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1	<a href="#">c3tebA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease/exonuclease/phosphatase; <b>PDBTitle:</b> endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
2	<a href="#">c3ngoA_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ccr4-not transcription complex subunit 6-like; <b>PDBTitle:</b> crystal structure of the human cnot6l nuclease domain in complex with2 poly(a) dna
3	<a href="#">c3g6sA_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative endonuclease/exonuclease/phosphatase <b>PDBTitle:</b> crystal structure of the2 endonuclease/exonuclease/phosphatase (bv0_0621) from3 bacteroides vulgatus. northeast structural genomics4 consortium target bvr56d
4	<a href="#">c3mprB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative endonuclease/exonuclease/phosphatase family <b>PDBTitle:</b> crystal structure of endonuclease/exonuclease/phosphatase family2 protein from bacteroides thetaiotaomicron, northeast structural3 genomics consortium target btr318a
5	<a href="#">c2j63B_</a>	 Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ap-endonuclease; <b>PDBTitle:</b> crystal structure of ap endonuclease lmap from leishmania2 major
6	<a href="#">c3l1wE_</a>	 Alignment		100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown conserved2 protein from enterococcus faecalis v583
7	<a href="#">d2ddra1</a>	 Alignment		100.0	19	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> Sphingomyelin phosphodiesterase-like
8	<a href="#">c1e9nB_</a>	 Alignment		100.0	21	<b>PDB header:</b> dna repair <b>Chain:</b> B: <b>PDB Molecule:</b> dna-(apurinic or apyrimidinic site) lyase; <b>PDBTitle:</b> a second divalent metal ion in the active site of a new2 crystal form of human apurinic/apyrimidinic endonuclease,3 ape1, and its implications for the catalytic mechanism
9	<a href="#">d1sr4b_</a>	 Alignment		100.0	17	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> DNase I-like
10	<a href="#">d1zwxal</a>	 Alignment		100.0	19	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> Sphingomyelin phosphodiesterase-like
11	<a href="#">d1akoa_</a>	 Alignment		100.0	21	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> DNase I-like

12	<a href="#">c2jc5A_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease; <b>PDBTitle:</b> apurinic apyrimidinic (ap) endonuclease (nape) from2 neisseria meningitidis
13	<a href="#">c3i46B_</a>	Alignment		100.0	16	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> beta-hemolysin; <b>PDBTitle:</b> crystal structure of beta toxin from staphylococcus aureus f277a,2 p278a mutant with bound calcium ions
14	<a href="#">c2voaB_</a>	Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> exodeoxyribonuclease iii; <b>PDBTitle:</b> structure of an ap endonuclease from archaeoglobus fulgidus
15	<a href="#">c3g0rA_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease; <b>PDBTitle:</b> complex of mth0212 and an 8bp dsdna with distorted ends
16	<a href="#">d1vyba_</a>	Alignment		99.9	16	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> DNase I-like
17	<a href="#">d2f1na1</a>	Alignment		99.9	16	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> DNase I-like
18	<a href="#">d1hd7a_</a>	Alignment		99.9	19	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> DNase I-like
19	<a href="#">c2jc4A_</a>	Alignment		99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease iii; <b>PDBTitle:</b> 3'-5' exonuclease (nexo) from neisseria meningitidis
20	<a href="#">d2a40b1</a>	Alignment		99.9	15	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> DNase I-like
21	<a href="#">d1wdua_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> DNase I-like
22	<a href="#">d2imqx1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> Inositol polyphosphate 5-phosphatase (IPP5)
23	<a href="#">c2ei9A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> non-ltr retrotransposon r1bmks orf2 protein; <b>PDBTitle:</b> crystal structure of r1bm endonuclease domain
24	<a href="#">c3mtcA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> type ii inositol-1,4,5-trisphosphate 5-phosphatase; <b>PDBTitle:</b> crystal structure of inpp5b in complex with phosphatidylinositol 4-2 phosphate
25	<a href="#">c3nr8A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2; <b>PDBTitle:</b> crystal structure of human ship2
26	<a href="#">c2xswB_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 72 kda inositol polyphosphate 5-phosphatase; <b>PDBTitle:</b> crystal structure of human inpp5e
27	<a href="#">d1i9za_</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> Inositol polyphosphate 5-phosphatase (IPP5)
28	<a href="#">d1emsa2</a>	Alignment	not modelled	83.9	7	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Nitrilase

29	<a href="#">c2w1vA</a>	Alignment	not modelled	61.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrilase homolog 2; <b>PDBTitle:</b> crystal structure of mouse nitrilase-2 at 1.4a resolution
30	<a href="#">c2vhiG</a>	Alignment	not modelled	61.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> cg3027-pa; <b>PDBTitle:</b> crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
31	<a href="#">d1f89a</a>	Alignment	not modelled	60.7	14	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Nitrilase
32	<a href="#">c3hkxA</a>	Alignment	not modelled	53.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> crystal structure analysis of an amidase from nesterenkonია sp.
33	<a href="#">c2plqA</a>	Alignment	not modelled	47.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aliphatic amidase; <b>PDBTitle:</b> crystal structure of the amidase from geobacillus pallidus rapc8
34	<a href="#">c1emsB</a>	Alignment	not modelled	45.2	7	<b>PDB header:</b> antitumor protein <b>Chain:</b> B: <b>PDB Molecule:</b> nit-fragile histidine triad fusion protein; <b>PDBTitle:</b> crystal structure of the c. elegans nitfhit protein
35	<a href="#">c3ilvA</a>	Alignment	not modelled	31.7	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
36	<a href="#">c2e2kC</a>	Alignment	not modelled	29.2	5	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> formamidase; <b>PDBTitle:</b> helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
37	<a href="#">c3n05B</a>	Alignment	not modelled	26.6	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
38	<a href="#">d1uf5a</a>	Alignment	not modelled	22.8	14	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Carbamilase
39	<a href="#">d3bula2</a>	Alignment	not modelled	20.4	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
40	<a href="#">c2e11B</a>	Alignment	not modelled	16.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
41	<a href="#">d1xrsb1</a>	Alignment	not modelled	14.3	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
42	<a href="#">c1chmA</a>	Alignment	not modelled	13.6	12	<b>PDB header:</b> creatinase <b>Chain:</b> A: <b>PDB Molecule:</b> creatine amidinohydrolase; <b>PDBTitle:</b> enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
43	<a href="#">c1y80A</a>	Alignment	not modelled	12.9	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted cobalamin binding protein; <b>PDBTitle:</b> structure of a corrinoid (factor iiii)-binding protein from2 moorella thermoacetica
44	<a href="#">c1xrsB</a>	Alignment	not modelled	12.3	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-lysine 5,6-aminomutase beta subunit; <b>PDBTitle:</b> crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
45	<a href="#">c3tliC</a>	Alignment	not modelled	10.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> double-strand break repair protein mre11a; <b>PDBTitle:</b> crystal structure of human mre11: understanding tumorigenic mutations
46	<a href="#">c3jvvA</a>	Alignment	not modelled	10.4	11	<b>PDB header:</b> atp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> twitching mobility protein; <b>PDBTitle:</b> crystal structure of p. aeruginosa pilt with bound amp-ppp
47	<a href="#">d7reqa2</a>	Alignment	not modelled	10.1	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
48	<a href="#">d1edqa1</a>	Alignment	not modelled	9.8	20	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
49	<a href="#">d1ccwa</a>	Alignment	not modelled	9.3	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
50	<a href="#">d1j31a</a>	Alignment	not modelled	9.2	18	<b>Fold:</b> Carbon-nitrogen hydrolase <b>Superfamily:</b> Carbon-nitrogen hydrolase <b>Family:</b> Carbamilase
51	<a href="#">c1bmtB</a>	Alignment	not modelled	8.5	21	<b>PDB header:</b> methyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
52	<a href="#">c2yxbA</a>	Alignment	not modelled	8.4	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
53	<a href="#">c3nrbD</a>	Alignment	not modelled	8.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
54	<a href="#">c1k98A</a>	Alignment	not modelled	8.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> adomet complex of meth c-terminal fragment

55	<a href="#">c3menC_</a>	Alignment	not modelled	8.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> acetylpolymine aminohydrolase; <b>PDBTitle:</b> crystal structure of acetylpolymine aminohydrolase from burkholderia2 pseudomallei, iodide soak
56	<a href="#">c2eyuA_</a>	Alignment	not modelled	7.3	11	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> twitching motility protein pilt; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
57	<a href="#">c3n0vD_</a>	Alignment	not modelled	7.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
58	<a href="#">c2qlvB_</a>	Alignment	not modelled	7.0	39	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> protein sip2; <b>PDBTitle:</b> crystal structure of the heterotrimer core of the s.2 cerevisiae ampk homolog snf1
59	<a href="#">c3ezxA_</a>	Alignment	not modelled	6.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monomethylamine corrinoid protein 1; <b>PDBTitle:</b> structure of methanosarcina barkeri monomethylamine2 corrinoid protein
60	<a href="#">c3obiC_</a>	Alignment	not modelled	6.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
61	<a href="#">c3o1lB_</a>	Alignment	not modelled	6.6	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
62	<a href="#">d3bzka5</a>	Alignment	not modelled	6.5	6	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Tex RuvX-like domain-like
63	<a href="#">c3louB_</a>	Alignment	not modelled	6.5	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
64	<a href="#">d2qlvb1</a>	Alignment	not modelled	6.5	39	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> AMPK-beta glycogen binding domain-like
65	<a href="#">d1g6oa_</a>	Alignment	not modelled	6.5	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
66	<a href="#">c3p9xB_</a>	Alignment	not modelled	6.4	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
67	<a href="#">c2i2xD_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> methyltransferase 1; <b>PDBTitle:</b> crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
68	<a href="#">d1p9ra_</a>	Alignment	not modelled	6.1	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
69	<a href="#">d2eg6a1</a>	Alignment	not modelled	5.6	50	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Dihydroorotase
70	<a href="#">d1fmfa_</a>	Alignment	not modelled	5.5	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
71	<a href="#">c3pn9C_</a>	Alignment	not modelled	5.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> proline dipeptidase; <b>PDBTitle:</b> crystal structure of a proline dipeptidase from streptococcus2 pneumoniae tigr4
72	<a href="#">d1hjra_</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> RuvC resolvase
73	<a href="#">c3o5vA_</a>	Alignment	not modelled	5.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> x-pro dipeptidase; <b>PDBTitle:</b> the crystal structure of the creatinase/prolidase n-terminal domain of2 an x-pro dipeptidase from streptococcus pyogenes to 1.85a
74	<a href="#">d1z0na1</a>	Alignment	not modelled	5.2	40	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> AMPK-beta glycogen binding domain-like
75	<a href="#">d1q8ia1</a>	Alignment	not modelled	5.1	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> DnaQ-like 3'-5' exonuclease
76	<a href="#">c3i7mA_</a>	Alignment	not modelled	5.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xaa-pro dipeptidase; <b>PDBTitle:</b> n-terminal domain of xaa-pro dipeptidase from lactobacillus brevis.