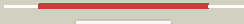



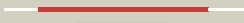




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3205c (-) _3581623_3582501
Date	Thu Aug 8 16:20:40 BST 2019
Unique Job ID	c7726f443c801b53

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ppqa1	 Alignment		99.6	14	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: APH phosphotransferases
2	c4ockA	 Alignment		99.6	18	PDB header: transferase Chain: A: PDB Molecule: n-acetylhexosamine 1-phosphate kinase; PDBTitle: n-acetylhexosamine 1-phosphate kinase in complex with glcnac and2 amppnp
3	c6ef6A	 Alignment		99.5	20	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside phosphotransferase; PDBTitle: structure of the microcompartment-associated aminopropanol kinase
4	d1zyla1	 Alignment		99.4	17	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: APH phosphotransferases
5	c4pdyA	 Alignment		99.3	16	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside phosphotransferase; PDBTitle: crystal structure of aminoglycoside phosphotransferase from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
6	c3ovcA	 Alignment		99.2	13	PDB header: transferase/antibiotic Chain: A: PDB Molecule: hygromycin-b 4-o-kinase; PDBTitle: crystal structure of aminoglycoside phosphotransferase aph(4)-ia
7	c2q83A	 Alignment		99.0	14	PDB header: transferase Chain: A: PDB Molecule: ytaa protein; PDBTitle: crystal structure of ytaa (2635576) from bacillus subtilis at 2.50 a2 resolution
8	c3jr1A	 Alignment		99.0	11	PDB header: transferase Chain: A: PDB Molecule: putative fructosamine-3-kinase; PDBTitle: crystal structure of putative fructosamine-3-kinase (yp_719053.1) from2 haemophilus somnus 129pt at 2.32 a resolution
9	c3dxqB	 Alignment		98.9	16	PDB header: transferase Chain: B: PDB Molecule: choline/ethanolamine kinase family protein; PDBTitle: crystal structure of choline/ethanolamine kinase family protein2 (np_106042.1) from mesorhizobium loti at 2.55 a resolution
10	c3dxaA	 Alignment		98.8	11	PDB header: transferase Chain: A: PDB Molecule: putative acyl-coa dehydrogenase; PDBTitle: crystal structure of a putative aminoglycoside phosphotransferase2 (reut_a1007) from ralstonia eutropha jmp134 at 2.32 a resolution
11	c3f7wA	 Alignment		98.8	15	PDB header: transferase Chain: A: PDB Molecule: putative fructosamine-3-kinase; PDBTitle: crystal structure of putative fructosamine-3-kinase (yp_290396.1) from2 thermobifida fusca yx-er1 at 1.85 a resolution

12	d1nd4a_	Alignment		98.8	12	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: APH phosphotransferases
13	c3i0oA_	Alignment		98.8	13	PDB header: transferase Chain: A: PDB Molecule: spectinomycin phosphotransferase; PDBTitle: crystal structure of spectinomycin phosphotransferase,2 aph(9)-ia, in complex with adp and spectinomycin
14	c6fucA_	Alignment		98.7	14	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside phosphotransferase; PDBTitle: structure of aminoglycoside phosphotransferase aph(3"-id from2 streptomyces rimosus atcc10970
15	d1j7la_	Alignment		98.7	9	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: APH phosphotransferases
16	c5igwA_	Alignment		98.7	12	PDB header: transferase Chain: A: PDB Molecule: macrolide 2'-phosphotransferase ii; PDBTitle: macrolide 2'-phosphotransferase type ii - complex with gdp and2 clarithromycin
17	c3tdvB_	Alignment		98.6	14	PDB header: transferase Chain: B: PDB Molecule: gentamicin resistance protein; PDBTitle: structure of the gdp complex of wild-type aminoglycoside 2'-2 phosphotransferase-iiiia
18	c5jy7K_	Alignment		98.6	18	PDB header: isomerase/transferase Chain: K: PDB Molecule: maltokinase; PDBTitle: complex of mycobacterium smegmatis trehalose synthase with maltokinase
19	c3lzhA_	Alignment		98.6	13	PDB header: transferase Chain: A: PDB Molecule: aph(2'')-id/aph(2'')-iva; PDBTitle: crystal structure of aminoglycoside phosphotransferase aph(2'')-2 id/aph(2'')-iva
20	c4h05B_	Alignment		98.6	15	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside-o-phosphotransferase viii; PDBTitle: crystal structure of aminoglycoside-3'-phosphotransferase of type viii
21	c3hamA_	Alignment	not modelled	98.4	12	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside phosphotransferase; PDBTitle: structure of the gentamicin-aph(2'')-iia complex
22	c5igrA_	Alignment	not modelled	98.4	15	PDB header: transferase/antibiotic Chain: A: PDB Molecule: macrolide 2'-phosphotransferase; PDBTitle: macrolide 2'-phosphotransferase type i - complex with gdp and2 oleandomycin
23	c5uxbA_	Alignment	not modelled	98.4	13	PDB header: transferase Chain: A: PDB Molecule: macrolide 2'-phosphotransferase mpph; PDBTitle: crystal structure of macrolide 2'-phosphotransferase mpph from2 brachy bacterium faecium, apoenzyme
24	c4r77A_	Alignment	not modelled	98.4	9	PDB header: transferase Chain: A: PDB Molecule: choline kinase; PDBTitle: crystal structure of choline kinase lica from streptococcus pneumoniae
25	c4o7oB_	Alignment	not modelled	98.2	25	PDB header: transferase Chain: B: PDB Molecule: maltokinase; PDBTitle: crystal structure of mycobacterium tuberculosis maltose kinase mak
26	d2pula1	Alignment	not modelled	98.2	12	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: APH phosphotransferases
27	c4wzyA_	Alignment	not modelled	98.2	22	PDB header: transferase Chain: A: PDB Molecule: maltokinase; PDBTitle: structure of mycobacterial maltokinase, the missing link in the2 essential glge-pathway (atp complex)
28	c4orkB_	Alignment	not modelled	98.1	10	PDB header: transferase Chain: B: PDB Molecule: bifunctional aac/aph; PDBTitle: crystal structure of the phosphotransferase domain of the bifunctional2 aminoglycoside resistance enzyme aac(6')-ie-aph(2'')-ia PDB header: isomerase/transferase

29	c5jy7L_	Alignment	not modelled	98.1	21	Chain: I; PDB Molecule: maltokinase; PDBTitle: complex of mycobacterium smegmatis trehalose synthase with maltokinase
30	c3attA_	Alignment	not modelled	98.1	12	PDB header: transferase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of rv3168 with atp
31	c3r78B_	Alignment	not modelled	98.0	13	PDB header: transferase Chain: B; PDB Molecule: aminoglycoside 3'-phosphotransferase apha1-1ab; PDBTitle: crystal structure of the aminoglycoside phosphotransferase aph(3')-ia,2 atp-bound
32	c3csvA_	Alignment	not modelled	98.0	8	PDB header: transferase Chain: A; PDB Molecule: aminoglycoside phosphotransferase; PDBTitle: crystal structure of a putative aminoglycoside phosphotransferase2 (yp_614837.1) from silicibacter sp. tm1040 at 2.15 a resolution
33	c3f2rA_	Alignment	not modelled	97.6	12	PDB header: transferase Chain: A; PDB Molecule: choline kinase alpha; PDBTitle: crystal structure of human choline kinase alpha in complex with2 hemicholinium-3
34	c2ig7A_	Alignment	not modelled	97.5	14	PDB header: transferase Chain: A; PDB Molecule: choline/ethanolamine kinase; PDBTitle: crystal structure of human choline kinase b
35	c3mesB_	Alignment	not modelled	97.4	11	PDB header: transferase Chain: B; PDB Molecule: choline kinase; PDBTitle: crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
36	c3f2rB_	Alignment	not modelled	97.4	12	PDB header: transferase Chain: B; PDB Molecule: choline kinase alpha; PDBTitle: crystal structure of human choline kinase alpha in complex with2 hemicholinium-3
37	c1nw1A_	Alignment	not modelled	97.4	14	PDB header: transferase Chain: A; PDB Molecule: choline kinase (49.2 kd); PDBTitle: crystal structure of choline kinase
38	d1nw1a_	Alignment	not modelled	97.4	14	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Choline kinase
39	c2pywA_	Alignment	not modelled	97.3	12	PDB header: transferase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: structure of a. thaliana 5-methylthioribose kinase in complex with adp2 and mtr
40	c3c5iD_	Alignment	not modelled	97.2	10	PDB header: transferase Chain: D; PDB Molecule: choline kinase; PDBTitle: crystal structure of plasmodium knowlesi choline kinase, pkh_134520
41	c2ckpB_	Alignment	not modelled	96.2	14	PDB header: transferase Chain: B; PDB Molecule: choline kinase alpha; PDBTitle: crystal structure of human choline kinase alpha-2 in2 complex with adp
42	c2ckpA_	Alignment	not modelled	96.1	14	PDB header: transferase Chain: A; PDB Molecule: choline kinase alpha; PDBTitle: crystal structure of human choline kinase alpha-2 in2 complex with adp
43	c6hwlB_	Alignment	not modelled	91.9	29	PDB header: transferase Chain: B; PDB Molecule: glucosamine kinase; PDBTitle: glucosamine kinase in complex with glucosamine, adp and inorganic2 phosphate
44	c1zp9A_	Alignment	not modelled	91.9	15	PDB header: transferase Chain: A; PDB Molecule: rio1 kinase; PDBTitle: crystal structure of full-length a.fulgidus rio1 serine kinase bound2 to atp and mn2+ ions.
45	c2qg7A_	Alignment	not modelled	90.6	22	PDB header: transferase Chain: A; PDB Molecule: ethanolamine kinase pv091845; PDBTitle: plasmodium vivax ethanolamine kinase pv091845
46	c4pedA_	Alignment	not modelled	88.7	6	PDB header: transferase Chain: A; PDB Molecule: chaperone activity of bc1 complex-like, mitochondrial; PDBTitle: mitochondrial adck3 employs an atypical protein kinase-like fold to2 enable coenzyme q biosynthes
47	c3byvA_	Alignment	not modelled	88.4	17	PDB header: transferase Chain: A; PDB Molecule: rhoptry kinase; PDBTitle: crystal structure of toxoplasma gondii specific rhoptry2 antigen kinase domain
48	c1tqmA_	Alignment	not modelled	87.1	38	PDB header: ribosome Chain: A; PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a. fulgidus rio2 serine protein kinase bound to2 amppnp
49	c5yk2A_	Alignment	not modelled	86.9	33	PDB header: transport protein Chain: A; PDB Molecule: probable conserved atp-binding protein abc transporter; PDBTitle: the complex structure of rv3197-erythromycin from mycobacterium2 tuberculosis
50	c3en9B_	Alignment	not modelled	86.3	30	PDB header: hydrolase Chain: B; PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
51	c6fdnA_	Alignment	not modelled	84.8	20	PDB header: nuclear protein Chain: A; PDB Molecule: serine/threonine-protein kinase rio2; PDBTitle: rio2 structure
52	c2pziA_	Alignment	not modelled	84.0	13	PDB header: transferase Chain: A; PDB Molecule: probable serine/threonine-protein kinase pkng; PDBTitle: crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
53	d1zara2	Alignment	not modelled	84.0	38	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like)

						Family:RIO1-like kinases
54	c6g51v_	Alignment	not modelled	83.9	20	PDB header: ribosome Chain: V: PDB Molecule: 40s ribosomal protein s21; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state d
55	c4ww7A_	Alignment	not modelled	83.2	17	PDB header: transferase Chain: A: PDB Molecule: ekc/keops complex subunit bud32; PDBTitle: crystal structure of binary complex bud32-cgi121 in complex with amp
56	c4gygA_	Alignment	not modelled	81.3	36	PDB header: transferase Chain: A: PDB Molecule: rio2 kinase; PDBTitle: crystal structure of the rio2 kinase from chaetomium thermophilum
57	c4azsA_	Alignment	not modelled	81.1	16	PDB header: transferase Chain: A: PDB Molecule: methyltransferase wbdd; PDBTitle: high resolution (2.2 a) crystal structure of wbdd.
58	c4jrnA_	Alignment	not modelled	80.3	21	PDB header: transferase Chain: A: PDB Molecule: rhoptry kinase family protein; PDBTitle: rop18 kinase domain in complex with amp-pnp and sucrose
59	c6emlr_	Alignment	not modelled	78.1	19	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s2; PDBTitle: cryo-em structure of a late pre-40s ribosomal subunit from <i>Saccharomyces cerevisiae</i>
60	c4bvua_	Alignment	not modelled	78.1	24	PDB header: transferase/ligase/protein binding Chain: A: PDB Molecule: protein kinase ospg; PDBTitle: structure of shigella effector ospg in complex with host ubch5c-2 ubiquitin conjugate
61	c4azwA_	Alignment	not modelled	77.5	16	PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: crystal structure of monomeric wbdd.
62	c3dzoA_	Alignment	not modelled	77.1	17	PDB header: transferase Chain: A: PDB Molecule: rhoptry kinase domain; PDBTitle: crystal structure of a rhoptry kinase from <i>Toxoplasma gondii</i>
63	c4ci6B_	Alignment	not modelled	76.8	20	PDB header: transferase/structural protein Chain: B: PDB Molecule: protein kinase yopo; PDBTitle: mechanisms of crippling actin-dependent phagocytosis by yopo
64	c6df1A_	Alignment	not modelled	76.4	18	PDB header: hydrolase Chain: A: PDB Molecule: lipopolysaccharide core heptose(i) kinase rfap; PDBTitle: waap in complex with acyl carrier protein
65	c3q60A_	Alignment	not modelled	75.4	20	PDB header: transferase Chain: A: PDB Molecule: rop5b; PDBTitle: crystal structure of virulent allele rop5b pseudokinase domain bound2 to atp
66	c5dfzB_	Alignment	not modelled	74.7	21	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase vps15; PDBTitle: structure of vps34 complex ii from <i>S. cerevisiae</i> .
67	c2yleA_	Alignment	not modelled	73.1	15	PDB header: actin-binding protein Chain: A: PDB Molecule: protein spire homolog 1; PDBTitle: crystal structure of the human spir-1 kind fsi domain in2 complex with the fsi peptide
68	c5ckwA_	Alignment	not modelled	73.1	15	PDB header: transferase Chain: A: PDB Molecule: legk4; PDBTitle: crystal structure of legk4_ amppnp kinase
69	c5clrB_	Alignment	not modelled	73.0	15	PDB header: transferase Chain: B: PDB Molecule: legk4; PDBTitle: crystal structure of legk4_ apo kinase
70	c4otpA_	Alignment	not modelled	72.5	30	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase rio1; PDBTitle: crystal structure of the catalytic domain of the human riok1 atypical2 protein kinase in complex with adp/mg2+
71	c6g4jA_	Alignment	not modelled	70.5	20	PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase yabt; PDBTitle: structure of the protein kinase yabt from <i>Bacillus subtilis</i> in complex2 with an alpharep crystallization helper
72	c6m7zE_	Alignment	not modelled	70.2	10	PDB header: transferase Chain: E: PDB Molecule: bradyzoite pseudokinase 1; PDBTitle: a divergent kinase lacking the glycine-rich loop regulates membrane2 ultrastructure of the <i>Toxoplasma parasitophorous vacuole</i>
73	c4o96D_	Alignment	not modelled	70.2	20	PDB header: hydrolase Chain: D: PDB Molecule: type iii effector protein kinase; PDBTitle: 2.60 angstrom resolution crystal structure of a protein kinase domain2 of type iii effector nleh2 (ecs1814) from <i>Escherichia coli</i> o157:h73 str. sakai
74	c4im2A_	Alignment	not modelled	70.1	24	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: serine/threonine-protein kinase tbk1; PDBTitle: structure of tank-binding kinase 1
75	c3c4wB_	Alignment	not modelled	67.4	19	PDB header: transferase Chain: B: PDB Molecule: rhodopsin kinase; PDBTitle: crystal structure of g protein coupled receptor kinase 1 bound to atp2 and magnesium chloride at 2.7a
76	c4uw0A_	Alignment	not modelled	65.0	17	PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: low resolution structure of wbdd with c-terminal bundle ordered to2 residue 505
77	c3nyoB_	Alignment	not modelled	64.2	24	PDB header: transferase Chain: B: PDB Molecule: g protein-coupled receptor kinase 6; PDBTitle: crystal structure of g protein-coupled receptor kinase 6 in complex2 with amp
78	c4ix5B_	Alignment	not modelled	64.1	13	PDB header: transferase Chain: B: PDB Molecule: msstt7d protein; PDBTitle: crystal structure of a stt7 homolog from <i>Micromonas</i> algae in complex2 with amp-pnp

79	c3e7eA_	Alignment	not modelled	61.3	15	PDB header: transferase Chain: A: PDB Molecule: mitotic checkpoint serine/threonine-protein kinase bub1; PDBTitle: structure and substrate recruitment of the human spindle checkpoint2 kinase bub
80	c6bhcA_	Alignment	not modelled	60.5	20	PDB header: transferase Chain: A: PDB Molecule: pseudopodium-enriched atypical kinase 1; PDBTitle: crystal structure of pseudokinase peak1 (sugen kinase 269)
81	c6eqiC_	Alignment	not modelled	58.2	32	PDB header: transferase Chain: C: PDB Molecule: serine/threonine-protein kinase pink1, putative; PDBTitle: structure of pink1 bound to ubiquitin
82	c5nclA_	Alignment	not modelled	57.4	12	PDB header: signaling protein Chain: A: PDB Molecule: serine/threonine-protein kinase cbk1; PDBTitle: crystal structure of the cbk1-mob2 kinase-coactivator complex with an2 ssd1 peptide
83	c2acxB_	Alignment	not modelled	57.0	24	PDB header: transferase Chain: B: PDB Molecule: g protein-coupled receptor kinase 6; PDBTitle: crystal structure of g protein coupled receptor kinase 6 bound to2 amppnp
84	c4myiA_	Alignment	not modelled	56.9	20	PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase, putative; PDBTitle: crystal structure of pvx_084705
85	c1ym7C_	Alignment	not modelled	55.6	24	PDB header: transferase Chain: C: PDB Molecule: beta-adrenergic receptor kinase 1; PDBTitle: g protein-coupled receptor kinase 2 (grk2)
86	c4wb7B_	Alignment	not modelled	54.2	24	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: dnaj homolog subfamily b member 1,camp-dependent protein PDBTitle: crystal structure of a chimeric fusion of human dnaj (hsp40) and camp-2 dependent protein kinase a (catalytic alpha subunit)
87	c4yhjA_	Alignment	not modelled	53.8	21	PDB header: transferase Chain: A: PDB Molecule: g protein-coupled receptor kinase 4; PDBTitle: structure and function of the hypertension variant a486v of g protein-2 coupled receptor kinase 4 (grk4)
88	c4oauC_	Alignment	not modelled	53.7	11	PDB header: hydrolase/rna Chain: C: PDB Molecule: 2-5a-dependent ribonuclease; PDBTitle: complete human rnase l in complex with biological activators.
89	c4wnkA_	Alignment	not modelled	53.4	24	PDB header: ligase Chain: A: PDB Molecule: g protein-coupled receptor kinase 5; PDBTitle: crystal structure of bovine g protein coupled-receptor kinase 5 in2 complex with ccg215022
90	c3tkuB_	Alignment	not modelled	50.7	24	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: serine/threonine-protein kinase mrck beta; PDBTitle: mrck beta in complex with fasudil
91	c2j0kB_	Alignment	not modelled	50.3	22	PDB header: transferase Chain: B: PDB Molecule: focal adhesion kinase 1; PDBTitle: crystal structure of a fragment of focal adhesion kinase containing2 the ferm and kinase domains.
92	c4btfA_	Alignment	not modelled	49.9	16	PDB header: transferase Chain: A: PDB Molecule: mixed lineage kinase domain-like protein; PDBTitle: structure of mlkl
93	c3c4yA_	Alignment	not modelled	49.6	24	PDB header: transferase Chain: A: PDB Molecule: rhodopsin kinase; PDBTitle: crystal structure of apo form of g protein coupled receptor kinase 12 at 7.51a
94	c2vuwA_	Alignment	not modelled	48.8	19	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase haspin; PDBTitle: structure of human haspin kinase domain
95	c3otvC_	Alignment	not modelled	48.6	12	PDB header: transferase Chain: C: PDB Molecule: probable conserved transmembrane protein; PDBTitle: crystal structure of the intracellular domain of rv3910 from2 mycobacterium tuberculosis
96	c5uuuA_	Alignment	not modelled	45.4	24	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: beta-adrenergic receptor kinase 1; PDBTitle: 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
97	c6ccfB_	Alignment	not modelled	43.8	24	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: calcium/calmodulin-dependent protein kinase kinase 1; PDBTitle: crystal structure of the human camkk1a in complex with hesperadin
98	c2rsvA_	Alignment	not modelled	42.9	28	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase vrk1; PDBTitle: solution structure of human full-length vaccinia related kinase 12 (vrk1)
99	c5oatF_	Alignment	not modelled	41.3	33	PDB header: kinase Chain: F: PDB Molecule: serine/threonine-protein kinase pink1, mitochondrial-like PDBTitle: pink1 structure
100	c4c0tA_	Alignment	not modelled	40.8	32	PDB header: transferase Chain: A: PDB Molecule: likely protein kinase; PDBTitle: candida albicans pkh kinase domain
101	c3qa8H_	Alignment	not modelled	40.4	21	PDB header: immune system, signaling protein Chain: H: PDB Molecule: mgc80376 protein; PDBTitle: crystal structure of inhibitor of kappa b kinase beta
102	c2jiiA_	Alignment	not modelled	40.3	11	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase vrk3 molecule: vaccinia PDBTitle: structure of vaccinia related kinase 3
103	c3qa8A_	Alignment	not modelled	40.1	21	PDB header: immune system, signaling protein Chain: A: PDB Molecule: mgc80376 protein; PDBTitle: crystal structure of inhibitor of kappa b kinase beta

104	c2vwiC	Alignment	not modelled	39.9	28	PDB header: transferase Chain: C: PDB Molecule: serine/threonine-protein kinase osr1; PDBTitle: structure of the osr1 kinase, a hypertension drug target
105	c5ebzF	Alignment	not modelled	38.1	15	PDB header: transferase/transferase inhibitor Chain: F: PDB Molecule: inhibitor of nuclear factor kappa-b kinase subunit alpha; PDBTitle: crystal structure of human ikk1
106	c3vwaA	Alignment	not modelled	37.7	17	PDB header: hydrolase Chain: A: PDB Molecule: cytoplasmic export protein 1; PDBTitle: crystal structure of cex1p
107	c4oliA	Alignment	not modelled	34.8	18	PDB header: transferase Chain: A: PDB Molecule: non-receptor tyrosine-protein kinase tyk2; PDBTitle: the pseudokinase/kinase protein from jak-family member tyk2
108	c4eutA	Alignment	not modelled	34.2	15	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: serine/threonine-protein kinase tbk1; PDBTitle: structure of bx-795 complexed with unphosphorylated human tbk1 kinase-2 uld domain
109	c4umkA	Alignment	not modelled	32.1	26	PDB header: dna binding protein/dna Chain: A: PDB Molecule: probable chromosome-partitioning protein parb; PDBTitle: the complex of spo0j and pars dna in chromosomal partition system
110	c3op5B	Alignment	not modelled	31.8	28	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase vrk1; PDBTitle: human vaccinia-related kinase 1
111	c4i6hA	Alignment	not modelled	29.8	21	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: serine/threonine-protein kinase plk2; PDBTitle: selective & brain-permeable polo-like kinase-2 (plk-2) inhibitors that2 reduce alpha-synuclein phosphorylation in rat brain
112	c3ckxA	Alignment	not modelled	29.8	20	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase 24; PDBTitle: crystal structure of sterile 20-like kinase 3 (mst3, stk24) in complex2 with staurosporine
113	c6jkmA	Alignment	not modelled	29.6	16	PDB header: transferase Chain: A: PDB Molecule: mitotic checkpoint control protein kinase bub1; PDBTitle: crystal structure of bubr1 kinase domain
114	c4y93A	Alignment	not modelled	28.4	24	PDB header: transferase Chain: A: PDB Molecule: non-specific protein-tyrosine kinase,non-specific protein- PDBTitle: crystal structure of the ph-th-kinase construct of bruton's tyrosine2 kinase (btk)
115	c2wu6A	Alignment	not modelled	26.7	21	PDB header: transferase Chain: A: PDB Molecule: dual specificity protein kinase clk3; PDBTitle: crystal structure of the human clk3 in complex with dki
116	c4bwxB	Alignment	not modelled	26.0	9	PDB header: gene regulation Chain: B: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan-3; PDBTitle: structure of neurospora crassa pan3 pseudokinase mutant
117	d3boja1	Alignment	not modelled	25.7	50	Fold: CdCA1 repeat-like Superfamily: CdCA1 repeat-like Family: CdCA1 repeat-like
118	d3boea1	Alignment	not modelled	25.1	57	Fold: CdCA1 repeat-like Superfamily: CdCA1 repeat-like Family: CdCA1 repeat-like
119	c2ozoA	Alignment	not modelled	24.3	28	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase zap-70; PDBTitle: autoinhibited intact human zap-70
120	c4czuC	Alignment	not modelled	23.1	20	PDB header: transferase Chain: C: PDB Molecule: cbl-interacting serine/threonine-protein kinase 23; PDBTitle: crystal structure of the kinase domain of cipk23 t190d mutant