Phyre^2

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Description	P09348
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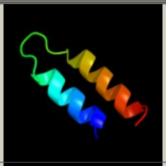
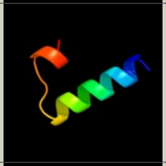
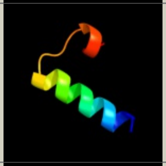
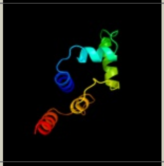
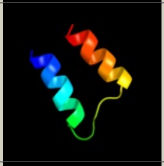
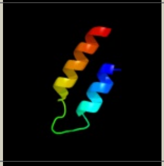
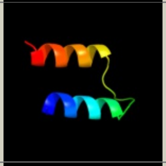
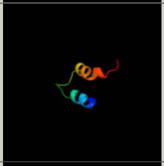
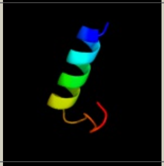
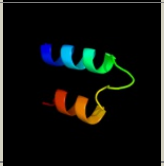
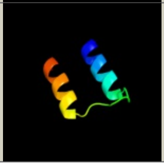
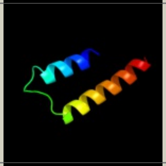
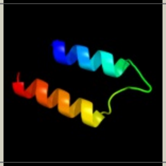
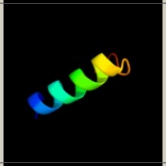
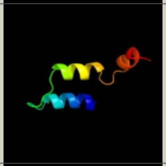
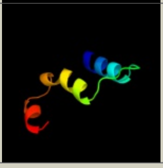
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1byga_	Alignment		59.4	32	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
2	d2hepa1	Alignment		57.4	21	**Fold:**Long alpha-hairpin **Superfamily:**YnzC-like **Family:**YznC-like
3	c2hepA_	Alignment		57.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** solution nmr structure of the upf0291 protein ynzc from2 bacillus subtilis. northeast structural genomics target3 sr384.
4	c2w1iB_	Alignment		56.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**jak2; **PDBTitle:** structure determination of aurora kinase in complex with2 inhibitor
5	d1u46a_	Alignment		55.3	16	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
6	d1vjya_	Alignment		49.1	6	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
7	d1iasa_	Alignment		48.7	6	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
8	d1p4oa_	Alignment		46.9	27	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
9	c2jvdA_	Alignment		46.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynzc from bacillus subtilis. northeast3 structural genomics target sr384-1-46
10	c3zzwA_	Alignment		46.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase transmembrane receptor ror2; **PDBTitle:** crystal structure of the kinase domain of ror2
11	c2bujA_	Alignment		45.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase 16; **PDBTitle:** crystal structure of the human serine-threonine kinase 162 in complex with staurosporine

12	c1ciiA_	Alignment		43.8	12	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
13	c3cc6A_	Alignment		41.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein tyrosine kinase 2 beta; **PDBTitle:** crystal structure of kinase domain of protein tyrosine kinase 2 beta2 (ptk2b)
14	c1k9aB_	Alignment		41.5	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carboxyl-terminal src kinase; **PDBTitle:** crystal structure analysis of full-length carboxyl-terminal2 src kinase at 2.5 a resolution
15	c3cblA_	Alignment		41.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fes/fps; **PDBTitle:** crystal structure of human feline sarcoma viral oncogene homologue (v-2 fes) in complex with staurosporine and a consensus peptide
16	c3bhpA_	Alignment		38.7	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** crystal structure of upf0291 protein ynzc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
17	c2xbaA_	Alignment		38.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alk tyrosine kinase receptor; **PDBTitle:** structure of human anaplastic lymphoma kinase in complex2 with pha-e429
18	c3c1xA_	Alignment		37.3	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor receptor; **PDBTitle:** crystal structure of the tyrosine kinase domain of the2 hepatocyte growth factor receptor c-met in complex with a3 pyrrolotriazine based inhibitor
19	c2c0iA_	Alignment		36.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase hck; **PDBTitle:** src family kinase hck with bound inhibitor a-420983
20	c3lvpD_	Alignment		36.8	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**insulin-like growth factor 1 receptor; **PDBTitle:** crystal structure of bisphosphorylated igf1-r kinase domain (2p) in2 complex with a bis-azaindole inhibitor
21	c3d4qA_	Alignment	not modelled	36.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**b-raf proto-oncogene serine/threonine-protein kinase; **PDBTitle:** pyrazole-based inhibitors of b-raf kinase
22	c3lxnA_	Alignment	not modelled	34.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**non-receptor tyrosine-protein kinase tyk2; **PDBTitle:** structural and thermodynamic characterization of the tyk2 and jak32 kinase domains in complex with cp-690550 and cmp-6
23	c2yhvA_	Alignment	not modelled	34.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alk tyrosine kinase receptor; **PDBTitle:** structure of l1196m mutant anaplastic lymphoma kinase
24	c3lxkA_	Alignment	not modelled	33.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase jak3; **PDBTitle:** structural and thermodynamic characterization of the tyk2 and jak32 kinase domains in complex with cp-690550 and cmp-6
25	c2qofA_	Alignment	not modelled	33.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin receptor; **PDBTitle:** human epha3 kinase and juxtamembrane region, y596f mutant
26	c3mtfB_	Alignment	not modelled	31.8	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**activin receptor type-1; **PDBTitle:** crystal structure of the acvr1 kinase in complex with a 2-2 aminopyridine inhibitor
27	c2j0kB_	Alignment	not modelled	30.8	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**focal adhesion kinase 1; **PDBTitle:** crystal structure of a fragment of focal adhesion kinase2 containing the ferm and kinase domains.
						PDB header:transferase

28	c2qluA_	Alignment	not modelled	30.0	16	**Chain:** A: **PDB Molecule:**activin receptor type iib; **PDBTitle:** crystal structure of activin receptor type ii kinase domain2 from human
29	c3fupB_	Alignment	not modelled	29.4	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**tyrosine-protein kinase jak2; **PDBTitle:** crystal structures of jak1 and jak2 inhibitor complexes
30	c3s95A_	Alignment	not modelled	29.0	26	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**lim domain kinase 1; **PDBTitle:** crystal structure of the human limk1 kinase domain in complex with2 staurosporine
31	c3kmuA_	Alignment	not modelled	28.8	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin-linked kinase; **PDBTitle:** crystal structure of the ilk/alpha-parvin core complex (apo)
32	c2oidA_	Alignment	not modelled	27.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**interleukin-1 receptor-associated kinase 4; **PDBTitle:** crystal structure of irak4 kinase domain complexed with2 amppnp
33	c3mdyC_	Alignment	not modelled	27.2	6	**PDB header:**transferase/isomerase **Chain:** C: **PDB Molecule:**bone morphogenetic protein receptor type-1b; **PDBTitle:** crystal structure of the cytoplasmic domain of the bone morphogenetic2 protein receptor type-1b (bmpr1b) in complex with fkbp12 and ldn-3 193189
34	c3sxrA_	Alignment	not modelled	26.8	13	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**cytoplasmic tyrosine-protein kinase bmx; **PDBTitle:** crystal structure of bmx non-receptor tyrosine kinase complex with2 dasatinib
35	c3eygA_	Alignment	not modelled	26.6	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase; **PDBTitle:** crystal structures of jak1 and jak2 inhibitor complexes
36	d1mp8a_	Alignment	not modelled	25.9	26	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
37	c3g2fB_	Alignment	not modelled	25.9	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bone morphogenetic protein receptor type-2; **PDBTitle:** crystal structure of the kinase domain of bone morphogenetic protein2 receptor type ii (bmpr2) at 2.35 a resolution
38	c2qkwB_	Alignment	not modelled	25.4	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein kinase; **PDBTitle:** structural basis for activation of plant immunity by2 bacterial effector protein avrpto
39	c3ll6B_	Alignment	not modelled	25.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cyclin g-associated kinase; **PDBTitle:** crystal structure of the human cyclin g associated kinase (gak)
40	d1r0pa_	Alignment	not modelled	24.5	26	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
41	c2h8hA_	Alignment	not modelled	24.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase src; **PDBTitle:** src kinase in complex with a quinazoline inhibitor
42	c2ozoA_	Alignment	not modelled	23.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase zap-70; **PDBTitle:** autoinhibited intact human zap-70
43	d1uwha_	Alignment	not modelled	23.8	17	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
44	d3bu3a1	Alignment	not modelled	23.7	21	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
45	d1opja_	Alignment	not modelled	23.3	26	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
46	c1yvjA_	Alignment	not modelled	23.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase jak3; **PDBTitle:** crystal structure of the jak3 kinase domain in complex with2 a staurosporine analogue
47	d1jpaa_	Alignment	not modelled	21.8	16	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
48	d1sm2a_	Alignment	not modelled	20.2	13	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
49	c2pvfA_	Alignment	not modelled	19.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fibroblast growth factor receptor 2; **PDBTitle:** crystal structure of tyrosine phosphorylated activated fgf2 receptor 2 (fgfr2) kinase domain in complex with atp3 analog and substrate peptide
50	d1u59a_	Alignment	not modelled	19.2	28	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
51	d1mqba_	Alignment	not modelled	19.1	16	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
52	c1y57A_	Alignment	not modelled	18.8	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase src; **PDBTitle:** structure of unphosphorylated c-src in complex with an inhibitor
						PDB header:structural protein/cell adhesion

53	c2kbrA_	Alignment	not modelled	18.7	11	**Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** solution structure of harmonin n terminal domain in complex2 with a internal peptide of cadherin23
54	c3dtcA_	Alignment	not modelled	17.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mitogen-activated protein kinase kinase kinase 9; **PDBTitle:** crystal structure of mixed-lineage kinase mlk1 complexed2 with compound 16
55	c2y4iB_	Alignment	not modelled	17.4	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**kinase suppressor of ras 2; **PDBTitle:** ksr2-mek1 heterodimer
56	c3qupA_	Alignment	not modelled	17.3	17	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**tyrosine-protein kinase receptor tyro3; **PDBTitle:** inhibitor bound structure of the kinase domain of the murine receptor2 tyrosine kinase tyro3 (sky)
57	d1fgka_	Alignment	not modelled	16.9	33	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
58	c3db8A_	Alignment	not modelled	16.8	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polo-like kinase 1; **PDBTitle:** crystal structure of an activated (thr->asp) polo-like2 kinase 1 (plk1) catalytic domain in complex with compound3 041
59	d2psqa1	Alignment	not modelled	16.8	23	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
60	c2psqA_	Alignment	not modelled	16.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fibroblast growth factor receptor 2; **PDBTitle:** crystal structure of unphosphorylated unactivated wild type2 fgf receptor 2 (fgfr2) kinase domain
61	c3mogA_	Alignment	not modelled	16.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxybutyryl-coa dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
62	c2wqmA_	Alignment	not modelled	16.2	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase nek7; **PDBTitle:** structure of apo human nek7
63	c3h9rA_	Alignment	not modelled	16.1	7	**PDB header:**isomerase/protein kinase **Chain:** A: **PDB Molecule:**activin receptor type-1; **PDBTitle:** crystal structure of the kinase domain of type i activin receptor2 (acvr1) in complex with fkbp12 and dorsomorphin
64	d1fmka3	Alignment	not modelled	15.8	20	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
65	d1qpca_	Alignment	not modelled	15.7	21	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
66	d1cm8a_	Alignment	not modelled	15.7	24	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
67	c2qobA_	Alignment	not modelled	15.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin receptor; **PDBTitle:** human epha3 kinase domain, base structure
68	c3brbB_	Alignment	not modelled	14.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**proto-oncogene tyrosine-protein kinase mer; **PDBTitle:** crystal structure of catalytic domain of the proto-oncogene tyrosine-2 protein kinase mer in complex with adp
69	c1ua2A_	Alignment	not modelled	14.5	11	**PDB header:**cell cycle, transferase **Chain:** A: **PDB Molecule:**cell division protein kinase 7; **PDBTitle:** crystal structure of human cdk7
70	d1ua2a_	Alignment	not modelled	14.5	11	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
71	d1csna_	Alignment	not modelled	14.4	18	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
72	d1h8ba_	Alignment	not modelled	14.4	20	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
73	c3o6xC_	Alignment	not modelled	14.3	13	**PDB header:**ligase **Chain:** C: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
74	c2dylA_	Alignment	not modelled	14.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dual specificity mitogen-activated protein **PDBTitle:** crystal structure of human mitogen-activated protein kinase2 kinase 7 activated mutant (s287d, t291d)
75	c3p86B_	Alignment	not modelled	13.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase ctr1; **PDBTitle:** crystal structure of ctr1 kinase domain mutant d676n in complex with2 staurosporine
76	c1y6aA_	Alignment	not modelled	13.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vascular endothelial growth factor receptor 2; **PDBTitle:** crystal structure of vegfr2 in complex with a 2-anilino-5-aryl-oxazole2 inhibitor
77	d1xbba_	Alignment	not modelled	13.5	29	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
78	d1ckia_	Alignment	not modelled	13.3	17	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit

79	c2evaA_	Alignment	not modelled	12.7	15	**PDB header:**transferase/transferase activator **Chain:** A: **PDB Molecule:**tak1 kinase - tab1 chimera fusion protein; **PDBTitle:** structural basis for the interaction of tak1 kinase with2 its activating protein tab1
80	d1xwsa_	Alignment	not modelled	12.5	32	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
81	d1lufa_	Alignment	not modelled	12.1	20	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
82	c1lufA_	Alignment	not modelled	12.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**muscle-specific tyrosine kinase receptor musk; **PDBTitle:** crystal structure of the musk tyrosine kinase: insights2 into receptor autoregulation
83	d1fvra_	Alignment	not modelled	11.9	17	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
84	c3jzdA_	Alignment	not modelled	11.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
85	d1ctda_	Alignment	not modelled	11.7	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
86	c2x58B_	Alignment	not modelled	11.5	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** the crystal structure of mfe1 liganded with coa
87	c3kexA_	Alignment	not modelled	11.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** crystal structure of the catalytically inactive kinase2 domain of the human epidermal growth factor receptor 33 (her3)
88	d1kqfb2	Alignment	not modelled	10.5	36	**Fold:**Single transmembrane helix **Superfamily:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor **Family:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
89	c3hkoA_	Alignment	not modelled	10.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calcium/calmodulin-dependent protein kinase with a kinase **PDBTitle:** crystal structure of a cdpk kinase domain from cryptosporidium parvum,2 cgd7_40
90	c2a1aB_	Alignment	not modelled	10.4	19	**PDB header:**protein synthesis/transferase **Chain:** B: **PDB Molecule:**interferon-induced, double-stranded rna-activated protein **PDBTitle:** pkr kinase domain-eif2alpha complex
91	d1k2pa_	Alignment	not modelled	10.4	20	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
92	c2c47D_	Alignment	not modelled	10.1	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**casein kinase 1 gamma 2 isoform; **PDBTitle:** structure of casein kinase 1 gamma 2
93	c1zy5B_	Alignment	not modelled	10.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase gcn2; **PDBTitle:** crystal structure of eif2alpha protein kinase gcn2: r794g2 hyperactivating mutant complexed with amppnp.
94	c3k6jA_	Alignment	not modelled	9.9	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence; **PDBTitle:** crystal structure of the dehydrogenase part of multifuctional enzyme 12 from c.elegans
95	d1f0ya1	Alignment	not modelled	9.7	15	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
96	c1oplA_	Alignment	not modelled	9.7	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase; **PDBTitle:** structural basis for the auto-inhibition of c-abl tyrosine2 kinase
97	c2vy9A_	Alignment	not modelled	9.6	18	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**anti-sigma-factor antagonist; **PDBTitle:** molecular architecture of the stressosome, a signal2 integration and transduction hub
98	c3famA_	Alignment	not modelled	9.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbon catabolite-derepressing protein kinase; **PDBTitle:** crystal structure of the protein kinase domain of yeast amp-2 activated protein kinase snf1
99	d2f05a1	Alignment	not modelled	9.3	16	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain