Phyre^2

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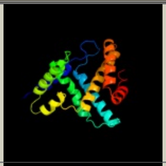
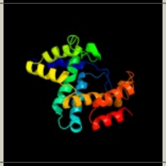
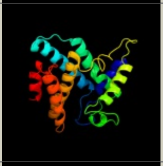
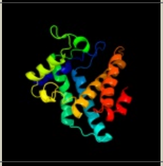
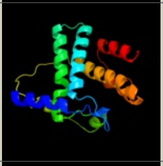
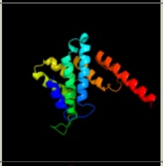
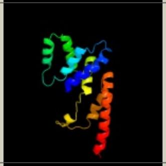
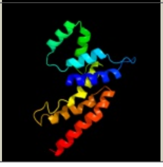
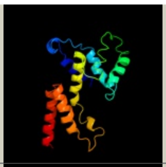
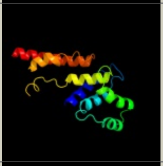
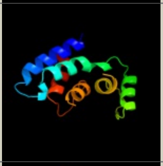
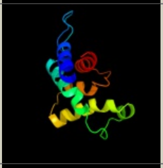
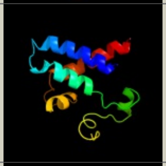
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2paqa1	Alignment		100.0	96	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
2	c3mzoA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lin2634 protein; **PDBTitle:** crystal structure of a hd-domain phosphohydrolase (lin2634) from2 listeria innocua at 1.98 a resolution
3	c3kh1B_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**predicted metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of predicted metal-dependent2 phosphohydrolase (zp_00055740.2) from magnetospirillum3 magnetotacticum ms-1 at 1.37 a resolution
4	d1xx7a_	Alignment		100.0	26	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
5	c2cqzA_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long hypothetical protein; **PDBTitle:** crystal structure of ph0347 protein from pyrococcus horikoshii ot3
6	d1ynba1	Alignment		100.0	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
7	d2gz4a1	Alignment		99.9	26	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
8	d2pq7a1	Alignment		99.1	13	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
9	d2qgsa1	Alignment		98.9	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
10	d3b57a1	Alignment		98.9	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
11	d2pjqa1	Alignment		98.9	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain

12	c3gw7A_	Alignment		98.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein yedj; **PDBTitle:** crystal structure of a metal-dependent phosphohydrolase2 with conserved hd domain (yedj) from escherichia coli in3 complex with nickel ions. northeast structural genomics4 consortium target er63
13	d3dtoa1	Alignment		98.8	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
14	d3djba1	Alignment		98.7	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
15	c2ogiA_	Alignment		98.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein sag1661; **PDBTitle:** crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
16	c3ccgA_	Alignment		98.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd superfamily hydrolase; **PDBTitle:** crystal structure of predicted hd superfamily hydrolase involved in2 nad metabolism (np_347894.1) from clostridium acetobutylicum at 1.503 a resolution
17	c2o08B_	Alignment		98.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh1327 protein; **PDBTitle:** crystal structure of a putative hd superfamily hydrolase (bh1327) from2 bacillus halodurans at 1.90 a resolution
18	c3m1tA_	Alignment		97.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of putative phosphohydrolase (yp_929327.1) from2 shewanella amazonensis sb2b at 1.62 a resolution
19	c2dqbB_	Alignment		97.5	18	**PDB header:**hydrolase, dna binding protein **Chain:** B: **PDB Molecule:**deoxyguanosinetriphosphate triphosphohydrolase, putative; **PDBTitle:** crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
20	c3i7aA_	Alignment		97.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of putative metal-dependent phosphohydrolase2 (yp_926882.1) from shewanella amazonensis sb2b at 2.06 a resolution
21	c3hc1A_	Alignment	not modelled	97.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized hdod domain protein; **PDBTitle:** crystal structure of hdod domain protein with unknown function2 (np_953345.1) from geobacter sulfurreducens at 1.90 a resolution
22	c3memA_	Alignment	not modelled	96.9	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative signal transduction protein; **PDBTitle:** crystal structure of a putative signal transduction protein2 (maqu_0641) from marinobacter aquaeolei vt8 at 2.25 a resolution
23	c3nqwB_	Alignment	not modelled	96.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
24	c3nr1A_	Alignment	not modelled	96.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain-containing protein 3; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
25	d2heka1	Alignment	not modelled	96.5	22	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
26	c2o6iA_	Alignment	not modelled	96.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain protein; **PDBTitle:** structure of an enterococcus faecalis hd domain phosphohydrolase
27	d2o6ia1	Alignment	not modelled	96.5	23	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
28	d1vqra_	Alignment	not modelled	96.4	10	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**modified HD domain

29	c2q14A_	Alignment	not modelled	96.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase; **PDBTitle:** crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
30	c3u1nC_	Alignment	not modelled	96.3	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** structure of the catalytic core of human samhd1
31	c3ljvA_	Alignment	not modelled	95.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mmoq response regulator; **PDBTitle:** crystal structure of mmoq response regulator (fragment 29-302) from2 methylococcus capsulatus str. bath, northeast structural genomics3 consortium target mcr175m
32	c2pgsA_	Alignment	not modelled	95.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyguanosinetriphosphate triphosphohydrolase; **PDBTitle:** crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
33	d1vj7a1	Alignment	not modelled	94.0	21	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
34	c3bg2A_	Alignment	not modelled	93.7	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dgtp triphosphohydrolase; **PDBTitle:** crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
35	c1vj7B_	Alignment	not modelled	93.3	23	**PDB header:**hydrolase, transferase **Chain:** B: **PDB Molecule:**bifunctional rela/spot; **PDBTitle:** crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
36	c3skdA_	Alignment	not modelled	88.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein tthb187; **PDBTitle:** crystal structure of the thermus thermophilus cas3 hd domain in the2 presence of ni2+
37	c3kq5A_	Alignment	not modelled	84.6	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical cytosolic protein; **PDBTitle:** crystal structure of an uncharacterized protein from coxiella burnetii
38	d1u6za1	Alignment	not modelled	78.5	12	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**Ppx associated domain
39	c1xotB_	Alignment	not modelled	70.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**camp-specific 3',5'-cyclic phosphodiesterase 4b; **PDBTitle:** catalytic domain of human phosphodiesterase 4b in complex with2 vardenafil
40	d1y2ka1	Alignment	not modelled	70.8	14	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
41	c3m5fA_	Alignment	not modelled	66.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent phosphohydrolase; **PDBTitle:** structure of mj0384, a cas3 protein from methanocaldococcus jannaschii
42	d1taza_	Alignment	not modelled	65.3	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
43	c2r8qA_	Alignment	not modelled	63.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i phosphodiesterase pdeb1; **PDBTitle:** structure of lmjpdeb1 in complex with ibmx
44	c1xozA_	Alignment	not modelled	63.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil
45	d3dy8a1	Alignment	not modelled	60.5	14	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
46	d3bxda1	Alignment	not modelled	59.6	24	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
47	c2huoA_	Alignment	not modelled	59.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inositol oxygenase; **PDBTitle:** crystal structure of mouse myo-inositol oxygenase in complex with2 substrate
48	d1f0ja_	Alignment	not modelled	58.5	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
49	c2o8hA_	Alignment	not modelled	57.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase-10a; **PDBTitle:** crystal structure of the catalytic domain of rat2 phosphodiesterase 10a
50	d2h44a1	Alignment	not modelled	55.5	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
51	c3qi4A_	Alignment	not modelled	54.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high affinity cgmp-specific 3',5'-cyclic phosphodiesterase **PDBTitle:** crystal structure of pde9a(q453e) in complex with ibmx
52	c3ibjB_	Alignment	not modelled	53.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
53	d2ibna1	Alignment	not modelled	51.9	28	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
						PDB header:hydrolase

54	c2ounA_	Alignment	not modelled	51.2	12	**Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic **PDBTitle:** crystal structure of pde10a2 in complex with amp
55	c2floA_	Alignment	not modelled	49.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
56	c1z1lA_	Alignment	not modelled	48.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** the crystal structure of the phosphodiesterase 2a catalytic2 domain
57	c2k0nA_	Alignment	not modelled	37.7	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription **PDBTitle:** solution structure of yeast gal11p kix domain
58	c3rv0C_	Alignment	not modelled	30.1	36	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**k. polysporus dcr1; **PDBTitle:** crystal structure of k. polysporus dcr1 without the c-terminal dsrbd
59	d1so2a_	Alignment	not modelled	16.9	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
60	c3g3nA_	Alignment	not modelled	15.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high affinity camp-specific 3',5'-cyclic **PDBTitle:** pde7a catalytic domain in complex with 3-(2,6-2 difluorophenyl)-2-(methylthio)quinazolin-4(3h)-one
61	d1tbfa_	Alignment	not modelled	14.3	12	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
62	c3r84O_	Alignment	not modelled	13.8	19	**PDB header:**transcription **Chain:** O: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 11; **PDBTitle:** structure of the mediator head subcomplex med11/22
63	d2dlda1	Alignment	not modelled	12.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
64	c3bjcA_	Alignment	not modelled	12.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of the pde5a catalytic domain in complex2 with a novel inhibitor
65	c2wukD_	Alignment	not modelled	12.0	10	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
66	d1j4aa1	Alignment	not modelled	11.6	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
67	c3hi0B_	Alignment	not modelled	11.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative exopolyphosphatase; **PDBTitle:** crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
68	d1ygya2	Alignment	not modelled	10.0	16	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
69	c3ecmA_	Alignment	not modelled	9.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high affinity camp-specific and ibmx-insensitive **PDBTitle:** crystal structure of the unliganded pde8a catalytic domain
70	d1odfa_	Alignment	not modelled	8.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
71	d1dxya2	Alignment	not modelled	8.3	11	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
72	c1z65A_	Alignment	not modelled	7.7	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**prion-like protein doppel; **PDBTitle:** mouse doppel 1-30 peptide
73	c3rv1B_	Alignment	not modelled	6.7	38	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**k. polysporus dcr1; **PDBTitle:** crystal structure of the n-terminal and rnase iii domains of k.2 polysporus dcr1 e224q mutant
74	c2k4vA_	Alignment	not modelled	5.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1076; **PDBTitle:** solution structure of uncharacterized protein pa1076 from2 pseudomonas aeruginosa. northeast structural genomics3 consortium (nesg) target pat3, ontario center for4 structural proteomics target pa1076 .
75	d1sc6a2	Alignment	not modelled	5.8	13	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
76	c1zklA_	Alignment	not modelled	5.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high-affinity camp-specific 3',5'-cyclic **PDBTitle:** multiple determinants for inhibitor selectivity of cyclic2 nucleotide phosphodiesterases
77	d1mvfd_	Alignment	not modelled	5.6	21	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
						PDB header:hydrolase

78	c2wdfA_	Alignment	not modelled	5.3	27	**Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb