

Protocol S1

Semiquantitative Scoring System for Immunopathology of Guinea Pig Tissues. Hematoxylin & Eosin-stained lung sections from guinea pigs infected with *M. tuberculosis* were scored individually based on the above system. The Total Lung Score for each animal represents the summation of the scores for each criterion; the maximum score for each animal is 24.

Percent of lung affected estimated at low magnification (2-4X obj.); scored as follows:

- 0 - no lesions in lung sections
- 1 - up to 25% of lung involved
- 2 - up to 50 % of lung involved
- 3 - Up to 75% of lung involved
- 4 - Above 75% of lung involved

Character of lesions were scores as follows:

Primary lesions

- 0 - No primary lesions present at section level
- 1 - A single primary lesion
- 2 - Two or more primary lesions, multifocal
- 3 - Two or more primary lesions, multifocal to coalescing
- 4 - Primary lesions, coalescing and extensive

Secondary lesions

- 1 - Up to 25% of lung involved
- 2 - Up to 50% of lung involved
- 3 - Up to 75% of lung involved
- 4 - Above 75% of lung involved

Necrosis

- 0 - No apparent necrosis present
- 1 - A single focus of necrosis present
- 2 - Two or more foci of necrosis, multifocal
- 3 - Two or more foci of necrosis, multifocal to coalescing
- 4 - Coalescing foci of necrosis that are extensive

Mineralization

- 0 - No mineralization present at section level
- 1 - A single focus of mineralization present
- 2 - Two or more foci of mineralization, multifocal
- 3 - Two or more foci of mineralization, multifocal to coalescing
- 4 - Coalescing foci of mineralization that are extensive

Fibrosis (scored relative to the cellularity of primary and secondary lesions)

- 0 - No fibrosis present
- 1 - Minimal fibrosis present
- 2 - Equal area of cellularity and fibrosis
- 3 - More fibrosis than cellularity
- 4 - Extensive fibrosis with low cellularity

Maximum lung score: 24

Crystallography: Summary of Data Collection and Refinement Statistics.

Space Group	C222₁
Unit Cell Parameters (Å)	<i>a</i> = 173.0 <i>b</i> = 241.5 <i>c</i> = 241.7
Data Collection Statistics:	
Wavelength (Å)	1.08
Resolution (Å)	140- 2.9
Reflections measures	694890
Unique reflections	111196
^a R_{merge} (%)	^b9.5(37.3)
Completeness (%)	99.2(98.4)
Refinement Statistics	
Total number of atoms	19011
Protein	18139
ATP	496
Mg²⁺	16
Solvent	360
Average Thermal Factors (Å²)	
Protein	47.6
ATP	32.8
Mg²⁺	31.5
Solvent	41.7
RMS Deviation from Ideality	
Bond lengths (Å)	0.01
Bond Angles (°)	0.98
Ramachandran Plot Regions (%)	
Most favored	91.1
Additional allowed	8.3
Generously allowed	0.6
^c R_{factor}/^dR_{free} (%)	25.0/26.8 (35.0/40.1)

^a $R_{\text{merge}} (\%) = \frac{\sum_{hkl} \sum_i |I_{hkl} - \langle I \rangle_{hkl}|}{\sum_{hkl} \sum_i \langle I \rangle_{hkl}} \times 100$; where I_{hkl} is the intensity measurement of a given reflection and $\langle I \rangle_{hkl}$ is the average intensity for multiple measurements of this reflection.

^bValues in parentheses refer to the highest resolution bin.

^c $R_{\text{factor}} (\%) = \frac{|F_{o_{hkl}} - F_{c_{hkl}}|}{|F_{o_{hkl}}|} \times 100$; where $F_{o_{hkl}}$ is the observed structure factor amplitude and $F_{c_{hkl}}$ is the calculated structure factor amplitude.

^d R_{free} was calculated for 5 % of the diffraction data and monitored throughout refinement.