Phyre^2

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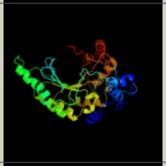
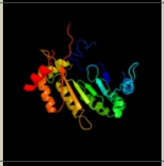
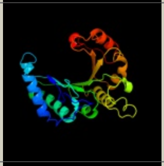
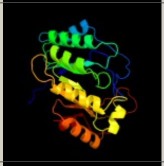
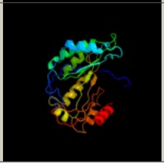
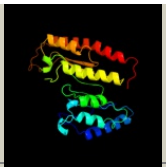
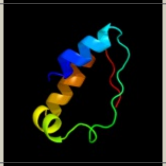
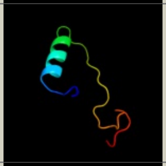
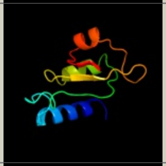
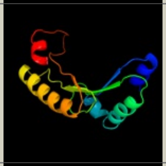
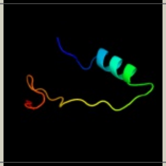
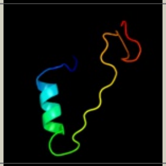
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rfaA_	Alignment		100.0	100	**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
2	c2a5hC_	Alignment		100.0	17	**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).
3	c2yx0A_	Alignment		99.9	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1
4	c3c8fA_	Alignment		99.9	20	**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
5	c3canA_	Alignment		99.8	19	**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
6	d1tv8a_	Alignment		99.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**MoCo biosynthesis proteins
7	c1r30A_	Alignment		99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
8	d1r30a_	Alignment		99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase
9	c2z2uA_	Alignment		99.7	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**upf0026 protein mj0257; **PDBTitle:** crystal structure of archaeal tyw1
10	c3t7vA_	Alignment		99.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
11	c3cixA_	Alignment		99.7	14	**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

12	c2qgqF_	Alignment		99.6	12	**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
13	d1olta_	Alignment		99.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
14	c3k1dA_	Alignment		81.5	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**1,4-alpha-glucan-branching enzyme; **PDBTitle:** crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
15	d1tz7a1	Alignment		77.8	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
16	c3fa4D_	Alignment		76.9	24	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
17	d1rvga_	Alignment		76.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
18	d1x1na1	Alignment		71.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
19	d1eswa_	Alignment		67.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
20	c2zq0B_	Alignment		65.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb); **PDBTitle:** crystal structure of susb complexed with acarbose
21	c3eooL_	Alignment	not modelled	59.5	15	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
22	c3amkA_	Alignment	not modelled	55.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
23	c3lyeA_	Alignment	not modelled	55.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
24	d3elga1	Alignment	not modelled	55.2	9	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
25	c2x4bA_	Alignment	not modelled	54.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**limit dextrinase; **PDBTitle:** barley limit dextrinase in complex with beta-cyclodextrin
26	c1zcoA_	Alignment	not modelled	54.7	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase; **PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
27	c1vs1B_	Alignment	not modelled	54.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-deoxy-7-phosphoheptulonate synthase; **PDBTitle:** crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
28	d1nfpa_	Alignment	not modelled	53.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)

29	c2dh3A_	Alignment	not modelled	51.8	12	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
30	d2duya1	Alignment	not modelled	50.2	8	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
31	c3lotC_	Alignment	not modelled	48.1	15	**PDB header:**structure genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
32	c3ktcB_	Alignment	not modelled	46.2	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
33	c3amlA_	Alignment	not modelled	45.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
34	c1m7xC_	Alignment	not modelled	45.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
35	c3blpX_	Alignment	not modelled	44.4	17	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
36	d2bhua3	Alignment	not modelled	44.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
37	d1a9xb2	Alignment	not modelled	41.9	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
38	d2aq0a1	Alignment	not modelled	41.6	18	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
39	c1keeH_	Alignment	not modelled	41.2	25	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
40	c3lfjB_	Alignment	not modelled	40.9	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, mannose/fructose/n- **PDBTitle:** crystal structure of manxb from thermoanaerobacter tengcongensis
41	c2l69A_	Alignment	not modelled	40.4	19	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
42	d1hl2a_	Alignment	not modelled	39.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
43	c3c6cA_	Alignment	not modelled	39.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
44	c3m07A_	Alignment	not modelled	38.9	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative alpha amylase; **PDBTitle:** 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhimurium.
45	c1ehaA_	Alignment	not modelled	38.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
46	d1wkya2	Alignment	not modelled	38.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
47	c3no5C_	Alignment	not modelled	37.5	14	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
48	c2v9dB_	Alignment	not modelled	36.6	17	**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
49	c3noeA_	Alignment	not modelled	36.6	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
50	c3e02A_	Alignment	not modelled	36.2	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849; **PDBTitle:** crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
51	d1muma_	Alignment	not modelled	35.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
52	d1cmwa2	Alignment	not modelled	35.2	13	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
53	c3jugA_	Alignment	not modelled	35.0	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-mannanase; **PDBTitle:** crystal structure of endo-beta-1,4-mannanase from the

						alkaliphilic2 bacillus sp. n16-5
54	c3e96B_	Alignment	not modelled	34.6	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
55	c1lwhA_	Alignment	not modelled	34.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
56	c3efyB_	Alignment	not modelled	34.0	23	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cif (cell cycle inhibiting factor); **PDBTitle:** structure of the cyclomodulin cif from pathogenic2 escherichia coli
57	c3fkkA_	Alignment	not modelled	33.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
58	d1lwha2	Alignment	not modelled	33.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
59	c3k8kB_	Alignment	not modelled	33.7	23	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg
60	c1x60A_	Alignment	not modelled	33.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine **PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
61	c1cmwA_	Alignment	not modelled	33.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
62	c3b4uB_	Alignment	not modelled	33.2	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
63	d1lvaa3	Alignment	not modelled	32.9	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
64	d1gvfa_	Alignment	not modelled	32.7	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
65	c2fhfA_	Alignment	not modelled	32.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
66	c3dx5A_	Alignment	not modelled	32.1	8	**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
67	d1sgga_	Alignment	not modelled	32.0	7	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
68	c2dl0A_	Alignment	not modelled	31.9	2	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sam-domain of the sam and sh32 domain containing protein 1
69	c3a47A_	Alignment	not modelled	31.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
70	c3dz1A_	Alignment	not modelled	31.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
71	d3bzka1	Alignment	not modelled	31.3	6	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
72	d1gxja_	Alignment	not modelled	31.0	19	**Fold:**Smc hinge domain **Superfamily:**Smc hinge domain **Family:**Smc hinge domain
73	d1m1nb_	Alignment	not modelled	30.9	7	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
74	d2dvta1	Alignment	not modelled	30.6	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
75	d2a1ja1	Alignment	not modelled	30.5	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
76	c3f46A_	Alignment	not modelled	30.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydromethanopterin hydrogenase; **PDBTitle:** the crystal structure of c176a mutated [fe]-hydrogenase (hmd)2 holoenzyme from methanocaldococcus jannaschii
77	c3n2xB_	Alignment	not modelled	30.2	17	**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
78	c1zjaB_	Alignment	not modelled	30.1	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
						Fold:TIM beta/alpha-barrel

79	d1m7xa3	Alignment	not modelled	30.0	21	**Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
80	c3t4cD_	Alignment	not modelled	29.2	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 1; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
81	c1uokA_	Alignment	not modelled	29.0	17	**PDB header:**glucosidase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of b. cereus oligo-1,6-glucosidase
82	d1avaa2	Alignment	not modelled	28.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
83	c1xyzA_	Alignment	not modelled	28.7	10	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**1,4-beta-d-xylan-xylanohydrolase; **PDBTitle:** a common protein fold and similar active site in two2 distinct families of beta-glycanases
84	d1xyza_	Alignment	not modelled	28.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
85	d2qswa1	Alignment	not modelled	28.5	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
86	c3pm6B_	Alignment	not modelled	28.4	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
87	c1qysA_	Alignment	not modelled	28.3	23	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
88	d1ujqa_	Alignment	not modelled	27.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
89	c1zrjA_	Alignment	not modelled	27.0	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**e1b-55kda-associated protein 5 isoform c; **PDBTitle:** solution structure of the sap domain of human e1b-55kda-2 associated protein 5 isoform c
90	c3c52B_	Alignment	not modelled	26.9	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
91	c3hilB_	Alignment	not modelled	26.8	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** sam domain of human ephrin type-a receptor 1 (epha1)
92	c2jvfA_	Alignment	not modelled	26.7	28	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
93	d1wg8a1	Alignment	not modelled	26.4	18	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
94	c2by0A_	Alignment	not modelled	26.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
95	d1thta_	Alignment	not modelled	26.3	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
96	c3elfA_	Alignment	not modelled	26.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** structural characterization of tetrameric mycobacterium tuberculosis2 fructose 1,6-bisphosphate aldolase - substrate binding and catalysis3 mechanism of a class iia bacterial aldolase
97	c1bf2A_	Alignment	not modelled	26.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
98	c2fmmE_	Alignment	not modelled	26.2	18	**PDB header:**transcription **Chain:** E: **PDB Molecule:**protein emsy; **PDBTitle:** crystal structure of emsy-hp1 complex
99	d2b0ja2	Alignment	not modelled	26.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
100	d1gjwa2	Alignment	not modelled	25.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
101	c2k4pA_	Alignment	not modelled	24.7	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**phosphatidylinositol-3,4,5-trisphosphate 5- **PDBTitle:** solution structure of ship2-sam
102	d1eh9a3	Alignment	not modelled	24.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
103	c3p3vB_	Alignment	not modelled	24.4	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts system, n-acetylgalactosamine-specific iib component; **PDBTitle:** crystal structure of a pts dependent n-acetyl-galactosamine-iib2 component (agav, spy_0631) from streptococcus pyogenes at 1.65 a3 resolution
104	d2do1a1	Alignment	not modelled	24.4	14	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain

						Family:SAP domain
105	c2wanA_	Alignment	not modelled	24.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
106	c1bagA_	Alignment	not modelled	24.3	19	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
107	c3l51B_	Alignment	not modelled	24.3	16	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**structural maintenance of chromosomes protein 4; **PDBTitle:** crystal structure of the mouse condensin hinge domain
108	c3h5dD_	Alignment	not modelled	24.3	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
109	d2fmme1	Alignment	not modelled	24.1	18	**Fold:**ENT-like **Superfamily:**ENT-like **Family:**Emsy N terminal (ENT) domain-like
110	d2jgra1	Alignment	not modelled	23.6	24	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
111	c1s5lu_	Alignment	not modelled	23.0	20	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
112	d2fmpa1	Alignment	not modelled	23.0	13	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
113	c2zdsB_	Alignment	not modelled	22.9	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
114	c2rfgB_	Alignment	not modelled	22.8	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
115	c3cuxA_	Alignment	not modelled	22.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
116	d1qh8b_	Alignment	not modelled	22.6	5	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
117	d1iv0a_	Alignment	not modelled	22.5	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
118	d1o5ka_	Alignment	not modelled	22.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
119	d1pcaa1	Alignment	not modelled	22.1	18	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
120	c3nwcA_	Alignment	not modelled	21.9	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**smc protein; **PDBTitle:** crystal structure of the pyrococcus furiosus smc protein hinge domain