Phyre2

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Description	P52119
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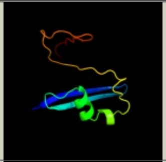
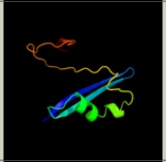
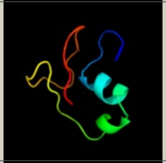
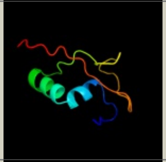
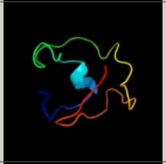
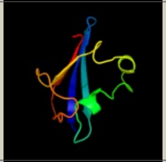
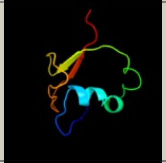
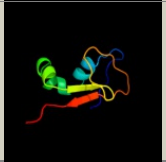
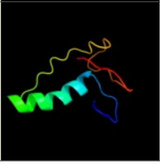
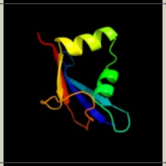
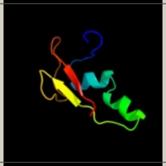
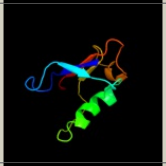
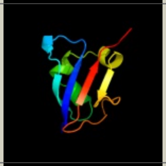
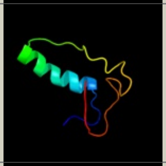
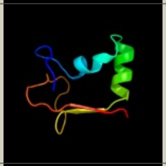
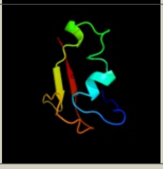
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hj1A_	Alignment		100.0	52	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
2	d2hj1a1	Alignment		100.0	52	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
3	c3hvzB_	Alignment		97.3	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
4	c2kmmA_	Alignment		97.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'- **PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
5	c2ekiA_	Alignment		96.8	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**developmentally-regulated gtp-binding protein 1; **PDBTitle:** solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
6	d1vjka_	Alignment		96.7	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
7	d1zud21	Alignment		96.6	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
8	d1wxqa2	Alignment		96.5	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
9	c2qieB_	Alignment		96.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
10	c3po0A_	Alignment		95.9	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1; **PDBTitle:** crystal structure of samp1 from haloferax volcanii
11	d1tkea1	Alignment		95.8	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain

12	d1wgka_	Alignment		94.9	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
13	c3cwiA_	Alignment		94.8	23	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
14	c2qjlA_	Alignment		94.5	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
15	c2kl0A_	Alignment		93.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
16	c2g1eA_	Alignment		93.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
17	c2l52A_	Alignment		92.9	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**methanosarcina acetivorans samp1 homolog; **PDBTitle:** solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
18	d1nyra2	Alignment		92.8	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
19	d2cu3a1	Alignment		92.7	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
20	d1tygb_	Alignment		91.9	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
21	d1xo3a_	Alignment	not modelled	91.5	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
22	d1fm0d_	Alignment	not modelled	91.0	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
23	c3dwmA_	Alignment	not modelled	90.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
24	c3u7zA_	Alignment	not modelled	89.8	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative metal binding protein rumgna_00854; **PDBTitle:** crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
25	c1tygG_	Alignment	not modelled	89.1	23	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
26	c2dwqB_	Alignment	not modelled	89.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**gtp-binding protein; **PDBTitle:** thermus thermophilus ychf gtp-binding protein
27	d1v8ca1	Alignment	not modelled	88.4	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
28	c1wxqA_	Alignment	not modelled	88.2	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3

29	c2k9xA_	Alignment	not modelled	87.2	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
30	d1rwsa_	Alignment	not modelled	86.8	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
31	c1v8cA_	Alignment	not modelled	86.4	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**moad related protein; **PDBTitle:** crystal structure of moad related protein from thermus2 thermophilus hb8
32	c3rpfC_	Alignment	not modelled	86.4	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**molybdopterin converting factor, subunit 1 (moad); **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
33	c1jalA_	Alignment	not modelled	84.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ychf protein; **PDBTitle:** ychf protein (hi0393)
34	c2ohfA_	Alignment	not modelled	82.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein 9; **PDBTitle:** crystal structure of human ola1 in complex with amppcp
35	c1wwtA_	Alignment	not modelled	81.3	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase
36	c1dm9A_	Alignment	not modelled	70.7	17	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
37	d1dm9a_	Alignment	not modelled	70.7	17	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
38	c1ni3A_	Alignment	not modelled	70.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ychf gtp-binding protein; **PDBTitle:** structure of the schizosaccharomyces pombe ychf gtpase
39	c3kt9A_	Alignment	not modelled	64.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
40	c2eh0A_	Alignment		64.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**kinesin-like protein kif1b; **PDBTitle:** solution structure of the fha domain from human kinesin-2 like protein kif1b
41	d1czpa_	Alignment	not modelled	59.5	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
42	c2k6pA_	Alignment	not modelled	56.7	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
43	c1yj5C_	Alignment	not modelled	55.7	29	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
44	d2fy8a2	Alignment	not modelled	52.0	13	**Fold:**TrkA C-terminal domain-like **Superfamily:**TrkA C-terminal domain-like **Family:**TrkA C-terminal domain-like
45	c2bs2E_	Alignment	not modelled	51.6	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
46	d1frda_	Alignment	not modelled	50.7	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
47	d1xr4a1	Alignment	not modelled	49.4	40	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
48	d1yjma1	Alignment	not modelled	49.0	28	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
49	c2wlbB_	Alignment	not modelled	45.6	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
50	d1offa_	Alignment	not modelled	45.5	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
51	c3fm8A_	Alignment	not modelled	45.5	14	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
52	c1tkeA_	Alignment	not modelled	44.2	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
53	d2fug33	Alignment	not modelled	41.0	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
						Fold: Alpha-L RNA-binding motif

54	d1p9ka_	Alignment	not modelled	40.3	8	**Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
55	d1krha3	Alignment	not modelled	38.4	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
56	d1pfda_	Alignment	not modelled	37.7	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
57	c3p42D_	Alignment	not modelled	37.6	10	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**predicted protein; **PDBTitle:** structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
58	d1doia_	Alignment	not modelled	37.2	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
59	c2e6zA_	Alignment	not modelled	37.0	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
60	d3c8ya2	Alignment	not modelled	36.5	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
61	d2cjoa_	Alignment	not modelled	34.6	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
62	c1c4cA_	Alignment	not modelled	34.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase); **PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
63	d1wlna1	Alignment	not modelled	34.4	8	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
64	d2bt6a1	Alignment	not modelled	33.1	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
65	d4fxca_	Alignment	not modelled	31.5	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
66	d2vbua1	Alignment	not modelled	30.8	40	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
67	d2g1la1	Alignment	not modelled	29.4	8	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
68	d1rp5a2	Alignment	not modelled	28.9	12	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
69	d1iuea_	Alignment	not modelled	28.6	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
70	c2fugC_	Alignment	not modelled	28.3	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
71	c3l5aA_	Alignment	not modelled	28.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
72	c3dh3C_	Alignment	not modelled	26.4	25	**PDB header:**isomerase/rna **Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
73	d1awda_	Alignment	not modelled	26.0	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
74	d1i7ha_	Alignment	not modelled	25.6	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
75	c3gqsB_	Alignment	not modelled	25.3	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
76	d1yvca1	Alignment	not modelled	25.2	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TRAM domain
77	d1ujxa_	Alignment	not modelled	23.9	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
78	c2bknA_	Alignment	not modelled	23.9	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein ph0236; **PDBTitle:** structure analysis of unknown function protein
79	c3ah7A_	Alignment	not modelled	23.7	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**[2fe-2s]ferredoxin; **PDBTitle:** crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
80	d2affa1	Alignment	not modelled	22.9	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain

						Family:FHA domain
81	d1frra_	Alignment	not modelled	22.8	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
82	d2jioa1	Alignment	not modelled	22.7	25	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
83	d1fxia_	Alignment	not modelled	22.6	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
84	d1vioa2	Alignment	not modelled	22.3	15	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
85	d1e0za_	Alignment	not modelled	22.2	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
86	d2brfa1	Alignment	not modelled	21.4	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
87	d1jq4a_	Alignment	not modelled	21.1	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
88	d1vyra_	Alignment	not modelled	20.6	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
89	c3lzkC_	Alignment	not modelled	20.5	44	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
90	d1iyjb4	Alignment	not modelled	19.7	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
91	d2iv2x1	Alignment	not modelled	18.5	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
92	d2ff4a3	Alignment	not modelled	18.2	22	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
93	d1uhta_	Alignment	not modelled	17.5	25	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
94	d2f06a1	Alignment	not modelled	17.2	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
95	d1k25a2	Alignment	not modelled	17.2	11	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
96	d2q1ma1	Alignment	not modelled	17.0	36	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
97	d1i94q_	Alignment	not modelled	16.7	42	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
98	d1t0ya_	Alignment	not modelled	16.3	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
99	c1t0yA_	Alignment	not modelled	16.3	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**tubulin folding cofactor b; **PDBTitle:** solution structure of a ubiquitin-like domain from tubulin-2 binding cofactor b