

Fold ID	SPIRED	OmegaFold	ESMFold	Fold Name
g.61	0.3193	0.2186	0.2152	Apical membrane antigen 1
d.372	0.2205	0.3752	0.2232	YqaI-like
d.196	0.2447	0.3818	0.2265	Outer capsid protein sigma 3
e.83	0.2442	0.2406	0.229	Coronavirus S1 beta-rich region
b.126	0.2117	0.235	0.2329	Adsorption protein p2
g.94	0.2573	0.2662	0.2402	Complement C3 linker domain-like
d.394	0.215	0.1945	0.2416	N-terminal domain of Prp8 / Spp42
f.50	0.3236	0.1724	0.2431	Connexin43
b.164	0.3249	0.298	0.2457	SARS ORF9b-like
f.12	0.237	0.2262	0.2458	Head and neck region of the ectodomain of NDV fusion glycoprotein
f.64	0.6526	0.226	0.2469	Filovirus surface glycoprotein-like
a.176	0.251	0.2319	0.2476	N-terminal domain of bifunctional PutA protein
a.300	0.2897	0.2314	0.25	Arenavirus nucleocapsid protein-like
e.82	0.2275	0.2467	0.2524	Influenza virus PB2 N-terminal region
f.47	0.2346	0.253	0.2568	VP4 membrane interaction domain
a.260	0.2419	0.2651	0.2578	Rhabdovirus nucleoprotein-like
d.364	0.4933	0.2885	0.2579	PA1123-like
d.184	0.4826	0.2839	0.2586	Non-globular alpha+beta subunits of globular proteins
d.339	0.2824	0.2839	0.2621	ORC1-binding domain
a.220	0.342	0.3363	0.2625	Hypothetical protein At3g22680
d.302	0.5158	0.2727	0.2629	Coronavirus NSP8-like
e.42	0.1962	0.2166	0.2641	L-A virus major coat protein
d.402	0.2555	0.2209	0.2654	B domain from Cmr1-like
e.77	0.2706	0.2248	0.2673	PA C-terminal domain-like
d.318	0.6756	0.3128	0.2699	SARS receptor-binding domain-like
e.75	0.4766	0.2678	0.2714	Flu NP-like
a.120	0.692	0.3644	0.2733	gene 59 helicase assembly protein
d.397	0.505	0.3072	0.2738	Influenza virus PB2 cap binding domain-like
a.170	0.2798	0.2954	0.2745	BRCA2 helical domain
a.206	0.284	0.2668	0.2755	P40 nucleoprotein
d.401	0.3039	0.2876	0.2769	Cas3 C-terminal domain-like
d.172	0.9582	0.8876	0.2775	gp120 core
g.82	0.4347	0.2773	0.2794	Expressed protein At2g23090/F21P24.15

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g.86	0.5364	0.3028	0.282	Coronavirus NSP10-like
b.27	0.5284	0.3492	0.2859	Soluble secreted chemokine inhibitor, VCCI
g.103	0.3087	0.3052	0.2866	Protein-only RNase P central domain-like
e.48	0.2299	0.2574	0.2869	Major capsid protein VP5
d.346	0.3845	0.3898	0.2878	SARS Nsp1-like
b.75	0.6079	0.263	0.2912	Bacteriochlorophyll A protein
a.15	0.5306	0.3611	0.2938	TAF(II)230 TBP-binding fragment
d.259	0.3023	0.7892	0.2958	Hypothetical protein HI1480
a.255	0.8851	0.9816	0.2998	Rv1873-like
e.41	0.2925	0.2893	0.3026	Adenylylcyclase toxin (the edema factor)
e.47	0.8853	0.4472	0.3051	39 kda initiator binding protein, IBP39, C-terminal domains
f.26	0.6561	0.4398	0.3064	Bacterial photosystem II reaction centre, L and M subunits
g.70	0.3152	0.3608	0.3086	Necrosis inducing protein 1, NIP1
g.21	0.3889	0.2916	0.3112	Methylamine dehydrogenase, L chain
f.29	0.2989	0.3632	0.3129	Photosystem I subunits PsaA/PsaB
e.2	0.312	0.3156	0.3131	Replication terminator protein (Tus)
a.115	0.3004	0.3188	0.3139	A virus capsid protein alpha-helical domain
g.101	0.6586	0.7748	0.3155	Triquetra knot
g.88	0.3049	0.3013	0.3155	Intrinsically disordered proteins
d.384	0.2608	0.2906	0.3179	SV5-V core-like
d.236	0.6377	0.4092	0.3184	DNA-binding protein Tfx
e.80	0.2568	0.2586	0.3201	Protospace-adjacent motif(PAM)-interacting domain from Cas9/Csn1
d.174	0.8063	0.2872	0.3212	Nitric oxide (NO) synthase oxygenase domain
a.178	0.4004	0.2677	0.3216	Soluble domain of poliovirus core protein 3a
a.291	0.7133	0.3632	0.3234	MG296-like
d.361	0.2704	0.2959	0.3264	PB2 C-terminal domain-like
a.225	0.8691	0.7393	0.3291	Hypothetical protein MG354
a.148	0.4304	0.3248	0.3294	Arp2/3 complex 21 kDa subunit ARPC3
d.255	0.6773	0.33	0.3297	Tombusvirus P19 core protein, VP19
d.168	0.3213	0.8661	0.3299	Catalytic domain of succinate dehydrogenase/fumarate reductase flavoprotein
d.275	0.7263	0.3159	0.3309	Hut operon positive regulatory protein HutP
d.213	0.6773	0.4088	0.3312	VSV matrix protein
d.102	0.7671	0.3269	0.3318	Regulatory factor Nef

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a.49	0.3846	0.3345	0.3321	C-terminal domain of B transposition protein
a.244	0.3088	0.3671	0.3332	EF2947-like
b.181	0.3013	0.3585	0.3335	Handle domain of Transferrin binding protein TbpB-like
g.63	0.6291	0.4119	0.3337	Mollusk pheromone
a.164	0.6686	0.6334	0.3339	C-terminal domain of DFF45/ICAD (DFF-C domain)
g.32	0.4464	0.3554	0.3341	GLA-domain
a.210	0.3619	0.2824	0.3352	Eukaryotic initiation factor 4f subunit eIF4g, eIF4e-binding domain
b.110	0.3872	0.3474	0.3362	Cloacin translocation domain
g.92	0.6501	0.3678	0.337	T-antigen specific domain-like
g.30	0.2891	0.3172	0.3375	Carboxypeptidase inhibitor
a.89	0.3619	0.3524	0.3386	Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
b.147	0.4765	0.3085	0.339	BTV NS2-like ssRNA-binding domain
d.256	0.7017	0.3178	0.3394	Ta1353-like
d.353	0.3207	0.3279	0.3407	AMPKBI-like
g.69	0.6857	0.3254	0.3409	Plant proteinase inhibitors
d.180	0.6041	0.3964	0.3415	Conserved core of transcriptional regulatory protein vp16
d.35	0.8736	0.344	0.3427	Heme-binding protein A (HasA)
d.293	0.6831	0.3765	0.3453	Phosphoprotein M1, C-terminal domain
d.374	0.5235	0.7139	0.3508	TTHC002-like
d.385	0.3939	0.3493	0.3508	DNA gyrase B, insert domain-like
a.296	0.3961	0.3076	0.3538	PMT central region-like
b.116	0.2647	0.3168	0.3562	Viral chemokine binding protein m3
g.51	0.3438	0.3323	0.3571	Zn-binding domains of ADDBP
d.396	0.7525	0.3669	0.3578	Influenza virus PB2 '627' domain-like
d.254	0.5019	0.3829	0.3587	Nucleocapsid protein dimerization domain
g.58	0.7183	0.8045	0.3603	Pheromone ER-23
a.85	0.3933	0.3635	0.3613	Hemocyanin, N-terminal domain
b.28	0.4961	0.3347	0.3618	Baculovirus p35 protein
a.166	0.3053	0.4551	0.3623	RuBisCo LSMT C-terminal, substrate-binding domain
b.168	0.823	0.9799	0.3628	HisI-like
b.91	0.7302	0.3212	0.3634	E2 regulatory, transactivation domain
a.299	0.7929	0.3033	0.3665	Tenuivirus/Phlebovirus nucleocapsid protein-like
e.84	0.2516	0.2628	0.3668	N-terminal helical domains from Cas12a / Cpf1-like

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a.262	0.631	0.3256	0.3669	PriB N-terminal domain-like
b.148	0.8165	0.2866	0.3677	Coronavirus RNA-binding domain
d.349	0.2472	0.3365	0.3692	CPE0013-like
e.34	0.777	0.3386	0.3705	NSP3 homodimer
d.216	0.3111	0.3751	0.3706	Rotavirus NSP2 fragment, N-terminal domain
e.70	0.4834	0.4229	0.3708	MalF N-terminal region-like
d.365	0.5525	0.445	0.3713	Ava3019-like
a.109	0.5792	0.4222	0.3717	Class II MHC-associated invariant chain ectoplasmic trimerization domain
f.45	0.3631	0.3199	0.3722	Mitochondrial ATP synthase coupling factor 6
d.352	0.7426	0.7452	0.3723	FlaG-like
a.168	0.7116	0.3399	0.3734	SopE-like GEF domain
a.195	0.4731	0.3757	0.3734	YutG-like
b.31	0.3501	0.3919	0.3735	EV matrix protein
a.267	0.6032	0.3999	0.3741	Topoisomerase V catalytic domain-like
b.63	0.6913	0.4262	0.379	Oncogene products
d.311	0.2956	0.5137	0.3794	ImmE5-like
a.54	0.3532	0.4841	0.3806	Domain of early E2A DNA-binding protein, ADDBP
d.280	0.4998	0.3826	0.383	Sulfolobus fructose-1,6-bisphosphatase-like
b.156	0.3603	0.3685	0.3867	Atu1913-like
d.253	0.6243	0.513	0.3879	Hypothetical protein YoaG
d.299	0.8305	0.3894	0.3884	Ns1 effector domain-like
a.153	0.4407	0.4959	0.3896	Nuclear receptor coactivator interlocking domain
d.337	0.2404	0.4159	0.3904	AF2331-like
a.292	0.5882	0.5	0.3905	HP0242-like
e.15	0.5286	0.6081	0.3916	Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
e.74	0.3127	0.9373	0.3922	HI0933 insert domain-like
d.368	0.6067	0.3989	0.3934	YonK-like
d.345	0.503	0.475	0.3945	NRDP1 C-terminal domain-like
a.243	0.7086	0.5067	0.4002	Type III secretion system domain
b.120	0.2598	0.3841	0.4009	Tp47 lipoprotein, N-terminal domain
b.54	0.9206	0.6083	0.4024	Core binding factor beta, CBF
a.282	0.789	0.7356	0.4049	RPA2825-like
a.53	0.6059	0.468	0.4106	p53 tetramerization domain

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d.214	0.5646	0.4676	0.411	Hypothetical protein MTH1880
a.293	0.3674	0.3805	0.4117	SMc04008-like
g.34	0.6025	0.481	0.4129	HIV-1 VPU cytoplasmic domain
a.279	0.4805	0.3902	0.4143	Jann4075-like
a.242	0.7421	0.4312	0.4179	Dcp2 domain-like
b.21	0.7674	0.4099	0.4182	Virus attachment protein globular domain
d.85	0.7567	0.3587	0.4188	RNA bacteriophage capsid protein
d.321	0.7045	0.4446	0.4201	STIV B116-like
a.41	0.4292	0.3694	0.4208	Domain of poly(ADP-ribose) polymerase
a.135	0.7356	0.9207	0.4209	Tetraspanin
d.403	0.4174	0.4276	0.4232	Lewis(b) antigen binding domain of BabA-like
e.63	0.7065	0.4433	0.4259	E2F-DP heterodimerization region
a.83	0.3816	0.5062	0.4262	Guanido kinase N-terminal domain
a.257	0.843	0.4571	0.428	SipA N-terminal domain-like
d.249	0.333	0.4261	0.4296	Hypothetical protein Ta1206
a.297	0.2835	0.4296	0.4298	DDB1 C-terminal-like
a.263	0.731	0.3	0.431	DNA terminal protein
d.350	0.625	0.651	0.431	YcgL-like
d.362	0.4337	0.3669	0.4325	BLRF2-like
d.238	0.3447	0.4168	0.4336	Hypothetical protein TM0875
a.94	0.3898	0.3956	0.4351	Ribosomal protein L19 (L19e)
a.171	0.316	0.5514	0.4364	BRCA2 tower domain
d.398	0.2556	0.3324	0.4375	NUC domain from Cas12a / Cpf1-like
f.55	0.3311	0.5448	0.4378	Photosystem II antenna protein-like
d.179	0.3779	0.8122	0.4382	Substrate-binding domain of HMG-CoA reductase
g.40	0.5405	0.4416	0.44	Retrovirus zinc finger-like domains
b.32	0.7934	0.451	0.4407	gp9
d.56	0.3969	0.8715	0.4423	GroEL-intermediate domain like
b.140	0.5703	0.5183	0.443	Replicase NSP9
d.200	0.4176	0.4841	0.4435	Integrin beta tail domain
a.137	0.605	0.5135	0.4441	Non-globular all-alpha subunits of globular proteins
a.200	0.4681	0.457	0.4443	Hypothetical protein MTH393
d.399	0.809	0.465	0.4471	Ebola nucleoprotein C-terminal domain-like
d.197	0.3511	0.4495	0.4532	Protein-L-isoaspartyl O-methyltransferase, C-terminal domain
a.241	0.5609	0.4433	0.4536	TraM-like

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e.32	0.7451	0.5036	0.4538	Phase 1 flagellin
a.62	0.8364	0.7275	0.4546	Hepatitis B viral capsid (hbcag)
b.127	0.4572	0.1964	0.4584	Baseplate structural protein gp8
a.212	0.444	0.4941	0.4656	KRAB domain (Kruppel-associated box)
a.63	0.9081	0.6392	0.4668	Apolipoprotein III
b.104	0.4368	0.5465	0.4671	P-domain of calnexin/calreticulin
f.18	0.7919	0.4681	0.4689	F1F0 ATP synthase subunit A
d.246	0.2556	0.586	0.4697	mRNA decapping enzyme DcpS N-terminal domain
e.76	0.4554	0.1865	0.4715	Viral glycoprotein ectodomain-like
a.66	0.3739	0.9446	0.4725	Transducin (alpha subunit), insertion domain
a.226	0.9009	0.3883	0.4734	Her-1
b.133	0.3333	0.326	0.4788	Dextranase, N-terminal domain
a.302	0.3704	0.3943	0.4809	Putative dsDNA-binding domain from Cas12a / Cpf1-like
a.190	0.5941	0.496	0.4811	Flavivirus capsid protein C
d.22	0.9594	0.5768	0.4845	GFP-like
a.131	0.6164	0.5415	0.487	Peridinin-chlorophyll protein
g.99	0.3457	0.7416	0.489	Pre-mRNA splicing factor Cwf14-like
b.174	0.3421	0.4649	0.4895	YopT-like
d.263	0.8074	0.6597	0.4922	Hypothetical protein Yml108w
e.66	0.483	0.229	0.4926	Api92-like
d.390	0.4983	0.4763	0.4933	KS-to-AT linker domain from 6-deoxyerythronolide B synthase (DEBS)-like
a.151	0.4426	0.4864	0.4936	Glutamyl tRNA-reductase dimerization domain
g.5	0.6552	0.6415	0.495	Midkine
b.162	0.6517	0.4727	0.4954	At5g01610-like
a.162	0.3585	0.8939	0.4956	Pre-protein crosslinking domain of SecA
d.393	0.3806	0.2906	0.4983	Target recognition (REC) lobe from Cas9/Csn1