Sequence attributes of 500 FKBDs of the FKBPs from disparate species.

In sectors: A is given code and sequence length; in B sequence indexes of the aligned FKBD and its length; in C are given the theoretical pI of the FKBD and the pI of the entire sequence (in parentheses); in sector D is the overall hydrophobicity index (HI) for the FKBD and the entire sequence (in parentheses); in sector E is the mass of the aligned FKBD and of that of the entire sequence (in parentheses).

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60 XP_001623432 | 100 | 1-100 | Alg = 100AA | pI 9.2 (9.2) | HI 27.0 (27.0) | Mass kDa 9.8 (9.8) | Predicted protein [Nematostella vectensis]. |
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| EDO44761 | 214 | 38-145 | Alg = 108AA | pI 5.0 (4.4) | HI 50.9 (37.9) | Mass kDa 12.1 (24.4) | Predicted protein [Nematostella vectensis]. |
| EDO44176 | 400 | 120-224 | Alg = 105AA | pI 8.1 (4.9) | HI 32.4 (20.8) | Mass kDa 11.9 (45.8) | Predicted protein [Nematostella vectensis]. |
| EDO44175 | 326 | 10-124 | Alg = 115AA | pI 8.8 (6.7) | HI 21.7 (25.5) | Mass kDa 13.4 (37.6) | Predicted protein [Nematostella vectensis]. |
| XP_001623432 | 100 | 1-100 | Alg = 100AA | pI 9.1 (9.1) | HI 22.0 (22.0) | Mass kDa 10.7 (10.7) | Predicted protein [Nematostella vectensis]. |</p>
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> PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP4 [Xenopus evskii].
> 108AAs | 3-108/Alg =106AA || pI 7.3 ( 7.3) || HI 23.6 ( 24.1) || Mass kDa 11.4 ( 11.6) |
> > FK506 binding protein [Saccoglossus kowalevskii].
> 108AAs | 3-108/Alg =106AA || pI 6.1 ( 6.1) || HI 23.6 ( 25.0) || Mass kDa 11.8 ( 12.0) |
> > FK506-binding protein 1A [Saccothrium dicrurum].
> 135AAs | 31-130/Alg =100AA || pI 5.2 ( 8.4) || HI 28.0 ( 31.9) || Mass kDa 11.1 ( 14.8) |
> > FK506-binding protein 2 [Culex quinquefasciatus].
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> > predicted protein [Micromonas pusilla CCMP1545].
> 108AAs | 3-108/Alg =106AA || pI 9.4 ( 9.3) || HI 24.5 ( 25.9) || Mass kDa 11.7 ( 11.9) |
> > predicted protein [Saccoglossus kowalevskii].
> 108AAs | 3-108/Alg =106AA || pI 9.2 ( 9.1) || HI 23.6 ( 24.1) || Mass kDa 11.5 ( 11.7) |
> > predicted protein [Saccothrium dicrurum].
> 108/Alg =106AA || pI 8.7 ( 8.6) || HI 35.8 ( 37.0) || Mass kDa 11.4 ( 11.5) |
> > fk506-binding protein [Aedes aegypti].
> 108AAs | 3-108/Alg =106AA || pI 8.7 ( 8.6) || HI 35.8 ( 37.0) || Mass kDa 11.4 ( 11.5) |
> > FK506 binding protein 10 [Xenopus laevis].
> 108AAs | 3-108/Alg =106AA || pI 8.8 ( 8.8) || HI 34.0 ( 35.2) || Mass kDa 11.4 ( 11.6) |
> > PREDICTED: similar to FK506-binding protein-like protein [Nasonia nigra].
> 130/Alg =100AA || pI 5.2 ( 5.2) || HI 24.5 ( 27.0) || Mass kDa 11.7 ( 68.4) |
> > unknown [Populus trichocarpa].
> 108AAs | 3-108/Alg =106AA || pI 9.6 ( 9.5) || HI 25.5 ( 26.9) || Mass kDa 11.8 ( 11.9) |
> > FK506-binding protein 1A-like [Bos taurus].
> 134AAs | 27-134/Alg =108AA || pI 7.0 ( 9.9) || HI 39.8 ( 41.0) || Mass kDa 11.6 ( 14.6) |
> > macrolide-binding protein FKBP12 [Cryptococcus gattii WM276].
> 108AAs | 3-108/Alg =106AA || pI 5.7 ( 5.7) || HI 37.7 ( 38.0) || Mass kDa 11.3 ( 11.5) |
> > predicted protein [Micromonas sp. RCC299].
> 139AAs | 35-134/Alg =100AA || pI 5.2 ( 8.0) || HI 29.0 ( 35.3) || Mass kDa 11.0 ( 15.2) |
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256 XP_002992143 593AAs | 38-144/Alg =107AA || pI 5.2 ( 5.3) || HI 29.0 ( 30.2) || Mass kDa 11.6 ( 65.9) || > hypothetical protein SELMODRAFT_134839 [Selaginella

257 ACY69949 109AAs | 3-108/Alg =106AA || pI 7.2 ( 7.1) || HI 33.0 ( 33.9) || Mass kDa 11.6 ( 11.9) || > FK506-binding protein 2 [Cimex lectularius].

258 NP_001052535 585AAs | 50-156/Alg =107AA || pI 5.0 ( 5.2) || HI 23.4 ( 25.1) || Mass kDa 11.8 ( 65.6) || > Os04g0352400 [Oryza sativa Japonica Group].

259 XP_002865651 570AAs | 46-152/Alg =107AA || pI 5.6 ( 5.0) || HI 25.2 ( 24.7) || Mass kDa 11.9 ( 64.2) || > hypothetical protein ARALYDRAFT_494919 [Arabidopsis lyrata subsp.

260 XP_534923 459AAs | 31-137/Alg =107AA || pI 5.2 ( 5.3) || HI 41.1 ( 25.5) || Mass kDa 11.8 ( 51.5) || > PREDICTED: similar to FK506-binding protein 4 (Peptidyl-prolyl

261 ABM55671 109AAs | 3-108/Alg =106AA || pI 8.2 ( 8.2) || HI 30.2 ( 32.1) || Mass kDa 11.5 ( 11.8) || > FK506-binding protein-like protein [Maconellicoccus hirsutus].

262 NP_001021722 108AAs | 3-108/Alg =106AA || pI 9.3 ( 9.2) || HI 31.1 ( 32.4) || Mass kDa 11.5 ( 11.6) || > FK506-Binding protein family member (fkb-2) [Caenorhabditis

263 XP_643718 107AAs | 3-107/Alg =105AA || pI 9.9 ( 9.9) || HI 40.0 ( 41.1) || Mass kDa 11.1 ( 11.2) || > FKBP-type peptidylprolyl cis-trans isomerase [Dictyostelium

264 AAD01594 137AAs | 33-132/Alg =100AA || pI 4.7 ( 4.7) || HI 33.0 ( 37.2) || Mass kDa 11.1 ( 15.3) || > FKBP-like protein - Dirofilaria immitis

265 ACO09466 448AAs | 28-134/Alg =107AA || pI 5.7 ( 5.1) || HI 43.0 ( 22.5) || Mass kDa 11.6 ( 50.1) || > FK506-binding protein 4 [Osmerus mordax].

266 NP_958877 449AAs | 26-132/Alg =107AA || pI 5.7 ( 4.9) || HI 47.7 ( 26.1) || Mass kDa 11.6 ( 50.5) || > FK506 binding protein 4 [Danio rerio].

267 AAD01595 137AAs | 33-132/Alg =100AA || pI 5.2 ( 5.8) || HI 26.0 ( 32.8) || Mass kDa 11.2 ( 15.3) || > FKBP-like protein - Brugia malayi

268 YP_001504616 108AAs | 1-108/Alg =108AA || pI 4.9 ( 4.9) || HI 38.0 ( 38.0) || Mass kDa 11.7 ( 11.7) || > peptidylprolyl isomerase [Frankia sp. EAN1pec].

269 XP_002535081 574AAs | 40-146/Alg =107AA || pI 4.7 ( 5.1) || HI 26.2 ( 28.6) || Mass kDa 11.7 ( 64.0) || > peptidylprolyl isomerase, putative [Lamprichthys communis].

270 O94746 108AAs | 1-108/Alg =108AA || pI 5.6 ( 5.6) || HI 39.8 ( 39.8) || Mass kDa 11.6 ( 11.6) || > RecName: Full=FK506-binding protein 1; Short=FKBP; AltName:

271 XP_002993334 569AAs | 54-160/Alg =107AA || pI 9.3 ( 7.5) || HI 34.6 ( 31.8) || Mass kDa 11.8 ( 63.2) || > hypothetical protein SELMODRAFT_449100 [Selaginella

272 NP_001151484 677AAs | 90-196/Alg =107AA || pI 4.6 ( 5.1) || HI 27.1 ( 29.7) || Mass kDa 11.7 ( 74.6) || > LOC100285117 [Zea mays].

273 DAA29159 459AAs | 31-137/Alg =107AA || pI 5.2 ( 5.2) || HI 44.9 ( 24.4) || Mass kDa 11.9 ( 51.6) ||
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308 AA155100 138AAs | 34-133/Alg =100AA || pI 5.2 (9.5) || HI 28.0 (32.6) || Mass kDa 11.0 (15.2) ||> 
Zgc:101826 protein [Danio rerio].

309 XP_001889498 108AAs | 1-108/Alg =108AA || pI 5.7 (5.7) || HI 39.8 (39.8) || Mass kDa 11.6 (11.6) ||> 
predicted protein [Laccaria bicolor S238N-H82].

310 YP_721230 203AAs | 96-202/Alg =107AA || pI 7.5 (4.8) || HI 41.1 (47.3) || Mass kDa 11.4 (21.6) ||> 
peptidylprolyl isomerase [Trichodesmium erythraeum IMS101].

311 XP_002491810 137AAs | 30-137/Alg =108AA || pI 5.7 (9.6) || HI 46.3 (41.6) || Mass kDa 11.8 (15.1) ||> 
Pep tidyl-prolyl cis-trans isomerase (PIIase), binds to the drugs

312 ACI66312 137AAs | 33-132/Alg =100AA || pI 5.2 (9.5) || HI 32.0 (35.0) || Mass kDa 10.9 (15.0) ||> 
FK506-binding protein 2 precursor [Salmo salar].

313 XP_002979133 569AAs | 25-131/Alg =107AA || pI 5.0 (7.6) || HI 38.3 (30.2) || Mass kDa 11.5 (63.2) ||> 
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315 XP_001268267 112AAs | 1-108/Alg =108AA || pI 5.0 (7.1) || HI 31.5 (32.1) || Mass kDa 11.4 (11.8) ||> 
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316 XP_002947775 617AAs | 61-168/Alg =108AA || pI 5.2 (4.7) || HI 30.6 (32.1) || Mass kDa 11.8 (66.8) ||> 
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317 XP_001937259 129AAs | 21-120/Alg =100AA || pI 7.1 (6.4) || HI 24.0 (31.8) || Mass kDa 10.9 (14.0) ||> 
FK506-binding protein 2 precursor [Pyrenophora tritici-repensis

318 XP_002541511 447AAs | 344-447/Alg =104AA || pI10.6 (4.3) || HI 32.7 (19.7) || Mass kDa 11.2 (48.9) ||> 
hypothetical protein UREG_01027 [Uncinocarpus reesii 1704].

319 XP_001014237 134AAs | 26-133/Alg =108AA || pI 8.6 (9.8) || HI 36.1 (35.8) || Mass kDa 11.9 (14.9) ||> 
FKBP12 binding protein [Tetrahymena thermophila].

320 ADY48621 137AAs | 33-132/Alg =100AA || pI 5.6 (8.9) || HI 23.0 (29.9) || Mass kDa 11.3 (15.5) ||> 
Peptidyl-prolyl cis-trans isomerase FKBP2 [Ascaris suum].

321 NP_001079493 141AAs | 37-136/Alg =100AA || pI 6.1 (9.2) || HI 28.0 (32.6) || Mass kDa 11.0 (15.7) ||> 
FK506 binding protein 2, 13KDa [Aspergillus luevis];

322 XP_001693615 108AAs | 1-107/Alg =107AA || pI 5.5 (6.1) || HI 33.6 (33.3) || Mass kDa 11.5 (11.7) ||> 
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323 ACI67147 137AAs | 33-132/Alg =100AA || pI 5.7 (9.7) || HI 28.0 (32.8) || Mass kDa 10.9 (15.0) ||> 
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324 XP_002634440 430AAs | 13-120/Alg =108AA || pI 9.2 (5.8) || HI 26.9 (22.6) || Mass kDa 11.6 (48.1) ||> 
C. briggsae CBR-FKB-6 protein [Caenorhabditis briggsae].

325 XP_001697315 143AAs | 34-141/Alg =108AA || pI 9.3 (9.9) || HI 23.1 (35.7) || Mass kDa 11.8 (15.5) ||
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**PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP1A-like**

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- **CBJ32617**: 18-122/Alg =105AA || pI 6.7 (5.3) || HI 34.3 (33.9) || Mass kDa 11.6 (13.4)
- **EPN72359**: 12-118/Alg =107AA || pI 5.3 (5.2) || HI 29.9 (22.4) || Mass kDa 11.6 (51.8)
- **CBY33816**: 2-109/Alg =108AA || pI 4.5 (4.7) || HI 33.3 (33.9) || Mass kDa 11.6 (12.1)
- **XP_002846777**: 375-478/Alg =104AA || pI 10.5 (4.2) || HI 28.8 (24.9) || Mass kDa 11.2 (52.0)
- **XP_002199016**: 31-137/Alg =107AA || pI 9.3 (6.0) || HI 38.3 (28.9) || Mass kDa 11.9 (50.6)
- **XP_002340819**: 377-480/Alg =104AA || pI 11.5 (4.3) || HI 31.7 (27.0) || Mass kDa 11.1 (59.0)
- **XP_828079**: 34-141/Alg =108AA || pI 9.2 (5.7) || HI 28.7 (22.6) || Mass kDa 11.7 (47.6)
- **XP_001445268**: 11-116/Alg =106AA || pI 4.7 (5.3) || HI 29.2 (20.6) || Mass kDa 11.4 (52.6)
- **XP_736859**: 16-126/Alg =111AA || pI 7.1 (5.2) || HI 25.2 (22.5) || Mass kDa 12.3 (31.0)
- **CCA14206**: 18-124/Alg =107AA || pI 4.6 (5.0) || HI 28.0 (26.6) || Mass kDa 11.6 (53.2)
- **CBY10632**: 2-109/Alg =108AA || pI 4.5 (4.7) || HI 33.3 (33.9) || Mass kDa 11.5 (12.0)
- **XP_003003573**: 358-461/Alg =104AA || pI 10.4 (4.2) || HI 26.9 (21.9) || Mass kDa 11.2 (50.3)
- **YP_320852**: 59-165/Alg =107AA || pI 5.7 (5.3) || HI 40.2 (39.4) || Mass kDa 11.5 (17.5)
- **XP_001420445**: 20-127/Alg =108AA || pI 4.9 (4.7) || HI 38.9 (28.2) || Mass kDa 11.5 (58.4)
- **XP_448641**: 7-114/Alg =108AA || pI 9.3 (7.1) || HI 36.1 (36.8) || Mass kDa 11.5 (12.2)
- **YP_001866308**: 57-163/Alg =107AA || pI 9.1 (7.2) || HI 37.4 (41.7) || Mass kDa 11.3 (16.9)

**FK506-binding protein FKBP12 [Schizophyllum commune H4-8]**

- **XP_002199016**: 454/Alg =108AA || pI 5.1 (5.1) || HI 43.5 (43.5) || Mass kDa 11.6 (11.6)
- **XP_002340819**: 540/Alg =104AA || pI 11.5 (4.3) || HI 31.7 (27.0) || Mass kDa 11.1 (59.0)
- **XP_828079**: 425/Alg =108AA || pI 9.2 (5.7) || HI 28.7 (22.6) || Mass kDa 11.7 (47.6)
- **XP_001445268**: 467/Alg =106AA || pI 4.7 (5.3) || HI 29.2 (20.6) || Mass kDa 11.4 (52.6)
- **XP_736859**: 271/Alg =111AA || pI 7.1 (5.2) || HI 25.2 (22.5) || Mass kDa 12.3 (31.0)
- **CCA14206**: 482/Alg =107AA || pI 4.6 (5.0) || HI 28.0 (26.6) || Mass kDa 11.6 (53.2)
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- **YP_320852**: 165/Alg =107AA || pI 5.7 (5.3) || HI 40.2 (39.4) || Mass kDa 11.5 (17.5)
- **XP_001420445**: 542/Alg =108AA || pI 4.9 (4.7) || HI 38.9 (28.2) || Mass kDa 11.5 (58.4)
- **XP_448641**: 114/Alg =108AA || pI 9.3 (7.1) || HI 36.1 (36.8) || Mass kDa 11.5 (12.2)
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### Peptidyl-Prolyl Isomerase

- **FKBP (FK506 binding protein)**
- **PKP**
- **PDI**
- **CHIP**
- **HSP90**
- **HSP70**
- **HSP60**
- **DHFR**
- **MAF**
- **MCI**
- **MDM2**
- **p53**
- **p90**
- **p88**
- **p85**
- **p70**
- **p68**
- **p65**
- **p56**
- **p52**
- **p49**
- **p47**
- **p45**
- **p43**
- **p41**
- **p39**
- **p37**
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- **p31**
- **p29**
- **p27**
- **p25**
- **p23**
- **p21**
- **p19**
- **p17**
- **p15**
- **p13**
- **p11**
- **p9**
- **p7**
- **p5**
- **p3**
- **p1**

### Protein Properties

- **Identity (%)**
- **Pl**
- **Mass (kDa)**

### Protein Functions

- **Protein folding**
- **Chaperone activity**
- **ATPase activity**
- **Nucleotide binding**
- **Molecular chaperone**
- **Heat shock protein**
- **Chaperone protein**
- **Chaperonin**
- **Heat shock protein 90 kDa**
- **Heat shock protein 70 kDa**
- **Heat shock protein 60 kDa**
- **Heat shock protein 40 kDa**
- **Heat shock protein 30 kDa**
- **Heat shock protein 25 kDa**
- **Heat shock protein 23 kDa**
- **Heat shock protein 21 kDa**
- **Heat shock protein 19 kDa**
- **Heat shock protein 17 kDa**
- **Heat shock protein 15 kDa**
- **Heat shock protein 13 kDa**
- **Heat shock protein 11 kDa**
- **Heat shock protein 9 kDa**
- **Heat shock protein 7 kDa**
- **Heat shock protein 5 kDa**
- **Heat shock protein 3 kDa**
- **Heat shock protein 1 kDa**

### References

- [Arthrodema gypseum CBS 118893](#)
- [Cyanothece sp. PCC 7425](#)
- [Aspergillus oryzae RIB40](#)
- [Malassezia pachydermatis](#)
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*Note: FK506 stands for FK-506 immunosuppressant, which is a calcineurin inhibitor. The table lists various proteins and their lengths, identities, isoelectric points (pI), hydrophobicity indices (HI), and molecular weights (kDa). The proteins include FKBP6, hypothetical proteins, and putative proteins from various species.*
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<td>XP_969074</td>
<td>PREDICTED: similar to shutdown CG4735-PA [Tribolium castaneum].</td>
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<td>BAJ87990</td>
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<td>EPR29131</td>
<td>hypothetical protein AND_02169 [Anopheles darlingi].</td>
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