

Enhanced features of *Dictyoglomus turgidum* Cellulase A engineered with carbohydrate binding module 11 from *Clostridium thermocellum*.

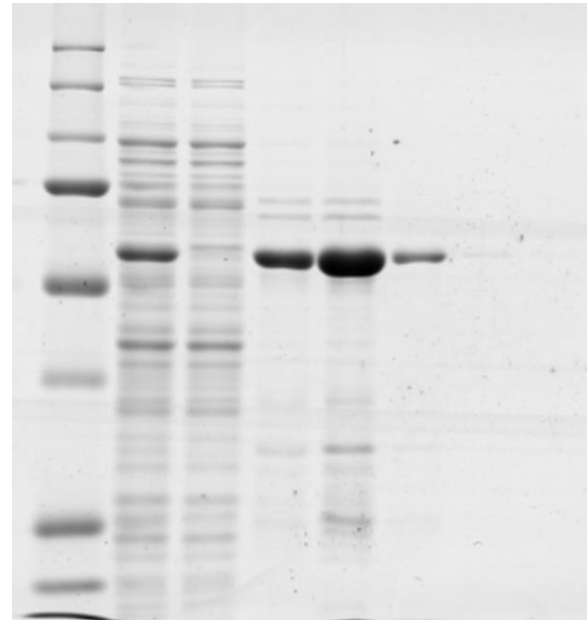
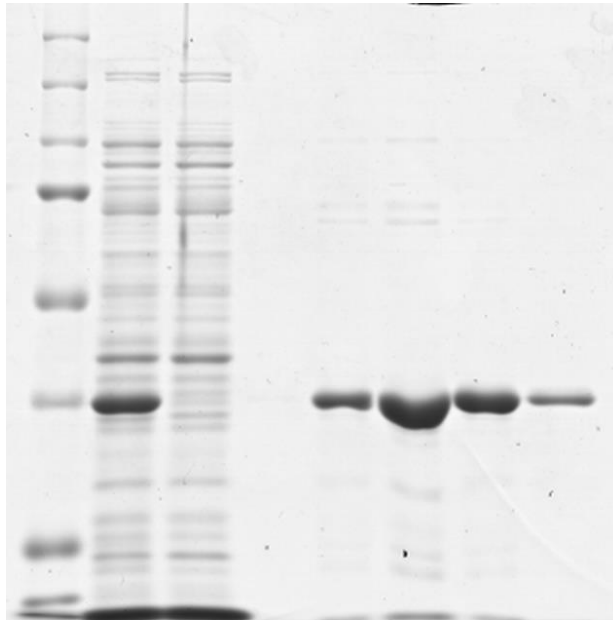
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Supplementary file 1: SDS-PAGE of native (left) and chimeric (right) Dtur CelA after purification by affinity chromatography. Lane 1: Molecular weight markers; lane 2: total protein extract; lane 3: flow through; lanes 4-7: elution fractions. The gels were Coomassie stained.



Supplementary file 2: MS sequence of spot 1 (Dtur CelA)

1	MNNLPIK RGI	NFGDALEAPY	EGAWSGYIIK	DEYFK IVKDA	GFDHVRIP IK
51	WSVYTQKEAP	YSIEKRIFDR	VDHLIEEGLK	NNLHVIINIH	HYEEIMEDPL
101	GEKERFLAIW	RQISEHYKDY	PNNLYFELLN	EPTQNLSEL	WNQFLK EAIE
151	VIRRTNPERK	IIVGPDNWS	LYNLEKLIIP	ENDENIIITF	HYYNPFPPFTH
201	QGAGWVKIDL	PVGVKWLGTE	EKREIEREL	DMAVSWAEH	GNIPLYMGEF
251	GAYSKADMES	RVRWTDFFAR	SAEKRGIAWS	YWEFYSGFGV	FDPEKNEWRT
301	PLLRALIPER	NI			

Supplementary file 3: MS sequence of spot 2 (Dtur CelA)

1	MNNLPIK RGI	NFGDALEAPY	EGAWSGYIIK	DEYFK IVKDA	GFDHVRIP IK
51	WSVYTQKEAP	YSIEKRIFDR	VDHLIEEGLK	NNLHVIINIH	HYEEIMEDPL
101	GEKERFLAIW	RQISEHYKDY	PNNLYFELLN	EPTQNLSEL	WNQFLK EAIE
151	VIRRTNPERK	IIVGPDNWS	LYNLEKLIIP	ENDENIIITF	HYYNPFPPFTH
201	QGAGWVKIDL	PVGVKWLGTE	EKREIEREL	DMAVSWAEH	GNIPLYMGEF
251	GAYSKADMES	RVRWTDFFAR	SAEKRGIAWS	YWEFYSGFGV	FDPEKNEWRT
301	PLLRALIPER	NI			

Peptides identified by LC-MS/MS analysis are in bold red

Supplementary file 4: MS sequence of spot 3 (Chimeric Dtur CelA)

Glycoside hydrolase 5 from *D. turgidum*

1 MNNLPIKR**GI NFGDALEAPY EGAWSGYIIK DEYFKIVKDA GFDHVRIPK**
51 **WSVYTQKEAP** YSIEKR**IFDR VDHLIEEGLK** NNLHVIINIH HYEEDIMEDPL
101 GEKERFLAIW RQISEHYKDY PNNLYFELLN EPTQNLSEL WNQFLKEAIE
151 VIRRTNPER**K IIVGPDNWS LYNLEKLIIP** ENDENIITF HYYPFPFTH
201 QGAGWVK**IDL PVGVK**WLGTE EEKREIER**EL DMAVSWAEH GNIPLYMGEF**
251 **GAYSK**ADMES RVRWTFVAR SAEKRGIAWS YWEFYSGFGV FDPEKNEWRT
301 PLLRALIPER NI

Carbohydrate-binding family 11 protein of Cel H from *C. thermocellum*

1 MKKRLLVSFL VLSIIVGLLS FQSLGNYSNG LKIGAWVGTQ PSESAIKSFQ
51 ELQGRKLDIV HQFINWSTDF SWVRPYADAV YNNGSILMIT WEPWEYNTVD
101 IKNGKADAYI TRMAQDMKAY GKEIWLRLPH EANGDWYPWA IGYSSRVNTN
151 ETYIAAFRHI VDI FRANGAT NVKWVENVNC DNVGNGTSYL GHYPGDNYVD
201 YTSIDGYNWG TTQSWG SQWQ SFDQVFSRAY QALASINKPI IIAEFASAEI
251 GGNKARWITE AYNSIRTSYN KVIAAVWFHE NKETDWRINS SPEALAAAYRE
301 AIGAGSSNPT PTPTWTSTPP SSSPKAVDPF EMVRKMGMGT NLGNTLEAPY
351 EGSWSKSAME YYFDDFKAAG YKNVRIPVRW DNHTMRTPY TIDKAFLDRV
401 EQVVDWSLSR GFVTIINSHH DDWIKEDYNG NIERFEKIWE QIAERFKNKS
451 ENLLFEIMNE PFGNITDEQI DDMNSRILKI IRKTNPTRIV IIGGGYWSY
501 NTLVNIKIPD DPYLIGTFHY YDPYEFTHKW RGTWGTQEDM DTVVRVDFV
551 KSWSDRNNIP VYFGEFAVMA YADRTSRVKW YDFISDALE RGFACSVWDN
601 GVFGSLDNDM AIYNRDTRTF DTEILNALFN PGTYPSPK PSPTPRPTKP
651 PVTPAVGE**KM LDDFEGVLNW GSYSSEGAKV** STKIVSGKTG NGMEVSYTGT
701 TDGYWGTVYS LPDGDWSKWL KISFDIKSVD GSANEIRFMI AEK**SINGVD**
751 **GEHWYSITP DSSWKTIEIP FSSFRRLDY** QPPGQDMSGT LDLDNIDSIH
801 FMYANNKSGK **FVVDNIKLI ATSDPTPSIK** HGDLNFDNAV NSTDLMLKR
851 YILKSLELGT SEQEEKFKKA ADLNRDNKVD STDLTILKRY LLKAISEIPI
901

Peptides identified by LC-MS/MS analysis are in bold red

Supplementary file 5: MS sequence of spot 4 (Chimeric Dtur CelA)

Glycoside hydrolase 5 from *D. turgidum*

1 **MNNLPIKRG**I **NFGDALEAPY** **EGAWSGYIIK** **DEYFKIVKDA** **GFDHVRIP**IK
 51 **WSVYTQKEAP** **YSIEKRIFDR** **VDHLIEEGLK** **NNLHVIINIH** **HYEEIMEDPL**
 101 **GEKER**FLAIW **RQISEHYKDY** **PNNLYFELLN** **EPTQNLSSSEL** **WNQFLKEAIE**
 151 **VIRRTNPERK** **IIVGPDNWN**S **LYNLEKLIIP** **ENDENIIITF** **HYYNPFPPFT**H
 201 **QGAGWVKIDL** **PVGVKWLGTE** **EEKREIEREL** **DMAVSWAEEH** **GNIPLYMGEF**
 251 **GAYSKADMES** **RVRWTD**FVAR **SAEKRGIAWS** **YWEFYSGFGV** **FDPEKNEWRT**
 301 PLLRALIPER NI

Carbohydrate-binding family 11 protein of Cel H from *C. thermocellum*

1 MKKRLLVSFLL VLSIIVGLLS FQSLGNYNSG LKIGAWVGTQ PSESAIKSFQ
 51 ELQGRKLDIV HQFINWSTDF SWVRPYADAV YNNGSILMIT WEPWEYNTVD
 101 IKNGKADAYI TRMAQDMKAY GKEIWLRLPH EANGDWYPWA IGYSSRVNTN
 151 ETYIAAFRHI VDIFRANGAT NVKWVFNVC DNVGNGTSYL GHYPGDNYVD
 201 YTSIDGYNWG TTQSWGSSQWQ SFDQVFSRAY QALASINKPI IIAEFASAEI
 251 GGNKARWITE AYNSIRTSYN KVIAAVWFHE NKETDWRINS SPEALAAAYRE
 301 AIGAGSSNPT PTPTWTSTPP SSSPKAVDPF EMVRKMGMGT NLGNTLEAPY
 351 EGSWSKSAME YYFDDFKAAG YKNVRIPVRW DNHTMRTYPY TIDKAFLDRV
 401 EQVVDWLSLR GFVTIINSHH DDWIKEDYNG NIERFEKIWE QIAERFKNKS
 451 ENLLFEIMNE PFGNITDEQI DDMNSRILKI IRKTNPTRIV IIGGGYWNSY
 501 NTLVNIKIPD DPYLIGTFHY YDPYEFTHKW RGTWGTQEDM DTVVRVDFDV
 551 KSWSDRNNIP VYFGEFAVMA YADRTSRVKW YDFISDAALE RGFACSVWDN
 601 GVFGSLDNDM AIYNRDTR**TF** **DTEILNALFN** **PGTYPSPSPK** **PSPTPRPTKP**
 651 **PVTPAVGEKM** **LDDFEGVLNW** **GSYSGEGAKV** **STKIVSGKTG** **NGMEVSYTGT**
 701 **TDGYWGTVYS** **LPDGDWSKWL** **KISFDIKSVD** **GSANEIRFMI** **AEKSINGVGD**
 751 **GEHWYSITP** **DSSWKTIEIP** **FSSFRRRLDY** **QPPGQDMSGT** **LDLDNIDSIH**
 801 **FMYANNKSGK** **FVVDNIKLI**G **ATSDPTPSIK** **HGDLNFDNAV** **NSTDLLMLKR**
 851 YILKSLELGT SEQEEKFKKA ADLNRDNKVD STDLTILKRY LLKAISEIPI
 901

Peptides identified by LC-MS/MS analysis are in bold red

Supplementary file 6: MS sequence of spot 5 (Chimeric Dtur CelA)

Glycoside hydrolase 5 from *D. turgidum*

1 **MNNLPIKRG**I **NFGDALEAP**Y **EGAWSGYIIK** **DEYFKIVKDA** **GFDHVRIPIK**
 51 **WSVYTQKEAP** **YSIEKRIFDR** **VDHLIEEGLK** **NNLHVIINIH** **HYEEIMEDPL**
 101 **GEKER**FLAIW RQISEHYKDY PNNLYFELLN EPTQNLSSSEL WNQFLK**EAIE**
 151 **VIRRTNPERK** **IIVGPDNWS** **LYNLEKLIIP** **ENDENIITF** **HYYNPFPTH**
 201 **QGAGWVKIDL** **PVGKWLGT**E **EKEIREL** **DMAVSWAEEH** **GNIPLYMG**F
 251 **GAYSKADMES** RVR**WTDFVAR** SAEKR**GIAWS** **YWEFYSGFGV** **FDPEKNEWRT**
 301 PLLRALIPER NI

Carbohydrate-binding family 11 protein of Cel H from *C. thermocellum*

1 MKKRLVLSFL VLSIIIVGLLS FQSLGNYSNG LKIGAWVGTQ PSESAIKSFQ
 51 ELQGRKLDIV HQFINWSTDF SWVRPYADAV YNNGSILMIT WEPWEYNTVD
 101 IKNGKADAYI TRMAQDMKAY GKEIWLRLPH EANGDWYPWA IGYSSRVNTN
 151 ETYIAAFRHI VDIFRANGAT NVKWFNVNC DNVGNGTSYL GHYPGDNYVD
 201 YTSIDGYNWG TTQSWGSSQWQ SFDQVFSRAY QALASINKPI IIAEFASAEI
 251 GGNKARWITE AYNSIRTSYN KVIAAVWFHE NKETDWRINS SPEALAAAYRE
 301 AIGAGSSNPT PTPTWTSTPP SSSPKAVDPF EMVRKMGMGT NLGNTLEAPY
 351 EGWSKKSAME YYFDDFKAAG YKNVRIPVRW DNHTMRTYPY TIDKAFLDRV
 401 EQVVDWSLSR GFVTIINSHH DDWIKEDYNG NIERFEKIWE QIAERFKNKS
 451 ENLLFEIMNE PFGNITDEQI DDMNSRILKI IRKTNPTRIV IIGGGYWNSY
 501 NTLVNIKIPD DPYLIGTFHY YDPYEFTHKW RGTWGTQEDM DTVVRVDFV
 551 KSWSDRNNIP VYFGEFAVMA YADRTSRVKW YDFISDALE RGFACSVWDN
 601 GVFGSLDNDM AIYNRDTR**TF** **DTEILNALFN** **PGTYPSPK** **PSPTPRPTK**
 651 **PVTPAVGEKM** **LDDFEGVLNW** **GSYSGEGAKV** STKIVSGKTG NGMEVSYTGT
 701 TDGYWGTVYS LPDGDWSKWL **KISFDIKSVD** **GSANEIREMI** **AEKSINGVGD**
 751 **GEHWVYSITP** **DSSWKTIEIP** **FSSFRRLDY** **QPPGQDMSGT** **LDLDNIDSIH**
 801 **FMYANNKSGK** **FVVDNIKLI**G **ATSDPTPSIK** HGDNLNFDNAV NSTDLMLLKR
 851 YILKSLELGT SEQEEKFKKA ADLNRDNKVD STDLTILKRY LLKAISEIPI
 901

Peptides identified by LC-MS/MS analysis are in bold red

Supplementary file 7: MS sequence of spot 6 (Chimeric Dtur CelA)

Glycoside hydrolase 5 from *D. turgidum*

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1 MNNLPIKRGI NFGDALEAPY EGAWSGYIIK DEYFKIVKDA GFDHVRIPK
51 WSVYTQKEAP YSIEKRIFDR VDHLIEEGLK NNLHVIINIH HYEIIMEDPL
101 GEKERFLAIW RQISEHYKDY PNNLYFELLN EPTQNLSEL WNQFLKEAIE
151 VIRRTNPERK IIVGPDNWNLS LYNLEKLIIP ENDENIITF HYYNPFPPFTH
201 QGAGWVKIDL PVGVKWLGTE EEKREIEREL DMAVSWAEH GNIPLYMGFEF
251 GAYSKADMES RVRWTD FVAR SAEKRGIAWS YWEFYSGFGV FDPEKNEWRT
301 PLLRALIPER NI

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Carbohydrate-binding family 11 protein of Cel H from *C. thermocellum*

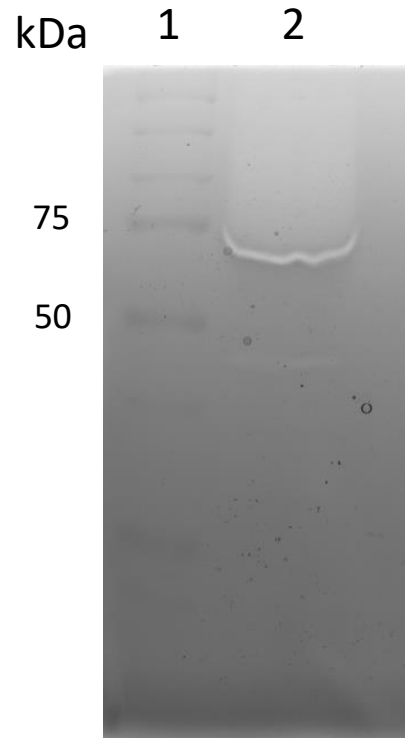
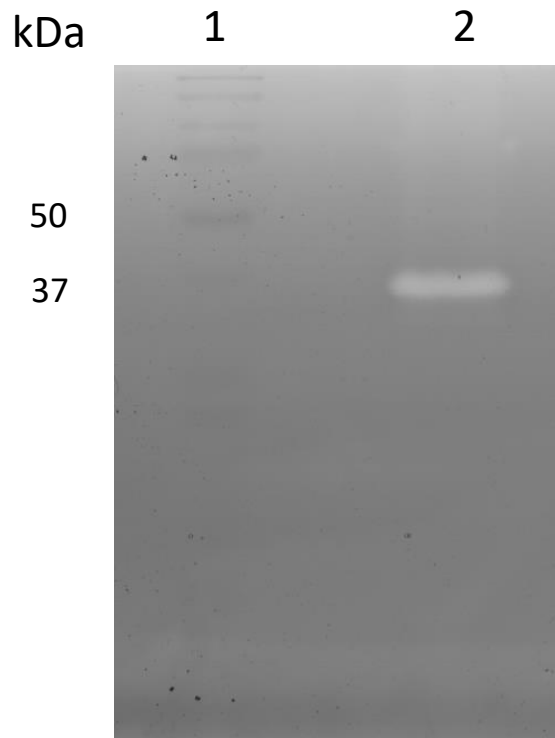
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1 MKKRLLSVFL VLSIIVGLLS FQSLGNYNSG LKIGAWVGTQ PSESAIKSFQ
51 ELQGRKLDIV HQFINWSTDF SWVRPYADAV YNNGSILMIT WEPWEYNTVD
101 IKNGKADAYI TRMAQDMKAY GKEIWLRLPH EANGDWYPWA IGYSSRVNTN
151 ETYIAAFRHI VDIFRANGAT NVKWFVFNVC DNVGNGTSYL GHYPGDNYVD
201 YTSIDGYNWG TTQSWGSSQWQ SFDQVFSRAY QALASINKPI IIAEFASAEI
251 GGNKARWITE AYNSIRTSYN KVIAAVWFHE NKETDWRINS SPEALAAYRE
301 AIGAGSSNPT PTPTWTSTPP SSSPKAVDPF EMVRKMGMT NLGNTLEAPY
351 EGSWSKSAME YYFDDFKAAG YKNVRIPVRW DNHTMRTYPY TIDKAFLDRV
401 EQVVDWLSLR GFVTIINSHH DDWIKEDYNG NIERFEKIWE QIAERFKNKS
451 ENLLFEIMNE PFGNITDEQI DDMNSRILKI IRKTNPTRIV IIGGGYWNYSY
501 NTLVNIKIPD DPYLIGTFHY YDPYEFTHKW RGTWGTQEDM DTVVRVDFDV
551 KWSDRNNIP VYFGEFAVMA YADRTSRVKW YDFISDALE RGFACSVWDN
601 GVFGSLDNDM AIYNRDTRTF DTEILNALFN PGTYPSPSPK PSPTPRPTKP
651 PVTPAVGEKM LDDFEGVLNW GSYSGEGAKV STKIVSGKTG NGMEVSYTGT
701 TDGYWGTVYS LPDGDWSKWL KISFDIKSVD GSANEIRFMI AEKSINGVGD
751 GEHWVYSITP DSSWKTIEIP FSSFRRLDY QPPGQDMSGT LDLDNIDSIH
801 FMYANNKSGK FVVDNIKLIG ATSDPTPSIK HGDNLNFDNAV NSTDLLMLKR
851 YILKSLELGT SEQEEKFKKA ADLNRDNKVD STDLTILKRY LLKAISEIPI
901

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Peptides identified by LC-MS/MS analysis are in bold red

Supplementary file 8: Zymography on 0.4% AZO-CMC of native (left) and chimeric (right) Dtur CelA. Lane 1: Molecular weight marker; lane 2: purified recombinant enzyme.



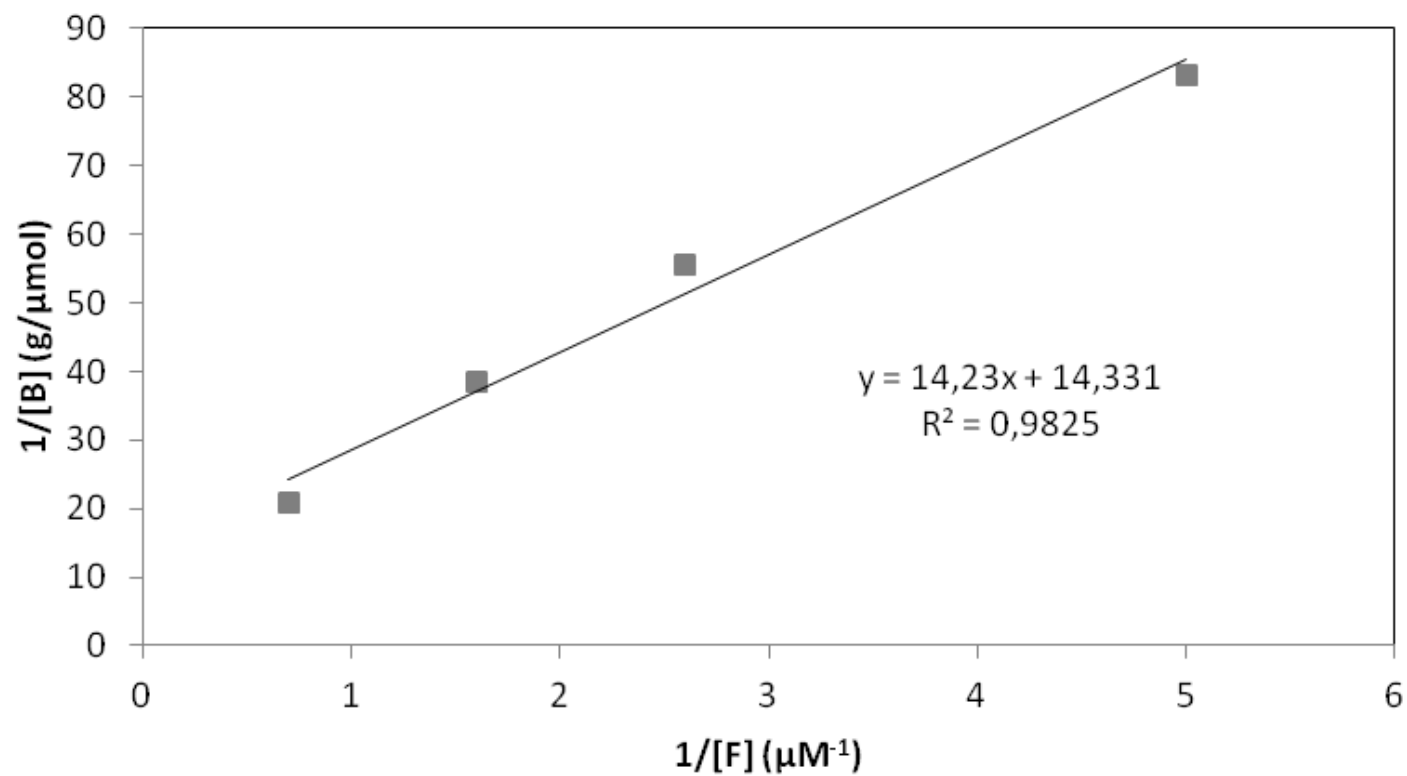
Supplementary file 9: Dtur CelA activity on barley beta-glucan vs time (days after protein production)

Enzyme	Time after production (days)	enzyme dilution (mg/ml)	Mean of enzyme activity (U/mg)	Standard Error	p<0.05
CelA	0	0.013	838,055	57,992	no
CelA	270	0.013	671,516	57,618	

Supplementary file 10: Chimeric Dtur CelA activity on barley beta-glucan vs time (days after protein production)

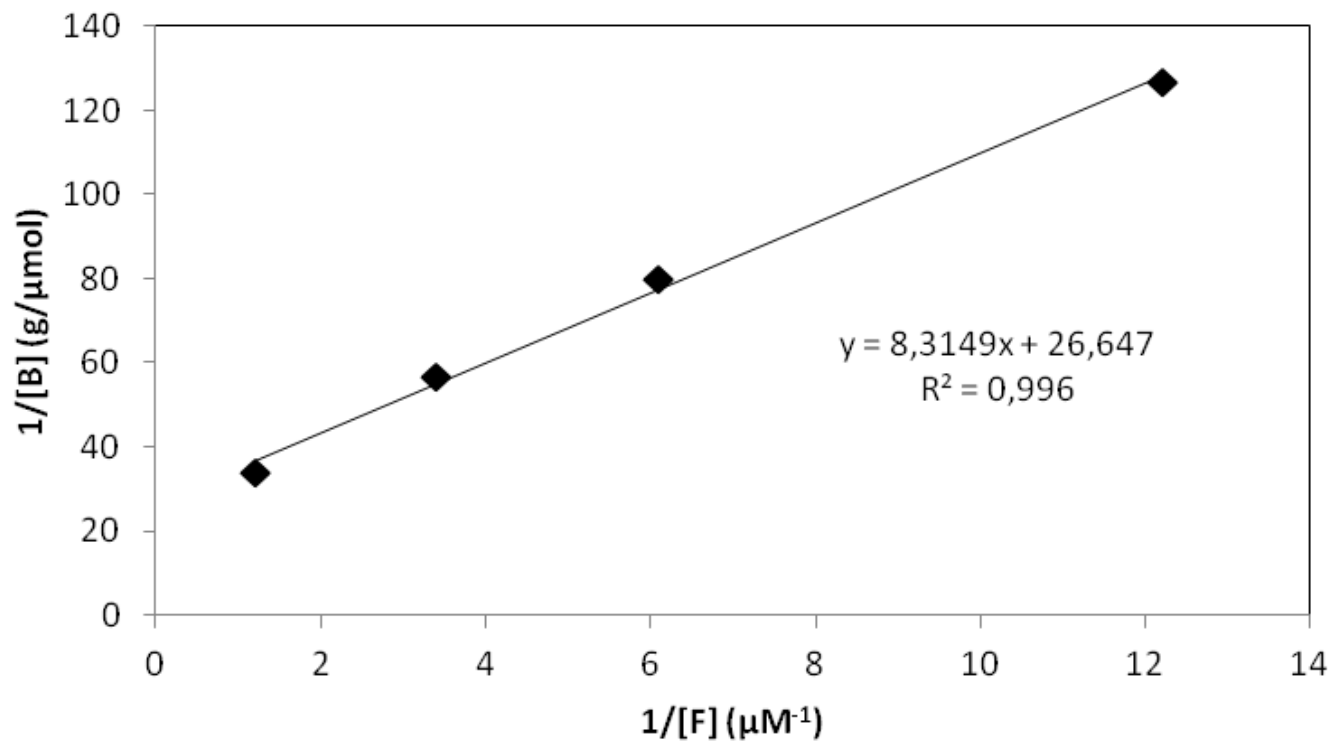
Enzyme	Time after production (days)	enzyme dilution (mg/ml)	Mean of enzyme activity (U/mg)	Standard Error	p<0.05
chimeric-CelA	0	0.013	157,288	6,064	no
chimeric-CelA	270	0.013	136,571	9,07	

Supplementary file 11: Dtur CelA binding to Avicel



Double reciprocal plot of bound (B) versus free (F) protein.

Supplementary file 12: Chimeric Dtur CelA binding to Avicel



Double reciprocal plot of bound (B) versus free (F) protein.