
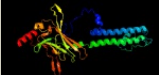
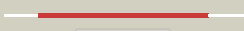
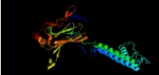











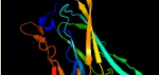

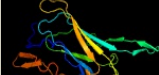



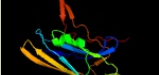




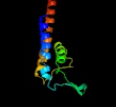


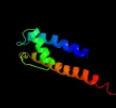
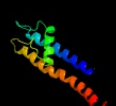


Phyre2

Email	m.sternberg@imperial.ac.uk
Description	KCJ11_HUMAN_ATP-sensitive_inward_rectifier_potassium_channel_11_
Date	Wed Jun 17 23:05:45 BST 2015
Unique Job ID	a9ffd763295ff236

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3syaA_	 Alignment		100.0	50	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
2	c3jycA_	 Alignment		100.0	51	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
3	c2qksA_	 Alignment		100.0	45	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
4	c1xl6B_	 Alignment		100.0	28	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
5	c2xkyl_	 Alignment		100.0	50	PDB header: metal transport Chain: I: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: single particle analysis of kir2.1nc_4 in negative stain
6	c1p7bB_	 Alignment		100.0	27	PDB header: metal transport Chain: B: PDB Molecule: integral membrane channel and cytosolic domains; PDBTitle: crystal structure of an inward rectifier potassium channel
7	c2gixC_	 Alignment		100.0	49	PDB header: metal transport Chain: C: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: cytoplasmic domain structure of kir2.1 containing2 andersen's mutation r218q and rescue mutation t309k
8	d1n9pa_	 Alignment		100.0	48	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
9	c2e4fA_	 Alignment		100.0	47	PDB header: transport protein Chain: A: PDB Molecule: g protein-activated inward rectifier potassium channel 2; PDBTitle: crystal structure of the cytoplasmic domain of g-protein-gated inward2 rectifier potassium channel kir3.2
10	c1u4fD_	 Alignment		100.0	51	PDB header: allergen Chain: D: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: crystal structure of cytoplasmic domains of irk1 (kir2.1)2 channel
11	d1xl4a1	 Alignment		100.0	30	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel

12	d1p7ba1	Alignment		100.0	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
13	d1xl4a2	Alignment		99.9	27	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
14	d1p7ba2	Alignment		99.9	26	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
15	d2a9ha1	Alignment		99.1	15	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
16	d1f6ga_	Alignment		99.0	13	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
17	d1r3jc_	Alignment		99.0	12	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
18	c3ifxB_	Alignment		98.9	17	PDB header: membrane protein Chain: B: PDB Molecule: voltage-gated potassium channel; PDBTitle: crystal structure of the spin-labeled kcsa mutant v48r1
19	c4h33A_	Alignment		98.9	16	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
20	c3lnmD_	Alignment		98.9	19	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
21	c2a79B_	Alignment	not modelled	98.8	19	PDB header: membrane protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily a PDBTitle: mammalian shaker kv1.2 potassium channel- beta subunit2 complex
22	c2r9rH_	Alignment	not modelled	98.8	17	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
23	c4chwB_	Alignment	not modelled	98.7	20	PDB header: transport protein Chain: B: PDB Molecule: cyclic nucleotide-gated potassium channel ml3241; PDBTitle: the electron crystallography structure of the camp-free2 potassium channel mlok1
24	c2kb1A_	Alignment	not modelled	98.6	15	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
25	c3behA_	Alignment	not modelled	98.6	19	PDB header: membrane protein Chain: A: PDB Molecule: ml3241 protein; PDBTitle: structure of a bacterial cyclic nucleotide regulated ion channel
26	c3e8gB_	Alignment	not modelled	98.6	10	PDB header: membrane protein Chain: B: PDB Molecule: potassium channel protein; PDBTitle: crystal structure of the the open nak channel-na+/ca2+ complex
27	c4gx5D_	Alignment	not modelled	98.5	22	PDB header: transport protein Chain: D: PDB Molecule: trka domain protein; PDBTitle: gsuk channel

28	c4gx2B_	Alignment	not modelled	98.5	21	PDB header: transport protein Chain: B: PDB Molecule: strka domain protein; PDBTitle: gsuk channel bound to nad
29	c3vouB_	Alignment	not modelled	98.5	12	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
30	c4bw5D_	Alignment	not modelled	98.2	17	PDB header: transport protein Chain: D: PDB Molecule: potassium channel subfamily k member 10; PDBTitle: crystal structure of human two pore domain potassium ion2 channel trek2 (k2p10.1)
31	d1orqc_	Alignment	not modelled	98.1	15	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
32	c3um7B_	Alignment	not modelled	98.0	25	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)
33	c4twkB_	Alignment	not modelled	98.0	18	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)
34	c3ukmB_	Alignment	not modelled	98.0	16	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)
35	d1lnqa2	Alignment	not modelled	97.6	16	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
36	d2h8pc1	Alignment	not modelled	97.0	16	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
37	c1lnqC_	Alignment	not modelled	96.0	18	PDB header: metal transport Chain: C: PDB Molecule: potassium channel related protein; PDBTitle: crystal structure of mthk at 3.3 a
38	c4tlmC_	Alignment	not modelled	81.5	22	PDB header: signaling protein Chain: C: PDB Molecule: receptor subunit glun1; PDBTitle: crystal structure of glun1/glun2b nmda receptor, structure 2
39	c4j7cK_	Alignment	not modelled	50.8	12	PDB header: transport protein Chain: K: PDB Molecule: ktr system potassium uptake protein b; PDBTitle: ktrab potassium transporter from bacillus subtilis
40	c2zxeB_	Alignment	not modelled	46.2	15	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: na+,k+-atpase beta subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
41	c3kdpD_	Alignment	not modelled	42.4	19	PDB header: hydrolase Chain: D: PDB Molecule: sodium/potassium-transporting atpase subunit beta-1; PDBTitle: crystal structure of the sodium-potassium pump
42	c2yn9B_	Alignment	not modelled	42.2	15	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: cryo-em structure of gastric h+,k+-atpase with bound rubidium
43	c2xzbB_	Alignment	not modelled	32.5	15	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h,k-atpase with bound bef and sch28080
44	c2a1sC_	Alignment	not modelled	29.3	29	PDB header: hydrolase Chain: C: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of native parn nuclease domain
45	c2hg5D_	Alignment	not modelled	27.5	7	PDB header: membrane protein Chain: D: PDB Molecule: kcsa channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
46	c3ixzB_	Alignment	not modelled	26.1	15	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
47	c4b0sA_	Alignment	not modelled	25.1	16	PDB header: hydrolase Chain: A: PDB Molecule: deamidase-depupylase dop; PDBTitle: structure of the deamidase-depupylase dop of the2 prokaryotic ubiquitin-like modification pathway in complex3 with atp
48	d1hywa_	Alignment	not modelled	24.6	17	Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW
49	c3j5pB_	Alignment	not modelled	24.1	20	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily v PDBTitle: structure of trpv1 ion channel determined by single particle electron2 cryo-microscopy
50	c3vcmP_	Alignment	not modelled	21.1	43	PDB header: hydrolase Chain: P: PDB Molecule: prorenin; PDBTitle: crystal structure of human prorenin
51	c3d45B_	Alignment	not modelled	19.3	29	PDB header: hydrolase Chain: B: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of mouse parn in complex with m7gpppg
52	c3pjzA_	Alignment	not modelled	19.2	23	PDB header: transport protein Chain: A: PDB Molecule: potassium uptake protein trkh; PDBTitle: crystal structure of the potassium transporter trkh from vibrio2 parahaemolyticus
53	c3h8sB_	Alignment	not modelled	16.5	10	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: sodium/potassium-transporting atpase

53	c308eB	Alignment	not modelled	10.3	19	subunit PDBTitle: crystal structure of the sodium-potassium pump
54	c4ltpC	Alignment	not modelled	15.6	11	PDB header: transport protein Chain: C: PDB Molecule: ion transport protein; PDBTitle: bacterial sodium channel in high calcium, i222 space group, crystal 2
55	c2xznQ	Alignment	not modelled	15.3	28	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein s17 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
56	c1ciiA	Alignment	not modelled	14.9	6	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
57	d1rh5a	Alignment	not modelled	14.4	10	Fold: Preprotein translocase SecY subunit Superfamily: Preprotein translocase SecY subunit Family: Preprotein translocase SecY subunit
58	c3pjzB	Alignment	not modelled	13.5	23	PDB header: transport protein Chain: B: PDB Molecule: potassium uptake protein trkh; PDBTitle: crystal structure of the potassium transporter trkh from vibrio2 parahaemolyticus
59	c4evxA	Alignment	not modelled	12.4	60	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative phage endolysin; PDBTitle: crystal structure of putative phage endolysin from s. enterica
60	c2o4wA	Alignment	not modelled	11.2	80	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: t4 lysozyme circular permutant
61	c3a0bX	Alignment	not modelled	10.9	38	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
62	c3a0hx	Alignment	not modelled	10.9	38	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
63	c3a0hX	Alignment	not modelled	10.9	38	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
64	c3a0bx	Alignment	not modelled	10.9	38	PDB header: electron transport Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
65	d1j2ga2	Alignment	not modelled	10.7	28	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
66	c3zeyE	Alignment	not modelled	10.6	34	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal proteins s11, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
67	c4ainB	Alignment	not modelled	10.4	9	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
68	c2qb0D	Alignment	not modelled	10.3	80	PDB header: hydrolase regulator Chain: D: PDB Molecule: telsam domain - lysozyme chimera; PDBTitle: structure of the 2tel crystallization module fused to t4 lysozyme with2 an ala-gly-pro linker.
69	c2w8aC	Alignment	not modelled	10.2	9	PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
70	d1lpya	Alignment	not modelled	10.1	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
71	d2ibaa2	Alignment	not modelled	10.0	38	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
72	d1p5ca	Alignment	not modelled	10.0	80	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
73	c1s5lx	Alignment	not modelled	9.7	38	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem ii psbx protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
74	d2hjea1	Alignment	not modelled	9.5	25	Fold: Profilin-like Superfamily: Sensory domain-like Family: LuxQ-periplasmic domain-like
75	d169la	Alignment	not modelled	9.3	31	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
76	c2anxB	Alignment	not modelled	9.1	29	PDB header: hydrolase Chain: B: PDB Molecule: lysozyme; PDBTitle: crystal structure of bacteriophage p22 lysozyme mutant i87m
77	c3he1F	Alignment	not modelled	9.1	50	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: major exported hcp3 protein; PDBTitle: secreted protein hcp3 from pseudomonas aeruginosa.
78	c2e76G	Alignment	not modelled	9.0	21	PDB header: photosynthesis Chain: G: PDB Molecule: cytochrome b6-f complex subunit 5; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
79	c3j3aL	Alignment	not modelled	9.0	28	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s11; PDBTitle: structure of the human 40s ribosomal proteins

80	d1l64a_	Alignment	not modelled	8.9	80	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
81	c1r56H_	Alignment	not modelled	8.7	38	PDB header: oxidoreductase Chain: H: PDB Molecule: uricase; PDBTitle: uncomplexed urate oxidase from aspergillus flavus
82	c2uwjF_	Alignment	not modelled	8.5	27	PDB header: chaperone Chain: F: PDB Molecule: type iii export protein pscf; PDBTitle: structure of the heterotrimeric complex which regulates2 type iii secretion needle formation
83	c4iapB_	Alignment	not modelled	8.5	80	PDB header: lipid binding protein/ hydrolase Chain: B: PDB Molecule: lysozyme, oxysterol-binding protein homolog 3; PDBTitle: crystal structure of ph domain of osh3 from saccharomyces cerevisiae
84	d2yzca2	Alignment	not modelled	8.2	34	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
85	c2vyxA_	Alignment	not modelled	8.1	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein, gk0453; PDBTitle: crystal structure of hypothetical conserved protein, gk0453
86	c3rzeA_	Alignment	not modelled	8.1	14	PDB header: hydrolase Chain: A: PDB Molecule: histamine h1 receptor, lysozyme chimera; PDBTitle: structure of the human histamine h1 receptor in complex with doxepin
87	c4pkfB_	Alignment	not modelled	8.1	29	PDB header: lyase Chain: B: PDB Molecule: tutg; PDBTitle: benzylsuccinate synthase alpha-beta-gamma complex
88	c3wx6A_	Alignment	not modelled	8.0	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of type six secretion system protein
89	c3fokH_	Alignment	not modelled	8.0	10	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein cg10159; PDBTitle: crystal structure of cg10159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
90	d2f2qa1	Alignment	not modelled	8.0	80	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
91	d1swya_	Alignment	not modelled	7.9	31	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
92	c2bruC_	Alignment	not modelled	7.8	26	PDB header: oxidoreductase Chain: C: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
93	d1k28a3	Alignment	not modelled	7.5	80	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
94	d1xjua_	Alignment	not modelled	7.4	60	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
95	d1e42a1	Alignment	not modelled	7.3	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Alpha-adaptin ear subdomain-like
96	c1j2gC_	Alignment	not modelled	7.3	28	PDB header: oxidoreductase Chain: C: PDB Molecule: uricase; PDBTitle: crystal structure of urate oxidase from bacillus sp. tb-90 co-2 crystallized with 8-azaxanthine
97	d1d4oa_	Alignment	not modelled	7.2	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
98	d1pnoa_	Alignment	not modelled	7.1	26	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
99	c3uonA_	Alignment	not modelled	7.1	14	PDB header: signaling protein/antagonist Chain: A: PDB Molecule: human m2 muscarinic acetylcholine, receptor t4 lysozyme PDBTitle: structure of the human m2 muscarinic acetylcholine receptor bound to2 an antagonist