

SaAM	-----	0
TaAM	-----	0
AtDPE1	-----	0
D-enzyme	-----MAIHTCFSLIPSSFS-SPK	18
EcAM	MESKR-LDNAALAAGISPNYINAHGKPQSI SAETKRRL-----	38
CgAM	MTARRFLNELADLYGVATS YTDYKGAHIEVSDDTLVKILRALGVNLDTSNLPNDDAIQRC	60

SaAM	-----	0
TaAM	-----	0
AtDPE1	---MH---HHHHHGKPIPNPLGLDSTENLY---FQGIDPFTMEVVSS-----	39
D-enzyme	LP-YP---KNTTFQSPIP-----KLS-RPTFM---FDRKGSF-----	47
EcAM	--DAMHQRTATKVAVTPVPNVMVYTS GKKM--PMVVEGSGEYSWLLTTE-----	83
CgAM	I ALFH DRE---FTRPLPSSVVAVEGDELVPVHVHDGSPADVHIELEDGTQRDVSQVEN	116

SaAM	-----MAKK	4
TaAM	-----MELP	4
AtDPE1	-----NSTCLSSISVGEDFPSEYEQ-----WLPVPDPESR	69
D-enzyme	-----QNGTAAVPAVGEDFPIDYAD-----WLPKRPDNR	77
EcAM	--EGTQYKGHVTGGKAFNLP TKLPEGYHTLTLTQDDQRAHCRVIVAPKRC YEPQALLNKQ	141
CgAM	WTAPREIDGIRWGEASF KIPGDLPLGWHKHLKSNERSAECGLIITPARLSTADKYLDSP	176

SaAM	RASGVL MHITSLPG--DLGIGTFGREAYAFVDFLVETDQKFWQILPLTTTS----FGDSP	58
TaAM	RAFGLLLHPTSLPG--PYGVVLGREARDFLRFLKEAGGRYQVLPPLGPTG----YGDSP	58
AtDPE1	RRAGVLLHPTSFRG--PHGIGDLGEEAFRIDWLHSTGCSVWQVLPPLVPPD---EGGSP	123
D-enzyme	RRAGILLHPTSFPG--PYGIGDLGPQAFKFLDWLHLAGCSLWQVLPPLVPPGKRG NEDGSP	135
EcAM	KLWGACVQLYTLRSEKNWGI GDFGDLKAMLV-DVAKRGGSFIGNPIHALYPANPESASP	200
CgAM	-RSGVMAQIYSVRSTLSWGMGDFNDLGNLAS-VVAQDGADFLINPMHAAEPLPPTEDSP	234
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SaAM	YQSFSAVAGNTHLIDFDLLTLEGFISKDD-----YQNISFGQDPEVVDYAGLFEKRR	110
TaAM	YQSFSAFAGNPYLIDLRPLAERGYVRLED-----PG----FPQGRVDYGLLYAWKW	105
AtDPE1	YAGQDANCNTLLISLDELVKDGLLIKDE-----LPQ---PIDADSVNYQTANKLKS	172
D-enzyme	YSGQDANCNTLLISLEELVDDGLLKMEE-----LPE---PLPTDRVNYSTISEIKD	184
EcAM	YSPSSRRWLVNIYIDVNAVEDFHLSEEQAQWQLPTTQQTQQARDADWDVYSTVTALKM	260
CgAM	YLPTRRFINPIYIRVEDIPEFNQLEIDLRDDIAEMAAEFRENRNLTSDIERNVDVYAAKL	294
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SaAM	PVLEKAVKNFLKEERAT--RMLSDF---LQEEKWVTDFAEFMA-----IKEHFNGKALQE	160
TaAM	PALKEAFRGFKEKASPEEREAF AAFRE--REAWWLEDYALFMA-----LKGAGGLPWNR	158
AtDPE1	PLITKAAKRLIDGN-GELKSKLLDFRNDPSISCWLEDAAYFAA-----IDNTLNAYSWE	226
D-enzyme	PLITKAAKRLLSSE-GELKDQLENFRDRPNISSWLEDAAYFAA-----IDNSVNTISWYD	238
EcAM	TALRMAWKGF AQRDDEQ-MAAFRQFVAE--QGDSLFWQA AFDALHAQQVKEDEM RWG WPA	317
CgAM	QVLRAIFE--MPRSSER-EANFVSFVQR--EGQGLID-----FAT	329
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SaAM	WDDKAIIRREEEALAGYRQKLSEVIKYHEVTQYFFYKQWFELKEYANDKG--IQIIGDMP	218
TaAM	WPLP-LRKREEKALREAKSALAE EVA FHAFTQWLFFRQWGALKAEAEALG--IRIIGDMP	215
AtDPE1	WPEP-LKNRHLSALEAIYESQKEFIDLFIAKQFLFQRQWQKVREYARRQG--VDIMGDMP	283
D-enzyme	WPEP-LKNRHLSALEE VYQSEKDFIDIFIAQQFLFQRQWKKVRDYARSKG--ISIMGDMP	295
EcAM	WPEM-YQNVDSPEVRQFCEEHRDDVDFYWLWLQWLAYSQFAACWEISQGYEMP IGLYRDLA	376
CgAM	WCAD-RETAQSES VHGTEPDRDELTMFYMWLQWLCDEQLAA AQRAVDAGMSIGIMADLA	388
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SaAM	IYVSADSVEVWTMP ELFKLDRDKQPLAIAGVPADDFSDDGQLWGNPIYNWDYHKESDFDW	278
TaAM	IFVAEDSAE VWAHP EWFHLDEEGRPTV VAGVPPDYFSETGQRWGNPLYRWDVLEREGFSF	275
AtDPE1	IYVGYSADVWANKKHFLLNKKGFP LLVSGVPPDLFSETGQLWGSPLYDWKAMESDQYSW	343
D-enzyme	IYVGYSADVWANKKQFLNLRKGFP LIVSGVPPDAFSETGQLWGSPLYDWKAMEKDGFSW	355
EcAM	VGVAEGGAETWCDRELYCLK-----ASVGAPPDILGPLGQNWGLPPMDPHIITARAYEP	430
CgAM	VGVHPGGADAQNL SHVLAPD-----ASVGAPPDGYNQQGQDWSQPPWHPVRLAEEGYIP	442
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SaAM	WIYRIQSGVKMYDYLRIDHFKGFS	DIWEIRGDYQTANDGSWQPAPGP	ELFA--TIKEKLG	336		
TaAM	WIRRLEKALELFLHLVRIDHFRGF	EAYWEIPASCPTAVEGRWVKAPGE	KLFQ--KIQEVFG	333		
AtDPE1	WVNRIIRAQDLYDECRIDHFRGF	AGFWAVPSEAKVAMVGRWKVGP	GKSLFD--AISKGVG	401		
D-enzyme	WVRRIQRATDLFDEFRIDHFRGF	AGFWAVPSEEKIAILGRWKVGP	GKPLFD--AILQAVG	413		
EcAM	FIELLRANMQNCALRIDHVM	SMLRLWWIPIYGE-TADQGAYVHY	PVDDLLSILALESKRH	489		
CgAM	WRNLLRTVLRHSGGIRVDHVLGL	RFLRFVMPRMQ-SPATGTYIRFDH	NALVGLALEAELA	501		
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SaAM	DLPIIAENLGYIDERAERLLAGT	GFPGMKIMEFGFYDTTGN	SIDIPHNYTE--NTIAYAG	394		
TaAM	EVPVLAEDLGVITPEVEALRDR	FGLPGMKVLQFAFDDGMEN-P	FLPHNYPAHGRVVVYTG	392		
AtDPE1	KIKIIAEDLGVITKDVVELRKS	IGAPGMAVLQFAFGGADN-P	HLPHNHEV--NQVVYSG	458		
D-enzyme	KINIIAEDLGVITEDVVQLRKS	IEAPGMAVLQFAFGSDAEN-P	HLPHNHEQ--NQVVYTG	470		
EcAM	RCMVIGEDLGTVPVEIVGKL	RSSGVYSYKVLYFENDHEKT--	FRAPKAYPE--QSMAVAA	545		
CgAM	GAVVIGEDLGTTFEPWVQDALA	QRGIMGTSILWFEHSPSQPG-	PRRQEEYRP--LALTTVT	558		
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SaAM	THDNEVINGWFENLTVEQKAYA	ENYMRR-----		422		
TaAM	THDNDTTLGWYRTATPHEKA	FMARYLAD-----WGIT-----	F	425		
AtDPE1	THDNDTIRGWWDTLDQEEKS	KAMKYLSI-----		486		
D-enzyme	THDNDTIRGWWDTLTPQEEKS	NVLKYLSN-----		498		
EcAM	THDLPTLRGYWECGDLTLGKT	LGLYPDEVVLRGLYQDRELAKQ	GLLDALHKYGCLPKRA-	604		
CgAM	THDLPTAGYLEGEHIALRERL	GVLNTDPAEEL-AEDLQ-WQAE	ILDVAASANALPAREY	616		
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SaAM	L-----	PNEPITETVLR	TLYATVSQTTITCMQDLLDKPADSRM	NMPNTVG-GNWQWR	473	
TaAM	R-----	EEEEVPWALMHLMG	KSVARLAVYPVQDVLALGSEARMNYPGR	PS-GNWAWR	476	
AtDPE1	A-----	GEDDISWSVIQA	AFSSSTAQTAIIPMQDILGLGSSARMNT	PATEV-GNWGWR	537	
D-enzyme	I-----	EEEEISRGLIEG	AVSSVARI	IIPMQDVLGLGSDSRMNI	PATQF-GNWSWR	549
EcAM	-GHKAS	LMSMTPTLN	RGLQRYIAD--SNSALLGLQPEDWLDMAE	FPVNIPGTS-YQYKNWR	660	
CgAM	VGLERD	QRGELAE	LEGLHTFAK--TPSALT	CVCLVDMVGEKRAQNPQGTTRDMYPNWC	674	
	:	:	: : :	* *	*	
SaAM	MRKEDLTENRK---	AFLKEITTIYNRGNKLEHHHHHH	-----	507		
TaAM	LLPGELSPEH---	GARLRAMAEATERL	-----	500		
AtDPE1	IPSSTSFDNLETES	DRLRDLSLYGRL	-----	564		
D-enzyme	IPSSTSFDNLD	AEAKKL	RDILATYGRL	-----	576	
EcAM	RKLSATLES	MFADDGVNKLKDLDRRRRS	SAHHHHHH	-----	696	
CgAM	IPLCDSE-----	GNSVLIES	RENELYHRVAKASKRDL	LEHHHHHH	714	
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Figure S1. Sequence alignment of various AMs and disproportionation enzymes. Yellow colours represent the catalytic triad residues. The N-terminal region is shown in green, while the dimerization arm is highlighted in cyan.

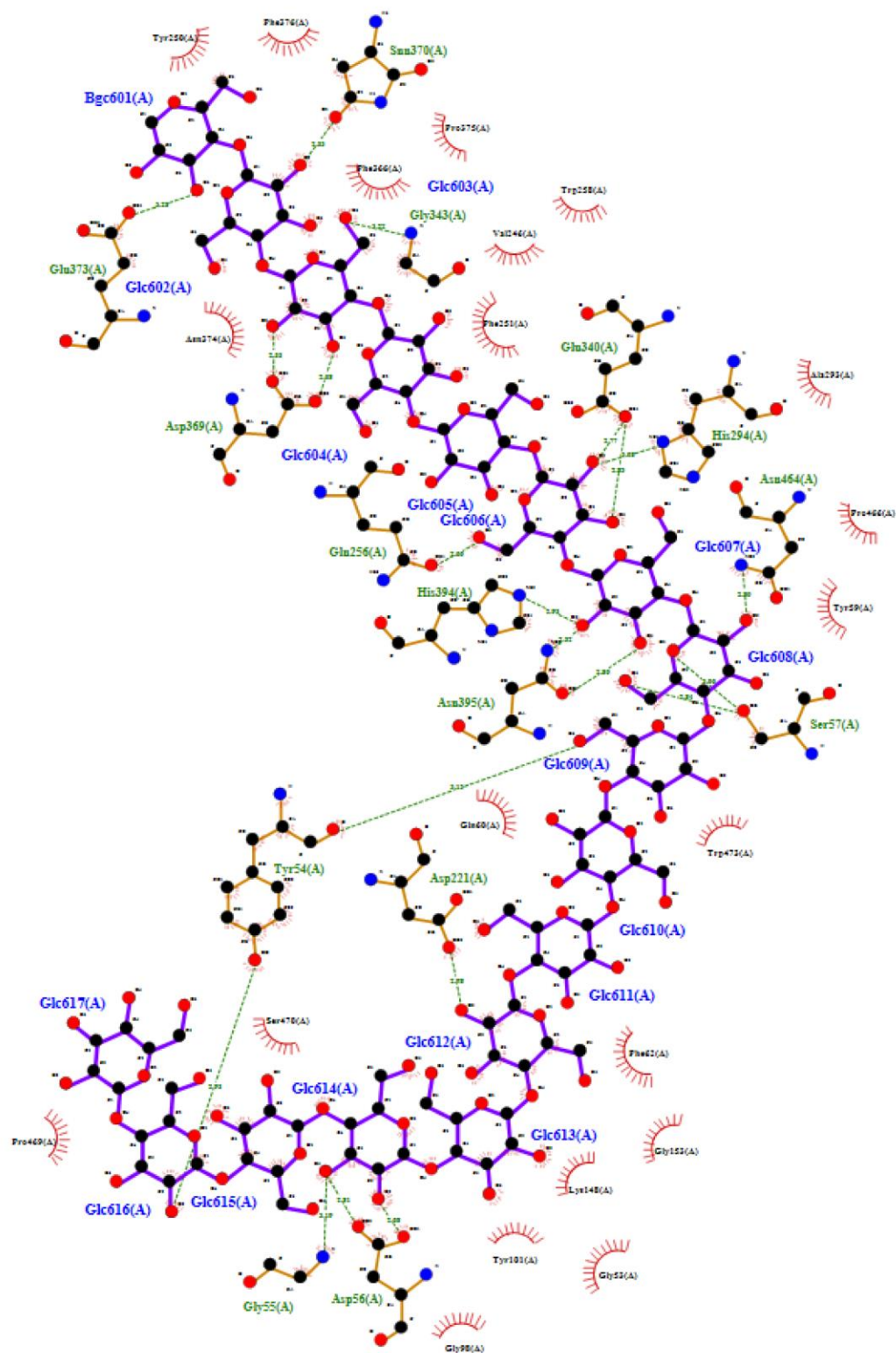


Figure S2. LigPlot of Interaction between *TaAM* and 17 mer glucan. The structure PDB: 5JIW is analyzed by LigPlot software.