



Title	Characterization of Ruminococcus albus cellodextrin phosphorylase and identification of a key phenylalanine residue for acceptor specificity and affinity to the phosphate group
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Type	journal article
File Information	Fig. s1.pdf, Supplement data



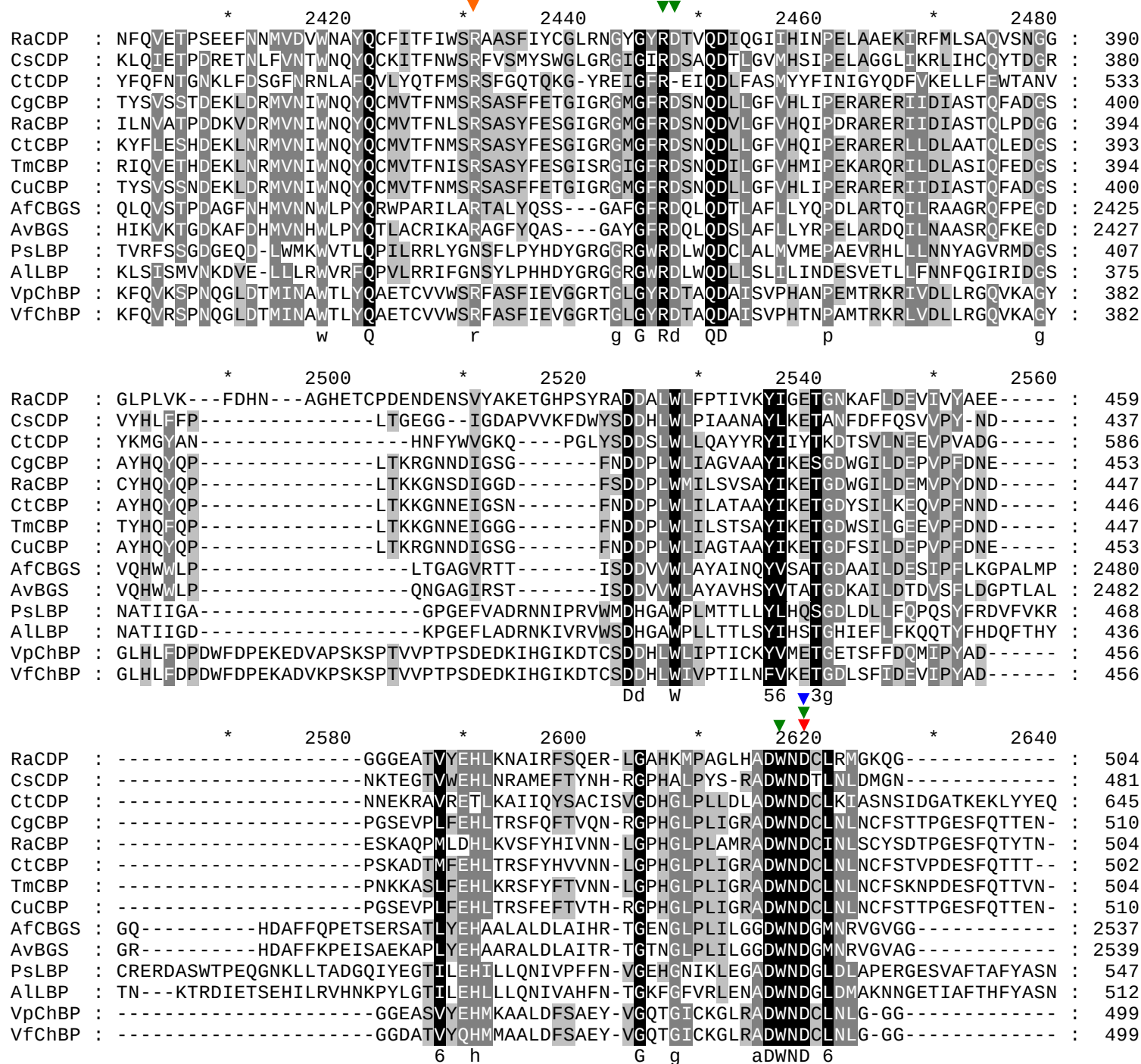


Figure S1. Multiple sequence alignment of catalytic domain of GH94 enzymes.

Multiple sequence alignment was constructed using ClustalW program (<http://www.genome.jp/tools/clustalw/>). Residues with black, dark gray, and light gray backgrounds are 100, 80, and 60 of conserved percent, respectively. Alphabets below the sequence indicate conserved or major residues. 1, D or E; 2, E or Q; 3, S or T; 4, K or R; 5, F, Y, or W; 6, L, I, V, or M. The catalytic residues are indicated by red triangle. The residues involved in the formation of subsites -1 and +1 are indicated by green and blue triangles, respectively. Amino acid residues forming phosphate binding site are shown by orange triangles. CsCDP, *Clostridium stercorarium* CDP (AAC45511.1); CtCDP A, *Clostridium thermocellum* YM4 CDP (BAB71818.1); CgCBP, *C. gilvus* CBP (GenBank ID, BAA28631.1); RaCBP, *R. albus* NE1 CBP (ADU20744.1); CtCBP, *Clostridium thermocellum* YM4 CBP (AAL67138.1); TmCBP, *Thermotoga maritima* MSB8 CBP (AAD36910.1); CuCBP, *Cellulomonas uda* CBP (AAQ20920.1); AfCBGS, *Agrobacterium fabrum* C58 cyclic β -1,2-glucan synthetase (AAK73356.1); AvBGS, *Agrobacterium vitis* F2/5 β -1,2-glucan synthetase (AAQ08605.1); PsLBP, *Paenibacillus* sp. YM1 laminaribiose phosphorylase (BAJ10826.1); AllBP, *Acholeplasma laidlawii* PG-8A laminaribiose phosphorylase (ABX81345.1); VpChBP, *Vibrio proteolyticus* ChBP (BAC87867.1); VfChBP, *Vibrio furnissii* ChBP (AAG23740.1).

	*	2660	*	2680	*	2700	*	2720	
RaCDP	:	-----	-----	-----	-----	ESTFVAFQLYYAMSVIKGYAEER-KD	TDYI-EYITKA	:	539
CsCDP	:	-----	-----	-----	-----	G-----IAETLFTSMLFSEP--PLKRFR	CRISDKRIAT-KYRYWY	:	518
CtCDP	:	LKKTNG-----	-----	-----	-----	KYGDRFMSDYSESVINAFLLKL	AIDHLAEIATLDNDTQLAQ	MSELS	698
CgCBP	:	-----	-----	-----	-----	QAGG-----VAESVFTAAQFVLYGAE	YATLAERRGLADVAT-EARKYV	:	552
RaCBP	:	-----	-----	-----	-----	PKFAAEGGYSKVAESVMATLFTYT	GPNYVAILKHLGKDDEAA-AAQAEI	:	553
CtCBP	:	-----	-----	-----	-----	SKDG-----KVAESVMIAGMFVFI	GKDYVKLCEYMGLEEEAR-KAQQHI	:	545
TmCBP	:	-----	-----	-----	-----	ALDG-----RVAESVFTAGLFVL	AGKEFVEICKRRGLEEEAR-EAEKHV	:	547
CuCBP	:	-----	-----	-----	-----	QAGG-----VAESTFTAAQFVLYGEQ	YAEALAARRGLADVAD-RARGHV	:	552
AfCBGS	:	-----	-----	-----	-----	KGTSVWL	GWFLAGALRAFHRDRREARRYRPGSGKWASHR	:	2576
AvBGS	:	-----	-----	-----	-----	RGESVWL	GWFLANALTVFTP-FAEERK	DSSRVKAWAKYL	2577
PsLBP	:	LMELSELLLELQKRTGKDSL	DAEEMALLDLTGKPI	SYDSIQE	KRSL	LD	RYDAVTPRVSGKKLLLDIRKVAEDL	KRKA	627
AllBP	:	LMKMAEVIEKINRPVR-----	-----	-----	-----	LFKSL-----YDLIFETID	KT-FFDNVS-DFKDTTVEVDATKLSYQLVELY	:	573
VpChBP	:	-----	-----	-----	-----	ESSMV	SFLHFWALQEFIDLAKFLGKDQDVN-TYTEMA	:	535
VfChBP	:	-----	-----	-----	-----	ESAMV	SFLHFWALEAFLELARHRQDAAAI	D-KYQAMA	535

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	*	2740	*	2760	*	2780	*	2800				
RaCDP	:	QAELGKALADCWDED-----	-----	-----	-----	RFIRGIRDNGVVVGAKKDPEAS	WLNPSWAVITSGFASKEQA-----	EKSL	600			
CsCDP	:	DEMKAINEWCWDGE-----	-----	-----	-----	WYIRAFDDEGNVLGSGKNRYGKIF	INSWAVLSMVAPEEYA-----	KKCL	579			
CtCDP	:	KEVTDRIQKHAWKENFFARV	LINRYKDG	SYTYLGAKGDKLSADPNIDGVYF	INSFAWSVLSDVATDEQI-----	-----	-----	AIMV	771			
CgCBP	:	DEVRAAVLEHGWDGQ-----	-----	-----	-----	WFLRAYDYYGNPVGTD	AKPEGKIWI	EPQGF	AVMAGIGVGE	PPDDADAPAVKA	620	
RaCBP	:	DKMKKNVMESAWDGN-----	-----	-----	-----	WFLRAYDANGEKMG	SKECEEGQIF	EPQGF	AIMSEIGKEQGA-----	DKKTL	615	
CtCBP	:	DAMKEAILKYG	YDGE-----	-----	-----	WFLRAYDDFGRK	VGSKE	NEEGKIF	IESGFCVMAEIGLEDGK-----	ALKAL	607	
TmCBP	:	NKMIETTLKYG	WDGE-----	-----	-----	WFLRAYDAFGRK	VGSKE	CEEGKIF	EPQGM	CMVAGIGVDNGY-----	AEKAL	609
CuCBP	:	AEMRDALLTDGWDGS-----	-----	-----	-----	WFLRAYDYYGNPI	GTDAHDEGKIWI	EPQGF	AVMAGVGVGE	GPQD	TAPAIKA	620
AfCBGS	:	EKL RHVLETAGWDGS-----	-----	-----	-----	YYRRGYFDDG	TPLGS	ASSEECQ	IDLGSWSVLSGEGEEGRS-----	RQAM	2637	
AvBGS	:	KSLKAAL	EKAGWDGD-----	-----	-----	HYRRGYFDDGD	PLGSDQ	SDECR	DAIAQSWSVLSGFAEPERQ-----	QQAM	2638	
PsLBP	:	DWAVAHLRGSEW	IQSKEG-----	-----	-----	YAWFNGYYNND	GERVEGD	HPDGV	MITL	TGVFAIMGGVATDEQT-----	EKIS	693
AllBP	:	KKRIDHINENAWIKDTH-----	-----	-----	-----	LQSYITDSN--	VFLDTAD--	TML	TG	AMALLNETLTMSQA-----	KSAV	631
VpChBP	:	ANVREACETHLWDDGG-----	-----	-----	-----	WYIRGLTKNGDK	IGTAQQ	QEGRVH	LESNTL	AVLSGLASQERG-----	EQAM	598
VfChBP	:	NGVREACETHLWDDNGG-----	-----	-----	-----	WYIRGLTKNGDK	IGTTEQ	QEGKVH	ESNTL	AVLSGAVSQRG-----	EKAM	598

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	*	2820	*	2840	*	2860	*	2880					
RaCDP	:	EKVHEILNTPYG--VKIMDP	PPYVDHYFDGALMHI	FNPDTKENG	GIF	SQTQGWII	LAESLMCHGNRAFEY	FMESAPAS---	675				
CsCDP	:	ESVYRHLN	TKYG--IVKVYP	PAYPEYNPKIGGM	TTYP	PAKENG	GIFAHTNPWMIAECMM	GNRRAYQYYRQILPLT---	654				
CtCDP	:	DVIKHHLL	TPYG--LRLVTP	ADLNKIANDTATGHYFFG	DRENGAVFK	ASMMAVAALIKAAKV	KDNE	LAKEMARIAYFM	849				
CgCBP	:	DSVNEM	LGT	PHG--LVLQYP	PAT	TYTQIELGEV	STYP	PGYKENG	GIFCHNNPWIIAETV	VGRGAQAFDY	KRITPAY---	695	
RaCBP	:	AAIDERL	N	TKFG--LVLNNP	AF	TKYIYQYGEI	STYP	PGYKENG	GIFTHNNAWIICAAYAGEG	DAFKYYSEI	APAF---	690	
CtCBP	:	DSVKKYL	D	TPYG--LVLQNP	AF	TRYIYIEYGEI	STYP	PGYKENG	GIFCHNNAWIICAETV	VGRGDMAFDY	RKIAPAY---	682	
TmCBP	:	DSVKKYL	D	TPYG--LVLQQP	P	AYSRYIYELGEI	SSYP	PGYKENG	GIFCHNNPWIIAETV	IGRGDRAFEI	YRKITPAY---	684	
CuCBP	:	DSVNEM	L	ADHG--MVLQYP	P	AT	TYTQVHMG	EVSTYP	PGYKENG	GIFCHNNPWIIAETV	VGRGGA	AFDYKRITPAY---	695
AfCBGS	:	DAVMEHL	V	DEKTGI	IRLFT	PPFSRASHDPGYIKGYPPGV	RENGGQYTHAAT	WVLALAKQ	GRAQ	EAWNCFKLLNPV	NHAL	2717	
AvBGS	:	NSVVGRL	I	D	EVGIVRLFT	PPFEKSRLDPGYIKSYPPGV	RENGGQYTHAAT	WTGLLETVS---	RLAWKV	F	SMNPNV	HAE	2715
PsLBP	:	QAVNRYL	K	DERIG-YRLNSR-FGGI	QNLGRAFG	AFGHKENG	AMF	SMTV	MYANALYKR	GFVQEGFEV	LDSIYRLS	ADF	771
AllBP	:	DTTKKLF	N	KDNGG	YHNSN-YHKIMDM	GRAFG	FSYNH	KENG	AVFSHMAIMY	YGLYN	NLVQLG	NEGYSLI-MRAIH	709
VpChBP	:	DAVDEHL	F	SPYG--LHLNAPS	F	STPNDIGFVTRVYQGV	KENG	AF	FSHPNP	WAWAETK	LRGDRAMKFY	DALNPYN---	673
VfChBP	:	DAVYEYL	F	SPYG--LHLNAPS	F	ATPNDIGFVTRVYQGV	KENG	AF	FSHPNP	WAWAETK	LRGDRAMEFY	DALNPYN---	673

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	*	2900	*	2920	*	2940	*	2960				
RaCDP	:	MNDKAEQRVME	EPYVHGQFTESTRS-----	-----	-----	PYAGRSHVHWL	TGTGSTVMVGCVEGTCGMR	PNAEGLVISPSTIP----	A	743		
CsCDP	:	RNDDADLLEVE	EPYVYCNILGKEH-----	-----	-----	PQFGIGRNSWL	TGTAANMVAVSQYILGIR	PEYDGLTVDPCIP----	P	722		
CtCDP	:	IDLVLPYKNLE	NPFQVAGNPRICTQYIN----	-----	-----	TD	TGENIGPLSGTATWLN	LNLSLAGIEYTRDGISFNPILR----	E	920		
CgCBP	:	REDISDTHKLE	PYVYAQMIAGKEA-----	-----	-----	VRAGEAKNSWL	TGTAANFVAVSQYLLGVR	PDYDGLVDPQIG----	P	763		
RaCBP	:	TEDTSDIHKTE	PYVYGMIIGK	DAGADIGRPGKNFGQ	GKNSWL	TGTAANMVAISQYILGVP	PDFDGLKIDPSTIP----	S	766			
CtCBP	:	IEDVSDIHKLE	PYVYAQMVAGKDA-----	-----	-----	KRHGEAKNSWL	TGTAANFVAISQYILGV	KPDYDGLKIDPSTIP----	K	750		
TmCBP	:	LEDISEIHRTE	PYVYAQMVAGKDA-----	-----	-----	PRHGEAKNSWL	TGTAANFVAITQHILGIR	PTYDSLVDPCIP----	K	752		
CuCBP	:	REDISDVHRL	EPYVYAQMIAGKEA-----	-----	-----	VRHGEAKNSWL	TGTAANFVTVSQYLLGVR	PEYDGLVDPQIG----	P	763		
AfCBGS	:	DAASSETYRVE	PYVVTADVYGEGA-----	-----	-----	YAGRGGWSWY	TGSAGWLYRAAVEGILGIT	TRTDGKLHSPSLP----	E	2784		
AvBGS	:	TTDEADRYRVE	PYVVAADVYGGPG-----	-----	-----	YEGRGGWTWY	TGSAGWLYRFALEGFLGI	HRQEGGITLKPALP----	S	2782		
PsLBP	:	ENSRIYPGVPE	YIN-----	-----	-----	ERGRGMYTYL	TGSASWLLLTQLTEYGV	KGRFGDLRL	LEPKLVQAQFD	:	832	
AllBP	:	PDAHTVLGIPE	YFYFT-----	-----	-----	DKGVGKYL	YLTGSASWLLKLLQEY	FGITFY	YGKLTLPKLV	REDFI	:	770
VpChBP	:	QNDIIEKRIAE	PYSYVQFIMGRDH-----	-----	-----	QDHGRANHPWL	TGSGWAYFAVTNYILGV	QSGFTGLSDPCIP----	S	741		
VfChBP	:	QNDIIEKRIAE	PYSYVQFIMGRDH-----	-----	-----	QDHGRANHPWL	TGSGWAYYATTNFI	LGVRTG	FDTLTVDP	CIP----	A	741

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