Phyre^2

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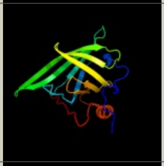
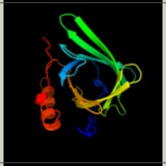
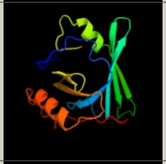
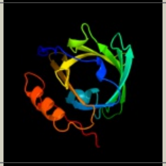
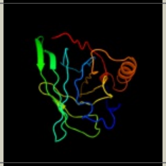
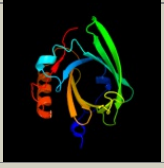
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qwda_	Alignment		100.0	98	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
2	c3cqrB_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**violaxanthin de-epoxidase, chloroplast; **PDBTitle:** crystal structure of the lipocalin domain of violaxanthin2 de-epoxidase (vde) at ph5
3	d1jyda_	Alignment		100.0	19	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
4	c3fmzB_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**retinol-binding protein 4; **PDBTitle:** crystal structure of retinol-binding protein 4 (rbp4) in2 complex with non-retinoid ligand
5	d1bbpa_	Alignment		100.0	23	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
6	d1kt7a_	Alignment		100.0	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
7	d1iiua_	Alignment		100.0	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
8	d1gkab_	Alignment		100.0	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
9	c3ebwA_	Alignment		100.0	21	**PDB header:**allergen **Chain:** A: **PDB Molecule:**per a 4 allergen; **PDBTitle:** crystal structure of major allergens, per a 4 from2 cockroaches
10	d1n0sa_	Alignment		100.0	24	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
11	d1i4ua_	Alignment		100.0	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like

12	c2hzqA_	Alignment		100.0	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**apolipoprotein d; **PDBTitle:** crystal structure of human apolipoprotein d (apod) in2 complex with progesterone
13	d1z24a1	Alignment		100.0	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
14	d1kxoa_	Alignment		100.0	23	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
15	d1x71a1	Alignment		100.0	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
16	d1qabe_	Alignment		100.0	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
17	c2l5pA_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipocalin 12; **PDBTitle:** solution nmr structure of protein lipocalin 12 from rat epididymis
18	c2k23A_	Alignment		99.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipocalin 2; **PDBTitle:** solution structure analysis of the rlcn2
19	c3by0B_	Alignment		99.9	13	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**neutrophil gelatinase-associated lipocalin; **PDBTitle:** crystal structure of siderocalin (ngal, lipocalin 2) w79a-r81a2 complexed with ferric enterobactin
20	d1lf7a_	Alignment		99.9	16	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
21	c2e4jA_	Alignment	not modelled	99.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**prostaglandin-h2 d-isomerase; **PDBTitle:** solution structure of mouse lipocalin-type prostaglandin d2 synthase
22	d1ew3a_	Alignment	not modelled	99.9	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
23	c2xstA_	Alignment	not modelled	99.9	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipocalin 15; **PDBTitle:** crystal structure of the human lipocalin 15
24	d1epba_	Alignment	not modelled	99.9	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
25	d1pm1x_	Alignment	not modelled	99.9	16	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
26	d1znda1	Alignment	not modelled	99.9	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
27	d1yupa1	Alignment	not modelled	99.9	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
28	d2a2ua_	Alignment	not modelled	99.9	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
29	d1beba_	Alignment	not modelled	99.9	18	**Fold:**Lipocalins **Superfamily:**Lipocalins

						Family: Retinol binding protein-like
30	d1exsa_	Alignment	not modelled	99.9	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
31	d1gm6a_	Alignment	not modelled	99.9	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
32	d1jzua_	Alignment	not modelled	99.9	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
33	c3l4rA_	Alignment	not modelled	99.9	14	**PDB header:**allergen, lipid binding protein **Chain:** A: **PDB Molecule:**minor allergen can f 2; **PDBTitle:** crystal structure of the dog lipocalin allergen can f 2 and2 implications for cross-reactivity to the cat allergen fel d 4
34	d1u17a1	Alignment	not modelled	99.9	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
35	d1x8qa_	Alignment	not modelled	99.9	18	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
36	c3bx6A_	Alignment	not modelled	99.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**alpha-1-acid glycoprotein; **PDBTitle:** crystal structure of human alpha 1 acid glycoprotein
37	d1avgi_	Alignment	not modelled	99.8	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Thrombin inhibitor
38	c2r73C_	Alignment	not modelled	99.7	17	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**trichosurin; **PDBTitle:** crystal structure of the possum milk whey lipocalin2 trichosurin at ph 8.2
39	d1gt1a_	Alignment	not modelled	99.6	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
40	c3fiqA_	Alignment	not modelled	99.6	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**odorant-binding protein 1f; **PDBTitle:** odorant binding protein obp1
41	d1bj7a_	Alignment	not modelled	99.6	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
42	d1e5pa_	Alignment	not modelled	99.5	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
43	d1xkia_	Alignment	not modelled	99.5	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
44	d1dzka_	Alignment	not modelled	99.4	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
45	c2wewA_	Alignment	not modelled	99.2	12	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipoprotein m; **PDBTitle:** crystal structure of human apom in complex with myristic2 acid
46	c3ebkA_	Alignment	not modelled	97.7	23	**PDB header:**allergen **Chain:** A: **PDB Molecule:**allergen bla g 4; **PDBTitle:** crystal structure of major allergens, bla g 4 from2 cockroaches
47	d1pgsa1	Alignment	not modelled	58.3	41	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**PHM/PNGase F **Family:**Glycosyl-asparaginase
48	c2k29A_	Alignment	not modelled	46.0	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
49	d2hsga1	Alignment	not modelled	44.0	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
50	d1lcda_	Alignment	not modelled	38.2	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
51	d2bjca1	Alignment	not modelled	36.1	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
52	d1qpza1	Alignment	not modelled	32.6	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
53	c2lcvA_	Alignment	not modelled	32.4	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
54	c2l8nA_	Alignment	not modelled	32.3	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
55	d1efaa1	Alignment	not modelled	31.2	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
56	d2cpga_	Alignment	not modelled	28.0	25	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like

57	d1uxca_	Alignment	not modelled	18.1	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
58	c2k5jB_	Alignment	not modelled	16.8	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
59	c3h5tA_	Alignment	not modelled	14.5	29	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum
60	c2eq9C_	Alignment	not modelled	14.1	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
61	c2kebA_	Alignment	not modelled	14.0	4	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
62	d3e9va1	Alignment	not modelled	13.3	22	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
63	d2z15a1	Alignment	not modelled	13.0	56	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
64	d1uxda_	Alignment	not modelled	12.9	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
65	c3brnA_	Alignment	not modelled	12.7	16	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**lipocalin; **PDBTitle:** crystal structure of am182 serotonin complex
66	d2b78a1	Alignment	not modelled	12.3	10	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
67	c2eq8C_	Alignment	not modelled	11.9	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
68	c2xlfA_	Alignment	not modelled	10.8	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**sll1785 protein; **PDBTitle:** structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
69	c2eq7C_	Alignment	not modelled	10.7	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
70	c3kjxD_	Alignment	not modelled	10.3	29	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from silicibacter pomeroyi
71	c1zvvA_	Alignment	not modelled	10.2	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
72	c3dv0I_	Alignment	not modelled	10.2	18	**PDB header:**oxidoreductase/transferase **Chain:** I: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
73	d2cyua1	Alignment	not modelled	9.5	14	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
74	d2hzab1	Alignment	not modelled	9.3	20	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
75	d1w85i_	Alignment	not modelled	8.8	18	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
76	d1xn7a_	Alignment	not modelled	8.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein YhgG
77	c1w3dA_	Alignment	not modelled	8.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
78	d2bsqe1	Alignment	not modelled	8.0	13	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Trafficking protein A-like
79	c3jv1A_	Alignment	not modelled	8.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**p22 protein; **PDBTitle:** crystal structure of the trypanosoma brucei p22 protein
80	d1yqfa1	Alignment	not modelled	8.0	9	**Fold:**Mitochondrial glycoprotein MAM33-like **Superfamily:**Mitochondrial glycoprotein MAM33-like **Family:**Mitochondrial glycoprotein MAM33-like
						PDB header:recombination, dna binding protein

81	c3c1dA_	Alignment	not modelled	7.9	6	**Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** x-ray crystal structure of recx
82	d1w4ha1	Alignment	not modelled	7.4	14	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
83	d1hmsa_	Alignment	not modelled	7.3	50	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
84	c2cooA_	Alignment	not modelled	7.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
85	c3eyiB_	Alignment	not modelled	7.2	15	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**z-dna-binding protein 1; **PDBTitle:** the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
86	c3qv0A_	Alignment	not modelled	7.1	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**mitochondrial acidic protein mam33; **PDBTitle:** crystal structure of saccharomyces cerevisiae mam33
87	d2hzaa1	Alignment	not modelled	7.1	20	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
88	d1p32a_	Alignment	not modelled	6.9	9	**Fold:**Mitochondrial glycoprotein MAM33-like **Superfamily:**Mitochondrial glycoprotein MAM33-like **Family:**Mitochondrial glycoprotein MAM33-like
89	c1zwvA_	Alignment	not modelled	6.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
90	c1w4kA_	Alignment	not modelled	6.6	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase e2; **PDBTitle:** peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
91	d2bj7a1	Alignment	not modelled	6.3	10	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
92	d1qfta_	Alignment	not modelled	6.1	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
93	d1myla_	Alignment	not modelled	6.0	29	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
94	d1wh7a_	Alignment	not modelled	6.0	48	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
95	c2zf8A_	Alignment	not modelled	5.9	5	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
96	d1fdqa_	Alignment	not modelled	5.9	25	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
97	d1bwya_	Alignment	not modelled	5.9	38	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
98	c2z0rA_	Alignment	not modelled	5.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0547; **PDBTitle:** crystal structure of hypothetical protein ttha0547
99	d1o8va_	Alignment	not modelled	5.7	50	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like