Phyre^2

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Description	Q47147
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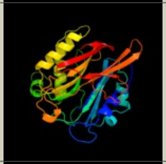
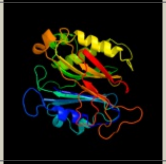
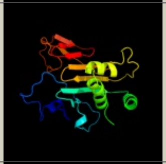
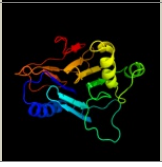
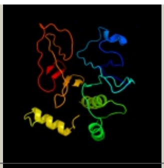
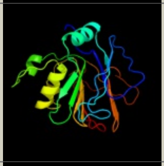
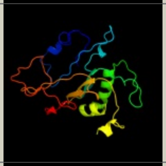
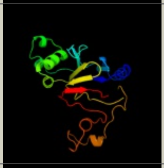
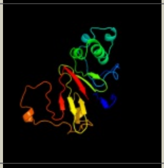
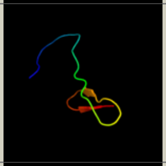
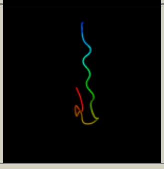
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1te5a_	Alignment		100.0	60	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
2	c3mdnD_	Alignment		100.0	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamine aminotransferase class-ii domain protein; **PDBTitle:** structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
3	d1ecfa2	Alignment		100.0	22	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
4	c1ecjB_	Alignment		100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
5	d1gph12	Alignment		100.0	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
6	c1gph1_	Alignment		100.0	21	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
7	d1xffa_	Alignment		100.0	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
8	c1jxaA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate synthase; **PDBTitle:** glucosamine 6-phosphate synthase with glucose 6-phosphate
9	c1ct9D_	Alignment		99.9	17	**PDB header:**ligase **Chain:** D: **PDB Molecule:**asparagine synthetase b; **PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli
10	d1ofda3	Alignment		99.9	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
11	d1ct9a2	Alignment		99.8	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases

12	d1ea0a3	Alignment		99.8	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
13	d1jgta2	Alignment		99.7	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
14	c1m1zB_	Alignment		99.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
15	c2vdcF_	Alignment		99.5	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glutamate synthase [nadph] large chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
16	c1lm1A_	Alignment		99.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-dependent glutamate synthase; **PDBTitle:** structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
17	c1q15A_	Alignment		99.4	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase
18	d1q15a2	Alignment		99.3	14	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
19	c2rprA_	Alignment		33.4	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**flywch-type zinc finger-containing protein 1; **PDBTitle:** solution structure of the fifth flywch domain of flywch-type2 zinc finger-containing protein 1
20	c2oqbA_	Alignment		26.4	32	**PDB header:**transferase,gene regulation **Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** crystal structure of the n-terminal domain of coactivator-associated2 methyltransferase 1 (carm1)
21	c2jraB_	Alignment	not modelled	17.6	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein rpa2121; **PDBTitle:** a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
22	d2ot2a1	Alignment	not modelled	15.5	19	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
23	c3pubA_	Alignment	not modelled	14.1	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**30kda protein; **PDBTitle:** crystal structure of the bombyx mori low molecular weight lipoprotein2 7 (bmlp7)
24	c2je2A_	Alignment	not modelled	13.3	5	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cytochrome p460; **PDBTitle:** cytochrome p460 from nitrosomonas europaea - probable2 nonphysiological oxidized form
25	d2gu2a1	Alignment	not modelled	11.8	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
26	d1qvpa_	Alignment	not modelled	11.2	33	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
27	c3nh8A_	Alignment	not modelled	11.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartoacylase-2; **PDBTitle:** crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine
28	c3mlhA_	Alignment	not modelled	10.8	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of the 2009 h1n1 influenza virus hemagglutinin2 receptor-binding domain

29	d2i3ca1	Alignment	not modelled	10.8	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
30	d1t0ga_	Alignment	not modelled	10.8	13	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Steroid-binding domain
31	c1y8aA_	Alignment	not modelled	10.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1437; **PDBTitle:** structure of gene product af1437 from archaeoglobus fulgidus
32	d2z1ca1	Alignment	not modelled	10.1	27	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
33	d2visc_	Alignment	not modelled	9.9	20	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
34	c2hc8A_	Alignment	not modelled	9.3	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
35	c3hshA_	Alignment	not modelled	8.7	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**collagen alpha-1(xviii) chain; **PDBTitle:** crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)
36	c3bbo1_	Alignment	not modelled	8.5	25	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**ribosomal protein l31; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
37	c3d3rA_	Alignment	not modelled	8.3	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
38	d3d3ra1	Alignment	not modelled	8.1	20	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
39	d1rvxa_	Alignment	not modelled	7.1	25	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
40	d2viua_	Alignment	not modelled	7.1	20	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
41	d1mqma_	Alignment	not modelled	6.9	20	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
42	d1mjta_	Alignment	not modelled	6.8	14	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
43	c3eykA_	Alignment	not modelled	6.8	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin ha1 chain; **PDBTitle:** structure of influenza haemagglutinin in complex with an2 inhibitor of membrane fusion
44	c2aukA_	Alignment	not modelled	6.8	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
45	c2j034_	Alignment	not modelled	6.7	43	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
46	d2j0141	Alignment	not modelled	6.7	43	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L31p
47	d1jsda_	Alignment	not modelled	6.7	20	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
48	d1rv0h_	Alignment	not modelled	6.6	30	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
49	d1rd8a_	Alignment	not modelled	6.5	25	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
50	c3qqiB_	Alignment	not modelled	6.4	15	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of the ha1 receptor binding domain of h22 hemagglutinin
51	d1xl7a2	Alignment	not modelled	6.3	13	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
52	d1pj5a3	Alignment	not modelled	6.2	21	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
53	d2ibxa1	Alignment	not modelled	6.1	20	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
54	d1jsma_	Alignment	not modelled	6.0	20	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
55	d1t1ua2	Alignment	not modelled	6.0	19	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase

56	c2q82A_	Alignment	not modelled	6.0	30	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**core protein p7; **PDBTitle:** crystal structure of core protein p7 from pseudomonas phage2 phi12. northeast structural genomics target oc1
57	d1soxa2	Alignment	not modelled	5.9	6	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
58	d3b55a1	Alignment	not modelled	5.8	29	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**EreA-like
59	d1vs6z1	Alignment	not modelled	5.7	43	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L31p
60	d1ti8a1	Alignment	not modelled	5.7	20	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
61	d1gmua1	Alignment	not modelled	5.7	19	**Fold:**Urease metallochaperone UreE, N-terminal domain **Superfamily:**Urease metallochaperone UreE, N-terminal domain **Family:**Urease metallochaperone UreE, N-terminal domain
62	c2b664_	Alignment	not modelled	5.6	43	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
63	d1nm8a2	Alignment	not modelled	5.6	17	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
64	c2radB_	Alignment	not modelled	5.6	29	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**succinoglycan biosynthesis protein; **PDBTitle:** crystal structure of the succinoglycan biosynthesis2 protein. northeast structural genomics consortium target3 bcr135
65	c2a45L_	Alignment	not modelled	5.6	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** L: **PDB Molecule:**fibrinogen gamma chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin
66	c2rfuA_	Alignment	not modelled	5.6	10	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**influenza b hemagglutinin (ha); **PDBTitle:** crystal structure of influenza b virus hemagglutinin in complex with2 lstc receptor analog
67	c2kijA_	Alignment	not modelled	5.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the actuator domain of the copper-2 transporting atpase atp7a
68	c1nh1A_	Alignment	not modelled	5.3	23	**PDB header:**avirulence protein **Chain:** A: **PDB Molecule:**avirulence b protein; **PDBTitle:** crystal structure of the type iii effector avrb from2 pseudomonas syringae.
69	d1nh1a_	Alignment	not modelled	5.3	23	**Fold:**Antivirulence factor **Superfamily:**Antivirulence factor **Family:**Antivirulence factor
70	d1m7va_	Alignment	not modelled	5.2	26	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
71	d1ewqa3	Alignment	not modelled	5.2	50	**Fold:**Ribonuclease H-like motif **Superfamily:**DNA repair protein MutS, domain II **Family:**DNA repair protein MutS, domain II
72	d1nosa_	Alignment	not modelled	5.2	24	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain