

[BLAST®](#) » [blastp suite](#) » RID-9JG20JT0014

BLAST Results

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PSI blast Iteration 1

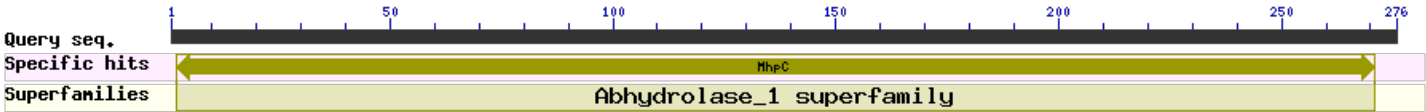
Job title: T0951 ShHTL7, Striga hermonthica, 276 residues|

| | | | |
|---------------|--|---------------|----------------------|
| RID | 9JG20JT0014 (Expires on 03-27 04:55 am) | Database Name | pdb |
| Query ID | lcIIQuery_66224 | Description | PDB protein database |
| Description | T0951 ShHTL7, Striga hermonthica, 276 residues | Program | BLASTP 2.9.0+ |
| Molecule type | amino acid | | |
| Query Length | 276 | | |

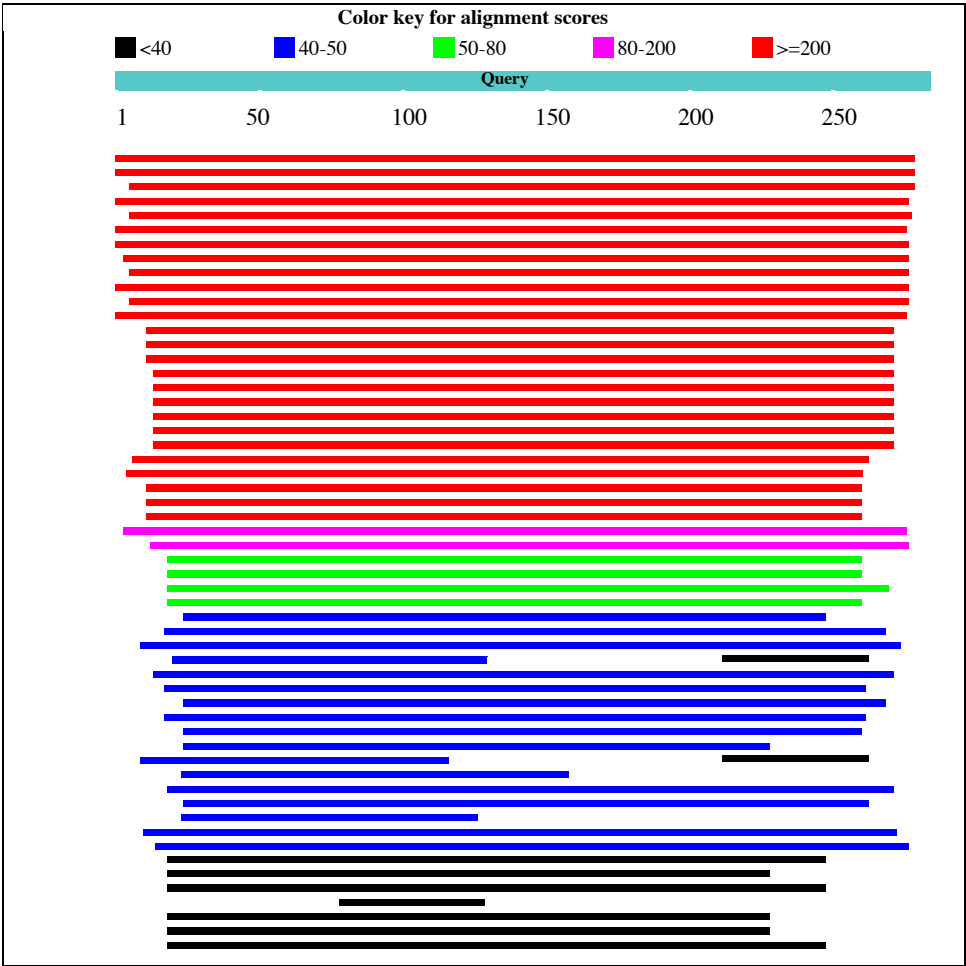
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Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 100 Blast Hits on 100 subject sequences



Descriptions

| Description | Max score | Total score | Query cover | E value | Perc. ident | Accession | Select for PSI blast | Used to build PSSM |
|---|-----------|-------------|-------------|---------|-------------|---|----------------------|--------------------|
| Chain A, Structural basis for specific inhibition of highly sensitive ShHTL7 receptor | 568 | 568 | 100% | 0.0 | 100.00% | 5Z82_A (scored below threshold on previous iteration) | | |
| Chain A, Structural basis for specific inhibition of highly sensitive ShHTL7 receptor | 567 | 567 | 100% | 0.0 | 99.64% | 5Z89_A (scored below threshold on previous iteration) | | |
| Chain A, Hyposensitive to light 7 | 558 | 558 | 98% | 0.0 | 100.00% | 5Z7Y_A (scored below threshold on previous iteration) | | |
| Chain A, Hyposensitive to light 4 | 427 | 427 | 99% | 1e-152 | 72.63% | 5Z7X_A (scored below threshold on previous iteration) | | |
| Chain A, Crystal Structure Of The Strigolactone Receptor Shhtl5 From Striga Hermonthica | 404 | 404 | 97% | 3e-143 | 68.89% | 5CBK_A (scored below threshold on previous iteration) | | |
| Chain A, Crystal Structure Of Striga Kai2-like Protein In Complex With Karrikin | 364 | 364 | 98% | 1e-127 | 61.90% | 5DNU_A (scored below threshold on previous iteration) | | |
| Chain A, Crystal Structure Of Arabidopsis Thaliana Dwarf14 Like (atd14l) | 353 | 353 | 99% | 2e-123 | 60.22% | 3W06_A (scored below threshold on previous iteration) | | |
| Chain A, Crystal Structure Of Kai2 | 353 | 353 | 98% | 2e-123 | 60.52% | 4HRX_A (scored below threshold on previous iteration) | | |
| Chain A, Crystal Structure Of Karrikin Insensitive 2 (kai2) From Arabidopsis Thaliana | 352 | 352 | 97% | 8e-123 | 60.59% | 4IH1_A (scored below threshold on previous iteration) | | |
| Chain A, Hyposensitive to light 1 | 350 | 350 | 99% | 4e-122 | 60.58% | 5Z7W_A (scored below threshold on previous iteration) | | |
| Chain A, Crystal structure of KAI2_ply2(A219V) | 343 | 343 | 97% | 2e-119 | 60.59% | 5Z9H_A (scored below threshold on previous iteration) | | |
| Chain A, PpKAI2-like C | 323 | 323 | 98% | 2e-111 | 53.11% | 6ATX_A (scored below threshold on previous iteration) | | |
| Chain A, Pp-KAI2-like E | 315 | 315 | 93% | 3e-108 | 54.26% | 6AZC_A (scored below threshold on previous iteration) | | |
| Chain A, Pp-KAI2-like E | 315 | 315 | 93% | 3e-108 | 54.26% | 6AZB_A (scored below threshold on previous iteration) | | |
| Chain A, PpKAI2-like H | 273 | 273 | 93% | 5e-92 | 50.38% | 6AZD_A (scored below threshold on previous iteration) | | |
| Chain A, Crystal Structure Of Rice Dwarf14 In Complex With Synthetic Strigolactone Gr24 | 265 | 265 | 92% | 2e-88 | 47.27% | 5DJ5_A (scored below threshold on previous iteration) | | |
| Chain A, Crystal Structure of rice D14 bound to 2-(2-methyl-3-nitroanilino)benzoic acid | 265 | 265 | 92% | 2e-88 | 47.27% | 6AP8_A (scored below threshold on previous iteration) | | |
| Chain A, Crystal Structure Of Rice Dwarf14 (d14) In Complex With A Gr24 Hydrolysis Intermediate | 264 | 264 | 92% | 2e-88 | 47.27% | 4IHA_A (scored below threshold on previous iteration) | | |

| | | | | | | | |
|---|------|------|-----|-------|--------|---|--|
| Chain A, Crystal Structure Of Oryza Sativa Dwarf14 (d14) | 264 | 264 | 92% | 2e-88 | 47.27% | 3W04_A (scored below threshold on previous iteration) | |
| Chain A, D3-CTH-D14-D-ring | 265 | 265 | 92% | 2e-88 | 47.27% | 6BRT_A (scored below threshold on previous iteration) | |
| Chain A, Crystal structure of OsD14 | 264 | 264 | 92% | 4e-88 | 47.27% | 3VXK_A (scored below threshold on previous iteration) | |
| Chain A, Dwarf 14 | 261 | 261 | 92% | 4e-87 | 48.03% | 5Z7Z_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of Arabidopsis Dwarf14 Orthologue, Atd14 | 260 | 260 | 92% | 1e-86 | 46.85% | 4IH4_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure of DAD2 in complex with tolfenamic acid | 260 | 260 | 89% | 1e-86 | 47.77% | 6AP6_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of Dad2 | 258 | 258 | 89% | 9e-86 | 47.77% | 4DNP_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of Dad2 S96a Mutant | 256 | 256 | 89% | 2e-85 | 47.37% | 4DNQ_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of Rsbq | 162 | 162 | 97% | 1e-48 | 32.47% | 1WOM_A (scored below threshold on previous iteration) | |
| Chain A, The Structure Of Olei00960, A Hydrolase From Oleispira Antarctica | 145 | 145 | 94% | 9e-42 | 30.80% | 3QVM_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of Bioh At 1.7 A | 53.9 | 53.9 | 86% | 3e-08 | 23.08% | 1M33_A (scored below threshold on previous iteration) | |
| Chain A, Structure Of The Enzyme-Acp Substrate Gatekeeper Complex Required For Biotin Synthesis | 53.5 | 53.5 | 86% | 6e-08 | 22.18% | 4ETW_A (scored below threshold on previous iteration) | |
| Chain A, The Structure Of Rv0554 From Mycobacterium Tuberculosis | 50.4 | 50.4 | 90% | 6e-07 | 20.74% | 3E3A_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of Carboxylesterase Bioh From Salmonella Enterica | 50.1 | 50.1 | 86% | 9e-07 | 23.14% | 4NMW_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of The Enol-Lactonase From Burkholderia Xenovorans Lb400 | 49.3 | 49.3 | 80% | 1e-06 | 18.75% | 2XUA_A (scored below threshold on previous iteration) | |
| Chain A, Crystal structure of an alpha/beta hydrolase fold protein from Burkholderia ambifaria | 48.9 | 48.9 | 90% | 2e-06 | 21.85% | 5W15_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of Alpha/beta Hydrolase From Rhodopseudomonas Palustris Cga009 | 48.9 | 48.9 | 94% | 2e-06 | 22.60% | 4PSU_A (scored below threshold on previous iteration) | |
| Chain C, Crystal Structure Of Epoxide Hydrolase A From Mycobacterium Thermoresistibile | 47.4 | 47.4 | 39% | 8e-06 | 27.83% | 5CW2_C (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure of E-2-(Acetamidomethylene)succinate Hydrolase | 47.4 | 47.4 | 92% | 8e-06 | 24.91% | 3KXP_A (scored below threshold on previous iteration) | |
| Chain A, Crystal structure of DxnB2, a carbon - carbon bond | 46.2 | 46.2 | 87% | 2e-05 | 24.42% | 4LXG_A (scored below threshold on previous iteration) | |

| | | | | | | | |
|---|------|------|-----|-------|--------|---|--|
| hydrolase from Sphingomonas wittichii RW1 | | | | | | previous iteration) | |
| Chain A, The Crystal Structure Of A Hydrolase From Pseudomonas Aeruginosa Pa01 | 45.4 | 45.4 | 87% | 3e-05 | 20.72% | 3OM8_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure of the S105A mutant of a carbon-carbon bond hydrolase, DxnB2 from Sphingomonas wittichii RW1, in complex with 3-Cl HOPDA | 45.4 | 45.4 | 87% | 3e-05 | 24.03% | 4LXH_A (scored below threshold on previous iteration) | |
| Chain A, Est816 As An N-acyl Homoserine Lactone Degrading Enzyme | 44.3 | 44.3 | 84% | 7e-05 | 19.76% | 5EGN_A (scored below threshold on previous iteration) | |
| Chain A, Crystal structure of bromoperoxidase from Bacillus anthracis | 43.9 | 43.9 | 73% | 1e-04 | 26.70% | 3FOB_A (scored below threshold on previous iteration) | |
| Chain A, 2.22 Angstrom Resolution Crystal Structure of a Putative Acyltransferase from Salmonella enterica | 43.5 | 43.5 | 38% | 1e-04 | 27.10% | 4NVR_A (scored below threshold on previous iteration) | |
| Chain A, Crystal structure of a probable hydrolytic enzyme (PA3053) from Pseudomonas aeruginosa PAO1 at 1.50 A resolution | 42.7 | 42.7 | 48% | 2e-04 | 22.96% | 4F0J_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of The C-C Bond Hydrolase Mhpc | 42.4 | 42.4 | 90% | 3e-04 | 20.22% | 1U2E_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure of the putative alpha/beta hydrolase RutD from E.coli | 42.0 | 42.0 | 85% | 4e-04 | 24.70% | 3V48_A (scored below threshold on previous iteration) | |
| Chain A, Peroxisomal Alpha-Beta-Hydrolase Lpx1 (Yor084w) From Saccharomyces Cerevisiae (Crystal Form II) | 42.0 | 42.0 | 36% | 5e-04 | 29.17% | 2Y6U_A (scored below threshold on previous iteration) | |
| Chain A, 2-Hydroxy-6-Oxo-6-Phenylhexa-2,4-Dienoate Hydrolase (Bphd) From Rhodococcus Sp. Strain Rha1 | 40.8 | 40.8 | 94% | 0.001 | 21.30% | 1C4X_A (scored below threshold on previous iteration) | |
| Chain A, Esterase (eaest) From Exiguobacterium Antarcticum | 40.0 | 40.0 | 94% | 0.001 | 19.01% | 5H3H_A (scored below threshold on previous iteration) | |
| Chain A, Bromoperoxidase A2 | 38.5 | 38.5 | 82% | 0.005 | 22.59% | 1BRO_A (scored below threshold on previous iteration) | |

Select:AllNone Selected:0

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| Description | Max score | Total score | Query cover | E value | Perc. ident | Accession | Select for PSI blast | Used to build PSSM |
|--|-----------|-------------|-------------|---------|-------------|---|----------------------|--------------------|
| Chain A, Switching Catalysis From Hydrolysis To Perhydrolysis In P. Fluorescens Esterase | 38.5 | 38.5 | 75% | 0.006 | 20.36% | 3HI4_A (scored below threshold on previous iteration) | | |
| Chain A, Non-haem bromoperoxidase BPO-A2, Matrix protein 1 | 38.5 | 38.5 | 82% | 0.006 | 23.01% | 4IQ4_A (scored below threshold on previous iteration) | | |

| | | | | | | | |
|---|------|------|-----|-------|--------|---|--|
| Chain A, 1.1 Resolution Structure Of Ybff, A New Esterase From Escherichia Coli: A Unique Substrate-binding Crevise Generated By Domain Arrangement | 38.1 | 38.1 | 17% | 0.007 | 34.69% | 3BF7_A (scored below threshold on previous iteration) | |
| Chain A, The L29pL124I MUTATION OF PSEUDOMONAS FLUORESCENS ESTERASE | 38.1 | 38.1 | 75% | 0.008 | 20.36% | 3HEA_A (scored below threshold on previous iteration) | |
| Chain A, Pseudomonas Fluorescens Aryl Esterase | 37.7 | 37.7 | 75% | 0.010 | 20.36% | 1VA4_A (scored below threshold on previous iteration) | |
| Chain A, Haloalkane Dehalogenase With 1-hexanol | 37.7 | 37.7 | 82% | 0.010 | 22.62% | 4C6H_A (scored below threshold on previous iteration) | |
| Chain A, Haloalkane Dehalogenase | 37.7 | 37.7 | 82% | 0.010 | 22.62% | 4BRZ_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of The Fluoroacetate Dehalogenase D104 Mutant From Burkholderia Sp. Fa1 In Complex With Fluoroacetate | | | | | | I2_A (scored below threshold on previous iteration) | |
| Chain A, Pseudomonas Fluorescens Esterase Complexed To The R-Enantiomer Of A Sulfonate Transition State Analog | | | | | | 2_A (scored below threshold on previous iteration) | |
| Chain A, L29i Mutation In An Aryl Esterase From Pseudomonas Fluorescens Leads To Unique Peptide Flip And Increased Activity | | | | | | U_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of A His-Tagged Serine Hydrolase Involved In The Carbazole Degradation (Carc Enzyme) | | | | | | I_A (scored below threshold on previous iteration) | |
| Chain A, Structure Of A Putative Epoxide Hydrolase From Pseudomonas Aeruginosa | 37.4 | 37.4 | 42% | 0.012 | 23.73% | 4B9A_A (scored below threshold on previous iteration) | |
| Chain A, Structure Of A Putative Epoxide Hydrolase Q244e Mutant From Pseudomonas Aeruginosa | 37.4 | 37.4 | 42% | 0.012 | 23.73% | 4BAZ_A (scored below threshold on previous iteration) | |
| Chain A, Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1 | 37.4 | 37.4 | 80% | 0.015 | 22.32% | 3VDX_A (scored below threshold on previous iteration) | |
| Chain A, Structure Of Fluoroacetate Dehalogenase From Burkholderia Sp. Fa1 | 37.0 | 37.0 | 43% | 0.016 | 22.22% | 1Y37_A (scored below threshold on previous iteration) | |
| Chain A, Structural Studies Of A Thermophilic Esterase From Thermogutta Terrifontis (native) | 37.0 | 37.0 | 89% | 0.017 | 20.75% | 4UHC_A (scored below threshold on previous iteration) | |
| Chain A, 1.1 Resolution Structure Of Ybff, A New Esterase From Escherichia Coli: A Unique Substrate-binding Crevise Generated By Domain Arrangement | 37.0 | 37.0 | 17% | 0.017 | 34.69% | 3BF8_A (scored below threshold on previous iteration) | |
| Chain A, Chloroperoxidase T | 37.0 | 37.0 | 82% | 0.018 | 22.18% | 1A7U_A (scored below threshold on previous iteration) | |
| Chain A, Structure of a putative epoxide hydrolase t131d mutant from Pseudomonas aeruginosa, with bound MFA | 37.0 | 37.0 | 42% | 0.018 | 23.73% | 4BAU_A (scored below threshold on previous iteration) | |
| Chain A, Structural Studies Of A | | | | | | 4UHH_A (scored | |

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No Thanks

Give Feedback

| | | | | | | | |
|--|------|------|-----|-------|--------|---|---|
| Thermophilic Esterase From Thermogutta Terrifontis (cacodylate Complex) | 37.0 | 37.0 | 89% | 0.019 | 21.51% | below threshold on previous iteration) | ✓ |
| Chain A, Crystal Structure Of Human Monoglyceride Lipase | 37.0 | 37.0 | 88% | 0.022 | 23.74% | 3HJU_A (scored below threshold on previous iteration) | ✓ |
| Chain A, X-Ray Structure Of The Epoxide Hydrolase From Agrobacterium Radiobacter Ad1 | 36.6 | 36.6 | 31% | 0.022 | 29.89% | 1EHY_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Crystal Structure Of Human Mono-Glyceride Lipase In Complex With Sar629 | 36.6 | 36.6 | 88% | 0.024 | 23.74% | 3JWE_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Monoglyceride lipase | 36.6 | 36.6 | 88% | 0.025 | 23.17% | 5ZUN_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Crystal Structure of a soluble form of human MGLL in complex with an inhibitor | 36.6 | 36.6 | 88% | 0.026 | 23.17% | 3PE6_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Structure Of A Thermophilic Esterase | 36.2 | 36.2 | 86% | 0.026 | 23.48% | 5FRD_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Structure of human monoacylglycerol lipase bound to a covalent inhibitor | 36.6 | 36.6 | 88% | 0.029 | 23.74% | 6AX1_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Crystal Structure Of A Stereoselective Esterase From Pseudomonas Putida Ifo12996 | 36.2 | 36.2 | 42% | 0.033 | 26.23% | 1ZOI_A (scored below threshold on previous iteration) | ✓ |
| Chain A, The Crystal Structure Of Epoxide Hydrolase B (Rv1938) From Mycobacterium Tuberculosis At 2.1 Angstrom | 36.2 | 36.2 | 36% | 0.034 | 23.76% | 2E3J_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Crystal Structure Of Mycobacterium Tuberculosis Epoxide Hydrolase B Complexed With An Inhibitor | 36.2 | 36.2 | 36% | 0.034 | 23.76% | 2ZJF_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Thioesterase Domain From Curacin Biosynthetic Pathway | 35.8 | 35.8 | 39% | 0.043 | 28.32% | 3QIT_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Laboratory Evolved Variant R-c1b1d33 Of Potato Epoxide Hydrolase Steh1 | 35.8 | 35.8 | 41% | 0.047 | 29.41% | 4UFP_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Crystal Structure Of Alr0039, A Putative Alpha/beta Hydrolase From Nostoc Sp Pcc 7120 | 35.8 | 35.8 | 45% | 0.047 | 21.58% | 3QYJ_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Crystal structure of a novel Pyrethroid Hydrolase PytH (S78A) | 35.4 | 35.4 | 18% | 0.049 | 34.00% | 5Y5V_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Laboratory Evolved Variant R-c1b1 Of Potato Epoxide Hydrolase Steh1 | 35.8 | 35.8 | 41% | 0.050 | 29.41% | 4UFN_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Laboratory Evolved Variant R-c1b1d33e6 Of Potato Epoxide Hydrolase Steh1 | 35.4 | 35.4 | 41% | 0.053 | 29.41% | 4UFO_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Crystal structure of aCif-D158S | 35.4 | 35.4 | 31% | 0.060 | 31.46% | 4MEB_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Structure Of A Y149f Mutant Of Epoxide Hydrolase From Solanum Tuberosum | 35.0 | 35.0 | 41% | 0.073 | 29.41% | 3CXU_A (scored below threshold on previous iteration) | ✓ |
| Chain A, Structure Of Potato (Solanum Tuberosum) Epoxide Hydrolase I (Steh1) | 35.0 | 35.0 | 41% | 0.074 | 29.41% | 2CJP_A (scored below threshold on previous iteration) | ✓ |

| | | | | | | | |
|---|------|------|-----|-------|--------|---|--|
| Chain A, Structure Of An H300n Mutant Of Potato Epoxide Hydrolase, Steh1 | 35.0 | 35.0 | 41% | 0.075 | 29.41% | 4Y9S_A (scored below threshold on previous iteration) | |
| Chain A, Laboratory Evolved Variant R-c1 Of Potato Epoxide Hydrolase Steh1 | 35.0 | 35.0 | 41% | 0.075 | 29.41% | 4UHB_A (scored below threshold on previous iteration) | |
| Chain A, Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera | 35.0 | 35.0 | 82% | 0.081 | 22.59% | 4QES_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structure Of Non-Heme Chloroperoxidase From Burkholderia Cenocepacia | 34.7 | 34.7 | 82% | 0.11 | 22.83% | 4DGQ_A (scored below threshold on previous iteration) | |
| Chain A, Crystal structure of the Cif epoxide hydrolase from Acinetobacter nosocomialis | 33.5 | 33.5 | 31% | 0.22 | 30.34% | 4MEA_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structures Of The Luciferase And Green Fluorescent Protein From Renilla Reniformis | 33.1 | 33.1 | 31% | 0.31 | 25.56% | 2PSJ_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structures Of The Luciferase And Green Fluorescent Protein From Renilla Reniformis | 33.1 | 33.1 | 31% | 0.32 | 25.56% | 2PSF_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structures Of The Luciferase And Green Fluorescent Protein From Renilla Reniformis | 33.1 | 33.1 | 31% | 0.32 | 25.56% | 2PSD_A (scored below threshold on previous iteration) | |
| Chain A, Crystal Structures Of The Luciferase And Green Fluorescent Protein From Renilla Reniformis | 33.1 | 33.1 | 31% | 0.32 | 25.56% | 2PSH_A (scored below threshold on previous iteration) | |
| Chain A, Crystal structure of an esterase RhEst1 from Rhodococcus sp. ECU1013 | 32.7 | 32.7 | 78% | 0.38 | 21.34% | 4RNC_A (scored below threshold on previous iteration) | |
| Chain A, Crystal structure of PytH_H230A | 32.7 | 32.7 | 18% | 0.43 | 32.00% | 5Y51_A (scored below threshold on previous iteration) | |

Alignments

Chain A, Structural basis for specific inhibition of highly sensitive ShHTL7 receptor
Sequence ID: **5Z82_A** Length: 276 Number of Matches: 1

See 2 more title(s)
Range 1: 1 to 276

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|----------------|--------|--|--------------------------------------|---------------|-----------|-------|
| 568 bits(1465) | 0.0() | Compositional matrix adjust. | 276/276(100%) | 276/276(100%) | 0/276(0%) | |
| Features: | | | | | | |
| Query | 1 | GPLGSMSSIGLAHNVTILGSGETT | VVLGHGYGTDQSVWKLLVPYLVDDYKVLLYDHMGAG | 60 | | |
| Sbjct | 1 | GPLGSMSSIGLAHNVTILGSGETT | VVLGHGYGTDQSVWKLLVPYLVDDYKVLLYDHMGAG | 60 | | |
| Query | 61 | TTNPDYDFDRYSSLEGYSYDLIAILEEFQVSKCIYVGHSMSMAAAVASIFRPDLFHKL | 120 | | | |
| Sbjct | 61 | TTNPDYDFDRYSSLEGYSYDLIAILEEFQVSKCIYVGHSMSMAAAVASIFRPDLFHKL | 120 | | | |
| Query | 121 | VMISPTPRLINTEEYGGFEQKVMDETLRSLDENFKSLSLGTAPLLLACDLESAAMQEYC | 180 | | | |
| Sbjct | 121 | VMISPTPRLINTEEYGGFEQKVMDETLRSLDENFKSLSLGTAPLLLACDLESAAMQEYC | 180 | | | |
| Query | 181 | RTLFNMRPDIACCITRMICGLDLRPYLGHVTVPCHHIQSSNDIMVPVAVGEYLRKNLGGP | 240 | | | |
| Sbjct | 181 | RTLFNMRPDIACCITRMICGLDLRPYLGHVTVPCHHIQSSNDIMVPVAVGEYLRKNLGGP | 240 | | | |
| Query | 241 | SVVEVMPTEGHLPHLSMPEVTIPVVLRHIRQDITDH | 276 | | | |
| Sbjct | 241 | SVVEVMPTEGHLPHLSMPEVTIPVVLRHIRQDITDH | 276 | | | |

Chain A, Structural basis for specific inhibition of highly sensitive ShHTL7 receptor

Sequence ID: **5Z89_A** Length: 276 Number of Matches: 1
Range 1: 1 to 276

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|----------------|--------|------------------------------|---------------------------|----------------------|-----------|-------|
| 567 bits(1461) | 0.0() | Compositional matrix adjust. | 275/276(99%) | 275/276(99%) | 0/276(0%) | |
| Features: | | | | | | |
| Query 1 | | GPLGSMSSIGLAHNVTILGSGETT | VVLGHGYGTDQSVWKL | LVPLYVDDYKVLLYDHMGAG | | 60 |
| Sbjct 1 | | GPLGSMSSIGLAHNVTILGSGETT | VVLGHGYGTDQSVWKL | LVPLYVDDYKVLLYDHMGAG | | 60 |
| Query 61 | | TTNPDYFDFDRYSSLEGYSYDLIA | ILEEFQVSKCIYVGHSMSSMAA | AVASIFRPDLFHKL | | 120 |
| Sbjct 61 | | TTNPDYFDFDRYSSLEGYSYDLIA | ILEEFQVSKCIYVGHSMSSMAA | AVASIFRPDLFHKL | | 120 |
| Query 121 | | VMISPTPRLINTEEYGGFEQKVMDE | TLRSLDENFKSLSLGTAPLLLACD | LESAAMQEYC | | 180 |
| Sbjct 121 | | VMISPTPRLINTEEYGGFEQKVMDE | TLRSLDENFKSLSLGTAPLLLACD | LESAAMQEYC | | 180 |
| Query 181 | | RTLNFMRPDIACCITRMICGLDLRP | YLGHVTPCHIIQSSNDIMVPVAVGE | YLRKKNLGGP | | 240 |
| Sbjct 181 | | RTLNFMRPDIACCITRMICGLDLRP | YLGHVTPCHIIQSSNDIMVPVAVGE | YLRKKNLGGP | | 240 |
| Query 241 | | SVVEVMPTEGHLPHLSMPEVTIPV | LRHIRQDITDH | 276 | | |
| Sbjct 241 | | SVVEVMPTEGHLPHLSMPEVTIPV | LRHIRQDITDH | 276 | | |

Chain A, Hyposensitive to light 7

Sequence ID: **5Z7Y_A** Length: 281 Number of Matches: 1

See 3 more title(s)
Range 1: 3 to 273

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|----------------|--------|------------------------------|---------------------------|----------------------|-----------|-------|
| 558 bits(1438) | 0.0() | Compositional matrix adjust. | 271/271(100%) | 271/271(100%) | 0/271(0%) | |
| Features: | | | | | | |
| Query 6 | | MSSIGLAHNVTILGSGETT | VVLGHGYGTDQSVWKL | LVPLYVDDYKVLLYDHMGAG | TNPD | 65 |
| Sbjct 3 | | MSSIGLAHNVTILGSGETT | VVLGHGYGTDQSVWKL | LVPLYVDDYKVLLYDHMGAG | TNPD | 62 |
| Query 66 | | YFDFDRYSSLEGYSYDLIAILEEFQ | VSKCIYVGHSMSSMAA | AVASIFRPDLFHKLV | MISP | 125 |
| Sbjct 63 | | YFDFDRYSSLEGYSYDLIAILEEFQ | VSKCIYVGHSMSSMAA | AVASIFRPDLFHKLV | MISP | 122 |
| Query 126 | | TPRLINTEEYGGFEQKVMDE | TLRSLDENFKSLSLGTAPLLLACD | LESAAMQEYCR | TLFN | 185 |
| Sbjct 123 | | TPRLINTEEYGGFEQKVMDE | TLRSLDENFKSLSLGTAPLLLACD | LESAAMQEYCR | TLFN | 182 |
| Query 186 | | MRPDIACCITRMICGLDLRP | YLGHVTPCHIIQSSNDIMVPVAVGE | YLRKKNLGGPSV | VVEV | 245 |
| Sbjct 183 | | MRPDIACCITRMICGLDLRP | YLGHVTPCHIIQSSNDIMVPVAVGE | YLRKKNLGGPSV | VVEV | 242 |
| Query 246 | | MPTEGHLPHLSMPEVTIPV | LRHIRQDITDH | 276 | | |
| Sbjct 243 | | MPTEGHLPHLSMPEVTIPV | LRHIRQDITDH | 273 | | |

Chain A, Hyposensitive to light 4

Sequence ID: **5Z7X_A** Length: 274 Number of Matches: 1
Range 1: 1 to 274

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|----------------|----------|------------------------------|---------------------------|----------------------|-----------|-------|
| 427 bits(1099) | 1e-152() | Compositional matrix adjust. | 199/274(73%) | 241/274(87%) | 0/274(0%) | |
| Features: | | | | | | |
| Query 1 | | GPLGSMSSIGLAHNVTILGSGETT | VVLGHGYGTDQSVWKL | LVPLYVDDYKVLLYDHMGAG | | 60 |
| Sbjct 1 | | GPLGSMSSIGLAHNVTILGSGETT | VVLGHGYGTDQSVWKL | LVPLYVDDYKVLLYDHMGAG | | 60 |
| Query 61 | | TTNPDYFDFDRYSSLEGYSYDLIA | ILEEFQVSKCIYVGHSMSSMAA | AVASIFRPDLFHKL | | 120 |
| Sbjct 61 | | TTNPDCYDFERYSSLEGHSNDLIA | ILDHVTTCIYVGHSLSSMAA | AVSSIFRPDLFRKV | | 120 |
| Query 121 | | VMISPTPRLINTEEYGGFEQKVMDE | TLRSLDENFKSLSLGTAPLLLACD | LESAAMQEYC | | 180 |
| Sbjct 121 | | VMISPTPRLINTEEYGGFEQKVMDE | TLRSLDENFKSLSLGTAPLLLACD | LESAAMQEYC | | 180 |
| Query 181 | | RTLNFMRPDIACCITRMICGLDLRP | YLGHVTPCHIIQSSNDIMVPVAVGE | YLRKKNLGGP | | 240 |
| Sbjct 181 | | RTLNFMRPDIACCITRMICGLDLRP | YLGHVTPCHIIQSSNDIMVPVAVGE | YLRKKNLGGP | | 240 |
| Query 241 | | SVVEVMPTEGHLPHLSMPEVTIPV | LRHIRQDIT | 274 | | |

Sbjct 241 SVVE++PTEGHLPHLS PE+TIPV++RHI+ DI
SVVELIPTEGHLPHLSAPELTIPVLVRHIKHDIA 274

Chain A, Crystal Structure Of The Strigolactone Receptor Shhtl5 From Striga Hermonthica
Sequence ID: **5CBK_A** Length: 271 Number of Matches: 1
Range 1: 1 to 270

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|--|--------|--------------------------|------------------------|--------------------------------|-------------------|------------------|
| 404 bits(1037) 3e-143() Compositional matrix adjust. 186/270(69%) 230/270(85%) 0/270(0%) | | | | | | |
| Features: | | | | | | |
| Query 6 | | MSSIGLAHNVTILGSGETT | VVLGHGYGTDQSVWKL | LVPYL | VDDYKVLLYDH | MGAGTTNPD 65 |
| Sbjct 1 | | MS++G AHNVT+LGSGETT | VVLGHG+GTDQSVWK | LVP+L DDY+VLLYD | +MGAGTT+P+ MSTVGS | AHNVTVLGSGETT 60 |
| Query 66 | | YDFD | RYSSLEGYSYDLIAILEEF | QVSKCIYVGHS | MSSMAAAVASIFR | PDLFHKLVMISP 125 |
| Sbjct 61 | | +DF+RYSSLEG+S DLIAILEEF | V+KCI+VGHS+SSM AV+SIFR | PDLF K+VMIS LYDFERYSSLE | GHSQDLIAILEEFH | VT |
| Query 126 | | TPRLINTEEYYGGFEQ | KVMDETLRSLDENFK | SLSLGTAPLLLACD | LESAA | MQEYCR |
| Sbjct 121 | | PR+ N +++YYGGFE++ +++ | +++ENF+++ G AP+++ DLES | AMQE+ RTLFN CPRVANADDYY | GGFEEDVNQLYG | AMEENFQ |
| Query 186 | | MRPDIACCITRMICGL | DLRPYLGHVTPCHIIQ | SSNDIMVPVAVGEY | LRK | NLGGPSVVEV 245 |
| Sbjct 181 | | MRPDIA I RMI G DLRPYL | G V +PCHIIQSS D +VPVAV | EYL +N GG SVVE+ MRPDIALSICRMIS | GYDLRPYLGLV | VIPCHIIQSSKDKL |
| Query 246 | | MPTEGHLPHLSMPEVT | TIPVLRHIRQDITD | 275 | | |
| Sbjct 241 | | +PTEGHLPHLS P++TIPV++RHI | QDI D | | | |
| | | IPTEGHLPHLSAPDITIPVL | IRHINQDIAD | 270 | | |

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