



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:27 PM GMT

PDB ID : 1TSJ  
Title : Crystal structure of protein from Staphylococcus aureus  
Authors : Min, T.; Gorman, J.; Shapiro, L.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)  
Deposited on : 2004-06-21  
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

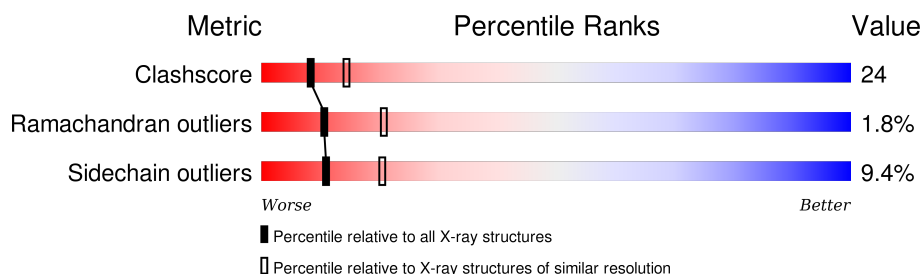
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	139	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 924 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called conserved hypothetical protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	117	Total	C	N	O	S	Se	0	0	0
			902	590	138	167	1	6			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MSE	MET	MODIFIED RESIDUE	UNP Q8NX24
A	35	MSE	MET	MODIFIED RESIDUE	UNP Q8NX24
A	62	MSE	MET	MODIFIED RESIDUE	UNP Q8NX24
A	?	-	MET	DELETION	UNP Q8NX24
A	?	-	ASN	DELETION	UNP Q8NX24
A	?	-	PRO	DELETION	UNP Q8NX24
A	?	-	ALA	DELETION	UNP Q8NX24
A	90	MSE	MET	MODIFIED RESIDUE	UNP Q8NX24
A	105	MSE	MET	MODIFIED RESIDUE	UNP Q8NX24
A	110	MSE	MET	MODIFIED RESIDUE	UNP Q8NX24
A	134	GLU	-	CLONING ARTIFACT	UNP Q8NX24
A	135	GLY	-	CLONING ARTIFACT	UNP Q8NX24
A	136	GLY	-	CLONING ARTIFACT	UNP Q8NX24
A	137	SER	-	CLONING ARTIFACT	UNP Q8NX24
A	138	HIS	-	EXPRESSION TAG	UNP Q8NX24
A	139	HIS	-	EXPRESSION TAG	UNP Q8NX24
A	140	HIS	-	EXPRESSION TAG	UNP Q8NX24
A	141	HIS	-	EXPRESSION TAG	UNP Q8NX24
A	138	HIS	-	EXPRESSION TAG	UNP Q8NX24
A	139	HIS	-	EXPRESSION TAG	UNP Q8NX24

- Molecule 2 is water.

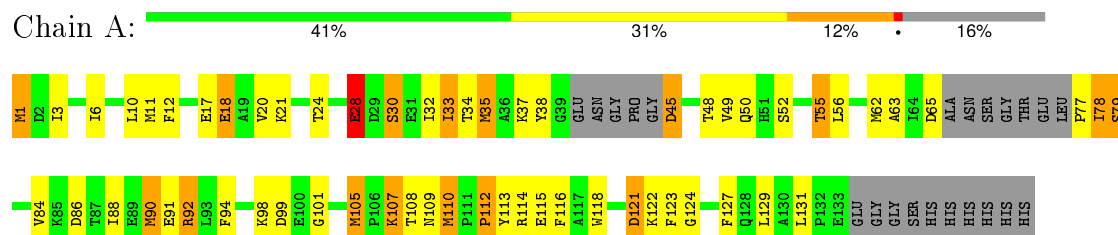
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	22	Total	O	0	0
			22	22		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: conserved hypothetical protein



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.85Å 83.85Å 36.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	100.0 (20.00-2.60)	Depositor
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC 5.1.9999	Depositor
R, $R_{free}$	0.189 , 0.264	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	924	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	2.06	29/916 (3.2%)	1.50	10/1229 (0.8%)

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	18	GLU	CD-OE1	10.86	1.37	1.25
1	A	91	GLU	CD-OE1	9.01	1.35	1.25
1	A	110	MSE	SE-CE	8.51	2.45	1.95
1	A	18	GLU	CD-OE2	8.50	1.35	1.25
1	A	38	TYR	CD1-CE1	-7.39	1.28	1.39
1	A	28	GLU	CD-OE2	7.29	1.33	1.25
1	A	118	TRP	CE3-CZ3	6.92	1.50	1.38
1	A	115	GLU	CD-OE1	6.83	1.33	1.25
1	A	123	PHE	CB-CG	-6.72	1.40	1.51
1	A	38	TYR	CG-CD2	6.07	1.47	1.39
1	A	30	SER	CB-OG	-6.00	1.34	1.42
1	A	118	TRP	CE2-CZ2	5.91	1.49	1.39
1	A	92	ARG	CG-CD	5.90	1.66	1.51
1	A	105	MSE	SE-CE	5.89	2.30	1.95
1	A	92	ARG	NE-CZ	5.71	1.40	1.33
1	A	124	GLY	C-O	-5.66	1.14	1.23
1	A	122	LYS	CE-NZ	5.54	1.62	1.49
1	A	18	GLU	CG-CD	5.52	1.60	1.51
1	A	21	LYS	CD-CE	5.45	1.64	1.51
1	A	127	PHE	CD2-CE2	-5.38	1.28	1.39
1	A	30	SER	C-O	-5.33	1.13	1.23
1	A	113	TYR	CE2-CZ	-5.32	1.31	1.38
1	A	112	PRO	N-CA	5.28	1.56	1.47
1	A	91	GLU	CD-OE2	5.21	1.31	1.25
1	A	116	PHE	CE2-CZ	5.16	1.47	1.37
1	A	92	ARG	CZ-NH1	5.14	1.39	1.33
1	A	115	GLU	CD-OE2	5.09	1.31	1.25
1	A	24	THR	CA-CB	5.08	1.66	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	77	PRO	CA-C	5.02	1.62	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	121	ASP	CB-CG-OD2	7.86	125.38	118.30
1	A	6	ILE	CG1-CB-CG2	-5.74	98.78	111.40
1	A	21	LYS	CD-CE-NZ	5.49	124.33	111.70
1	A	79	SER	N-CA-C	5.46	125.75	111.00
1	A	78	ILE	CG1-CB-CG2	-5.32	99.71	111.40
1	A	108	THR	OG1-CB-CG2	-5.26	97.91	110.00
1	A	86	ASP	CB-CG-OD1	5.17	122.95	118.30
1	A	55	THR	OG1-CB-CG2	-5.14	98.18	110.00
1	A	45	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	45	ASP	N-CA-CB	5.08	119.75	110.60

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	902	0	876	43	0
2	A	22	0	0	4	0
All	All	924	0	876	43	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

All (43) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:SD	1:A:1:MET:CE	2.03	1.46
1:A:62:MSE:CE	1:A:62:MSE:SE	2.18	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:MSE:CE	1:A:11:MSE:SE	2.21	1.39
1:A:105:MSE:CE	1:A:105:MSE:SE	2.30	1.29
1:A:110:MSE:CE	1:A:110:MSE:SE	2.45	1.14
1:A:10:LEU:N	1:A:10:LEU:HD12	1.91	0.83
1:A:78:ILE:O	1:A:78:ILE:HG12	1.88	0.74
1:A:88:ILE:O	1:A:92:ARG:HG3	1.90	0.72
1:A:17:GLU:HA	1:A:35:MSE:HE1	1.73	0.69
1:A:114:ARG:HB3	1:A:131:LEU:HD22	1.74	0.69
1:A:50:GLN:HG2	2:A:147:HOH:O	1.95	0.67
1:A:30:SER:HB2	1:A:55:THR:O	1.95	0.67
1:A:45:ASP:HB2	2:A:160:HOH:O	1.98	0.63
1:A:84:VAL:HG11	1:A:90:MSE:HG2	1.80	0.61
1:A:107:LYS:HD2	2:A:146:HOH:O	2.01	0.59
1:A:33:ILE:HD12	1:A:33:ILE:O	2.03	0.57
1:A:48:THR:HG22	1:A:49:VAL:N	2.19	0.57
1:A:78:ILE:O	1:A:78:ILE:CG1	2.53	0.57
1:A:34:THR:O	1:A:52:SER:HA	2.06	0.56
1:A:3:ILE:HD12	1:A:62:MSE:CE	2.39	0.53
1:A:10:LEU:N	1:A:10:LEU:CD1	2.68	0.53
1:A:20:VAL:HG12	1:A:32:ILE:HD11	1.90	0.52
1:A:121:ASP:C	1:A:121:ASP:OD1	2.47	0.52
1:A:90:MSE:HE1	1:A:129:LEU:HD12	1.93	0.50
1:A:48:THR:HG23	1:A:65:ASP:C	2.32	0.50
1:A:10:LEU:O	1:A:63:ALA:HA	2.12	0.49
1:A:1:MET:SD	1:A:1:MET:N	2.73	0.48
1:A:99:ASP:C	1:A:101:GLY:N	2.66	0.48
1:A:55:THR:O	1:A:56:LEU:HD23	2.14	0.48
1:A:30:SER:HB2	1:A:56:LEU:HA	1.96	0.47
1:A:30:SER:CB	1:A:56:LEU:HA	2.45	0.47
1:A:65:ASP:CB	2:A:148:HOH:O	2.63	0.47
1:A:28:GLU:O	1:A:30:SER:N	2.48	0.46
1:A:48:THR:CG2	1:A:49:VAL:N	2.79	0.45
1:A:37:LYS:HA	1:A:48:THR:O	2.17	0.45
1:A:88:ILE:HD12	1:A:88:ILE:H	1.81	0.45
1:A:94:PHE:CE2	1:A:107:LYS:HE2	2.52	0.45
1:A:3:ILE:HD12	1:A:62:MSE:HE1	2.00	0.44
1:A:10:LEU:H	1:A:10:LEU:HD12	1.78	0.44
1:A:48:THR:CG2	1:A:65:ASP:HA	2.47	0.44
1:A:107:LYS:HE3	1:A:107:LYS:HB2	1.88	0.42
1:A:12:PHE:HE1	1:A:63:ALA:HB1	1.84	0.42
1:A:105:MSE:CE	1:A:105:MSE:HB2	2.50	0.42



There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	111/139 (80%)	103 (93%)	6 (5%)	2 (2%)	11 21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	79	SER
1	A	28	GLU

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	96/114 (84%)	87 (91%)	9 (9%)	11 20

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	18	GLU
1	A	33	ILE
1	A	35	MSE
1	A	90	MSE
1	A	98	LYS

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Mol	Chain	Res	Type
1	A	107	LYS
1	A	109	ASN
1	A	112	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	GLN
1	A	57	ASN
1	A	109	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.