Phyre2

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Description	RVBD1734c_(-)_1960781_1961023
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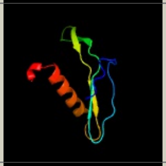
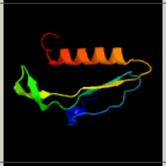
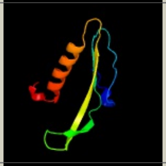
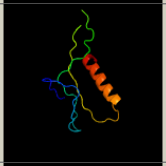
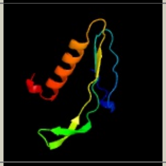
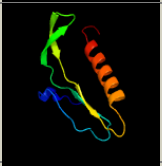
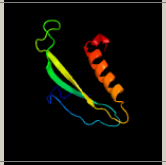
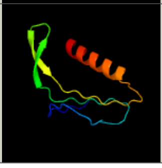
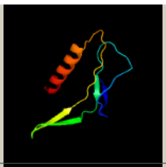
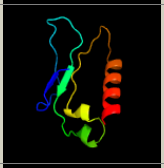
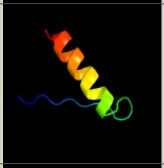
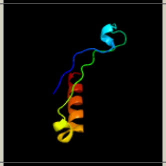
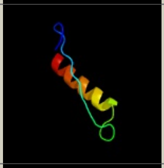
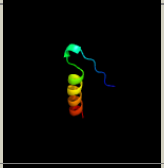
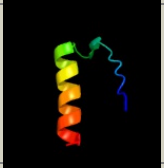
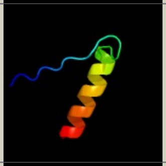
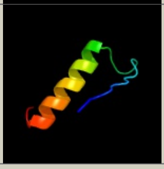
Unique Job ID	edb48cee630d63a1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b5sa_	Alignment		100.0	25	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
2	c4n72B_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate dehydrogenase (dihydrolipoyltransacetylase **PDBTitle:** catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
3	c3l60A_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**branched-chain alpha-keto acid dehydrogenase; **PDBTitle:** crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from mycobacterium tuberculosis
4	d1dpba_	Alignment		100.0	16	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
5	c2ii4C_	Alignment		100.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**lipoamide acyltransferase component of branched-chain **PDBTitle:** crystal structure of a cubic core of the dihydrolipoamide2 acyltransferase (e2b) component in the branched-chain alpha-ketoacid3 dehydrogenase complex (bckdc), coenzyme a-bound form
6	c3b8kA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase; **PDBTitle:** structure of the truncated human dihydrolipoyl acetyltransferase (e2)
7	d1scza_	Alignment		100.0	27	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
8	c3maeA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-oxoisovalerate dehydrogenase e2 component, **PDBTitle:** crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
9	c6h60A_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component, mitochondrial; **PDBTitle:** pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex
10	c3rqcB_	Alignment		99.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable lipoamide acyltransferase; **PDBTitle:** crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
11	d1q23a_	Alignment		99.7	7	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like

12	d3claa_	Alignment		99.7	15	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
13	c2i9dC_	Alignment		99.7	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** chloramphenicol acetyltransferase
14	c2zbaD_	Alignment		80.5	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trichothecene 3-o-acetyltransferase; **PDBTitle:** crystal structure of f. sporotrichioides tri101 complexed with2 coenzyme a and t-2
15	c2xt6B_	Alignment		78.8	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
16	c3fotA_	Alignment		77.9	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**15-o-acetyltransferase; **PDBTitle:** structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
17	c2e1uA_	Alignment		75.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl transferase; **PDBTitle:** crystal structure of dendranthema morifolium dmat
18	c4ke4A_	Alignment		74.5	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydroxycinnamoyl-coa:shikimate hydroxycinnamoyl **PDBTitle:** elucidation of the structure and reaction mechanism of sorghum bicolor2 hydroxycinnamoyltransferase and its structural relationship to other3 coa-dependent transferases and synthases
19	c3b2sA_	Alignment		72.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trichothecene 3-o-acetyltransferase; **PDBTitle:** crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
20	c4g0bA_	Alignment		68.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydroxycinnamoyl-coa shikimate/quinate **PDBTitle:** structure of native hct from coffea canephora
21	c2xr7A_	Alignment	not modelled	63.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyltransferase; **PDBTitle:** crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
22	c2bghA_	Alignment	not modelled	62.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vinorine synthase; **PDBTitle:** crystal structure of vinorine synthase
23	c5t3eA_	Alignment	not modelled	53.4	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**bacillamide synthetase heterocyclization domain; **PDBTitle:** crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
24	c4j7hA_	Alignment	not modelled	40.2	24	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**evaa 2,3-dehydratase; **PDBTitle:** crystal structure of evaa, a 2,3-dehydratase in complex with dtdp-2 benzene and dtdp-rhamnose
25	d1q9ja1	Alignment	not modelled	39.7	29	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
26	d1ysja2	Alignment	not modelled	39.1	6	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
27	d1z2la2	Alignment	not modelled	38.4	16	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
28	c6cgoB_	Alignment	not modelled	37.9	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**condensation domain protein; **PDBTitle:** molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase

29	c5m6pB_	Alignment	not modelled	37.3	7	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**tyrocidine synthase 2; **PDBTitle:** crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
30	c4znmB_	Alignment	not modelled	36.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**c-domain type ii peptide synthetase; **PDBTitle:** crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
31	c1q9jA_	Alignment	not modelled	35.9	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**polyketide synthase associated protein 5; **PDBTitle:** structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
32	d1vgya2	Alignment	not modelled	35.8	9	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
33	d1cg2a2	Alignment	not modelled	33.8	18	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
34	c6aefB_	Alignment	not modelled	33.2	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyketide synthase associated protein papa2; **PDBTitle:** papa2 acyl transferase
35	c2jgpA_	Alignment	not modelled	32.7	3	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrocidine synthetase 3; **PDBTitle:** structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
36	c5dijA_	Alignment	not modelled	32.2	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**tqaa; **PDBTitle:** the crystal structure of ct
37	c3v46A_	Alignment	not modelled	31.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cell division control protein 73; **PDBTitle:** crystal structure of yeast cdc73 c-terminal domain
38	c3d3rA_	Alignment	not modelled	29.7	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
39	d1r3na2	Alignment	not modelled	28.8	10	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
40	c6ad3A_	Alignment	not modelled	28.6	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**lovastatin nonaketide synthase moka; **PDBTitle:** structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
41	d1l5aa2	Alignment	not modelled	27.7	7	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
42	c4tx3B_	Alignment	not modelled	26.4	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide synthetase, module 7; **PDBTitle:** complex of the x-domain and oxyb from teicoplanin biosynthesis
43	c2fy2A_	Alignment	not modelled	26.0	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline o-acetyltransferase; **PDBTitle:** structures of ligand bound human choline acetyltransferase provide2 insight into regulation of acetylcholine synthesis
44	d3d3ra1	Alignment	not modelled	25.6	13	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
45	c2xhgA_	Alignment	not modelled	25.2	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tyrocidine synthetase a; **PDBTitle:** crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
46	c1l5aA_	Alignment	not modelled	24.7	7	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**amide synthase; **PDBTitle:** crystal structure of vibh, an nrps condensation enzyme
47	c6m7lB_	Alignment	not modelled	24.3	9	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**putative non-ribosomal peptide synthetase; **PDBTitle:** complex of oxya with the x-domain from gpa biosynthesis
48	c5t81A_	Alignment	not modelled	22.6	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**epob; **PDBTitle:** rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
49	d1l5aa1	Alignment	not modelled	22.3	21	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
50	d2z1ca1	Alignment	not modelled	21.9	16	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
51	d1nm8a1	Alignment	not modelled	21.8	12	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
52	c4jn3B_	Alignment	not modelled	19.8	0	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cda peptide synthetase i; **PDBTitle:** crystal structures of the first condensation domain of the cda2 synthetase
53	d1ndba1	Alignment	not modelled	19.1	11	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
54	c6dd2A_	Alignment	not modelled	18.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable hydroxycinnamoyl transferase; **PDBTitle:** crystal structure of selaginella moellendorffii hct
						Fold: CoA-dependent acyltransferases

55	d1t1ua1	Alignment	not modelled	16.5	8	**Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
56	c4hvmC_	Alignment	not modelled	15.5	7	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**tlmii; **PDBTitle:** crystal structure of tallysomycin biosynthesis protein tlmii
57	c1t7qA_	Alignment	not modelled	14.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine acetyltransferase; **PDBTitle:** crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
58	d1xl7a1	Alignment	not modelled	14.4	11	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
59	c3lfjB_	Alignment	not modelled	12.8	4	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, mannose/fructose/n- **PDBTitle:** crystal structure of manxb from thermoanaerobacter tengcongensis
60	c1xl8B_	Alignment	not modelled	12.1	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**peroxisomal carnitine o-octanoyltransferase; **PDBTitle:** crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
61	c4mmoB_	Alignment	not modelled	12.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sso-cp2 metallo-carboxypetidase; **PDBTitle:** the crystal structure of a m20 family metallo-carboxypeptidase sso-cp22 from sulfolobus solfataricus
62	c5t17A_	Alignment	not modelled	10.8	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphocarrier protein npr; **PDBTitle:** nmr structure of the e. coli protein npr, residues 1-85
63	c4zxjA_	Alignment	not modelled	10.7	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**enterobactin synthase component f; **PDBTitle:** crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
64	c3pfoB_	Alignment	not modelled	10.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative acetylornithine deacetylase (rpa2325)2 from rhodopseudomonas palustris cga009 at 1.90 a resolution
65	d1zvvj1	Alignment	not modelled	10.4	0	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
66	d2ot2a1	Alignment	not modelled	10.2	14	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
67	d1cm3a_	Alignment	not modelled	9.4	5	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
68	c4pxeB_	Alignment	not modelled	9.3	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ureidoglycolate hydrolase; **PDBTitle:** the crystal structure of atuah in complex with glyoxylate
69	c5u89A_	Alignment	not modelled	9.2	12	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**amino acid adenylation domain protein; **PDBTitle:** crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
70	d1ptfa_	Alignment	not modelled	9.1	17	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
71	c3n5fB_	Alignment	not modelled	8.8	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-carbamoyl-l-amino acid hydrolase; **PDBTitle:** crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
72	c6ozvA_	Alignment	not modelled	8.7	22	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**txo1; **PDBTitle:** the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
73	c1vsqC_	Alignment	not modelled	8.7	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannose-specific phosphotransferase enzyme iib component; **PDBTitle:** solution nmr structure of the productive complex between iiamannose2 and iibmannose of the mannose transporter of the e. coli3 phosphotransferase system
74	c3ihsB_	Alignment	not modelled	8.7	0	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
75	c6chjB_	Alignment	not modelled	8.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diacylglycerol o-acyltransferase; **PDBTitle:** wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
76	c1q6xA_	Alignment	not modelled	8.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline o-acetyltransferase; **PDBTitle:** crystal structure of rat choline acetyltransferase
77	d1mo1a_	Alignment	not modelled	8.5	0	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
78	c5d6aA_	Alignment	not modelled	8.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase of the abc class; **PDBTitle:** 2.7 angstrom crystal structure of abc transporter atpase from vibrio2 vulnificus in complex with adenylyl-imidodiphosphate (amp-pnp)
79	c2imoA_	Alignment	not modelled	8.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoate amidohydrolase; **PDBTitle:** crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6

80	c2pokB_	Alignment	not modelled	8.2	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae
81	c2memA_	Alignment	not modelled	8.0	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sex comb on midleg-like protein 2; **PDBTitle:** solution nmr structure of sled domain of scml2
82	c2zogA_	Alignment	not modelled	7.3	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic non-specific dipeptidase; **PDBTitle:** crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
83	c2fyoA_	Alignment	not modelled	7.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine o-palmitoyltransferase ii, mitochondrial; **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
84	c3fz0C_	Alignment	not modelled	6.9	8	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nucleoside hydrolase, putative; **PDBTitle:** inosine-guanosine nucleoside hydrolase (ig-nh)
85	c2f7vA_	Alignment	not modelled	6.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aectylcitrulline deacetylase; **PDBTitle:** structure of acetylcitrulline deacetylase complexed with2 one co
86	c5tp4B_	Alignment	not modelled	6.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidase, hydantoinase/carbamoylase family; **PDBTitle:** crystal structure of a hydantoinase/carbamoylase family amidase from2 burkholderia ambifaria
87	c3le1B_	Alignment	not modelled	6.5	5	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, hpr-related proteins; **PDBTitle:** crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis
88	d2oo3a1	Alignment	not modelled	6.4	38	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**LPG1296-like
89	d1ka5a_	Alignment	not modelled	6.3	9	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
90	c2v8gD_	Alignment	not modelled	6.1	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-alanine synthase; **PDBTitle:** crystal structure of beta-alanine synthase from2 saccharomyces kluyveri in complex with the product beta-3 alanine
91	c3eyeA_	Alignment	not modelled	6.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system n-acetylgalactosamine-specific iib component 1; **PDBTitle:** crystal structure of pts system n-acetylgalactosamine-specific iib2 component 1 from escherichia coli
92	c2h4tB_	Alignment	not modelled	5.7	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carnitine o-palmitoyltransferase ii, mitochondrial; **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase ii
93	d2hpra_	Alignment	not modelled	5.5	5	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
94	c6mbcB_	Alignment	not modelled	5.4	23	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**df4; **PDBTitle:** human bfl-1 in complex with the designed peptide df4
95	c3io1B_	Alignment	not modelled	5.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminobenzoyl-glutamate utilization protein; **PDBTitle:** crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
96	c5ij7T_	Alignment	not modelled	5.1	8	**PDB header:**transferase/transferase inhibitor **Chain:** T: **PDB Molecule:**polycomb protein suz12; **PDBTitle:** structure of hs/acprc2 in complex with a pyridone inhibitor