



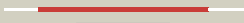



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3d32a1	 Alignment		100.0	57	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like
2	c3h9dB_	 Alignment		100.0	54	PDB header: structural protein Chain: B: PDB Molecule: microtubule-associated protein 1a/1b, light chain 3, PDBTitle: crystal structure of trypanosoma brucei atg8
3	d1eo6a_	 Alignment		100.0	60	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like
4	c6aagF_	 Alignment		100.0	72	PDB header: membrane protein Chain: F: PDB Molecule: transmembrane protein 184 homolog ykr051w,autophagy-related PDBTitle: crystal structure of budding yeast atg8 complexed with the helical aim2 of hfl1.
5	c5azhA_	 Alignment		100.0	34	PDB header: protein binding Chain: A: PDB Molecule: eeeweel peptide,protein lgg-2; PDBTitle: crystal structure of lgg-2 fused with an eeeweel peptide
6	c3vvwB_	 Alignment		100.0	45	PDB header: protein transport Chain: B: PDB Molecule: microtubule-associated proteins 1a/1b light chain 3c; PDBTitle: ndp52 in complex with lc3c
7	d2zjda1	 Alignment		100.0	37	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like
8	c2zpnB_	 Alignment		100.0	72	PDB header: protein transport Chain: B: PDB Molecule: autophagy-related protein 8; PDBTitle: the crystal structure of saccharomyces cerevisiae atg8-2 atg19(412-415) complex
9	c3w1yA_	 Alignment		100.0	36	PDB header: transport protein/ribosomal protein Chain: A: PDB Molecule: microtubule-associated protein 1a/1b, light chain 3; PDBTitle: crystal structure of t brucei atg8.2 in complex with e coli s10
10	c4eoyB_	 Alignment		100.0	47	PDB header: transport protein Chain: B: PDB Molecule: microtubule-associated protein 1 light chain 3; PDBTitle: plasmodium falciparum atg8 in complex with plasmodium falciparum atg32 peptide
11	d1klva_	 Alignment		100.0	60	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like

12	c4gdkA_	Alignment		100.0	24	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin-like protein atg12; PDBTitle: crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
13	d1wz3a1	Alignment		99.9	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: APG12-like
14	c3w1sC_	Alignment		99.8	16	PDB header: ligase Chain: C: PDB Molecule: ubiquitin-like protein atg12; PDBTitle: crystal structure of saccharomyces cerevisiae atg12-atg5 conjugate2 bound to the n-terminal domain of atg16
15	c2dymE_	Alignment		96.7	20	PDB header: protein turnover/protein turnover Chain: E: PDB Molecule: autophagy protein 5; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
16	c3vqiE_	Alignment		96.6	19	PDB header: protein transport Chain: E: PDB Molecule: atg5; PDBTitle: crystal structure of kluyveromyces marxianus atg5
17	c4hpmB_	Alignment		96.3	17	PDB header: transcription Chain: B: PDB Molecule: polycomb group ring finger protein 1; PDBTitle: pcgf1 ub fold (rawul)/bcor1 pufd complex
18	c2na1A_	Alignment		96.2	19	PDB header: transcription Chain: A: PDB Molecule: polycomb complex protein bmi-1, polyhomeotic-like 2; PDBTitle: uld complex
19	c4gdkB_	Alignment		96.1	16	PDB header: protein binding Chain: B: PDB Molecule: autophagy protein 5; PDBTitle: crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
20	c3goeA_	Alignment		85.9	11	PDB header: recombination, replication Chain: A: PDB Molecule: dna repair protein rad60; PDBTitle: molecular mimicry of sumo promotes dna repair
21	c5ejsA_	Alignment	not modelled	83.0	10	PDB header: motor protein Chain: A: PDB Molecule: myosin-i heavy chain; PDBTitle: structure of dictyostelium discoideum myosin vii myth4-ferm mf22 domain, mutant 1
22	d1wz0a1	Alignment	not modelled	79.6	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
23	c5xqmA_	Alignment	not modelled	78.4	8	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin-related modifier; PDBTitle: nmr solution structure of smo1, sumo homologue in caenorhabditis2 elegans
24	c2k8hA_	Alignment	not modelled	78.3	8	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin protein; PDBTitle: solution structure of sumo from trypanosoma brucei
25	d2uyzb1	Alignment	not modelled	77.8	6	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
26	c5jp1B_	Alignment	not modelled	76.7	6	PDB header: hydrolase Chain: B: PDB Molecule: small ubiquitin-related modifier; PDBTitle: structure of xanthomonas campestris effector protein xopd bound to2 tomato sumo
27	c2l76A_	Alignment	not modelled	73.7	10	PDB header: transcription Chain: A: PDB Molecule: nfatc2-interacting protein; PDBTitle: solution nmr structure of human nfatc2ip ubiquitin-like domain,2 nfatc2ip_244_338, nesg target ht65a/ocsp target hs00387_244_338/sgc-3 toronto
28	c3a4rB_	Alignment	not modelled	73.7	12	PDB header: transcription Chain: B: PDB Molecule: nfatc2-interacting protein; PDBTitle: the crystal structure of sumo-like domain 2 in nip45

29	c6l0lA_	Alignment	not modelled	71.1	10	PDB header: de novo protein Chain: A: PDB Molecule: hydra-1ubq; PDBTitle: hydra-1ubq de nova designed by hydra based on ubiquitin
30	c1yx5B_	Alignment	not modelled	69.5	6	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin; PDBTitle: solution structure of s5a uim-1/ubiquitin complex
31	c6izgA_	Alignment	not modelled	69.4	5	PDB header: endocytosis Chain: A: PDB Molecule: ubiquitin-fold modifier 1; PDBTitle: solution structure of ufm1 protein from trypanosoma brucei
32	c2jxxA_	Alignment	not modelled	69.3	13	PDB header: protein binding Chain: A: PDB Molecule: nfatc2-interacting protein; PDBTitle: nmr solution structure of ubiquitin-like domain of nfatc2ip, northeast2 structural genomics consortium target hr5627
33	c2kdiA_	Alignment	not modelled	67.2	6	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin, vacuolar protein sorting-associated protein 27 PDBTitle: solution structure of a ubiquitin/uim fusion protein
34	c5y3tA_	Alignment	not modelled	66.4	25	PDB header: ligase Chain: A: PDB Molecule: ranbp-type and c3hc4-type zinc finger-containing protein 1; PDBTitle: crystal structure of hetero-trimeric core of lubac: hoip double-uba2 complexed with hoil-1l ubl and sharpin ubl
35	d1a5ra_	Alignment	not modelled	66.4	8	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
36	c5ycaA_	Alignment	not modelled	66.3	6	PDB header: membrane protein Chain: A: PDB Molecule: ubiquitin-like protein smt3,bouquet formation protein 4; PDBTitle: crystal structure of inner membrane protein bqt4 in complex with lem2
37	c5gjlA_	Alignment	not modelled	65.8	8	PDB header: protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of sumo from plasmodium falciparum
38	d1wmha_	Alignment	not modelled	65.2	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
39	c2al6A_	Alignment	not modelled	64.5	9	PDB header: transferase Chain: A: PDB Molecule: focal adhesion kinase 1; PDBTitle: ferm domain of focal adhesion kinase
40	d1wh3a_	Alignment	not modelled	64.1	4	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
41	c2klcA_	Alignment	not modelled	63.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr solution structure of human ubiquitin-like domain of ubiquilin 1,2 northeast structural genomics consortium (nesg) target ht5a
42	c2n7dA_	Alignment	not modelled	63.4	16	PDB header: unknown function Chain: A: PDB Molecule: protein ddi1 homolog 2; PDBTitle: solution structure of the ubl domain of human ddi2
43	d1wjna_	Alignment	not modelled	62.7	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
44	d1euvb_	Alignment	not modelled	62.5	4	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
45	d1ud7a_	Alignment	not modelled	62.2	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
46	d1j0ga_	Alignment	not modelled	61.9	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: BM-002-like
47	d1ndda_	Alignment	not modelled	61.2	4	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
48	d1l7ya_	Alignment	not modelled	60.5	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: BM-002-like
49	c5xq0B_	Alignment	not modelled	60.3	16	PDB header: signaling protein Chain: B: PDB Molecule: fermitin family homolog 2,integrin beta-1; PDBTitle: structural basis of kindlin-mediated integrin recognition and2 activation
50	d1iyfa_	Alignment	not modelled	59.6	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
51	c2dziA_	Alignment	not modelled	59.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquitin-like protein 4a; PDBTitle: 2dzi/solution structure of the n-terminal ubiquitin-like2 domain in human ubiquitin-like protein 4a (gdx)
52	c2mlbA_	Alignment	not modelled	58.9	17	PDB header: de novo protein Chain: A: PDB Molecule: redesigned ubiquitin; PDBTitle: nmr solution structure of a computational designed protein based on2 template of human erythrocytic ubiquitin
53	c3au5B_	Alignment	not modelled	58.3	11	PDB header: motor protein Chain: B: PDB Molecule: myosin-x; PDBTitle: structure of the human myosin-x myth4-ferm cassette
54	c6gf2A_	Alignment	not modelled	57.5	13	PDB header: immune system Chain: A: PDB Molecule: ubiquitin d; PDBTitle: the structure of the ubiquitin-like modifier fat10 reveals a novel2 targeting mechanism for degradation by the 26s proteasome
						Fold: beta-Grasp (ubiquitin-like)

55	d1yqba1	Alignment	not modelled	57.3	18	Superfamily: Ubiquitin-like Family: Ubiquitin-related
56	d1j8ca	Alignment	not modelled	56.6	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
57	c2ekeC	Alignment	not modelled	56.5	4	PDB header: ligase/protein binding Chain: C: PDB Molecule: ubiquitin-like protein smt3; PDBTitle: structure of a sumo-binding-motif mimic bound to smt3p-2 ubc9p: conservation of a noncovalent ubiquitin-like3 protein-e2 complex as a platform for selective4 interactions within a sumo pathway
58	d1wm3a	Alignment	not modelled	55.5	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
59	d1c3ta	Alignment	not modelled	54.5	6	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
60	d1wxsa1	Alignment	not modelled	54.4	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: BM-002-like
61	d1sifa	Alignment	not modelled	53.2	4	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
62	c6jl3A	Alignment	not modelled	52.8	12	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin domain-containing protein dsk2,putative; PDBTitle: crystal structure of the ubl domain of plasmodium falciparum dsk2
63	d2zeqa1	Alignment	not modelled	52.7	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
64	c2kk8A	Alignment	not modelled	50.1	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at4g05270; PDBTitle: nmr solution structure of a putative uncharacterized protein obtained2 from arabidopsis thaliana: northeast structural genomics consortium3 target ar3449a
65	d1bt0a	Alignment	not modelled	50.1	4	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
66	c3pgeA	Alignment	not modelled	49.9	9	PDB header: dna binding protein Chain: A: PDB Molecule: sumo-modified proliferating cell nuclear antigen; PDBTitle: structure of sumoylated pcna
67	c3q3fA	Alignment	not modelled	49.3	6	PDB header: hydrolase, protein binding Chain: A: PDB Molecule: ribonuclease/ubiquitin chimeric protein; PDBTitle: engineering domain-swapped binding interfaces by mutually exclusive2 folding: insertion of ubiquitin into position 103 of barnase
68	c2mqjA	Alignment	not modelled	48.1	17	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like protein; PDBTitle: solution structure of ubiquitin-like protein from caldiarchaeum2 subterraneum
69	c5f3yA	Alignment	not modelled	47.3	14	PDB header: motor protein/protein binding Chain: A: PDB Molecule: unconventional myosin-viib; PDBTitle: crystal structure of myo7b n-myth4-ferm-sh3 in complex with anks4b cen
70	c2lrwA	Alignment	not modelled	47.1	6	PDB header: cell cycle Chain: A: PDB Molecule: ubiquitin, putative; PDBTitle: solution structure of a ubiquitin-like protein from trypanosoma brucei
71	d2io3b1	Alignment	not modelled	47.1	8	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
72	d1zkha1	Alignment	not modelled	46.7	8	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
73	c5y3tC	Alignment	not modelled	46.3	17	PDB header: ligase Chain: C: PDB Molecule: sharpin; PDBTitle: crystal structure of hetero-trimeric core of lubac: hoip double-uba2 complexed with hoil-1l ubl and sharpin ubl
74	c2k25A	Alignment	not modelled	44.6	7	PDB header: unknown function Chain: A: PDB Molecule: ubb; PDBTitle: automated nmr structure of the ubb by fapsy
75	d1wx9a1	Alignment	not modelled	44.2	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
76	c6wajA	Alignment	not modelled	43.4	14	PDB header: protein binding Chain: A: PDB Molecule: nle1; PDBTitle: crystal structure of the ubl domain of human nle1
77	d2faza1	Alignment	not modelled	43.3	5	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
78	d1v5oa	Alignment	not modelled	43.0	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
79	c1ttnA	Alignment	not modelled	43.0	9	PDB header: signaling protein Chain: A: PDB Molecule: dendritic cell-derived ubiquitin-like protein; PDBTitle: solution structure of the ubiquitin-like domain of human dc-2 ubp from dendritic cells
80	d1ttna1	Alignment	not modelled	43.0	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related

81	c3pvlA	 Alignment	not modelled	42.8	19	PDB header: motor protein/protein transport Chain: A: PDB Molecule: myosin viia isoform 1; PDBTitle: structure of myosin viia myth4-ferm-sh3 in complex with the cen1 of2 sans
82	c3pzdA	 Alignment	not modelled	42.1	11	PDB header: motor protein/apoptosis Chain: A: PDB Molecule: myosin-x; PDBTitle: structure of the myosin x myth4-ferm/dcc complex
83	d1z2ma2	 Alignment	not modelled	41.3	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
84	d1wy8a1	 Alignment	not modelled	40.1	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
85	c6v9gB	 Alignment	not modelled	39.9	14	PDB header: blood clotting Chain: B: PDB Molecule: fermitin family homolog 3; PDBTitle: kindlin-3 double deletion mutant long form
86	c2mrpA	 Alignment	not modelled	39.9	12	PDB header: ubiquitin-binding protein Chain: A: PDB Molecule: dna damage-inducible protein 1; PDBTitle: nmr solution structure of the ubiquitin like domain (ubl) of dna-2 damage-inducible 1 protein (ddi1)
87	c3m62B	 Alignment	not modelled	39.7	10	PDB header: ligase/protein binding Chain: B: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of rad23
88	d1wjua	 Alignment	not modelled	39.2	8	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
89	c3v7oB	 Alignment	not modelled	39.2	4	PDB header: transcription Chain: B: PDB Molecule: minor nucleoprotein vp30; PDBTitle: crystal structure of the c-terminal domain of ebola virus vp30 (strain2 reston-89)
90	c2ojrA	 Alignment	not modelled	39.0	8	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin; PDBTitle: structure of ubiquitin solved by sad using the lanthanide-binding tag
91	c3ivfA	 Alignment	not modelled	38.1	18	PDB header: structural protein Chain: A: PDB Molecule: taln-1; PDBTitle: crystal structure of the talin head ferm domain
92	d1wx7a1	 Alignment	not modelled	37.6	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
93	c3tixA	 Alignment	not modelled	37.3	4	PDB header: gene regulation/protein binding Chain: A: PDB Molecule: ubiquitin-like protein smt3,rna-induced transcriptional PDBTitle: crystal structure of the chp1-tas3 complex core
94	c4dbgA	 Alignment	not modelled	36.7	19	PDB header: ligase Chain: A: PDB Molecule: ranbp-type and c3hc4-type zinc finger-containing protein 1; PDBTitle: crystal structure of hoil-1l-ubl complexed with a hoip-uba derivative
95	d2bwfa1	 Alignment	not modelled	36.1	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
96	c5ejvA	 Alignment	not modelled	35.8	14	PDB header: motor protein Chain: A: PDB Molecule: myosin-i heavy chain; PDBTitle: structure of dictyostelium discoideum myosin vii myth4-ferm mf1 domain
97	c3m63B	 Alignment	not modelled	35.4	14	PDB header: ligase/protein binding Chain: B: PDB Molecule: ubiquitin domain-containing protein dsk2; PDBTitle: crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of dsk2
98	c3ai5A	 Alignment	not modelled	35.1	6	PDB header: fluorescent protein, transcription Chain: A: PDB Molecule: yeast enhanced green fluorescent protein,ubiquitin; PDBTitle: crystal structure of yeast enhanced green fluorescent protein-2 ubiquitin fusion protein
99	c5n9vA	 Alignment	not modelled	33.6	13	PDB header: transferase Chain: A: PDB Molecule: nad(p)(+)--arginine adp-ribosyltransferase; PDBTitle: nmr solution structure of ubl5 domain from polyubiquitin locus of2 t.thermophila.
100	c2qieB	 Alignment	not modelled	32.7	21	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
101	d1wx8a1	 Alignment	not modelled	31.9	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
102	c2n9pC	 Alignment	not modelled	31.7	12	PDB header: ligase Chain: C: PDB Molecule: large proline-rich protein bag6; PDBTitle: solution structure of rnf126 n-terminal zinc finger domain in complex2 with bag6 ubiquitin-like domain
103	c2kc2A	 Alignment	not modelled	31.5	17	PDB header: structural protein Chain: A: PDB Molecule: taln-1; PDBTitle: nmr structure of the f1 domain (residues 86-202) of the2 talin
104	c6cs2A	 Alignment	not modelled	30.7	22	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibrin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
105	c2j0kB	 Alignment	not modelled	30.4	9	PDB header: transferase Chain: B: PDB Molecule: focal adhesion kinase 1; PDBTitle: crystal structure of a fragment of focal adhesion kinase containing2 the ferm and kinase domains.
106	c2dzmA	 Alignment	not modelled	26.7	10	PDB header: structural genomics unknown function Chain: A: PDB Molecule: fas-associated factor 1; PDBTitle: solution structure of the ubiquitin-like domain in human2

					fas-associated factor 1 (hfaf1) PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin-like protein smt3,1108aa long hypothetical cell PDBTitle: crystal structure of phocdc21-1 intein
107	c6rpqA_	Alignment	not modelled	26.2	6
108	d2npta1	Alignment	not modelled	25.3	22
109	c2l7rA_	Alignment	not modelled	24.7	14
110	c2jwlB_	Alignment	not modelled	24.6	24
111	c1y7oE_	Alignment	not modelled	24.5	12
112	c3h8hA_	Alignment	not modelled	24.1	12
113	c2w9nA_	Alignment	not modelled	23.9	6
114	c6girA_	Alignment	not modelled	23.8	20
115	c5e9oC_	Alignment	not modelled	23.5	26
116	c4pyzA_	Alignment	not modelled	22.2	9
117	d1wxva1	Alignment	not modelled	21.7	18
118	d1ip9a_	Alignment	not modelled	21.5	18
119	c6mdhA_	Alignment	not modelled	21.1	13
120	c6a42A_	Alignment	not modelled	21.0	7