Phyre^2

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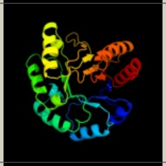
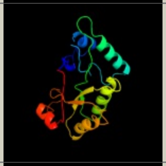
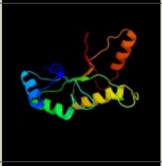
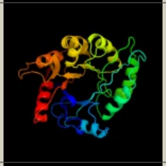
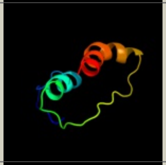
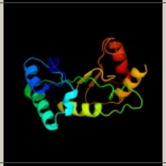
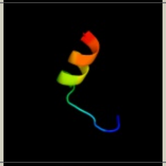
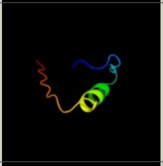
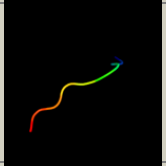
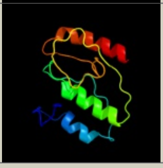
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vpqa_	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**TM1631-like **Family:**TM1631-like
2	d1vpya_	Alignment		100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**TM1631-like **Family:**TM1631-like
3	c3lmzA_	Alignment		93.2	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
4	c3l23A_	Alignment		87.7	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
5	c3cnyA_	Alignment		82.4	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**inositol catabolism protein iole; **PDBTitle:** crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
6	d1yx1a1	Alignment		73.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
7	c3dx5A_	Alignment		68.9	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
8	c2x7vA_	Alignment		59.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable endonuclease 4; **PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
9	d2cx6a1	Alignment		56.1	17	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
10	c2hk1D_	Alignment		51.5	14	**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
11	c2ou4C_	Alignment		50.2	10	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii

12	c2imgA_	Alignment		45.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 23; **PDBTitle:** crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
13	c3p6lA_	Alignment		39.7	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
14	d1edga_	Alignment		34.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
15	d1rh6a_	Alignment		28.6	25	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
16	c2zvrA_	Alignment		26.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uncharacterized protein tm_0416; **PDBTitle:** crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
17	d1ay7b_	Alignment		24.9	38	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
18	d2gs5a1	Alignment		24.7	20	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
19	c3obeB_	Alignment		21.6	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
20	d1yoba1	Alignment		21.4	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
21	d1tpna_	Alignment	not modelled	20.9	19	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
22	c3ngfA_	Alignment	not modelled	19.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family 2; **PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis
23	d1i60a_	Alignment	not modelled	18.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
24	d2do8a1	Alignment	not modelled	18.5	20	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
25	d1wjwa_	Alignment	not modelled	17.3	17	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
26	d1jpma1	Alignment	not modelled	17.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
27	d2gzoa1	Alignment	not modelled	17.2	30	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
28	c2l82A_	Alignment	not modelled	14.9	19	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein or32; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
						PDB header:transcription

29	c2dn5A_	Alignment	not modelled	14.8	28	**Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
30	c2pebB_	Alignment	not modelled	14.3	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative dioxygenase; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f1925) from nostoc2 punctiforme pcc 73102 at 1.46 a resolution
31	c2xrfA_	Alignment	not modelled	14.1	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
32	c3bjeA_	Alignment	not modelled	13.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside phosphorylase, putative; **PDBTitle:** crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
33	c2d99A_	Alignment	not modelled	12.6	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
34	c3ceuA_	Alignment	not modelled	12.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268
35	c2qz5A_	Alignment	not modelled	12.5	19	**PDB header:**signaling protein, lipid binding protein **Chain:** A: **PDB Molecule:**axin interactor, dorsalization associated **PDBTitle:** crystal structure of the c-terminal domain of aida
36	d1nuia1	Alignment	not modelled	12.1	10	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**Primase fragment of primase-helicase protein
37	c2e3lA_	Alignment	not modelled	11.5	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor gtf2ird2 beta; **PDBTitle:** solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna
38	c2dzrA_	Alignment	not modelled	11.0	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
39	c2ejeA_	Alignment	not modelled	10.8	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
40	d1u83a_	Alignment	not modelled	10.7	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
41	c1u83A_	Alignment	not modelled	10.7	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
42	c3eufC_	Alignment	not modelled	10.1	38	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase 1; **PDBTitle:** crystal structure of bau-bound human uridine phosphorylase 1
43	c3hefB_	Alignment	not modelled	9.9	29	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
44	c3sjnB_	Alignment	not modelled	9.9	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of enolase spea_3858 (target efi-500646) from2 shewanella pealeana with magnesium bound
45	d1m3ga_	Alignment	not modelled	9.9	14	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
46	c3b73A_	Alignment	not modelled	9.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phih1 repressor-like protein; **PDBTitle:** crystal structure of the phih1 repressor-like protein from2 haloarcula marismortui
47	d1nwba_	Alignment	not modelled	9.5	14	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
48	d2pb9a1	Alignment	not modelled	9.2	18	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**Phosphomethylpyrimidine kinase C-terminal domain-like
49	c3iz3D_	Alignment	not modelled	9.2	17	**PDB header:**virus **Chain:** D: **PDB Molecule:**viral structural protein 5; **PDBTitle:** cryoem structure of cytoplasmic polyhedrosis virus
50	d1kyqa2	Alignment	not modelled	9.0	9	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
51	c3eezA_	Alignment	not modelled	8.9	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative mandelate racemase/muconate lactonizing **PDBTitle:** crystal structure of a putative mandelate racemase/muconate2 lactonizing enzyme from silicibacter pomeroyi
52	c3izxE_	Alignment	not modelled	8.8	17	**PDB header:**virus **Chain:** E: **PDB Molecule:**viral structural protein 5; **PDBTitle:** 3.1 angstrom cryoem structure of cytoplasmic polyhedrosis virus
53	d1q60a_	Alignment	not modelled	8.6	21	**Fold:**GTF2I-like repeat **Superfamily:**GTF2I-like repeat **Family:**GTF2I-like repeat

54	c2yvaB_	Alignment	not modelled	8.6	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
55	c2ed2A_	Alignment	not modelled	8.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
56	c2pfcA_	Alignment	not modelled	8.3	63	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv0098/mt0107; **PDBTitle:** structure of mycobacterium tuberculosis rv0098
57	c2qsxB_	Alignment	not modelled	8.1	3	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** crystal structure of putative transcriptional regulator lysr from2 vibrio parahaemolyticus
58	c2b5dX_	Alignment	not modelled	7.8	24	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
59	c2qgyA_	Alignment	not modelled	7.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**enolase from the environmental genome shotgun **PDBTitle:** crystal structure of an enolase from the environmental2 genome shotgun sequencing of the sargasso sea
60	d1autl1	Alignment	not modelled	7.5	27	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
61	d2p8ia1	Alignment	not modelled	7.4	11	**Fold:**Ferredoxin-like **Superfamily:**DOPA-like **Family:**DOPA dioxygenase-like
62	c2j37W_	Alignment	not modelled	7.3	8	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
63	c3tdqB_	Alignment	not modelled	7.3	43	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**pily2 protein; **PDBTitle:** crystal structure of a fimbrial biogenesis protein pily22 (pily2_pa4555) from pseudomonas aeruginosa pao1 at 2.10 a resolution
64	c2iy3A_	Alignment	not modelled	7.2	14	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
65	d2mnra1	Alignment	not modelled	7.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
66	c2jm3A_	Alignment	not modelled	6.9	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the thap domain from c. elegans c-2 terminal binding protein (ctbp)
67	c2htdB_	Alignment	not modelled	6.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**predicted flavin-nucleotide-binding protein from cog3576 **PDBTitle:** crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution
68	c3emuA_	Alignment	not modelled	6.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine rich repeat and phosphatase domain **PDBTitle:** crystal structure of a leucine rich repeat and phosphatase2 domain containing protein from entamoeba histolytica
69	d1dgsa3	Alignment	not modelled	6.7	12	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
70	d2q02a1	Alignment	not modelled	6.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
71	d1qwga_	Alignment	not modelled	6.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
72	c3icgD_	Alignment	not modelled	6.3	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase d; **PDBTitle:** crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
73	c2dn4A_	Alignment	not modelled	6.3	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
74	d1qtwa_	Alignment	not modelled	6.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
75	c3iraA_	Alignment	not modelled	6.2	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
76	d1iuka_	Alignment	not modelled	6.1	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
77	d2choa2	Alignment	not modelled	5.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
78	c2k4zA_	Alignment	not modelled	5.7	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dsrr; **PDBTitle:** solution nmr structure of allochromatium vinosum dsrr:2

						northeast structural genomics consortium target op5
79	c2dzqA_	Alignment	not modelled	5.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
80	d1h4pa_	Alignment	not modelled	5.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
81	c2esbA_	Alignment	not modelled	5.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 18; **PDBTitle:** crystal structure of human dusp18
82	c2duwA_	Alignment	not modelled	5.3	13	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
83	d1h41a1	Alignment	not modelled	5.2	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
84	c3bb5B_	Alignment	not modelled	5.2	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**stress responsive alpha-beta protein; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution