Phyre2

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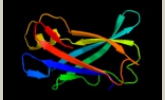
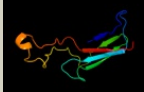
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2h1xB_	Alignment		100.0	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5-hydroxyisourate hydrolase (formerly known as **PDBTitle:** crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
2	c2gpzC_	Alignment		100.0	77	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** transthyretin-like protein from salmonella dublin
3	d1ttaa_	Alignment		100.0	32	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
4	d1oo2a_	Alignment		100.0	38	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
5	d1kgia_	Alignment		100.0	36	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
6	d1f86a_	Alignment		100.0	33	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
7	d1tfpa_	Alignment		100.0	39	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
8	c2h0eA_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transthyretin-like protein pucm; **PDBTitle:** crystal structure of pucm in the absence of substrate
9	c3qvaB_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
10	c2azqA_	Alignment		94.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
11	c3n9tA_	Alignment		94.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pnpc; **PDBTitle:** cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4

12	c3kptA_	Alignment		93.8	21	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**collagen adhesion protein; **PDBTitle:** crystal structure of bcpa, the major pilin subunit of2 bacillus cereus
13	d3pccm_	Alignment		93.4	24	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
14	c1tmxA_	Alignment		92.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyquinol 1,2-dioxygenase; **PDBTitle:** crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardioides simplex 3e
15	d1cwva1	Alignment		92.3	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
16	c2pz4A_	Alignment		92.2	22	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein gbs052; **PDBTitle:** crystal structure of spab (gbs52), the minor pilin in gram-positive2 pathogen streptococcus agalactiae
17	d1h8la1	Alignment		91.9	22	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
18	c1h8lA_	Alignment		91.8	22	**PDB header:**carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
19	c3hj8A_	Alignment		90.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol
20	d2burb1	Alignment		90.7	22	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
21	d1s9aa_	Alignment	not modelled	90.6	15	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
22	d1dmha_	Alignment	not modelled	90.6	16	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
23	c2boyC_	Alignment	not modelled	90.4	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-chlorocatechol 1,2-dioxygenase; **PDBTitle:** crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp
24	c3mn8A_	Alignment	not modelled	89.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
25	c2xsuA_	Alignment	not modelled	89.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2 dioxygenase; **PDBTitle:** crystal structure of the a72g mutant of acinetobacter2 radioresistens catechol 1,2 dioxygenase
26	c3e8vA_	Alignment	not modelled	88.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible transglutaminase-family protein; **PDBTitle:** crystal structure of a possible transglutaminase-family2 protein proteolytic fragment from bacteroides fragilis
27	c3irpX_	Alignment	not modelled	88.0	33	**PDB header:**cell adhesion **Chain:** X: **PDB Molecule:**uro-adherence factor a; **PDBTitle:** crystal structure of functional region of uafa from staphylococcus2 saprophyticus at 1.50 angstrom resolution
28	d1f00i1	Alignment	not modelled	87.7	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments

29	d1nkga1	Alignment	not modelled	85.5	19	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Rhamnogalacturonase B, RhgB, middle domain
30	d1uwya1	Alignment	not modelled	85.3	18	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
31	c2nsmA_	Alignment	not modelled	85.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
32	c1uwyA_	Alignment	not modelled	85.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
33	c2ww8A_	Alignment	not modelled	79.9	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell wall surface anchor family protein; **PDBTitle:** structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae
34	d2bura1	Alignment	not modelled	79.8	19	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
35	c2x5pA_	Alignment	not modelled	78.3	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibronectin binding protein; **PDBTitle:** crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
36	c1cwvA_	Alignment	not modelled	77.3	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**invasin; **PDBTitle:** crystal structure of invasin: a bacterial integrin-binding protein
37	d3pcca_	Alignment	not modelled	74.9	13	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
38	c2p9rA_	Alignment	not modelled	66.0	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**alpha-2-macroglobulin; **PDBTitle:** human alpha2-macroglogulin is composed of multiple domains,2 as predicted by homology with complement component c3
39	d1cwva2	Alignment	not modelled	62.5	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
40	c2xtlB_	Alignment	not modelled	55.5	18	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**cell wall surface anchor family protein; **PDBTitle:** structure of the major pilus backbone protein from streptococcus2 agalactiae
41	c3htlX_	Alignment	not modelled	50.2	25	**PDB header:**structural protein, cell adhesion **Chain:** X: **PDB Molecule:**putative surface-anchored fimbrial subunit; **PDBTitle:** structure of the corynebacterium diphtheriae major pilin2 spaa points to a modular pilus assembly with stabilizing3 isopeptide bonds
42	c2zxcA_	Alignment	not modelled	48.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**neutral ceramidase; **PDBTitle:** seramidase complexed with c2
43	d1cwva3	Alignment	not modelled	44.9	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
44	d2dmca1	Alignment	not modelled	42.7	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
45	d1ix2a_	Alignment	not modelled	30.0	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
46	c2xicB_	Alignment	not modelled	25.5	11	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**ancillary protein 1; **PDBTitle:** pilus-presented adhesin, spy0125 (cpa), p212121 form (esrf data)
47	d2yzca2	Alignment	not modelled	21.7	25	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
48	c2x9yA_	Alignment	not modelled	19.6	22	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell wall surface anchor family protein; **PDBTitle:** structure of the pilus backbone (rrgb) from streptococcus2 pneumoniae
49	c2yzbA_	Alignment	not modelled	18.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uricase; **PDBTitle:** crystal structure of uricase from arthrobacter globiformis2 in complex with uric acid (substrate)
50	c3hlkB_	Alignment	not modelled	16.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
51	d2q3za1	Alignment	not modelled	16.6	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
52	c2v1lA_	Alignment	not modelled	15.2	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein
53	c2w56B_	Alignment	not modelled	14.7	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**vc0508; **PDBTitle:** structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
						PDB header:cell adhesion

54	c3rpkA_	Alignment	not modelled	12.9	22	**Chain:** A: **PDB Molecule:**backbone pilus subunit; **PDBTitle:** structure of the full-length major pilin rrgb from streptococcus2 pneumoniae
55	c2jmbA_	Alignment	not modelled	12.7	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu4866; **PDBTitle:** solution structure of the protein atu4866 from agrobacterium2 tumefaciens
56	c3cu7A_	Alignment	not modelled	12.4	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement c5; **PDBTitle:** human complement component 5
57	d2c9qa1	Alignment	not modelled	12.2	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
58	d1vrma1	Alignment	not modelled	12.0	53	**Fold:**T-fold **Superfamily:**ApbE-like **Family:**ApbE-like
59	c3lznA_	Alignment	not modelled	11.7	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**p19 protein; **PDBTitle:** crystal structure analysis of the apo p19 protein from campylobacter2 jejuni at 1.59 a at ph 9
60	d1ju3a1	Alignment	not modelled	11.5	19	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**PepX C-terminal domain-like
61	c2ougC_	Alignment	not modelled	11.4	18	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional activator rfah; **PDBTitle:** crystal structure of the rfah transcription factor at 2.1a2 resolution
62	c2jh3C_	Alignment	not modelled	11.0	26	**PDB header:**ribosomal protein **Chain:** C: **PDB Molecule:**ribosomal protein s2-related protein; **PDBTitle:** the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
63	c2djcA_	Alignment	not modelled	11.0	57	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**growth-blocking peptide; **PDBTitle:** solution structure of growth-blocking peptide of the2 tobacco cutworm, spodoptera litura
64	d1vjja1	Alignment	not modelled	10.8	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
65	d1olma2	Alignment	not modelled	10.7	30	**Fold:**Supernatant protein factor (SPF), C-terminal domain **Superfamily:**Supernatant protein factor (SPF), C-terminal domain **Family:**Supernatant protein factor (SPF), C-terminal domain
66	c1c8uA_	Alignment	not modelled	10.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coa thioesterase ii; **PDBTitle:** crystal structure of the e.coli thioesterase ii, a2 homologue of the human nef-binding enzyme
67	c1irrA_	Alignment	not modelled	10.2	57	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**paralytic peptide; **PDBTitle:** solution structure of paralytic peptide of the silkworm,2 bombyx mori
68	c3pvmB_	Alignment	not modelled	10.0	29	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cobra venom factor; **PDBTitle:** structure of complement c5 in complex with cvf
69	c1hrlA_	Alignment	not modelled	9.2	57	**PDB header:**toxin **Chain:** A: **PDB Molecule:**paralytic peptide i; **PDBTitle:** structure of a paralytic peptide from an insect, manduca2 sexta
70	c1v28A_	Alignment	not modelled	8.9	57	**PDB header:**toxin **Chain:** A: **PDB Molecule:**paralytic peptide; **PDBTitle:** solution structure of paralytic peptide of the wild2 silkmoth, antheraea yamamai
71	d1qhda2	Alignment	not modelled	8.6	16	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
72	c2dj9A_	Alignment	not modelled	8.6	57	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**growth-blocking peptide; **PDBTitle:** solution structure of growth-blocking peptide of the2 cabbage armyworm, mamestra brassicae
73	c2y7uM_	Alignment	not modelled	8.3	18	**PDB header:**virus **Chain:** M: **PDB Molecule:**coat protein; **PDBTitle:** x-ray structure of the grapevine fanleaf virus
74	d1zxqa1	Alignment	not modelled	8.3	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C2 set domains
75	c2zxqA_	Alignment	not modelled	8.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** crystal structure of endo-alpha-n-acetylgalactosaminidase2 from bifidobacterium longum (engbf)
76	c1nkgA_	Alignment	not modelled	8.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rhamnogalacturonase b; **PDBTitle:** rhamnogalacturonan lyase from aspergillus aculeatus
77	d1c8ua1	Alignment	not modelled	7.8	14	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-CoA thioesterase
78	c1o7dC_	Alignment	not modelled	7.6	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
79	d2g3ra1	Alignment	not modelled	7.2	23	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
80	d1fcda2	Alignment	not modelled	7.1	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain

80	d1fcda2	Alignment	not modelled	7.1	19	**Family:**FAD/NAD-linked reductases, N-terminal and central domains
81	d1rm6a2	Alignment	not modelled	7.1	20	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
82	d1z0mb1	Alignment	not modelled	6.9	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
83	d1t2sa_	Alignment	not modelled	6.9	18	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
84	c1zpuE_	Alignment	not modelled	6.8	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**iron transport multicopper oxidase fet3; **PDBTitle:** crystal structure of fet3p, a multicopper oxidase that functions in2 iron import
85	d2vera1	Alignment	not modelled	6.7	27	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Dr-family adhesin
86	d1zdxa1	Alignment	not modelled	6.4	21	**Fold:**FimD N-terminal domain-like **Superfamily:**FimD N-terminal domain-like **Family:**Usher N-domain
87	c1fi8E_	Alignment	not modelled	6.3	40	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** E: **PDB Molecule:**ecotin; **PDBTitle:** rat granzyme b [n66q] complexed to ecotin [81-84 iepd]
88	c1d2pA_	Alignment	not modelled	6.3	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen adhesin; **PDBTitle:** crystal structure of two b repeat units (b1b2) of the2 collagen binding protein (cna) of staphylococcus aureus
89	d1v6ea_	Alignment	not modelled	6.2	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
90	c2o6dB_	Alignment	not modelled	5.8	33	**PDB header:**membrane protein, protein binding **Chain:** B: **PDB Molecule:**34 kda membrane antigen; **PDBTitle:** structure of native rtp34 from treponema pallidum
91	c1kv3F_	Alignment	not modelled	5.7	17	**PDB header:**transferase **Chain:** F: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** human tissue transglutaminase in gdp bound form
92	d1eala_	Alignment	not modelled	5.5	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
93	c1t3qB_	Alignment	not modelled	5.5	34	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**quinoline 2-oxidoreductase large subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
94	d1m7xa2	Alignment	not modelled	5.4	15	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
95	c3nrqB_	Alignment	not modelled	5.4	25	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**periplasmic protein-probably involved in high-affinity fe2+ **PDBTitle:** crystal structure of copper-reconstituted fetp from uropathogenic2 escherichia coli strain f11
96	d1a9xa1	Alignment	not modelled	5.4	63	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
97	c3ecqA_	Alignment	not modelled	5.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** endo-alpha-n-acetylgalactosaminidase from streptococcus pneumoniae:2 semet structure
98	d1lnsa2	Alignment	not modelled	5.3	9	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**PepX C-terminal domain-like
99	d2p0ma2	Alignment	not modelled	5.3	40	**Fold:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Superfamily:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Family:**Lipoxigenase N-terminal domain