Phyre2

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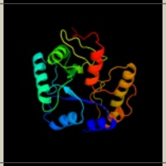
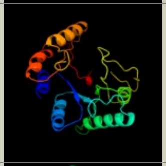
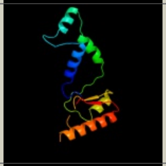
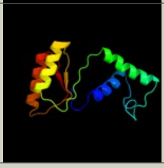
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qv5A_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
2	d2nlya1	Alignment		100.0	30	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
3	c2vyoA_	Alignment		98.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitooligosaccharide deacetylase; **PDBTitle:** chitin deacetylase family member from encephalitozoon2 cuniculi
4	c2c1iA_	Alignment		98.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase; **PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
5	d2iw0a1	Alignment		98.2	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
6	c1w17A_	Alignment		98.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
7	c2iw0A_	Alignment		98.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
8	d2c1ia1	Alignment		98.1	20	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
9	d1ny1a_	Alignment		97.9	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
10	d2j13a1	Alignment		97.9	13	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
11	c2w3zA_	Alignment		97.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase

12	d2c71a1	Alignment		97.8	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
13	d2cc0a1	Alignment		97.8	14	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
14	c3rxzA_	Alignment		97.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**polysaccharide deacetylase; **PDBTitle:** crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
15	d2i5ia1	Alignment		96.8	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**YdjC-like
16	c3qbuD_	Alignment		96.6	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of putative peptidoglyacn deactelyase (hp0310) from2 helicobacter pylori
17	c3s6oD_	Alignment		96.3	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**polysaccharide deacetylase family protein; **PDBTitle:** crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
18	d1z7aa1	Alignment		95.9	10	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**PA1517-like
19	c2q6tB_	Alignment		88.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
20	c2vyeA_	Alignment		83.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
21	d1v6ta_	Alignment	not modelled	80.7	20	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
22	c2dt8A_	Alignment	not modelled	79.8	12	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** fatty acid binding of a degv family protein from thermus thermophilus
23	c3qjaA_	Alignment	not modelled	78.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
24	c2recB_	Alignment	not modelled	77.9	9	**PDB header:**helicase **PDB COMPND:**
25	d3dhwc1	Alignment	not modelled	77.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
26	c3lupA_	Alignment	not modelled	77.2	10	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
27	d1mgpa_	Alignment	not modelled	74.5	7	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
28	c1mgpA_	Alignment	not modelled	74.5	7	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm841; **PDBTitle:** hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
						PDB header:transcription

29	c2q5cA_	Alignment	not modelled	72.1	16	**Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
30	c2e67D_	Alignment	not modelled	71.9	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein tthb029; **PDBTitle:** crystal structure of the hypothetical protein tthb029 from thermus2 thermophilus hb8
31	c3ktsA_	Alignment	not modelled	69.8	17	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein; **PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
32	c2pjuD_	Alignment	not modelled	67.8	22	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
33	c3uoaB_	Alignment	not modelled	67.3	21	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**mucosa-associated lymphoid tissue lymphoma translocation **PDBTitle:** crystal structure of the malt1 paracaspase (p21 form)
34	d1jz8a5	Alignment	not modelled	66.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
35	d2pjua1	Alignment	not modelled	63.6	20	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
36	d2gwga1	Alignment	not modelled	61.2	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
37	d1cr2a_	Alignment	not modelled	60.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
38	c3nyiA_	Alignment	not modelled	59.0	18	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fat acid-binding protein; **PDBTitle:** the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
39	d2f6ka1	Alignment	not modelled	58.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
40	c2c3zA_	Alignment	not modelled	58.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
41	d1pzxa_	Alignment	not modelled	57.4	13	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
42	c3bgwD_	Alignment	not modelled	57.1	13	**PDB header:**replication **Chain:** D: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase
43	d1i4na_	Alignment	not modelled	56.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
44	c2e21A_	Alignment	not modelled	53.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
45	c2g7zB_	Alignment	not modelled	53.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein spy1493; **PDBTitle:** conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
46	d1a53a_	Alignment	not modelled	53.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
47	c1vlvA_	Alignment	not modelled	51.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
48	c3cixA_	Alignment		50.8	16	**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
49	d1vjia_	Alignment	not modelled	49.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
50	d1piia2	Alignment	not modelled	48.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
51	c3ij6A_	Alignment	not modelled	48.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase; **PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from lactobacillus acidophilus
52	c3fdiA_	Alignment	not modelled	47.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein from eubacterium2 ventriosum atcc 27560.
53	c2fdsA_	Alignment	not modelled	46.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**orotidine-monophosphate-decarboxylase; **PDBTitle:** crystal structure of plasmodium berghei orotidine 5'-2 monophosphate decarboxylase (ortholog of plasmodium3

						falciparum pf10_0225)
54	d2fdsa1	Alignment	not modelled	46.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
55	c3uj2C_	Alignment	not modelled	45.5	21	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** crystal structure of an enolase from anaerostipes caccae (efi target2 efi-502054) with bound mg and sulfate
56	c3hdtB_	Alignment	not modelled	45.4	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase from clostridium symbiosum atcc2 14940
57	c3fysA_	Alignment	not modelled	45.4	13	**PDB header:**fatty acid-binding protein **Chain:** A: **PDB Molecule:**protein degv; **PDBTitle:** crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis
58	d1ni5a1	Alignment	not modelled	45.2	8	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
59	d2dfaa1	Alignment	not modelled	45.1	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
60	c2aamA_	Alignment	not modelled	43.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein tm1410; **PDBTitle:** crystal structure of a putative glycosidase (tm1410) from thermotoga2 maritima at 2.20 a resolution
61	d2aama1	Alignment	not modelled	43.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**TM1410-like
62	c3c8fA_	Alignment	not modelled	43.4	8	**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
63	c3r89A_	Alignment	not modelled	42.3	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548
64	c3cmgA_	Alignment	not modelled	41.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
65	c2xt6B_	Alignment	not modelled	40.6	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
66	c2k6xA_	Alignment	not modelled	39.3	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
67	c3ngkA_	Alignment	not modelled	39.2	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**propanediol utilization protein pdua; **PDBTitle:** pdua from salmonella enterica typhimurium
68	d2ffca1	Alignment	not modelled	38.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
69	c3lpgA_	Alignment	not modelled	38.8	10	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** structure of e. coli beta-glucuronidase bound with a novel, potent2 inhibitor 3-(2-fluorophenyl)-1-(2-hydroxyethyl)-1-((6-methyl-2-oxo-1,3 2-dihydroquinolin-3-yl)methyl)urea
70	d1vc4a_	Alignment	not modelled	38.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
71	d2ihta3	Alignment	not modelled	38.6	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
72	c3sggA_	Alignment	not modelled	36.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical hydrolase; **PDBTitle:** crystal structure of a hypothetical hydrolase (bt_2193) from2 bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
73	d2q02a1	Alignment	not modelled	35.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
74	d1wy5a1	Alignment	not modelled	35.5	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
75	d2nu7b1	Alignment	not modelled	35.4	13	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
76	c2vf7B_	Alignment	not modelled	35.4	15	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
77	c3otrC_	Alignment	not modelled	35.4	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase; **PDBTitle:** 2.75 angstrom crystal structure of enolase 1 from toxoplasma gondii
78	d2ffea1	Alignment	not modelled	35.3	11	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
79	d1o98a1	Alignment	not modelled	34.6	23	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent

79	d1o98a1	Alignment	not modelled	34.6	23	phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
80	d1j5ta_	Alignment	not modelled	34.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
81	d1yq2a5	Alignment	not modelled	34.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
82	d2ptza1	Alignment	not modelled	33.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
83	d1xi9a_	Alignment	not modelled	33.2	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
84	c2pa6A_	Alignment	not modelled	32.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of mj0232 from methanococcus jannaschii
85	c2yciX_	Alignment	not modelled	32.8	19	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
86	d1nlfa_	Alignment	not modelled	32.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
87	c2ztsB_	Alignment	not modelled	32.4	12	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein ph0186; **PDBTitle:** crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
88	d2g0wa1	Alignment	not modelled	31.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
89	d2akza1	Alignment	not modelled	31.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
90	c3gkaB_	Alignment	not modelled	30.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
91	d1v43a3	Alignment	not modelled	30.0	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
92	c1xp8A_	Alignment	not modelled	28.6	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
93	c3qocD_	Alignment	not modelled	27.0	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative metallopeptidase; **PDBTitle:** crystal structure of n-terminal domain (creatinase/prolidase like2 domain) of putative metallopeptidase from corynebacterium diphtheriae
94	d1m5wa_	Alignment	not modelled	26.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
95	c3tqpA_	Alignment	not modelled	26.8	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** structure of an enolase (eno) from coxiella burnetii
96	d1ru8a_	Alignment	not modelled	26.7	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
97	c3i6pF_	Alignment	not modelled	26.7	22	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**ethanolamine utilization protein eutm; **PDBTitle:** ethanolamine utilization microcompartment shell subunit, eutm
98	c1l8pC_	Alignment	not modelled	26.0	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** mg-phosphonoacetohydroxamate complex of s39a yeast enolase 1
99	d1iyxa1	Alignment	not modelled	26.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
100	c3ox4D_	Alignment	not modelled	25.7	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
101	d2al1a1	Alignment	not modelled	25.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
102	d1oxxk2	Alignment	not modelled	25.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
103	c1knwA_	Alignment	not modelled	25.3	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase
104	c3obaA_	Alignment	not modelled	25.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis
105	d1vpla_	Alignment	not modelled	25.2	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family:ABC transporter ATPase domain-like
106	c3bijC_	Alignment	not modelled	25.0	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein gsu0716; **PDBTitle:** crystal structure of protein gsu0716 from geobacter2 sulfurreducens. northeast structural genomics target gsr13
107	c3pl5A_	Alignment	not modelled	24.7	10	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** fatty acid binding protein
108	c1o98A_	Alignment	not modelled	23.2	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
109	c3eglC_	Alignment	not modelled	23.2	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of degv family protein cg2579 from corynebacterium2 glutamicum
110	c2we7A_	Alignment	not modelled	23.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
111	c2fymA_	Alignment	not modelled	22.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of e. coli enolase complexed with the2 minimal binding segment of rnase e.
112	c1q57G_	Alignment	not modelled	22.7	15	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
113	c3ke8A_	Alignment	not modelled	22.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
114	d1efvb_	Alignment	not modelled	21.9	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
115	d1n0wa_	Alignment	not modelled	21.3	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
116	c1w8gA_	Alignment	not modelled	21.2	12	**PDB header:**plp-binding protein **Chain:** A: **PDB Molecule:**hypothetical upf0001 protein yggs; **PDBTitle:** crystal structure of e. coli k-12 yggs
117	d1chma1	Alignment	not modelled	20.9	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
118	d1b0ua_	Alignment	not modelled	20.5	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
119	c3mv14_	Alignment	not modelled	20.5	17	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium
120	c3ms5A_	Alignment	not modelled	20.4	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gamma-butyrobetaine dioxygenase; **PDBTitle:** crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)