Phyre^2

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Description	P77147
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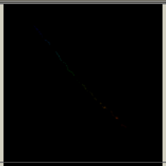
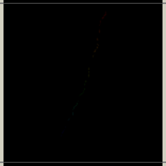
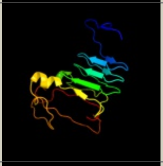
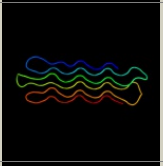
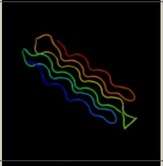
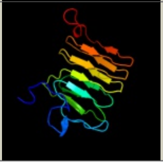
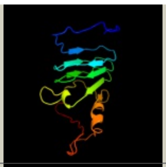
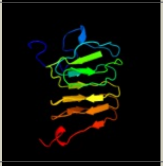
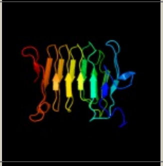
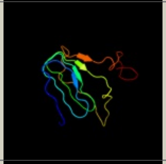
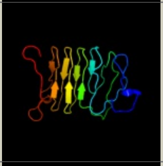
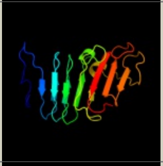
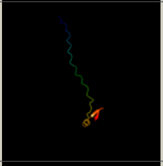
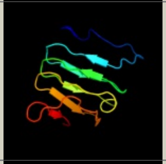
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygvA_	Alignment		99.2	13	**PDB header:**structural protein/contractile protein **Chain:** A: **PDB Molecule:**collagen i alpha 1; **PDBTitle:** the structure of collagen type i. single type i collagen2 molecule: rigid refinment
2	c1y0fB_	Alignment		98.8	13	**PDB header:**structural protein/contractile protein **Chain:** B: **PDB Molecule:**collagen i alpha 2; **PDBTitle:** the structure of collagen type i. single type i collagen2 molecule
3	c2qubG_	Alignment		97.7	13	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**extracellular lipase; **PDBTitle:** crystal structure of extracellular lipase lipa from serratia2 marcescens
4	c2zj6A_	Alignment		97.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
5	c1satA_	Alignment		97.0	16	**PDB header:**hydrolase (serine protease) **Chain:** A: **PDB Molecule:**serratia protease; **PDBTitle:** crystal structure of the 50 kda metallo protease from s.2 marcescens
6	c3bogB_	Alignment		96.6	13	**PDB header:**antifreeze protein **Chain:** B: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein quasi-racemate
7	c3bogA_	Alignment		96.6	13	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein quasi-racemate
8	c2pneA_	Alignment		96.5	14	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** crystal structure of the snow flea antifreeze protein
9	c3boiB_	Alignment		96.5	14	**PDB header:**antifreeze protein **Chain:** B: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein racemate
10	c3boiA_	Alignment		96.5	14	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein racemate
11	d1kapp1	Alignment		95.5	14	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**beta-Roll **Family:**Serralysin-like metalloprotease, C-terminal domain

12	c1k7qA_	Alignment		95.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**secreted protease c; **PDBTitle:** prtc from erwinia chrysanthemi: e189a mutant
13	d1g9ka1	Alignment		94.6	16	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**beta-Roll **Family:**Serralysin-like metalloprotease, C-terminal domain
14	d1sata1	Alignment		94.3	12	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**beta-Roll **Family:**Serralysin-like metalloprotease, C-terminal domain
15	c2agmA_	Alignment		93.6	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**poly(beta-d-mannuronate) c5 epimerase 4; **PDBTitle:** solution structure of the r-module from alge4
16	d1k7ia1	Alignment		93.0	12	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**beta-Roll **Family:**Serralysin-like metalloprotease, C-terminal domain
17	c1om8A_	Alignment		92.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serralysin; **PDBTitle:** crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallyzed with 10 mm edta
18	c1nayC_	Alignment		92.1	8	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen-like peptide; **PDBTitle:** gpp-foldon:x-ray structure
19	c1jiwP_	Alignment		91.8	20	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
20	c3p4gD_	Alignment		62.9	14	**PDB header:**antifreeze protein **Chain:** D: **PDB Molecule:**antifreeze protein; **PDBTitle:** x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
21	d1ic8a2	Alignment		62.9	38	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
22	c1ezyA_	Alignment	not modelled	41.5	11	**PDB header:**signaling protein inhibitor **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 4; **PDBTitle:** high-resolution solution structure of free rgs4 by nmr
23	c2wauA_	Alignment	not modelled	39.2	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**erythrocyte membrane protein 1 (pfemp1); **PDBTitle:** structure of dbl6 epsilon domain from var2csa
24	d1zroa2	Alignment	not modelled	37.6	30	**Fold:**Duffy binding domain-like **Superfamily:**Duffy binding domain-like **Family:**Duffy binding domain
25	d1h8ba_	Alignment	not modelled	36.3	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
26	d1a9xa1	Alignment	not modelled	34.7	20	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
27	c2c6jA_	Alignment	not modelled	30.8	30	**PDB header:**receptor **Chain:** A: **PDB Molecule:**duffy receptor, alpha form; **PDBTitle:** structure of p. knowlesi dbl domain capable of binding2

						human duffy antigen
28	d2c6ja1	Alignment	not modelled	30.8	30	**Fold:**Duffy binding domain-like **Superfamily:**Duffy binding domain-like **Family:**Duffy binding domain
29	c2xu0A_	Alignment	not modelled	30.5	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**erythrocyte membrane protein 1; **PDBTitle:** crystal structure of the nts-dbl1(alpha-1) domain of the plasmodium2 falciparum membrane protein 1 (pfemp1) from the varo strain.
30	c3cpzA_	Alignment	not modelled	29.8	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**erythrocyte membrane protein 1; **PDBTitle:** crystal structure of var2csa dbl3x domain in the presence of2 dodecasaccharide of csa
31	d1zroa1	Alignment	not modelled	26.9	10	**Fold:**Duffy binding domain-like **Superfamily:**Duffy binding domain-like **Family:**Duffy binding domain
32	c1e17A_	Alignment	not modelled	23.9	36	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
33	c1kzzA_	Alignment	not modelled	19.9	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor associated factor 3; **PDBTitle:** downstream regulator tank binds to the cd40 recognition2 site on traf3
34	c2rngA_	Alignment	not modelled	19.8	7	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**big defensin; **PDBTitle:** solution structure of big defensin
35	d3bpya1	Alignment	not modelled	19.8	42	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
36	d1kq8a_	Alignment	not modelled	19.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
37	c1kq8A_	Alignment	not modelled	19.6	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 3 forkhead homolog 1; **PDBTitle:** solution structure of winged helix protein hfh-1
38	c3g73A_	Alignment	not modelled	19.1	42	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**forkhead box protein m1; **PDBTitle:** structure of the foxm1 dna binding
39	d1czya1	Alignment	not modelled	18.4	25	**Fold:**TRAF domain-like **Superfamily:**TRAF domain-like **Family:**MATH domain
40	c3chxG_	Alignment	not modelled	17.4	24	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**pmoc; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
41	d1l0aa1	Alignment	not modelled	17.1	25	**Fold:**TRAF domain-like **Superfamily:**TRAF domain-like **Family:**MATH domain
42	c1ca9D_	Alignment	not modelled	16.5	25	**PDB header:**tnf signaling **Chain:** D: **PDB Molecule:**protein (tnf receptor associated factor 2); **PDBTitle:** structure of tnf receptor associated factor 2 in complex2 with a peptide from tnf-r2
43	d1d5va_	Alignment	not modelled	16.4	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
44	d1lb6a_	Alignment	not modelled	15.8	19	**Fold:**TRAF domain-like **Superfamily:**TRAF domain-like **Family:**MATH domain
45	d2prva1	Alignment	not modelled	15.8	36	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
46	c1zroB_	Alignment	not modelled	15.7	10	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**erythrocyte binding antigen region ii; **PDBTitle:** crystal structure of eba-175 region ii (rii) crystallized2 in the presence of (alpha)2,3-sialyllactose
47	d2icga1	Alignment	not modelled	14.9	27	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
48	d1n1xa_	Alignment	not modelled	14.8	29	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
49	c3i7fA_	Alignment	not modelled	14.6	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
50	c1fllA_	Alignment	not modelled	14.6	25	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor associated factor 3; **PDBTitle:** molecular basis for cd40 signaling mediated by traf3
51	c2jrrA_	Alignment	not modelled	14.2	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q5lls5 from silicibacter2 pomeroyi. northeast structural genomics consortium target3 sir90
52	c3nuhB_	Alignment	not modelled	13.9	31	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
53	c3co7C_	Alignment	not modelled	13.6	25	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
						Fold:RNase A-like

54	d1b6va_	Alignment	not modelled	13.0	29	**Superfamily:**RNase A-like **Family:**Ribonuclease A-like
55	c2hkyA_	Alignment	not modelled	12.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease 7; **PDBTitle:** nmr solution structure of human rnase 7
56	d2c6ya1	Alignment	not modelled	12.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
57	d2a07f1	Alignment	not modelled	12.7	45	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
58	d1srna_	Alignment	not modelled	12.7	29	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
59	d1lq9a_	Alignment	not modelled	12.4	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Actinorhodin biosynthesis monooxygenase ActVa-Orf6
60	d1gqva_	Alignment	not modelled	11.2	29	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
61	c1ceuA_	Alignment	not modelled	11.1	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hiv-1 regulatory protein n-terminal **PDBTitle:** nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
62	c2kz6A_	Alignment	not modelled	11.0	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2
63	d1h8xa_	Alignment	not modelled	10.8	29	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
64	d2hfha_	Alignment	not modelled	10.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
65	c3fofD_	Alignment	not modelled	10.5	27	**PDB header:**isomerase/dna **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit b; **PDBTitle:** structural insight into the quinolone-dna cleavage complex2 of type iia topoisomerases
66	d1e7ua4	Alignment	not modelled	10.4	16	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Phoshoinositide 3-kinase (PI3K), catalytic domain
67	d1id3c_	Alignment	not modelled	10.3	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
68	d1agre_	Alignment	not modelled	10.1	11	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
69	c1agrE_	Alignment	not modelled	10.1	11	**PDB header:**complex (signal transduction/regulator) **Chain:** E: **PDB Molecule:**rgs4; **PDBTitle:** complex of alf4-activated gi-alpha-1 with rgs4
70	d1rraa_	Alignment	not modelled	10.0	29	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
71	c2z9fC_	Alignment	not modelled	9.9	12	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**cellulose synthase operon protein d; **PDBTitle:** crystal structure of axcesd protein from acetobacter xylinum
72	c1iojA_	Alignment	not modelled	9.9	26	**PDB header:**apolipoprotein **Chain:** A: **PDB Molecule:**apoc-i; **PDBTitle:** human apolipoprotein c-i, nmr, 18 structures
73	d1f7ca_	Alignment	not modelled	9.9	13	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
74	c1f7cA_	Alignment	not modelled	9.9	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rhogap protein; **PDBTitle:** crystal structure of the bh domain from graf, the gtpase2 regulator associated with focal adhesion kinase
75	d1tzya_	Alignment	not modelled	9.7	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
76	c3hwpA_	Alignment	not modelled	9.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phlg; **PDBTitle:** crystal structure and computational analyses provide insights into the2 catalytic mechanism of 2, 4-diacetylphloroglucinol hydrolase phlg3 from pseudomonas fluorescens
77	c3fbyC_	Alignment	not modelled	9.4	53	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**cartilage oligomeric matrix protein; **PDBTitle:** the crystal structure of the signature domain of cartilage oligomeric2 matrix protein.
78	c2zjtB_	Alignment	not modelled	9.3	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** crystal structure of dna gyrase b' domain sheds lights on2 the mechanism for t-segment navigation
79	c3ifuA_	Alignment	not modelled	9.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**non-structural protein; **PDBTitle:** the crystal structure of porcine reproductive and2 respiratory syndrome virus (prrsv) leader protease nsp1
						Fold: Heme oxygenase-like

80	d1j77a_	Alignment	not modelled	9.1	16	**Superfamily:**Heme oxygenase-like **Family:**Heme oxygenase HemO (PigA)
81	c3qwlA_	Alignment	not modelled	9.0	32	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**tbc1 domain family member 7; **PDBTitle:** crystal structure of human tbc1 domain family member 7
82	d1u35c1	Alignment	not modelled	9.0	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
83	c2kn6A_	Alignment	not modelled	8.8	23	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis-associated speck-like protein containing a card; **PDBTitle:** structure of full-length human asc (apoptosis-associated speck-like2 protein containing a card)
84	c2oq2B_	Alignment	not modelled	8.7	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
85	d1dy5a_	Alignment	not modelled	8.4	29	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
86	c3fqdA_	Alignment	not modelled	8.4	23	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**5'-3' exoribonuclease 2; **PDBTitle:** crystal structure of the s. pombe rat1-rai1 complex
87	c3bwvB_	Alignment	not modelled	8.3	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative 5'(3')-deoxyribonucleotidase; **PDBTitle:** crystal structure of deoxyribonucleotidase-like protein (np_764060.1)2 from staphylococcus epidermidis atcc 12228 at 1.55 a resolution
88	c3id6A_	Alignment	not modelled	8.2	67	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pre mrna splicing protein; **PDBTitle:** crystal structure of sulfolobus solfataricus nop5 (1-262) and2 fibrillarin complex
89	c2zpoA_	Alignment	not modelled	8.1	57	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** crystal structure of green turtle egg white ribonuclease
90	d1pbwa_	Alignment	not modelled	7.9	17	**Fold:**GTPase activation domain, GAP **Superfamily:**GTPase activation domain, GAP **Family:**BCR-homology GTPase activation domain (BH-domain)
91	d1kx3c_	Alignment	not modelled	7.8	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
92	d1juqa_	Alignment	not modelled	7.7	23	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
93	d1fx0b2	Alignment	not modelled	7.5	40	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
94	d1ucpa_	Alignment	not modelled	7.4	23	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Pyrin domain, PYD
95	d1ztda1	Alignment	not modelled	7.4	46	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**PF0609-like
96	d1dyta_	Alignment	not modelled	7.4	29	**Fold:**RNase A-like **Superfamily:**RNase A-like **Family:**Ribonuclease A-like
97	c1yo8A_	Alignment	not modelled	7.3	47	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thrombospondin-2; **PDBTitle:** structure of the c-terminal domain of human thrombospondin-2
98	c1f66C_	Alignment	not modelled	7.3	30	**PDB header:**structural protein/dna **Chain:** C: **PDB Molecule:**histone h2a.z; **PDBTitle:** 2.6 a crystal structure of a nucleosome core particle2 containing the variant histone h2a.z
99	d1f66c_	Alignment	not modelled	7.3	30	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones