

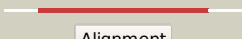













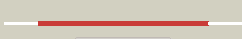












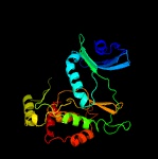
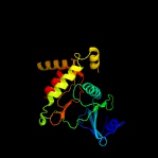


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3817 (- )_4281825_4282580
Date	Fri Aug 9 18:20:52 BST 2019
Unique Job ID	d76ac4ddce49c9de

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3r78B_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside 3'-phosphotransferase aph1-ia-b; <b>PDBTitle:</b> crystal structure of the aminoglycoside phosphotransferase aph(3')-ia,2 atp-bound
2	<a href="#">c4h05B_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside-o-phosphotransferase viii; <b>PDBTitle:</b> crystal structure of aminoglycoside-3'- phosphotransferase of type viii
3	<a href="#">c6fucA_</a>	 Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of aminoglycoside phosphotransferase aph(3''- id from2 streptomyces rimosus atcc10970
4	<a href="#">d1j7la_</a>	 Alignment		100.0	21	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
5	<a href="#">d1nd4a_</a>	 Alignment		100.0	29	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
6	<a href="#">c3dxaA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative aminoglycoside phosphotransferase2 (reut_a1007) from ralstonia eutropha jmp134 at 2.32 a resolution
7	<a href="#">c3ovcA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> hygromycin-b 4-o-kinase; <b>PDBTitle:</b> crystal structure of aminoglycoside phosphotransferase aph(4)-ia
8	<a href="#">c3attA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of rv3168 with atp
9	<a href="#">c3csvA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> crystal structure of a putative aminoglycoside phosphotransferase2 (yp_614837.1) from silicibacter sp. tm1040 at 2.15 a resolution
10	<a href="#">c3lzhA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aph(2'')-id/aph(2'')-iva; <b>PDBTitle:</b> crystal structure of aminoglycoside phosphotransferase aph(2'')-2 id/aph(2'')-iva
11	<a href="#">c3tdvB_</a>	 Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> gentamicin resistance protein; <b>PDBTitle:</b> structure of the gdp complex of wild-type aminoglycoside 2'-2 phosphotransferase-iiiia

12	<a href="#">c5igrA</a>	Alignment		100.0	22	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide 2'-phosphotransferase; <b>PDBTitle:</b> macrolide 2'-phosphotransferase type i - complex with gdp and 2 oleandomycin
13	<a href="#">c6ef6A</a>	Alignment		99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of the microcompartment-associated aminopropanol kinase
14	<a href="#">c5uxbA</a>	Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide 2'-phosphotransferase mphh; <b>PDBTitle:</b> crystal structure of macrolide 2'-phosphotransferase mphh from 2 brachybacterium faecium, apoenzyme
15	<a href="#">c5igwA</a>	Alignment		99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide 2'-phosphotransferase ii; <b>PDBTitle:</b> macrolide 2'-phosphotransferase type ii - complex with gdp and 2 clarithromycin
16	<a href="#">c3dxbB</a>	Alignment		99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> choline/ethanolamine kinase family protein; <b>PDBTitle:</b> crystal structure of choline/ethanolamine kinase family protein2 (np_106042.1) from mesorhizobium loti at 2.55 a resolution
17	<a href="#">d2ppqa1</a>	Alignment		99.9	13	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
18	<a href="#">c4orkB</a>	Alignment		99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional aac/aph; <b>PDBTitle:</b> crystal structure of the phosphotransferase domain of the bifunctional 2 aminoglycoside resistance enzyme aac(6')-ie-aph(2'')-ia
19	<a href="#">c3jr1A</a>	Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fructosamine-3-kinase; <b>PDBTitle:</b> crystal structure of putative fructosamine-3-kinase (yp_719053.1) from 2 haemophilus somnus 129pt at 2.32 a resolution
20	<a href="#">d2pula1</a>	Alignment		99.9	13	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
21	<a href="#">c4r77A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline kinase; <b>PDBTitle:</b> crystal structure of choline kinase lica from streptococcus pneumoniae
22	<a href="#">c3i0oA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> spectinomycin phosphotransferase; <b>PDBTitle:</b> crystal structure of spectinomycin phosphotransferase, 2 aph(9)-ia, in complex with adp and spectinomycin
23	<a href="#">c3f7wA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fructosamine-3-kinase; <b>PDBTitle:</b> crystal structure of putative fructosamine-3-kinase (yp_290396.1) from 2 thermobifida fusca yx-er1 at 1.85 a resolution
24	<a href="#">d1zyla1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
25	<a href="#">c3hamA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of the gentamicin-aph(2'')-ia complex
26	<a href="#">c2pywA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of a. thaliana 5-methylthioribose kinase in complex with adp2 and mtr
27	<a href="#">c3c5iD</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> choline kinase; <b>PDBTitle:</b> crystal structure of plasmodium knowlesi choline kinase, pkh_134520
28	<a href="#">c2ig7A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline/ethanolamine kinase; <b>PDBTitle:</b> crystal structure of human choline kinase b
						<b>PDB header:</b> transferase

29	<a href="#">c3mesB_</a>	Alignment	not modelled	99.9	14	<b>Chain:</b> B; <b>PDB Molecule:</b> choline kinase; <b>PDBTitle:</b> crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3 2030
30	<a href="#">c4ockA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> n-acetylhexosamine 1-phosphate kinase; <b>PDBTitle:</b> n-acetylhexosamine 1-phosphate kinase in complex with glcnac and2 amppnp
31	<a href="#">c1nw1A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> choline kinase (49.2 kd); <b>PDBTitle:</b> crystal structure of choline kinase
32	<a href="#">d1nw1a_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Choline kinase
33	<a href="#">c2q83A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> yttaa protein; <b>PDBTitle:</b> crystal structure of yttaa (2635576) from bacillus subtilis at 2.50 a2 resolution
34	<a href="#">c3f2rA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha in complex with2 hemicholinium-3
35	<a href="#">c2ckpB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha-2 in2 complex with adp
36	<a href="#">c2ckpA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha-2 in2 complex with adp
37	<a href="#">c4pdyA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> crystal structure of aminoglycoside phosphotransferase from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
38	<a href="#">c3f2rB_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha in complex with2 hemicholinium-3
39	<a href="#">c2qg7A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ethanolamine kinase pv091845; <b>PDBTitle:</b> plasmodium vivax ethanolamine kinase pv091845
40	<a href="#">c5jy7K_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> isomerase/transferase <b>Chain:</b> K; <b>PDB Molecule:</b> maltokinase; <b>PDBTitle:</b> complex of mycobacterium smegmatis trehalose synthase with maltokinase
41	<a href="#">c2pziA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable serine/threonine-protein kinase pkng; <b>PDBTitle:</b> crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
42	<a href="#">c3en9B_</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> o-sialoglycoprotein endopeptidase/protein kinase; <b>PDBTitle:</b> structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
43	<a href="#">c4pedA_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> chaperone activity of bc1 complex-like, mitochondrial; <b>PDBTitle:</b> mitochondrial adck3 employs an atypical protein kinase-like fold to2 enable coenzyme q biosynthes
44	<a href="#">c5yk2A_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> probable conserved atp-binding protein abc transporter; <b>PDBTitle:</b> the complex structure of rv3197-erythromycin from mycobacterium2 tuberculosis
45	<a href="#">c5jy7I_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> isomerase/transferase <b>Chain:</b> I; <b>PDB Molecule:</b> maltokinase; <b>PDBTitle:</b> complex of mycobacterium smegmatis trehalose synthase with maltokinase
46	<a href="#">c5ebzF_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> F; <b>PDB Molecule:</b> inhibitor of nuclear factor kappa-b kinase subunit alpha; <b>PDBTitle:</b> crystal structure of human ikk1
47	<a href="#">c4o7oB_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> maltokinase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis maltose kinase mak
48	<a href="#">c6g51v_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> ribosome <b>Chain:</b> V; <b>PDB Molecule:</b> 40s ribosomal protein s21; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state d
49	<a href="#">c4azwA_</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> wbdd; <b>PDBTitle:</b> crystal structure of monomeric wbdd.
50	<a href="#">c4im2A_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> serine/threonine-protein kinase tbk1; <b>PDBTitle:</b> structure of tank-binding kinase 1
51	<a href="#">c4wzyA_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> maltokinase; <b>PDBTitle:</b> structure of mycobacterial maltokinase, the missing link in the2 essential glge-pathway (atp complex)
52	<a href="#">c3qa8A_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> immune system, signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> mgc80376 protein; <b>PDBTitle:</b> crystal structure of inhibitor of kappa b kinase beta
53	<a href="#">c4azsA_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> methyltransferase wbdd; <b>PDBTitle:</b> high resolution (2.2 a) crystal structure of wbdd.
						<b>PDB header:</b> nuclear protein

54	<a href="#">c6fdnA</a>	Alignment	not modelled	99.3	14	<b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase rio2; <b>PDBTitle:</b> rio2 structure
55	<a href="#">c3qa8H</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> immune system, signaling protein <b>Chain:</b> H: <b>PDB Molecule:</b> mgc80376 protein; <b>PDBTitle:</b> crystal structure of inhibitor of kappa b kinase beta
56	<a href="#">c4uw0A</a>	Alignment	not modelled	99.2	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wbdd; <b>PDBTitle:</b> low resolution structure of wbdd with c-terminal bundle ordered to2 residue 505
57	<a href="#">c4c0tA</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> likely protein kinase; <b>PDBTitle:</b> candida albicans pkh kinase domain
58	<a href="#">c1tqmA</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of a. fulgidus rio2 serine protein kinase bound to2 amppnp
59	<a href="#">c3pfaA</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c beta type; <b>PDBTitle:</b> crystal structure and allosteric activation of protein kinase c beta2 ii
60	<a href="#">c1ym7C</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-adrenergic receptor kinase 1; <b>PDBTitle:</b> g protein-coupled receptor kinase 2 (grk2)
61	<a href="#">c4gygA</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rio2 kinase; <b>PDBTitle:</b> crystal structure of the rio2 kinase from chaetomium thermophilum
62	<a href="#">c4wnkA</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> g protein-coupled receptor kinase 5; <b>PDBTitle:</b> crystal structure of bovine g protein coupled-receptor kinase 5 in2 complex with ccg215022
63	<a href="#">c3tkuB</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase mrck beta; <b>PDBTitle:</b> mrck beta in complex with fasudil
64	<a href="#">c4czuC</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> cbl-interacting serine/threonine-protein kinase 23; <b>PDBTitle:</b> crystal structure of the kinase domain of cipk23 t190d mutant
65	<a href="#">c3c4wB</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> rhodopsin kinase; <b>PDBTitle:</b> crystal structure of g protein coupled receptor kinase 1 bound to atp2 and magnesium chloride at 2.7a
66	<a href="#">c2acxB</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> g protein-coupled receptor kinase 6; <b>PDBTitle:</b> crystal structure of g protein coupled receptor kinase 6 bound to2 amppnp
67	<a href="#">c4yhjA</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> g protein-coupled receptor kinase 4; <b>PDBTitle:</b> structure and function of the hypertension variant a486v of g protein-2 coupled receptor kinase 4 (grk4)
68	<a href="#">c5dfzB</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase vps15; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
69	<a href="#">c1zpqA</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rio1 kinase; <b>PDBTitle:</b> crystal structure of full-length a.fulgidus rio1 serine kinase bound2 to atp and mn2+ ions.
70	<a href="#">c3nyoB</a>	Alignment	not modelled	99.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> g protein-coupled receptor kinase 6; <b>PDBTitle:</b> crystal structure of g protein-coupled receptor kinase 6 in complex2 with amp
71	<a href="#">c5uuuA</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> beta-adrenergic receptor kinase 1; <b>PDBTitle:</b> design, synthesis, and evaluation of the first selective and potent g-2 protein-coupled receptor kinase 2 (grk2) inhibitor for the potential3 treatment of heart failure
72	<a href="#">c5ckwA</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> legk4; <b>PDBTitle:</b> crystal structure of legk4_ amppnp kinase
73	<a href="#">c3c4yA</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodopsin kinase; <b>PDBTitle:</b> crystal structure of apo form of g protein coupled receptor kinase 12 at 7.51a
74	<a href="#">c2vwiC</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine-protein kinase osr1; <b>PDBTitle:</b> structure of the osr1 kinase, a hypertension drug target
75	<a href="#">c4wb7B</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> dnaj homolog subfamily b member 1,camp-dependent protein <b>PDBTitle:</b> crystal structure of a chimeric fusion of human dnaj (hsp40) and camp-2 dependent protein kinase a (catalytic alpha subunit)
76	<a href="#">c4cfhA</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-amp-activated protein kinase catalytic subunit alpha-1; <b>PDBTitle:</b> structure of an active form of mammalian ampk
77	<a href="#">c3ckxA</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase 24; <b>PDBTitle:</b> crystal structure of sterile 20-like kinase 3 (mst3, stk24) in complex2 with staurosporine
78	<a href="#">c6emlr</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 40s ribosomal protein s2; <b>PDBTitle:</b> cryo-em structure of a late pre-40s ribosomal subunit from2 saccharomyces cerevisiae
79	<a href="#">c4oauC</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> 2-5a-dependent ribonuclease; <b>PDBTitle:</b> complete human rnase l in complex with biological

						activators.
80	<a href="#">c6ccfB</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase kinase 1; <b>PDBTitle:</b> crystal structure of the human camkk1a in complex with hesperadin
81	<a href="#">c6df1A</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipopolysaccharide core heptose(i) kinase rfp; <b>PDBTitle:</b> waap in complex with acyl carrier protein
82	<a href="#">d1zara2</a>	Alignment	not modelled	98.9	12	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> RIO1-like kinases
83	<a href="#">c2fo0A</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase abl1 (1b isoform); <b>PDBTitle:</b> organization of the sh3-sh2 unit in active and inactive forms of the2 c-abl tyrosine kinase
84	<a href="#">c4eutA</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase tbk1; <b>PDBTitle:</b> structure of bx-795 complexed with unphosphorylated human tbk1 kinase-2 uld domain
85	<a href="#">c4i6hA</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase plk2; <b>PDBTitle:</b> selective & brain-permeable polo-like kinase-2 (plk-2) inhibitors that2 reduce alpha-synuclein phosphorylation in rat brain
86	<a href="#">c4myiA</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-dependent protein kinase, putative; <b>PDBTitle:</b> crystal structure of pvx_084705
87	<a href="#">c6c9dB</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase mark1,serine/threonine- <b>PDBTitle:</b> crystal structure of ka1-autoinhibited mark1 kinase
88	<a href="#">c5nclA</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase cbk1; <b>PDBTitle:</b> crystal structure of the cbk1-mob2 kinase-coactivator complex with an2 ssd1 peptide
89	<a href="#">c4ci6B</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> transferase/structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein kinase yopo; <b>PDBTitle:</b> mechanisms of crippling actin-dependent phagocytosis by yopo
90	<a href="#">c3vwaA</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic export protein 1; <b>PDBTitle:</b> crystal structure of cex1p
91	<a href="#">c6g4jA</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable serine/threonine-protein kinase yabt; <b>PDBTitle:</b> structure of the protein kinase yabt from bacillus subtilis in complex2 with an alpharep crystallization helper
92	<a href="#">c4dn5A</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 14; <b>PDBTitle:</b> crystal structure of nf-kb-inducing kinase (nik)
93	<a href="#">c1oplA</a>	Alignment	not modelled	98.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase; <b>PDBTitle:</b> structural basis for the auto-inhibition of c-abl tyrosine2 kinase
94	<a href="#">c3otvC</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> probable conserved transmembrane protein; <b>PDBTitle:</b> crystal structure of the intracellular domain of rv3910 from2 mycobacterium tuberculosis
95	<a href="#">c4mvfA</a>	Alignment	not modelled	98.8	11	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-dependent protein kinase 2; <b>PDBTitle:</b> crystal structure of plasmodium falciparum cdpk2 complexed with2 inhibitor staurosporine
96	<a href="#">c1koaA</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> kinase <b>Chain:</b> A: <b>PDB Molecule:</b> twitchin; <b>PDBTitle:</b> twitchin kinase fragment (c.elegans), autoregulated protein2 kinase and immunoglobulin domains
97	<a href="#">c4y93A</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> non-specific protein-tyrosine kinase,non-specific protein- <b>PDBTitle:</b> crystal structure of the ph-th-kinase construct of bruton's tyrosine2 kinase (btk)
98	<a href="#">c3fbvL</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> serine/threonine-protein kinase/endoribonuclease ire1; <b>PDBTitle:</b> crystal structure of the oligomer formed by the kinase-ribonuclease2 domain of ire1
99	<a href="#">c3q5iA</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase; <b>PDBTitle:</b> crystal structure of pbanka_031420
100	<a href="#">c4xi2A</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase btk; <b>PDBTitle:</b> crystal structure of an auto-inhibited form of bruton's tryrosine2 kinase
101	<a href="#">c3d9vA</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rho-associated protein kinase 1; <b>PDBTitle:</b> crystal structure of rock i bound to h-1152p a di-2 methylated variant of fasudil
102	<a href="#">c3e7eA</a>	Alignment	not modelled	98.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitotic checkpoint serine/threonine-protein kinase bub1; <b>PDBTitle:</b> structure and substrate recruitment of the human spindle checkpoint2 kinase bub
103	<a href="#">c4o96D</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> type iii effector protein kinase; <b>PDBTitle:</b> 2.60 angstrom resolution crystal structure of a protein kinase domain2 of type iii effector nleh2 (ecs1814) from escherichia

						coli o157:h73 str. sakai
104	<a href="#">c2y7jB_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphorylase b kinase gamma catalytic chain, testis/liver <b>PDBTitle:</b> structure of human phosphorylase kinase, gamma 2
105	<a href="#">c4bvua_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> transferase/ligase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase ospg; <b>PDBTitle:</b> structure of shigella effector ospg in complex with host ubc5c-2 ubiquitin conjugate
106	<a href="#">c5hnvA_</a>	Alignment	not modelled	98.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ppka n terminal; <b>PDBTitle:</b> crystal structure of ppka
107	<a href="#">c6hwIB_</a>	Alignment	not modelled	98.7	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine kinase; <b>PDBTitle:</b> glucosamine kinase in complex with glucosamine, adp and inorganic2 phosphate
108	<a href="#">d1phka_</a>	Alignment	not modelled	98.7	18	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
109	<a href="#">c2ozoA_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase zap-70; <b>PDBTitle:</b> autoinhibited intact human zap-70
110	<a href="#">c2a1aB_</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> protein synthesis/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> interferon-induced, double-stranded rna-activated protein <b>PDBTitle:</b> pkr kinase domain-eif2alpha complex
111	<a href="#">c3p23B_</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> kinase/threonine-protein kinase/endoribonuclease ire1; <b>PDBTitle:</b> crystal structure of the human kinase and rnase domains in complex2 with adp
112	<a href="#">c2j0kB_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> focal adhesion kinase 1; <b>PDBTitle:</b> crystal structure of a fragment of focal adhesion kinase containing2 the ferm and kinase domains.
113	<a href="#">c3q60A_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rop5b; <b>PDBTitle:</b> crystal structure of virulent allele rop5b pseudokinase domain bound2 to atp
114	<a href="#">c4bwxB_</a>	Alignment	not modelled	98.6	10	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> pab-dependent poly(a)-specific ribonuclease subunit pan-3; <b>PDBTitle:</b> structure of neurospora crassa pan3 pseudokinase mutant
115	<a href="#">c4eqmE_</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> protein kinase; <b>PDBTitle:</b> structural analysis of staphylococcus aureus serine/threonine kinase2 pknb
116	<a href="#">c6jkmA_</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitotic checkpoint control protein kinase bub1; <b>PDBTitle:</b> crystal structure of bubr1 kinase domain
117	<a href="#">c4fijA_</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 4; <b>PDBTitle:</b> catalytic domain of human pak4
118	<a href="#">c4xhgA_</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> similar to uniprot p29295 saccharomyces cerevisiae ypl204w
119	<a href="#">c4fieB_</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 4; <b>PDBTitle:</b> full-length human pak4
120	<a href="#">c2c30A_</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 6; <b>PDBTitle:</b> crystal structure of the human p21-activated kinase 6