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BLAST Results

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PSI blast Iteration 1

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

RID [77X2XU7501N](#) (Expires on 02-26 20:57 pm)

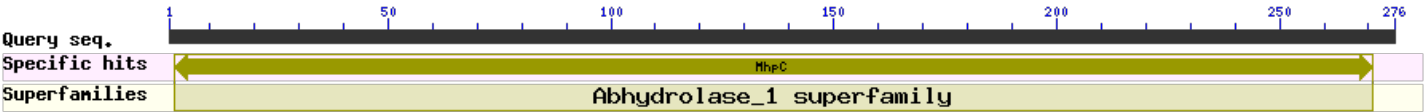
Query ID [IcIIQuery\\_320279](#)  
Description T0951 ShHTL7, Striga hermonthica, 276 residues|  
Molecule type amino acid  
Query Length 276

Database Name [pdb](#)  
Description PDB protein database  
Program BLASTP 2.8.1+

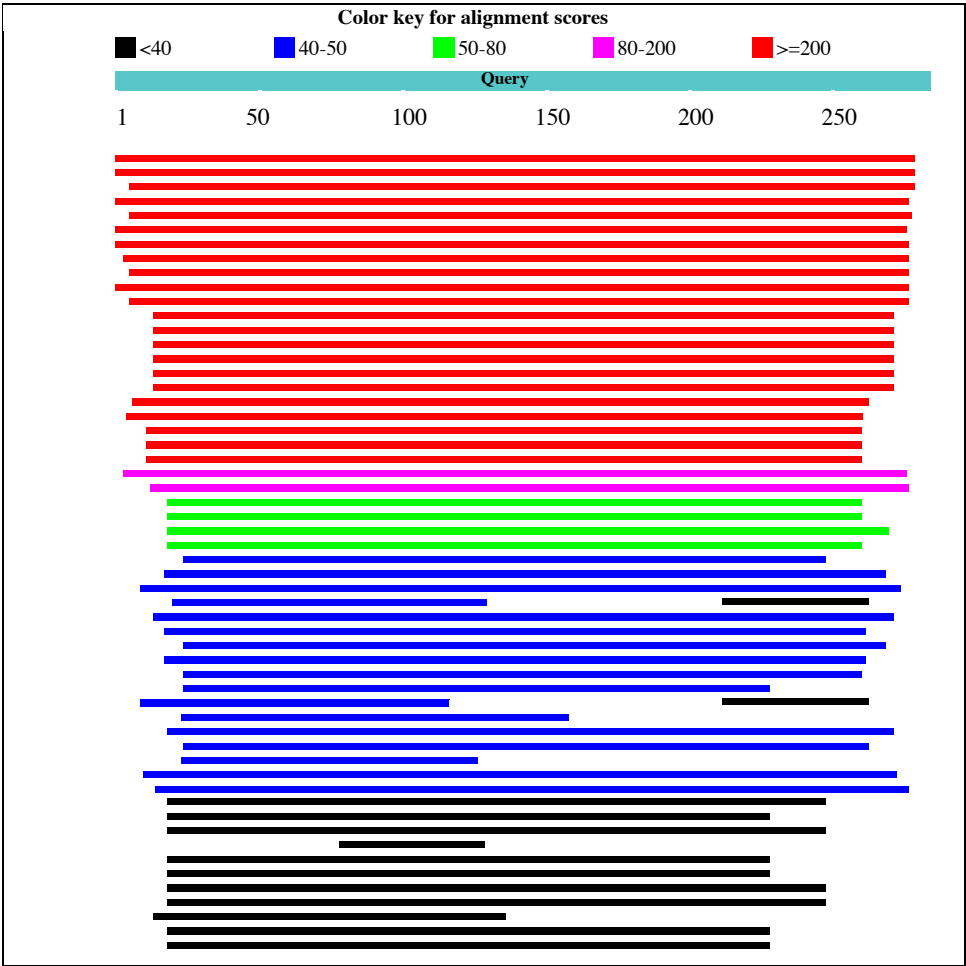
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Graphic Summary

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	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%	<a href="#">5Z82_A</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%	<a href="#">5Z89_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal structure of Striga hermonthica HTL7 (ShHTL7)	558	558	98%	0.0	100.00%	<a href="#">5Z7Y_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal structure of Striga hermonthica HTL4 (ShHTL4)	427	427	99%	1e-152	72.63%	<a href="#">5Z7X_A</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%	<a href="#">5CBK_A</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%	<a href="#">5DNU_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal Structure Of Arabidopsis Thaliana Dwarf14 Like (atd14l)	353	353	99%	2e-123	60.22%	<a href="#">3W06_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal Structure Of Kai2	353	353	98%	2e-123	60.52%	<a href="#">4HRX_A</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%	<a href="#">4IH1_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal structure of Striga hermonthica HTL1 (ShHTL1)	350	350	99%	3e-122	60.58%	<a href="#">5Z7W_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal structure of KAI2_ply2(A219V)	343	343	97%	2e-119	60.59%	<a href="#">5Z9H_A</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%	<a href="#">5DJ5_A</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%	<a href="#">6AP8_A</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%	<a href="#">4IHA_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal Structure Of Oryza Sativa Dwarf14 (d14)	264	264	92%	2e-88	47.27%	<a href="#">3W04_A</a> (scored below threshold on previous iteration)		
Chain A, D3-CTH-D14-D-ring	265	265	92%	2e-88	47.27%	<a href="#">6BRT_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal structure of OsD14	264	264	92%	4e-88	47.27%	<a href="#">3VXK_A</a> (scored below threshold on previous iteration)		
Chain A, Crystal structure of Striga hermonthica Dwarf14 (ShD14)	261	261	92%	4e-87	48.03%	<a href="#">5Z7Z_A</a> (scored below threshold on previous iteration)		

Chain A, Crystal Structure Of Arabidopsis Dwarf14 Orthologue, Atd14	260	260	92%	1e-86	46.85%	<a href="#">4IH4_A</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%	<a href="#">6AP6_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal Structure Of Dad2	258	258	89%	9e-86	47.77%	<a href="#">4DNP_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal Structure Of Dad2 S96a Mutant	256	256	89%	2e-85	47.37%	<a href="#">4DNQ_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal Structure Of Rsbq	162	162	97%	1e-48	32.47%	<a href="#">1WOM_A</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%	<a href="#">3QVM_A</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%	<a href="#">1M33_A</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%	<a href="#">4ETW_A</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%	<a href="#">3E3A_A</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%	<a href="#">4NMW_A</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%	<a href="#">2XUA_A</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%	<a href="#">5W15_A</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%	<a href="#">4PSU_A</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%	<a href="#">5CW2_C</a> (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%	<a href="#">3KXP_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal structure of DxnB2, a carbon - carbon bond hydrolase from Sphingomonas wittichii RW1	46.2	46.2	87%	2e-05	24.42%	<a href="#">4LXG_A</a> (scored below threshold on previous iteration)	
Chain A, The Crystal Structure Of A Hydrolase From Pseudomonas Aeruginosa Pa01	45.4	45.4	87%	3e-05	20.72%	<a href="#">3OM8_A</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%	<a href="#">4LXH_A</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%	<a href="#">5EGN_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal structure of bromoperoxidase from Bacillus	43.9	43.9	73%	1e-04	26.70%	<a href="#">3FOB_A</a> (scored below threshold on previous iteration)	

anthracis						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%	<a href="#">4NVR_A</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%	<a href="#">4F0J_A</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%	<a href="#">1U2E_A</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%	<a href="#">3V48_A</a> (scored below threshold on previous iteration)	
Chain A, Peroxisomal Alpha-Beta-Hydrolase Lpx1 (Yor084w) From Saccharomyces Cerevisiae (Crystal Form li)	42.0	42.0	36%	5e-04	29.17%	<a href="#">2Y6U_A</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%	<a href="#">1C4X_A</a> (scored below threshold on previous iteration)	
Chain A, Esterase (eaest) From Exiguobacterium Antarcticum	40.0	40.0	94%	0.001	19.01%	<a href="#">5H3H_A</a> (scored below threshold on previous iteration)	
Chain A, Bromoperoxidase A2	38.5	38.5	82%	0.005	22.59%	<a href="#">1BRQ_A</a> (scored below threshold on previous iteration)	

Select:[AllNone](#) Selected:0
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Description	Max score	Total score	Query cover	E value	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%	<a href="#">3HI4_A</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%	<a href="#">4IQ4_A</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 Crevice Generated By Domain Arrangement	38.1	38.1	17%	0.007	34.69%	<a href="#">3BF7_A</a> (scored below threshold on previous iteration)		
Chain A, The L29pL124I MUTATION OF PSEUDOMONAS FLUORESCENS ESTERASE	38.1	38.1	75%	0.007	20.36%	<a href="#">3HEA_A</a> (scored below threshold on previous iteration)		
Chain A, Pseudomonas Fluorescens Aryl Esterase	37.7	37.7	75%	0.010	20.36%	<a href="#">1VA4_A</a> (scored below threshold on previous iteration)		
Chain A, Haloalkane Dehalogenase With 1-hexanol	37.7	37.7	82%	0.010	22.62%	<a href="#">4C6H_A</a> (scored below threshold on previous iteration)		

Chain A, Haloalkane Dehalogenase	37.7	37.7	82%	0.010	22.62%	<a href="#">4BRZ_A</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	37.7	37.7	43%	0.010	22.22%	<a href="#">3B12_A</a> (scored below threshold on previous iteration)	
Chain A, Pseudomonas Fluorescens Esterase Complexed To The R-Enantiomer Of A Sulfonate Transition State Analog	37.7	37.7	75%	0.010	20.36%	<a href="#">3IA2_A</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	37.7	37.7	75%	0.010	20.36%	<a href="#">3T4U_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal Structure Of A His-Tagged Serine Hydrolase Involved In The Carbazole Degradation (Carc Enzyme)	37.7	37.7	80%	0.011	22.61%	<a href="#">1J1I_A</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%	<a href="#">4B9A_A</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%	<a href="#">4BAZ_A</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%	<a href="#">3VDX_A</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%	<a href="#">1Y37_A</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%	<a href="#">4UHC_A</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 Crevice Generated By Domain Arrangement	37.0	37.0	17%	0.017	34.69%	<a href="#">3BF8_A</a> (scored below threshold on previous iteration)	
Chain A, Chloroperoxidase T	37.0	37.0	82%	0.017	22.18%	<a href="#">1A7U_A</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%	<a href="#">4BAU_A</a> (scored below threshold on previous iteration)	
Chain A, Structural Studies Of A Thermophilic Esterase From Thermogutta Terrifontis (cacodylate Complex)	37.0	37.0	89%	0.019	21.51%	<a href="#">4UHH_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal Structure Of Human Monoglyceride Lipase	37.0	37.0	88%	0.022	23.74%	<a href="#">3HJU_A</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%	<a href="#">1EHY_A</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%	<a href="#">3JWE_A</a> (scored below threshold on previous iteration)	
Chain A, Monoglyceride lipase	36.6	36.6	88%	0.025	23.17%	<a href="#">5ZUN_A</a> (scored below threshold on previous iteration)	

						previous iteration)	
Chain A, Crystal Structure of a soluble form of human MGLL in complex with an inhibitor	36.6	36.6	88%	0.025	23.17%	<a href="#">3PE6_A</a> (scored below threshold on previous iteration)	
Chain A, Structure Of A Thermophilic Esterase	36.2	36.2	86%	0.025	23.48%	<a href="#">5FRD_A</a> (scored below threshold on previous iteration)	
Chain A, Structure of human monoacylglycerol lipase bound to a covalent inhibitor	36.6	36.6	88%	0.028	23.74%	<a href="#">6AX1_A</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%	<a href="#">1ZOI_A</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%	<a href="#">2E3J_A</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%	<a href="#">2ZJF_A</a> (scored below threshold on previous iteration)	
Chain A, Thioesterase Domain From Curacin Biosynthetic Pathway	35.8	35.8	39%	0.042	28.32%	<a href="#">3QIT_A</a> (scored below threshold on previous iteration)	
Chain A, Laboratory Evolved Variant R-c1b1d33 Of Potato Epoxide Hydrolase Steh1	35.8	35.8	41%	0.046	29.41%	<a href="#">4UFP_A</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%	<a href="#">3QYJ_A</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%	<a href="#">5Y5V_A</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%	<a href="#">4UFN_A</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%	<a href="#">4UFO_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal structure of aCif-D158S	35.4	35.4	31%	0.060	31.46%	<a href="#">4MEB_A</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%	0.072	29.41%	<a href="#">3CXU_A</a> (scored below threshold on previous iteration)	
Chain A, Structure Of Potato (Solanum Tuberosum) Epoxide Hydrolase I (Steh1)	35.0	35.0	41%	0.073	29.41%	<a href="#">2CJP_A</a> (scored below threshold on previous iteration)	
Chain A, Structure Of An H300n Mutant Of Potato Epoxide Hydrolase, Steh1	35.0	35.0	41%	0.074	29.41%	<a href="#">4Y9S_A</a> (scored below threshold on previous iteration)	
Chain A, Laboratory Evolved Variant R-c1 Of Potato Epoxide Hydrolase Steh1	35.0	35.0	41%	0.074	29.41%	<a href="#">4UHB_A</a> (scored below threshold on previous iteration)	
Chain A, Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera	35.0	35.0	82%	0.080	22.59%	<a href="#">4QES_A</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%	<a href="#">4DGQ_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal structure of the Cif epoxide hydrolase from	33.5	33.5	31%	0.22	30.34%	<a href="#">4MEA_A</a> (scored below threshold on	

Acinetobacter nosocomialis						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%	<a href="#">2PSJ_A</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%	<a href="#">2PSF_A</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%	<a href="#">2PSD_A</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%	<a href="#">2PSH_A</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%	<a href="#">4RNC_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal structure of PytH_H230A	32.7	32.7	18%	0.42	32.00%	<a href="#">5Y51_A</a> (scored below threshold on previous iteration)	
Chain A, X-ray crystal structure of Halotag bound to the P1 benzoxadiazole fluorogenic ligand	32.7	32.7	62%	0.43	21.67%	<a href="#">5VNP_A</a> (scored below threshold on previous iteration)	
Chain A, X-ray crystal structure of apo Halotag	32.3	32.3	62%	0.50	21.67%	<a href="#">5UY1_A</a> (scored below threshold on previous iteration)	
Chain A, Structure Of Haloalkane Dehalogenase Variant Dhaa101	32.3	32.3	35%	0.50	24.78%	<a href="#">5FLK_A</a> (scored below threshold on previous iteration)	
Chain A, Crystal Structure Of Human Mono-Glyceride Lipase	32.3	32.3	88%	0.52	23.55%	<a href="#">3JW8_A</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	GPLGSMSSIGLAHNVTILGSGETTVVLGHGYGTDQSVWKLLVPYLVDYKVLLYDHMGAG				60
Sbjct	1	GPLGSMSSIGLAHNVTILGSGETTVVLGHGYGTDQSVWKLLVPYLVDYKVLLYDHMGAG				60
Query	61	TTNPDYDFD DRYSSLEGYSYDLIAILEEFQVSKCIYVGHSMSMAAAVASIFRPDLFHKL				120
Sbjct	61	TTNPDYDFD DRYSSLEGYSYDLIAILEEFQVSKCIYVGHSMSMAAAVASIFRPDLFHKL				120
Query	121	VMISPTPRLINTEEYYGGFEQKVMDET L RSLDENFKSLSLGTAPLLLACDLESAAMQEYC				180
Sbjct	121	VMISPTPRLINTEEYYGGFEQKVMDET L RSLDENFKSLSLGTAPLLLACDLESAAMQEYC				180
Query	181	RTLFNMRPDIACCI TRMICGLDLRPYLGHVTVPCII IQSSNDIMVPVAVGEYLRKNLGGP				240
Sbjct	181	RTLFNMRPDIACCI TRMICGLDLRPYLGHVTVPCII IQSSNDIMVPVAVGEYLRKNLGGP				240
Query	241	SVVEVMPTEGHLPHLSMPEVTIPVVL RHIRQDITDH			276	
Sbjct	241	SVVEVMPTEGHLPHLSMPEVTIPVVL RHIRQDITDH			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	VVLGHGYGTDQSVWKLLVPYL	VDDYKVLLYDHMGAG		60
Sbjct	1	GPLGSMSSIGLAHNVTILGSGETT	VVLGHGYGTDQSVWKLLVPYL	VDDYKVLLYDHMGAG		60
Query	61	TTNPDYFDFDRYSSLEGYSYDLIA	ILEEFQVSKCIYVGHSMSMAAAVAS	IFRPDLFHKL		120
Sbjct	61	TTNPDYFDFDRYSSLEGYSYDLIA	ILEEFQVSKCIYVGHSMSMAAAVAS	IFRPDLFHKL		120
Query	121	VMISPTPRLINTEEYGGFEQKVMDE	TLRSLDENFKSLSLGTAPLLLACDLESAAMQ	EYC		180
Sbjct	121	VMISPTPRLINTEEYGGFEQKVMDE	TLRSLDENFKSLSLGTAPLLLACDLESAAMQ	EYC		180
Query	181	RTLNFMRPDIAACITRMICGLDLR	PYLGHVTVPCIIQSSNDIMVPVAVGEYLRK	NLGGP		240
Sbjct	181	RTLNFMRPDIAACITRMICGLDLR	PYLGHVTVPCIIQSSNDIMVPVAVGEYLRK	NLGGP		240
Query	241	SVVEVMPTEGHLPHLSMPEVTIPV	VLRHIRQDITDH	276		
Sbjct	241	SVVEVMPTEGHLPHLSMPEVTIPV	VLRHIRQDITDH	276		

Chain A, Crystal structure of Striga hermonthica HTL7 (ShHTL7)  
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	VVLGHGYGTDQSVWKLLVPYL	VDDYKVLLYDHMGAG	TNPD	65
Sbjct	3	MSSIGLAHNVTILGSGETT	VVLGHGYGTDQSVWKLLVPYL	VDDYKVLLYDHMGAG	TNPD	62
Query	66	YFDFDRYSSLEGYSYDLIAILEEF	QVSKCIYVGHSMSMAAAVAS	IFRPDLFHKLV	MISP	125
Sbjct	63	YFDFDRYSSLEGYSYDLIAILEEF	QVSKCIYVGHSMSMAAAVAS	IFRPDLFHKLV	MISP	122
Query	126	TPRLINTEEYGGFEQKVMDE	TLRSLDENFKSLSLGTAPLLLACDLESAAMQ	EYCR	TLFN	185
Sbjct	123	TPRLINTEEYGGFEQKVMDE	TLRSLDENFKSLSLGTAPLLLACDLESAAMQ	EYCR	TLFN	182
Query	186	MRPDIAACITRMICGLDLR	PYLGHVTVPCIIQSSNDIMVPVAVGEYLRK	NLGGPSV	VEV	245
Sbjct	183	MRPDIAACITRMICGLDLR	PYLGHVTVPCIIQSSNDIMVPVAVGEYLRK	NLGGPSV	VEV	242
Query	246	MPTEGHLPHLSMPEVTIPV	VLRHIRQDITDH	276		
Sbjct	243	MPTEGHLPHLSMPEVTIPV	VLRHIRQDITDH	273		

Chain A, Crystal structure of Striga hermonthica HTL4 (ShHTL4)  
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	VVLGHGYGTDQSVWKLLVPYL	VDDYKVLLYDHMGAG		60
Sbjct	1	GPLGSMSSIGLAHNVTILGSGETT	VVLGHGYGTDQSVWKLLVPYL	VDDYKVLLYDHMGAG		60
Query	61	TTNPDDF+RYSSLEG+S	DLIAIL++F V+KCIYVGHS+SSMAAAV+S	IFRPDLF K+		120
Sbjct	61	TTNPDCYDFERYSSLEGHSNDLIA	ILDHVTTCIYVGHSLSMAAAVSS	IFRPDLFRKV		120
Query	121	VMISPTPRLINTEEYGGFEQKVMDE	TLRSLDENFKSLSLGTAPLLLACDLESAAMQ	EYC		180
Sbjct	121	VMIS TPR+ NTE+YGGFEQ+ +++	+++ENFK++ +G AP+++ DLES A+QE+			180
Query	181	RTLNFMRPDIAACITRMICGLDLR	PYLGHVTVPCIIQSSNDIMVPVAVGEYLRK	NLGGP		240
Sbjct	181	RTLNFMRPDIAACITRMICGLDLR	PYLGHVTVPCIIQSSNDIMVPVAVGEYLRK	NLGGP		240
Query	241	SVVEVMPTEGHLPHLSMPEVTIPV	VLRHIRQDIT	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	VDDYKVLLYDHM	GAGTTNPD 65
Sbjct 1		MS++G AHNVT+LGSGETT	VVLGHG+GTDQSVWK	LVP+L DDY+VLLYD	+MGAGTT+P+ MSTVGS	AHNVT+LGSGETT 60
Query 66		YDFD	RYSSLEGYSYDLIAILEEF	QVSKCIYVGHS	MSSMAAAVASIFR	PDLFHKLVMISP 125
Sbjct 61		+DF+RYSSLEG+S DLIAILEEF	V+KCI+VGHS+SSM AV+SIFR	PDLF K+VMIS LYDFERYSS	LEGHSQDLIAILEEFHVT	KCIFVGHSLSMVGAVSSI 120
Query 126		TPRLINTEEYYGGFEQ	KVMDETLRSLDENFK	SLSLGTAPLLLACD	LESAA	MQEYCRTLFN 185
Sbjct 121		PR+ N +++YYGGFE++ +++	+++ENF+++ G AP+++ DLES	AMQE+ RTLFN CPRVANADDYY	GGFEEDVNQLYGAMEEN	FQTMMTGYAPIVVGGDLESEAMQEF 180
Query 186		MRPDIACCITRMICGL	DLRPYLGHVTVPC	HIQSSNDIMVPVAV	GEYLRK	NLGGPSVVEV 245
Sbjct 181		MRPDIA I RMI G DLRPYLG	V +PCHIIQSS D +VPVAV	EYL +N GG SVVE+ MRPDIALSICRMIS	GYDLRPYLGLVVIPCHIIQSS	KDKLVPVAVAEYLHRNFGGKSVVEL 240
Query 246		MPTEGHLPHLSMPEVT	TIPVVLRHIRQDITD	275		
Sbjct 241		+PTEGHLPHLS P++TIPV++RHI	QDI D			
		IPTEGHLPHLSAPDIT	TIPVLIRHINQDIAD	270		

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Page 9 of 9