

Table S1. The result of a BLAST search using the uncharacterized domain of Tc-ChiD

GenomeNet BLAST search (<http://www.genome.jp/tools/blast/>)
 Query: Tc-ChiD (321-805)
 Protein library:KEGG genes

	Entry	Description	Bits	E-value
1	cbi:CLJ_B3058	hypothetical protein	366	7.00E-116
2	cby:CLM_3195	hypothetical protein	366	8.00E-116
3	cbj:H04402_02911	chitinase Jessie 3	363	6.00E-115
4	cbm:CBF_2873	hypothetical protein	362	2.00E-114
5	cbf:CLI_2881	hypothetical protein	362	2.00E-114
6	cbb:CLD_1743	hypothetical protein	359	3.00E-113
7	cbh:CLC_2708	hypothetical protein	358	4.00E-113
8	cba:CLB_2775	hypothetical protein	358	4.00E-113
9	cbo:CBO2831	hypothetical protein	358	4.00E-113
10	clid:CLSPO_c29070	chitinase A-like protein	358	1.00E-112
11	cbl:CLK_2219	hypothetical protein	355	9.00E-112
12	cbk:CLL_A1377	putative secreted chitodextrinase	335	7.00E-104
13	ehi:EHI_152170	2.t00133; chitinase Jessie 3	96.3	3.00E-18
14	edi:EDI_038370	chitin binding lectin	95.9	4.00E-18
15	eiv:EIN_066080	chitin binding lectin, putative	89.7	3.00E-16
16	eiv:EIN_095550	chitin binding lectin, putative	87.8	1.00E-15
17	edi:EDI_333670	chitin binding lectin	67.4	6.00E-10
18	ehi:EHI_015750	chitinase Jessie3	67	7.00E-10
19	aci:ACIAD0436	ahpC; alkyl hydroperoxide reductase, C22 subunit	37.7	3.2
20	oar:OA238_c13710	hypothetical protein	38.9	3.4
21	fve:101306474	protein transport protein SEC16B homolog	38.5	4.5
22	ccs:CCNA_00607	TonB-dependent receptor	37.7	8.2
23	ccr:CC_0571	TonB-dependent receptor	37.7	8.2
24	pri:PRIO_3348	putative membrane protein	37.7	8.4
25	hab:SG26_01490	hypothetical protein	37	8.6

*Group of proteins showing high similarities to each other are shown in colored backgrounds

Horiuchi et al., Fig. S1

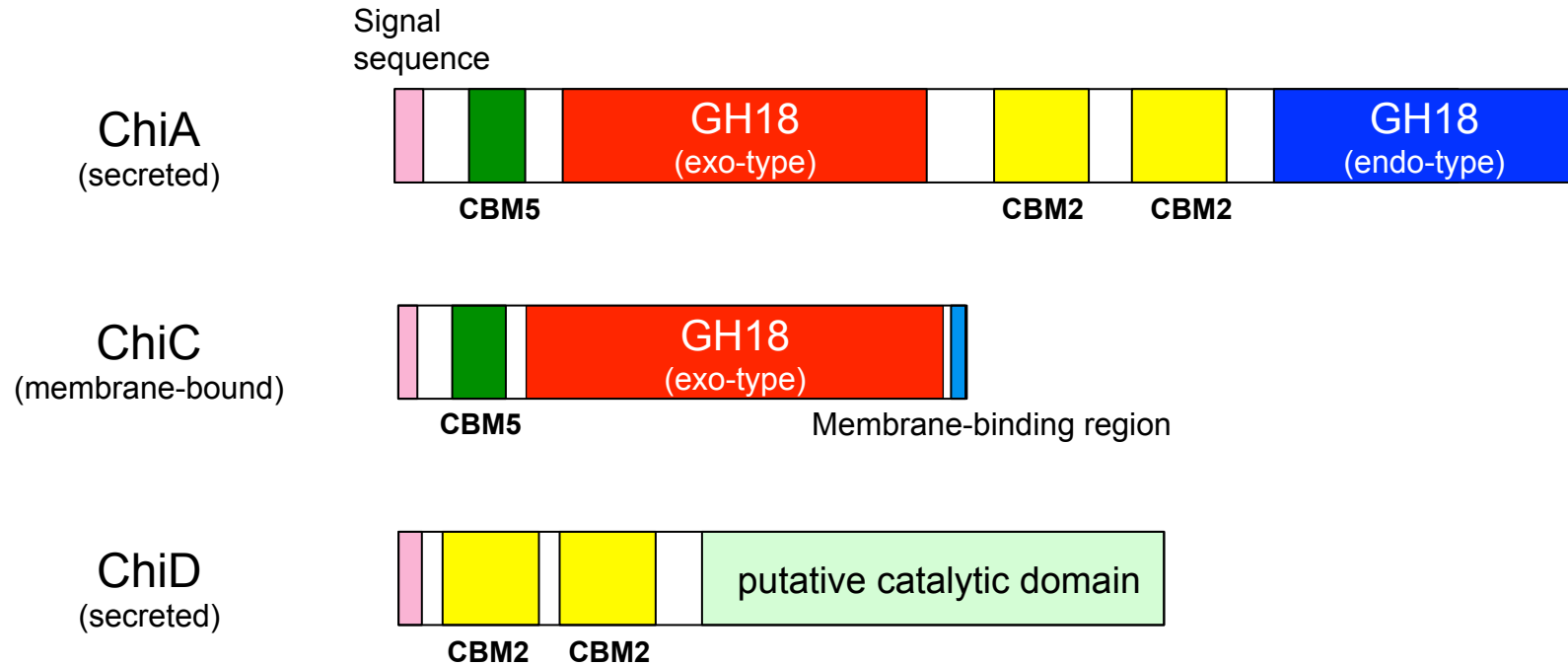


Figure S1. Schematic description of putative chitinases identified on the genome of *T. chitonophagus*.

Horiuchi et al., Fig. S2

>TcChiA

MNTKSKIAALLVVLVAIGVVPPLVTVPLVSAETQIQLSAYPIAWDIVNLTWTPVSNVSGYEIYRST SPE
GIISPQNLIVYVNWSSYPQYEPGKTY YQGDIVEYNGKIYRAKYWTTSQPSDDPYGAWELLGEAEPTTNY
LDQYGLQPETTYYYVVPVFKDGSKGTPSNVVEVTPPKKFRVVVYIISWGIYARKFY PEDIPFDKVTH
VLYAFLKPEQDGSVVMYDTWADPQNLEKFKELKKKYPQVKILISVGGWTL SKYFSVIAADPAKRQ RFAE
TALEIIRKYDLGDVIDWEYPGGGMEGNYVSPDDGKNFVLLLKTVREVL DQAEKEDKKHYLLTAAVPA
DPVKAARINWTEAMKYLDFINVMTYDYHGAWENITGHNAPLYADPNAPYTDPNVKWNFN VNASIQWYLH
HGVAPEKISLGLPFYGRSFANVPPENGLYQPFQGTDPDGTWGPASETYGVM DYWDIEEKKASGQYNYW
DPVAMVPWLYSPSLKIFISYDDQKSIGIKVDYALKYKLGGMVWEITADRKPGTNNHPLLDTI IQHIEQ
GGGVPTPAPQPSPTPTQTTTTTTTTTSVPTTTTTTTTTTTTTTSVPTTTTTTTTTTTTTTATPAPT TTTTTTTTTT
SAPTQTTTTTTTTTSPTATSTSTQTTTTTSSAGSPVKPGSMSVKVNDWGTGGQFDITLNLGAQYDWVVKV
QLDSSTQMGN YWGVQKSQEGDWVVF TPLSWNKGPTASFGFIVNGPVSGVKQIILEINGEVWDVWPEVSQ
VPSETGTTTTVTTTTTTTTTTTTTSVPTTSTTTVTTTTTTTTTTTTTTTVTSTTTASTTTSTVTTTTTSSAGSPVKP
GSM SVKVNDWGTGGQFDITLNLGGQYDWVVKVQLDSSTQMGN YWGVQKSQEGDWVVF TPLSWNKGPTAS
FGFIVNGPVSGVKQIILEINGE IWDVWPSSGEATTTTSTTTTTTTTTTTTTTTATPAPT TTTTTTTTTTSTPT
QTTTTTTTTQTEVPAPVGANPIPEHFFAPYIDMTLSVHKPLTEYAQLTGTKYFTLAFI IYSSAYGPSWGG
ALPLDTFVQEVN DLRKMGGEV IIAFGGAVGPYLCQQAQSAEQLAQWYIQIIDMYNATYLD FDI ESYVDA
NMLADALLIVQRERPWKISFTLPSDPGVGLT GSGYSLIKTMVEKGVKIDRVNAMTMDY YWTPSNAENA
IKVAQNLFNQLKQLYPNKTDEEIWGMIGLTPMIGVNDDKSVFTLQDAQTLVDWAIQYKIRALAFWSVDR
DHPGPEGQV SPLHRGTSDPDWAYSHVFVKFMEAFGYQPVTQQAVSST

Figure S2. Amino acid sequence of *Tc*-ChiA.

Horiuchi et al., Fig. S3

>TcChiC

MRFIGVTCMKRALALTLVVIVILFATPTPVLSKSEIKLKAQPIAWDAVNLTWTPLSNVKAYEVYRSTNP
RDVYSSPNLIFVVNWSNYTKYKENWNYLPGEIVEYQGYLWKAKKVTSQPPQEGDYWEKLGPIPTNTAV
DYFNVGTNTTYYYIVVPVFKDGKDGKRGTPSNVIKVTTPPQPYRIVVYYISWGIYARAFSPYDVPFENV
THVNYAFLKLENGTVTWADPWADPMNLEAFKELKSRYPAVKFLISVGGWTLISKYFSPVAADPKKRQEF
IKSAIAIIRKYNLDGIDIDWEYPGGGGMEGNYVSPDDPRNFIVLLKEFRKALDDVGREDHKHYLLTVAA
PANLEIASRIDWKEASKYLDFINVMTYDYIGPWSPVTGHNAPLYRNPNGPDYGSVDQTIKWYIEHVPDR
TKIVLGIPFYARSFANVPPKNHGLFQPYKGTAGTWGSAAETHGIMDYWDVADKAKTGEYEYFWDNYSK
VPWLYSESKRIFITFDDPRSILIKTQYMLNQSLGGVMIWEITADRKPGTSSHPLLAHVLEGLQEKPPVW
IPDKYVLGSNVPSNITIPKPETVPTKRGGVCGPAAILIVALFVLLKRNS

Figure S3. Amino acid sequence of *Tc-ChiC*.

Horiuchi et al., Fig. S4

>TcChiD

MGLKRLLVLVVAVVVLSSGINFSWALGNRPSEGTGVAGKLSFKATFWNTGGQYTVDMKLDSPAEWKVYV
KIENGELGNYWNTGQVYREKDYYVFPAASWNKGPMAFSGFIVTGSEAVVSEILLVVGSEIVDRWSMENT
STSTTTYTTTSQTPTQTPTTQTPTTTTSTPVTSTTTSAPPSLVKPGSMSVKVTSWTGASQYDVTLN
LGEALDWMVKVKLSPGARLGSYWSVNRAEEDGWIIFTPLTWNKGPTASFGFIVQNGEAESIALIVNNQI
WDIWPENAPVPSVPSPAPEQSPVSQPSQGLVNIITDPNDPDELYAAYRIVSETGDKITVELTLANKNTHY
VWNGWCFDIKNITFETTGVLSIKYADGGEPVYNVNGNLVTIDLTRGIFHLNNTVKIIIEIQKSGDNP
YPHNFKIHYLRGESIIYPTIGELPASWKPGNFTLSDLIADPKSYYPHVKPHQNGFIMYNPPHPTQIIII
GLADIDYPLNLASSARMWVPNKYFAMGLALAYEWFKVNPNFLMALAAKENWGTAVTKDPAFKGYKVIID
EEYYWPVQIDHPDGIFQVESGNFNQIKAYYPDIFPDTADHDDYMKVSLDPNDTAWITSPIVAAVSLTM
ERELLYAAVGDKYNEFLRLAKDPWAETEIIDFGYNRGVGAIEALKIFSDNWEKAINAEVLWKEFNMEGF
GGHVPTVINITATMDMETERIYDANLTWDDIEYFFTVVRQKFFRPGAISDEEWNAMMRDVKRAYDLLSQ
HWGGDHISYRYDFLTILRVAMKHWPEPHIPRPTGDDWYYHARNYNP

Figure S4. Amino acid sequence of *Tc-ChiD*.

Horiuchi et al., Fig. S5

```

Tc-ChiD_1    -GTGVAGKLSFKATFWNTGGQYTVDMKLDSPAEWKVYVKIENG-ELGNYWNTGQVYREKD
Tc-ChiD_2    PSLVKPGSMSVKVTSWTGASQYDVTNLNLGEALDWMVKVLSPGARLGSYWSVNRAE-EDG
Pf-ChiB      TPVPVSGSLEVKVNDWGSGAEYDVTNLNLGDQYDWTVKVKLAPGATVGSFWSANKQE-GNG
Tk-ChiA_2    GDFVKPGSLSVKVTDWGN-TEYDVTNLNLGGTYDWVVKVCLKDGSSVSSFWSANKAE-EGG
Tk-ChiA_3    GDLVKPDAFSVKIQDWGS-TEYDVTNLNLGGTYDWVVKVCLKDGSAVSSVWSANKAE-EGG
              .. :..*   *       :* *  ::* .   :* * ** :   *   :.. *...:   .

Tc-ChiD_1    YYVFPAASWNKGPMASFGFIVTG-SEAVVSEILLVVGSEIVDRW
Tc-ChiD_2    WIIFTPLTWNKGPTASFGFIVQN---GEAESIALIVNNQIWDIW
Pf-ChiB      YVIFTTPVSWNKGPTATFGFIVNGPQDKVEEITLEINGQVIDIW
Tk-ChiA_2    YVVFTPVSWNRGPTATFGFIATG--SESVEAIYLYVDGQLWDAW
Tk-ChiA_3    YVVFTPVSWNKGPTATFGFIATG--SEPVEAMYLYVNDQLWDVW
              :  :*..  :**:** *:*:**. .           .. : * :...: * *

```

Figure S5. Alignment of ChBD amino acid sequences from hyperthermophilic archaea. The sequences of ChBD1 and ChBD2 of *Tc*-ChiD (residues 33-133 and 181-280), ChBD of *Pf*-ChiB (residues 259-361) and ChBD2 and ChBD3 of *Tk*-ChiA (residues 621-720 and 764-863) are shown aligned by the Clustal W program. The conserved Trp residues corresponding to Trp²⁷⁴, Trp³⁰⁸ and Trp³²⁶ of *Pf*-ChiB are indicated in red.