Supplementary Materials

Exploring intrinsic disorder in human synucleins and associated proteins

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Suppelemtary **Table S1:** Amino acid sequences of α-, β-, and γ-synucleins analyzed in this study

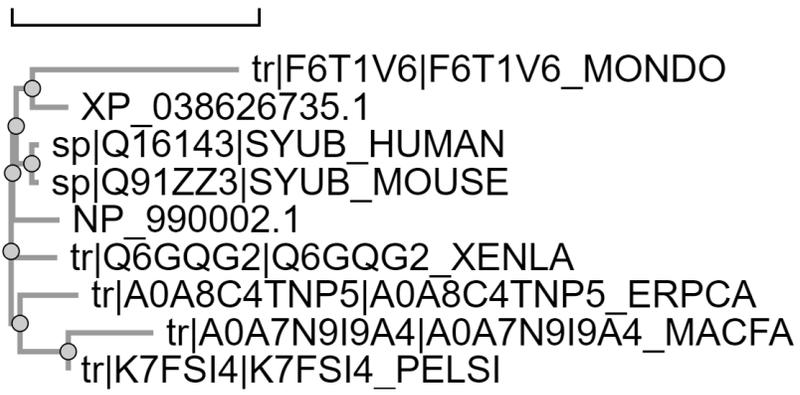| Species	Amino acid sequence (FASTA format)
	α-synuclein
Homo sapiens	>sp|P37840|SYUA_HUMAN Alpha-synuclein OS=Homo sapiens OX=9606 GN=SNCA PE=1 SV=1 MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTN VGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSE EGYQDYEPEA
	>tr|G7P5X2|G7P5X2_MACFA Alpha-synuclein OS=Macaca fascicularis OX=9541 GN=EGM_14544 PE=3 SV=1 MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQV TNVGGAVVTGVTAVAQKTVEGAGSIAAATGFIKKDQLGKNEEGAPQEGILQDMPVDPDNEAYE MPSEEGYQDYEPEA
	>sp|O55042|SYUA_MOUSE Alpha-synuclein OS=Mus musculus OX=10090 GN=Snca PE=1 SV=2 MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTKEQV TNVGGAVVTGVTAVAQKTVEGAGNIAAATGFVKKDQMGKGEEGYPQEGILEDMPVDPGSEAYE MPSEEGYQDYEPEA
	Sequence is not available

	Sequence is not available
	>tr|Q9I9H1|Q9I9H1_CHICK Alpha-synuclein OS=Gallus gallus OX=9031 GN=SNCA PE=1 SV=1 MDVFMKGLNKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSRTKEGVVHGVTTVAEKTKEQV SNVGGAVVTGVTAVAQKTVEGAGNIAAATGLVKKDQLAKQNEEGFLQEGMVNNTDIPVDPENE AYEMPPEEEYQDYEPEA
	>tr|K7FW98|K7FW98_PELSI Alpha-synuclein OS=Pelodiscus sinensis OX=13735 GN=SNCA PE=3 SV=1 MDVFMKGLSKAKEGVVAAAEKTKQGMAEAAGKTKEGVLYVGSRTREGVVHGVTTMAEKTKEQV SNVGGAVVTGVTAVAHKTVEGAGNIAAATGLVKKDQMAKQNEEGLSQEGMMDSTDMPMDPDNE AYEMPPEEEYQDYEPEA
	>tr|Q7SZ02|Q7SZ02_XENLA Alpha-synuclein OS=Xenopus laevis OX=8355 GN=snca.L PE=2 SV=1 MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTKEQV SNVGGAVVTGVTAVAHKTVEGAGNFAAATGLVKKDQKNESGFGPEGTMENSENMPVNPNNETY EMPPEEEYQDYDPEA
	>tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA Alpha-synuclein OS=Erpetoichthys calabaricus OX=27687 GN=SNCA PE=3 SV=1 MDVLMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVMYVGTKTKDGVTSVAEKTKEQVSNVG GAVVTGVTAVAHKTVEGAGNIAAATGLVKRDHLGKQNEDMLSQEGLMDNTADYPLDPDDTYDM PPEDDCQEYQPNA
β-synuclein	
Homo sapiens	>sp|Q16143|SYUB_HUMAN Beta-synuclein OS=Homo sapiens OX=9606 GN=SNCB PE=1 SV=1 MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGSKTREGVVQGVASVAEKTKEQAS HLGGAVFSGAGNIAAATGLVKREEFPTDLKPEEVAQEAAEEPLIEPLMEPEGESYEDPPQEEYQ EYEPEA
	>tr|A0A7N9I9A4|A0A7N9I9A4_MACFA Beta-synuclein OS=Macaca fascicularis OX=9541 GN=SNCB PE=3 SV=1 GPATQAPDPGPIPTPAPSPPRPGLAEPPRPPAAATVPSPAPAPHPGSKTREGVVQGVASVAEK TKEQASHLGGAVFSGAGNIAAATGLVKREEFPTDLKPEEVAQEAAEEPLIEPLMEPEGESYED PPQEEYQEYEPEA
	>sp|Q91ZZ3|SYUB_MOUSE Beta-synuclein OS=Mus musculus OX=10090 GN=Sncb PE=1 SV=1 MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGSKTSGVVQGVASVAEKTKEQAS HLGGAVFSGAGNIAAATGLVKKEEFPTDLKPEEVAQEAAEEPLIEPLMEPEGESYEDSPQEEY QEYEPEA

	>tr|F6T1V6|F6T1V6_MONDO Beta-synuclein OS=Monodelphis domestica OX=13616 GN=SNCB PE=3 SV=1 MDMFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGSEIRSKDRARGSGSVVRDQSNE STEGITMGGIRGDDGSSVGVGRVLVKSSQWWHGIPEEVGQEVGEEPMAEPLLDTEGESYEEPP QEEYQEYEPEA
	>XP_038626735.1 beta-synuclein [Tachyglossus aculeatus] MDMFMKGLNMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGNRTREGVVQSVASVAEKTKEQA SQLGGAVFSGAGNIAAATGLMKKEDLPADVKPEEVGQEAGEEPLIEPLLEPEGESYEDPTQEE YQEYEPEA
	>NP_990002.1 beta-synuclein [Gallus gallus] MEVFMKGLSKAKEGVVAAAEKTKQGVAEAAEKTKEGVLYVGSKTQGVVQGVTSVAEKAKEQAS QLGEAAFSGAGNIAAATGLVKKEEFPADLKAEEVAQEAVEEPLVEPLLEPEGESYEESPQEEY QEYEPEA
	>tr|K7FSI4|K7FSI4_PELSI Beta-synuclein-like OS=Pelodiscus sinensis OX=13735 GN=SNCB PE=3 SV=1 VAEKTKEQASQLGGAVMSGAGNIAAATGLVKKEEFPTDLKPEEVGQEAGEEPLSEPLLEPEGE AYEEPPQ
	>tr|Q6GQG2|Q6GQG2_XENLA Beta-synuclein OS=Xenopus laevis OX=8355 GN=sncb.S PE=2 SV=1 MDVFMKGFSKAKEGVVAAAEKTKQGVAEAAEKTKEGVLYVGNKTRDGVVQGVTSVAEKTKEQA SHLGGAVMSGAGNIAAATGLVKKDEFPTDLKPEEEAQEALEEPAAEPLLEPEGESYEDPQDDY QEYEPEA
	>tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA Beta-synuclein OS=Erpetoichthys calabaricus OX=27687 GN=sncb PE=3 SV=1 MDVLMKGLSKAKEGMAAAAEKTKEGVAVAAEKTKEGVLYVGNMTKEGVVQGVASVAEKTKEQA SQLGGAVFSGAGNIAAATGLMKKEEFPTDIKPEELGQEAVEEPLGEPIMEPEGEAYEEAPQDE YQEYEPEA
	γ-synuclein
Homo sapiens	>sp|O76070|SYUG_HUMAN Gamma-synuclein OS=Homo sapiens OX=9606 GN=SNCG PE=1 SV=2 MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKTKENVVQSVTSVAEKTKEQANA VSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRPSAPQQEGEASKEKEEVAEEAQSGGD
	>tr|G7PEV7|G7PEV7_MACFA Gamma-synuclein OS=Macaca fascicularis OX=9541 GN=EGM_17995 PE=3 SV=1 MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGTKTKENVVHSVTSVAEKTKEQA NAVSEAVVSSVNTVAAKTVEEAENIAVTSGVVRKEDLKPSAPQQEGEAAKEKEEVAEEAQSGG D

>sp|Q9Z0F7|SYUG_MOUSE Gamma-synuclein OS=Mus musculus OX=10090 GN=Sncg PE=1 SV=1

MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGTKTKENVVQSVTSVAEKTKEQA
NAVSEAVVSSVNTVANKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEENEEAKSGED

>tr|A0A5F8G4U8|A0A5F8G4U8_MONDO Gamma-synuclein OS=Monodelphis domestica OX=13616 GN=SNCG PE=3 SV=1

MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGTKTKEGVVQSVTSVAEKTKEQA
NLVSDVMVASVNTVANKTVEEAENIVVTSGIVRKEDLVNPAQPEHGAPEEQPAEAAEVTEEVG
APDAFFPLSPGLDRFSLFSPLLPASWASVTAAIRGAEEKGFPPCGLFSLLLSPFILP

>XP_038599981.1 gamma-synuclein [Tachyglossus aculeatus]

MDVFKKGFSIAMDGVVAAAEKTKQGVTEAAEKTKEGVMYVGTKTKEGVVQSVSSVAEKTKEQA
SAVSEAMVASVNTVASKTVEGAESIVVTAGVVKKEDLLRPDQLEEAAAEENPAEAPAEVPEAT
EKEDNGGN

>tr|Q9I9H0|Q9I9H0_CHICK Gamma-synuclein OS=Gallus gallus OX=9031 GN=SNCG1 PE=1 SV=1

MDVFKKGFSIAKEGVVAAAEKTKQGVTEAAEKTKEGVMYVGTKTKEGVVQSVTSVAEKTKEQA
NVVGEAVVASVNTVANKTVEGAETIVATTGVVKKEDLAPQQPAAEGEAAIPGSTEGGGEGENE
GN

>tr|K7FIG2|K7FIG2_PELSI Gamma-synuclein OS=Pelodiscus sinensis OX=13735 GN=SNCG PE=3 SV=1

MDVFKKGFSIAKEGVVAAAEKTKQGVTEAAEKTKEGVMYVGAKTKEGVVHSVSSVAEKTKEQA
NMVGEAVVASVNTVAGKTVEGAENIVTTTGIVKKEELSHPEHPAEPAAAEEEPPAEDIKATGE
GESESN

>tr|Q7SYT8|Q7SYT8_XENLA Gamma-synuclein OS=Xenopus laevis OX=8355 GN=sncg.S PE=2 SV=1

MDVFKKGFSMAKEGVVAAAEKTKQGVTEAAEKTKEGVMYVGAKTKEGVVHSVNTVAEKTKEQA
NVVGGAVVSGVNQVSSKTVEGTENVVSSTGLVKKEDLHPDQPEEPAAEEPAVEATESIEQVGD
GEN

>tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA Gamma-synuclein OS=Erpetoichthys calabaricus OX=27687 GN=sncg PE=3 SV=1

MDVFKKGFSMAKEGVVAAAEKTKHGVEEAAAKTKEGVMYVGTKTKEGVAHSVNAVAEKTKEQA
NIVGDAVVSSATQVSAKTVEGVENVAATGGLIKKDEQEGELVQNPAENESEEDAQAAEQVGN

Supplementary Figure S2. CLUSTAL O(1.2.4) multiple sequence alignment of alpha-synucleins

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tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA    MDVLMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVMYVGTKTKDG----VTSVAEKTK  56
tr|K7FW98|K7FW98_PELSI             MDVFMKGLSKAKEGVVAAAEKTKQGMAEAAGKTKEGVLYVGSRTREGVVHGVTTMAEKTK  60
tr|Q7SZ02|Q7SZ02_XENLA            MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTK  60
sp|O55042|SYUA_MOUSE              MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTK  60
tr|G7P5X2|G7P5X2_MACFA            MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTK  60
sp|P37840|SYUA_HUMAN              MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTK  60
tr|Q9I9H1|Q9I9H1_CHICK            MDVFMKGLNKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSRTKEGVVHGVTTVAEKTK  60
                                  ***:****.*****************:************:***::*::*   *::*****

tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA    EQVSNVGGAVVTGVTAVAHKTVEGAGNIAAATGLVKRDHLGKQNEDMLSQEGLMDNTADY  116
tr|K7FW98|K7FW98_PELSI             EQVSNVGGAVVTGVTAVAHKTVEGAGNIAAATGLVKKDQMAKQNEEGLSQEG-MMDSTDM  119
tr|Q7SZ02|Q7SZ02_XENLA            EQVSNVGGAVVTGVTAVAHKTVEGAGNFAAATGLVKKDQK---NESGFGPEGTMENSENM  117
sp|O55042|SYUA_MOUSE              EQVTNVGGAVVTGVTAVAQKTVEGAGNIAAATGFVKKDQMGKG-EEGYPQEG-IL--EDM  116
tr|G7P5X2|G7P5X2_MACFA            EQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFIKKDQLGKN-EEGAPQEG-IL--QDM  116
sp|P37840|SYUA_HUMAN              EQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKN-EEGAPQEG-IL--EDM  116
tr|Q9I9H1|Q9I9H1_CHICK            EQVSNVGGAVVTGVTAVAQKTVEGAGNIAAATGLVKKDQLAKQNEEGFLQEG-MVNNTDI  119
                                  ***:***************:*******.:*****::*:*:     *.   ** :   :

tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA    PLDPD-DTYDMPPEDDCQEYQPNA       139
tr|K7FW98|K7FW98_PELSI             PMDPDNEAYEMPPEEEYQDYEPEA       143
tr|Q7SZ02|Q7SZ02_XENLA            PVNPNNETYEMPPEEEYQDYDPEA       141
sp|O55042|SYUA_MOUSE              PVDPGSEAYEMPSEEGYQDYEPEA       140
tr|G7P5X2|G7P5X2_MACFA            PVDPDNEAYEMPSEEGYQDYEPEA       140
sp|P37840|SYUA_HUMAN              PVDPDNEAYEMPSEEGYQDYEPEA       140
tr|Q9I9H1|Q9I9H1_CHICK            PVDPENEAYEMPPEEEYQDYEPEA       143
                                  *::*  ::*:** *:  *:*:*:*
```

```
#  Percent Identity  Matrix - created by Clustal2.1
#
   1: tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA   100.00    78.26    77.21    76.30    75.56    76.30    78.26
   2: tr|K7FW98|K7FW98_PELSI            78.26   100.00    86.43    86.43    85.00    85.71    90.21
   3: tr|Q7SZ02|Q7SZ02_XENLA           77.21    86.43   100.00    86.13    83.94    85.40    87.86
   4: sp|O55042|SYUA_MOUSE             76.30    86.43    86.13   100.00    93.57    95.00    87.86
   5: tr|G7P5X2|G7P5X2_MACFA           75.56    85.00    83.94    93.57   100.00    98.57    87.14
   6: sp|P37840|SYUA_HUMAN             76.30    85.71    85.40    95.00    98.57   100.00    87.86
   7: tr|Q9I9H1|Q9I9H1_CHICK           78.26    90.21    87.86    87.86    87.14    87.86   100.00
```

Supplementary Figure S2. CLUSTAL O(1.2.4) multiple sequence alignment of beta-synucleins

```
tr|F6T1V6|F6T1V6_MONDO            MDMFMKGLSMAK--EGVVA--AAEKTKQGVTE-------AAEKTKEGVLYVGSEIRSKDR    49
NP_990002.1                       MEVFMKGLSKAK--EGVVA--AAEKTKQGVAE-------AAEKTKEGVLYVGSKT-QGVV    48
tr|Q6GQG2|Q6GQG2_XENLA            MDVFMKGFSKAK--EGVVA--AAEKTKQGVAE-------AAEKTKEGVLYVGNKTRDGVV    49
XP_038626735.1                    MDMFMKGLNMAK--EGVVA--AAEKTKQGVTE-------AAEKTKEGVLYVGNRTREGVV    49
tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA    MDVLMKGLSKAK--EGMAA--AAEKTKEGV-------AVAAEKTKEGVLYVGNMTKEGVV    49
tr|A0A7N9I9A4|A0A7N9I9A4_MACFA    ------GPATQAPDPGPIPTPAPSPPRPGLAEPPRPPAAATVPSPAPAPHPGSKTREGVV    54
sp|Q16143|SYUB_HUMAN              MDVFMKGLSM--AKEGVVA--AAEKTKQGVTE-------AAEKTKEGVLYVGSKTREGVV    49
sp|Q91ZZ3|SYUB_MOUSE              MDVFMKGLSM--AKEGVVA--AAEKTKQGVTE-------AAEKTKEGVLYVGSKT-SGVV    48
tr|K7FSI4|K7FSI4_PELSI            ----------------------------------------------------------    0


tr|F6T1V6|F6T1V6_MONDO            ARGSGSVVRDQSNESTEGITMGGIRGDDGSSVGVGRVLVKSSQW-WHGIPEEVGQEVGEE   108
NP_990002.1                       -QGVTSVAEKA-KE--QASQLGEAAFSGAGNIAAATGLVKKEEFPADLKAEEVAQEAVEE   104
tr|Q6GQG2|Q6GQG2_XENLA            -QGVTSVAEKT-KE--QASHLGGAVMSGAGNIAAATGLVKKDEFPTDLKPEEEAQEALEE   105
XP_038626735.1                    -QSVASVAEKT-KE--QASQLGGAVFSGAGNIAAATGLMKKEDLPADVKPEEVGQEAGEE   105
tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA    -QGVASVAEKT-KE--QASQLGGAVFSGAGNIAAATGLMKKEEFPTDIKPEELGQEAVEE   105
tr|A0A7N9I9A4|A0A7N9I9A4_MACFA    -QGVASVAEKT-KE--QASHLGGAVFSGAGNIAAATGLVKREEFPTDLKPEEVAQEAAEE   110
sp|Q16143|SYUB_HUMAN              -QGVASVAEKT-KE--QASHLGGAVFSGAGNIAAATGLVKREEFPTDLKPEEVAQEAAEE   105
sp|Q91ZZ3|SYUB_MOUSE              -QGVASVAEKT-KE--QASHLGGAVFSGAGNIAAATGLVKKEEFPTDLKPEEVAQEAAEE   104
tr|K7FSI4|K7FSI4_PELSI            ------VAEKT-KE--QASQLGGAVMSGAGNIAAATGLVKKEEFPTDLKPEEVGQEAGEE    51
                                        *... :*  :. :*    .......:..  *:* .:  .   ** .**. **


tr|F6T1V6|F6T1V6_MONDO            PMAEPLLDTEGESYEEPPQEEYQEYEPEA    137
NP_990002.1                       PLVEPLLEPEGESYEESPQEEYQEYEPEA    133
tr|Q6GQG2|Q6GQG2_XENLA            PAAEPLLEPEGESYEDP-QDDYQEYEPEA    133
XP_038626735.1                    PLIEPLLEPEGESYEDPTQEEYQEYEPEA    134
tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA    PLGEPIMEPEGEAYEEAPQDEYQEYEPEA    134
tr|A0A7N9I9A4|A0A7N9I9A4_MACFA    PLIEPLMEPEGESYEDPPQEEYQEYEPEA    139
sp|Q16143|SYUB_HUMAN              PLIEPLMEPEGESYEDPPQEEYQEYEPEA    134
sp|Q91ZZ3|SYUB_MOUSE             PLIEPLMEPEGESYEDSPQEEYQEYEPEA    133
tr|K7FSI4|K7FSI4_PELSI            PLSEPLLEPEGEAYEEPPQ----------    70
                                  *  **::: ***:**:  *
```

Percent Identity Matrix - created by Clustal 2.1

```
#
 1: tr|F6T1V6|F6T1V6_MONDO           100.00    58.33    57.58    60.90    52.67    38.58    61.07    60.77    44.93
 2: NP_990002.1                       58.33   100.00    84.85    81.95    81.68    67.72    87.02    88.55    84.29
 3: tr|Q6GQG2|Q6GQG2_XENLA            57.58    84.85   100.00    81.95    80.92    68.50    87.79    87.69    86.96
 4: XP_038626735.1                    60.90    81.95    81.95   100.00    81.82    67.19    87.88    87.02    85.71
 5: tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA    52.67    81.68    80.92    81.82   100.00    65.62    83.85    84.50    87.14
 6: tr|A0A7N9I9A4|A0A7N9I9A4_MACFA    38.58    67.72    68.50    67.19    65.62   100.00    78.12    75.59    87.14
 7: sp|Q16143|SYUB_HUMAN              61.07    87.02    87.79    87.88    83.85    78.12   100.00    97.74    87.14
 8: sp|Q91ZZ3|SYUB_MOUSE              60.77    88.55    87.69    87.02    84.50    75.59    97.74   100.00    87.14
 9: tr|K7FSI4|K7FSI4_PELSI            44.93    84.29    86.96    85.71    87.14    87.14    87.14    87.14   100.00
```

tr|F6T1V6|F6T1V6_MONDO
XP_038626735.1
sp|Q16143|SYUB_HUMAN
sp|Q91ZZ3|SYUB_MOUSE
NP_990002.1
tr|Q6GQG2|Q6GQG2_XENLA
tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA
tr|A0A7N9I9A4|A0A7N9I9A4_MACFA
tr|K7FSI4|K7FSI4_PELSI

Supplementary Figure S3. CLUSTAL O(1.2.4) multiple sequence alignment of gamma-synucleins

```
tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA      MDVFKKGFSMAKEGVVAAAEKTKHGVEEAAAKTKEGVMYVGTKTKEGVAHSVNAVAEKTK   60
tr|Q7SYT8|Q7SYT8_XENLA              MDVFKKGFSMAKEGVVAAAEKTKQGVTEAAEKTKEGVMYVGAKTKEGVVHSVNTVAEKTK   60
tr|Q9I9H0|Q9I9H0_CHICK              MDVFKKGFSIAKEGVVAAAEKTKQGVTEAAEKTKEGVMYVGTKTKEGVVQSVTSVAEKTK   60
tr|K7FIG2|K7FIG2_PELSI              MDVFKKGFSIAKEGVVAAAEKTKQGVTEAAEKTKEGVMYVGAKTKEGVVHSVSSVAEKTK   60
XP_038599981.1                      MDVFKKGFSIAMDGVVAAAEKTKQGVTEAAEKTKEGVMYVGTKTKEGVVQSVSSVAEKTK   60
tr|A0A5F8G4U8|A0A5F8G4U8_MONDO      MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGTKTKEGVVQSVTSVAEKTK   60
sp|Q9Z0F7|SYUG_MOUSE                MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGTKTKENVVQSVTSVAEKTK   60
sp|O76070|SYUG_HUMAN                MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKTKENVVQSVTSVAEKTK   60
tr|G7PEV7|G7PEV7_MACFA              MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGTKTKENVVHSVTSVAEKTK   60
                                    *********:* :***.*.****:** *** **********:****.*.:**.:******


tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA      EQANIVGDAVVSSATQVSAKTVEGVENVAATGGLIKKDEQEGELVQNPAENESEED---A   117
tr|Q7SYT8|Q7SYT8_XENLA              EQANVVGGAVVSGVNQVSSKTVEGTENVVSSTGLVKKEDLHPDQPEE-PAAE-EPAVEAT  118
tr|Q9I9H0|Q9I9H0_CHICK              EQANVVGEAVVASVNTVANKTVEGAETIVATTGVVKKEDLAPQQPAAE----GEAAIP--  114
tr|K7FIG2|K7FIG2_PELSI              EQANMVGEAVVASVNTVAGKTVEGAENIVTTTGIVKKEELSHPEHPAEPAAAEEEPPA--  118
XP_038599981.1                      EQASAVSEAMVASVNTVASKTVEGAESIVVTAGVVKKEDLLRPDQLEEAAAEENPAEAPA  120
tr|A0A5F8G4U8|A0A5F8G4U8_MONDO      EQANLVSDVMVASVNTVANKTVEEAENIVVTSGIVRKEDLVNPAQPEHGAPEEQPAEAAE  120
sp|Q9Z0F7|SYUG_MOUSE                EQANAVSEAVVSSVNTVANKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEENE----  116
sp|O76070|SYUG_HUMAN                EQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRPSAPQQEGEASKEKEEVAE  120
tr|G7PEV7|G7PEV7_MACFA              EQANAVSEAVVSSVNTVAAKTVEEAENIAVTSGVVRKEDLKPSAPQQEGEAAKEKEEVAE  120
                                    ***. *. .:*:... *: **** .*.:. : *:::*::            :


tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA      QAAEQVGN----------------------------------------------------  125
tr|Q7SYT8|Q7SYT8_XENLA              ESIEQVGDGEN-------------------------------------------------  129
tr|Q9I9H0|Q9I9H0_CHICK              GSTEGGGEGENEGN----------------------------------------------  128
tr|K7FIG2|K7FIG2_PELSI              EDIKATGEGESESN----------------------------------------------  132
XP_038599981.1                      EVPEATEKEDNGGN----------------------------------------------  134
tr|A0A5F8G4U8|A0A5F8G4U8_MONDO      VT-------EEVGAPDAFFPLSPGLDRFSLFSPLLPASWASVTAAIRGAEEKGFPPCGLF  173
sp|Q9Z0F7|SYUG_MOUSE                EA-------KSGED----------------------------------------------  123
sp|O76070|SYUG_HUMAN                EA-------QSGGD----------------------------------------------  127
tr|G7PEV7|G7PEV7_MACFA              EA-------QSGGD----------------------------------------------  127


tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA      ----------        125
tr|Q7SYT8|Q7SYT8_XENLA              ----------        129
tr|Q9I9H0|Q9I9H0_CHICK              ----------        128
tr|K7FIG2|K7FIG2_PELSI              ----------        132
XP_038599981.1                      ----------        134
tr|A0A5F8G4U8|A0A5F8G4U8_MONDO      SLLLSPFILP        183
sp|Q9Z0F7|SYUG_MOUSE                ----------        123
sp|O76070|SYUG_HUMAN                ----------        127
tr|G7PEV7|G7PEV7_MACFA              ----------        127
```
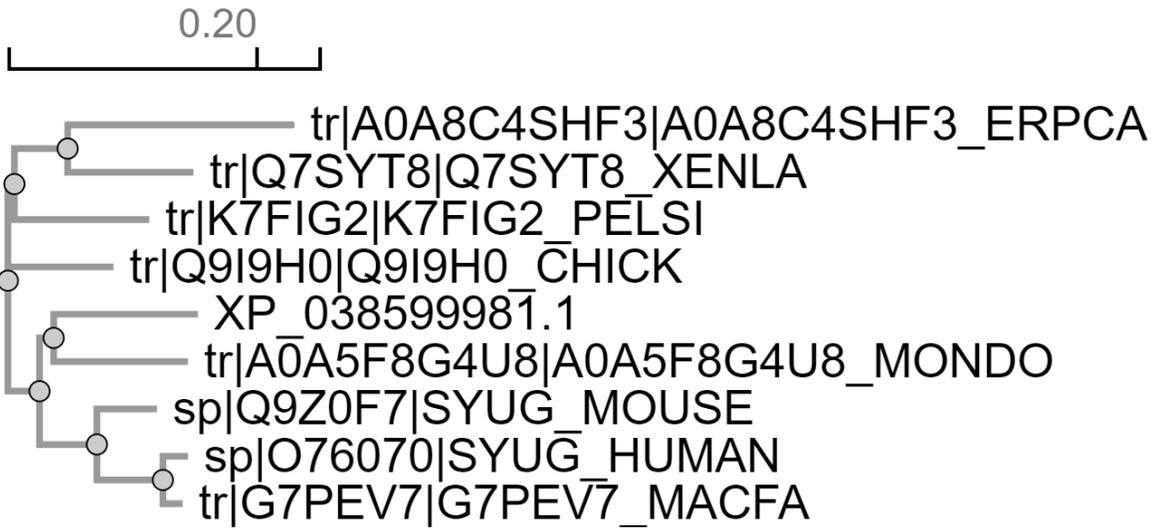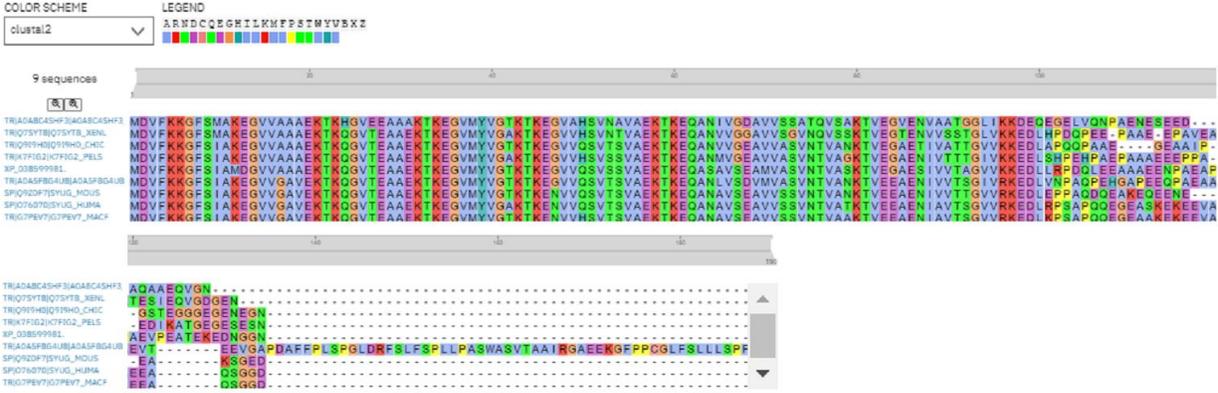
Percent Identity Matrix - created by Clustal 2.1

```
    1: tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA   100.00   69.11   64.17   62.90   57.60   57.98   61.86   61.34   63.87
    2: tr|Q7SYT8|Q7SYT8_XENLA            69.11  100.00   76.42   73.23   66.67   67.21   68.64   68.03   68.03
    3: tr|Q9I9H0|Q9I9H0_CHICK            64.17   76.42  100.00   78.12   74.22   74.38   78.15   75.21   75.21
    4: tr|K7FIG2|K7FIG2_PELSI            62.90   73.23   78.12  100.00   72.73   72.00   73.98   71.20   72.00
    5: XP_038599981.1                    57.60   66.67   74.22   72.73  100.00   75.59   75.61   70.87   70.87
    6: tr|A0A5F8G4U8|A0A5F8G4U8_MONDO    57.98   67.21   74.38   72.00   75.59  100.00   78.05   75.59   75.59
    7: sp|Q9Z0F7|SYUG_MOUSE              61.86   68.64   78.15   73.98   75.61   78.05  100.00   86.99   86.99
    8: sp|O76070|SYUG_HUMAN              61.34   68.03   75.21   71.20   70.87   75.59   86.99  100.00   96.06
    9: tr|G7PEV7|G7PEV7_MACFA            63.87   68.03   75.21   72.00   70.87   75.59   86.99   96.06  100.00
```

Supplementary Figure S4. CLUSTAL O(1.2.4) multiple sequence alignment of all synucleins

```
tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA      ---------MDVFKKGFSMAKEGVVAAAEKTKHGVEEAAAKTKEGVMYVGTKTKEGVA-H      50
tr|Q7SYT8|Q7SYT8_XENLA              ---------MDVFKKGFSMAKEGVVAAAEKTKQGVTEAAEKTKEGVMYVGAKTKEGVV-H      50
tr|Q9I9H0|Q9I9H0_CHICK              ---------MDVFKKGFSIAKEGVVAAAEKTKQGVTEAAEKTKEGVMYVGTKTKEGVV-Q      50
tr|K7FIG2|K7FIG2_PELSI              ---------MDVFKKGFSIAKEGVVAAAEKTKQGVTEAAEKTKEGVMYVGAKTKEGVV-H      50
XP_038599981.1                      ---------MDVFKKGFSIAMDGVVAAAEKTKQGVTEAAEKTKEGVMYVGTKTKEGVV-Q      50
tr|A0A5F8G4U8|A0A5F8G4U8_MONDO      ---------MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGTKTKEGVV-Q      50
sp|Q9Z0F7|SYUG_MOUSE                ---------MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGTKTKENVV-Q      50
sp|O76070|SYUG_HUMAN                ---------MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKTKENVV-Q      50
tr|G7PEV7|G7PEV7_MACFA              ---------MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGTKTKENVV-H      50
tr|F6T1V6|F6T1V6_MONDO              ---------MDMFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGSEIRSKDRAR      51
tr|Q6GQG2|Q6GQG2_XENLA              ---------MDVFMKGFSKAKEGVVAAAEKTKQGVAEAAEKTKEGVLYVGNKTRDGVV-Q      50
XP_038626735.1                      ---------MDMFMKGLNMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGNRTREGVV-Q      50
NP_990002.1                         ---------MEVFMKGLSKAKEGVVAAAEKTKQGVAEAAEKTKEGVLYVGSKT-QGVV-Q      49
sp|Q16143|SYUB_HUMAN                ---------MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGSKTREGVV-Q      50
sp|Q91ZZ3|SYUB_MOUSE                ---------MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGSKT-SGVV-Q      49
tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA      ---------MDVLMKGLSKAKEGMAAAAEKTKEGVAVAAEKTKEGVLYVGNMTKEGVV-Q      50
tr|A0A7N9I9A4|A0A7N9I9A4_MACFA      GPATQAPDPGPIPTPAPSPPRPGLAEPPRP----PAAATVPSPAPAPHPGSKTREGVV-Q      55
tr|K7FSI4|K7FSI4_PELSI              ------------------------------------------------------------       0
tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA      ---------MDVLMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVMYVGTKTKDG----      47
tr|Q7SZ02|Q7SZ02_XENLA              ---------MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGV-H      50
sp|O55042|SYUA_MOUSE                ---------MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGV-H      50
sp|P37840|SYUA_HUMAN                ---------MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGV-H      50
tr|G7P5X2|G7P5X2_MACFA              ---------MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGV-H      50
tr|Q9I9H1|Q9I9H1_CHICK              ---------MDVFMKGLNKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSRTKEGVV-H      50
tr|K7FW98|K7FW98_PELSI              ---------MDVFMKGLSKAKEGVVAAAEKTKQGMAEAAGKTKEGVLYVGSRTREGVV-H      50


tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA      SVNAVAEKTKEQANIVGDAVVSSATQVSAKTVEGVENVAATGGLIKKDEQEGELVQNPAE     110
tr|Q7SYT8|Q7SYT8_XENLA              SVNTVAEKTKEQANVVGGAVVSGVNQVSSKTVEGTENVVSSTGLVKKEDLHPDQPEE-PA     109
tr|Q9I9H0|Q9I9H0_CHICK              SVTSVAEKTKEQANVVGEAVVASVNTVANKTVEGAETIVATTGVVKKEDLAPQQPAAE--     108
tr|K7FIG2|K7FIG2_PELSI              SVSSVAEKTKEQANMVGEAVVASVNTVAGKTVEGAENIVTTTGIVKKEELSHPEHPAEPA     110
XP_038599981.1                      SVSSVAEKTKEQASAVSEAMVASVNTVASKTVEGAESIVVTAGVVKKEDLLRPDQLEEAA     110
tr|A0A5F8G4U8|A0A5F8G4U8_MONDO      SVTSVAEKTKEQANLVSDVMVASVNTVANKTVEEAENIVVTSGIVRKEDLVNPAQPEHGA     110
sp|Q9Z0F7|SYUG_MOUSE                SVTSVAEKTKEQANAVSEAVVSSVNTVANKTVEGVIVTTGVVRKEDLEPPAQDQEAK      110
sp|O76070|SYUG_HUMAN                SVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRPSAPQQEGE     110
tr|G7PEV7|G7PEV7_MACFA              SVTSVAEKTKEQANAVSEAVVSSVNTVAAKTVEEAENIAVTSGVVRKEDLKPSAPQQEGE     110
tr|F6T1V6|F6T1V6_MONDO              GSGSVVRDQSNE--STEGITMGGIRGD------DGSSVGVGRVLVKSSQWWH-GIPEEVG     102
tr|Q6GQG2|Q6GQG2_XENLA              GVTSVAEKTKEQASHLGGAVMS----------GAGNIAAATGLVKKDEFPTDLKPEEEA      99
XP_038626735.1                      SVASVAEKTKEQASQLGGAVFS----------GAGNIAAATGLMKKEDLPADVKPEEVG      99
NP_990002.1                         GVTSVAEKAKEQASQLGEAAFS----------GAGNIAAATGLVKKEEFPADLKAEEVA      98
sp|Q16143|SYUB_HUMAN                GVASVAEKTKEQASHLGGAVFS----------GAGNIAAATGLVKREEFPTDLKPEEVA      99
sp|Q91ZZ3|SYUB_MOUSE                GVASVAEKTKEQASHLGGAVFS----------GAGNIAAATGLVKREEFPTDLKPEEVA      98
tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA      GVASVAEKTKEQASQLGGAVFS----------GAGNIAAATGLMKKEEFPTDIKPEELG      99
tr|A0A7N9I9A4|A0A7N9I9A4_MACFA      GVASVAEKTKEQASHLGGAVFS----------GAGNIAAATGLVKREEFPTDLKPEEVA     104
tr|K7FSI4|K7FSI4_PELSI              ----VAEKTKEQASQLGGAVMS----------GAGNIAAATGLVKKEEFPTDLKPEEVG      45
tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA      -VTSVAEKTKEQVSNVGGAVVTGVTAVAHKTVEGAGNIAAATGLVKRDHLGKQN-EDMLS     105
tr|Q7SZ02|Q7SZ02_XENLA              GVTTVAEKTKEQVSNVGGAVVTGVTAVAHKTVEGAGNFAAATGLVKKDQK---N-ESGFG     106
sp|O55042|SYUA_MOUSE                GVTTVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGNIAAATGFVKKDQMGK-G-EEGYP     108
sp|P37840|SYUA_HUMAN                GVATVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGK-N-EEGAP     108
tr|G7P5X2|G7P5X2_MACFA              GVATVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFIKKDQLGK-N-EEGAP     108
tr|Q9I9H1|Q9I9H1_CHICK              GVTTVAEKTKEQVSNVGGAVVTGVTAVAQKTVEGAGNIAAATGLVKKDQLAKQN-EEGFL     109
tr|K7FW98|K7FW98_PELSI              GVTTMAEKTKEQVSNVGGAVVTGVTAVAHKTVEGAGNIAAATGLVKKDQMAKQN-EEGLS     109
                                      :... .::       .                  ..       .:: ..


tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA      NESEED---AQAAEQVGN----------------------------------------     125
tr|Q7SYT8|Q7SYT8_XENLA              AE-EPAVEATESIEQVGDGEN-------------------------------------     129
tr|Q9I9H0|Q9I9H0_CHICK              --GEAAIP--GSTEGGGEGENEGN----------------------------------     128
tr|K7FIG2|K7FIG2_PELSI              AAEEEPPA--EDIKATGEGESESN----------------------------------     132
XP_038599981.1                      AEENPAEAPAEVPEATEKEDNGGN----------------------------------     134
tr|A0A5F8G4U8|A0A5F8G4U8_MONDO      PEEQPAEAAEVT------EEVGAPDAFFPLSPGLDRFSLFSPLLPASWASVTAAIRGAE     163
sp|Q9Z0F7|SYUG_MOUSE                EQEENE----EA-------KSGED----------------------------------     123
sp|O76070|SYUG_HUMAN                ASKEKEEVAEEA-------QSGGD----------------------------------     127
tr|G7PEV7|G7PEV7_MACFA              AAKEKEEVAEEA-------QSGGD----------------------------------     127
tr|F6T1V6|F6T1V6_MONDO              QEVGEEPMAEPLLDTEGESYEE----------PPQEEYQEYEPEA-------------     137
tr|Q6GQG2|Q6GQG2_XENLA              QEALEEPAAEPLLEPEGESYED----------PQDDYQEYEPEA-------------     133
XP_038626735.1                      QEAGEEPLIEPLLEPEGESYED----------PTQEEYQEYEPEA-------------     134
NP_990002.1                         QEAVEEPLVEPLLEPEGESYEE----------SPQEEYQEYEPEA-------------     133
sp|Q16143|SYUB_HUMAN                QEAAEEPLIEPLMEPEGESYED----------PPQEEYQEYEPEA-------------     134
```

```
sp|Q91ZZ3|SYUB_MOUSE                QEAAEEPLIEPLMEPEGESYED---------SPQEEYQEYEPEA--------------    133
tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA      QEAVEEPLGEPIMEPEGEAYEE---------APQDEYQEYEPEA--------------    134
tr|A0A7N9I9A4|A0A7N9I9A4_MACFA      QEAEEEPLIEPLMEPEGESYED---------PPQEEYQEYEPEA--------------    139
tr|K7FSI4|K7FSI4_PELSI              QEAGEEPLSEPLLEPEGEAYEE---------PPQ-----------------------    70
tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA      QEGLMDNTADYPLDPD-DTYDM---------PPEDDCQEYQPNA--------------    139
tr|Q7SZ02|Q7SZ02_XENLA              PEGTMENSENMPVNPNNETYEM---------PPEEEYQDYDPEA--------------    141
sp|O55042|SYUA_MOUSE                QEGIL-E--DMPVDPGSEAYEM---------PSEEGYQDYEPEA--------------    140
sp|P37840|SYUA_HUMAN                QEGIL-E--DMPVDPNEAYEM---------PSEEGYQDYEPEA--------------    140
tr|G7P5X2|G7P5X2_MACFA              QEGIL-Q--DMPVDPNEAYEM---------PSEEGYQDYEPEA--------------    140
tr|Q9I9H1|Q9I9H1_CHICK              QEGMV-NNTDIPVDPENEAYEM---------PPEEEYQDYEPEA--------------    143
tr|K7FW98|K7FW98_PELSI              QEGMM-DSTDMPMDPDNEAYEM---------PPEEEYQDYEPEA--------------    143


tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA      --------------------    125
tr|Q7SYT8|Q7SYT8_XENLA              --------------------    129
tr|Q9I9H0|Q9I9H0_CHICK              --------------------    128
tr|K7FIG2|K7FIG2_PELSI              --------------------    132
XP_038599981.1                      --------------------    134
tr|A0A5F8G4U8|A0A5F8G4U8_MONDO      EKGFPPCGLFSLLLSPFILP    183
sp|Q9Z0F7|SYUG_MOUSE                --------------------    123
sp|O76070|SYUG_HUMAN                --------------------    127
tr|G7PEV7|G7PEV7_MACFA              --------------------    127
tr|F6T1V6|F6T1V6_MONDO              --------------------    137
tr|Q6GQG2|Q6GQG2_XENLA              --------------------    133
XP_038626735.1                      --------------------    134
NP_990002.1                         --------------------    133
sp|Q16143|SYUB_HUMAN                --------------------    134
sp|Q91ZZ3|SYUB_MOUSE                --------------------    133
tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA      --------------------    134
tr|A0A7N9I9A4|A0A7N9I9A4_MACFA      --------------------    139
tr|K7FSI4|K7FSI4_PELSI              --------------------    70
tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA      --------------------    139
tr|Q7SZ02|Q7SZ02_XENLA              --------------------    141
sp|O55042|SYUA_MOUSE                --------------------    140
sp|P37840|SYUA_HUMAN                --------------------    140
tr|G7P5X2|G7P5X2_MACFA              --------------------    140
tr|Q9I9H1|Q9I9H1_CHICK              --------------------    143
tr|K7FW98|K7FW98_PELSI              --------------------    143
```

```
#  Percent Identity  Matrix - created by Clustal2.1
#
#
    1: tr|A0A8C4SHF3|A0A8C4SHF3_ERPCA  100.00   69.11   64.17   62.90   57.60   57.98   61.86   61.34   63.87   35.34   59.65   56.14   55.75   58.77   59.29   54.39   32.73   45.00   57.98   58.68   57.38   57.38   58.20   56.10   54.47
    2: tr|Q7SYT8|Q7SYT8_XENLA           69.11  100.00   76.42   73.23   66.67   67.21   68.64   68.03   68.03   40.00   61.02   61.02   57.26   61.86   62.39   55.08   34.21   43.75   59.35   60.80   61.29   61.29   60.48   59.84   57.48
    3: tr|Q9I9H0|Q9I9H0_CHICK           64.17   76.42  100.00   78.12   74.22   74.38   78.15   75.21   75.21   37.61   61.74   61.74   62.28   61.74   62.28   57.39   34.23   44.26   61.67   60.66   62.30   61.48   60.66   61.29   58.87
    4: tr|K7FIG2|K7FIG2_PELSI           62.90   73.23   78.12  100.00   72.73   72.00   73.98   71.20   72.00   39.67   62.18   59.66   60.17   62.18   62.71   57.14   35.65   46.15   56.45   57.94   58.73   58.73   57.94   57.03   54.69
    5: XP_038599981.1                   57.60   66.67   74.22   72.73  100.00   75.59   75.61   70.87   70.87   34.96   55.37   54.55   54.17   55.37   55.83   49.59   30.77   34.33   53.17   52.34   54.33   56.69   55.12   52.31   50.00
    6: tr|A0A5F8G4U8|A0A5F8G4U8_MONDO   57.98   67.21   74.38   72.00   75.59  100.00   78.05   75.59   75.59   35.66   54.76   51.97   50.00   52.76   52.38   47.24   29.27   34.92   51.88   51.49   53.38   52.63   51.13   50.74   48.53
    7: sp|Q9Z0F7|SYUG_MOUSE             61.86   68.64   78.15   73.98   75.61   78.05  100.00   86.99   86.99   35.71   58.18   58.18   56.88   58.18   58.72   52.73   31.13   39.29   56.90   57.26   56.78   56.78   55.93   55.46   52.94
    8: sp|O76070|SYUG_HUMAN             61.34   68.03   75.21   71.20   70.87   75.59   86.99  100.00   96.06   36.21   57.89   57.02   55.75   57.02   57.52   51.75   30.91   38.33   55.00   55.37   56.67   55.83   54.17   53.66   51.22
    9: tr|G7PEV7|G7PEV7_MACFA           63.87   68.03   75.21   72.00   70.87   75.59   86.99   96.06  100.00   36.21   57.02   56.14   54.87   56.14   56.64   50.88   30.00   38.33   55.83   55.37   56.67   57.50   56.67   54.47   52.03
   10: tr|F6T1V6|F6T1V6_MONDO           35.34   40.00   37.61   39.67   34.96   35.66   35.71   36.21   36.21  100.00   57.69   60.31   57.69   61.07   60.77   51.15   34.65   44.78   42.31   46.62   46.97   46.97   46.21   47.76   47.01
   11: tr|Q6GQG2|Q6GQG2_XENLA           59.65   61.02   61.74   62.18   55.37   54.76   58.18   57.89   57.02   57.69  100.00   81.20   85.61   81.20   81.20   65.12   36.96   67.72   61.72   67.44   67.97   66.41   65.62   67.94   67.18
   12: XP_038626735.1                   56.14   61.02   61.74   59.66   54.55   51.97   58.18   57.02   56.14   60.31   81.20  100.00   81.95   88.06   87.22   60.60   63.08   85.71   58.59   63.85   63.57   64.34   64.34   67.42   64.39
   13: NP_990002.1                      55.75   57.26   62.28   60.17   54.17   50.00   56.88   55.75   54.87   57.69   85.61   81.95  100.00   87.22   88.72   81.20   64.34   84.29   60.63   66.67   66.41   64.84   64.06   67.18   65.65
   14: sp|Q16143|SYUB_HUMAN             58.77   61.86   61.74   62.18   55.37   52.76   58.18   57.02   56.14   61.07   87.97   88.06   87.22  100.00   97.74   82.84   74.62   87.14   61.72   67.69   67.44   67.44   66.67   68.18   68.18
   15: sp|Q91ZZ3|SYUB_MOUSE             59.29   62.39   62.28   62.71   55.83   52.38   58.72   57.52   56.64   60.77   88.64   87.22   88.72   97.74  100.00   83.46   72.09   87.14   60.63   67.44   67.19   67.19   66.41   67.94   67.18
   16: tr|A0A8C4TNP5|A0A8C4TNP5_ERPCA   54.39   55.08   57.39   57.14   49.59   47.24   52.73   51.75   50.88   51.15   65.12   60.60   81.20   82.84   83.46  100.00   63.85   83.46   60.16   63.85   63.85   63.57   63.57   65.15   64.39
   17: tr|A0A7N9I9A4|A0A7N9I9A4_MACFA   32.73   34.21   34.23   35.65   30.77   29.27   31.13   30.91   30.00   34.65   65.12   63.08   64.34   74.62   72.09   63.85  100.00   87.14   38.71   43.65   43.20   43.20   42.40   44.53   45.31
   18: tr|K7FSI4|K7FSI4_PELSI           45.00   43.75   44.26   46.15   34.33   34.92   39.29   38.33   38.33   44.78   86.96   85.71   84.29   87.14   87.14   83.46   87.14  100.00   48.53   53.03   52.31   50.77   49.23   55.88   52.94
   19: tr|A0A8C4RPQ9|A0A8C4RPQ9_ERPCA   57.98   59.35   61.67   56.45   53.17   51.88   56.90   55.00   55.83   42.31   67.72   60.63   61.72   60.63   60.16   38.71   48.53  100.00   77.21   76.30   77.04   76.30   77.54   78.26
   20: tr|Q7SZ02|Q7SZ02_XENLA           58.68   60.80   60.66   57.94   52.34   51.49   57.26   55.37   56.20   46.62   67.44   63.85   66.67   67.69   67.44   63.85   43.65   53.03   77.21  100.00   84.78   84.78   84.06   87.14   86.43
   21: sp|O55042|SYUA_MOUSE             57.38   61.29   62.30   58.73   54.33   53.38   56.78   56.67   57.50   46.97   67.97   63.57   66.41   67.44   67.19   63.57   43.20   52.31   76.30   84.78  100.00   95.00   93.57   87.86   86.43
   22: sp|P37840|SYUA_HUMAN             57.38   61.29   61.48   58.73   56.69   52.63   56.78   55.83   56.67   46.97   66.41   64.34   64.84   67.44   67.19   63.57   43.20   50.77   77.04   84.78   95.00  100.00   98.57   88.57   86.43
   23: tr|G7P5X2|G7P5X2_MACFA           58.20   60.48   60.66   57.94   55.12   51.13   55.93   54.17   55.00   46.21   65.62   64.34   64.06   66.67   66.41   63.57   42.40   49.23   76.30   84.06   93.57   98.57  100.00   87.86   85.71
   24: tr|Q9I9H1|Q9I9H1_CHICK           56.10   59.84   61.29   57.03   52.31   50.74   55.46   53.66   54.47   47.76   67.94   67.42   67.18   68.18   67.94   65.15   44.53   55.88   77.54   87.14   87.86   88.57   87.86  100.00   90.21
   25: tr|K7FW98|K7FW98_PELSI           54.47   57.48   58.87   54.69   50.00   48.53   52.94   51.22   52.03   47.01   67.18   64.39   65.65   68.18   67.18   64.39   45.31   52.94   78.26   86.43   86.43   86.43   85.71   90.21  100.00
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