Phyre^2

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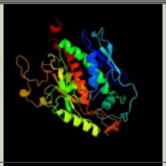
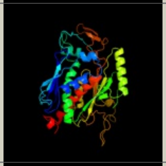
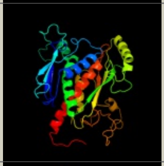
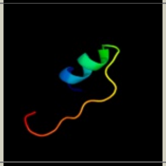
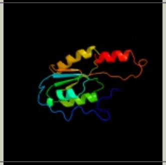
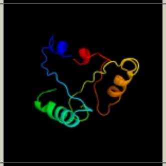
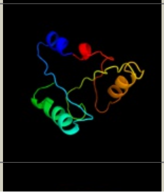
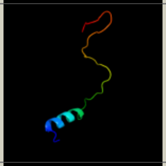
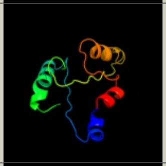
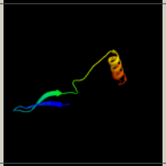
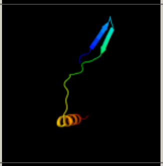
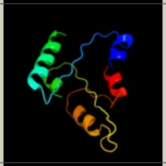
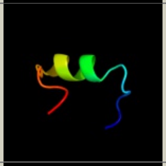
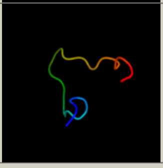
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1um0a_	Alignment		100.0	45	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
2	d1qxoa_	Alignment		100.0	38	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
3	c1ztbA_	Alignment		100.0	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**chorismate synthase; **PDBTitle:** crystal structure of chorismate synthase from mycobacterium2 tuberculosis
4	d1q1la_	Alignment		100.0	41	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
5	d1sq1a_	Alignment		100.0	45	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
6	d1r53a_	Alignment		100.0	51	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
7	c2k1hA_	Alignment		76.4	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ser13; **PDBTitle:** solution nmr structure of ser13 from staphylococcus epidermidis.2 northeast structural genomics consortium target ser13
8	d2ffma1	Alignment		73.0	13	**Fold:**Hypothetical protein SAV1430 **Superfamily:**Hypothetical protein SAV1430 **Family:**Hypothetical protein SAV1430
9	c3r3sD_	Alignment		61.2	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase; **PDBTitle:** structure of the ygha oxidoreductase from salmonella enterica
10	d1o4va_	Alignment		61.1	25	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
11	c3lp6D_	Alignment		58.6	31	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution

12	d1qcza_	Alignment		54.8	21	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
13	c1m1gB_	Alignment		53.4	28	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
14	d1xmpa_	Alignment		44.9	23	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
15	c2ekmC_	Alignment		40.6	24	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein st1511; **PDBTitle:** structure of st1219 protein from sulfolobus tokodaii
16	d1vgga_	Alignment		39.1	23	**Fold:**Ta1353-like **Superfamily:**Ta1353-like **Family:**Ta1353-like
17	c3trhI_	Alignment		35.4	24	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
18	c2xznF_	Alignment		35.4	13	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**eif1; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
19	c2lhuA_	Alignment		32.7	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
20	d1ciya1	Alignment		31.1	33	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
21	d1ji6a1	Alignment	not modelled	29.3	24	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
22	c2d16B_	Alignment	not modelled	27.9	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph1918; **PDBTitle:** crystal structure of ph1918 protein from pyrococcus horikoshii ot3
23	c3orsD_	Alignment	not modelled	26.5	16	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
24	c3rggD_	Alignment	not modelled	23.0	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
25	d1dlca1	Alignment	not modelled	22.6	29	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
26	d1qlwa_	Alignment	not modelled	22.6	28	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**A novel bacterial esterase
27	c2ywxA_	Alignment	not modelled	17.8	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
28	d2za7a1	Alignment	not modelled	16.0	42	**Fold:**Ferritin-like **Superfamily:**Ferritin-like

						Family: Ferritin
29	d1z6om1	Alignment	not modelled	15.9	32	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
30	c2w3pB_	Alignment	not modelled	13.9	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**benzoyl-coa-dihydrodiol lyase; **PDBTitle:** boxc crystal structure
31	c2ejeA_	Alignment	not modelled	13.7	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
32	c3mcaB_	Alignment	not modelled	13.1	20	**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
33	c2dn5A_	Alignment	not modelled	13.0	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
34	c2a73B_	Alignment	not modelled	12.7	16	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement c3; **PDBTitle:** human complement component c3
35	c2dzrA_	Alignment	not modelled	12.3	58	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
36	d1q60a_	Alignment	not modelled	12.1	42	**Fold:**GTF2I-like repeat **Superfamily:**GTF2I-like repeat **Family:**GTF2I-like repeat
37	c2d99A_	Alignment	not modelled	12.1	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
38	c1w99A_	Alignment	not modelled	12.1	24	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidial crystal protein cry4ba; **PDBTitle:** mosquito-larvicidal toxin cry4ba from bacillus2 thuringiensis ssp. israelensis
39	c3b8hA_	Alignment	not modelled	11.9	50	**PDB header:**biosynthetic protein/transferase **Chain:** A: **PDB Molecule:**elongation factor 2; **PDBTitle:** structure of the eef2-exoa(e546a)-nad+ complex
40	c2dn4A_	Alignment	not modelled	11.7	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
41	d1r03a_	Alignment	not modelled	11.4	43	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
42	d1g9pa_	Alignment	not modelled	11.3	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
43	c1g9pA_	Alignment	not modelled	11.3	100	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omega-atracotoxin-hv2a; **PDBTitle:** solution structure of the insecticidal calcium channel2 blocker omega-atracotoxin-hv2a
44	c2c9kA_	Alignment	not modelled	11.1	38	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidal crystal protein cry4aa; **PDBTitle:** structure of the functional form of the mosquito-larvicidal2 cry4aa toxin from bacillus thuringiensis at 2.8 a3 resolution
45	c2k4mA_	Alignment	not modelled	11.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0146 protein mth_1000; **PDBTitle:** solution nmr structure of m. thermoautotrophicum protein2 mth_1000, northeast structural genomics consortium target3 tr8
46	c2e3lA_	Alignment	not modelled	10.8	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor gtf2ird2 beta; **PDBTitle:** solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna
47	c2ed2A_	Alignment	not modelled	10.7	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
48	d2ceia1	Alignment	not modelled	10.5	40	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
49	c2dzqA_	Alignment	not modelled	10.4	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
50	d1rcda_	Alignment	not modelled	10.0	32	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
51	d1x52a1	Alignment	not modelled	9.7	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
52	d2fzcb1	Alignment	not modelled	9.3	30	**Fold:**Ferredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain
						PDB header:transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase

53	c2h3eB_	Alignment	not modelled	8.7	28	regulatory chain; **PDBTitle:** structure of wild-type e. coli aspartate transcarbamoylase in the2 presence of n-phosphonacetyl-l-isoasparagine at 2.3a resolution
54	d1pg5b1	Alignment	not modelled	8.6	40	**Fold:**Ferredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain
55	d1nz9a_	Alignment	not modelled	8.6	53	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
56	c2b39B_	Alignment	not modelled	8.5	17	**PDB header:**immune system **Chain:** B: **PDB Molecule:**c3; **PDBTitle:** structure of mammalian c3 with an intact thioester at 3a resolution
57	c3izq1_	Alignment	not modelled	8.3	33	**PDB header:**ribosomal protein,hydrolase **Chain:** 1: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** structure of the dom34-hbs1-gdpnp complex bound to a translating2 ribosome
58	c3degC_	Alignment	not modelled	8.1	26	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
59	d2do3a1	Alignment	not modelled	8.1	47	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
60	c2be7E_	Alignment	not modelled	7.9	15	**PDB header:**transferase **Chain:** E: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** crystal structure of the unliganded (t-state) aspartate2 transcarbamoylase of the psychrophilic bacterium moritella profunda
61	c1pg5B_	Alignment	not modelled	7.7	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius
62	c2oghA_	Alignment	not modelled	7.7	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1; **PDBTitle:** solution structure of yeast eif1
63	c2ywfA_	Alignment	not modelled	7.6	24	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
64	c3bdeA_	Alignment	not modelled	7.2	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**mll5499 protein; **PDBTitle:** crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from mesorhizobium loti maff303099 at 1.79 a resolution
65	c2xg8D_	Alignment	not modelled	7.2	38	**PDB header:**transcription **Chain:** D: **PDB Molecule:**pipx; **PDBTitle:** structural basis of gene regulation by protein pii: the2 crystal complex of pii and pipx from synechococcus3 elongatus pcc 7942
66	c3n5bB_	Alignment	not modelled	7.1	38	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**asr0485 protein; **PDBTitle:** the complex of pii and pipx from anabaena
67	d2vgna3	Alignment	not modelled	7.1	7	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
68	c3cb4D_	Alignment	not modelled	7.1	31	**PDB header:**translation **Chain:** D: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** the crystal structure of lepa
69	c3kopB_	Alignment	not modelled	7.0	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
70	c2diuA_	Alignment	not modelled	6.9	28	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0430 protein; **PDBTitle:** solution structure of the rrm domain of kiaa0430 protein
71	c3seeA_	Alignment	not modelled	6.8	18	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**hypothetical sugar binding protein; **PDBTitle:** crystal structure of a hypothetical sugar binding protein (bt_4411)2 from bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
72	c3ebkA_	Alignment	not modelled	6.7	50	**PDB header:**allergen **Chain:** A: **PDB Molecule:**allergen bla g 4; **PDBTitle:** crystal structure of major allergens, bla g 4 from2 cockroaches
73	d1nppa2	Alignment	not modelled	6.6	43	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
74	c2xexA_	Alignment	not modelled	6.5	60	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g
75	d1l5oa_	Alignment	not modelled	6.5	21	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
76	c3tr5C_	Alignment	not modelled	6.5	47	**PDB header:**translation **Chain:** C: **PDB Molecule:**peptide chain release factor 3; **PDBTitle:** structure of a peptide chain release factor 3 (prfc) from

						coxiella2 burnetii
77	c2ywwA_	Alignment	not modelled	6.5	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** crystal structure of aspartate carbamoyltransferase2 regulatory chain from methanocaldococcus jannaschii
78	c1ciyA_	Alignment	not modelled	6.2	32	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cryia(a); **PDBTitle:** insecticidal toxin: structure and channel formation
79	c1dlcA_	Alignment	not modelled	5.9	28	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-endotoxin cryiiia; **PDBTitle:** crystal structure of insecticidal delta-endotoxin from2 bacillus thuringiensis at 2.5 angstroms resolution
80	d2atcb1	Alignment	not modelled	5.9	20	**Fold:**Ferredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain
81	c3bb5B_	Alignment	not modelled	5.8	9	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**stress responsive alpha-beta protein; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution
82	c2zxeG_	Alignment	not modelled	5.6	33	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
83	c1ji6A_	Alignment	not modelled	5.4	19	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidial crystal protein cry3bb; **PDBTitle:** crystal structure of the insecticidal bacterial del2 endotoxin cry3bb1 bacillus thuringiensis
84	d1vqot1	Alignment	not modelled	5.3	35	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
85	c1zn0B_	Alignment	not modelled	5.1	60	**PDB header:**translation/biosynthetic protein/rna **Chain:** B: **PDB Molecule:**elongation factor g; **PDBTitle:** coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdpnp) and rrf