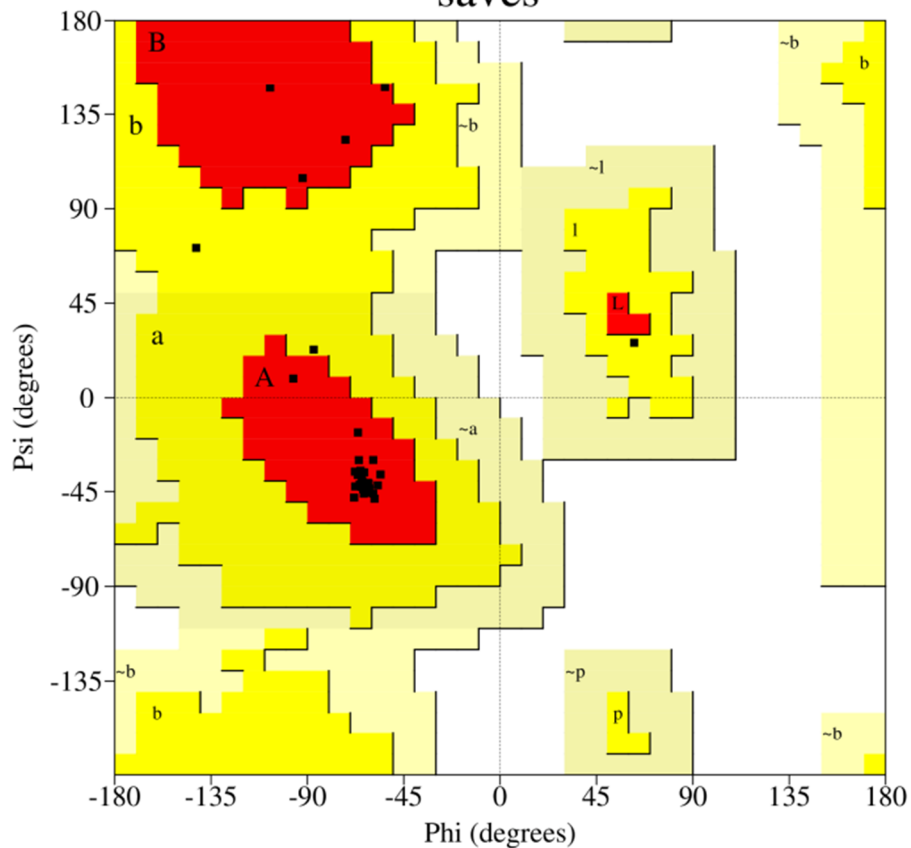


PROCHECK

# (a) Ramachandran Plot

saves



## Plot statistics

Residues in most favoured regions [A,B,L]	36	92.3%
Residues in additional allowed regions [a,b,l,p]	3	7.7%
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	39	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	1	
Number of proline residues	1	
-----		
Total number of residues	43	

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.

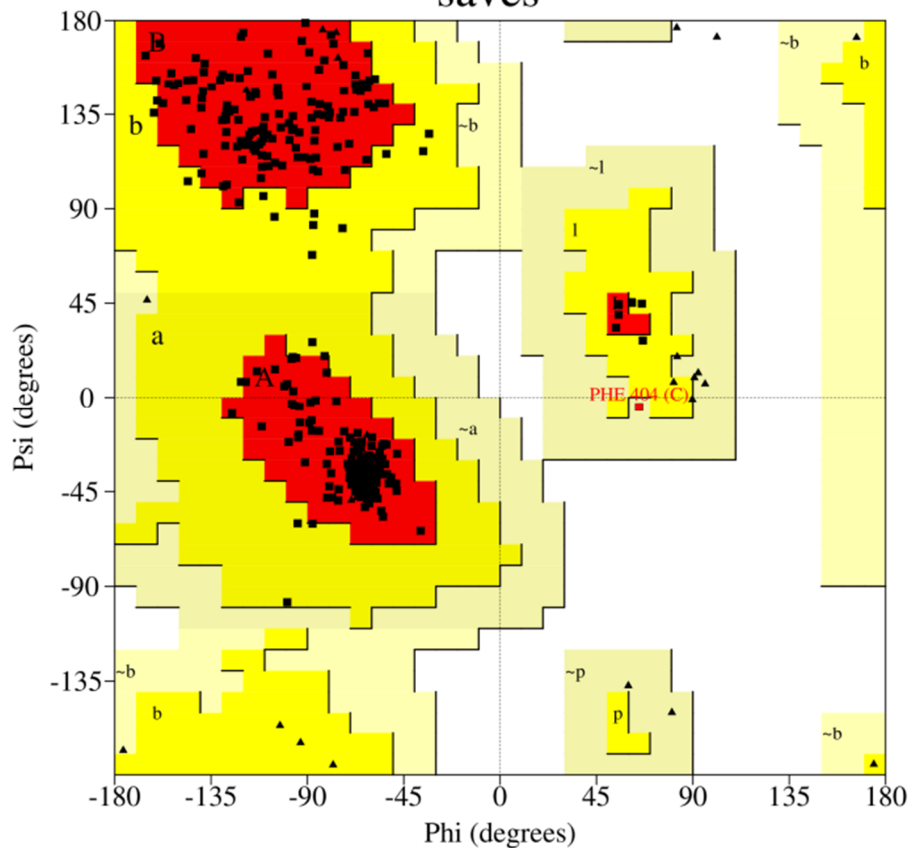
saves\_01.ps

PROCHECK

(b)

# Ramachandran Plot

saves



## Plot statistics

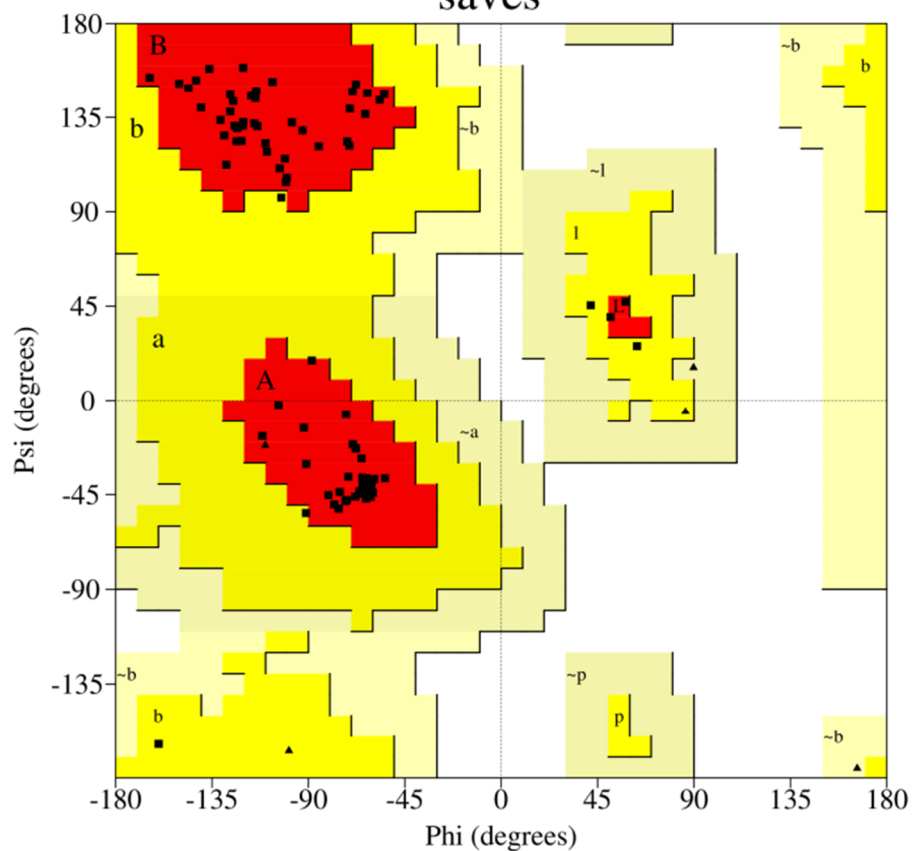
Residues in most favoured regions [A,B,L]	362	94.3%
Residues in additional allowed regions [a,b,l,p]	21	5.5%
Residues in generously allowed regions [-a,-b,-l,-p]	1	0.3%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	384	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	35	
Number of proline residues	20	
-----		
Total number of residues	440	

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.

saves\_01.ps

PROCHECK

# (c) Ramachandran Plot saves



## Plot statistics

Residues in most favoured regions [A,B,L]	87	94.6%
Residues in additional allowed regions [a,b,l,p]	5	5.4%
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	92	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	6	
Number of proline residues	7	
-----		
Total number of residues	107	

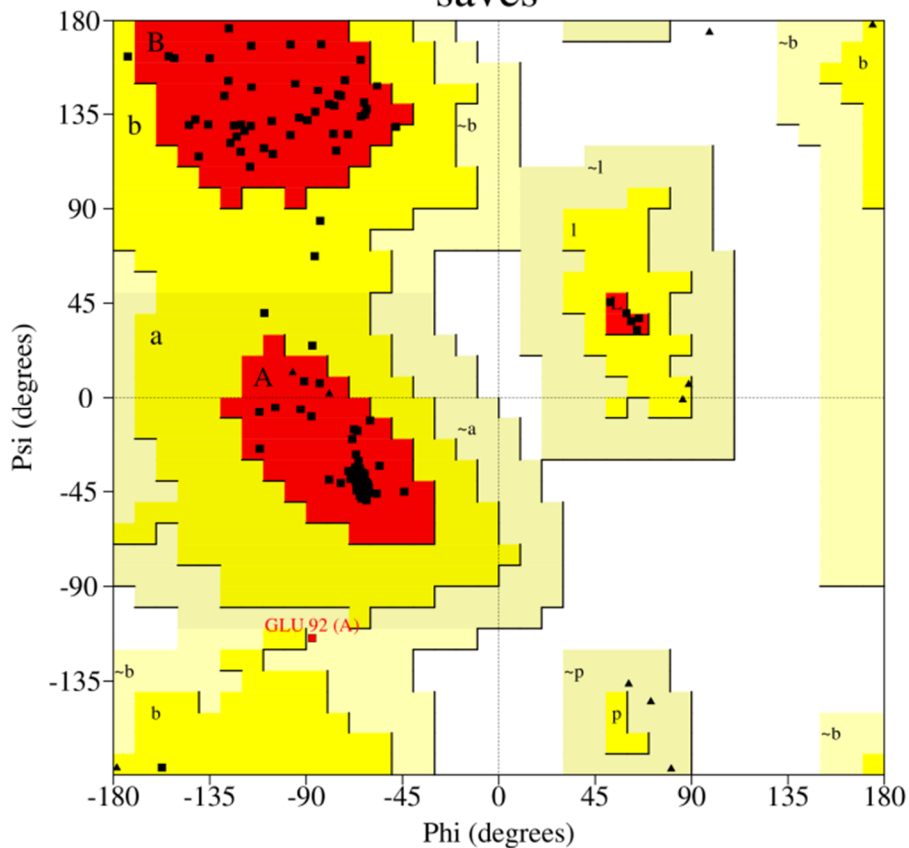
Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

PROCHECK

(d)

# Ramachandran Plot

saves



## Plot statistics

Residues in most favoured regions [A,B,L]	114	94.2%
Residues in additional allowed regions [a,b,l,p]	6	5.0%
Residues in generously allowed regions [-a,-b,-l,-p]	1	0.8%
Residues in disallowed regions	0	0.0%
-----		
Number of non-glycine and non-proline residues	121	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	11	
Number of proline residues	5	
-----		
Total number of residues	139	

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.

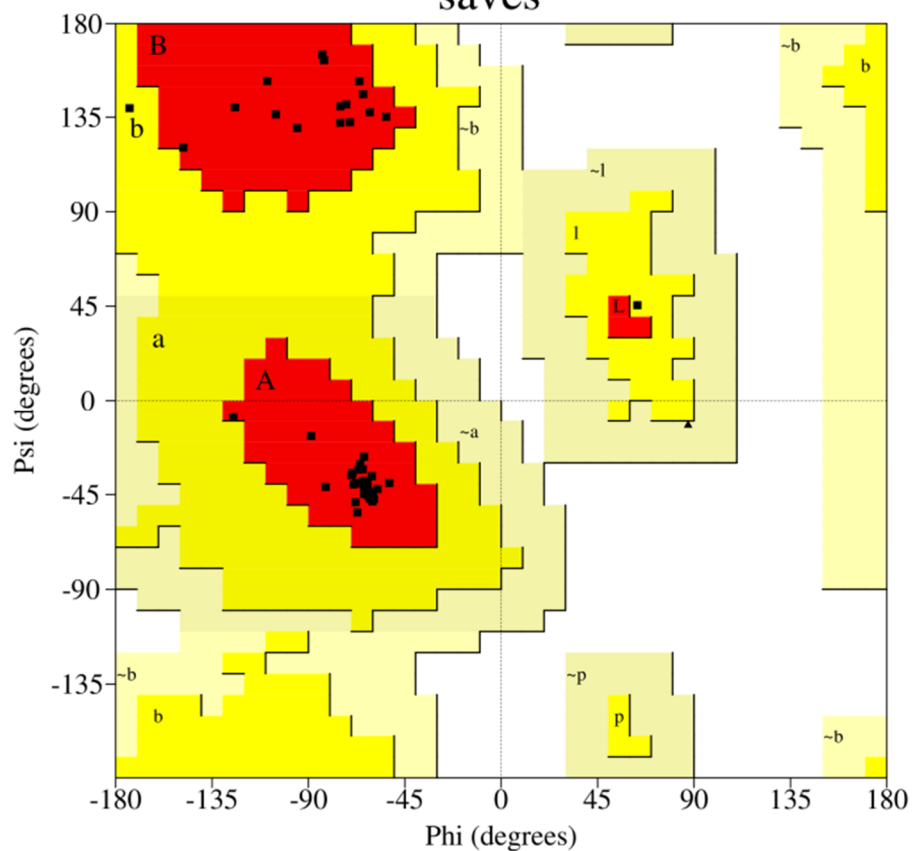
saves\_01.ps

PROCHECK

(e)

# Ramachandran Plot

saves



## Plot statistics

Residues in most favoured regions [A,B,L]	54	96.4%
Residues in additional allowed regions [a,b,l,p]	2	3.6%
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	56	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	61	

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.

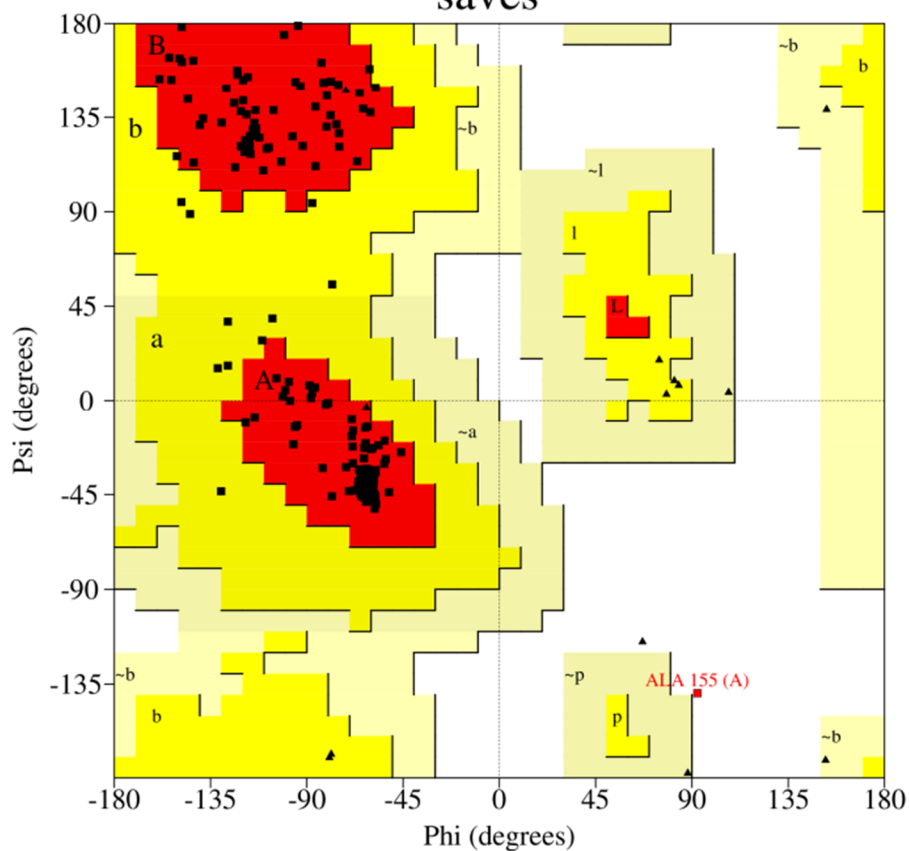
saves\_01.ps

PROCHECK

(f)

# Ramachandran Plot

saves



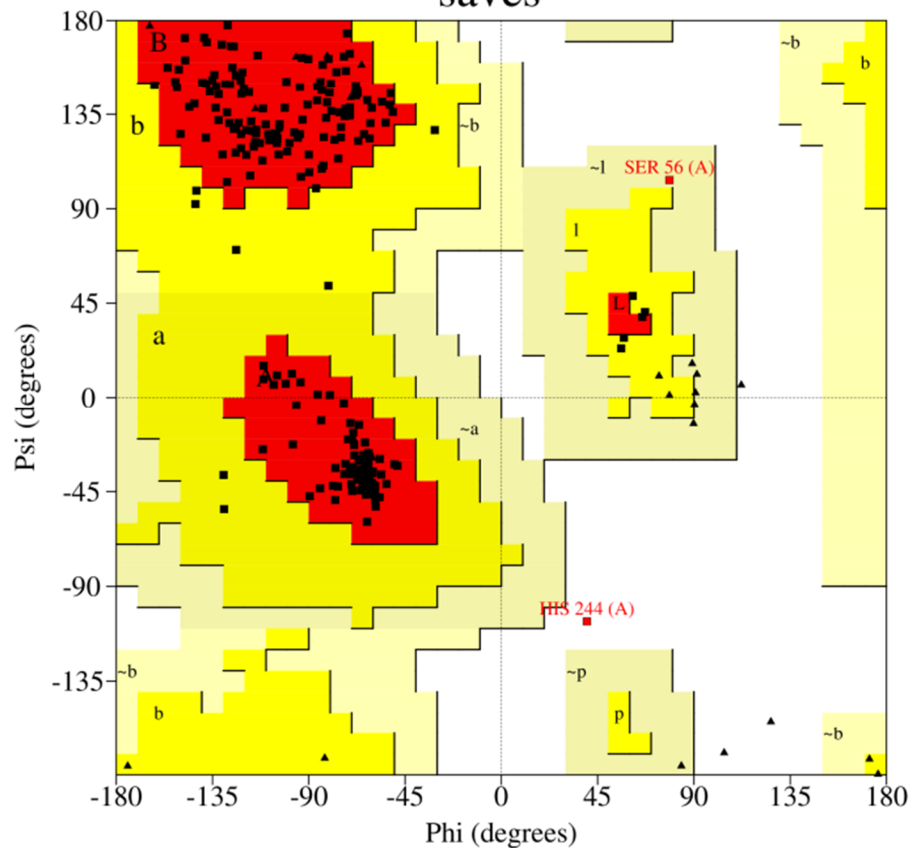
## Plot statistics

Residues in most favoured regions [A,B,L]	172	93.5%
Residues in additional allowed regions [a,b,l,p]	11	6.0%
Residues in generously allowed regions [-a,-b,-l,-p]	0	0.0%
Residues in disallowed regions	1	0.5%
-----		
Number of non-glycine and non-proline residues	184	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	17	
Number of proline residues	4	
-----		
Total number of residues	207	

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.

PROCHECK

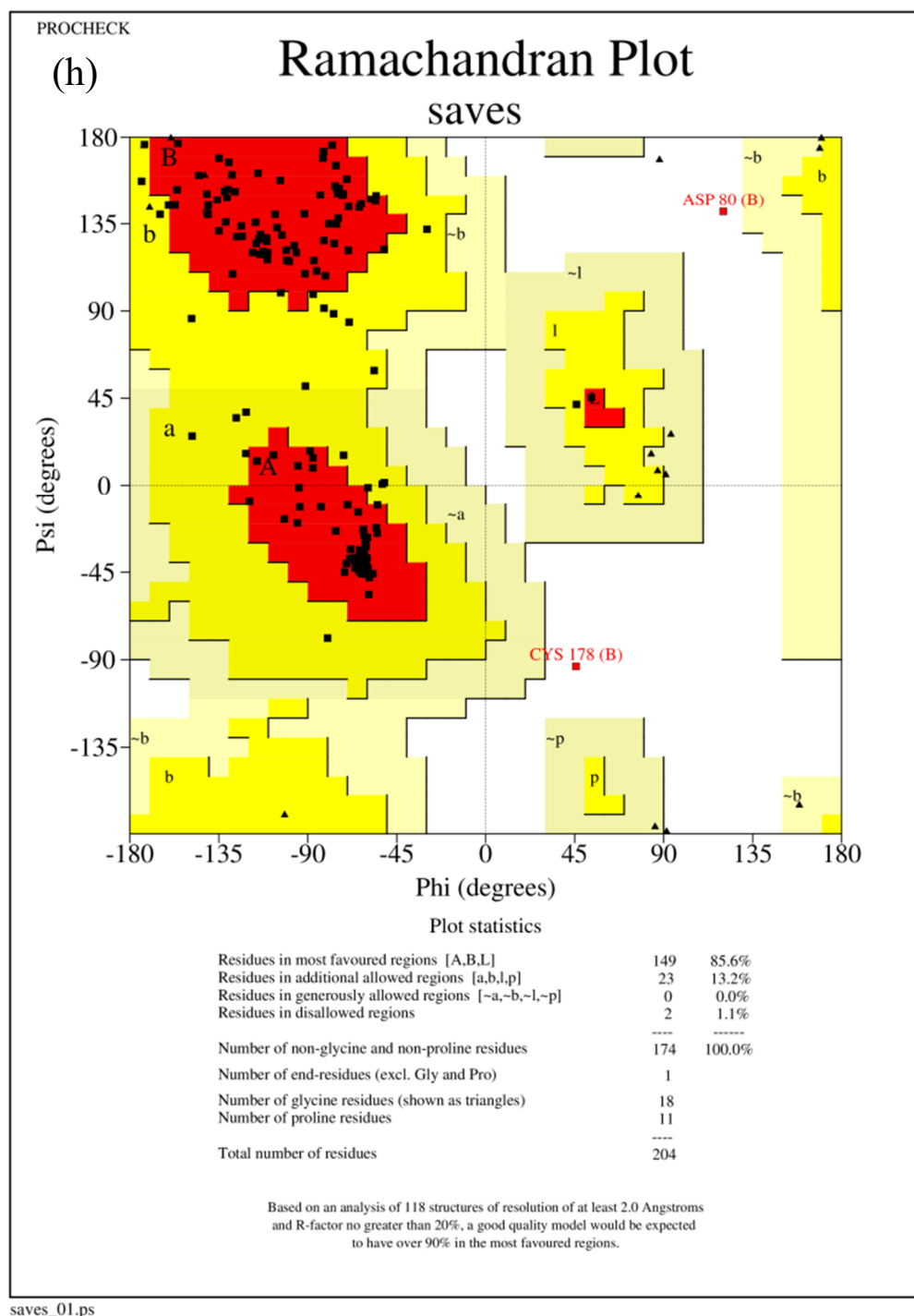
# (g) Ramachandran Plot



## Plot statistics

Residues in most favoured regions [A,B,L]	219	94.0%
Residues in additional allowed regions [a,b,l,p]	12	5.2%
Residues in generously allowed regions [-a,-b,-l,-p]	1	0.4%
Residues in disallowed regions	1	0.4%
-----		
Number of non-glycine and non-proline residues	233	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	25	
Number of proline residues	16	
-----		
Total number of residues	276	

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 S1.** Ramachandran plot analysis of **a**: Acetylcholinesterase, **b**:  $\alpha$ -tubulin, **c**: Actin, **d**: Argenin kinase, **e**: Histone subunit 3, **f**: Hsp90, **g**: Elongation factor and **h**: Carbamoyl phosphate synthase. Here, the red color indicates a region that is favored energetically and structurally, yellow region for allowed, light yellow shows generously allowed region, and white for disallowed region. Phi ( $\Phi$ ) and Psi ( $\Psi$ ) angles determine torsion angles. Based on an analysis of the structures of resolution of at least 2.0 Å and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.