

SUPPLEMENTARY FIGURES AND TABLES

A. Module 1

4WZF_B Beta-1,3-glucanase; Mycobacterium tuberculosis, Rv0315, GH16 laminarinases; HET: EDO; 1.699A {Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)} SCOP: I.1.1.1, b.29.1.0; Related PDB entries: 4WZF_A ; Related PDB entries: 4WZF_A
Probability: 95.89%, E-value: 2.8, Score: 40.13, Aligned cols: 202, Identities: 15%, Similarity: 0.072

B. Module 2

3AZY_D Laminarinase (E.C.3.2.1.39); beta-jelly roll fold, Glycosyl hydrolase; HET: SO4; 1.65A {Thermotoga maritima} SCOP: b.29.1.2; Related PDB entries: 3AZX_A 3AZX_B 3AZY_A 3AZY_B 3AZY_C 3AZZ_A 3AZZ_B 3AZZ_D 3AZZ_C 3B00_A 3B00_B 3B00_D 3B00_C 3B01_A 3B01_B 3B01_D 3B01_C 4DF5_A 4DF5_B
Probability: 97.87%, E-value: 0.017, Score: 49.14, Aligned cols: 209, Identities: 13%, Similarity: 0.146

Q ss_pred		cCCCCCCCCChheEEEEeCCCCceeeEcCCC-----CEEEEeCCEEEEEEccceeCCCCcCCCCcceeEEEeceEEC		
Q WP_067651170	5	DDFAGGADEVPARWFQELEVTGPGEAWYADPA-----AVTVAAGGAVAVRIFPEFLACPAQIILDNPKSTAEFDL	78	(235)
Q Consensus	5	ddf~g~ld~r~w~l~pl~DG~w~y~e~P-----A~v~v~dG~l~v~i~Ftr~Hd~v~Q~DN~K~m~S~e~f~v	78	(235)
T Consensus	16	+ .+..+.++ ...+.+.+++.++ ..-.+..-.-.+.		
T 3AZY_D	16	DGF~~~~~W~~~~~W~~~~~W~~~~~W~~~~~W~~~~~W~~~~~W~~~~~W~~~~~W~~~~~W~~~~~W~~~~~W~~~~~	94	(272)
T ss_dssp		QEFDDGVIDPNIWNFEINGNHAKGIPGWGNGELEYTYTDENADEVNGCLVIEARKEQSDE-YGTYDYSARTMTECKFEI	94	(272)
T ss_pred		ECCCSSCTTCTECECCSSGGTGGGTTCEEECSSEEEETTEEEEEECS-SCEECEEECEEECTTCEE		
Q ss_pred		eCCCCCCCCccccEEeeecCCCCCCCCCCCCCcCcEEEEEcCcEEEEEccCc-cceeeeeEEeCCccee		
Q WP_067651170	79	CCcceeEEEEEEeEcCCCCcccccccccEEEEEeCCc-----eEEE-EecCcEEEEEcccccCCCCCCCCcccccc		
Q Consensus	79	TAGFDFGVGRMAATNLGADGADYRGDFAAFNVLDMATAQ-----VFDA-IATGRHAYAERFVGPGVVDPAFFTH	149	(235)
p~G~t~f~v~k~m~a~a~m~g~p~Dl~DGfaa~nvl~d~tg~v~fvd~a~at~d~v~av~e~l~p~Pg~p~v~th		p~v~f~d~v~a~v~e~l~p~Pg~p~v~th	149	(235)
T Consensus	95	.. .+..+.++-.-+.... -+ +=...+....+-+...+.... .		
T 3AZY_D	95	~~G~~~e~r~k~~~~~g~~~a~w~~~~~Eidi~E~~~~~E~~~~~E~~~~~E~~~~~E~~~~~E~~~~~E~~~~~	161	(272)
T ss_dssp		KYGKIEIRAKLPLKG-----KGWI PALWMLGNNGNIGEVGVGWTCEGIDIMEMLGHDTRTVGTAHGP GYSGG---ASI	161	(272)
T ss_pred		SSEEEEEECCCS-----TTEEEEEEETTHHHHCTTTCEEEEEEETCTCTTEEEEEEEETBTBCGG---GCE		
Q ss_pred		ecEEEEEECCCC-----CCcceeEEEEecCC		
Q WP_067651170	150	EEcccc-cCCCCCCCCcEEEEECCCCBEEEEECCCEEeeEcCc-----CC-CceEEEEEecccCCCC-ce		
Q Consensus	150	VVHAPL-VGEAVKAGEFQHYAVTIDRAERWEVRAAGTPYAVRAAA-----LP-ERVRIGFGIITLHPLADGR-ST	218	(235)
~v~p~l~v~d~p~g~b~y~I~t~d~r~v~w~v~D~g~v~p~v~p~v~g~G~i~T~p~l~g~S~		v~p~v~g~G~i~T~p~l~g~S~	218	(235)
T Consensus	162++++ + .+.+ ...++ ++ ++ +..... + ...+ - +..... .+		
T 3AZY_D	162	~~~~~h~y~~~~~w~----~i~idg~v~~~~~~v~~~~~~v~~~~~~v~~~~~~v~~~~~~v~~~~~~v~~~~~~	239	(272)
T ss_dssp		GVAYHLPEGVPDFSFEDHIFI5IEW--DDEEWVYWDQQLYHVLSKDELABLGELEWFDPFFLILNVAVGGWPGYPDET	239	(272)
T ss_pred		EEEEECCTTSCTTSCCEESEE-----CSSEEEEEEETTEEEEEEHHHHHTCCCCCSCCEESEESEECCCTTCCCCCT		
eeeeeeCCCCCCCCccccCcEEEEE-----ECCEEEEEECCCEESEEHHHHHhhccccccCcCEESEESEEeCCCCCCCCCc				
Q ss_pred		eeccCcceeEee		
Q WP_067651170	219	SLRGQLAAW 229 (235)		
Q Consensus	219	S~hHQG~g~W 229 (235)		
.....+.=				
T Consensus	240	~~~~~v~d~	250	(272)
T 3AZY_D	240	TQFPQRMYIDY 250 (272)		
T ss_dssp		CCSSEEEEEE		
T ss_pred		CCCCCCEESEE		

C. Module 3

1O4Y_A beta-agarase A (E.C.3.2.1.81); BETA-AGARASE, GLYCOSIDE HYDROLASE FAMILY 16; HET: SO4; 1.48A {Zobellia galactanivorans} SCOP: b.29.1.2; Related PDB entries: 1URX_A ; Related PDB entries: 1URX_A
Probability: 81.76%, E-value: 69, Score: 29.46, Aligned cols: 188, Identities: 16%, Similarity: 0.189

Q ss_pred		HcHHHHHhcCCcccCCCCCce--EEEeCCCCcHHH-----HHcccCCCCCCC-----cccCCCCccccCCCeEEEEecC	
Q WP_009778041	15	IAGLPATLAASPAEASKPSVT--TTVYDTFDGSESD-----YAAKWDNPYGG-----EMAAGGTRTHDGSTFRASAL	80 (340)
Q Consensus	15	a~~~~~a~~~~~a~~~~~v~YDs~~~yslae----Y~~kWan~YGp-----ema~~~Trs~~~g~f~vs~	80 (340)
T Consensus	3	++.-....+...++...-.+.+ + ++...+.+ ...+++.+.+ ..++ ..	
T 1O4Y_A	3	IAQDWNGIPVPANPGNGMTWQLQDNVSDSFNYTSSEGNRPTAFTSWKWPYSINGWTGPGSTIFNAPQAWTNGSQLAIQAO	82 (288)
T ss_dssp		-CCCTTCCSSCCCTTEEECGGGCBCCCSEEBTTBCCHHHHTEESSSSCCSTTEECCGGGEEEESSCEEEEEEE	82 (288)
T ss_pred		ccccccCccCCCCCCCCCceEECCccccccCCCCCCCCCCCCccccccCCCCCCCCCCCCccccCccceEECcEEEEee	
Q ss_pred		CccCCCCCchhhhhhEE~-EcceCccEeeeeEEecCCCCCcEcceecCCCCCcCcCcCcCcChhhhhh	
Q WP_009778041	81	PFRTGADFSVDHIKYLG~-VSROVFTVPDKGSVTFSLTIDADTVGTDPAAGRVIHGKVYGPVGCAADDPACAADAKPWQALA	158 (340)
Q Consensus	81	PF~tg~DfSVfdH1KY~a~~v~s~~~F~VP~~~GsvtFs~~I~A~TpGt~~~G~Vv~G~Y~~pG~~~a~~~akpy~a~~	158 (340)
T Consensus	83	+..+..+..+.. .+. +++.++... +++.++..+..	
T 1O4Y_A	83	PAGNGK---SYNGITSKNKI---QYP~VYMEIKAKIMDQV---LANAFWTLD---	127 (288)
T ss_dssp		EETTTE---EEEEEESCB---CSS-EEEEEEECSSS---SEESEEECTT---	127 (288)
T ss_pred		cCCCCC-----eeEEEeCcce---eCc-eEEEEEEeCCCC-----cccccccCCC-----	
Q ss_pred		hchhhHHhEEEccccc---eeeeccCceeeeHHcccccc---CCCCccccHHhheeeeCCCC--CEEEEEE	
Q WP_009778041	159	LEGQQAGATLHMIDFRTGQL--FDWFVSGTTAFALIERLPAVTI---GSPDGGTRDTMYTQIIKEIFVFDG--PHRVSIIT	231 (340)
Q Consensus	159	LEGQQAgvvnlnIdF-TGOL--FDWFVsg~AF~LIERLPS~Vt---~p~VG1d~~YTQI1k~ipi~pG~~~H~val~	231 (340)
T Consensus	128	...+++. ++-.----.-+...+. +...----- +...+	
T 1O4Y_A	128	-----~p1D1~E~g-----~p~V~y~f~y~	192 (288)
T ss_dssp		-----ETQEIDIMEGYGSDRGCTWAFQRMHLSHTFIRNPFTDYQPMDATWYNGTPWRSAYHYGCY	192 (288)
T ss_pred		-----SCEEEEEEECCGGGCHHHHTEEEEEEETTTTEEECCCCGGGEEECTTCGGGSCEECCCC	
Q ss_pred		EecCCCCceEEEEECCCEEEEEEee	
Q WP_009778041	232	FSRNAGSSHVDYTIDGKRVARVGK 255 (340)	
Q Consensus	232	y~r~g~sv~Y~lDG~Va~v~ 255 (340)	
T Consensus	193	++...+. ++ +.!.++.+	
T 1O4Y_A	193	w~~~~~i~~~vDg~~~v~~~~ 213 (288)	
T ss_dssp		WKDPF---TLEYYIDGVKVRTVTR 213 (288)	
T ss_pred		EEETT---EEEEEETTEEEEEECH	
		EeCC---EEEEECCCEECCCCe	

Supplementary figure 1. Results of the HHpred search seeded with the multiple sequence alignments prepared from proteins in module 1 (A), 2 (B) and 3 (C). H(h), α -helix; C(c), coil; Q, query; T, target; ss, secondary structure.

Supplementary figure 2. Multiple sequence alignment of GH16 family proteins and their inactive derivatives. Enzymatically active GH16 family proteins for which X-ray structures available are shown in red and indicated with the corresponding PDB identifiers. Inactivated GH16 derivatives encoded by diverse bacteria and giant viruses are indicated with green and red fonts, respectively. Note that bacterial sequences include representatives of all 3 modules defined in Figure 2A. Long, non-conserved insertions are not shown for clarity, with the exact number of omitted residues indicated in parenthesis.

Supplementary table 1. Composition of the Modules 1 to 3.

Accession #	Organism name	Taxon
Module 1		
WP_004001160	Streptomyces viridochromogenes	Actinobacteria
WP_013422495	Frankia inefficax	Actinobacteria
WP_018542795	unclassified Streptomyces	Actinobacteria
WP_019070481	Streptomyces hokutonensis	Actinobacteria
WP_019524852	unclassified Streptomyces	Actinobacteria
WP_019524853	unclassified Streptomyces	Actinobacteria
WP_033294507	Amycolatopsis jejuensis	Actinobacteria
WP_036346721	Micromonospora	Actinobacteria
WP_043667143	Streptomyces xylophagus	Actinobacteria
WP_051763122	Streptomyces virginiae	Actinobacteria
WP_051773929	Streptomyces sp. NRRL S-237	Actinobacteria
WP_051782626	unclassified Streptomyces	Actinobacteria
WP_051816291	Streptomyces sp. NRRL WC-3744	Actinobacteria
WP_051818725	Streptomyces	Actinobacteria
WP_051848524	Streptomyces sp. NRRL WC-3725	Actinobacteria
WP_051854226	unclassified Streptomyces	Actinobacteria
WP_052021393	Actinokineospora sphecospongiae	Actinobacteria
WP_052183290	Streptomyces sp. UNC401CLCol	Actinobacteria
WP_052681576	Saccharothrix sp. ST-888	Actinobacteria
WP_053211603	Streptomyces antibioticus	Actinobacteria
WP_055613714	Streptomyces phaeochromogenes	Actinobacteria
WP_055613717	Streptomyces phaeochromogenes	Actinobacteria
WP_066927533	Streptomyces sp. NBRC 110611	Actinobacteria
WP_073215198	Streptomyces sp. NBRC 110465	Actinobacteria
WP_073496364	Streptomyces phaeoluteigriseus	Actinobacteria
WP_073904122	Streptomyces sp. CB02009	Actinobacteria
WP_078637708	Streptomyces	Actinobacteria
WP_079134226	unclassified Streptomyces	Actinobacteria
WP_079134227	unclassified Streptomyces	Actinobacteria
WP_079141677	Streptomyces sp. LUP30	Actinobacteria
WP_079149609	Streptomyces sp. EN27	Actinobacteria
WP_079180745	Streptomyces sp. CB02058	Actinobacteria
WP_079180747	Streptomyces sp. CB02058	Actinobacteria
WP_079185489	Streptomyces sp. NBRC 110465	Actinobacteria
WP_079188286	Streptomyces sp. CB0200	Actinobacteria
WP_079192651	Streptomyces sp. CB01883	Actinobacteria
WP_083753708	Actinosynnema sp. ALI-1.44	Actinobacteria
WP_087924989	Streptomyces albireticuli] 134	Actinobacteria
WP_088961757	Micromonospora purpureochromogenes	Actinobacteria
WP_091451464	Alloactinosynnema iranicum	Actinobacteria
WP_092650511	Actinopolymorpha singaporense	Actinobacteria
WP_092886397	Actinopolymorpha cephalotaxi	Actinobacteria
WP_093471991	unclassified Streptomyces	Actinobacteria
WP_093627747	Streptomyces sp. 3213.3	Actinobacteria

WP_093736433	unclassified Streptomyces	Actinobacteria
WP_093908613	Streptomyces sp. Cf386	Actinobacteria
WP_095578871	Streptomyces albireticuli	Actinobacteria
WP_100825925	Streptomyces sp. 69	Actinobacteria
WP_106246877	Allonocardiopsis opalescens	Actinobacteria
WP_106432501	unclassified Streptomyces	Actinobacteria
WP_107072723	Streptomyces sp. NRRL B-1568	Actinobacteria
WP_109497567	Streptomyces sp. Act143	Actinobacteria
WP_110079847	Actinokineospora mzabensis	Actinobacteria
WP_116021934	Actinomadura umbrina	Actinobacteria
WP_116021939	Actinomadura umbrina	Actinobacteria
WP_116180669	Kutzneria buriramensis	Actinobacteria
WP_121801026	Streptomyces griseocarneus	Actinobacteria
WP_123440892	Streptomyces sp. PanSC9	Actinobacteria
WP_125594626	Streptomyces sp. WAC07061	Actinobacteria
WP_125814831	Streptomyces sp. WAC07149	Actinobacteria
WP_129593328	Streptomyces sp. C	Actinobacteria
WP_130876631	Streptomyces netropsis	Actinobacteria
WP_138043881	Streptomyces sp. NEAU-C151	Actinobacteria
WP_141208225	Streptomyces griseorubiginosus	Actinobacteria
WP_141561871	Micromonospora sp. WMMA1996	Actinobacteria
WP_141684583	Micromonospora sediminicola	Actinobacteria
WP_143593014	Streptomyces albireticuli	Actinobacteria
WP_145788523	Kitasatospora atroaurantiaca	Actinobacteria
WP_146045455	Streptomyces eurocidicus	Actinobacteria
WP_146238386	Streptomyces sp. Act143	Actinobacteria
WP_146238387	Streptomyces sp. Act143	Actinobacteria
WP_147472096	Streptomyces griseocarneus	Actinobacteria
WP_148349770	Actinomadura syzygii	Actinobacteria
WP_148349773	Actinomadura syzygii	Actinobacteria
WP_148767260	Actinomadura sp. CYP1-5	Actinobacteria
WP_148767263	Actinomadura sp. CYP1-5	Actinobacteria
WP_153278161	Saccharothrix syringae	Actinobacteria
WP_153541889	Streptomyces sp. RB17	Actinobacteria
WP_154936519	Micromonospora palomenae	Actinobacteria
WP_154936522	Micromonospora palomenae	Actinobacteria
WP_157745954	Micromonospora purpureochromogenes	Actinobacteria
WP_159042716	Streptomyces curacoi	Actinobacteria
WP_159395205	Streptomyces albireticuli	Actinobacteria
WP_161069931	Streptomyces sp. HUCO-GS316	Actinobacteria
WP_161108180	Streptomyces sp. XHT-2	Actinobacteria
WP_161108181	Streptomyces sp. XHT-2	Actinobacteria
WP_161231499	Streptomyces sp. SID4956	Actinobacteria
WP_161241892	Streptomyces sp. SID2888	Actinobacteria
WP_161241895	Streptomyces sp. SID2888	Actinobacteria
WP_161241896	Streptomyces sp. SID2888	Actinobacteria
WP_161290971	Streptomyces sp. SID1046	Actinobacteria

WP_168211442	Actinosynnema sp. ALI-1.44	Actinobacteria
WP_053601342	Bacillus sp. FJAT-18017	Firmicutes
WP_066204414	Bacillus sp. FJAT-27225	Firmicutes
WP_099355020	Bacillus onubensis	Firmicutes
WP_099364288	Bacillus onubensis	Firmicutes
WP_011952500	Sphingomonas wittichii	Proteobacteria
WP_016746823	Sphingomonas wittichii	Proteobacteria
WP_047168197	Sphingomonas sp. Y57	Proteobacteria
WP_052420046	Hyalangium minutum	Proteobacteria
WP_056354592	unclassified Sphingomonas	Proteobacteria
WP_132145912	Luteibacter rhizovicinus	Proteobacteria
WP_146728083	Minicystis rosea	Proteobacteria
WP_170328229	Ruegeria arenilitoris	Proteobacteria
WP_170609244	Ruegeria conchae	Proteobacteria

Module 2

WP_068013487	Nocardia mexicana	Actinobacteria
WP_024802787	Nocardia sp. BMG51109	Actinobacteria
WP_146251404	Nocardia tenerifensis	Actinobacteria
WP_138666465	Nonomuraea turkmeniaca	Actinobacteria
WP_028931974	Pseudonocardia asaccharolytica	Actinobacteria
WP_009478479	Rhodococcus sp. JVH1	Actinobacteria
WP_055722186	Streptomyces	Actinobacteria
WP_050371984	Streptomyces acidiscabies	Actinobacteria
WP_075730970	Streptomyces acidiscabies	Actinobacteria
WP_053210749	Streptomyces antibioticus	Actinobacteria
WP_037701643	Streptomyces atratus	Actinobacteria
WP_062050432	Streptomyces canus	Actinobacteria
WP_050782599	Streptomyces griseoflavus	Actinobacteria
WP_073502273	Streptomyces paucisporeus	Actinobacteria
WP_100203414	Streptomyces sp. TRM SA0054	Actinobacteria
WP_018839510	unclassified Streptomyces	Actinobacteria
WP_098503344	Thermoflexus hugenholtzii	Chloroflexi
WP_151729905	Thermogemmatispora aurantia	Chloroflexi
WP_066289961	Fictibacillus arsenicus	Firmicutes
WP_066394060	Fictibacillus phosphorivorans	Firmicutes
WP_019637377	Paenibacillus fonticola	Firmicutes
WP_144873436	Paenibacillus ihbetae	Firmicutes
WP_127588546	Paenibacillus kolevorans	Firmicutes
WP_076287080	Paenibacillus odorifer	Firmicutes
WP_091167356	Paenibacillus sp. 1_12	Firmicutes
WP_053375461	Paenibacillus sp. FJAT-27812	Firmicutes
WP_039879466	Paenibacillus sp. FSL R7-0273	Firmicutes
WP_036692278	Paenibacillus sp. FSL R7-269	Firmicutes
WP_129437925	Paenibacillus sp. FW100M-2	Firmicutes
WP_057314481	Paenibacillus sp. Soil766	Firmicutes
WP_150270317	Paenibacillus sp. SYSU G01001	Firmicutes

WP_038699482	Paenibacillus stellifer	Firmicutes
WP_093338107	Salibacterium halotolerans	Firmicutes
WP_006159786	Cupriavidus basilensis	Proteobacteria
WP_013954189	Cupriavidus necator	Proteobacteria
WP_013954198	Cupriavidus necator	Proteobacteria
WP_116263445	Pseudomonas sp. OV081	Proteobacteria

Module 3

WP_009778041	Janibacter sp. HTCC2649	Actinobacteria
WP_091356076	Frankineae bacterium MT45	Actinobacteria
WP_096304281	Jatrophihabitans sp. GAS493	Actinobacteria
WP_135839310	Nocardioides sp. MMS17-SY213	Actinobacteria
WP_139131788	Micromonospora chersina	Actinobacteria
WP_141844292	Humibacillus xanthopallidus	Actinobacteria
WP_148616077	Nocardioides rubriscoriae	Actinobacteria
WP_151461420	Micromonospora sp. AMSO31t	Actinobacteria
WP_124897093	Haloplanus aerogenes	Halobacteria
WP_056193950	Pelomonas sp. Root1237	Proteobacteria
WP_056264676	unclassified Pelomonas	Proteobacteria
WP_057300625	Pelomonas sp. Root1217	Proteobacteria
WP_100922660	Candidatus Thiodictyon syntrophicum	Proteobacteria