


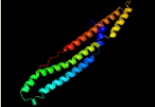

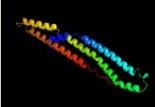

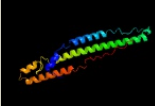

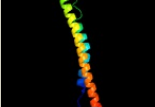

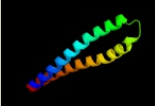










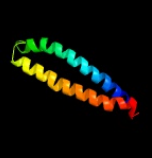



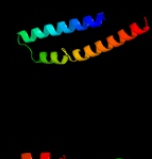

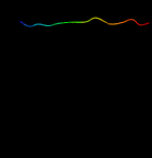

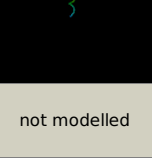


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1789_(PPE26)_2026797_2027978
Date	Fri Aug 2 13:30:39 BST 2019
Unique Job ID	de5a4abc88d6cfa7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	60	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38B_	 Alignment		100.0	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	33	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	19	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		98.1	20	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.7	13	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.6	19	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
8	c3gvmA_	 Alignment		97.6	11	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	c3zbhC_	 Alignment		97.4	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.7	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.0	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		94.2	24	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	Alignment		94.2	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	Alignment		93.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B	Alignment		87.7	18	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xJ	Alignment		40.6	28	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	d1ui5a2	Alignment		28.9	24	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c1bkvA	Alignment		20.5	44	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvC	Alignment		19.6	44	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvB	Alignment		19.6	44	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
21	c5frgA	Alignment	not modelled	17.9	75	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
22	c4xb6D	Alignment	not modelled	12.2	33	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
23	c6aokA	Alignment	not modelled	12.0	22	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
24	c2ke4A	Alignment	not modelled	11.2	75	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cjp4
25	c2nviA	Alignment	not modelled	11.1	40	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit a from2 the yeast proton v-atpase
26	c6cgjA	Alignment	not modelled	11.1	33	PDB header: hydrolase Chain: A: PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
27	c2lkqA	Alignment	not modelled	9.7	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
28	c3sjrB	Alignment	not modelled	8.5	6	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknown function protein cv_1783 from2 chromobacterium violaceum atcc 12472

29	c1vytF_	Alignment	not modelled	7.9	38	PDB header: transport protein Chain: F; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
30	c6q5IA_	Alignment	not modelled	7.7	23	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-I24h; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24h
31	c6q5IB_	Alignment	not modelled	7.7	23	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-I24h; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24h
32	c5l85B_	Alignment	not modelled	7.7	36	PDB header: signaling protein Chain: B; PDB Molecule: nuclear fragile x mental retardation-interacting protein 1; PDBTitle: solution structure of the complex between human znhit3 and nufip12 proteins
33	c5bv9A_	Alignment	not modelled	7.6	31	PDB header: hydrolase Chain: A; PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of bacillus pumilus gh48 in complex with cellobiose
34	c6q5hA_	Alignment	not modelled	7.6	23	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-I24d; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24d
35	c6gp2A_	Alignment	not modelled	7.6	4	PDB header: oxidoreductase Chain: A; PDB Molecule: ribonucleoside-diphosphate reductase beta chain; PDBTitle: ribonucleotide reductase class ie r2 from mesoplasma florum, dopa-2 active form
36	c6q5iB_	Alignment	not modelled	7.6	23	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-I24e; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24e
37	c6q5mB_	Alignment	not modelled	7.6	23	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-I24dab; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24dab
38	c6q5kA_	Alignment	not modelled	7.5	23	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-I24k; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24k
39	c6q5mA_	Alignment	not modelled	7.4	23	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-I24dab; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24dab
40	c6nbiP_	Alignment	not modelled	7.4	60	PDB header: signaling protein Chain: P; PDB Molecule: long-acting parathyroid hormone analog; PDBTitle: cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
41	c6q5jE_	Alignment	not modelled	7.2	23	PDB header: de novo protein Chain: E; PDB Molecule: cc-hex*-I24e; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24e
42	c3r47I_	Alignment	not modelled	7.2	23	PDB header: de novo protein Chain: I; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
43	c3r47B_	Alignment	not modelled	7.2	23	PDB header: de novo protein Chain: B; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
44	c3r47J_	Alignment	not modelled	7.2	23	PDB header: de novo protein Chain: J; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
45	c1bzgA_	Alignment	not modelled	7.1	0	PDB header: hormone Chain: A; PDB Molecule: parathyroid hormone-related protein; PDBTitle: the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
46	c6q5jF_	Alignment	not modelled	7.0	23	PDB header: de novo protein Chain: F; PDB Molecule: cc-hex*-I24e; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24e
47	c6q5kB_	Alignment	not modelled	7.0	23	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-I24k; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24k
48	c2iu1A_	Alignment	not modelled	6.9	17	PDB header: transcription Chain: A; PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
49	c3r47F_	Alignment	not modelled	6.9	23	PDB header: de novo protein Chain: F; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
50	c3r47C_	Alignment	not modelled	6.9	23	PDB header: de novo protein Chain: C; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
51	c3r47L_	Alignment	not modelled	6.9	23	PDB header: de novo protein Chain: L; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
52	c3r47M_	Alignment	not modelled	6.9	23	PDB header: de novo protein Chain: M; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
53	c4mveB_	Alignment	not modelled	6.8	21	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of tcur_1030 protein from thermomonospora curvata PDB header: de novo protein

54	c6q5hB_	Alignment	not modelled	6.8	23	Chain: B; PDB Molecule: cc-hex*-I24d; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24d
55	c6q5nG_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: G; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
56	c6q5nE_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: E; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
57	c6q5nC_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: C; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
58	c6q5nD_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: D; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
59	c6q5nI_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: I; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
60	c6q5nK_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: K; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
61	c6q5nF_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: F; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
62	c6q5nH_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: H; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
63	c6q5nB_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
64	c6q5nA_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
65	c6q5nJ_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: J; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
66	c6q5nL_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: L; PDB Molecule: cc-hex*-I24nle; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-I24nle
67	c4kvtE_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: E; PDB Molecule: 6-helix coiled coil cc-hex-I24c peptide; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-I24c
68	c4kvtF_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: F; PDB Molecule: 6-helix coiled coil cc-hex-I24c peptide; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-I24c
69	c4kvtA_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: A; PDB Molecule: 6-helix coiled coil cc-hex-I24c peptide; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-I24c
70	c4kvtB_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: B; PDB Molecule: 6-helix coiled coil cc-hex-I24c peptide; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-I24c
71	c4kvtC_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: C; PDB Molecule: 6-helix coiled coil cc-hex-I24c peptide; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-I24c
72	d1vlfn1	Alignment	not modelled	6.7	80	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
73	c3r47K_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: K; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
74	c3r47H_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: H; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
75	c3r48F_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: F; PDB Molecule: coiled coil helix w22-I24h; PDBTitle: crystal structure of a hetero-hexamer coiled coil
76	c3r47G_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: G; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
77	c3r47A_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: A; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
78	c3r47E_	Alignment	not modelled	6.7	23	PDB header: de novo protein Chain: E; PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
79	c5uc0B_	Alignment	not modelled	6.7	60	PDB header: hydrolase Chain: B; PDB Molecule: uncharacterized protein cog5400; PDBTitle: crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
80	c3r46E_	Alignment	not modelled	6.6	23	PDB header: de novo protein Chain: E; PDB Molecule: coiled coil helix I24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24

81	c3r46C_	Alignment	not modelled	6.6	23	PDB header: de novo protein Chain: C: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
82	c3r46F_	Alignment	not modelled	6.6	23	PDB header: de novo protein Chain: F: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
83	c3r46A_	Alignment	not modelled	6.6	23	PDB header: de novo protein Chain: A: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
84	c3r46G_	Alignment	not modelled	6.6	23	PDB header: de novo protein Chain: G: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
85	c3r46B_	Alignment	not modelled	6.6	23	PDB header: de novo protein Chain: B: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
86	c2fulE_	Alignment	not modelled	6.6	28	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
87	d1zeeal	Alignment	not modelled	6.5	25	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
88	c4kvtD_	Alignment	not modelled	6.5	23	PDB header: de novo protein Chain: D: PDB Molecule: 6-helix coiled coil cc-hex-l24c peptide; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-l24c
89	c3r48A_	Alignment	not modelled	6.5	23	PDB header: de novo protein Chain: A: PDB Molecule: coiled coil helix w22-l24h; PDBTitle: crystal structure of a hetero-hexamer coiled coil
90	c3r48G_	Alignment	not modelled	6.5	23	PDB header: de novo protein Chain: G: PDB Molecule: coiled coil helix w22-l24h; PDBTitle: crystal structure of a hetero-hexamer coiled coil
91	c6q5iA_	Alignment	not modelled	6.5	23	PDB header: de novo protein Chain: A: PDB Molecule: cc-hex*-l24e; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-l24e
92	c2kg7A_	Alignment	not modelled	6.3	47	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
93	c6q5jD_	Alignment	not modelled	6.3	23	PDB header: de novo protein Chain: D: PDB Molecule: cc-hex*-l24e; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-l24e
94	c6q5jB_	Alignment	not modelled	6.3	23	PDB header: de novo protein Chain: B: PDB Molecule: cc-hex*-l24e; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-l24e
95	c6q5jC_	Alignment	not modelled	6.3	23	PDB header: de novo protein Chain: C: PDB Molecule: cc-hex*-l24e; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-l24e
96	c6q5iA_	Alignment	not modelled	6.3	23	PDB header: de novo protein Chain: A: PDB Molecule: cc-hex*-l24e; PDBTitle: crystal structure of a cc-hex mutant that forms a parallel six-helix2 coiled coil cc-hex*-l24e
97	c2y5tG_	Alignment	not modelled	6.3	67	PDB header: immune system Chain: G: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
98	c5lzkB_	Alignment	not modelled	6.1	9	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
99	c1vytE_	Alignment	not modelled	6.1	38	PDB header: transport protein Chain: E: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid