Phyre^2

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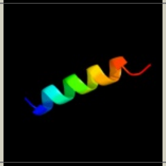
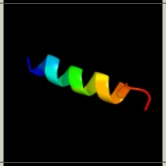
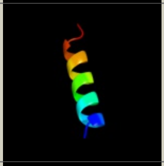
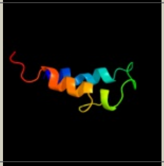
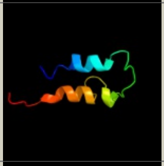
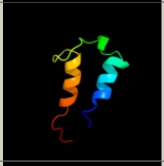
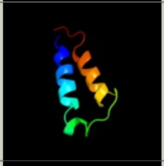
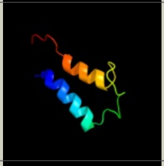
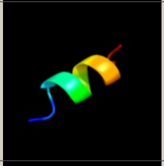
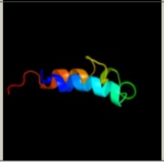
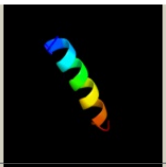
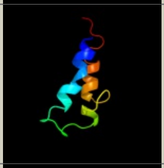
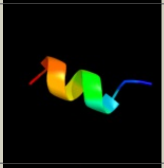
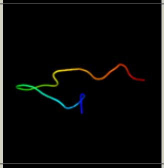
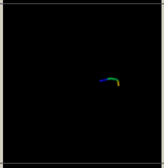
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ca1a1	Alignment		40.5	32	**Fold:**Phospholipase C/P1 nuclease **Superfamily:**Phospholipase C/P1 nuclease **Family:**Phospholipase C
2	d1olpa1	Alignment		31.2	33	**Fold:**Phospholipase C/P1 nuclease **Superfamily:**Phospholipase C/P1 nuclease **Family:**Phospholipase C
3	c1gygA_	Alignment		26.9	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase c; **PDBTitle:** r32 closed form of alpha-toxin from clostridium perfringens2 strain cer89l43
4	d1khoa1	Alignment		26.7	33	**Fold:**Phospholipase C/P1 nuclease **Superfamily:**Phospholipase C/P1 nuclease **Family:**Phospholipase C
5	d1y2ka1	Alignment		18.8	23	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
6	c1xotB_	Alignment		18.0	23	**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
7	c2r8qA_	Alignment		13.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i phosphodiesterase pdeb1; **PDBTitle:** structure of lmjpdeb1 in complex with ibmx
8	c3ecmA_	Alignment		12.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high affinity camp-specific and ibmx-insensitive **PDBTitle:** crystal structure of the unliganded pde8a catalytic domain
9	c1z1lA_	Alignment		12.8	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** the crystal structure of the phosphodiesterase 2a catalytic2 domain
10	c3ec2A_	Alignment		11.9	18	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication protein dnac; **PDBTitle:** crystal structure of the dnac helicase loader
11	d3dy8a1	Alignment		11.5	19	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase

12	d1ah7a_	Alignment		11.2	32	**Fold:**Phospholipase C/P1 nuclease **Superfamily:**Phospholipase C/P1 nuclease **Family:**Phospholipase C
13	d1f0ja_	Alignment		11.1	23	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
14	c3bjcA_	Alignment		11.0	17	**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
15	c2w58B_	Alignment		10.4	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**primosome component (helicase loader); **PDBTitle:** crystal structure of the dnai
16	c2qgzA_	Alignment		10.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative primosome component; **PDBTitle:** crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
17	c3cvgC_	Alignment		9.5	21	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**putative metal binding protein; **PDBTitle:** crystal structure of a periplasmic putative metal binding protein
18	d1p3qq_	Alignment		9.0	44	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
19	d1tbfa_	Alignment		8.9	19	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
20	c1xozA_	Alignment		8.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil
21	c1olpB_	Alignment	not modelled	8.4	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-toxin; **PDBTitle:** alpha toxin from clostridium absonum
22	c3qi4A_	Alignment	not modelled	8.4	19	**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
23	c1wqdA_	Alignment	not modelled	8.3	56	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omtx2; **PDBTitle:** an unusual fold for potassium channel blockers: nmr2 structure of three toxins from the scorpion opisthacanthus3 madagascariensis
24	c1zklA_	Alignment	not modelled	8.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high-affinity camp-specific 3',5'-cyclic **PDBTitle:** multiple determinants for inhibitor selectivity of cyclic2 nucleotide phosphodiesterases
25	d2h44a1	Alignment	not modelled	7.7	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
26	c2kjqA_	Alignment	not modelled	7.6	27	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnaa-related protein; **PDBTitle:** solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
27	c3g3nA_	Alignment	not modelled	7.4	21	**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
28	d1so2a_	Alignment	not modelled	7.3	24	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase

29	d1p3qr_	Alignment	not modelled	7.0	43	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
30	c2lf6A_	Alignment	not modelled	6.8	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**effector protein hopab1; **PDBTitle:** solution nmr structure of hopabpph1448_220_320 from pseudomonas2 syringae pv. phaseolicola str. 1448a, midwest center for structural3 genomics target apc40132.4 and northeast structural genomics4 consortium target pst3a
31	d1mn3a_	Alignment	not modelled	6.1	44	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
32	c3ibjB_	Alignment	not modelled	5.9	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
33	c2o8hA_	Alignment	not modelled	5.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase-10a; **PDBTitle:** crystal structure of the catalytic domain of rat2 phosphodiesterase 10a