Phyre^2

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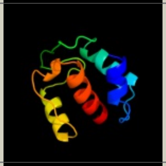
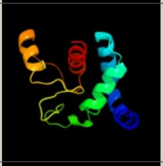
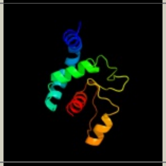
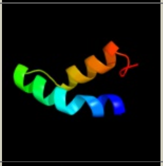
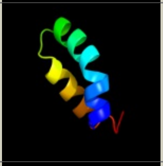
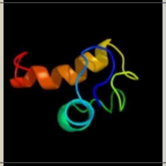
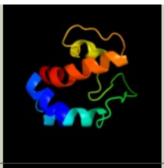
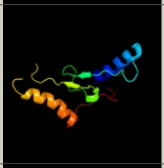
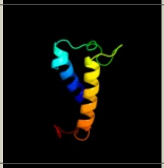
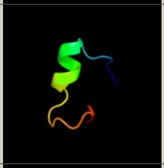
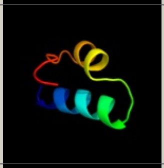
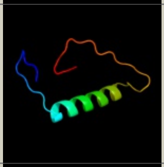
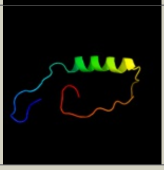
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qusa_	Alignment		100.0	99	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
2	d1qsaa2	Alignment		99.0	27	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
3	d1gbsa_	Alignment		98.9	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
4	c3gxkB_	Alignment		98.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**goose-type lysozyme 1; **PDBTitle:** the crystal structure of g-type lysozyme from atlantic cod2 (gadus morhua l.) in complex with nag oligomers sheds new3 light on substrate binding and the catalytic mechanism.4 native structure to 1.9
5	c2y8pA_	Alignment		98.9	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endo-type membrane-bound lytic murein transglycosylase a; **PDBTitle:** crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
6	c1slyA_	Alignment		98.7	27	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
7	c3mgwA_	Alignment		98.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
8	c3fi7A_	Alignment		96.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lmo1076 protein; **PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
9	c2zycA_	Alignment		95.6	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj; **PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
10	c1xsfA_	Alignment		90.0	17	**PDB header:**cell cycle, hydrolase **Chain:** A: **PDB Molecule:**probable resuscitation-promoting factor rpfb; **PDBTitle:** solution structure of a resuscitation promoting factor2 domain from mycobacterium tuberculosis
11	d1xsfa1	Alignment		89.5	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**RPF-like

12	c3bkhA_	Alignment		87.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
13	c3eo5A_	Alignment		85.9	21	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** crystal structure of the resuscitation promoting factor rpfb
14	d7reqb1	Alignment		49.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Methylmalonyl-CoA mutase, N-terminal (CoA-binding) domain
15	d3e9va1	Alignment		44.2	31	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
16	c3p0dD_	Alignment		42.3	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glycoside hydrolase family 9; **PDBTitle:** crystal structure of a multimodular ternary protein complex from2 clostridium thermocellum
17	d2coba1	Alignment		38.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
18	c6reqB_	Alignment		36.6	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**protein (methylmalonyl-coa mutase); **PDBTitle:** methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
19	d1lcia_	Alignment		33.8	13	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
20	c3gqwB_	Alignment		31.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fatty acid amp ligase; **PDBTitle:** crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
21	c3bjqA_	Alignment	not modelled	27.4	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phage-related protein; **PDBTitle:** crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
22	d1v25a_	Alignment	not modelled	24.7	13	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
23	c2djpA_	Alignment	not modelled	22.8	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sb145; **PDBTitle:** the solution structure of the lysm domain of human2 hypothetical protein sb145
24	c2zuxA_	Alignment	not modelled	21.2	40	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yesw protein; **PDBTitle:** crystal structure of rhamnogalacturonan lyase yesw2 complexed with rhamnose
25	d1zfsa1	Alignment	not modelled	21.2	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
26	c1g3wA_	Alignment	not modelled	20.4	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
27	c2zuyA_	Alignment	not modelled	20.3	40	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yesx protein; **PDBTitle:** crystal structure of exotype rhamnogalacturonan lyase yesx
28	c3fcuB_	Alignment	not modelled	20.2	16	**PDB header:**cell adhesion/blood clotting **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** structure of headpiece of integrin aiibb3 in open conformation
						PDB header:hydrolase

29	c1lnsA_	Alignment	not modelled	18.6	36	**Chain:** A: **PDB Molecule:**x-prolyl dipeptidyl aminopetidase; **PDBTitle:** crystal structure analysis of the x-prolyl dipeptidyl2 aminopeptidase from lactococcus lactis
30	c1zx4B_	Alignment	not modelled	18.3	17	**PDB header:**translation **Chain:** B: **PDB Molecule:**plasmid partition par b protein; **PDBTitle:** structure of parb bound to dna
31	c2c4dA_	Alignment	not modelled	17.5	40	**PDB header:**lectin **Chain:** A: **PDB Molecule:**psathyrella velutina lectin pvl; **PDBTitle:** 2.6a crystal structure of psathyrella velutina lectin in2 complex with n-acetylglucosamine
32	d1ohzb_	Alignment	not modelled	16.1	21	**Fold:**Type I dockerin domain **Superfamily:**Type I dockerin domain **Family:**Type I dockerin domain
33	c3etcB_	Alignment	not modelled	15.9	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-binding protein; **PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
34	d1nvma1	Alignment	not modelled	15.8	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
35	d1e0ga_	Alignment	not modelled	15.5	15	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
36	d1aqta1	Alignment	not modelled	15.5	47	**Fold:**Long alpha-hairpin **Superfamily:**Epsilon subunit of F1F0-ATP synthase C-terminal domain **Family:**Epsilon subunit of F1F0-ATP synthase C-terminal domain
37	d2cclb1	Alignment	not modelled	14.5	21	**Fold:**Type I dockerin domain **Superfamily:**Type I dockerin domain **Family:**Type I dockerin domain
38	c2vkzH_	Alignment	not modelled	13.9	26	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
39	d1nxca_	Alignment	not modelled	13.8	27	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
40	c2uval_	Alignment	not modelled	13.8	23	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
41	d1k0ga_	Alignment	not modelled	13.6	16	**Fold:**ADC synthase **Superfamily:**ADC synthase **Family:**ADC synthase
42	d1dava_	Alignment	not modelled	13.2	31	**Fold:**Type I dockerin domain **Superfamily:**Type I dockerin domain **Family:**Type I dockerin domain
43	d1twfa_	Alignment	not modelled	12.9	35	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta-prime
44	d1uwsa_	Alignment	not modelled	12.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
45	c3pn8A_	Alignment	not modelled	11.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phospho-beta-glucosidase; **PDBTitle:** the crystal structure of 6-phospho-beta-glucosidase from streptococcus2 mutans ua159
46	c2xhyD_	Alignment	not modelled	11.6	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**6-phospho-beta-glucosidase bgla; **PDBTitle:** crystal structure of e.coli bgla
47	d1c7va_	Alignment	not modelled	11.6	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
48	c3r74B_	Alignment	not modelled	11.6	13	**PDB header:**lyase, biosynthetic protein **Chain:** B: **PDB Molecule:**anthranilate/para-aminobenzoate synthases component i; **PDBTitle:** crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
49	d3c1va1	Alignment	not modelled	11.4	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
50	c2pmzQ_	Alignment	not modelled	11.3	36	**PDB header:**translation, transferase **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase subunit a; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
51	c2aaoA_	Alignment	not modelled	11.1	45	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calcium-dependent protein kinase, isoform ak1; **PDBTitle:** regulatory apparatus of calcium dependent protein kinase from2 arabidopsis thaliana
52	c3k8kB_	Alignment	not modelled	11.0	28	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg
53	c2it0A_	Alignment	not modelled	10.9	15	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
						PDB header:cell adhesion

54	c2vn5B_	Alignment	not modelled	10.7	21	**Chain:** B: **PDB Molecule:**endoglucanase a; **PDBTitle:** the clostridium cellulolyticum dockerin displays a dual2 binding mode for its cohesin partner
55	d2z15a1	Alignment	not modelled	10.6	35	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
56	c2d1tA_	Alignment	not modelled	10.5	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**luciferin 4-monooxygenase; **PDBTitle:** crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
57	c2lcvA_	Alignment	not modelled	10.4	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
58	c2vrgA_	Alignment	not modelled	10.2	20	**PDB header:**transport **Chain:** A: **PDB Molecule:**multiple coagulation factor deficiency protein 2; **PDBTitle:** structure of human mcfd2
59	c3lcpC_	Alignment	not modelled	10.0	40	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**multiple coagulation factor deficiency protein 2; **PDBTitle:** crystal structure of the carbohydrate recognition domain of lman1 in2 complex with mcfd2
60	c2y5iF_	Alignment	not modelled	9.9	11	**PDB header:**metal-binding protein **Chain:** F: **PDB Molecule:**s100 calcium binding protein z; **PDBTitle:** s100z from zebrafish in complex with calcium
61	c3ggzC_	Alignment	not modelled	9.7	25	**PDB header:**protein transport, endocytosis **Chain:** C: **PDB Molecule:**increased sodium tolerance protein 1; **PDBTitle:** crystal structure of s.cerevisiae ist1 n-terminal domain in2 complex with did2 mim motif
62	c3hruA_	Alignment	not modelled	9.5	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
63	c3h4sE_	Alignment	not modelled	9.3	20	**PDB header:**motor protein/calcium binding protein **Chain:** E: **PDB Molecule:**kcbp interacting ca2+-binding protein; **PDBTitle:** structure of the complex of a mitotic kinesin with its2 calcium binding regulator
64	c3rqcB_	Alignment	not modelled	9.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable lipoamide acyltransferase; **PDBTitle:** crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
65	c2l8nA_	Alignment	not modelled	9.3	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
66	d1a4pa_	Alignment	not modelled	9.2	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
67	d1lwub1	Alignment	not modelled	9.2	17	**Fold:**Fibrinogen C-terminal domain-like **Superfamily:**Fibrinogen C-terminal domain-like **Family:**Fibrinogen C-terminal domain-like
68	d1f86a_	Alignment	not modelled	9.1	23	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
69	d1a03a_	Alignment	not modelled	9.1	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
70	c3fovA_	Alignment	not modelled	9.0	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0102 protein rpa0323; **PDBTitle:** crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris
71	c2da4A_	Alignment	not modelled	9.0	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
72	d1ynjd1	Alignment	not modelled	8.9	35	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta-prime
73	d1j55a_	Alignment	not modelled	8.9	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
74	c2y3nB_	Alignment	not modelled	8.4	42	**PDB header:**structrual protein/hydrolase **Chain:** B: **PDB Molecule:**cellulosomal family-48 processive glycoside hydrolase; **PDBTitle:** type ii cohesin-dockerin domain from bacteroides cellulosolvens
75	c3ct5A_	Alignment	not modelled	8.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
76	c2g8yB_	Alignment	not modelled	8.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate/l-lactate dehydrogenases; **PDBTitle:** the structure of a putative malate/lactate dehydrogenase from e. coli.
77	d1uxda_	Alignment	not modelled	8.2	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
78	d1boda_	Alignment	not modelled	8.2	36	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calbindin D9K
						PDB header:hydrolase **Chain:** B: **PDB Molecule:**5-hydroxyisourate hydrolase (formerly

79	c2h1xB_	Alignment	not modelled	8.1	19	known as **PDBTitle:** crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
80	c2fcdA_	Alignment	not modelled	7.9	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**myosin light chain 1; **PDBTitle:** solution structure of n-lobe myosin light chain from2 saccharomices cerevisiae
81	d1u5ta1	Alignment	not modelled	7.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
82	d4icba_	Alignment	not modelled	7.8	40	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calbindin D9K
83	c3kztB_	Alignment	not modelled	7.7	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_812423.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
84	c1u8cB_	Alignment	not modelled	7.7	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** a novel adaptation of the integrin psi domain revealed from its2 crystal structure
85	c2oznB_	Alignment	not modelled	7.7	29	**PDB header:**toxin **Chain:** B: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** the cohesin-dockerin complex of nagj and nagh from clostridium2 perfringens
86	c2kq5A_	Alignment	not modelled	7.7	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**avirulence protein; **PDBTitle:** solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha
87	d1bw6a_	Alignment	not modelled	7.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
88	c3h0gA_	Alignment	not modelled	7.6	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb1; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
89	c3ptkB_	Alignment	not modelled	7.6	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase os4bglu12; **PDBTitle:** the crystal structure of rice (oryza sativa l.) os4bglu12
90	c1irjG_	Alignment	not modelled	7.5	20	**PDB header:**metal binding protein **Chain:** G: **PDB Molecule:**migration inhibitory factor-related protein 14; **PDBTitle:** crystal structure of the mrp14 complexed with chaps
91	d1nsha_	Alignment	not modelled	7.5	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
92	c1g6iA_	Alignment	not modelled	7.4	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i alpha-1,2-mannosidase; **PDBTitle:** crystal structure of the yeast alpha-1,2-mannosidase with bound 1-2 deoxymannojirimycin at 1.59 a resolution
93	c1bdhA_	Alignment	not modelled	7.3	5	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (purine repressor); **PDBTitle:** purine repressor mutant-hypoxanthine-palindromic operator2 complex
94	c1i6hA_	Alignment	not modelled	7.3	35	**PDB header:**transcription/dna-rna hybrid **Chain:** A: **PDB Molecule:**dna-directed rna polymerase ii largest subunit; **PDBTitle:** rna polymerase ii elongation complex
95	d1tyea_	Alignment	not modelled	7.3	42	**Fold:**7-bladed beta-propeller **Superfamily:**Integrin alpha N-terminal domain **Family:**Integrin alpha N-terminal domain
96	c1vbiA_	Alignment	not modelled	7.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type 2 malate/lactate dehydrogenase; **PDBTitle:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
97	d1qpza1	Alignment	not modelled	7.2	3	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
98	d1snla_	Alignment	not modelled	7.2	36	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
99	d1dl2a_	Alignment	not modelled	7.1	31	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain