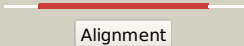

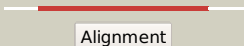

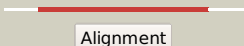







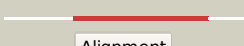












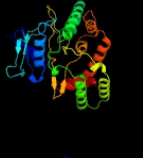




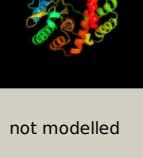


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0127 (- )_154230_155597
Date	Tue Jul 23 14:50:17 BST 2019
Unique Job ID	e7ab1336572e9a43

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4o7oB_</a>	 Alignment		100.0	100	<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
2	<a href="#">c4wzyA_</a>	 Alignment		100.0	61	<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)
3	<a href="#">c5jy7I_</a>	 Alignment		100.0	67	<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
4	<a href="#">c6hwIB_</a>	 Alignment		100.0	26	<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
5	<a href="#">c5jy7K_</a>	 Alignment		100.0	71	<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
6	<a href="#">d2ppqa1</a>	 Alignment		99.9	16	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
7	<a href="#">d1zyla1</a>	 Alignment		99.9	19	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
8	<a href="#">c6ef6A_</a>	 Alignment		99.8	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
9	<a href="#">c4pdyA_</a>	 Alignment		99.8	20	<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
10	<a href="#">c4ockA_</a>	 Alignment		99.8	17	<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
11	<a href="#">c3jr1A_</a>	 Alignment		99.7	12	<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) from2 haemophilus somnus 129pt at 2.32 a resolution

12	<a href="#">c5uxbA</a>	Alignment		99.7	16	<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 <i>brachybacterium faecium</i> , apoenzyme
13	<a href="#">c5igwA</a>	Alignment		99.7	13	<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
14	<a href="#">c4orkB</a>	Alignment		99.7	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
15	<a href="#">c3lzhA</a>	Alignment		99.7	10	<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
16	<a href="#">d2pula1</a>	Alignment		99.7	19	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
17	<a href="#">c3i0oA</a>	Alignment		99.7	18	<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
18	<a href="#">c2q83A</a>	Alignment		99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ytaa protein; <b>PDBTitle:</b> crystal structure of ytaa (2635576) from <i>bacillus subtilis</i> at 2.50 a2 resolution
19	<a href="#">c5igrA</a>	Alignment		99.7	20	<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
20	<a href="#">c3tdvB</a>	Alignment		99.7	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-iiiA
21	<a href="#">c2pywA</a>	Alignment	not modelled	99.6	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
22	<a href="#">c3hamA</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of the gentamicin-aph(2'')-iia complex
23	<a href="#">c4h05B</a>	Alignment	not modelled	99.6	22	<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
24	<a href="#">d1nd4a</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
25	<a href="#">c3dxpA</a>	Alignment	not modelled	99.6	14	<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 <i>ralstonia eutropha</i> jmp134 at 2.32 a resolution
26	<a href="#">c3ovcA</a>	Alignment	not modelled	99.6	17	<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
27	<a href="#">c4r77A</a>	Alignment	not modelled	99.6	16	<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 <i>streptococcus pneumoniae</i>
28	<a href="#">c3f7wA</a>	Alignment	not modelled	99.6	21	<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 <i>thermobifida fusca</i> yx-er1 at 1.85 a resolution

29	<a href="#">c3r78B_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside 3'-phosphotransferase apha1-iab; <b>PDBTitle:</b> crystal structure of the aminoglycoside phosphotransferase aph(3')-ia,2 atp-bound
30	<a href="#">c3attA_</a>	Alignment	not modelled	99.5	16	<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
31	<a href="#">d1j7la_</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
32	<a href="#">c3dxqB_</a>	Alignment	not modelled	99.5	21	<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
33	<a href="#">c3csvA_</a>	Alignment	not modelled	99.5	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
34	<a href="#">c3c5iD_</a>	Alignment	not modelled	99.5	18	<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
35	<a href="#">c3mesB_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <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
36	<a href="#">c6fucA_</a>	Alignment	not modelled	99.4	21	<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
37	<a href="#">c2ckpA_</a>	Alignment	not modelled	99.3	18	<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
38	<a href="#">c2ig7A_</a>	Alignment	not modelled	99.3	15	<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
39	<a href="#">c2ckpB_</a>	Alignment	not modelled	99.3	18	<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
40	<a href="#">d1nw1a_</a>	Alignment	not modelled	99.3	22	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Choline kinase
41	<a href="#">c1nw1A_</a>	Alignment	not modelled	99.3	22	<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
42	<a href="#">c2qg7A_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ethanolamine kinase pv091845; <b>PDBTitle:</b> plasmodium vivax ethanolamine kinase pv091845
43	<a href="#">c3f2rA_</a>	Alignment	not modelled	99.2	15	<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
44	<a href="#">c3f2rB_</a>	Alignment	not modelled	99.2	16	<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
45	<a href="#">c3en9B_</a>	Alignment	not modelled	98.6	19	<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
46	<a href="#">c1tqmA_</a>	Alignment	not modelled	97.1	25	<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
47	<a href="#">d1zara2</a>	Alignment	not modelled	97.1	32	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> RIO1-like kinases
48	<a href="#">c4azsA_</a>	Alignment	not modelled	97.0	22	<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.
49	<a href="#">c6fdnA_</a>	Alignment	not modelled	96.9	21	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase rio2; <b>PDBTitle:</b> rio2 structure
50	<a href="#">c6df1A_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipopolysaccharide core heptose(i) kinase rfap; <b>PDBTitle:</b> waap in complex with acyl carrier protein
51	<a href="#">c5yk2A_</a>	Alignment	not modelled	96.8	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
52	<a href="#">c4pedA_</a>	Alignment	not modelled	96.7	11	<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 biosynthesis
53	<a href="#">c4ci6B_</a>	Alignment	not modelled	96.4	18	<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

54	<a href="#">c6g51v</a>	Alignment	not modelled	96.3	17	<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
55	<a href="#">c2pziA</a>	Alignment	not modelled	96.2	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable serine/threonine-protein kinase pkgng; <b>PDBTitle:</b> crystal structure of protein kinase pkgng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
56	<a href="#">c6emlr</a>	Alignment	not modelled	96.0	18	<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
57	<a href="#">c4bwxB</a>	Alignment	not modelled	96.0	17	<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
58	<a href="#">c4gygA</a>	Alignment	not modelled	95.7	26	<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
59	<a href="#">c4bvua</a>	Alignment	not modelled	95.3	48	<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 host2 ubch5c-ubiquitin conjugate
60	<a href="#">c5dfzB</a>	Alignment	not modelled	95.3	25	<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.
61	<a href="#">c4uw0A</a>	Alignment	not modelled	95.0	22	<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
62	<a href="#">c1zp9A</a>	Alignment	not modelled	94.7	29	<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.
63	<a href="#">c4o96D</a>	Alignment	not modelled	94.5	22	<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
64	<a href="#">c6g4jA</a>	Alignment	not modelled	93.7	27	<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
65	<a href="#">c3byvA</a>	Alignment	not modelled	93.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhoptry kinase; <b>PDBTitle:</b> crystal structure of toxoplasma gondii specific rhoptry2 antigen kinase domain
66	<a href="#">c4otpA</a>	Alignment	not modelled	93.1	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase rio1; <b>PDBTitle:</b> crystal structure of the catalytic domain of the human rio1 atypical2 protein kinase in complex with adp/mg2+
67	<a href="#">c4ww7A</a>	Alignment	not modelled	92.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ekc/keops complex subunit bud32; <b>PDBTitle:</b> crystal structure of binary complex bud32-cgi121 in complex with amp
68	<a href="#">c3vwaA</a>	Alignment	not modelled	92.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic export protein 1; <b>PDBTitle:</b> crystal structure of cex1p
69	<a href="#">c6m7zE</a>	Alignment	not modelled	92.0	16	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> bradyzoite pseudokinase 1; <b>PDBTitle:</b> a divergent kinase lacking the glycine-rich loop regulates membrane2 ultrastructure of the toxoplasma parasitophorous vacuole
70	<a href="#">c4jrnA</a>	Alignment	not modelled	91.9	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhoptry kinase family protein; <b>PDBTitle:</b> rop18 kinase domain in complex with amp-pnp and sucrose
71	<a href="#">c6bhcA</a>	Alignment	not modelled	91.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pseudopodium-enriched atypical kinase 1; <b>PDBTitle:</b> crystal structure of pseudokinase peak1 (sugen kinase 269)
72	<a href="#">c4azwA</a>	Alignment	not modelled	91.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wbdd; <b>PDBTitle:</b> crystal structure of monomeric wbdd.
73	<a href="#">c3e7eA</a>	Alignment	not modelled	91.3	16	<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
74	<a href="#">c3q60A</a>	Alignment	not modelled	90.2	26	<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
75	<a href="#">c3dzoA</a>	Alignment	not modelled	90.1	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhoptry kinase domain; <b>PDBTitle:</b> crystal structure of a rhoptry kinase from toxoplasma gondii
76	<a href="#">c6eqiC</a>	Alignment	not modelled	89.8	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine-protein kinase pink1, putative; <b>PDBTitle:</b> structure of pink1 bound to ubiquitin
77	<a href="#">c4eutA</a>	Alignment	not modelled	89.0	24	<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 <b>PDB header:</b> transferase

78	<a href="#">c2jiiA_</a>	Alignment	not modelled	87.9	18	<b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase vrk3 <b>molecule:</b> vaccinia <b>PDBTitle:</b> structure of vaccinia related kinase 3
79	<a href="#">c5oatF_</a>	Alignment	not modelled	87.7	20	<b>PDB header:</b> kinase <b>Chain:</b> F: <b>PDB Molecule:</b> serine/threonine-protein kinase pink1, mitochondrial-like <b>PDBTitle:</b> pink1 structure
80	<a href="#">c4im2A_</a>	Alignment	not modelled	87.6	23	<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
81	<a href="#">c3qa8A_</a>	Alignment	not modelled	87.6	26	<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
82	<a href="#">c4bwpA_</a>	Alignment	not modelled	87.4	9	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> pab-dependent poly(a)-specific ribonuclease subunit pan-3; <b>PDBTitle:</b> structure of drosophila melanogaster pan3 pseudokinase
83	<a href="#">c4ix5B_</a>	Alignment	not modelled	87.4	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> msstt7d protein; <b>PDBTitle:</b> crystal structure of a stt7 homolog from micromonas algae in complex2 with amp-pnp
84	<a href="#">c3qa8H_</a>	Alignment	not modelled	87.1	26	<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
85	<a href="#">c4c0tA_</a>	Alignment	not modelled	86.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> likely protein kinase; <b>PDBTitle:</b> candida albicans pkh kinase domain
86	<a href="#">c5ebzF_</a>	Alignment	not modelled	86.4	21	<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
87	<a href="#">c3dfaA_</a>	Alignment	not modelled	85.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-dependent protein kinase cgd3_920; <b>PDBTitle:</b> crystal structure of kinase domain of calcium-dependent protein kinase2 cgd3_920 from cryptosporidium parvum
88	<a href="#">c5nclA_</a>	Alignment	not modelled	84.6	22	<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="#">c6jkmA_</a>	Alignment	not modelled	83.8	20	<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
90	<a href="#">c5clrB_</a>	Alignment	not modelled	82.6	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> legk4; <b>PDBTitle:</b> crystal structure of legk4_apo kinase
91	<a href="#">c1e8zA_</a>	Alignment	not modelled	82.3	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase catalytic subunit; <b>PDBTitle:</b> structure determinants of phosphoinositide 3-kinase2 inhibition by wortmannin, ly294002, quercetin, myricetin3 and staurosporine
92	<a href="#">c3op5B_</a>	Alignment	not modelled	81.7	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase vrk1; <b>PDBTitle:</b> human vaccinia-related kinase 1
93	<a href="#">c2vuwA_</a>	Alignment	not modelled	81.2	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase haspin; <b>PDBTitle:</b> structure of human haspin kinase domain
94	<a href="#">c1ym7C_</a>	Alignment	not modelled	80.9	20	<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)
95	<a href="#">c3tkuB_</a>	Alignment	not modelled	80.0	32	<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
96	<a href="#">c2ozoA_</a>	Alignment	not modelled	79.9	22	<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
97	<a href="#">c5ckwA_</a>	Alignment	not modelled	79.6	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> legk4; <b>PDBTitle:</b> crystal structure of legk4_ammnp kinase
98	<a href="#">c3nyoB_</a>	Alignment	not modelled	79.5	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 in complex2 with amp
99	<a href="#">c4myiA_</a>	Alignment	not modelled	79.1	27	<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
100	<a href="#">c2vwiC_</a>	Alignment	not modelled	78.7	30	<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
101	<a href="#">d1e7ua4</a>	Alignment	not modelled	78.4	29	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Phosphoinositide 3-kinase (PI3K), catalytic domain
102	<a href="#">c3c4wB_</a>	Alignment	not modelled	77.9	20	<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
103	<a href="#">c4cyiH_</a>	Alignment	not modelled	77.4	9	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> pab-dependent poly(a)-specific ribonuclease subunit pan3- <b>PDBTitle:</b> chaetomium thermophilum pan3 <b>PDB header:</b> transferase

104	<a href="#">c3otvC_</a>	Alignment	not modelled	77.3	13	<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
105	<a href="#">c4wnkA_</a>	Alignment	not modelled	77.0	16	<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
106	<a href="#">c4yknA_</a>	Alignment	not modelled	76.3	29	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha, <b>PDBTitle:</b> pi3k alpha lipid kinase with active site inhibitor
107	<a href="#">c2v62A_</a>	Alignment	not modelled	75.9	30	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine/threonine-protein kinase vrk2; <b>PDBTitle:</b> structure of vaccinia-related kinase 2
108	<a href="#">c4q8jE_</a>	Alignment	not modelled	75.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> pab-dependent poly(a)-specific ribonuclease subunit pan3; <b>PDBTitle:</b> structure of the saccharomyces cerevisiae pan2-pan3 core complex
109	<a href="#">c5is5A_</a>	Alignment	not modelled	74.9	29	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> discovery and pharmacological characterization of novel quinazoline-2 based pi3k delta-selective inhibitors
110	<a href="#">c2rsvA_</a>	Alignment	not modelled	74.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine/threonine-protein kinase vrk1; <b>PDBTitle:</b> solution structure of human full-length vaccinia related kinase 12 (vrk1)
111	<a href="#">c2wxoA_</a>	Alignment	not modelled	74.5	29	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> the crystal structure of the murine class ia pi 3-kinase p110delta in2 complex with as5.
112	<a href="#">c4czuC_</a>	Alignment	not modelled	74.4	26	<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
113	<a href="#">c4wb7B_</a>	Alignment	not modelled	73.4	21	<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)
114	<a href="#">c4cdaA_</a>	Alignment	not modelled	73.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrosine kinase as - a common ancestor of src and abl; <b>PDBTitle:</b> tyrosine kinase as - a common ancestor of src and abl
115	<a href="#">c2acxB_</a>	Alignment	not modelled	73.3	13	<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
116	<a href="#">c4btfA_</a>	Alignment	not modelled	73.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> mixed lineage kinase domain-like protein; <b>PDBTitle:</b> structure of mlkl
117	<a href="#">c4oauC_</a>	Alignment	not modelled	73.0	24	<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.
118	<a href="#">c4oliA_</a>	Alignment	not modelled	72.8	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> non-receptor tyrosine-protein kinase tyk2; <b>PDBTitle:</b> the pseudokinase/kinase protein from jak-family member tyk2
119	<a href="#">c6ccfB_</a>	Alignment	not modelled	72.7	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
120	<a href="#">c2rd0A_</a>	Alignment	not modelled	72.1	29	<b>PDB header:</b> transferase/oncoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic <b>PDBTitle:</b> structure of a human p110alpha/p85alpha complex