Phyre2

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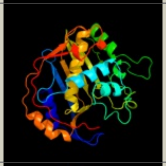
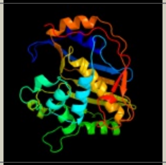
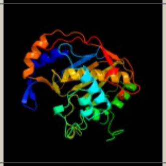
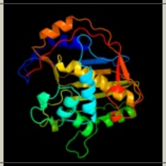
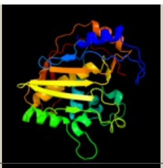
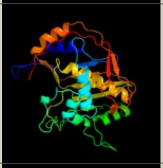
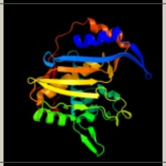
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oipE_	Alignment		100.0	51	**PDB header:**transferase, oxidoreductase **Chain:** E: **PDB Molecule:**chain a, crystal structure of dhfr; **PDBTitle:** crystal structure of the s290g active site mutant of ts-2 dhfr from cryptosporidium hominis
2	d1qzfa2	Alignment		100.0	51	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
3	d1j3kc_	Alignment		100.0	48	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
4	c3jsuA_	Alignment		100.0	48	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**dihydrofolate reductase-thymidylate synthase; **PDBTitle:** quadruple mutant(n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase(pfdhfr-ts) complexed3 with qn254, nadph, and dump
5	d1tswa_	Alignment		100.0	60	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
6	c3k2hA_	Alignment		100.0	49	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrofolate reductase/thymidylate synthase; **PDBTitle:** co-crystal structure of dihydrofolate reductase/thymidylate synthase2 from babesia bovis with dump, pemetrexed and nadp
7	d2g8oa1	Alignment		100.0	100	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
8	c3qj7D_	Alignment		100.0	66	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis thymidylate2 synthase (thya) bound to dump
9	c3clbA_	Alignment		100.0	51	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**dhfr-ts; **PDBTitle:** structure of bifunctional tcdhfr-ts in complex with tmq
10	d1hvya_	Alignment		100.0	56	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
11	d1seja2	Alignment		100.0	51	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase

12	c2aazG_	Alignment		100.0	49	**PDB header:**transferase **Chain:** G: **PDB Molecule:**thymidylate synthase; **PDBTitle:** cryptococcus neoformans thymidylate synthase complexed with2 substrate and an antifolate
13	d1f28a_	Alignment		100.0	49	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
14	d2tsra_	Alignment		100.0	55	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
15	d1bkpa_	Alignment		100.0	37	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
16	d1tisa_	Alignment		100.0	50	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
17	c1hw3A_	Alignment		100.0	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate synthase; **PDBTitle:** structure of human thymidylate synthase suggests advantages of2 chemotherapy with noncompetitive inhibitors
18	c1hw4A_	Alignment		100.0	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate synthase; **PDBTitle:** structure of thymidylate synthase suggests advantages of chemotherapy2 with noncompetitive inhibitors
19	c3ix6B_	Alignment		100.0	66	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of thymidylate synthase thya from brucella2 melitensis
20	c3kgbA_	Alignment		100.0	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate synthase 1/2; **PDBTitle:** crystal structure of thymidylate synthase 1/2 from encephalitozoon2 cuniculi at 2.2 a resolution
21	d1b5ea_	Alignment	not modelled	100.0	24	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
22	c2vsvB_	Alignment	not modelled	42.0	9	**PDB header:**protein-binding **Chain:** B: **PDB Molecule:**rhophilin-2; **PDBTitle:** crystal structure of the pdz domain of human rhophilin-2
23	c2q3gA_	Alignment	not modelled	35.1	22	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**pdz and lim domain protein 7; **PDBTitle:** structure of the pdz domain of human pdlim7 bound to a c-2 terminal extension from human beta-tropomyosin
24	c3o46A_	Alignment	not modelled	28.1	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**maguk p55 subfamily member 7; **PDBTitle:** crystal structure of the pdz domain of mpp7
25	d1r6ja_	Alignment	not modelled	28.0	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
26	c1r6jA_	Alignment	not modelled	28.0	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**syntenin 1; **PDBTitle:** ultrahigh resolution crystal structure of syntenin pdz2
27	c1nteA_	Alignment	not modelled	28.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure analysis of the second pdz domain of2 syntenin
28	c3diwB_	Alignment	not modelled	27.5	19	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
29	c2jjkB	Alignment	not modelled	27.2	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**synaptojanin-2 binding protein;

29	c2jrkB_	Alignment	not modelled	27.2	16	**PDBTitle:** crystal structure of pdz domain of synaptojanin-2 binding2 protein
30	d1ueza_	Alignment	not modelled	26.2	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
31	c2eeiA_	Alignment	not modelled	25.9	6	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 1; **PDBTitle:** solution structure of second pdz domain of pdz domain2 containing protein 1
32	d1w9ea1	Alignment	not modelled	25.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
33	d1wi2a_	Alignment	not modelled	24.4	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
34	c3khfA_	Alignment	not modelled	24.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**microtubule-associated serine/threonine-protein **PDBTitle:** the crystal structure of the pdz domain of human microtubule2 associated serine/threonine kinase 3 (mast3)
35	d1tp5a1	Alignment	not modelled	23.3	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
36	d1fc6a3	Alignment	not modelled	23.1	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
37	d1vaea_	Alignment	not modelled	22.8	9	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
38	c2d8iA_	Alignment	not modelled	21.4	16	**PDB header:**immune system, signaling protein **Chain:** A: **PDB Molecule:**t-cell lymphoma invasion and metastasis 1 **PDBTitle:** solution structure of the pdz domain of t-cell lymphoma2 invasion and metastasis 1 varian
39	c2dkrA_	Alignment	not modelled	20.1	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**lin-7 homolog b; **PDBTitle:** solution structure of the pdz domain from human lin-72 homolog b
40	c2jxoA_	Alignment	not modelled	19.3	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ezrin-radixin-moesin-binding phosphoprotein 50; **PDBTitle:** structure of the second pdz domain of nherf-1
41	c2kv8A_	Alignment	not modelled	18.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 12; **PDBTitle:** solution structure ofrgs12 pdz domain
42	c2fneB_	Alignment	not modelled	17.0	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 13th pdz domain of mpdz
43	c2d90A_	Alignment	not modelled	16.8	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pdz domain containing protein 1; **PDBTitle:** solution structure of the third pdz domain of pdz domain2 containing protein 1
44	d1kwaa_	Alignment	not modelled	15.0	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
45	d1y7na1	Alignment	not modelled	14.7	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
46	c3shuB_	Alignment	not modelled	14.4	22	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3
47	c2ejyA_	Alignment	not modelled	14.4	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**55 kda erythrocyte membrane protein; **PDBTitle:** solution structure of the p55 pdz t85c domain complexed2 with the glycophorin c f127c peptide
48	d1wi4a1	Alignment	not modelled	13.9	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
49	c2e7kA_	Alignment	not modelled	13.9	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**maguk p55 subfamily member 2; **PDBTitle:** solution structure of the pdz domain from human maguk p552 subfamily member 2
50	d1p1da2	Alignment	not modelled	13.3	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
51	d1t2ma1	Alignment	not modelled	13.3	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
52	d1nowa1	Alignment	not modelled	13.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
53	c1w9qB_	Alignment	not modelled	13.1	12	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the pdz tandem of human syntenin in2 complex with tnefaf peptide
54	d1ihja_	Alignment	not modelled	12.5	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
55	c2kjdA_	Alignment	not modelled	11.8	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchange regulatory cofactor nhe- **PDBTitle:** solution structure of extended pdz2 domain from nherf1

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56	c3qglD_	Alignment	not modelled	11.8	11	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**sorting nexin-27; **PDBTitle:** crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3
57	d1uepa_	Alignment	not modelled	11.6	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
58	c2v90E_	Alignment	not modelled	11.5	8	**PDB header:**protein-binding **Chain:** E: **PDB Molecule:**pdz domain-containing protein 3; **PDBTitle:** crystal structure of the 3rd pdz domain of intestine- and2 kidney-enriched pdz domain ikepp (pdzd3)
59	c2d92A_	Alignment	not modelled	11.2	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the fifth pdz domain of inad-like2 protein
60	c2iwnA_	Alignment	not modelled	11.1	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 3rd pdz domain of multiple pdz domain protein mpdz (casp2 target)
61	c2z17A_	Alignment	not modelled	11.0	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pleckstrin homology sec7 and coiled-coil domains- **PDBTitle:** crystal sturcture of pdz domain from human pleckstrin2 homology, sec7
62	c3l4fD_	Alignment	not modelled	10.8	17	**PDB header:**signaling protein/protein binding **Chain:** D: **PDB Molecule:**sh3 and multiple ankyrin repeat domains protein **PDBTitle:** crystal structure of betapix coiled-coil domain and shank2 pdz complex
63	c1u3bA_	Alignment	not modelled	10.4	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding, **PDBTitle:** auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
64	c2eehA_	Alignment	not modelled	10.2	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 7; **PDBTitle:** solution structure of first pdz domain of pdz domain2 containing protein 7
65	d1uita_	Alignment	not modelled	10.2	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
66	c2gzvA_	Alignment	not modelled	10.1	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** the cystal structure of the pdz domain of human pick1 (casp target)
67	d2byga1	Alignment	not modelled	10.0	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
68	c2jilA_	Alignment	not modelled	9.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate receptor interacting protein-1; **PDBTitle:** crystal structure of 2nd pdz domain of glutamate receptor2 interacting protein-1 (grip1)
69	c2egkC_	Alignment	not modelled	9.9	13	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**general receptor for phosphoinositides 1- **PDBTitle:** crystal structure of tamalin pdz-intrinsic ligand fusion2 protein
70	d1jaka1	Alignment	not modelled	9.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
71	d1wh1a_	Alignment	not modelled	9.7	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
72	d2fcfa1	Alignment	not modelled	9.7	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
73	d2o7ta1	Alignment	not modelled	9.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
74	c3qikA_	Alignment	not modelled	9.5	14	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phosphatidylinositol 3,4,5-trisphosphate-dependent rac **PDBTitle:** crystal structure of the first pdz domain of prex1
75	d1jt6a1	Alignment	not modelled	9.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
76	c3m4rA_	Alignment	not modelled	9.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of the n-terminal class ii aldolase domain of a conserved2 protein from thermoplasma acidophilum
77	c3rcnA_	Alignment	not modelled	9.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
78	d1lcya1	Alignment	not modelled	9.4	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
79	d1be9a_	Alignment	not modelled	9.3	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
80	d1q3oa_	Alignment	not modelled	9.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain

81	d1ky9b2	Alignment	not modelled	9.1	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
82	d2f5ya1	Alignment	not modelled	9.0	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
83	c2ka9A_	Alignment	not modelled	8.9	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**disks large homolog 4; **PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide
84	d1pi1a_	Alignment	not modelled	8.9	31	**Fold:**Bromodomain-like **Superfamily:**Mob1/phocein **Family:**Mob1/phocein
85	c1m04A_	Alignment	not modelled	8.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
86	d2gjxa1	Alignment	not modelled	8.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
87	c2yuyA_	Alignment	not modelled	8.5	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho gtpase activating protein 21; **PDBTitle:** solution structure of pdz domain of rho gtpase activating2 protein 21
88	c2yubA_	Alignment	not modelled	8.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lim domain kinase 2; **PDBTitle:** solution structure of the pdz domain from mouse lim domain2 kinase
89	d1u3ba2	Alignment	not modelled	8.3	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
90	c2dm8A_	Alignment	not modelled	8.1	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the eighth pdz domain of human inad-2 like protein
91	d1qaua_	Alignment	not modelled	8.0	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
92	c1obyA_	Alignment	not modelled	7.9	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the complex of pdz2 of syntenin with2 a syndecan-4 peptide.
93	c1nouA_	Alignment	not modelled	7.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase beta chain; **PDBTitle:** native human lysosomal beta-hexosaminidase isoform b
94	c2hjnA_	Alignment	not modelled	7.7	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**maintenance of ploidy protein mob1; **PDBTitle:** structural and functional analysis of saccharomyces2 cerevisiae mob1
95	d1iyjb4	Alignment	not modelled	7.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
96	d1wj2a_	Alignment	not modelled	7.4	38	**Fold:**WRKY DNA-binding domain **Superfamily:**WRKY DNA-binding domain **Family:**WRKY DNA-binding domain
97	c3lfhF_	Alignment	not modelled	7.3	62	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
98	c3enhD_	Alignment	not modelled	7.3	22	**PDB header:**hydrolase/unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein mj0187; **PDBTitle:** crystal structure of cgi121/bud32/kae1 complex
99	c4a8aI_	Alignment	not modelled	7.3	27	**PDB header:**hydrolase/hydrolase **Chain:** I: **PDB Molecule:**periplasmic ph-dependent serine endoprotease degq; **PDBTitle:** asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme