Phyre2

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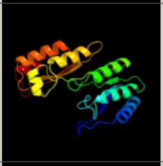
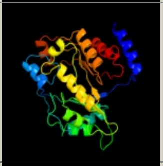
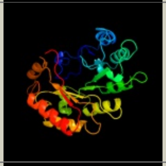
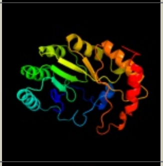
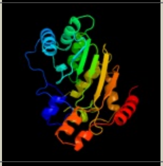
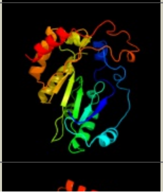
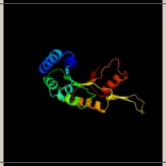
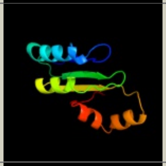
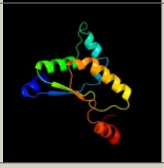
Description	P0ADW6
Date	Thu Jan 5 11:21:59 GMT 2012
Unique Job ID	44467d66f96a0fe1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1olta_	Alignment		100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
2	c3cixA_	Alignment		100.0	15	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
3	c3t7vA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
4	c2qgqF_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**protein tm_1862; **PDBTitle:** crystal structure of tm_1862 from thermotoga maritima.2 northeast structural genomics consortium target vr77
5	c1r30A_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
6	d1r30a_	Alignment		99.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase
7	c3rfaA_	Alignment		99.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase n; **PDBTitle:** x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
8	d1tv8a_	Alignment		99.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**MoCo biosynthesis proteins
9	c2a5hC_	Alignment		99.5	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-lysine 2,3-aminomutase; **PDBTitle:** 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
10	c2yx0A_	Alignment		99.3	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1
11	c3c8fA_	Alignment		99.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate formate-lyase 1-activating enzyme; **PDBTitle:** 4fe-4s-pyruvate formate-lyase activating enzyme with2 partially disordered adomet

12	c3canA_	Alignment		96.8	8	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
13	c2z2uA_	Alignment		96.5	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**upf0026 protein mj0257; **PDBTitle:** crystal structure of archaeal tyw1
14	c3bleA_	Alignment		95.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
15	c3ivuB_	Alignment		92.3	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
16	c3gnoA_	Alignment		92.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**os03g0212800 protein; **PDBTitle:** crystal structure of a rice os3bglu6 beta-glucosidase
17	c1x7fA_	Alignment		91.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein
18	c3lerA_	Alignment		90.7	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
19	d1x7fa2	Alignment		90.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
20	c2rgmA_	Alignment		89.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** rice bglu1 beta-glucosidase, a plant exoglucanase/beta-glucosidase
21	c1jibA_	Alignment	not modelled	89.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**neopullulanase; **PDBTitle:** complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.
22	c2ftpA_	Alignment	not modelled	88.9	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
23	c3s5oA_	Alignment	not modelled	88.7	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
24	d1vffa1	Alignment	not modelled	88.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
25	c2ehhE_	Alignment	not modelled	88.4	14	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
26	d1xxxa1	Alignment	not modelled	88.2	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
27	d1h3ga3	Alignment	not modelled	88.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
28	c2r94B_	Alignment	not modelled	87.9	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax

29	d1yx1a1	Alignment	not modelled	87.9	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
30	d1wzla3	Alignment	not modelled	87.8	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
31	c2zoxA_	Alignment	not modelled	87.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic beta-glucosidase; **PDBTitle:** crystal structure of the covalent intermediate of human cytosolic2 beta-glucosidase
32	c2yxgD_	Alignment	not modelled	87.4	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
33	c3ahxC_	Alignment	not modelled	87.1	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** crystal structure of beta-glucosidase a from bacterium clostridium2 cellulovorans
34	d2j78a1	Alignment	not modelled	87.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
35	c3bi8A_	Alignment	not modelled	86.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
36	d1cgta4	Alignment	not modelled	86.6	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
37	d1h4pa_	Alignment	not modelled	86.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
38	c3pueA_	Alignment	not modelled	86.5	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
39	c1qhoA_	Alignment	not modelled	86.5	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
40	d1oy0a_	Alignment	not modelled	86.2	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
41	c3fiyA_	Alignment	not modelled	86.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of bglb
42	c1bagA_	Alignment	not modelled	85.9	20	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
43	c1ehaA_	Alignment	not modelled	85.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
44	c3czkA_	Alignment	not modelled	85.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
45	d1gvia3	Alignment	not modelled	85.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
46	d2bhua3	Alignment	not modelled	84.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
47	c2j75A_	Alignment	not modelled	84.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase a; **PDBTitle:** beta-glucosidase from thermotoga maritima in complex with2 noeuromycin
48	c3cqkB_	Alignment	not modelled	84.7	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-ribulose-5-phosphate 3-epimerase ulae; **PDBTitle:** crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
49	d1i60a_	Alignment	not modelled	84.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
50	c3lciA_	Alignment	not modelled	84.4	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
51	d1avaa2	Alignment	not modelled	84.4	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
52	c3eb2A_	Alignment	not modelled	84.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
53	d1hl2a_	Alignment	not modelled	84.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
54	d1j0ha3	Alignment	not modelled	84.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
55	d1e43a2	Alignment	not modelled	84.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

56	d1gnxa_	Alignment	not modelled	84.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
57	c2dgaA_	Alignment	not modelled	84.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of hexameric beta-glucosidase in wheat
58	c1nvmG_	Alignment	not modelled	84.0	12	**PDB header:**lyase/oxidoreductase **Chain:** G: **PDB Molecule:**4-hydroxy-2-oxovalerate aldolase; **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
59	d1ea9c3	Alignment	not modelled	83.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
60	d1gcya2	Alignment	not modelled	83.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
61	d1e4ia_	Alignment	not modelled	83.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
62	d1xkya1	Alignment	not modelled	83.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
63	c1jdaA_	Alignment	not modelled	83.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
64	c1jd7A_	Alignment	not modelled	82.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
65	c3fluD_	Alignment	not modelled	82.8	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
66	d1o5ka_	Alignment	not modelled	82.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
67	d1ua7a2	Alignment	not modelled	82.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
68	c1mwoA_	Alignment	not modelled	82.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase; **PDBTitle:** crystal structure analysis of the hyperthermostable2 pyrocoocus woesei alpha-amylase
69	d1qhoa4	Alignment	not modelled	82.1	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
70	c1lwhA_	Alignment	not modelled	82.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
71	d2gjpa2	Alignment	not modelled	81.9	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
72	d1ud2a2	Alignment	not modelled	81.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	c2rfgB_	Alignment	not modelled	81.7	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
74	d1g5aa2	Alignment	not modelled	81.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
75	d2d3na2	Alignment	not modelled	81.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
76	c2jf7B_	Alignment	not modelled	81.5	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**strictosidine-o-beta-d-glucosidase; **PDBTitle:** structure of strictosidine glucosidase
77	c2v9dB_	Alignment	not modelled	81.4	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
78	d1ht6a2	Alignment	not modelled	81.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
79	c3si9B_	Alignment	not modelled	81.4	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
80	c3k2gA_	Alignment		81.2	17	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
81	d1ob0a2	Alignment	not modelled	81.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

82	c2vc6A_	Alignment	not modelled	81.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
83	c2ou4C_	Alignment	not modelled	81.1	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
84	c3n2xB_	Alignment	not modelled	81.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
85	d2a6na1	Alignment	not modelled	81.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
86	c2nuxB_	Alignment	not modelled	81.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
87	c1jgiA_	Alignment	not modelled	80.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of the active site mutant glu328gln of2 amylosucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose
88	d1w3ia_	Alignment	not modelled	80.7	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
89	c3bdkB_	Alignment	not modelled	80.3	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
90	d1vjza_	Alignment	not modelled	80.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
91	d1g94a2	Alignment	not modelled	80.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
92	c3noeA_	Alignment	not modelled	79.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
93	c1e40A_	Alignment	not modelled	79.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a
94	c3cprB_	Alignment	not modelled	79.1	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
95	c1ud8A_	Alignment	not modelled	79.0	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
96	c2hk1D_	Alignment	not modelled	78.7	12	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**d-psicose 3-epimerase; **PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
97	d1mxga2	Alignment	not modelled	78.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
98	c3navB_	Alignment	not modelled	78.3	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
99	c3daqB_	Alignment	not modelled	78.2	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
100	c3dhuC_	Alignment	not modelled	78.2	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
101	c3fkkA_	Alignment	not modelled	77.8	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
102	c1wpcA_	Alignment	not modelled	77.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltohexaosidase; **PDBTitle:** crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose
103	c2wcsA_	Alignment	not modelled	77.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
104	c1hvxA_	Alignment	not modelled	77.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** bacillus stearothermophilus alpha-amylase
105	c3aicC_	Alignment	not modelled	77.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucosyltransferase-si; **PDBTitle:** crystal structure of glucansucrase from streptococcus mutans
106	d1lwha2	Alignment	not modelled	76.7	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
107	c2aaaA_	Alignment	not modelled	76.6	12	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** calcium binding in alpha-amylases: an x-ray diffraction2

						study at 2.1 angstroms resolution of two enzymes from3 aspergillus
108	c3na8A_	Alignment	not modelled	76.4	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
109	c2e3zB_	Alignment	not modelled	76.1	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of intracellular family 1 beta-2 glucosidase bgl1a from the basidiomycete phanerochaete3 chrysosporium in substrate-free form
110	d1ug6a_	Alignment	not modelled	75.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
111	d1v08a_	Alignment	not modelled	75.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
112	c3dx5A_	Alignment	not modelled	75.6	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
113	c3ptkB_	Alignment	not modelled	75.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase os4bglu12; **PDBTitle:** the crystal structure of rice (oryza sativa l.) os4bglu12
114	c3ewbX_	Alignment	not modelled	75.1	12	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
115	c3g0sA_	Alignment	not modelled	74.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
116	c2dh3A_	Alignment	not modelled	74.6	17	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
117	d1hvxa2	Alignment	not modelled	74.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
118	c1gviA_	Alignment	not modelled	74.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd
119	c2x7vA_	Alignment	not modelled	74.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable endonuclease 4; **PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
120	d2guya2	Alignment	not modelled	74.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain