

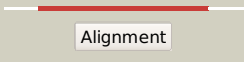

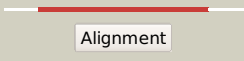

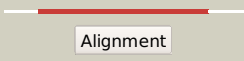

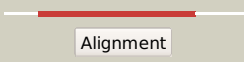

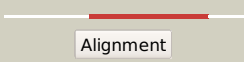

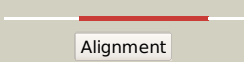

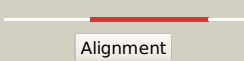

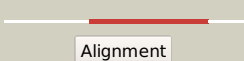

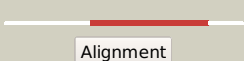

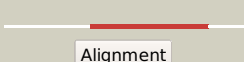












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3200c (-) _3572599_3573666
Date	Thu Aug 8 16:20:39 BST 2019
Unique Job ID	1f7e27b0806c7b26

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4gx2B_	 Alignment		100.0	22	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: gsuk channel bound to nad
2	c5tj6A_	 Alignment		100.0	20	PDB header: membrane protein Chain: A: PDB Molecule: high conductance calcium-activated potassium channel; PDBTitle: ca2+ bound aplasia slo1
3	c1lnqC_	 Alignment		100.0	24	PDB header: metal transport Chain: C: PDB Molecule: potassium channel related protein; PDBTitle: crystal structure of mthk at 3.3 a
4	c5u76A_	 Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: potassium channel subfamily t member 1; PDBTitle: chicken slo2.2 in a closed conformation vitrified in the presence of2 300 mm nacl
5	c4gx5D_	 Alignment		100.0	24	PDB header: transport protein Chain: D: PDB Molecule: trka domain protein; PDBTitle: gsuk channel
6	c2fy8A_	 Alignment		100.0	27	PDB header: transport protein Chain: A: PDB Molecule: calcium-gated potassium channel mthk; PDBTitle: crystal structure of mthk rck domain in its ligand-free gating-ring2 form
7	c4gvlB_	 Alignment		100.0	24	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: crystal structure of the gsuk rck domain
8	c4g65A_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: trk system potassium uptake protein trka; PDBTitle: potassium transporter peripheral membrane component (trka) from vibrio2 vulnificus
9	c4hpfB_	 Alignment		100.0	18	PDB header: membrane protein, transport protein Chain: B: PDB Molecule: potassium channel subfamily u member 1; PDBTitle: structure of the human slo3 gating ring
10	c3u6nC_	 Alignment		100.0	16	PDB header: transport protein Chain: C: PDB Molecule: high-conductance ca2+-activated k+ channel protein; PDBTitle: open structure of the bk channel gating ring
11	c4j7cA_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: ktr system potassium uptake protein a; PDBTitle: ktrab potassium transporter from bacillus subtilis

12	c3mt5A_	Alignment		100.0	17	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: potassium large conductance calcium-activated channel, PDBTitle: crystal structure of the human bk gating apparatus
13	c3nafA_	Alignment		100.0	14	PDB header: ion transport Chain: A: PDB Molecule: calcium-activated potassium channel subunit alpha-1, PDBTitle: structure of the intracellular gating ring from the human high-2 conductance ca2+ gated k+ channel (bk channel)
14	c3l4bG_	Alignment		99.9	18	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
15	c5a6eC_	Alignment		99.9	18	PDB header: transport Chain: C: PDB Molecule: gating ring of potassium channel subfamily t member 1; PDBTitle: cryo-em structure of the slo2.2 na-activated k channel
16	c3eywA_	Alignment		99.9	25	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
17	c3fwzA_	Alignment		99.9	23	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ybal; PDBTitle: crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
18	d1ld1a_	Alignment		99.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
19	c5nc8B_	Alignment		99.9	22	PDB header: transport protein Chain: B: PDB Molecule: potassium efflux system protein; PDBTitle: shewanella denitrificans kef ctd in amp bound form
20	d2fy8a1	Alignment		99.9	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
21	d1lssa_	Alignment	not modelled	99.9	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
22	c3c85A_	Alignment	not modelled	99.9	16	PDB header: transport protein Chain: A: PDB Molecule: putative glutathione-regulated potassium-efflux system PDBTitle: crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
23	d2hmva1	Alignment	not modelled	99.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
24	c3llvA_	Alignment	not modelled	99.8	17	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
25	c2g1uA_	Alignment	not modelled	99.8	19	PDB header: transport protein Chain: A: PDB Molecule: hypothetical protein tm1088a; PDBTitle: crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
26	c5butG_	Alignment	not modelled	99.8	20	PDB header: membrane protein Chain: G: PDB Molecule: ktr system potassium uptake protein a,ktr system potassium PDBTitle: crystal structure of inactive conformation of ktrab k+ transporter
27	c3vouB_	Alignment	not modelled	99.3	23	PDB header: transport protein Chain: B: PDB Molecule: ion transport 2 domain protein, voltage-gated sodium PDBTitle: the crystal structure of nak-navsulp chimera channel
						Fold: Voltage-gated potassium channels

28	d1f6ga_	Alignment	not modelled	99.3	19	Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
29	c3e8gB_	Alignment	not modelled	99.2	26	PDB header: membrane protein Chain: B: PDB Molecule: potassium channel protein; PDBTitle: crystal structure of the the open nak channel-na+/ca2+ complex
30	d1r3jc_	Alignment	not modelled	99.2	18	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
31	c5a6eB_	Alignment	not modelled	99.2	19	PDB header: transport Chain: B: PDB Molecule: pore domain of potassium channel subfamily t member 1; PDBTitle: cryo-em structure of the slo2.2 na-activated k channel
32	d2a9ha1	Alignment	not modelled	99.1	22	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
33	c5cbfA_	Alignment	not modelled	99.1	17	PDB header: transport protein Chain: A: PDB Molecule: ion transport 2 domain protein; PDBTitle: structural and functional characterization of a calcium-activated2 cation channel from tsukamurella paurometabola
34	c5vknA_	Alignment	not modelled	99.1	15	PDB header: transport protein Chain: A: PDB Molecule: potassium channel subfamily k member 2; PDBTitle: k2p2.1(trek-1):ml335 complex
35	c3behA_	Alignment	not modelled	99.1	22	PDB header: membrane protein Chain: A: PDB Molecule: ml3241 protein; PDBTitle: structure of a bacterial cyclic nucleotide regulated ion channel
36	c3lnmD_	Alignment	not modelled	99.0	12	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: f233w mutant of the kv2.1 paddle-kv1.2 chimera; PDBTitle: f233w mutant of the kv2.1 paddle-kv1.2 chimera channel
37	c4chwB_	Alignment	not modelled	99.0	25	PDB header: transport protein Chain: B: PDB Molecule: cyclic nucleotide-gated potassium channel ml3241; PDBTitle: the electron crystallography structure of the camp-free potassium2 channel mlok1
38	c2qksA_	Alignment	not modelled	99.0	20	PDB header: metal transport Chain: A: PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera
39	c2kb1A_	Alignment	not modelled	99.0	16	PDB header: membrane protein Chain: A: PDB Molecule: wsk3; PDBTitle: nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsa
40	c4bw5D_	Alignment	not modelled	99.0	21	PDB header: transport protein Chain: D: PDB Molecule: potassium channel subfamily k member 10; PDBTitle: crystal structure of human two pore domain potassium ion channel trek22 (k2p10.1)
41	c3ifxB_	Alignment	not modelled	99.0	20	PDB header: membrane protein Chain: B: PDB Molecule: voltage-gated potassium channel; PDBTitle: crystal structure of the spin-labeled kcsa mutant v48r1
42	c4h33A_	Alignment	not modelled	99.0	22	PDB header: membrane protein Chain: A: PDB Molecule: lmo2059 protein; PDBTitle: crystal structure of a voltage-gated k+ channel pore module in a2 closed state in lipid membranes, tetragonal crystal form
43	c3ukmB_	Alignment	not modelled	99.0	19	PDB header: membrane protein Chain: B: PDB Molecule: potassium channel subfamily k member 1; PDBTitle: crystal structure of the human two pore domain potassium ion channel2 k2p1 (twik-1)
44	c2a79B_	Alignment	not modelled	99.0	13	PDB header: membrane protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily a PDBTitle: mammalian shaker kv1.2 potassium channel- beta subunit2 complex
45	c2r9rH_	Alignment	not modelled	99.0	12	PDB header: membrane protein, transport protein Chain: H: PDB Molecule: paddle chimera voltage gated potassium channel kv1.2-kv2.1; PDBTitle: shaker family voltage dependent potassium channel (kv1.2-kv2.1 paddle2 chimera channel) in association with beta subunit
46	c1xl6B_	Alignment	not modelled	98.9	14	PDB header: metal transport Chain: B: PDB Molecule: inward rectifier potassium channel; PDBTitle: intermediate gating structure 2 of the inwardly rectifying k+ channel2 kirbac3.1
47	c3um7B_	Alignment	not modelled	98.9	24	PDB header: metal transport Chain: B: PDB Molecule: potassium channel subfamily k member 4; PDBTitle: crystal structure of the human two pore domain k+ ion channel traak2 (k2p4.1)
48	d1xl4a2	Alignment	not modelled	98.9	14	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
49	c4twkB_	Alignment	not modelled	98.8	15	PDB header: transport protein Chain: B: PDB Molecule: potassium channel subfamily k member 2; PDBTitle: crystal structure of human two pore domain potassium ion channel trek12 (k2p2.1)
50	d1p7ba2	Alignment	not modelled	98.8	20	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
51	c6cnmA_	Alignment	not modelled	98.8	17	PDB header: membrane protein Chain: A: PDB Molecule: intermediate conductance calcium-activated potassium PDBTitle: cryo-em structure of the human sk4/calmodulin channel complex
52	c5vmsA_	Alignment	not modelled	98.8	16	PDB header: transport protein, calcium binding prote Chain: A: PDB Molecule: potassium voltage-gated channel subfamily kqt member 1;

						PDBTitle: cryoem structure of xenopus kcnq1 channel PDB header: transport protein Chain: G: PDB Molecule: atp-sensitive inward rectifier potassium channel 11; PDBTitle: cryo-em structure of the pancreatic atp-sensitive k+ channel2 sur1/kir6.2 in the presence of atp and glibenclamide
53	c5twvG_	Alignment	not modelled	98.7	13	
54	d1e5qa1	Alignment	not modelled	98.7	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
55	d1orqc_	Alignment	not modelled	98.7	29	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
56	c1p7bB_	Alignment	not modelled	98.6	21	PDB header: metal transport Chain: B: PDB Molecule: integral membrane channel and cytosolic domains; PDBTitle: crystal structure of an inward rectifier potassium channel
57	c4xttA_	Alignment	not modelled	98.6	19	PDB header: transport protein Chain: A: PDB Molecule: putative potassium transport protein; PDBTitle: structural studies of potassium transport protein ktra regulator of 2 conductance of k+ (rck) c domain in complex with cyclic diadenosine3 monophosphate (c-di-amp)
58	c5k7lA_	Alignment	not modelled	98.5	14	PDB header: metal transport/calcium binding protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: single particle cryo-em structure of the voltage-gated k+ channel eag12 bound to the channel inhibitor calmodulin
59	c3c85D_	Alignment	not modelled	98.4	17	PDB header: transport protein Chain: D: PDB Molecule: putative glutathione-regulated potassium-efflux system PDBTitle: crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
60	c3syaA_	Alignment	not modelled	98.4	16	PDB header: metal transport Chain: A: PDB Molecule: g protein-activated inward rectifier potassium channel 2; PDBTitle: crystal structure of the g protein-gated inward rectifier k+ channel2 girk2 (kir3.2) in complex with sodium and pip2
61	d1lnqa2	Alignment	not modelled	98.4	30	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
62	c3jycA_	Alignment	not modelled	98.4	14	PDB header: metal transport Chain: A: PDB Molecule: inward-rectifier k+ channel kir2.2; PDBTitle: crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
63	d2fy8a2	Alignment	not modelled	98.4	26	Fold: TrkA C-terminal domain-like Superfamily: TrkA C-terminal domain-like Family: TrkA C-terminal domain-like
64	c4ys2A_	Alignment	not modelled	98.3	15	PDB header: immune system Chain: A: PDB Molecule: na+/h+ antiporter-like protein; PDBTitle: rck domain with cda
65	d1vcta2	Alignment	not modelled	98.3	25	Fold: TrkA C-terminal domain-like Superfamily: TrkA C-terminal domain-like Family: TrkA C-terminal domain-like
66	c5v4sB_	Alignment	not modelled	98.3	21	PDB header: transport protein Chain: B: PDB Molecule: transporter, cation channel family / cyclic nucleotide- PDBTitle: cryoem structure of a prokaryotic cyclic nucleotide-gated ion channel
67	c3jxoB_	Alignment	not modelled	98.2	25	PDB header: transport protein Chain: B: PDB Molecule: trka-n domain protein; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
68	c5va1A_	Alignment	not modelled	98.2	15	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: cryo-em structure of the human ether-a-go-go related k+ channel
69	c2bknA_	Alignment	not modelled	98.2	25	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical protein ph0236; PDBTitle: structure analysis of unknown function protein
70	c5u6pA_	Alignment	not modelled	98.1	12	PDB header: transport protein Chain: A: PDB Molecule: potassium/sodium hyperpolarization-activated cyclic PDBTitle: structure of the human hcn1 hyperpolarization-activated cyclic2 nucleotide-gated ion channel in complex with camp
71	d1pjqa1	Alignment	not modelled	97.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
72	c6cjtB_	Alignment	not modelled	97.7	19	PDB header: transport protein Chain: B: PDB Molecule: sthk cyclic nucleotide-gated potassium channel; PDBTitle: structure of the sthk cyclic nucleotide-gated potassium channel in2 complex with cgmp
73	d2h8pc1	Alignment	not modelled	97.7	28	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
74	c5h3oA_	Alignment	not modelled	97.7	16	PDB header: transport protein Chain: A: PDB Molecule: cyclic nucleotide-gated cation channel; PDBTitle: structure of a eukaryotic cyclic nucleotide-gated channel
75	c3ic5A_	Alignment	not modelled	97.2	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
76	c2axqA_	Alignment	not modelled	96.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2

						forming) from <i>saccharomyces cerevisiae</i>
77	c1e5IA	Alignment	not modelled	96.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from <i>magnaporthe grisea</i>
78	c2zcuA	Alignment	not modelled	96.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized oxidoreductase ytfg; PDBTitle: crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from <i>escherichia coli</i>
79	c5hm8C	Alignment	not modelled	96.4	22	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from <i>2 cryptosporidium parvum</i> in complex with adenosine and nad.
80	c3dhyC	Alignment	not modelled	96.3	17	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of <i>mycobacterium tuberculosis</i> s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and 3 inhibitors
81	d1xgka	Alignment	not modelled	96.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	c3ktdC	Alignment	not modelled	96.3	11	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cg10226)2 from <i>corynebacterium glutamicum</i> atcc 13032 at 2.60 a resolution
83	d2pgda2	Alignment	not modelled	96.2	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
84	c3n58D	Alignment	not modelled	96.2	20	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from <i>brucella2 melitensis</i> in ternary complex with nad and adenosine, orthorhombic3 form
85	c2qx7A	Alignment	not modelled	96.2	11	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from <i>ocimum basilicum</i>
86	c4rl6A	Alignment	not modelled	96.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04l03_strp2 protein from <i>streptococcus2 pneumoniae</i> . northeast structural genomics consortium target spr105
87	c3triB	Alignment	not modelled	96.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from <i>coxiella2 burnetii</i>
88	d1pjca1	Alignment	not modelled	96.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
89	c2rirA	Alignment	not modelled	96.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from <i>bacillus2 subtilis</i>
90	c1v8bA	Alignment	not modelled	96.0	16	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
91	c5v96A	Alignment	not modelled	95.9	16	PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from <i>2 naegleria fowleri</i> with bound nad and adenosine
92	c3d4oA	Alignment	not modelled	95.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from <i>bacillus halodurans</i> at 2.10 a resolution
93	c4o19A	Alignment	not modelled	95.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of putative 2-dehydropantoate 2-reductase pane from <i>2 mycobacterium tuberculosis</i> complexed with nadp and oxamate
94	c4tlmC	Alignment	not modelled	95.7	11	PDB header: signaling protein Chain: C: PDB Molecule: receptor subunit glun1; PDBTitle: crystal structure of glun1/glun2b nmda receptor, structure 2
95	c2x4gA	Alignment	not modelled	95.7	15	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar epimerase2 from <i>pseudomonas aeruginosa</i>
96	c6f3oC	Alignment	not modelled	95.7	18	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from <i>2 pseudomonas aeruginosa</i> complexed with adenine, k+ and zn2+ cations
97	c2vrcD	Alignment	not modelled	95.6	16	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the <i>citrobacter</i> sp. triphenylmethane2 reductase complexed with nadp(h)
98	c3oneA	Alignment	not modelled	95.6	27	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of <i>lupinus luteus</i> s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
99	c5g6sD	Alignment	not modelled	95.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from <i>aspergillus oryzae</i> in complex with nadp(h) and 2 (r)-rasagiline
100	c3x2fA	Alignment	not modelled	95.5	19	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
						PDB header: isomerase

101	c2c20D_	Alignment	not modelled	95.5	30	Chain: D: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase
102	c3fwnB_	Alignment	not modelled	95.5	9	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
103	c2ew2B_	Alignment	not modelled	95.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase, putative; PDBTitle: crystal structure of the putative 2-dehydropantoate 2-reductase from 2 enterococcus faecalis
104	c5uowB_	Alignment	not modelled	95.4	11	PDB header: membrane protein Chain: B: PDB Molecule: n-methyl-d-aspartate receptor subunit nr2a; PDBTitle: triheteromeric nmda receptor glun1/glun2a/glun2b in complex with 2 glycine, glutamate, mk-801 and a glun2b-specific fab, at ph 6.5
105	c3gvpB_	Alignment	not modelled	95.4	21	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
106	c6aphA_	Alignment	not modelled	95.3	20	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
107	c6aqjB_	Alignment	not modelled	95.3	15	PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadh(+)); PDBTitle: crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that 3 have biocidal activity.
108	c2g5cD_	Alignment	not modelled	95.3	9	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
109	c2f1kD_	Alignment	not modelled	95.3	21	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
110	c1bg6A_	Alignment	not modelled	95.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; PDBTitle: crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
111	c6jczL_	Alignment	not modelled	95.2	18	PDB header: isomerase Chain: L: PDB Molecule: putative ketol-acid reductoisomerase 2; PDBTitle: cryo-em structure of sulfolobus solfataricus ketol-acid2 reductoisomerase (sso-kari) in complex with mg2+, nadph, and cpd at 3 ph7.5
112	c2iz1C_	Alignment	not modelled	95.2	9	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
113	c3e48B_	Alignment	not modelled	95.2	7	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
114	c5l3zA_	Alignment	not modelled	95.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide ketoreductase simc7; PDBTitle: polyketide ketoreductase simc7 - binary complex with nadp+
115	c4tskA_	Alignment	not modelled	95.2	18	PDB header: oxidoreductase, isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
116	d1bg6a2	Alignment	not modelled	95.1	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
117	c1d4fD_	Alignment	not modelled	95.1	17	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
118	c5y8mA_	Alignment	not modelled	95.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthbadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
119	c3wj7B_	Alignment	not modelled	95.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2253
120	c3b1fA_	Alignment	not modelled	95.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans