































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r9da_	 Alignment		100.0	17	Fold: PFL-like glycyl radical enzymes Superfamily: PFL-like glycyl radical enzymes Family: PFL-like
2	c2y8nC_	 Alignment		100.0	16	PDB header: lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate decarboxylase large subunit; PDBTitle: crystal structure of glycyl radical enzyme
3	c2f3oB_	 Alignment		100.0	17	PDB header: unknown function Chain: B: PDB Molecule: pyruvate formate-lyase 2; PDBTitle: crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
4	d1h16a_	 Alignment		100.0	18	Fold: PFL-like glycyl radical enzymes Superfamily: PFL-like glycyl radical enzymes Family: PFL-like
5	c1hk8A_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dntp
6	d1hk8a_	 Alignment		100.0	18	Fold: PFL-like glycyl radical enzymes Superfamily: PFL-like glycyl radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
7	d1qhma_	 Alignment		100.0	16	Fold: PFL-like glycyl radical enzymes Superfamily: PFL-like glycyl radical enzymes Family: PFL-like
8	c2wghA_	 Alignment		97.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large PDBTitle: human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
9	c2cvuA_	 Alignment		97.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large chain PDBTitle: structures of yeast ribonucleotide reductase i
10	c3hnfA_	 Alignment		97.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large subunit; PDBTitle: crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
11	c1xjeA_	 Alignment		96.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleotide reductase, b12-dependent; PDBTitle: structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dntp-gdp complex

12	c3r1rB_	Alignment		96.0	14	PDB header: complex (oxidoreductase/peptide) Chain: B: PDB Molecule: ribonucleotide reductase r1 protein; PDBTitle: ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
13	c1pemA_	Alignment		95.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase 2 alpha PDBTitle: ribonucleotide reductase protein r1e from salmonella2 typhimurium
14	d1peqa2	Alignment		95.3	14	Fold: PFL-like glycol radical enzymes Superfamily: PFL-like glycol radical enzymes Family: R1 subunit of ribonucleotide reductase, C-terminal domain
15	d1rlra2	Alignment		94.0	10	Fold: PFL-like glycol radical enzymes Superfamily: PFL-like glycol radical enzymes Family: R1 subunit of ribonucleotide reductase, C-terminal domain
16	d1l1la_	Alignment		72.6	14	Fold: PFL-like glycol radical enzymes Superfamily: PFL-like glycol radical enzymes Family: B12-dependent (class II) ribonucleotide reductase
17	c3a9rA_	Alignment		41.5	17	PDB header: isomerase Chain: A: PDB Molecule: d-arabinose isomerase; PDBTitle: x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
18	c2vg2C_	Alignment		39.1	13	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with i pp
19	d1ueha_	Alignment		39.0	16	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
20	c3ugsB_	Alignment		36.6	8	PDB header: transferase Chain: B: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
21	d1vioa2	Alignment	not modelled	26.2	21	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
22	c1jp3A_	Alignment	not modelled	25.3	16	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of e.coli undecaprenyl pyrophosphate synthase
23	d1j6wa_	Alignment	not modelled	24.6	11	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
24	c3vjja_	Alignment	not modelled	23.0	24	PDB header: viral protein Chain: A: PDB Molecule: p9-1; PDBTitle: crystal structure analysis of the p9-1
25	c3gxxB_	Alignment	not modelled	22.5	13	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt6; PDBTitle: structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
26	c2pd0D_	Alignment	not modelled	22.3	13	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: protein cgd2_2020 from cryptosporidium parvum
27	d2cb5a_	Alignment	not modelled	22.1	14	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Papain-like
28	c3gr1A_	Alignment	not modelled	21.6	12	PDB header: membrane protein Chain: A: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
29	d1j6xa_	Alignment	not modelled	21.6	11	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase

						Family: Autoinducer-2 production protein LuxS
30	c3mf2B_	Alignment	not modelled	20.2	8	PDB header: ligase Chain: B: PDB Molecule: blI0957 protein; PDBTitle: crystal structure of class ii aars homologue (blI0957) complexed with2 amp
31	d1dm9a_	Alignment	not modelled	18.5	17	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kD
32	c1dm9A_	Alignment	not modelled	18.5	17	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka PDBTitle: heat shock protein 15 kd
33	d1f75a_	Alignment	not modelled	16.6	6	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
34	d1vh4a_	Alignment	not modelled	16.5	14	Fold: Single-stranded right-handed beta-helix Superfamily: Stabilizer of iron transporter SufD Family: Stabilizer of iron transporter SufD
35	c3mx2A_	Alignment	not modelled	16.2	21	PDB header: nuclear protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: lassa fever virus nucleoprotein complexed with dttp
36	d1loua_	Alignment	not modelled	15.8	10	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Endonuclease I
37	c2vfwB_	Alignment	not modelled	14.2	10	PDB header: transferase Chain: B: PDB Molecule: short-chain z-isoprenyl diphosphate synthetase; PDBTitle: rv1086 native
38	d1pugb_	Alignment	not modelled	14.1	16	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
39	d2c1wa1	Alignment	not modelled	14.0	19	Fold: EndoU-like Superfamily: EndoU-like Family: Eukaryotic EndoU ribonuclease
40	c3f42A_	Alignment	not modelled	13.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hp0035; PDBTitle: crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
41	c3gr0D_	Alignment	not modelled	13.4	12	PDB header: membrane protein Chain: D: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
42	d1frba_	Alignment	not modelled	12.9	24	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
43	d1dq3a4	Alignment	not modelled	12.5	14	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
44	c2h5gA_	Alignment	not modelled	11.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: delta 1-pyrroline-5-carboxylate synthetase; PDBTitle: crystal structure of human pyrroline-5-carboxylate synthetase
45	d1j08a2	Alignment	not modelled	11.2	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
46	c3ofgA_	Alignment	not modelled	10.5	7	PDB header: chaperone Chain: A: PDB Molecule: boca/mesd chaperone for ywtd beta-propeller-egf protein 1; PDBTitle: structured domain of caenorhabditis elegans bmy-1
47	d1l8na1	Alignment	not modelled	10.5	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
48	d2rh3a1	Alignment	not modelled	10.1	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VirC2-like
49	d1h21a_	Alignment	not modelled	10.0	17	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
50	c1mqrA_	Alignment	not modelled	9.7	11	PDB header: hydrolase Chain: A: PDB Molecule: alpha-d-glucuronidase; PDBTitle: the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 stearrowthermophilus t-6
51	c3erpA_	Alignment	not modelled	9.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
52	c2i9sa_	Alignment	not modelled	9.5	13	PDB header: chaperone Chain: A: PDB Molecule: mesoderm development candidate 2; PDBTitle: the solution structure of the core of mesoderm development2 (mesd).
53	c3ofeB_	Alignment	not modelled	9.3	6	PDB header: chaperone Chain: B: PDB Molecule: ldlr chaperone boca; PDBTitle: structured domain of drosophila melanogaster boca p41 2 2 crystal form
54	c3ry0A_	Alignment	not modelled	9.3	8	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
55	c1gqkB_	Alignment	not modelled	9.1	11	PDB header: hydrolase Chain: B: PDB Molecule: alpha-d-glucuronidase; PDBTitle: structure of pseudomonas cellulosa alpha-d-glucuronidase2 complexed with glucuronic acid

56	d1z41a1	Alignment	not modelled	8.8	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
57	d1lv3a_	Alignment	not modelled	8.5	16	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Hypothetical zinc finger protein YacG
58	c1zxb_	Alignment	not modelled	8.4	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein mg377 homolog; PDBTitle: crystal structure of the hypthetical mycoplasma protein,2 mpm555
59	c1ybxA_	Alignment	not modelled	8.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: conserved hypothetical protein cth-383 from clostridium thermocellum
60	d1mi3a_	Alignment	not modelled	8.3	20	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
61	c2cqjA_	Alignment	not modelled	8.3	7	PDB header: rna binding protein Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein PDBTitle: solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
62	c2f7cA_	Alignment	not modelled	8.2	13	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: catm effector binding domain with its effector cis,cis-muconate
63	d1mp9a1	Alignment	not modelled	8.2	7	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
64	d1jvaa3	Alignment	not modelled	8.0	8	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
65	c1sjiA_	Alignment	not modelled	7.9	18	PDB header: metal binding protein Chain: A: PDB Molecule: calsequestrin, cardiac muscle isoform; PDBTitle: comparing skeletal and cardiac calsequestrin structures and2 their calcium binding: a proposed mechanism for coupled3 calcium binding and protein polymerization
66	c2h9qC_	Alignment	not modelled	7.9	13	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: crystal structure of the effector binding domain of a catm2 variant (r156h)
67	d1hw6a_	Alignment	not modelled	7.8	17	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
68	d1q2za_	Alignment	not modelled	7.7	12	Fold: alpha-alpha superhelix Superfamily: C-terminal domain of Ku80 Family: C-terminal domain of Ku80
69	d1c9wa_	Alignment	not modelled	7.7	19	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
70	c3r6fA_	Alignment	not modelled	7.4	10	PDB header: hydrolase Chain: A: PDB Molecule: hit family protein; PDBTitle: crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
71	c3t4aG_	Alignment	not modelled	7.3	23	PDB header: immune system Chain: G: PDB Molecule: fibrinogen-binding protein; PDBTitle: structure of a truncated form of staphylococcal complement inhibitor b2 bound to human c3c at 3.4 angstrom resolution
72	d1bjpa_	Alignment	not modelled	7.3	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
73	c2xzeA_	Alignment	not modelled	7.2	17	PDB header: hydrolase/protein transport Chain: A: PDB Molecule: stam-binding protein; PDBTitle: structural basis for amsh-escrt-iii chmp3 interaction
74	d1w2za2	Alignment	not modelled	7.2	21	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
75	c3ol0C_	Alignment	not modelled	7.2	8	PDB header: de novo protein Chain: C: PDB Molecule: de novo designed monomer trefoil-fold sub-domain which PDBTitle: crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
76	d1nj1a3	Alignment	not modelled	6.9	4	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
77	d2fm8a1	Alignment	not modelled	6.9	2	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
78	c3mixA_	Alignment	not modelled	6.8	12	PDB header: protein transport Chain: A: PDB Molecule: flagellar biosynthesis protein flha; PDBTitle: crystal structure of the cytosolic domain of b. subtilis flha
79	c3n4pA_	Alignment	not modelled	6.7	18	PDB header: dna binding protein Chain: A: PDB Molecule: terminase subunit ul89 protein; PDBTitle: human cytomegalovirus terminase nuclease domain
80	c3abfB_	Alignment	not modelled	6.7	10	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
81	d1u7za_	Alignment	not modelled	6.6	7	Fold: Ribokinase-like Superfamily: CoaB-like

					Family: CoaB-like
82	d2g2xa1	Alignment	not modelled	6.5	20 Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
83	c2d2ra	Alignment	not modelled	6.4	13 PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
84	c2qffa	Alignment	not modelled	6.3	23 PDB header: hydrolase inhibitor Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of staphylococcal complement inhibitor
85	d2z1ca1	Alignment	not modelled	6.2	7 Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
86	c3dh3C	Alignment	not modelled	6.0	21 PDB header: isomerase/rna Chain: C: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
87	c3inpA	Alignment	not modelled	6.0	14 PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
88	c2op8A	Alignment	not modelled	5.9	16 PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
89	d1dzfa2	Alignment	not modelled	5.8	26 Fold: RPB5-like RNA polymerase subunit Superfamily: RPB5-like RNA polymerase subunit Family: RPB5
90	c2kkvA	Alignment	not modelled	5.8	19 PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: solution nmr structure of an integrase domain from protein2 spa4288 from salmonella enterica, northeast structural3 genomics consortium target slr105h
91	c3u1nC	Alignment	not modelled	5.8	19 PDB header: hydrolase Chain: C: PDB Molecule: sam domain and hd domain-containing protein 1; PDBTitle: structure of the catalytic core of human samhd1
92	d1qnaa1	Alignment	not modelled	5.8	18 Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
93	d1qnaa2	Alignment	not modelled	5.7	11 Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
94	d1aisa1	Alignment	not modelled	5.7	4 Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
95	c2h9bB	Alignment	not modelled	5.7	17 PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
96	d1x3ca1	Alignment	not modelled	5.6	19 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
97	c3o0kB	Alignment	not modelled	5.5	20 PDB header: oxidoreductase Chain: B: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo/keto reductase from brucella melitensis
98	c3cwzB	Alignment	not modelled	5.5	11 PDB header: transport protein Chain: B: PDB Molecule: rab6-interacting protein 1; PDBTitle: strucure of rab6(gtp)-r6ip1 complex
99	d1f54a	Alignment	not modelled	5.5	4 Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like