Phyre^2

Email	l.a.kelley@imperial.ac.uk
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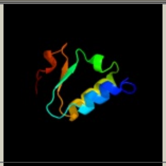
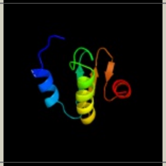
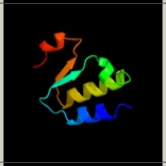
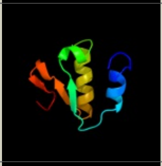
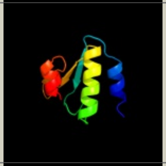
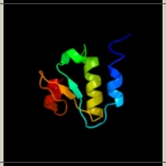
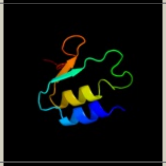
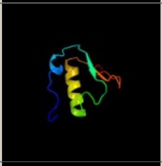
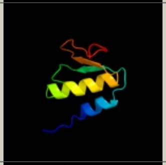
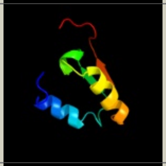
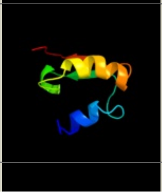
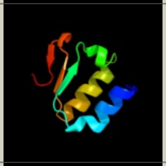
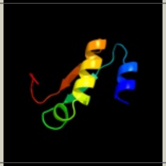
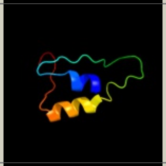
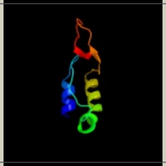
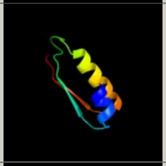
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pkzK_	Alignment		99.4	17	**PDB header:**recombination **Chain:** K: **PDB Molecule:**recombinase sin; **PDBTitle:** structural basis for catalytic activation of a serine recombinase
2	c3g13B_	Alignment		99.4	14	**PDB header:**recombination **Chain:** B: **PDB Molecule:**putative conjugative transposon recombinase; **PDBTitle:** crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
3	c2r0qF_	Alignment		99.4	18	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
4	d2rsla_	Alignment		99.2	30	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
5	c2gm4B_	Alignment		99.2	29	**PDB header:**recombination, dna **Chain:** B: **PDB Molecule:**transposon gamma-delta resolvase; **PDBTitle:** an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
6	c3ploX_	Alignment		99.2	46	**PDB header:**recombination **Chain:** X: **PDB Molecule:**dna-invertase; **PDBTitle:** crystal structure of the fis-independent mutant of gin
7	d1hx7a_	Alignment		99.2	29	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
8	d2gm4a2	Alignment		99.1	31	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
9	d1gdta2	Alignment		99.0	28	**Fold:**Resolvase-like **Superfamily:**Resolvase-like **Family:**gamma,delta resolvase, catalytic domain
10	c3lhkA_	Alignment		98.8	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna binding protein mj0014; **PDBTitle:** crystal structure of putative dna binding protein from2 methanocaldococcus jannaschii.
11	c3lhfC_	Alignment		98.8	23	**PDB header:**recombination **Chain:** C: **PDB Molecule:**serine recombinase; **PDBTitle:** the crystal structure of a serine recombinase from2 sulfolobus solfataricus to 2.3a

12	c3guvA_	Alignment		98.7	21	**PDB header:**recombination **Chain:** A: **PDB Molecule:**site-specific recombinase, resolvase family protein; **PDBTitle:** crystal structure of a resolvase family site-specific recombinase from2 streptococcus pneumoniae
13	c3bvpB_	Alignment		98.7	26	**PDB header:**recombination **Chain:** B: **PDB Molecule:**tp901-1 integrase; **PDBTitle:** crystal structure of the n-terminal catalytic domain of tp901-12 integrase
14	d2obba1	Alignment		85.3	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
15	c3trjC_	Alignment		82.2	20	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
16	c3shoA_	Alignment		78.1	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
17	d2c71a1	Alignment		77.1	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
18	d2cc0a1	Alignment		74.9	11	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
19	c2x3yA_	Alignment		72.6	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
20	d1x92a_	Alignment		72.5	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
21	d2c1ia1	Alignment	not modelled	70.1	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
22	d1x94a_	Alignment	not modelled	69.6	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
23	c2xhzC_	Alignment	not modelled	69.1	5	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
24	c2yvaB_	Alignment	not modelled	67.9	22	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
25	d1jeoa_	Alignment	not modelled	63.7	8	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
26	d1tk9a_	Alignment	not modelled	58.8	10	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
27	c1w17A_	Alignment	not modelled	56.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
28	c3fxaA_	Alignment	not modelled	55.9	10	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution

29	d1vima_	Alignment	not modelled	55.7	12	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
30	d1m3sa_	Alignment	not modelled	55.4	10	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
31	d1ny1a_	Alignment	not modelled	54.9	13	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
32	d2p8ta2	Alignment	not modelled	48.8	10	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**PH0730 C-terminal domain-like
33	c3etnD_	Alignment	not modelled	47.4	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative phosphosugar isomerase involved in capsule **PDBTitle:** crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
34	c2c1iA_	Alignment	not modelled	47.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase; **PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
35	d1j8fa_	Alignment	not modelled	40.1	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
36	c2vyoA_	Alignment	not modelled	36.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitooligosaccharide deacetylase; **PDBTitle:** chitin deacetylase family member from encephalitozoon2 cuniculi
37	c3cvjB_	Alignment	not modelled	35.5	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
38	c1q14A_	Alignment	not modelled	35.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
39	c2puwA_	Alignment	not modelled	32.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isomerase domain of glutamine-fructose-6-phosphate **PDBTitle:** the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
40	d2jfga2	Alignment	not modelled	30.4	16	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
41	d2j13a1	Alignment	not modelled	28.1	24	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
42	d2nlya1	Alignment	not modelled	27.8	14	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
43	c3pryA_	Alignment	not modelled	26.9	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp 90-beta; **PDBTitle:** crystal structure of the middle domain of human hsp90-beta refined at2 2.3 a resolution
44	c3glsC_	Alignment	not modelled	26.5	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
45	d1q1aa_	Alignment	not modelled	24.5	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
46	c2hjhB_	Alignment	not modelled	22.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
47	c2w3zA_	Alignment	not modelled	22.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
48	c2zj3A_	Alignment	not modelled	19.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
49	c3pkiF_	Alignment	not modelled	17.7	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
50	c3k35D_	Alignment	not modelled	15.3	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
51	c1gqqA_	Alignment	not modelled	14.5	13	**PDB header:**cell wall biosynthesis **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
52	d1xdpa3	Alignment	not modelled	13.9	12	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
53	c2odkD_	Alignment	not modelled	13.6	5	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
54	c2gq0B_	Alignment	not modelled	13.1	20	**PDB header:**chaperone, hydrolase **Chain:** B: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of the middle domain of htpg, the e. coli2 hsp90
						PDB header:hydrolase

55	c3kw0D_	Alignment	not modelled	12.7	13	**Chain:** D: **PDB Molecule:**cysteine peptidase; **PDBTitle:** crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
56	c3ipzA_	Alignment	not modelled	12.5	14	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
57	d1usua_	Alignment	not modelled	12.5	12	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Hsp90 middle domain
58	d1x52a1	Alignment	not modelled	12.3	25	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
59	d1ofla_	Alignment	not modelled	11.7	17	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Chondroitinase B
60	c3efhB_	Alignment	not modelled	11.5	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
61	d1p3da2	Alignment	not modelled	11.5	14	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
62	c3e7nB_	Alignment	not modelled	11.4	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**d-ribose high-affinity transport system; **PDBTitle:** crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
63	c2a3nA_	Alignment	not modelled	11.4	12	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative glucosamine-fructose-6-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
64	c1hk7A_	Alignment	not modelled	11.3	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp82; **PDBTitle:** middle domain of hsp90
65	c3mvnA_	Alignment	not modelled	10.9	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamayl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamayl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
66	c2o1wB_	Alignment	not modelled	10.7	14	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
67	c1dbgA_	Alignment	not modelled	10.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase b; **PDBTitle:** crystal structure of chondroitinase b
68	d1x9aa_	Alignment	not modelled	10.1	14	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrH-like
69	c2p5dA_	Alignment	not modelled	10.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0310 protein mjecl36; **PDBTitle:** crystal structure of mjecl36 from methanocaldococcus2 jannaschii dsm 2661
70	d1ps9a1	Alignment	not modelled	9.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
71	d1ogda_	Alignment	not modelled	9.6	15	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
72	c3p13B_	Alignment	not modelled	9.6	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribose pyranase; **PDBTitle:** complex structure of d-ribose pyranase sa240 with d-ribose
73	c2o14A_	Alignment	not modelled	9.5	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yxim; **PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595
74	d1e8ca2	Alignment	not modelled	9.3	17	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
75	c3hs2H_	Alignment	not modelled	8.9	19	**PDB header:**antitoxin **Chain:** H: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
76	d1x9ia_	Alignment	not modelled	8.7	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
77	c1dkrB_	Alignment	not modelled	8.7	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
78	c3hryA_	Alignment	not modelled	8.6	19	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**prevent host death protein; **PDBTitle:** crystal structure of phd in a trigonal space group and partially2 disordered
79	d2iw0a1	Alignment	not modelled	8.4	11	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase

80	d2odka1	Alignment	not modelled	8.0	5	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
81	d1q45a_	Alignment	not modelled	7.9	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
82	d2gbsa1	Alignment	not modelled	7.9	14	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
83	c2wztA_	Alignment	not modelled	7.8	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of a mycobacterium aldo-keto reductase in2 its apo and liganded form
84	d2hd9a1	Alignment	not modelled	7.6	18	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
85	d1vjia_	Alignment	not modelled	7.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
86	d2ob5a1	Alignment	not modelled	7.4	15	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
87	d1zcea1	Alignment	not modelled	7.1	14	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
88	d1hw6a_	Alignment	not modelled	7.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
89	c1xkmC_	Alignment	not modelled	7.0	24	**PDB header:**antibiotic **Chain:** C: **PDB Molecule:**distinctin chain a; **PDBTitle:** nmr structure of antimicrobial peptide distinctin in water
90	c1pgjA_	Alignment	not modelled	7.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
91	c1y6zA_	Alignment	not modelled	6.9	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**heat shock protein, putative; **PDBTitle:** middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
92	c3hn7A_	Alignment	not modelled	6.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
93	c3mvkA_	Alignment	not modelled	6.9	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein fucu; **PDBTitle:** the crystal structure of fucu from bifidobacterium longum to 1.65a
94	c3iz6V_	Alignment	not modelled	6.8	20	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**40s ribosomal protein s25 (s25e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
95	c2o8rA_	Alignment	not modelled	6.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
96	c1xkmA_	Alignment	not modelled	6.5	29	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**distinctin chain a; **PDBTitle:** nmr structure of antimicrobial peptide distinctin in water
97	d1a6fa_	Alignment	not modelled	6.5	7	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**RNase P protein
98	c3hjcA_	Alignment	not modelled	6.3	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 83-1; **PDBTitle:** crystal structure of the carboxy-terminal domain of hsp90 from2 leishmania major, lmjf33.0312
99	c2iw0A_	Alignment	not modelled	6.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum