

Table 1. Human query proteins and select functional domains for sequence similarity evaluation across species. ^aType of Domain Hit defined by the NCBI CDD: Specific hits (S) meet or exceed a domain-specific e-value threshold and represent a very high confidence that the query sequence belongs to the same protein family as the sequences used to create the domain model; non-specific hits (N) meet or exceed the RPS-BLAST (reverse-position specific-Basic Local Alignment Search Tool) threshold for statistical significance (default E-value cutoff of 0.01). National Center for Biotechnology Information (NCBI); Conserved Domain Database (CDD); amino acid (aa).

Target Molecule	NCBI Protein Accession	NCBI CDD Accession	Domain Description (Summary)	^a Type of Hit	Domain Length (Residues)	% of Primary aa Sequence Covered by Selected Domains
Aryl hydrocarbon receptor	NP_001612.1	cd00083	Helix-loop-helix domain, found in DNA-binding proteins that act as transcription factors	S	42	5.0%
Caspase 8	NP_203519.1	cd00032 cd08333	Caspase, interleukin-1 beta converting enzyme Death effector domain, repeat 1, of Caspase-8	S S	253 82	69.9%
C-C motif chemokine 2	NP_002973.1	cd00272	Chemokine_CC: 1 of 4 subgroup designations of two N-terminal cysteine residues	S	58	58.6%
C-X-C motif chemokine 10	NP_001556.2	cd00273	Chemokine_CXC: 1 of 4 subgroup designations of two N-terminal cysteine residues	S	65	65.7%
C-X-C motif	NP_002407.1	cd00273	Chemokine_CXC:	S	63	50.4%

chemokine 9			1 of 4 subgroup designations of two N-terminal cysteine residues			
Ephrin type-A receptor 1	EAL23789.1	cd09542 cd05033 cd10479	SAM (sterile alpha motif) domain of EPH-A1 Catalytic domain Ligand Binding Domain of Ephrin type-A Receptor 1	S N S	63 266 177	51.8%
Ephrin type-A receptor 2	NP_004422.2	cd05063 cd09543 cd10480	Catalytic domain SAM (sterile alpha motif) domain of EPH-A2 Ligand Binding Domain of Ephrin type-A Receptor 2	S S S	269 70 174	52.6%
Ephrin type-B receptor 1	NP_004432.1	cd05065 cd09551 cd10476	Catalytic domain SAM (sterile alpha motif) domain of EPH-B1 Ligand Binding Domain of Ephrin type-B Receptor 1	S S S	269 68 176	52.1%
Estrogen receptor alpha	NP_000116.2	cd06949 cd07171	Ligand binding domain DNA-binding domain	S S	238 82	53.8%
Fibroblast growth factor receptor 1	NP_075598.2	cd05098	Catalytic domain	S	302	36.7%

Hypoxia-inducible	NP_001521.1	cd00083	Helix-loop-helix	S	54	15.5%
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factor 1 alpha		pfam08778	domain, found in	S	40	
		pfam11413	DNA- binding	S	34	
			proteins that act			
			as transcription			
			factors			
			HIF-1 alpha C			
			terminal			
			transactivation			
			domain			
			Hypoxia-inducible			
			factor-1			
Interleukin 1, alpha	NP_000566.3	cd00100	Interleukin-1	S	135	90.0%
		pfam02394	homologes	S	109	
			Interleukin-1			
			propeptide			
Interleukin 6	NP_000591.1	pfam00489	Interleukin-6/G-	S	154	42.6%
			CSF/MGF family			
Interleukin 8	NP_000575.1	cd00273	Chemokine_CXC:	S	64	64.6%
			1 of 4 subgroup			
			designations of			
			two N-terminal			
			cysteine residues			
Matrix metalloproteinase 2	NP_004521.1	cd04278	Zinc-dependent	S	318	48.2%
		cd00062	metalloprotease	S	48	
			Fibronectin Type II			
			domain			
Matrix metalloproteinase 9	AAM97934.1	cd04278	Zinc-dependent	S	330	46.7%
		cd00062	metalloprotease	S	48	
			Fibronectin Type II			
			domain			
Nuclear factor kappa-light- chain-enhancer of activated B cells	NP_068810.3	cd07885	N-terminal sub-	S	169	48.3%
		cd01177	domain of the Rel	S	97	
			homology domain			
			(RHD) of RelA			
			IPT domain of the			
			transcription factor			
			NFkappaB			

Plasminogen	NP_000593.1	cd02051	Plasminogen	N	378	94.0%
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activator inhibitor-1			activator inhibitor-1_like			
Protein tyrosine phosphatase, non-receptor type 11	NP_002825.3	cd00047 cd10340 cd09931	Catalyze the dephosphorylation of phosphotyrosine peptides N-terminal Src homology 2 (N-SH2) domain C-terminal Src homology 2 (C-SH2) domain	S S S	244 99 108	76.1%
Protein tyrosine phosphatase, non-receptor type 12	NP_002826.3	cd00047	Catalyze the dephosphorylation of phosphotyrosine peptides	S	233	29.9%
T-box A2	NP_005985.3	cd00182 pfam12598	T-box DNA binding domain T-box transcription factor	S S	186 78	37.1%
Transforming growth factor beta	P01137.2	pfam00019 pfam00688	Transforming growth factor beta like domain TGF-beta propeptide	S S	101 234	85.9%
Angiopoietin-1 receptor	NP_000450.2	cd05088	Catalytic domain	S	303	27.0%
Tumor necrosis factor alpha	NP_000585.2	cd00184	Tumor Necrosis Factor	S	144	61.8%
Urokinase-type plasminogen activator receptor	NP_002650.1	cd00117	Ly-6 antigen/uPA receptor -like domain	S	82	24.5%

Urokinase-type	NP_002649.1	cd00190	Trypsin-like serine	S	244	56.6%
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plasminogen
activator isoform
1

protease

Vascular cell adhesion molecule 1	NP_001069.1	cd07689	Second immunoglobulin (Ig)-like domain	S	99	13.4%
Vascular endothelial growth factor receptor 1	NP_002010.2	cd14207 cd07702 cd05742	Catalytic domain Second immunoglobulin (Ig)-like domain First immunoglobulin (Ig)-like domain	S S S	339 72 78	36.5%
Vascular endothelial growth factor receptor 2	NP_002244.1	cd05103 cd05862 cd05864	Catalytic domain Second immunoglobulin (Ig)-like domain First immunoglobulin (Ig)-like domain	S S S	342 88 70	36.9%
Vascular endothelial growth factor receptor 3	NP_891555.2	cd05102 cd05862 cd05863	Catalytic domain Second immunoglobulin (Ig)-like domain First immunoglobulin (Ig)-like domain	S S S	340 85 67	36.1%
