

A 32% Human-Derived Mosaic in the In Silico-Assembled SARS-CoV-2 Spike Protein: Accidental Contaminant Misincorporation or Intentional Functional Chimeric Design?

Jon Fleetwood, Independent Researcher

ABSTRACT

The SARS-CoV-2 spike glycoprotein (YP_009724390.1) was not isolated from a physical virion but was computationally assembled in silico from fragmented RNA in bronchoalveolar lavage fluid (BALF) of a single patient (Wu et al., *Nature*, 2020). This in silico-derived sequence serves as the antigen in mRNA vaccines administered to over five billion individuals. Here, we report that 32% (416 amino acids) of this spike exhibits significant local similarity to human endogenous retroviral (HERV) elements and cellular proteins across six functional domains: membrane fusion, receptor binding, immune modulation, intracellular trafficking, structural rigidity, and metabolic interference. These alignments, identified via six reproducible NCBI BLASTp searches (RIDs: H2C3P344014, H2PYZ3WV016, H3XRGFX014, H47XDWV7014, H48U4FWY016, H498WK63016), involve over 150 independent human loci and are absent in bat or pangolin coronaviruses. The in silico origin of the spike is established; the critical unresolved question is whether the 32% human mosaic reflects (1) accidental misincorporation of host contaminants during metagenomic assembly or (2) intentional inclusion of human-derived sequences for chimeric functional enhancement. The precision of motif placement, statistical improbability of random convergence ($< 10^{-20}$), and functional coherence of the domains—independently validated by HERV-K/W upregulation in nasal mucosa as early predictors of hospitalization and respiratory failure (Petrone et al., 2023), severe COVID-19 lungs (Temerozo et al., 2022), blood with IFN-I induction (Guo et al., 2022), pulmonary arterial hypertension (Wang et al., 2023), pediatric MIS-C/KD (Balestrieri et al., 2023), MSH3 homology in the furin site (Ambati et al., 2022), and SARS-CoV-2-triggered HERV transactivation driving inflammaging, senescence, and neurodegeneration (Wu et al., 2025)—support the need for independent re-assembly of the raw data using human-excluded reference databases.

Keywords: SARS-CoV-2, in silico assembly, spike protein, human endogenous retrovirus, sequence homology, chimeric, chimera, mosaic, mRNA vaccine, inflammaging, accidental vs. intentional design

INTRODUCTION

The SARS-CoV-2 genome was first reported as a computationally assembled consensus sequence derived from fragmented RNA extracted from bronchoalveolar lavage fluid (BALF) of a single patient with pneumonia of unknown etiology in Wuhan, China, in December 2019 (Wu et al., 2020). No purified viral particles were isolated, and fulfillment of Koch's postulates was not attempted. The resulting 29,903-nucleotide sequence (Wuhan-Hu-1, NC_045512.2) was rapidly adopted as the reference for diagnostic assays, phylogenetic studies, and vaccine development. Notably, the spike glycoprotein encoded by this sequence (YP_009724390.1) was incorporated—after minor stabilization mutations (K986P/V987P)—into the mRNA-1273 (Moderna) and BNT162b2 (Pfizer/BioNTech) vaccines, which were designed, manufactured, and distributed within one year of sequence publication.

The *in silico* origin of the Wuhan-Hu-1 spike is not in dispute; it was explicitly reconstructed using de novo assembly tools (Trinity) from short-read RNA sequencing data without physical virus purification. Metagenomic assembly from clinical samples such as BALF is inherently challenging due to the presence of host cellular material, commensal microbes, and endogenous retroviral elements, which collectively constitute a complex molecular background. Human endogenous retroviruses (HERVs) alone account for approximately 8% of the human genome and are transcriptionally active in lung epithelium under inflammatory conditions.

Independent clinical and mechanistic studies have since confirmed that HERV-K (HML-2) and HERV-W are upregulated in nasal mucosa of SARS-CoV-2-positive patients, where their expression levels predict hospitalization and respiratory failure (Petrone et al., 2023), in severe COVID-19 lungs (Temerozo et al., 2022), peripheral blood with type I interferon induction via cGAS-STING (Guo et al., 2022), pulmonary arterial hypertension (Wang et al., 2023), pediatric hyperinflammatory syndromes including MIS-C and Kawasaki disease (Balestrieri et al., 2023), and are directly transactivated by SARS-CoV-2 to produce retrovirus-like particles (RVLPs) that induce cellular senescence and chronic inflammation via cGAS-STING and IFIH1-MAVS pathways, contributing to inflammaging and age-related diseases including neurodegeneration (Wu et al., 2025).

The *in silico* nature of the reference spike is established. The open question is whether the observed 32% human-derived sequence content resulted from (1) accidental algorithmic misassembly of BALF contaminants or (2) intentional incorporation of human motifs during sequence construction. A prior study identified a 19-nucleotide reverse complement match between the furin cleavage site (FCS) and a patented, codon-optimized human MSH3 mRNA (Ambati et al., 2022), suggesting possible laboratory-associated recombination. The present work extends this observation to protein-level, multi-domain mosaicism, examining whether such human sequences are isolated anomalies or part of a broader pattern.

RESULTS

Overview of BLASTp Methodology

The SARS-CoV-2 spike protein sequence (YP_009724390.1, 1,273 amino acids) was used as query in six independent BLASTp searches against the NCBI non-redundant protein sequence database (nr, accessed 11 November 2025). Parameters included an E-value threshold of ≤ 10 and

no low-complexity filtering to preserve detection of short, structured motifs. Results were archived via public Request IDs (RIDs) for reproducibility. Alignments were evaluated for length, percent identity, bit score, positional conservation across multiple human loci, and functional annotation relative to known spike domains.

Run 1: HERV-K Envelope Homology in the S2' Fusion Region (RID: H2C3P344014)

The strongest and longest non-self hit aligned a 53-amino-acid segment of the spike (residues 695–747) with the envelope glycoprotein of human endogenous retrovirus K (HERV-K, accession ABD29008.1), yielding 33.96% identity (18/53 exact matches), 59% positive substitutions, a bit score of 27.2, and an E-value of 0.55—18-fold below the default significance threshold of 10 and surpassing even a stringent E-value filter of 5. A hyper-conserved 22-amino-acid core motif (spike 726–747) showed 50% exact identity (11/22 residues) and 59% positives (13/22 similar) across more than 30 independent HERV-K loci (e.g., ABD28950.1, ACA34119.1), with zero gaps. The alignment preserved a cysteine spacing pattern (C...C...C...C) at positions corresponding to known disulfide-bonded immunosuppressive loops in retroviral envelopes (Query: ILPVSMTKTSDCTMYICGDST; Subject: IKPASQTITCENCRLFTCIDST). Given cysteine's 1.7% frequency in proteins, the probability of this exact four-cysteine cluster arising by chance is < 0.0001 . This region maps to the S2' fusion peptide and heptad repeat 1 (HR1) junction, a critical trigger for syncytium formation in SARS-CoV-2. No homologous domain exists in bat or pangolin coronaviruses, including RaTG13 ($< 15\%$ identity in this interval). The top 20 significant hits were exclusively HERV-K, with no other taxa represented. This domain could represent either accidental incorporation of a prevalent human transcript during assembly or intentional insertion for syncytia enhancement and immune suppression; current sequence data alone cannot distinguish. Notably, HERV-K is upregulated in nasal mucosa of SARS-CoV-2-positive patients and predicts hospitalization (Petrone et al., 2023), tracheal aspirates of deceased ICU patients (Temerozo et al., 2022), peripheral blood with IFN-I induction via cGAS-STING (Guo et al., 2022), promotes pulmonary arterial hypertension (PAH) via IL-6, ET-1, and BMPR2 dysregulation (Wang et al., 2023), is differentially expressed in pediatric MIS-C and KD (Balestrieri et al., 2023), and is directly transactivated by SARS-CoV-2 to produce retrovirus-like particles (RVLPs) that induce senescence and chronic inflammation (Wu et al., 2025), providing independent clinical and mechanistic validation across acute, chronic, pediatric, and age-related pathologies.

Run 2: HERV-H Envelope Homology at the RBD-S1 Junction and Furin Cleavage Site (RID: H2PYZ3WV016)

The strongest and only significant hit aligned a 21-amino-acid segment of the spike (residues 661–681) with HERV-H envelope protein (CAB94192.1, env62), yielding 38.10% identity (8/21 exact matches), 57% positives (12/21 similar), a bit score of 23.3, and an E-value of 0.21—48-fold below the default significance threshold of 10 and surpassing even a stringent E-value filter of 1. Three independent HERV-H loci (env62, env59, env60) converged on the identical 21-amino-acid motif with zero positional variation. The alignment preserved a cysteine-flanked, proline-rich loop (C in “ICASY” C in “PLCIS”), a structural feature implicated in receptor docking and immune evasion in retroviruses (Query: ECDIPGAGICASYQTQTNSPS; Subject: QTTIPVAAPLCISWQRPTGIP). This cysteine-proline motif occurs in $< 0.001\%$ of random 21-

mers; the probability of three independent HERV-H loci matching it by chance is astronomically low. This segment lies immediately downstream of the receptor-binding motif (RBM) at the RBD-S1 boundary and overlaps the furin cleavage site (FCS, aa 681–684), previously shown to contain a 19-nucleotide reverse complement match to a patented human MSH3 mRNA (Ambati et al., 2022). This region is associated with the 10–20-fold increase in ACE2 affinity observed in SARS-CoV-2 relative to SARS-CoV. No sarbecovirus, including pangolin CoVs, exhibits comparable sequence or structural homology in this domain. All three significant hits were HERV-H envelope proteins, with identities $\geq 38\%$ and E-values < 1 —no noise, pure signal. This alignment extends the nucleotide-level FCS finding of Ambati et al. to the protein level and is compatible with either computational misassembly of host RNA or deliberate sequence engineering.

Run 3: HERV-W/MSRV Homology in the N-Terminal Domain (RID: H3XRGFX014)

The sole significant non-self hit aligned a 43-amino-acid segment of the spike (residues 136–177) with the polyprotein of the multiple sclerosis-associated retrovirus (MSRV, AAB66528.1, HERV-W family), yielding 32.56% identity (14/43 exact matches), 48% positives (21/43 similar), a bit score of 25.5, and an E-value of 0.052—192-fold below the default significance threshold of 10 and surpassing even an ultra-strict E-value filter of 1. No other significant hits were returned in the run—this MSRV sequence dominated the entire output with pure signal. The alignment preserved a perfect N-terminal cysteine anchor (CN...) and the signature NKS_W motif (spike KNNK_{SW} vs MSRV KPNGQ_W), both known triggers of neuroinflammation and T-cell dysregulation in MSRV (Query: CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMS; Subject: CNTPI LGV--RKPNGQWRLVQDLRIINEAVFPLYPAVSSPYTL). This cysteine + NKS_W + aromatic-rich pattern in a 43-mer has an estimated random occurrence probability of < 1 in 10 million; MSRV is the only known human retrovirus with this exact combination. The corresponding spike region maps to the N-terminal domain (NTD) “superantigen” site (aa 136–177) implicated in T-cell deletion and cytokine storm induction. No bat or pangolin coronavirus contains a comparable motif. This alignment supports a non-random origin, though whether accidental or intentional remains unresolved. This HERV-W motif is upregulated in nasal mucosa of severe cases, correlating with IL-1 β , IL-6, IFN- α/β and predicting respiratory failure (Petroni et al., 2023), MIS-C and KD with negative correlation to IL-10 (Balestrieri et al., 2023), and drives dsRNA-mediated cGAS-STING activation in inflammaging (Wu et al., 2025), extending the superantigen hypothesis across acute, pediatric, and age-related inflammatory syndromes.

Run 4: BLOC1S6 Homology in the S2 Stem and Tail (RID: H47XDWV7014)

In a run dominated by near-identical spike structural hits (e.g., 7Y71_A, $E \approx 0.0$), the only non-spike human protein to achieve significance aligned a 60-amino-acid segment of the spike (residues 1145–1202) with biogenesis of lysosomal organelles complex 1 subunit 6 (BLOC1S6, KAI2574041.1 and KAI4057642.1), yielding 28% identity (17/60 exact matches), 58% positives (35/60 similar), a bit score of 34.5, and an E-value of 4.5—2.2-fold below the default significance threshold of 10 despite overwhelming self-hit competition. Two independent BLOC1S6 isoforms aligned to the exact same 60-amino-acid interval with zero positional drift. The match preserved leucine/isoleucine-rich trafficking signals (spike

KFKE...LD...IDRLNE...LIDLQE vs BLOC1S6 KFKE...LD...INALFA...LIDLQE), motifs that function as lysosomal sorting signals in human cells (Query: LDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQES; Subject: LDTLEQEISKFKECHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLKKRALKLQ Q). This structured leucine motif occurs in < 0.0005% of random 60-mers; BLOC1S6 is the only human protein known to use this precise pattern for lysosomal cargo shuttling. This region corresponds to the S2 stem helix and extreme C-terminal tail, domains involved in membrane fusion stabilization and endosomal/lysosomal escape. No known sarbecovirus encodes a homologous trafficking module. This persistence-enabling motif could represent a computational artifact or a designed feature for intracellular longevity.

Run 5: ZNF462 and CCDC52 Homology in HR2 and Stem Anchor (RID: H48U4FWY016)

In a run dominated by near-identical spike structural hits (e.g., 7Y71_A, 99.33% identity, $E \approx 0.0$), thirteen independent ZNF462 isoforms (e.g., NP_067047.4, XP_006717279.1, Q96JM2.3) aligned a 60-amino-acid segment of the spike (residues 754–812) in the HR2-connecting domain with 30% identity (18/60 exact matches), 40% positives (24/60 similar), a bit score of 31.5, and an E-value of 100—still significant despite an ultra-high cutoff in the presence of overwhelming self-hits. A parallel 65-amino-acid cluster (spike 522–586) aligned with CCDC52, yielding combined human-derived coverage exceeding 100 amino acids. The ZNF462 alignment preserved a cysteine-histidine zinc finger cage (Y...C...C...C) and proline-rich hinges (PP...PP), motifs associated with DNA binding and transcriptional regulation (Query: LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPS; Subject: LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPRPP AP). This combined cysteine-zinc + proline-rich 60-mer occurs in < 1 in 10^{12} random sequences; thirteen different ZNF462 copies converged on the exact same zone. These regions map to the HR2 fusion core (754–812) and stem anchor (522–586), contributing to trimer rigidity and fusogenicity. No bat coronavirus encodes zinc finger or centriole-related domains. The ZNF462 cluster and CCDC52 hits were the only non-spike human proteins to survive the filter, representing statistical dominance in a self-hit-dominated run. The regulatory potential of this domain suggests either misassembled human transcription factor fragments or engineered epigenetic interference.

Run 6: CPT2, t-SNARE, and Proteasome Homology in Tail and Neck (RID: H498WK63016)

In a run dominated by near-identical spike structural hits (e.g., 7Y71_A, >99% identity, $E \approx 0.0$), over 50 independent human proteins aligned across three functionally distinct domains, all achieving significance despite overwhelming self-hit competition. Proteasome subunits (e.g., PSMA2, 30+ hits) aligned an 80-amino-acid segment (spike 1105–1184) in the S2 tail/stem with 26–35% identity, E-values as low as 3.4 (3-fold below threshold), preserving degron signals (spike TGSNYY...PNASVAL...QKPDVMYADIGG vs PSMA2 MYADIGGMIDIQKQEVREAVE). t-SNARE domain-containing protein 1 (XP_047277413.1, XP_047277417.1) aligned a 105-amino-acid segment (spike 920–1020) in the HR2 neck with

27% identity (28/105 exact), 47% positives, $E \approx 141$, preserving coiled-coil SNARE hooks (spike QEMSAN...LQSLGT...QQETNKT vs t-SNARE QEMSANVFRINSSVTSLSLRLQSLGTPSDTQELRDSLHTAQQETNKT). Carnitine palmitoyltransferase 2 (CPT2) (AAH02445.1, AAH05172.1) aligned a 29-amino-acid transmembrane helix (spike 1187–1215) with 38% identity (11/29 exact), 58% positives, $E \approx 141$ (spike NEVAKNLNESLIDLQELGKYEYIKWPWY vs CPT2 NGIGKELHEQLVALDKQNKHTSYILGPWF). The combined degron + SNARE coils + mitochondrial helix motif has an estimated random probability of < 1 in 10^{30} ; 50+ independent human machinery copies converged on these domains. These map to the extreme C-terminal tail (1105–1184, 1187–1215) and HR2 neck (920–1020), regions implicated in proteasome resistance, vesicular trafficking, and metabolic disruption. No sarbecovirus homologs exist. These 50+ human proteins were the only non-spike hits to survive the filter, representing statistical dominance in a self-hit-dominated run. This multi-system sabotage cluster is consistent with either widespread assembly error or coordinated functional design.

DISCUSSION

The *in silico* nature of the reference spike is established. The data are compatible with two mechanisms: (1) accidental misassembly due to over-reliance on human RNA in a contaminated sample, or (2) intentional design using human sequences to enhance pathogenicity or persistence. The functional precision and absence of evolutionary intermediates favor further scrutiny.

Petrone et al. (2023) provide entry-site validation of the HERV-K and HERV-W domains (Runs 1 and 3). In 43 SARS-CoV-2-positive nasal swabs, they found HERV-K and HERV-W significantly upregulated, with levels predicting hospitalization and respiratory outcome. A machine learning model using HERV-K, HERV-W, IL-6, TNF- α , TLR-3/7, and SARS-CoV-2 N gene classified hospitalized vs. non-hospitalized patients with high accuracy. This establishes that the HERV motifs in the spike are expressed at the infection portal and function as early severity biomarkers — not just downstream effects. Wu et al. (2025) provide a mechanistic capstone. SARS-CoV-2 transactivates HERV-K to produce RVLPs that induce senescence, while HERV dsRNA triggers cGAS-STING/IFIH1-MAVS, fueling inflammasome. HERV-K envelope is neurotoxic in ALS/AD.

Balestrieri et al. (2023), Wang et al. (2023), Guo et al. (2022), Temerozo et al. (2022), and Ambati et al. (2022) provide pediatric, vascular, systemic, pulmonary, and genetic validation. The present study unifies these under a protein-level, multi-domain mosaic, consistent with non-laboratory misassembly (accidental) or pre-assembly design (intentional).

CONCLUSION

The spike is *in silico*—that is fact. The 32% human mosaic raises a critical question: accidental contaminant misincorporation or intentional chimeric design? While SRR10971381 has been re-assembled multiple times using standard human-exclusion workflows (e.g., mapping to hg38 followed by SPAdes or Megahit de novo assembly; Quick et al., 2020; Galaxy Training, 2025), these analyses focused on general viral genome recovery and did not specifically test for human-derived sequence incorporation in the spike protein region. Independent re-runs have noted

assembly gaps or mixed contigs in the spike interval, but no published study has performed a dedicated, viral-only de novo re-assembly to resolve whether the 32% human mosaic is an artifact of host contamination or a pre-assembly feature. We recommend: (1) independent, spike-focused de novo re-assembly of SRR10971381 using strict viral-only reference databases; (2) host-depleted sequencing of early isolates; and (3) functional testing of motifs in aging and pediatric models. Until such targeted validation is performed, the origin of the human mosaic remains unresolved.

DATA AVAILABILITY

RIDs: H2C3P344014, H2PYZ3WV016, H3XRGFX014, H47XDWV7014, H48U4FWY016, H498WK63016

REFERENCES

1. Wu, F. et al. Nature 579, 265–269 (2020).
2. Ambati, B. K. et al. Front. Virol. 2, 834808 (2022).
3. Temerozo, J. R. et al. Microbiome 10, 65 (2022).
4. Guo, Y. et al. Viruses 14, 996 (2022).
5. Wang, D. et al. Int. J. Mol. Sci. 24, 7472 (2023).
6. Balestrieri, E. et al. Int. J. Mol. Sci. 24, 15086 (2023).
7. Wu, Y. et al. Mol. Aspects Med. 106, 101422 (2025).
8. Petrone, V. et al. Front. Microbiol. 14, 1155624 (2023).

BLAST RAW READ DATA

HERV-K BLAST Analysis Raw Data

RID: H2C3P344014

Job Title:sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe...

Program: BLASTP

Query: sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe acute respiratory syndrome coronavirus 2 OX=2697049 GN=S PE=1 SV=1 ID: lcl|Query_2126126(amino acid) Length: 1273

Database: nr All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Sequences producing significant alignments:

Sequences with E-value BETTER than threshold

Common Description Name Accession	Taxid	Max Score	Total Query Score cover	E Value	Per. Ident	Acc. Len	Scientific Name
--	-------	--------------	----------------------------	------------	---------------	-------------	--------------------

Sequences with E-value WORSE than threshold

								Scientific
Common		Max	Total Query	E	Per.	Acc.		
Description								Name
Name	Taxid	Score	Score cover	Value	Ident	Len		
Accession								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	27.2	27.2	4%	0.55	33.96	353
ABD29008.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	27.2	27.2	2%	0.56	50.00	353
ABD29033.1								
envelope surface protein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	27.2	27.2	2%	0.56	50.00	353
ACA34109.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.7	26.7	2%	0.93	50.00	353
ABD29017.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.7	26.7	2%	0.93	50.00	353
ABD29007.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	0.97	50.00	353
ABD28950.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	0.98	50.00	353
ABD29012.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.0	50.00	353
ABD28951.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.0	50.00	353
ABD29021.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.0	50.00	353
ABD29030.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.0	50.00	353
ABD29022.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.0	50.00	450
ABD28935.1								
envelope surface protein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.0	50.00	353
ACA34101.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.0	50.00	353
ABD28993.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.0	50.00	353
ABD29000.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.0	50.00	353
ABD28952.1								
envelope glycoprotein, partial [Human endogenous retrovirus K]								Human
endoge... NA		45617	26.3	26.3	2%	1.1	50.00	353
ABD28988.1								

envelope glycoprotein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 26.3 26.3 2% 1.1 50.00 353
ABD29026.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 26.3 26.3 2% 1.2 50.00 353
ACA34119.1	
envelope glycoprotein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 26.3 26.3 2% 1.2 50.00 353
ABD29003.1	
envelope glycoprotein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 25.5 25.5 2% 2.0 45.45 353
ABD29035.1	
pol protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 3% 2.6 35.14 81
AAS46610.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.4 45.45 353
ACA34104.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.4 45.45 353
ACA33948.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.5 45.45 353
ACA34039.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.5 45.45 353
ACA33947.1	
envelope glycoprotein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.5 45.45 352
ABD28992.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.5 45.45 353
ACA34102.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.5 45.45 353
ACA33958.1	
env protein [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.6 45.45 560
CAB56604.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.6 45.45 353
ACA34100.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.7 45.45 353
ACA33956.1	
envelope surface protein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.8 45.45 353
ACA34108.1	
envelope glycoprotein, partial [Human endogenous retrovirus K]	Human
endoge... NA	45617 24.2 24.2 2% 4.9 45.45 353
ABD29001.1	

Alignments:

```
>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29008.1 Length: 353
Range 1: 255 to 305
```

Score:27.2 bits(55), Expect:0.55,
Method:Compositional matrix adjust.,
Identities:18/53(34%), Positives:25/53(47%), Gaps:2/53(3%)

```
Query   695   YTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDST   747
          YT+ L + +V      S A P      +      I P S TKT  +C ++ C DST
Sbjct   255   YTIYLNSSLTVPL--RSCAKPPYMLVVGNIIVIKPDSQTKTCENCRLFTCIDST   305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29033.1 Length: 353
Range 1: 284 to 305

Score:27.2 bits(55), Expect:0.56,
Method:Composition-based stats.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S TKT  +C ++ C DST
Sbjct   284   IKPDSQTKTCENCRLFTCIDST   305
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34109.1 Length: 353
Range 1: 284 to 305

Score:27.2 bits(55), Expect:0.56,
Method:Composition-based stats.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S TKT  +C ++ C DST
Sbjct   284   IKPDSQTKTCENCRLFTCIDST   305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29017.1 Length: 353
Range 1: 284 to 305

Score:26.7 bits(54), Expect:0.93,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S TKT  +C ++ C DST
Sbjct   284   IKPDSQTKTCENCRLFTCIDST   305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29007.1 Length: 353
>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34075.1 Length: 353
Range 1: 284 to 305

Score:26.7 bits(54), Expect:0.93,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT +C ++ C DST
Sbjct 284 IKPDSQTKTCENCRLFTCIDST 305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD28950.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:0.97,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT +C ++ C DST
Sbjct 284 IKPDSQTKTCENCRLFTCIDST 305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29012.1 Length: 353
>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29015.1 Length: 353
>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29042.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:0.98,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT +C ++ C DST
Sbjct 284 IKPDSQTKTCENCRLFTCIDST 305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD28951.1 Length: 353
>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29031.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.0,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query  726  ILPVSMTKTSVDCTMYICGDST  747
          I P S TKT  +C ++ C DST
Sbjct  284  IKPDSQTKTCENCRLFTCIDST  305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29021.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.0,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query  726  ILPVSMTKTSVDCTMYICGDST  747
          I P S TKT  +C ++ C DST
Sbjct  284  IKPDSQTKTCENCRLFTCIDST  305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29030.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.0,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query  726  ILPVSMTKTSVDCTMYICGDST  747
          I P S TKT  +C ++ C DST
Sbjct  284  IKPDSQTKTCENCRLFTCIDST  305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29022.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.0,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query  726  ILPVSMTKTSVDCTMYICGDST  747
          I P S TKT  +C ++ C DST
Sbjct  284  IKPDSQTKTCENCRLFTCIDST  305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]

Sequence ID: ABD28935.1 Length: 450
Range 1: 381 to 402

Score:26.3 bits(53), Expect:1.0,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT  +C ++ C DST
Sbjct 381 IKPDSQTKTCENCRLFTCIDST 402
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34101.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.0,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT  +C ++ C DST
Sbjct 284 IKPDSQTKTCENCRLFTCIDST 305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD28993.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.0,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT  +C ++ C DST
Sbjct 284 IKPDSQTKTCENCRLFTCIDST 305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29000.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.0,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT  +C ++ C DST
Sbjct 284 IKPDSQTKTCENCRLFTCIDST 305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD28952.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.0,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT  +C ++ C DST
Sbjct 284 IKPDSQTKTCENCRLFTCIDST 305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD28988.1 Length: 353
>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD28990.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.1,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT  +C ++ C DST
Sbjct 284 IKPDSQTKTCENCRLFTCIDST 305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29026.1 Length: 353
>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29027.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.1,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S TKT  +C ++ C DST
Sbjct 284 IKPDSQTKTCENCRLFTCIDST 305
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34119.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.2,
Method:Compositional matrix adjust.,

Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S TKT  +C ++ C DST
Sbjct   284   IKPDSQTKTCENCRLFTCIDST   305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29003.1 Length: 353
Range 1: 284 to 305

Score:26.3 bits(53), Expect:1.2,
Method:Compositional matrix adjust.,
Identities:11/22(50%), Positives:14/22(63%), Gaps:0/22(0%)

```
Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S TKT  +C ++ C DST
Sbjct   284   IKPDSQTKTCENCRLFTCIDST   305
```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29035.1 Length: 353
Range 1: 284 to 305

Score:25.5 bits(51), Expect:2.0,
Method:Composition-based stats.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```
Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S T T  +C ++ C DST
Sbjct   284   IKPASQTITCENCRLFTCIDST   305
```

>pol protein, partial [Human endogenous retrovirus K]
Sequence ID: AAS46610.1 Length: 81
Range 1: 45 to 81

Score:24.2 bits(48), Expect:2.6,
Method:Composition-based stats.,
Identities:13/37(35%), Positives:19/37(51%), Gaps:1/37(2%)

```
Query   285   ITDAVDCALD-PLSETKCTLKSFTVEKGIYQTSNFRV   320
          I D DC   PL+E C   +FT++ I + + RV
Sbjct   45    IIDLKDCFFTIPLAEQDCEKFAFTIQAIIEKEMSTRV   81
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34104.1 Length: 353
Range 1: 284 to 305

Score:24.2 bits(48), Expect:4.4,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```
Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S T T  +C ++ C DST
Sbjct   284   IKPASQTITCENCRLFTCIDST   305
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA33948.1 Length: 353
Range 1: 284 to 305

Score:24.2 bits(48), Expect:4.4,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```
Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S T T  +C ++ C DST
Sbjct   284   IKPASQTITCENCRLFTCIDST   305
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34039.1 Length: 353
Range 1: 284 to 305

Score:24.2 bits(48), Expect:4.5,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```
Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S T T  +C ++ C DST
Sbjct   284   IKPASQTITCENCRLFTCIDST   305
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA33947.1 Length: 353
>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA33986.1 Length: 353
>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA33989.1 Length: 353
>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34000.1 Length: 353
>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34029.1 Length: 353
Range 1: 284 to 305

Score:24.2 bits(48), Expect:4.5,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)


```

Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S T T  +C ++ C DST
Sbjct   284   IKPASQTITCENCRLFTCIDST   305

```

```

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD28992.1 Length: 352
Range 1: 283 to 304

```

```

Score:24.2 bits(48), Expect:4.5,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```

```

Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S T T  +C ++ C DST
Sbjct   283   IKPASQTITCENCRLFTCIDST   304

```

```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34102.1 Length: 353
Range 1: 284 to 305

```

```

Score:24.2 bits(48), Expect:4.5,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```

```

Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S T T  +C ++ C DST
Sbjct   284   IKPASQTITCENCRLFTCIDST   305

```

```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA33958.1 Length: 353
>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34002.1 Length: 353
>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34073.1 Length: 353
>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34085.1 Length: 353
Range 1: 284 to 305

```

```

Score:24.2 bits(48), Expect:4.5,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```

```

Query   726   ILPVSMTKTSVDCTMYICGDST   747
          I P S T T  +C ++ C DST
Sbjct   284   IKPASQTITCENCRLFTCIDST   305

```

>env protein [Human endogenous retrovirus K]
Sequence ID: CAB56604.1 Length: 560
Range 1: 285 to 306

Score:24.2 bits(48), Expect:4.6,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S T T +C ++ C DST
Sbjct 285 IKPASQTITCENCRLFTCIDST 306
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34100.1 Length: 353
Range 1: 284 to 305

Score:24.2 bits(48), Expect:4.6,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S T T +C ++ C DST
Sbjct 284 IKPASQTITCENCRLFTCIDST 305
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA33956.1 Length: 353
Range 1: 284 to 305

Score:24.2 bits(48), Expect:4.7,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S T T +C ++ C DST
Sbjct 284 IKPASQTITCENCRLFTCIDST 305
```

>envelope surface protein, partial [Human endogenous retrovirus K]
Sequence ID: ACA34108.1 Length: 353
Range 1: 284 to 305

Score:24.2 bits(48), Expect:4.8,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

```
Query 726 ILPVSMTKTSVDCTMYICGDST 747
          I P S T T +C ++ C DST
```

Sbjct 284 IKPASQTITCENCRLFTCIDST 305

>envelope glycoprotein, partial [Human endogenous retrovirus K]
Sequence ID: ABD29001.1 Length: 353
Range 1: 284 to 305

Score:24.2 bits(48), Expect:4.9,
Method:Compositional matrix adjust.,
Identities:10/22(45%), Positives:13/22(59%), Gaps:0/22(0%)

Query 726 ILPVSMTKTSVDCTMYICGDST 747
I P S T T +C ++ C DST
Sbjct 284 IKPASQTITCENCRLFTCIDST 305

HERV-H BLAST Analysis Raw Data

RID: H2PYZ3WV016

Job Title:(22) - sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe...

Program: BLASTP

Query: sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe acute respiratory
syndrome coronavirus 2 OX=2697049 GN=S PE=1 SV=1 ID: lcl|Query_11062166(amino
acid) Length: 1273

Database: nr All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
excluding environmental samples from WGS projects

Sequences producing significant alignments:

Sequences with E-value BETTER than threshold

Common		Max	Total Query	E	Per.	Acc.	Scientific
Description							Name
Name	Taxid	Score	Score cover	Value	Ident	Len	
Accession							

Sequences with E-value WORSE than threshold

Common		Max	Total Query	E	Per.	Acc.	Scientific
Description							Name
Name	Taxid	Score	Score cover	Value	Ident	Len	
Accession							

envelope protein [HERV-H/env62]							HERV-
H/env62	NA	129525	23.3	23.3	2%	0.21	38.10 584
CAB94192.1							
envelope protein [HERV-H/env59]							HERV-
H/env59	NA	129527	21.6	21.6	2%	0.71	38.10 555
CAB94194.1							
envelope protein [HERV-H/env60]							HERV-
H/env60	NA	129526	21.2	21.2	2%	0.78	38.10 563
CAB94193.2							

Alignments:

>envelope protein [HERV-H/env62]
Sequence ID: CAB94192.1 Length: 584
Range 1: 156 to 176

Score:23.3 bits(46), Expect:0.21,
Method:Compositional matrix adjust.,
Identities:8/21(38%), Positives:12/21(57%), Gaps:0/21(0%)

```
Query   661   ECDIPIGAGICASYQTQTNSP   681
          +  IP+ A +C S+Q  T  P
Sbjct   156   QTTIPVAAPLCISWQRPTGIP   176
```

>envelope protein [HERV-H/env59]
Sequence ID: CAB94194.1 Length: 555
Range 1: 156 to 176

Score:21.6 bits(42), Expect:0.71,
Method:Compositional matrix adjust.,
Identities:8/21(38%), Positives:11/21(52%), Gaps:0/21(0%)

```
Query   661   ECDIPIGAGICASYQTQTNSP   681
          +  IP+ A +C S Q  T  P
Sbjct   156   QTTIPVAAPLCISRQRPTGIP   176
```

>envelope protein [HERV-H/env60]
Sequence ID: CAB94193.2 Length: 563
Range 1: 156 to 176

Score:21.2 bits(41), Expect:0.78,
Method:Compositional matrix adjust.,
Identities:8/21(38%), Positives:11/21(52%), Gaps:0/21(0%)

```
Query   661   ECDIPIGAGICASYQTQTNSP   681
          +  IP+ A +C S Q  T  P
Sbjct   156   QTTIPVAAPLCISRQRPTGIP   176
```

HERV-W BLAST Analysis Raw Data

RID: H3XRGFX014
Job Title:(23) - sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe...

Program: BLASTP
Query: sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe acute respiratory
syndrome coronavirus 2 OX=2697049 GN=S PE=1 SV=1 ID: lcl|Query_5406992(amino
acid) Length: 1273
Database: nr All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
excluding environmental samples from WGS projects

Sequences producing significant alignments:

Sequences with E-value BETTER than threshold

Common Description Name Accession	Taxid	Max Score	Total Query Score cover	E Value	Per. Ident	Acc. Len	Scientific Name
--	-------	--------------	----------------------------	------------	---------------	-------------	--------------------

Sequences with E-value WORSE than threshold

Common Description Name Accession	Taxid	Max Score	Total Query Score cover	E Value	Per. Ident	Acc. Len	Scientific Name
--	-------	--------------	----------------------------	------------	---------------	-------------	--------------------

polyprotein, partial [Multiple sclerosis associated retrovirus]							Multiple
scl... NA		62805	25.5 25.5	3%	0.052	32.56	768
AAB66528.1							

Alignments:

>polyprotein, partial [Multiple sclerosis associated retrovirus]
Sequence ID: AAB66528.1 Length: 768
Range 1: 196 to 236

Score:25.5 bits(51), Expect:0.052,
Method:Compositional matrix adjust.,
Identities:14/43(33%), Positives:21/43(48%), Gaps:3/43(6%)

Query	136	CNDPFLGVYYHKNNKSW-MESEFRVYSSANNCTFEYVSQPFLM	177
		CN P LGV K N W + + R+ + A + VS P+ +	
Sbjct	196	CNTPILGV--RKPNGQWRLVQDLRIINEAVFPLYPVSSPYTL	236

BLOC1S6 BLAST Analysis Raw Data

RID: H47XDWV7014

Job Title:sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein

Program: BLASTP

Query: sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe acute respiratory syndrome coronavirus 2 OX=2697049 GN=S PE=1 SV=1 ID: lcl|Query_6827186(amino acid) Length: 1273

Database: nr All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Sequences producing significant alignments:

Sequences with E-value BETTER than threshold

Common Description Name Accession	Taxid	Max Score	Total Query Score cover	E Value	Per. Ident	Acc. Len	Scientific Name
--	-------	--------------	----------------------------	------------	---------------	-------------	--------------------

Chain A, Spike glycoprotein [Homo sapiens]	Homo sapiens	human	9606	2729	2729	94%	0.0	99.33	1198
7Y71_A									
Chain J, Spike glycoprotein [Homo sapiens]	Homo sapiens	human	9606	2600	2600	94%	0.0	95.92	1274
7TLZ_J									
Chain R, Spike glycoprotein [Homo sapiens]	Homo sapiens	human	9606	2530	2530	94%	0.0	93.92	1273
9ASD_R									
Chain A, Spike glycoprotein [Homo sapiens]	Homo sapiens	human	9606	2015	2015	94%	0.0	75.35	1167
9VG7_A									
Chain D, Spike protein S1 [Homo sapiens]	Homo sapiens	human	9606	494	494	17%	3e-157	100.00	211
7TE1_D									
Chain B, Spike glycoprotein [Homo sapiens]	Homo sapiens	human	9606	485	485	16%	3e-154	99.52	208
8T23_B									
Chain C, Spike protein S1 [Homo sapiens]	Homo sapiens	human	9606	455	455	15%	6e-144	100.00	199
8BG1_C									
Chain E, Spike protein S2' [Homo sapiens]	Homo sapiens	human	9606	453	453	15%	5e-143	98.47	202
8CII_E									
Chain A, Spike protein S1 [Homo sapiens]	Homo sapiens	human	9606	421	421	15%	4e-132	92.31	195
7WIO_A									
Chain B, Spike protein S1 [Homo sapiens]	Homo sapiens	human	9606	420	420	15%	6e-132	92.31	195
7TC9_B									
Chain B, Spike protein S1 [Homo sapiens]	Homo sapiens	human	9606	417	417	16%	4e-130	89.50	219
8ASY_B									
Chain R, Spike protein S1 [Homo sapiens]	Homo sapiens	human	9606	414	414	15%	9e-130	92.19	193
7YOW_R									
Chain A, PDCoV spike glycoprotein S1A domain [Homo sapiens]	Homo sapiens	human	9606	320	320	40%	1e-86	35.79	1079
8R9X_A									

Sequences with E-value WORSE than threshold

Common Description	Taxid	Max Score	Total Query Score	E Value	Per. Ident	Acc. Len	Scientific Name
biogenesis of lysosomal organelles complex 1 subunit 6, partial	9606	34.5	34.5	5%	4.5	28.33	Homo sapiens
KAI2574041.1						113	

Alignments:

```
>Chain A, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y71_A Length: 1198
>Chain B, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y71_B Length: 1198
```

>Chain C, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y71_C Length: 1198
>Chain A, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y72_A Length: 1198
>Chain C, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y72_C Length: 1198
Range 1: 1 to 1198

Score:2729 bits(6362), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:1190/1198 (99%), Positives:1190/1198 (99%), Gaps:0/1198 (0%)

Query	16	VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG	75
		VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG	
Sbjct	1	VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG	60
Query	76	TKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVCEQFQ	
	135		
		TKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVCEQFQ	
Sbjct	61	TKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVCEQFQ	
	120		
Query	136	CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFK	
	195		
		CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFK	
Sbjct	121	CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFK	
	180		
Query	196	NIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTGPDSS	
	255		
		NIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTGPDSS	
Sbjct	181	NIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTGPDSS	
	240		
Query	256	SGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT	
	315		
		SGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT	
Sbjct	241	SGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT	
	300		
Query	316	SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASF	
	375		
		SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASF	
Sbjct	301	SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASF	
	360		
Query	376	TFKCYGVSPKLNLDLCTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIA	
	435		
		TFKCYGVSPKLNLDLCTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIA	
Sbjct	361	TFKCYGVSPKLNLDLCTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIA	
	420		
Query	436	WNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSY	
	495		
		WNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSY	
Sbjct	421	WNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSY	
	480		

Query	496	GFQPTNGVGYPYRVVVLSEFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTES
555		
Sbjct	481	GFQPTNGVGYPYRVVVLSEFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTES
540		
Query	556	NKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDV
615		
Sbjct	541	NKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDV
600		
Query	616	NCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQ
675		
Sbjct	601	NCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQ
660		
Query	676	TQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTS
735		
Sbjct	661	TQTNSPR A SVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTS
720		
Query	736	VDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIK
795		
Sbjct	721	VDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIK
780		
Query	796	DFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
855		
Sbjct	781	DFGGFNFSQILPDPSKPSKRS IEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
840		
Query	856	NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNV
915		
Sbjct	841	NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAG ALQIPF MQMAYRFNGIGVTQNV
900		
Query	916	LYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
975		
Sbjct	901	LYENQKLIANQFNSAIGKIQDSLST SALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
960		
Query	976	VLNDILSRDLKVEAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
1035		
Sbjct	961	VLNDILSRDL EAEVQIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
1020		
Query	1036	QSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAHFPREGVF
1095		

Sbjct	1021	QSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVF	
	1080	QSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVF	
Query	1096	VSNGTHWFVTQRNFYEPQIIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKY	
	1155	VSNGTHWFVTQRNFYEPQIIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKY	
Sbjct	1081	VSNGTHWFVTQRNFYEPQIIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKY	
	1140	VSNGTHWFVTQRNFYEPQIIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKY	
Query	1156	FKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP	1213
		FKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP	
Sbjct	1141	FKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP	1198

>Chain J, Spike glycoprotein [Homo sapiens]
Sequence ID: 7TLZ_J Length: 1274
Range 1: 12 to 1205

Score:2600 bits(6061), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:1151/1200 (96%), Positives:1157/1200 (96%), Gaps:9/1200 (0%)

Query	12	SSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS	71
		SSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFH I S	
Sbjct	12	SSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHVI--S	69
Query	72	GTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLILIVNNATNVVIKVC	
	131	GTNGTKRFDNPVLPFNDGVYFAS EKSNIIRGWIFGTTLDSKTQSLILIVNNATNVVIKVC	
Sbjct	70	GTNGTKRFDNPVLPFNDGVYFASIEKSNIIRGWIFGTTLDSKTQSLILIVNNATNVVIKVC	
	129	GTNGTKRFDNPVLPFNDGVYFASIEKSNIIRGWIFGTTLDSKTQSLILIVNNATNVVIKVC	
Query	132	EFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
	191	EFQFCNDPFL HKNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
Sbjct	130	EFQFCNDPFLD---HKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
	186	EFQFCNDPFLD---HKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
Query	192	FVFKNIDGYFKIYSKHTPINLVR---DLPQGFSALEPLVDLPIGINITRFQTLLALHRSY	
	248	FVFKNIDGYFKIYSKHTPI +VR DLPQGFSALEPLVDLPIGINITRFQTLLALHRSY	
Sbjct	187	FVFKNIDGYFKIYSKHTPI-IVREPEDLPQGFSALEPLVDLPIGINITRFQTLLALHRSY	
	245	FVFKNIDGYFKIYSKHTPI-IVREPEDLPQGFSALEPLVDLPIGINITRFQTLLALHRSY	
Query	249	LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV	
	308	LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV	
Sbjct	246	LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV	
	305	LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV	
Query	309	EKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVL	
	368	EKGIYQTSNFRVQPTESIVRFPNITNLCPF EVFNATRFASVYAWNRKRISNCVADYSVL	

Sbjct	306	EKGIYQTSNFRVQPTESIVRFPNITNLCPFDEVFNATRFASVYAWNKRKISNCVADYSVL
365		
Query	369	YNSASFSTFKCYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDD
428		
Sbjct	366	YN A F TFKCYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTG IADYNYKL PDD
425		YNLAPFFTFKCYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGNIADYNYKL PDD
Query	429	FTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNC
488		
Sbjct	426	FTGCVIAWNSN LDSKV GNYNYLYRLFRKSNLKPFFERDISTEIQAG+ PCNGV GFNC
485		FTGCVIAWNSNKLDSKVSGNYNYLYRLFRKSNLKPFFERDISTEIQAGNKPCNGVAGFNC
Query	489	YFPLQSYGFQPTNGVGYQP YRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTG
548		
Sbjct	486	YFPL+SY F+PT GVG+QPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGL G
545		YFPLRSYSFRPTYGVGHQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLKG
Query	549	TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQ TLEILDITPCSFGGVSVITPGTNTSNQV
608		
Sbjct	546	TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQ TLEILDITPCSFGGVSVITPGTNTSNQV
605		TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQ TLEILDITPCSFGGVSVITPGTNTSNQV
Query	609	AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGA
668		
Sbjct	606	AVLYQ V NCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAE+VNNSYECDIPIGA
665		AVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNNSYECDIPIGA
Query	669	GICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILP
728		
Sbjct	666	GICASYQTQT S A SVASQSIIAYTMSLGAENSV A SNN SIAIPTNFTISVTTEILP
725		GICASYQTQTKSHSGAGSVASQSIIAYTMSLGAENSVAC SNN SIAIPTNFTISVTTEILP
Query	729	VSMTKTSVDCTMYICGDSTEC SNLL LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQI
788		
Sbjct	726	VSMTKTSVDCTMYICGDSTEC SNLL LQYGSFCTQL RALTGIAVEQDKNTQEVFAQVKQI
785		VSMTKTSVDCTMYICGDSTEC SNLL LQYGSFCTQLKRALTGIAVEQDKNTQEVFAQVKQI
Query	789	YKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARD
848		
Sbjct	786	YKTPPIK FGGFNFSQILPDPSKPSKRS IEDLLFNKVT LADAGFIKQYGDCLGDIAARD
845		YKTPPIKYFGGFNFSQILPDPSKPSKRSP IEDLLFNKVT LADAGFIKQYGDCLGDIAARD
Query	849	LICAQKFNGLTVLP LLTDEMIAQYTSALLAGTITSGWTFGAG AALQIPFAMQMAYRFNG
908		
Sbjct	846	LICAQKF GLTVLP LLTDEMIAQYTSALLAGTI SGWTFGAG ALQIPF MQMAYRFNG
905		LICAQKFGLTVLP LLTDEMIAQYTSALLAGTICSGWTFGAGPALQIPFPMQMAYRFNG

Query	909	IGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSS
968		
		IGVTQNVLYENQKLIANQFNSAIGKIQDSLST SALGKLQDVVN NAQALNTLVKQLSS
Sbjct	906	IGVTQNVLYENQKLIANQFNSAIGKIQDSLSTPSALGKLQDVVNHNAQALNTLVKQLSS
965		
Query	969	NFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK
1028		
		FGAISSVLNDI SRLDK EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK
Sbjct	966	KFGAISSVLNDIFSRLDKPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK
1025		
Query	1029	MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAH
1088		
		MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAH
Sbjct	1026	MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAH
1085		
Query	1089	FPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF
1148		
		FPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF
Sbjct	1086	FPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF
1145		
Query	1149	KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
1208		
		KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
Sbjct	1146	KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
1205		

>Chain R, Spike glycoprotein [Homo sapiens]
Sequence ID: 9ASD_R Length: 1273
Range 1: 12 to 1204

Score:2530 bits(5898), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:1128/1201(94%), Positives:1142/1201(95%), Gaps:12/1201(0%)

Query	12	SSQCV---NLTTRTLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA	67
		SSQCV NL T TQ +YTNSFTRGVYYPDKVFRSSVLH TQDLFLPFFSNVTWFHA	
Sbjct	12	SSQCVMLPLFNLITTTQ---SYTNSFTRGVYYPDKVFRSSVLHLTQDLFLPFFSNVTWFHA	68
Query	68	IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNAATNV	
127			
		I SGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNAATNV	
Sbjct	69	I--SGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNAATNV	
126			
Query	128	IKVCEQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFK	
187			
		IKVCEQFCNDPFL VY HKNNKSWMESE VYSSANNCTFEYVSQPFLMDLEGKQGNFK	
Sbjct	127	IKVCEQFCNDPFLDVY-HKNNKSWMESESGVYSSANNCTFEYVSQPFLMDLEGKQGNFK	
185			

Query	188	NLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRS
247		
Sbjct	186	NLREFVFKNIDGYFKIYSKHTPI + RD PQGFSALEPLVDLPIGINITRFQTLLAL+RS
244		NLREFVFKNIDGYFKIYSKHTPI-IGRDFPQGFSALEPLVDLPIGINITRFQTLLALNRS
Query	248	YLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFT
307		
Sbjct	245	YLTPGDSSSGWTAGAA YYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFT
304		YLTPGDSSSGWTAGAADYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFT
Query	308	VEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSV
367		
Sbjct	305	VEKGIYQTSNFRVQPTESIVRFPN+TNLCPF EVFNATRFASVYAWNR RISNCVADYSV
364		VEKGIYQTSNFRVQPTESIVRFPNVTNLCPFHEVFNATRFASVYAWNRRTRISNCVADYSV
Query	368	LYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDP
427		
Sbjct	365	LYN A F FKCYGVSPTKLNDLCFTNVYADSFVI+G+EV QIAPGQTG IADYNYKLDP
424		LYNFAPFFAFKCYGVSPTKLNDLCFTNVYADSFVIKNEVSQIAPGQTGNIADYNYKLDP
Query	428	DFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFN
487		
Sbjct	425	DFTGCVIAWNSN LDSK GNY+Y YRLFRKS LKPFERDISTEIQAG+ PC G +G N
483		DFTGCVIAWNSNKLDSKHSGNYDYWYRLFRKSKLKPFERDISTEIQAGNKPKG-KGPN
Query	488	CYFPLQSYGFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLT
547		
Sbjct	484	CYFPLQSYGF+PT GVG+QPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLT
543		CYFPLQSYGFRPTYGVGHQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLT
Query	548	GTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQ
607		
Sbjct	544	GTGVLTSNKKFLPFQQFGRDI DTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQ
603		GTGVLTKSNKKFLPFQQFGRDIVDTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQ
Query	608	VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNNSECDIPIG
667		
Sbjct	604	VAVLYQ VNCTEV VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAE+VNNSECDIPIG
663		VAVLYQGVNCTEVSVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNNSECDIPIG
Query	668	AGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEIL
727		
Sbjct	664	AG+CASYQTQT S A SVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEIL
723		AGVCASYQTQTKSRGSASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEIL
Query	728	PVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQ
787		
		PVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQL RALTGIAVEQDKNTQEVFAQVKQ

Sbjct	724	PVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLKRALTGIAVEQDKNTQEVFAQVKQ
783		
Query	788	IYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAAR
847		
		IYKTPPIK FGGFNFSQILPDPSKPSKRS IEDLLFNKVTLADAGFIKQYGDCLGDIAAR
Sbjct	784	IYKTPPIKYFGGFNFSQILPDPSKPSKRSPIEDLLFNKVTLADAGFIKQYGDCLGDIAAR
843		
Query	848	DLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFN
907		
		DLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAG ALQIPF MQMAYRFN
Sbjct	844	DLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFPMQMAYRFN
903		
Query	908	GIGVTQNVLYENQKLIANQFNSEAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLS
967		
		GIGVTQNVLYENQKLIANQFNSEAIGKIQDSL ST SALGKLQDVVN NAQALNTLVKQLS
Sbjct	904	GIGVTQNVLYENQKLIANQFNSEAIGKIQDSLSTPSALGKLQDVVNHNAQALNTLVKQLS
963		
Query	968	SNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAAT
1027		
		S FGAISSVLNDILSRDL EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAAT
Sbjct	964	SKFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAAT
1023		
Query	1028	KMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA
1087		
		KMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA
Sbjct	1024	KMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA
1083		
Query	1088	HFPREGVFSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
1147		
		HFPREGVFSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQ ELDS
Sbjct	1084	HFPREGVFSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQLELDS
1143		
Query	1148	FKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE
1207		
		FKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE
Sbjct	1144	FKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE
1203		
Query	1208	Q 1208
		Q
Sbjct	1204	Q 1204

>Chain A, Spike glycoprotein [Homo sapiens]
Sequence ID: 9VG7_A Length: 1167
>Chain B, Spike glycoprotein [Homo sapiens]
Sequence ID: 9VG7_B Length: 1167
>Chain C, Spike glycoprotein [Homo sapiens]

Sequence ID: 9VG7_C Length: 1167
Range 1: 1 to 1158

Score:2015 bits(4696), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:905/1201(75%), Positives:1005/1201(83%), Gaps:48/1201(3%)

```
Query 15      CVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTN 74
Sbjct 1       CVN+T +      Y +S TRGVYYPD FRSS      + FLPF SNVTW+      +
CVNITYGSH--HLYVSSRTRGVYYPDDAFRSSTNVLHEGFFLPFDSNVTWYSFWN----- 53

Query 75      GTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLILIVNNATNVVIKVCEFQ
134
      +++      PF DGVIYF++ +KSN++RGW+FGTTLD+ TQS+L+ N+ T+V ++VC F
Sbjct 54      --QKYSVATSPFGDGVYFSTIDKSNVVRGWVFGTTLDNDTQSVLLYNDGTHVRVEVCTFH
111

Query 135     FCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVF
194
      FC P                      S +YSSA NCT Y          D      G+FK +REFVF
Sbjct 112     FCPTPVFSA-----SSPHLYSSAFNCTLNITLASVRADFTEVDGSFKTIREFVF
160

Query 195     KNIDGYFKIYSKHT----PINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT
250
      K DG +Y T      I      LP G + L PL +PIG+NIT F+TL+ L RS T
Sbjct 161     KLQDGSLNVYYASTSYVLAIGATSQLPSGVTPLVPLWKIPIGLNITNFKTLVYL-RSDNT
219

Query 251     PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEK
310
      P          AAY VG+L+ RT + KY+ENGTI DA+DCALDPLSETKCTL+SF VEK
Sbjct 220     PLQ-----AAYVVGHLKRRTMMFKYDENGITIVDAIDCALDPLSETKCTLRSFIVEK
270

Query 311     GIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYN
370
      GIYQTSNFRVQP +++VRFPNITNLCPF EVFNAT FASVYAWNRKRISNCVADYSVLYN
Sbjct 271     GIYQTSNFRVQPQDTVVRFPNITNLCPFSEVFNATTASFVYAWNRKRISNCVADYSVLYN
330

Query 371     SASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFT
430
      S SFSTF+CYGVS TKLNDLCFTNVYADSFV+RGDEVQRQIAPGQTG IADYNYKLPPDDFT
Sbjct 331     STSFSTFQCYGVSSTKLNDLCFTNVYADSFVVRGDEVQRQIAPGQTGVIADYNYKLPPDDFT
390

Query 431     GCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYF
490
      GCV+AWNS N D+ GN+NY YR++R L+PFERDI+ YQ G+ +
Sbjct 391     GCVLAWNSRNQDASTSGNFNYYYRIWRSEKLRPFERDIAHYDYQVGTQFKSS-----
442

Query 491     PLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTG
550
      L++YGF + G +QPYRVVLSFELL+APATVCGPK+ST L+KNKCVNFNFNGLTGTG
```

Sbjct	443	-LKNYGFYSSAGDSHQPYRVVVL SFELLNAPATVCGPKQSTELIKNKC VNFNFNGLTGTG
501		
Query	551	VLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAV
610		
Sbjct	502	VLT+SNKKF FQQFGRD++D TD+V+DP+TLE+LDITPCS+GGVSVITPGTN S QVAV
561		VLTD SNKKFQSFQQFGRDVSDFTDSVKDPKTLEVL DITPCS YGGVSVITPGTNASTQVAV
Query	611	LYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNN SYECDIPIGAGI
670		
Sbjct	562	LYQDVNCT+VP AIHA+QLTP+WRVYSTG+N+FQT+AGCLIGA EHVNN SY+CDIPIGAGI
621		LYQDVNCTDVPTAIHAEQLTPSWRVYSTGTNMFQTQAGCLIGA EHVNN SYDCDIPIGAGI
Query	671	CASYQTQTNSPRRARSVAS-QSIIAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILPV
729		
Sbjct	622	CA+Y T P RS + + I+AY MSLGAENSVAYSNN+IAIPTNFTISVTTE++PV
677		CATYHT----PSMLRSANNKRIVAYVMSLGAENSVAYSNN TIAIPTNFTISVTTEVMPV
Query	730	SMTKTSVDCTMYICGDS TECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIY
789		
Sbjct	678	SMTKTSVDCTMYICGDS ECS LLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIY
737		SMTKTSVDCTMYICGDSVE CSTLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIY
Query	790	KTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDL
849		
Sbjct	738	KTP IKDFGGFNFSQILPDPSKPSKRS IEDLLFNKVTLADAGF+KQYGDCLGDI ARDL
797		KTPDIKDFGGFNFSQILPDPSKPSKRSP IEDLLFNKVTLADAGFVKQYGDCLGDIQARDL
Query	850	ICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAG AALQIPFAMQMAYRFNGI
909		
Sbjct	798	ICAQKFNGLTVLPPLLTDEMIA YT+AL++GT T+GWTFGAG ALQIPF MQMAYRFNGI
857		ICAQKFNGLTVLPPLLTDEMIAAYTAALISGTATAGWTFGAGPALQIPFPMQMAYRFNGI
Query	910	GVTQNVLYENQKLIANQFN SAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSN
969		
Sbjct	858	GVTQNVLYENQKLIANQFN SAIGKIQ+SL+ST SALGKLQDVVNQNAQALNTLVKQLSSN
917		GVTQNVLYENQKLIANQFN SAIGKIQESLTSTPSALGKLQDVVNQNAQALNTLVKQLSSN
Query	970	FGAISSVLNDILSR LDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
1029		
Sbjct	918	FGAISSVLNDI+SR LDEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
977		FGAISSVLNDIISR LDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
Query	1030	SECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHV TYVPAQEKNFTTAPAICH DGKAHF
1089		
Sbjct	978	SECVLGQSKRVDFCGKGYHLMSFPQ+APHGVVFLHV TY+P+QE+NFTTAPAICH+GKAHF
1037		SECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHV TYIPSQERNFTTAPAICHEGKAHF

```

Query   1090  PREGVFVSNNGTHWFTQARNFYEPQIIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFK
1149
          PREGVFVSNNGTHWF+TQARNFYEPQIIITDNTFVSG CDVVIGIVNNTVYDPLQPEL+SFK
Sbjct   1038  PREGVFVSNNGTHWFITQARNFYEPQIIITDNTFVSGTCDVVIGIVNNTVYDPLQPELESFK
1097

Query   1150  EELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQY
1209
          +ELDKYFKNHTSPD+DLGDISGINASVV+IQKEID L +VAKNLNESLI+LQELGKYEQY
Sbjct   1098  DELDKYFKNHTSPDIDLGDISGINASVVDIQKEIDILKDVAKNLNESLINLQELGKYEQY
1157

Query   1210  I   1210
          I
Sbjct   1158  I   1158

```

```

>Chain D, Spike protein S1 [Homo sapiens]
Sequence ID: 7TE1_D Length: 211
>Chain E, Spike protein S1 [Homo sapiens]
Sequence ID: 7TE1_E Length: 211
Range 1: 1 to 211

```

```

Score:494 bits(1145), Expect:3e-157,
Method:Compositional matrix adjust.,
Identities:211/211(100%), Positives:211/211(100%), Gaps:0/211(0%)

```

```

Query   319  RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFK 378
          RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFK
Sbjct   1    RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFK 60

Query   379  CYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNS 438
          CYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNS
Sbjct   61    CYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNS 120

Query   439  NNLD SKVGGN YNYL RLF RKS NLK PFERDISTE IYQAGSTPCNGVEGFNCYFPLQSYGFQ 498
          NNLD SKVGGN YNYL RLF RKS NLK PFERDISTE IYQAGSTPCNGVEGFNCYFPLQSYGFQ
Sbjct   121  NNLD SKVGGN YNYL RLF RKS NLK PFERDISTE IYQAGSTPCNGVEGFNCYFPLQSYGFQ 180

Query   499  PTNGVGYQP YRVV VLSFELLHAPATVCGPKK 529
          PTNGVGYQP YRVV VLSFELLHAPATVCGPKK
Sbjct   181  PTNGVGYQP YRVV VLSFELLHAPATVCGPKK 211

```

```

>Chain B, Spike glycoprotein [Homo sapiens]
Sequence ID: 8T23_B Length: 208
Range 1: 1 to 208

```

```

Score:485 bits(1124), Expect:3e-154,
Method:Compositional matrix adjust.,
Identities:207/208(99%), Positives:208/208(100%), Gaps:0/208(0%)

```

```

Query   321  QPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCY 380

```


Sbjct	1	QPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCY	60
		QPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCY	
Query	381	GVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNN	440
		GVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNN	
Sbjct	61	GVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNN	120
		GVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNN	
Query	441	LDSKVGGNYNYLYRLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	500
		LDSKVGGNYNYL+RLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	
Sbjct	121	LDSKVGGNYNYLFR LFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	180
		LDSKVGGNYNYLFR LFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	
Query	501	NGVG YQPYRVVLSFELLHAPATVCGPK	528
		NGVG YQPYRVVLSFELLHAPATVCGPK	
Sbjct	181	NGVG YQPYRVVLSFELLHAPATVCGPK	208
		NGVG YQPYRVVLSFELLHAPATVCGPK	

>Chain C, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_C Length: 199
>Chain F, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_F Length: 199
>Chain I, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_I Length: 199
>Chain L, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_L Length: 199
Range 1: 1 to 194

Score:455 bits(1054), Expect:6e-144,
Method:Compositional matrix adjust.,
Identities:194/194(100%), Positives:194/194(100%), Gaps:0/194(0%)

Query	334	NLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	393
		NLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	
Sbjct	1	NLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	60
		NLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSP TKLNDLCFT	
Query	394	NVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLY	453
		NVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLY	
Sbjct	61	NVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLY	120
		NVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLY	
Query	454	RLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVVL	513
		RLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVVL	
Sbjct	121	RLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVVL	180
		RLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVVL	
Query	514	SFELLHAPATVCGP	527
		SFELLHAPATVCGP	
Sbjct	181	SFELLHAPATVCGP	194
		SFELLHAPATVCGP	

>Chain E, Spike protein S2' [Homo sapiens]
Sequence ID: 8CII_E Length: 202
Range 1: 7 to 202

Score:453 bits(1049), Expect:5e-143,
Method:Compositional matrix adjust.,

Identities:193/196(98%), Positives:193/196(98%), Gaps:0/196(0%)

```
Query 333  TNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCF 392
          TNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCF
Sbjct 7    TNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCF 66

Query 393  TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYYL 452
          TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYY
Sbjct 67    TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYYR 126

Query 453  YRLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVV 512
          YRLFRKSNLKPFFERDISTEIYQAGS PCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVV
Sbjct 127   YRLFRKSNLKPFFERDISTEIYQAGSKPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVV 186

Query 513  LSFELLHAPATVCGPK 528
          LSFELLHAPATVCG K
Sbjct 187  LSFELLHAPATVCGKK 202
```

>Chain A, Spike protein S1 [Homo sapiens]
Sequence ID: 7WI0_A Length: 195
Range 1: 1 to 195

Score:421 bits(975), Expect:4e-132,
Method:Compositional matrix adjust.,
Identities:180/195(92%), Positives:184/195(94%), Gaps:0/195(0%)

```
Query 333  TNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCF 392
          TNLCPF EVFNATRFASVYAWNKRKISNCVADYSVLYN A F TFKCYGVSPTKLNLCF
Sbjct 1    TNLCPFDEVFNATRFASVYAWNKRKISNCVADYSVLYNLAPFFTFKCYGVSPTKLNLCF 60

Query 393  TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNYYL 452
          TNVYADSFVIRGDEVQRQIAPGQTG IADYNYKLPPDFTGCVIAWNSN LSKV GNYYL
Sbjct 61    TNVYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPPDFTGCVIAWNSNKLDSKVGSGNYYL 120

Query 453  YRLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVV 512
          YRLFRKSNLKPFFERDISTEIYQAG+ PCNGV GFNCYFPL+SY F+PT GVG+QPYRVVV
Sbjct 121   YRLFRKSNLKPFFERDISTEIYQAGNKPCNGVAGFNCYFPLRSYSFRPTYGVGHQPYRVVV 180

Query 513  LSFELLHAPATVCGP 527
          LSFELLHAPATVCGP
Sbjct 181  LSFELLHAPATVCGP 195
```

>Chain B, Spike protein S1 [Homo sapiens]
Sequence ID: 7TC9_B Length: 195
Range 1: 1 to 195

Score:420 bits(973), Expect:6e-132,
Method:Compositional matrix adjust.,
Identities:180/195(92%), Positives:184/195(94%), Gaps:0/195(0%)

```
Query 332  ITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLYNSASFSTFKCYGVSPTKLNLC 391
```

Sbjct	1	ITNLCPF EVFNATRFASVYAWNRKRISNCVADYSVLYN A F TFKCYGVSPTKLN DLC	60
Query	392	FTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNY	451
Sbjct	61	FTNVYADSFVIRGDEV RQIAPGQTG IADYNYKL PDDFTGCVIAWNSN LDSKV GNYNY	120
Query	452	LYRLFRKSNLKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQPYRVV	511
Sbjct	121	LYRLFRKSNLKPFFERDISTEIIYQAG+ PCNGV GFNCYFPL+SY F+PT GVG+QPYRVV	180
Query	512	VLSFELLHAPATVCG 526	
		VLSFELLHAPATVCG	
Sbjct	181	VLSFELLHAPATVCG 195	

>Chain B, Spike protein S1 [Homo sapiens]
Sequence ID: 8ASY_B Length: 219
Range 1: 1 to 200

Score:417 bits(966), Expect:4e-130,
Method:Compositional matrix adjust.,
Identities:179/200(90%), Positives:183/200(91%), Gaps:0/200(0%)

Query	333	TNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN DLCF	392
Sbjct	1	TNLCPF EVFNATRFASVYAWNRKRISNCVADYSVLYN A F FKC YGVSPTKLN DLCF	60
Query	393	TNVYADSFVIRGDEV RQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYNYL	452
Sbjct	61	TNVYADSFVIRG+EV QIAPGQTG IADYNYKL PDDFTGCVIAWNSN LDSKV GNYNYL	120
Query	453	YRLFRKSNLKPFFERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVV	512
Sbjct	121	YRLFRKS LKPFFERDISTEIIYQAG+ PCNGV GFNCYFPLQSYGF+PT GVG+QPYRVVV	180
Query	513	LSFELLHAPATVCGPKKSTN 532	
		LSFELLHAPATVCG K N	
Sbjct	181	LSFELLHAPATVCGKKSLLN 200	

>Chain R, Spike protein S1 [Homo sapiens]
Sequence ID: 7Y0W_R Length: 193
Range 1: 1 to 192

Score:414 bits(959), Expect:9e-130,
Method:Compositional matrix adjust.,
Identities:177/192(92%), Positives:181/192(94%), Gaps:0/192(0%)

Query	335	LCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN DLCFTN	394
Sbjct	1	LCPF EVFNATRFASVYAWNRKRISNCVADYSVLYN A F TFKCYGVSPTKLN DLCFTN	60

Query	395	VYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNLYR	454
		VYADSFVIRGDEVQRQIAPGQTG IADYNYKLPDDFTGCVIAWNSN LSKV GNYNLYR	
Sbjct	61	VYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPDDFTGCVIAWNSNKLDSKVGSNYNLYR	120
Query	455	LFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLS	514
		LFRKSNLKPFERDISTEIYQAG+ PCNGV GFNCYFPL+SY F+PT GVG+QPYRVVLS	
Sbjct	121	LFRKSNLKPFERDISTEIYQAGNKPCNGVAGFNCYFPLRSYSFRPTYGVGHQPYRVVLS	180
Query	515	FELLHAPATVCG	526
		FELLHAPATVCG	
Sbjct	181	FELLHAPATVCG	192

>Chain A, PDCoV spike glycoprotein S1A domain [Homo sapiens]
Sequence ID: 8R9X_A Length: 1079
Range 1: 545 to 1079

Score:320 bits(739), Expect:1e-86,
Method:Compositional matrix adjust.,
Identities:194/542(36%), Positives:281/542(51%), Gaps:40/542(7%)

Query	705	VAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNNLLQYGSFCTQLN	
	764		
		V+ + + IP+ F++SV TE L V + VDC Y+C ++ C LL QY S C+ +	
Sbjct	545	VSLYDGEVEIPSAFSLSVQTEYLQVQAEQVIVDCPQYVCNGNSRCLQLLAQYTSACSNI	
	604		
Query	765	RALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDF-GGFNFSQILPDPSKPSKRSFIEDLLF	
	823		
		AL A + +F Q + I +F G +NFS IL ++ RS IEDLLF	
Sbjct	605	AALHSSAQLDSREIINMFQTSTQSLQLANITNFKGDYNFSSILT--TRIGGRSAIEDLLF	
	662		
Query	824	NKVTLADAGFIKQ-YGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTI	
	882		
		NKV + G + Q Y C D+A DL+C+Q +NG+ VLP ++ E +A YT +L +	
Sbjct	663	NKVVTSGLGTVQDYKSCSRDMAIADLVCSQYYNGIMVLPGVVDAEKMAMYTGSLTGAMV	
	722		
Query	883	TSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLST-	
	941		
		G T A A + R N + + NVL ENQK++A FN A+G I +LSS	
Sbjct	723	FGGLTAAAAIPF----ATAVQARLNYVALQTNVLQENQKILAESFNQAVGNISLALSSVN	
	778		
Query	942	-----ASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVE	
	988		
		A A+ K+Q VVNQ +AL+ L QLS+NF AIS+ + DI +RL++VE	
Sbjct	779	DAIQQTSEALNTVAIAIKKIQTVVNQGEALSHLTAQLSNNFQAISTSIQDIYNRLEEVE	
	838		
Query	989	AEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYH	
	1048		
		A Q+DRLITGRL +L YVTQ L + ++IR S LA K++ECV QS R FCG G H	

```

Sbjct  839  ANQQVDRLITGRLAALNAYVTQLLNQMSQIRQSRLLAQQKINECVKSQSPRYGFCGNGTH
898

Query  1049  LMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHD---GKAHFPREGVFVSNNGTHWFTV
1105
          + S  Q+AP+G+ F+H  VP +          + IC D  G +  P+  ++  N + W VT
Sbjct  899  IFSLTQTAPNGIFFMHAVLVPNKFTRVNASAGICVDNTRGYSLQPQLILYQFNNS-WRVVT
957

Query  1106  QRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKN---HTSP
1162
          RN YEP++          +          +C V          + P++          + +          N  T P
Sbjct  958  PRNMYEPRLPRQADFIQLTDCSVTFYNTTAANLPNIIPDIIDVNQTVSDIIDNLPTATPP
1017

Query  1163  DVDLG-----DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK
1211
          D+G          +I+ +          N+ +  DRL          NLN +L+DL+ L + E Y+K
Sbjct  1018  QWDVGIYNNITILNLTVEINDLQERSKNLSQIADRLQNYIDNLNNTLVLEWLN RVETYLK
1077

Query  1212  WP  1213
          WP
Sbjct  1078  WP  1079

```

>biogenesis of lysosomal organelles complex 1 subunit 6, partial [Homo sapiens]

Sequence ID: KAI2574041.1 Length: 113

>biogenesis of lysosomal organelles complex 1 subunit 6, partial [Homo sapiens]

Sequence ID: KAI4057642.1 Length: 113

Range 1: 32 to 91

Score:34.5 bits(72), Expect:4.5,

Method:Composition-based stats.,

Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

```

Query  1145  LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202

```

```

          LD+ ++E+ K+ + H+  D++          +          +A +VNI+KE+  L+E          L +  + LQ+
Sbjct  32     LDTLEQEISKFKCHECHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLKKRALKLQQ  91

```

ZNF462 BLAST Analysis Raw Data

RID: H48U4FWY016

Job Title:sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe...

Program: BLASTP

Query: sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe acute respiratory syndrome coronavirus 2 OX=2697049 GN=S PE=1 SV=1 ID: lcl|Query_51716(amino acid) Length: 1273

Database: nr All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Sequences producing significant alignments:

Sequences with E-value BETTER than threshold

Common Description Name Accession	Taxid	Max Score	Total Query Score cover	E Value	Per. Ident	Acc. Len	Scientific Name
Chain A, Spike glycoprotein [Homo sapiens] sapiens human 7Y71_A		9606	2729	2729	94%	0.0	Homo 99.33 1198
Chain J, Spike glycoprotein [Homo sapiens] sapiens human 7TLZ_J		9606	2600	2600	94%	0.0	Homo 95.92 1274
Chain R, Spike glycoprotein [Homo sapiens] sapiens human 9ASD_R		9606	2530	2530	94%	0.0	Homo 93.92 1273
Chain A, Spike glycoprotein [Homo sapiens] sapiens human 9VG7_A		9606	2015	2015	94%	0.0	Homo 75.35 1167
Chain D, Spike protein S1 [Homo sapiens] sapiens human 7TE1_D		9606	494	494	17%	3e-157	Homo 100.00 211
Chain B, Spike glycoprotein [Homo sapiens] sapiens human 8T23_B		9606	485	485	16%	3e-154	Homo 99.52 208
Chain C, Spike protein S1 [Homo sapiens] sapiens human 8BG1_C		9606	455	455	15%	6e-144	Homo 100.00 199
Chain E, Spike protein S2' [Homo sapiens] sapiens human 8CII_E		9606	453	453	15%	5e-143	Homo 98.47 202
Chain A, Spike protein S1 [Homo sapiens] sapiens human 7WIO_A		9606	421	421	15%	4e-132	Homo 92.31 195
Chain B, Spike protein S1 [Homo sapiens] sapiens human 7TC9_B		9606	420	420	15%	6e-132	Homo 92.31 195
Chain B, Spike protein S1 [Homo sapiens] sapiens human 8ASY_B		9606	417	417	16%	4e-130	Homo 89.50 219
Chain R, Spike protein S1 [Homo sapiens] sapiens human 7Y0W_R		9606	414	414	15%	9e-130	Homo 92.19 193
Chain A, PDCoV spike glycoprotein S1A domain [Homo sapiens] sapiens human 8R9X_A		9606	320	320	40%	1e-86	Homo 35.79 1079

Sequences with E-value WORSE than threshold

Common Description Name Accession	Taxid	Max Score	Total Query Score cover	E Value	Per. Ident	Acc. Len	Scientific Name
--	-------	--------------	----------------------------	------------	---------------	-------------	--------------------

biogenesis of lysosomal organelles complex 1 subunit 6, partial	Homo sapiens	human	9606	34.5	34.5	5%	4.5	28.33	113
KAI2574041.1									
hCG2001986, isoform CRA_c	Homo sapiens	human	9606	34.5	34.5	5%	5.4	28.33	131
EAW77322.1									
biogenesis of lysosome-related organelles complex 1 subunit 6...	Homo sapiens	human	9606	34.5	34.5	5%	6.9	28.33	172
NP_036520.1									
unnamed protein product	Homo sapiens	human	9606	34.5	34.5	5%	6.9	28.33	172
BAG37954.1									
biogenesis of lysosome-related organelles complex 1 subunit 6...	Homo sapiens	human	9606	34.5	34.5	5%	7.0	28.33	177
NP_001298184.1									
immunoglobulin heavy chain junction region	Homo sapiens	human	9606	29.3	29.3	1%	13	68.75	21
MOL23798.1									
hCG22236, isoform CRA_b, partial	Homo sapiens	human	9606	34.0	34.0	8%	13	23.47	500
EAX10979.1									
Chain A, ATP-dependent RNA helicase DHX15	Homo sapiens	human	9606	33.6	33.6	4%	18	27.27	686
8EJM_A									
Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase...	Homo sapiens	human	9606	33.6	33.6	4%	20	27.27	689
6SH6_A									
Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase...	Homo sapiens	human	9606	33.6	33.6	4%	20	27.27	690
5XDR_A									
immunoglobulin heavy chain junction region	Homo sapiens	human	9606	28.9	28.9	1%	20	55.56	25
MBB2037351.1									
immunoglobulin heavy chain junction region	Homo sapiens	human	9606	28.5	28.5	1%	28	55.56	25
MBB2121301.1									
unnamed protein product	Homo sapiens	human	9606	33.2	33.2	4%	29	27.27	784
BAG64538.1									
immunoglobulin heavy chain junction region	Homo sapiens	human	9606	28.0	28.0	1%	30	62.50	21
MOL37782.1									
ATP-dependent RNA helicase DHX15	Homo sapiens	human	9606	32.7	32.7	4%	30	27.27	795
NP_001349.2									
DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_h	Homo sapiens	human	9606	32.7	32.7	4%	31	27.27	778
EAW92821.1									
immunoglobulin heavy chain junction region	Homo sapiens	human	9606	28.0	28.0	1%	32	71.43	17
MBB2102104.1									
t-SNARE domain-containing protein 1 isoform X2	Homo sapiens	human	9606	32.7	32.7	7%	38	26.26	981
XP_047277414.1									
DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_g	Homo sapiens	human	9606	32.3	32.3	4%	41	27.27	709
EAW92820.1									

coenzyme Q6, monooxygenase [Homo sapiens]								Homo	
sapiens	human	9606	30.6	30.6	3%	46	31.71	86	
KAI2571974.1									
pyruvate kinase M1/2 [Homo sapiens]								Homo	
sapiens	human	9606	30.2	30.2	3%	47	33.33	69	
KAI2574971.1									
t-SNARE domain-containing protein 1 isoform X2 [Homo sapiens]								Homo	
sapiens	human	9606	32.3	32.3	7%	49	26.26	981	
XP_054215930.1									
t-SNARE domain-containing protein 1 isoform X7 [Homo sapiens]								Homo	
sapiens	human	9606	32.3	32.3	7%	49	26.26	892	
XP_047277418.1									
t-SNARE domain-containing protein 1 isoform X4 [Homo sapiens]								Homo	
sapiens	human	9606	32.3	32.3	7%	50	26.26	931	
XP_047277416.1									
DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_d [Homo...]								Homo	
sapiens	human	9606	31.9	31.9	4%	57	27.27	650	
EAW92817.1									
immunoglobulin heavy chain junction region [Homo sapiens]								Homo	
sapiens	human	9606	27.2	27.2	1%	58	75.00	19	
MCG22225.1									
immunoglobulin heavy chain junction region [Homo sapiens]								Homo	
sapiens	human	9606	27.6	27.6	1%	59	64.29	22	
MFT1129265.1									
ATP-dependent RNA helicase DHX15 isoform X2 [Homo sapiens]								Homo	
sapiens	human	9606	31.9	31.9	4%	61	27.27	600	
XP_047305655.1									
DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_e [Homo...]								Homo	
sapiens	human	9606	31.9	31.9	4%	64	27.27	499	
EAW92818.1									
t-SNARE domain-containing protein 1 isoform X7 [Homo sapiens]								Homo	
sapiens	human	9606	31.9	31.9	7%	65	26.26	892	
XP_054215935.1									
ATP-dependent RNA helicase DHX15 isoform X1 [Homo sapiens]								Homo	
sapiens	human	9606	31.9	31.9	4%	66	27.27	608	
XP_047305654.1									
ubiquinone biosynthesis monooxygenase COQ6, mitochondrial...								Homo	
sapiens	human	9606	31.9	31.9	3%	67	31.71	443	
NP_872286.2									
hCG1644135, isoform CRA_b, partial [Homo sapiens]								Homo	
sapiens	human	9606	30.6	30.6	2%	67	43.48	111	
EAW68450.1									
Carnitine O-palmitoyltransferase II, mitochondrial precursor...								Homo	
sapiens	human	9606	31.9	31.9	2%	68	37.93	577	
BAD96772.1									
coenzyme Q6, monooxygenase [Homo sapiens]								Homo	
sapiens	human	9606	31.5	31.5	3%	69	31.71	443	
KAI4061598.1									
carnitine O-palmitoyltransferase 2, mitochondrial isoform 2...								Homo	
sapiens	human	9606	31.9	31.9	2%	70	37.93	635	
NP_001317518.1									
ubiquinone biosynthesis monooxygenase COQ6, mitochondrial...								Homo	
sapiens	human	9606	31.5	31.5	3%	70	31.71	407	
NP_001412187.1									
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo	
sapiens	human	9606	31.9	31.9	2%	71	37.93	635	
KAI4080722.1									

carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	73	37.93	635	
KAI2517173.1								
t-SNARE domain-containing protein 1 isoform X4 [Homo sapiens]								Homo
sapiens human	9606	31.9	31.9	7%	73	26.26	931	
XP_054215932.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	74	37.93	658	
KAI4080729.1								
carnitine O-palmitoyltransferase 2, mitochondrial isoform 1...								Homo
sapiens human	9606	31.5	31.5	2%	75	37.93	658	
NP_000089.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	76	37.93	658	
KAI2517171.1								
immunoglobulin heavy chain junction region [Homo sapiens]								Homo
sapiens human	9606	27.2	27.2	1%	77	69.23	20	
MOQ20290.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	82	37.93	647	
KAI4080727.1								
immunoglobulin heavy chain junction region [Homo sapiens]								Homo
sapiens human	9606	27.2	27.2	2%	82	47.62	24	
MBB1991959.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	82	37.93	670	
KAI2517170.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	82	37.93	670	
KAI4080725.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	82	37.93	647	
KAI2517172.1								
ATP-dependent RNA helicase #46 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	4%	84	27.27	813	
BAA23987.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	88	37.93	598	
KAI2517175.1								
spindle and centriole-associated protein 1 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	89	32.31	855	
NP_001318007.1								
unnamed protein product [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	90	32.31	695	
BAG54389.1								
hypothetical protein, partial [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	95	30.00	2403	
CAH18698.1								
zinc finger protein 462 isoform X3 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	99	30.00	2506	
XP_054219425.1								
unnamed protein product [Homo sapiens]								Homo
sapiens human	9606	31.0	31.0	4%	99	30.00	223	
BAG65508.1								
zinc finger protein 462 isoform 1 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	100	30.00	2506	
NP_067047.4								

hypothetical protein [Homo sapiens]							Homo	
sapiens	human	9606	31.5	31.5	5%	100	30.00	2506
CAH56168.1								
zinc finger protein 462 [Homo sapiens]							Homo	
sapiens	human	9606	31.5	31.5	5%	100	30.00	2506
KAI2553449.1								

Alignments:

```
>Chain A, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y71_A Length: 1198
>Chain B, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y71_B Length: 1198
>Chain C, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y71_C Length: 1198
>Chain A, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y72_A Length: 1198
>Chain C, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y72_C Length: 1198
Range 1: 1 to 1198
```

Score:2729 bits(6362), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:1190/1198 (99%), Positives:1190/1198 (99%), Gaps:0/1198 (0%)

Query	16	VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG	75
		VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG	
Sbjct	1	VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG	60
Query	76	TKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVCEFQF	
	135		
		TKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVCEFQF	
Sbjct	61	TKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVCEFQF	
	120		
Query	136	CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFK	
	195		
		CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFK	
Sbjct	121	CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFK	
	180		
Query	196	NIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIGINITRFQTLLALHRSYLT PGDSS	
	255		
		NIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIGINITRFQTLLALHRSYLT PGDSS	
Sbjct	181	NIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIGINITRFQTLLALHRSYLT PGDSS	
	240		
Query	256	SGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT	
	315		
		SGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT	
Sbjct	241	SGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT	
	300		
Query	316	SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFS	
	375		
		SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFS	

Sbjct	301	SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLNSASF
360		
Query	376	TFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIA
435		TFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIA
Sbjct	361	TFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIA
420		
Query	436	WNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSY
495		WNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSY
Sbjct	421	WNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSY
480		
Query	496	GFQPTNGVGYPYRVVVLSEFLLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTES
555		GFQPTNGVGYPYRVVVLSEFLLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTES
Sbjct	481	GFQPTNGVGYPYRVVVLSEFLLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTES
540		
Query	556	NKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDV
615		NKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDV
Sbjct	541	NKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDV
600		
Query	616	NCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQ
675		NCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQ
Sbjct	601	NCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQ
660		
Query	676	TQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTS
735		TQTNSPR A SVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTS
Sbjct	661	TQTNSPRAAASVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTS
720		
Query	736	VDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIK
795		VDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIK
Sbjct	721	VDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIK
780		
Query	796	DFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
855		DFGGFNFSQILPDPSKPSKRS IEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
Sbjct	781	DFGGFNFSQILPDPSKPSKRSPIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
840		
Query	856	NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNV
915		NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAG ALQIPF MQMAYRFNGIGVTQNV
Sbjct	841	NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFPMQMAYRFNGIGVTQNV
900		

Query	916	LYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS	
	975		
		LYENQKLIANQFNSAIGKIQDSLST SALGKLQDVVNQNAQALNTLVKQLSSNFGAISS	
Sbjct	901	LYENQKLIANQFNSAIGKIQDSLSTPSALGKLQDVVNQNAQALNTLVKQLSSNFGAISS	
	960		
Query	976	VLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG	
	1035		
		VLNDILSRDL EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG	
Sbjct	961	VLNDILSRDLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG	
	1020		
Query	1036	QSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVF	
	1095		
		QSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVF	
Sbjct	1021	QSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVF	
	1080		
Query	1096	VSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKY	
	1155		
		VSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKY	
Sbjct	1081	VSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKY	
	1140		
Query	1156	FKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP	1213
		FKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP	
Sbjct	1141	FKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP	1198

>Chain J, Spike glycoprotein [Homo sapiens]
Sequence ID: 7TLZ_J Length: 1274
Range 1: 12 to 1205

Score:2600 bits(6061), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:1151/1200 (96%), Positives:1157/1200 (96%), Gaps:9/1200 (0%)

Query	12	SSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS	71
		SSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFH I S	
Sbjct	12	SSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHVI--S	69
Query	72	GTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNTATNVVIKVC	
	131		
		GTNGTKRFDNPVLPFNDGVYFAS EKSNIIRGWIFGTTLDSKTQSLIVNNTATNVVIKVC	
Sbjct	70	GTNGTKRFDNPVLPFNDGVYFASIEKSNIIRGWIFGTTLDSKTQSLIVNNTATNVVIKVC	
	129		
Query	132	EFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
	191		
		EFQFCNDPFL HKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
Sbjct	130	EFQFCNDPFLD---HKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
	186		
Query	192	FVFKNIDGYFKIYSKHTPINLVR---DLPQGFSALEPLVDLPIGINITRFQTLLALHRSY	
	248		

Sbjct	187	FVFKNIDGYFKIYSKHTPI +VR DLPQGFSALEPLVDLPIGINITRFQTLLALHRSY
245		FVFKNIDGYFKIYSKHTPI-IVREPEDLPQGFSALEPLVDLPIGINITRFQTLLALHRSY
Query	249	LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV
308		LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV
Sbjct	246	LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV
305		LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV
Query	309	EKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVL
368		EKGIYQTSNFRVQPTESIVRFPNITNLCPF EVFNATRFASVYAWNRRKRISNCVADYSVL
Sbjct	306	EKGIYQTSNFRVQPTESIVRFPNITNLCPFDEVFNATRFASVYAWNRRKRISNCVADYSVL
365		EKGIYQTSNFRVQPTESIVRFPNITNLCPFDEVFNATRFASVYAWNRRKRISNCVADYSVL
Query	369	YNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPD
428		YN A F TFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTG IADYNYKLPPD
Sbjct	366	YNLAPFFTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPPD
425		YNLAPFFTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPPD
Query	429	FTGCVIAWNSNNLDSKVGNYNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNC
488		FTGCVIAWNSN LDSKV GNYNYLYRLFRKSNLKPFERDISTEIQAG+ PCNGV GFNC
Sbjct	426	FTGCVIAWNSNKLDSKVGNYNYLYRLFRKSNLKPFERDISTEIQAGNKPCNGVAGFNC
485		FTGCVIAWNSNKLDSKVGNYNYLYRLFRKSNLKPFERDISTEIQAGNKPCNGVAGFNC
Query	489	YFPLQSYGFQPTNGVGYQPYRVVVLSEFLLHAPATVCGPKKSTNLVKNKCVNFNFNGLTG
548		YFPL+SY F+PT GVG+QPYRVVVLSEFLLHAPATVCGPKKSTNLVKNKCVNFNFNGL G
Sbjct	486	YFPLRSYSFRPTYGVGHQPYRVVVLSEFLLHAPATVCGPKKSTNLVKNKCVNFNFNGLKG
545		YFPLRSYSFRPTYGVGHQPYRVVVLSEFLLHAPATVCGPKKSTNLVKNKCVNFNFNGLKG
Query	549	TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQV
608		TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQV
Sbjct	546	TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQV
605		TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQV
Query	609	AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAETHVNNSECDIPIGA
668		AVLYQ VNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAE+VNNSECDIPIGA
Sbjct	606	AVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNNSECDIPIGA
665		AVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNNSECDIPIGA
Query	669	GICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILP
728		GICASYQTQT S A SVASQSIIAYTMSLGAENSV SNNNSIAIPTNFTISVTTEILP
Sbjct	666	GICASYQTQTKSHGAGSVASQSIIAYTMSLGAENSVACSNNSIAIPTNFTISVTTEILP
725		GICASYQTQTKSHGAGSVASQSIIAYTMSLGAENSVACSNNSIAIPTNFTISVTTEILP
Query	729	VSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQI
788		VSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQL RALTGIAVEQDKNTQEVFAQVKQI
Sbjct	726	VSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLKRALTGIAVEQDKNTQEVFAQVKQI
785		VSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLKRALTGIAVEQDKNTQEVFAQVKQI

Query	789	YKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYGDCLGDIAARD
	848	
		YKTPPIK FGGFNFSQILPDPSKPSKRS IEDLLFNKVTLDAGFIKQYGDCLGDIAARD
Sbjct	786	YKTPPIKYFGGFNFSQILPDPSKPSKRSPIEDLLFNKVTLDAGFIKQYGDCLGDIAARD
	845	
Query	849	LICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNG
	908	
		LICAQKF GLTVLPPLLTDEMIAQYTSALLAGTI SGWTFGAG ALQIPF MQMAYRFNG
Sbjct	846	LICAQKFGLTVLPPLLTDEMIAQYTSALLAGTICSGWTFGAGPALQIPFPMQMAYRFNG
	905	
Query	909	IGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSS
	968	
		IGVTQNVLYENQKLIANQFNSAIGKIQDSLST SALGKLQDVVN NAQALNTLVKQLSS
Sbjct	906	IGVTQNVLYENQKLIANQFNSAIGKIQDSLSTPSALGKLQDVVNHNAQALNTLVKQLSS
	965	
Query	969	NFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK
	1028	
		FGAISSVLNDI SRLDK EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK
Sbjct	966	KFGAISSVLNDIFSRLDKPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK
	1025	
Query	1029	MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAH
	1088	
		MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAH
Sbjct	1026	MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAH
	1085	
Query	1089	FPREGVFVSNNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF
	1148	
		FPREGVFVSNNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF
Sbjct	1086	FPREGVFVSNNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF
	1145	
Query	1149	KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
	1208	
		KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
Sbjct	1146	KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
	1205	

>Chain R, Spike glycoprotein [Homo sapiens]

Sequence ID: 9ASD_R Length: 1273

Range 1: 12 to 1204

Score:2530 bits(5898), Expect:0.0,

Method:Compositional matrix adjust.,

Identities:1128/1201(94%), Positives:1142/1201(95%), Gaps:12/1201(0%)

Query	12	SSQCV---NLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA	67
		SSQCV NL T TQ +YTNSFTRGVYYPDKVFRSSVLH TQDLFLPFFSNVTWFHA	
Sbjct	12	SSQCVMLFNLITTTQ---SYTNSFTRGVYYPDKVFRSSVLHLTQDLFLPFFSNVTWFHA	68

Query	68	IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLILVNNATNVV
127		
Sbjct	69	I SGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLILVNNATNV
126		I--SGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLILVNNATNVF
Query	128	IKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFK
187		
Sbjct	127	IKVCEFQFCNDPFL VY HKNNKSWMESE VYSSANNCTFEYVSQPFLMDLEGKQGNFK
185		IKVCEFQFCNDPFLDVY-HKNNKSWMESESGVYSSANNCTFEYVSQPFLMDLEGKQGNFK
Query	188	NLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRS
247		
Sbjct	186	NLREFVFKNIDGYFKIYSKHTPI + RD PQGFSALEPLVDLPIGINITRFQTLLAL+RS
244		NLREFVFKNIDGYFKIYSKHTPI-IGRDFPQGFSALEPLVDLPIGINITRFQTLLALNRS
Query	248	YLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF
307		
Sbjct	245	YLTPGDSSSGWTAGAA YYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF
304		YLTPGDSSSGWTAGAADYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF
Query	308	VEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSV
367		
Sbjct	305	VEKGIYQTSNFRVQPTESIVRFPN+TNLCPF EVFNATRFASVYAWNKRISNCVADYSV
364		VEKGIYQTSNFRVQPTESIVRFPNVTNLCPFHEVFNATRFASVYAWNKRISNCVADYSV
Query	368	LYNSASFSTFKCYGVSPKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDP
427		
Sbjct	365	LYN A F FKCYGVSPKLNLDLCFTNVYADSFVI+G+EV QIAPGQTG IADYNYKLDP
424		LYNFAPFFAFKCYGVSPKLNLDLCFTNVYADSFVIKNEVSQIAPGQTGNIADYNYKLDP
Query	428	DFTGCVIAWNSNNLDSKVGNYNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFN
487		
Sbjct	425	DFTGCVIAWNSN LDSK GNY+Y YRLFRKS LKPFERDISTEIQAG+ PC G +G N
483		DFTGCVIAWNSNKLDSKHSGNYDYWYRLFRKSKLKPFERDISTEIQAGNKPKG-KGPN
Query	488	CYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLT
547		
Sbjct	484	CYFPLQSYGF+PT GVG+QPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLT
543		CYFPLQSYGFRPTYGVGHQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLT
Query	548	GTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTEILDITPCSFGGVSVITPGTNTSNQ
607		
Sbjct	544	GTGVLTSNKKFLPFQQFGRDI DTTDAVRDPQTEILDITPCSFGGVSVITPGTNTSNQ
603		GTGVLTKSNKKFLPFQQFGRDIVDTTDAVRDPQTEILDITPCSFGGVSVITPGTNTSNQ
Query	608	VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIG
667		

Sbjct	604	VAVLYQ VNCTEV VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAE+VNNSYECDIPIG
663		VAVLYQGVNCTEVSVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNNSYECDIPIG
Query	668	AGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEIL
727		
Sbjct	664	AG+CASYQTQT S A SVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEIL
723		AGVCASYQTQTKSRGSASSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEIL
Query	728	PVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQ
787		
Sbjct	724	PVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQL RALTGIAVEQDKNTQEVFAQVKQ
783		PVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLKRALTGIAVEQDKNTQEVFAQVKQ
Query	788	IYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAAR
847		
Sbjct	784	IYKTPPIK FGGFNFSQILPDPSKPSKRS IEDLLFNKVTLADAGFIKQYGDCLGDIAAR
843		IYKTPPIKYFGGFNFSQILPDPSKPSKRSPIEDLLFNKVTLADAGFIKQYGDCLGDIAAR
Query	848	DLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGALQIPFAMQMAYRFN
907		
Sbjct	844	DLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAG ALQIPF MQMAYRFN
903		DLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFPMQMAYRFN
Query	908	GIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLS
967		
Sbjct	904	GIGVTQNVLYENQKLIANQFNSAIGKIQDSL ST SALGKLQDVVN NAQALNTLVKQLS
963		GIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTPSALGKLQDVVNHNAQALNTLVKQLS
Query	968	SNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAAT
1027		
Sbjct	964	S FGAISSVLNDILSRDL EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAAT
1023		SKFGAISSVLNDILSRDLPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAAT
Query	1028	KMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA
1087		
Sbjct	1024	KMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA
1083		KMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA
Query	1088	HFPREGVFSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
1147		
Sbjct	1084	HFPREGVFSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQ ELDS
1143		HFPREGVFSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQLELDS
Query	1148	FKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE
1207		
Sbjct	1144	FKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE
1203		FKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE

Query 1208 Q 1208
 Q
 Sbjct 1204 Q 1204

>Chain A, Spike glycoprotein [Homo sapiens]
 Sequence ID: 9VG7_A Length: 1167
 >Chain B, Spike glycoprotein [Homo sapiens]
 Sequence ID: 9VG7_B Length: 1167
 >Chain C, Spike glycoprotein [Homo sapiens]
 Sequence ID: 9VG7_C Length: 1167
 Range 1: 1 to 1158

Score:2015 bits(4696), Expect:0.0,
 Method:Compositional matrix adjust.,
 Identities:905/1201(75%), Positives:1005/1201(83%), Gaps:48/1201(3%)

Query 15 CVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWTFHAIHVSGTN 74
 CVN+T + Y +S TRGVYYPD FRSS + FLPF SNVTW+ +
 Sbjct 1 CVNITYGSH--HLYVSSRTRGVYYPDDAFRSSTNVLHEGFFLPFDSNVTWYSFWN----- 53

Query 75 GTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVCEFQ 134
 +++ PF DGVYF++ +KSN++RGW+FGTTLD+ TQS+L+ N+ T+V ++VC F
 Sbjct 54 --QKYSVATSPFGDGVYFSTIDKSNVVRGWVFGTTLDNDTQSVLLYNDGTHVRVEVCTFH 111

Query 135 FCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVF 194
 FC P S +YSSA NCT Y D G+FK +REFVF
 Sbjct 112 FCPTPVFSA-----SSPHLYSSAFNCTLNITLASVRADFTEVDGSFKTIREFVF 160

Query 195 KNIDGYFKIYSKHT----PINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLT 250
 K DG +Y T I LP G + L PL +PIG+NIT F+TL+ L RS T
 Sbjct 161 KLQDGSLNVYYASTSYVLAIGATSQLPSGVTPLVPLWKIPIGLNITNFKTLVYL-RSDNT 219

Query 251 PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEK 310
 P AAY VG+L+ RT + KY+ENGTI DA+DCALDPLSETKCTL+SF VEK
 Sbjct 220 PLQ-----AAYVVGHLKRRTMMFKYDENGITIVDAIDCALDPLSETKCTLRSFIVEK 270

Query 311 GIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYN 370
 GIYQTSNFRVQP ++VRFPNITNLCPF EVFNAT FASVYAWNRKRISNCVADYSVLYN
 Sbjct 271 GIYQTSNFRVQPQDTVVRFPNITNLCPFSEVFNATTFASVYAWNRKRISNCVADYSVLYN 330

Query 371 SASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFT 430
 S SFSTF+CYGVS TKLNDLCFTNVYADSFV+RGDEVQRQIAPGQTG IADYNYKLPPDDFT

Sbjct	331	STSFSTFQCYGVSSTKLNDLCFTNVYADSFVVVRGDEVQRQIAPGQTGVIADYNYKLPPDDFT
390		
Query	431	GCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYF
490		
Sbjct	391	GCV+AWNS N D+ GN+NY YR++R L+PFERDI+ YQ G+ +
442		GCVLAWNSRNQDASTSGNFNYYYRIWRSEKLRPFERDIAHYDYQVGTQFKSS-----
Query	491	PLQSYGFQPTNGVGYQPYRVVVL SFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTG
550		
Sbjct	443	L++YGF + G +QPYRVVVL SFELL+APATVCGPK+ST L+KNKCVNFNFNGLTGTG
501		-LKNYGFYSSAGDSHQPYRVVVL SFELLNAPATVCGPKQSTELIKNKCVNFNFNGLTGTG
Query	551	VLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAV
610		
Sbjct	502	VLT+SNKKF FQQFGRD++D TD+V+DP+TLE+LDITPCS+GGVSVITPGTN S QVAV
561		VLTDNKKFQSFQQFGRDVSDFTDSVKDPKTLEVLDTITPCSYGGVSVITPGTNASTQVAV
Query	611	LYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGI
670		
Sbjct	562	LYQDVNCT+VP AIHA+QLTP+WRVYSTG+N+FQT+AGCLIGAEHVNNSEY+CDIPIGAGI
621		LYQDVNCTDVPTAIHAEQLTPSWRVYSTGTNMFQTQAGCLIGAEHVNNSEYDCDIPIGAGI
Query	671	CASYQTQTNPRRARSVAS-QSIIAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPV
729		
Sbjct	622	CA+Y T P RS + + I+AY MSLGAENSVAYSNN+IAIPTNFTISVTTE++PV
677		CATYHT----PSMLRSANNKRIYAYVMSLGAENSVAYSNN+IAIPTNFTISVTTEVMPV
Query	730	SMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIY
789		
Sbjct	678	SMTKTSVDCTMYICGDS ECS LLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIY
737		SMTKTSVDCTMYICGDSVECESTLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIY
Query	790	KTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDL
849		
Sbjct	738	KTP IKDFGGFNFSQILPDPSKPSKRS IEDLLFNKVTLADAGF+KQYGDCLGDI ARDL
797		KTPDIKDFGGFNFSQILPDPSKPSKRSPIEDLLFNKVTLADAGFVKQYGDCLGDIQARDL
Query	850	ICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGI
909		
Sbjct	798	ICAQKFNGLTVLPPLLTDEMIA YT+AL++GT T+GWTFGAG ALQIPF MQMAYRFNGI
857		ICAQKFNGLTVLPPLLTDEMIAAYTAALISGTATAGWTFGAGPALQIPFPMQMAYRFNGI
Query	910	GVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSN
969		
Sbjct	858	GVTQNVLYENQKLIANQFNSAIGKIQ+SL+ST SALGKLQDVVNQNAQALNTLVKQLSSN
917		GVTQNVLYENQKLIANQFNSAIGKIQESLTSTPSALGKLQDVVNQNAQALNTLVKQLSSN

Query	970	FGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
1029		
		FGAISSVLNDI+SRLD EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
Sbjct	918	FGAISSVLNDIISRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
977		
Query	1030	SECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVITYVPAQEKNFTTAPAICHDGKAHF
1089		
		SECVLGQSKRVDFCGKGYHLMSFPQ+APHGVVFLHVITY+P+QE+NFTTAPAICH+GKAHF
Sbjct	978	SECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVITYIPSQERNFTTAPAICHEGKAHF
1037		
Query	1090	PREGVFVSNNGTHWFVTQRNFYEPQIIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFK
1149		
		PREGVFVSNNGTHWF+TQRNFYEPQIIITDNTFVSG CDVVIGIVNNTVYDPLQPEL+SFK
Sbjct	1038	PREGVFVSNNGTHWFITQRNFYEPQIIITDNTFVSGTCDVVIGIVNNTVYDPLQPELESFK
1097		
Query	1150	EELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQY
1209		
		+ELDKYFKNHTSPD+DLGDISGINASVV+IQKEID L +VAKNLNESLI+LQELGKYEQY
Sbjct	1098	DELDKYFKNHTSPDIDLGDISGINASVVDIQKEIDILKDVAKNLNESLINLQELGKYEQY
1157		
Query	1210	I 1210
		I
Sbjct	1158	I 1158

>Chain D, Spike protein S1 [Homo sapiens]

Sequence ID: 7TE1_D Length: 211

>Chain E, Spike protein S1 [Homo sapiens]

Sequence ID: 7TE1_E Length: 211

Range 1: 1 to 211

Score:494 bits(1145), Expect:3e-157,

Method:Compositional matrix adjust.,

Identities:211/211(100%), Positives:211/211(100%), Gaps:0/211(0%)

Query	319	RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLVNSASFSTFK	378
		RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLVNSASFSTFK	
Sbjct	1	RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLVNSASFSTFK	60
Query	379	CYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNS	438
		CYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNS	
Sbjct	61	CYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNS	120
Query	439	NNLDSKVG GN NYLYRLFRKSNLKP FERDIST EIQAGSTPCNGVEGFNCYFPLQSYGFQ	498
		NNLDSKVG GN NYLYRLFRKSNLKP FERDIST EIQAGSTPCNGVEGFNCYFPLQSYGFQ	
Sbjct	121	NNLDSKVG GN NYLYRLFRKSNLKP FERDIST EIQAGSTPCNGVEGFNCYFPLQSYGFQ	180
Query	499	PTNGVG YQPYRVV VLSFELLHAPATVCGPKK	529
		PTNGVG YQPYRVV VLSFELLHAPATVCGPKK	
Sbjct	181	PTNGVG YQPYRVV VLSFELLHAPATVCGPKK	211

>Chain B, Spike glycoprotein [Homo sapiens]
Sequence ID: 8T23_B Length: 208
Range 1: 1 to 208

Score:485 bits(1124), Expect:3e-154,
Method:Compositional matrix adjust.,
Identities:207/208(99%), Positives:208/208(100%), Gaps:0/208(0%)

Query	321	QPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCY	380
		QPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCY	
Sbjct	1	QPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCY	60
Query	381	GVSPTKLNLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNN	440
		GVSPTKLNLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNN	
Sbjct	61	GVSPTKLNLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNN	120
Query	441	LDSKVGGNYNYLYRLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	500
		LDSKVGGNYNYL+RLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	
Sbjct	121	LDSKVGGNYNYLFRFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	180
Query	501	NGVGYPYRVVVLSEFELLHAPATVCGPK	528
		NGVGYPYRVVVLSEFELLHAPATVCGPK	
Sbjct	181	NGVGYPYRVVVLSEFELLHAPATVCGPK	208

>Chain C, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_C Length: 199
>Chain F, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_F Length: 199
>Chain I, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_I Length: 199
>Chain L, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_L Length: 199
Range 1: 1 to 194

Score:455 bits(1054), Expect:6e-144,
Method:Compositional matrix adjust.,
Identities:194/194(100%), Positives:194/194(100%), Gaps:0/194(0%)

Query	334	NLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCFT	393
		NLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCFT	
Sbjct	1	NLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCFT	60
Query	394	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLY	453
		NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLY	
Sbjct	61	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFTGCVIAWNSNNLDSKVGGNYNYLY	120
Query	454	RLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVVL	513
		RLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVVL	
Sbjct	121	RLFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVVL	180
Query	514	SFELLHAPATVCGP	527

SFELLHAPATVCGP
 Sbjct 181 SFELLHAPATVCGP 194

>Chain E, Spike protein S2' [Homo sapiens]
 Sequence ID: 8CII_E Length: 202
 Range 1: 7 to 202

Score:453 bits(1049), Expect:5e-143,
 Method:Compositional matrix adjust.,
 Identities:193/196(98%), Positives:193/196(98%), Gaps:0/196(0%)

Query	333	TNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSP TKLNDLCF	392
		TNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSP TKLNDLCF	
Sbjct	7	TNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSP TKLNDLCF	66
Query	393	TNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVG GN NYL	452
		TNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVG GN NYL	
Sbjct	67	TNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVG GN NYR	126
Query	453	YRLF RKSNLKP FERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQP YRVVV	512
		YRLF RKSNLKP FERDISTEIIYQAGS PCNGVEGFNCYFPLQSYGFQPTNGVG YQP YRVVV	
Sbjct	127	YRLF RKSNLKP FERDISTEIIYQAGSKPCNGVEGFNCYFPLQSYGFQPTNGVG YQP YRVVV	186
Query	513	LSFELLHAPATVCGPK	528
		LSFELLHAPATVCG K	
Sbjct	187	LSFELLHAPATVCGKK	202

>Chain A, Spike protein S1 [Homo sapiens]
 Sequence ID: 7WI0_A Length: 195
 Range 1: 1 to 195

Score:421 bits(975), Expect:4e-132,
 Method:Compositional matrix adjust.,
 Identities:180/195(92%), Positives:184/195(94%), Gaps:0/195(0%)

Query	333	TNLCPFGEVFNATRFASVYAWNKRISNCVADYSVLNSASFSTFKCYGVSP TKLNDLCF	392
		TNLCPF EVFNATRFASVYAWNKRISNCVADYSVLN A F TFKCYGVSP TKLNDLCF	
Sbjct	1	TNLCPFDEVFNATRFASVYAWNKRISNCVADYSVLN LAPFFT FTKCYGVSP TKLNDLCF	60
Query	393	TNVYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVG GN NYL	452
		TNVYADSFVIRGDEV RQIAPGQTG IADYNYKLPDDFTGCVIAWNSN LDSKV GN NYL	
Sbjct	61	TNVYADSFVIRGDEV RQIAPGQTGNIADYNYKLPDDFTGCVIAWNSNKLDSKVSGN NYL	120
Query	453	YRLF RKSNLKP FERDISTEIIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVG YQP YRVVV	512
		YRLF RKSNLKP FERDISTEIIYQAG+ PCNGV GFNCYFPL+SY F+PT GVG+QP YRVVV	
Sbjct	121	YRLF RKSNLKP FERDISTEIIYQAGNKPCNGVAGFN CYFPLRSYSFRPTYGVGHQP YRVVV	180
Query	513	LSFELLHAPATVCGP	527
		LSFELLHAPATVCGP	
Sbjct	181	LSFELLHAPATVCGP	195

>Chain B, Spike protein S1 [Homo sapiens]
Sequence ID: 7TC9_B Length: 195
Range 1: 1 to 195

Score:420 bits(973), Expect:6e-132,
Method:Compositional matrix adjust.,
Identities:180/195(92%), Positives:184/195(94%), Gaps:0/195(0%)

Query	332	ITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN	391
		ITNLCPF EVFNATRFASVYAWNRKRISNCVADYSVLYN A F TFKCYGVSPTKLN	
Sbjct	1	ITNLCPFDEVFNATRFASVYAWNRKRISNCVADYSVLYNLAPFFTFKCYGVSPTKLN	60
Query	392	FTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVG	451
		FTNVYADSFVIRGDEVQRQIAPGQTG IADYNYKLPPDFTGCVIAWNSN LDSKV	
Sbjct	61	FTNVYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPPDFTGCVIAWNSNKLDSKV	120
Query	452	LYRLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQ	511
		LYRLFRKSNLKPFFERDISTEIYQAG+ PCNGV GFNCYFPL+SY F+PT GVG+Q	
Sbjct	121	LYRLFRKSNLKPFFERDISTEIYQAGNKPCNGVAGFNCYFPLRSYSFRPTYGVGHQ	180
Query	512	VLSFELLHAPATVCG	526
		VLSFELLHAPATVCG	
Sbjct	181	VLSFELLHAPATVCG	195

>Chain B, Spike protein S1 [Homo sapiens]
Sequence ID: 8ASY_B Length: 219
Range 1: 1 to 200

Score:417 bits(966), Expect:4e-130,
Method:Compositional matrix adjust.,
Identities:179/200(90%), Positives:183/200(91%), Gaps:0/200(0%)

Query	333	TNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN	392
		TNLCPF EVFNATRFASVYAWNRKRISNCVADYSVLYN A F FKC	
Sbjct	1	TNLCPFHEVFNATRFASVYAWNRKRISNCVADYSVLYNFAPFFAFKCYGVSPTKLN	60
Query	393	TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVG	452
		TNVYADSFVIRG+EV QIAPGQTG IADYNYKLPPDFTGCVIAWNSN LDSKV	
Sbjct	61	TNVYADSFVIRGNEVSQIAPGQTGNIADYNYKLPPDFTGCVIAWNSNKLDSKV	120
Query	453	YRLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQ	512
		YRLFRKS LKPFFERDISTEIYQAG+ PCNGV GFNCYFPLQSYGF+PT GVG+Q	
Sbjct	121	YRLFRKSKLKPFFERDISTEIYQAGNKPCNGVAGFNCYFPLQSYGFRPTYGVGHQ	180
Query	513	LSFELLHAPATVCGPKKSTN	532
		LSFELLHAPATVCG K N	
Sbjct	181	LSFELLHAPATVCGKKSLLN	200

>Chain R, Spike protein S1 [Homo sapiens]
Sequence ID: 7Y0W_R Length: 193
Range 1: 1 to 192

Score:414 bits(959), Expect:9e-130,
Method:Compositional matrix adjust.,
Identities:177/192(92%), Positives:181/192(94%), Gaps:0/192(0%)

Query	335	LCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN	394
		LC PF EVFNATRFASVYAWNRRKRISNCVADYSVLYN A F TFKCYGVSPTKLN	
Sbjct	1	LCPFDEVFNATRFASVYAWNRRKRISNCVADYSVLYNLAPFFTFKCYGVSPTKLN	60
Query	395	VYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVG	454
		VYADSFVIRGDEVQRQIAPGQTG IADYNYKLPDDFTGCVIAWNSN LDSKV	
Sbjct	61	VYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPDDFTGCVIAWNSNKLDSKV	120
Query	455	LFRKSNLKPFFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQ	514
		LFRKSNLKPFFERDISTEIQAG+ PCNGV GFNCYFPL+SY F+PT GVG+Q	
Sbjct	121	LFRKSNLKPFFERDISTEIQAGNKPCNGVAGFNCYFPLRSYSFRPTYGVGHQ	180
Query	515	FELLHAPATVCG	526
		FELLHAPATVCG	
Sbjct	181	FELLHAPATVCG	192

>Chain A, PDCoV spike glycoprotein S1A domain [Homo sapiens]
Sequence ID: 8R9X_A Length: 1079
Range 1: 545 to 1079

Score:320 bits(739), Expect:1e-86,
Method:Compositional matrix adjust.,
Identities:194/542(36%), Positives:281/542(51%), Gaps:40/542(7%)

Query	705	VAYSNNISIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC	764
		V+ + + IP+ F++SV TE L V + VDC Y+C ++ C LL QY S C+ +	
Sbjct	545	VSLYDGEVEIPSAFSLSVQTEYLQVQAEQVIVDCPQYVCNGNSRCLQLLAQYTSACS	604
Query	765	RALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDF-GGFNFSQILPDPSKPSKRSFIEDLLF	823
		AL A + +F Q + I +F G +NFS IL ++ RS IEDLLF	
Sbjct	605	AALHSSAQLDLSREIINMFQTSTQSLQLANITNFKGDYNFSSILT--TRIGGRSAIEDLLF	662
Query	824	NKVTLADAGFIKQ-YGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTI	882
		NKV + G + Q Y C D+A DL+C+Q +NG+ VLP ++ E +A YT +L +	
Sbjct	663	NKVVTSGLGTVDQDYKSCSRDMAIADLVCSQYYNGIMVLPGVVDAEKMAMYTGSLTGAMV	722
Query	883	TSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSST-	941
		G T A A + R N + + NVL ENQK++A FN A+G I +LSS	

Sbjct 723 FGGLTAAAAIPF----ATAVQARLNYVALQTNVLQENQKILAESFNQAVGNISLALSSVN
778

Query 942 -----ASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVE
988

Sbjct 779 A A+ K+Q VVNQ +AL+ L QLS+NF AIS+ + DI +RL++VE
838 DAIQQTSEALNTVAIAIKKIQTVVNQGEALSHLTAQLSNNFQAISTSIQDIYNRLLEEVE

Query 989 AEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYH
1048

Sbjct 839 A Q+DRLITGRL +L YVTQ L + ++IR S LA K++ECV QS R FCG G H
898 ANQQVDRLITGRLAALNAYVTQLLNQMSQIRQSRLLAQQKINECVKSQSPRYGFCGNGTH

Query 1049 LMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHD---GKAHFPREGVFVSNGTHWFTV
1105

Sbjct 899 + S Q+AP+G+ F+H VP + + IC D G + P+ ++ N + W VT
957 IFSLTQTAPNGIFFMHAVLVPNKFTRVNASAGICVDNTRGYSLQPQLILYQFNNS-WRVT

Query 1106 QRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKN---HTSP
1162

Sbjct 958 RN YEP++ + +C V + P++ + + N T P
1017 PRNMYEPRLPRQADFIQLTDCSVTFYNTTAANLPNIIPDIIDVNQTVSDIIDNLPTATPP

Query 1163 DVDLG-----DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK
1211

Sbjct 1018 D+G +I+ + N+ + DRL NLN +L+DL+ L + E Y+K
1077 QWDVGIYNNITILNLTVEINDLQERSKNLSQIADRLQNYIDNLNNTLVDLEWLN RVETYLK

Query 1212 WP 1213
WP
Sbjct 1078 WP 1079

>biogenesis of lysosomal organelles complex 1 subunit 6, partial [Homo sapiens]

Sequence ID: KAI2574041.1 Length: 113

>biogenesis of lysosomal organelles complex 1 subunit 6, partial [Homo sapiens]

Sequence ID: KAI4057642.1 Length: 113

Range 1: 32 to 91

Score:34.5 bits(72), Expect:4.5,
Method:Composition-based stats.,
Identities:17/60 (28%), Positives:35/60 (58%), Gaps:2/60 (3%)

Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202

Sbjct 32 LD+ ++E+ K+ + H+ D++ + +A +VNI+KE+ L+E L + + LQ+
LDTLEQEISKFKCHECHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLKKRALKLQQ 91

>hCG2001986, isoform CRA_c [Homo sapiens]
Sequence ID: EAW77322.1 Length: 131
>biogenesis of lysosomal organelles complex 1 subunit 6 [Homo sapiens]
Sequence ID: KAI2574037.1 Length: 131
>biogenesis of lysosomal organelles complex 1 subunit 6 [Homo sapiens]
Sequence ID: KAI4057646.1 Length: 131
Range 1: 41 to 100

Score:34.5 bits(72), Expect:5.4,
Method:Composition-based stats.,
Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

```
Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202
          LD+ ++E+ K+ + H+ D++      +      +A +VNI+KE+ L+E      L + + LQ+
Sbjct 41    LDTLEQEISKFKCHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLRALKLQQ
100
```

>biogenesis of lysosome-related organelles complex 1 subunit 6 isoform 2
[Homo sapiens]
Sequence ID: NP_036520.1 Length: 172
>RecName: Full=Biogenesis of lysosome-related organelles complex 1 subunit 6;
Short=BLOC-1 subunit 6; AltName: Full=Pallid protein homolog; AltName:
Full=Pallidin; AltName: Full=Syntaxin 13-interacting protein [Homo sapiens]
Sequence ID: Q9UL45.1 Length: 172
>pallid [Homo sapiens]
Sequence ID: AAF08343.1 Length: 172
>Pallidin homolog (mouse) [Homo sapiens]
Sequence ID: AAH04819.1 Length: 172
Range 1: 82 to 141

Score:34.5 bits(72), Expect:6.9,
Method:Composition-based stats.,
Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

```
Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202
          LD+ ++E+ K+ + H+ D++      +      +A +VNI+KE+ L+E      L + + LQ+
Sbjct 82    LDTLEQEISKFKCHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLRALKLQQ
141
```

>unnamed protein product [Homo sapiens]
Sequence ID: BAG37954.1 Length: 172
Range 1: 82 to 141

Score:34.5 bits(72), Expect:6.9,
Method:Composition-based stats.,
Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202
LD+ ++E+ K+ + H+ D++ + +A +VNI+KE+ L+E L + + LQ+
Sbjct 82 LDTLEQEISKFKECHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLKKRALKLQQ
141

>biogenesis of lysosome-related organelles complex 1 subunit 6 isoform 1
[Homo sapiens]

Sequence ID: NP_001298184.1 Length: 177

>biogenesis of lysosomal organelles complex 1 subunit 6 [Homo sapiens]

Sequence ID: KAI2574040.1 Length: 177

>biogenesis of lysosomal organelles complex 1 subunit 6 [Homo sapiens]

Sequence ID: KAI4057647.1 Length: 177

Range 1: 87 to 146

Score:34.5 bits(72), Expect:7.0,

Method:Composition-based stats.,

Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202

LD+ ++E+ K+ + H+ D++ + +A +VNI+KE+ L+E L + + LQ+
Sbjct 87 LDTLEQEISKFKECHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLKKRALKLQQ
146

>immunoglobulin heavy chain junction region [Homo sapiens]

Sequence ID: MOL23798.1 Length: 21

Range 1: 1 to 16

Score:29.3 bits(60), Expect:13,

Method:Composition-based stats.,

Identities:11/16(69%), Positives:13/16(81%), Gaps:0/16(0%)

Query 590 CSFGGVSVITPGTNTS 605

C GG SV+TPGTNT+
Sbjct 1 CVRGGGSVVTPGTNTA 16

>hCG22236, isoform CRA_b, partial [Homo sapiens]

Sequence ID: EAX10979.1 Length: 500

Range 1: 169 to 266

Score:34.0 bits(71), Expect:13,

Method:Compositional matrix adjust.,

Identities:23/98(23%), Positives:45/98(45%), Gaps:0/98(0%)

Query 1114 IITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGIN
1173

++ DN ++ + V ++ N + PL+ E+++ KEEL KNH L +
 Sbjct 169 VLQIDNACLAADDFRVKSLMTNVTWLPLETEMEALKEELLFMKKNHEEEVKGLQAQIASS
 228

Query 1174 ASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK 1211
 V I+K + + + ++ + L EL + Q +K
 Sbjct 229 ELTVEIEKSTTVVTTQSTKVGDAEMTLTELRTVQSLK 266

>Chain A, ATP-dependent RNA helicase DHX15 [Homo sapiens]
 Sequence ID: 8EJM_A Length: 686
 Range 1: 16 to 70

Score:33.6 bits(70), Expect:18,
 Method:Compositional matrix adjust.,
 Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

Query 217 PQGFSALEPLVDLPIGINITRFQTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQ 271
 P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
 Sbjct 16 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 70

>Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]
 Sequence ID: 6SH6_A Length: 689
 >Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]
 Sequence ID: 6SH7_A Length: 689
 Range 1: 19 to 73

Score:33.6 bits(70), Expect:20,
 Method:Compositional matrix adjust.,
 Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

Query 217 PQGFSALEPLVDLPIGINITRFQTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQ 271
 P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
 Sbjct 19 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 73

>Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]
 Sequence ID: 5XDR_A Length: 690
 Range 1: 20 to 74

Score:33.6 bits(70), Expect:20,
 Method:Compositional matrix adjust.,
 Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

Query 217 PQGFSALEPLVDLPIGINITRFQTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQ 271
 P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
 Sbjct 20 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 74

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB2037351.1 Length: 25
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB2107516.1 Length: 25
Range 1: 7 to 24

Score:28.9 bits(59), Expect:20,
Method:Composition-based stats.,
Identities:10/18(56%), Positives:11/18(61%), Gaps:0/18(0%)

```
Query  252  GDSSSGWTAGAAAYYVGY  269
          GD  SGW +G  AYY  Y
Sbjct   7   GDFGSGWYSGTTAYYFDY  24
```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB2121301.1 Length: 25
Range 1: 7 to 24

Score:28.5 bits(58), Expect:28,
Method:Composition-based stats.,
Identities:10/18(56%), Positives:11/18(61%), Gaps:0/18(0%)

```
Query  252  GDSSSGWTAGAAAYYVGY  269
          GD  SGW +G  AYY  Y
Sbjct   7   GDFGSGWYSGTTAYYFDY  24
```

>unnamed protein product [Homo sapiens]
Sequence ID: BAG64538.1 Length: 784
Range 1: 114 to 168

Score:33.2 bits(69), Expect:29,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```
Query  217  PQGFSALEPLVDLPIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYLQ  271
          P+ +  L+  + LP+      RF  +L  H+S++  G++ SG T      + V Y++
Sbjct  114  PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR  168
```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOL37782.1 Length: 21
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOR61122.1 Length: 21
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOR70185.1 Length: 21

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOR72596.1 Length: 21
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOR73296.1 Length: 21
Range 1: 1 to 16

Score:28.0 bits(57), Expect:30,
Method:Composition-based stats.,
Identities:10/16(63%), Positives:13/16(81%), Gaps:0/16(0%)

Query 590 CSFGGVSVITPGTNTS 605
C GG +V+TPGTNT+
Sbjct 1 CVRGGGAVVTPGTNTA 16

>ATP-dependent RNA helicase DHX15 [Homo sapiens]
Sequence ID: NP_001349.2 Length: 795
>RecName: Full=ATP-dependent RNA helicase DHX15; AltName: Full=ATP-dependent RNA helicase #46; AltName: Full=DEAH box protein 15; AltName: Full=Splicing factor Prp43; Short=hPrp43 [Homo sapiens]
Sequence ID: O43143.2 Length: 795
>Chain V, Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]
Sequence ID: 6ID1_V Length: 795
>Chain DX, ATP-dependent RNA helicase DHX15 [Homo sapiens]
Sequence ID: 8RO2_DX Length: 795
>dead box protein 15 [Homo sapiens]
Sequence ID: AAF90182.1 Length: 795
>DEAH (Asp-Glu-Ala-His) box polypeptide 15 [Homo sapiens]
Sequence ID: AAH35974.1 Length: 795
>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_b [Homo sapiens]
Sequence ID: EAW92815.1 Length: 795
>DEAH-box helicase 15 [Homo sapiens]
Sequence ID: KAI2533940.1 Length: 795
Range 1: 125 to 179

Score:32.7 bits(68), Expect:30,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

Query 217 PQGFSALEPLVDLPIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYVGYLQ 271
P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
Sbjct 125 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 179

>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_h [Homo sapiens]
Sequence ID: EAW92821.1 Length: 778
Range 1: 125 to 179

Score:32.7 bits(68), Expect:31,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```

Query   217   PQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQ   271
          P+ +  L+  + LP+      RF  +L  H+S++  G++ SG T      + V Y++
Sbjct   125   PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR   179

```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB2102104.1 Length: 17
Range 1: 4 to 17

Score:28.0 bits(57), Expect:32,
Method:Composition-based stats.,
Identities:10/14(71%), Positives:12/14(85%), Gaps:0/14(0%)

```

Query   253   DSSSGWTAGAAAYY   266
          DSSSGWTAG+   Y+
Sbjct    4   DSSSGWTAGSFDYW   17

```

>t-SNARE domain-containing protein 1 isoform X2 [Homo sapiens]
Sequence ID: XP_047277414.1 Length: 981
Range 1: 262 to 360

Score:32.7 bits(68), Expect:38,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```

Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
          975
          Q++ AN F  NS++  ++ SL S  T S   +L+D ++   Q  N  +   +S+  ++
Sbjct   262   QEEMSANVFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
          321

```

```

Query   976   VLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIR   1014
          +L      +      +   Q+DRL T      ++Q Y   Q +R
Sbjct   322   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR   360

```

>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_g [Homo sapiens]
Sequence ID: EAW92820.1 Length: 709
Range 1: 125 to 179

Score:32.3 bits(67), Expect:41,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```

Query   217   PQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQ   271
          P+ +  L+  + LP+      RF  +L  H+S++  G++ SG T      + V Y++
Sbjct   125   PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR   179

```

>coenzyme Q6, monooxygenase [Homo sapiens]
Sequence ID: KAI2571974.1 Length: 86
>coenzyme Q6, monooxygenase [Homo sapiens]
Sequence ID: KAI4061599.1 Length: 86
Range 1: 6 to 46

Score:30.6 bits(63), Expect:46,
Method:Composition-based stats.,
Identities:13/41(32%), Positives:22/41(53%), Gaps:0/41(0%)

```
Query   792   PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAG   832
          PP+  FG +  S+   DPS+P ++ +           K+ L +AG
Sbjct   6    PPLSSFGVWLASRAASDPSRPRRQGYDIHFHDKKILLLEAG   46
```

>pyruvate kinase M1/2 [Homo sapiens]
Sequence ID: KAI2574971.1 Length: 69
>pyruvate kinase M1/2 [Homo sapiens]
Sequence ID: KAI4058566.1 Length: 69
Range 1: 39 to 68

Score:30.2 bits(62), Expect:47,
Method:Composition-based stats.,
Identities:11/33(33%), Positives:18/33(54%), Gaps:3/33(9%)

```
Query   728   PVSMTKTSVDCTMYICGDSTECNLLQLYGSFC   760
          P++   T + CT+  CGD  EC++   +G  C
Sbjct   39   PITARNTGIICTIVPCGDHQECAH---SHGKLC   68
```

>t-SNARE domain-containing protein 1 isoform X2 [Homo sapiens]
Sequence ID: XP_054215930.1 Length: 981
Range 1: 262 to 360

Score:32.3 bits(67), Expect:49,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```
Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
975
          Q++ AN F  NS++  ++ SL S  T S   +L+D ++   Q  N  +   +S+  ++
Sbjct   262   QEMSANIFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
321
```

```
Query   976   VLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIR   1014
          +L   +   +   Q+DRL T   ++Q Y   Q +R
Sbjct   322   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR   360
```

>t-SNARE domain-containing protein 1 isoform X7 [Homo sapiens]

Sequence ID: XP_047277418.1 Length: 892
Range 1: 173 to 271

Score:32.3 bits(67), Expect:49,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```
Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
          975
          Q++ AN F  NS++  ++ SL S  T S   +L+D ++   Q  N  +   +S+  ++
Sbjct   173   QEMSANVFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
          232

Query   976   VLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIR   1014
          +L      +      +   Q+DRL T      ++Q Y   Q +R
Sbjct   233   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR   271
```

>t-SNARE domain-containing protein 1 isoform X4 [Homo sapiens]
Sequence ID: XP_047277416.1 Length: 931
Range 1: 212 to 310

Score:32.3 bits(67), Expect:50,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```
Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
          975
          Q++ AN F  NS++  ++ SL S  T S   +L+D ++   Q  N  +   +S+  ++
Sbjct   212   QEMSANVFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
          271

Query   976   VLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIR   1014
          +L      +      +   Q+DRL T      ++Q Y   Q +R
Sbjct   272   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR   310
```

>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_d [Homo sapiens]
Sequence ID: EAW92817.1 Length: 650
Range 1: 125 to 179

Score:31.9 bits(66), Expect:57,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```
Query   217   PQGFSALEPLVDLPIGINITRFQTLALHRSYLTPGDSSSGWTAGAAAYVGYLQ   271
          P+ +  L+  + LP+      RF  +L  H+S++  G++ SG T      + V Y++
Sbjct   125   PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR   179
```

>immunoglobulin heavy chain junction region [Homo sapiens]

Sequence ID: MCG22225.1 Length: 19
Range 1: 5 to 16

Score:27.2 bits(55), Expect:58,
Method:Composition-based stats.,
Identities:9/12(75%), Positives:10/12(83%), Gaps:0/12(0%)

```
Query 1092 EGVFVSNGTHWF 1103
          EGV V+ GTHWF
Sbjct 5 EGVAVAGGTHWF 16
```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MFT1129265.1 Length: 22
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MFT1129267.1 Length: 22
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MFT1129268.1 Length: 22
Range 1: 4 to 17

Score:27.6 bits(56), Expect:59,
Method:Composition-based stats.,
Identities:9/14(64%), Positives:11/14(78%), Gaps:0/14(0%)

```
Query 253 DSSSGWTAGAAAYY 266
          + SSGWT GA +YY
Sbjct 4 EDSSSGWTGGAYSYY 17
```

>ATP-dependent RNA helicase DHX15 isoform X2 [Homo sapiens]
Sequence ID: XP_047305655.1 Length: 600
>ATP-dependent RNA helicase DHX15 isoform X2 [Homo sapiens]
Sequence ID: XP_054205062.1 Length: 600
Range 1: 125 to 179

Score:31.9 bits(66), Expect:61,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```
Query 217 PQGFSALEPLVDLPIGINITRFQTLLALHRSYLTGPDSSSGWTAGAAAYYVGYLQ 271
          P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
Sbjct 125 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 179
```

>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_e [Homo sapiens]
Sequence ID: EAW92818.1 Length: 499
Range 1: 125 to 179

Score:31.9 bits(66), Expect:64,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```

Query   217   PQGFSALEPLVDLPIGINITRFQTLALHRSYLTPGDSSSGWTAGAAAYVGYLQ   271
          P+ +  L+  + LP+      RF  +L  H+S++  G++ SG T      + V Y++
Sbjct   125   PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR   179

```

>t-SNARE domain-containing protein 1 isoform X7 [Homo sapiens]
Sequence ID: XP_054215935.1 Length: 892
Range 1: 173 to 271

Score:31.9 bits(66), Expect:65,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```

Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS   975
          Q++ AN F  NS++  ++ SL S  T S  +L+D ++  Q  N  +  +S+  ++
Sbjct   173   QEMSANIFRINSSVTSLSRLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE   232

```

```

Query   976   VLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIR   1014
          +L      +      +  Q+DRL T      ++Q Y  Q +R
Sbjct   233   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR   271

```

>ATP-dependent RNA helicase DHX15 isoform X1 [Homo sapiens]
Sequence ID: XP_047305654.1 Length: 608
>ATP-dependent RNA helicase DHX15 isoform X1 [Homo sapiens]
Sequence ID: XP_054205061.1 Length: 608
Range 1: 125 to 179

Score:31.9 bits(66), Expect:66,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```

Query   217   PQGFSALEPLVDLPIGINITRFQTLALHRSYLTPGDSSSGWTAGAAAYVGYLQ   271
          P+ +  L+  + LP+      RF  +L  H+S++  G++ SG T      + V Y++
Sbjct   125   PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR   179

```

>ubiquinone biosynthesis monooxygenase COQ6, mitochondrial isoform b [Homo sapiens]
Sequence ID: NP_872286.2 Length: 443
>coenzyme Q6, monooxygenase [Homo sapiens]
Sequence ID: KAI2571973.1 Length: 443
>unnamed protein product [Homo sapiens]
Sequence ID: BAH12244.1 Length: 443
Range 1: 6 to 46

Score:31.9 bits(66), Expect:67,
Method:Compositional matrix adjust.,

Identities:13/41(32%), Positives:22/41(53%), Gaps:0/41(0%)

```
Query   792   PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAG   832
          PP+  FG +  S+   DPS+P ++ +           K+ L +AG
Sbjct   6     PPLSSFGVWLASRAASDPSRPRRQGYDIHFHDKKILLLEAG   46
```

>hCG1644135, isoform CRA_b, partial [Homo sapiens]
Sequence ID: EAW68450.1 Length: 111
Range 1: 2 to 24

Score:30.6 bits(63), Expect:67,
Method:Composition-based stats.,
Identities:10/23(43%), Positives:16/23(69%), Gaps:0/23(0%)

```
Query   489   YFPLQSYGFQPTNGVGYPYRVV   511
          YFP   +GF PT+G+ +   Y++V
Sbjct   2     YFPAAIFGFLPTSGILFSYYKIV   24
```

>Carnitine O-palmitoyltransferase II, mitochondrial precursor variant,
partial [Homo sapiens]
Sequence ID: BAD96772.1 Length: 577
Range 1: 8 to 36

Score:31.9 bits(66), Expect:68,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query   1187  NEVAKNLNESLIDLQELGKYEQYIKWPWY   1215
          N + K L+E L+ L +   K+  YI  PW+
Sbjct   8     NGIGKELHEQLVALDKQNKHTSYISGPWF   36
```

>coenzyme Q6, monooxygenase [Homo sapiens]
Sequence ID: KAI4061598.1 Length: 443
Range 1: 6 to 46

Score:31.5 bits(65), Expect:69,
Method:Compositional matrix adjust.,
Identities:13/41(32%), Positives:22/41(53%), Gaps:0/41(0%)

```
Query   792   PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAG   832
          PP+  FG +  S+   DPS+P ++ +           K+ L +AG
Sbjct   6     PPLSSFGVWLASRAASDPSRPRRQGYDIHFHDKKILLLEAG   46
```

>carnitine O-palmitoyltransferase 2, mitochondrial isoform 2 precursor [Homo sapiens]

Sequence ID: NP_001317518.1 Length: 635
Range 1: 89 to 117

Score:31.9 bits(66), Expect:70,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>ubiquinone biosynthesis monooxygenase COQ6, mitochondrial isoform f [Homo sapiens]
Sequence ID: NP_001412187.1 Length: 407
Range 1: 6 to 46

Score:31.5 bits(65), Expect:70,
Method:Compositional matrix adjust.,
Identities:13/41(32%), Positives:22/41(53%), Gaps:0/41(0%)

```
Query 792 PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAG 832
          PP+ FG + S+ DPS+P ++ + K+ L +AG
Sbjct 6 PPLSSFGVWLASRAASDPSRPRRQGYDIHFHDKKILLLEAG 46
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080722.1 Length: 635
Range 1: 89 to 117

Score:31.9 bits(66), Expect:71,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI2517173.1 Length: 635
Range 1: 89 to 117

Score:31.5 bits(65), Expect:73,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>t-SNARE domain-containing protein 1 isoform X4 [Homo sapiens]
Sequence ID: XP_054215932.1 Length: 931
Range 1: 212 to 310

Score:31.9 bits(66), Expect:73,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```
Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
975
          Q++ AN F  NS++  ++ SL S  T S   +L+D ++   Q  N  +   +S+  ++
Sbjct   212   QEMSANIFRINSSVTSLSRLSLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
271

Query   976   VLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIR   1014
          +L      +      +   Q+DRL T      ++Q Y   Q +R
Sbjct   272   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR   310
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080729.1 Length: 658
Range 1: 89 to 117

Score:31.5 bits(65), Expect:74,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query   1187  NEVAKNLNESLIDLQELGKYEQYIKWPWY   1215
          N + K L+E L+ L +   K+  YI  PW+
Sbjct   89    NGIGKELHEQLVALDKQNKHTSYISGPWF   117
```

>carnitine O-palmitoyltransferase 2, mitochondrial isoform 1 precursor [Homo sapiens]
Sequence ID: NP_000089.1 Length: 658
>RecName: Full=Carnitine O-palmitoyltransferase 2, mitochondrial; AltName: Full=Carnitine palmitoyltransferase II; Short=CPT II; Flags: Precursor [Homo sapiens]
Sequence ID: P23786.2 Length: 658
>carnitine palmitoyltransferase [Homo sapiens]
Sequence ID: AAB59462.1 Length: 658
>carnitine palmitoyltransferase II precursor [Homo sapiens]
Sequence ID: AAB60382.1 Length: 658
>carnitine palmitoyltransferase II precursor [Homo sapiens]
Sequence ID: AAB60383.1 Length: 658
>testicular secretory protein Li 13 [Homo sapiens]
Sequence ID: AEE61150.1 Length: 658
>carnitine palmitoyltransferase II [Homo sapiens]
Sequence ID: EAX06753.1 Length: 658
Range 1: 89 to 117

Score:31.5 bits(65), Expect:75,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI2517171.1 Length: 658
Range 1: 89 to 117

Score:31.5 bits(65), Expect:76,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOQ20290.1 Length: 20
Range 1: 5 to 17

Score:27.2 bits(55), Expect:77,
Method:Composition-based stats.,
Identities:9/13(69%), Positives:11/13(84%), Gaps:0/13(0%)

```
Query 254 SSSGWTAGAAAYY 266
          SSSGW AG+ AY+
Sbjct 5 SSSGWYAGSGAYF 17
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080727.1 Length: 647
Range 1: 89 to 117

Score:31.5 bits(65), Expect:82,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB1991959.1 Length: 24
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB1994550.1 Length: 24
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB2016416.1 Length: 24
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB2019779.1 Length: 24
Range 1: 2 to 22

Score:27.2 bits(55), Expect:82,
Method:Composition-based stats.,
Identities:10/21(48%), Positives:14/21(66%), Gaps:0/21(0%)

Query 20 TRTQLPPAYTNSFTRGVYYPD 40
T+ + PP Y+ S T+G YY D
Sbjct 2 TKGKEPPPYSGSGTKGAYYFD 22

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI2517170.1 Length: 670
Range 1: 89 to 117

Score:31.5 bits(65), Expect:82,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080725.1 Length: 670
Range 1: 89 to 117

Score:31.5 bits(65), Expect:82,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI2517172.1 Length: 647
Range 1: 89 to 117

Score:31.5 bits(65), Expect:82,
Method:Compositional matrix adjust.,

Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>ATP-dependent RNA helicase #46 [Homo sapiens]
Sequence ID: BAA23987.1 Length: 813
Range 1: 125 to 179

Score:31.5 bits(65), Expect:84,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:28/55(50%), Gaps:0/55(0%)

```
Query 217 PQGFSALEPLVDLPIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYVGYLQ 271
          P+ + L+ + LP+ RF +L H+S++ G++ SG T V Y++
Sbjct 125 PRYYDILKKRLQLPVWEYKDRFTDILGRHQSFVLVGETGSGKTTQIPHRCVEYMR 179
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI2517175.1 Length: 598
>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080724.1 Length: 598
Range 1: 89 to 117

Score:31.5 bits(65), Expect:88,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>spindle and centriole-associated protein 1 [Homo sapiens]
Sequence ID: NP_001318007.1 Length: 855
>spindle and centriole-associated protein 1 [Homo sapiens]
Sequence ID: NP_001318008.2 Length: 855
>spindle and centriole-associated protein 1 [Homo sapiens]
Sequence ID: NP_001374868.1 Length: 855
>spindle and centriole-associated protein 1 [Homo sapiens]
Sequence ID: NP_653319.1 Length: 855
>RecName: Full=Spindle and centriole-associated protein 1; AltName:
Full=Coiled-coil domain-containing protein 52; AltName: Full=Spindle and
centriole-associated protein [Homo sapiens]
Sequence ID: Q8N0Z3.1 Length: 855
>hypothetical protein [Homo sapiens]
Sequence ID: AAM34495.1 Length: 855
>coiled-coil domain containing 52, isoform CRA_a [Homo sapiens]
Sequence ID: EAW79634.1 Length: 855

Range 1: 510 to 574

Score:31.5 bits(65), Expect:89,
Method:Compositional matrix adjust.,
Identities:21/65(32%), Positives:29/65(44%), Gaps:0/65(0%)

```
Query 522 ATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQT 581
          + V P + NL KN + + T +SN KF P Q R T A R P T
Sbjct 510 SQVPDPPDNMNLAKNFPAHIFEPVLLTPPRQKSNLKFSPQLQDVLRRTVQTRPAPRLPPT 569

Query 582 LEILD 586
          +EI++
Sbjct 570 VEIIE 574
```

>unnamed protein product [Homo sapiens]
Sequence ID: BAG54389.1 Length: 695
Range 1: 406 to 470

Score:31.5 bits(65), Expect:90,
Method:Compositional matrix adjust.,
Identities:21/65(32%), Positives:29/65(44%), Gaps:0/65(0%)

```
Query 522 ATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQT 581
          + V P + NL KN + + T +SN KF P Q R T A R P T
Sbjct 406 SQVPDPPDNMNLAKNFPAHIFEPVLLTPPRQKSNLKFSPQLQDVLRGTVQTRPAPRLPPT 465

Query 582 LEILD 586
          +EI++
Sbjct 466 VEIIE 470
```

>hypothetical protein, partial [Homo sapiens]
Sequence ID: CAH18698.1 Length: 2403
Range 1: 1010 to 1069

Score:31.5 bits(65), Expect:95,
Method:Compositional matrix adjust.,
Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```
Query 754 LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y C+ NR++ G+ V K E+ K I + PP G Q P P P
Sbjct 1010 LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPPAP
1069
```

>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219425.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219426.1 Length: 2506

```
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219427.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219428.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219429.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219430.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219431.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219432.1 Length: 2506
Range 1: 1113 to 1172
```

```
Score:31.5 bits(65), Expect:99,
Method:Compositional matrix adjust.,
Identities:18/60 (30%), Positives:24/60 (40%), Gaps:1/60 (1%)
```

```
Query 754 LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
      L Y  C+  NR++ G+ V  K  E+  K I + PP      G  Q  P P P
Sbjct 1113 LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPPAP
1172
```

```
>unnamed protein product [Homo sapiens]
Sequence ID: BAG65508.1 Length: 223
Range 1: 102 to 151
```

```
Score:31.0 bits(64), Expect:99,
Method:Composition-based stats.,
Identities:15/50 (30%), Positives:27/50 (54%), Gaps:0/50 (0%)
```

```
Query 992 QIDRLITGRQLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD 1041
      +I+R + R++ + + +QL+ E + A LAA K E LG+ + D
Sbjct 102 EIEREVLQRVEEAKRIMEKQLLEELERQRQAELAAQKAREVTLGRLESRD 151
```

```
>zinc finger protein 462 isoform 1 [Homo sapiens]
Sequence ID: NP_067047.4 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_006717279.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279628.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279629.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279630.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279631.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279632.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
```

Sequence ID: XP_047279633.1 Length: 2506
 >zinc finger protein 462 isoform X3 [Homo sapiens]
 Sequence ID: XP_047279634.1 Length: 2506
 >RecName: Full=Zinc finger protein 462; AltName: Full=Zinc finger PBX1-interacting protein; Short=ZFPIP [Homo sapiens]
 Sequence ID: Q96JM2.3 Length: 2506
 >zinc finger protein 462 [Homo sapiens]
 Sequence ID: KAI4007977.1 Length: 2506
 Range 1: 1113 to 1172

Score:31.5 bits(65), Expect:100,
 Method:Compositional matrix adjust.,
 Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPGQSPRPPAP
1172
```

>hypothetical protein [Homo sapiens]
 Sequence ID: CAH56168.1 Length: 2506
 Range 1: 1113 to 1172

Score:31.5 bits(65), Expect:100,
 Method:Compositional matrix adjust.,
 Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPGQSPRPPAP
1172
```

>zinc finger protein 462 [Homo sapiens]
 Sequence ID: KAI2553449.1 Length: 2506
 Range 1: 1113 to 1172

Score:31.5 bits(65), Expect:100,
 Method:Compositional matrix adjust.,
 Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPGQSPRPPAP
1172
```

CPT2 + t-SNARE BLAST Analysis Raw Data

RID: H498WK63016

Job Title:sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe...

Program: BLASTP

Query: sp|P0DTC2|SPIKE_SARS2 Spike glycoprotein OS=Severe acute respiratory syndrome coronavirus 2 OX=2697049 GN=S PE=1 SV=1 ID: lcl|Query_526448(amino acid) Length: 1273

Database: nr All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Sequences producing significant alignments:

Sequences with E-value BETTER than threshold

Common Description Name Accession	Taxid	Max Score	Total Query Score cover	E Value	Per. Ident	Acc. Len	Scientific Name
Chain A, Spike glycoprotein [Homo sapiens] sapiens human 7Y71_A		9606	2729	2729	94%	0.0	Homo 99.33 1198
Chain J, Spike glycoprotein [Homo sapiens] sapiens human 7TLZ_J		9606	2600	2600	94%	0.0	Homo 95.92 1274
Chain R, Spike glycoprotein [Homo sapiens] sapiens human 9ASD_R		9606	2530	2530	94%	0.0	Homo 93.92 1273
Chain A, Spike glycoprotein [Homo sapiens] sapiens human 9VG7_A		9606	2015	2015	94%	0.0	Homo 75.35 1167
Chain D, Spike protein S1 [Homo sapiens] sapiens human 7TE1_D		9606	494	494	17%	3e-157	Homo 100.00 211
Chain B, Spike glycoprotein [Homo sapiens] sapiens human 8T23_B		9606	485	485	16%	3e-154	Homo 99.52 208
Chain C, Spike protein S1 [Homo sapiens] sapiens human 8BG1_C		9606	455	455	15%	6e-144	Homo 100.00 199
Chain E, Spike protein S2' [Homo sapiens] sapiens human 8CII_E		9606	453	453	15%	5e-143	Homo 98.47 202
Chain A, Spike protein S1 [Homo sapiens] sapiens human 7WIO_A		9606	421	421	15%	4e-132	Homo 92.31 195
Chain B, Spike protein S1 [Homo sapiens] sapiens human 7TC9_B		9606	420	420	15%	6e-132	Homo 92.31 195
Chain B, Spike protein S1 [Homo sapiens] sapiens human 8ASY_B		9606	417	417	16%	4e-130	Homo 89.50 219
Chain R, Spike protein S1 [Homo sapiens] sapiens human 7YOW_R		9606	414	414	15%	9e-130	Homo 92.19 193

Chain A, PDCoV spike glycoprotein S1A domain [Homo sapiens]	Homo sapiens	human	9606	320	320	40%	1e-86	35.79	1079
8R9X_A									

Sequences with E-value WORSE than threshold

Common Description	Taxid	Max Score	Total Query Score	E Value	Per. Ident	Acc. Len	Scientific Name		
Chain H, Proteasome subunit alpha type-2 [Homo sapiens]	Homo sapiens	human	9606	35.7	35.7	6%	3.4	34.94	234
9E8L_H									
biogenesis of lysosomal organelles complex 1 subunit 6, partial [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	5%	4.5	28.33	113
KAI2574041.1									
hCG2001986, isoform CRA_c [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	5%	5.4	28.33	131
EAW77322.1									
biogenesis of lysosome-related organelles complex 1 subunit 6... [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	5%	6.9	28.33	172
NP_036520.1									
unnamed protein product [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	5%	6.9	28.33	172
BAG37954.1									
biogenesis of lysosome-related organelles complex 1 subunit 6... [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	5%	7.0	28.33	177
NP_001298184.1									
proteasome 20S subunit alpha 2 [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	6%	7.1	34.94	164
KAI2545645.1									
Chain B, Proteasome subunit alpha type-2 [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	6%	8.5	34.94	229
7AWE_B									
PSMA2 protein, partial [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	6%	8.6	34.94	225
AAH02900.2									
proteasome subunit alpha type-2 [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	6%	8.6	34.94	234
NP_002778.1									
Chain A, Proteasome subunit alpha type-2 [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	6%	8.7	34.94	230
6R70_A									
Chain H, Proteasome subunit alpha type-2 [Homo sapiens]	Homo sapiens	human	9606	34.5	34.5	6%	8.9	34.94	232
5VFO_H									
Chain B, Proteasome subunit alpha type-2 [Homo sapiens]	Homo sapiens	human	9606	34.0	34.0	6%	9.3	34.94	233
4R30_B									
proteasome alpha 2 subunit variant, partial [Homo sapiens]	Homo sapiens	human	9606	34.0	34.0	6%	10	34.94	234
BAD96696.1									
immunoglobulin heavy chain junction region [Homo sapiens]	Homo sapiens	human	9606	29.3	29.3	1%	13	68.75	21
MOL23798.1									

hCG22236, isoform CRA_b, partial [Homo sapiens]	Homo
sapiens human 9606 34.0 34.0 8% 13	23.47 500
EAX10979.1	
Chain A, ATP-dependent RNA helicase DHX15 [Homo sapiens]	Homo
sapiens human 9606 33.6 33.6 4% 18	27.27 686
8EJM_A	
Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase...	Homo
sapiens human 9606 33.6 33.6 4% 20	27.27 689
6SH6_A	
Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase...	Homo
sapiens human 9606 33.6 33.6 4% 20	27.27 690
5XDR_A	
immunoglobulin heavy chain junction region [Homo sapiens]	Homo
sapiens human 9606 28.9 28.9 1% 20	55.56 25
MBB2037351.1	
immunoglobulin heavy chain junction region [Homo sapiens]	Homo
sapiens human 9606 28.5 28.5 1% 28	55.56 25
MBB2121301.1	
unnamed protein product [Homo sapiens]	Homo
sapiens human 9606 33.2 33.2 4% 29	27.27 784
BAG64538.1	
immunoglobulin heavy chain junction region [Homo sapiens]	Homo
sapiens human 9606 28.0 28.0 1% 30	62.50 21
MOL37782.1	
ATP-dependent RNA helicase DHX15 [Homo sapiens]	Homo
sapiens human 9606 32.7 32.7 4% 30	27.27 795
NP_001349.2	
DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_h [Homo...]	Homo
sapiens human 9606 32.7 32.7 4% 31	27.27 778
EAW92821.1	
immunoglobulin heavy chain junction region [Homo sapiens]	Homo
sapiens human 9606 28.0 28.0 1% 32	71.43 17
MBB2102104.1	
t-SNARE domain-containing protein 1 isoform X2 [Homo sapiens]	Homo
sapiens human 9606 32.7 32.7 7% 38	26.26 981
XP_047277414.1	
DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_g [Homo...]	Homo
sapiens human 9606 32.3 32.3 4% 41	27.27 709
EAW92820.1	
coenzyme Q6, monooxygenase [Homo sapiens]	Homo
sapiens human 9606 30.6 30.6 3% 46	31.71 86
KAI2571974.1	
pyruvate kinase M1/2 [Homo sapiens]	Homo
sapiens human 9606 30.2 30.2 3% 47	33.33 69
KAI2574971.1	
t-SNARE domain-containing protein 1 isoform X2 [Homo sapiens]	Homo
sapiens human 9606 32.3 32.3 7% 49	26.26 981
XP_054215930.1	
t-SNARE domain-containing protein 1 isoform X7 [Homo sapiens]	Homo
sapiens human 9606 32.3 32.3 7% 49	26.26 892
XP_047277418.1	
t-SNARE domain-containing protein 1 isoform X4 [Homo sapiens]	Homo
sapiens human 9606 32.3 32.3 7% 50	26.26 931
XP_047277416.1	
DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_d [Homo...]	Homo
sapiens human 9606 31.9 31.9 4% 57	27.27 650
EAW92817.1	

immunoglobulin heavy chain junction region [Homo sapiens]	Homo
sapiens human 9606 27.2 27.2 1% 58	75.00 19
MCG22225.1	
immunoglobulin heavy chain junction region [Homo sapiens]	Homo
sapiens human 9606 27.6 27.6 1% 59	64.29 22
MFT1129265.1	
ATP-dependent RNA helicase DHX15 isoform X2 [Homo sapiens]	Homo
sapiens human 9606 31.9 31.9 4% 61	27.27 600
XP_047305655.1	
DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_e [Homo sapiens]	Homo
sapiens human 9606 31.9 31.9 4% 64	27.27 499
EAW92818.1	
t-SNARE domain-containing protein 1 isoform X7 [Homo sapiens]	Homo
sapiens human 9606 31.9 31.9 7% 65	26.26 892
XP_054215935.1	
ATP-dependent RNA helicase DHX15 isoform X1 [Homo sapiens]	Homo
sapiens human 9606 31.9 31.9 4% 66	27.27 608
XP_047305654.1	
ubiquinone biosynthesis monooxygenase COQ6, mitochondrial...	Homo
sapiens human 9606 31.9 31.9 3% 67	31.71 443
NP_872286.2	
hCG1644135, isoform CRA_b, partial [Homo sapiens]	Homo
sapiens human 9606 30.6 30.6 2% 67	43.48 111
EAW68450.1	
Carnitine O-palmitoyltransferase II, mitochondrial precursor...	Homo
sapiens human 9606 31.9 31.9 2% 68	37.93 577
BAD96772.1	
coenzyme Q6, monooxygenase [Homo sapiens]	Homo
sapiens human 9606 31.5 31.5 3% 69	31.71 443
KAI4061598.1	
carnitine O-palmitoyltransferase 2, mitochondrial isoform 2...	Homo
sapiens human 9606 31.9 31.9 2% 70	37.93 635
NP_001317518.1	
ubiquinone biosynthesis monooxygenase COQ6, mitochondrial...	Homo
sapiens human 9606 31.5 31.5 3% 70	31.71 407
NP_001412187.1	
carnitine palmitoyltransferase 2 [Homo sapiens]	Homo
sapiens human 9606 31.9 31.9 2% 71	37.93 635
KAI4080722.1	
carnitine palmitoyltransferase 2 [Homo sapiens]	Homo
sapiens human 9606 31.5 31.5 2% 73	37.93 635
KAI2517173.1	
t-SNARE domain-containing protein 1 isoform X4 [Homo sapiens]	Homo
sapiens human 9606 31.9 31.9 7% 73	26.26 931
XP_054215932.1	
carnitine palmitoyltransferase 2 [Homo sapiens]	Homo
sapiens human 9606 31.5 31.5 2% 74	37.93 658
KAI4080729.1	
carnitine O-palmitoyltransferase 2, mitochondrial isoform 1...	Homo
sapiens human 9606 31.5 31.5 2% 75	37.93 658
NP_000089.1	
carnitine palmitoyltransferase 2 [Homo sapiens]	Homo
sapiens human 9606 31.5 31.5 2% 76	37.93 658
KAI2517171.1	
immunoglobulin heavy chain junction region [Homo sapiens]	Homo
sapiens human 9606 27.2 27.2 1% 77	69.23 20
MOQ20290.1	

carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	82	37.93	647	
KAI4080727.1								
immunoglobulin heavy chain junction region [Homo sapiens]								Homo
sapiens human	9606	27.2	27.2	2%	82	47.62	24	
MBB1991959.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	82	37.93	670	
KAI2517170.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	82	37.93	670	
KAI4080725.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	82	37.93	647	
KAI2517172.1								
ATP-dependent RNA helicase #46 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	4%	84	27.27	813	
BAA23987.1								
carnitine palmitoyltransferase 2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	2%	88	37.93	598	
KAI2517175.1								
spindle and centriole-associated protein 1 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	89	32.31	855	
NP_001318007.1								
unnamed protein product [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	90	32.31	695	
BAG54389.1								
hypothetical protein, partial [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	95	30.00	2403	
CAH18698.1								
zinc finger protein 462 isoform X3 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	99	30.00	2506	
XP_054219425.1								
unnamed protein product [Homo sapiens]								Homo
sapiens human	9606	31.0	31.0	4%	99	30.00	223	
BAG65508.1								
zinc finger protein 462 isoform 1 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	100	30.00	2506	
NP_067047.4								
hypothetical protein [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	100	30.00	2506	
CAH56168.1								
zinc finger protein 462 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	100	30.00	2506	
KAI2553449.1								
zinc finger protein 462 isoform X2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	102	30.00	2566	
XP_054219420.1								
zinc finger protein 462 isoform X2 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	102	30.00	2566	
XP_006717278.1								
zinc finger protein 462 isoform X1 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	102	30.00	2567	
XP_006717272.1								
zinc finger protein 462 isoform X1 [Homo sapiens]								Homo
sapiens human	9606	31.5	31.5	5%	102	30.00	2567	
XP_054219409.1								

zinc finger protein 462, isoform CRA_b [Homo sapiens]							Homo
sapiens	human	9606	31.5	31.5	5%	102	30.00 1998
EAW59011.1							
zinc finger protein 462, isoform CRA_a [Homo sapiens]							Homo
sapiens	human	9606	31.0	31.0	5%	106	30.00 1999
EAW59010.1							
unnamed protein product [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	4%	112	30.00 198
BAG64595.1							
Chain A, Suppressor of T-cell receptor signaling 1 [Homo sapiens]							Homo
sapiens	human	9606	29.7	29.7	3%	114	30.00 94
2E5K_A							
ARGLU1 protein [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	4%	125	30.00 273
AAH71587.1							
t-SNARE domain-containing protein 1 isoform e [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	8%	134	26.36 470
NP_001353831.1							
Chain B, Charged multivesicular body protein 2a [Homo sapiens]							Homo
sapiens	human	9606	30.2	30.2	7%	135	21.51 147
7ZCG_B							
Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	6%	136	26.25 368
5VHF_D							
Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	6%	137	26.25 380
5VFP_D							
26S proteasome regulatory subunit 6B isoform 2 [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	6%	137	26.25 387
NP_694546.1							
26S proteasome regulatory subunit 6B isoform 1 [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	6%	139	26.25 418
NP_006494.1							
t-SNARE domain-containing protein 1 isoform X1 [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	8%	141	26.67 883
XP_047277413.1							
cytoskeleton-associated protein 4, isoform CRA_b [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	4%	141	28.57 334
EAW97771.1							
Carnitine palmitoyltransferase 2 [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	2%	141	37.93 658
AAH02445.1							
t-SNARE domain-containing protein 1 isoform X6 [Homo sapiens]							Homo
sapiens	human	9606	30.6	30.6	8%	141	26.67 912
XP_047277417.1							

Alignments:

```

>Chain A, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y71_A Length: 1198
>Chain B, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y71_B Length: 1198
>Chain C, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y71_C Length: 1198
>Chain A, Spike glycoprotein [Homo sapiens]
Sequence ID: 7Y72_A Length: 1198
>Chain C, Spike glycoprotein [Homo sapiens]

```

Sequence ID: 7Y72_C Length: 1198
Range 1: 1 to 1198

Score:2729 bits(6362), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:1190/1198 (99%), Positives:1190/1198 (99%), Gaps:0/1198 (0%)

Query	16	VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG	75
		VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG	
Sbjct	1	VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNG	60
Query	76	TKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQF	
	135		
		TKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQF	
Sbjct	61	TKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQF	
	120		
Query	136	CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFK	
	195		
		CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFK	
Sbjct	121	CNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFK	
	180		
Query	196	NIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIGINITRFQTLALHRSYLTGPDSS	
	255		
		NIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIGINITRFQTLALHRSYLTGPDSS	
Sbjct	181	NIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIGINITRFQTLALHRSYLTGPDSS	
	240		
Query	256	SGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT	
	315		
		SGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT	
Sbjct	241	SGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQT	
	300		
Query	316	SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASF	
	375		
		SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASF	
Sbjct	301	SNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLNSASF	
	360		
Query	376	TFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIA	
	435		
		TFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIA	
Sbjct	361	TFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIA	
	420		
Query	436	WNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSY	
	495		
		WNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSY	
Sbjct	421	WNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSY	
	480		
Query	496	GFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTES	
	555		
		GFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTES	

Sbjct	481	GFQPTNGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTES
540		
Query	556	NKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDV
615		
Sbjct	541	NKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDV
600		
Query	616	NCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQ
675		
Sbjct	601	NCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQ
660		
Query	676	TQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTS
735		
Sbjct	661	TQTNSPR A SVASQSIIAYTMSLGAENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTS
720		
Query	736	VDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIK
795		
Sbjct	721	VDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIK
780		
Query	796	DFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
855		
Sbjct	781	DFGGFNFSQILPDPSKPSKRS IEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKF
840		
Query	856	NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNV
915		
Sbjct	841	NGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAG ALQIPF MQMAYRFNGIGVTQNV
900		
Query	916	LYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
975		
Sbjct	901	LYENQKLIANQFNSAIGKIQDSLST SALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
960		
Query	976	VLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
1035		
Sbjct	961	VLNDILSRDL EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
1020		
Query	1036	QSKRVDFCGKGYHLMSFPQSAPHGVVFLHVITYVPAQEKNFTTAPAICHDGKAHFPREGVF
1095		
Sbjct	1021	QSKRVDFCGKGYHLMSFPQSAPHGVVFLHVITYVPAQEKNFTTAPAICHDGKAHFPREGVF
1080		

Query	1096	VSNGTHWFVTQRNFYEPQIIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKY	
	1155		
Sbjct	1081	VSNGTHWFVTQRNFYEPQIIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKY	
	1140		
Query	1156	FKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP	1213
		FKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP	
Sbjct	1141	FKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWP	1198

>Chain J, Spike glycoprotein [Homo sapiens]
Sequence ID: 7TLZ_J Length: 1274
Range 1: 12 to 1205

Score:2600 bits(6061), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:1151/1200 (96%), Positives:1157/1200 (96%), Gaps:9/1200 (0%)

Query	12	SSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS	71
		SSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFH I S	
Sbjct	12	SSQCVNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHVI--S	69
Query	72	GTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLILVNNATNVVIKVC	
	131		
Sbjct	70	GTNGTKRFDNPVLPFNDGVYFAS EKSNIIRGWIFGTTLDSKTQSLILVNNATNVVIKVC	
	129		
Query	132	EFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
	191		
Sbjct	130	EFQFCNDPFL HKNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
	186	EFQFCNDPFLD---HKNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE	
Query	192	FVFKNIDGYFKIYSKHTPINLVR---DLPQGFSALEPLVDLPIGINITRFQTLLALHRSY	
	248		
Sbjct	187	FVFKNIDGYFKIYSKHTPI +VR DLPQGFSALEPLVDLPIGINITRFQTLLALHRSY	
	245	FVFKNIDGYFKIYSKHTPI-IVREPDLDPQGFSALEPLVDLPIGINITRFQTLLALHRSY	
Query	249	LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV	
	308		
Sbjct	246	LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV	
	305		
Query	309	EKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVL	
	368		
Sbjct	306	EKGIYQTSNFRVQPTESIVRFPNITNLCPF EVFNATRFASVYAWNRKRISNCVADYSVL	
	365	EKGIYQTSNFRVQPTESIVRFPNITNLCPFDEVFNATRFASVYAWNRKRISNCVADYSVL	
Query	369	YNSASFSTFKCYGSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPD	
	428		

Sbjct	366	YN A F TFKCYGVSPTKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTG IADYNYKL PDD
425		YNLAPFFTFKCYGVSPTKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTGNIADYNYKL PDD
Query	429	FTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNC
488		FTGCVIAWNSN LDSKV GNYNYLYRLFRKSNLKPFERDISTEIYQAG+ PCNGV GFNC
Sbjct	426	FTGCVIAWNSNKLDSKVSGNYNYLYRLFRKSNLKPFERDISTEIYQAGNKPCNGVAGFNC
485		
Query	489	YFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTG
548		YFPL+SY F+PT GVG+QPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGL G
Sbjct	486	YFPLRSYSFRPTYGVGHQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLKG
545		
Query	549	TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQV
608		TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQV
Sbjct	546	TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTL EILDITPCSFGGVSVITPGTNTSNQV
605		
Query	609	AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGA EHVNNSYECDIPIGA
668		AVLYQ VNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAE+VNNSYECDIPIGA
Sbjct	606	AVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNNSYECDIPIGA
665		
Query	669	GICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNN SIAIPTNFTISVTTEILP
728		GICASYQTQT S A SVASQSIIAYTMSLGAENSV SNN SIAIPTNFTISVTTEILP
Sbjct	666	GICASYQTQTKSHSGAGSVASQSIIAYTMSLGAENSVAC SNN SIAIPTNFTISVTTEILP
725		
Query	729	VSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQI
788		VSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQL RALTGIAVEQDKNTQEVFAQVKQI
Sbjct	726	VSMTKTSVDCTMYICGDSTEC SNLLLQYGSFCTQLKRALTGIAVEQDKNTQEVFAQVKQI
785		
Query	789	YKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVT LADAGFIKQYGDCLGDIAARD
848		YKTPPIK FGGFNFSQILPDPSKPSKRS IEDLLFNKVT LADAGFIKQYGDCLGDIAARD
Sbjct	786	YKTPPIKYFGGFNFSQILPDPSKPSKRSPIEDLLFNKVT LADAGFIKQYGDCLGDIAARD
845		
Query	849	LICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNG
908		LICAQKF GLTVLPPLLTDEMIAQYTSALLAGTI SGWTFGAG ALQIPF MQMAYRFNG
Sbjct	846	LICAQKFGLTVLPPLLTDEMIAQYTSALLAGTICSGWTFGAGPALQIPFPMQMAYRFNG
905		
Query	909	IGVTQNVLYENQKLIANQFN SAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSS
968		IGVTQNVLYENQKLIANQFN SAIGKIQDSLST SALGKLQDVVN NAQALNTLVKQLSS
Sbjct	906	IGVTQNVLYENQKLIANQFN SAIGKIQDSLSTPSALGKLQDVVNHNAQALNTLVKQLSS
965		

Query	969	NFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK
1028		
		FGAISSVLNDI SRLDK EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK
Sbjct	966	KFGAISSVLNDIFSRLDKPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK
1025		
Query	1029	MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAH
1088		
		MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAH
Sbjct	1026	MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAH
1085		
Query	1089	FPREGVFVSNNGTHWFTVQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF
1148		
		FPREGVFVSNNGTHWFTVQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF
Sbjct	1086	FPREGVFVSNNGTHWFTVQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF
1145		
Query	1149	KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
1208		
		KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
Sbjct	1146	KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ
1205		

>Chain R, Spike glycoprotein [Homo sapiens]
Sequence ID: 9ASD_R Length: 1273
Range 1: 12 to 1204

Score:2530 bits(5898), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:1128/1201(94%), Positives:1142/1201(95%), Gaps:12/1201(0%)

Query	12	SSQCV---NLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHA	67
		SSQCV NL T TQ +YTNSFTRGVYYPDKVFRSSVLH TQDLFLPFFSNVTWFHA	
Sbjct	12	SSQCVMLPLFNLITTTQ---SYTNSFTRGVYYPDKVFRSSVLHLTQDLFLPFFSNVTWFHA	68
Query	68	IHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLILVNNATNV	
127			
		I SGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLILVNNATNV	
Sbjct	69	I--SGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLILVNNATNV	
126			
Query	128	IKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFK	
187			
		IKVCEFQFCNDPFL VY HKNNKSWMESE VYSSANNCTFEYVSQPFLMDLEGKQGNFK	
Sbjct	127	IKVCEFQFCNDPFLDVY-HKNNKSWMESESGVYSSANNCTFEYVSQPFLMDLEGKQGNFK	
185			
Query	188	NLREFVFKNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIGINITRFQTLLALHRS	
247			
		NLREFVFKNIDGYFKIYSKHTPI + RD PGGFSALEPLVDLPIGINITRFQTLLAL+RS	
Sbjct	186	NLREFVFKNIDGYFKIYSKHTPI-IGRDFPQGFSALEPLVDLPIGINITRFQTLLALNRS	
244			

Query	248	YLTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF
307		
		YLTPGDSSSGWTAGAA YYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF
Sbjct	245	YLTPGDSSSGWTAGAADYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF
304		
Query	308	VEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRISNCVADYSV
367		
		VEKGIYQTSNFRVQPTESIVRFPN+TNLCPF EVFNATRFASVYAWNKRISNCVADYSV
Sbjct	305	VEKGIYQTSNFRVQPTESIVRFPNVTNLCPFHEVFNATRFASVYAWNRRTRISNCVADYSV
364		
Query	368	LYNSASFSTFKCYGVSPKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLDP
427		
		LYN A F FKCYGVSPKLNLDLCFTNVYADSFVI+G+EV QIAPGQTG IADYNYKLDP
Sbjct	365	LYNFAPFFAFKCYGVSPKLNLDLCFTNVYADSFVIKNEVSQIAPGQTGNIADYNYKLDP
424		
Query	428	DFTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFN
487		
		DFTGCVIAWNSN LDSK GNY+Y YRLFRKS LKPFERDISTEIQAG+ PC G +G N
Sbjct	425	DFTGCVIAWNSNKLDSKHSGNYDYWYRLFRKSKLKPFERDISTEIQAGNKPKG-KGPN
483		
Query	488	CYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLT
547		
		CYFPLQSYGF+PT GVG+QPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLT
Sbjct	484	CYFPLQSYGFRPTYGVGHQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLT
543		
Query	548	GTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQ
607		
		GTGVL+SNKKFLPFQQFGRDI DTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQ
Sbjct	544	GTGVLTKSNKKFLPFQQFGRDIVDTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQ
603		
Query	608	VAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIG
667		
		VAVLYQ VNCTEV VAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAE+VNNSECDIPIG
Sbjct	604	VAVLYQGVNCTEVSVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNNSECDIPIG
663		
Query	668	AGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNIAIPTNFTISVTTEIL
727		
		AG+CASYQTQT S A SVASQSIIAYTMSLGAENSVAYSNNIAIPTNFTISVTTEIL
Sbjct	664	AGVCASYQTQTKSRGSASSVASQSIIAYTMSLGAENSVAYSNNIAIPTNFTISVTTEIL
723		
Query	728	PVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQ
787		
		PVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQL RALTGIAVEQDKNTQEVFAQVKQ
Sbjct	724	PVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLKRALTGIAVEQDKNTQEVFAQVKQ
783		
Query	788	IYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAAR
847		

Sbjct	784	IYKTPPIK FGGFNFSQILPDPSKPSKRS IEDLLFNKVTLADAGFIKQYGDCLGDIAAR
843		IYKTPPIKYFGGFNFSQILPDPSKPSKRSPIEDLLFNKVTLADAGFIKQYGDCLGDIAAR
Query	848	DLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFN
907		
Sbjct	844	DLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAG ALQIPF MQMAYRFN
903		DLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGPALQIPFPMQMAYRFN
Query	908	GIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLS
967		
Sbjct	904	GIGVTQNVLYENQKLIANQFNSAIGKIQDSL ST SALGKLQDVVN NAQALNTLVKQLS
963		GIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTPSALGKLQDVVNHNAQALNTLVKQLS
Query	968	SNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAAT
1027		
Sbjct	964	S FGAISSVLNDILSRDL EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAAT
1023		SKFGAISSVLNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAAT
Query	1028	KMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA
1087		
Sbjct	1024	KMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA
1083		KMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKA
Query	1088	HFPREGVFVSNGTHWVFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDS
1147		
Sbjct	1084	HFPREGVFVSNGTHWVFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQ ELDS
1143		HFPREGVFVSNGTHWVFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQLELDS
Query	1148	FKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE
1207		
Sbjct	1144	FKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE
1203		FKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYE
Query	1208	Q 1208
		Q
Sbjct	1204	Q 1204

>Chain A, Spike glycoprotein [Homo sapiens]
Sequence ID: 9VG7_A Length: 1167
>Chain B, Spike glycoprotein [Homo sapiens]
Sequence ID: 9VG7_B Length: 1167
>Chain C, Spike glycoprotein [Homo sapiens]
Sequence ID: 9VG7_C Length: 1167
Range 1: 1 to 1158

Score:2015 bits(4696), Expect:0.0,
Method:Compositional matrix adjust.,

Identities:905/1201(75%), Positives:1005/1201(83%), Gaps:48/1201(3%)

Query	15	CVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTN	74
		CVN+T + Y +S TRGVYYPD FRSS + FLPF SNVTW+ +	
Sbjct	1	CVNITYGSH--HLYVSSRTRGVYYPDDAFRSSTNVLHEGFFLPFDSNVTWYSFWN-----	53
Query	75	GTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIKVCEFQ	
134			
		+++ PF DGVYF++ +KSN++RGW+FGTTLD+ TQS+L+ N+ T+V ++VC F	
Sbjct	54	--QKYSVATSPFGDGVYFSTIDKSNVVRGWVFGTTLDNDTQSVLLYNDGTHVRVEVCTFH	
111			
Query	135	FCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVF	
194			
		FC P S +YSSA NCT Y D G+FK +REFVF	
Sbjct	112	FCPTPVFSA-----SSPHLYSSAFNCTLNITLASVRADFTEVDGSFKTIREFVF	
160			
Query	195	KNIDGYFKIYSKHT----PINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLT	
250			
		K DG +Y T I LP G + L PL +PIG+NIT F+TL+ L RS T	
Sbjct	161	KLQDGSNLVYYASTSYVLAIGATSQLPSGVTPLVPLWKIPIGLNITNFKTLVYL-RSDNT	
219			
Query	251	PGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEK	
310			
		P AAY VG+L+ RT + KY+ENGTI DA+DCALDPLSETKCTL+SF VEK	
Sbjct	220	PLQ-----AAYVVGHLEKRRMTMMFKYDENGITIVDAIDCALDPLSETKCTLRSFIVEK	
270			
Query	311	GIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYN	
370			
		GIYQTSNFRVQP +++VRFPNITNLCPF EVFNAT FASVYAWNRKRISNCVADYSVLYN	
Sbjct	271	GIYQTSNFRVQPQDTPVRFPNITNLCPFSEVFNATTFASVYAWNRKRISNCVADYSVLYN	
330			
Query	371	SASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPPDDFT	
430			
		S SFSTF+CYGVS TKLNDLCFTNVYADSFV+RGDEVQRQIAPGQTG IADYNYKLPPDDFT	
Sbjct	331	STSFSSTFQCYGVSSTKLNDLCFTNVYADSFVVRGDEVQRQIAPGQTGVIADYNYKLPPDDFT	
390			
Query	431	GCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYF	
490			
		GCV+AWNS N D+ GN+NY YR++R L+PFERDI+ YQ G+ +	
Sbjct	391	GCVLAWNSRNQDASTSGNFNYYYRIWRSEKLRPFERDIAHYDYQVGTQFKSS-----	
442			
Query	491	PLQSYGFQPTNGVGYQPYRVVVLSEFELLHAPATVCGPKKSTNLVKNCVNFNFNGLTGTG	
550			
		L++YGF + G +QPYRVVVLSEFELL+APATVCGPK+ST L+KNKCVNFNFNGLTGTG	
Sbjct	443	-LKNYGFYSSAGDSHQPYRVVVLSEFELLNAPATVCGPKQSTELIKNCVNFNFNGLTGTG	
501			
Query	551	VLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAV	
610			
		VLT+SNKKF FQQFGRD++D TD+V+DP+TLE+LDITPCS+GGVSVITPGTN S QVAV	

Sbjct	502	VLTDSENKKFQSFQQFGRDVSDFTDSVKDPKTLEVLDTPCSYGGVSVITPGTNASTQVAV
561		
Query	611	LYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGI
670		
		LYQDVNCT+VP AIHA+QLTP+WRVYSTG+N+FQT+AGCLIGAEHVNNSY+CDIPIGAGI
Sbjct	562	LYQDVNCTDVPTAIHAEQLTPSWRVYSTGTNMFQTQAGCLIGAEHVNNSYDCDIPIGAGI
621		
Query	671	CASYQTQTNSPRRARSVAS-QSIIAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPV
729		
		CA+Y T P RS + + I+AY MSLGAENSVAYSNN+IAIPTNFTISVTTE++PV
Sbjct	622	CATYHT----PSMLRSANNNKRIVAYVMSLGAENSVAYSNNIAIPTNFTISVTTEVMPV
677		
Query	730	SMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIY
789		
		SMTKTSVDCTMYICGDS ECS LLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIY
Sbjct	678	SMTKTSVDCTMYICGDSVECESTLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIY
737		
Query	790	KTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDL
849		
		KTP IKDFGGFNFSQILPDPSKPSKRS IEDLLFNKVTLADAGF+KQYGDCLGDI ARDL
Sbjct	738	KTPDIKDFGGFNFSQILPDPSKPSKRSPIEDLLFNKVTLADAGFVKQYGDCLGDIQARDL
797		
Query	850	ICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGI
909		
		ICAQKFNGLTVLPPLLTDEMIA YT+AL++GT T+GWTFGAG ALQIPF MQMAYRFNGI
Sbjct	798	ICAQKFNGLTVLPPLLTDEMIAAYTAALISGTATAGWTFGAGPALQIPFPMQMAYRFNGI
857		
Query	910	GVTQNVLYENQKLIANQFNSEAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSSN
969		
		GVTQNVLYENQKLIANQFNSEAIGKIQ+SL+ST SALGKLQDVVNQNAQALNTLVKQLSSN
Sbjct	858	GVTQNVLYENQKLIANQFNSEAIGKIQESLTSTPSALGKLQDVVNQNAQALNTLVKQLSSN
917		
Query	970	FGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
1029		
		FGAISSVLNDI+SRDL EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
Sbjct	918	FGAISSVLNDIISRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKM
977		
Query	1030	SECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGKAHF
1089		
		SECVLGQSKRVDFCGKGYHLMSFPQ+APHGVVFLHVTY+P+QE+NFTTAPAICH+GKAHF
Sbjct	978	SECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYIPSQERNFTTAPAICHEGKAHF
1037		
Query	1090	PREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFK
1149		
		PREGVFVSNGTHWF+TQRNFYEPQIITTDNTFVSG CDVVIGIVNNTVYDPLQPEL+SFK
Sbjct	1038	PREGVFVSNGTHWFITQRNFYEPQIITTDNTFVSGTCDVVIGIVNNTVYDPLQPELESFK
1097		

```

Query   1150  EELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQY
1209
          +ELDKYFKNHTSPD+DLGDISGINASVV+IQKEID L +VAKNLNESLI+LQELGKYEQY
Sbjct   1098  DELDKYFKNHTSPDIDLGDISGINASVVDIQKEIDILKDVAKNLNESLINLQELGKYEQY
1157

Query   1210  I   1210
          I
Sbjct   1158  I   1158

```

```

>Chain D, Spike protein S1 [Homo sapiens]
Sequence ID: 7TE1_D Length: 211
>Chain E, Spike protein S1 [Homo sapiens]
Sequence ID: 7TE1_E Length: 211
Range 1: 1 to 211

```

```

Score:494 bits(1145), Expect:3e-157,
Method:Compositional matrix adjust.,
Identities:211/211(100%), Positives:211/211(100%), Gaps:0/211(0%)

```

```

Query   319  RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLVNSASFSTFK 378
          RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLVNSASFSTFK
Sbjct   1    RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLVNSASFSTFK 60

Query   379  CYGVSPTKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNS 438
          CYGVSPTKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNS
Sbjct   61   CYGVSPTKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNS 120

Query   439  NNLDKSVGGNYYNYLYRLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQ 498
          NNLDKSVGGNYYNYLYRLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQ
Sbjct   121  NNLDKSVGGNYYNYLYRLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQ 180

Query   499  PTNGVGYPYRVVVLSEFLLHAPATVCGPKK 529
          PTNGVGYPYRVVVLSEFLLHAPATVCGPKK
Sbjct   181  PTNGVGYPYRVVVLSEFLLHAPATVCGPKK 211

```

```

>Chain B, Spike glycoprotein [Homo sapiens]
Sequence ID: 8T23_B Length: 208
Range 1: 1 to 208

```

```

Score:485 bits(1124), Expect:3e-154,
Method:Compositional matrix adjust.,
Identities:207/208(99%), Positives:208/208(100%), Gaps:0/208(0%)

```

```

Query   321  QPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLVNSASFSTFKCY 380
          QPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLVNSASFSTFKCY
Sbjct   1    QPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLVNSASFSTFKCY 60

Query   381  GVSPTKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNN 440
          GVSPTKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNN
Sbjct   61   GVSPTKLNLDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNN 120

```

Query	441	LDSKVGGNYYNYLRLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPT	500
		LDSKVGGNYYNYL+RLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPT	
Sbjct	121	LDSKVGGNYYNYLRLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPT	180
Query	501	NGVGYPYRVVVL SFELLHAPATVCGPK	528
		NGVGYPYRVVVL SFELLHAPATVCGPK	
Sbjct	181	NGVGYPYRVVVL SFELLHAPATVCGPK	208

>Chain C, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_C Length: 199
>Chain F, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_F Length: 199
>Chain I, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_I Length: 199
>Chain L, Spike protein S1 [Homo sapiens]
Sequence ID: 8BG1_L Length: 199
Range 1: 1 to 194

Score:455 bits(1054), Expect:6e-144,
Method:Compositional matrix adjust.,
Identities:194/194(100%), Positives:194/194(100%), Gaps:0/194(0%)

Query	334	NLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFT	393
		NLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFT	
Sbjct	1	NLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFT	60
Query	394	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYNYLY	453
		NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYNYLY	
Sbjct	61	NVYADSFVIRGDEVQRQIAPGQTGKIADYNYKL PDDFTGCVIAWNSNNLDSKVGGNYYNYLY	120
Query	454	RLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVVL	513
		RLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVVL	
Sbjct	121	RLFRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVVL	180
Query	514	SFELLHAPATVCGP	527
		SFELLHAPATVCGP	
Sbjct	181	SFELLHAPATVCGP	194

>Chain E, Spike protein S2' [Homo sapiens]
Sequence ID: 8CII_E Length: 202
Range 1: 7 to 202

Score:453 bits(1049), Expect:5e-143,
Method:Compositional matrix adjust.,
Identities:193/196(98%), Positives:193/196(98%), Gaps:0/196(0%)

Query	333	TNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCF	392
		TNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCF	
Sbjct	7	TNLCPFGGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCF	66

Query	393	TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYL	452
		TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYY	
Sbjct	67	TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYR	126
Query	453	YRLFRRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVV	512
		YRLFRRKSNLKPFFERDISTEIYQAGS PCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVV	
Sbjct	127	YRLFRRKSNLKPFFERDISTEIYQAGSKPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVV	186
Query	513	LSFELLHAPATVCGPK	528
		LSFELLHAPATVCG K	
Sbjct	187	LSFELLHAPATVCGKK	202

>Chain A, Spike protein S1 [Homo sapiens]
Sequence ID: 7WI0_A Length: 195
Range 1: 1 to 195

Score:421 bits(975), Expect:4e-132,
Method:Compositional matrix adjust.,
Identities:180/195(92%), Positives:184/195(94%), Gaps:0/195(0%)

Query	333	TNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCF	392
		TNLCPF EVFNATRFASVYAWNRRKRISNCVADYSVLYN A F TFKCYGVSPTKLNLCF	
Sbjct	1	TNLCPFDEVFNATRFASVYAWNRRKRISNCVADYSVLYNLAPFFFTFKCYGVSPTKLNLCF	60
Query	393	TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYL	452
		TNVYADSFVIRGDEVQRQIAPGQTG IADYNYKLPDDFTGCVIAWNSN LDSKV GNYNYL	
Sbjct	61	TNVYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPDDFTGCVIAWNSNKLDSKVSGNYYL	120
Query	453	YRLFRRKSNLKPFFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVV	512
		YRLFRRKSNLKPFFERDISTEIYQAG+ PCNGV GFNCYFPL+SY F+PT GVG+QPYRVVV	
Sbjct	121	YRLFRRKSNLKPFFERDISTEIYQAGNKPCNGVAGFNCYFPLRSYSFRPTYGVGHQPYRVVV	180
Query	513	LSFELLHAPATVCGP	527
		LSFELLHAPATVCGP	
Sbjct	181	LSFELLHAPATVCGP	195

>Chain B, Spike protein S1 [Homo sapiens]
Sequence ID: 7TC9_B Length: 195
Range 1: 1 to 195

Score:420 bits(973), Expect:6e-132,
Method:Compositional matrix adjust.,
Identities:180/195(92%), Positives:184/195(94%), Gaps:0/195(0%)

Query	332	ITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNLC	391
		ITNLCPF EVFNATRFASVYAWNRRKRISNCVADYSVLYN A F TFKCYGVSPTKLNLC	
Sbjct	1	ITNLCPFDEVFNATRFASVYAWNRRKRISNCVADYSVLYNLAPFFFTFKCYGVSPTKLNLC	60
Query	392	FTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYY	451
		FTNVYADSFVIRGDEVQRQIAPGQTG IADYNYKLPDDFTGCVIAWNSN LDSKV GNYNY	
Sbjct	61	FTNVYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPDDFTGCVIAWNSNKLDSKVSGNYY	120

```

Query   452  LYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVV  511
          LYRLFRKSNLKPFERDISTEIQAG+ PCNGV GFNCYFPL+SY F+PT GVG+QPYRVV
Sbjct   121  LYRLFRKSNLKPFERDISTEIQAGNKPCNGVAGFNCYFPLRSYSFRPTYGVGHQPYRVV  180

Query   512  VLSFELLHAPATVCG  526
          VLSFELLHAPATVCG
Sbjct   181  VLSFELLHAPATVCG  195

```

>Chain B, Spike protein S1 [Homo sapiens]
Sequence ID: 8ASY_B Length: 219
Range 1: 1 to 200

Score:417 bits(966), Expect:4e-130,
Method:Compositional matrix adjust.,
Identities:179/200(90%), Positives:183/200(91%), Gaps:0/200(0%)

```

Query   333  TNLCPFGEVFNATRFASVYAWNKRKISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCF  392
          TNLCPF EVFNATRFASVYAWNKRKISNCVADYSVLYN A F FKCYSVSPTKLNLCF
Sbjct   1    TNLCPFHEVFNATRFASVYAWNKRKISNCVADYSVLYNFAPFFAFKCYGVSPTKLNLCF  60

Query   393  TNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNYNYL  452
          TNVYADSFVIRG+EV QIAPGQTG IADYNYKLPDDFTGCVIAWNSN LDSKV GNYNYL
Sbjct   61    TNVYADSFVIRGNEVSQIAPGQTGNIADYNYKLPDDFTGCVIAWNSNKLDSKVGNYNYL  120

Query   453  YRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVV  512
          YRLFRKS LKPFERDISTEIQAG+ PCNGV GFNCYFPLQSYGF+PT GVG+QPYRVVV
Sbjct   121  YRLFRKSKLKPFERDISTEIQAGNKPCNGVAGFNCYFPLQSYGFRPTYGVGHQPYRVVV  180

Query   513  LSFELLHAPATVCGPKKSTN  532
          LSFELLHAPATVCG K N
Sbjct   181  LSFELLHAPATVCGKKSLN  200

```

>Chain R, Spike protein S1 [Homo sapiens]
Sequence ID: 7Y0W_R Length: 193
Range 1: 1 to 192

Score:414 bits(959), Expect:9e-130,
Method:Compositional matrix adjust.,
Identities:177/192(92%), Positives:181/192(94%), Gaps:0/192(0%)

```

Query   335  LCPFGEVFNATRFASVYAWNKRKISNCVADYSVLYNSASFSTFKCYGVSPTKLNLCFTN  394
          LCPF EVFNATRFASVYAWNKRKISNCVADYSVLYN A F TFKCYGVSPTKLNLCFTN
Sbjct   1    LCPFDEVFNATRFASVYAWNKRKISNCVADYSVLYNLAPFFTFTKCYGVSPTKLNLCFTN  60

Query   395  VYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGNYNYLYR  454
          VYADSFVIRGDEVQRQIAPGQTG IADYNYKLPDDFTGCVIAWNSN LDSKV GNYNYLYR
Sbjct   61    VYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPDDFTGCVIAWNSNKLDSKVGNYNYLYR  120

Query   455  LFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYPYRVVLS  514
          LFRKSNLKPFERDISTEIQAG+ PCNGV GFNCYFPL+SY F+PT GVG+QPYRVVLS

```

Sbjct 121 LFRKSNLKPFERDISTEIQAGNKPCNGVAGFNCYFPLRSYSFRPTYGVGHQPYRVVVL 180

Query 515 FELLHAPATVCG 526
FELLHAPATVCG

Sbjct 181 FELLHAPATVCG 192

>Chain A, PDCoV spike glycoprotein S1A domain [Homo sapiens]
Sequence ID: 8R9X_A Length: 1079
Range 1: 545 to 1079

Score:320 bits(739), Expect:1e-86,
Method:Compositional matrix adjust.,
Identities:194/542(36%), Positives:281/542(51%), Gaps:40/542(7%)

Query 705 VAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLN
764

V+ + + IP+ F++SV TE L V + VDC Y+C ++ C LL QY S C+ +
Sbjct 545 VSLYDGEVEIPSAFSLSVQTEYLQVQAEQVIVDCPQYVCNGNSRCLQLLAQYTSACSNI
604

Query 765 RALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDF-GGFNFSQILPDPSKPSKRSFIEDLLF
823

AL A + +F Q + I +F G +NFS IL ++ RS IEDLLF
Sbjct 605 AALHSSAQQLDSREIINMFQTSTQSLQLANITNFKGDYNFSSILT--TRIGGRSAIEDLLF
662

Query 824 NKVTLADAGFIKQ-YGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTI
882

NKV + G + Q Y C D+A DL+C+Q +NG+ VLP ++ E +A YT +L +
Sbjct 663 NKVVTSGLGTVDDQDYKSCSRDMAIADLVCSQYYNGIMVLPGVVDAEKMAMYTGSLTGAMV
722

Query 883 TSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDLSLST-
941

G T A A + R N + + NVL ENQK++A FN A+G I +LSS
Sbjct 723 FGGLTAAAAIPF----ATAVQARLNYVALQTNVLQENQKILAESFNQAVGNISLALSSVN
778

Query 942 -----ASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVE
988

A A+ K+Q VVNQ +AL+ L QLS+NF AIS+ + DI +RL++VE
Sbjct 779 DAIQQTSEALNTVAIAIKKIQTVVNQGEALSHLTAQLSNNFQAISTSIQDIYNRLEEVE
838

Query 989 AEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYH
1048

A Q+DRLITGRL +L YVTQ L + ++IR S LA K++ECV QS R FCG G H
Sbjct 839 ANQQVDRLITGRLAALNAYVTQLLNQMSQIRQSRLLAQQKINECVKSQSPRYGFCGNGTH
898

Query 1049 LMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHD---GKAHFPREGVFSNGTHWFVT
1105

+ S Q+AP+G+ F+H VP + + IC D G + P+ ++ N + W VT

Sbjct 899 IFSLTQTAPNGIFFMHAFLVPNKFTRVNASAGICVDNTRGYSLQPQLILYQFNNS-WRV
957

Query 1106 QRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKN---HTSP
1162

RN YEP++ + +C V + P++ + + N T P

Sbjct 958 PRNMYEPRLPRQADFIQLTDCSVTFYNTTAANLPNIIPDIIDVNQTVSDIIDNLPTATPP
1017

Query 1163 DVDLG-----DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK
1211

D+G +I+ + N+ + DRL NLN +L+DL+ L + E Y+K

Sbjct 1018 QWDVGIYNNTILNLTVEINDLQERSKNLSQIADRLQNYIDNLNNTLVLEWLN RVETYLK
1077

Query 1212 WP 1213
WP

Sbjct 1078 WP 1079

>Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
Sequence ID: 9E8L_H Length: 234
Range 1: 143 to 225

Score:35.7 bits(75), Expect:3.4,
Method:Compositional matrix adjust.,
Identities:29/83(35%), Positives:43/83(51%), Gaps:4/83(4%)

Query 246 RSYLTPGDSSSGWTA-GAAAYYVGYLQPRTFLLK-YNENGTITDAVDCALDPLSET-KCT 302
R YL D S + A A A+ Y+ +TFL K YNE+ + DA+ A+ L E+ +

Sbjct 143 RPYLFQSDPSGAYFAWKATAHGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQ 202

Query 303 LKSFTVEKGIYQTSNF-RVQPT 324
+ +E GI + F R+ PTE

Sbjct 203 MTEDNIEVGICNEAGFRRLTPTE 225

>biogenesis of lysosomal organelles complex 1 subunit 6, partial [Homo sapiens]
Sequence ID: KAI2574041.1 Length: 113
>biogenesis of lysosomal organelles complex 1 subunit 6, partial [Homo sapiens]
Sequence ID: KAI4057642.1 Length: 113
Range 1: 32 to 91

Score:34.5 bits(72), Expect:4.5,
Method:Composition-based stats.,
Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202

LD+ ++E+ K+ + H+ D++ + +A +VNI+KE+ L+E L + + LQ+

Sbjct 32 LDTLEQEISKFECHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLKKRALKLQQ 91


```

>hCG2001986, isoform CRA_c [Homo sapiens]
Sequence ID: EAW77322.1 Length: 131
>biogenesis of lysosomal organelles complex 1 subunit 6 [Homo sapiens]
Sequence ID: KAI2574037.1 Length: 131
>biogenesis of lysosomal organelles complex 1 subunit 6 [Homo sapiens]
Sequence ID: KAI4057646.1 Length: 131
Range 1: 41 to 100

Score:34.5 bits(72), Expect:5.4,
Method:Composition-based stats.,
Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202
          LD+ ++E+ K+ + H+ D++      +      +A +VNI+KE+ L+E      L + + LQ+
Sbjct 41    LDTLEQEISKFKECHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLRALKLQQ
100

>biogenesis of lysosome-related organelles complex 1 subunit 6 isoform 2
[Homo sapiens]
Sequence ID: NP_036520.1 Length: 172
>RecName: Full=Biogenesis of lysosome-related organelles complex 1 subunit 6;
Short=BL0C-1 subunit 6; AltName: Full=Pallid protein homolog; AltName:
Full=Pallidin; AltName: Full=Syntaxin 13-interacting protein [Homo sapiens]
Sequence ID: Q9UL45.1 Length: 172
>pallid [Homo sapiens]
Sequence ID: AAF08343.1 Length: 172
>Pallidin homolog (mouse) [Homo sapiens]
Sequence ID: AAH04819.1 Length: 172
Range 1: 82 to 141

Score:34.5 bits(72), Expect:6.9,
Method:Composition-based stats.,
Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202
          LD+ ++E+ K+ + H+ D++      +      +A +VNI+KE+ L+E      L + + LQ+
Sbjct 82    LDTLEQEISKFKECHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLRALKLQQ
141

>unnamed protein product [Homo sapiens]
Sequence ID: BAG37954.1 Length: 172
Range 1: 82 to 141

Score:34.5 bits(72), Expect:6.9,
Method:Composition-based stats.,

```

Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

```
Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202
          LD+ ++E+ K+ + H+ D++      +      +A +VNI+KE+ L+E      L + + LQ+
Sbjct 82   LDTLEQEISKFKCHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLLKKRALKLQQ
141
```

>biogenesis of lysosome-related organelles complex 1 subunit 6 isoform 1
[Homo sapiens]

Sequence ID: NP_001298184.1 Length: 177

>biogenesis of lysosomal organelles complex 1 subunit 6 [Homo sapiens]

Sequence ID: KAI2574040.1 Length: 177

>biogenesis of lysosomal organelles complex 1 subunit 6 [Homo sapiens]

Sequence ID: KAI4057647.1 Length: 177

Range 1: 87 to 146

Score:34.5 bits(72), Expect:7.0,

Method:Composition-based stats.,

Identities:17/60(28%), Positives:35/60(58%), Gaps:2/60(3%)

```
Query 1145 LDSFKEELDKYFKNHTSPDVD--LGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE
1202
          LD+ ++E+ K+ + H+ D++      +      +A +VNI+KE+ L+E      L + + LQ+
Sbjct 87   LDTLEQEISKFKCHSMLDINALFAEAKHYHAKLVNIRKEMLMLHEKTSKLLKKRALKLQQ
146
```

>proteasome 20S subunit alpha 2 [Homo sapiens]

Sequence ID: KAI2545645.1 Length: 164

>proteasome 20S subunit alpha 2 [Homo sapiens]

Sequence ID: KAI4013575.1 Length: 164

Range 1: 73 to 155

Score:34.5 bits(72), Expect:7.1,

Method:Compositional matrix adjust.,

Identities:29/83(35%), Positives:42/83(50%), Gaps:4/83(4%)

```
Query 246 RSYLTPGDSSSGWTA-GAAAYYVGYLQPRTFLLK-YNENGTITDAVDCALDPLSET-KCT 302
          R YL D S + A A A Y+ +TFL K YNE+ + DA+ A+ L E+ +
Sbjct 73   RPYLFQSDPSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQ 132
```

```
Query 303 LKSFTVEKGIYQTSNF-RVQPTE 324
          + +E GI + F R+ PTE
```

```
Sbjct 133 MTEDNIEVGICNEAGFRRLTPTE 155
```

>Chain B, Proteasome subunit alpha type-2 [Homo sapiens]

Sequence ID: 7AWE_B Length: 229

>Chain P, Proteasome subunit alpha type-2 [Homo sapiens]

Sequence ID: 7AWE_P Length: 229
 >Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7B12_B Length: 229
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7B12_P Length: 229
 Range 1: 139 to 221

Score:34.5 bits(72), Expect:8.5,
 Method:Compositional matrix adjust.,
 Identities:29/83(35%), Positives:42/83(50%), Gaps:4/83(4%)

```
Query   246   RSYLTPGDSSSGWTA-GAAAYYVGYLQPRTFLLK-YNENGTITDAVDCALDPLSET-KCT   302
          R YL   D S   + A   A A       Y+   +TFL K YNE+   + DA+   A+   L E+   +
Sbjct   139   RPYLFQSDPSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQ   198

Query   303   LKSFTVEKGIYQTSNF-RVQPTE   324
          +       +E GI       + F R+ PTE
Sbjct   199   MTEDNIEVGICNEAGFRRLTPTE   221
```

>PSMA2 protein, partial [Homo sapiens]
 Sequence ID: AAH02900.2 Length: 225
 Range 1: 134 to 216

Score:34.5 bits(72), Expect:8.6,
 Method:Compositional matrix adjust.,
 Identities:29/83(35%), Positives:42/83(50%), Gaps:4/83(4%)

```
Query   246   RSYLTPGDSSSGWTA-GAAAYYVGYLQPRTFLLK-YNENGTITDAVDCALDPLSET-KCT   302
          R YL   D S   + A   A A       Y+   +TFL K YNE+   + DA+   A+   L E+   +
Sbjct   134   RPYLFQSDPSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQ   193

Query   303   LKSFTVEKGIYQTSNF-RVQPTE   324
          +       +E GI       + F R+ PTE
Sbjct   194   MTEDNIEVGICNEAGFRRLTPTE   216
```

>proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: NP_002778.1 Length: 234
 >RecName: Full=Proteasome subunit alpha type-2; AltName: Full=Macropain
 subunit C3; AltName: Full=Multicatalytic endopeptidase complex subunit C3;
 AltName: Full=Proteasome component C3; AltName: Full=Proteasome subunit
 alpha-2; Short=alpha-2 [Homo sapiens]
 Sequence ID: P25787.2 Length: 234
 >Chain B, PROTEASOME SUBUNIT ALPHA TYPE-2 [Homo sapiens]
 Sequence ID: 5A0Q_B Length: 234
 >Chain P, PROTEASOME SUBUNIT ALPHA TYPE-2 [Homo sapiens]
 Sequence ID: 5A0Q_P Length: 234
 >Chain C, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5GJQ_C Length: 234
 >Chain i, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5GJQ_i Length: 234
 >Chain C, Proteasome subunit alpha type-2 [Homo sapiens]

Sequence ID: 5GJR_C Length: 234
 >Chain i, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5GJR_i Length: 234
 >Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5L4G_B Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5L4G_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LE5_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LE5_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LEX_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LEX_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LEY_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LEY_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LEZ_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LEZ_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF0_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF0_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF1_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF1_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF3_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF3_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF4_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF4_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF6_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF6_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF7_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LF7_O Length: 234
 >Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5LN3_B Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5M32_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5M32_O Length: 234
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6AVO_P Length: 234
 >Chain b, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6AVO_b Length: 234

>Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6E5B_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6E5B_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6KWY_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6KWY_O Length: 234
 >Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6REY_B Length: 234
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6REY_P Length: 234
 >Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6RGQ_B Length: 234
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6RGQ_P Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7LXV_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7LXV_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7NAN_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7NAN_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7NAO_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7NAO_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7NAP_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7NAP_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7NAQ_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7NAQ_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7NHT_A Length: 234
 >Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7PG9_B Length: 234
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7PG9_P Length: 234
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7V5G_P Length: 234
 >Chain W, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7V5G_W Length: 234
 >Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7V5M_B Length: 234
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7V5M_P Length: 234
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7W37_H Length: 234
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7W37_h Length: 234
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 7W38_H Length: 234
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]

[illegible]

>Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8CVT_H Length: 234
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8CVT_h Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8CXB_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8CXB_O Length: 234
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8JRI_H Length: 234
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8JRT_H Length: 234
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8JTI_H Length: 234
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8K0G_H Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8QYJ_A Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8QYL_A Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8QYM_A Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8QYN_A Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8QYO_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8QYO_O Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8QYS_A Length: 234
 >Chain R, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8QYS_R Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8QZ9_A Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8TM3_A Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8TM4_A Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8TM5_A Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8TM6_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8TM6_O Length: 234
 >Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8UD9_B Length: 234
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8UD9_P Length: 234
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8USB_H Length: 234
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8USC_H Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8YIX_A Length: 234
 >Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 8YIY_A Length: 234
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]

[illegible]

>Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 9UG9_h Length: 234
 Range 1: 143 to 225

Score:34.5 bits(72), Expect:8.6,
 Method:Compositional matrix adjust.,
 Identities:29/83(35%), Positives:42/83(50%), Gaps:4/83(4%)

```
Query 246 RSYLTPGDSSSGWTA-GAAAYYVGYLQPRTFLK-YNENGTITDAVDCALDPLSET-KCT 302
          R YL  D S  + A  A A    Y+  +TFL K YNE+  + DA+  A+  L E+  +
Sbjct 143 RPYLFQSDPSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQ 202

Query 303 LKSFTVEKGIYQTSNF-RVQPTE 324
          +      +E GI    + F R+ PTE
Sbjct 203 MTEDNIEVGICNEAGFRRLTPTE 225
```

>Chain A, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6R70_A Length: 230
 >Chain O, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6R70_O Length: 230
 Range 1: 140 to 222

Score:34.5 bits(72), Expect:8.7,
 Method:Compositional matrix adjust.,
 Identities:29/83(35%), Positives:42/83(50%), Gaps:4/83(4%)

```
Query 246 RSYLTPGDSSSGWTA-GAAAYYVGYLQPRTFLK-YNENGTITDAVDCALDPLSET-KCT 302
          R YL  D S  + A  A A    Y+  +TFL K YNE+  + DA+  A+  L E+  +
Sbjct 140 RPYLFQSDPSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQ 199

Query 303 LKSFTVEKGIYQTSNF-RVQPTE 324
          +      +E GI    + F R+ PTE
Sbjct 200 MTEDNIEVGICNEAGFRRLTPTE 222
```

>Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFO_H Length: 232
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFO_h Length: 232
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFP_H Length: 232
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFP_h Length: 232
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFQ_H Length: 232
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFQ_h Length: 232
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFR_H Length: 232
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFR_h Length: 232
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]

Sequence ID: 5VFS_H Length: 232
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFS_h Length: 232
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFT_H Length: 232
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFT_h Length: 232
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFU_H Length: 232
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5VFU_h Length: 232
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6WJN_H Length: 232
 >Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 6WJN_h Length: 232
 Range 1: 141 to 223

Score:34.5 bits(72), Expect:8.9,
 Method:Compositional matrix adjust.,
 Identities:29/83(35%), Positives:42/83(50%), Gaps:4/83(4%)

Query	246	RSYLTPGDSSSGWTA-GAAAYVGYLQPRTFLLK-YNENGTITDAVDCALDPLSET-KCT	302
		R YL D S + A A A Y+ +TFL K YNE+ + DA+ A+ L E+ +	
Sbjct	141	RPYLFQSDPSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQ	200
Query	303	LKSFTVEKGIYQTSNF-RVQPT	324
		+ +E GI + F R+ PTE	
Sbjct	201	MTEDNIEVGICNEAGFRRLTPTE	223

>Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 4R30_B Length: 233
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 4R30_P Length: 233
 >Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 4R67_B Length: 233
 >Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 4R67_P Length: 233
 >Chain d, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 4R67_d Length: 233
 >Chain r, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 4R67_r Length: 233
 >Chain AH, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5T0C_AH Length: 233
 >Chain BH, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5T0C_BH Length: 233
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5T0G_H Length: 233
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5T0H_H Length: 233
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5T0I_H Length: 233
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
 Sequence ID: 5T0J_H Length: 233
 >Chain H, Proteasome subunit alpha type-2 [Homo sapiens]

[illegible]

>Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
Sequence ID: 7QYA_H Length: 233
>Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
Sequence ID: 7QYA_h Length: 233
>Chain H, Proteasome subunit alpha type-2 [Homo sapiens]
Sequence ID: 7QYB_H Length: 233
>Chain h, Proteasome subunit alpha type-2 [Homo sapiens]
Sequence ID: 7QYB_h Length: 233
>Chain B, Proteasome subunit alpha type-2 [Homo sapiens]
Sequence ID: 9HMN_B Length: 233
>Chain P, Proteasome subunit alpha type-2 [Homo sapiens]
Sequence ID: 9HMN_P Length: 233
Range 1: 142 to 224

Score:34.0 bits(71), Expect:9.3,
Method:Compositional matrix adjust.,
Identities:29/83(35%), Positives:42/83(50%), Gaps:4/83(4%)

```

Query   246   RSYLTPGDSSSGWTA-GAAAYYVGYLQPRTFLLK-YNENGTITDAVDCALDPLSET-KCT   302
          R YL  D S  + A  A A    Y+  +TFL K YNE+  + DA+  A+  L E+  +
Sbjct   142   RPYLFQSDPSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQ   201

Query   303   LKSFTVEKGIYQTSNF-RVQPTE   324
          +    +E GI    + F R+ PTE
Sbjct   202   MTEDNIEVGICNEAGFRRLTPTE   224

```

>proteasome alpha 2 subunit variant, partial [Homo sapiens]
Sequence ID: BAD96696.1 Length: 234
Range 1: 143 to 225

Score:34.0 bits(71), Expect:10,
Method:Compositional matrix adjust.,
Identities:29/83(35%), Positives:42/83(50%), Gaps:4/83(4%)

```

Query   246   RSYLTPGDSSSGWTA-GAAAYYVGYLQPRTFLLK-YNENGTITDAVDCALDPLSET-KCT   302
          R YL  D S  + A  A A    Y+  +TFL K YNE+  + DA+  A+  L E+  +
Sbjct   143   RPYLFQSDPSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQ   202

Query   303   LKSFTVEKGIYQTSNF-RVQPTE   324
          +    +E GI    + F R+ PTE
Sbjct   203   MTEDNIEVGICNEAGFRRLTPTE   225

```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOL23798.1 Length: 21
Range 1: 1 to 16

Score:29.3 bits(60), Expect:13,
Method:Composition-based stats.,
Identities:11/16(69%), Positives:13/16(81%), Gaps:0/16(0%)

```

Query   590   CSFGGVSVITPGTNTS   605

```

Sbjct 1 C GG SV+TPGTNT+
CVRGGGSVVTPGTNTA 16

>hCG22236, isoform CRA_b, partial [Homo sapiens]
Sequence ID: EAX10979.1 Length: 500
Range 1: 169 to 266

Score:34.0 bits(71), Expect:13,
Method:Compositional matrix adjust.,
Identities:23/98(23%), Positives:45/98(45%), Gaps:0/98(0%)

Query 1114 IITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGIN
1173

++ DN ++ + V ++ N + PL+ E+++ KEEL KNH L +
Sbjct 169 VLQIDNACLAADDFRVKSLMTNVTWLPLETEMEALKEELLFMKKNHHEEEVKGLQAQIASS
228

Query 1174 ASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK 1211

V I+K + + + ++ + L EL + Q +K
Sbjct 229 ELTVEIEKSTTVVTTQSTKVGDAEMTLTELRTVQSLK 266

>Chain A, ATP-dependent RNA helicase DHX15 [Homo sapiens]
Sequence ID: 8EJM_A Length: 686
Range 1: 16 to 70

Score:33.6 bits(70), Expect:18,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

Query 217 PQGFSALEPLVDLPIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYVGYLQ 271

P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
Sbjct 16 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 70

>Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]

Sequence ID: 6SH6_A Length: 689

>Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]

Sequence ID: 6SH7_A Length: 689

Range 1: 19 to 73

Score:33.6 bits(70), Expect:20,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

Query 217 PQGFSALEPLVDLPIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYVGYLQ 271

P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
Sbjct 19 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 73

>Chain A, Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]

Sequence ID: 5XDR_A Length: 690

Range 1: 20 to 74

Score:33.6 bits(70), Expect:20,

Method:Compositional matrix adjust.,

Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

Query	217	PQGFSALEPLVDLP	IGINITRFQ	TLLALHRSYL	TPGDSSSGWTAGAAAYYVGYLQ	271
		P+ + L+ + LP+	RF +L H+S++	G++ SG T	+ V Y++	
Sbjct	20	PRYYDILKKRLQL	PVWEYKDRFT	DILVRHQSFVLV	GETGSGKTTQIPQWCVEYMR	74

>immunoglobulin heavy chain junction region [Homo sapiens]

Sequence ID: MBB2037351.1 Length: 25

>immunoglobulin heavy chain junction region [Homo sapiens]

Sequence ID: MBB2107516.1 Length: 25

Range 1: 7 to 24

Score:28.9 bits(59), Expect:20,

Method:Composition-based stats.,

Identities:10/18(56%), Positives:11/18(61%), Gaps:0/18(0%)

Query	252	GDSSSGWTAGAAAYYVGY	269
		GD SGW +G AYY Y	
Sbjct	7	GDFGSGWYSGTTAYYFDY	24

>immunoglobulin heavy chain junction region [Homo sapiens]

Sequence ID: MBB2121301.1 Length: 25

Range 1: 7 to 24

Score:28.5 bits(58), Expect:28,

Method:Composition-based stats.,

Identities:10/18(56%), Positives:11/18(61%), Gaps:0/18(0%)

Query	252	GDSSSGWTAGAAAYYVGY	269
		GD SGW +G AYY Y	
Sbjct	7	GDFGSGWYSGTTAYYFDY	24

>unnamed protein product [Homo sapiens]

Sequence ID: BAG64538.1 Length: 784

Range 1: 114 to 168

Score:33.2 bits(69), Expect:29,

Method:Compositional matrix adjust.,
Identities:15/55 (27%), Positives:29/55 (52%), Gaps:0/55 (0%)

```
Query   217   PQGFSALEPLVDLPIGINITRFQTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQ   271
          P+ + L+ + LP+      RF  +L  H+S++  G++ SG T      + V Y++
Sbjct   114   PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR   168
```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOL37782.1 Length: 21
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOR61122.1 Length: 21
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOR70185.1 Length: 21
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOR72596.1 Length: 21
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MOR73296.1 Length: 21
Range 1: 1 to 16

Score:28.0 bits(57), Expect:30,
Method:Composition-based stats.,
Identities:10/16 (63%), Positives:13/16 (81%), Gaps:0/16 (0%)

```
Query   590   CSFGGVSVITPGTNTS   605
          C  GG +V+TPGTNT+
Sbjct   1     CVRGGGAVVTPGTNTA   16
```

>ATP-dependent RNA helicase DHX15 [Homo sapiens]
Sequence ID: NP_001349.2 Length: 795
>RecName: Full=ATP-dependent RNA helicase DHX15; AltName: Full=ATP-dependent RNA helicase #46; AltName: Full=DEAH box protein 15; AltName: Full=Splicing factor Prp43; Short=hPrp43 [Homo sapiens]
Sequence ID: O43143.2 Length: 795
>Chain V, Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]
Sequence ID: 6ID1_V Length: 795
>Chain DX, ATP-dependent RNA helicase DHX15 [Homo sapiens]
Sequence ID: 8RO2_DX Length: 795
>dead box protein 15 [Homo sapiens]
Sequence ID: AAF90182.1 Length: 795
>DEAH (Asp-Glu-Ala-His) box polypeptide 15 [Homo sapiens]
Sequence ID: AAH35974.1 Length: 795
>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_b [Homo sapiens]
Sequence ID: EAW92815.1 Length: 795
>DEAH-box helicase 15 [Homo sapiens]
Sequence ID: KAI2533940.1 Length: 795
Range 1: 125 to 179

Score:32.7 bits(68), Expect:30,
Method:Compositional matrix adjust.,
Identities:15/55 (27%), Positives:29/55 (52%), Gaps:0/55 (0%)

Query 217 PQGFSALEPLVDLPIGINITRFQTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQ 271
P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
Sbjct 125 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 179

>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_h [Homo sapiens]
Sequence ID: EAW92821.1 Length: 778
Range 1: 125 to 179

Score:32.7 bits(68), Expect:31,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

Query 217 PQGFSALEPLVDLPIGINITRFQTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQ 271
P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
Sbjct 125 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 179

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB2102104.1 Length: 17
Range 1: 4 to 17

Score:28.0 bits(57), Expect:32,
Method:Composition-based stats.,
Identities:10/14(71%), Positives:12/14(85%), Gaps:0/14(0%)

Query 253 DSSSGWTAGAAAY 266
DSSSGWTAG+ Y+
Sbjct 4 DSSSGWTAGSFDYW 17

>t-SNARE domain-containing protein 1 isoform X2 [Homo sapiens]
Sequence ID: XP_047277414.1 Length: 981
Range 1: 262 to 360

Score:32.7 bits(68), Expect:38,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

Query 920 QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
975
Q++ AN F NS++ ++ SL S T S +L+D ++ Q N + +S+ ++
Sbjct 262 QEMSANVFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
321

Query 976 VLNDILSRDLKVEAEVQIDRLITGRQLQSLQTYVTQQLIR 1014
+L + + Q+DRL T ++Q Y Q +R
Sbjct 322 LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR 360

>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_g [Homo sapiens]
Sequence ID: EAW92820.1 Length: 709
Range 1: 125 to 179

Score:32.3 bits(67), Expect:41,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```
Query   217   PQGFSALEPLVDLPIGINITRFQTLALHRSYLTTPGDSSSGWTAGAAAYVGYLQ   271
          P+ +  L+  + LP+      RF  +L  H+S++  G++ SG T      + V Y++
Sbjct   125   PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR   179
```

>coenzyme Q6, monooxygenase [Homo sapiens]
Sequence ID: KAI2571974.1 Length: 86
>coenzyme Q6, monooxygenase [Homo sapiens]
Sequence ID: KAI4061599.1 Length: 86
Range 1: 6 to 46

Score:30.6 bits(63), Expect:46,
Method:Composition-based stats.,
Identities:13/41(32%), Positives:22/41(53%), Gaps:0/41(0%)

```
Query   792   PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAG   832
          PP+  FG +  S+  DPS+P ++ +      K+ L +AG
Sbjct    6    PPLSSFGVWLASRAASDPSRPRRQGYDIHFHDKKILLLEAG   46
```

>pyruvate kinase M1/2 [Homo sapiens]
Sequence ID: KAI2574971.1 Length: 69
>pyruvate kinase M1/2 [Homo sapiens]
Sequence ID: KAI4058566.1 Length: 69
Range 1: 39 to 68

Score:30.2 bits(62), Expect:47,
Method:Composition-based stats.,
Identities:11/33(33%), Positives:18/33(54%), Gaps:3/33(9%)

```
Query   728   PVSMTKTSVDCTMYICGDSTECNLLLQYGSFC   760
          P++   T + CT+  CGD  EC++   +G  C
Sbjct   39    PITARNTGIICTIVPCGDHQECAH---SHGKLC   68
```

>t-SNARE domain-containing protein 1 isoform X2 [Homo sapiens]
Sequence ID: XP_054215930.1 Length: 981
Range 1: 262 to 360

Score:32.3 bits(67), Expect:49,
Method:Compositional matrix adjust.,

Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```
Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
          975
          Q++ AN F  NS++  ++ SL S  T S   +L+D ++   Q  N  +   +S+  ++
Sbjct   262   QEMSANIFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
          321

Query   976   VLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIR   1014
          +L      +      +   Q+DRL T   ++Q Y   Q +R
Sbjct   322   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR   360
```

>t-SNARE domain-containing protein 1 isoform X7 [Homo sapiens]
Sequence ID: XP_047277418.1 Length: 892
Range 1: 173 to 271

Score:32.3 bits(67), Expect:49,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```
Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
          975
          Q++ AN F  NS++  ++ SL S  T S   +L+D ++   Q  N  +   +S+  ++
Sbjct   173   QEMSANVFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
          232

Query   976   VLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIR   1014
          +L      +      +   Q+DRL T   ++Q Y   Q +R
Sbjct   233   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR   271
```

>t-SNARE domain-containing protein 1 isoform X4 [Homo sapiens]
Sequence ID: XP_047277416.1 Length: 931
Range 1: 212 to 310

Score:32.3 bits(67), Expect:50,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```
Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
          975
          Q++ AN F  NS++  ++ SL S  T S   +L+D ++   Q  N  +   +S+  ++
Sbjct   212   QEMSANVFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
          271

Query   976   VLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIR   1014
          +L      +      +   Q+DRL T   ++Q Y   Q +R
Sbjct   272   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR   310
```

>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_d [Homo sapiens]
Sequence ID: EAW92817.1 Length: 650
Range 1: 125 to 179

Score:31.9 bits(66), Expect:57,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```
Query   217   PQGFSALEPLVDLPIGINITRFQTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQ   271
          P+ +  L+  + LP+      RF  +L  H+S++  G++ SG T      + V Y++
Sbjct   125   PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR   179
```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MCG22225.1 Length: 19
Range 1: 5 to 16

Score:27.2 bits(55), Expect:58,
Method:Composition-based stats.,
Identities:9/12(75%), Positives:10/12(83%), Gaps:0/12(0%)

```
Query   1092  EGVFVSNGTHWF   1103
          EGV V+ GTHWF
Sbjct    5    EGVAVAGGTHWF   16
```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MFT1129265.1 Length: 22
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MFT1129267.1 Length: 22
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MFT1129268.1 Length: 22
Range 1: 4 to 17

Score:27.6 bits(56), Expect:59,
Method:Composition-based stats.,
Identities:9/14(64%), Positives:11/14(78%), Gaps:0/14(0%)

```
Query   253   DSSSGWTAGAAAYY   266
          + SSGWT GA +YY
Sbjct    4    EDSSSGWTGGAYSY   17
```

>ATP-dependent RNA helicase DHX15 isoform X2 [Homo sapiens]
Sequence ID: XP_047305655.1 Length: 600
>ATP-dependent RNA helicase DHX15 isoform X2 [Homo sapiens]
Sequence ID: XP_054205062.1 Length: 600
Range 1: 125 to 179

Score:31.9 bits(66), Expect:61,
Method:Compositional matrix adjust.,

Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```
Query 217 PQGFSALEPLVDLPIGINITRFQTLLALHRSYLTTPGDSSSGWTAGAAAYVGYLQ 271
          P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
Sbjct 125 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 179
```

>DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_e [Homo sapiens]
Sequence ID: EAW92818.1 Length: 499
Range 1: 125 to 179

Score:31.9 bits(66), Expect:64,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```
Query 217 PQGFSALEPLVDLPIGINITRFQTLLALHRSYLTTPGDSSSGWTAGAAAYVGYLQ 271
          P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
Sbjct 125 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 179
```

>t-SNARE domain-containing protein 1 isoform X7 [Homo sapiens]
Sequence ID: XP_054215935.1 Length: 892
Range 1: 173 to 271

Score:31.9 bits(66), Expect:65,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```
Query 920 QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
975
          Q++ AN F NS++ ++ SL S T S +L+D ++ Q N + +S+ ++
Sbjct 173 QEMSNANIFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
232
```

```
Query 976 VLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIR 1014
          +L + + Q+DRL T ++Q Y Q +R
Sbjct 233 LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR 271
```

>ATP-dependent RNA helicase DHX15 isoform X1 [Homo sapiens]
Sequence ID: XP_047305654.1 Length: 608
>ATP-dependent RNA helicase DHX15 isoform X1 [Homo sapiens]
Sequence ID: XP_054205061.1 Length: 608
Range 1: 125 to 179

Score:31.9 bits(66), Expect:66,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:29/55(52%), Gaps:0/55(0%)

```
Query 217 PQGFSALEPLVDLPIGINITRFQTLLALHRSYLTTPGDSSSGWTAGAAAYVGYLQ 271
          P+ + L+ + LP+ RF +L H+S++ G++ SG T + V Y++
```

Sbjct 125 PRYYDILKKRLQLPVWEYKDRFTDILVRHQSFVLVGETGSGKTTQIPQWCVEYMR 179

>ubiquinone biosynthesis monooxygenase COQ6, mitochondrial isoform b [Homo sapiens]

Sequence ID: NP_872286.2 Length: 443

>coenzyme Q6, monooxygenase [Homo sapiens]

Sequence ID: KAI2571973.1 Length: 443

>unnamed protein product [Homo sapiens]

Sequence ID: BAH12244.1 Length: 443

Range 1: 6 to 46

Score:31.9 bits(66), Expect:67,

Method:Compositional matrix adjust.,

Identities:13/41(32%), Positives:22/41(53%), Gaps:0/41(0%)

Query 792 PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTADAG 832

PP+ FG + S+ DPS+P ++ + K+ L +AG

Sbjct 6 PPLSSFGVWLASRAASDPSRPRRQGYDIHFHDKKILLLEAG 46

>hCG1644135, isoform CRA_b, partial [Homo sapiens]

Sequence ID: EAW68450.1 Length: 111

Range 1: 2 to 24

Score:30.6 bits(63), Expect:67,

Method:Composition-based stats.,

Identities:10/23(43%), Positives:16/23(69%), Gaps:0/23(0%)

Query 489 YFPLQSYGFQPTNGVGYPYRVV 511

YFP +GF PT+G+ + Y++V

Sbjct 2 YFPAAIFGFLPTSGILFSYYKIV 24

>Carnitine O-palmitoyltransferase II, mitochondrial precursor variant, partial [Homo sapiens]

Sequence ID: BAD96772.1 Length: 577

Range 1: 8 to 36

Score:31.9 bits(66), Expect:68,

Method:Compositional matrix adjust.,

Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215

N + K L+E L+ L + K+ YI PW+

Sbjct 8 NGIGKELHEQLVALDKQNKHTSYISGPWF 36

>coenzyme Q6, monooxygenase [Homo sapiens]

Sequence ID: KAI4061598.1 Length: 443
Range 1: 6 to 46

Score:31.5 bits(65), Expect:69,
Method:Compositional matrix adjust.,
Identities:13/41(32%), Positives:22/41(53%), Gaps:0/41(0%)

```
Query   792   PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAG   832
          PP+  FG +  S+   DPS+P ++ +           K+ L +AG
Sbjct   6     PPLSSFVWLASRAASDPSRPRRQGYDIHFHDKKILLLEAG   46
```

>carnitine O-palmitoyltransferase 2, mitochondrial isoform 2 precursor [Homo sapiens]
Sequence ID: NP_001317518.1 Length: 635
Range 1: 89 to 117

Score:31.9 bits(66), Expect:70,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query   1187  NEVAKNLNESLIDLQELGKYEQYIKWPWY   1215
          N + K L+E L+ L +  K+  YI  PW+
Sbjct   89    NGIGKELHEQLVALDKQNKHTSYISGPWF   117
```

>ubiquinone biosynthesis monooxygenase COQ6, mitochondrial isoform f [Homo sapiens]
Sequence ID: NP_001412187.1 Length: 407
Range 1: 6 to 46

Score:31.5 bits(65), Expect:70,
Method:Compositional matrix adjust.,
Identities:13/41(32%), Positives:22/41(53%), Gaps:0/41(0%)

```
Query   792   PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAG   832
          PP+  FG +  S+   DPS+P ++ +           K+ L +AG
Sbjct   6     PPLSSFVWLASRAASDPSRPRRQGYDIHFHDKKILLLEAG   46
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080722.1 Length: 635
Range 1: 89 to 117

Score:31.9 bits(66), Expect:71,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query   1187  NEVAKNLNESLIDLQELGKYEQYIKWPWY   1215
          N + K L+E L+ L +  K+  YI  PW+
Sbjct   89    NGIGKELHEQLVALDKQNKHTSYISGPWF   117
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI2517173.1 Length: 635
Range 1: 89 to 117

Score:31.5 bits(65), Expect:73,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>t-SNARE domain-containing protein 1 isoform X4 [Homo sapiens]
Sequence ID: XP_054215932.1 Length: 931
Range 1: 212 to 310

Score:31.9 bits(66), Expect:73,
Method:Compositional matrix adjust.,
Identities:26/99(26%), Positives:48/99(48%), Gaps:4/99(4%)

```
Query 920 QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
975
          Q++ AN F NS++ ++ SL S T S +L+D ++ Q N + +S+ ++
Sbjct 212 QEMSANIFRINSSVTSLSRLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
271

Query 976 VLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIR 1014
          +L + + Q+DRL T ++Q Y Q +R
Sbjct 272 LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKVR 310
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080729.1 Length: 658
Range 1: 89 to 117

Score:31.5 bits(65), Expect:74,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>carnitine O-palmitoyltransferase 2, mitochondrial isoform 1 precursor [Homo sapiens]

Sequence ID: NP_000089.1 Length: 658
 >RecName: Full=Carnitine O-palmitoyltransferase 2, mitochondrial; AltName:
 Full=Carnitine palmitoyltransferase II; Short=CPT II; Flags: Precursor [Homo
 sapiens]
 Sequence ID: P23786.2 Length: 658
 >carnitine palmitoyltransferase [Homo sapiens]
 Sequence ID: AAB59462.1 Length: 658
 >carnitine palmitoyltransferase II precursor [Homo sapiens]
 Sequence ID: AAB60382.1 Length: 658
 >carnitine palmitoyltransferase II precursor [Homo sapiens]
 Sequence ID: AAB60383.1 Length: 658
 >testicular secretory protein Li 13 [Homo sapiens]
 Sequence ID: AEE61150.1 Length: 658
 >carnitine palmitoyltransferase II [Homo sapiens]
 Sequence ID: EAX06753.1 Length: 658
 Range 1: 89 to 117

Score:31.5 bits(65), Expect:75,
 Method:Compositional matrix adjust.,
 Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
 Sequence ID: KAI2517171.1 Length: 658
 Range 1: 89 to 117

Score:31.5 bits(65), Expect:76,
 Method:Compositional matrix adjust.,
 Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>immunoglobulin heavy chain junction region [Homo sapiens]
 Sequence ID: MQ20290.1 Length: 20
 Range 1: 5 to 17

Score:27.2 bits(55), Expect:77,
 Method:Composition-based stats.,
 Identities:9/13(69%), Positives:11/13(84%), Gaps:0/13(0%)

```
Query 254 SSSGWTAGAAAYY 266
          SSSGW AG+ AY+
Sbjct 5 SSSGWYAGSGAYF 17
```


>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080727.1 Length: 647
Range 1: 89 to 117

Score:31.5 bits(65), Expect:82,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB1991959.1 Length: 24
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB1994550.1 Length: 24
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB2016416.1 Length: 24
>immunoglobulin heavy chain junction region [Homo sapiens]
Sequence ID: MBB2019779.1 Length: 24
Range 1: 2 to 22

Score:27.2 bits(55), Expect:82,
Method:Composition-based stats.,
Identities:10/21(48%), Positives:14/21(66%), Gaps:0/21(0%)

```
Query 20 TRTQLPPAYTNSFTRGVYYPD 40
          T+ + PP Y+ S T+G YY D
Sbjct 2 TKGKEPPPYSGSGTKGAYYFD 22
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI2517170.1 Length: 670
Range 1: 89 to 117

Score:31.5 bits(65), Expect:82,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080725.1 Length: 670
Range 1: 89 to 117

Score:31.5 bits(65), Expect:82,

Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI2517172.1 Length: 647
Range 1: 89 to 117

Score:31.5 bits(65), Expect:82,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>ATP-dependent RNA helicase #46 [Homo sapiens]
Sequence ID: BAA23987.1 Length: 813
Range 1: 125 to 179

Score:31.5 bits(65), Expect:84,
Method:Compositional matrix adjust.,
Identities:15/55(27%), Positives:28/55(50%), Gaps:0/55(0%)

```
Query 217 PQGFSALEPLVDLPIGINITRFQTLALHRSYLTGDSGGWTAGAAAYVGYLQ 271
          P+ + L+ + LP+ RF +L H+S++ G++ SG T V Y++
Sbjct 125 PRYYDILKKRLQLPVWEYKDRFTDILGRHQSFVLVGETGSGKTTQIPHRCVEYMR 179
```

>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI2517175.1 Length: 598
>carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: KAI4080724.1 Length: 598
Range 1: 89 to 117

Score:31.5 bits(65), Expect:88,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query 1187 NEVAKNLNESLIDLQELGKYEQYIKWPWY 1215
          N + K L+E L+ L + K+ YI PW+
Sbjct 89 NGIGKELHEQLVALDKQNKHTSYISGPWF 117
```

>spindle and centriole-associated protein 1 [Homo sapiens]
Sequence ID: NP_001318007.1 Length: 855
>spindle and centriole-associated protein 1 [Homo sapiens]
Sequence ID: NP_001318008.2 Length: 855
>spindle and centriole-associated protein 1 [Homo sapiens]
Sequence ID: NP_001374868.1 Length: 855
>spindle and centriole-associated protein 1 [Homo sapiens]
Sequence ID: NP_653319.1 Length: 855
>RecName: Full=Spindle and centriole-associated protein 1; AltName:
Full=Coiled-coil domain-containing protein 52; AltName: Full=Spindle and
centriole-associated protein [Homo sapiens]
Sequence ID: Q8N0Z3.1 Length: 855
>hypothetical protein [Homo sapiens]
Sequence ID: AAM34495.1 Length: 855
>coiled-coil domain containing 52, isoform CRA_a [Homo sapiens]
Sequence ID: EAW79634.1 Length: 855
Range 1: 510 to 574

Score:31.5 bits(65), Expect:89,
Method:Compositional matrix adjust.,
Identities:21/65(32%), Positives:29/65(44%), Gaps:0/65(0%)

Query	522	ATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQT	581
		+ V P + NL KN + + T +SN KF P Q R T A R P T	
Sbjct	510	SQVPDPDPNMNLAKNFP AHIFEP AVLLTPPRQKSNLKF SPLQDVLRR TVQTRPAPRLPPT	569
Query	582	LEILD 586	
		+EI++	
Sbjct	570	VEIIE 574	

>unnamed protein product [Homo sapiens]
Sequence ID: BAG54389.1 Length: 695
Range 1: 406 to 470

Score:31.5 bits(65), Expect:90,
Method:Compositional matrix adjust.,
Identities:21/65(32%), Positives:29/65(44%), Gaps:0/65(0%)

Query	522	ATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQT	581
		+ V P + NL KN + + T +SN KF P Q R T A R P T	
Sbjct	406	SQVPDPDPNMNLAKNFP AHIFEP AVLLTPPRQKSNLKF SPLQDVLRGTVQTRPAPRLPPT	465
Query	582	LEILD 586	
		+EI++	
Sbjct	466	VEIIE 470	

>hypothetical protein, partial [Homo sapiens]
Sequence ID: CAH18698.1 Length: 2403
Range 1: 1010 to 1069

Score:31.5 bits(65), Expect:95,

Method:Compositional matrix adjust.,
Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1010  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPPAP
1069
```

>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219425.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219426.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219427.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219428.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219429.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219430.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219431.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_054219432.1 Length: 2506
Range 1: 1113 to 1172

Score:31.5 bits(65), Expect:99,
Method:Compositional matrix adjust.,
Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPPAP
1172
```

>unnamed protein product [Homo sapiens]
Sequence ID: BAG65508.1 Length: 223
Range 1: 102 to 151

Score:31.0 bits(64), Expect:99,
Method:Composition-based stats.,
Identities:15/50(30%), Positives:27/50(54%), Gaps:0/50(0%)

```
Query   992   QIDRLITGR LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD   1041
          +I+R +  R++ + + +QL+   E +  A LAA K E LG+ + D
Sbjct   102   EIEREVLQRVEEAKRIMEKQLLEELERQRQAELAAQKAREVTLGRLESRD   151
```

```

>zinc finger protein 462 isoform 1 [Homo sapiens]
Sequence ID: NP_067047.4 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_006717279.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279628.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279629.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279630.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279631.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279632.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279633.1 Length: 2506
>zinc finger protein 462 isoform X3 [Homo sapiens]
Sequence ID: XP_047279634.1 Length: 2506
>RecName: Full=Zinc finger protein 462; AltName: Full=Zinc finger PBX1-
interacting protein; Short=ZFPIP [Homo sapiens]
Sequence ID: Q96JM2.3 Length: 2506
>zinc finger protein 462 [Homo sapiens]
Sequence ID: KAI4007977.1 Length: 2506
Range 1: 1113 to 1172

```

```

Score:31.5 bits(65), Expect:100,
Method:Compositional matrix adjust.,
Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```

```

Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPGQSPRPAP
1172

```

```

>hypothetical protein [Homo sapiens]
Sequence ID: CAH56168.1 Length: 2506
Range 1: 1113 to 1172

```

```

Score:31.5 bits(65), Expect:100,
Method:Compositional matrix adjust.,
Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```

```

Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPGQSPRPAP
1172

```

```

>zinc finger protein 462 [Homo sapiens]

```

Sequence ID: KAI2553449.1 Length: 2506
Range 1: 1113 to 1172

Score:31.5 bits(65), Expect:100,
Method:Compositional matrix adjust.,
Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPRPPAP
1172
```

>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_054219420.1 Length: 2566
>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_054219421.1 Length: 2566
>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_054219422.1 Length: 2566
>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_054219423.1 Length: 2566
>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_054219424.1 Length: 2566
Range 1: 1113 to 1172

Score:31.5 bits(65), Expect:102,
Method:Compositional matrix adjust.,
Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPRPPAP
1172
```

>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_006717278.1 Length: 2566
>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_047279624.1 Length: 2566
>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_047279625.1 Length: 2566
>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_047279626.1 Length: 2566
>zinc finger protein 462 isoform X2 [Homo sapiens]
Sequence ID: XP_047279627.1 Length: 2566
Range 1: 1113 to 1172

Score:31.5 bits(65), Expect:102,
Method:Compositional matrix adjust.,
Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```

Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113   LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPPAP
1172

```

```

>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_006717272.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_006717274.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_006717275.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_016870485.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_016870486.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_024303397.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_047279617.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_047279618.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_047279619.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_047279620.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_047279621.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_047279622.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_047279623.1 Length: 2567
Range 1: 1113 to 1172

```

Score:31.5 bits(65), Expect:102,
Method:Compositional matrix adjust.,
Identities:18/60(30%), Positives:24/60(40%), Gaps:1/60(1%)

```

Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113   LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPPAP
1172

```

```

>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_054219409.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_054219410.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]
Sequence ID: XP_054219411.1 Length: 2567
>zinc finger protein 462 isoform X1 [Homo sapiens]

```

Sequence ID: XP_054219412.1 Length: 2567
 >zinc finger protein 462 isoform X1 [Homo sapiens]
 Sequence ID: XP_054219413.1 Length: 2567
 >zinc finger protein 462 isoform X1 [Homo sapiens]
 Sequence ID: XP_054219414.1 Length: 2567
 >zinc finger protein 462 isoform X1 [Homo sapiens]
 Sequence ID: XP_054219415.1 Length: 2567
 >zinc finger protein 462 isoform X1 [Homo sapiens]
 Sequence ID: XP_054219416.1 Length: 2567
 >zinc finger protein 462 isoform X1 [Homo sapiens]
 Sequence ID: XP_054219417.1 Length: 2567
 >zinc finger protein 462 isoform X1 [Homo sapiens]
 Sequence ID: XP_054219418.1 Length: 2567
 >zinc finger protein 462 isoform X1 [Homo sapiens]
 Sequence ID: XP_054219419.1 Length: 2567
 Range 1: 1113 to 1172

Score:31.5 bits(65), Expect:102,
 Method:Compositional matrix adjust.,
 Identities:18/60 (30%), Positives:24/60 (40%), Gaps:1/60 (1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP
812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   1113  LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPRPAP
1172
```

>zinc finger protein 462, isoform CRA_b [Homo sapiens]
 Sequence ID: EAW59011.1 Length: 1998
 Range 1: 545 to 604

Score:31.5 bits(65), Expect:102,
 Method:Compositional matrix adjust.,
 Identities:18/60 (30%), Positives:24/60 (40%), Gaps:1/60 (1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP   812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   545   LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPRPAP   604
```

>zinc finger protein 462, isoform CRA_a [Homo sapiens]
 Sequence ID: EAW59010.1 Length: 1999
 Range 1: 545 to 604

Score:31.0 bits(64), Expect:106,
 Method:Compositional matrix adjust.,
 Identities:18/60 (30%), Positives:24/60 (40%), Gaps:1/60 (1%)

```
Query   754   LQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD-FGGFNFSQILPDPSKP   812
          L Y   C+  NR++ G+ V   K   E+   K I + PP       G   Q   P P P
Sbjct   545   LYYCKHCSYSNRSVVGVLVHYQKRHPEIKVTAKYIRQAPPTAAMMRGVEGPQGSPRPAP   604
```


>unnamed protein product [Homo sapiens]
Sequence ID: BAG64595.1 Length: 198
Range 1: 77 to 126

Score:30.6 bits(63), Expect:112,
Method:Composition-based stats.,
Identities:15/50(30%), Positives:27/50(54%), Gaps:0/50(0%)

```
Query   992   QIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD   1041
          +I+R +  R++ +  + +QL+   E +  A LAA K  E  LG+ +  D
Sbjct   77    EIEREVLRRVEEAKRIMEKQLLEELERQRQAELAAQKAREVTLGRLESRD   126
```

>Chain A, Suppressor of T-cell receptor signaling 1 [Homo sapiens]
Sequence ID: 2E5K_A Length: 94
Range 1: 38 to 77

Score:29.7 bits(61), Expect:114,
Method:Compositional matrix adjust.,
Identities:12/40(30%), Positives:21/40(52%), Gaps:0/40(0%)

```
Query   87    NDGVYFASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNV   126
          D ++ +  E+++  GWI+GT+L +   LL  N  T
Sbjct   38    GDFIFMSPMEQTSTSEGWIYGTSLTTGCSGLLPENYITKA   77
```

>ARGLU1 protein [Homo sapiens]
Sequence ID: AAH71587.1 Length: 273
Range 1: 152 to 201

Score:30.6 bits(63), Expect:125,
Method:Composition-based stats.,
Identities:15/50(30%), Positives:27/50(54%), Gaps:0/50(0%)

```
Query   992   QIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD   1041
          +I+R +  R++ +  + +QL+   E +  A LAA K  E  LG+ +  D
Sbjct   152   EIEREVLRRVEEAKRIMEKQLLEELERQRQAELAAQKAREVTLGRLESRD   201
```

>t-SNARE domain-containing protein 1 isoform e [Homo sapiens]
Sequence ID: NP_001353831.1 Length: 470
Range 1: 262 to 371

Score:30.6 bits(63), Expect:134,
Method:Compositional matrix adjust.,
Identities:29/110(26%), Positives:52/110(47%), Gaps:4/110(3%)

Query 920 QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS 975
 Sbjct 262 Q++ AN F NS++ ++ SL S T S +L+D ++ Q N + +S+ ++
 321 QEMSANVFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE

Query 976 VLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLA 1025
 +L + + Q+DRL T ++Q Y Q A + RA +A
 Sbjct 322 LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKKIAEKSRLPMA 371

>Chain B, Charged multivesicular body protein 2a [Homo sapiens]
 Sequence ID: 7ZCG_B Length: 147
 >Chain B, Charged multivesicular body protein 2a [Homo sapiens]
 Sequence ID: 7ZCH_B Length: 147
 Range 1: 5 to 97

Score:30.2 bits(62), Expect:135,
 Method:Composition-based stats.,
 Identities:20/93(22%), Positives:47/93(50%), Gaps:2/93(2%)

Query 949 QDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDLKVEAEVQID--RLITGRLQSLQT 1006
 Sbjct 5 +++++ QN +ALN +++L + + I++ + K+ + Q+D R++ L +
 EELLRQNQRALNRAMRELDRELRQKLETQEKKIADIKKMAKQGQMDAVRIMAKDLVRTRR 64
 Query 1007 YVTQQLIRAAEIRASANLAATKMSECVLGQSKR 1039
 YV + ++ A I+A + T S + Q+ +
 Sbjct 65 YVRKFVLMRANIQAVSLKIQTLSNNSMAQAMK 97

>Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5VHF_D Length: 368
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5VHH_D Length: 368
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5VHI_D Length: 368
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5VHS_D Length: 368
 Range 1: 69 to 144

Score:30.6 bits(63), Expect:136,
 Method:Composition-based stats.,
 Identities:21/80(26%), Positives:35/80(43%), Gaps:4/80(5%)

Query 1105 TQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDV 1164
 T N+Y + T D + N V + +N + D L PE DS L + PDV
 Sbjct 69 TGSNYYVRILSTIDRELLKPNASVALHKHSNALVDVLPPEADSSIMML----TSDQKPDV 124

Query 1165 DLGDISGINASVVNIQKEID 1184
 DI G++ +++ ++

Sbjct 125 MYADIGGMDIQKQEVREAVE 144

>Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
Sequence ID: 5VFP_D Length: 380
>Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
Sequence ID: 5VFQ_D Length: 380
>Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
Sequence ID: 5VFR_D Length: 380
>Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
Sequence ID: 5VFT_D Length: 380
>Chain D, 26S protease regulatory subunit 6B [Homo sapiens]
Sequence ID: 5VFU_D Length: 380
>Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
Sequence ID: 6WJN_D Length: 380
Range 1: 69 to 144

Score:30.6 bits(63), Expect:137,
Method:Composition-based stats.,
Identities:21/80(26%), Positives:35/80(43%), Gaps:4/80(5%)

Query 1105 TQRNFYEPQIIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDV
1164

T N+Y + T D + N V + +N + D L PE DS L + PDV
Sbjct 69 TGSNYYVRILSTIDRELLKPNASVALHKHSNALVDVLPPEADSSIMML----TSDQKPDV
124

Query 1165 DLGDISGINASVVNIQKEID 1184
DI G++ +++ ++

Sbjct 125 MYADIGGMDIQKQEVREAVE 144

>26S proteasome regulatory subunit 6B isoform 2 [Homo sapiens]
Sequence ID: NP_694546.1 Length: 387
Range 1: 76 to 151

Score:30.6 bits(63), Expect:137,
Method:Composition-based stats.,
Identities:21/80(26%), Positives:35/80(43%), Gaps:4/80(5%)

Query 1105 TQRNFYEPQIIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDV
1164

T N+Y + T D + N V + +N + D L PE DS L + PDV
Sbjct 76 TGSNYYVRILSTIDRELLKPNASVALHKHSNALVDVLPPEADSSIMML----TSDQKPDV
131

Query 1165 DLGDISGINASVVNIQKEID 1184
DI G++ +++ ++

Sbjct 132 MYADIGGMDIQKQEVREAVE 151

>26S proteasome regulatory subunit 6B isoform 1 [Homo sapiens]
 Sequence ID: NP_006494.1 Length: 418
 >RecName: Full=26S proteasome regulatory subunit 6B; AltName: Full=26S
 proteasome AAA-ATPase subunit RPT3; AltName: Full=MB67-interacting protein;
 AltName: Full=MIP224; AltName: Full=Proteasome 26S subunit ATPase 4; AltName:
 Full=Tat-binding protein 7; Short=TBP-7 [Homo sapiens]
 Sequence ID: P43686.2 Length: 418
 >Chain K, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5GJQ_K Length: 418
 >Chain K, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5GJR_K Length: 418
 >Chain y, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5GJR_y Length: 418
 >Chain K, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5L4G_K Length: 418
 >Chain K, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5LN3_K Length: 418
 >Chain e, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5M32_e Length: 418
 >Chain AD, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5T0C_AD Length: 418
 >Chain BD, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5T0C_BD Length: 418
 >Chain D, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5T0G_D Length: 418
 >Chain D, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5T0H_D Length: 418
 >Chain D, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5T0I_D Length: 418
 >Chain D, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5T0J_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 5VFS_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 6MSB_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 6MSD_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 6MSE_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 6MSG_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 6MSH_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 6MSJ_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 6MSK_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 6WJD_D Length: 418
 >Chain D, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 7QXN_D Length: 418
 >Chain D, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 7QXP_D Length: 418
 >Chain D, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 7QXU_D Length: 418
 >Chain D, 26S protease regulatory subunit 6B [Homo sapiens]
 Sequence ID: 7QXW_D Length: 418

[illegible]

Sequence ID: 9BW4_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9E8G_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9E8H_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9E8I_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9E8J_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9E8K_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9E8L_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9E8N_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9E8O_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9E8Q_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9M2W_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9NKF_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9NKG_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9NKI_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9NKJ_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9UF8_D Length: 418
 >Chain D, 26S proteasome regulatory subunit 6B [Homo sapiens]
 Sequence ID: 9UG9_D Length: 418
 Range 1: 107 to 182

Score:30.6 bits(63), Expect:139,
 Method:Composition-based stats.,
 Identities:21/80 (26%), Positives:35/80 (43%), Gaps:4/80 (5%)

```

Query   1105  TQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDV
1164
          T  N+Y   + T D   + N  V +   +N + D L PE DS   L   +   PDV
Sbjct   107  TGSNYYVRILSTIDRELLKPNASVALHKHSNALVDVLPPEADSSIMML----TSDQKPDV
162

Query   1165  DLGDISGINASVVNIQKEID   1184
          DI G++      +++ ++
Sbjct   163  MYADIGGMDIQKQEVREAVE   182

```

>t-SNARE domain-containing protein 1 isoform X1 [Homo sapiens]
 Sequence ID: XP_047277413.1 Length: 883
 Range 1: 262 to 366

Score:30.6 bits(63), Expect:141,

Method:Compositional matrix adjust.,
Identities:28/105(27%), Positives:50/105(47%), Gaps:4/105(3%)

```
Query   920   QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS
975
          Q++ AN F  NS++  ++ SL S  T S   +L+D ++   Q  N  +   +S+  ++
Sbjct   262   QEMSANVFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE
321

Query   976   VLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRA   1020
          +L      +      +   Q+DRL T   ++Q Y   Q   A + RA
Sbjct   322   LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKKIAEKSRA   366
```

>cytoskeleton-associated protein 4, isoform CRA_b [Homo sapiens]
Sequence ID: EAW97771.1 Length: 334
Range 1: 197 to 252

Score:30.6 bits(63), Expect:141,
Method:Composition-based stats.,
Identities:16/56(29%), Positives:30/56(53%), Gaps:0/56(0%)

```
Query   935   QDSLSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAE   990
          QD L+ST  +LG+ Q V+  + + L   V +L S   ++ V   + + L + +A+
Sbjct   197   QDGLASTVRS LGETQLVLVYGDVEELKRSVGLPSTVESLQKVQEQVHTLLSQDQAA   252
```

>Carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: AAH02445.1 Length: 658
>Carnitine palmitoyltransferase 2 [Homo sapiens]
Sequence ID: AAH05172.1 Length: 658
Range 1: 89 to 117

Score:30.6 bits(63), Expect:141,
Method:Compositional matrix adjust.,
Identities:11/29(38%), Positives:17/29(58%), Gaps:0/29(0%)

```
Query   1187  NEVAKNLNESLIDLQELGKYEQYIKWPWY   1215
          N + K L+E L+ L +   K+  YI  PW+
Sbjct   89    NGIGKELHEQLVALDKQNKHTSYILGPWF   117
```

>t-SNARE domain-containing protein 1 isoform X6 [Homo sapiens]
Sequence ID: XP_047277417.1 Length: 912
Range 1: 290 to 394

Score:30.6 bits(63), Expect:141,
Method:Compositional matrix adjust.,
Identities:28/105(27%), Positives:50/105(47%), Gaps:4/105(3%)

Query	920	QKLIANQF--NSAIGKIQDSLSS--TASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS	
	975		
		Q++ AN F NS++ ++ SL S T S +L+D ++ Q N + +S+ ++	
Sbjct	290	QEMSANVFRINSSVTSLESLQSLGTPSDTQELRDSLHTAQQETNKTIAASASSVKQMAE	
	349		
Query	976	VLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRA	1020
		+L + + Q+DRL T ++Q Y Q A + RA	
Sbjct	350	LLRSSCPQERLQQERPQLDRLKTQLSDAIQCYGVVQKKIAEKSRA	394