sion of the major pneumococcus toxin pneumolysin but does appear to be a transcription factor involved in pathogen fitness.[3] These studies indicate that Tex may play a role in gene expression or transcript maintenance of either specific toxin or general housekeeping genes.

Tex domain architecture and sequence conservation may extend beyond prokaryotes to the essential eukaryotic transcription elongation factor Spt6.[5–7] Tex is approximately half the size of Spt6 (e.g., 86 kDa for *P. aeruginosa* Tex *versus* 168 kDa for *Saccharomyces cerevisiae* Spt6), with sequence homology spanning the central region of Spt6. The flanking nonhomologous regions of Spt6 include a highly charged N-terminal region and a C-terminal SH2-like domain. Within the region of homology, Tex and Spt6 share ~25% pairwise sequence identity and have a similar predicted domain architecture; primary sequence analysis identified YqgF, HhH, and S1 RNA-binding domains in both proteins.[7] This level of sequence similarity falls in Doolittle's "twilight zone,"[8] indicating that Tex and Spt6 may have similar structures, although direct evidence is lacking.

The sequence similarity may also indicate that Tex and Spt6 have related cellular functions. Although current evidence suggests that Spt6 is a nucleosome chaperone,[9–11] a function unique to eukaryotes, recent studies have shown that Spt6 also interacts directly with both RNA polymerase (RNAP)[12] and mRNA processing factors, including the exosomal RNA degradation machinery.[13] Thus, beyond its role in nucleosome maintenance, Spt6 appears to provide a physical link between transcription and pre-mRNA surveillance, although the relationship between these critical processes is lacking in structural detail. Interestingly, we have recently observed similar interactions with Tex. *P. aeruginosa* Tex copurifies with RNAP, RNase E, and PNPase (I.V.-G. and S.L.D., unpublished data); RNase E and PNPase are components of the prokaryotic RNA degradosome, a 3′–5′ RNA degradation complex analogous to the eukaryotic exosome.[14]

In an effort to better understand the molecular function of Tex, and possibly to gain insight into Spt6, we have determined high-resolution crystal structures of the *P. aeruginosa* Tex protein in two crystal forms. These reveal four putative nucleic acid

Table 1. Data collection and refinement statistics

	Tex Se-Met: crystal form I	Tex native 1: crystal form I	Tex native 2: crystal form II
Data collection			
Beamline	NSLS X29	NSLS X29	Home source
Wavelength (Å)	0.978	1.10000	1.54178
Resolution (Å)	40–2.7	50–2.5	20–2.3
Outer shell (Å)	2.8–2.7	2.59–2.5	2.38–2.3
No. of reflections			
Unique	23,640	35,199	38,347
Total	273,923	448,770	343,965
Mean $I/\sigma(I)$	21.1 (4.8)	30.0 (4.2)	19.0 (3.3)
Completeness (%)	91.2 (61.7)	90.4 (64.8)	99.4 (99.3)
R_{sym}[a]	9.0 (32.0)	8.6 (40.3)	8.4 (50.7)
Space group	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$
Unit cell dimensions (Å)			
a	57.0	57.2	56.2
b	135.1	131.8	106.7
c	144.5	144.0	139.7
Phasing (40–3.4 Å)			
FOM, before DM (SOLVE)	0.320		
FOM, after DM (RESOLVE)	0.720		
Refinement			
R_{cryst}[b]/R_{free}[c] (%)		24.0/27.4	22.1/26.6
Nonhydrogen atoms			
Total		5692	5884
Solvent		73	256
RMSD from ideal geometry			
Bond lengths (Å)		0.004	0.004
Bond angles (°)		0.6	0.6
Average isotropic *B* value (Å^2)		66.7	27.4
Protein geometry[d]			
Ramachandran outliers (%)		0.0	0.0
Ramachandran favored (%)		96.2	98.5
Rotamer outliers (%)		0.2	0.2

Values in parentheses correspond to those in the outer resolution shell.
FOM, figure of merit; DM, density modification.
[a] $R_{sym} = (\sum|(I-\langle I\rangle)|)/(\sum I)$, where $\langle I\rangle$ is the average intensity of multiple measurements.
[b] $R_{cryst} = (\sum|F_{obs}-F_{calc}|)/(\sum|F_{obs}|)$.
[c] R_{free} is the *R*-factor based on 5% of the data excluded from refinement.
[d] Geometry statistics were determined by MolProbity.[15]