Phyre^2

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Description	P0ABV2
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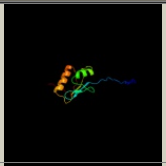
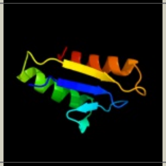
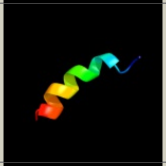
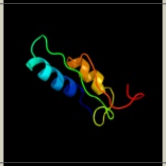
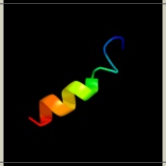
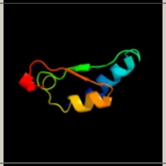
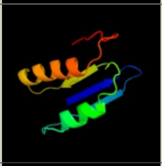
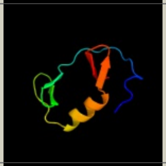
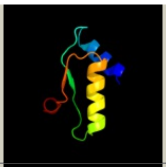
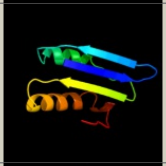
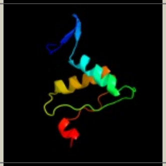
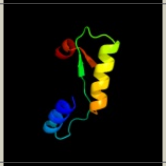
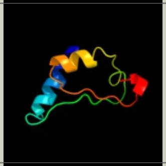
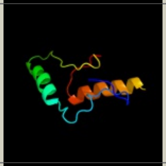
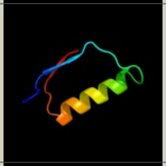
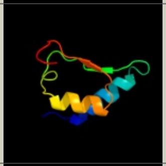
Unique Job ID	337d86223ff0c2e8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pfuA_	Alignment		99.8	100	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**biopolymer transport exbd protein; **PDBTitle:** nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
2	c2jwlB_	Alignment		99.4	28	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
3	d2axtk1	Alignment		49.0	31	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein K, PsbK **Family:**PsbK-like
4	c3a0bK_	Alignment		45.2	31	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
5	c3e6eC_	Alignment		35.6	10	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
6	c3a0bk_	Alignment		35.2	31	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
7	d1bd0a2	Alignment		29.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
8	c2jvfA_	Alignment		28.2	21	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
9	c2re3A_	Alignment		27.6	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
10	c3a0hk_	Alignment		26.0	31	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
11	d2e8aa1	Alignment		25.1	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70

12	d1jcea1	Alignment		25.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
13	c1qysA_	Alignment		22.5	17	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
14	d1dkgd1	Alignment		20.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
15	d1bupa1	Alignment		19.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
16	d1vfsa2	Alignment		19.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
17	c1ur8B_	Alignment		18.4	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**chitinase b; **PDBTitle:** interactions of a family 18 chitinase with the designed2 inhibitor hm508, and its degradation product,3 chitobiono-delta-lactone
18	c3ugsB_	Alignment		18.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
19	c1vftA_	Alignment		17.8	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
20	c3ghfA_	Alignment		17.5	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the septum site-determining protein2 minc from salmonella typhimurium
21	c3co8B_	Alignment	not modelled	16.6	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from oenococcus oeni
22	c3lupA_	Alignment	not modelled	16.5	18	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
23	c2c2xB_	Alignment	not modelled	16.3	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
24	d1edza2	Alignment	not modelled	16.1	9	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
25	c3me8B_	Alignment	not modelled	15.8	11	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of putative electron transfer protein aq_2194 from2 aquifex aeolicus vf5
26	c1niuA_	Alignment	not modelled	15.7	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** alanine racemase with bound inhibitor derived from l-2 cycloserine
27	d1qyia_	Alignment	not modelled	14.9	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
28	d1goia2	Alignment	not modelled	14.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase

29	c3oo2A_	Alignment	not modelled	13.6	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
30	d2d0oa1	Alignment	not modelled	12.5	17	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Swiveling domain of dehydratase reactivase alpha subunit **Family:**Swiveling domain of dehydratase reactivase alpha subunit
31	c3pm6B_	Alignment	not modelled	12.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
32	c3outC_	Alignment	not modelled	11.9	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
33	d1a9xa4	Alignment	not modelled	11.7	11	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
34	d2j9ga2	Alignment	not modelled	11.5	7	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
35	c2g7zB_	Alignment	not modelled	11.4	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein spy1493; **PDBTitle:** conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
36	c3iprC_	Alignment	not modelled	10.8	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
37	d1b0aa2	Alignment	not modelled	10.8	4	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
38	d1wd5a_	Alignment	not modelled	10.8	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
39	c1xfcB_	Alignment	not modelled	10.7	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** the 1.9 a crystal structure of alanine racemase from mycobacterium2 tuberculosis contains a conserved entryway into the active site
40	d2axth1	Alignment	not modelled	10.5	18	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II 10 kDa phosphoprotein PsbH **Family:**PsbH-like
41	d1ne9a1	Alignment	not modelled	10.5	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
42	d2p10a1	Alignment	not modelled	10.0	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
43	c2dy3B_	Alignment	not modelled	9.9	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from corynebacterium glutamicum
44	c2ra9A_	Alignment	not modelled	9.5	5	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf1285; **PDBTitle:** crystal structure of a duf1285 family protein (sbal_2486) from2 shewanella baltica os155 at 1.40 a resolution
45	c2odoC_	Alignment	not modelled	9.4	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of pseudomonas fluorescens alanine racemase
46	d1f75a_	Alignment	not modelled	9.2	19	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
47	c1p74B_	Alignment	not modelled	9.2	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
48	c3a0hY_	Alignment	not modelled	8.7	10	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
49	c3bz1y_	Alignment	not modelled	8.7	10	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii protein y; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
50	c3a0hy_	Alignment	not modelled	8.7	10	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
51	c3a0by_	Alignment	not modelled	8.5	10	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
52	d1gph11	Alignment	not modelled	8.4	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
53	c3arcY_	Alignment	not modelled	8.3	10	**PDB header:**electron transport, photosynthesis **Chain:** Y: **PDB Molecule:**protein ycf12; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
54	c3arcy_	Alignment	not modelled	8.3	10	**PDB header:**electron transport, photosynthesis **Chain:** Y: **PDB Molecule:**protein ycf12; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution

55	d1gvfa_	Alignment	not modelled	8.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
56	c1jp3A_	Alignment	not modelled	8.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of e.coli undecaprenyl pyrophosphate synthase
57	d1ecfa1	Alignment	not modelled	7.9	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
58	c3eooL_	Alignment	not modelled	7.8	15	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
59	d2nn6d2	Alignment	not modelled	7.7	8	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
60	d1hgxa_	Alignment	not modelled	7.6	8	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
61	d1rvga_	Alignment	not modelled	7.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
62	c3qm3C_	Alignment	not modelled	7.4	9	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
63	c3gmgB_	Alignment	not modelled	7.3	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rv1825/mt1873; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
64	c3o8qB_	Alignment	not modelled	7.2	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase i alpha; **PDBTitle:** 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
65	c2vfwB_	Alignment	not modelled	6.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**short-chain z-isoprenyl diphosphate synthetase; **PDBTitle:** rv1086 native
66	d1ueha_	Alignment	not modelled	6.8	10	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
67	d1zhva2	Alignment	not modelled	6.7	37	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
68	c3gycB_	Alignment	not modelled	6.7	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glycoside hydrolase; **PDBTitle:** crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
69	c3a0bY_	Alignment	not modelled	6.7	10	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
70	d1g8fa3	Alignment	not modelled	6.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
71	c2d2rA_	Alignment	not modelled	6.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
72	c2f40A_	Alignment	not modelled	6.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf1455; **PDBTitle:** structure of a novel protein from backbone-centered nmr data and nmr-2 assisted structure prediction
73	d1i5ea_	Alignment	not modelled	5.8	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
74	c2qlxA_	Alignment	not modelled	5.8	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**l-rhamnose mutarotase; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
75	c2qlwA_	Alignment	not modelled	5.8	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rhau; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
76	c2dcqA_	Alignment	not modelled	5.8	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative protein at4g01050; **PDBTitle:** fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
77	c3oo2B_	Alignment	not modelled	5.7	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
78	d1zzoa1	Alignment	not modelled	5.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
79	d2bz1a1	Alignment	not modelled	5.5	20	**Fold:**RibA-like **Superfamily:**RibA-like **Family:**RibA-like
80	d1x8da1	Alignment	not modelled	5.5	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YiiL-like
						PDB header:transferase

81	c1ecjB_	Alignment	not modelled	5.3	20	**Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
82	d1g9sa_	Alignment	not modelled	5.2	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
83	c1yfzA_	Alignment	not modelled	5.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
84	d1yfza1	Alignment	not modelled	5.2	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
85	c3l8cA_	Alignment	not modelled	5.2	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** structure of probable d-alanine--poly(phosphoribitol) ligase2 subunit-1 from streptococcus pyogenes
86	c3q94B_	Alignment	not modelled	5.2	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
87	c3navB_	Alignment	not modelled	5.1	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
88	d1xd7a_	Alignment	not modelled	5.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
89	d1aopa1	Alignment	not modelled	5.1	15	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
90	d1ujpa_	Alignment	not modelled	5.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
91	d1ulza2	Alignment	not modelled	5.1	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
92	d1rhsa1	Alignment	not modelled	5.1	10	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
93	d1zj8a1	Alignment	not modelled	5.0	14	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3