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Supplementary Information for

<u>Cryo-EM structure of acylpeptide hydrolase reveals substrate selection by multimerization and a</u> <u>multi-state serine-protease triad.</u>

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Detailed Methods

Cryo-EM data processing

Movies were subjected to beam-induced motion correction using RELION-3.0 [1] and contrast transfer function parameters were estimated by CTFFIND4 [2]. All of the following processes were performed using RELION-3.0. Particles were auto-picked and two rounds of reference-free two-dimensional (2D) classification was performed. In total, 345,001 particles from 1157 micrographs were auto-picked and subjected to 3D initial model building and 3D classification. 3D refinement was performed applying C2 and D2 symmetry. 50,604 particles were used for final reconstruction. The 3D map and particle set yielded from the D2 symmetry refinement were subjected to per-particle defocus refinement, beam-tilt refinement, Bayesian polishing and 3D refinement. Final 3D refinement and postprocessing yielded a map with an overall resolution of 3.27 Å, estimated by the gold-standard FSC = 0.143 criterion.

Reprocessing out data with cryoSPARC [3] yielded a map with no symmetry applied (C1) with overall resolution of 4.12 Å. 3D variability analysis [4] of this map was carried out to obtain a more thorough picture of the fluctuation of the flexible segments of our final model.



Figure S1. Overview of single-particle cryo-EM for AAP. A) Example cryo-EM micrograph for AAP with example particles circled in red. B) Reference-free 2D class averages of different particle orientations. C) C1 reconstruction of cryoEM map: 3D reconstruction of AAP specimen with no symmetry applied (resolution: 4.12Å). D) Local resolution of the D2 symmetry-averaged map (of overall 3.27Å resolution) contoured at a 0.010 threshold level (figure was made using UCSF Chimera [5]) calculated using ResMap [6]. The highest resolution region is observed in the hydrolase core. This map was used for structure determination. E) Map to map and F) model to map FSC curves calculated, the resolution of the map corresponding to FSC=0.143 is indicated.

Model building and refinement

The processed map was inverted by EMAN2 [7]. Automatic model building was carried out by ARP/wARP [8] and REFMAC5 [9] and manual finishing the monomer model in Coot [10] using the sequence and D2 point group symmetry of the tetramer was used. The tetramer was created by using Phenix Dock in Map [11], manually finished in Coot [10] and refined with real space refinement in Phenix [12].

Structure characterization

Analysis of interaction surfaces wax carried out with the PISA server [13]. Amyloidogenic properties were characterized using predictor servers: Aggrescan3D [14], Waltz [15], MetAmyl [16], RFAmyloids [17], BAP [18] and Zipper DB [19]. Sequence alignments were carried out in Uniprot [20].

Molecular dynamic simulations

Starting model for the molecular dynamics (MD) simulation was built from the cryo-EM determined structure. Missing residues were built manually and the longest of these new loops (residues 183-198) was subjected to 500 step MCMM-LMOD conformational search [21] as implemented in the Schrödinger Modeling Suite [22], keeping the rest of the model frozen. MD simulation was started from low energy conformers (for the entire tetrameric system, including the missing loop in identical conformation to all four chains) derived from the search, selecting the one that resulted in a structure most similar to the experimental result. The simulation was carried out suing GROMACS [23], applying the AMBER-ff99SBildnp* forcefield [24] with the OPC water model [25]. The total charge of the system was neutralized and physiological salt concentration was set using Na⁺ and Cl⁻ ions. Energy minimization of the starting structures was followed by relaxation of constraints on protein atoms in three steps, with an additional NVT step (all of 200 ps) to stabilize pressure. Trajectories of 500 ns NPT simulations at 310 K and 1 bar were recorded for analysis (collecting snapshots at every 4 ps). Snapshots from the last 300 ns of the most optimal simulation were clustered based on the conformation of the backbone of the protein components using a 1 Å cutoff both for the tetrameric system and the monomers alone (using all four chains of every snapshot independently). For analyzing proteinprotein contacts within the tetramer with PISA [9] a hybrid model was used: the cryo-EM structure attenuated with the missing residues in their most frequently sampled conformations (carrying out separate clustering for the missing residues of the 1st helix (residues 1-18), the inner gate (105-123) and the outer gating region (residues 171-201)). For determining the heterogeneity of the active site, clustering was carried out based on the conformation of residues 582-294, 673-677, 705-709. Figures showing conformational ensembles were composed using the mid-structures of the most populated clusters that account for over 95% of the snapshots. Principle component analysis was carried out based on main chain conformations along the full sequence using GROMACS. Hydrogen bonds were considered to be present when donor-acceptor distance did not exceed 3.2 Å.

Table S1. Sequence identity and similarity (in parentheses) among S9 family members as compared to human AAP. AAPs with available crystal structures were included and selected representatives of the S9 protease family. Comparison was calculated along the full sequence of human AAP (residues 1-732), the propeller domain (residues 22-461) and the hydrolase domain (residues 462-732, excluding the highly varying *N*-terminal segment (residues1-21)).

Protein name	full sequence	propeller	hydrolase
Sus scrofa (liver) AAP (pAAP)	92% (98%)	87% (92%)	91% (94%)
Pyrococcus horikoshii AAP (PhAAP)	15% (31%)	14% (28%)	21% (40%)
Aeropyrum pernix AAP (ApAAP)	18% (33%)	13% (27%)	26% (43%)
Sporosarcina psychrophila AAP (SpAAP)	13% (30%)	10% (24%)	20% (40%)
Streptomyces morookaense AAP (SmAAP)	16% (26%)	13% (21%)	23% (34%)
Deinococcus radiodurans R1 S9-carboxypeptidase (DrCP)	20% (33%)	16% (26%)	26% (45%)
human POP	12% (29%)	11% (27%)	18% (35%)
human DPP4	11% (27%)	10% (24%)	14% (34%)
Leishmania major OPB	13% (30%)	13% (28%)	14% (31%)

Table S2. Length and location of the blades of the propeller domains of the S9 serine proteases.

Protein		Propeller domain	Blade1	Blade2	Blade3	Blade4	Blade5	Blade6	Blade7	Blade8
AAP	Residue numbers	23-457	23-88	89-134	135-238	239-298	299-345	346-405	406-457	-
<i>(porcine)</i> PDB id: 7px8	No. of amino acids	435	66	46	104	60	47	60	52	-
POP	Residue numbers	72-426	72-114	115-168	169-227	228-284	285-330	331-377	378-426	-
<i>(human)</i> PDB id: 3ddu	No. of amino acids	355	43	54	59	57	46	47	49	-
ОРВ	Residue numbers	95-448	95-152	153-201	202-250	251-299	300-347	348-399	400-448	-
<i>(L. major)</i> PBD id: 2xe4	No. of amino acids	354	58	49	49	49	48	52	49	-
DPP4	Residue numbers	56-496	56-90	91-150	151-191	192-287	288-350	351-401	402-453	454-496
<i>(human)</i> PDB id: 1j2e	No. of amino acids	441	35	60	41	96	63	51	52	43
РТР	Residue numbers	50-471	50-107	108-145	146-192	193-282	283-331	332-379	380-427	428-471
(P. gingivalis) PDB id: 2eep	No. of amino acids	422	58	38	47	90	49	48	48	44
AAP	Residue numbers	23-320	23-62	63-109	110-149	150-191	192-232	233-281	282-320	-
<i>(A. pernix)</i> PDB id: 304g	No. of amino acids	298	40	47	40	42	41	49	39	-
AAP	Residue numbers	15-338	15-59	60-103	104-171	172-216	217-258	259-299	300-338	-
(P. horikoshii) PDB id: 4hxe	No. of amino acids	324	45	44	68	45	42	41	39	-
AAP	Residue numbers	16-331	16-59	60-106	107-152	153-199	200-244	245-287	288-331	-
(S. psychrophyla) PDB id: 5l8s	No. of amino acids	316	44	47	46	47	45	43	44	-
IsoP	Residue numbers	42-413	42-89	90-131	132-224	225-277	278-320	321-367	368-413	
(S. alaskensis) PDB id: 5jrk	No. of amino acids	372	48	42	93	53	43	47	46	-
AAP	Residue numbers	25-380	25-66	67-120	121-185	186-239	240-283	284-333	334-380	
(S. morookaensis) PDB id: 3azo	No. of amino acids	356	42	54	65	54	44	50	47	-
DrCP	Residue numbers	17-389	17-75	76-122	123-195	196-249	250-292	293-351	352-389	
<i>(D. radiodurans)</i> PDB id: 5yzn	No. of amino acids	373	59	47	73	54	43	59	38	-

Table S3. Residues participating in the formation of the substrate specificity pocket S1 of pAAP in comparison with other S9 oligopeptidases. (Based on the presently determined structure and PDB entries: 4hxe, 1ve6, 5yzn, 5l8s, 3azo, 5yzn, 3ddu, 1j2e, 2xe4).

hAAP*	Pro510	His588	Val613	Trp628	Glu632	Val678
pAAP (PDB id: 7px8)	cisPro510	His588	Val613	Trp628	Glu632	Val678
PhAAP (PDB id: 4hxe)	<i>cis</i> Pro388	Tyr467	lle491	Phe507	Val511	Cys549
ApAAP (PDB id: 1ve6)	cisPro370	Tyr446	Val471	Phe488	Leu492	Thr527
SpAAP (PDB id: 518s)	cisPro381	Tyr459	Pro484	Trp505	-	Val543
SmAAP (PDB id: 3azo)	cisPro434	Ala512	Val536	Tyr554	Leu588	Cys596
DrCP (PDB id: 5yzn)	cisPro436	Tyr515	lle539	Phe555	Glu559	Cys600
hPOP PDB id: 3ddu)	Phe476	Asn555	Val580	Trp595	Tyr599	Val644
hDPP4 (PDB id: 1j2e)	Pro550	Tyr631	Val656	Tyr666	Tyr670	Val711
LmOPB (PDB id: 2xe4)	Ser498	Ala578	Phe603	Glu621	Glu624	Val665

* estimated based on sequence alignment

Table S4. Predicted amyloidogenicity of the outermost β -strand of the central β -sheet of the hydrolase domain in proteins of the S9 serine protease family: amyloid propensity was evaluated from high to low probability and was visualized by coloring from red through yellow to green.

Enzyme name	PDB id	residue number *	sequence	Aggrescan3D ** (aa)	WALTZ ** (75<	MetAmyl ** (6aa)	RFAmyloid ** (Y/N)	BAP ** (6aa)	ZipperDB ** (6aa)	oligomeric state*	PISA CSS ***
pAAP (Sus scrofa)	7px8	695-704	VPVRLLLYPK	* + + +	score)	•	ł		÷	tetramer (edge-shielding)	1.000
POP (human)	3ddu	668-678	NPLLIHVDTK	<mark>++++</mark>	÷	++++	±	++++ <mark>-</mark>	+ <mark>+</mark>	monomer (intramolecular edge-shielding)	0.000
OPB (<i>L. major</i>)	2xe4	685-695	NEILLNIDMES	<mark>++++</mark>	+++	++ <mark>+</mark> +-	±	+++ <mark></mark>	+ <mark>-</mark> ++	monomer (intramolecular edge-shielding)	0.000
OPB (T. brucei)	4bp8	671-681	NEVLLKMDLES	<mark></mark>	++	1	H		-	monomer (intramolecular edge-shielding)/ dimer (non edge- shielding)	0.000
DPP4 (human)	1j2e	729-738	DFQAMWYTDE	<mark>++</mark> +	+++	+	+		+++	dimer (edge-shielding)	1.000
РТР	2eep	698-708	YPDYYVYPSH	<mark>++++</mark> +	++	+	+			dimer (edge-shielding)	0.561
AAP (A. pernix)	304g	545-553	TFEAHIIPD	++++	++	+	+		+	dimer (edge-shielding)	0.925
AAP (P.horikoshii)	4hxe	566-575	KEVYIAIFKK	+ <mark>++++</mark> +	+++	+++	+	+ <mark>-</mark> +++	++++ +	hexamer (edge-shielding)	0.892
AAP (S.psychrophyla)	518s	560-569	RDVEYLVLED	•	Ŧ	Ŧ	-	<mark><mark>++</mark>-</mark>	++++	dimer (non edge-shielding) /tetramer(could be edge- shielding- model)?	0.528
lsoP (S. alaskensis)	5jrk	673-682	VATQISYYPG	<mark>++++</mark> ╉╋╋	+++	+++	+		+++	dimer (edge-shielding)	1.000
PMH/AAP (S.morookaensis)	3azo	613-622	VPHAYLSFEG	++ <mark>++</mark>	++		Ŧ		+ +	monomer (intramolecular edge-shielding)	0.011
DrCP (D.radiodurans)	5yzn	618-625	VPVRFVRFPE	<mark>++</mark>	+	not available⁺	not available⁺	*- *	-	tetramer (edge-shielding)	1.000

* based on PDB structure

** Aggrescan3D [14] predicts from whole protein sequence for individual residues (A3D score,color coded in the sequence in column 4, column 5. for residues with A3D score = 0 and for residues with A3D score <0.</p>

**Waltz [15] predicts scores for aggregation propensities, number being higher than 75 indicates that submitted sequence is prone to amyloidtype aggregation. number being 75-80: 4, 80-90: ++, 90<+++ and - for number being <75.</p>

**MetAmyl [16] predicts amyloid hotspots from whole protein sequence. The score for the meta-prediction, p(x), is obtained using a logistic regression model, so that it can be interpreted as the probability for a fragment to form amyloid fiber. The score p(x) have been calculated for all possible hexapeptides. MetAmyl uses a sliding window to screen the whole submitted sequence. 0.6
If or each hexapeptide in the selected sequence (column4).

**RFAmyloid Server [17] predicts yes: //no: for submitted entries.

**The Budapest Amyloid Predictor (BAP) Server [18] predicts amyloidogenicity for hexapeptides yes: -/no: - (for every hexapeptide in sliding sequence).

**ZipperDB [19] predicts fibrinogen propensity for hexapeptides from a protein sequence. $\frac{1}{2}$ for high fibrillation propensity > -23kcal/mol, $\frac{1}{2}$ from -23kcal/mol – (-6 kcal/mol) and $\frac{1}{2}$ for no fibrillation propensity profile predicted for hexapeptides contained in the sequence (column 4).

***PISA [13] calculates interactions of molecular surfaces between submitted structures. The Complex Formation Significance Score for the interaction (CSS ranges from 0 to 1 as interface relevance to complex formation increases. Low CSS implies that the interface is not significant for complex formation and may be solely a result of crystal packing.

+ Servers not available in December 2021.

Table S5. Cryo-EM data collection, refinement and validation statistics

Data collection	
Magnification	X80,000
Voltage (kV)	300
Electron exposure (e/Å ²)	40
Defocus range (µm)	1-3
Pixel size (Å)	0.95
Data processing	EMD-13691, PDB 7px8
Symmetry imposed	D2
Initial particle images (no.)	345,001
Final particle images (no.)	50,604
Map resolution (Å)	3.27
FSC threshold	0.143
Refinement	
Model resolution (Å)	3.27
Model composition	•
Non-hydrogen atoms	21,409
Protein residues	2798
B-factors (min/max/mean)	
Protein	24.27/122.04/46.20
r.m.s. deviations	
Bond length (Å)	0.002
Bond angles (°)	0.529
Validation	
MolProbility score	1.18
Clashscore	3.45
Rotamer outliers (%)	0
CaBLAM outliers (%)	1.87
Ramachandran plot (%)	•
Outliers	0
Allowed	69 (2%)
Favored	2731 (98%)



Figure S2. Topology of blades and inserts of the propeller domains of the S9 serine proteases compared to the presently determined structure. Numbers indicate the length of the segments creating turns, loops and β -sheets. Distorted or partially unstructured β -strands are labeled with an asterisk (*). Insertions are colored orange. Insertions of pAAP referred to as insert1 and insert2 are the 12 residues long insert is in blade 1; and the 54 residues long insert is in blade 3, respectively.



Figure S3. Comparing the structures of S9 oligopeptidases with that of pAAP. Structural alignment of members of the S9 family reveals that insertions to the pAAP sequence create significant protrusions from the surface allowing them to form extra contact surfaces. Monomeric units of pAAP (shown in green: hydrolase lighter, propeller darker), *Pyrococcus horikoshii* AAP (PDB id: 4hxe), *Aeropyrum pernix* AAP (PDB id: 3o4g), *Sporosarcina psychrophila* AAP (PDB id: 5l8s), *Streptomyces morookaensis* AAP (PDB id: 3azo), *Deinococcus radiodurans R1* S9-peptidase (PDB id: 5yzn), human POP (PDB id: 3ddu), human DPP4 (PDB id: 1j2e) and *Leishmania major* OPB (PDB id: 2xe4) are overlaid, fitting their hydrolase domains. For representing pAAP the cryo-EM structure was used, completing missing segments (residues 1-9, 39, 110-115, 183-198, 496-497) (shown in red) based on the results of the MD simulations. The N-terminal segment – a highly variable region that belongs to the hydrolase but sequentially precedes the propeller domain is not shown for any of the structures, for clarity.



Figure S4. Destabilization of the catalytic Ser587. (*A*) Sequence alignment of the 4th strand of the hydrolase domain core β-sheet and the following loop (forming the oxyanion site) among the S9 protease family members (those with known structures) reveals that Pro506 of pAAP is rather unusual in this position (with the only one other such protein: *Sp*AAP). (*B*) Presence of Pro506 considerably shortens the 4th strand of the core of pAAP and also the adjacent 5th strand that leads up to the catalytic Ser587 (green: pAAP, grey: all other AAPs: *Ap*AAP, *Ph*AAP, *Sm*AAP, *Sp*AAP; PDB id: 304g, 4hxe, 3azo and 5l8s, respectively). (*C*) Comparison of pAAP (green) and *Sp*AAP (pink) shows that the closed and more compact fold of the *Sp*AAP monomer provides stabilization to the catalytic Ser, while in pAAP the loss of backbone H-bonds between the 4th and 5th strands allow destabilization of the loop holding the catalytic Ser because of the considerably more open structure, with reduced number of stabilizing propeller-hydrolase interactions.



Figures S5. Model building for the disordered Ser587-loop. A) 3D variability analysis (carried out using cryoSPARC [4] shows fluctuation of the C1 symmetry map near the active site (green and magenta backbone traces show the final models (active and latent state, respectively), the map is shown at a threshold of 0.015 (image created with Chimera)). B) Final model built in the D2 symmetry map with two conformers of the 584-591 segment is shown in the same orientation and coloring as of panel A. C -E) The "active" conformation (Conf.1) and the "latent" conformation (Conf.2.) of the Ser-loop in different orientations in the D2 symmetry map (contoured at treshold of 0.016. F) Local resolution (contoured at a 0.010 threshold level in Chimera, calculated by ResMap [6]) of the hydrolase domain core. Chain A was used to represent the averaged structures because of the D2 symmetry. (Panels C-E were created with PyMol [Schrödinger, L., & DeLano, W. (2020). *PyMOL*. Retrieved from http://www.pymol.org/pymol])



Figure S6. Substrate binding subsites of AAPs tailoring specificity. (*A*) Molecular surfaces of the S1 substrate specificity pocket of pAAP (left, green) is narrowed by Trp628 as compared to *Ap*AAP (right, grey; PDB id: 2hu7). Note: In oligopeptidase structures, beside pAAP (and the human variant) only POP and *Sp*AAP carry a Trp in this position. However, in POP, this Trp residue is in a different conformation forming a stacking interaction with P1 Pro residue by which it becomes the major determinant of specificity; in *Sp*AAP it is considerably shifted, widening the S1 pocket. (*B*) S2 and S3 subsites of pAAP (left, green) and *Ap*AAP (right, grey) are shown. The S3 subsite of pAAP is restricted by Phe274-Cys275 barrier, while this region of archaeal AAPs is open. Bound peptides overlaid are shown for different oligopeptidases: for *Ap*AAP in magenta (PDB id: 2hu7, 2hu8); backbone of the peptide fragment in cyan for OPB and POP (PDB ids: 4bp9; 5n4c, respectively).



Figure S7. Reported natural mutations of human AAP. (*A*) The location of the mutations is shown on the monomer: mutations not altering function in green, mutations leading to loss of enzyme activity in red. (*B*) The latter are shown on the tetramer (red), together with the position of the predicted phosphorylation site Ser187 (black). Trp336* terminates the sequence in the middle of blade 5 so the loss of enzyme activity is due to the absence of the entire hydrolase domain. Thr541Met mutation could result in catalytic Ser-loop disorder (Fig. S6). Pro470Leu and Ser451Phe mutations are on the outer surface of the tetramer not blocking the entrance or causing any disorder near the catalytic triad - although they could play an essential role in effecting interactions with other proteins or could lead to aggregation or misfolding and thus cause disfunction of the enzyme.



Figure S8. Possible structural effects of the Thr541Met mutation. (*A*) Hydrogen bonding network including Thr541 (green) and the catalytic triad (orange) is shown. There is a more hydrophilic and quite loose loop (residues 507-513) between the mutation site of Thr541 and the loop holding the catalytic Ser587. Methionine sulfur is known to form S...O interaction where the divalent sulfur serves as an electrophile, while it is also known to form H-bonds, especially with heterocyclic N-H moieties like the His sidechain [26]. (*B*) Possible changes caused by Thr541Met mutation (dark grey). The Met541...His511 side chain interaction could modify the 507-513 loop conformation. This may cause effectivity loss through repositioning the Gly509 residue (oxyanion binding site labeled with an asterisk), which will thus not be able to take part in stabilizing the transition state of the catalytic reaction.



Figure S9. The comparison of the cryo-EM structure of pAAP and the model generated by AlphaFold [27]. The domain opening was slightly underestimated, the *cis* conformation of Pro510 was not predicted, neither was the liberation of the Ser-loop - or the mode of tetramerization. (Cryo-EM structure: rainbow colors; the structure found in AlphaFold database: light blue).



Figure S10. The propeller channel of the mammalian AAP may serve as a pathway towards the catalytic cavity. Ligand binding sites along the channel calculated by the FTMap server [28] (yellow and orange) and within the substrate specificity pockets (S1 blue, S2 cyan) are shown ((*A*) side view and (*B*) top view).



Figure S11. MD-derived B-factors of pAAP. (*A*) B factors were calculated based on the average deviation of main-chain atoms (averaged over all chains of the tetramer, for the last 300ns of the molecular dynamics simulation). Red rectangles show the regions that could not be resolved in the cryo-EM map. Green rectangles show the three unique inserts characteristic to mammalian AAPs. (*B*) Conformational changes associated with the first component of the PCA or the MD trajectory (carried out for all monomers of the tetrameric assembly). The figure shows transition between the two endpoints of the fluctuations (green corresponding to the closed structure, blue to the open form), with the most significant variations in the insert 2 (residues 180-200) and the 110-118 regions. (*C*, *D*) Cluster mid-structures are shown for the monomeric unit (side and top view, respectively; hydrolase domain: light green, propeller domain: dark green, catalytic triad: orange). Two segments were found especially highly mobile during MD simulations (and also missing in the cryo-EM map): insert2 (red) and residues 110-117 (blue), respectively.



Figure S12. Structural elements shielding the sticky edge of the central β -sheet of the hydrolase domain in multimeric oligopeptidases. (*A*) In the dimeric structure of *Ap*AAP (PDB id: 3o4g) the two monomers (hydrolase domain in skyblue, propeller domain in green) create a 16-stranded large β -sheet (red). (*B*) In the *Ph*AAP (PDB id: 4hxg) hexamer and (*C*) in the *Dr*CP tetramer (PDB id: 5yzn) the β -edge is covered by a loop extension of the propeller of a neighboring monomer.

SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	MERQVLLSEPEEAAALYRGLSRQPALSAACLGPEVTTQYGGRYRTVHTEWTQRDLERMEN 6 MERQVLLSEPEEAAALYRGLSRQPALSAACLGPEVTTQYGGQYRTVHTEWTQRDLERMEN 6 ************************************	50 50
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	IRFCRQYLVFHDGDSVVFAGPAGNSVETRGELLSRESPSGTMKAVLRKAGGTGTAEEKQF 1 IRFCRQYLVFHDGDSVVFAGPAGNSVETRGELLSRESPSGTMKAVLRKAGGTGPGEEKQF 1	120 120
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	LEVWEKNRKLKSFNLSALEKHGPVYEDDCFGCLSWSHSETHLLY ADKKRPKAESFFQTK 1 LEVWEKNRKLKSFNLSALEKHGPVYEDDCFGCLSWSHSETHLLY AEKKRPKAESFFQTK 1	180 180
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	ALDVTGSDDEMARTKKPDQAIKGDQFLFYEDWGENMVSKS ALDVSASDDEIARLKKPDQAIKGDQFVFYEDWGENMVSKS ****: ****:** ************************	240 240
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	PESVSPGQAFWAPGDTGVVFVGWWHEPFRLGIRFCTNRRSALYYVDLTGGKCELLSDESV 3 PENVSPGQAFWAPGDAGVVFVGWWHEPFRLGIRFCTNRRSALYYVDLIGGKCELLSDDSL 3 **.**********************************	300 300
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	AVTSPRLSPDQCRIVYLRFPSLVPHQQCGQLCLYDWYTRVTSVVVDIVPRQLGEDFSGIY AVSSPRLSPDQCRIVYLQYPSLIPHHQCSQLCLYDWYTKVTSVVVDVVPRQLGENFSGIY **:**********************************	360 360
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	CSLLPLGCWSADSQRVVFDSPQRSRQDLFAVDTQMGSVTSLTAGGSGGSWKLLTIDRDLM 4 CSLLPLGCWSADSQRVVFDSAQRSRQDLFAVDTQVGTVTSLTAGGSGGSWKLLTIDQDLM 4	420 420
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	VVQFSTPSVPPSLKVGFLPPAGKEQAVSWVSLEEAEPFPDISWSIRVLQPPPQQEHVQYA 4 VAQFSTPSLPPTLKVGFLPSAGKEQSVLWVSLEEAEPIPDIHWGIRVLQPPPQENVQYA 4 *.******:**:**************************	180 180
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	GLDFEAILLQPSNSPEKTQVPMVVMPHGGPHSSFVTAWMLFPAMLCKMGFAVLLVNYRGS 5 GLDFEAILLQPGSPPDKTQVPMVVMPHGGPHSSFVTAWMLFPAMLCKMGFAVLLVNYRGS 5	540 540
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	TGFGQDSILSLPGNVGHQDVKDVQFAVEQVLQEEHFDAGRVALMGGSHGGFLSCHLIGQY 6 TGFGQDSILSLPGNVGHQDVKDVQFAVEQVLQEEHFDASHVALMGGSHGGFISCHLIGQY 6	500 500
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	PETYSACVVRNPVINIASMMGSTDIPDWCMVEAGFSYSSDCLPDLSVWAAMLDKSPIKYA 6 PETYRACVARNPVINIASMLGSTDIPDWCVVEAGFPFSSDCLPDLSVWAEMLDKSPIRYI 6 **** ***.****************************	560 560
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	PQVKTPLLLMLGQEDRRVPFKQGMEYYRVLKARNVPVRLLLYPKSTHALSEVEVESDSFM 7 PQVKTPLLLMLGQEDRRVPFKQGMEYYRALKTRNVPVRLLLYPKSTHALSEVEVESDSFM 7	720 720
SP P19205 ACPH_PIG SP P13798 ACPH_HUMAN	NAVLWLCTHLGS 732 NAVLWLRTHLGS 732	
91. 673 45 14	.9% sequence identity- Propeller domain3 identical positions- Hydrolase domainsimilar positions- Blade3 insertiondifferent positions* Catalytic triad	

Figure S13. Sequence alignment of porcine ((Uniprot [20] code P19205) and human AAP (P13798) with the positions of the domain border, as well as large insertion of propeller blade3 and the catalytic triad indicated.

Species ider	tity %	1	[0
Sus scrofa	100%		MERQ VILLSEP EEAAALYRGLSROPALSAACLGP EVIT OVGGOVET UTENTORD	
Macaca mulatta	91.9%			
Bos taurus	92.2%		<mark>MERQVLLSE</mark> PEEAAALYRGLSRQPALSAACLGPEVTTQYGGRYRTVHTEWTQRDL	
Rattus norvegicus	90.8%		MERQVLLSEP <mark>Q</mark> EAAALYRGLSRQP <mark>SLSAACLGPEVTTQYGGLYRTVHTEWTQRD</mark> L	
Mus musculus	90.7%		MEROVIL SEPOEAAALYRGLSROPSLSAACLGPEV HOYGGLYR VHTEMTORDL	
Canis Jupus familiaris	92.68		MEROVRARPAVPVAPAARAGPDPGVSPA VLLNEP EEAAALYRGLSROPALSAACLGPDV TTOYGGRYRTVITEWTORD	
10110 00000				
	1009	81	. 1	60
Homo sapiens	91.9%		EK YEN IRFORQYLVFHDODSVVFAGPAGNSVETROELLSRESPSGTMKAVLRKAGGTGTAEEKQFLEVWEKNKKLKSFNL	
Macaca mulatta	91.9%		ERMENTRECROYLVEHDCDSVVEAGPAGISVETRCELLSRESPSGSKAVLRKAGGTGPGEEKOELEVWEKNRKLKSEN	
Bos taurus	92.28		ER VENLIRF <mark>CR</mark> QYLVFHDCDSVVFAGPAGNSVETRCELLSRESPSGTMKAVLRKAGS <mark>TF-G</mark> EEKQFLEVWEKNRKLKSFN-	
Rattus norvegicus	90.8%		ERMENTRF <mark>CR</mark> QYLVFHDGDSVVFAGPAGNSVETRGELLSRESPSGTMKAVLRKAGGTVSG <mark>EEKQFLEVWEKNRKLKSFN</mark> L	
Mus musculus	90.7%		DR MENT RF <mark>C</mark> RQYLVFHDCDSVVFAGPAGNSVETRCELLSRESPSCTMKAVLRKAGGAVSGEEKQFLEVWEKNRKLKSFNL	
Canis lupus familiaris	92.68		EK MENLIKFORQYLVFHD ODSVVFSGPAG NSVETIK CELLSRUSPSGAM KAVLKKAGG ISPGEEK QFLEV MEKNIKKLKSFNL	
FEIIS Catus	52.20			
Sug garafa	100%	161		40
Homo sapiens	91 9%		SALEKH GPVYEDD CFGCL SWSHSETH LLYVADKKR FKAESFFOTKALDVTGSDDEMARTKKPDOATKGDOFL FYEDWGEN	
Macaca mulatta	91.9%		SVLEKI GPVYEDDCEGCLSWSISETH LLYVAERKRPKAESEFOTKALDVSASDDETARLKKPDOPTKGDOFVEDWGEN	
Bos taurus	92.28		SALEKH GPVYEDD <mark>CFGCL SWSHSETH LLYVAEKKR PKAESFFOTKALDISC SDDE MARPKK PDOAIK GDOFL FYEDWG EN</mark>	
Rattus norvegicus	90.8%		SALEKHGPVYEDD <mark>CFGCLSWSHSETHLLYVA</mark> EKKRPKAESFFQTKALDISASDDEMA <mark>RPKKPDQAIKGDQFVFYEDWG</mark> ET	
Mus musculus	90.7%		SALEKH GPVYEDD <mark>CFGCL SWSHSETH LLYVAEKKRPKAESFFQTKALDVSASDEEMARPKKPDQA I KGDQFVFYEDWGE</mark> T	
Canis lupus familiaris	92.68		SLIEKH GLYYEDD CFGCLSWSHSETH LLYVAEKKRYKTESFFOTKALD VSSSDEEMARPKKPD0ATKGD0FVFYEDWGEN	
Terrs Catas	52.20			
		241	:	20
Sus scrofa	100%		MVSKSTPVL <mark>CVLDI</mark> ESGNISVLEGVPESVSPGQAFWAPGDIGVVFVGWHEPF <mark>R</mark> LGI <mark>RF</mark> CINRRSALYYVDLIGG <mark>KC</mark> ELL	
Homo sapiens	91.9%		MVSKSTPVLCVLDVESGNLSVLEGVPENVSPGQAFWAPGDAGVVFVGWMHEPFRLGTRF <mark>CTNRR</mark> SALYYVDLTGG <mark>KC</mark> ELL	
Macaca mulatta	91.9%		MVSKSIPVLCVLDVESGNISVLEGVPENVSPGQAFWAPGDAGVVFVGWWHEPFRLGIRFCTNRRSALYYVDLIGGKCELL	
Rattus norvegicus	90.8%		MVSKOSVULVU DTES OT SVULOVPES SPOOA WAPOD OV POWINE PREGINCTINGSALTI VULI ODNOLULI MVSKSTPVI CVI DTDS OT SVILEGVPENVSPGOAEWAPGDTGVVEVGWHEPERI GTRVCTNRRSALTI VULI SGGKCELL	
Mus musculus	90.7%		MVSKSIPVLCVLDIESGNISVLEGVPENVSPGQAFWAPGDTGVVFVGWHEPFRLGIRYCTNRRSALYYVDLSGGKCELL	
Canis lupus familiaris	92.6%		MVSKSTPVLCVLDVESGNTSVLEGVPESVSPGQAFWAPGDTGVVFVGWMHEPFRLGT <mark>RFCTNRR</mark> SALYVVDLTGGQCELL	
Felis catus	92.2%		MV <mark>skst</mark> pvl <mark>ovldvesgnisvlegvpesvs</mark> pgqafwapgdtgvvfvgwwhepf <mark>r</mark> lgi <mark>rfctnrr</mark> salyyvdltggq <mark>c</mark> ell	
		221		00
Sus scrofa	100%	321	SDESVAVTSPILSDDOOTVYLDEDSLVDHOOCOLOLVDWYTRVTSVAVDTVDROLGEDESGTVCSLLDLGOVSADSOD	66
Homo sapiens	91.9%		SDDSLAVSS PRUS PDOCRTVYLOYPS TPHFOCSOLCLYDWYTKYTS VVVDVVPROLCENFS GIYCS LLPLGCWS ADSOR	
Macaca mulatta	91.9%		SDDSLAVSSPRLSPDQCRIVYLQYPSLIPHQCSQLCLYDWYTKVTSVVVDIVPRQLGENFSGIYCSLLPLGCWSADSQR	
Bos taurus	92.28		SDDSLAVTSPRLSPDQCRIVYLQFPSLVPHQQCGQLCLYDWYTRVTVVVDVVPRQLGENFSGIYCSLLPLGCWSADSQR	
Rattus norvegicus	90.8%		SD <mark>GSLAICSPRLSPDQC</mark> RIVYLQYPCLAPHHQCSQLCLYDWYTKVTSVVVDIVPRQLGESFSGIY <mark>C</mark> SLLPLGCWSADSQR	
Mus musculus	90.7%		SDESLAVCSPR_SPDQCR/VYLQYPSLAPHOCSQLFLYDWYTKVTSLVVD1VPRQLGESFSG1YCSLLPLGCNSADSQR	
Canis lupus familiaris	92.68		SUDSLAVSS PRIS PUCKLYPI AVPSLVPHOCSULCLYDWYTRV IS VVUVVPRUIGENES GLYCSLLPLGCASADSUR	
reiis catus	92.20		Soorthase Messole and the second	
		401		80
Sus scrofa	100%	401	4 VVFDSPQRSRQDLEANDTQNGSVTSLTAGGSGGSWKLLTTEDRDLHVVQFSTPSVPPSLKVGFLPPAGKEQAVSKVSLEEA	80
Sus scrofa Homo sapiens	100% 91.9%	401	4 VVFDSPQRSRQDLFAVDTQVGSVTSLTAGGSGGSMKLLTIDRDLHVVQFSTPSVPRSLKVGFLPPAGKEQAVSIVSLEEA VVFDSQQRSRQDLFAVDTQVGTVTSLTAGGSGSMKLLTIDQDLHVQQFSTPSUPPTLKVGFLPSAGKEQSVLHVSLEEA	80
Sus scrofa Homo sapiens Macaca mulatta	100% 91.9% 91.9%	401	4 VV FDS PQRSRQDL FAV DTOVICS V TSL T AGG SG SMKLL T DRDL HVV OF ST SVPPSL KVGFL PPAG (EQAVSH V SL EEA VV FDS AQRSRQDL FAV DTOVGTV TSL T AGG SG SMKLL T DODL HV AGF ST SUPPTL KVGFL PSAG KEQSVLM V SL EEA VV FDS AQRSRQDL FAV DTOVGTV TSL T AGG SG SMKLL T DRDL HV AGF ST SUPPTL KVGFL PSAG KEQSVLM V SL EEA	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus porvegicus	100% 91.9% 91.9% 92.2% 90.8%	401	4 V FDS PQRSRQD I FAV DTOMES YTS I TAGES GESMIK IL TE DRD HIV OF STES VPPS I XVEF I PDAGKEQ AV SAV STEEA W FDS PQRSRQD I FAV DTOWET YTS I TAGES GESMIK I TE DOL HV AVFSTES I PTT I XVEF I PS AVKEOS YTM STEEA V FDS PQRSRQD I FAV DTOWET YTS I TAGES GESMIK I TE DOL HV AVFSTES I PTT I XVEF I PS AVKEOS YTM STEEA W FDT AVRSRQD I FAV DTOWET YTS I TAGES GESMIK I TE DOL HV AVFSTES I PTT I XVEF I PS AVKEOS YTM STEEA W FDT AVRSRQD I FAV DTOWET YTS I TAGES GESMIK I TE DOL HV AVFSTES I PTT I XVEF I PDAGKEGS YTM STEEA W FDT AVRSRQD I FAV DTOWET YTD I TAGES GESMIK I TE DOL HV AVFSTEN I PTT I XVEF I PDAGKEGS YTM STEEA W FDT AVRSRDD I FAV DTOWET YTD I TAGES GESMIK I TO ROUT WAT STEN I DTOWET YTM STEEA I PTT I VIET I PDAGKEGS YTM STEEA	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus	100% 91.9% 91.9% 92.2% 90.8% 90.7%	401	4 VFDS*QRSRQDLFAVDTQNGSVTSLTAGGSGGSMKLLTEDRDLHVVQFSTSVPPSLXVGFLPPAGKEQAVSNSLEEA VFDSAQRSRQDLFAVDTQVTSTTSLTAGGSGSMKLLTEDDLHVQFSTSLDFTLXVGFLPSARKEQSVLNSLEEA VFDSAQRSRQDLFAVDTQNGTVTSLTAGGSGSMKLLTEDRDLHVQFSTSLDFTLXVGFLPSARKEQSVLNSLEEA VFDSAQRSRQDLFAVDTQNGTVTPLTAGGSGSMKLLTEDRDLHVAQFSTSNLPPCLXVGFLPPAGKEQSVLNSLEEA VFDSAQRSRQDLFAVDTQNGTVTPLTAGGSGSMKLLTEDRDLHVAQFSTSLDVSLKVGFLPPAGKEQSVLSSLSEEA VFDSAQRSRQDLFAVDTQNGTVTPLTAGGSGSMKLLTEDRDLHVAQFSTSLDVSLKVGFLPPAGKEQSVSNSLEEA VFDSAQRSRQDLFAVDTQNGTVTPLTAGGSGSMKLLTEDRDLHVAQFSTSLDVSLKVGFLPPAGKEQSVSNSLEEA	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus nozvegicus Mus musculus Canis lupus familiaris	100% 91.9% 92.2% 90.8% 90.7% 92.6%	401	4 W FDS-QRSRQD FAV DTQ/GS VTS LTAGG SG SMKLLT DRD LHVV QFST-SVPPSLKVGFLPPAGKEQAVSKVS LEA W FDS-QRSRQD FAV DTQVGTVTS LTAGG SG SMKLLT DQD JHVQ QFST-SLDPTL KVGFLPSAGKEQAVSKVS LEA V FDS-QRSRQD FAV DTQVGTVTS LTAGG SG SMKLLT DRD LHVQ QFST-SLDPTL KVGFLPSAGKEQS VLN S LEA W FDS-QRSRQD FAV DTQVGTVTD LTAGG SG SMKLLT DRD LHVQ PST-SLDPTL KVGFLPSAGKEQS VLN S LEA W FDS-QRSRQD FAV DTQVGTVTD LTAGG SG SMKLLT DRD LHVQ PST-SLDPSL KVGFLPPAGKEQEV VN S LEA W FDS-QRSRQD FAV DTQTGTSTTS LTAGG SG SMKLLT DRD LHVQ PST-SLDPSL KVGFLPPAGKEQEV SM S LEA W FDS-QRSRQD FAV DTQTG ST ST LTAGG SG SMKLLT DRD LHVQ PST-SLDPSL KVGFLPPAGKEQEV SM S LEA W FDS-QRSRQD FAV DTQTG ST ST LTAGG SG SMKLLT DRD LHVQ FST-SLDPSL KVGFLPPAGKEQT VN S LEA W FDS-QRSRQD FAV DTQTG ST ST LTAGG SG SMKLLT DRD LHVQ FST SLDPSL KVGFLPPAGKEQT VLN S LEA	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus	100% 91.9% 92.2% 90.8% 90.7% 92.6% 92.2%	401	4 W FDS-PQRSRQD FAV DTOVGS VTS LTAGG SG SMKLLT DRD HVV OFST SVPPS LVGFLPPAG (EQAUSIVS LEA W FDS-QRSRQD FAV DTOVGT VTS LTAGG SG SMK LLT DQD HVV OFST SLPHT LVGFLPSAG (EQAUSIVS LEA W FDS-QRSRQD FAV DTOVGT VTS LTAGG SG SMK LLT DRD HVV OFST SLPHT LVGFLPSAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOVGT VTS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS TAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLT DRD HVV OFST NLPSL VVGFLPAG (EQAUSIVS LEA V FDS-QRSRQD FAV DTOTG STS LTAGG SG SMK LLA DRD HVV OFST SLPSL VVGFLPAG (EQAUSIVS LEA	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus	100% 91.9% 91.9% 92.2% 90.8% 90.7% 92.6% 92.2%	401	4 V FDS PQRSRQD I FAV DTOMES VTS I TAGES GESMIK I UT DRD LHV OF ST S VPPS I XVEFLPPAG KEQ AV SAV S LEEA V FDS AQRSRQD I FAV DTOWET VTS I TAGES GESMIK I TO DO LHV AQF ST SLIPTI V VEFLPSAG KEQ AV SAV S LEEA V FDS AQRSRQD I FAV DTOWET VTS I TAGES GESMIK I TO DO HVA APST PAUDTI V VEFLPSAG KEQ AV SAV S LEEA V FDT AQRSRQD I FAV DTOWET VTS I TAGES GESMIK I TO DO HVA APST PAUDTI V VEFLPSAG KEQ AV SAV S LEEA V FDT AQRSRQD I FAV DTOTE STIS I TAGES GESMIK I TO DO HVA APST PAUDTI V VEFLPSAG KEQ AV SAV S LEEA V FDT AQRSRQD I FAV DTOTE STIS I TAGES GESMIK I TO DOL HVA APST PAUDTI V VEFLPFAG KEQ S VI S LEEA V FDS AQRSRQD I FAV DTOTE STIS I TAGES GESMIK I TO DOL HVA APST PSL PS I VVEFLPFAG KEQ S VI S LEEA V FDS AQRSRQD I FAV DTOTES VTS I TAGES GESMIK I TO DOL HVA APST PSL PS I VVEFLPFAG KEQ S VI S LEEA V FDS AQRSRQD I FAV DTOWES VTS I TAGES GESMIK I TO DOL HVA APST PSL PS I VVEFLPFAG KEQ S VI S LEEA V FDS AQRSRQD I FAV DTOWES VTS I TAGES GESMIK I TO DOL HVA APST PSL PS I VVEFLPFAG KEQ VI VI S LEEA V FDS AQRSRQD I FAV DTOWES VTS I TAGES GESMIK I TO DOL HVA APST PSL PS I VVEFLPFAG KEQ VI VI S LEEA	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa	100% 91.9% 92.2% 90.8% 90.7% 92.6% 92.2%	401	4 V FDS ORSROD L PAV DTONIS V TS LTAGG SIG SMKLLT DRDLHVV OF STO SVPPS L XVGFLPPAG KEQ AV SM S LEEA W FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DODLHVV OF STO SLIPTI, VVGFLPS AV REG V LW S LEEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRDLHVA OF STO SLIPTI, VVGFLPS AV REG V LW S LEEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRDLHVA OF STO SLIPTI, VVGFLPS AV REG V LW S LEEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRDLHVA OF STO SLIPTI, VVGFLPS AV REG V LW S LEEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRDLHVA OF STO SLIPTI, VVGFLPPAG KEQ SVM S LEEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRDLHVA OF STO SLIPTI, VVGFLPPAG KEQ SVM S LEEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRD HVA AQF STO SLIPTI, VVGFLPPAG KEQ SVM S LEEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRD HVA AQF STO SLIPTI, VVGFLPPAG KEQ SVM S LEEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRD HVA AQF STO SLIPTI, VVGFLPPAG KEQ SVM SU SEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRD HVA AQF STO SLIPTI, VVGFLPPAG KEQ SVM SU SEA V FDS AQRSROD L PAV DTOVIST IT S LTAGG SIG SMKLLT DRD HVA AQF STO SLIPTI S	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens	100% 91.9% 92.2% 90.8% 92.6% 92.6% 92.2% 100% 91.9%	401 481	4 W FDS-QRSRQD LFAV DTQ/RGS/TS_LTAGG SG SMKLLT DRD_HV/QFSTPSUPPSLKVGFLPPAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/GT/TS_LTAGG SG SMKLLT DQD_HV/QFSTPSLD/TT_KVGFLPSAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/GT/TS_LTAGG SG SMKLLT DQD_HV/QFSTPSLD/TT_KVGFLPSAGKEQAVL/NS_LEFA W FDS-QRSRQD LFAV DTQ/GT/TS_LTAGG SG SMKLLT DQD_HV/QFSTPSLD/ST_KVGFLPFAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/GTT/TS_LTAGG SG SMKLLT DQD_HV/QFSTPSLD/ST_KVGFLPFAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/TS_TS_TS_TAGG SG SMKLLT DQD_HV/QFSTPSLD/ST_KVGFLPFAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/TS_TS_TS_TAGG SG SMKLLT DQD_HV/QFSTPSLD/ST_KVGFLPFAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/TS_TS_TS_TAGG SG SMKLLT DQD_HV/QFSTPSLD/ST_KVGFLPFAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/TS_TS_TAGG SG SMKLLT DQD_HV/QFSTPSLD/ST_KVGFLPFAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/TS_TVS_TAGG SG SMKLLT DQD_HV/QFSTPSLD/ST_KVGFLPFAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/TS_TVS_TAGG SG SMKLLT DQD_HV/QFSTPSLD/ST_KVGFLPFAGKEQAVS/NS_LEFA W FDS-QRSRQD LFAV DTQ/TS_TVS_TAGG SG SMKLLT DQD_HV/QFSTPSLD/ST_KVGFLPFAGKEQAVS/NS_LEFA S = D = DM/GT/TV_DPD/DGH/TV/SGED HS_TVTA/NLFPAMLC/TVGFAVLLY = TD = DM/GT/TV_DOPD/GH/TV/SGED HS_TVTA/NLFPAMLC/TVGFAVLLY = TD = DM/GT/TV_DOPD/SGH/TV/SGED HS_TVTA/NLFPAMLC/TVGFAVLLY = TD = DM/GT/TV_DOPD/SGEN/TA/SGED HS_TVTA/NLFPAMLC/TVGFAVLLY = TD = DM/GT/TV_DOPD/DTS_TVTA/SGED HS_TVTA/NLFPAMLC/TVGFAVLLY = TD = DM/GT/TV_DOPD/SGEN/TA/NLFPAMLC/TVGFAVLLY = TD = DM/GT/TV_DOPD/SGEN/TA/NLFPAMLC/TVGFAVLLY = TD = DM/GT/TV_DOPD/SGEN/TS_DTS/NLFPAMLC/TVGFAVLLY = TD = DM/GT/TV_DOPD/SGEN/TS_DTS/NLFPAMLC/TVGFAVLLY = TD = DM/GT/TV_DDPS/DTD/SGEN/TS_DT	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta	100% 91.9% 92.2% 90.8% 90.7% 92.6% 92.2% 100% 91.9%	401 481	4 W EDS PQRSRQD I SAV DTOMES YTS I TAGES GESMIK ILT DRD LHV OFST S VPP S L XVEFLPAAKEQ V SAV S I EEA W EDS PQRSRQD I SAV DTOWET YTS I TAGES GESMIK ILT DRD LHV OFST S I PHT I XVEFLPSAKEQ S I W SI S EEA W EDS PQRSRQD I SAV DTOWET YTS I TAGES GESMIK ILT DRD LHV OFST S I PHT I XVEFLPSAKEQ S I W SI S EEA W FDT PARSRQD I SAV DTOWET YTS I TAGES GESMIK ILT DRD LHV OFST S I PHT I XVEFLPSAKEQ S I W SI S EEA W FDT PARSRQD I SAV DTOWET Y D'I TAGES GESMIK ILT DRD LHV OFST S I PHT I XVEFLPSAKEQ S I W SI S EEA W FDT PARSRQD I SAV DTOWET Y D'I TAGES GESMIK ILT DRD LHV OFST S I D'I'S I XVEFLPPAR VEGEV V SI EEA W FDS PQRSRQD I SAV DTOWES YTS I TAGES GESMIK ILT DRD LHV OFST SI D'I'S I XVEFLPPAR VEGEV V SI EEA W FDS PQRSRQD I SAV DTOWES YTS I TAGES GESMIK ILT DRD LHV OFST SI D'I'S I XVEFLPPAR VEGEV V SI EEA W FDS PQRSRQD I SAV DTOWES YTS I TAGES GESMIK ILT DRD LHV OFST SI D'I'S I XVEFLPPAR VEGEV V SI EEA W FDS PQRSRQD I SAV DTOWES YTS I TAGES GESMIK ILT DRD LHV OFST SI D'I'S I XVEFLPAR VEGT Y D'I'N SI EEA W FDS PQRSRQD I SAV DTOWES Y TS I TAGES GESMIK I TO DRD LHV OFST SI D'I'S I XVEFLPAR VEGT Y D'I'N SI EEA W FDS PQRSRQD I SAV DTOWES Y TS I TAGES GESMIK I TO DRD LHV OFST SI D'I'S I XVEFLPAR VEGT Y D'I'N SI EEA V FDS PQRSRQD I SAV DTOWES Y TS I TAGES GESMIK I TO DRD LHV OFST SI D'I'S I XVEFLPAR VEGT Y D'I'N SI EEA W FDS PQRSRD I SAV DTOWES Y TS I TAGES GESMIK I TO DRD LHV OFST SI D'I'S I XVEFLPAR VEGT Y D'I'N SI EEA W FDS PQRSRD I SAV DTOWES Y TS I TAGES GESMIK I TO DRD LHV OFST SI D'I'S I'N SI I'N SI E K WEFLPAR VEGT Y D'I'N SI EEA W FDS PARSRD I SAVI D'I'N SI I'N SI GES GESMIK I TO DRD LHV OFST SI D'I'S I'N SI I'N SI GEV SAVI SI D'I'N SI TAGES GESMIK I TO DRD LHV OFST SI D'I'N SI I'N SI I'N SI GEV SAVI SI TO I'N SI TAGES GESMIK I TO DRD LHV O'N SI GER SI'N N'I'N SI EEA S S S S S S S S S S S S S S S S S S S	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus	100% 91.9% 92.2% 90.8% 92.6% 92.6% 92.2% 100% 91.9% 91.9% 92.2%	401	4 V FDS PQRSRQD L PAV DTOM'S V TS LTAGG SOG SMK LLT DRD LHV QFST SUPPS L XVGFLPPAG KEQAV SM S L EEA W FDS AQRSRQD L PAV DTOW'ST TS LTAGG SOG SMK LLT DRD LHV QFST SLD PT L KVGFLPSAG KEQAV LM S L EEA W FDS AQRSRQD L PAV DTOM'ST TS LTAGG SOG SMK LLT DRD LHV QFST SLD PT L KVGFLPSAG KEQAV LM S L EEA W FDS AQRSRQD L PAV DTOTS DTS LTAGG SOG SMK LLT DRD HV AQFST SHLD PT L KVGFLPSAG KEQAV LM S L EEA W FDS AQRSRQD L PAV DTOTS DTS LTAGG SOG SMK LLT DRD HV AQFST SHLD PT L KVGFLPPAG KEQAV SM S L EEA W FDS AQRSRQD L PAV DTOTS S TS LTAGG SOG SMK LLT DRD HV AQFST SHLD SL KVGFLPPAG KEQAV SM S L EEA W FDS AQRSRQD L PAV DTOTS ST SL TAGG SOG SMK LLT DRD LHV AQFST SL PS L KVGFLPPAG KEQAV SM S L EEA W FDS AQRSRQD L PAV DTOTS ST SL TAGG SOG SMK LLT DRD LHV AQFST SL PS L KVGFLPPAG KEQAV SM S L EEA W FDS AQRSRQD L PAV DTOTS ST SL TAGG SOG SMK LLT DRD LHV AQFST SL PS L KVGFLPPAG KEQAV SM S L EEA W FDS AQRSRQD L PAV DTOTOS ST SL TAGG SOG SMK LLT DRD LHV AQFST SL PS L KVGFLPPAG KEQAV LM S L EEA W FDS AQRSRQD L PAV DTOTOG ST TS L TAGG SOG SMK LLT DRD LHV AQFST SL PS L KVGFLPPAG KEQAV LM S L EEA W FDS AQRSRQD L PAV DTOTOG ST TS L TAGG SOG SMK LLT DRD LHV AQFST SL PS L KVGFLPPAG KEQAV LM S L EEA V FDS AQRSRQD L PAV DTOTOG ST TS L TAGG SOG SMK LLT DRD LHV AQFST SL PS L KVGFLPPAG KEQT LM S L EEA V FDS AQRSRD L PAV DTOTOG ST TS L TAGG SOG SMK LLA DRD HV AQFST SL PS L KVGFLPPAG KEQT LM S L EEA V FDS AQRSRD L PAV DTOG MGT TS L TAGG SOG SMK LLA DRD HV AQFST SL PS L KVGFLPPAG KEQT LM S L EEA V FDS AQRSRD L FVL D PPH EQE V YAGL D FEATLL Q TOG PH STOTOV PMV VMPT GGPHSSFV TA ML FPAML GKVG FAULLY E TD D L MGT RVL OPPH EQE Y OYAGL D FEATLL Q TOG PH SKTOV PMV VMPT GGPHSSFV TA ML FPAML GKVG FAULLY E TD D L MGT RVL OPPH EQE Y OYAGL D FEATLL Q TOG PHO KTOVPMV VMPT GGPHSSFV TA ML FPAML GKVG FAULLY E TD D L MGT RVL OPPH EQE Y OYAGL D FEATLL Q TOG PHO KTOVPMV VMPT GGPHSSFV TA ML FPAML GKVG FAULLY E TD D L MGT RVL OPPH EQE Y OYAGL D FEATLL Q TOG PHO YMV PT GGPHSSFV TA ML L PAML CKVG FAULLY E TD D L MGT RVL OPPH EQE MOY GAU LEFA LL D TOTO S	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus	100% 91.9% 92.2% 90.8% 92.6% 92.6% 92.2% 100% 91.9% 91.9% 92.2% 90.8% 90.8%	401	4 V FDS ORSROD L PAUDIONS VTS LTAGS SOS MKLLT ORDLINV OF STOS VPS L XVEFLPPAG YEAVSIVS L EEA W FDS ARRADD L PAUDIOVET TIS LTAGS SOS MKLLT ODDLINV AFSTOS L PTT L XVEFLPSAG YEAVINS L EEA V FDS ARRADD L PAUDIOVET TIS LTAGS SOS MKLLT DRDLINV AFSTOS L PTTL XVEFLPSAG YEAVINS L EEA V FDS ARRADD L PAUDIOVET TIS LTAGS SOS MKLLT DRDLINV AFSTOS L PTTL XVEFLPSAG YEAVINS L EEA V FDS ARRADD L PAUDIOVES VTS LTAGS SOS MKLLT DRDLINV AFSTOS L PTSL XVEFLPPAG YEAVINS L EEA V FDS ARRADD L PAUDIOVES VTS LTAGS SOS MKLLT DRDLINV AFSTOS L PTSL XVEFLPPAG YEAVINS L EEA V FDS ARRADD L PAUDIOVES VTS LTAGS SOS MKLLT DRDLINV AFSTOS L PTSL XVEFLPPAG YEAVINS L EEA V FDS ARRADD L PAUDIOVES VTS LTAGS SOS MKLLT DRDLINV AFSTOS L PTSL XVEFLPPAG YEAVINS L EEA V FDS ARRADD L PAUDIOVES VTS LTAGS SOS MKLLT DRDLINV AFSTOS L PTSL XVEFLPPAG YEAVINS L EEA V FDS ARRADD L PAUDIOVES VTS L TAGS SOS MKLLT DRDLINV AFSTOS L PTSL XVEFLPPAG YEAVINS L EEA V FDS ARRADD L PAUDIOVES VTS L TAGS SOS MKLLT DRDLINV AFSTOS L PTSL XVEFLPPAG YEAVING YEA	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris	100% 91.9% 92.2% 90.7% 92.6% 92.2% 91.9% 91.9% 91.9% 91.9% 92.2% 90.8% 90.7% 90.7%	401	4 V FDS-QRSRQD LFAV DTQNG SV TS LTAGG SG SMKLLT DRDLHVVQFST SVPPSLXVGFLPPAGKEQAVSN SLEEA W FDS-QRSRQD LFAV DTQNG TV TS LTAGG SG SMKLLT DQDLHVVQFST SLDATT KVGFLPSAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG TV TS LTAGG SG SMKLLT DQDLHVVQFST SLDATT KVGFLPSAGKEQAVLN SLEEA W FDS-QRSRQD LFAV DTQNG TV TS LTAGG SG SMKLLT DQDLHVVQFST SLDATT KVGFLPSAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG TV TS LTAGG SG SMKLLT DQDLHVVQFST SLDATT KVGFLPPAGKEQAVLN SLEEA W FDS-QRSRQD LFAV DTQNG TS TS LTAGG SG SMKLLT DQDLHVVQFST SLDATT KVGFLPPAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG SV TS LTAGG SG SMKLLT DQDLHVVQFST SLDAS KVGFLPPAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG SV TS LTAGG SG SMKLLT DQDLHVQFST SLDAS KVGFLPPAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG SV TS LTAGG SG SMKLLT DQDLHVQFST SLDAS KVGFLPPAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG SV TS LTAGG SG SMKLLT DQDLHVQFST SLDAS KVGFLPPAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG SV TS LTAGG SG SMKLLT DQDLHVQFST SLDAS KVGFLPPAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG SV TS LTAGG SG SMKLLT DQDLHVQFST SLDAS KVGFLPPAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG SV TS LTAGG SG SMKLLT DQDLHVQFST SLDAS KVGFLPPAGKEQAVLN SLEEA V FDS-QRSRQD LFAV DTQNG SV TS LTAGG SG SMKLLT DQDLHVQFST SLDAS KVGFLPPAGKEQAVLN SLEEA S 5 5 5 5 5 5 5 5 5 5 5 5 5	80
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus	100% 91.9% 92.2% 90.7% 92.6% 92.2% 91.9% 91.9% 91.9% 92.2% 90.8% 90.7% 92.2%	401	4 V EDS PQRSRQD I SAV DTOMES VITS I TAGES GESMIK LITE DRD LINV OF STIPS VPP SLXVEFLPPAG KEQ VISAV SU EEA W EDS PQRSRQD I SAV DTOWET VITS I TAGES GESMIK LITE DRD LINV OF STIPS UP TI KVEFLPS ACKEOS VIDAV SI EEA V EDS PQRSRQD I SAV DTOWET VITS I TAGES GESMIK LITE DRD LINV OF STIPS UP TI KVEFLPS ACKEOS VIDAV SI EEA W FDT PARKEND I SAV DTOWET VIDE VITAGES GESMIK LITE DRD LINV OF STIPS UP TI KVEFLPS ACKEOS VIDAV SI EEA W FDT PARKEND I SAV DTOWET VIDE VITAGES GESMIK LITE DRD LINV OF STIPS UP TI KVEFLPS ACKEOS VIDAV SI EEA V FDS PQRSRQD I SAV DTOWES VITS I TAGES GESMIK LITE DRD LINV OF STIPS LIDES V KVEFLPPAG KEOVINA SI EEA V FDS PQRSRQD I SAV DTOWES VITS I TAGES GESMIK LITE DRD LINV OF STIPS LIDES V KVEFLPPAG KEOVINA SI EEA V FDS PQRSRQD I SAV DTOWES VITS I TAGES GESMIK LITE DRD LINV OF STIPS LIDES V KVEFLPPAG KEOVINA SI EEA V FDS PQRSRQD I SAV DTOWES VITS I TAGES GESMIK LITE DRD LINV OF STIPS LIDES V KVEFLPPAG KEOVINA SI EEA V FDS PQRSRQD I SAV DTOWES VITS I TAGES GESMIK LITE DRD LINV OF STIPS LIDES V KVEFLPPAG KEOVINA SI EEA V FDS PQRSRQD I SAV DTOWES VITS I TAGES GESMIK LITE DRD LINV OF STIPS LIDES V KVEFLPPAG KEOVINA SI EEA V FDS PQRSRQD I SAV DTOWES VITS I TAGES GESMIK LITE DRD LINV OF STIPS LIDES V KVEFLPPAG KEOVINA SI EEA V FDS PQRSRQD I SAV DTOWES VITS I TAGES GESMIK LITE DRD LINV OF STIPS LIDES V KVEFLPPAG KEOVINA SI EEA V FDS PQRSRQD I SAV DTOWES VITS I TAGES GESMIK LIDE DRD LINV OF STIPS SI VITA WILE PARME CKREPAUL V E TIDE I MOLENNI OPPROEN VOYAGI DEFAILLO SAME SKOTOV PMVVMPI GEPHSSEV VITA WILE PARME CKREPAUL V E TIDE I MOLENNI OPPROEN VOYAGI DEFAILLO SAME PROVOVINVIR GEPHSSEV VITA WILE PARME CKREPAUL V E TIDE I SMS I RVI OPPROEN VOYAGI DEFAILLO SAME PORTOV PMVVMIR I GEPHSSEV VITA WILE PARME CKREPAUL V E TIDE I SMS I RVI OPPROEN VOYAGI DEFAILLO SAME PORTOV PMVVMIR I GEPHSSEV VITA WILE PARME CKREPAUL V E TIDE I SMS I RVI OPPROEN VOYAGI DEFAILLO SAME PORTOV PMVVMIRI GEPHSSEV VITA WILE PARME CKREPAUL V E TIDE I SMS I RVI OPPROEN VOYAGI DEFAILLO SAME PORTOV PMVVMIRI GEPHSSEV VITA WILE PARME	60
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus	100% 91.9% 92.9% 90.8% 90.7% 92.6% 92.2% 100% 91.9% 91.9% 91.9% 90.8% 90.7% 92.6% 92.2%	401	4 V FDS PQRSRQD L PAV DTOMES VTS LTAGE SOGSMIKLUT DODLINV OF ST S VPP SLXVEFLPPAG KEQAV SN SLEEA W FDS AQRSRQD L PAV DTOMET VTS LTAGES GESMIKLUT DODLINV OF ST SLDATLIK VEFLPSAK KEQAV IN SLEEA V FDS AQRSRQD L PAV DTOMET VTS LTAGES GESMIKLUT DODLINV APST SLDATLIK VEFLPSAK KEQAVIN SLEEA W FDTAQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST ST DATLIK VEFLPSAK KEQAVIN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATLIK VEFLPSAK KEQAVIN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATLIK VEFLPPACKEQSVIN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPPACKEQSVIN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPPACKEQSVIN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPPACKEQSVIN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPACKEQT VEN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPACKEQT VEN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPACKEQT VEN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPACKEQT VEN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPACKEQT VEN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPACKEQT VEN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPACKEQT VEN VIN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES GESMIKLUT DODLINV APST SLDATS VEFLPACKEQT VEN SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES DE COLORIDATE ST SLDATS VEFLPACKEQT VE ST SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES ST SLAT VEFLPACKEQT VE ST SLEEA V FDS AQRSRQD L PAV DTOTE ST SLTAGES ST SLAT VEFLPACKEQT VE ST SLEAA V FDS AQRSRQD L PAV DTOTE ST SLTAGES ST SLAT VEFLPACKEQT VE ST SLAT VEFLPACKEQT VE ST SL SLEAA ST SLAT VLOPPP SOEN VERALD SLEAA SLOTE ST SLAT VEFLPACKEQT VE ST SLAT VEFLPACKEQT VE SLEAA SLEAA SLEAA SLEAA SLAT VLOPPH SOEN VER SLEAA SLOTE SLAT VEFLPACKEQT	60
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus	100% 91.9% 92.2% 90.8% 92.6% 92.2% 92.6% 92.2% 91.9% 92.2% 90.7% 92.2% 90.7% 92.2%	401 481 561	4 V FDS ORSROD LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV OFST S VPS LXVEFLPPAG KEQAV SM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV OFST S LPT LXVEFLPSAG KEQAV LM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMT LXVEFLPSAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMT LXVEFLPSAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMT LXVEFLPSAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPAG KEQAVLM S LEA V FDS ARRAND LAN DTOMS NTS LTAGG SOG SMKLLT DRDLMV APST SLDMS LXVEFLPAG KEQAVLM S LEA S S S S S S S S S S S S S S S S S S S	660
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Ecomo sapiens	100% 91.9% 92.2% 90.8% 92.3% 92.2% 92.2% 91.9% 91.9% 92.2% 90.7% 92.2% 90.78 92.2%	401 481 561	4 V FDS ORSROD LAN DTON'S VIS LIAGS SOS MKLLT DROLMV OF STOS VPS LXVEFLPPACKEO X SM S LEA V FDS ORSROD LAN DTON'S VIS LIAGS SOS MKLLT DOLLMV OF STOS UP TO KVEFLPS A KEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLT DOLLMV OF STOS UP TO KVEFLPS A KEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLT DROLMV OF STOS UP TO KVEFLPS A KEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLT DROLMV OF STOS UP TO KVEFLPS A KEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLT DROLMV A OF STOS UP TO KVEFLPS A KEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLT DROLMV A OF STOS UP S KVEFLPPACKEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLT DROLMV A OF STOS UP S KVEFLPPACKEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLT DROLMV A OF STOS UP S LV CFLPPACKEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLTA DROLMVA OF STOS UP S LV CFLPPACKEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLTA DROLMVA OF STOS UP S LV CFLPPACKEOS VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLTA DROLMVA OF STOS UP S LV CFLPACKEOA VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLTA DROLMVA OF STOS UP S LV CFLPACKEOA VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLTA DROLMVA OF STOS UP S LV CFLPACKEOA VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SOS MKLLTA DROLMVA OF STOS UP S LV CFLPACKEOA VID X S LEA V FDS A READ LAN DTON'S VIS LIAGS SON DE S VID Y VID Y VID Y TON VID Y S LONG VID Y VID Y S LONG Y S L VID Y S L VIC LAN U C PARA VID Y S L S L X S L VID Y S L VIC LAN U C V S L S L X S	660
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta	100% 91.9% 92.2% 90.8% 92.6% 92.6% 92.6% 91.9% 91.9% 90.7% 92.6% 92.2% 90.7% 92.6% 92.2%	401 481 561	4 V EDS PQRSRQD L FAV DTOMES VTS. T. AGG SG SMK.LLT DRD.LHV.QFST S.VPP SLXVGFLPPAGKEQ.V.SN.S.LEEA W EDS PQRSRQD L FAV DTOMET VTS. T. AGG SG SMK.LLT DRD.LHV.QFST SLPHT LKVGFLPSAGKEQ.V.SN.S.LEEA V EDS PQRSRQD L FAV DTOMET VTS. T. AGG SG SMK.LLT DRD.LHV.QFST SLPHT LKVGFLPSAGKEQ.V.LN.S.LEEA W EDS PQRSRQD L FAV DTOMES VTS. T. AGG SG SMK.LLT DRD.LHV.QFST SLPHT LKVGFLPSAGKEQ.V.LN.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTT LKVGFLPSAGKEQ.V.LN.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQ.V.SN.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQS.V.N.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQS.V.SN.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQS.V.N.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQT L W.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQT L W.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQT L W.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQT L W.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQT L W.S.LEEA W EDS PQRSRQD L FAV DTOTE STITS T. AGG SG SMK.LLT DRD.LHV.QFST SLDTS LKVGFLPPAGKEQT L W.S.LEEA W EDS PPOT SMST R.V.CPPP PQELD VGYAGL DEFAILL Q SNS PEKT QVPMVVMPI GGPHSSFV TAVIL EPAMLCK/GF FAVLLV E T.D D LNG R.N.CPPP FQELQVGVG DEFAILL Q SNS PEKT QVPMVVMPI FGFHSSFV TAVIL EPAMLCK/GF FAVLLV E T.D D LNG R.N.CPPP FQELQVGVG DEFAILL Q SNS PEKT QVPMVVMPI FGFHSSFV TAVIL EPAMLCK/GF FAVLLV E T.D D LNG R.N.LPPPH QELX/QYABL DEFAILL Q SNS PEKT QVPMVVMPI FGFHSSFV TAVIL EPAMLCK/GF FAVLLV E T.D D LNG R.N.LPPPH QELX/QYABL DEFAILL Q SNS PEKT QVPMVVMPI FGFHSSFV TAVIL EPAMLCK/GF FAVLLV E T.D D LNG R.N.LPPPH QELX/QYABL DEFAILL Q SNS PEKT QVPMVVMPI FGFHSSFV TAVIL EPAMLCK/GF FAVLLV E T.D D LNG R.N.LPPPH QE	60
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Mus auculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus	100% 91.9% 92.2% 90.8% 92.6% 92.6% 92.2% 91.9% 91.9% 92.2% 90.7% 92.2% 100% 91.9% 92.2%	401 481 561	4 V FDS PQR5RQD LFAV DTOMES VTS LTAGE SOG SMKLIT DODLINV QFST SUPPS LXVEFLPPAG KEQAV SM S LEEA W FDS AQR5RQD LFAV DTOMET VTS LTAGES GESMKLIT DODLINV QFST SLDVTLKVEFLPSAK KEQS VLM S LEEA V FDS AQR5RQD LFAV DTOTE STIS LTAGES GESMKLIT DODLINV QFST SLDVTLKVEFLPSAK KEQS VLM S LEEA W FDS AQR5RQD LFAV DTOTE STIS LTAGES GESMKLIT DOD WA APST MLDPC VKEFLPSAK KEQS VLM S LEEA W FDS AQR5RQD LFAV DTOTE STIS LTAGES GESMKLIT DOD WA APST MLDPC VKEFLPSAK KEQS VLM S LEEA W FDS AQR5RQD LFAV DTOTE STIS LTAGES GESMKLIT DOD WA APST MLDPC VKEFLPFAK KEQS VLM S LEEA W FDS AQR5RQD LFAV DTOTE STIS LTAGES GESMKLIT DOD WA APST MLDPC VKEFLPFAK KEQS VLM S LEEA W FDS AQR5RQD LFAV DTOTE STIS LTAGES GESMKLIT DOD LWA APST MLDPC VKEFLPFAK KEQT VLM S LEEA W FDS AQR5RQD LFAV DTOTE STIS LTAGES GESMKLIT DOD LWA APST SLDPS LKVEFLPFAK KEQT VLM S LEEA W FDS AQR5RQD LFAV DTOTE STIS LTAGES GESMKLIT DOD LWA APST SLDPS LKVEFLPFAK KEQT VLM S LEEA W FDS AQR5RQD LFAV DTOTE STIS LTAGES GESMKLIT DOD LWA APST SLDPS LKVEFLPFAK KEQT VLM S LEEA W FDS AQR5RD LFAV DTOTE STIS LTAGES GESMKLIT DOD LWA APST SLDPS LKVEFLPFAK KEQT VLM S LEEA W FDS AQR5RD LFAV DTOTE STIS LTAGES GESMKLIT DOD LWA APST SLDPS LKVEFLPAK KEQT VLM S LEEA W FDS AQR5RD LFAV DTOTE STIS LTAGES DE STAKLIN DOD LWA APST SLDPS LKVEFLPAK KEQT VLM S LEEA W FDS AQR5RD LFAV DTOTE STIS LTAGES DE STAKLING SMEDIA ET D D LMG R.N LOPPP SQEN VOYAGL DFEATLLO PONDER VDVMPT GGPHSSEV TAMLEPAML CKG FAULLV ET D D LMG R.N LOPPP SQEN VOYAGL DFEATLLO PONDER VDVMPT GGPHSSEV TAMLEPAML CKG FAULLV ET D D LMG R.N LOPPP SQEN VOYAGL DFEATLLO SND PONTOVMET GGPHSSEV TAMLEPAML CKG FAULLV ET D D LMG R.N LOPPP SQEN VOYAGL DFEATLLO SND PONTOVMET GGPHSSEV TAMLEPAML CKG FAULLV ET D D LMG R.N LOPPP SQEN VOYAGL DFEATLLO SND PONTOVMET GGPHSSEV TAMLEPAML CKG FAULLV ET D D LMG R.N LOPPP SQEN VOYAGL DFEATLLO SND PONTOVPMVVMET GGPHSSEV TAMLEPAML CKG FAULLV ET D D LMG R.N LOPPP SQEN VOYAGL DFEATLLO SND PONTOVPMVVMET GGPHSSEV TAMLEPAML CKG FAULLV ET D D SMALRN LOPPP SQEN VOYAGL DFEATLLO SND PONTOVPMVVMET GGPHSSEV TAMLEPAML CKG	660
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Ratus norvegicus	100% 91.9% 92.2% 90.8% 92.6% 92.2% 100% 91.9% 92.2% 90.8% 92.2% 100% 92.2%	401 481 561	4 V FDS ORSROD LAV DTOMS VITS LIAGS SOS MKLLT ORDUNVOFST S VPS LXVEFLPPACKEOX SN S LEA W FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD TI, KVEFLBS AK EQS VILN S LEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD TI, KVEFLBS AK EQS VILN S LEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD TI, KVEFLBS AK EQS VILN S LEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD TI, KVEFLBS AK EQS VILN S LEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD TI, KVEFLPACKEOS VILN S LEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS LEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS SUS LEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS V EEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS V EEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS V EEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS V EEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS V S EEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS V S EEA V FDS ARSROD LAV DTOMS VITS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS V S EEA V FDS ARSROD LAV DTOMS VIS LIAGS SOS MKLLT DODLIVA OFST SLD S LKVEFLPACKEOS VIS V S EEA V FDS ARSR VI OPPPOENT OVACID FEATLLO S SOP DK OV PMVVNPI GOPHSSEV TAVILE PAMI CAVE FAULLV E FI D LAVG R V OPPPOENT OVACID FEATLLO S SOP DK OV PMVVNPI GOPHSSEV TAVILE PAMI CAVE FAULLV E FI D TAVG R V OPPPOENT OVACID FEATLLO S SOP DK OV PMVVNPI GOPHSSEV TAVILE PAMI CAVE FAULLV E FI D S MALINI OPPPOENT OVACID FEATLLO S SOP DK OVAPVVNPI GOPHSSEV TAVILE PAMI CAVE FAULLV E FI D S MALINI OPPPOENT OVACID FEATLLO S SOP DK OVAPVVNPI GOPHSSEV TAVILE PAMI CAVE FAULLV E FI D S MALINI OPPPOENT OVACID FEATLLO S SOP DK OVAPVVNPI GOPHSSEV TAVIL PAMI CAVE FAULLV E FI D S MALINI OPPPOENT OVACID FEATLLO S SOP DK OVAPVVNPI HOR SOR SSEV TAVIL	660
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus	100% 91.9% 92.2% 90.8% 92.6% 92.2% 100% 91.9% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8% 92.2% 91.9% 92.2% 91.9% 92.2% 91.9% 92.2%	401 481 561	4 V FDS ORSROD FANDTON'S VIS LIAGS SOSMIKLUT ORDUNVOFSTOS VPS LIVOFUPPACKEON SIVS LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPT VIVOF LISAR KEOS VILN'S LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPT VIVOF LISAR KEOS VILN'S LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPT VIVOF LISAR KEOS VILN'S LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPT VIVOF LISAR KEOS VILN'S LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPT VIVOF LISAR KEOS VIN'S LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPT VIVOF LISAR KEOS VIN'S LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPS VIVOF LIPAR KEOS VIS VIS LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPS VIVOF LIPAR KEOS VIS VIS LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPS VIVOF LIPAR KEOS VIS VIS LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPS VIVOF LIPAR KEOS VIS VIS LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOFSTOS UPS VIVOF LIPAR KEOS VIS VIS LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOV VID LIGGPHSSEV VIA MLEPAR KEOS VIS VIS LEA V FDS ARRADD FANDTON'S VIS LIAGS SOSMIKLUT ODDUNVOV VID LIGGPHSSEV VIA MLEPAR (CA'GF ANLLUV E T D SINGTR'N OPPPOOL VOVAGLUP FAILLO 'S ND POKTOV PMVVVNP LIGGPHSSEV VIA MLEPAR (CA'GF ANLLUV E T D SINGTR'N OPPPOOL VOVAGLUP FAILLO 'S ND POKTOV PMVVVNP LIGGPHSSEV VIA MLEPAR (CA'GF ANLLUV E T D SINGTR'N OPPPOOL VOVAGLUP FAILLO SND POKTOV PMVVVNP LIGGPHSSEV VIA MLEPAR (CA'GF ANLLUV E T D SINGTR'N OPPPOOL VOVAGLUP FAILLO SND POKTOV PMVVVNP LIGGPHSSEV VIA MLEPAR (CA'GF ANLLUV E T D SINGTR'N OPPPOOL VOVAGLUP FAILLO SND POKTOV PMVVVNP LIGGPHSSEV VIA MLEPAR (CA'GF ANLLUV E T D SINGTR'N OPPPOOL VOVAGLUP FAILLO SND POKTOV PMVVVNP LIGHSSEV VIA MLEPAR (CA'GF ANLLUV E T D SINGTR'N OPPPOOL VOVAGLUP FAILLO SND POKTOV PMVVNP LIGHSSEV VIA MLEPAR (CA'GF ANLLUV E T D SINGTR'N OPPPOOL VOVAGLUP FAILLO SND POKTOV PMVVNP LIGHSSEV VIA MLEPAR (CA'GF ANLLUV E T D SINGTR'N OPPPOOL VOVAGLUP	880 660
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus auculus Canis lupus familiaris Palis catus	100% 91.9% 92.2% 90.8% 92.6% 92.2% 92.6% 91.9% 91.9% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8% 92.6% 92.6%	401 481 561	4 V FDS - QRSRQD I FAV DTOMES MTS I TAGE SO SANK LIT DRD LINV QFST - SVPP S LXVEFLPPAG KEQAN SAV S I EEA W FDS - QRSRQD I FAV DTOMET MTS I TAGES OG SANK LIT DRD LINV QFST S LIPTI, KVEFLPSAG KEQAN SAV S I EEA W FDS - QRSRQD I FAV DTOMET MTS I TAGES OG SANK LIT DRD LINV QFST S LIPTI, KVEFLPSAG KEQAN NA S I EEA W FDS - QRSRQD I FAV DTOTE S ITTS I TAGES OG SANK LIT DRD LINV QFST S LIPTI, KVEFLPSAG KEQAN NA S I EEA W FDS - QRSRQD I FAV DTOTE S ITTS I TAGES OG SANK LIT DRD LINV QFST S LIPTI, KVEFLPSAG KEQAN NA S I EEA W FDS - QRSRQD I FAV DTOTE S ITTS I TAGES OG SANK LIT DRD LINV QFST S LIPTI, KVEFLPSAG KEQAN NA S I EEA W FDS - QRSRQD I FAV DTOTE S ITTS I TAGES OG SANK LIT DRD LINV QFST S LIPTI, KVEFLPSAG KEQAN NA S I EEA W FDS - QRSRQD I FAV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA W FDS - QRSRQD I FAV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA W FDS - QRSRQD I FAV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA W FDS - QRSRQD I FAV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA W FDS - QRSRQD I FAV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA W FDS - QRSRQD I FAV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA W FDS - QRSRQD I FAV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA W FDS - QRSRQD I FAV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA W FDS - QRSRQD I FAV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA U FDS - QRSRQD I S AV DTOTE S I TTS I TAGES OG SANK LIT DRD LINV QFST S LIPTS I KVEFLPSAG KEQAN LIV S I EEA U FDS - QRSRQD I S VOTAG DE AT LILLO S SAN S FOR TO VPNVVNPI GGPHSSFV TAM LIPPAMI CAGE FAULLU E TID D I NGRNU OPPROEND OVEND D FATILLO S SAN PROCTO VPNVVNPI GGPHSSFV TAM LIPAMI CAGE FAULLU E TID D I NGRNU NI PPAPED C VOTAG DE FATILLO S SAN PROCTO VP	880 660
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Mus mucculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus caturus Rattus norvegicus Mus caturus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus	100% 91.9% 92.2% 90.8% 92.6% 92.2% 100% 91.9% 92.2% 90.8% 92.2% 100% 91.9% 92.2% 90.8% 92.2%	401 481 561	4 V FDS PQR5RQD LFAV DTOMES VTS LTAGE SOG SMK LTE DRDLHVAQFST SUPPLEXVEFLPAAKEQAV SM SLEEA W FDS AQR5RQD LFAV DTOMET VTS LTAGES GESMK LTE DDLHVAQFST SLDHTLKVEFLPSAKEQSVLM SLEEA V FDS AQR5RQD LFAV DTOT STISLTAGES GESMK LTE DDLHVAQFST SLDHTLKVEFLPSAKEQSVLM SLEEA W FDS AQR5RQD LFAV DTOT STISLTAGES GESMK LTE DDLHVAQFST SLDHTLKVEFLPSAKEQSVLM SLEEA V FDS AQR5RQD LFAV DTOT STISLTAGES GESMK LTE DDLHVAQFST SLDHTLKVEFLPSAKEQSVLM SLEEA W FDS AQR5RQD LFAV DTOT STISLTAGES GESMK LTE DDLHVAQFST SLDHTLKVEFLPSAKEQSVLM SLEEA V FDS AQR5RQD LFAV DTOT STISLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPPACKEQSVLM SLEEA V FDS AQR5RQD LFAV DTOT STISLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPPACKEQSVLM SLEEA V FDS AQR5RQD LFAV DTOT STISLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPPACKEQSVLM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPPACKEQSVLM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPACKEQSVLM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDLHVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDHLVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDHLVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDHLVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDHLVAQFST SLDHSLKVEFLPACKEQT VM SLEEA V FDS AQR5RQD LFAV DTOT GES VTSLTAGES GESMK LTE DDHLVAGES GESMK LTE DDHLVKGF GEN FT TD TMG TR TG FOODEN QPAVES DEALLO PSN FOR TO QPHVVNP TG GPHSSFV TAV ML FPAML QKG FAVLLLV FT TD TMG TR TG FOODEN QPAVES DA DEA	89 60
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Mus aulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis Lupus familiaris Felis catus	100% 91.9% 92.2% 90.8% 92.6% 92.2% 100% 91.9% 92.2% 100% 92.2% 100% 92.2% 100% 92.2% 100% 91.9% 92.8% 90.8% 92.2%	401 481 561 641	4 V FDS ORSROD LAV DTOMS VTS LTAGG SOG SMK LT DRDLINV OFST S VPS L XVG FLPPAG KEQAV SM S LEA W FDS ARRAND LAV DTOM TITS LTAGG SOG SMK LT DRDLINV OFST SLD TL KVG FLPSAG KEQAV SM S LEA W FDS ARRAND LAV DTOM TITS LTAGG SOG SMK LT DRD LINV APST SLD TL KVG FLPSAG KEQAV LM S LEA W FDS ARRAND LAV DTOM TITS LTAGG SOG SMK LT DRD LINV APST SLD TL KVG FLPSAG KEQAV LM S LEA W FDS ARRAND LAV DTOM TITS LTAGG SOG SMK LT DRD LINV APST SLD TL KVG FLPSAG KEQAV LM S LEA W FDS ARRAND LAV DTOM TITS LTAGG SOG SMK LT DRD LINV APST SLD TL KVG FLPPAG KEQAV SM S LEA W FDS ARRAND LAV DTOM TITS LTAGG SOG SMK LT DRD LINV APST SLD S LKVG FLPPAG KEQAV SM S LEA W FDS ARRAND LAV DTOM S VTS LTAGG SOG SMK LT DRD LINV APST SLD S LKVG FLPPAG KEQAV SM S LEA W FDS ARRAND LAV DTOM S VTS LTAGG SOG SMK LT DRD LINV APST SLD S LKVG FLPPAG KEQAV SM S LEA W FDS ARRAND LAV DTOM S VTS LTAGG SOG SMK LTA DRD LINV APST SLD S LKVG FLPPAG KEQAV SM S LEA W FDS ARRAND LAV DTOM S VTS LTAGG SOG SMK LTA DRD LINV APST SLD S LKVG FLPAG KEQT LNN S LEA W FDS ARRAND LAV DTOM S VTS LTAGG SOG SMK LTA DRD LINV APST SLD S LKVG FLPAG KEQT LNN S LEA W FDS ARRAND LAV DTOM S VTS LTAGG SOG SMK LTA DRD LINV APST SLD S LKVG FLPAG KEQT LNN S LEA W FDS ARRAND LAV DTOM S VTS LTAGG SOG SMK LTA DRD LINV APST SLD S LKVG FLPAG KEQT LNN S LEA W FDS ARRAND LAV DTOM S VTS LTAGG SOG SMK LLAV DRS VTG VPMVVMPT IGPHSSFV T NHL FPAML CK G FAULLV E PT D LNG TRV OPPPO CEN VAGI DFEATLLO SON POKTOVPMVVMPT IGPHSSFV T NHL FPAML CK G FAULLV E TT D LNG TRV OPPPO CEN VAGI DFEATLLO SON POKTOVPMVVMPT IGPHSSFV T NHL FPAML CK G FAULLV E TT D LNG TRV IVPPPO CEN VAND DFEATLLO SON POKTOVPMVVMPT IGPHSSFV T NHL FPAML CK G FAULLV E TT D LNG TRV IVPPPO CEN VAND DFEATLLO SON POKTOVPMVVMPT IGPHSSFV T NHL FPAML CK G FAULLV E TT D LNG TRV IVPPO CEN VAND DFEATLLO SON POKTOVPMVMPT IGPHSSFV T NHL FPAML CK G FAULLV E TT D LNG TRV IVPPO CEN VAND VND VND VND VND VND VND VND VND VND V	889 660 440
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus	100% 91.9% 92.2% 90.7% 92.6% 92.2% 100% 91.9% 92.2% 90.7% 92.2% 90.7% 92.2% 91.9% 92.2% 90.7% 92.2% 90.7% 92.2% 90.7% 92.2%	401 481 561 641	4 V EDS OR SROD LEAV DTOMES YTS LTAGES GESMIK LET DRD LINV OF STIS VPP SLXVEFLEPAGKEO VISAV SLEEA V EDS OR RENOU LEAV DTOMETY TS LTAGES GESMIK LET DRD LINV OF STIS LPHT LKVEFLESAGKEOS VILW SLEEA V EDS OR RENOU LEAV DTOWETY TS LTAGES GESMIK LET DRD LINV OF STIS LPHT LKVEFLESAGKEOS VILW SLEEA V EDS OR RENOU LEAV DTOWETY TS LTAGES GESMIK LET DRD LINV OF STIS LPHT LKVEFLESAGKEOS VILW SLEEA V EDS OR RENOU LEAV DTOWETY TS LTAGES GESMIK LET DRD LINV OF STIS LPHT LKVEFLESAGKEOS VILW SLEEA V EDS OR RENOU LEAV DTOWE VTB LTAGES GESMIK LET DRD LINV OF STIS LPHT LKVEFLESAGKEOS VILW SLEEA V EDS OR RENOU LEAV DTOWES VTS LTAGES GESMIK LET DRD LINV OF STIS LIPS LKVEFLESAGKEOS VILW SLEEA V EDS OR RENOU LEAV DTOWES VTS LTAGES GESMIK LET DRD LINV OF STIS LIPS LKVEFLESAGKEOTI LINV SLEEA V EDS OR RENOU LEAV DTOWES VTS LTAGES GESMIK LET DRD LINV OF STIS LIPS LKVEFLESAGKEOTI LINV SLEEA V EDS OR RENOU LEAV DTOWES VTS LTAGES GESMIK LET DRD LINV OF STIS LIPS LKVEFLESAGKEOTI LINV SLEEA V EDS OR RENOU LEAV DTOWES VTS LTAGES GESMIK LET DRD LINV OF STIS LIPS LKVEFLESAGKEOTI LINV SLEEA V EDS OR RENOU DE VOTOWES VTS LTAGES GESMIK LET DRD LINV OF STIS LIPS LKVEFLESAGKEOTI LINV SLEEA V EDS OR RENOU DE VOTOWES VERS LID GED FAILLO OF DR DKOVOWNY RENOT SLESS VTAMILE PAMIL GKVEFAULLV E TID D LINGERN OPPEDENT OVAEL DE FAILLO OF DR DKTOVPNVVME TEGENESSEV TAMILE PAMIL GKVEFAULLV E TID D LINGERN LIPPPEDENT OVAEL DE FAILLO OF DR DKTOVPNVVME TEGENESSEV TAMILE PAMIL GKVEFAULLV E TID D LINGERN LIPPPEDENT OVAEL DE FAILLO SINDE DKTOVPNVVME TEGENESSEV TAMILE PAMIL GKVEFAULLV E TID D LINGERN LIPPPEDENT OVAEL DE FAILLO SINDE DKTOVPNVVME TEGENESSEV TAMILE PAMIL GKVEFAULLV E TID D LINGERN LIPPPEDENT OVAEL DE FAILLO SINDE DKTOVPNVVME TEGENESSEV TAMILE PAMIL GKVEFAULLV E TID D LINGERN LIPPPEDENT OVAEL DE FAILLO SINDE DKTOVPNVVME TEGENESSEV TAMILE PAMIL GKVEFAULLV E TID D LINGERN LIPPPEDENT OVAEL DE FAILLO SINDE DKTOVPNVME TEGENESSEV TAMILE PAMIL GKVEFAULLV E TID D LINGERN LIPPPEDENT OVAEL DE FAILLO SINDE DKTOVPNVME TEGENESSEV TAMILE PAMIL GKVEFAU	80 60 440
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus causulus Canis lupus familiaris Felis catus Canis lupus familiaris Felis catus	100% 91.9% 92.2% 90.8% 92.6% 92.2% 91.9% 91.9% 92.2% 91.9% 92.2% 92.6% 92.2% 100% 91.9% 92.2% 90.8% 92.2% 90.8% 92.2%	401 481 561 641	4 V PDS PQRSRQD I PAV DTOMES VTS I TAGE SO SAK IL TO DRUHVOPST S VPP S XVEFLPPAG KEQAV SAV S I EFA V PDS PQRSRQD I PAV DTOMET VTS I TAGES OG SAK IL TO DRUHVOPST S UPT I XVEFLPSAG KEQAV SAV S I EFA V PDS PQRSRQD I PAV DTOMET VTS I TAGES OG SAK IL TO DRUHVOPST S UPT I XVEFLPSAG KEQAVI SAV S I EFA V PDS PQRSRQD I PAV DTOTES VTS I TAGES OG SAK IL TO DRUHVOPST S UPT I XVEFLPSAG KEQAVI VS I EFA V PDS PQRSRQD I PAV DTOTES VTS I TAGES OG SAK IL TO DRUHVOPST S UPT I XVEFLPSAG KEQAVI VS I EFA V PDS PQRSRQD I PAV DTOTES VTS I TAGES OG SAK IL TO DRUHVOPST S UPT I XVEFLPPAG KEQAVI VS I EFA V PDS PQRSRQD I PAV DTOTES VTS I TAGES OG SAK IL TO DRUHVOPST S UPT I XVEFLPPAG KEQAVI VS I EFA V PDS PQRSRQD I PAV DTOTES VTS I TAGES OG SAK IL TO DRUHVOPST S UPS I XVEFLPPAG KEQAVI VS I EFA V PDS PQRSRQD I PAV DTOTES VTS I TAGES OG SAK IL TO DRUHVOPST S UPS I XVEFLPPAG KEQAVI VS I EFA V PDS PQRSRQD I PAV DTOTES VTS I TAGES OG SAK IL TO DRUHVOPST S UPS I XVEFLPPAG KEQAVI VS I EFA V PDS PQRSRQD I PAV DTOTES VTS I TAGES OG SAK IL TO DRUHVOPST GEPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGERVI O PPP OGEN VOYAGI D FEATIL O TAGES PDCTO VPMVVNPT GGPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGERVI O PPP OGEN VOYAGI D FEATIL O TAGES PDCTO VPMVVNPT GGPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGERVI O PPP OGEN VOYAGI D FEATIL O TAGES PDCTO VPMVVNPT GGPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGERVI O PPP OGEN VOYAGI D FEATIL O TAGES PDCTO VPMVVNPT GGPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGERVI O PPP OGEN VOYAGI D FEATIL O SNO POCTO VPMVVNPT GGPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGERVI O PPP OGEN VOYAGI D FEATIL O SNO POCTO VPMVVNPT GGPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGERVI O PPP OGEN VOYAGI D FEATIL O SNO POCTO VPMVVNPT I GGPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGERVI O PPP OGEN VOYAGI D FEATIL O SNO POCTO VPMVVNPT I GGPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGERVI O PPP OGEN VOYAGI D FEATIL O SNO POCTO VPMVVNPT I GGPHSSEV V AN UF PAMI CAME FAULU E PTD D I NGENT V O PPP OGEN VOYAGI D FEATIL O SNO POCTO VPMVVNPT I GGPHSSEV V AN UF PA	80 60 40
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus	100% 91.9% 92.2% 90.7% 92.6% 92.2% 100% 91.9% 92.2% 90.8% 92.2% 100% 91.9% 92.2% 100% 91.9% 92.2% 100% 91.9% 92.2%	401 481 561 641	4 V PDS PQR5RQD LFAV DTOMES ITS LTAGE SO SAK LLT DRDLINV QFST SUPPS LXVEFLPPAG KEQA ISA S LEFA W PDS AQR5RQD LFAV DTOMET TS LTAGES GESAK LLT DRDLINV QFST SLD PT LXVEFLPSAG KEQS ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD PT LXVEFLPSAG KEQS ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD PT LXVEFLPSAG KEQS ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD PT LXVEFLPSAG KEQS ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD PT LXVEFLPFAG KEQS ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD SL KVEFLPFAG KEQS ISM SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD SL KVEFLPFAG KEQT ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD SL KVEFLPFAG KEQT ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD SL KVEFLPFAG KEQT ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD SL KVEFLPFAG KEQT ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD SL KVEFLPFAG KEQT ILW SLEFA W PDS AQR5RQD LFAV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD SL KVEFLPFAG KEQT ILW SLEFA W PDS AQR5RDD LFV DTOTE STITS LTAGES GESAK LLT DRDLINV QFST SLD SL KVEFLPFAG KEQT ILW SLEFA W PDS AQR5RDD LFV DTOTE STITS LTAGES DEST SLD SL KVEFLPFAG KEQT ILW SLEFA LV PDS AQR5RDD LFV DTOTE STITS LTAGES DEST SLD SL KVEFLPFAG KEQT ILW SLEFA LV PDS AQR5RDD LFV DTOTE STITS LTAGES DEST SLD SL KVEFLPFAG KEQT ILW SLEFA LV PDS AQR5RDD LFV DTOTE STITS LTAGES DEST STITS LTAGES DEST STITS ILP SL KVEFLPFAG KEQT ILW SLEFA LV PDS AQR5RDD LFV DTOTE STITS LTAGES DEST STITS LTAGES DEST STITS ILP SL KVEFLPAG KEQT ILW SLEFA LV PDS AQR5RDD LFV DTOTE STITS LTAGES DEST STITS	80 60 40
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis Lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Ratus norvegicus	100% 91.9% 92.2% 90.8% 92.6% 92.2% 100% 91.9% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8%	401 481 561 641	4 V PDS QRSRQD L AV DTOM'S YTS LTAGG SOG SMK LT TO DRUM QFST S VPS L XVG PLPPAG KEQAY SM S L EA W PDS AQRSRQD L AV DTOM'T YS LTAGG SOG SMK LT TO DRUM QFST S L PT L XVG PLPSAG KEQAY SM S L EA W PDS AQRSRQD L AV DTOM'T YS LTAGG SOG SMK LT TO DRUM QFST S L PT L XVG PLPSAG KEQAY L SK S W PDS AQRSRQD L AV DTOM'T YS LTAGG SOG SMK LT TO DRUM QFST S L PT L XVG PLPSAG KEQAY L SK S W PDS AQRSRQD L AV DTOM'S YTS L TAGG SOG SMK LT TO DRUM QFST S L PT L XVG PLPSAG KEQAY L SK S W PDS AQRSRQD L AV DTOM'S YTS L TAGG SOG SMK LT TO DRUM QFST S L PT L XVG PLPPAG KEQAY SM S L EA W PDS AQRSRQD L AV DTOM'S YTS LTAGG SOG SMK LT TO DRUM QFST S L PT S L XVG PLPPAG KEQAY SM S L EA W PDS AQRSRQD L AV DTOM'S YTS L TAGG S G SMK LT TO DRUM QFST S L PT S L XVG PLPPAG KEQAY SM S L EA W PDS AQRSRQD L AV DTOM'S YTS L TAGG S G SMK LT TO DRUM QFST S L PT S L XVG PLPPAG KEQAY SM S L EA W PDS AQRSRQD L AV DTOM'S YTS L TAGG S G SMK LT TO DRUM AV ST S L PT S L XVG PLPPAG KEQAY SM S L EA W PDS AQRSRQD L FV DTOM'S YTS L TAGG S G SMK LT TO RDUM AV ST S L PT S L XVG PLPPAG KEQAY SM S L EA W PDS AQRSRQD L FV DTOM'S Y TS L TAGG S G SMK LT TO RDUM AV ST S L PT S L Y S L Y S L XVG PLPAG KEQAY L S L EA W PDS AQRSRQD L FV DTOM'S Y TS L TAGG S G SMK LT A DRDUM AV SFT S L PT S L XVG PLPAG KEQAY L S L EA W PDS AQRSRQD L FV DTOM'S Y TS L TAGG S G S MK LT TO RDUM AV ST S L PT S L XVG PLPAG KEQAY L S L EA W PDS AQRSRQD L FV DTOM'S Y TS L TAGG S G S MK LT A DRDUM AV SFT S L PT S L XVG PLPAG KEQAY L S L EA W PDS AQRSRD L FV DTOM'S Y TS L TAGG S G S MK LT O'RDUM Y S T G F C AV L L Y ET D L S M L P PAN L C AV S L D PE AT L D S D PO CTOVPHVVMP T G PHSSEY T A M L PAML C AV G F AV L L Y E T D L M'G T N L O PPP QEN Y AV L D F AT L L D S M P D CTOVPHVVMP T G PHSSEY T A M L PAML C AV G F AU L L Y E T D L M'G T R C AV L L P PPP QEN Y AV D D F AT L D S ND PD CTOVPHVVMP T G PHSSEY T A M L PAML C AV G F AU L L Y E T D L M'G T R L O PPP QEN Y AV D D F AT L L D S ND PD CTOVPHVVMP T G PHSSEY T A M L PAML C AV G F AU L L Y E T D L M'G T R N L O PPP QEN Y AV D D F AT L D S ND PD CTOVP	80 660 440
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Mus caus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus	100% 91.9% 92.2% 90.7% 92.6% 92.2% 91.9% 91.9% 92.2% 90.8% 92.2% 90.8% 92.2% 90.7% 92.2% 90.7% 92.2% 90.7% 92.2% 90.7% 92.2% 90.7% 92.2%	401 481 561 641	4 V EDS PQRSRQD LFAV DTOMES VTS LTAGE SO SANK LLT DRD LHV QFST S VPP S LXVEFLPAAK KEQ V SAV S L EEA V EDS PQRSRQD LFAV DTOMES VTS LTAGES GESMK LLT DRD LHV QFST S LPT L KVEFLPSAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTOMES VTS LTAGES GESMK LLT DRD LHV QFST S LPT L KVEFLPSAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTOT VTP LTAGES GESMK LLT DRD LHV QFST S LPT L KVEFLPSAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTOT S T S LTAGES GESMK LLT DRD LHV QFST S LPT L KVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTOT S VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTOT S VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTOT S VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTOT S VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTOT NES VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTONES VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTONES VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTONES VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTONES VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PQRSRQD LFAV DTONES VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PDR S V PAR DTONES VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPFAK KEQ VLW S LEA V EDS PDR S V PAR DTONES VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPAK KEQ VLW S LEA V EDS PDR S V PAR DTONES VTS LTAGES GESMK LLT DRD LHV QFST S LDT S LKVEFLPAK KEQ VLW S LEA V EDS S V PAR V DPP QELV QYARD DFATLL Q S S PDR V QFVHVW NF IGGPHSS V TAM L PAML (KVEF AULLV E T D L NG K LHPPPDQEN QYA D LFATLL Q S ND PDK Q VPMVVMF IGGPHSS V TAM L PAML (KVEF AULLV E T D L S LK LT V PAR D ND ND Q PAV Q V D D KD Q PAV Q V V PMVVMF IGGPHSS V TAM L PAML (KVEF AULLV E T D D S MA R V Q PPR QELVQVG D FATLL Q S ND PDK Q VPMVVMF IGGPHSS V T	80 60 440
Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Mus musculus Canis lupus familiaris Felis catus Sus scrofa Homo sapiens Macaca mulatta Bos taurus Rattus norvegicus Mus musculus Canis lupus familiaris	100% 91.9% 92.2% 90.8% 92.6% 92.2% 91.9% 91.9% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8% 92.2% 90.8% 92.2% 91.9% 92.2% 91.9% 92.2% 90.8% 92.2%	401 481 561 641	4 V PDS PQR5RQD LFAV DTOMES ITS IT AGG SG SMK LIT DRD LINVQFST S VPP S XVGFLPPAG KEQA SM S LEEA W PDS AQR5RQD LFAV DTOMET ITS IT AGG SG SMK LIT DRD LINVQFST S LIPT I XVGFLP5AG KEQA ISM S LEEA W PDS AQR5RQD LFAV DTOT ST ITS IT AGG SG SMK LIT DRD LINVQFST S LIPT I XVGFLP5AG KEQA ISM S LEEA W PDS AQR5RQD LFAV DTOT S ITS IT AGG SG SMK LIT DRD LINVQFST S LIPT I XVGFLP5AG KEQA ILW S LEEA W PDS AQR5RQD LFAV DTOT S ITS IT AGG SG SMK LIT DRD LINVQFST NL PC X VGFLP5AG KEQA ILW S LEEA W PDS AQR5RQD LFAV DTOT S ITS IT AGG SG SMK LIT DRD LINVQFST NL PS I XVGFLP5AG KEQA ILW S LEEA W PDS AQR5RQD LFAV DTOT S ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQA ILW S LEEA W PDS AQR5RQD LFAV DTOT S ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQA ILW S LEEA W PDS AQR5RQD LFAV DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA W PDS AQR5RQD LFAV DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA W PDS AQR5RQD LFAV DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA W PDS AQR5RQD LFAV DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA W PDS AQR5RQD LFAV DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA W PDS AQR5RQD LFAV DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA W PDS AQR5RQD LFAV DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA W PDS AQR5RQ LIPY DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA W PDS AQR5RQ LIPY DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA W PDS AQR5RQ LIPY DTOT MS ITS IT AGG SG SMK LIT DRD LINVQFST S LIPS I XVGFLP5AG KEQT ILW S LEEA U PDS LINGGT NO PPROED VOTAG LDFATILLO S SM PAGT OVPMVNM F GG PHSSFV TAVM I PAMIC (KG FAULL V ET D I NMGR NU OPPP OEN VOTAG LDFATILLO S SM PAGT OVPMVNM F GG PHSSFV TAVM I PAMIC (KG FAULL V ET D I NMGR NU OPPP QEV VG AD DFATILLO S ND PAGT OVPMVNM F GG PHSSFV TAVM I PAMIC (KG FAULL V ET D ID MGR NU OPPP QEV VG VG	80 60 40
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Figure S14. Sequence alignment of AAPs of mammals. Results of sequence alignment carried out with Clustal Omega [29] are presented with MView [30]. Sequence identity % with porcine AAP is shown (backgrounds of residues identical with that of porcine AAP are colored). Uniprot IDs are as follows: Sus scrofa: P19205, Homo sapiens: P13798, Macaca mulatta: F7G744, Bos taurus: P80227, Rattus norvegicus: P13676, Mus musculus: Q8R146, Canis lupus familiaris: E2R7E8, Felis catus: A0A5F5XJB2.



Figure S15. Characterization of the AAP sample. A) Size exclusion chromatography (Superose6 30/100 column, 20 mM TRIS, pH=8, 0.15M NaCl, 1mM EDTA, 1mM DTT) shows the homogeneity and the main peak retention is corresponding to the approximate mass of the AAP tetramer (325 kDa), B) SDS-PAGE of the main peak fractions is shown. SDS disassembles the tetramer and the bands are corresponding to the mass of the monomer (81 kDa). C) Calibration of Superose6 30/100 column (20 mM TRIS, pH=8, 0.15M NaCl, 1mM EDTA, 1mM DTT) with Gel Filtration Molecular Weight Markers Kit for Molecular Weights 29,000-700,000 Da (Merck, recommended concentrations were used). From elution volume (V_e) of our AAP sample (same sample volume and flow rate was used). The calibration peaks obtained in Superose6 30/100 column calibration: column3 shows the peak centroids (integrated with UNICORNTM software) and the estimated M_w of our protein sample based on the calibration curves. Using the standard semilog calibration curve the molecular mass of AAP specimen was calculated to be 341 kDa.

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