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*Supplementary material*

# Immunoproteomic Analysis Reveals Novel Candidate Antigens for the Diagnosis of Paracoccidioidomycosis Due to *Paracoccidioides lutzii*

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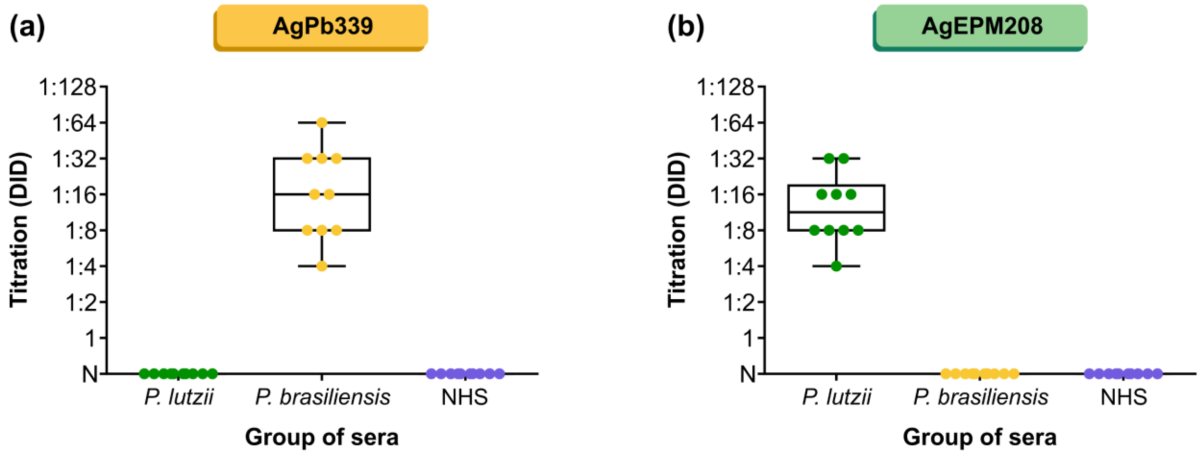
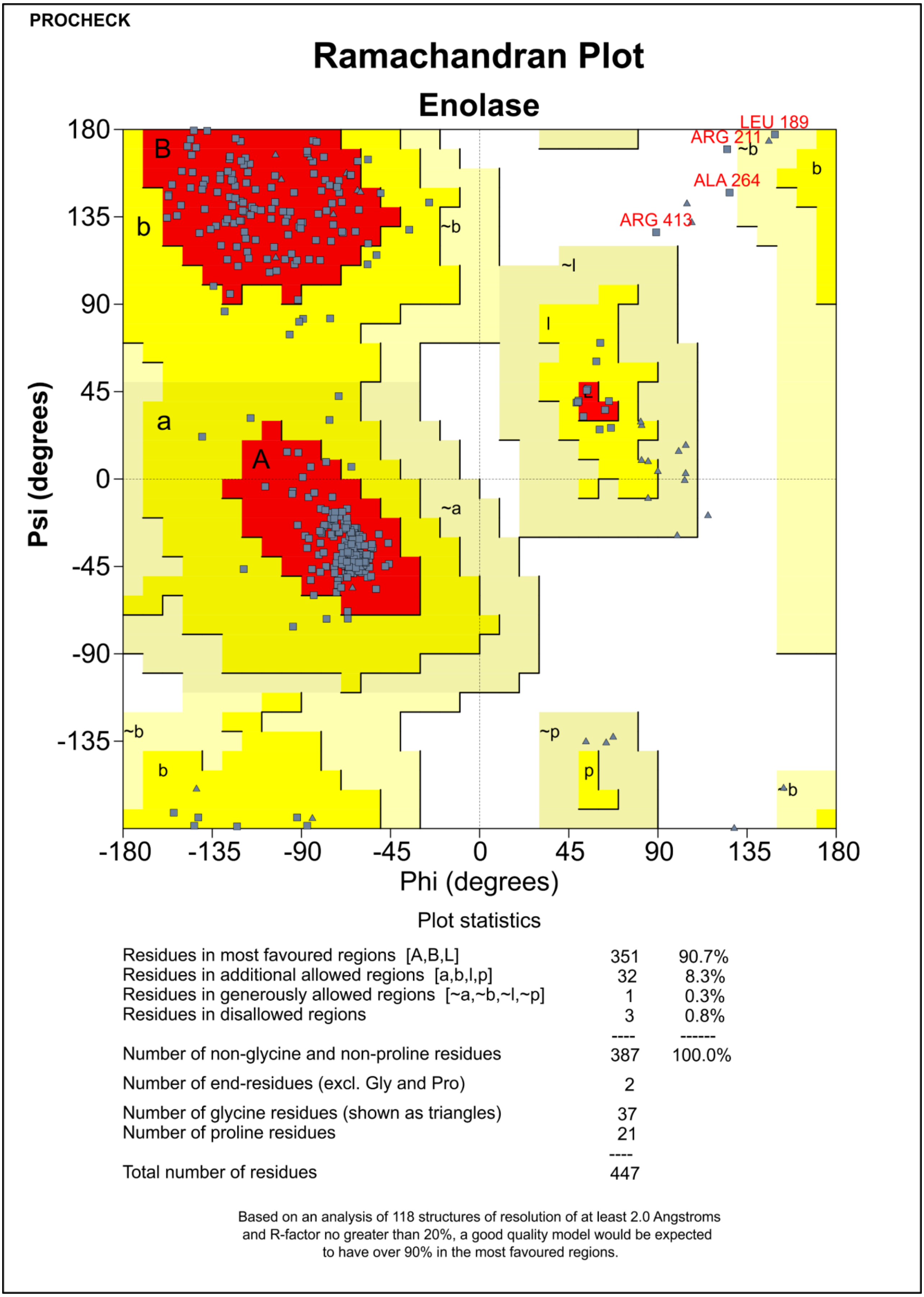


**Figure S1.** Anti-*Paracoccidioides* antibody titers in reactive sera of patients with paracoccidioidomycosis due to *P. brasiliensis sensu stricto* (S1; n=10) or *P. lutzii* (n=10). NHS: normal human serum (sera from the healthy normal donors; n=10). A quantitative double immunodiffusion assay (DID) was used to establish the titration of each patient's serum using **(a)** the exoantigens from the reference B-339 strain (AgPbB339; PS3) or **(b)** a *P. lutzii* CFA preparation derived from the reference isolate EPM208 as described earlier [1,2]. Each dot represents the result of a single patient. Bars represent the lowest (Min) and the highest (Max) value in each column.

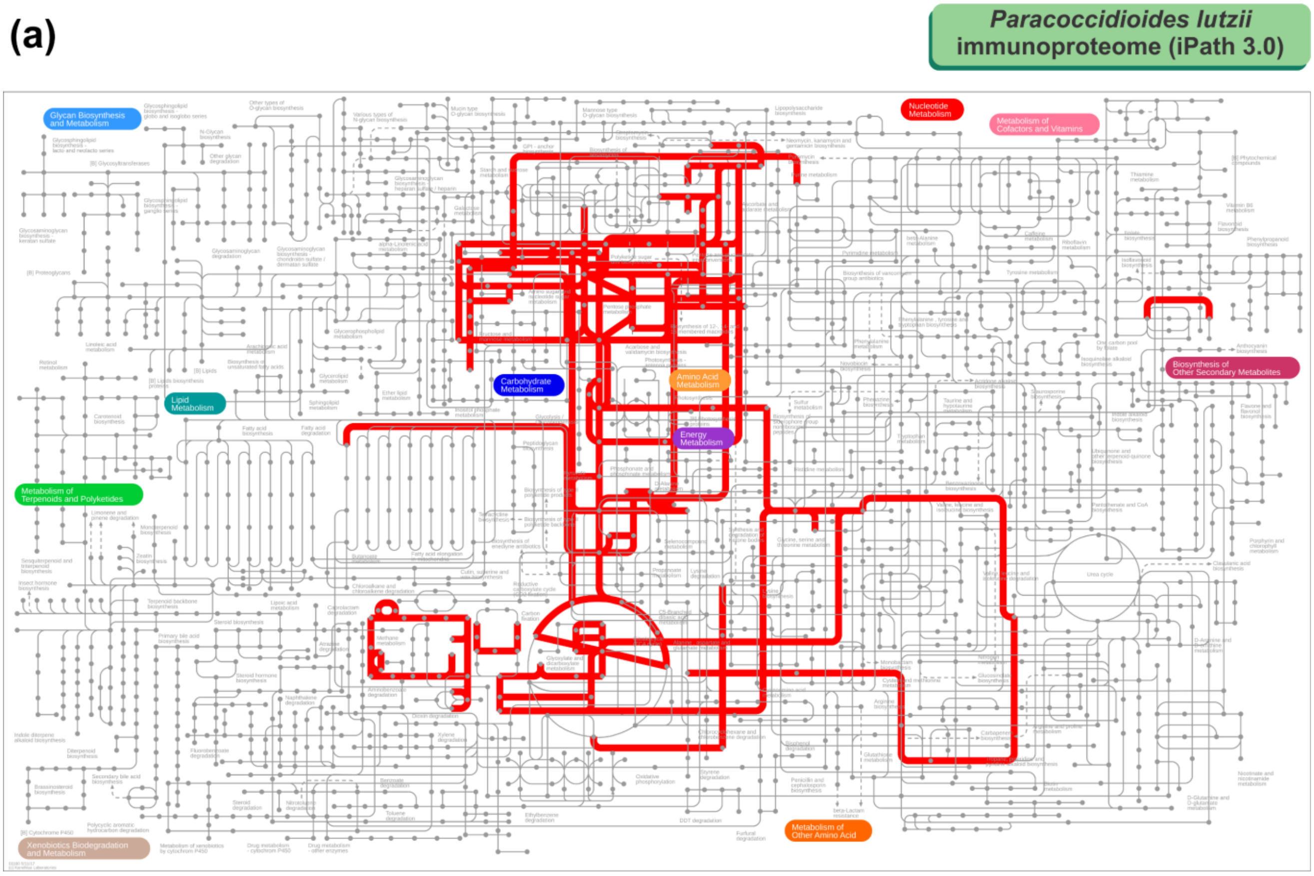


Plot statistics

| | | |
|---|---|---|
| Residues in most favoured regions [A,B,L] | 351 | 90.7% |
| Residues in additional allowed regions [a,b,l,p] | 32 | 8.3% |
| Residues in generously allowed regions [~a,~b,~l,~p] | 1 | 0.3% |
| Residues in disallowed regions | 3 | 0.8% |
| | ---- | ------ |
| Number of non-glycine and non-proline residues | 387 | 100.0% |
| Number of end-residues (excl. Gly and Pro) | 2 | |
| Number of glycine residues (shown as triangles) | 37 | |
| Number of proline residues | 21 | |
| | ---- | |
| Total number of residues | 447 | |

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

**Figure S2.** Ramachandran plot generated by PROCHECK validation server [3] showing the stereochemical quality of the *Paracoccidioides lutzii* enolase structure (accession number: XP_015703472).



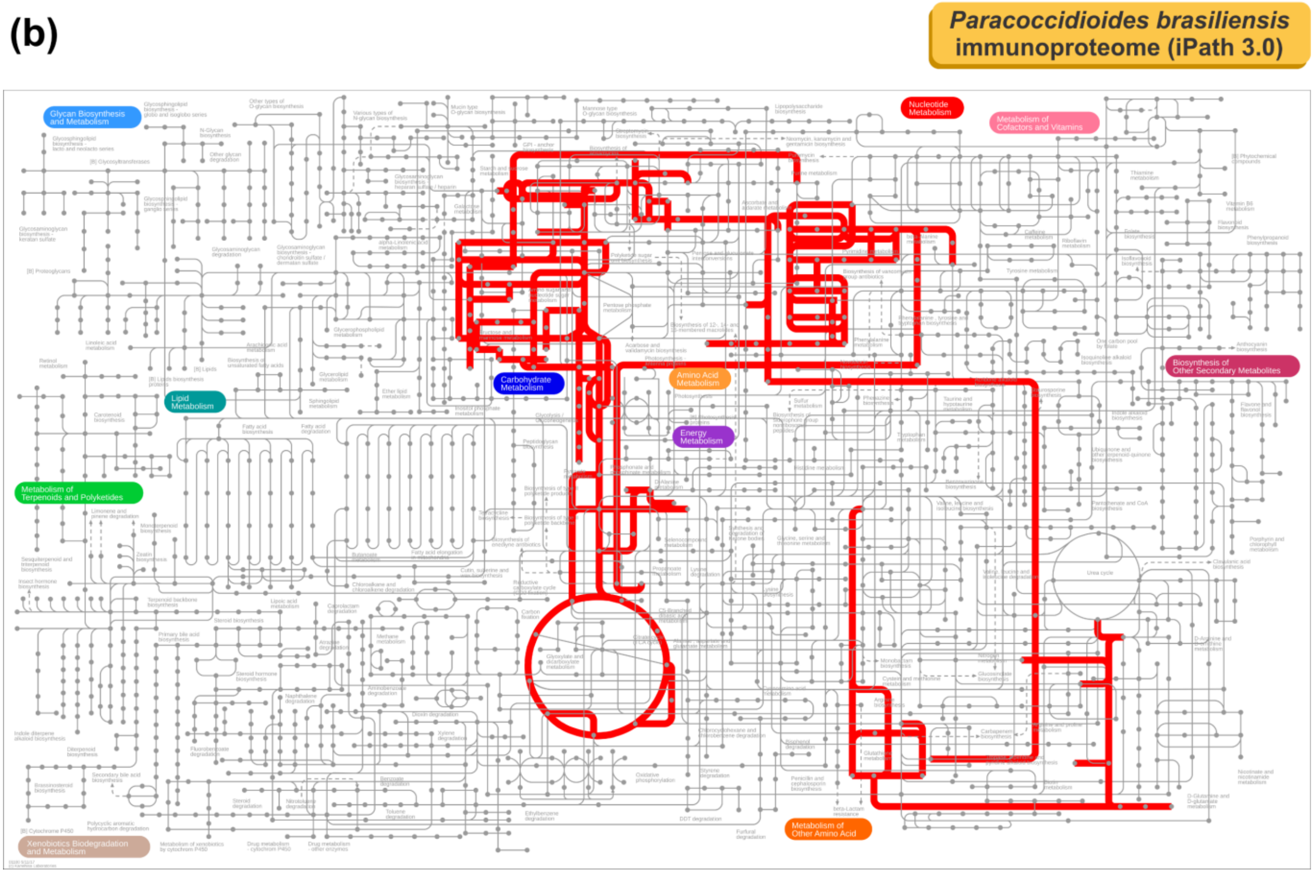


**Figure S3.** Overview of the metabolic pathways in **(a)** *P. lutzii* and **(b)** *P. brasiliensis* proteomes. The red lines represent proteins (IgG immunoreactive) that were highly enriched, and the boxes represent metabolic pathways. These metabolic maps were visualized and analyzed by the web-application iPath3.0 [4].

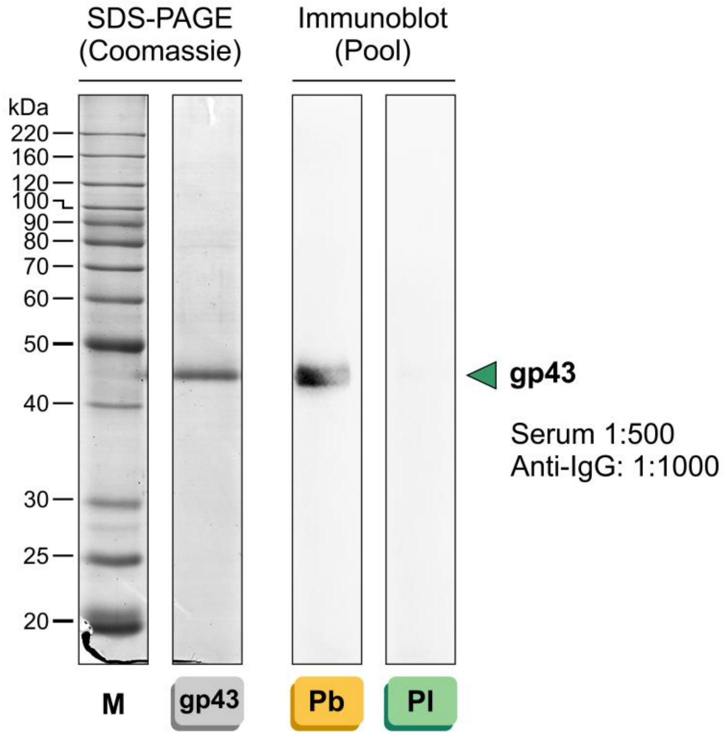


**Figure S4.** Representative immunoblot of purified gp43 antigen (B-339 strain) using sera from patients with confirmed paracoccidioidomycosis due to *P. brasiliensis s. str.* (Pb, yellow lane) or *P. lutzii* (Pl, green lane). For immunoblotting, gp43 (250 ng) was resolved with SDS-PAGE and transferred onto 0.45 polyvinylidene difluoride (PVDF) membranes (Bio-Rad, USA) at 25 V for 1 h with transfer buffer (25 mM Tris base, 192 mM glycine, 20% methanol; pH 8.3) using a Trans-Blot SD semi-dry transfer cell (Bio-Rad, USA). Membranes were probed individually with primary antibody diluted 1:500 (gold standard pooled human sera) at 25 °C for 2 h. Afterward, the membranes were washed three times with Tris-buffered saline (pH 7.5) containing 0.05% (v/v) Tween 20 (TBST) for 10 min and incubated with horseradish peroxidase (HRP)-conjugated goat anti-human IgG (1:1,000 dilution) for 2 h at room temperature. The membranes were then washed with TBST, and the signal was detected with an enhanced chemiluminescence detection kit (GE Healthcare, Uppsala, Sweden). Immunoblots were imaged in a transilluminator (Uvitec, Cambridge). Alliance software v. 4.7 was used to capture several images at different exposure times, reaching ten shots with a 2 s increment. M: marker.

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**Table S1.** BepiPred Linear Epitope Prediction 2.0 Results.

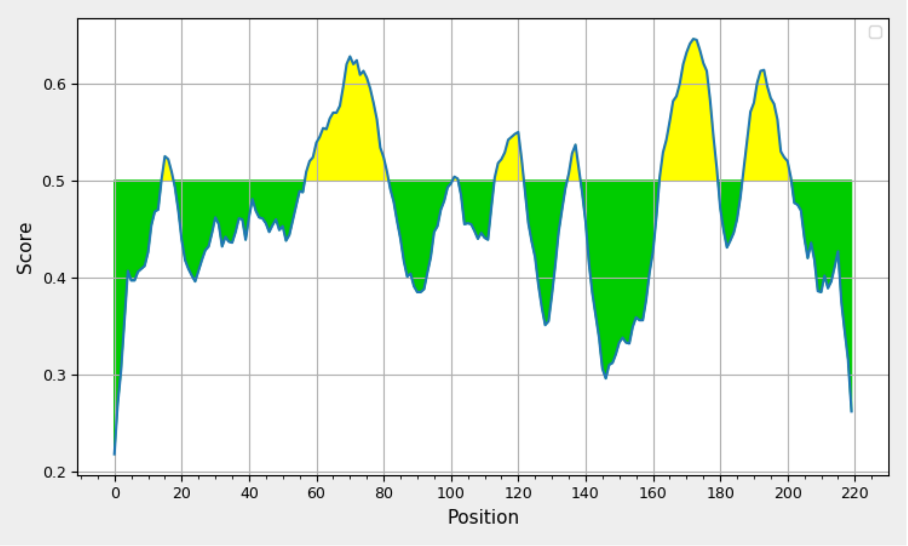
We used a high-throughput *in silico* prediction of protein antigenicity to compare linear B-cell epitopes between *P. brasiliensis* (Pb18) and *P. lutzii* (Pb01) immunoreactive proteins. Therefore, protein sequences were retrieved from NCBI and submitted to BepiPred [5] using the default parameters.

**Protein name: NAD(P)H: quinone oxidoreductase, type IV**

**Predicted peptides: XP_015702763 [Pb01]**

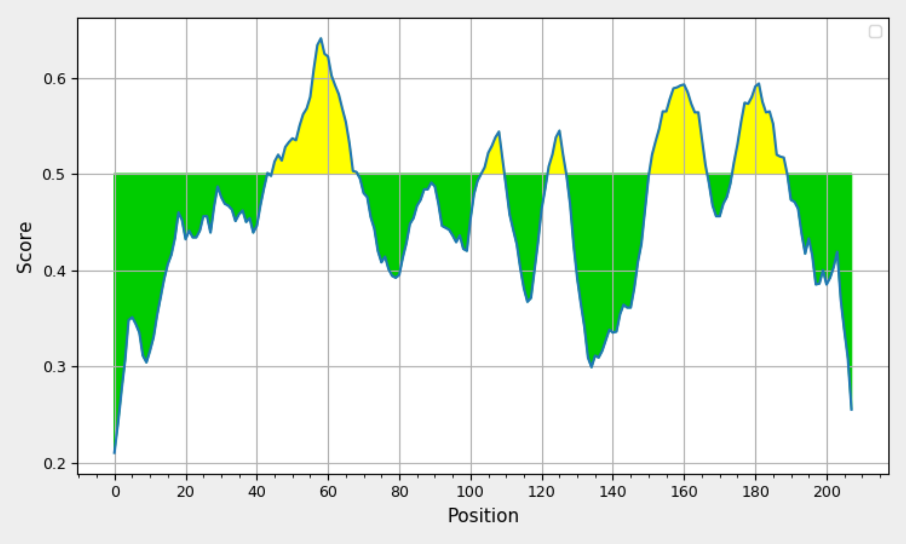
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 15 | 18 | FIPA | 4 |
| 2 | 58 | 82 | ETLPQEVLDKMHAPGKSSYPVAEPA | 25 |
| 3 | 102 | 103 | PG | 2 |
| 4 | 114 | 122 | GIWSTGGFW | 9 |
| 5 | 136 | 139 | GGGQ | 4 |
| 6 | 163 | 180 | KTTFPILANLNEVRGGSP | 18 |
| 7 | 188 | 202 | GADGSRQPSALELQL | 15 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010763025 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 44 | 44 | I | 1 |
| 2 | 46 | 69 | ETLPQEVLDKMHAPGKSSYPVAEP | 24 |
| 3 | 105 | 110 | STGGFW | 6 |
| 4 | 123 | 127 | PGGGQ | 5 |
| 5 | 152 | 167 | TTFPILANLDEVRGGS | 16 |
| 6 | 175 | 189 | AGADGSRQPSALELQ | 15 |

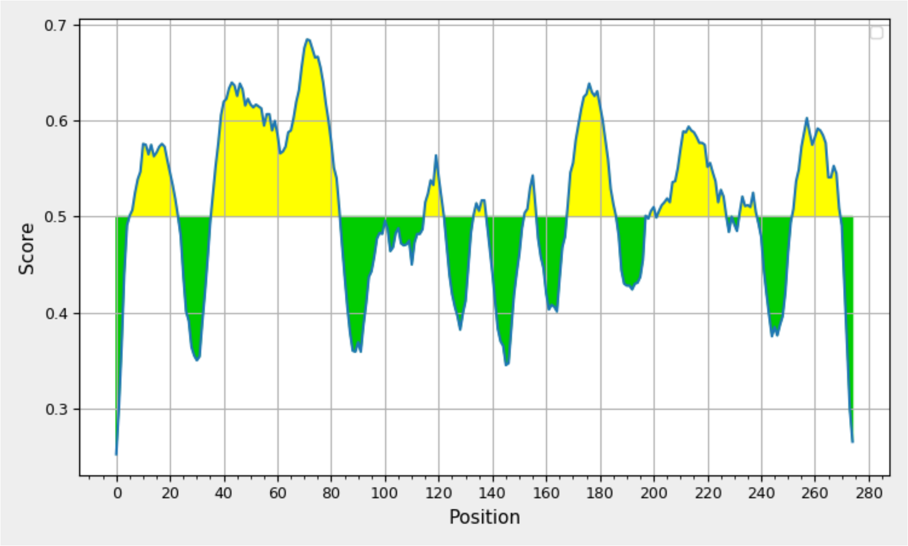


**Protein name: Uncharacterized protein (Thioredoxin-like Superfamily)**

**Predicted peptides: XP_015700719 [Pb01]**

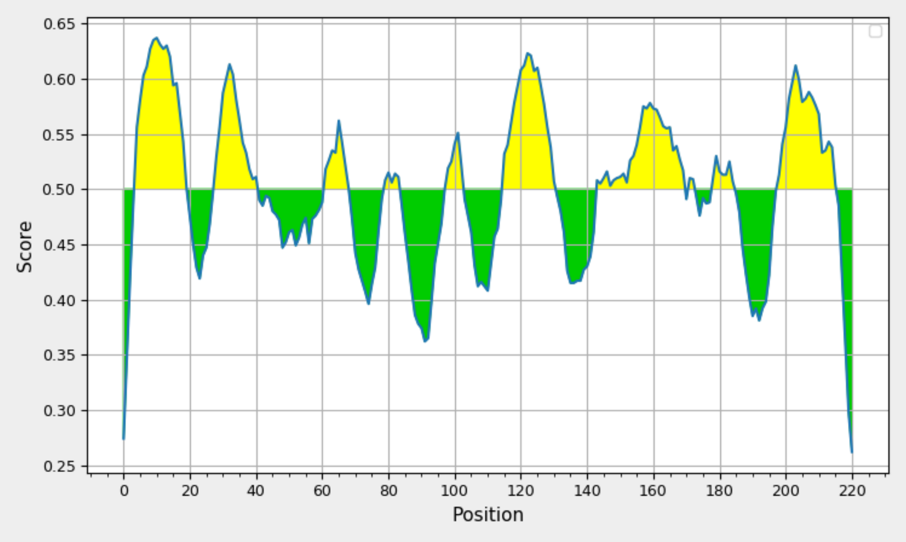
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 6 | 24 | ISRLTLHDPPVYSVAKQFP | 19 |
| 2 | 37 | 84 | PSNPPTLRTSQITSKTYHDSKSPIRRPEALPEWRHGDQAHAGIFTPSK | 48 |
| 3 | 116 | 122 | SKNPHYR | 7 |
| 4 | 134 | 138 | **QPWHP** | 5 |
| 5 | 153 | 157 | LAPEK | 5 |
| 6 | 169 | 186 | QTEFFDANVVNETRNETY | 18 |
| 7 | 198 | 198 | V | 1 |
| 8 | 200 | 201 | EA | 2 |
| 9 | 203 | 228 | LLKMLAVSDKPDEQGDLNGGNGVTGD | 26 |
| 10 | 230 | 230 | K | 1 |
| 11 | 233 | 239 | **VKASRLI** | 7 |
| 12 | 253 | 270 | **EERTISSRFTAEQWEKWL** | 18 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010758121 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 20 | PQFAGQKLSLSGGTET | 16 |
| 2 | 29 | 41 | LRTQKPDTNPATS | 13 |
| 3 | 62 | 69 | SKNAHYRD | 8 |
| 4 | 80 | 84 | **QPWHP** | 5 |
| 5 | 98 | 103 | KLAPEK | 6 |
| 6 | 116 | 131 | TEFFDANVVNETRNET | 16 |
| 7 | 144 | 170 | VDEAALLKMLAVSDKPDEQGDLNGGNG | 27 |
| 8 | 172 | 173 | TG | 2 |
| 9 | 179 | 185 | **VKASRLI** | 7 |
| 10 | 199 | 216 | **EERTISSRFTAEQWEKWL** | 18 |

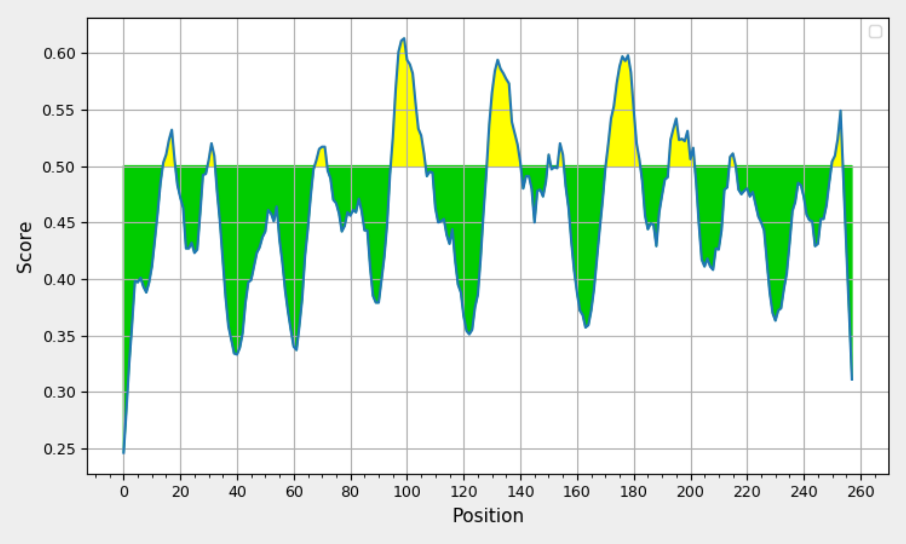


**Protein name: Triosephosphate isomerase**

**Bepipred Linear Epitope Prediction 2.0**

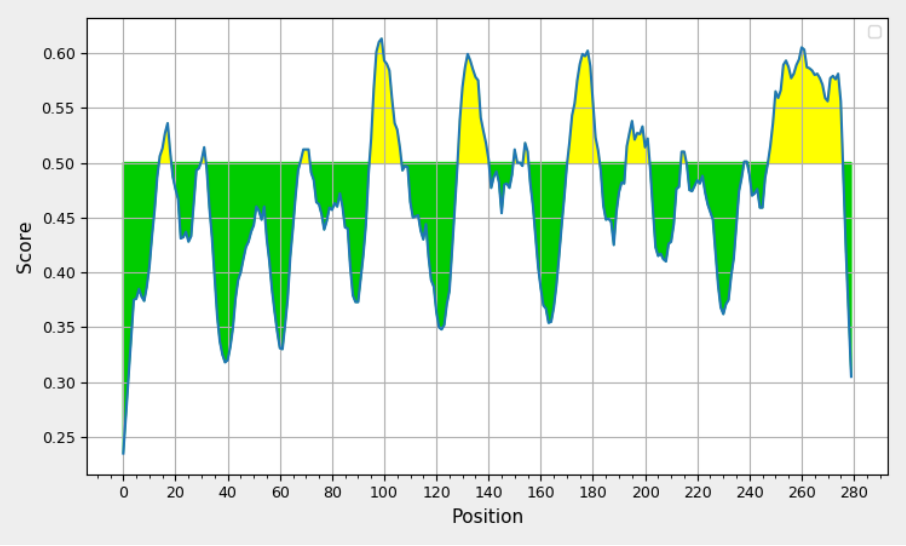
**Predicted peptides: XP_002795879 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 15 | 19 | **GTAKS** | 5 |
| 2 | 31 | 33 | KLD | 3 |
| 3 | 69 | 72 | **PNGA** | 4 |
| 4 | 96 | 107 | **ERRVLLREDDEF** | 12 |
| 5 | 130 | 141 | LEEREAGKTIDV | 12 |
| 6 | 151 | 151 | **E** | 1 |
| 7 | 155 | 156 | **PA** | 2 |
| 8 | 172 | 183 | **GTGKVATTEQAQ** | 12 |
| 9 | 194 | 202 | **NEKISPEAA** | 9 |
| 10 | 215 | 217 | ENN | 3 |
| 11 | 251 | 254 | GIPH | 4 |



**Predicted peptides: XP_010762134 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 15 | 19 | **GTAKS** | 5 |
| 2 | 31 | 32 | KL | 2 |
| 3 | 69 | 72 | **PNGA** | 4 |
| 4 | 96 | 107 | **ERRVLLREDDEF** | 12 |
| 5 | 130 | 141 | LEEREAGRTIDV | 12 |
| 6 | 151 | 151 | **E** | 1 |
| 7 | 153 | 153 | V | 1 |
| 8 | 155 | 156 | **PA** | 2 |
| 9 | 172 | 183 | **GTGKVATTEQAQ** | 12 |
| 10 | 194 | 202 | **NEKISPEAA** | 9 |
| 11 | 215 | 216 | ES | 2 |
| 12 | 239 | 240 | PA | 2 |
| 13 | 249 | 276 | MIGISYPANGQITNSSRSCRYHQRPFID | 28 |

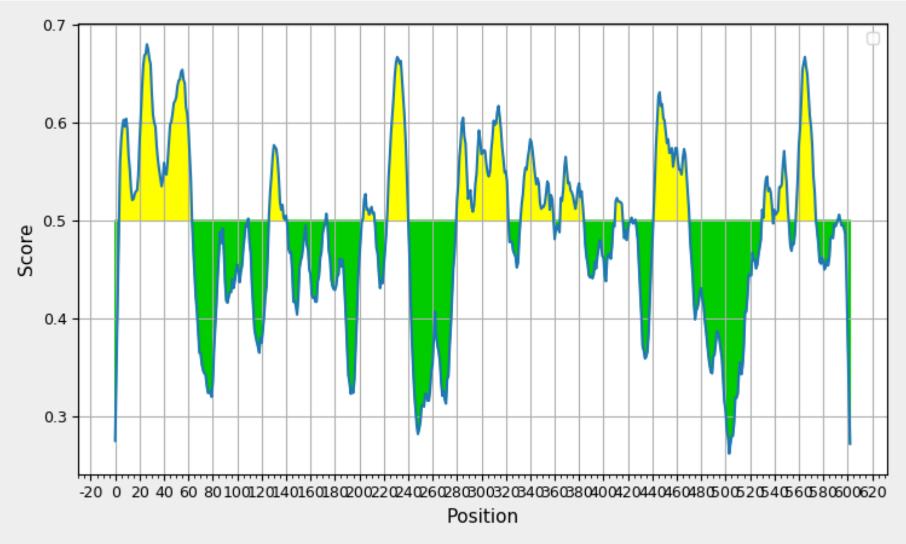


**Protein name: Phenylacetone monooxydase**

**Predicted peptides: XP_002797384 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 63 | ISNEVSFDPDVLKAKYIEERNKRIRDDG IKQYQAIDTDNFKFSVEDPYTKPGFSRAPID | 59 |
| 2 | 110 | 110 | Y | 1 |
| 3 | 127 | 141 | EELNYIPTEKYARAP | 15 |
| 4 | 174 | 174 | T | 1 |
| 5 | 204 | 213 | KLPGVPGIEK | 10 |
| 6 | 224 | 241 | WDYDYTGGDTRGGLSKLA | 18 |
| 7 | 281 | 323 | RLDQPTDPAWAASLKKGWQQKR MDNFNIIVSGGHQDEDLVHDG | 43 |
| 8 | 333 | 360 | VFGGADQPTAKKEAASAMQMA DFKKMEQ | 28 |
| 9 | 366 | 385 | DQIVKDPATAGRLKAYYNQF | 20 |
| 10 | 411 | 416 | GKGIEC | 6 |
| 11 | 424 | 424 | A | 1 |
| 12 | 427 | 427 | K | 1 |
| 13 | 442 | 471 | FSTDYSKRSGVEIKGLN | 30 |

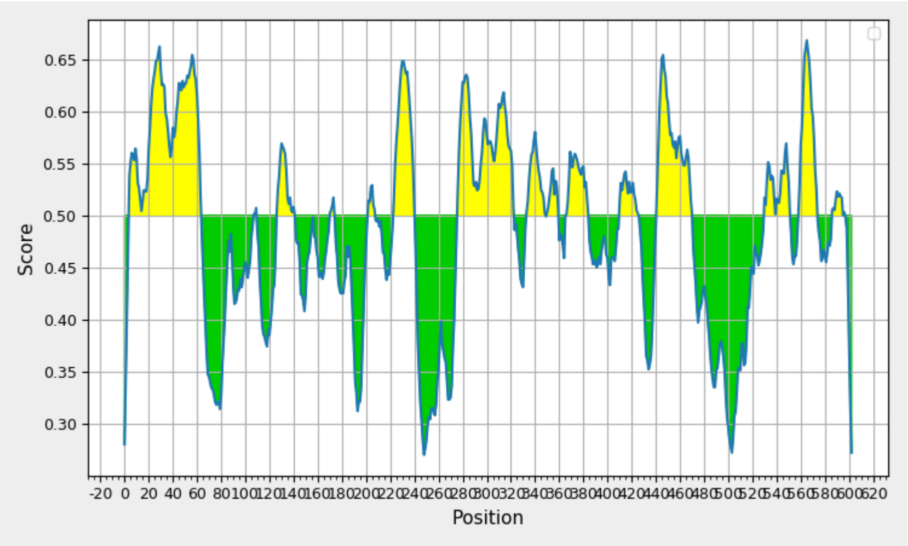
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| | | | GTTLTEKWEDGEK | |
| 14 | 531 | 539 | EAEEQWVKT | 9 |
| 15 | 541 | 552 | MEGGKLQQNFVK | 12 |
| 16 | 559 | 575 | YNQEGQITERALRNSNY | 17 |
| 17 | 593 | 595 | GKL | 3 |

**Predicted peptides: XP_010759514 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 64 | TSNEVTFDPDVLKAKYLEERNKRLRDDGI<br>KQYQAIETGNLKYSVEDPYTKPGFSRASIDE | 60 |
| 2 | 108 | 110 | NRY | 3 |
| 3 | 127 | 142 | EELNYIPTEKYARAPE | 16 |
| 4 | 171 | 174 | WDET | 4 |
| 5 | 203 | 208 | PKLPGV | 6 |
| 6 | 224 | 241 | WDYDYTGGDTTGGLSKLA | 18 |
| 7 | 277 | 323 | SVDIRLDQPTDPAWAASLQKGWQQ<br>KRMDNFNIIVSGGHQDEDLVQDG | 47 |
| 8 | 334 | 349 | YGGRDQPTAKKEAASA | 16 |
| 9 | 351 | 360 | QMADFKKMEQ | 10 |
| 10 | 367 | 385 | QIVKDPATAARLKAYYNQF | 19 |



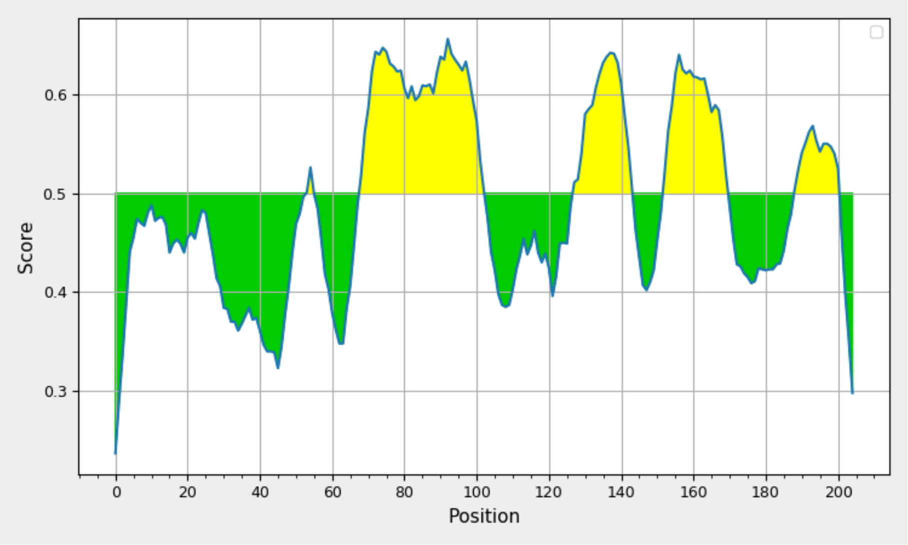
| | | | | |
|---|---|---|---|---|
| 11 | 411 | 426 | GKGIERITENGIVANG | 16 |
| 12 | 442 | 470 | FSTDYSKRSGIEIRGLNGTTLTEKWEDGE | 29 |
| 13 | 531 | 552 | EAEQQWVEAIMEGGKLQQNFVK | 22 |
| 14 | 559 | 574 | YNQEGQITERALRNSN | 16 |
| 15 | 587 | 595 | KDWREAGKL | 9 |
| 16 | 597 | 597 | G | 1 |

**Protein name: Uncharacterized Protein (PRTases type I Superfamily)**

**Predicted peptides: XP_015701261 [Pb01]**

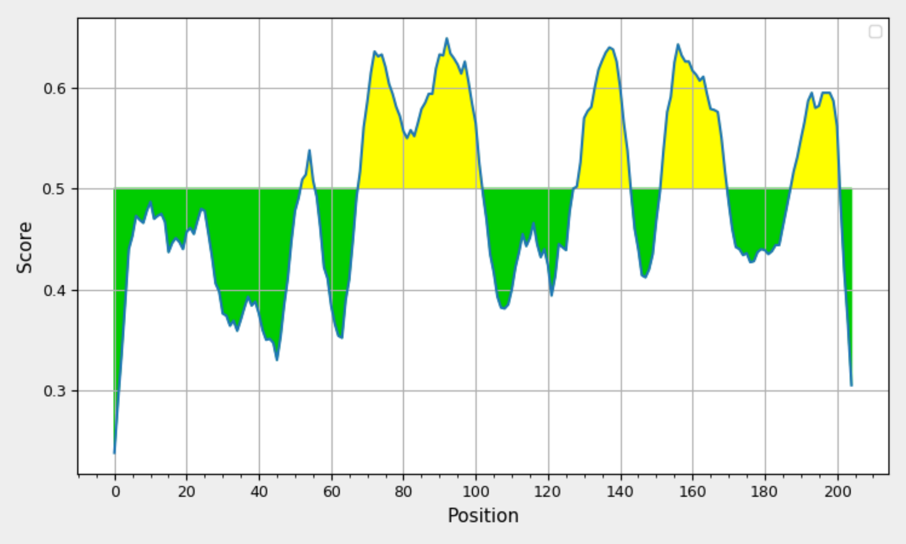
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 54 | 55 | DG | 2 |
| 2 | 69 | 103 | ENLGRDDDPVEQLGTKVTRTQWLDLSSLEMANLIG | 35 |
| 3 | 128 | 144 | KDVQVAQQQLGREGEKT | 17 |
| 4 | 153 | 170 | NKDKPKKGKLPADMLESG | 18 |
| 5 | 189 | 201 | AKDIDQHDQLAAE | 13 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010756299 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 53 | 56 | PDGA | 4 |
| 2 | 69 | 102 | ENLGRDDDPVEQLGTKVTRTQWLDLSSLEM ANLI | 34 |
| 3 | 129 | 143 | DVQVAQQQLGREGEK | 15 |
| 4 | 153 | 170 | NKDKLKKGKLPADMLESG | 18 |
| 5 | 189 | 201 | **AKDIDQHDQLAAE** | 13 |

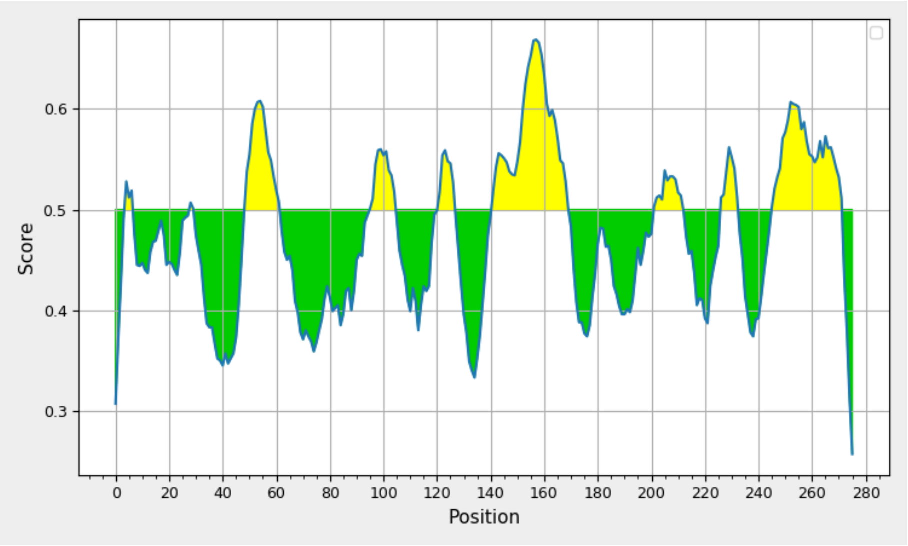


**Protein name: Proteasome subunit alpha**

**Predicted peptides: XP_002797532 [Pb01]**

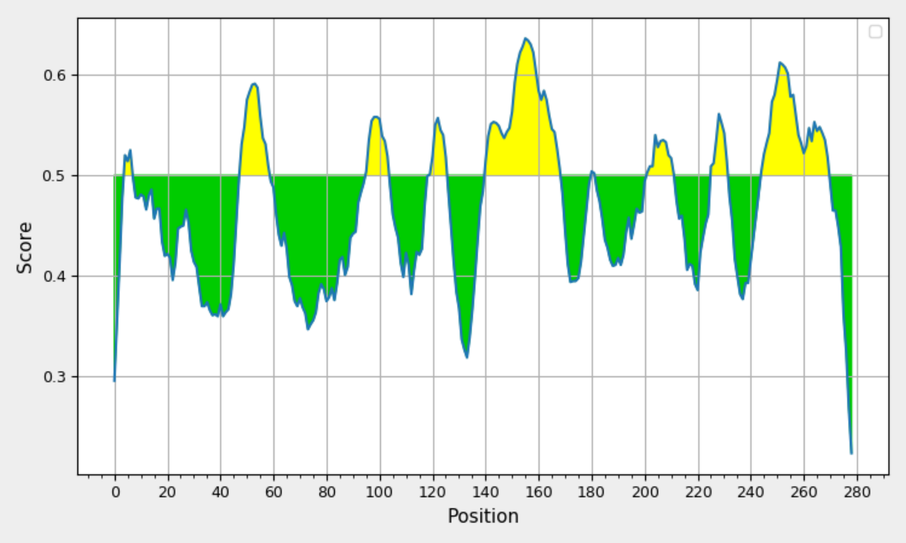
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 7 | **YSF** | 3 |
| 2 | 29 | 30 | NQ | 2 |
| 3 | 50 | 62 | KSSSPLIEPPSLS | 13 |
| 4 | 96 | 105 | AYKRIYNEYP | 10 |
| 5 | 122 | 127 | TQSGGV | 6 |
| 6 | 142 | 170 | GVKPIPAEGELDTNKKKASGKTGGILKGG | 29 |
| 7 | 202 | 212 | EKRYTEGLELE | 11 |
| 8 | 227 | 233 | **EGEMNGE** | 7 |
| 9 | 246 | 272 | HLLGYEGVEGARGPRFRKLSKEEIEDY | 27 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010762451 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 7 | **YSF** | 3 |
| 2 | 49 | 59 | KSSSPLIDPPS | 11 |
| 3 | 96 | 104 | YKRIYNEYP | 9 |
| 4 | 120 | 126 | ATQSGGV | 7 |
| 5 | 141 | 169 | GVEPTPVEGELDRNKKKASGKTGGILKGG | 29 |
| 6 | 181 | 182 | YF | 2 |
| 7 | 202 | 212 | KRYTEGLELED | 11 |
| 8 | 226 | 232 | **EGEMNGE** | 7 |
| 9 | 245 | 270 | HLLGYEGVEGARGPRFRKLSKEEIED | 26 |

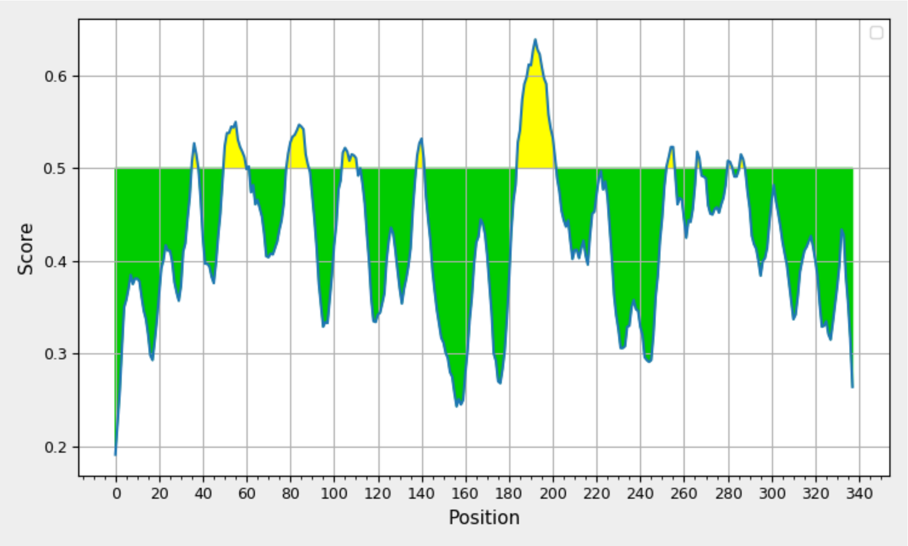


**Protein name: Glyceraldehyde-3-Phosphate dehydrogenase**

**Predicted peptides: Q8X1X3**

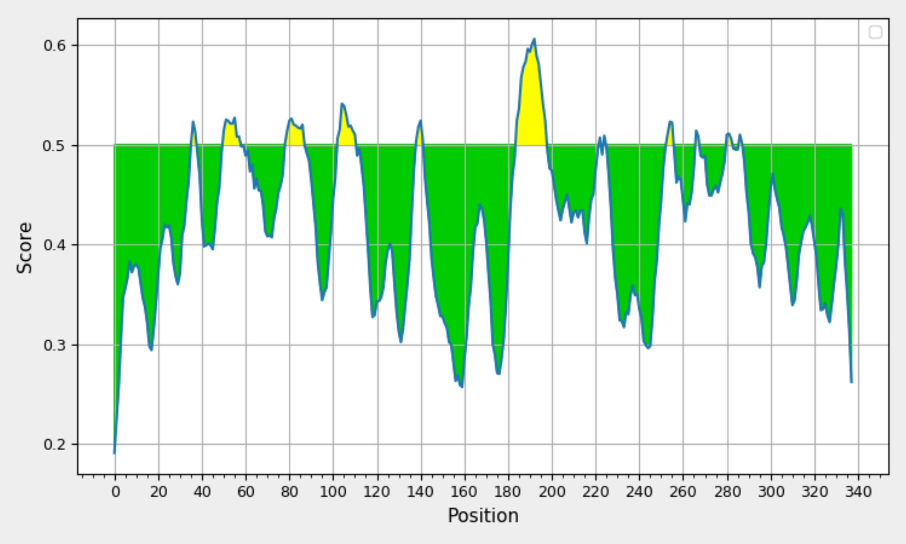
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 36 | 38 | **FIE** | 3 |
| 2 | 51 | 60 | THGQFKGDIQ | 10 |
| 3 | 62 | 62 | S | 1 |
| 4 | 80 | 89 | RDPANIPWGK | 10 |
| 5 | 105 | 111 | TEKAKAH | 7 |
| 6 | 139 | 142 | **SYRP** | 4 |
| 7 | 185 | 202 | QKTVDGPSHKDWRGGRTA | 18 |
| 8 | 253 | 256 | VTYD | 4 |
| 9 | 267 | 268 | **EG** | 2 |
| 10 | 281 | 283 | **LVS** | 3 |
| 11 | 287 | 288 | **NG** | 2 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010758444 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 36 | 38 | **FIE** | 3 |
| 2 | 51 | 58 | THGQFKGD | 8 |
| 3 | 79 | 87 | ERDPTNIPW | 9 |
| 4 | 103 | 111 | TTTEKAKAH | 9 |
| 5 | 139 | 142 | **SYRP** | 4 |
| 6 | 185 | 198 | QKTVDGPSHKDWRG | 14 |
| 7 | 223 | 223 | A | 1 |
| 8 | 225 | 225 | N | 1 |
| 9 | 254 | 256 | TYD | 3 |
| 10 | 267 | 268 | **EG** | 2 |
| 11 | 281 | 283 | **LVS** | 3 |
| 12 | 287 | 288 | **NG** | 2 |

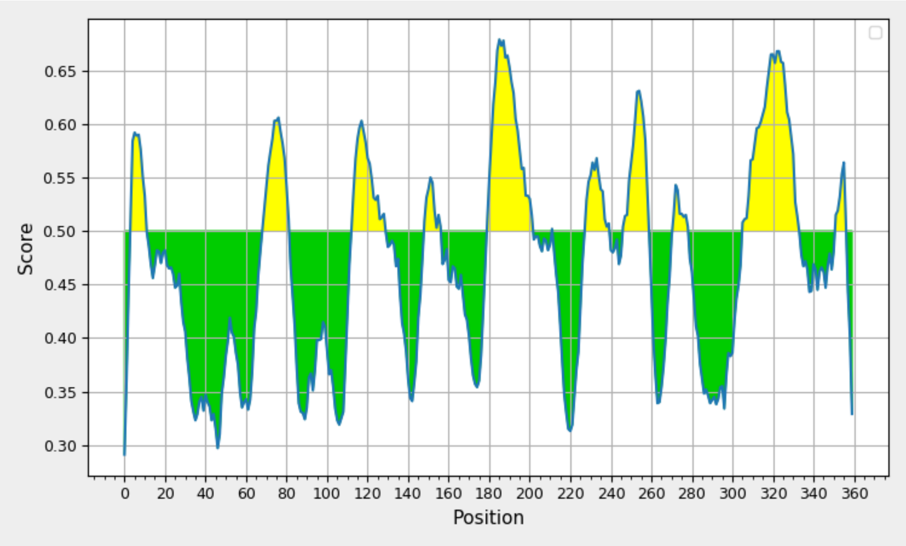


**Protein name: Fructose-bisphosphate aldolase 1**

**Bepipred Linear Epitope Prediction 2.0**

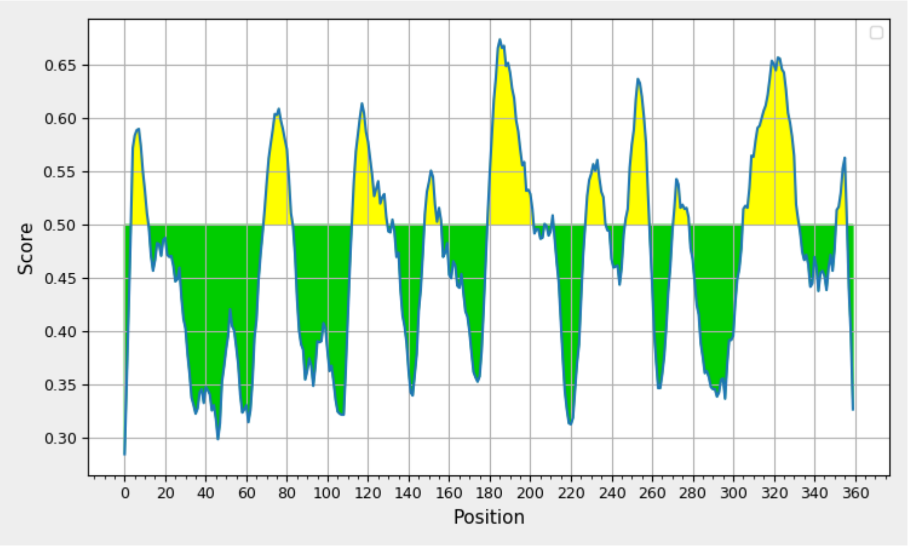
**Predicted peptides: XP_002796107 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 4 | 11 | KDILSRKT | 8 |
| 2 | 69 | 82 | FFAGKGVPNGKQEA | 14 |
| 3 | 113 | 129 | AKKLLPWLDGMLDADEC | 17 |
| 4 | 149 | 157 | **ESVEWNIET** | 9 |
| 5 | 180 | 202 | **GGEEDGVNNESVDNNSLYTQPED** | 23 |
| 6 | 212 | 212 | **A** | 1 |
| 7 | 229 | 240 | VYKPGNVRLHPE | 12 |
| 8 | 247 | 259 | AYVKEKTGSSKNK | 13 |
| 9 | 272 | 279 | **TKAEFKEA** | 8 |
| 10 | 306 | 333 | **LKKKDYLMSAVGNPEGEDKPNKKYFDPR** | 28 |
| 11 | 352 | 357 | **DDFNTS** | 6 |



**Predicted peptides: XP_010756450 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 12 | DILSRKTG | 8 |
| 2 | 70 | 83 | FAGKGVPNGNQEAS | 14 |
| 3 | 113 | 130 | AKKLLPWLDGMLDADERY | 18 |
| 4 | 133 | 133 | L | 1 |
| 5 | 149 | 157 | **ESVEWNIET** | 9 |
| 6 | 180 | 202 | **GGEEDGVNNESVDNNSLYTQPED** | 23 |
| 7 | 208 | 208 | K | 1 |
| 8 | 212 | 212 | **A** | 1 |
| 9 | 229 | 238 | VYKPGNVRLH | 10 |
| 10 | 248 | 259 | HVKEKTGSSKNK | 12 |
| 11 | 272 | 279 | **TKAEFKEA** | 8 |
| 12 | 306 | 333 | **LKKKDYLMSAVGNPEGEDKPNKKYFDPR** | 28 |
| 13 | 352 | 357 | **DDFNTS** | 6 |

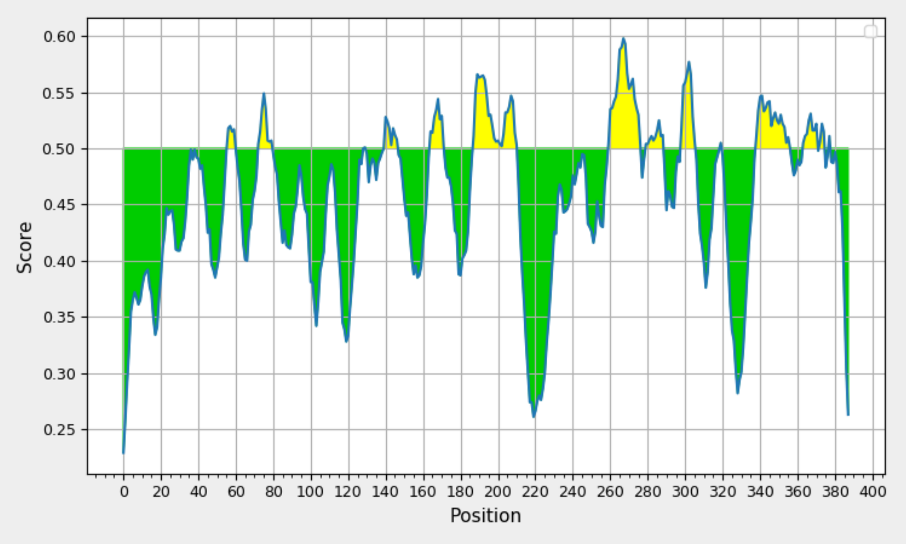


**Protein name: Mannitol-1-Phosphate 5-dehydrogenase**

**Predicted peptides: XP_002791734 [Pb01]**

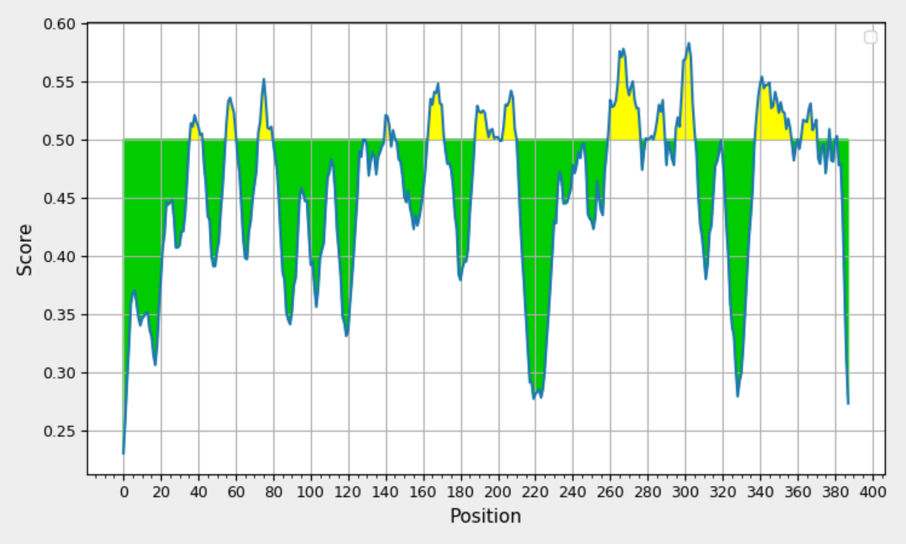
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 57 | 60 | GEHK | 4 |
| 2 | 73 | 80 | HNLDDVIK | 8 |
| 3 | 129 | 130 | TD | 2 |
| 4 | 141 | 147 | DESRRDS | 7 |
| 5 | 165 | 172 | TQDPNSGL | 8 |
| 6 | 188 | 211 | PFGDVGHPDIKAIHWVDNLEPYIE | 24 |
| 7 | 260 | 277 | IVEKHHIPAEEQHDYVQK | 18 |
| 8 | 280 | 289 | TRISNPYLED | 10 |
| 9 | 299 | 306 | LRKLSRKE | 8 |
| 10 | 320 | 320 | Q | 1 |
| 11 | 339 | 356 | PDDEESFELHKILKELSA | 18 |
| 12 | 364 | 371 | TDLEPDHP | 8 |
| 13 | 373 | 375 | YPR | 3 |
| 14 | 378 | 378 | E | 1 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010757428 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 37 | 43 | SVIDALQ | 7 |
| 2 | 56 | 61 | EGEHKK | 6 |
| 3 | 73 | 80 | **HNLDDVIK** | 8 |
| 4 | 141 | 143 | DES | 3 |
| 5 | 145 | 146 | RD | 2 |
| 6 | 164 | 172 | PTQDPNSGL | 9 |
| 7 | 189 | 201 | FGDVGHPDIKAIH | 13 |
| 8 | 204 | 211 | DNLEPYIE | 8 |
| 9 | 260 | 277 | IVEKHHIPAAEQHDYVQK | 18 |
| 10 | 280 | 290 | TRISNPYLEDV | 11 |
| 11 | 296 | 306 | RAPLRKLSRKE | 11 |
| 12 | 339 | 357 | PDDEESFELHKILKELSAA | 19 |
| 13 | 361 | 361 | T | 1 |
| 14 | 363 | 371 | LTDLEADHP | 9 |
| 15 | 378 | 378 | E | 1 |
| 16 | 382 | 382 | K | 1 |

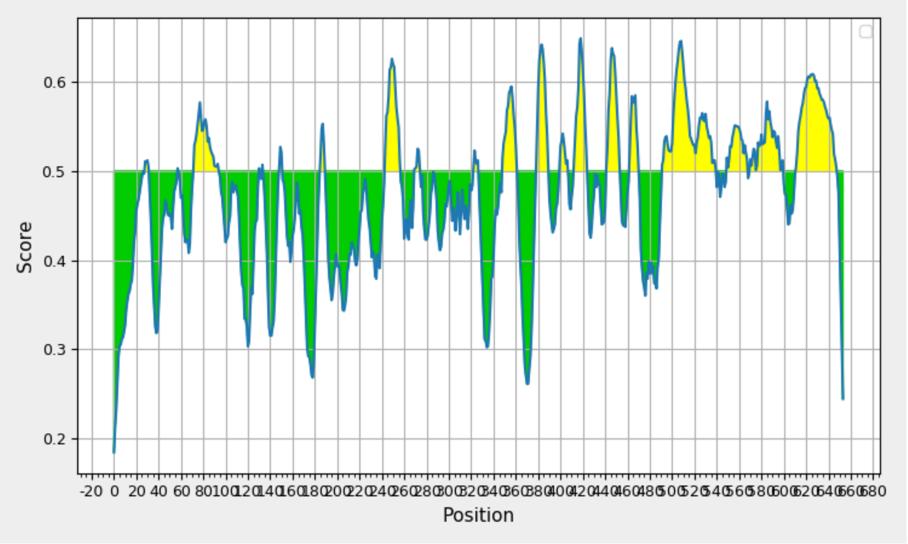


**Protein name: Hsp72-like protein**

**Predicted peptides: XP_002790117 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 29 | 32 | **NDQG** | 4 |
| 2 | 58 | 58 | A | 1 |
| 3 | 73 | 94 | GRKFADPEVQSDMKHFPFKVID | 22 |
| 4 | 131 | 131 | S | 1 |
| 5 | 134 | 134 | **G** | 1 |
| 6 | 149 | 151 | **NDS** | 3 |
| 7 | 186 | 190 | **KAEGE** | 5 |
| 8 | 244 | 257 | **KRKHKKDLSSNARA** | 14 |
| 9 | 270 | 275 | RTLSSA | 6 |
| 10 | 323 | 327 | KIDKS | 5 |
| 11 | 349 | 362 | SDFFNGKEPNKSIN | 14 |
| 12 | 380 | 390 | GDTTSKSTNEI | 11 |
| 13 | 400 | 407 | VGIETAGG | 8 |
| 14 | 413 | 424 | IKRNTTIPTKKS | 12 |
| 15 | 442 | 454 | FEGERARTKDNNL | 13 |
| 16 | 463 | 471 | IPPAPRGVP | 9 |

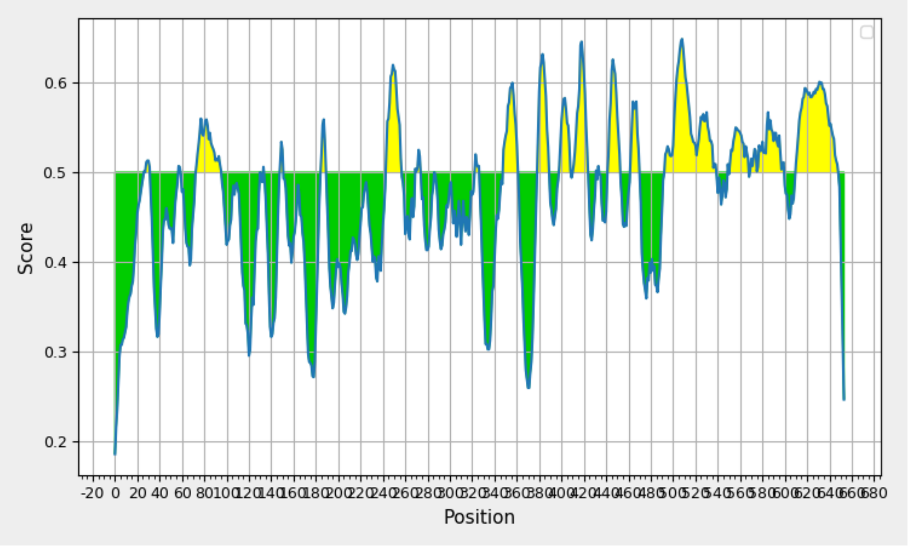
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 17 | 492 | 540 | KGTGKTNKIVITNDKGRLSKEEIERMLAE AEKYKAEDEAEASRISAKNG | 49 |
| 18 | 550 | 568 | NTISDSKVDEKLDASDKEK | 19 |
| 19 | 571 | 600 | TEIDKTVSWLDENQTATKEEFEAQQKELES | 30 |
| 20 | 612 | 648 | AGGEGGAPGAGFPGAGGPGGFPGA GAGGAHSGGDDGP | 37 |

**Predicted peptides: XP_010763478 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 27 | 27 | I | 1 |
| 2 | 29 | 32 | **NDQG** | 4 |
| 3 | 58 | 59 | AM | 2 |
| 4 | 74 | 96 | RKFADPEVQSDMKHFPFKVIDKA | 23 |
| 5 | 134 | 134 | **G** | 1 |
| 6 | 149 | 151 | **NDS** | 3 |
| 7 | 186 | 190 | **KAEGE** | 5 |
| 8 | 244 | 257 | **KRKHKKDLSSNARA** | 14 |
| 9 | 270 | 274 | RTLSS | 5 |
| 10 | 324 | 327 | IDKS | 4 |
| 11 | 349 | 361 | SDFFNGKEPNKSI | 13 |



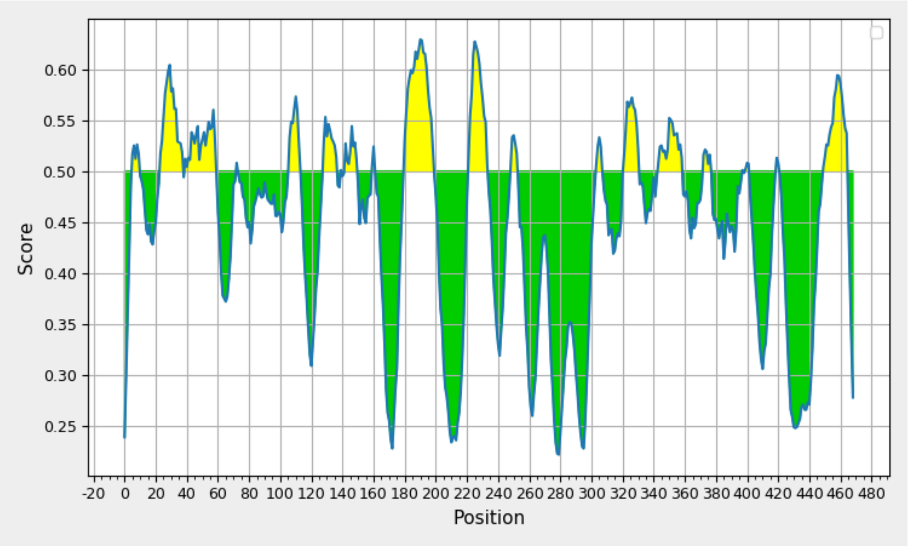
| | | | | |
|---|---|---|---|---|
| 12 | 380 | 389 | GDTTSKSTNE | 10 |
| 13 | 399 | 409 | SVGIETAGGVM | 11 |
| 14 | 411 | 424 | PLIKRNTTIPTKKS | 14 |
| 15 | 432 | 432 | D | 1 |
| 16 | 434 | 434 | Q | 1 |
| 17 | 443 | 453 | EGERARTKDNN | 11 |
| 18 | 463 | 470 | IPPAPRGV | 8 |
| 19 | 494 | 539 | TGKTNKIVITNDKGRLSKEEIERML AEAEKYKAEDEAEASRISAKN | 46 |
| 20 | 550 | 550 | N | 1 |
| 21 | 552 | 568 | ISDSKVDEKLDASDKEK | 17 |
| 22 | 570 | 600 | KTEIDKTVSWLDENQTATKEEFEAQQKELES | 31 |
| 23 | 611 | 648 | GAGGEGGAPGAGFPGAGGPG GFPGAGASGAHSGGDDGP | 38 |

**Protein name: Citrate synthase**

**Predicted peptides: XP_002793640 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 6 | 10 | RATRQ | 5 |
| 2 | 24 | 38 | SSRFYSTAESDLKTV | 15 |
| 3 | 40 | 59 | EKAIPAKKELFQEVKKRGED | 20 |
| 4 | 73 | 73 | M | 1 |
| 5 | 107 | 113 | **PKGTSGT** | 7 |
| 6 | 129 | 137 | **VPTTPQVRA** | 9 |
| 7 | 140 | 140 | S | 1 |
| 8 | 143 | 150 | AQKSHLPK | 8 |
| 9 | 160 | 161 | **PK** | 2 |
| 10 | 181 | 199 | KFAKAYADGLSKASYWEPT | 19 |
| 11 | 222 | 234 | **EIEKVGTQELDPT** | 13 |
| 12 | 249 | 253 | SKANE | 5 |
| 13 | 304 | 307 | LHGL | 4 |
| 14 | 322 | 331 | TIGNKFTDAD | 10 |
| 15 | 344 | 359 | QVVPGYGHGVLRKPDP | 16 |

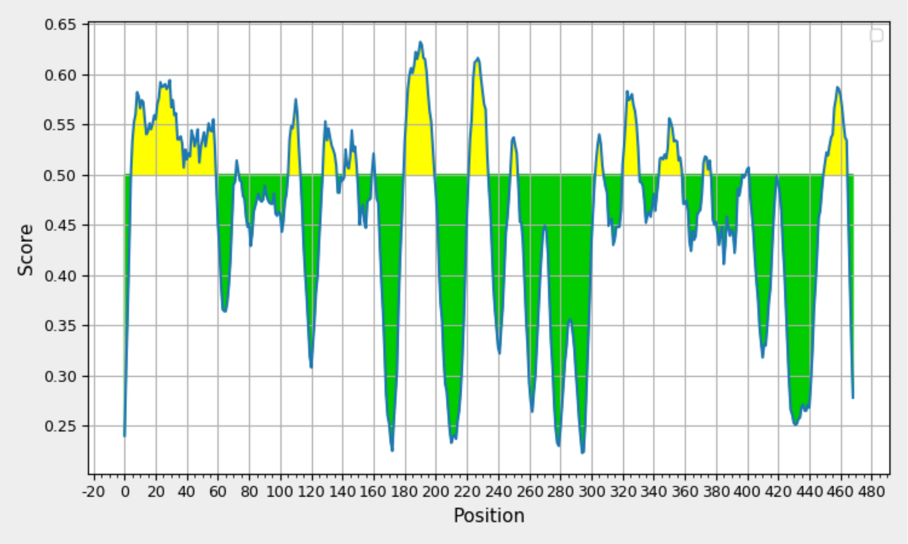
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 16 | 373 | 377 | **EIQAN** | 5 |
| 17 | 398 | 398 | **G** | 1 |
| 18 | 400 | 402 | TKN | 3 |
| 19 | 420 | 421 | FR | 2 |
| 20 | 450 | **465** | **LPIERPKSVNLQGLLD** | 16 |

**Predicted peptides: XP_010760342 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 6 | 59 | RATRQALKASQSAAWSFSSSRFYSTAESDL<br>KTVFEKAIPAKKELFQEVKKRGED | 54 |
| 2 | 73 | 74 | MR | 2 |
| 3 | 107 | 113 | **PKGTSGT** | 7 |
| 4 | 129 | 137 | **VPTTPQVRA** | 9 |
| 5 | 143 | 150 | AQKSHLPR | 8 |
| 6 | 160 | 161 | **PK** | 2 |
| 7 | 181 | 200 | KFAKAYADGLSKASYWEPTF | 20 |
| 8 | 222 | 234 | **EIEKVGTQELDPT** | 13 |
| 9 | 249 | 253 | SKVNE | 5 |
| 10 | 304 | 308 | LHGLA | 5 |
| 11 | 321 | 331 | STIGNKFTDAD | 11 |



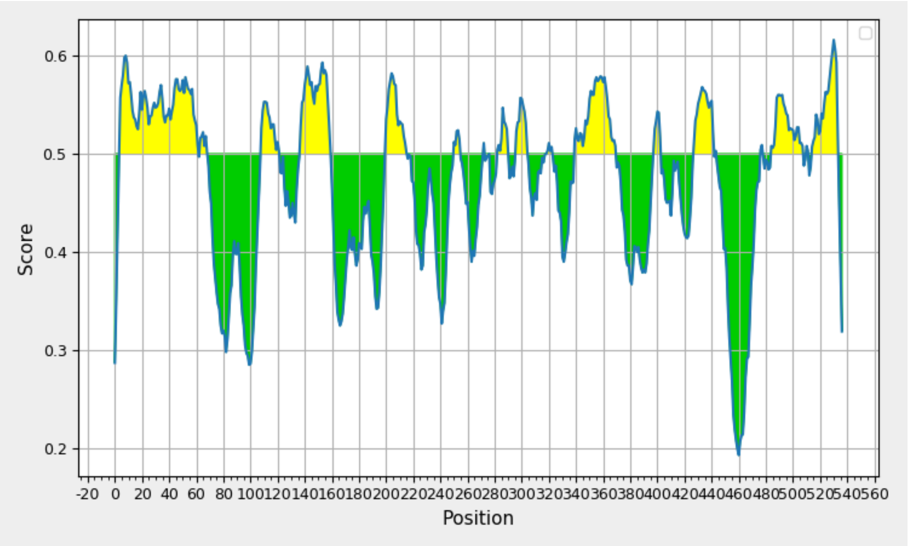
| | | | | |
|---|---|---|---|---|
| 12 | 345 | 359 | VVPGYGHGVLRKPDP | 15 |
| 13 | 373 | 377 | **EIQAN** | 5 |
| 14 | 398 | 398 | **G** | 1 |
| 15 | 401 | 402 | KN | 2 |
| 16 | 450 | 465 | **LPIERPKSVNLQGLLD** | 16 |

**Protein name: Isocitrate lyase**

**Predicted peptides: XP_002791040 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 62 | EQEDQKYWAEVQAVKEWWQDSRWRYTKRPFTAEQIVAKRGNLKIEYPSNVQSKKLWGI | 58 |
| 2 | 64 | 69 | EERFKN | 6 |
| 3 | 109 | 122 | DEPSPDLADYPMNT | 14 |
| 4 | 138 | 160 | DRKQREERLRAPKSQRASLPNID | 23 |
| 5 | 201 | 216 | PGTKKCGHMAGKVLVP | 16 |
| 6 | 251 | 255 | LITST | 5 |
| 7 | 273 | 273 | K | 1 |
| 8 | 277 | 277 | D | 1 |
| 9 | 283 | 290 | EQAGKNGA | 8 |
| 10 | 297 | 305 | DKWNAEAGL | 9 |
| 11 | 319 | 323 | SSIPN | 5 |
| 12 | 340 | 370 | NTEARAIAKKITGSDIYFDWDAARTREGFYR | 31 |
| 13 | 398 | 403 | LPDYAQ | 6 |

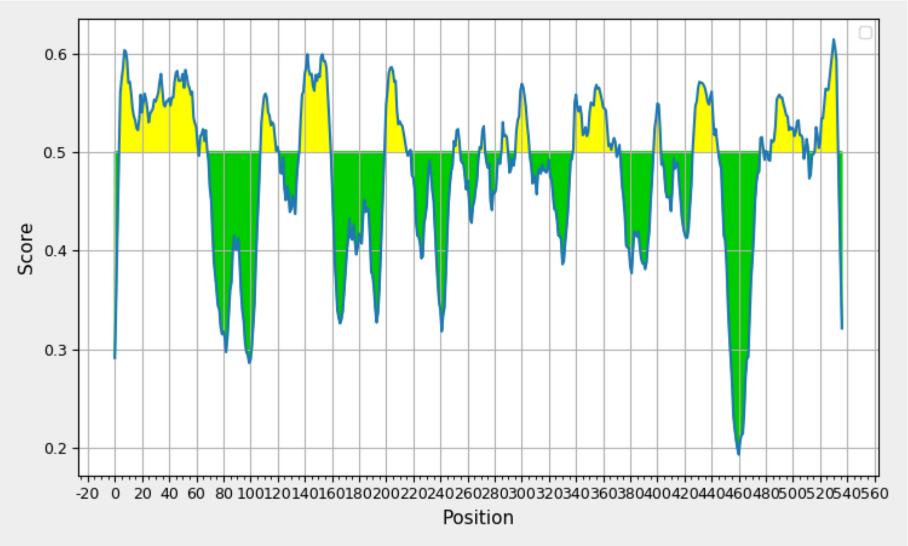
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 14 | 428 | 442 | FNWKAAMPRGEQETY | 15 |
| 15 | 444 | 444 | **R** | 1 |
| 16 | 477 | 478 | MN | 2 |
| 17 | 485 | 508 | ELVQEPEMENGVDVVTHQKWSGAN | 24 |
| 18 | 511 | 512 | DE | 2 |
| 19 | 515 | 534 | KMVSGGISSTSAMGKGVTED | 20 |

**Predicted peptides: XP_010757468 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 62 | **EQEDQKYWAEVQAVKEWWQD<br>SRWRYTKRPFTAEQIVAKR<br>GNLKIEYPSNVQSKKLWGI** | 58 |
| 2 | 64 | 69 | **EERFKN** | 6 |
| 3 | 109 | 121 | DEPSPDLADYPMN | 13 |
| 4 | 137 | 160 | HDRKQREERLRAPKSQRASLPNID | 24 |
| 5 | 200 | 216 | APGTKKCGHMAGKVLVP | 17 |
| 6 | 218 | 219 | SE | 2 |
| 7 | 251 | 255 | **LITST** | 5 |
| 8 | 270 | 273 | PNIK | 4 |
| 9 | 286 | 290 | GKNGA | 5 |



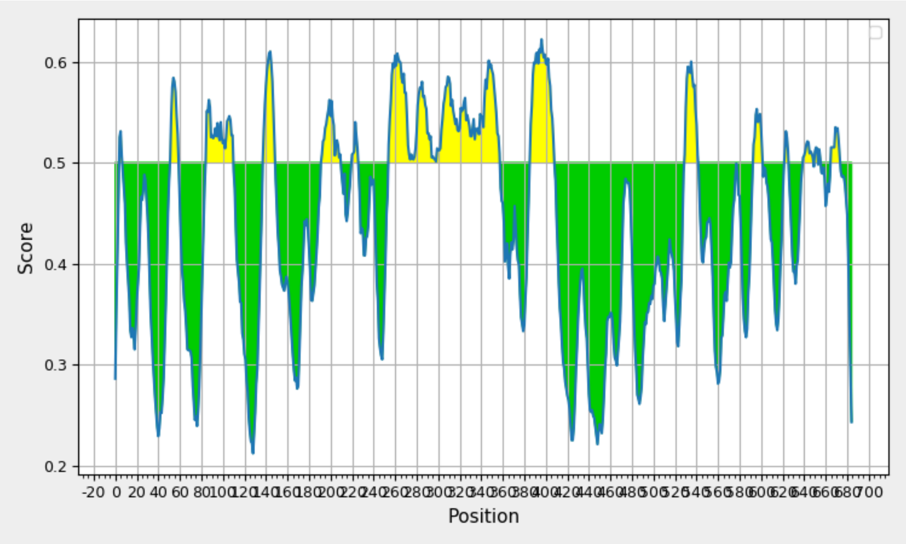
| | | | | |
|---|---|---|---|---|
| 10 | 297 | 306 | DKWNAEAGLK | 10 |
| 11 | 339 | 370 | SNTEARAIAKKITASDTYFDWDAARTREGFYR | 32 |
| 12 | 373 | 373 | G | 1 |
| 13 | 399 | 403 | PDYAQ | 5 |
| 14 | 427 | 445 | SFNWKAAMPRGEQETYIRR | 19 |
| 15 | 477 | 479 | TNG | 3 |
| 16 | 481 | 481 | **R** | 1 |
| 17 | 485 | 508 | ELVQEPEMENGIDVVTHQKWSGAN | 24 |
| 18 | 510 | 512 | VDE | 3 |
| 19 | 517 | 534 | VSGGISSTSAMGKGVTED | 18 |

**Protein name: Transketolase**

**Predicted peptides: XP_002793534 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 7 | **NDV** | 3 |
| 2 | 52 | 59 | NPKNPQWI | 8 |
| 3 | 85 | 110 | AVSLDDLKDFRRLDSITPGHPEAHDT | 26 |
| 4 | 138 | 149 | **GAVFNKPGFDLI** | 12 |
| 5 | 193 | 210 | IDGDTKVAFTEDVMKRFE | 18 |
| 6 | 221 | 226 | DGNNDL | 6 |
| 7 | 255 | 358 | GSELQGTGGVHGNPLKADDSKGVKK<br>RFGFDPEQSFVVPQQVYDLYHKK<br>AAEGAAKEQEWNALLQQYASKYPAEHA<br>DFTRRLSGKLPEGWEKNLPRYSPTDPAIA | 104 |
| 8 | 387 | 408 | SNNTRWKDAVDFQPPSTGLGDW | 22 |
| 9 | 530 | 542 | **NLPQLEASSIEKA** | 13 |
| 10 | 594 | 602 | **VFDVQDKEY** | 9 |
| 11 | 623 | 626 | GWDR | 4 |
| 12 | 640 | 649 | SGPYKEVYKK | 10 |
| 13 | 651 | 653 | **EFT** | 3 |

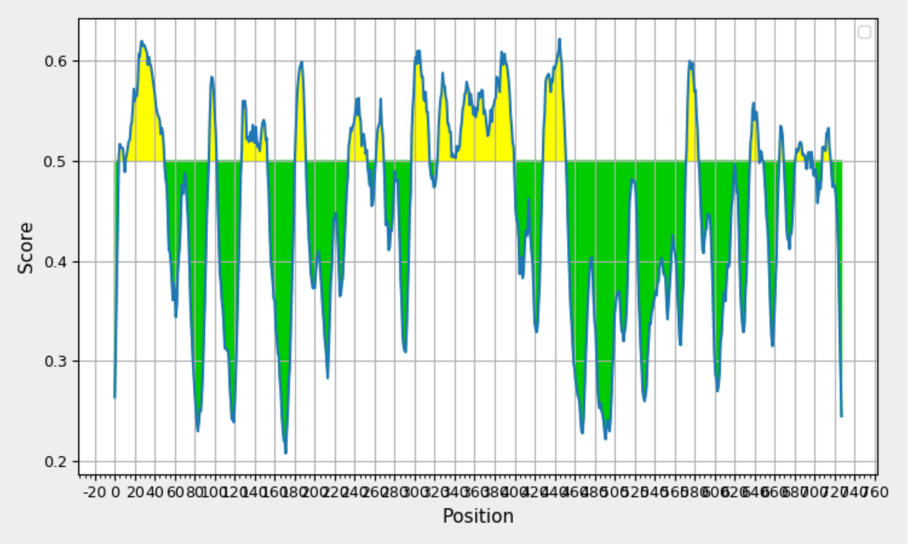
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 14 | 655 | 656 | EG | 2 |
| 15 | 666 | 674 | **EFYKGSPVL** | 9 |

**Predicted peptides: XP_010760067 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 10 | **NDVDQL** | 6 |
| 2 | 12 | 50 | INTIRVLAVSIFYLSTIITQSACPISQSVLFLKSRKITA | 39 |
| 3 | 95 | 102 | NPKNPQWI | 8 |
| 4 | 128 | 153 | AVSLDDLKDFRKLDSITPGHPEAHDT | 26 |
| 5 | 181 | 192 | **GAVFNKPGFDLI** | 12 |
| 6 | 235 | 253 | SIDGDTKVAFTEDVMKRFE | 19 |
| 7 | 262 | 270 | VEDGNNDLA | 9 |
| 8 | 298 | 315 | GSELQGTGGVHGNPLKAD | 18 |
| 9 | 324 | 400 | FGFDPEQSFVVPQQVYDLYHKKAAEGAAKEQEWNALLQQYASKYPAEHADFTRRLSGKLPEGWEKSLPRYSPTDPAI | 77 |
| 10 | 430 | 452 | SNNTRWKDAVDFQPPSTGLGDWT | 23 |
| 11 | 573 | 585 | **NLPQLEASSIEKA** | 13 |
| 12 | 637 | 645 | **VFDVQDKEY** | 9 |
| 13 | 647 | 649 | LSV | 3 |



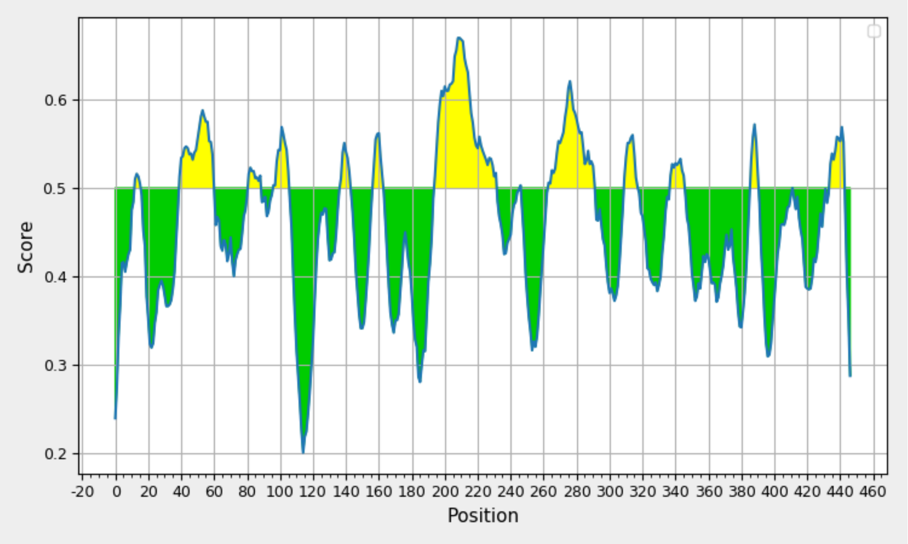
| | | | | |
|---|---|---|---|---|
| 14 | 666 | 670 | GWDRY | 5 |
| 15 | 682 | 692 | ASGPYKEVYKK | 11 |
| 16 | 694 | 696 | **EFT** | 3 |
| 17 | 698 | 698 | E | 1 |
| 18 | 709 | 717 | **EFYKGSPVL** | 9 |

**Protein name: Enolase**

**Bepipred Linear Epitope Prediction 2.0**

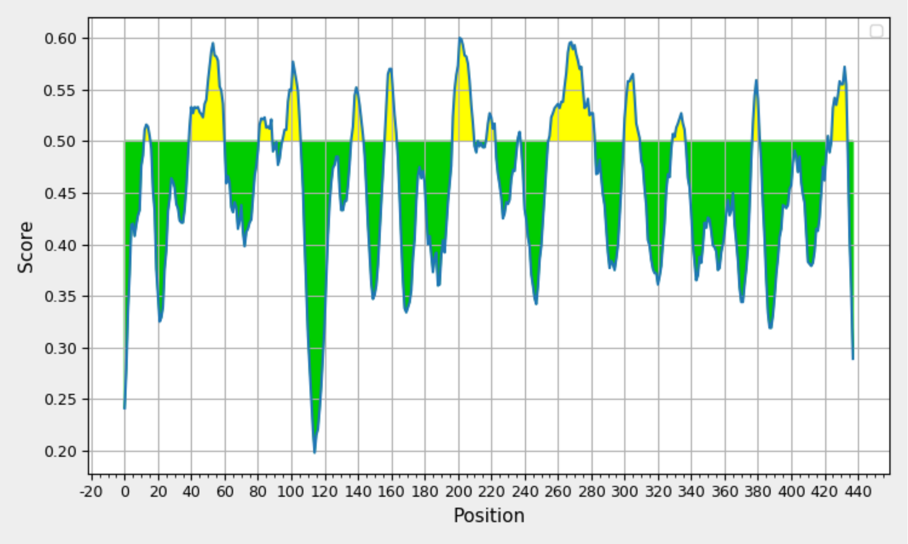
**Predicted peptides: XP_015703472 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 13 | 16 | **DSRG** | 4 |
| 2 | 40 | 60 | STGQHEACELRDGDQSKWLGK | 21 |
| 3 | 82 | 89 | **IDVKDQSK** | 8 |
| 4 | 97 | 106 | LDGTPNKSKL | 10 |
| 5 | 138 | 143 | AGTKKP | 6 |
| 6 | 158 | 163 | SHAGGR | 6 |
| 7 | 195 | 232 | RLRSLSQTEGPRQEEVRQSAGNVGDEG GVAPDIQTPEE | 38 |
| 8 | 247 | 247 | T | 1 |
| 9 | 264 | 292 | ADEKKYDLDFKNPDSDKSKWLTYEQLADL | 29 |
| 10 | 310 | 318 | AEDDWEAWS | 9 |
| 11 | 338 | 346 | PIRIKKAIE | 9 |
| 12 | 387 | 391 | **GETED** | 5 |
| 13 | 435 | 443 | **VYAGDKFRA** | 9 |



**Predicted peptides: XP_010759701 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 13 | 16 | **DSRG** | 4 |
| 2 | 40 | 60 | STGQHEACELRDGDKSKWLGK | 21 |
| 3 | 82 | 89 | **IDVKDQSK** | 8 |
| 4 | 96 | 106 | KLDGTPNKSKL | 11 |
| 5 | 137 | 144 | LAGTKKPY | 8 |
| 6 | 157 | 164 | GSHAGGRL | 8 |
| 7 | 198 | 210 | KKKYGQSAGNVGD | 13 |
| 8 | 218 | 223 | IQTPEE | 6 |
| 9 | 237 | 238 | YT | 2 |
| 10 | 256 | 283 | DEKKYDLDFKNPDSDKSKWLTYEQLADL | 28 |
| 11 | 301 | 310 | AEDDWEAWSY | 10 |
| 12 | 330 | 337 | IRIKKAIE | 8 |
| 13 | 378 | 382 | **GETED** | 5 |
| 14 | 423 | 423 | S | 1 |
| 15 | 426 | 434 | **VYAGDKFRA** | 9 |

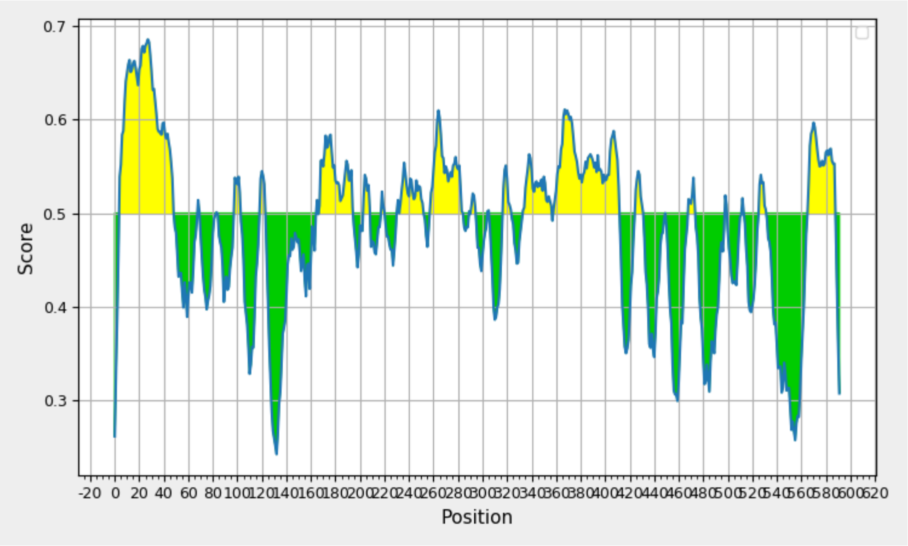


**Protein name: Heat shock protein 60, mitochondrial**

**Predicted peptides: XP_002789992 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 49 | FTSSRASVLSSASSTRAPLSRFRSAG<br>VGLQQQRFAHKELKFGVEA | 45 |
| 2 | 69 | 70 | GP | 2 |
| 3 | 84 | 84 | P | 1 |
| 4 | 99 | 103 | **LQDKF** | 5 |
| 5 | 120 | 123 | **EVAG** | 4 |
| 6 | 166 | 166 | E | 1 |
| 7 | 168 | 195 | LQTNKRDITTTEEIAQVATISANGDTHV | 28 |
| 8 | 204 | 209 | **EKVGKE** | 6 |
| 9 | 219 | 221 | TID | 3 |
| 10 | 231 | 232 | RF | 2 |
| 11 | 234 | 252 | RGYVSPYFITDTKAQKVEF | 19 |
| 12 | 258 | 284 | LLSEKKISAVQDIIPALEASTSLRRPL | 27 |
| 13 | 290 | 290 | D | 1 |
| 14 | 292 | 295 | EGEA | 4 |

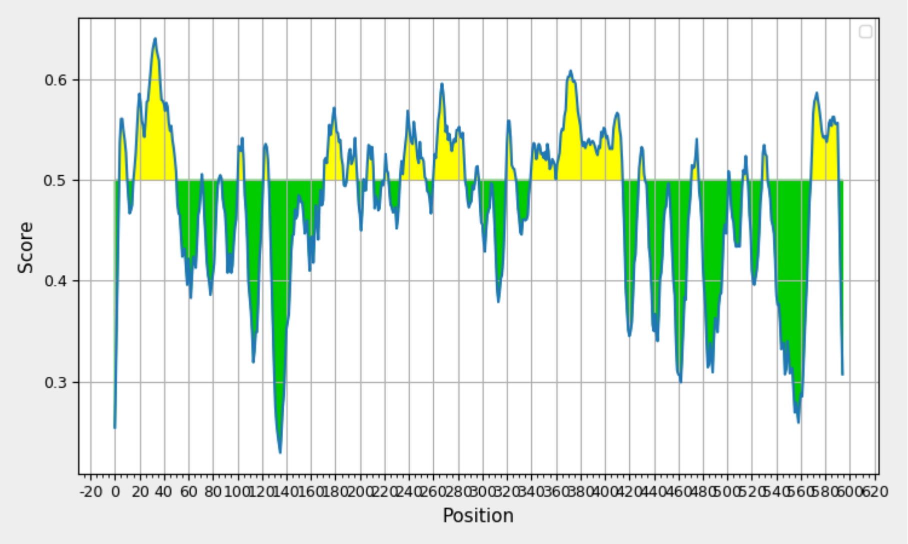
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 15 | 305 | 306 | RG | 2 |
| 16 | 318 | 324 | FGDNRKS | 7 |
| 17 | 334 | 357 | NATVFTDELDLKLEKATPDMLGST | 24 |
| 18 | 359 | 412 | SITITKEDTIILNGEGSKDAIAQRCEQIRSVISDPATSDYEKEKLQERLAKLSG | 54 |
| 19 | 426 | 432 | EVGEKKD | 7 |
| 20 | 450 | 450 | **L** | 1 |
| 21 | 469 | 474 | **NPTNFD** | 6 |
| 22 | 499 | 500 | LE | 2 |
| 23 | 513 | 514 | AG | 2 |
| 24 | 527 | 532 | YVDMIG | 6 |
| 25 | 567 | 588 | **PEEKVPAGSGAGGMGGGMGGMG** | 22 |

**Predicted peptides: XP_010763632 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 11 | FTSSRAL | 7 |
| 2 | 17 | 51 | SSASSTRAPLSRFRSAGVGLQQQRF AHKELKFGVE | 35 |
| 3 | 72 | 72 | G | 1 |
| 4 | 86 | 88 | SPK | 3 |
| 5 | 102 | 106 | **LQDKF** | 5 |
| 6 | 123 | 126 | **EVAG** | 4 |
| 7 | 172 | 187 | QANKRDITTTEEIAQV | 16 |
| 8 | 191 | 198 | SANGDTHV | 8 |
| 9 | 204 | 204 | N | 1 |
| 10 | 207 | 212 | **EKVGKE** | 6 |
| 11 | 221 | 224 | KTID | 4 |
| 12 | 234 | 255 | RFDRGYVSPYFITDTKAQKVEF | 22 |
| 13 | 261 | 286 | LLSEKKISAVQDIIPALEASTSLRRP | 26 |
| 14 | 296 | 298 | GEA | 3 |
| 15 | 321 | 328 | FGDNRKSI | 8 |
| 16 | 341 | 415 | FTDELDLKLEKATPDMLGSTGSITITK EDTIILNGEGSKDAIAQRCEQIRSVIS | 75 |



| | | | | |
|---|---|---|---|---|
| | | | DPATSDYEKEKLQERLAKLSG | |
| 17 | 429 | 433 | EVGEK | 5 |
| 18 | 472 | 477 | **NPTNFD** | 6 |
| 19 | 502 | 502 | **L** | 1 |
| 20 | 514 | 517 | DFAS | 4 |
| 21 | 530 | 533 | YVDM | 4 |
| 22 | 570 | 591 | **PEEKVPAGSGAGGMGGGMGGMG** | 22 |

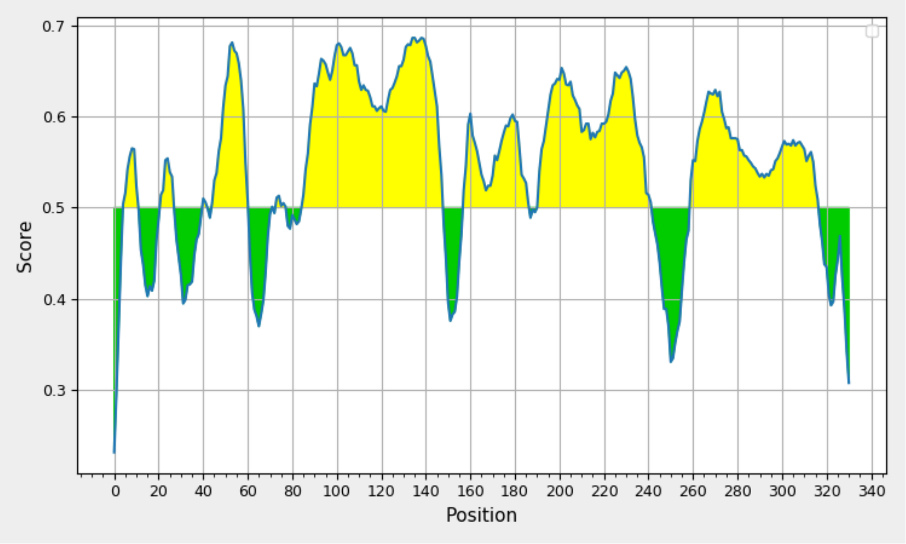
**Protein name: Uncharacterized protein**

**Predicted peptides: XP_002797075 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 11 | ATRQVVN | 7 |
| 2 | 22 | 27 | SPRTLV | 6 |
| 3 | 41 | 42 | EV | 2 |
| 4 | 45 | 61 | FLNLKNTPSPRARNTGR | 17 |
| 5 | 72 | 72 | A | 1 |
| 6 | 74 | 78 | NAAVE | 5 |
| 7 | 86 | 148 | IPSLSKLLPESSMFNSSKESYPT<br>KSALAKPRIKARTKEARRNRERDK<br>KREKKLADYGDGNSPE | 63 |
| 8 | 158 | 187 | SHHDHNVAVMQNPYYNAFHVAT<br>NSLEVQDL | 30 |
| 9 | 192 | 242 | TICSEGVGYSEAPTKSPGDLVLKPPPW<br>LQHMDCFPKKKRMFPFRHQANVLR | 51 |
| 10 | 260 | 317 | REVMEKLKVKKAMTSNEEANEMAQEQEQ<br>EQEQEQEQEQEQGQRREQEQEQEREMEGIR | 58 |

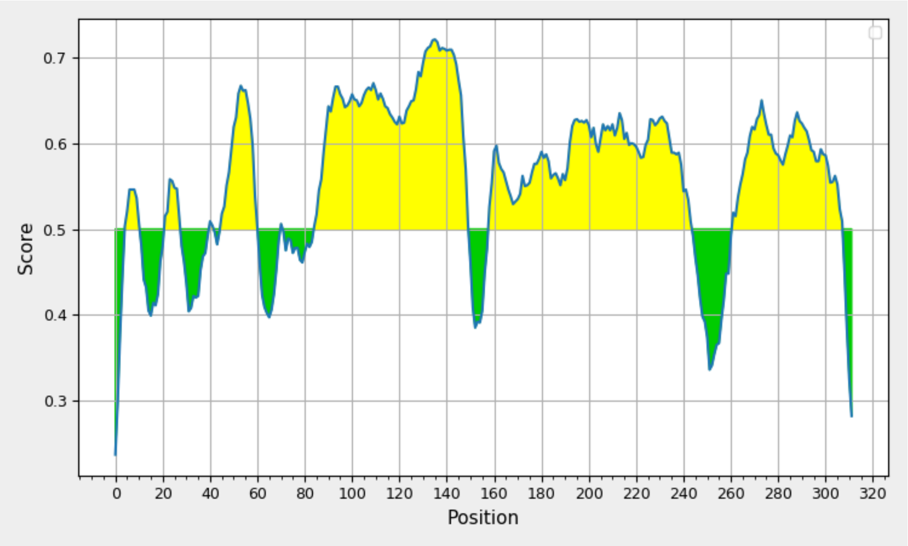
**Bepipred Linear Epitope Prediction 2.0**

**12**



**Predicted peptides: XP_010759641 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 11 | AARQVAN | 7 |
| 2 | 22 | 28 | SPRTLVE | 7 |
| 3 | 41 | 42 | **EV** | 2 |
| 4 | 46 | 61 | LNLKNTPSPRAMNTGR | 16 |
| 5 | 71 | 71 | D | 1 |
| 6 | 85 | 150 | PIPSLSKLLPESSMLNSGKESYPTKSTLAKPRIKARTREARRNRERAKKKRQNLADYDGDGSSPAP | 66 |
| 7 | 159 | 244 | SHHDHNVAVMQNPYYNAFHIATNLLEVQDLMKTATNCSEGVGYSEEPTKSLGDLVLKPPPWLQHMDCFPKKKRMFPFRHQGNVLRI | 86 |
| 8 | 262 | 308 | EVMEKLKVKKAMTSNKKANEMAQEKEQGQGQRIEQEQEQERESRELE | 47 |

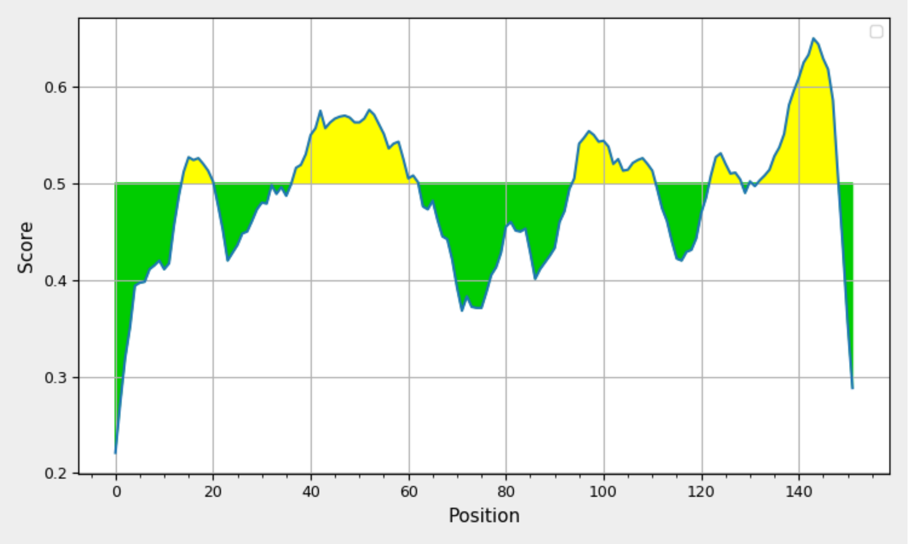


**Protein name: Nucleoside diphosphate kinase**

**Predicted peptides: XP_002794019 [Pb01]**

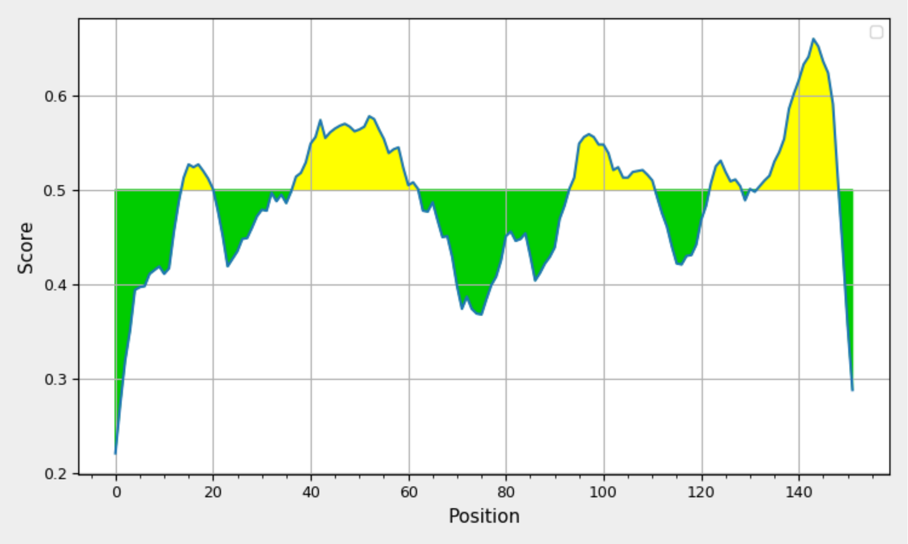
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 15 | 21 | **GVQRGLV** | 7 |
| 2 | 38 | 63 | **IKLVTPSKEHLEKHYEDLSSKPFFNG** | 26 |
| 3 | 95 | 111 | NPADSAPGTIRGDYAID | 17 |
| 4 | 123 | 129 | **VESAKKE** | 7 |
| 5 | 131 | 131 | **A** | 1 |
| 6 | 133 | 149 | **WFKPEELVKYEQSQANW** | 17 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010762888 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 15 | 21 | GVQRGLV | 7 |
| 2 | 38 | 63 | IKLVTPSKEHLEKHYEDLSSKPFFNG | 26 |
| 3 | 94 | 111 | TNPADSAPGTIRGDYAID | 18 |
| 4 | 123 | 129 | VESAKKE | 7 |
| 5 | 131 | 131 | A | 1 |
| 6 | 133 | 149 | WFKPEELVKYEQSQANW | 17 |

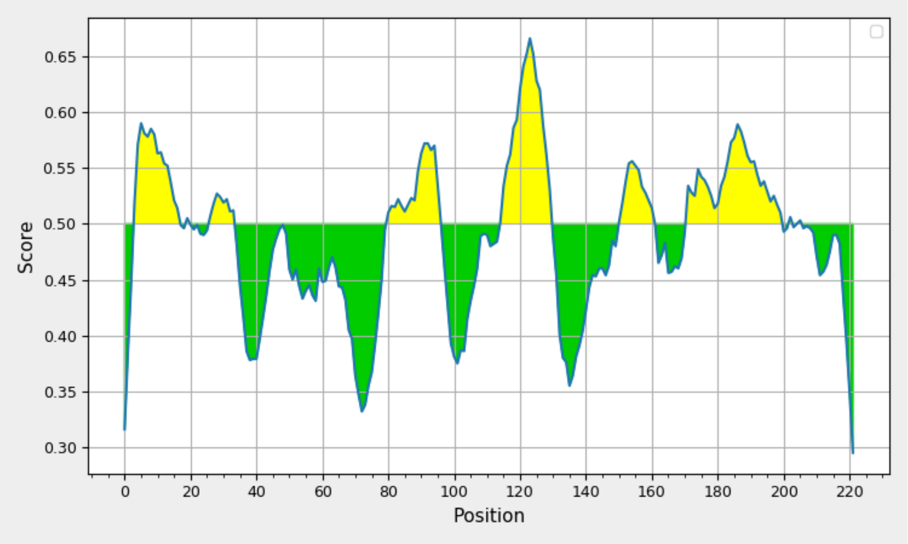


**Protein name: Uncharacterized protein (Thioredoxin-like superfamily)**

**Predicted peptides: XP_002794671 [Pb01]**

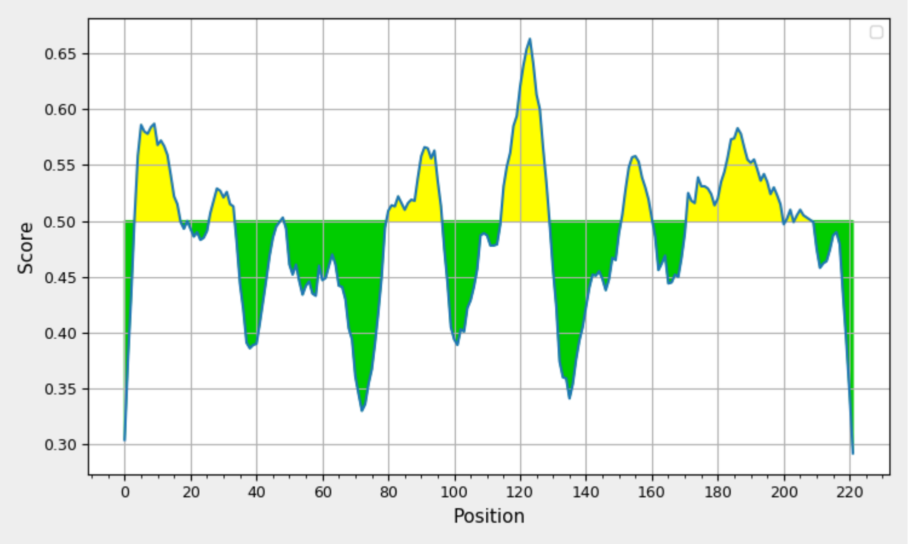
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 4 | 17 | EQRAPLRLGSTAPN | 14 |
| 2 | 20 | 20 | **A** | 1 |
| 3 | 27 | 34 | IDFHEFIG | 8 |
| 4 | 81 | 97 | **KSHYDWINDINEVTGSD** | 17 |
| 5 | 115 | 130 | DMIDYQDTTNVDEKGM | 16 |
| 6 | 151 | 161 | SYPASTGRNAA | 11 |
| 7 | 172 | 200 | **TTDKNGVNTPINWNVGDDVIIPPAVKTED** | 29 |
| 8 | 203 | 203 | K | 1 |
| 9 | 205 | 206 | FG | 2 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010758730 [Pb18]**

| ] | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 4 | 17 | EHRAPLRLGSTAPN | 14 |
| 2 | 20 | 20 | **A** | 1 |
| 3 | 27 | 34 | IDFYEFIG | 8 |
| 4 | 49 | 49 | P | 1 |
| 5 | 81 | 97 | **KSHYDWINDINEVTGSD** | 17 |
| 6 | 116 | 129 | MIDYQDTTNVDEKG | 14 |
| 7 | 152 | 161 | YPASTGRNAA | 10 |
| 8 | 172 | 200 | **TTDKNGVNTPINWNVGDDVIIPPAVKTED** | 29 |
| 9 | 202 | 203 | IK | 2 |
| 10 | 205 | 209 | FGDVR | 5 |

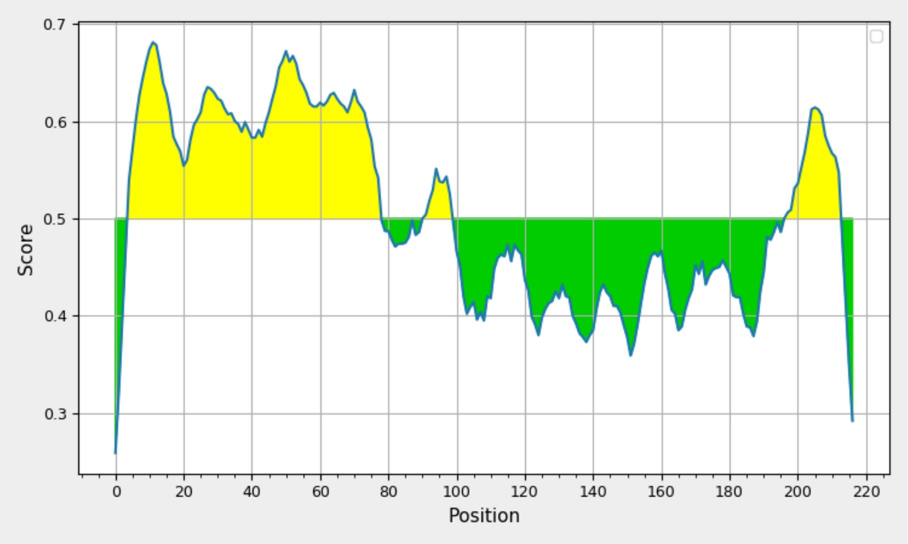


**Protein name: Deoxyuridine 5'-triphosphate nucleotidohydrolase**

**Predicted peptides: XP_002792326 [Pb01]**

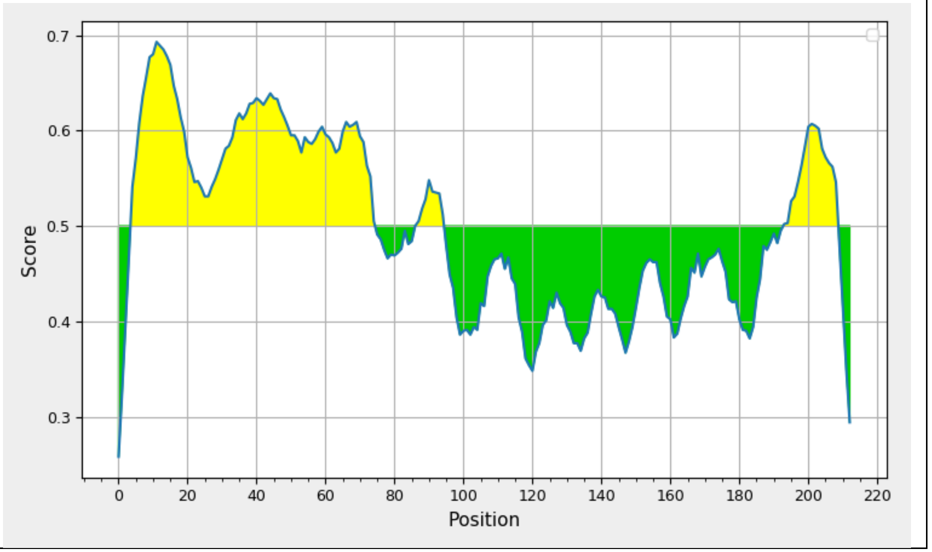
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 78 | TTPRPQTKASEESTTTNITANHP<br>PPSLPSSPLPKRAKITDMARATESSTA<br>PAAASSETATSTNPAVTSLSQLTP | 74 |
| 2 | 92 | 99 | APTRGSAF | 8 |
| 3 | 197 | 213 | VLEVEELEESVRGVGGF | 17 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010763035 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 75 | TTPRPQTKASAESTTVNHPP<br>PSLPSSPLPKRAKITDMAPATESFTAPA<br>AAYSETATSTNPAVTSLSQLTPP | 71 |
| 2 | 88 | 95 | APTRGSAF | 8 |
| 3 | 194 | 209 | LEVEELEESVRGVGGF | 16 |

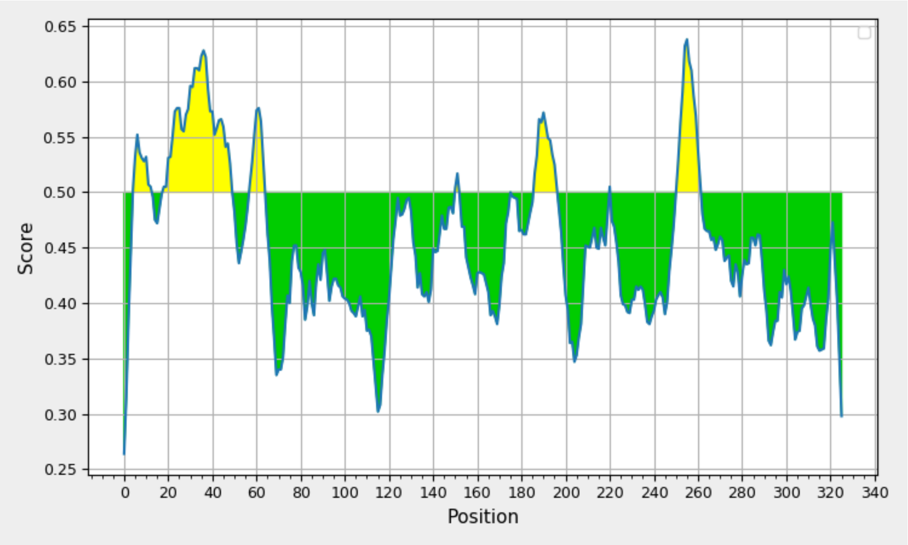


**Protein name: Proliferating cell nuclear antigen**

**Predicted peptides: XP_015700963 [Pb01]**

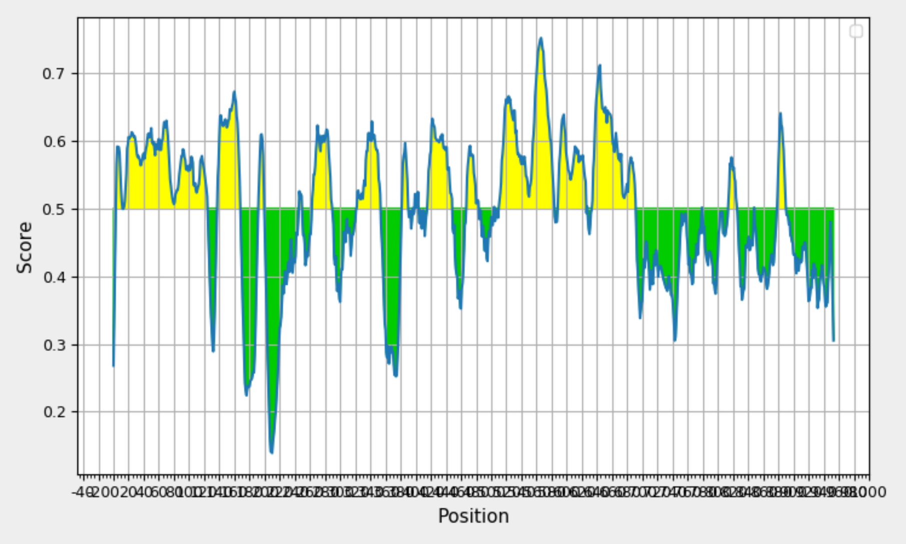
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 13 | LPQTLYSIP | 9 |
| 2 | 19 | 50 | IPTDTLNLSFTHISTTPGRTGAQYLHSTISPA | 32 |
| 3 | 58 | 64 | FNIYPPQ | 7 |
| 4 | 151 | 152 | QN | 2 |
| 5 | 187 | 197 | MDIDQEHLAIP | 11 |
| 6 | 221 | 221 | N | 1 |
| 7 | 251 | 262 | RQHTNVDKPDQN | 12 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010759909 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 12 | SRFSTDSA | 8 |
| 2 | 15 | 125 | TGEGEGQEDWALQEDLSPSQPPLDSSTANFAPRGPPTFQDRIRNRLPVPRQLKPLAKHQTLARISDFCKVWGRFFRFHDVDFPLLTGYTFRIDKAVVSTTIGKSENERFLE | 111 |
| 3 | 139 | 168 | EQCAPSYSAITGLLSNTRNNEDQSSTRAAN | 30 |
| 4 | 193 | 200 | SRQGSDWN | 8 |
| 5 | 247 | 250 | SFDS | 4 |
| 6 | 264 | 290 | LVSRGYRLSTPMPPITRLEEQTQTRRC | 27 |
| 7 | 323 | 354 | NLEKYYDIYDFSPEELEETNALLADSAMEDGT | 32 |
| 8 | 383 | 391 | EGGEADIAN | 9 |
| 9 | 397 | 397 | E | 1 |
| 10 | 400 | 404 | QRLVA | 5 |
| 11 | 417 | 449 | LNEQDHNMIPPNPQAKLAPNKDHHRAQLRRLNS | 33 |
| 12 | 468 | 484 | SDASLERATDDTDFGTT | 17 |
| 13 | 505 | 505 | A | 1 |
| 14 | 511 | 584 | FATLENSGRLSRPTSSLKSPASPTFS | 74 |



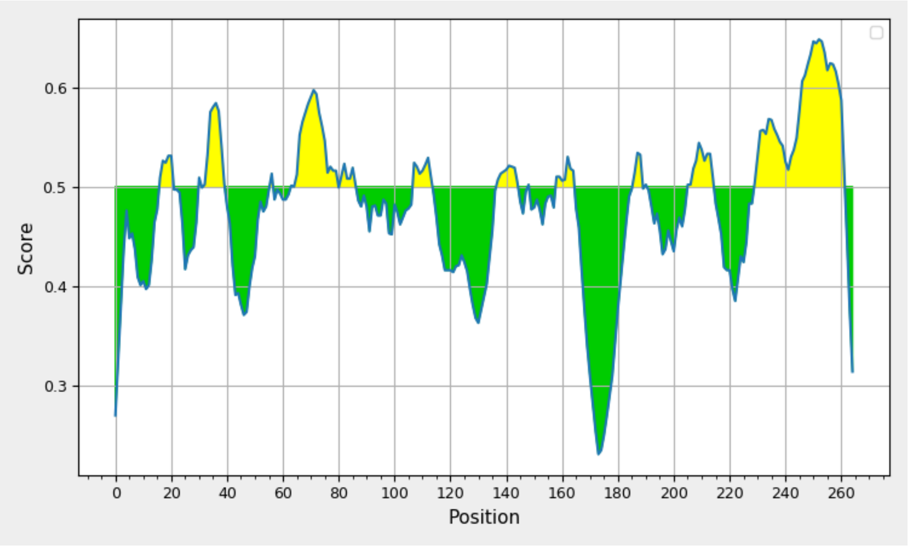
| | | | | |
|---|---|---|---|---|
| | | | LSGVTAVDGGPPEALRALTGEDQQQQQQQQQQHQQSLQSPDNNMDDDE | |
| 15 | 589 | 626 | IALPLKRNSMSREERIARMKEERARQAMVREKLDANTH | 38 |
| 16 | 628 | 628 | L | 1 |
| 17 | 635 | 692 | IKLRPRKKASSNGARLPLTRRDSCLATRRRALWPRKSSTAKLQLPSTLHRAPLSPTNS | 58 |
| 18 | 780 | 780 | **N** | 1 |
| 19 | 815 | 826 | MDIDQEHLAIPD | 12 |
| 20 | 849 | 849 | N | 1 |
| 21 | 880 | 891 | QHTNVDKPDQNV | 12 |

**Protein name: Uncharacterized protein (14-3-3 Superfamily)**

**Predicted peptides: XP_002791205 [Pb01]**

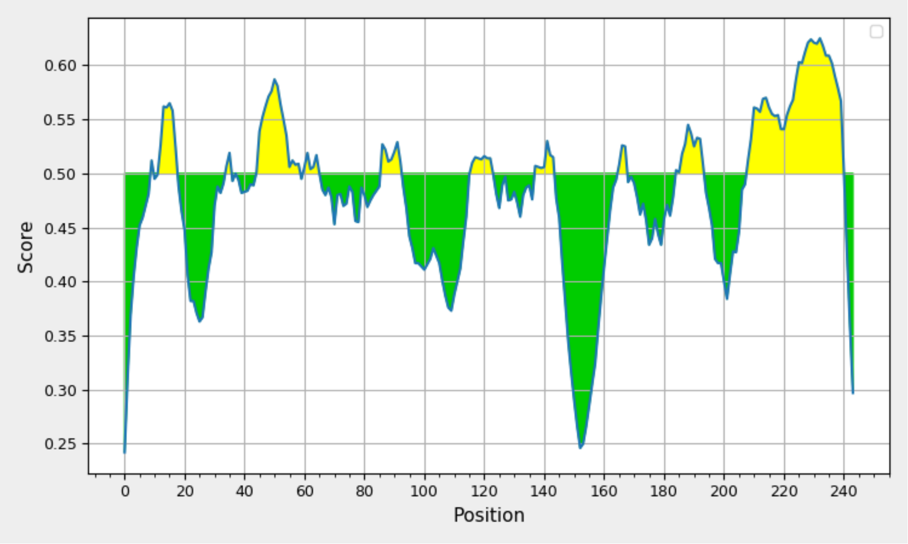
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 17 | 21 | ERYEE | 5 |
| 2 | 31 | 31 | **S** | 1 |
| 3 | 33 | 40 | DKELSVEE | 8 |
| 4 | 57 | 57 | A | 1 |
| 5 | 64 | 80 | SIEQKEESKGNEAQVAL | 17 |
| 6 | 82 | 87 | **KEYRQN** | 6 |
| 7 | 108 | 114 | **IASAETG** | 7 |
| 8 | 138 | 145 | DKRKDSAD | 8 |
| 9 | 149 | 149 | E | 1 |
| 10 | 159 | 165 | **QTDLAPT** | 7 |
| 11 | 187 | 189 | **PDQ** | 3 |
| 12 | 191 | 191 | C | 1 |
| 13 | 206 | 215 | **DTLSEESYKD** | 10 |
| 14 | 230 | 262 | WTSSEAEPAPEVAPAPAEQ<br>KDEAPASTSEDAPK | 33 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010759842 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 10 | 10 | **S** | 1 |
| 2 | 13 | 18 | KELSVE | 6 |
| 3 | 35 | 36 | RA | 2 |
| 4 | 38 | 38 | W | 1 |
| 5 | 45 | 59 | EQKEESKGNEAQVAL | 15 |
| 6 | 61 | 66 | **KEYRQN** | 6 |
| 7 | 87 | 93 | **IASAETG** | 7 |
| 8 | 117 | 123 | DKRKDSA | 7 |
| 9 | 138 | 144 | **QTDLAPT** | 7 |
| 10 | 166 | 168 | **PDQ** | 3 |
| 11 | 185 | 194 | **DTLSEESYKD** | 10 |
| 12 | 209 | 241 | WTSSEAEPAPEVAPAPSEQKDEA PAATSEDAPK | 33 |

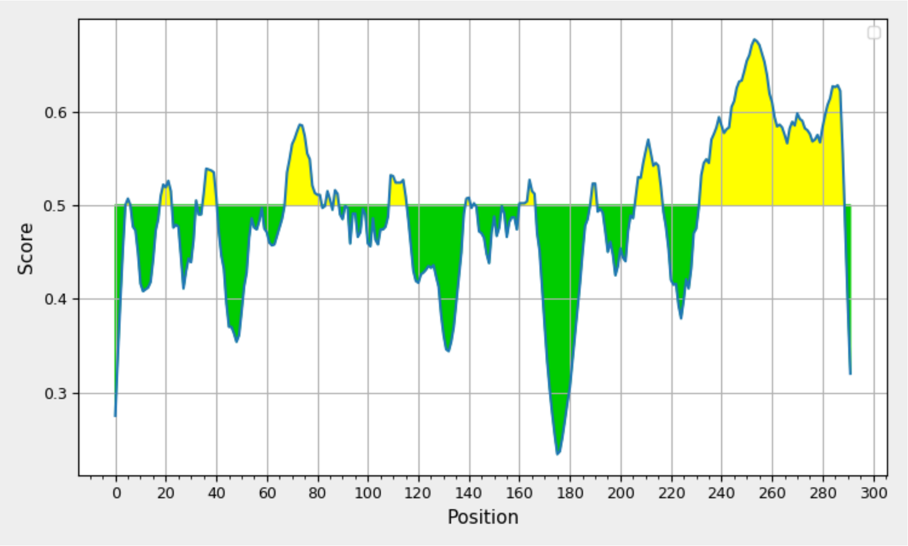


**Protein name: 14-3-3 family protein epsilon**

**Predicted peptides: XP_002796914 [Pb01]**

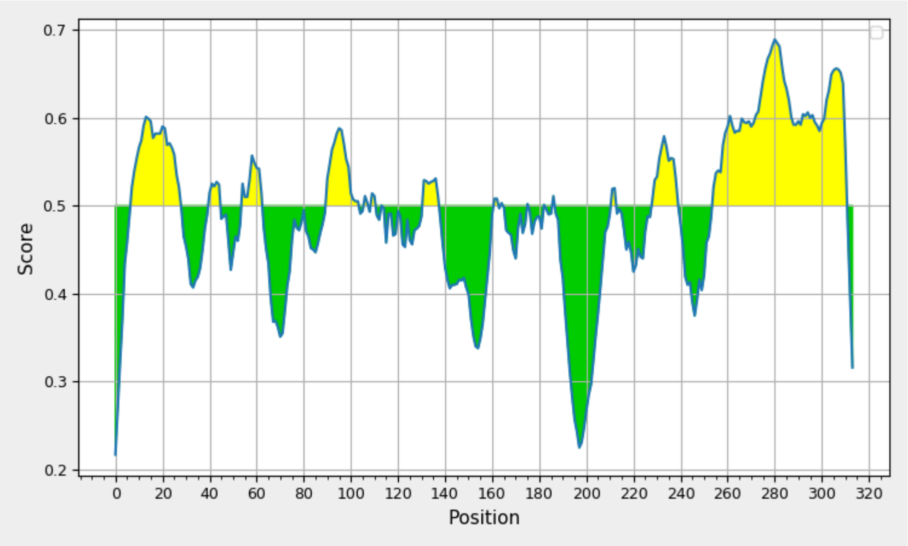
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 6 | RE | 2 |
| 2 | 19 | 23 | **ERYDE** | 5 |
| 3 | 33 | 33 | N | 1 |
| 4 | 36 | 41 | GELTVD | 6 |
| 5 | 69 | 82 | **QKEDSKGSEKHVAI** | 14 |
| 6 | 85 | 86 | **EY** | 2 |
| 7 | 88 | 89 | **QK** | 2 |
| 8 | 110 | 116 | **IPKAESG** | 7 |
| 9 | 140 | 141 | **NK** | 2 |
| 10 | 143 | 143 | **K** | 1 |
| 11 | 161 | 167 | QTELTPT | 7 |
| 12 | 189 | 191 | PDR | 3 |
| 13 | 207 | 217 | **LDSLSEESYRD** | 11 |
| 14 | 233 | 289 | TSSDGAEPEPVAAGDGKDDKTAEGEEGPATATTTDAPAPEEVAAPAAADEEPKKEGT | 57 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010759301 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 8 | 28 | LPPIHSSGVCRANYNLSYSVK | 21 |
| 2 | 41 | 45 | **ERYDE** | 5 |
| 3 | 55 | 63 | NLGGELTVD | 9 |
| 4 | 91 | 104 | **QKEDSKGSEKHVAI** | 14 |
| 5 | 107 | 108 | **EY** | 2 |
| 6 | 110 | 111 | **QK** | 2 |
| 7 | 132 | 138 | **IPKAESG** | 7 |
| 8 | 162 | 163 | **NK** | 2 |
| 9 | 165 | 165 | **K** | 1 |
| 10 | 176 | 176 | K | 1 |
| 11 | 183 | 183 | Q | 1 |
| 12 | 187 | 187 | T | 1 |
| 13 | 212 | 213 | DR | 2 |
| 14 | 229 | 239 | **LDSLSEESYRD** | 11 |
| 15 | 255 | 311 | TSSDGAEPEPAAAGDGKDDKTAEGEEGS<br>ATATTADPPAPEEMAAPAAADEEPKKEGT | 57 |

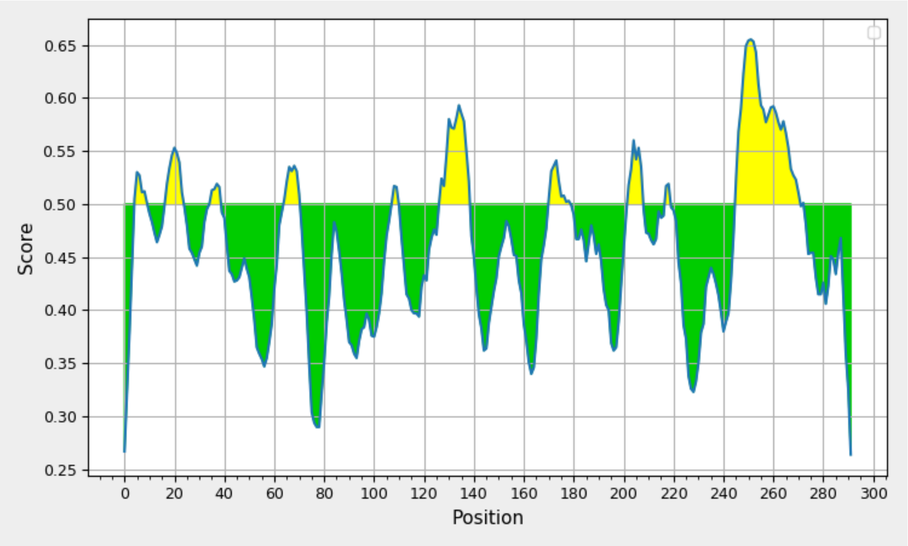


**Protein name: Spermidine synthase**

**Predicted peptides: XP_002793533 [Pb01]**

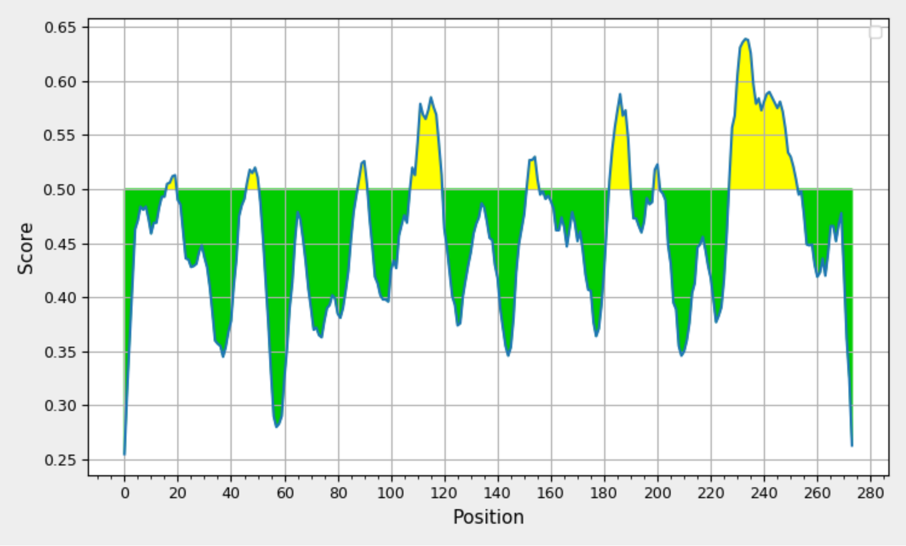
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 10 | THPTIK | 6 |
| 2 | 18 | 24 | SDMWPGQ | 7 |
| 3 | 35 | 39 | HHEKS | 5 |
| 4 | 65 | 71 | TERDEFS | 7 |
| 5 | 108 | 110 | ETV | 3 |
| 6 | 128 | 139 | **KYLPGMSVGFQH** | 12 |
| 7 | 171 | 179 | EGPAEALFQ | 9 |
| 8 | 203 | 208 | QWLHLS | 6 |
| 9 | 218 | 219 | RE | 2 |
| 10 | 246 | 271 | **KDSSRDVREPVRTWTREEEEKLCRYY** | 26 |
| 11 | 273 | 273 | K | 1 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010760066 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 17 | 20 | HEKS | 4 |
| 2 | 47 | 51 | ERDEF | 5 |
| 3 | 89 | 92 | ETVE | 4 |
| 4 | 109 | 120 | **KYLPGMSVGFQH** | 12 |
| 5 | 152 | 156 | EGPAE | 5 |
| 6 | 183 | 191 | ENQWLHLSL | 9 |
| 7 | 200 | 201 | **RE** | 2 |
| 8 | 228 | **253** | **KDSSRDVREPVRTWTREEEEKLCRYY** | 26 |

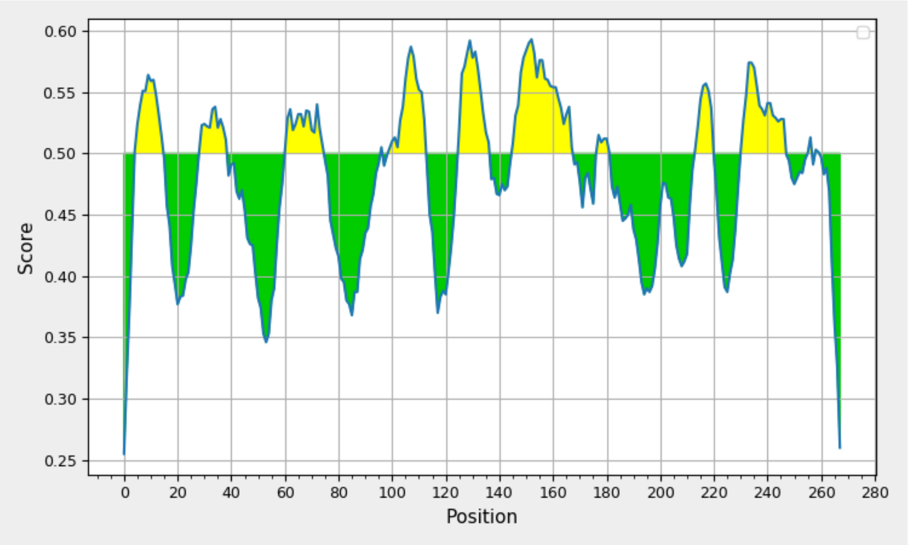


**Protein name: Phosphomannomutase**

**Predicted peptides: XP_002797030 [Pb01]**

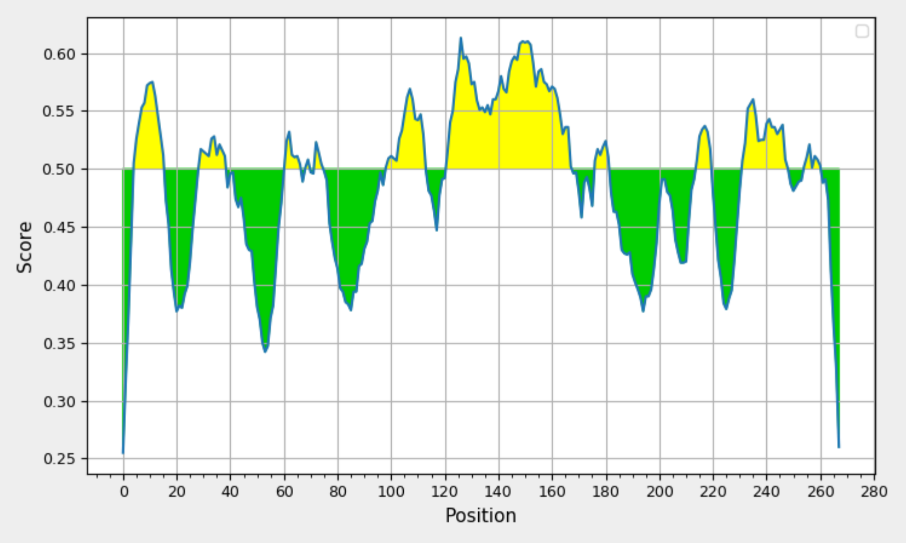
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 15 | AGVYPPLEARP | 11 |
| 2 | 29 | 39 | LTPARGTVAPE | 11 |
| 3 | 61 | 75 | LAKQQEQLGTQTTDV | 15 |
| 4 | 97 | 97 | M | 1 |
| 5 | 100 | 113 | NSFIKWLGEEKYQN | 14 |
| 6 | 126 | 137 | KLPRKRGTFVEY | 12 |
| 7 | 146 | 168 | PVGRSASVEERNEFEEFDKVHNI | 23 |
| 8 | 178 | 182 | KEFAD | 5 |
| 9 | 214 | 220 | EKNISGV | 7 |
| 10 | 231 | 247 | KCFKGGNDHEIYEDSRT | 17 |
| 11 | 256 | 257 | DD | 2 |
| 12 | 259 | 260 | MR | 2 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010759656 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 16 | AGVYPPLEARPL | 12 |
| 2 | 30 | 39 | TPARGTVAPE | 10 |
| 3 | 62 | 67 | AKQQEQ | 6 |
| 4 | 69 | 70 | GT | 2 |
| 5 | 73 | 75 | TDV | 3 |
| 6 | 99 | 113 | SNSFIKWLGEEKYQN | 15 |
| 7 | 122 | 168 | ISSVKLPRKRGTFVEYRNGMVNISPVGRSASVEERNEFEEFDKVHNI | 47 |
| 8 | 177 | 182 | RKEFAD | 6 |
| 9 | 215 | 220 | KNISGV | 6 |
| 10 | 232 | 249 | CFKGGNDHEIYEDSRTIG | 18 |
| 11 | 255 | 261 | PDDTMRQ | 7 |

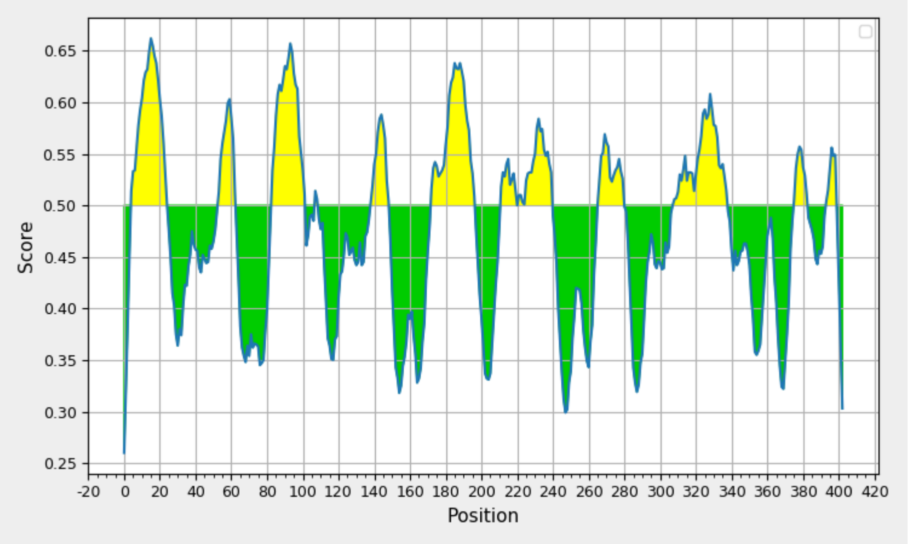


**Protein name: 4-hydroxyphenylpyruvate dioxygenase**

**Predicted peptides: XP_002789912 [Pb01]**

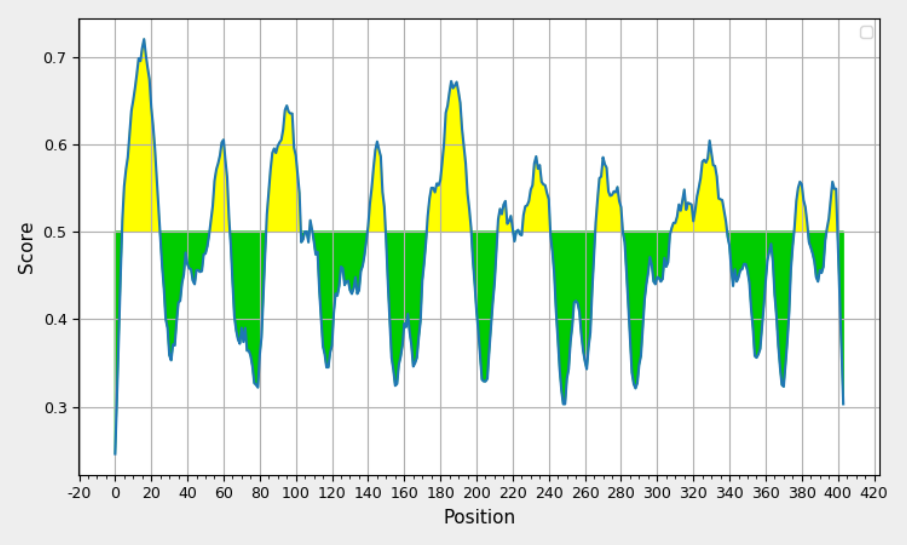
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 25 | AVSPPPSTRGTQQHNDLSSYK | 21 |
| 2 | 54 | 63 | AYRGLETGSR | 10 |
| 3 | 84 | 102 | RSLDDLSQFSPEEQALLTE | 19 |
| 4 | 108 | **109** | **EK** | 2 |
| 5 | 139 | 149 | VSGIKTLEDCQ | 11 |
| 6 | 173 | 197 | YNGIFLPGYREENTKDPLSSLLPPV | 25 |
| 7 | 212 | 240 | EEMEKVCEYYEKALGFHRFWSVDDKDICT | 29 |
| 8 | 266 | 280 | **KGKKQSQIEEYVNFY** | 15 |
| 9 | 309 | 338 | FIKVPETYYTEMKQRLERSGMKLKEDFEML | 30 |
| 10 | 376 | 383 | **NFSGFGAG** | 8 |
| 11 | 394 | 399 | **REQALR** | 6 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010763814 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 25 | AVSPPPTTRDTQQHNNDLSSY | 21 |
| 2 | 54 | 64 | IAYRGLETGSR | 11 |
| 3 | 85 | 103 | RSLDDLSQFSPEEQTLLTE | 19 |
| 4 | 106 | 107 | SH | 2 |
| 5 | 109 | 110 | **EK** | 2 |
| 6 | 141 | 150 | SSIKTLEDSQ | 10 |
| 7 | 174 | 198 | YKGIFLPGYREEHTKDPLSSLLPPV | 25 |
| 8 | 213 | 221 | EEMEKVCEY | 9 |
| 9 | 224 | 224 | K | 1 |
| 10 | 227 | 241 | GFHRFWSVDDKDICT | 15 |
| 11 | 267 | 281 | **KGKKQSQIEEYVNFY** | 15 |
| 12 | 309 | 339 | EFIKVPETYYTEMKQRLERSGMKLKEDFEML | 31 |
| 13 | 377 | 384 | **NFSGFGAG** | 8 |
| 14 | 395 | 400 | **REQALR** | 6 |

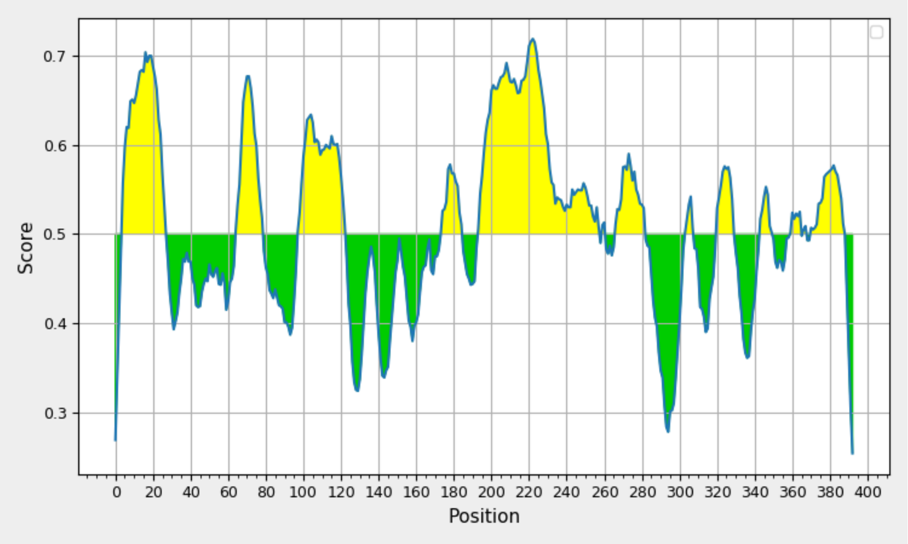


**Protein name: Uncharacterized protein (Cyclophilin superfamily )**

**Predicted peptides: XP_015701903 [Pb01]**

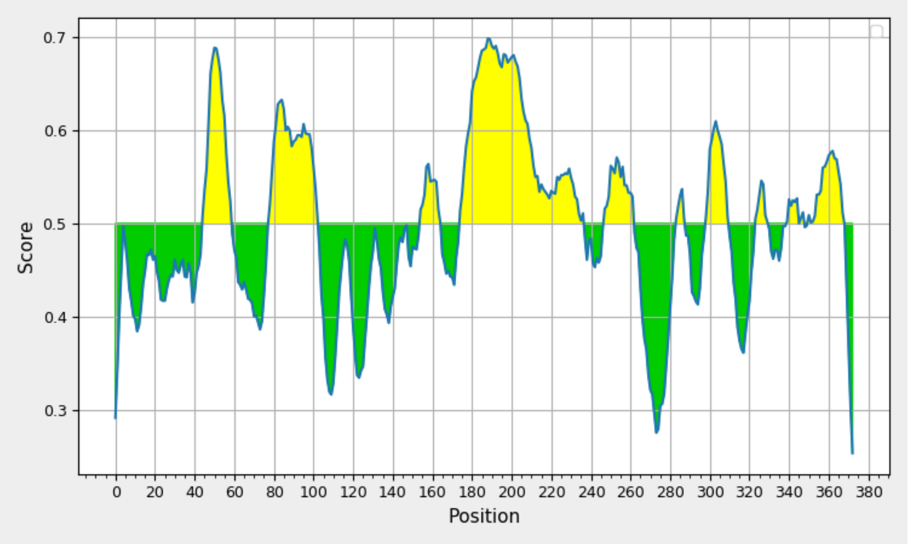
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 27 | TGTSSDSLPSNHTRSPRDALERR | 23 |
| 2 | 65 | 79 | TGEKGEGKSGKLLSY | 15 |
| 3 | 98 | 123 | FTAFNGTGGESIYGEKFDDENFDLKH | 26 |
| 4 | 175 | 185 | KSQTDTSDKPY | 11 |
| 5 | 194 | 258 | GQLSGDSYEAAKEVSVDETGDKYEDYPEDAGETLSGAEYYKIASEVKEFGNKAFKSGNLDLGLEK | 65 |
| 6 | 260 | 261 | QK | 2 |
| 7 | 267 | 282 | NECPEPSDSDPPELQG | 16 |
| 8 | 304 | 308 | **RFDDA** | 5 |
| 9 | 321 | 329 | AAQAKDTDR | 9 |
| 10 | 344 | 350 | **KDDEAAL** | 7 |
| 11 | 360 | 365 | **APGDAA** | 6 |
| 12 | 367 | 368 | **VS** | 2 |
| 13 | 371 | 388 | ARVKKTIAEQQRKEKEML | 18 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010761900 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 45 | 59 | TGEKGEGKSGKQLSY | 15 |
| 2 | 79 | 103 | TAFNGTGGESIYGEKFDDENFDLKH | 25 |
| 3 | 155 | 165 | KSPTDTSDKPH | 11 |
| 4 | 175 | 237 | QLSGDSYEAAKEVSVDETGDKYED<br>YPEDAGETLSGAEYYKIASEVK<br>EFGNKAFKSGNLDLGLE | 63 |
| 5 | 248 | 262 | ECPEPSDSDPPELQG | 15 |
| 6 | 284 | 288 | **RFDDA** | 5 |
| 7 | 299 | 310 | ATAAQAKDTDRA | 12 |
| 8 | 324 | 330 | **KDDEAAL** | 7 |
| 9 | 340 | 345 | **APGDAA** | 6 |
| 10 | 347 | 348 | **VS** | 2 |
| 11 | 351 | 368 | ARVKKSIAEQQRKEKEML | 18 |

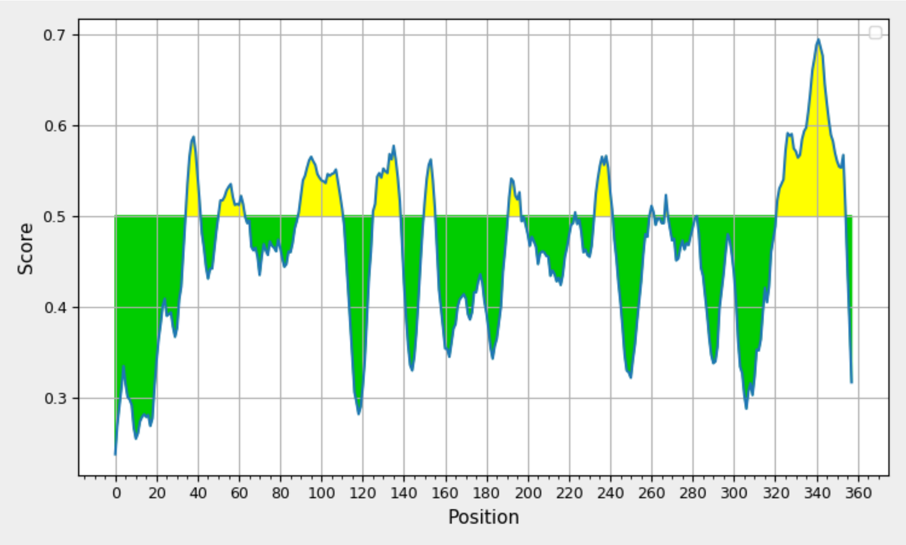


**Protein name: Thioredoxin reductase**

**Predicted peptides: XP_002791109 [Pb01]**

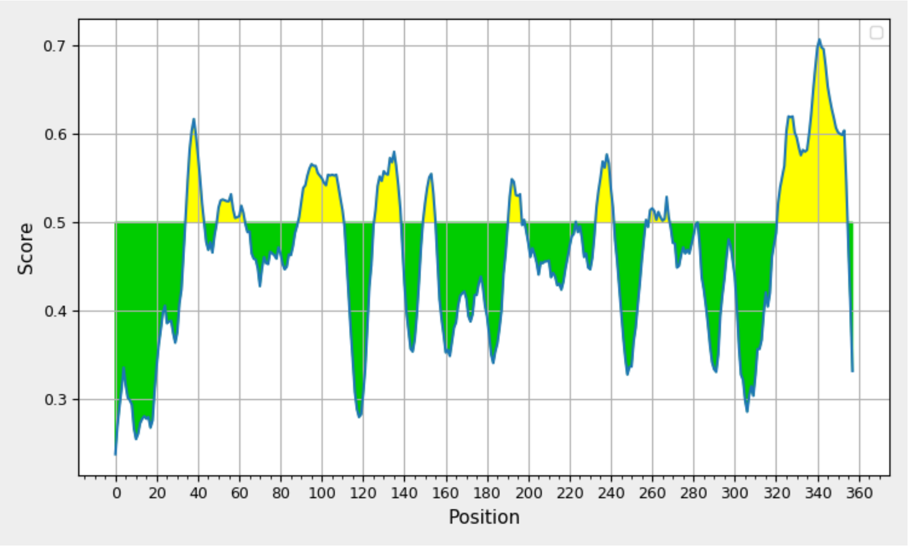
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 36 | 42 | MANGTAA | 7 |
| 2 | 52 | 63 | VENFPGFPHGIG | 12 |
| 3 | 90 | 111 | **VDLSCRPFKLWKEFSDGPDDAP** | 22 |
| 4 | 126 | 139 | ARRLDLPGEQQYWQ | 14 |
| 5 | 151 | 156 | AVPIFR | 6 |
| 6 | 192 | 197 | **LRASKT** | 6 |
| 7 | 224 | 224 | **A** | 1 |
| 8 | 234 | 242 | IKNVVSGVE | 9 |
| 9 | 260 | 262 | TAL | 3 |
| 10 | 268 | 268 | E | 1 |
| 11 | 283 | 283 | Y | 1 |
| 12 | 322 | 355 | AESEGGDEPPFVATSIEQSNQ GENAPPTLEYTSN | 34 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010756960 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 35 | 43 | MMANGTAAG | 9 |
| 2 | 51 | 63 | DIENFPGFPNGIG | 13 |
| 3 | 90 | 111 | **VDLSCRPFKLWKEFSDGPDDAP** | 22 |
| 4 | 127 | 139 | RRLDLPGEQQYWQ | 13 |
| 5 | 150 | 156 | GAVPIFR | 7 |
| 6 | 192 | 197 | **LRASKT** | 6 |
| 7 | 199 | 199 | A | 1 |
| 8 | 224 | 224 | **A** | 1 |
| 9 | 234 | 242 | IKNVVSGGE | 9 |
| 10 | 258 | 258 | P | 1 |
| 11 | 260 | 269 | TALVKGQIET | 10 |
| 12 | 322 | 355 | AESEGGDEPPLVATSIEQSNQG<br>ENAPPTLEYTSN | 34 |

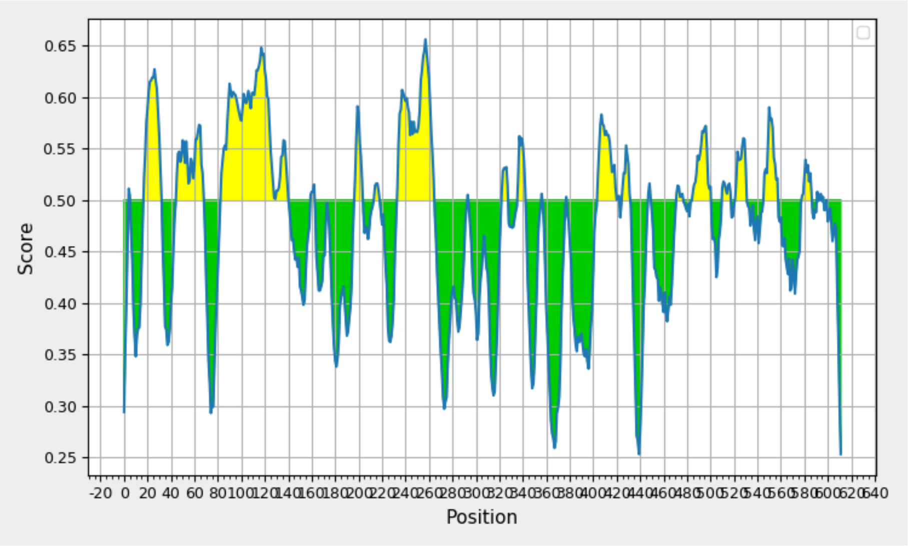


**Protein name: ATP synthase subunit beta**

**Predicted peptides: XP_002789970 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 6 | RY | 2 |
| 2 | 18 | 33 | LAANPIAQRPSESRFE | 16 |
| 3 | 46 | 69 | LTKIRSSHPHFLDSLTRNLAPHPV | 24 |
| 4 | 84 | 141 | SPFRQVPPPLLHITSIMFKSGVART FARSALARSSLRLPQNPALRSLASRYASTSSGQ | 58 |
| 5 | 160 | 163 | **EQLP** | 4 |
| 6 | 198 | 204 | **GTEGLVR** | 7 |
| 7 | 214 | 218 | PIMIP | 5 |
| 8 | 234 | 265 | PIDERGPIKHSKKAPIHAEAPEFVEQSTTAEV | 32 |
| 9 | 294 | 294 | **G** | 1 |
| 10 | 323 | 328 | **TREGND** | 6 |
| 11 | 337 | 343 | RVIQLDG | 7 |
| 12 | 357 | 357 | P | 1 |
| 13 | 378 | 378 | E | 1 |
| 14 | 405 | 423 | GRIPSAVGYQPTLAVDMGG | 19 |

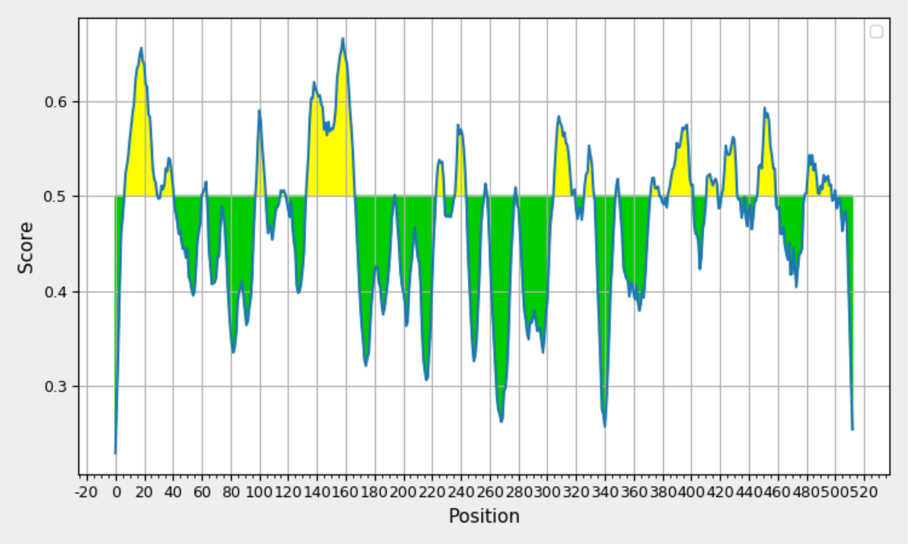
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 15 | 426 | 432 | **ERITTTT** | 7 |
| 16 | 448 | 450 | DLT | 3 |
| 17 | 472 | 477 | SELGIY | 6 |
| 18 | 486 | 501 | KSRMLDPRIVGEEHYE | 16 |
| 19 | 511 | 518 | **QEYKSLQD** | 8 |
| 20 | 522 | 531 | **ILGMDELSEA** | 10 |
| 21 | 547 | 558 | SQPFTVAQVFTG | 12 |
| 22 | 579 | 587 | GEGDDLPEA | 9 |
| 23 | 592 | 592 | V | 1 |
| 24 | 594 | 595 | DF | 2 |
| 25 | 597 | 597 | S | 1 |

**Predicted peptides: XP_010763627 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 8 | 30 | RTFARSALARHSLRLPQNPALRS | 23 |
| 2 | 33 | 41 | SRYASTSSG | 9 |
| 3 | 61 | 64 | **EQLP** | 4 |
| 4 | 99 | 105 | **GTEGLVR** | 7 |
| 5 | 116 | 119 | IMIP | 4 |
| 6 | 134 | 167 | DPIDERGPIKHSKKAPIHAEAPEFVEQSTTAEVL | 34 |
| 7 | 195 | 195 | **G** | 1 |
| 8 | 224 | 229 | **TREGND** | 6 |
| 9 | 237 | 244 | TRVIQLDG | 8 |
| 10 | 258 | 259 | PP | 2 |
| 11 | 279 | 279 | **E** | 1 |
| 12 | 306 | 320 | GRIPSAVGYQPTLAV | 15 |
| 13 | 327 | 333 | **ERITTTT** | 7 |
| 14 | 349 | 350 | DL | 2 |
| 15 | 373 | 379 | SELGIYP | 7 |
| 16 | 385 | 402 | DSKSRMLDPRIVGEEHYE | 18 |



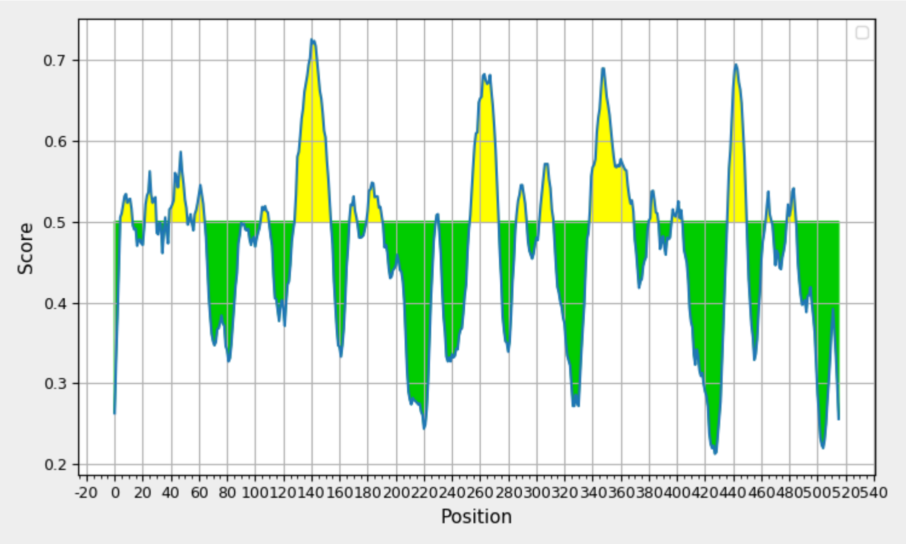
| | | | | |
|---|---|---|---|---|
| 17 | 412 | 419 | **QEYKSLQD** | 8 |
| 18 | 423 | 432 | **ILGMDELSEA** | 10 |
| 19 | 447 | 459 | LSQPFTVAQVFTG | 13 |
| 20 | 480 | 498 | GEGDDLPEAAFYMVGDFES | 19 |
| 21 | 501 | 501 | A | 1 |

**Protein name: Hexokinase**

**Bepipred Linear Epitope Prediction 2.0**

**Predicted peptides: XP_002791907 [Pb01]**

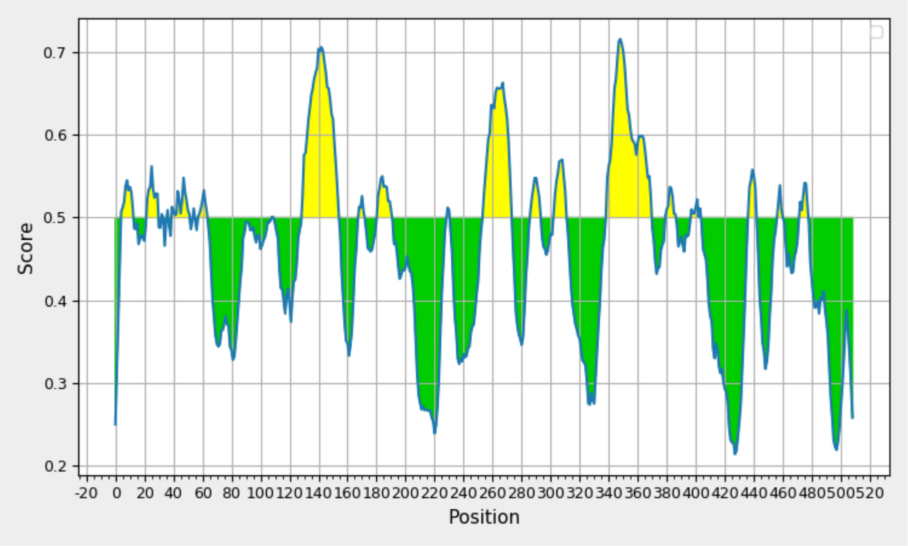
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 13 | SSSSSVLDE | 9 |
| 2 | 23 | 30 | YSAEELNR | 8 |
| 3 | 37 | 37 | **R** | 1 |
| 4 | 40 | 52 | **HEGLEEEGATLRQ** | 13 |
| 5 | 54 | 55 | PT | 2 |
| 6 | 58 | 65 | TAVPEGTE | 8 |
| 7 | 105 | 110 | LMTTKN | 6 |
| 8 | 129 | 154 | HQSEHFDLHIKKRQTGQITAPYTDDH | 26 |
| 9 | 168 | 173 | QHGINS | 6 |
| 10 | 181 | 191 | KGFDIKEAVGK | 11 |
| 11 | 230 | 231 | **GP** | 2 |
| 12 | 254 | 274 | RVTKLDKKNGDSAAAKYDRAT | 21 |
| 13 | 287 | 294 | **DNHLSVLP** | 8 |
| 14 | 304 | 313 | NDSVNPGIQM | 10 |
| 15 | 339 | 370 | AVKLFSNDSAARQNGLVTIIPADSGLHKQWGI | 32 |



| | | | | |
|---|---|---|---|---|
| 16 | 381 | 387 | DDSPAFD | 7 |
| 17 | 398 | 404 | **GIENAST** | 7 |
| 18 | 437 | 450 | GRLRGEGEVEKGDG | 14 |
| 19 | 465 | 468 | PGFE | 4 |
| 20 | 480 | 485 | **GIGENG** | 6 |

**Predicted peptides: XP_010763342 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 13 | SSSSPVLDE | 9 |
| 2 | 23 | 30 | YPAEELNR | 8 |
| 3 | 33 | 34 | RE | 2 |
| 4 | 37 | 37 | **R** | 1 |
| 5 | 40 | 52 | **HEGLEEEGATLRQ** | 13 |
| 6 | 55 | 55 | T | 1 |
| 7 | 58 | 64 | TAVPEGT | 7 |
| 8 | 109 | 110 | KN | 2 |
| 9 | 130 | 155 | QSEHFDLHIKKRQTGEITAPYTDDHI | 26 |
| 10 | 169 | 172 | HGIN | 4 |
| 11 | 182 | 191 | GFDIKEAVGK | 10 |
| 12 | 230 | 231 | **GP** | 2 |



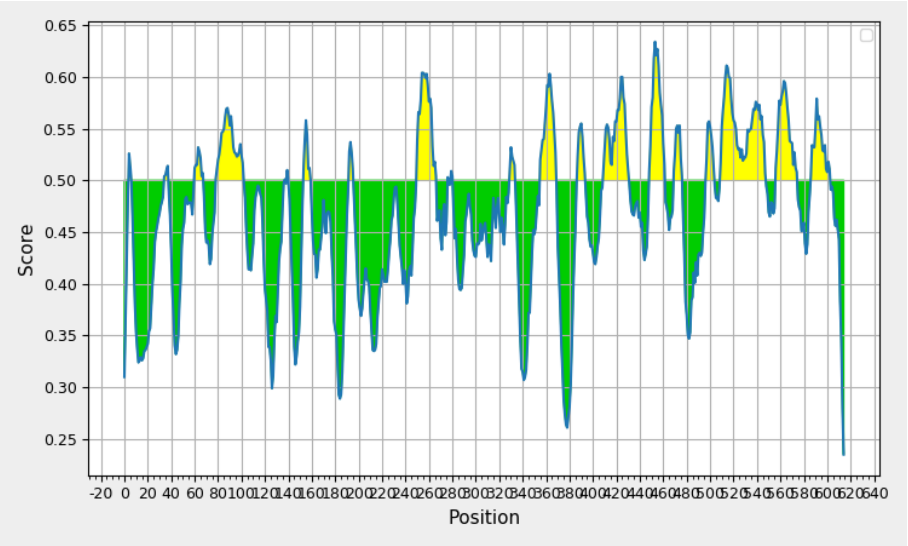
| | | | | |
|---|---|---|---|---|
| 13 | 254 | 274 | RVTKLDKKNGNSADAKYDRAT | 21 |
| 14 | 287 | 294 | **DNHLSVLP** | 8 |
| 15 | 303 | 312 | DNDSVNPGIQ | 10 |
| 16 | 339 | 370 | AVMLFNNDSAAGQNGLVTIIP<br>ADSDLHKQWGI | 32 |
| 17 | 380 | 387 | ADDSPAFD | 8 |
| 18 | 398 | 404 | **GIENAST** | 7 |
| 19 | 437 | 442 | DRLRGD | 6 |
| 20 | 457 | 461 | YPGFE | 5 |
| 21 | 473 | 478 | **GIGENG** | 6 |

**Protein name: Hsp75-like protein**

**Predicted peptides: XP_015700721 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 6 | **EV** | 2 |
| 2 | 35 | 38 | **NEQG** | 4 |
| 3 | 61 | 68 | NQAAMNPQ | 8 |
| 4 | 79 | 102 | GRRFDDPVVKKDVESWPFKVVDQG | 24 |
| 5 | 138 | 138 | **K** | 1 |
| 6 | 140 | 140 | **A** | 1 |
| 7 | 154 | 159 | FNDNQR | 6 |
| 8 | 193 | 196 | RSEK | 4 |
| 9 | 251 | 267 | **ERKTKKDLSGDPRALRR** | 17 |
| 10 | 277 | 277 | R | 1 |
| 11 | 280 | 281 | SN | 2 |
| 12 | 330 | 334 | **NIDKS** | 5 |
| 13 | 356 | 369 | SDFFNGKKLEKSIN | 14 |
| 14 | 388 | 394 | QATSADT | 7 |
| 15 | 410 | 431 | AMEGNIFAPVVPRGQTVPTIKK | 22 |

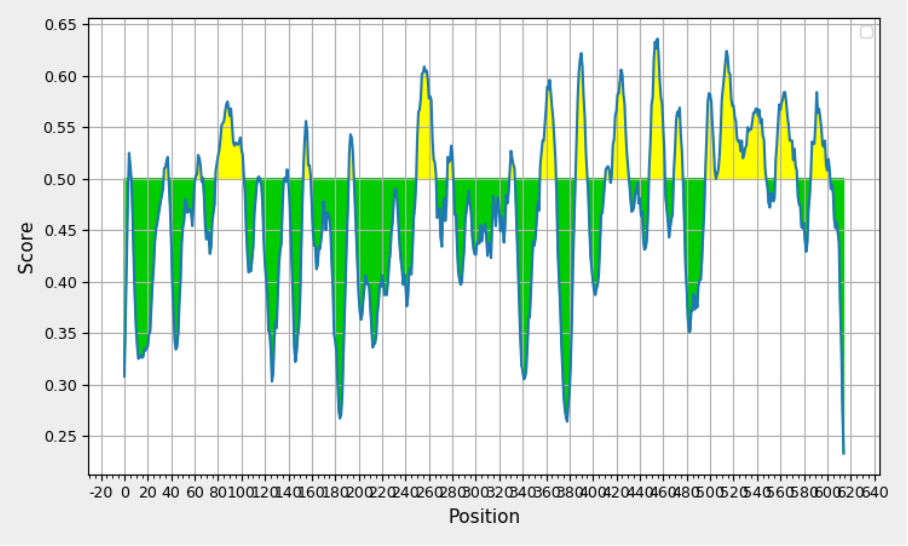
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 16 | 449 | 462 | **YQGERTNCEDNTSL** | 14 |
| 17 | 470 | 477 | **IPPMKAGD** | 8 |
| 18 | 498 | 504 | EKSSGRS | 7 |
| 19 | 510 | 548 | SNAVGKLSSTEIENMINDAARFKSSDEAFSKRFESRQQL | 39 |
| 20 | 557 | 575 | **EIISDPTMSLKIKRGNKEK** | 19 |
| 21 | 587 | 603 | **LEIEDSSPEDLKKKELA** | 17 |

**Predicted peptides: XP_010758595 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 6 | **EV** | 2 |
| 2 | 35 | 38 | **NEQG** | 4 |
| 3 | 62 | 66 | QAAMN | 5 |
| 4 | 68 | 68 | Q | 1 |
| 5 | 79 | 103 | GRRFDDPVVKKDVESWPFKVVDQGG | 25 |
| 6 | 115 | 116 | TK | 2 |
| 7 | 138 | 138 | **K** | 1 |
| 8 | 140 | 140 | **A** | 1 |
| 9 | 154 | 160 | FNDNQRQ | 7 |
| 10 | 193 | 197 | RSEKE | 5 |



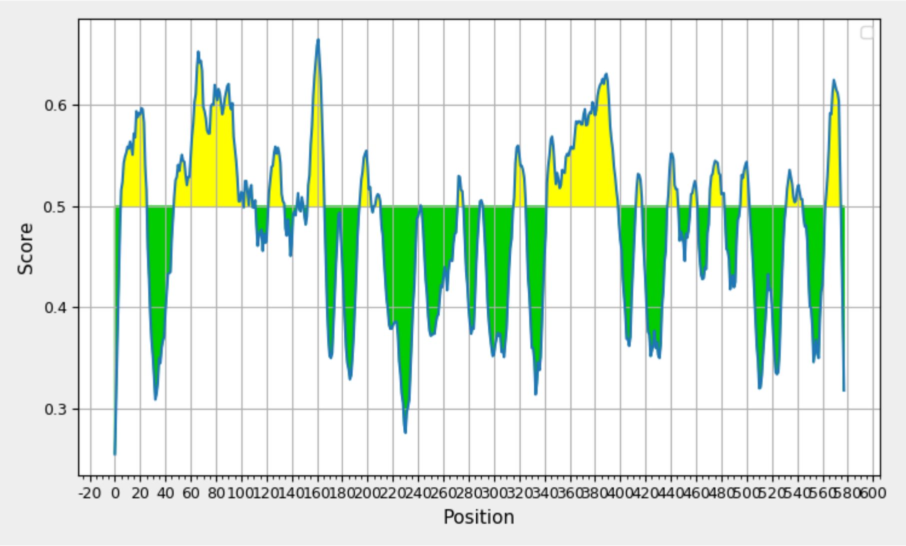
| | | | | |
|---|---|---|---|---|
| 11 | 251 | 267 | **ERKTKKDLSGDPRALRR** | 17 |
| 12 | 277 | 281 | RTLSN | 5 |
| 13 | 330 | 334 | **NIDKS** | 5 |
| 14 | 356 | 369 | **SDFFNGKKLEKSIN** | 14 |
| 15 | 387 | 396 | GQATSADTND | 10 |
| 16 | 412 | 415 | EGNI | 4 |
| 17 | 417 | 431 | APVVPRGQTVPTIKK | 15 |
| 18 | 449 | 462 | **YQGERTNCEDNTSL** | 14 |
| 19 | 470 | 477 | **IPPMKAGD** | 8 |
| 20 | 497 | 548 | TEKSSGRSANITISNAVGKLSSTEIE<br>NMINDAAKFKSSDEAFSKRFESRQQL | 52 |
| 21 | 557 | 575 | **EIISDPTMSLKIKRGNKEK** | 19 |
| 22 | 587 | 603 | **LEIEDSSPEDLKKKELA** | 17 |

**Protein name: (M20_dimer domain-containing protein)**

**Predicted peptides: XP_002789172 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 6 | 26 | LPISRIAASLPPPTRLRAAVQ | 21 |
| 2 | 48 | 102 | PSPYPSSSFYPLSIPRAVRPPSPSTSTVTRI<br>HRRSFYANIDDPKMAPQLEPFFKE | 55 |
| 3 | 104 | 109 | DNLQDA | 6 |
| 4 | 112 | 112 | **D** | 1 |
| 5 | 123 | 135 | VSAQDDKRKDVVK | 13 |
| 6 | 145 | 146 | KR | 2 |
| 7 | 149 | 150 | **AE** | 2 |
| 8 | 154 | 166 | **RPLGKEHGREHLD** | 13 |
| 9 | 195 | 204 | **ALLEDGWNTE** | 10 |
| 10 | 207 | 211 | KLTVD | 5 |
| 11 | 243 | 243 | **V** | 1 |
| 12 | 273 | 276 | KKFF | 4 |
| 13 | 290 | 292 | LGT | 3 |
| 14 | 317 | 326 | **DLHSGVFGGS** | 10 |

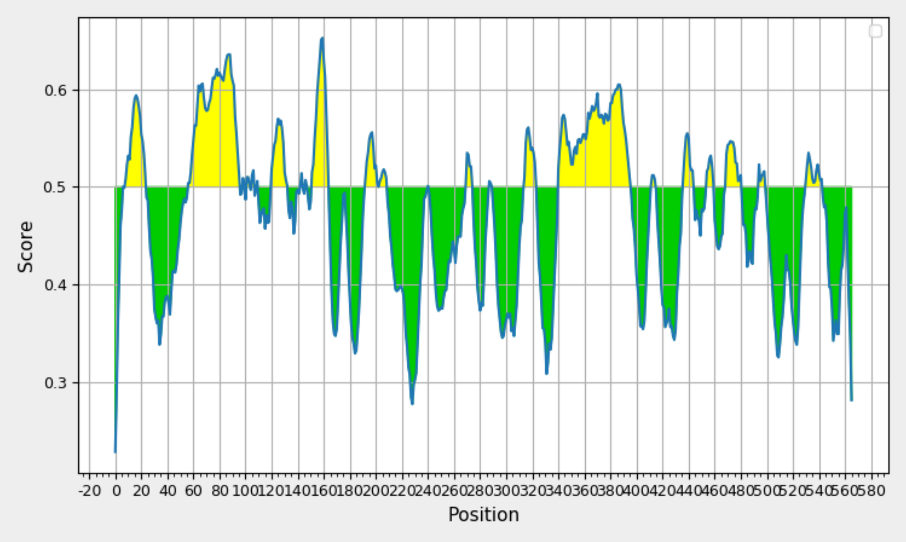
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 15 | 343 | 399 | DVQGNILIPGINELVAPLTEDEKGLYKDIAFSMENLYESLGSTTSIFSDKEPTLMRR | 57 |
| 16 | 414 | 418 | YSAPG | 5 |
| 17 | 439 | 446 | **MESEDVNK** | 8 |
| 18 | 457 | 462 | **AKLNSK** | 6 |
| 19 | 472 | 483 | **DGKWWVASPKHW** | 12 |
| 20 | 496 | 503 | FGVEPDFT | 8 |
| 21 | 533 | 545 | **DMAHSTNEKLDKR** | 13 |
| 22 | 564 | 575 | EPIKEQINTDNV | 12 |

**Predicted peptides: XP_010761260 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 9 | 24 | AASLPPPIRLRRAAVQ | 16 |
| 2 | 57 | 96 | LSLPRTIRPPSPSTSTVIRIHRRSFYANIDDPKMAPQLEP | 40 |
| 3 | 99 | 100 | KE | 2 |
| 4 | 102 | 104 | DIL | 3 |
| 5 | 106 | 107 | DA | 2 |
| 6 | 110 | 110 | **D** | 1 |
| 7 | 121 | 133 | VSAQDDNRKDVVK | 13 |



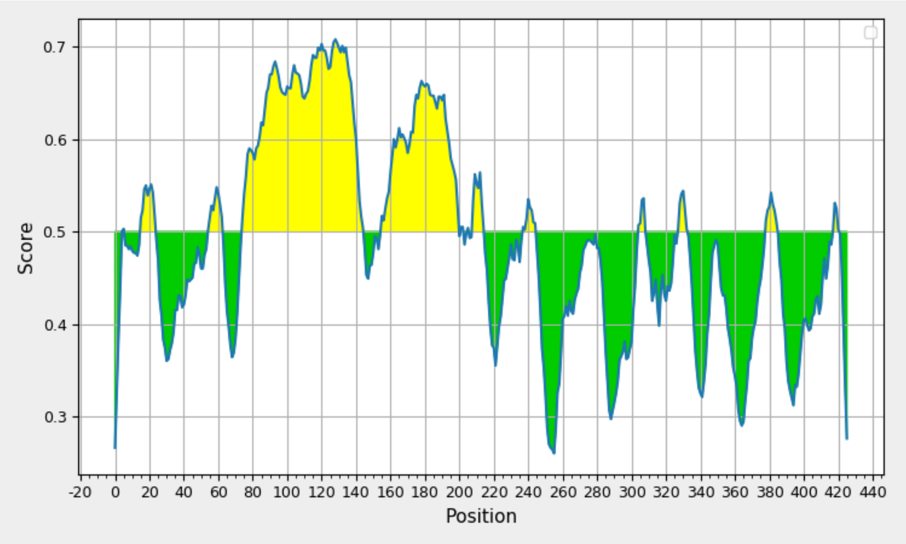
| | | | | |
|---|---|---|---|---|
| 8 | 143 | 144 | RR | 2 |
| 9 | 147 | 148 | **AE** | 2 |
| 10 | 152 | 164 | **RPLGKEHGREHLD** | 13 |
| 11 | 193 | 202 | **ALLEDGWNTE** | 10 |
| 12 | 204 | 209 | FKLTVD | 6 |
| 13 | 241 | 241 | **V** | 1 |
| 14 | 270 | 274 | SKKYF | 5 |
| 15 | 288 | 290 | **LGT** | 3 |
| 16 | 315 | 324 | **DLHSGVFGGS** | 10 |
| 17 | 341 | 396 | DVQGNILIPGINELVAPLTEDEKGLYKDIAFSMENLYESLGSTTSIFSEKEPTLMR | 56 |
| 18 | 412 | 415 | YSAP | 4 |
| 19 | 437 | 444 | **MESEDVNK** | 8 |
| 20 | 455 | 460 | **AKLNSK** | 6 |
| 21 | 470 | 481 | **DGKWWVASPKHW** | 12 |
| 22 | 495 | 499 | GVEPD | 5 |
| 23 | 531 | 543 | **DMAHSTNEKLDKR** | 13 |

**Protein name: Acetyltransferase component of pyruvate dehydrogenase complex**

**Predicted peptides: XP_002797511 [Pb01]**

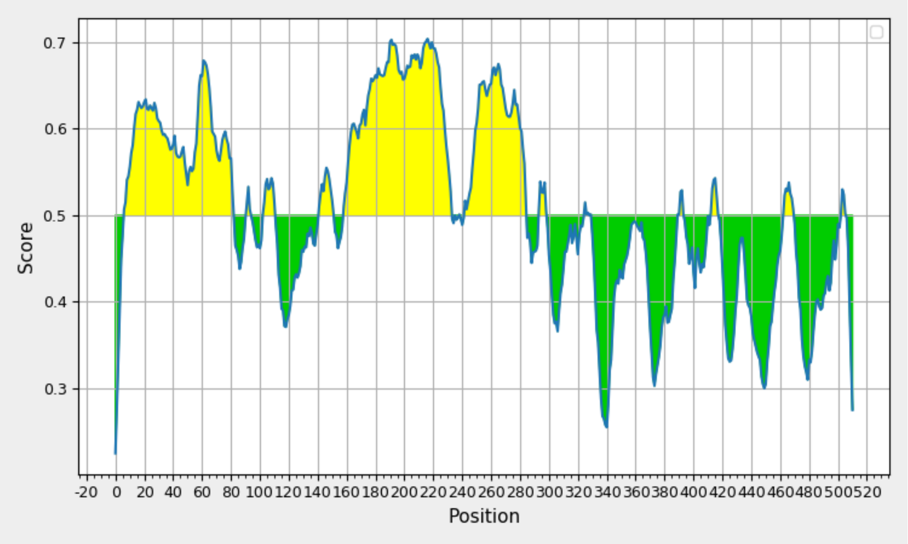
| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 6 | 6 | P | 1 |
| 2 | 16 | 24 | **WQKKVGDAL** | 9 |
| 3 | 55 | 63 | REAGEKDIA | 9 |
| 4 | 75 | 145 | GTDITPFESFSLEDAGGEKSSALK<br>EPEQPKKELKVAPAAPKEESTPAA<br>EEEPVSTGERLQPSLDRESFIAP | 71 |
| 5 | 156 | 200 | VPLKDIKGTGPGGRVTKNDVEK<br>YQPAGTAVSASGPAFEDIPASSM | 45 |
| 6 | 202 | 203 | KI | 2 |
| 7 | 206 | 206 | N | 1 |
| 8 | 209 | 215 | VQSMREN | 7 |
| 9 | 238 | 245 | NSADGKYK | 8 |
| 10 | 305 | 309 | **AHTLG** | 5 |
| 11 | 328 | 333 | **KLKPEE** | 6 |
| 12 | 379 | 385 | GEDGTSV | 7 |
| 13 | 418 | 421 | **VENP** | 4 |

**Bepipred Linear Epitope Prediction 2.0**



**Predicted peptides: XP_010762465 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 7 | 82 | SRSASCRSLFSRSPPTCIRESGHMYRLRDASRYGQCSRIWLLSLMFTLILVVHRGRRQLPAFAALARFYASKSYPP | 76 |
| 2 | 92 | 94 | SPT | 3 |
| 3 | 103 | 111 | **WQKKVGDAL** | 9 |
| 4 | 142 | 152 | REAGEKDVTVG | 11 |
| 5 | 159 | 233 | VEEGTDITPFESFSLEDAGGEKAPTLKQPEQPKEELKVAPAAPKEESTPAAEEEPVSTGERLQPSLDRESFIAPA | 75 |
| 6 | 239 | 239 | L | 1 |
| 7 | 243 | 285 | VPLKDIKGTGPGGRVTKNDVEKYQPAGTAVSGPPYEDIPASSM | 43 |
| 8 | 294 | 299 | LQSMRE | 6 |
| 9 | 326 | 328 | NGK | 3 |
| 10 | 330 | 330 | K | 1 |
| 11 | 390 | 394 | **AHTLG** | 5 |
| 12 | 413 | 418 | **KLKPEE** | 6 |
| 13 | 464 | 470 | GEDSTSV | 7 |
| 14 | 503 | 506 | **VENP** | 4 |

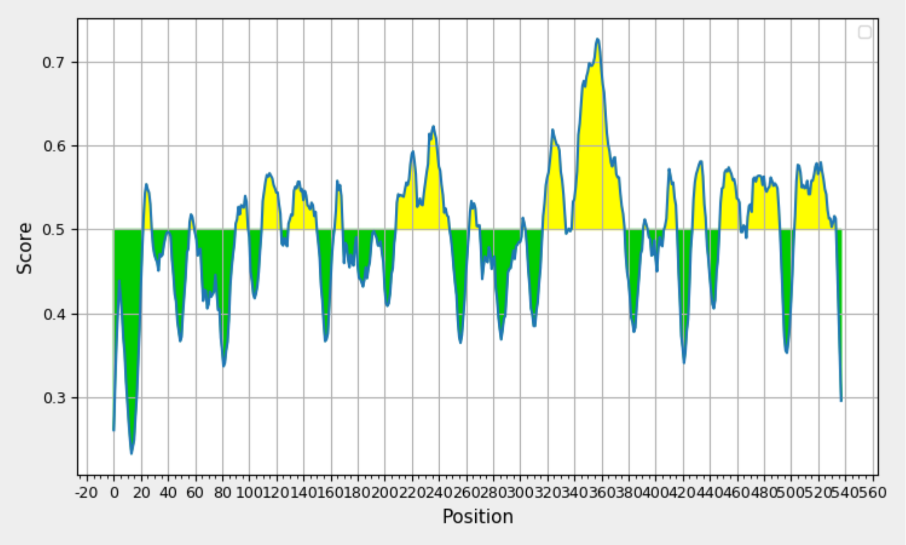


**Protein name: Protein disulfide-isomerase**

**Predicted peptides: XP_002797127 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 23 | 29 | ADEAASD | 7 |
| 2 | 57 | 60 | **CGHC** | 4 |
| 3 | 91 | 100 | **ELCQEYGVEG** | 10 |
| 4 | 111 | 124 | EQVKPYSGPRKSSS | 14 |
| 5 | 130 | 150 | VKQSLPAVTVVTVDNLEDVKT | 21 |
| 6 | 164 | 170 | DKATNET | 7 |
| 7 | 210 | 248 | DEGKTVYKGELTQEQVTSFIKLSSTPL IGELGPHTYAGY | 39 |
| 8 | 264 | 271 | EEREEFSK | 8 |
| 9 | 303 | 304 | LK | 2 |
| 10 | 318 | 334 | NNKKYPFDQELKITHDT | 17 |
| 11 | 337 | 337 | **T** | 1 |
| 12 | 339 | 378 | VQDVLDGKVEPSIKSEPIPEKQEGP VTVVVARSYQELVID | 40 |
| 13 | 392 | 395 | CGHC | 4 |
| 14 | 408 | 416 | LYADNPEFA | 9 |

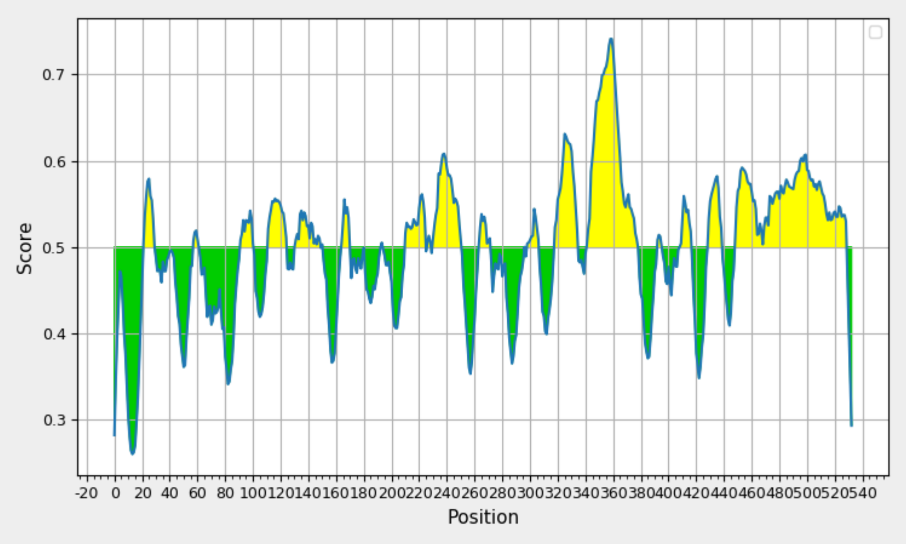
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 15 | 429 | 438 | **NDVPEEIQGF** | 10 |
| 16 | 449 | 463 | KDKPFDYQGLRTIQG | 15 |
| 17 | 466 | 467 | DF | 2 |
| 18 | 469 | 492 | RDNGKHKVDAYDESKVNEDDDDDD | 24 |
| 19 | 504 | 534 | SSSSTKTAEKKKDSKTTSSAAPKDTAAESAR | 31 |

**Predicted peptides: XP_010759621 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 22 | 30 | AADEAAVSD | 9 |
| 2 | 58 | 61 | **CGHC** | 4 |
| 3 | 92 | 101 | **ELCQEYGVEG** | 10 |
| 4 | 112 | 125 | EQVKPYSGPRKSAS | 14 |
| 5 | 132 | 149 | KQSLPAVTVVTVDNLEDV | 18 |
| 6 | 151 | 151 | **T** | 1 |
| 7 | 165 | 170 | DKATNE | 6 |
| 8 | 194 | 194 | A | 1 |
| 9 | 211 | 225 | DEGKAVYSGELTQEQ | 15 |
| 10 | 227 | 229 | TSF | 3 |
| 11 | 231 | 251 | KLSSTPLIGELGPHTYARYIQ | 21 |
| 12 | 264 | 272 | PEEREEFSK | 9 |



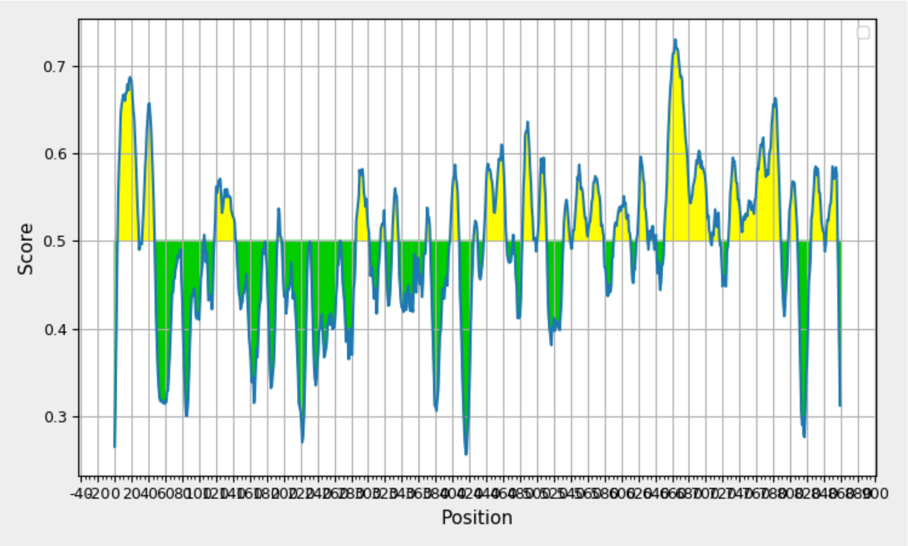
| | | | | |
|---|---|---|---|---|
| 13 | 299 | 307 | AGNLNLKVD | 9 |
| 14 | 319 | 335 | NNKKYPFDQELKITHDI | 17 |
| 15 | 342 | 378 | DVLDGKVEPSIKSEPIPEKQEGPV<br>TVVVAHSYQELVI | 37 |
| 16 | 393 | 396 | CGHC | 4 |
| 17 | 410 | 417 | YADNPEFA | 8 |
| 18 | 430 | 439 | **NDVPEEIQGF** | 10 |
| 19 | 449 | 529 | SKDKPFDYQGSRTIQGLAEFVRDNGKH<br>KVDAYDESKVTEDDDVTETPASPSSSSTKA<br>ADEKKETKTTSSAAPKDTAAEGAR | 81 |

**Protein name: HSP7-like protein**

**Predicted peptides: XP_015703361 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 29 | RFSRALPRAVPSFARSSSRSSAYKL | 25 |
| 2 | 34 | 48 | FRRWNSTEGGEEKVK | 15 |
| 3 | 107 | 107 | V | 1 |
| 4 | 119 | 144 | LIGRKFTDPECQRDLKEVPYKIVQHA | 26 |
| 5 | 194 | 198 | **NDSQR** | 5 |
| 6 | 287 | 302 | KKESGIDLSNDRMAIQ | 16 |
| 7 | 316 | 321 | SSALQT | 6 |
| 8 | 330 | 337 | **ADSSGAKH** | 8 |
| 9 | 370 | 374 | **NLQAK** | 5 |
| 10 | 398 | 408 | IFGRDPAKSVN | 11 |
| 11 | 426 | 430 | GEVTD | 5 |
| 12 | 438 | 464 | PLSLGIETLGGVFTRLINRNTTIPTKK | 27 |
| 13 | 473 | 473 | D | 1 |
| 14 | 484 | 499 | QGERELVRDNKLLGNF | 16 |
| 15 | 502 | 512 | VGIPPAHRGVP | 11 |

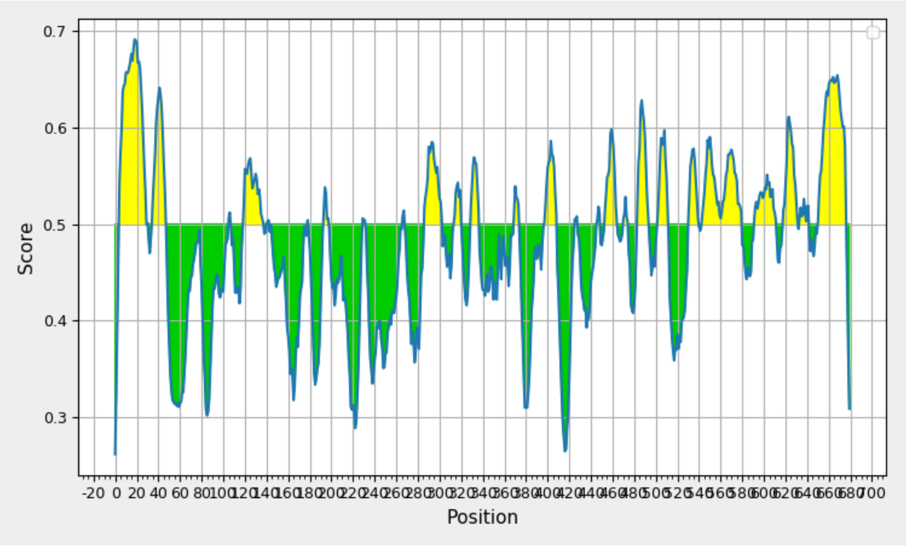
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 16 | 533 | 540 | KSTGKDQS | 8 |
| 17 | 544 | 580 | ASGSGLSDTEIQNMVDDAEKFGAQDKERKAAIEAANR | 37 |
| 18 | 592 | 611 | LKEFEDKLDKTEADQIKEKI | 20 |
| 19 | 619 | 632 | **AKSQSGEGSITADE** | 14 |
| 20 | 634 | 639 | KAKVDE | 6 |
| 21 | 641 | 642 | QN | 2 |
| 22 | 652 | 706 | HKARSEEGQQQQSQQSNEGQQGDSNLLTETFDLIVSPANSFGRLDSAFNGAISRA | 55 |
| 23 | 709 | 717 | LPHHNYNSF | 9 |
| 24 | 728 | 789 | RWRGYAPPGSCTLVPFPAEIAWTAPWVHCVRLCGCRSVEGVERGGRVQGEGDREGDGGERKR | 62 |
| 25 | 799 | 809 | VVGVGNVSKEK | 11 |
| 26 | 826 | 841 | ERTERWRRLEWSMLGR | 16 |
| 27 | 844 | 857 | FEVKKTWREKQKAW | 14 |

**Predicted peptides: XP_010756347 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 29 | RFSRALPRAVPSFARSSARSSAYKL | 25 |
| 2 | 31 | 31 | A | 1 |
| 3 | 35 | 47 | RRWNSTEGGEEKV | 13 |
| 4 | 106 | 107 | VV | 2 |
| 5 | 120 | 138 | IGRKFTDPECQRDLKEVPY | 19 |
| 6 | 142 | 143 | QH | 2 |
| 7 | 179 | 179 | G | 1 |
| 8 | 194 | 198 | **NDSQR** | 5 |
| 9 | 230 | 232 | REQ | 3 |
| 10 | 267 | 268 | TH | 2 |
| 11 | 287 | 303 | KKESGIDLSNDRMAIQR | 17 |
| 12 | 315 | 321 | LSSALQT | 7 |
| 13 | 330 | 337 | **ADSSGAKH** | 8 |
| 14 | 370 | 374 | **NLQAK** | 5 |
| 15 | 398 | 409 | IFGRDPAKSVNP | 12 |
| 16 | 426 | 428 | GEV | 3 |
| 17 | 447 | 449 | GGV | 3 |



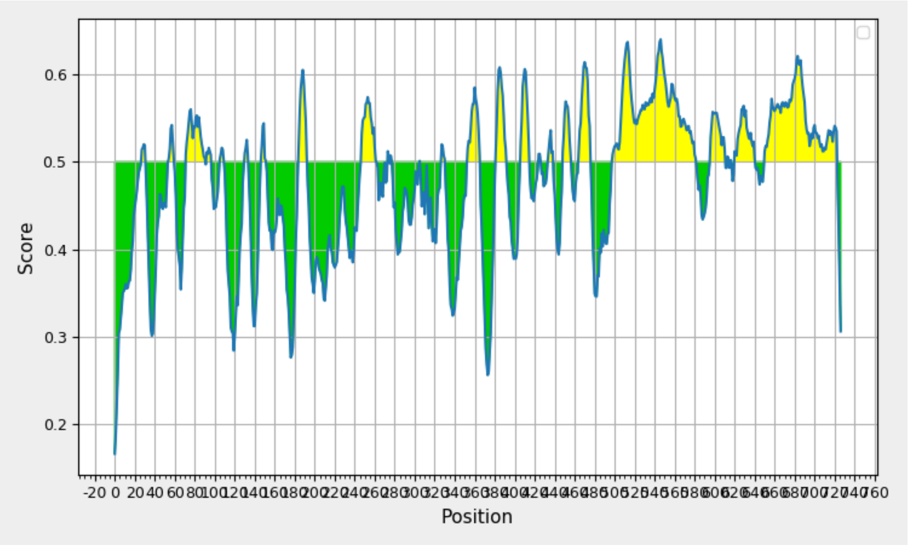
| | | | | |
|---|---|---|---|---|
| 18 | 454 | 465 | INRNTTIPTKKS | 12 |
| 19 | 471 | 475 | AADFQ | 5 |
| 20 | 484 | 494 | QGERELVRDNK | 11 |
| 21 | 503 | 512 | GIPPAHRGVP | 10 |
| 22 | 531 | 540 | KDKSTGKDQS | 10 |
| 23 | 544 | 580 | ASGSGLSDAEIQNMVDDAEKFG<br>AQDKERKAAIEAANR | 37 |
| 24 | 592 | 612 | LKEFEDKLDKTEADQIKEKIA | 21 |
| 25 | 619 | 632 | **AKSQSGEGSITADE** | 14 |
| 26 | 634 | 642 | KAKVDELQN | 9 |
| 27 | 651 | 677 | MHKARSEDGQQQQSQQSNEGQQSGEGE | 27 |

**Protein name: Uncharacterized protein (NBD sugar kinase HSP70 actin superfamily)**

**Predicted peptides: XP_002790451 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 28 | 31 | NEVS | 4 |
| 2 | 55 | 60 | QEISNL | 6 |
| 3 | 72 | 91 | GRSFNDPDVQIEQDYNSATL | 20 |
| 4 | 93 | 97 | DVNGE | 5 |
| 5 | 106 | 110 | GKKEQ | 5 |
| 6 | 131 | 134 | **ELKL** | 4 |
| 7 | 147 | 152 | FTDAQR | 6 |
| 8 | 185 | 193 | FDLPTAEEK | 9 |
| 9 | 248 | 262 | KEKFNIDIKTNLKAW | 15 |
| 10 | 274 | 275 | KI | 2 |
| 11 | 277 | 278 | SA | 2 |
| 12 | 306 | 306 | **E** | 1 |
| 13 | 328 | 331 | LKPE | 4 |
| 14 | 354 | 366 | **EFFGKPLSFTLNQ** | 13 |
| 15 | 382 | 392 | SPVFRVRDFSV | 11 |

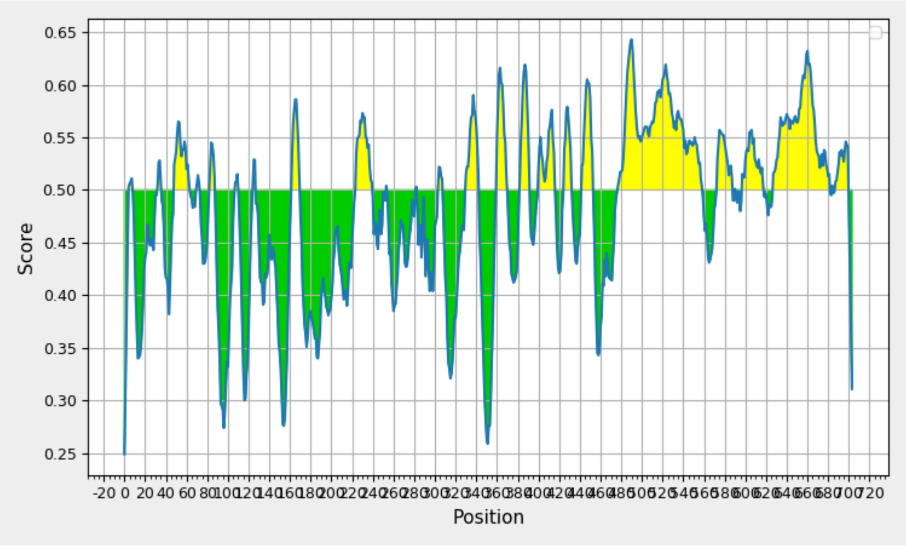
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 16 | 407 | 415 | APDIPDEAT | 9 |
| 17 | 425 | 427 | VMP | 3 |
| 18 | 434 | 439 | FYRKQP | 6 |
| 19 | 449 | 457 | IDGLPGKTN | 9 |
| 20 | 465 | 476 | VKGITESSDGDF | 12 |
| 21 | 499 | 582 | VEDVEVEEPIPEKEGDAMDTDAPNG<br>DAEDGKPKMRKVKKQVRKGDLPVSGGTA<br>GLDPESKERLTEKENAMYMEDKLVADTEDKK | 84 |
| 22 | 597 | 611 | DGVYSEFASDEEKTK | 15 |
| 23 | 614 | 614 | **T** | 1 |
| 24 | 617 | 617 | D | 1 |
| 25 | 621 | 641 | **DWLYEDGEDTTKAVYISKMDD** | 21 |
| 26 | 651 | 723 | QRYTDKVEAERAAAQKAQEEAAAKR<br>REEQEAAQEAAKKAAGPPPAADAEM<br>KDMDAAAPAGEVDKNADESMAEV | 73 |

**Predicted peptides: XP_010758132 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 5 | 8 | DKLS | 4 |
| 2 | 33 | 36 | EISN | 4 |
| 3 | 49 | 64 | GRSFNDPDVQIEQDYN | 16 |
| 4 | 71 | 73 | VNG | 3 |
| 5 | 83 | 88 | GKKEQF | 6 |
| 6 | 108 | 111 | **ELKL** | 4 |
| 7 | 125 | 127 | TODA | 3 |
| 8 | 163 | 170 | DLPTAEEK | 8 |
| 9 | 224 | 240 | FKEKFNIDIKTNLKAWT | 17 |
| 10 | 254 | 254 | S | 1 |
| 11 | 283 | 283 | **E** | 1 |
| 12 | 304 | 308 | DLKPE | 5 |
| 13 | 331 | 343 | **EFFGKPLSFTLNQ** | 13 |
| 14 | 360 | 370 | PVFRVRDFSVH | 11 |
| 15 | 383 | 392 | RAPDIPDEAT | 10 |
| 16 | 401 | 417 | NVMPSTKILTFYRKQPF | 17 |
| 17 | 426 | 433 | IDRLPGKT | 8 |



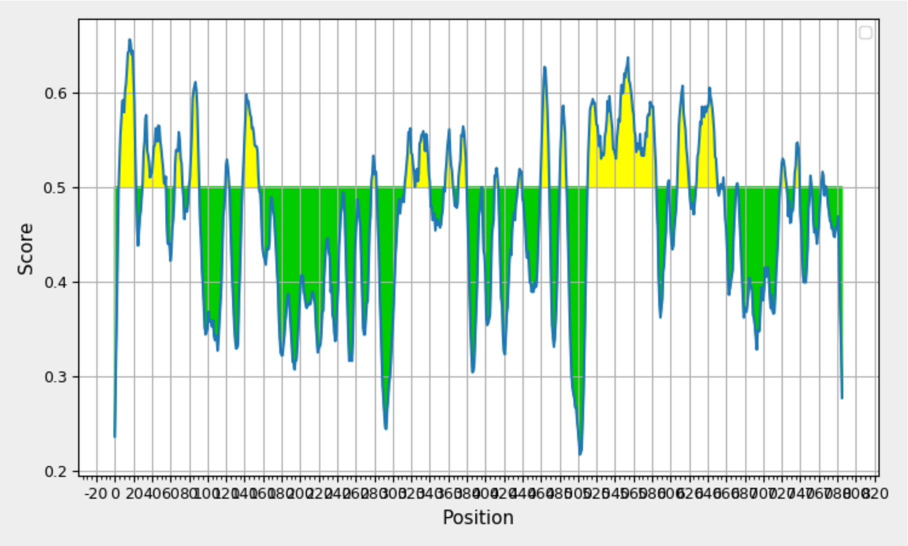
| | | | | |
|---|---|---|---|---|
| 18 | 443 | 453 | KGITESSDGDF | 11 |
| 19 | 478 | 559 | DVEVEEPIPEKEGDAMDTDAPNGDAEDGKPKMRKVKKQVRKGDLPVSGGTAGLDAESKERLTEKENAMYMEDKLVADTEDKK | 82 |
| 20 | 573 | 588 | IDGVYSEFASDEEKTK | 16 |
| 21 | 591 | 591 | **T** | 1 |
| 22 | 598 | 618 | **DWLYEDGEDTTKAVYISKMDD** | 21 |
| 23 | 628 | 682 | QRYTDKVEAERAAAQKAQEEAAAKRREEQEAAEEAAKKAAGPPPAADAEMKDMDA | 55 |
| 24 | 685 | 685 | P | 1 |
| 25 | 688 | 700 | EVDKNADESMAEV | 13 |

**Protein name: Aconitate hydratase, mitochondrial**

**Predicted peptides: XP_015699682 [Pb01]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 6 | 23 | RFARVGALASKSRNLLGA | 18 |
| 2 | 31 | 56 | ENPLDKKVEMCNYEKGNYINYKKMAE | 26 |
| 3 | 66 | 74 | NRPLTYAEK | 9 |
| 4 | 81 | 92 | DDPHEQDIHRGK | 12 |
| 5 | 121 | 124 | MPSV | 4 |
| 6 | 139 | 156 | QVGGEKDLARANEINKEV | 18 |
| 7 | 278 | 283 | VNSLSC | 6 |
| 8 | 314 | 341 | **KATKRQAIGDFARSYAHSLREDEGAEYD** | 28 |
| 9 | 358 | 366 | PFTPDLATP | 9 |
| 10 | 372 | 380 | DAVKENGWP | 9 |
| 11 | 397 | 397 | E | 1 |
| 12 | 411 | 414 | **DHGI** | 4 |
| 13 | 436 | 440 | **DGQLK** | 5 |
| 14 | 461 | 470 | **WDRRDVKKGE** | 10 |
| 15 | 482 | 488 | **FTGRNDA** | 7 |

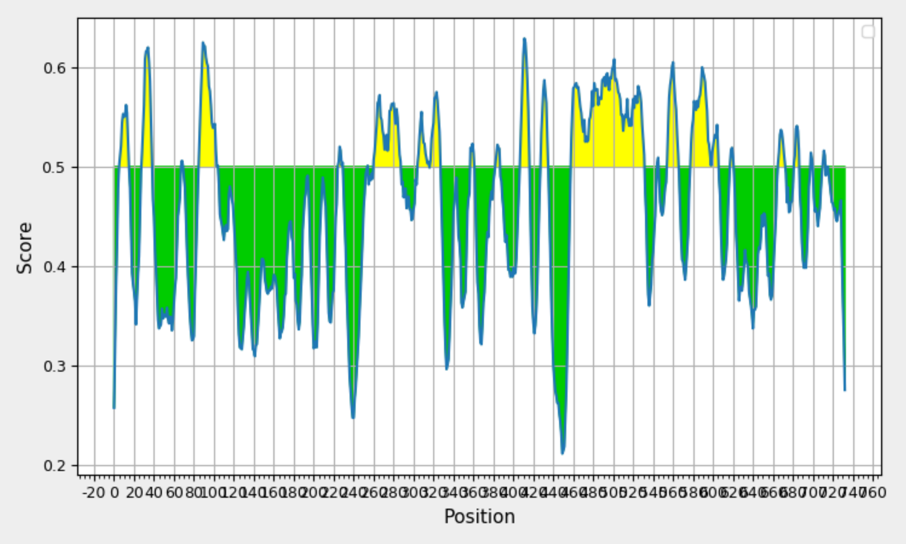
**Bepipred Linear Epitope Prediction 2.0**



| | | | | |
|---|---|---|---|---|
| 16 | 512 | 585 | **NFNPLTDTLKDKDGKEFKLKEPTG<br>AGLPANGYDPGRDTYQAPPKDRSSIS<br>VAVSPTSDRLQILKAFQPWDGKDA** | 74 |
| 17 | 598 | 599 | **TT** | 2 |
| 18 | 608 | 620 | PWLKYRGHLDNIS | 13 |
| 19 | 629 | 651 | NAENGEANKVKNFKTGEYGPVPA | 23 |
| 20 | 655 | 656 | DY | 2 |
| 21 | 658 | 658 | A | 1 |
| 22 | 672 | 673 | GE | 2 |
| 23 | 720 | 726 | DYDRIRP | 7 |
| 24 | 735 | 740 | **TELAVG** | 6 |
| 25 | 752 | 753 | **GK** | 2 |
| 26 | 764 | 766 | **NEP** | 3 |
| 27 | 768 | 769 | LQ | 2 |

**Predicted peptides: XP_010760563 [Pb18]**

| No. | Start | End | Peptide | Length |
|---|---|---|---|---|
| 1 | 6 | 15 | DIVRSRLNRP | 10 |
| 2 | 29 | 39 | DPHEQDIHRGK | 11 |
| 3 | 69 | 70 | PS | 2 |
| 4 | 86 | 105 | QVGGEKDLARANEINKEVYD | 20 |
| 5 | 226 | 230 | NSLSC | 5 |
| 6 | 255 | 255 | R | 1 |
| 7 | 261 | 288 | **KATKRQAIGDFARSYAHSLREDEGAEYD** | 28 |
| 8 | 305 | 316 | PFTPDLATPISK | 12 |
| 9 | 318 | 328 | KDAVKENGWPE | 11 |
| 10 | 358 | 361 | **DHGI** | 4 |
| 11 | 383 | 387 | **DGQLK** | 5 |
| 12 | 408 | 417 | **WDRRDVKKGE** | 10 |
| 13 | 429 | 435 | **FTGRNDA** | 7 |
| 14 | 459 | 532 | **NFNPLTDTLKDKDGKEFKLKEPT<br>GAGLPANGYDPGRDTYQAPPKDRSS<br>ISVAVSPTSDRLQILKAFQPWDGKDA** | 74 |
| 15 | 545 | 546 | **TT** | 2 |
| 16 | 555 | 566 | PWLKYRGHLDNI | 12 |



| | | | | |
|---|---|---|---|---|
| 17 | 579 | 606 | NGEANKVKNFKTGEYGPVPATARDYKAR | 28 |
| 18 | 618 | 621 | YGEG | 4 |
| 19 | 666 | 673 | ADYDRIRP | 8 |
| 20 | 682 | 687 | **TELAVG** | 6 |
| 21 | 699 | 700 | **GK** | 2 |
| 22 | 711 | 713 | **NEP** | 3 |
| 23 | 716 | 716 | Q | 1 |

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