Phyre^2

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Description	P0ADN0
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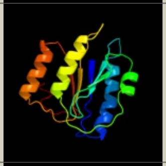
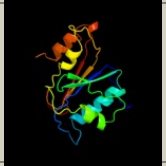
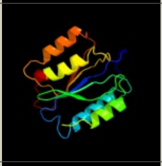
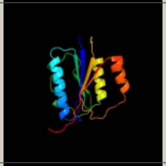
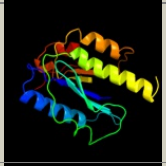
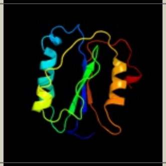
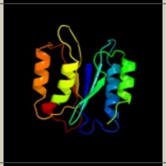
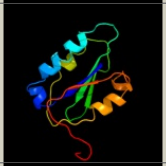
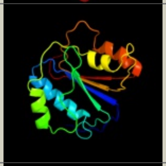
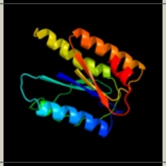
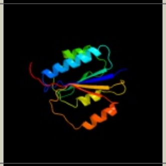
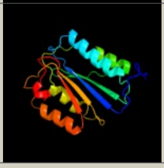
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yvra2	Alignment		99.6	16	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**RoRNP C-terminal domain-like
2	c2x5nA_	Alignment		99.6	10	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**26s proteasome regulatory subunit rpn10; **PDBTitle:** crystal structure of the sprpn10 vwa domain
3	c2nvoA_	Alignment		99.5	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ro sixty-related protein, rsr; **PDBTitle:** crystal structure of deinococcus radiodurans ro (rsr) protein
4	d2ok5a1	Alignment		99.5	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
5	d1jeyb2	Alignment		99.5	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Ku80 subunit N-terminal domain
6	c1rs0A_	Alignment		99.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement factor b; **PDBTitle:** crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
7	c2i6sA_	Alignment		99.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement c2a fragment; **PDBTitle:** complement component c2a
8	d1jeya2	Alignment		99.5	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Ku70 subunit N-terminal domain
9	c2x31F_	Alignment		99.5	22	**PDB header:**ligase **Chain:** F: **PDB Molecule:**magnesium-chelatase 60 kda subunit; **PDBTitle:** modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang
10	c2ok5A_	Alignment		99.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement factor b; **PDBTitle:** human complement factor b
11	c3ibsA_	Alignment		99.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein batb; **PDBTitle:** crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron

12	d1shux_	Alignment		99.3	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
13	c2iueA_	Alignment		99.3	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pactolus i-domain; **PDBTitle:** pactolus i-domain: functional switching of the rossmann2 fold
14	c1yvrA_	Alignment		99.3	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**60-kda ss-a/ro ribonucleoprotein; **PDBTitle:** ro autoantigen
15	c3n2nC_	Alignment		99.3	16	**PDB header:**toxin receptor **Chain:** C: **PDB Molecule:**anthrax toxin receptor 1; **PDBTitle:** the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain
16	c2xggB_	Alignment		99.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**microneme protein 2; **PDBTitle:** structure of toxoplasma gondii micronemal protein 2 a_i2 domain
17	d1q0pa_	Alignment		99.2	13	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
18	c2b2xB_	Alignment		99.2	11	**PDB header:**immune system **Chain:** B: **PDB Molecule:**integrin alpha-1; **PDBTitle:** vla1 rdeltah i-domain complexed with a quadruple mutant of the aqc22 fab
19	c1jeyB_	Alignment		99.1	12	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**ku80; **PDBTitle:** crystal structure of the ku heterodimer bound to dna
20	d1ijba_	Alignment		99.1	10	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
21	d1atza_	Alignment	not modelled	99.0	12	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
22	d1v7pc_	Alignment	not modelled	99.0	13	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
23	d1u0oc1	Alignment	not modelled	99.0	9	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
24	d1n3ya_	Alignment	not modelled	99.0	16	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
25	d1mf7a_	Alignment	not modelled	98.9	17	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
26	c3gxbB_	Alignment	not modelled	98.9	12	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**von willebrand factor; **PDBTitle:** crystal structure of vwf a2 domain
27	d1mjna_	Alignment	not modelled	98.9	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
28	d1ck4a_	Alignment	not modelled	98.9	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
29	d1pt6a_	Alignment	not modelled	98.8	12	**Fold:**vWA-like **Superfamily:**vWA-like

						Family: Integrin A (or I) domain
30	d1pd0a3	Alignment	not modelled	98.7	11	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Trunk domain of Sec23/24
31	d1tyeb2	Alignment	not modelled	98.4	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
32	c3ragA_	Alignment	not modelled	98.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
33	c1jeqA_	Alignment	not modelled	98.0	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ku70; **PDBTitle:** crystal structure of the ku heterodimer
34	c3fcuB_	Alignment	not modelled	97.8	14	**PDB header:**cell adhesion/blood clotting **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** structure of headpiece of integrin aiibb3 in open conformation
35	c1m2oA_	Alignment	not modelled	96.8	17	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
36	c1u8cB_	Alignment	not modelled	96.8	17	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** a novel adaptation of the integrin psi domain revealed from its2 crystal structure
37	c1pd0A_	Alignment	not modelled	96.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
38	c3eg9A_	Alignment	not modelled	96.1	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec23a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
39	c3egxB_	Alignment	not modelled	96.0	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
40	d2qtva3	Alignment	not modelled	95.8	17	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Trunk domain of Sec23/24
41	c3eg9B_	Alignment	not modelled	95.2	18	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sec24 related gene family, member d; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
42	c1m2vB_	Alignment	not modelled	95.2	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
43	c3k6sB_	Alignment	not modelled	95.0	21	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
44	c3eh2B_	Alignment	not modelled	94.4	17	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24c; **PDBTitle:** crystal structure of the human copii-coat protein sec24c
45	c3fniA_	Alignment	not modelled	41.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
46	d2hy5a1	Alignment	not modelled	40.5	8	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
47	c2yhsA_	Alignment	not modelled	34.5	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
48	c2h6jI_	Alignment	not modelled	32.4	19	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**proteasome beta-type subunit 1; **PDBTitle:** crystal structure of the beta f145a rhodococcus proteasome (casp2 target)
49	c3gehA_	Alignment	not modelled	31.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
50	d1ccwa_	Alignment	not modelled	30.4	12	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
51	d1jx7a_	Alignment	not modelled	30.4	11	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
52	d1xzpa1	Alignment	not modelled	29.7	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**TrmE connector domain **Family:**TrmE connector domain
53	c3nzxK_	Alignment	not modelled	29.4	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** K: **PDB Molecule:**proteasome component pre2; **PDBTitle:** crystal structure of the yeast 20s proteasome in complex with ligand2 2c
54	c3r84O_	Alignment	not modelled	27.7	16	**PDB header:**transcription **Chain:** O: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 11; **PDBTitle:** structure of the mediator head subcomplex med11/22
						Fold: Ntn hydrolase-like

55	d1rypl_	Alignment	not modelled	26.8	15	**Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
56	d1ofua1	Alignment	not modelled	26.5	14	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
57	d1skye1	Alignment	not modelled	25.5	32	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
58	d1ja1a2	Alignment	not modelled	23.4	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
59	d1fx0b1	Alignment	not modelled	22.4	28	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
60	d2bo4a1	Alignment	not modelled	22.1	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
61	d1g6ha_	Alignment	not modelled	21.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
62	c2f9iC_	Alignment	not modelled	20.9	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
63	d2a7sa2	Alignment	not modelled	19.8	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
64	d1vmea1	Alignment	not modelled	19.7	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
65	c3hlyA_	Alignment	not modelled	19.1	10	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
66	d2d1pa1	Alignment	not modelled	18.0	11	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
67	d2vapa1	Alignment	not modelled	18.0	14	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
68	c3glmD_	Alignment	not modelled	17.9	19	**PDB header:**lyase **Chain:** D: **PDB Molecule:**glutaconyl-coa decarboxylase subunit a; **PDBTitle:** glutaconyl-coa decarboxylase a subunit from clostridium2 symbiosum co-crystallized with crotonyl-coa
69	c1on3E_	Alignment	not modelled	17.7	19	**PDB header:**transferase **Chain:** E: **PDB Molecule:**methylmalonyl-coa carboxyltransferase 12s **PDBTitle:** transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
70	d1xnya2	Alignment	not modelled	17.5	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
71	c1vrgE_	Alignment	not modelled	16.4	21	**PDB header:**ligase **Chain:** E: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of propionyl-coa carboxylase, beta subunit (tm0716)2 from thermotoga maritima at 2.30 a resolution
72	d1l7vc_	Alignment	not modelled	16.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
73	d1p9pa_	Alignment	not modelled	16.4	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
74	c3pdiG_	Alignment	not modelled	16.0	14	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
75	c2cnwF_	Alignment	not modelled	15.8	15	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
76	d1fhea1	Alignment	not modelled	15.6	10	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
77	d2jdid1	Alignment	not modelled	15.5	20	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
78	c3cbnA_	Alignment	not modelled	15.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mth639; **PDBTitle:** crystal structure of a conserved protein (mth639) from2 methanobacterium thermoautotrophicum
79	d1qwga_	Alignment	not modelled	15.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
						Fold: ClpP/crotonase

80	d1pixa3	Alignment	not modelled	14.9	19	**Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
81	d1b8pa1	Alignment	not modelled	14.8	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
82	c1w57A_	Alignment	not modelled	14.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
83	d7mdha1	Alignment	not modelled	14.3	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
84	d1t98a2	Alignment	not modelled	14.2	18	**Fold:**STAT-like **Superfamily:**MukF C-terminal domain-like **Family:**MukF C-terminal domain-like
85	c1x0uB_	Alignment	not modelled	14.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical methylmalonyl-coa decarboxylase alpha subunit; **PDBTitle:** crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfolobus tokodaii
86	d1xw6a1	Alignment	not modelled	13.9	8	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
87	c2vliB_	Alignment	not modelled	13.2	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**antibiotic resistance protein; **PDBTitle:** structure of deinococcus radiodurans tunicamycin resistance2 protein
88	d5mdha1	Alignment	not modelled	13.1	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
89	d1n2za_	Alignment	not modelled	13.1	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
90	d1on3a2	Alignment	not modelled	13.1	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
91	c2r2vB_	Alignment	not modelled	13.1	28	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**gcn4 leucine zipper; **PDBTitle:** sequence determinants of the topology of the lac repressor2 tetrameric coiled coil
92	d1oyja1	Alignment	not modelled	12.9	13	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
93	c2a7sD_	Alignment	not modelled	12.9	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**probable propionyl-coa carboxylase beta chain 5; **PDBTitle:** crystal structure of the acyl-coa carboxylase, accd5, from2 mycobacterium tuberculosis
94	c3mtvA_	Alignment	not modelled	12.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**papain-like cysteine protease; **PDBTitle:** the crystal structure of the prrsv nonstructural protein nsp1
95	d1q5rh_	Alignment	not modelled	12.1	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
96	c3td4D_	Alignment	not modelled	12.0	24	**PDB header:**membrane protein,peptide binding protein **Chain:** D: **PDB Molecule:**outer membrane protein omp38; **PDBTitle:** crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate
97	d1civa1	Alignment	not modelled	11.7	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
98	d1irug_	Alignment	not modelled	11.7	13	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
99	d2i71a1	Alignment	not modelled	11.6	18	**Fold:**SSO1389-like **Superfamily:**SSO1389-like **Family:**Cas DxTHG