



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2MZW
Title : Staphylococcus aureus FusB:EF-GC3 complex
Authors : Tomlinson, J.H.; Thompson, G.S.; Kalverda, A.P.; Zhuravleva, A.; O'Neill, A.
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This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.23.1
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.1

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

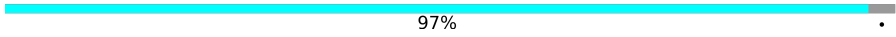

The overall completeness of chemical shifts assignment is 13%.

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)	NMR archive (#Entries)
Clashscore	158937	12864

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	301	 97% .
2	B	233	 91% 9%

2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8050 atoms, of which 4018 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms						Trace
1	A	292	Total	C	H	N	O	S	0
			4471	1417	2214	378	445	17	

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	693	GLU	-	expression tag	UNP W8UT26
A	694	LEU	-	expression tag	UNP W8UT26
A	695	GLU	-	expression tag	UNP W8UT26
A	696	HIS	-	expression tag	UNP W8UT26
A	697	HIS	-	expression tag	UNP W8UT26
A	698	HIS	-	expression tag	UNP W8UT26
A	699	HIS	-	expression tag	UNP W8UT26
A	700	HIS	-	expression tag	UNP W8UT26
A	701	HIS	-	expression tag	UNP W8UT26

- Molecule 2 is a protein called Far1.

Mol	Chain	Residues	Atoms						Trace
2	B	213	Total	C	H	N	O	S	0
			3578	1143	1804	291	332	8	

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	expression tag	UNP Q8GNY5
B	-18	GLY	-	expression tag	UNP Q8GNY5
B	-17	SER	-	expression tag	UNP Q8GNY5
B	-16	SER	-	expression tag	UNP Q8GNY5
B	-15	HIS	-	expression tag	UNP Q8GNY5
B	-14	HIS	-	expression tag	UNP Q8GNY5
B	-13	HIS	-	expression tag	UNP Q8GNY5
B	-12	HIS	-	expression tag	UNP Q8GNY5
B	-11	HIS	-	expression tag	UNP Q8GNY5
B	-10	HIS	-	expression tag	UNP Q8GNY5
B	-9	SER	-	expression tag	UNP Q8GNY5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	SER	-	expression tag	UNP Q8GNY5
B	-7	GLY	-	expression tag	UNP Q8GNY5
B	-6	LEU	-	expression tag	UNP Q8GNY5
B	-5	VAL	-	expression tag	UNP Q8GNY5
B	-4	PRO	-	expression tag	UNP Q8GNY5
B	-3	ASN	-	expression tag	UNP Q8GNY5
B	-2	GLY	-	expression tag	UNP Q8GNY5
B	-1	SER	-	expression tag	UNP Q8GNY5
B	0	HIS	-	expression tag	UNP Q8GNY5

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
3	B	1	Total	Zn
			1	1

5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 200 calculated structures, 1 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR NIH	structure solution	2.33.0
X-PLOR NIH	refinement	2.33.0
HADDOCK	structure solution	2.1
HADDOCK	refinement	2.1

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	2
Total number of shifts	812
Number of shifts mapped to atoms	812
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	13%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	0	0	0	0
2	B	0	0	0	0
3	B	1	0	0	0
All	All	1	0	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 -.

There are no clashes.

6.3 Torsion angles [i](#)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	0	-	-	-	-

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	0	-	-	-	-
All	All	0	-	-	-	-

There are no Ramachandran outliers.

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	0	-	-	-
2	B	0	-	-	-
All	All	0	-	-	-

There are no protein residues with a non-rotameric sidechain to report.

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 13% for the well-defined parts and 13% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *C3_assigned_chem_shift_list*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	560
Number of shifts mapped to atoms	560
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	129	0.35 ± 0.19	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	117	0.12 ± 0.17	None needed (< 0.5 ppm)
^{15}N	157	-0.33 ± 0.36	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 9%, i.e. 560 atoms were assigned a chemical shift out of a possible 6300. 0 out of 72 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	560/2485 (23%)	157/990 (16%)	246/1010 (24%)	157/485 (32%)
Sidechain	0/3326 (0%)	0/1953 (0%)	0/1230 (0%)	0/143 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	0/489 (0%)	0/255 (0%)	0/213 (0%)	0/21 (0%)
Overall	560/6300 (9%)	157/3198 (5%)	246/2453 (10%)	157/649 (24%)

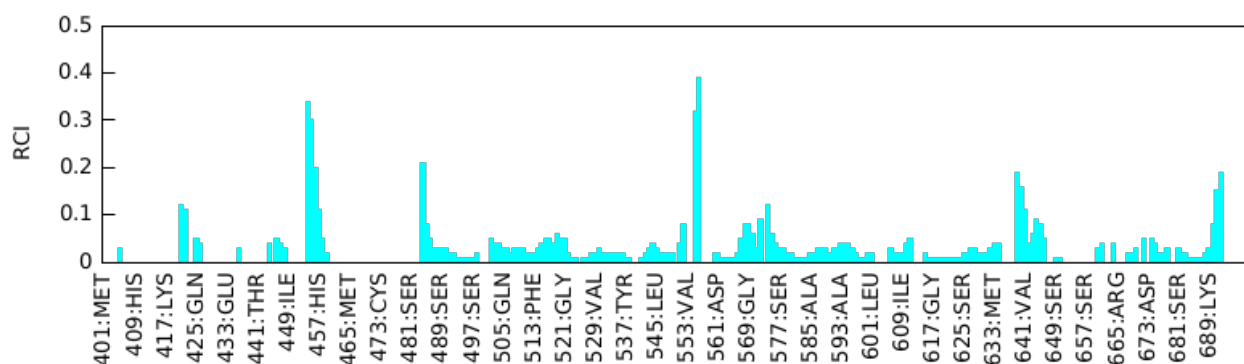
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:



7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: C3_assigned_chem_shift_list_dup

7.2.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	252
Number of shifts mapped to atoms	252
Number of unparsed shifts	0

Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.2.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	126	-0.22 ± 0.23	None needed (< 0.5 ppm)

7.2.3 Completeness of resonance assignments ⓘ

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 4%, i.e. 248 atoms were assigned a chemical shift out of a possible 6300. 0 out of 72 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	248/2485 (10%)	124/990 (13%)	0/1010 (0%)	124/485 (26%)
Sidechain	0/3326 (0%)	0/1953 (0%)	0/1230 (0%)	0/143 (0%)
Aromatic	0/489 (0%)	0/255 (0%)	0/213 (0%)	0/21 (0%)
Overall	248/6300 (4%)	124/3198 (4%)	0/2453 (0%)	124/649 (19%)

7.2.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.2.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain B:

