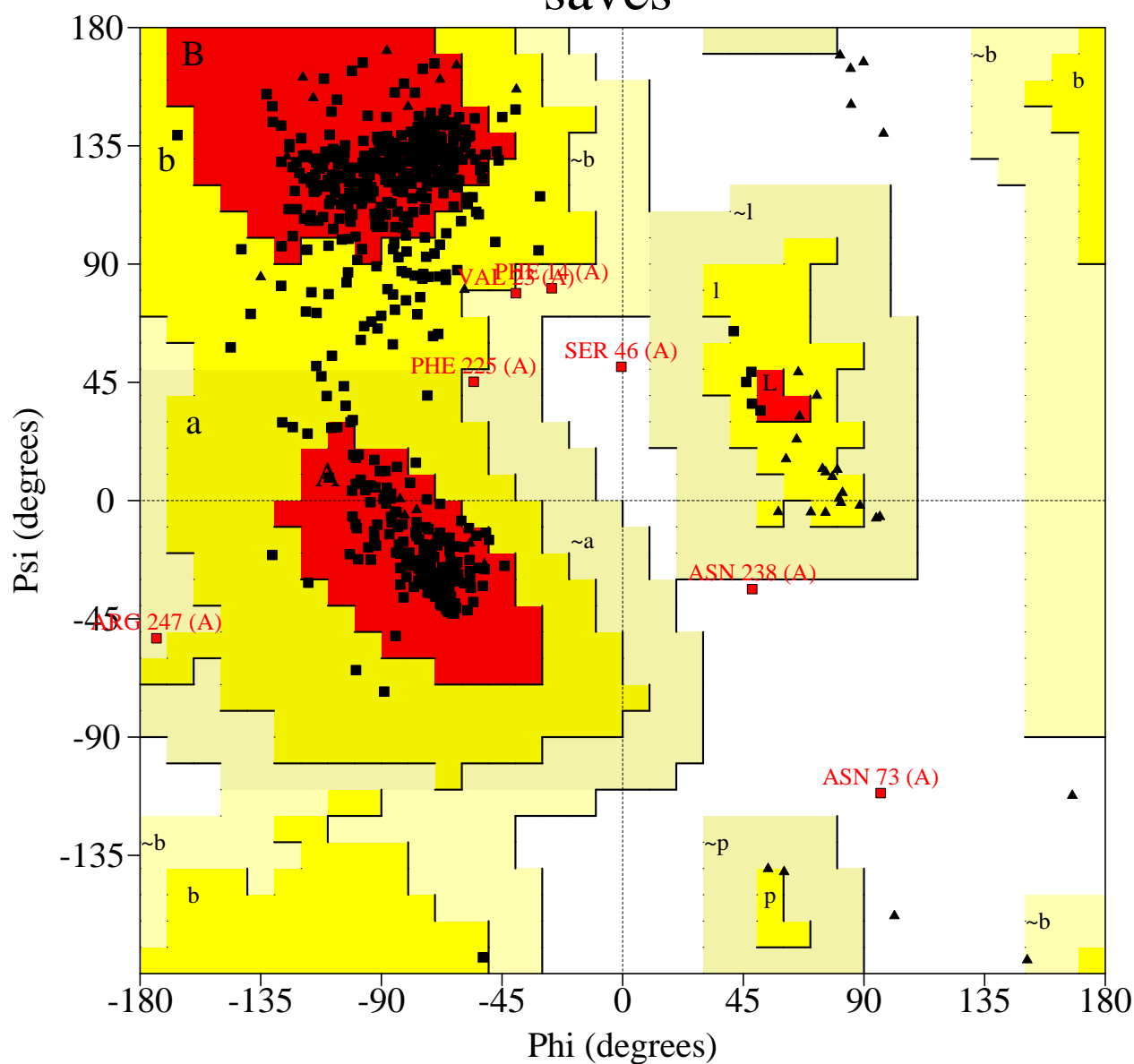


# Ramachandran Plot

saves



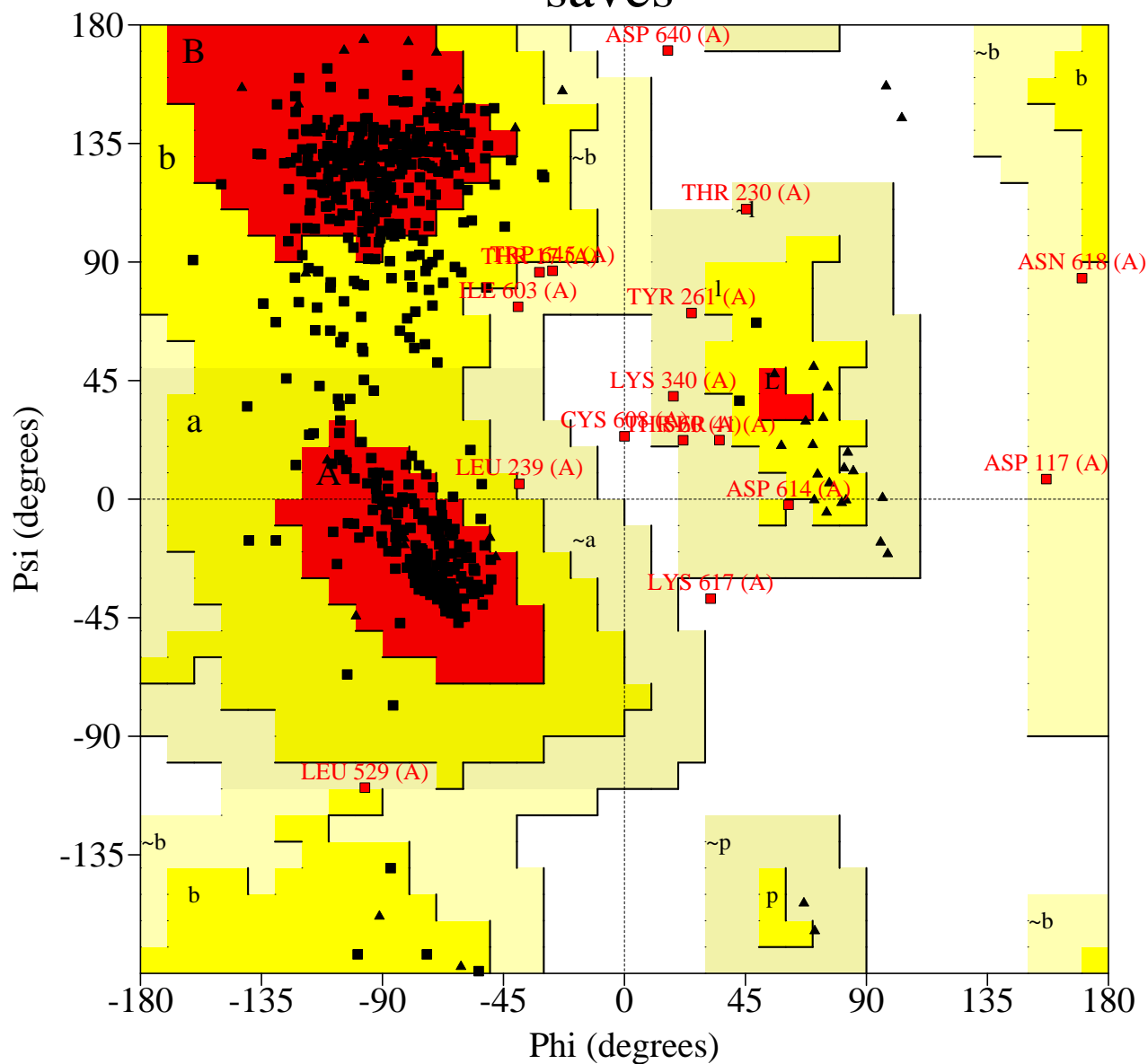
## Plot statistics

Residues in most favoured regions [A,B,L]	498	85.0%
Residues in additional allowed regions [a,b,l,p]	81	13.8%
Residues in generously allowed regions [~a,~b,~l,~p]	4	0.7%
Residues in disallowed regions	3	0.5%
-----		
Number of non-glycine and non-proline residues	586	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	53	
Number of proline residues	35	
-----		
Total number of residues	676	

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.

# Ramachandran Plot

saves



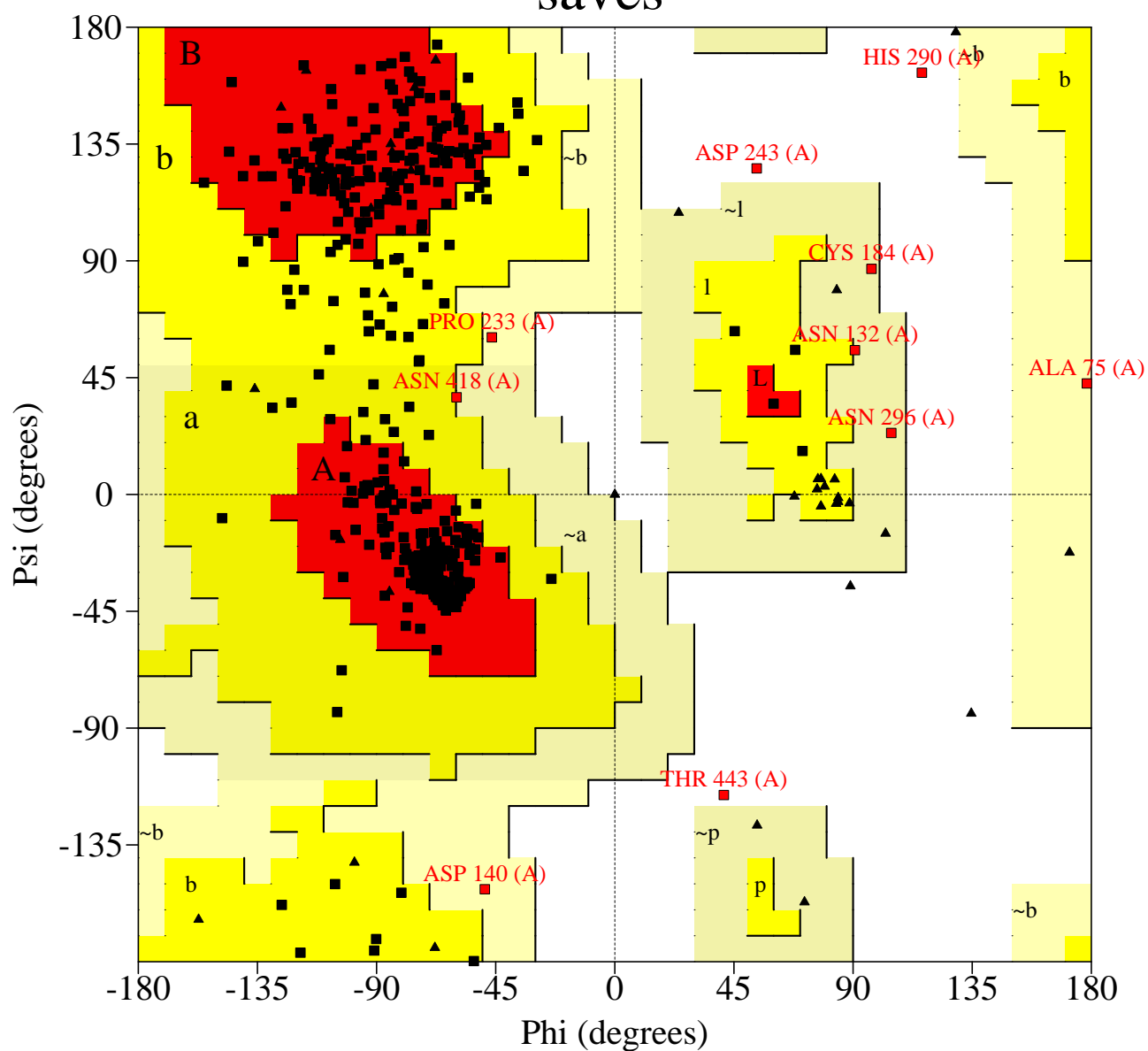
## Plot statistics

Residues in most favoured regions [A,B,L]	490	83.5%
Residues in additional allowed regions [a,b,l,p]	81	13.8%
Residues in generously allowed regions [~a,~b,~l,~p]	13	2.2%
Residues in disallowed regions	3	0.5%
-----		
Number of non-glycine and non-proline residues	587	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	53	
Number of proline residues	34	
-----		
Total number of residues	676	

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.

# Ramachandran Plot

saves



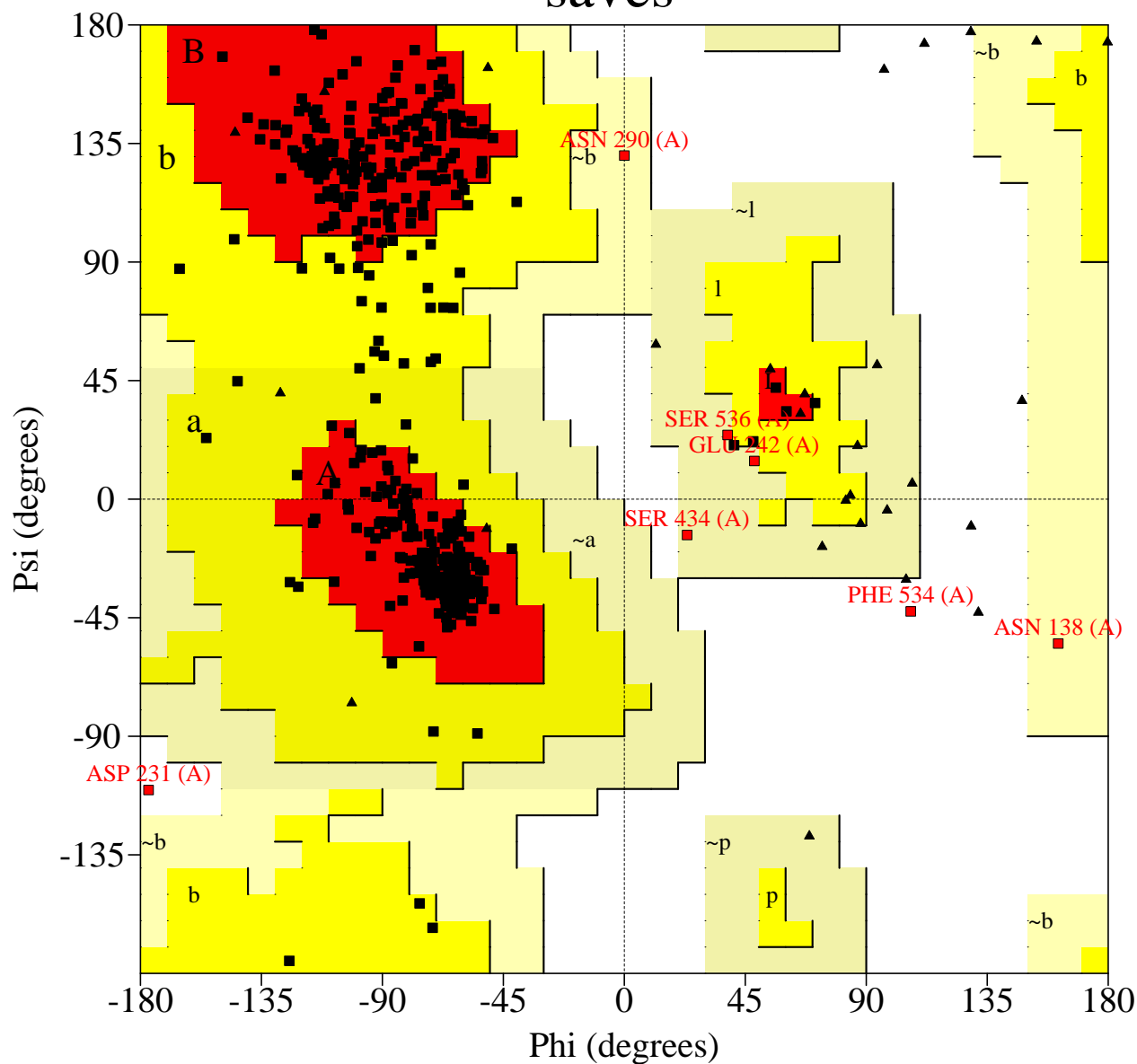
## Plot statistics

Residues in most favoured regions [A,B,L]	407	84.6%
Residues in additional allowed regions [a,b,l,p]	65	13.5%
Residues in generously allowed regions [~a,~b,~l,~p]	6	1.2%
Residues in disallowed regions	3	0.6%
-----		
Number of non-glycine and non-proline residues	481	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	37	
Number of proline residues	14	
-----		
Total number of residues	534	

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.

# Ramachandran Plot

saves



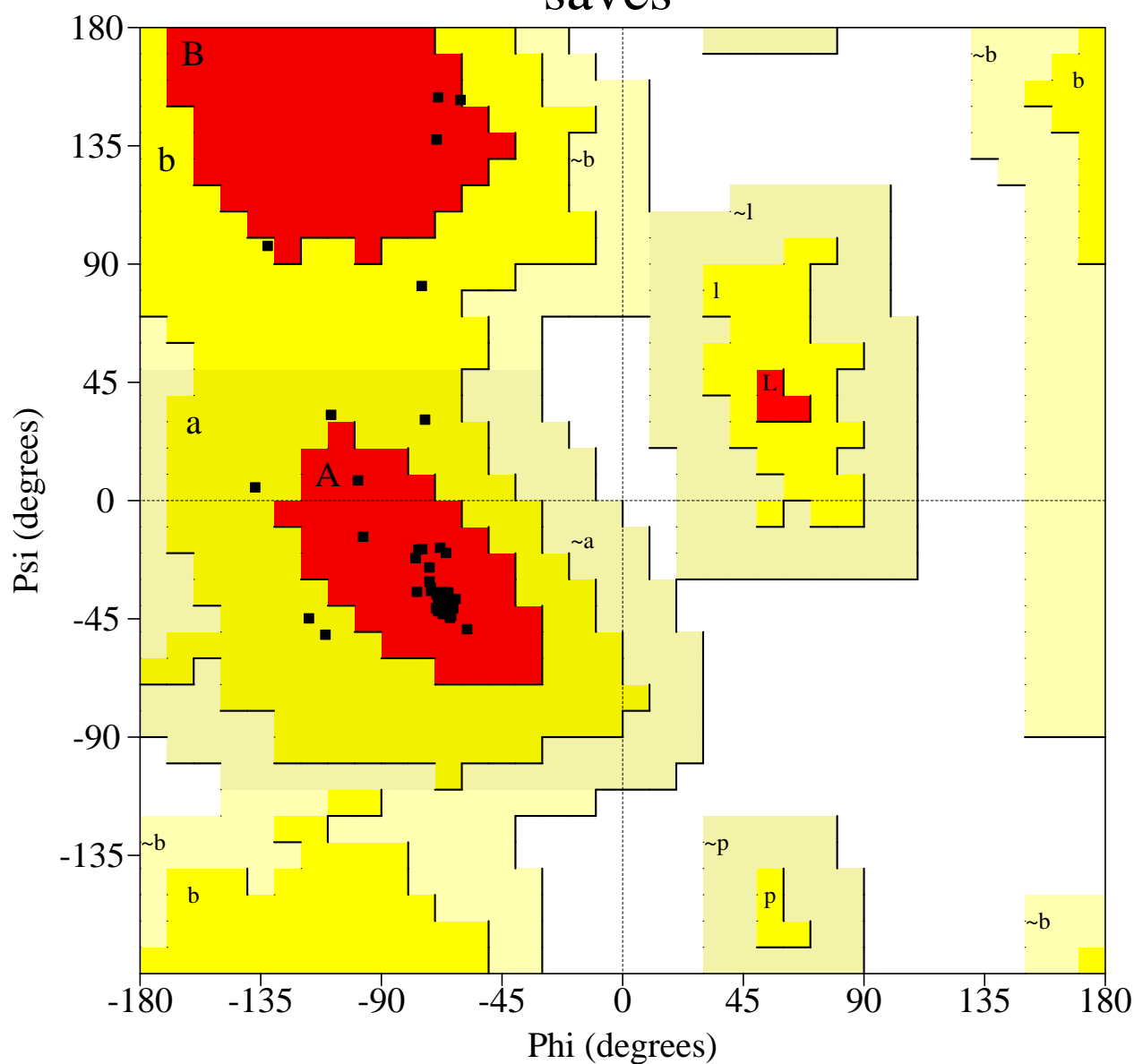
## Plot statistics

Residues in most favoured regions [A,B,L]	452	89.9%
Residues in additional allowed regions [a,b,l,p]	44	8.7%
Residues in generously allowed regions [~a,~b,~l,~p]	5	1.0%
Residues in disallowed regions	2	0.4%
-----		
Number of non-glycine and non-proline residues	503	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	30	
Number of proline residues	32	
-----		
Total number of residues	567	

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.

# Ramachandran Plot

saves



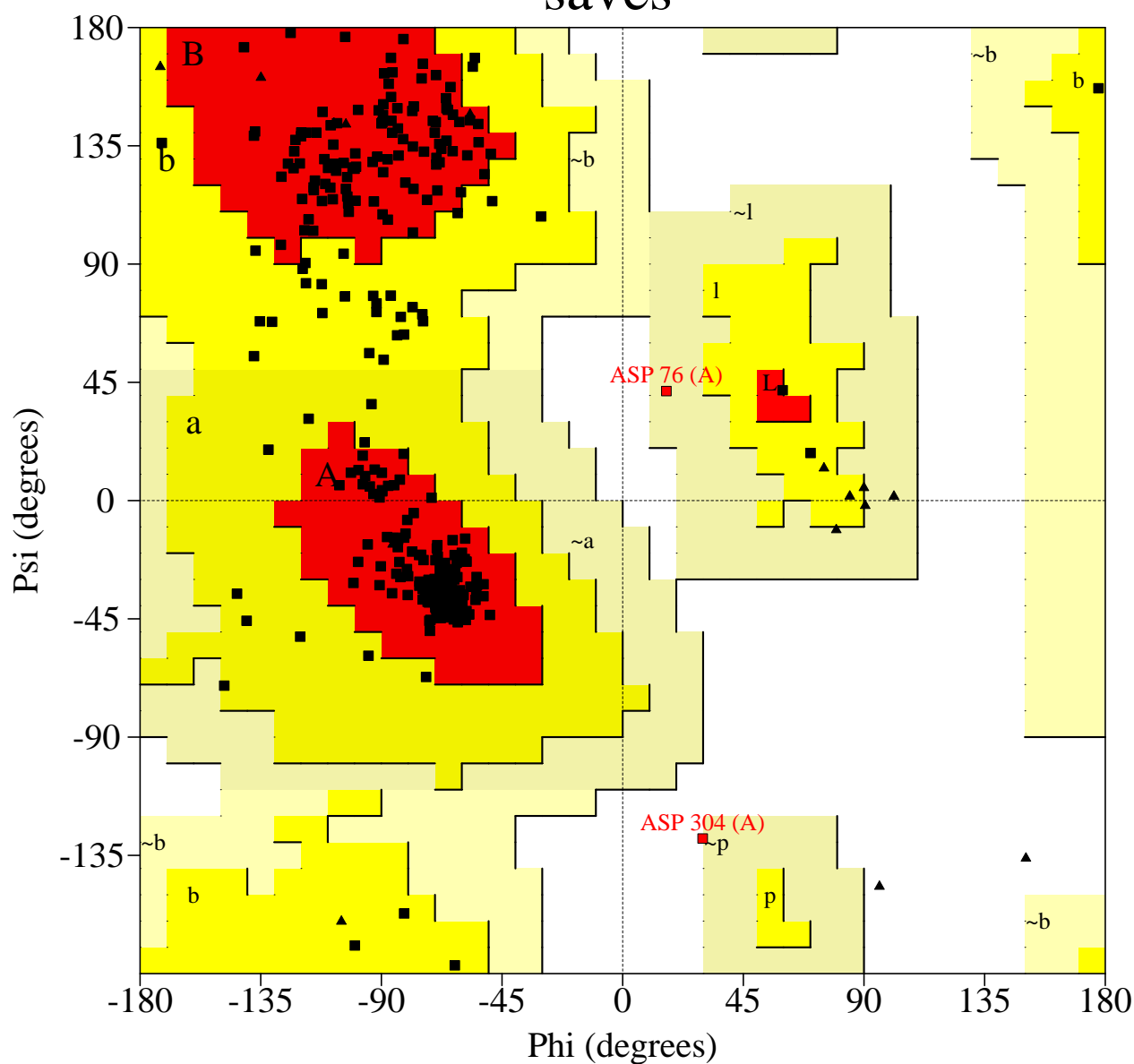
## Plot statistics

Residues in most favoured regions [A,B,L]	34	82.9%
Residues in additional allowed regions [a,b,l,p]	7	17.1%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	41	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	1	
Number of proline residues	3	
-----		
Total number of residues	46	

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.

# Ramachandran Plot

saves



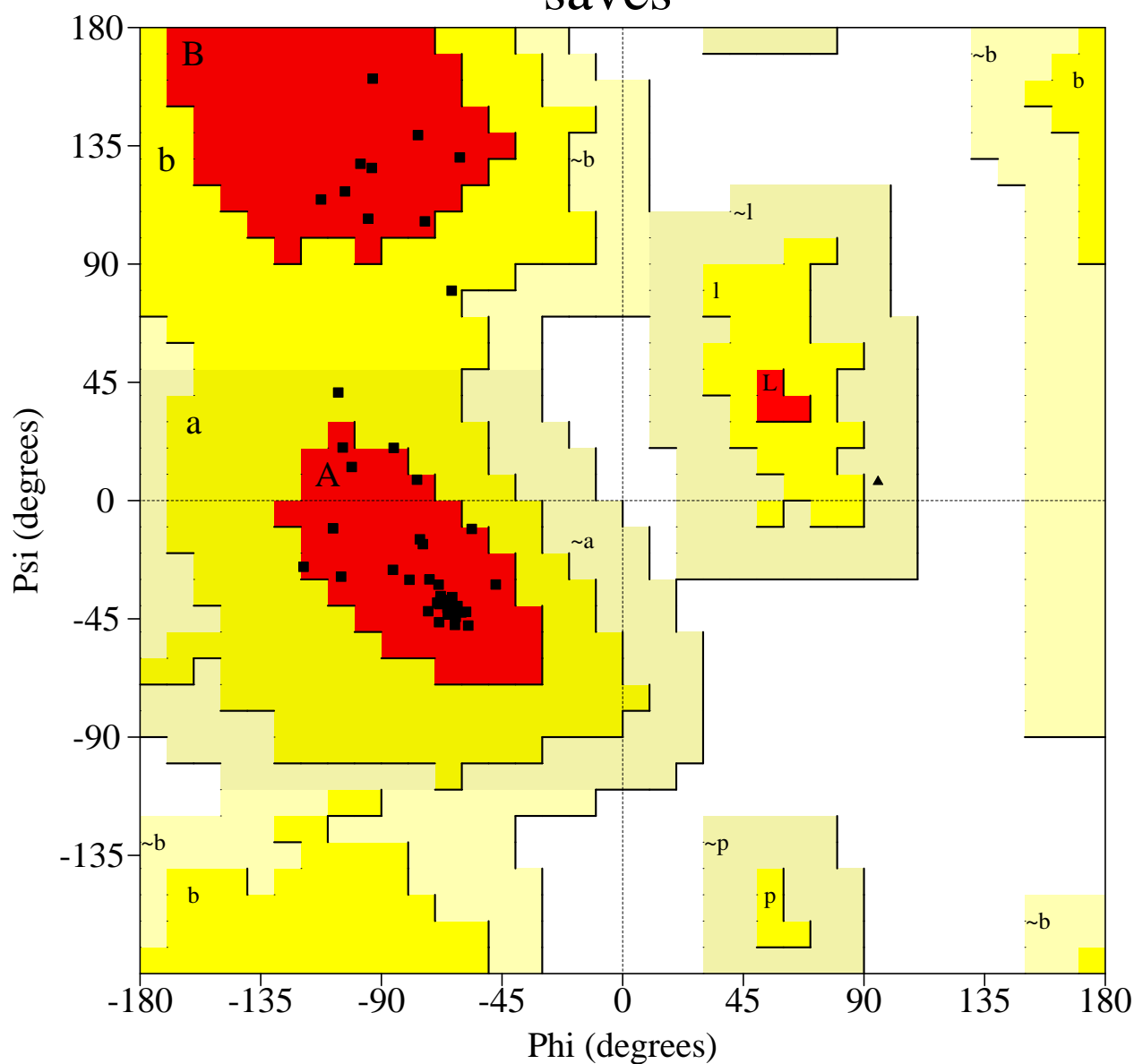
## Plot statistics

Residues in most favoured regions [A,B,L]	295	87.5%
Residues in additional allowed regions [a,b,l,p]	40	11.9%
Residues in generously allowed regions [~a,~b,~l,~p]	1	0.3%
Residues in disallowed regions	1	0.3%
-----		
Number of non-glycine and non-proline residues	337	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	23	
Number of proline residues	20	
-----		
Total number of residues	382	

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.

# Ramachandran Plot

saves



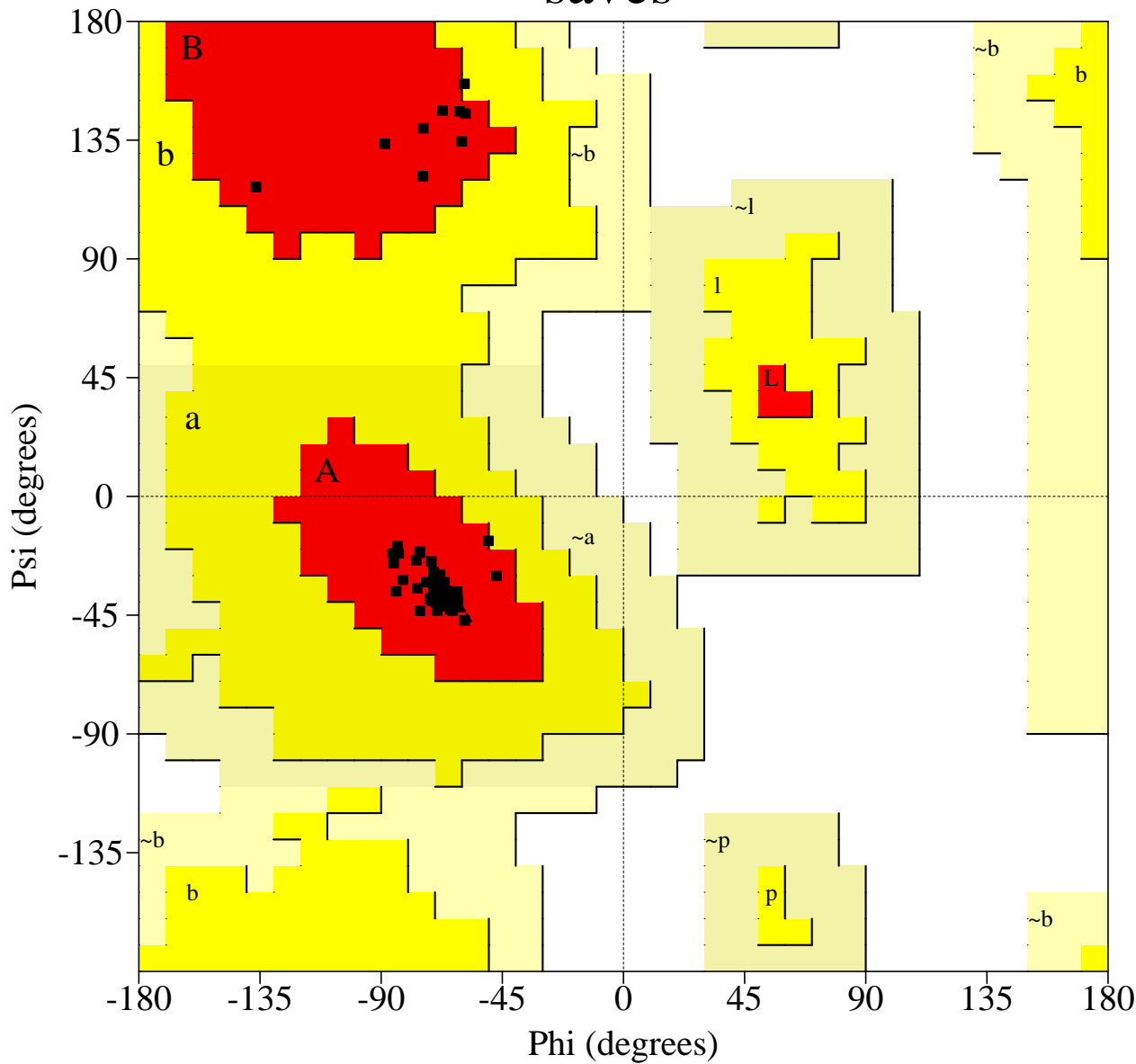
## Plot statistics

Residues in most favoured regions [A,B,L]	43	95.6%
Residues in additional allowed regions [a,b,l,p]	2	4.4%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	45	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	2	
Number of proline residues	2	
-----		
Total number of residues	50	

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.

# Ramachandran Plot

saves



## Plot statistics

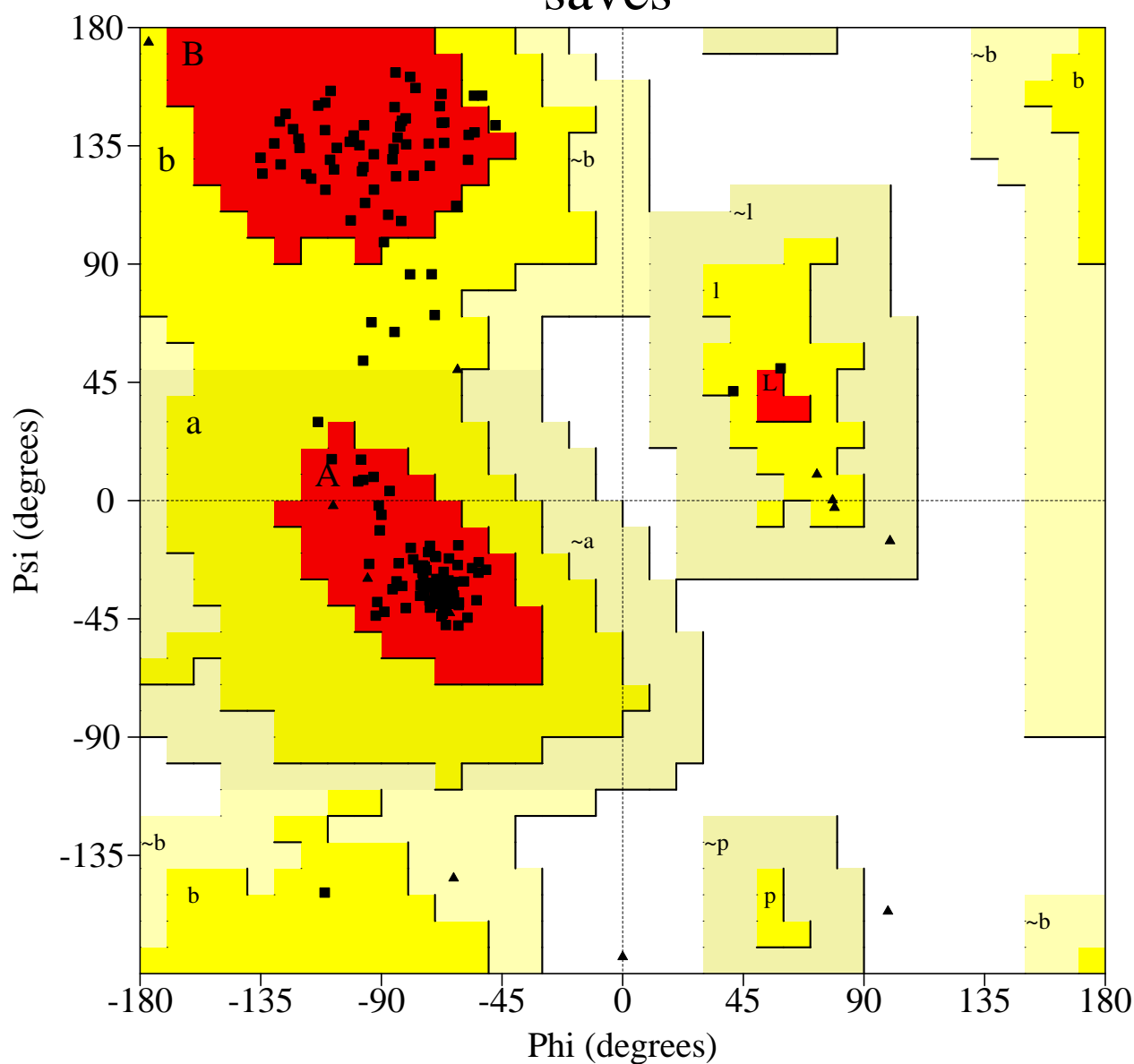
Residues in most favoured regions [A,B,L]	58	100.0%
Residues in additional allowed regions [a,b,l,p]	0	0.0%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	58	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	4	
Number of proline residues	7	
-----		
Total number of residues	70	

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.



# Ramachandran Plot

saves



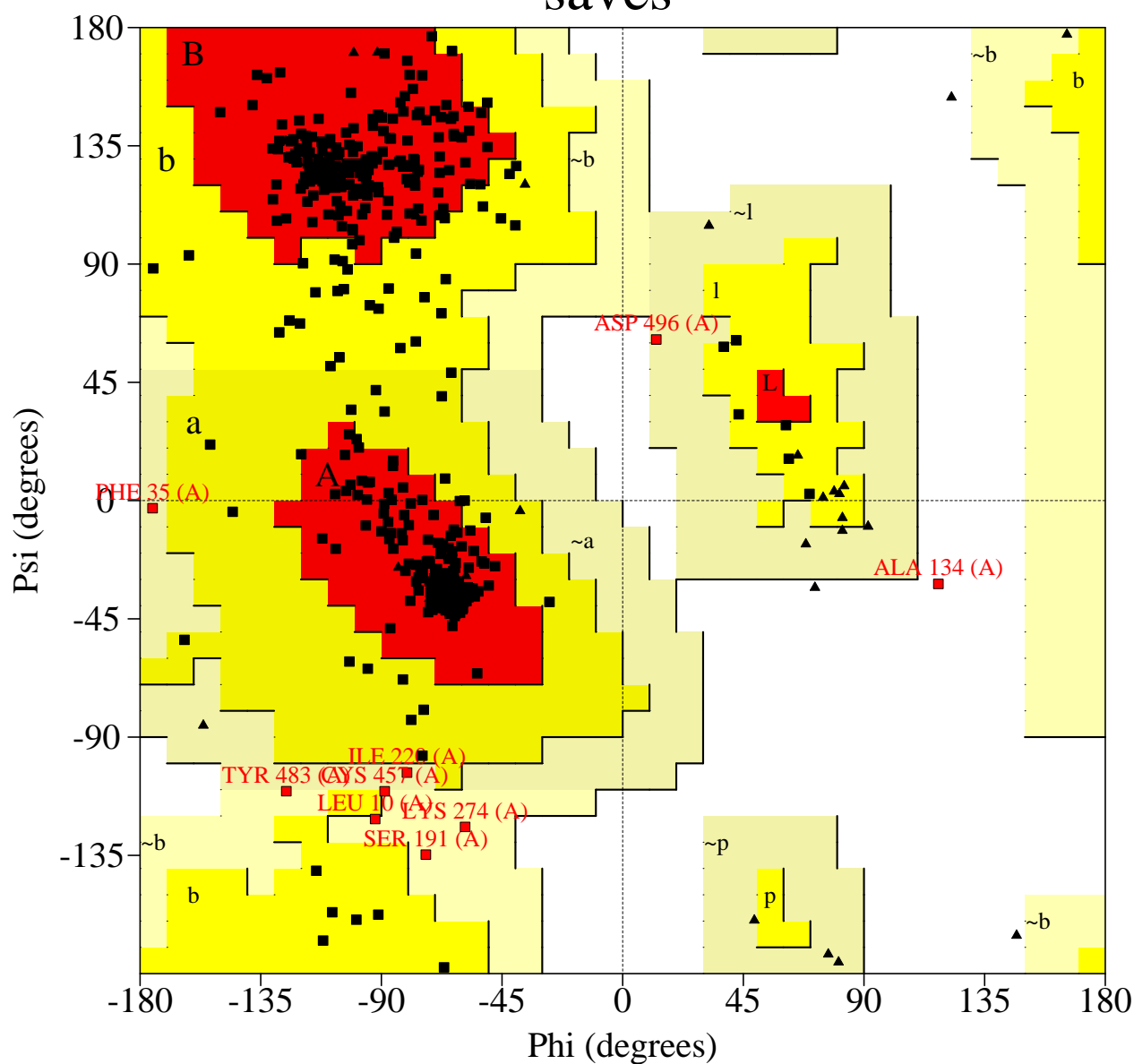
## Plot statistics

Residues in most favoured regions [A,B,L]	132	90.4%
Residues in additional allowed regions [a,b,l,p]	14	9.6%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	146	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	14	
Number of proline residues	5	
-----		
Total number of residues	167	

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.

# Ramachandran Plot

saves



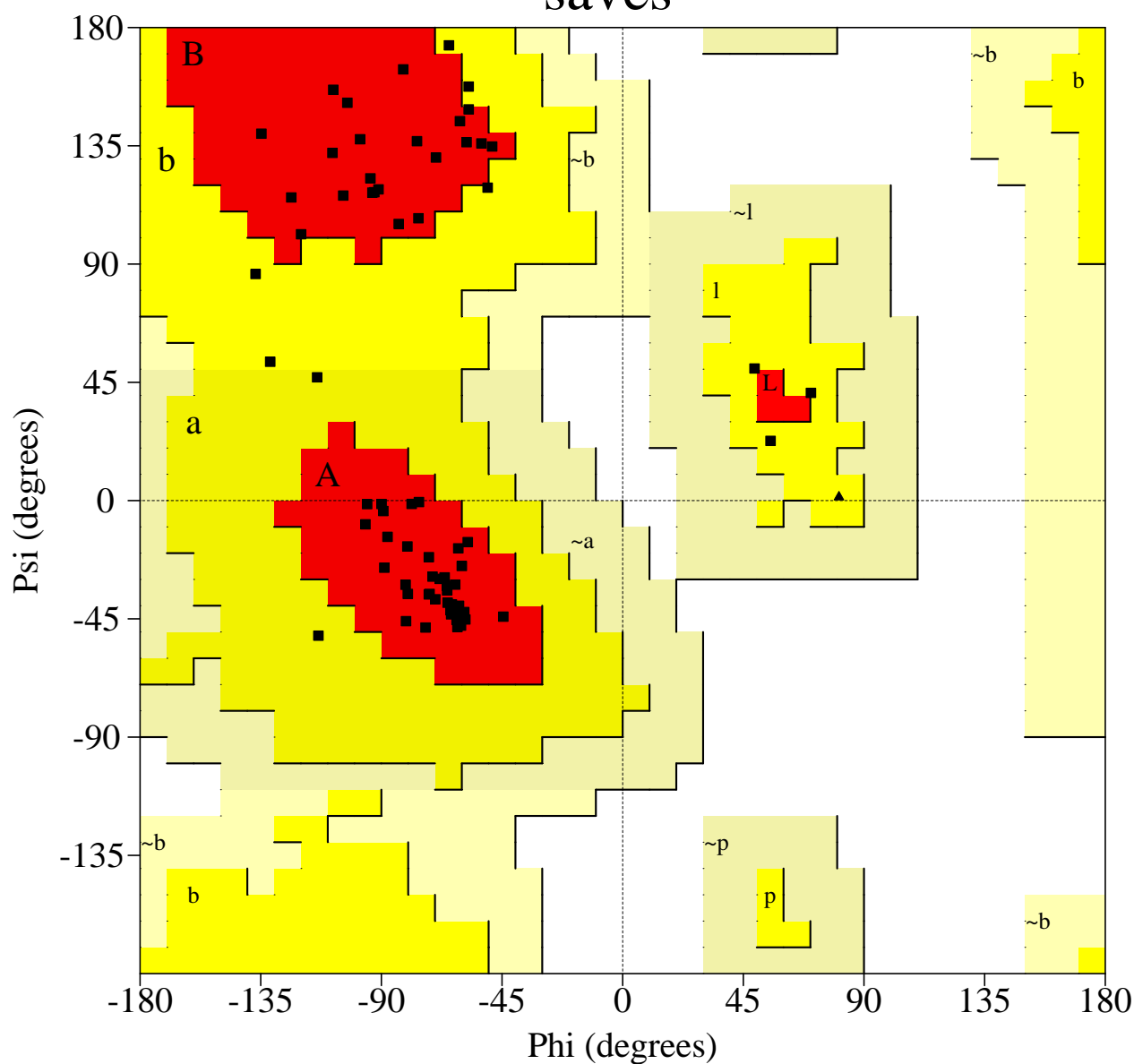
## Plot statistics

Residues in most favoured regions [A,B,L]	419	85.7%
Residues in additional allowed regions [a,b,l,p]	61	12.5%
Residues in generously allowed regions [~a,~b,~l,~p]	8	1.6%
Residues in disallowed regions	1	0.2%
-----		
Number of non-glycine and non-proline residues	489	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	33	
Number of proline residues	20	
-----		
Total number of residues	544	

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.

# Ramachandran Plot

saves



## Plot statistics

Residues in most favoured regions [A,B,L]	59	88.1%
Residues in additional allowed regions [a,b,l,p]	8	11.9%
Residues in generously allowed regions [~a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	67	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	1	
Number of proline residues	8	
-----		
Total number of residues	77	

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.