

Fold ID	SPIRED	OmegaFold	ESMFold	Fold Name
e.42	0.1962	0.2166	0.2641	L-A virus major coat protein
b.126	0.2117	0.235	0.2329	Adsorption protein p2
d.394	0.215	0.1945	0.2416	N-terminal domain of Prp8 / Spp42
d.372	0.2205	0.3752	0.2232	YqaI-like
e.82	0.2275	0.2467	0.2524	Influenza virus PB2 N-terminal region
e.48	0.2299	0.2574	0.2869	Major capsid protein VP5
f.47	0.2346	0.253	0.2568	VP4 membrane interaction domain
f.12	0.237	0.2262	0.2458	Head and neck region of the ectodomain of NDV fusion glycoprotein
d.337	0.2404	0.4159	0.3904	AF2331-like
a.260	0.2419	0.2651	0.2578	Rhabdovirus nucleoprotein-like
e.83	0.2442	0.2406	0.229	Coronavirus S1 beta-rich region
d.196	0.2447	0.3818	0.2265	Outer capsid protein sigma 3
d.349	0.2472	0.3365	0.3692	CPE0013-like
a.176	0.251	0.2319	0.2476	N-terminal domain of bifunctional PutA protein
e.84	0.2516	0.2628	0.3668	N-terminal helical domains from CRISPR-associated protein Cas12a / Cpf1-like
d.402	0.2555	0.2209	0.2654	B domain from Cmr1-like
d.398	0.2556	0.3324	0.4375	NUC domain from Cas12a / Cpf1-like
d.246	0.2556	0.586	0.4697	mRNA decapping enzyme DcpS N-terminal domain
e.80	0.2568	0.2586	0.3201	Protospacer-adjacent motif(PAM)-interacting domain from Cas9/Csn1
g.94	0.2573	0.2662	0.2402	Complement C3 linker domain-like
b.120	0.2598	0.3841	0.4009	Tp47 lipoprotein, N-terminal domain
d.384	0.2608	0.2906	0.3179	SV5-V core-like
b.116	0.2647	0.3168	0.3562	Viral chemokine binding protein m3
d.361	0.2704	0.2959	0.3264	PB2 C-terminal domain-like
e.77	0.2706	0.2248	0.2673	PA C-terminal domain-like
a.170	0.2798	0.2954	0.2745	BRCA2 helical domain
d.339	0.2824	0.2839	0.2621	ORC1-binding domain
a.297	0.2835	0.4296	0.4298	DDB1 C-terminal-like
a.206	0.284	0.2668	0.2755	P40 nucleoprotein
g.30	0.2891	0.3172	0.3375	Carboxypeptidase inhibitor
a.300	0.2897	0.2314	0.25	Arenavirus nucleocapsid protein-like

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e.41	0.2925	0.2893	0.3026	Adenylylcyclase toxin (the edema factor)
d.311	0.2956	0.5137	0.3794	ImmE5-like
f.29	0.2989	0.3632	0.3129	Photosystem I subunits PsaA/PsaB
a.115	0.3004	0.3188	0.3139	A virus capsid protein alpha-helical domain
b.181	0.3013	0.3585	0.3335	Handle domain of Transferrin binding protein TbpB-like
d.259	0.3023	0.7892	0.2958	Hypothetical protein HI1480
d.401	0.3039	0.2876	0.2769	Cas3 C-terminal domain-like
g.88	0.3049	0.3013	0.3155	Intrinsically disordered proteins
a.166	0.3053	0.4551	0.3623	RuBisCo LSMT C-terminal, substrate-binding domain
g.103	0.3087	0.3052	0.2866	Protein-only RNase P central domain-like
a.244	0.3088	0.3671	0.3332	EF2947-like
d.216	0.3111	0.3751	0.3706	Rotavirus NSP2 fragment, N-terminal domain
e.2	0.312	0.3156	0.3131	Replication terminator protein (Tus)
e.74	0.3127	0.9373	0.3922	HI0933 insert domain-like
g.70	0.3152	0.3608	0.3086	Necrosis inducing protein 1, NIP1
a.171	0.316	0.5514	0.4364	BRCA2 tower domain
g.61	0.3193	0.2186	0.2152	Apical membrane antigen 1
d.353	0.3207	0.3279	0.3407	AMPKBI-like
d.168	0.3213	0.8661	0.3299	Catalytic domain of succinate dehydrogenase/fumarate reductase flavoprotein
f.50	0.3236	0.1724	0.2431	Connexin43
b.164	0.3249	0.298	0.2457	SARS ORF9b-like
f.55	0.3311	0.5448	0.4378	Photosystem II antenna protein-like
d.249	0.333	0.4261	0.4296	Hypothetical protein Ta1206
b.133	0.3333	0.326	0.4788	Dextranase, N-terminal domain
a.220	0.342	0.3363	0.2625	Hypothetical protein At3g22680
b.174	0.3421	0.4649	0.4895	YopT-like
g.51	0.3438	0.3323	0.3571	Zn-binding domains of ADDBP
d.238	0.3447	0.4168	0.4336	Hypothetical protein TM0875
g.99	0.3457	0.7416	0.489	Pre-mRNA splicing factor Cwf14-like
b.31	0.3501	0.3919	0.3735	EV matrix protein
d.197	0.3511	0.4495	0.4532	Protein-L-isoaspartyl O-methyltransferase, C-terminal domain
a.54	0.3532	0.4841	0.3806	Domain of early E2A DNA-binding protein, ADDBP

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a.162	0.3585	0.8939	0.4956	Pre-protein crosslinking domain of SecA
b.156	0.3603	0.3685	0.3867	Atu1913-like
a.210	0.3619	0.2824	0.3352	Eukaryotic initiation factor 4f subunit eIF4g, eIF4e-binding domain
a.89	0.3619	0.3524	0.3386	Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
f.45	0.3631	0.3199	0.3722	Mitochondrial ATP synthase coupling factor 6
a.249	0.3634	0.4176	0.7619	YfmB-like
a.293	0.3674	0.3805	0.4117	SMc04008-like
a.187	0.368	0.6841	0.5308	HAND domain of the nucleosome remodeling ATPase ISWI
g.102	0.3683	0.6872	0.5697	Jumonji C-terminal domain-like
a.302	0.3704	0.3943	0.4809	Putative dsDNA-binding domain from Cas12a / Cpf1-like
a.66	0.3739	0.9446	0.4725	Transducin (alpha subunit), insertion domain
d.179	0.3779	0.8122	0.4382	Substrate-binding domain of HMG-CoA reductase
d.393	0.3806	0.2906	0.4983	Target recognition (REC) lobe of Cas9/Csn1
a.83	0.3816	0.5062	0.4262	Guanido kinase N-terminal domain
d.272	0.3825	0.4602	0.6421	Dystroglycan, domain 2
d.346	0.3845	0.3898	0.2878	SARS Nsp1-like
a.49	0.3846	0.3345	0.3321	C-terminal domain of B transposition protein
b.110	0.3872	0.3474	0.3362	Cloacin translocation domain
g.21	0.3889	0.2916	0.3112	Methylamine dehydrogenase, L chain
a.94	0.3898	0.3956	0.4351	Ribosomal protein L19 (L19e)
f.30	0.3923	0.7194	0.6053	Photosystem I reaction center subunit X, PsaK
a.85	0.3933	0.3635	0.3613	Hemocyanin, N-terminal domain
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
d.56	0.3969	0.8715	0.4423	GroEL-intermediate domain like
a.178	0.4004	0.2677	0.3216	Soluble domain of poliovirus core protein 3a
d.403	0.4174	0.4276	0.4232	Lewis(b) antigen binding domain of BabA-like
d.200	0.4176	0.4841	0.4435	Integrin beta tail domain
g.100	0.4194	0.6474	0.6342	Pre-mRNA splicing factor Cwf5-like
b.94	0.4256	0.3196	0.5608	Olfactory marker protein
a.41	0.4292	0.3694	0.4208	Domain of poly(ADP-ribose) polymerase
a.148	0.4304	0.3248	0.3294	Arp2/3 complex 21 kDa subunit ARPC3
d.362	0.4337	0.3669	0.4325	BLRF2-like

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g.82	0.4347	0.2773	0.2794	Expressed protein At2g23090/F21P24.15
b.104	0.4368	0.5465	0.4671	P-domain of calnexin/calreticulin
a.270	0.439	0.4649	0.5158	Hermes dimerisation domain
a.153	0.4407	0.4959	0.3896	Nuclear receptor coactivator interlocking domain
a.151	0.4426	0.4864	0.4936	Glutamyl tRNA-reductase dimerization domain
a.212	0.444	0.4941	0.4656	KRAB domain (Kruppel-associated box)
d.341	0.4453	0.6486	0.8776	Peptidoglycan deacetylase N-terminal noncatalytic region
g.32	0.4464	0.3554	0.3341	GLA-domain
e.76	0.4554	0.1865	0.4715	Viral glycoprotein ectodomain-like
b.127	0.4572	0.1964	0.4584	Baseplate structural protein gp8
a.214	0.4593	0.6178	0.5471	NbIA-like
b.56	0.4598	0.6396	0.5302	Transcription factor IIA (TFIIA), beta-barrel domain
g.66	0.4621	0.4232	0.5933	CCCH zinc finger
d.332	0.4638	0.7254	0.5736	RGC domain-like
a.200	0.4681	0.457	0.4443	Hypothetical protein MTH393
f.68	0.4703	0.5242	0.5656	Anoctamin (TMEM16)-like
a.69	0.4728	0.8816	0.5632	Left-handed superhelix
a.195	0.4731	0.3757	0.3734	YutG-like
b.147	0.4765	0.3085	0.339	BTV NS2-like ssRNA-binding domain
e.75	0.4766	0.2678	0.2714	Flu NP-like
d.342	0.4776	0.3426	0.6247	PH1570-like
d.281	0.4777	0.4519	0.6269	Hemolytic lectin CEL-III, C-terminal domain
a.279	0.4805	0.3902	0.4143	Jann4075-like
d.335	0.4817	0.7649	0.7332	L,D-transpeptidase pre-catalytic domain-like
d.184	0.4826	0.2839	0.2586	Non-globular alpha+beta subunits of globular proteins
e.66	0.483	0.229	0.4926	Api92-like
e.70	0.4834	0.4229	0.3708	MalF N-terminal region-like
d.247	0.4875	0.646	0.7807	Chromosomal protein MC1
d.325	0.4906	0.547	0.5851	L28p-like
g.19	0.4926	0.4868	0.5925	Crisp domain-like
d.364	0.4933	0.2885	0.2579	PA1123-like
b.28	0.4961	0.3347	0.3618	Baculovirus p35 protein
d.390	0.4983	0.4763	0.4933	KS-to-AT linker domain from 6-deoxyerythronolide B synthase (DEBS)-like

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d.280	0.4998	0.3826	0.383	Sulfolobus fructose-1,6-bisphosphatase-like