Phyre2

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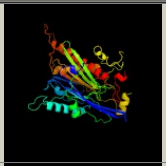
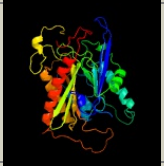
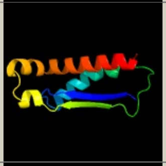
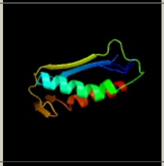
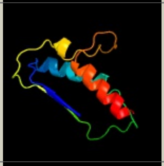
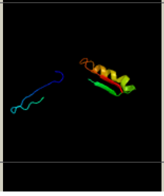
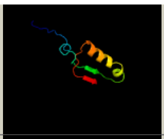
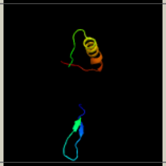
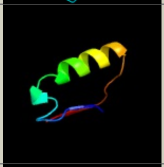
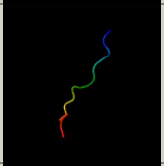
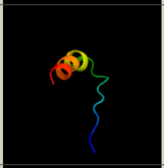
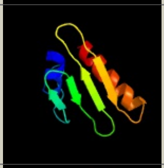
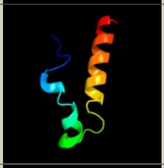
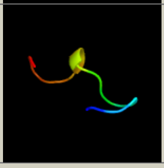
Description	RVBD1333_(-)_1501605_1502639
Date	Wed Jul 31 22:05:43 BST 2019
Unique Job ID	a02b06a50546b5be

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3s3uB_	Alignment		100.0	52	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cysteine transferase; **PDBTitle:** crystal structure of uncleaved thnt t282c
2	c3n5iC_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-peptidyl aminopeptidase; **PDBTitle:** crystal structure of the precursor (s250a mutant) of the n-terminal2 beta-aminopeptidase bapa
3	d1b65a_	Alignment		100.0	24	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**DmpA-like
4	c2drhD_	Alignment		100.0	25	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**361aa long hypothetical d-aminopeptidase; **PDBTitle:** crystal structure of the ph0078 protein from pyrococcus horikoshii ot3
5	c3axgN_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** N: **PDB Molecule:**endotype 6-aminohexanoat-oligomer hydrolase; **PDBTitle:** structure of 6-aminohexanoate-oligomer hydrolase
6	c5tzbA_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-aminopeptidase; **PDBTitle:** burkholderia sp. beta-aminopeptidase
7	c3it4B_	Alignment		95.3	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj **PDBTitle:** the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
8	d1vz6a_	Alignment		95.2	19	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**ArgJ-like
9	c1vraB_	Alignment		94.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arginine biosynthesis bifunctional protein argj; **PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
10	c2vzkD_	Alignment		92.6	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamate n-acetyltransferase 2 beta chain; **PDBTitle:** structure of the acyl-enzyme complex of an n-terminal nucleophile2 (ntn) hydrolase, oat2
11	c4qmkB_	Alignment		87.8	38	**PDB header:**toxin **Chain:** B: **PDB Molecule:**type iii secretion system effector protein exou; **PDBTitle:** crystal structure of type iii effector protein exou (exou)

12	c3tu3B_	Alignment		83.2	42	**PDB header:**toxin/toxin chaperone **Chain:** B: **PDB Molecule:**exou; **PDBTitle:** 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
13	c4akxB_	Alignment		70.7	38	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**exou; **PDBTitle:** structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
14	c5fyaA_	Alignment		54.5	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**patatin-like protein, plpd; **PDBTitle:** cubic crystal of the native plpd
15	c4akfA_	Alignment		50.3	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vipd; **PDBTitle:** crystal structure of vipd from legionella pneumophila
16	c3geiB_	Alignment		29.8	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp
17	c2m4mA_	Alignment		19.4	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the rrm domain of the hypothetical protein2 cagl0m09691g from candida glabrata
18	c2jpiA_	Alignment		17.6	19	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
19	c2vg2C_	Alignment		15.2	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
20	c1osxA_	Alignment		14.5	54	**PDB header:**immune system **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily **PDBTitle:** solution structure of the extracellular domain of blys2 receptor 3 (br3)
21	d1osxa_	Alignment	not modelled	14.5	54	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
22	c1p0tA_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
23	c1p0tU_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** U: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
24	c1p0tx_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** X: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
25	c1p0tN_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** N: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
26	c1p0tC_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
27	c1p0tk_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** K: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
28	c1p0t3_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** 3: **PDB Molecule:** **PDB Fragment:**residues 1-63; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
29	c1p0tL_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** L: **PDB Molecule:**tumor necrosis factor receptor

29		Alignment	not modelled	14.4	54	superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
30	c1p0tV_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** V: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
31	c1p0tW_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** W: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
32	c1p0tp_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** P: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
33	c1p0tX_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** X: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
34	c1p0t9_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** 9: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
35	c1p0tJ_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** J: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
36	c1p0tB_	Alignment	not modelled	14.4	54	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
37	d1qy9a1	Alignment	not modelled	14.3	22	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
38	c1p0tK_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** K: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
39	c1p0te_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
40	c1p0t7_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** 7: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
41	c1p0t0_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** 0: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
42	c1p0tZ_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** Z: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
43	c1p0tt_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** T: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
44	c1p0tO_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** O: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
45	c1p0tq_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** Q: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
46	c1p0tn_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** N: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
47	c1p0t6_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** 6: **PDB Molecule:** **PDB Fragment:**residues 1-63; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
48	c1p0tF_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
49	c1p0t1_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** 1: **PDB Molecule:** **PDB Fragment:**residues 1-63; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
50	c1p0t8_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** 8: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
51	c1p0tf_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
52	c1p0tR_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** R: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
53	c1p0ta_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
54	c1p0tw_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** W: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
55	c1p0ts_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** S: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)

56	c1p0ti_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** I: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
57	c1p0td_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
58	c1p0th_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
59	c1p0tT_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** T: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
60	c1p0tE_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
61	c1p0tM_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** M: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
62	c1p0tm_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** M: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
63	c1p0t4_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** 4: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
64	c1p0tH_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
65	c1p0tI_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** I: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
66	c1p0tr_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** R: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
67	c1p0to_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** O: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
68	c1p0tS_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** S: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
69	c1p0tv_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** V: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
70	c1p0tY_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** Y: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
71	c1p0t5_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** 5: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
72	c1p0tj_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** J: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
73	c1p0tP_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** P: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
74	c1p0tc_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
75	c1p0tD_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
76	c1p0tG_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
77	c1p0t2_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** 2: **PDB Molecule:** **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
78	c1p0tb_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
79	c1p0tL_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** L: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
80	c1p0tg_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
81	c1p0tQ_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** Q: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)

82	c1p0tu_	Alignment	not modelled	14.1	54	**PDB header:**protein binding **Chain:** U: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of the baff-baff-r complex (part ii)
83	d1oqen_	Alignment	not modelled	13.9	54	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
84	c1oqeN_	Alignment	not modelled	13.9	54	**PDB header:**immune system **Chain:** N: **PDB Molecule:**tumor necrosis factor receptor superfamily member 13c; **PDBTitle:** crystal structure of stall-1 with baff-r
85	c1pjtB_	Alignment	not modelled	13.5	12	**PDB header:**transferase/oxidoreductase/lyase **Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatase for3 siroheme synthesis
86	d1xuba1	Alignment	not modelled	13.1	25	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
87	c4m55E_	Alignment	not modelled	12.3	20	**PDB header:**lyase **Chain:** E: **PDB Molecule:**udp-glucuronic acid decarboxylase 1; **PDBTitle:** crystal structure of human udp-xylose synthase r236h substitution
88	c4yn3B_	Alignment	not modelled	10.5	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cucumisin; **PDBTitle:** crystal structure of cucumisin complex with pro-peptide
89	c5uazB_	Alignment	not modelled	9.7	50	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**nucleoporin nup53; **PDBTitle:** crystal structure of the yeast nucleoporin
90	d1ws6a1	Alignment	not modelled	9.1	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
91	c1kyqC_	Alignment	not modelled	9.0	16	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
92	c4u3fV_	Alignment	not modelled	8.9	26	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** V: **PDB Molecule:**cytochrome b-c1 complex subunit rieske, mitochondrial; **PDBTitle:** cytochrome bc1 complex from chicken with designed inhibitor bound
93	c5gukA_	Alignment	not modelled	8.7	27	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cyclolavandulyl diphosphate synthase; **PDBTitle:** crystal structure of apo form of cyclolavandulyl diphosphate synthase2 (clds) from streptomyces sp. cl190
94	c3h1kI_	Alignment	not modelled	8.6	20	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**cytochrome b-c1 complex subunit rieske, mitochondrial; **PDBTitle:** chicken cytochrome bc1 complex with zn++ and an iodinated derivative2 of kresoxim-methyl bound
95	c3sxpD_	Alignment	not modelled	8.2	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**adp-l-glycero-d-mannoheptose-6-epimerase; **PDBTitle:** crystal structure of helicobacter pylori adp-l-glycero-d-manno-2 heptose-6-epimerase (rfad, hp0859)
96	c3h1lV_	Alignment	not modelled	7.8	26	**PDB header:**oxidoreductase **Chain:** V: **PDB Molecule:**cytochrome b-c1 complex subunit rieske, mitochondrial; **PDBTitle:** chicken cytochrome bc1 complex with ascochlorin bound at qo and qi2 sites
97	c3cwbV_	Alignment	not modelled	7.5	26	**PDB header:**oxidoreductase **Chain:** V: **PDB Molecule:**mitochondrial ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
98	d2o0ma1	Alignment	not modelled	7.5	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
99	c2o0mA_	Alignment	not modelled	7.5	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, sorc family; **PDBTitle:** the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis