	N*	S*	RW*		Charged/hydrophilic
446 R	KMNRST	T	K	G*	K		
450 E	DEQV	N*	K*	H*	E	Charged/hydrophilic	
455 D	DKNS	S	K	I*	A*		
456 P	ALPST	S	Y*	L	V*		
457 I	AINQT	E*	S*	T	S*		
458 N	DENQRS	F*	F*	D	D		

¹Residue observed in the model structure of thermosome subunit A from *T. acidophilum*; ²Residues observed in all human CCT subunits; ³Residues observed in human BBS and CCT8L proteins; *Residue-types not observed in any human CCT subunit.