Phyre^2

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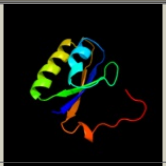
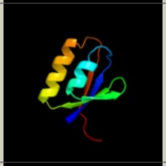
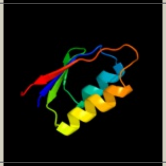
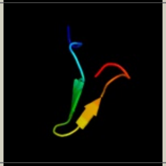
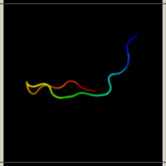
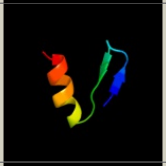
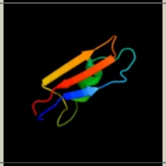
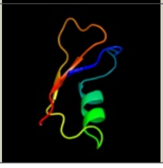
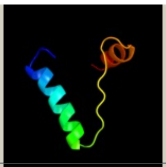
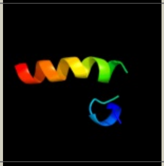
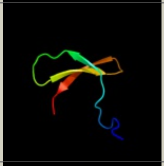
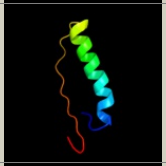
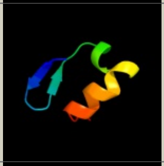
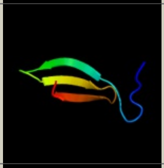
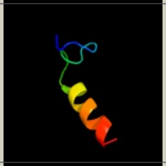
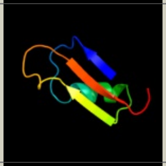
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3oq2A_	Alignment		71.3	14	**PDB header:**immune system **Chain:** A: **PDB Molecule:**crispr-associated protein cas2; **PDBTitle:** structure of a crispr associated protein cas2 from desulfovibrio2 vulgaris
2	d1zpwx1	Alignment		56.3	17	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
3	d2i0xa1	Alignment		44.4	24	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
4	d2ivya1	Alignment		39.2	16	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
5	c1yz4A_	Alignment		34.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase-like 15 isoform a; **PDBTitle:** crystal structure of dusp15
6	c2p4dA_	Alignment		29.1	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** structure-assisted discovery of variola major h12 phosphatase inhibitors
7	d1m3ga_	Alignment		22.5	12	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
8	c2e5jA_	Alignment		22.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**methenyltetrahydrofolate synthetase domain **PDBTitle:** solution structure of rna binding domain in2 methenyltetrahydrofolate synthetase domain containing
9	c1zzwA_	Alignment		21.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of catalytic domain of human map kinase2 phosphatase 5
10	d1h4vb1	Alignment		20.8	13	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
11	d1wf0a_	Alignment		20.5	23	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD

12	d1x52a1	Alignment		20.4	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
13	c3cwvB_	Alignment		20.0	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase, b subunit, truncated; **PDBTitle:** crystal structure of b-subunit of the dna gyrase from myxococcus2 xanthus
14	c2dgyA_	Alignment		19.8	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
15	d1f20a2	Alignment		19.5	8	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
16	c2r0bA_	Alignment		19.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine/tyrosine-interacting protein; **PDBTitle:** crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
17	c2oqkA_	Alignment		16.3	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
18	c3lnuA_	Alignment		15.7	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
19	c1no8A_	Alignment		15.7	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**aly; **PDBTitle:** solution structure of the nuclear factor aly rbd domain
20	d1no8a_	Alignment		15.7	13	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
21	c2osrA_	Alignment	not modelled	14.7	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolar protein 3; **PDBTitle:** nmr structure of rrm-2 of yeast npl3 protein
22	c2esbA_	Alignment	not modelled	14.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 18; **PDBTitle:** crystal structure of human dusp18
23	c3d0jA_	Alignment	not modelled	14.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ca_c3497; **PDBTitle:** crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
24	c2e0tA_	Alignment	not modelled	14.3	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 26; **PDBTitle:** crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
25	c3pgwP_	Alignment	not modelled	14.3	14	**PDB header:**splicing/dna/rna **Chain:** P: **PDB Molecule:**u1-a; **PDBTitle:** crystal structure of human u1 snrnp
26	c2wgpA_	Alignment	not modelled	14.2	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 14; **PDBTitle:** crystal structure of human dual specificity phosphatase 14
27	c2y96A_	Alignment	not modelled	13.4	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase dupd1; **PDBTitle:** structure of human dual-specificity phosphatase 27
28	c2oudA_	Alignment	not modelled	13.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the catalytic domain of human mkp5
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase;

29	c2hcmA_	Alignment	not modelled	13.2	17	**PDBTitle:** crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural genomics3 consortium
30	c1wrmA_	Alignment	not modelled	12.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 22; **PDBTitle:** crystal structure of jsp-1
31	c3ek1C_	Alignment	not modelled	12.6	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
32	d1jl0a_	Alignment	not modelled	12.4	12	**Fold:**S-adenosylmethionine decarboxylase **Superfamily:**S-adenosylmethionine decarboxylase **Family:**S-adenosylmethionine decarboxylase
33	c3jz4C_	Alignment	not modelled	11.8	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
34	d2f9da1	Alignment	not modelled	10.9	18	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
35	d1pvga2	Alignment	not modelled	10.6	24	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
36	c1qzrA_	Alignment	not modelled	10.1	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase ii; **PDBTitle:** crystal structure of the atpase region of saccharomyces cerevisiae2 topoisomerase ii bound to icrf-187 (dexrazoxane)
37	d2vgna3	Alignment	not modelled	10.1	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
38	c3emuA_	Alignment	not modelled	10.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine rich repeat and phosphatase domain **PDBTitle:** crystal structure of a leucine rich repeat and phosphatase2 domain containing protein from entamoeba histolytica
39	d1mkpa_	Alignment	not modelled	9.9	21	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
40	d2ghpa2	Alignment	not modelled	9.8	13	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
41	d1vhra_	Alignment	not modelled	9.6	38	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
42	c1zxnB_	Alignment	not modelled	9.4	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme; **PDBTitle:** human dna topoisomerase iia atpase/adp
43	d1uawa_	Alignment	not modelled	9.2	19	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
44	c2kkuA_	Alignment	not modelled	9.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein af2351 from archaeoglobus2 fulgidus. northeast structural genomics consortium target3 att9/ontario center for structural proteomics target af2351
45	d1o04a_	Alignment	not modelled	8.8	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
46	c3pgwS_	Alignment	not modelled	8.7	12	**PDB header:**splicing/dna/rna **Chain:** S: **PDB Molecule:**u1-70k; **PDBTitle:** crystal structure of human u1 snrnp
47	c2g6zB_	Alignment	not modelled	8.5	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 5; **PDBTitle:** crystal structure of human dusp5
48	c1flcB_	Alignment	not modelled	8.5	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**haemagglutinin-esterase-fusion glycoprotein; **PDBTitle:** x-ray structure of the haemagglutinin-esterase-fusion glycoprotein of2 influenza c virus
49	c2e44A_	Alignment	not modelled	8.3	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**insulin-like growth factor 2 mrna binding **PDBTitle:** solution structure of rna binding domain in insulin-like2 growth factor 2 mrna binding protein 3
50	d2cq3a1	Alignment	not modelled	8.2	20	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
51	d1sqwa1	Alignment	not modelled	8.0	14	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
52	d1vpqa_	Alignment	not modelled	8.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**TM1631-like **Family:**TM1631-like
53	c2gwoC_	Alignment	not modelled	7.9	33	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dual specificity protein phosphatase 13; **PDBTitle:** crystal structure of tmdp
54	c3ifgH_	Alignment	not modelled	7.6	21	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of succinate-semialdehyde

						dehydrogenase from2 burkholderia pseudomallei, part 1 of 2
55	d2cpja1	Alignment	not modelled	7.6	23	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
56	c3lyrA_	Alignment	not modelled	7.6	13	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**transcription factor coe1; **PDBTitle:** human early b-cell factor 1 (ebf1) dna-binding domain
57	c1s16B_	Alignment	not modelled	7.4	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of e. coli topoisomerase iv pare 43kda subunit2 complexed with adpnp
58	c2nt2C_	Alignment	not modelled	7.3	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein phosphatase slingshot homolog 2; **PDBTitle:** crystal structure of slingshot phosphatase 2
59	c2vgmA_	Alignment	not modelled	7.2	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dom34; **PDBTitle:** structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
60	c3ed6B_	Alignment	not modelled	6.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
61	c3b4wA_	Alignment	not modelled	6.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
62	c3s01A_	Alignment	not modelled	6.8	11	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein l; **PDBTitle:** crystal structure of a heterogeneous nuclear ribonucleoprotein l2 (hnrpl) from mus musculus at 2.15 a resolution
63	c3bs9A_	Alignment	not modelled	6.8	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolysin tia-1 isoform p40; **PDBTitle:** x-ray structure of human tia-1 rrm2
64	d1fjca_	Alignment	not modelled	6.7	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
65	c2hvzA_	Alignment	not modelled	6.7	23	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor, arginine/serine-rich 7; **PDBTitle:** solution structure of the rrm domain of sr rich factor 9g8
66	c3p6yD_	Alignment	not modelled	6.7	7	**PDB header:**rna binding protein/rna **Chain:** D: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 6; **PDBTitle:** cf im25-cf im68-uguaa complex
67	d1y0na_	Alignment	not modelled	6.6	14	**Fold:**YehU-like **Superfamily:**YehU-like **Family:**YehU-like
68	d1x4aa1	Alignment	not modelled	6.5	19	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
69	d1fnxh1	Alignment	not modelled	6.5	10	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
70	c2fhoB_	Alignment	not modelled	6.4	17	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**spliceosomal protein p14; **PDBTitle:** nmr solution structure of the human spliceosomal protein2 complex p14-sf3b155
71	c2i38A_	Alignment	not modelled	6.3	23	**PDB header:**rna binding protein/chimera **Chain:** A: **PDB Molecule:**fusion protein consists of immunoglobin g- **PDBTitle:** solution structure of the rrm of srp20
72	c3mlpE_	Alignment	not modelled	6.2	13	**PDB header:**transcription/dna **Chain:** E: **PDB Molecule:**transcription factor coe1; **PDBTitle:** early b-cell factor 1 (ebf1) bound to dna
73	c2zamA_	Alignment	not modelled	6.1	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
74	c3r31A_	Alignment	not modelled	6.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
75	c2e5gA_	Alignment	not modelled	6.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**u6 snrna-specific terminal uridylyltransferase 1; **PDBTitle:** solution structure of rna binding domain in rna binding2 motif protein 21
76	d2ghpa3	Alignment	not modelled	6.0	11	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
77	d2qwva1	Alignment	not modelled	5.9	29	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
78	c2krbA_	Alignment	not modelled	5.8	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 3 **PDBTitle:** solution structure of eif3b-rrm bound to eif3j peptide
79	d2cqia1	Alignment	not modelled	5.8	17	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
80	c1ei1B_	Alignment	not modelled	5.8	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase b; **PDBTitle:** dimerization of e. coli dna gyrase b provides a structural mechanism2 for activating the atpase catalytic center

81	c2vroB_	Alignment	not modelled	5.7	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
82	c2dngA_	Alignment	not modelled	5.7	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 4h; **PDBTitle:** solution structure of rna binding domain in eukaryotic2 translation initiation factor 4h
83	c1t90B_	Alignment	not modelled	5.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable methylmalonate-semialdehyde **PDBTitle:** crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
84	d1bxsa_	Alignment	not modelled	5.6	19	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
85	c3ep3A_	Alignment	not modelled	5.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**s-adenosylmethionine decarboxylase alpha chain; **PDBTitle:** human adometdc d174n mutant with no putrescine bound
86	c3mcaB_	Alignment	not modelled	5.5	14	**PDB header:**translation regulation/hydrolase **Chain:** B: **PDB Molecule:**protein dom34; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
87	d1fjeb2	Alignment	not modelled	5.5	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
88	d1wi8a_	Alignment	not modelled	5.5	12	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
89	d1a4sa_	Alignment	not modelled	5.4	20	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
90	d1ynya1	Alignment	not modelled	5.3	15	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
91	d1o89a2	Alignment	not modelled	5.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
92	d3dhwc1	Alignment	not modelled	5.3	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
93	d1x0fa1	Alignment	not modelled	5.2	28	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
94	c3cp0A_	Alignment	not modelled	5.2	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein implicated in regulation of membrane **PDBTitle:** crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
95	d1ky8a_	Alignment	not modelled	5.2	21	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
96	c2fc9A_	Alignment	not modelled	5.2	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ncl protein; **PDBTitle:** solution structure of the rrm_1 domain of ncl protein
97	c2fc8A_	Alignment	not modelled	5.1	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ncl protein; **PDBTitle:** solution structure of the rrm_1 domain of ncl protein