Phyre^2

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Description	P0A7E3
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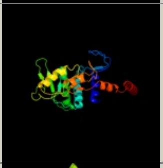
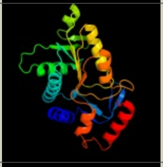
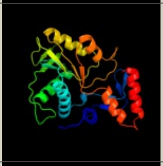
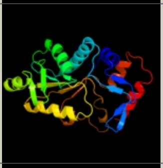
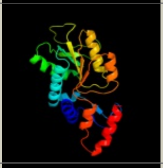
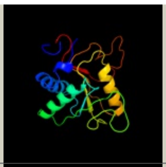
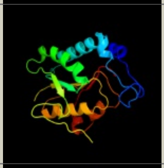
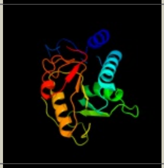
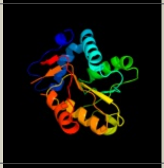
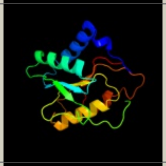
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lh0a_	Alignment		100.0	97	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
2	c3n2lA_	Alignment		100.0	80	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
3	c2przB_	Alignment		100.0	47	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase 1; **PDBTitle:** s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
4	c3mjdA_	Alignment		100.0	45	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
5	c2wnsB_	Alignment		100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
6	c3qw4B_	Alignment		100.0	24	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
7	c3dezA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
8	d2aeea1	Alignment		100.0	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
9	c3m3hA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
10	c2yzkC_	Alignment		100.0	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
11	d1mzva_	Alignment		100.0	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)

12	c2p1zA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase; **PDBTitle:** crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
13	d1qb7a_	Alignment		100.0	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
14	d1y0ba1	Alignment		100.0	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
15	d1o57a2	Alignment		99.9	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
16	c2dy0A_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
17	c1o57A_	Alignment		99.9	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
18	d1zn7a1	Alignment		99.9	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
19	d1l1qa_	Alignment		99.9	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
20	d1g2qa_	Alignment		99.9	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
21	d1vcha1	Alignment	not modelled	99.8	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
22	d1vdma1	Alignment	not modelled	99.8	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
23	d2igba1	Alignment	not modelled	99.8	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
24	d1ufra_	Alignment	not modelled	99.7	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
25	d1hgxa_	Alignment	not modelled	99.7	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
26	d1w30a_	Alignment	not modelled	99.7	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
27	c3o7mD_	Alignment	not modelled	99.7	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
28	d1a3ca_	Alignment	not modelled	99.7	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)

29	d1g9sa_	Alignment	not modelled	99.7	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
30	c2ywtA_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
31	d1j7ja_	Alignment	not modelled	99.7	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
32	d1z7ga1	Alignment	not modelled	99.7	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
33	d1pzma_	Alignment	not modelled	99.7	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
34	d1tc1a_	Alignment	not modelled	99.7	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
35	c3kb8A_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
36	c1pzmB_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
37	d1yfza1	Alignment	not modelled	99.6	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
38	c1yfzA_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
39	d1p17b_	Alignment	not modelled	99.6	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
40	c2jkzB_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
41	d1ecfa1	Alignment	not modelled	99.5	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
42	d1nula_	Alignment	not modelled	99.5	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
43	d1gph11	Alignment	not modelled	99.5	25	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
44	c2jbhA_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase domain-containing protein 1; **PDBTitle:** human phosphoribosyl transferase domain containing 1
45	c3lpnB_	Alignment	not modelled	99.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
46	c1ecjB_	Alignment	not modelled	99.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
47	d1wd5a_	Alignment	not modelled	99.4	24	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
48	c3efhB_	Alignment	not modelled	99.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
49	d1fsga_	Alignment	not modelled	99.4	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
50	d1cjba_	Alignment	not modelled	99.4	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
51	c1gph1_	Alignment	not modelled	99.4	26	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
52	c1dkrB_	Alignment	not modelled	99.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis

						phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
53	c2c4kD_	Alignment	not modelled	99.2	17	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
54	d1dkua2	Alignment	not modelled	99.2	24	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
55	d1u9ya2	Alignment	not modelled	99.2	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
56	d2c4ka2	Alignment	not modelled	99.2	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
57	c1u9yD_	Alignment	not modelled	99.1	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
58	c3dahB_	Alignment	not modelled	98.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
59	d1dqna_	Alignment	not modelled	98.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
60	c2ehjA_	Alignment	not modelled	98.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of uracil phosphoribosyl transferase
61	d1o5oa_	Alignment	not modelled	98.2	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
62	c2e55D_	Alignment	not modelled	98.2	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of aq2163 protein from aquifex aeolicus
63	d1i5ea_	Alignment	not modelled	98.1	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
64	d1xtta1	Alignment	not modelled	97.7	9	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
65	d1bd3a_	Alignment	not modelled	97.7	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
66	c3dmpD_	Alignment	not modelled	97.6	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
67	d1v9sa1	Alignment	not modelled	97.4	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
68	d1g57a_	Alignment	not modelled	91.5	25	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
69	d1tksa_	Alignment	not modelled	90.8	14	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
70	d1snna_	Alignment	not modelled	89.5	8	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
71	c3mioA_	Alignment	not modelled	89.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase; **PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
72	d1k4ia_	Alignment	not modelled	83.5	20	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
73	d1s8na_	Alignment	not modelled	79.4	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
74	d1u9ya1	Alignment	not modelled	69.7	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
75	c2vspA_	Alignment	not modelled	62.3	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 1; **PDBTitle:** crystal structure of the fourth pdz domain of pdz domain-2 containing protein 1
76	d1vaea_	Alignment	not modelled	60.4	12	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
77	c3l4fD_	Alignment	not modelled	59.9	18	**PDB header:**signaling protein/protein binding **Chain:** D: **PDB Molecule:**sh3 and multiple ankyrin repeat domains protein **PDBTitle:** crystal structure of betapix coiled-coil domain and shank2 pdz complex

78	c2vsvB_	Alignment	not modelled	57.2	12	**PDB header:**protein-binding **Chain:** B: **PDB Molecule:**rhophilin-2; **PDBTitle:** crystal structure of the pdz domain of human rhophilin-2
79	d2c4ka1	Alignment	not modelled	57.1	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
80	d1m5za_	Alignment	not modelled	54.8	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
81	c3eggC_	Alignment	not modelled	54.4	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**spinophilin; **PDBTitle:** crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
82	c2d90A_	Alignment	not modelled	54.1	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pdz domain containing protein 1; **PDBTitle:** solution structure of the third pdz domain of pdz domain2 containing protein 1
83	c3r2uC_	Alignment	not modelled	52.6	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
84	c2jxoA_	Alignment	not modelled	52.6	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ezrin-radixin-moesin-binding phosphoprotein 50; **PDBTitle:** structure of the second pdz domain of nherf-1
85	c3mmnA_	Alignment	not modelled	51.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine kinase homolog; **PDBTitle:** crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
86	c1a2oB_	Alignment	not modelled	51.5	20	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
87	d1q3oa_	Alignment	not modelled	51.3	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
88	c2o2tB_	Alignment	not modelled	50.8	10	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 1st pdz domain of mpdz
89	c3diwB_	Alignment	not modelled	48.2	10	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
90	c2kjdA_	Alignment	not modelled	47.5	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchange regulatory cofactor nhe- **PDBTitle:** solution structure of extended pdz2 domain from nherf1 (150-2 270)
91	d1ihja_	Alignment	not modelled	47.5	6	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
92	c3qglD_	Alignment	not modelled	47.2	20	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**sorting nexin-27; **PDBTitle:** crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3
93	c1r6jA_	Alignment	not modelled	47.1	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**syntenin 1; **PDBTitle:** ultrahigh resolution crystal structure of syntenin pdz2
94	d1r6ja_	Alignment	not modelled	47.1	10	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
95	c1nteA_	Alignment	not modelled	47.1	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure analysis of the second pdz domain of2 syntenin
96	c1j6uA_	Alignment	not modelled	46.6	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-alanine ligase murc; **PDBTitle:** crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
97	c2eeiA_	Alignment	not modelled	46.2	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 1; **PDBTitle:** solution structure of second pdz domain of pdz domain2 containing protein 1
98	c1obyA_	Alignment	not modelled	46.0	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the complex of pdz2 of syntenin with2 a syndecan-4 peptide.
99	d1dcfa_	Alignment	not modelled	44.9	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
100	d1vi2a1	Alignment	not modelled	44.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
101	d1dkua1	Alignment	not modelled	44.2	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
102	c2kv8A_	Alignment	not modelled	43.8	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 12; **PDBTitle:** solution structure ofrgs12 pdz domain
103	c2he4A_	Alignment	not modelled	43.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf2;

						PDBTitle: the crystal structure of the second pdz domain of human2 nherf-2 (slc9a3r2) interacting with a mode 1 pdz binding3 motif
104	c2z17A_	Alignment	not modelled	43.5	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pleckstrin homology sec7 and coiled-coil domains- **PDBTitle:** crystal sturcture of pdz domain from human pleckstrin2 homology, sec7
105	d1v6ba_	Alignment	not modelled	43.0	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
106	d2fe5a1	Alignment	not modelled	40.6	8	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
107	d1g9oa_	Alignment	not modelled	40.6	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
108	d1y7na1	Alignment	not modelled	40.2	10	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
109	c3k1rA_	Alignment	not modelled	40.0	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
110	c2edzA_	Alignment	not modelled	40.0	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 1; **PDBTitle:** solution structures of the pdz domain of mus musculus pdz2 domain-containing protein 1
111	c2krgA_	Alignment	not modelled	39.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf1; **PDBTitle:** solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
112	c2pkuA_	Alignment	not modelled	39.9	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** solution structure of pick1 pdz in complex with the2 carboxyl tail peptide of glur2
113	d1u3ba2	Alignment	not modelled	39.8	11	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
114	c2dmzA_	Alignment	not modelled	39.7	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the third pdz domain of human inad-2 like protein
115	c1obyB_	Alignment	not modelled	39.3	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the complex of pdz2 of syntenin with2 a syndecan-4 peptide.
116	d1obxa_	Alignment	not modelled	39.3	10	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
117	c1obxA_	Alignment	not modelled	39.3	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the complex of pdz2 of syntenin with2 an interleukin 5 receptor alpha peptide.
118	d2j01f1	Alignment	not modelled	38.9	13	**Fold:**Ribosomal protein L4 **Superfamily:**Ribosomal protein L4 **Family:**Ribosomal protein L4
119	d1uita_	Alignment	not modelled	38.1	10	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
120	d1wjla_	Alignment	not modelled	38.1	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain