























Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1s2jA_	 Alignment		100.0	43	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan recognition protein sa cg11709-pa; PDBTitle: crystal structure of the drosophila pattern-recognition2 receptor pgrp-sa
2	d1sxra_	 Alignment		100.0	43	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
3	d2f2la1	 Alignment		100.0	32	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
4	d2cb3a1	 Alignment		100.0	44	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
5	d1ycka1	 Alignment		100.0	45	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
6	c2rkaA_	 Alignment		100.0	40	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein-sd; PDBTitle: crystal structure of drosophila peptidoglycan recognition2 protein sd (pgrp-sd)
7	d2f2lx1	 Alignment		100.0	45	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
8	c2xz4A_	 Alignment		100.0	37	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein lf; PDBTitle: crystal structure of the lfz ectodomain of the2 peptidoglycan recognition protein lf
9	d1ohta_	 Alignment		100.0	38	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
10	c1ohtA_	 Alignment		100.0	38	PDB header: hydrolase Chain: A: PDB Molecule: cg14704 protein; PDBTitle: peptidoglycan recognition protein-lb
11	d1sk4a_	 Alignment		100.0	77	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like

12	c3ep1B_	Alignment		100.0	31	PDB header: immune system Chain: B: PDB Molecule: pgrp-hd - peptidoglycan recognition protein PDBTitle: structure of the pgrp-hd from alvinella pompejana
13	c2xz8A_	Alignment		100.0	30	PDB header: immune system Chain: A: PDB Molecule: peptidoglycan-recognition protein lf; PDBTitle: crystal structure of the lfw ectodomain of the2 peptidoglycan recognition protein lf
14	d1lbaa_	Alignment		100.0	27	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
15	d2bgxa2	Alignment		99.9	15	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
16	d1yb0a1	Alignment		99.9	11	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
17	c3hmaA_	Alignment		99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase xlya; PDBTitle: amidase from bacillus subtilis
18	d1j3ga_	Alignment		99.8	13	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
19	c4bolA_	Alignment		99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: ampdh2; PDBTitle: crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
20	c2bh7A_	Alignment		99.7	21	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: crystal structure of a semet derivative of amid at 2.22 angstroms
21	c3latB_	Alignment	not modelled	98.9	14	PDB header: hydrolase Chain: B: PDB Molecule: bifunctional autolysin; PDBTitle: crystal structure of staphylococcus peptidoglycan hydrolase2 amie
22	d2b3ya2	Alignment		52.4	21	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
23	d1whqa_	Alignment	not modelled	51.4	17	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
24	d2etla1	Alignment	not modelled	48.3	24	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin carboxyl-terminal hydrolase UCH-L
25	c2b3yB_	Alignment	not modelled	45.6	21	PDB header: lyase Chain: B: PDB Molecule: iron-responsive element binding protein 1; PDBTitle: structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
26	c4iq7A_	Alignment	not modelled	33.0	19	PDB header: hydrolase/signaling protein Chain: A: PDB Molecule: ubiquitin c-terminal hydrolase 37; PDBTitle: crystal structure of trichinella spiralis uch37 bound to ubiquitin2 vinyl methyl ester
27	c2yzhD_	Alignment	not modelled	25.6	24	PDB header: oxidoreductase Chain: D: PDB Molecule: probable thiol peroxidase; PDBTitle: crystal structure of peroxiredoxin-like protein from aquifex aeolicus PDB header: oxidoreductase

28	c2lrtA	Alignment	not modelled	25.6	24	Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the uncharacterized thioredoxin-like protein2 buv_1432 from bacteroides vulgatus
29	d1xd3a	Alignment	not modelled	24.7	47	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin carboxyl-terminal hydrolase UCH-L
30	d1a9xb1	Alignment	not modelled	24.2	32	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Carbamoyl phosphate synthetase, small subunit N-terminal domain Family: Carbamoyl phosphate synthetase, small subunit N-terminal domain
31	c2ywiA	Alignment	not modelled	24.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
32	d1cmxa	Alignment	not modelled	18.0	32	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin carboxyl-terminal hydrolase UCH-L
33	d1zzoa1	Alignment	not modelled	17.5	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
34	d1zj8a1	Alignment	not modelled	17.1	22	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
35	c2k6xA	Alignment	not modelled	16.6	24	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
36	c3lorB	Alignment	not modelled	14.3	16	PDB header: isomerase Chain: B: PDB Molecule: thiol-disulfide isomerase and thioredoxins; PDBTitle: the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
37	c1keeH	Alignment	not modelled	13.5	32	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
38	d1knga	Alignment	not modelled	13.1	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
39	d1t23a	Alignment	not modelled	13.1	43	Fold: Chromosomal protein MC1 Superfamily: Chromosomal protein MC1 Family: Chromosomal protein MC1
40	d1xm8a	Alignment	not modelled	12.9	13	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
41	c3kebB	Alignment	not modelled	12.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: probable thiol peroxidase; PDBTitle: thiol peroxidase from throbacterium violaceum
42	c1y88A	Alignment	not modelled	12.2	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1548; PDBTitle: crystal structure of protein of unknown function af1548
43	c3uinD	Alignment	not modelled	11.9	13	PDB header: ligase/isomerase/protein binding Chain: D: PDB Molecule: e3 sumo-protein ligase ranbp2; PDBTitle: complex between human rangap1-sumo2, ubc9 and the ir1 domain from2 ranbp2
44	c1u3eM	Alignment	not modelled	11.3	53	PDB header: dna binding protein/dna Chain: M: PDB Molecule: hnh homing endonuclease; PDBTitle: dna binding and cleavage by the hnh homing endonuclease i-hmui
45	c1r6tA	Alignment	not modelled	11.1	15	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of human tryptophanyl-trna synthetase
46	d1zofa1	Alignment	not modelled	10.8	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
47	c2lvIA	Alignment	not modelled	10.5	36	PDB header: lantibiotic-binding-protein Chain: A: PDB Molecule: spai; PDBTitle: nmr structure the lantibiotic immunity protein spai
48	c3gknA	Alignment	not modelled	10.2	31	PDB header: oxidoreductase Chain: A: PDB Molecule: bacterioferritin comigratory protein; PDBTitle: insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
49	c3t2dA	Alignment	not modelled	9.9	19	PDB header: lyase, hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphate aldolase/phosphatase; PDBTitle: fructose-1,6-bisphosphate aldolase/phosphatase from thermoproteus2 neutrophilus, fbp-bound form
50	c2ywnA	Alignment	not modelled	9.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxiredoxin-like protein; PDBTitle: crystal structure of peroxiredoxin-like protein from2 sulfolobus tokodaii
51	c2p5qA	Alignment	not modelled	9.6	47	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 5; PDBTitle: crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
52	c4fo5A	Alignment	not modelled	9.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-like protein; PDBTitle: crystal structure of a thioredoxin-like protein (bdi_1100) from2 parabacteroides distazonis atcc 8503 at 2.02 a resolution PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin family protein;

53	c4evmA	Alignment	not modelled	9.4	5	PDBTitle: 1.5 angstrom crystal structure of soluble domain of membrane-anchored2 thioredoxin family protein from streptococcus pneumoniae strain3 canada mdr_19a
54	c3cynC	Alignment	not modelled	9.2	25	PDB header: oxidoreductase Chain: C: PDB Molecule: probable glutathione peroxidase 8; PDBTitle: the structure of human gpX8
55	c3dvwB	Alignment	not modelled	9.2	25	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione peroxidase-like protein; PDBTitle: glutathione peroxidase-type tryparedoxin peroxidase, oxidized form
56	c2obiA	Alignment	not modelled	8.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: phospholipid hydroperoxide glutathione peroxidase3 (gpX4) PDBTitle: crystal structure of the selenocysteine to cysteine mutant2 of human phospholipid hydroperoxide glutathione peroxidase3 (gpX4)
57	c3u5rG	Alignment	not modelled	8.4	21	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein smc02350 from2 sinorhizobium meliloti 1021
58	d1jfua	Alignment	not modelled	8.2	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
59	d2hq4a1	Alignment	not modelled	8.1	14	Fold: PH1570-like Superfamily: PH1570-like Family: PH1570-like
60	d1r6ta2	Alignment	not modelled	8.1	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
61	c1lrjA	Alignment	not modelled	8.0	16	PDB header: hormone/growth factor Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
62	c1d0rA	Alignment	not modelled	8.0	24	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon-like peptide-1-(7-36)-amide; PDBTitle: solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
63	d1gp1a	Alignment	not modelled	7.8	67	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
64	c3a7sA	Alignment	not modelled	7.7	24	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase isozyme I5; PDBTitle: catalytic domain of uch37
65	c2ls5A	Alignment	not modelled	7.5	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a putative protein disulfide isomerase from2 bacteroides thetaiotaomicron
66	c2wdtA	Alignment	not modelled	7.4	21	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase I3; PDBTitle: crystal structure of plasmodium falciparum uchI3 in complex2 with the suicide inhibitor ubvme
67	c1z5sD	Alignment	not modelled	7.2	13	PDB header: ligase Chain: D: PDB Molecule: ran-binding protein 2; PDBTitle: crystal structure of a complex between ubc9, sumo-1,2 rangap1 and nup358/ranbp2
68	d1xhoa	Alignment	not modelled	7.2	20	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
69	c1xhoB	Alignment	not modelled	7.2	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: chorismate mutase; PDBTitle: chorismate mutase from clostridium thermocellum cth-682
70	c2r37A	Alignment	not modelled	7.1	24	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 3; PDBTitle: crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
71	d2f8aa1	Alignment	not modelled	6.8	67	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
72	c2l5oA	Alignment	not modelled	6.8	31	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin; PDBTitle: solution structure of a putative thioredoxin from neisseria2 meningitidis
73	c2kgsA	Alignment	not modelled	6.6	21	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein rv0899/mt0922; PDBTitle: solution structure of the amino-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
74	d1zyea1	Alignment	not modelled	6.5	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
75	c4hdeA	Alignment	not modelled	6.5	38	PDB header: lipid binding protein Chain: A: PDB Molecule: sco1/senc family lipoprotein; PDBTitle: the crystal structure of a sco1/senc family lipoprotein from bacillus2 anthracis str. ames
76	c3tueB	Alignment	not modelled	6.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: tryparedoxin peroxidase; PDBTitle: the structure of tryparedoxin peroxidase i from leishmania major
77	c3ewlA	Alignment	not modelled	6.3	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein bf1870; PDBTitle: crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
78	d1vl6a1	Alignment	not modelled	6.3	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain PDB header: transferase

79	c2fyoA_	Alignment	not modelled	6.3	21	Chain: A: PDB Molecule: carnitine o-palmitoyltransferase ii, PDBTitle: crystal structure of rat carnitine palmitoyltransferase 22 in space group p43212
80	c2ke4A_	Alignment	not modelled	6.0	5	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
81	d1pj3a1	Alignment	not modelled	6.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
82	c2b1kA_	Alignment	not modelled	6.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbe; PDBTitle: crystal structure of e. coli ccmg protein
83	c4eo3A_	Alignment	not modelled	5.9	31	PDB header: oxidoreductase Chain: A: PDB Molecule: bacterioferritin comigratory protein/nadh dehydrogenase; PDBTitle: peroxiredoxin nitroreductase fusion enzyme
84	c2h66G_	Alignment	not modelled	5.9	30	PDB header: structural genomics/oxidoreductase Chain: G: PDB Molecule: pv-pf14_0368; PDBTitle: the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
85	c2he3A_	Alignment	not modelled	5.8	26	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 2; PDBTitle: crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gpx2)
86	c3eurA_	Alignment	not modelled	5.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the c-terminal domain of uncharacterized protein2 from bacteroides fragilis nctc 9343
87	c4ka0C_	Alignment	not modelled	5.7	12	PDB header: oxidoreductase Chain: C: PDB Molecule: putative thiol-disulfide oxidoreductase; PDBTitle: crystal structure of a putative thiol-disulfide oxidoreductase from2 bacteroides vulgatus (target nysgrc-011676), space group p21221
88	d1m98a1	Alignment	not modelled	5.6	14	Fold: Orange carotenoid protein, N-terminal domain Superfamily: Orange carotenoid protein, N-terminal domain Family: Orange carotenoid protein, N-terminal domain
89	c4htyA_	Alignment	not modelled	5.5	13	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of a metagenome-derived cellulase cel5a
90	d1o0sa1	Alignment	not modelled	5.5	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
91	d1lu4a_	Alignment	not modelled	5.5	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
92	c2p18A_	Alignment	not modelled	5.5	11	PDB header: hydrolase Chain: A: PDB Molecule: glyoxalase ii; PDBTitle: crystal structure of the leishmania infantum glyoxalase ii
93	c2lrnA_	Alignment	not modelled	5.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: solution structure of a thiol:disulfide interchange protein from2 bacteroides sp.
94	c2bmxB_	Alignment	not modelled	5.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxidase c; PDBTitle: mycobacterium tuberculosis ahpc
95	c2p7jA_	Alignment	not modelled	5.3	25	PDB header: transcription Chain: A: PDB Molecule: putative sensory box/ggdef family protein; PDBTitle: crystal structure of the domain of putative sensory box/ggdef family2 protein from vibrio parahaemolyticus
96	c2m72A_	Alignment	not modelled	5.3	31	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized thioredoxin-like protein; PDBTitle: solution structure of uncharacterized thioredoxin-like protein pg_21752 from porphyromonas gingivalis
97	c4je1A_	Alignment	not modelled	5.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: probable thiol peroxidase; PDBTitle: crystal structure of thiol peroxidase from burkholderia cenocepacia2 j2315
98	d1gq2a1	Alignment	not modelled	5.2	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
99	c2j8aA_	Alignment	not modelled	5.2	18	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-4 PDBTitle: x-ray structure of the n-terminus rrm domain of set1