

Fold ID	SPIRED	OmegaFold	ESMFold	Fold Name
f.50	0.3236	0.1724	0.2431	Connexin43
e.76	0.4554	0.1865	0.4715	Viral glycoprotein ectodomain-like
d.394	0.215	0.1945	0.2416	N-terminal domain of Prp8 / Spp42
b.127	0.4572	0.1964	0.4584	Baseplate structural protein gp8
e.42	0.1962	0.2166	0.2641	L-A virus major coat protein
g.61	0.3193	0.2186	0.2152	Apical membrane antigen 1
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
f.64	0.6526	0.226	0.2469	Filovirus surface glycoprotein-like
f.12	0.237	0.2262	0.2458	Head and neck region of the ectodomain of NDV fusion glycoprotein
f.60	0.7876	0.2264	0.6923	Anthrax protective antigen C-terminal-like
f.10	0.852	0.2287	0.7409	Viral glycoprotein, central and dimerisation domains
e.66	0.483	0.229	0.4926	Api92-like
a.300	0.2897	0.2314	0.25	Arenavirus nucleocapsid protein-like
a.176	0.251	0.2319	0.2476	N-terminal domain of bifunctional PutA protein
b.126	0.2117	0.235	0.2329	Adsorption protein p2
e.83	0.2442	0.2406	0.229	Coronavirus S1 beta-rich region
a.235	0.8614	0.2433	0.9241	ATP-dependent DNA ligase DNA-binding domain
e.82	0.2275	0.2467	0.2524	Influenza virus PB2 N-terminal region
e.68	0.8362	0.2524	0.9325	YacF-like
f.47	0.2346	0.253	0.2568	VP4 membrane interaction domain
e.48	0.2299	0.2574	0.2869	Major capsid protein VP5
e.80	0.2568	0.2586	0.3201	Protospace-adjacent motif (PAM)-interacting domain from Cas9/Csn1
a.119	0.8559	0.2586	0.9162	Lipoxigenase
e.81	0.8991	0.2589	0.9478	CRISPR associated protein CasA/Cse1-like
d.209	0.9109	0.2609	0.8654	LCCL domain
b.131	0.8737	0.2612	0.8307	SPOC domain-like
e.84	0.2516	0.2628	0.3668	N-terminal helical domains from Cas12a / Cpf1-like
b.75	0.6079	0.263	0.2912	Bacteriochlorophyll A protein
a.260	0.2419	0.2651	0.2578	Rhabdovirus nucleoprotein-like
g.94	0.2573	0.2662	0.2402	Complement C3 linker domain-like
a.206	0.284	0.2668	0.2755	P40 nucleoprotein

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a.198	0.9735	0.2671	0.9792	YcfC-like
d.260	0.9532	0.2677	0.9602	Suppressor of Fused, N-terminal domain
a.178	0.4004	0.2677	0.3216	Soluble domain of poliovirus core protein 3a
e.75	0.4766	0.2678	0.2714	Flu NP-like
d.382	0.8236	0.2701	0.8943	PSTPO5379-like
d.302	0.5158	0.2727	0.2629	Coronavirus NSP8-like
g.82	0.4347	0.2773	0.2794	Expressed protein At2g23090/F21P24.15
d.182	0.6751	0.2823	0.5639	Baseplate structural protein gp11
a.210	0.3619	0.2824	0.3352	Eukaryotic initiation factor 4f subunit eIF4g, eIF4e-binding domain
b.57	0.9163	0.2838	0.8067	Herpes virus serine proteinase, assemblin
d.339	0.2824	0.2839	0.2621	ORC1-binding domain
d.184	0.4826	0.2839	0.2586	Non-globular alpha+beta subunits of globular proteins
b.148	0.8165	0.2866	0.3677	Coronavirus RNA-binding domain
d.174	0.8063	0.2872	0.3212	Nitric oxide (NO) synthase oxygenase domain
d.401	0.3039	0.2876	0.2769	Cas3 C-terminal domain-like
d.364	0.4933	0.2885	0.2579	PA1123-like
e.41	0.2925	0.2893	0.3026	Adenylylcyclase toxin (the edema factor)
b.102	0.9328	0.2903	0.9608	Methuselah ectodomain
d.384	0.2608	0.2906	0.3179	SV5-V core-like
d.393	0.3806	0.2906	0.4983	Target recognition (REC) lobe from Cas9/Csn1
g.21	0.3889	0.2916	0.3112	Methylamine dehydrogenase, L chain
a.170	0.2798	0.2954	0.2745	BRCA2 helical domain
d.361	0.2704	0.2959	0.3264	PB2 C-terminal domain-like
b.164	0.3249	0.298	0.2457	SARS ORF9b-like
a.263	0.731	0.3	0.431	DNA terminal protein
g.88	0.3049	0.3013	0.3155	Intrinsically disordered proteins
g.86	0.5364	0.3028	0.282	Coronavirus NSP10-like
a.299	0.7929	0.3033	0.3665	Tenuivirus/Phlebovirus nucleocapsid protein-like
g.103	0.3087	0.3052	0.2866	Protein-only RNase P central domain-like
d.397	0.505	0.3072	0.2738	Influenza virus PB2 cap binding domain-like
e.27	0.9206	0.3072	0.8448	Upper collar protein gp10 (connector protein)
a.296	0.3961	0.3076	0.3538	PMT central region-like
b.147	0.4765	0.3085	0.339	BTB NS2-like ssRNA-binding domain
d.262	0.9291	0.3086	0.6832	NinB

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d.318	0.6756	0.3128	0.2699	SARS receptor-binding domain-like
e.2	0.312	0.3156	0.3131	Replication terminator protein (Tus)
d.275	0.7263	0.3159	0.3309	Hut operon positive regulatory protein HutP
b.116	0.2647	0.3168	0.3562	Viral chemokine binding protein m3
g.30	0.2891	0.3172	0.3375	Carboxypeptidase inhibitor
d.256	0.7017	0.3178	0.3394	Ta1353-like
b.134	0.9314	0.3186	0.9087	Smp-1-like
a.115	0.3004	0.3188	0.3139	A virus capsid protein alpha-helical domain
b.94	0.4256	0.3196	0.5608	Olfactory marker protein
f.45	0.3631	0.3199	0.3722	Mitochondrial ATP synthase coupling factor 6
b.91	0.7302	0.3212	0.3634	E2 regulatory, transactivation domain
c.147	0.8666	0.3234	0.9055	CAC2185-like
a.148	0.4304	0.3248	0.3294	Arp2/3 complex 21 kDa subunit ARPC3
g.69	0.6857	0.3254	0.3409	Plant proteinase inhibitors
e.69	0.6718	0.3256	0.5291	Poly(A) polymerase catalytic subunit-like
a.262	0.631	0.3256	0.3669	PriB N-terminal domain-like
b.133	0.3333	0.326	0.4788	Dextranase, N-terminal domain
a.84	0.858	0.3261	0.7004	Scaffolding protein gpD of bacteriophage procapsid
d.102	0.7671	0.3269	0.3318	Regulatory factor Nef
d.353	0.3207	0.3279	0.3407	AMPKBI-like
d.255	0.6773	0.33	0.3297	Tombusvirus P19 core protein, VP19
b.20	0.8591	0.3304	0.6998	ENV polyprotein, receptor-binding domain
a.233	0.7814	0.332	0.7334	YfbU-like
g.51	0.3438	0.3323	0.3571	Zn-binding domains of ADDBP
d.398	0.2556	0.3324	0.4375	NUC domain from Cas12a / Cpf1-like
a.49	0.3846	0.3345	0.3321	C-terminal domain of B transposition protein
b.28	0.4961	0.3347	0.3618	Baculovirus p35 protein
a.220	0.342	0.3363	0.2625	Hypothetical protein At3g22680
d.349	0.2472	0.3365	0.3692	CPE0013-like
d.294	0.5805	0.3372	0.7133	EndoU-like
e.34	0.777	0.3386	0.3705	NSP3 homodimer
a.168	0.7116	0.3399	0.3734	SopE-like GEF domain
d.381	0.9275	0.3401	0.8991	ATP12-like
b.65	0.6042	0.3414	0.6188	triple barrel
b.19	0.9203	0.3425	0.5595	Viral protein domain

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d.342	0.4776	0.3426	0.6247	PH1570-like
d.35	0.8736	0.344	0.3427	Heme-binding protein A (HasA)
b.110	0.3872	0.3474	0.3362	Cloacin translocation domain
b.27	0.5284	0.3492	0.2859	Soluble secreted chemokine inhibitor, VCCI
d.385	0.3939	0.3493	0.3508	DNA gyrase B, insert domain-like
a.89	0.3619	0.3524	0.3386	Methyl-coenzyme reductase alpha and beta chain C-terminal domain
c.102	0.7902	0.3551	0.8504	Cell-division inhibitor MinC, N-terminal domain
d.103	0.9464	0.3554	0.8252	CytB endotoxin-like
g.32	0.4464	0.3554	0.3341	GLA-domain
f.53	0.9017	0.3562	0.6856	ATP synthase D chain-like
f.7	0.7846	0.3581	0.8033	Lipovitellin-phosvitin complex; beta-sheet shell regions
b.181	0.3013	0.3585	0.3335	Handle domain of Transferrin binding protein TbpB-like
d.85	0.7567	0.3587	0.4188	RNA bacteriophage capsid protein
g.70	0.3152	0.3608	0.3086	Necrosis inducing protein 1, NIP1
a.15	0.5306	0.3611	0.2938	TAF(II)230 TBP-binding fragment
d.165	0.968	0.3625	0.9038	Ribosome inactivating proteins (RIP)
f.29	0.2989	0.3632	0.3129	Photosystem I subunits PsaA/PsaB
a.291	0.7133	0.3632	0.3234	MG296-like
a.85	0.3933	0.3635	0.3613	Hemocyanin, N-terminal domain
a.120	0.692	0.3644	0.2733	gene 59 helicase assembly protein
d.396	0.7525	0.3669	0.3578	Influenza virus PB2 '627' domain-like
d.362	0.4337	0.3669	0.4325	BLRF2-like
a.244	0.3088	0.3671	0.3332	EF2947-like
g.92	0.6501	0.3678	0.337	T-antigen specific domain-like
a.294	0.711	0.3682	0.6238	Tex N-terminal region-like
b.156	0.3603	0.3685	0.3867	Atu1913-like
a.41	0.4292	0.3694	0.4208	Domain of poly(ADP-ribose) polymerase
a.234	0.8762	0.374	0.6862	Hypothetical protein MPN330
d.216	0.3111	0.3751	0.3706	Rotavirus NSP2 fragment, N-terminal domain
d.372	0.2205	0.3752	0.2232	YqaI-like
a.195	0.4731	0.3757	0.3734	YutG-like
a.256	0.7019	0.3758	0.7872	RUN domain-like

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d.293	0.6831	0.3765	0.3453	Phosphoprotein M1, C-terminal domain
a.293	0.3674	0.3805	0.4117	SMc04008-like
d.196	0.2447	0.3818	0.2265	Outer capsid protein sigma 3
d.280	0.4998	0.3826	0.383	Sulfolobus fructose-1,6-bisphosphatase-like
d.254	0.5019	0.3829	0.3587	Nucleocapsid protein dimerization domain
a.72	0.5791	0.3832	0.8349	Functional domain of the splicing factor Prp18
b.120	0.2598	0.3841	0.4009	Tp47 lipoprotein, N-terminal domain
d.135	0.8971	0.3847	0.8985	The spindle assembly checkpoint protein mad2
a.226	0.9009	0.3883	0.4734	Her-1
d.299	0.8305	0.3894	0.3884	Ns1 effector domain-like
d.346	0.3845	0.3898	0.2878	SARS Nsp1-like
a.279	0.4805	0.3902	0.4143	Jann4075-like
b.31	0.3501	0.3919	0.3735	EV matrix protein
d.360	0.7949	0.3935	0.7353	PG1857-like
a.302	0.3704	0.3943	0.4809	Putative dsDNA-binding domain from Cas12a / Cpf1-like
a.94	0.3898	0.3956	0.4351	Ribosomal protein L19 (L19e)
d.180	0.6041	0.3964	0.3415	Conserved core of transcriptional regulatory protein vp16
d.324	0.8982	0.3973	0.8908	DUSP-like
d.368	0.6067	0.3989	0.3934	YonK-like
a.267	0.6032	0.3999	0.3741	Topoisomerase V catalytic domain-like
e.57	0.8953	0.3999	0.9609	Vacuolar ATP synthase subunit C
e.43	0.9472	0.4014	0.879	Subunits of heterodimeric actin filament capping protein Capz
d.62	0.9433	0.4022	0.8745	Pepsin inhibitor-3
a.222	0.9723	0.405	0.9843	VPS9 domain
d.213	0.6773	0.4088	0.3312	VSV matrix protein
d.236	0.6377	0.4092	0.3184	DNA-binding protein Tfx
b.21	0.7674	0.4099	0.4182	Virus attachment protein globular domain
g.63	0.6291	0.4119	0.3337	Mollusk pheromone
d.147	0.9565	0.4156	0.9768	Methenyltetrahydromethanopterin cyclohydrolase
d.337	0.2404	0.4159	0.3904	AF2331-like
d.238	0.3447	0.4168	0.4336	Hypothetical protein TM0875
a.249	0.3634	0.4176	0.7619	YfmB-like
a.254	0.7342	0.4177	0.7316	PA2201 C-terminal domain-like
d.288	0.867	0.4194	0.8725	GTF2I-like repeat

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a.109	0.5792	0.4222	0.3717	Class II MHC-associated invariant chain ectoplasmic trimerization domain
e.70	0.4834	0.4229	0.3708	MalF N-terminal region-like
g.66	0.4621	0.4232	0.5933	CCCH zinc finger
a.185	0.8652	0.4251	0.54	Gametocyte protein Pfg27
d.105	0.8892	0.4258	0.9382	Subdomain of clathrin and coatamer appendage domain
d.249	0.333	0.4261	0.4296	Hypothetical protein Ta1206
b.63	0.6913	0.4262	0.379	Oncogene products
d.403	0.4174	0.4276	0.4232	Lewis(b) antigen binding domain of BabA-like
a.219	0.9495	0.4279	0.866	Hypothetical protein YhaI
a.193	0.5453	0.4292	0.6024	GRIP domain
a.297	0.2835	0.4296	0.4298	DDB1 C-terminal-like
a.242	0.7421	0.4312	0.4179	Dcp2 domain-like
a.202	0.6643	0.432	0.5005	Superantigen MAM
e.46	0.7204	0.4333	0.5359	Virulence-associated V antigen
d.378	0.7237	0.4367	0.5021	Phosphoprotein oligomerization domain-like
b.182	0.8187	0.4374	0.868	U5 small nuclear riboprotein particle assembly factor Aar2 N-terminal domain-like
f.26	0.6561	0.4398	0.3064	Bacterial photosystem II reaction centre, L and M subunits
g.40	0.5405	0.4416	0.44	Retrovirus zinc finger-like domains
e.63	0.7065	0.4433	0.4259	E2F-DP heterodimerization region
a.241	0.5609	0.4433	0.4536	TraM-like
d.221	0.9496	0.4444	0.9886	Nuclease A inhibitor (NuiA)
d.321	0.7045	0.4446	0.4201	STIV B116-like
d.365	0.5525	0.445	0.3713	Ava3019-like
d.354	0.8776	0.4452	0.9571	Shew3726-like
d.329	0.8918	0.4465	0.9337	PF0523-like
e.47	0.8853	0.4472	0.3051	39 kda initiator binding protein, IBP39, C-terminal domains
d.197	0.3511	0.4495	0.4532	Protein-L-isoaspartyl O-methyltransferase, C-terminal domain
b.32	0.7934	0.451	0.4407	gp9
a.227	0.9175	0.4518	0.8736	ERO1-like
d.281	0.4777	0.4519	0.6269	Hemolytic lectin CEL-III, C-terminal domain
d.228	0.9128	0.4523	0.9667	Replication modulator SeqA, C-terminal DNA-binding domain
a.166	0.3053	0.4551	0.3623	RuBisCo LSMT C-terminal, substrate-binding domain
a.200	0.4681	0.457	0.4443	Hypothetical protein MTH393

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a.257	0.843	0.4571	0.428	SipA N-terminal domain-like
d.272	0.3825	0.4602	0.6421	Dystroglycan, domain 2
b.108	0.521	0.4611	0.6225	Triple-stranded beta-helix
b.174	0.3421	0.4649	0.4895	YopT-like
a.270	0.439	0.4649	0.5158	Hermes dimerisation domain
d.399	0.809	0.465	0.4471	Ebola nucleoprotein C-terminal domain-like
a.205	0.9168	0.4671	0.757	Hsp90 co-chaperone CDC37
d.214	0.5646	0.4676	0.411	Hypothetical protein MTH1880
a.53	0.6059	0.468	0.4106	p53 tetramerization domain
f.18	0.7919	0.4681	0.4689	F1F0 ATP synthase subunit A
b.162	0.6517	0.4727	0.4954	At5g01610-like
d.345	0.503	0.475	0.3945	NRDP1 C-terminal domain-like
b.90	0.9313	0.476	0.8754	Head-binding domain of phage P22 tailspike protein
d.390	0.4983	0.4763	0.4933	KS-to-AT linker domain from 6-deoxyerythronolide B synthase (DEBS)-like
c.154	0.907	0.4771	0.6615	CdCA1 repeat-like
g.34	0.6025	0.481	0.4129	HIV-1 VPU cytoplasmic domain
a.150	0.7103	0.4818	0.7377	Anti-sigma factor AsiA
a.237	0.5884	0.483	0.6208	DNA polymerase III theta subunit-like
a.54	0.3532	0.4841	0.3806	Domain of early E2A DNA-binding protein, ADDBP
d.200	0.4176	0.4841	0.4435	Integrin beta tail domain
a.151	0.4426	0.4864	0.4936	Glutamyl tRNA-reductase dimerization domain
g.19	0.4926	0.4868	0.5925	Crisp domain-like
a.212	0.444	0.4941	0.4656	KRAB domain (Kruppel-associated box)
a.153	0.4407	0.4959	0.3896	Nuclear receptor coactivator interlocking domain
a.190	0.5941	0.496	0.4811	Flavivirus capsid protein C