

## Sally Special gp 5 and 6 Lysin A genes

SallySpecial gp 5 called as Lysin A, protease M15 domain BUT that sounds different than a peptidoglycan binding domain which is a separate gene in the plyC operon (Lysin A genes encoded in two genes) of strept phage C1. See HHPRED results below.

Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
<input type="checkbox"/> 1	2RKQ_A	Peptidoglycan-recognition protein-SD; innate immunity Toll ; 1.5A {Drosophila melanogaster} SCOP: l.1.1.1, d.118.1.0	99.63	2e-17	11.8	117	169
<input checked="" type="checkbox"/> 2	1S2J_A	Peptidoglycan recognition protein SA CG11709-PA; mixed beta-sheet, pi-helix (one turn); HET: PO4; 2.2A {Drosophila melanogaster} SCOP: d.118.1.1, l.1.1.1	99.61	3.8e-17	11.9	118	209
<input type="checkbox"/> 3	2XZ4_B	PEPTIDOGLYCAN-RECOGNITION PROTEIN LF; IMMUNE SYSTEM, INNATE IMMUNITY; HET: EDO, 1PG; 1.72A {DROSOPHILA MELANOGASTER} SCOP: d.118.1.0	99.6	6e-17	11.7	119	180
<input checked="" type="checkbox"/> 4	4Z8I_A	peptidoglycan recognition protein 3 (E.C.3.5.1.28); peptidoglycan recognition protein, chitin-binding domain; 2.701A {Branchiostoma belcheri tsingtauense}	99.59	7e-17	11.8	120	236
<input type="checkbox"/> 5	1SXR_B	Peptidoglycan recognition protein SA CG11709-PA; Pattern Recognition Receptor, peptidoglycan, innate; HET: SO4, EDO; 1.56A {Drosophila melanogaster} SCOP: d.118.1.1, l.1.1.1	99.59	1e-16	12.3	119	183

1. [Template alignment](#) | [Template 3D structure](#) | [PDBe](#)  
**2RKQ\_A Peptidoglycan-recognition protein-SD; innate immunity Toll ; 1.5A {Drosophila melanogaster} SCOP: I.1.1.1, d.118.1.0**  
 Probability: 99.63 E-value: 2.0E-17 Score: 116.65 Aligned Cols: 117 Identities: 17% Similarity: 0.204

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Q ss_pred          CCCCCcCCccccCCCC----cCCccEEEEecCCCCc-----hHHHHhCCCCCCCCceeeEE
Q SS_5            28  GLPVVEHAGWRERGHG----FLDIRGVLCHHTAGGGAN-----DWRIVQNGRPDLPGPLAQLV 82 (155)
Q Consensus       28  ~~~~~w~~~~~iViH~T~~~~~h~~ 82 (155)
                   ++.++.+.|.++.+. .+.+.||+||+++... ..+.+.+.+.+.||+
T Consensus       1   ~~~~~w~~~~~iVH~t~~~~~h~~ 70 (169)
T 2RKQ_A          1   EVPITVTRAEWNAKPPNGAIDSMVTLPRAVIAHTAGGACADDVTCSQHMRNLQNFQMSKQKFSDIGYHYL 70 (169)
T ss_dssp         CCEECTGGGTCCCCSCCCBCCSSEEEEEEECCSCCCSHHHHHHHHHHHHHHTSCSSSCSE
T ss_pred         CCEEECHHHhCCCCCCCCcCCCEEEEECCCCCCCCHHHHHHHHHHHHhCCCCCCCC
  
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Q ss_pred          ECCCCeEEEE--eCeeccCCCCCCCCCCCCcCeEEEEccCCCCCCHHHHHHHHHHHHHHH
Q SS_5            83  LEKDGTVRII--AVGVCHWAGRGAWPGWPTNNANHYHTIGIEAVSRGDGKDWTAVQLRNYRILCAALLNAL 150 (155)
Q Consensus       83  i~dG~i~-----w~g~-----N~sigIe~-----t~q~-----l~l~----- 150 (155)
                   |+.||.+++ .+.+|+++ ..|.+.+||+++...+.+.+.+.+.+.|+++|+++|
T Consensus       71  i~dG~i~-----N~i~i~g~-----q~a~-----l~l~----- 130 (169)
T 2RKQ_A          71  IGGNGKVYEGRSPSQRGAFAG-----PNNDGSLGIAFIGNFEERAPNKEALDAAKELEQAVKQA 130 (169)
T ss_dssp         ECTTSEEEESCCTTBCCSSG-----GGCTTEEEEESSCCSSCCCHHHHHHHHHHHHHHTT
T ss_pred         ECCCCeEECCChhccccC-----CcCCCeEEEEccCCCCCCHHHHHHHHHHHHHh
  
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Q ss_pred          CCCC
Q SS_5            151  GLEG 154 (155)
Q Consensus       151  gi~~ 154 (155)
                   +|++
T Consensus       131  ~i~~ 134 (169)
T 2RKQ_A          131  QLVE 134 (169)
T ss_dssp         SEEE
T ss_pred         CCCC
  
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## Sally Special gp 6 called as Lysin A, glycosyl hydrolase domain

1. [Template alignment](#) | [Template 3D structure](#) | [PDBe](#)  
**2Y28\_B 1,6-ANHYDRO-N-ACETYLMURAMYL-L-ALANINE AMIDASE AMPD (E.C.3.5.1.28); HYDROLASE, PEPTIDOGLYCAN AMIDASE, AMIDASE\_2 FAMILY; HET: MSE; 1.8A {CITROBACTER FREUNDII} SCOP: d.118.1.1; Related PDB entries: 1J3G\_A 2Y28\_C 2Y28\_A 2Y2B\_C 2Y2B\_B 2Y2B\_A 2Y2C\_C 2Y2C\_B 2Y2C\_A 2Y2D\_C 2Y2D\_B 2Y2D\_A 2Y2E\_C 2Y2E\_B 2Y2E\_A**  
 Probability: 95.02 E-value: 0.012 Score: 44.37 Aligned Cols: 37 Identities: 30% Similarity: 0.356

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Q ss_pred          ceecchhhcCCCCCCC-CCCHHHHHHHHHHcCCCC
Q SS_6            3   NVVGHKEYSAEGKIDPA-GIDMAAFGRDVQALIKGGND 39 (178)
Q Consensus       3   sVIGHKEWSaQKwDPG-GFDMD~FRARVAaRLaG~p~ 39 (178)
                   .|+|.||...+|.||+ .|+|.|++|.+.+.+.
T Consensus       150  ~i~H~~~~~cPg~~~~~v~~~~~ 187 (187)
T 2Y28_B          150  NMTGHCNIAPERKTDPGPSFDWARFRALVTPSSHKEMT 187 (187)
T ss_dssp         CEEHHHHSTTTCTTCTTCHHHHHHC-----
T ss_pred         heeehhHcCCCCCCCCCCCCCHHHHHHhchhhcCCC
  
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