Phyre^2

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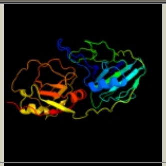
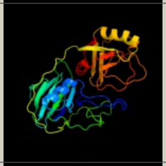
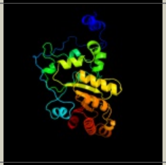
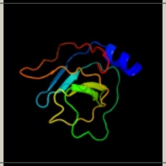
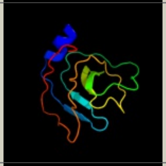
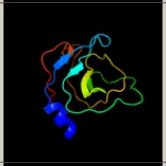
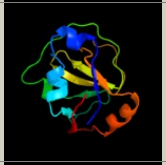
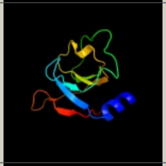
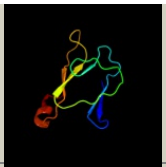
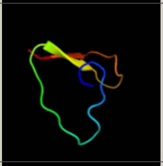
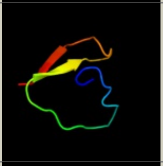
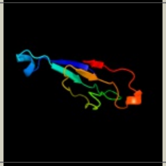
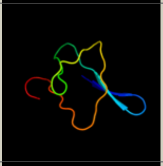
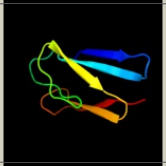
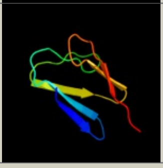
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mmlE_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**allophanate hydrolase subunit 2; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
2	c3oepA_	Alignment		100.0	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0988; **PDBTitle:** crystal structure of ttha0988 in space group p43212
3	c2qf7A_	Alignment		97.3	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
4	c2phcB_	Alignment		96.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
5	d2phcb1	Alignment		95.6	15	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
6	c2zp2B_	Alignment		95.4	16	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
7	c2p0oA_	Alignment		93.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf871; **PDBTitle:** crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
8	c1x7fA_	Alignment		91.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein
9	d1x7fa1	Alignment		91.9	13	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**Outer surface protein, C-terminal domain
10	c3mmlD_	Alignment		89.6	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
11	c3elsA_	Alignment		86.3	17	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** crystal structure of yeast pml1p, residues 51-204

12	d2piea1	Alignment		84.9	10	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
13	c1gxcA_	Alignment		81.4	15	**PDB header:**phosphoprotein-binding domain **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase chk2; **PDBTitle:** fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
14	d1gxca_	Alignment		81.4	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
15	c2jkdB_	Alignment		80.1	10	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** structure of the yeast pml1 splicing factor and its2 integration into the res complex
16	d1uhta_	Alignment		69.2	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
17	c2jpeA_	Alignment		68.0	2	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear inhibitor of protein phosphatase 1; **PDBTitle:** fha domain of nipp1
18	c3gmgB_	Alignment		67.8	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rv1825/mt1873; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
19	d2brfa1	Alignment		66.5	13	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
20	d1ujxa_	Alignment		65.8	7	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
21	c1yj5C_	Alignment	not modelled	62.8	11	**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
22	c3poaA_	Alignment	not modelled	62.3	10	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
23	c3kt9A_	Alignment	not modelled	61.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
24	d1g3ga_	Alignment	not modelled	61.5	16	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
25	d2g1la1	Alignment	not modelled	54.2	20	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
26	c3fm8A_	Alignment	not modelled	53.9	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)
27	c3kf6B_	Alignment	not modelled	47.4	20	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**protein ten1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
28	c2eh0A_	Alignment	not modelled	47.2	12	**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

29	d1g6ga_	Alignment	not modelled	46.7	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
30	d1dmza_	Alignment	not modelled	43.4	17	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
31	d1kf6b2	Alignment	not modelled	41.4	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
32	d1yjma1	Alignment	not modelled	40.1	9	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
33	c3hx1B_	Alignment	not modelled	38.4	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1951 protein; **PDBTitle:** crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
34	c1zeqX_	Alignment	not modelled	38.0	15	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
35	c2o55A_	Alignment	not modelled	37.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative glycerophosphodiester phosphodiesterase; **PDBTitle:** crystal structure of a putative glycerophosphodiester2 phosphodiesterase from galdieria sulphuraria
36	d1dm9a_	Alignment	not modelled	36.4	11	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
37	c1dm9A_	Alignment	not modelled	36.4	11	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
38	d2cu3a1	Alignment	not modelled	34.5	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
39	c2k6pA_	Alignment	not modelled	34.2	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
40	c2kklA_	Alignment	not modelled	34.0	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
41	c3ks6A_	Alignment	not modelled	30.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens3 str. c58 (dupont) at 1.80 a resolution
42	d1nekb2	Alignment	not modelled	29.8	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
43	c2l55A_	Alignment	not modelled	29.8	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three **PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
44	c3gqsB_	Alignment	not modelled	29.6	12	**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
45	d1snoa_	Alignment	not modelled	28.2	19	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
46	d2affa1	Alignment	not modelled	27.9	9	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
47	d2ff4a3	Alignment	not modelled	27.6	5	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
48	d1w96c1	Alignment	not modelled	27.5	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
49	d1rkna_	Alignment	not modelled	26.5	17	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
50	d1mzka_	Alignment	not modelled	26.4	9	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
51	c2jqlA_	Alignment	not modelled	25.6	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna damage response protein kinase dun1; **PDBTitle:** nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
52	c3uotB_	Alignment	not modelled	25.6	3	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1; **PDBTitle:** crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
53	c3rlgA_	Alignment	not modelled	25.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a;

						PDBTitle: crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant
54	d1zud21	Alignment	not modelled	24.7	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
55	c2zplA_	Alignment	not modelled	24.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain a
56	d2oyza1	Alignment	not modelled	24.2	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**VPA0057-like
57	c1r21A_	Alignment	not modelled	23.9	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
58	d1lgpa_	Alignment	not modelled	22.9	10	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
59	c3rggD_	Alignment	not modelled	22.9	28	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
60	d2bs2b2	Alignment	not modelled	22.6	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
61	c2g1eA_	Alignment	not modelled	22.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
62	c2kl0A_	Alignment	not modelled	22.4	24	**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
63	c2nnzA_	Alignment	not modelled	21.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
64	c3eo6B_	Alignment	not modelled	21.2	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of unknown function (duf1255); **PDBTitle:** crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455 at3 0.97 a resolution
65	d1wlna1	Alignment	not modelled	21.0	12	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
66	d1k92a1	Alignment	not modelled	21.0	33	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
67	c3cwiA_	Alignment	not modelled	20.5	13	**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
68	c3rleA_	Alignment	not modelled	20.5	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**golgi reassembly-stacking protein 2; **PDBTitle:** crystal structure of grasp55 grasp domain (residues 7-208)
69	d2z1ca1	Alignment	not modelled	18.9	9	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
70	d1v10a2	Alignment	not modelled	17.7	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
71	c3i10A_	Alignment	not modelled	16.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (np_812074.1) from bacteroides thetaiotaomicron3 vpi-5482 at 1.35 a resolution
72	c2jrtA_	Alignment	not modelled	16.4	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
73	d2soba_	Alignment	not modelled	15.9	16	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
74	c3hvzB_	Alignment	not modelled	15.0	23	**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
75	c3ju0A_	Alignment	not modelled	14.8	38	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** structure of the arm-type binding domain of hai7 integrase
76	d1u1ha1	Alignment	not modelled	14.6	44	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase
77	c3r6oA_	Alignment	not modelled	14.3	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; **PDBTitle:** crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus

78	d1zcca1	Alignment	not modelled	14.1	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
79	c2aanA_	Alignment	not modelled	13.9	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**auracyanin a; **PDBTitle:** auracyanin a: a "blue" copper protein from the green thermophilic2 photosynthetic bacterium,chloroflexus aurantiacus
80	d2pyta1	Alignment	not modelled	13.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**EutQ-like
81	d1tygb_	Alignment	not modelled	13.7	3	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
82	d2bh1x1	Alignment	not modelled	13.5	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**EspE N-terminal domain-like **Family:**GSPII protein E N-terminal domain-like
83	c2bh1Y_	Alignment	not modelled	13.5	13	**PDB header:**transport protein **Chain:** Y: **PDB Molecule:**general secretion pathway protein e,; **PDBTitle:** x-ray structure of the general secretion pathway complex of2 the n-terminal domain of epse and the cytosolic domain of3 epsl of vibrio cholerae
84	c3rlhA_	Alignment	not modelled	13.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a; **PDBTitle:** crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
85	d1tkea1	Alignment	not modelled	13.3	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
86	d1nyra2	Alignment	not modelled	13.3	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
87	c2vgmA_	Alignment	not modelled	13.2	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dom34; **PDBTitle:** structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
88	c1kh2D_	Alignment	not modelled	13.0	35	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
89	c1tygG_	Alignment	not modelled	12.8	0	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
90	c3rpfB_	Alignment	not modelled	12.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase catalytic subunit; **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
91	d1j20a1	Alignment	not modelled	12.5	35	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
92	c3hqxA_	Alignment	not modelled	12.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0345 protein aciad0356; **PDBTitle:** crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1
93	d2oa4a1	Alignment	not modelled	12.4	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
94	d1vl2a1	Alignment	not modelled	12.0	31	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
95	c2zpmA_	Alignment	not modelled	12.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
96	c2x4iA_	Alignment	not modelled	11.6	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein 114; **PDBTitle:** orf 114a from sulfolobus islandicus rudivirus 1
97	c3r7kB_	Alignment	not modelled	11.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable acyl coa dehydrogenase; **PDBTitle:** crystal structure of a probable acyl coa dehydrogenase from2 mycobacterium abscessus atcc 19977 / dsm 44196
98	d1tt2a_	Alignment	not modelled	11.5	19	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
99	c3no3A_	Alignment	not modelled	11.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphodiester phosphodiesterase2 (bdi_0402) from parabacteroides distasonis atcc 8503 at 1.89 a3 resolution