Electronic Supplementary Material (ESI) for Metallomics
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Supporting Materials

Calciomics: integrative studies of Ca^{2+}-binding proteins and their interactomes in biological systems

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Supplementary Table 1. Summary of predicted EF-hand-containing proteins in prokaryotes.

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF01799660	Bifunctional protein	165-193	1	*Acinetobacter sp. ADP3*
NF01800980	Hypothetical protein	134-162	1	*Acinetobacter sp. ADP4*
NF00596974	AGR_C_660p	166-194	1	*Agrobacterium tumefaciens*
NF00854152	Hypothetical protein Atu0377	147-175	1	*Agrobacterium tumefaciens*
NF00853975	Potassium-transporting ATPase B chain	555-583	1	*Agrobacterium tumefaciens*
NF00854754	Two component response regulator	273-301	1	*Agrobacterium tumefaciens*
NF00601861	AGR_C_1956p	288-316	1	*Agrobacterium tumefaciens*
NF02630316	Haloacid dehalogenase-like hydrolase:E1-E2 ATPase-associated region	556-584	1	*Anaeromyxobacter dehalogenans*
NF02630616	DNA gyrase, subunit A precursor	501-529	1	*Anaeromyxobacter dehalogenans*
NF02632976	Twin-arginine translocation pathway signal precursor	227-255	1	*Anaeromyxobacter dehalogenans*
NF02633157	TPR repeat precursor	343-371	1	*Anaeromyxobacter dehalogenans*
NF02633311	Aminotransferase, putative	153-181	1	*Anaeromyxobacter dehalogenans*
NF02145020	Prolyl-tRNA synthetase	220-248	1	*Anaplasma marginale*
NF00005240	Na^+:solute symporter	266-294	1	*Aquifex aeolicus*
NF02418698	Initiation factor 2:Small GTP-binding protein domain	712-740	1	*Arthrobacter sp. FB24*
NF02419170	Regulatory protein, LysR:LysR, substrate-binding	188-216	1	*Arthrobacter sp. FB24*
NF02420554	Amino acid-binding ACT:Prephenate dehydrogenase	325-353	1	*Arthrobacter sp. FB24*
NF02183774	Hypothetical protein	129-157	1	*Azoarcus sp. EbN2*
NF02110613	AcrA/AcrE family putative membrane-fusion protein	57-85	1	*Azoarcus sp. EbN3*
NF02111329	Isoleucyl-tRNA synthetase	608-636	1	*Azoarcus sp. EbN4*
NF02599343	Hypothetical protein	333-361	1	*Azotobacter vinelandii*
NF02601050	Glycine cleavage system P-protein	678-706	1	*Azotobacter vinelandii*
NF01002531	Polysaccharide deacetylase-like protein	229-257	1	*Bacillus anthracis*
NF01003358	Multidrug resistance protein, putative	174-202	1	*Bacillus anthracis*
NF01293886	Acetyltransferase, GNAT family	61-89	1	*Bacillus anthracis*
NF00452066	hypothetical protein pxo2_15	123-151	1	*Bacillus anthracis*
NF01293170	Oxidoreductase, short-chain dehydrogenase/reductase family	195-223	1	*Bacillus anthracis*
NF01968462	Probable multidrug efflux transporter	174-202	1	*Bacillus cereus*
NF01692216	Isoleucyl-tRNA synthetase	583-611	1	*Bacillus cereus*
NF02763311	Polysaccharide deacetylase family protein, putative	229-257	1	*Bacillus cereus*
NF01693845	Acetyltransferase, GNAT family	61-89	1	*Bacillus cereus*
NF01694384	IS231-related transposase	241-269	1	*Bacillus cereus*
NF01269023	3-oxoacyl-[acyl-carrier protein] reductase	195-223	1	*Bacillus cereus*
NF02058262	3-oxoacyl-[acyl-carrier-protein] reductase	191-219	1	*Bacillus clausii*
NF00639248	Ribonuclease G (Cytosolic axial filament protein)	291-319	1	*Bacillus halodurans*
NF01942957	Hypothetical protein (D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain)	227-255	1	*Bacillus licheniformis*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF01943135	Putative L-2,4-diaminobutyrate decarboxylase	216-244	1	*Bacillus licheniformis*
NF00459033	Hypothetical oxidoreductase yoxD	191-219	1	*Bacillus subtilis*
NF01847653	Probable multidrug efflux transporter	174-202		*Bacillus thuringiensis*
NF01850556	Acetyltransferase, GNAT family	61-89	1	*Bacillus thuringiensis*
NF02232249	Hypothetical protein	740-768	1	*Bacillus thuringiensis*
NF01852124	Short chain dehydrogenase	195-223	1	*Bacillus thuringiensis*
NF01982311	Hypothetical protein	9-37	1	*Bacteroides fragilis*
NF02360737	Putative glycosyl hydrolase	1087-1115 1123-1151	2	*Bacteroides fragilis*
NF01983199	K^+-transporting ATPase B chain	545-573	1	*Bacteroides fragilis*
NF01984037	Putative outer membrane protein	889-917	1	*Bacteroides fragilis*
NF02360881	Putative AraC-family transcriptional regulator	67-95	1	*Bacteroides fragilis*
NF01247854	Putative outer membrane protein	856-884	1	*Bacteroides thetaiotaomicron*
NF01244792	Alpha-xylosidase	1093-1121 1129-1157	2	*Bacteroides thetaiotaomicron*
NF01247957	Hypothetical protein	57-85	1	*Bacteroides thetaiotaomicron*
NF01243332	K^+-transporting ATPase B chain	540-568	1	*Bacteroides thetaiotaomicron*
NF01632112	Ribonuclease G	309-337	1	*Bdellovibrio bacteriovorus*
NF01633060	Probable GTP-binding protein	120-148	1	*Bdellovibrio bacteriovorus*
NF01125245	BglX	745-773	1	*Bifidobacterium longum*
NF01125387	5'-nucleotidase family protein	412-440	1	*Bifidobacterium longum*
NF01125928	Solute binding protein of ABC transporter for branched-chain amino acids	360-388	1	*Bifidobacterium longum*
NF01356204	Putative outer membrane protein	133-161	1	*Bordetella bronchiseptica*
NF01357346	Putative exported protein	53-81	1	*Bordetella bronchiseptica*
NF01358260	Putative exported protein	193-221	1	*Bordetella bronchiseptica*
NF01360429	Potassium-transporting ATPase B chain	582-610	1	*Bordetella bronchiseptica*
NF01857138	Decorin binding protein B	94-122	1	*Borrelia garinii*
NF01347842	Potassium-transporting ATPase B chain	582-610	1	*Bordetella parapertussis*
NF01348670	Putative exported protein	53-81	1	*Bordetella parapertussis*
NF01349793	Putative exported protein	193-221	1	*Bordetella parapertussis*
NF01351614	Potassium-transporting ATPase B chain	582-610	1	*Bordetella pertussis*
NF01354467	Putative exported protein	198-226	1	*Bordetella pertussis*
NF01143994	Bll5001 protein	92-120	1	*Bradyrhizobium japonicum*
NF01144916	Bll3714 protein	4088-4116	1	*Bradyrhizobium japonicum*
NF01146006	Bll6206 protein	28-56 77-105	2	*Bradyrhizobium japonicum*
NF01145264	Bsr4957 protein	28-56	1	*Bradyrhizobium japonicum*
NF01138884	Potassium-transporting ATPase B chain	567-595	1	*Bradyrhizobium japonicum*
NF01145262	Bll5679 protein	105-133 139-167	2	*Bradyrhizobium japonicum*
NF02362000	Hypothetical protein	187-215	1	*Brucella melitensis*
NF02362472	Chaperone protein DnaK	173-201	1	*Brucella melitensis*
NF00882038	Cobalt-zinc-cadmium resistance protein CZCD	213-241	1	*Brucella melitensis*
NF00882425	Transporter	172-200	1	*Brucella melitensis*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF00729490	Acid-shock protein, putative	63-91 120-148	2	*Brucella melitensis*
NF01092664	Hypothetical protein	191-219	1	*Brucella melitensis*
NF01013862	Exodeoxyribonuclease V beta chain	542-570	1	*Buchnera aphidicola*
NF00001599	Cell division protein ftsY homolog	20-48	1	*Buchnera aphidicola*
NF02558178	Haloacid dehalogenase-like hydrolase:E1-E2 ATPase-associated region	555-583	1	*Burkholderia cenocepacia*
NF02562763	Pyridoxal-dependent decarboxylase	150-178	1	*Burkholderia cenocepacia*
NF01994075	Hypothetical protein	100-128	1	*Burkholderia mallei*
NF01995267	AMP nucleosidase	136-164	1	*Burkholderia mallei*
NF01997459	K$^+$-transporting ATPase, B subunit	556-584	1	*Burkholderia mallei*
NF01974439	Putative exported protein	110-138	1	*Burkholderia pseudomallei*
NF01975408	Potassium-transporting ATPase b chain	547-575	1	*Burkholderia pseudomallei*
NF01976188	AMP nucleosidase	136-164	1	*Burkholderia pseudomallei*
NF02692726	Iron-sulfur cluster binding protein	285-313	1	*Campylobacter coli*
NF02628440	Cj81-040 (Fragment)	130-158	1	*Campylobacter jejuni*
NF02271643	Dihydroorotase, putative	157-185	1	*Campylobacter jejuni*
NF00555721	Potassium-transporting ATPase B chain	539-567	1	*Campylobacter jejuni*
NF00556942	Hemin ABC transporter	101-129	1	*Campylobacter jejuni*
NF02581023	Uncharacterized ACR, COG1427	169-197	1	*Campylobacter lari*
NF02581415	Iron-sulfur cluster binding protein	282-310	1	*Campylobacter lari*
NF02513884	Hypothetical protein	155-183	1	*Campylobacter upsaliensis*
NF02514058	Hypothetical protein	48-76	1	*Campylobacter upsaliensis*
NP_419996	hypothetical protein CC1180	96-124 120-148 197-225 221-249	4	*Caulobacter crescentus*
NP_420996	hypothetical protein CC2193	36-64 77-105 191-219	3	*Caulobacter crescentus*
NP_421029	EF hand domain protein	33-61 59-87	2	*Caulobacter crescentus*
NP_421548	EF hand domain protein	294-322 319-337	2	*Caulobacter crescentus*
NF00922900	Potassium-transporting ATPase B chain	547-575	1	*Caulobacter vibrioides*
NF00923077	Hypothetical protein CC1180	96-124	1	*Caulobacter vibrioides*
NF00921487	Hypothetical protein CC2193	319-347	1	*Caulobacter vibrioides*
NF00921074	TonB-dependent receptor	282-310	1	*Caulobacter vibrioides*
NF00920950	EF hand domain protein	33-61	1	*Caulobacter vibrioides*
NF00919601	EF hand domain protein	36-64	1	*Caulobacter vibrioides*
NF00920207	dnaK-type molecular chaperone dnaK	173-201	1	*Caulobacter vibrioides*
NF00170276	Hypothetical protein CPn0045	460-488	1	*Chlamydophila pneumoniae*
NF01414521	Potassium-transporting ATPase B chain	566-594	1	*Chromobacterium violaceum*
NF01415832	Flagellar hook-associated protein	130-158	1	*Chromobacterium violaceum*
NF01417084	Acid phosphatase	38-66	1	*Chromobacterium violaceum*
NF00462703	DnaK protein	184-212	1	*Clostridium acetobutylicum*
NF00464732	General secretion pathway protein E, ATPase	4-32	1	*Clostridium acetobutylicum*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF00463611	Membrane flavodoxin oxidoreductase	367-395	1	*Clostridium acetobutylicum*
NF00464531	dockerin domain	394-422	1	*Clostridium acetobutylicum*
NF00462598	Possible non-processive endoglucanase family 5, secreted; CelA homolog secreted; dockerin domain	418-446 450-478	2	*Clostridium acetobutylicum*
NF00464704	Probably secreted sialidase; several ASP-boxes and dockerin domain	768-796 800-828	2	*Clostridium acetobutylicum*
NF00461910	Cellulase CelE ortholog; dockerin domain	805-833 837-865	2	*Clostridium acetobutylicum*
NF00464704	dockerin and cellulose-binding domain	647-675 679-707	2	*Clostridium acetobutylicum*
NF00465242	dockerin and cellulose-binding domain	628-656 660-688	2	*Clostridium acetobutylicum*
NF00464378	dockerin domain	662-690 696-724	2	*Clostridium acetobutylicum*
NF00872981	Probable thioredoxin reductase	367-395	1	*Clostridium perfringens*
NF01191711	Encapsulation protein capA	25-53	1	*Clostridium tetani*
NF01192507	Putative cardiolipin synthetase 2	436-464	1	*Clostridium tetani*
NF01190826	RNA polymerase sigma factor for flagellar operon fliA	156-184	1	*Clostridium tetani*
NF01191088	Putative S-layer protein	438-466	1	*Clostridium tetani*
NF02636675	transcriptional regulator, LysR family	143-171	1	*Colwellia psychrerythraea*
NF02635517	hypothetical protein CPS_0266	258-286	1	*Colwellia psychrerythraea*
NF02635672	DNA polymerase III, gamma/tau subunit	72-100	1	*Colwellia psychrerythraea*
NF02637464	EF hand domain protein	22-50	1	*Colwellia psychrerythraea*
NF02637914	EF hand domain protein	6-34 42-70	2	*Colwellia psychrerythraea*
NF02638565	hypothetical protein CPS_4268	89-117	1	*Colwellia psychrerythraea*
NF02638842	patatin-like phospholipase family protein	435-463	1	*Colwellia psychrerythraea*
NF01120262	TnpC protein	21-49	1	*Corynebacterium efficiens*
NF00925376	Conserved hypothetical secreted protein	163-191	1	*Corynebacterium glutamicum*
NF02423383	Putative surface-anchored protein	537-565	1	*Corynebacterium jeikeium*
NF02421939	Hypothetical protein	136-164 304-332	2	*Corynebacterium jeikeium*
NF02421622	ATP-dependent DNA helicase	287-315	1	*Corynebacterium jeikeium*
NF02421112	Thiol-disulfide isomerase/thioredoxin precursor	59-87	1	*Corynebacterium jeikeium*
NF02492865	Calcium-binding EF-hand	70-98 136-164	2	*Cupriavidus necator*
NF02493293	ATP-binding region, ATPase-like:Histidine kinase A, N-terminal	426-454	1	*Cupriavidus necator*
NF02493847	Fungal/archaeal/bacterial haem catalase/peroxidase	518-546	1	*Cupriavidus necator*
NF02495396	Outer membrane autotransporter barrel	496-524	1	*Cupriavidus necator*
NF02497227	Histidine kinase, HAMP region:Bacterial chemotaxis sensory transducer	349-377	1	*Cupriavidus necator*
NF02497778	ATPase, E1-E2 type:Potassium-translocating P-type ATPase, B subunit	600-628	1	*Cupriavidus necator*
NF02274727	hypothetical protein DET1403	195-223	1	*Dehalococcoides ethenogenes*
NF02696634	Calcium-binding EF-hand	46-74	1	*Dechloromonas aromatica*
NF02697139	Glycine cleavage system P-protein	613-641	1	*Dechloromonas aromatica*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF02274727	hypothetical protein DET1403	195-223	1	*Dehalococcoides ethenogenes*
NF02650500	Similar to High-affinity K^+ transport system ATPase chain B precursor	26-54	1	*Deinococcus geothermalis*
NF02648532	Hypothetical protein precursor	120-148	1	*Deinococcus geothermalis*
NF00437343	Ribonuclease II family protein	88-116	1	*Deinococcus radiodurans*
NF00435709	Hypothetical protein DR0685	179-207	1	*Deinococcus radiodurans*
NF00438084	Hypothetical protein DR1404	14-42	1	*Deinococcus radiodurans*
NF00435967	Hypothetical protein DR2551	191-219	1	*Deinococcus radiodurans*
NF01898379	Hypothetical protein	161-189	1	*Desulfotalea psychrophila*
NF01900066	Hypothetical protein	277-305 384-412 491-519	3	*Desulfotalea psychrophila*
NF01899559	Probable high affinity sulfate transporter (SulP)	560-588	1	*Desulfotalea psychrophila*
NF01722462	K^+-transporting ATPase, B subunit	539-567	1	*Desulfovibrio vulgaris*
NF01723330	EF hand domain protein	19-47	1	*Desulfovibrio vulgaris*
NF01724660	EF hand domain protein	51-79 152-180	2	*Desulfovibrio vulgaris*
NF01239980	Glycosyl hydrolase, family 31/fibronectin type III domain protein	1162-1190	1	*Enterococcus faecalis*
NF02746267	DnaK molecular chaperone	173-201	1	*Erythrobacter litoralis*
NF02746140	Hypothetical protein	97-125	1	*Erythrobacter litoralis*
NF02746586	Hypothetical protein	93-121	1	*Erythrobacter litoralis*
NF00704786	Hypothetical protein ECs5257	4-32	1	*Escherichia coli*
NF00695695	N-acetylmuramoyl-L-alanine amidase amiB precursor	379-407	1	*Escherichia coli*
NF01134307	Rhamnulokinase	324-352	1	*Escherichia coli*
NF01744738	Putative glycosyltransferase	174-202	1	*Escherichia coli*
NF00692267	Resolvase family recombinase	6-34	1	*Escherichia coli*
NF01491630	Zn-dependent hydrolase	462-490	1	*Fusobacterium nucleatum*
NF01492715	Protease	388-416	1	*Fusobacterium nucleatum*
NF02148420	Hypothetical conserved protein	73-101	1	*Geobacillus kaustophilus*
NF01553463	EF hand domain protein	22-50 59-87	2	*Geobacter sulfurreducens*
NF01551775	EF hand domain/PKD domain protein	1723-1751	1	*Geobacter sulfurreducens*
NF01553119	Salmonella virulence plasmid 65kDa B protein	1363-1391	1	*Geobacter sulfurreducens*
NF01553013	Potassium-transporting ATPase	552-580	1	*Geobacter sulfurreducens*
NF01419166	Gll3319 protein	106-134	1	*Gloeobacter violaceus*
NF01422150	Glr3888 protein	757-785	1	*Gloeobacter violaceus*
NF01420350	Transaldolase	357-385	1	*Gloeobacter violaceus*
NF02258009	Cation efflux system protein	211-239	1	*Gluconobacter oxydans*
NF01345996	Cell division protein FtsZ	259-287	1	*Haemophilus ducreyi*
NF01345965	Hypothetical protein	60-88	1	*Haemophilus ducreyi*
NF01744248	Adhesin	286-314	1	*Haemophilus influenzae*
NF00736924	Hypothetical protein HI1594	179-207	1	*Haemophilus influenzae*
NF02647744	Exodeoxyribonuclease V gamma chain	469-497	1	*Haemophilus influenzae*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF02647997	DNA translocase FtsK	290-318	1	*Haemophilus influenzae*
NF01331967	Bacterial cell division topological specificity factor MinE	51-79	1	*Helicobacter hepaticus*
NF01331990	Aconitate hydratase	404-432	1	*Helicobacter hepaticus*
NF00574925	Ulcer associated adenine specific DNA methyltransferase	290-318	1	*Helicobacter pylori*
NF00572083	Hypothetical protein alpB	248-276	1	*Helicobacter pylori*
NF02103893	DNA-directed RNA polymerase beta subunit	405-433	1	*Idiomarina loihiensis*
NF02104158	RND family efflux system membrane fusion protein	62-90	1	*Idiomarina loihiensis*
NF02105366	GntP family permease	335-363	1	*Idiomarina loihiensis*
NF02106157	Outer membrane protein	535-563	1	*Idiomarina loihiensis*
NF01526365	TnpR recombinase	29-57	1	*Klebsiella pneumoniae*
NF02267084	Iron-sulfur cofactor synthesis protein	113-141	1	*Lactobacillus acidophilus*
NF02266040	Alpha-glucosidase	953-981	1	*Lactobacillus acidophilus*
NF01324779	Cysteine sulfinate desulfinase/cysteine desulfurase	114-142	1	*Lactobacillus johnsonii*
NF01585065	Hypothetical protein	330-358	1	*Lactobacillus johnsonii*
NF01210549	Cation transporting P-type ATPase	9339-367	1	*Lactobacillus plantarum*
NF01211534	Phosphoglucosamine mutase	234-262	1	*Lactobacillus plantarum*
NF00449250	Maltose ABC transporter substrate binding protein	111-139	1	*Lactococcus lactis*
NF02043787	RNA polymerase beta' subunit	1365-1393	1	*Legionella pneumophila*
NF00628534	O-methyltransferase, SAM-dependent	132-160	1	*Legionella pneumophila*
NF02048951	DNA-directed RNA polymerase beta' subunit	1379-1407	1	*Legionella pneumophila*
NF01698417	Hypothetical protein	12-40	1	*Leptospira interrogans*
NF01085961	Potassium-transporting ATPase B chain	548-576	1	*Leptospira interrogans*
NF00554020	Preprotein translocase SecY	41-69	1	*Leptospira interrogans*
NF00844705	Potassium-transporting ATPase B chain 2	543-571	1	*Listeria innocua*
NF00813533	Lin0875 protein	48-76	1	*Listeria innocua*
NF00813673	Lin2223 protein	232-260	1	*Listeria innocua*
NF01748822	GGDEF domain protein	152-180	1	*Listeria monocytogenes*
NF01746930	Transketolase	338-366	1	*Listeria monocytogenes*
NF00812586	Lmo1869 protein	228-256	1	*Listeria monocytogenes*
NF00604651	Mlr9645 protein	129-157 152-180	2	*Mesorhizobium loti*
NF00606972	Mll5457 protein	69-97 102-130	2	*Mesorhizobium loti*
NF00610956	Potassium-transporting ATPase B chain	551-579	1	*Mesorhizobium loti*
NF02036858	DNA gyrase, A subunit	518-546	1	*Methylococcus capsulatus*
NF02038758	Hypothetical protein	209-237	1	*Methylococcus capsulatus*
NF01628109	GyrA	496-524	1	*Mycobacterium avium*
NF01628325	Hypothetical protein	76-104	1	*Mycobacterium avium*
NF01324088	Potassium-transporting ATPase B chain	570-598	1	*Mycobacterium bovis*
NF01321371	DNA gyrase subunit A	495-523	1	*Mycobacterium bovis*
NF00480640	probable DNA gyrase subunit A	916-944	1	*Mycobacterium leprae*
NF00484231	P450 heme-thiolate protein	335-363	1	*Mycobacterium tuberculosis*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF00485681	Potassium-transporting ATPase B chain	570-598	1	*Mycobacterium tuberculosis*
NF01586715	Mannitol-permease IIBC component	43-71	1	*Mycoplasma mycoides*
NF01587410	Hypothetical protein	9-37	1	*Mycoplasma mycoides*
NF00630859	Putative type II restriction endonuclease NlaIV	119-147	1	*Neisseria gonorrhoeae*
NF01296409	DEAD/DEAH box helicase:HD domain	624-652	1	*Nitrosomonas europaea*
NF01294890	Hypothetical protein	6-34	1	*Nitrosomonas europaea*
NF01296468	Site-specific recombinase	215-243	1	*Nitrosomonas europaea*
NF02020754	Putative potassium transporter B subunit	544-572	1	*Nocardia farcinica*
NF02023298	Hypothetical protein	23-51	1	*Nocardia farcinica*
NF02024201	Putative resolvase	3-31	1	*Nocardia farcinica*
NF00818483	All5017 protein	190-218	1	*Nostoc sp. PCC 7120*
NF00819095	Alr7304 protein	3336-3364	1	*Nostoc sp. PCC 7120*
NF00817274	RND multidrug efflux transporter	87-115	1	*Nostoc sp. PCC 7120*
NF00817119	Asr1131 protein	45-73	1	*Nostoc sp. PCC 7120*
NF01061743	NADH-dependent flavin oxidoreductase	52-80	1	*Oceanobacillus iheyensis*
NF01776242	Putative pyridoxal-dependent decarboxylase	150-178	1	*Pectobacterium atrosepticum*
NF01829006	Hypothetical methylamine utilization protein	5-33	1	*Photobacterium profundum*
NF01830545	Phosphoglycerate transport system transcription regulator	250-278	1	*Photobacterium profundum*
NF01831581	Hypothetical protein	500-528	1	*Photobacterium profundum*
NF01833037	Hypothetical small protein A	21-49	1	*Photobacterium profundum*
NF01831267	Hypothetical protein	278-306	1	*Photobacterium profundum*
NF01423716	Similar to proteins involved in antibiotics biosynthesis	1476-1504	1	*Photorhabdus luminescens*
NF01426461	Hypothetical protein	106-134	1	*Photorhabdus luminescens*
NF01427112	LsrR DNA-binding protein	13-41	1	*Photorhabdus luminescens*
NF01410240	Secretion activator protein, putative	35-63	1	*Porphyromonas gingivalis*
NF02499786	carboxysome shell protein CsoS2	102-130	1	*Prochlorococcus marinus*
NF02499308	ornithine carbamoyltransferase	16-44	1	*Prochlorococcus marinus*
NF01372938	Hypothetical protein precursor	38-66	1	*Prochlorococcus marinus*
NF02498817	hypothetical protein PMN2A_0622	557-585	1	*Prochlorococcus marinus*
NF01854896	Cobalamin biosynthesis protein CobN	130-158	1	*Propionibacterium acnes*
NF01010095	Similar to Histidine biosynthesis protein	165-193	1	*Pseudomonas aeruginosa*
NF00582290	Chaperone protein htpG	404-432	1	*Pseudomonas aeruginosa*
NF00579604	TnpR protein (Fragment)	6-34	1	*Pseudomonas aeruginosa*
NF00585284	Hypothetical protein	79-107	1	*Pseudomonas aeruginosa*
NF00580099	Heat shock protein 66-kDa	187-215	1	*Pseudomonas aeruginosa*
NF00584502	Hypothetical protein	203-231	1	*Pseudomonas aeruginosa*
NF02412314	Calcium-binding protein	24-52 60-88 98-126	3	*Pseudomonas fluorescens*
NF02409575	K^+-transporting ATPase, B subunit	551-579	1	*Pseudomonas fluorescens*
NF01130810	Chaperone protein hscA homolog	187-215	1	*Pseudomonas putida*
NF00593298	Resolvase	6-34	1	*Pseudomonas putida*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF01131075	Hypothetical protein	39-67	1	*Pseudomonas putida*
NF01128446	Glycine dehydrogenase	613-641	1	*Pseudomonas putida*
NF01131319	EF hand domain protein	143-171	1	*Pseudomonas putida*
NF02715683	calcium-binding protein	101-159 134-162 180-208	3	*Pseudomonas savastanoi*
NF02713698	heat shock protein HtpG	405-433	1	*Pseudomonas savastanoi*
NF02713796	hypothetical protein PSPPH_1452	119-147	1	*Pseudomonas savastanoi*
NF02715540	type IV pilus-associated protein, putative	990-1018	1	*Pseudomonas savastanoi*
NF02713796	hypothetical protein PSPPH_1452	119-147	1	*Pseudomonas savastanoi*
NF02518859	Calcium-binding EF-hand precursor	63-91 100-128 133-161 179-207	4	*Pseudomonas syringae*
NF02518864	Heat shock protein Hsp90:ATP-binding region, ATPase-like	407-435	1	*Pseudomonas syringae*
NF02517892	Type IV pilus-associated protein, putative precursor	989-1017	1	*Pseudomonas syringae*
NF01447618	Chaperone protein htpG	405-433	1	*Pseudomonas syringae group genomosp. 3*
NF01447738	Type IV pilus-associated protein, putative	989-1017	1	*Pseudomonas syringae group genomosp. 3*
NF01447731	Hypothetical protein	143-171	1	*Pseudomonas syringae group genomosp. 3*
NF01444486	EF hand domain protein	4-32 316-344 391-419	3	*Pseudomonas syringae group genomosp. 3*
NF02500531	Calcium-binding EF-hand precursor	63-91 100-128 135-161 179-207	4	*Pseudomonas syringae*
NF01410240	Secretion activator protein, putative	35-63	1	*Porphyromonas gingivalis*
NF00853288	Potassium-transporting ATPase B chain	605-633	1	*Ralstonia solanacearum*
NF00849451	Hypothetical protein RSc1742	295-323	1	*Ralstonia solanacearum*
NF00850536	Putative calcium binding signal peptide protein	74-102, 113-141	2	*Ralstonia solanacearum*
AAG21376	Calsymin	79-107 122-150 157-185 189-217 236-264 269-297	6	*Rhizobium etli*
NF01530872	Calcium-binding EF-hand precursor	94-122 128-156	2	*Rhodopseudomonas palustris*
NF01643065	Similar to CaM-like protein-putative secreted, membrane associated or paryphoplasmic Ca(2+)-binding protein	50-78	1	*Rhodopirellula baltica*
NF01643299	Hypothetical protein	257-285	1	*Rhodopirellula baltica*
NF01649307	Hypothetical protein	103-131	1	*Rhodopirellula baltica*
NF01643065	putative secreted, membrane associated or paryphoplasmic Ca^{2+}-binding protein	50-78	1	*Rhodopirellula baltica*
NF01644848	Hypothetical protein	214-242 340-368 417-445	3	*Rhodopirellula baltica*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF01647263	Matrix metalloproteinase	516-544	1	*Rhodopirellula baltica*
NF01647900	Probable lipase/esterase	76-104	1	*Rhodopirellula baltica*
NF01643609	Alkaline phosphatase	1576-1604	1	*Rhodopirellula baltica*
NF01649041	Putative ABC transporter integral membrane protein	42-70	1	*Rhodopirellula baltica*
NF01644544	Probable calmodulin	347-375	1	*Rhodopirellula baltica*
NF01644969	Hypothetical protein	71-99	1	*Rhodopirellula baltica*
NF01528433	Hypothetical protein precursor	64-92	1	*Rhodopseudomonas palustris*
:NF01529160	Potassium-transporting atpase b chain, KdpB	570-598	1	*Rhodopseudomonas palustris*
NF01530032	Hypothetical protein precursor	26-54	1	*Rhodopseudomonas palustris*
NF01530456	Hypothetical protein	245-273	1	*Rhodopseudomonas palustris*
NF01530872	Calcium-binding EF-hand precursor	94-122 128-156	2	*Rhodopseudomonas palustris*
NF01531759	Glycosyl hydrolase	64-92	1	*Rhodopseudomonas palustris*
NF01532507	DUF218	94-122	1	*Rhodopseudomonas palustris*
NF02577387	DnaK protein	172-200	1	*Rickettsia felis*
P06495	Calerythrin	9-37 60-88 104-132 138-164	4	*Saccharopolyspora erythrea*
NF00806470	probable glycogen debranching protein	35-63	1	*Salmonella enterica*
NF02097096	Putative glycogen debranching protein homolog	35-63	1	*Salmonella paratyphi*
NF01911344	Putative glycogen debranching protein	35-63	1	*Salmonella typhi*
NF00861463	Putative glycosyl hydrolase	35-63	1	*Salmonella typhimurium*
NF01074234	Pyruvate formate-lyase 1 activating enzyme	35-63	1	*Shewanella oneidensis*
NF01074109	RTX toxin, putative	461-489	1	*Shewanella oneidensis*
NF02205755	EF hand domain protein	30-58	1	*Silicibacter pomeroyi*
NF02206123	Type I secretion target repeat protein	7295-7323	1	*Silicibacter pomeroyi*
NF00616675	Potassium-transporting ATPase B chain	541-569	1	*Sinorhizobium meliloti*
NF00612473	Hypothetical protein SMc01708	784-812	1	*Sinorhizobium meliloti*
NF00617441	Hypothetical protein SMb21413	137-165	1	*Sinorhizobium meliloti*
NF00431107	Transposase B	519-547	1	*Staphylococcus aureus*
NF02262335	LysM domain protein	235-263	1	*Staphylococcus aureus*
NF01789691	Putative dihydrolipoamide dehydrogenase	153-181	1	*Staphylococcus aureus*
NF00433953	Similar to Zn-dependent hydrolase	465-493	1	*Staphylococcus aureus*
NF01166407	Secretory antigen SsaA	108-136	1	*Staphylococcus epidermidis*
NF00434602	HMG-CoA reductase	297-325	1	*Staphylococcus epidermidis*
NF02269390	Tn554, transposase B	519-547	1	*Staphylococcus epidermidis*
NF01165622	Hydroxymethylglutaryl-CoA reductase	297-325	1	*Staphylococcus epidermidis*
NF01167423	Hypothetical protein SE0148	85-113	1	*Staphylococcus epidermidis*
NF01165840	Hypothetical protein SE0787	465-493	1	*Staphylococcus epidermidis*
NF02607639	Capsular polysaccharide synthesis enzyme CapE	299-327	1	*Staphylococcus haemolyticus*
NF02608469	Homoserine dehydrogenase	393-421	1	*Staphylococcus haemolyticus*
NF02663555	Similar to unknown protein	465-493	1	*Staphylococcus haemolyticus*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF01048375	Proteinase, putative	626-654	1	*Streptococcus agalactiae*
NF01049107	Hypothetical protein gbs1919	194-222	1	*Streptococcus agalactiae*
NF01049640	Hypothetical protein gbs1489	371-399	1	*Streptococcus agalactiae*
NF01113363	Hypothetical protein gbs1332	210-238	1	*Streptococcus agalactiae*
NF00439678	Putative type II restriction endonuclease	263-291	1	*Streptococcus thermophilus*
NF01280369	Putative calcium binding protein	9-37 88-137 137-165	3	*Streptomyces avermitilis*
NF01277143	Hypothetical protein	24-52	1	*Streptomyces avermitilis*
NF01281064	Putative chitinase C	413-441	1	*Streptomyces avermitilis*
NF01278333	Putative high-affinity potassium transport system	555-583	1	*Streptomyces avermitilis*
NF01277145	Putative calcium binding protein	6-34	1	*Streptomyces avermitilis*
NF00543258	Putative calcium binding protein	10-38 60-88	2	*Streptomyces coelicolor*
NF00549617	Putative calcium-binding protein	9-37 60-88 98-126 132-160	4	*Streptomyces coelicolor*
NF00550219	Putative calcium binding protein	9-37 60-88 103-131 137-165	4	*Streptomyces coelicolor*
NF00543851	ChiC (Chitinase C) (Putative secreted protein) (Fragment)	415-443	1	*Streptomyces coelicolor*
NF00549644	Potassium-transporting ATPase B chain	567-595	1	*Streptomyces coelicolor*
NF00548721	SCO5464 protein	6-34	1	*Streptomyces coelicolor*
NF00543475	Hypothetical protein SCO4859	126-154	1	*Streptomyces coelicolor*
NF00928474	Hypothetical protein spyM18_1868	523-551	1	*Streptococcus pyogenes*
NF01861114	Putative Fe^{3+}-siderophore transport protein	525-553	1	*Streptococcus pyogenes*
NF01223601	Putative PBP 5 synthesis repressor	63-91	1	*Streptococcus pyogenes*
NF00442096	Penicillin-binding protein 3	167-195	1	*Streptococcus pneumoniae*
NF01965281	Hypothetical protein	196-224	1	*Symbiobacterium thermophilum*
NF02172090	Transaldolase	358-386	1	*Synechococcus elongatus*
NF02171539	Carboxyl-terminal protease	152-180	1	*Synechococcus elongatus*
P72797	Transaldolase	333-361 356-384	2	*Synechocystis sp.*
NF00423899	Slr0366 protein	171-199 277-305 383-411 489-517	4	*Synechocystis sp. PCC 6803*
NF00424738	Cation or drug efflux system protein	87-115	1	*Synechocystis sp. PCC 6803*
NF00425666	Sulfate adenylyltransferase	99-127	1	*Synechocystis sp. PCC 6803*
NF00968263	Septum formation inhibitor-activating ATPase	28-56	1	*Thermoanaerobacter tengcongensis*
NF02549883	calcium-binding EF-hand	61-89 97-125	2	*Thermobifida fusca*
NF01023077	transaldolase	356-384	1	*Thermosynechococcus elongatus*
NF00578072	50S Ribosomal Protein L4	1-28	1	*Thermus thermophilus*
NF01703216	Hypothetical conserved protein	240-268	1	*Thermus thermophilus*
NF00723911	Hemolysin-related protein	54-82	1	*Vibrio cholerae*

Accession ID	**Protein Name**	**Sequence Range**	**EF-hand number**	***Organism***
NF00722357	Hypothetical protein VCA0849	3164-3192	1	*Vibrio cholerae*
NF01185821	FlgA	125-153	1	*Vibrio fischeri*
NF02302098	Iron-regulated protein FrpC	344-372	1	*Vibrio fischeri*
NF01230959	Chemotaxis protein CheV	133-161	1	*Vibrio parahaemolyticus*
NF01234459	Putative outer membrane protein	42-70	1	*Vibrio parahaemolyticus*
NF01147763	Autotransporter adhesin	1196-1224 2841-2869	2	*Vibrio vulnificus*
NF01149533	Multidrug resistance efflux pump	128-156	1	*Vibrio vulnificus*
NF01147763	Autotransporter adhesin	887-915 990-1018 1093-1121 1196-1224 2841-2869	5	*Vibrio vulnificus*
NF01147228	FOG: Ankyrin repeat	310-338	1	*Vibrio vulnificus*
NF01150679	ATPase component of various ABC-type transport system	353-381	1	*Vibrio vulnificus*
NF01149533	Multidrug resistance efflux pump	128-156	1	*Vibrio vulnificus*
NF01411038	Hypothetical protein	214-242		*Wolinella succinogenes*
NF01840495	exopolysaccharide synthesis protein ExoD-related protein	16-44	1	*Wolbachia sp. wMel*
NF01840821	Exopolysaccharide synthesis protein ExoD-related protein	16-44	1	*Wolbachia sp. wMel*
NF01189636	Metallopeptidase	56-84	1	*Xylella fastidiosa*
NF00981304	Calcium-binding protein	38-66 74-102 112-140 143-171	4	*Xanthomonas axonopodis*
NF01010603	NodB-like protein	662-690	1	*Xanthomonas campestris*
NF00974448	Hypothetical protein XCC0163	30-58	1	*Xanthomonas campestris*
NF00977416	Polysaccharide deacetylase	714-742	1	*Xanthomonas campestris*
NF00974241	Hypothetical protein XCC1206	172-200	1	*Xanthomonas campestris*
NF02292841	EF hand domain protein	617-645	1	*Xanthomonas oryzae*
NF02292473	Phage-related protein	342-370	1	*Xanthomonas oryzae*
NF02292388	Polysaccharide deacetylase	662-690	1	*Xanthomonas oryzae*
NF02294838	Hypothetical protein	88-116	1	*Xanthomonas oryzae*
NF02293741	Hypothetical protein	505-533	1	*Xanthomonas oryzae*
NF01189016	Hypothetical protein	36-64	1	*Xylella fastidiosa*
NF02140272	DnaK molecular chaperone	173-201	1	*Zymomonas mobilis*
NF02139509	Hypothetical protein	51-79	1	*Zymomonas mobilis*
NF02139489	Hypothetical protein	58-86	1	*Zymomonas mobilis*
NF02139845	Putative RTX family exoprotein	2479-2507	1	*Zymomonas mobilis*

Supplementary Table 2. Putative EF-hand and EF-hand like Ca^{2+}-binding motifs in viral genomes.

Virus	**Accession ID**	**Protein name**	**Match Ranges**	**Sequences**
	EF-hand motifs			**1** 2 **3** 4 **5** 6 **7** 8 **9** 10 11 **12**
(+) ssRNA viruses				
MHV	Q5ICX2/Q83331	Spike protein	727-738	**D** N **S** T **E** Q **S** V **D** A C **D**
Rat coronavirus	Q9IKD1	Spike protein	726-737	**D** N **S** T **E** Q **S** V **D** A C **D**
Rubella virus	P13889	NSP (Protease)	1206-1217	**D** A **S** P **D** G **T** G **D** P L **D**
VEEV	P36327	NSP (mRNA-capping enzyme nsP1)	401-412	**D** Q **E** D **E** R **P** L **G** L R **D**
WEEV	P13896	NSP (mRNA-capping enzyme nsP1)	399-410	**D** L **D** D **E** K **E** L **G** V R **E**
Sindbis virus	P27283	NSP (mRNA-capping enzyme nsP1)	402-413	**D** L **D** N **E** K **M** L **G** T R **E**
SFV	P08411	NSP (mRNA-capping enzyme nsP1)	402-413	**D** L **D** D **E** K **P** L **G** V R **E**
RRV	P13887	NSP (mRNA-capping enzyme nsP1)	402-413	**D** L **D** N **E** K **M** L **G** T R **E**
SqMV	P36341	Movement protein	218-229	**N** N **S** G **D** N **E** V **E** F S **E**
SBLV	Q8JW06	3a protein	52-63	**N** L **S** S **D** N **R** L **N** F I **D**
Nora virus	Q27YG9	Replication polyprotein	462-473	**N** K **S** P **D** K **S** V **T** I E **D**
Tobamovirus (RMV/TMV/TVCV/YoMV)	Q1L1D7/Q88604/ Q88920/Q66220	RNA polymerase	1358-1369/ 1362-1373	**D** L **D** S **T** Q **A** M **E** I L **E**
TTV	A1XIP9/A6NA62	Polyportein/ RNA polymerase	1535-1546/ 196-207	**D** V **S** S **S** K **M** L **D** L S **E**
BSBMV	Q9IF43	29K protein	222-233	**D** D **D** G **D** G **V** V **G** D D **D**
BYSV	Q65858	Coat protein	11-22	**D** S **S** A **S** Q **T** M **T** A K **D**
PRV	Q98WK3	Coat protein	50-61	**D** K **D** N **D** G **A** C **D** G N **D**
SMoV	Q8UYV9	Polyprotein	1388-1399	**D** K **D** G **D** R **W** V **A** K D **E**
(-) ssRNA viruses				
HRSV-A	P28887/O36635/ Q82021/Q82027	RNA Polymerase (subunit L)	1557-1568	**D** M **N** T **S** D **L** L **C** V L **E**
HRSV-B	P24567/O42062	Phosphoprotein	229-240	**D** N **D** S **D** N **D** L **S** L D **D**
BRSV	P33454/Q77KZ1	Phosphoprotein	229-240	**D** E **S** S **D** N **D** L **S** L E **D**

Virus	Accession ID	Protein name	Match Ranges	Sequences
PPRV	Q4PIR9/Q91QS4	Phosphoprotein	74-85	**D** M **S** P **E** D **N** L **G** F R **E**
BEFV	P32595/Q56I18	Spike protein	400-411	**D** K **N** E **D** G **Y** I **D** I Q **E**
Puumala virus	Q6QTA9	RNA polymerase	1975-1986	**D** S **D** E **D** D **D** V **S** Q L **D**
NDV	A0SZV5	RNA polymerase	1529-1540	**N** H **D** G **S** H **Q** L **A** D T **D**
Influenza A virus	Q1I0S8	Neuraminidase	68-79	**N** I **S** N **T** K **I** V **N** V Q **D**
	Q0P290	Neuraminidase	68-79	**N** I **N** N **T** N **V** V **A** G K **D**
(+) ssRNA viruses require DNA intermediates				
HIV-1	Q2PNG6	Envelope protein	29-41	**D** N **S** T **E** G **T** V **G** G G **E**
	Q2PN97		29-41	**N** T **S** T **G** G **T** V **G** G G **E**
	Q2PN98		29-41	**N** N **S** T **G** G **T** V **G** G G **E**
	A1Z0A9		132-143	**D** L **N** T **T** N **T** I **N** S S **D**
	Q6EJM9		28-39	**N** T **N** N **S** R **I** M **E** G G **E**
	Q8AF19		139-150	**N** S **S** S **E** N **K** M **E** I G **E**
	P19549/Q03807		141-152	**N** N **S** S **G** G **T** V **E** K E **E**
	Q1G4R9		151-162	**N** N **S** S **G** Q **I** M **E** K G **E**
	Q1HSZ5		137-148	**N** S **S** S **G** K **M** M **E** E G **E**
	Q2NN71		137-148	**N** S **S** S **E** R **T** M **E** K G **E**
	Q1HSY3		143-154	**N** S **S** R **G** K **M** M **E** K G **E**
	Q1HT34		155-166	**N** N **S** G **G** G **T** V **E** E R **E**
	Q1HT21		149-160	**N** N **S** S **G** R **T** M **E** E R **E**
	QIHT20		147-158	**N** N **S** S **G** R **T** I **E** E R **E**
	Q2PN97		147-158	**N** T **S** S **T** G **G** T **V** G G **E**
	Q6QBL0		32-43	**N** N **N** S **E** G **R** I **E** R G **E**
	Q6QUE1		34-45	**N** T **S** S **E** G **M** V **E** K G **E**
	Q71129		24-35	**N** N **S** S **G** K **L** I **E** L G **E**
	Q71313		17-28	**N** S **S** D **E** G **K** I **E** K G **E**
CYMV	Q91B26	Putative protein	129-140	**N** R **D** H **E** Q **L** C **E** V V **E**
dsRNA viruses				
PsV-F	Q4G3H1	Capsid protein	294-305	**D** E **D** R **S** D **L** L **T** T L **D**
AHSV-6	Q64913	VP6 protein	144-155	**N** D **D** A **T** R **N** V **G** S S **E**

Virus	Accession ID	Protein name	Match Ranges	Sequences
ssDNA viruses				
FPV	P04864/P24840	Coat protein VP1	658-669	**S** A **N** M **S** R **I** V **T** Y S **D**
MEV	P27437	Coat protein VP1	653-664	**S** A **N** M **S** R **I** V **T** Y S **D**
dsDNA viruses				
Megalocytivirus (RBIV/DGIV/ISKNV/OSGIV/RSIV)	Q8B4N1/Q65858/Q8QUT8/Q1X6P8/Q71G61	Putative Phosphatase	80-91	**D** M **S** Q **D** G **F** V **N** Y Q **D**
Ranavirus (ATSV/FV-3)	Q6YH54/Q6GZT5	Orf2-like protein	327-338	**D** P **D** A **S** H **V** M **Q** T D **E**
LCDV	Q677V5	Purative protein	31-42	**D** I **N** N **S** Q **I** I **T** V S **D**
EHV-1	P28925	ICP4	733-744	**D** S **D** P **T** H **R** L **G** S D **E**
FeHV-1	Q86665/Q90050	Glycoprotein B	871-882/876-887	**D** F **D** E **E** K **L** M **Q** A R **E**
WSSV	Q8JNB7/Q8JNC2	ORF2735/ORF4162	312-323/281-292	**D** D **D** D **D** D **D** C **E** G M **D**
CPV	Q80DU9/Q8QMS8	A27L	383-394/57-68	**D** D **D** D **D** D **V** I **D** D D **D**
Squirrelpox virus	Q1HTR0	C3R	22-33	**D** D **D** T **D** G **E** L **E** S K **D**
Ectromelia virus	Q9PXN5	C11R	32-43	**N** R **N** S **T** H **K** I **Q** E N **E**
MOCV-1	Q98173	MC002L	251-262	**N** T **N** E **N** G **A** M **S** S A **E**
Nucleopolyhedrovirus (AgMNPV/Cfdef/CfNMPV)	Q06KP7/Q6VTX1/Q7TLX0	Putative protein	63-74/61-72/61-72	**D** D **N** N **G** R **C** C **N** V V **D** / **D** D **S** A **N** R **C** C **S** V V **D**
Granulovirus		Alk-exo	350-361	**N** L **N** E **S** Q **T** L **S** L S **E**
PBCV-1	Q84528	A208R	214-225	**D** D **D** S **D** D **D** I **N** D N **D**
ESV	Q9J3U5	EsV-1-56	333-344	**D** V **S** G **N** D **L** L **N** V S **D**
Sulfolobus virus	Q684G2	Adenine-specific DNA methylase	151-162	**D** D **D** A **E** G **Y** I **G** T W **E**
Archaeal BJ1 virus	A0ZYT1	Putative protein	18-29	**D** I **S** D **T** N **V** L **A** A A **E**
AFV-2	Q573C5	Putative protein	85-96	**D** S **S** S **S** Q **E** V **T** I P **D**

Virus	Accession ID	Protein name	Match Ranges	Sequences
HZV-1	Q8JKJ1	Microtubule-associated-like protein	423-434	**D** T **D** G **S** N **D** L **A** K L **D**
Others				
ABV	A4ZUC5	ORF188	169-180	**D** P **N** Q **N** Q **T** I **S** E S **E**
		EF-hand-like motifs		
(+) ssRNA viruses				
EEEV	Q306W6	NSP	2401-2414	**D** D **D** Q **D** G **D** R **R** R A L Y **D**
CSFV	P19712	Genome polyprotein	929-942	**D** C **N** R **D** G **V** V **I** S T E G **E**
(-) ssRNA viruses				
Influenza A virus	Q6XV43	Neuraminidase	385-398	**D** K **D** S **N** G **V** Q **D** I I D N **D**
	P21427/Q0A2K9/O89750/Q0A2Q7	RNA polymerase subunit P2	294-306	**D** P **S** H **E** G **E** G **I** P L Y **D**
HPIV-1	P16017	Hemagglutinin-neuraminidase	281-293	**D** Y **S** S **E** G **I** E **D** L V F **D**
Sendai virus	Q783Y1/P19758/P03425/Q88261	Hemagglutinin-neuraminidase	281-293	**D** Y **S** S **D** G **I** E **D** L V L **D**
VHSV				
dsRNA viruses				
AHSV-4	Q64929	VP4 core protein	263-276	**D** V **S** A **D** G **L** K **G** T I E W **E**
(+) ssRNA viruses require DNA intermediates				
HIV-2	P24103	Negative factor Nef	181-194	**D** T **S** Q **E** G **E** D **T** E T D T **E**
MPMV	P07567	Gag polyprotein	133-146	**D** S **D** D **E** G **A** K **S** S S L Q **D**
dsDNA viruses				
BoHV-1	P29128	Trans-acting transcriptional protein ICP0	287-300	**D** S **D** S **E** G **S** E **D** D S W S **E**
HHV-1	P10211/P06347	Glycoprotein B precursor	824-837	**D** A **S** G **E** G **E** E **G** G D F D **E**
HHV-2	P07918	DNA polymerase	675-688	**D** D **D** E **D** G **D** E **D** G D E R **E**

Virus	Accession ID	Protein name	Match Ranges	Sequences
HHV-3	P09255	Transcriptional transactivator IE63	164-177	**D** S **D** D **D** G **S** T **P** S D V I **E**
HHV-6	Q01350	Protein U3	284-297	**D** N **D** E **D** G **R** P **R** F V A **E**
HHV-7	P52520	Protein U3	299-311	**D** N **D** P **D** G **N** L **T** F I A **E**
CeHV-9	Q04548	Glycoprotein E precursor	40-53	**D** M **D** E **D** G **V** Y **G** D D I Q **D**
PRV	P24827	Immediate-early protein RSP40	224-237	**D** E **D** E **E** G **E** E **E** E D E E **E**
			335-348	**D** E **D** E **D** G **E** G **E** E G G K **D**
	P24381	Serine/threonine-protein kinase	77-90	**D** G **D** G **D** G **D** S **S** G D E D **D**
EBV	P12977	Nuclear antigen 3	711-724	**D** E **S** G **E** G **S** D **T** S E P C **E**
	P03210	Putative protein BRRF2	492-505	**D** E **D** E **D** G **S** E **D** G E F S **D**
BmNPV	P41712	DNA polymerase	955-967	**D** D **D** D **D** G **C** D **S** S D S **E**
SlNPV	O57030	DNA-directed RNA polymerase beta chain	422-435	**D** E **D** E **N** G **S** G **G** D D D D **D**

Abbreviations: MHV, murine hepatitis virus; VEEV, Venezuelan equine encephalitis virus; WEEV, western equine encephalitis virus; SFV, Semliki forest virus; RRV, Ross river virus; SqMV, squash mosaic virus; SBLV, spring beauty latent virus; RMV, ribgrass mosaic virus; TMV, tobacco mosaic virus; TVCV, turnip vein-clearing virus; YoMV, youcai mosaic virus; TTV, tomato torrado virus; BSBMV, beet soil-borne mosaic virus; BYSV, beet yellow stunt virus: PYV, papaya ringspot virus; SMoV, strawberry mottle virus; HRSV, human respiratory syncytial virus; BRSV, bovine respiratory syncytial virus; PPRV, peste-des-petits-ruminants virus; BEFV, bovine ephemeral fever virus; NDV, Newcastle disease virus; HIV, human immunodeficiency virus; BSV, banana streak virus; DBV, dioscorea bacilliform virus; CYMV, citrus yellow mosaic virus; GVBV, gooseberry vein banding virus; KTSV, kalanchoe top-spotting virus; PsV-F, penicillium stoloniferum virus; AHSV, African horse sickness virus; FPV, feline panleukopenia virus; MEV, mink enteritis virus; RBIV, rock bream iridovirus; DGIV, dwarf gourami iridovirus; ISKNV, infectious spleen and kidney necrosis virus; OSGIV, orange-spotted grouper iridovirus; RSIV, red sea bream iridovirus; ATSV, ambystoma tigrinum stebbensi virus; FV, frog virus; LCDV, lymphocystis disease virus; FeHV, feline herpesvirus; EHV, equine herpesvirus; WSSV, white spot syndrome virus; CPV, cowpox virus; MOCV, mollucum ontagiosum virus; AgMNPV, anticarsia gemmatalis nuclear polyhedrosis virus; Cfdef, choristoneura fumiferana defective polyhedrosis virus; CfNMPV, choristoneura fumiferana nuclear polyhedrosis virus; PBCV, paramecium bursaria chlorella virus; ESV, ectocarpus siliculosus virus; AFV, acidianus filamentous virus; HZV, heliothis zea virus; ABV, acidianus bottle-shaped virus; EEEV, Eastern equine encephalomyelitis virus; CSFV, classical swine fever virus; HPIV, human parainfluenza 1 virus; VHSV, viral hemorrhagic septicemia virus; MPMV, Mason-Pfizer monkey virus; BoHV, bovine herpesvirus; HHV, human herpesvirus; CeHV, Cercopithecine herpesvirus; PRV, pseudorabies virus; EBV, Epstein-Barr virus ; BmNPV, Bombyx mori nuclear polyherosis virus; SlNPV, spodoptera littoralis nuclear polyherosis vírus.