Phyre^{2}

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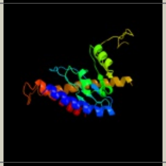
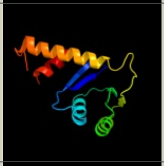
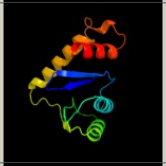
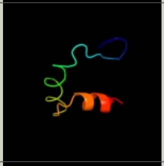
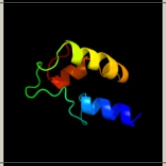
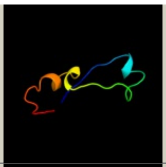
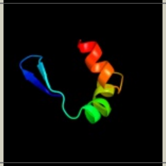
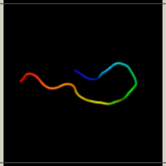
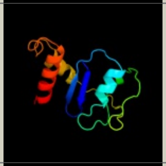
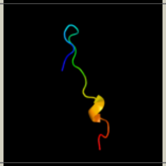
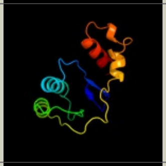
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	Alignment		98.3	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	Alignment		97.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
3	d1cxqa_	Alignment		76.7	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
4	d1asua_	Alignment		75.9	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
5	c3nf9A_	Alignment		53.5	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
6	d1c0ma2	Alignment		49.1	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
7	c3hefB_	Alignment		44.3	15	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
8	d2htsa_	Alignment		43.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-shock transcription factor
9	d1hksa_	Alignment		40.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-shock transcription factor
10	d1a9xa1	Alignment		39.8	14	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
11	c1c0mA_	Alignment		34.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (integrase); **PDBTitle:** crystal structure of rsv two-domain integrase

12	d1d5ra1	Alignment		29.4	26	**Fold:**C2 domain-like **Superfamily:**C2 domain (Calcium/lipid-binding domain, CaLB) **Family:**PLC-like (P variant)
13	c2lduA_	Alignment		28.7	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock factor protein 1; **PDBTitle:** solution nmr structure of heat shock factor protein 1 dna binding2 domain from homo sapiens, northeast structural genomics consortium3 target hr3023c
14	c2e0yB_	Alignment		28.2	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of the samarium derivative of mature gamma-2 glutamyltranspeptidase from escherichia coli
15	c3pvpA_	Alignment		24.2	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
16	d1hyva_	Alignment		23.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
17	c2nqoB_	Alignment		22.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of helicobacter pylori gamma-glutamyltranspeptidase
18	d1exqa_	Alignment		18.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
19	c3f9kV_	Alignment		18.4	12	**PDB header:**viral protein, recombination **Chain:** V: **PDB Molecule:**integrase; **PDBTitle:** two domain fragment of hiv-2 integrase in complex with ledgf ibd
20	c3eplA_	Alignment		15.3	10	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna isopentenyltransferase; **PDBTitle:** crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
21	c2v36D_	Alignment	not modelled	15.1	30	**PDB header:**transferase **Chain:** D: **PDB Molecule:**gamma-glutamyltranspeptidase small chain; **PDBTitle:** crystal structure of gamma-glutamyl transferase from2 bacillus subtilis
22	c2o8kA_	Alignment	not modelled	15.0	27	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
23	d1mnga2	Alignment	not modelled	14.3	18	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
24	c1p7gL_	Alignment	not modelled	13.5	5	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**superoxide dismutase; **PDBTitle:** crystal structure of superoxide dismutase from pyrobaculum2 aerophilum
25	d1bsma2	Alignment	not modelled	13.4	11	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
26	d1slma1	Alignment	not modelled	13.2	27	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
27	d1c6va_	Alignment	not modelled	12.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
28	d1p7ga2	Alignment	not modelled	12.6	5	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain

29	d1kkca2	Alignment	not modelled	12.5	5	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
30	d1b06a2	Alignment	not modelled	11.9	5	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
31	d1ma1a2	Alignment	not modelled	11.6	13	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
32	d1idsa2	Alignment	not modelled	11.1	13	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
33	c3g7pA_	Alignment	not modelled	10.9	17	**PDB header:**unknown function **Chain: A: PDB Molecule:**nitrogen fixation protein; **PDBTitle:** crystal structure of a nifx-associated protein of unknown function2 (afe_1514) from acidithiobacillus ferrooxidans atcc at 2.00 a3 resolution
34	d2vo1a1	Alignment	not modelled	9.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
35	c3nj2B_	Alignment	not modelled	9.8	17	**PDB header:**unknown function **Chain: B: PDB Molecule:**duf269-containing protein; **PDBTitle:** crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
36	d1jr9a2	Alignment	not modelled	9.7	13	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
37	d1wb8a2	Alignment	not modelled	9.7	5	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
38	c3d3kD_	Alignment	not modelled	9.2	12	**PDB header:**protein binding **Chain: D: PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
39	d2i3oa1	Alignment	not modelled	9.2	25	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Gamma-glutamyltranspeptidase-like
40	d1gv3a2	Alignment	not modelled	9.0	11	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
41	d2nyba2	Alignment	not modelled	8.9	8	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
42	c3ceiA_	Alignment	not modelled	8.8	9	**PDB header:**oxidoreductase **Chain: A: PDB Molecule:**superoxide dismutase; **PDBTitle:** crystal structure of superoxide dismutase from helicobacter2 pylori
43	d2p4ka2	Alignment	not modelled	8.8	11	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
44	d2nlza1	Alignment	not modelled	8.7	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Gamma-glutamyltranspeptidase-like
45	c3n0aA_	Alignment	not modelled	8.6	29	**PDB header:**hydrolase **Chain: A: PDB Molecule:**tyrosine-protein phosphatase auxilin; **PDBTitle:** crystal structure of auxilin (40-400)
46	c1y67D_	Alignment	not modelled	8.5	11	**PDB header:**oxidoreductase **Chain: D: PDB Molecule:**manganese superoxide dismutase; **PDBTitle:** crystal structure of manganese superoxide dismutase from2 deinococcus radiodurans
47	c2kvcA_	Alignment	not modelled	8.1	20	**PDB header:**unknown function **Chain: A: PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
48	d1y67a2	Alignment	not modelled	7.9	11	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
49	c3d3jA_	Alignment	not modelled	7.4	12	**PDB header:**protein binding **Chain: A: PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
50	d1s1ma2	Alignment	not modelled	7.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
51	c3ga9S_	Alignment	not modelled	7.2	36	**PDB header:**hydrolase **Chain: S: PDB Molecule:**capsule biosynthesis protein capd; **PDBTitle:** crystal structure of bacillus anthracis transpeptidase enzyme capd,2 crystal form ii
52	c1k6yB_	Alignment	not modelled	7.1	15	**PDB header:**transferase **Chain: B: PDB Molecule:**integrase; **PDBTitle:** crystal structure of a two-domain fragment of hiv-1 integrase
53	d1j1va_	Alignment	not modelled	6.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV

54	d1sfka_	Alignment	not modelled	6.4	24	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
55	d1vcoa2	Alignment	not modelled	6.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
56	c1cojA_	Alignment	not modelled	6.2	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (superoxide dismutase); **PDBTitle:** fe-sod from aquifex pyrophilus, a hyperthermophilic bacterium
57	d1su3a1	Alignment	not modelled	6.1	28	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
58	d2fug11	Alignment	not modelled	5.9	19	**Fold:**Bromodomain-like **Superfamily:**Nqo1C-terminal domain-like **Family:**Nqo1C-terminal domain-like
59	d1b48a1	Alignment	not modelled	5.9	44	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
60	d1coja2	Alignment	not modelled	5.8	8	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
61	c1m6vE_	Alignment	not modelled	5.8	14	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
62	c1dt0A_	Alignment	not modelled	5.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**superoxide dismutase; **PDBTitle:** cloning, sequence, and crystallographic structure of2 recombinant iron superoxide dismutase from pseudomonas3 ovalis
63	c2jg6A_	Alignment	not modelled	5.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
64	c3kksB_	Alignment	not modelled	5.6	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**integrase; **PDBTitle:** crystal structure of catalytic core domain of biv integrase in crystal2 form ii
65	c3eusB_	Alignment	not modelled	5.6	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
66	c2vkpA_	Alignment	not modelled	5.5	12	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**btb/poz domain-containing protein 6; **PDBTitle:** crystal structure of btb domain from btbd6
67	d1uera2	Alignment	not modelled	5.2	15	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
68	d1ix9a2	Alignment	not modelled	5.1	13	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
69	d1v77a_	Alignment	not modelled	5.1	7	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**RNase P subunit p30