Phyre2

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Description	P76298
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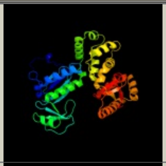
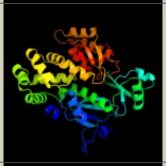
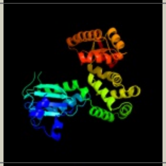
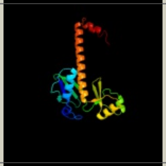
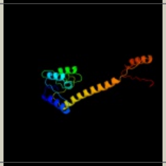
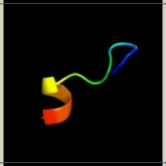
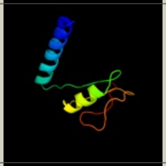
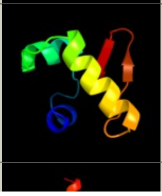
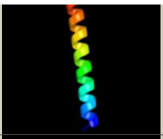
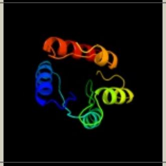
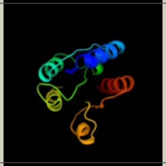
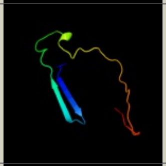
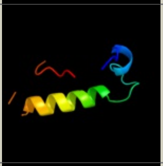
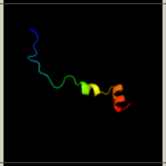
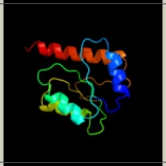
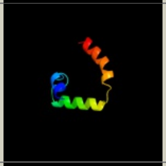
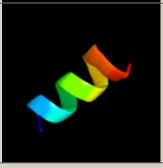
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a5iB_	Alignment		100.0	96	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha
2	c3mydA_	Alignment		100.0	38	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha from helicobacter pylori
3	c2x49A_	Alignment		100.0	22	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**invasion protein inva; **PDBTitle:** crystal structure of the c-terminal domain of inva
4	c3mixA_	Alignment		100.0	36	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** crystal structure of the cytosolic domain of b. subtilis flha
5	c3lw9B_	Alignment		100.0	18	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**invasion protein inva; **PDBTitle:** structure of a cytoplasmic domain of salmonella inva
6	c1ny5A_	Alignment		48.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
7	d1lm5a_	Alignment		47.8	18	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Plakin repeat **Family:**Plakin repeat
8	c3gz6A_	Alignment		41.5	18	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of shewanella oneidensis nrtr complexed2 with a 27mer dna
9	c2jobA_	Alignment		39.9	38	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
10	d1ovma1	Alignment		37.8	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
11	d1wi9a_	Alignment		37.2	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)

12	c3mtuD_	Alignment		32.8	23	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**tropomyosin alpha-1 chain, microtubule-associated protein **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
13	c3t6kB_	Alignment		29.0	22	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator receiver; **PDBTitle:** crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
14	d1zh2a1	Alignment		29.0	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
15	d1jhna4	Alignment		27.2	16	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Calnexin/calreticulin
16	d2h9fa2	Alignment		23.2	24	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PA0793-like
17	c1b35D_	Alignment		23.0	22	**PDB header:**virus **Chain:** D: **PDB Molecule:**protein (cricket paralysis virus, vp4); **PDBTitle:** cricket paralysis virus (crpv)
18	c3cfyA_	Alignment		22.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative luxo repressor protein; **PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
19	d2fswa1	Alignment		21.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**HxlR-like
20	c1iijA_	Alignment		21.0	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**erbb-2 receptor protein-tyrosine kinase; **PDBTitle:** solution structure of the neu/erbb-2 membrane spanning2 segment
21	c3kmgE_	Alignment	not modelled	20.8	50	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator-1; **PDBTitle:** the x-ray crystal structure of ppar-gamma in complex with an indole2 derivative modulator, gsk538, and an src-1 peptide
22	c2q2kA_	Alignment	not modelled	20.1	34	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of nucleic-acid binding protein
23	c2rjnA_	Alignment	not modelled	19.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
24	c2zwmA_	Alignment	not modelled	19.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
25	c2dd4H_	Alignment	not modelled	18.4	26	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**thiocyanate hydrolase beta subunit; **PDBTitle:** thiocyanate hydrolase (scnase) from thiobacillus thioparus2 recombinant apo-enzyme
26	c2cdqB_	Alignment	not modelled	17.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
27	c4a5mH_	Alignment	not modelled	17.4	20	**PDB header:**transcription **Chain:** H: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yybr; **PDBTitle:** redox regulator hypr in its oxidized form
28	d1qhma_	Alignment	not modelled	17.1	50	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
						PDB header:apoptosis

29	c2o2fA_	Alignment	not modelled	17.1	16	**Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
30	c2yhsA_	Alignment	not modelled	16.6	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
31	d1zgza1	Alignment	not modelled	16.3	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
32	c3dnfB_	Alignment	not modelled	16.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
33	c2lkyA_	Alignment	not modelled	15.2	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
34	c3rg0A_	Alignment	not modelled	15.1	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**calreticulin; **PDBTitle:** structural and functional relationships between the lectin and arm2 domains of calreticulin
35	c1vj7B_	Alignment	not modelled	14.9	17	**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	c2lbgA_	Alignment	not modelled	14.9	56	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**major prion protein; **PDBTitle:** structure of the chr of the prion protein in dpc micelles
37	c2oviA_	Alignment	not modelled	14.5	21	**PDB header:**ligand binding protein, metal transport **Chain:** A: **PDB Molecule:**hypothetical protein chux; **PDBTitle:** structure of the heme binding protein chux
38	c2hfpB_	Alignment	not modelled	14.5	54	**PDB header:**transcription **Chain:** B: **PDB Molecule:**src peptide fragment; **PDBTitle:** crystal structure of ppar gamma with n-sulfonyl-2-indole2 carboxamide ligands
39	c1fm9E_	Alignment	not modelled	14.3	54	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and gi262570 and co-activator peptides.
40	c1fm6E_	Alignment	not modelled	14.3	54	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides.
41	c1k74E_	Alignment	not modelled	14.3	54	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.3 angstrom resolution crystal structure of the2 heterodimer of the human ppargamma and rxralpha ligand3 binding domains respectively bound with gw409544 and 9-cis4 retinoic acid and co-activator peptides.
42	d1h16a_	Alignment	not modelled	14.2	50	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
43	c3ke8A_	Alignment	not modelled	14.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
44	c1fm6V_	Alignment	not modelled	14.0	54	**PDB header:**transcription **Chain:** V: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides.
45	c3hjlA_	Alignment	not modelled	13.7	14	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** the structure of full-length flig from aquifex aeolicus
46	d2fb1a1	Alignment	not modelled	13.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Nudix-associated domain
47	c1jscA_	Alignment	not modelled	13.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetohydroxy-acid synthase; **PDBTitle:** crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
48	d1pvda1	Alignment	not modelled	13.2	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
49	c1p8dC_	Alignment	not modelled	13.1	50	**PDB header:**membrane protein/protein binding **Chain:** C: **PDB Molecule:**nuclear receptor coactivator 1 isoform 3; **PDBTitle:** x-ray crystal structure of lxr ligand binding domain with 24(s),25-2 epoxycholesterol
50	d2f2ea1	Alignment	not modelled	13.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**HxlR-like
51	c2cu5C_	Alignment	not modelled	12.9	21	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved hypothetical protein tt1486; **PDBTitle:** crystal structure of the conserved hypothetical protein tt1486 from2 thermus thermophilus hb8
52	d1zpda1	Alignment	not modelled	12.4	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain

						Family: Pyruvate oxidase and decarboxylase, middle domain
53	c2qzjC_	Alignment	not modelled	12.3	8	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
54	c2peoA_	Alignment	not modelled	12.3	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**rbcx protein; **PDBTitle:** crystal structure of rbcx from anabaena ca
55	d2peoa1	Alignment	not modelled	12.3	16	**Fold:**RbcX-like **Superfamily:**RbcX-like **Family:**RbcX-like
56	d1rh5a_	Alignment	not modelled	12.1	20	**Fold:**Preprotein translocase SecY subunit **Superfamily:**Preprotein translocase SecY subunit **Family:**Preprotein translocase SecY subunit
57	c3s93B_	Alignment	not modelled	12.0	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tudor domain-containing protein 5; **PDBTitle:** crystal structure of conserved motif in tdrd5
58	d1a68a_	Alignment	not modelled	11.8	25	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
59	c1mhsA_	Alignment	not modelled	11.3	24	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
60	c1nw3A_	Alignment	not modelled	11.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone methyltransferase dot1l; **PDBTitle:** structure of the catalytic domain of human dot1l, a non-set2 domain nucleosomal histone methyltransferase
61	d1nw3a_	Alignment	not modelled	11.2	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Catalytic, N-terminal domain of histone methyltransferase Dot1l
62	c2kvcA_	Alignment	not modelled	11.2	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
63	d1ugpa_	Alignment	not modelled	11.2	29	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
64	c2prgC_	Alignment	not modelled	11.1	54	**PDB header:**complex (thiazolidinedione/receptor) **Chain:** C: **PDB Molecule:**nuclear receptor coactivator src-1; **PDBTitle:** ligand-binding domain of the human peroxisome proliferator2 activated receptor gamma
65	d1xhfa1	Alignment	not modelled	10.7	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
66	c3ktsA_	Alignment	not modelled	10.6	20	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein; **PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
67	c2c9eA_	Alignment	not modelled	10.6	18	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**peridinin-chlorophyll a protein; **PDBTitle:** peridinin-chlorophyll a protein, high-salt form
68	d1niga_	Alignment	not modelled	10.5	23	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Hypothetical protein Ta1238
69	c2z99A_	Alignment	not modelled	10.3	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of scpb from mycobacterium tuberculosis
70	d1y8oa1	Alignment	not modelled	10.2	17	**Fold:**Bromodomain-like **Superfamily:**alpha-ketoacid dehydrogenase kinase, N-terminal domain **Family:**alpha-ketoacid dehydrogenase kinase, N-terminal domain
71	c3cgxA_	Alignment	not modelled	10.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotide-diphospho-sugar transferase; **PDBTitle:** crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
72	c2qr3A_	Alignment	not modelled	10.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**two-component system response regulator; **PDBTitle:** crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
73	c1pjtB_	Alignment	not modelled	10.0	11	**PDB header:**transferase/oxidoreductase/lyase **Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
74	d1d8ba_	Alignment	not modelled	9.9	23	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
75	c3df8A_	Alignment	not modelled	9.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible hxlr family transcriptional factor; **PDBTitle:** the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1
76	c6paxA_	Alignment	not modelled	9.8	29	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6;

76	c6paxA_	Alignment	not modelled	9.8	29	**PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
77	c2q9qF_	Alignment	not modelled	9.8	16	**PDB header:**replication **Chain:** F: **PDB Molecule:**gins complex subunit 4; **PDBTitle:** the crystal structure of full length human gins complex
78	d1qkka_	Alignment	not modelled	9.7	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
79	d1dsxa_	Alignment	not modelled	9.7	27	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
80	d1orna_	Alignment	not modelled	9.7	17	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
81	d1b0na1	Alignment	not modelled	9.4	38	**Fold:**Dimerisation interlock **Superfamily:**SinR repressor dimerisation domain-like **Family:**SinR repressor dimerisation domain-like
82	d1wfra_	Alignment	not modelled	9.3	27	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
83	c2ph0A_	Alignment	not modelled	9.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q6d2t7_erwct protein from erwinia2 carotovora. nesg target ewr41.
84	c1cpbA_	Alignment	not modelled	9.1	24	**PDB header:**hydrolase (c-terminal peptidase) **Chain:** A: **PDB Molecule:**carboxypeptidase b; **PDBTitle:** structure of carboxypeptidase b at 2.8 angstroms resolution
85	d1iuka_	Alignment	not modelled	9.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
86	c2f3oB_	Alignment	not modelled	8.9	25	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
87	d1ni5a1	Alignment	not modelled	8.9	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
88	c3hv2B_	Alignment	not modelled	8.9	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator/hd domain protein; **PDBTitle:** crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5
89	c3dzdA_	Alignment	not modelled	8.9	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
90	c4ktqA_	Alignment	not modelled	8.8	25	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (large fragment of dna polymerase i); **PDBTitle:** binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna
91	c1p8dD_	Alignment	not modelled	8.7	55	**PDB header:**membrane protein/protein binding **Chain:** D: **PDB Molecule:**nuclear receptor coactivator 1 isoform 3; **PDBTitle:** x-ray crystal structure of lxr ligand binding domain with 24(s),25-2 epoxycholesterol
92	d2cdqa1	Alignment	not modelled	8.6	13	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
93	c2pw0A_	Alignment	not modelled	8.6	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**prpf methylaconitate isomerase; **PDBTitle:** crystal structure of trans-aconitate bound to methylaconitate2 isomerase prpf from shewanella oneidensis
94	c3r0jA_	Alignment	not modelled	8.5	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
95	d1ckqa_	Alignment	not modelled	8.5	15	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRI
96	c1k7lD_	Alignment	not modelled	8.4	55	**PDB header:**transcription **Chain:** D: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.5 angstrom resolution crystal structure of the human2 pparalpha ligand binding domain bound with gw409544 and a3 co-activator peptide.
97	c1k7lB_	Alignment	not modelled	8.4	55	**PDB header:**transcription **Chain:** B: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.5 angstrom resolution crystal structure of the human2 pparalpha ligand binding domain bound with gw409544 and a3 co-activator peptide.
98	c1k7lF_	Alignment	not modelled	8.4	55	**PDB header:**transcription **Chain:** F: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.5 angstrom resolution crystal structure of the human2 pparalpha ligand binding domain bound with gw409544 and a3 co-activator peptide.
99	c1k7lH_	Alignment	not modelled	8.4	55	**PDB header:**transcription **Chain:** H: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.5 angstrom resolution crystal structure of the human2 pparalpha ligand binding domain bound with gw409544 and a3 co-activator peptide.