wwPDB NMR Structure Validation Summary Report (i)

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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
http://wwpdb.org/validation/2016/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

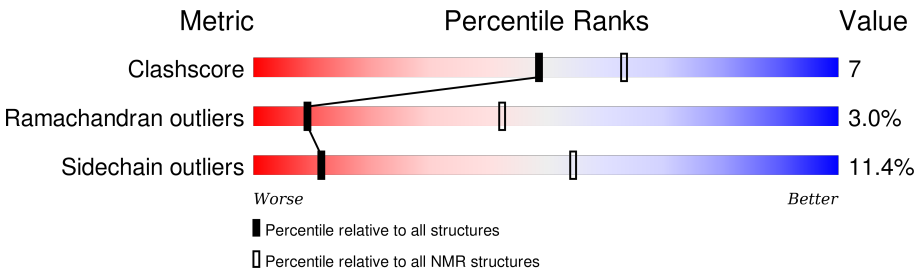
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

1 Overall quality at a glance (i)

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	301	66% 26% • • •
2	B	233	76% 14% • 9%

2 Ensemble composition and analysis (i)

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
			Total	C	H	N	O	S	
1	A	292	4471	1417	2214	378	445	17	0

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
			Total	C	H	N	O	S	
2	B	213	3578	1143	1804	291	332	8	0

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).

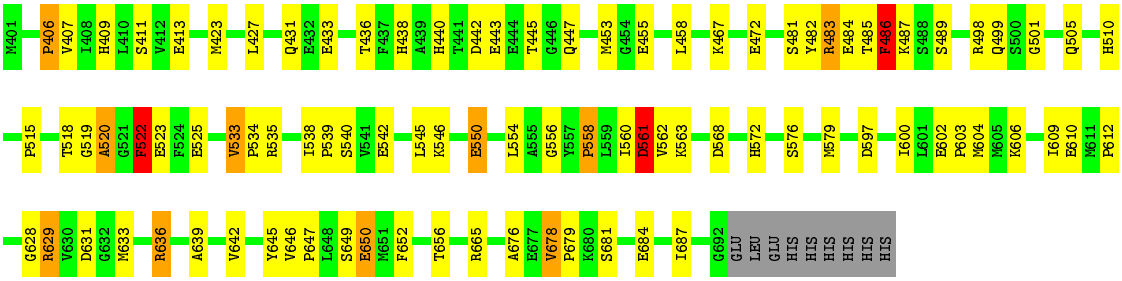
Mol	Chain	Residues	Atoms	
			Total	Zn
3	B	1	1	1

4 Residue-property plots (i)

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

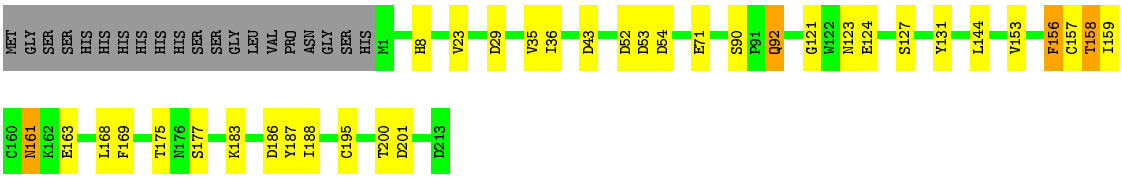
- Molecule 1: Elongation factor G

Chain A:



- Molecule 2: Far1

Chain B:



5 Refinement protocol and experimental data overview (i)

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)	2mzw_cs.str
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%

No validations of the models with respect to experimental NMR restraints is performed at this time.

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	2257	2214	2204	51
2	B	1774	1804	1805	21
3	B	1	0	0	2
All	All	4032	4018	4009	60

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 7.

5 of 60 clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
2:B:169:PHE:HB2	2:B:188:ILE:HG12	0.90	1.40
1:A:525:GLU:HG2	2:B:183:LYS:HB2	0.82	1.49
1:A:525:GLU:HA	2:B:183:LYS:HD3	0.73	1.58
2:B:195:CYS:SG	3:B:301:ZN:ZN	0.72	1.77
1:A:533:VAL:HB	1:A:534:PRO:HD3	0.70	1.63

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	290/301 (96%)	232 (80%)	44 (15%)	14 (5%)	5 28
2	B	211/233 (91%)	199 (94%)	11 (5%)	1 (0%)	38 79
All	All	501/534 (94%)	431 (86%)	55 (11%)	15 (3%)	9 42

5 of 15 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	650	GLU
1	A	633	MET
1	A	522	PHE
1	A	406	PRO
1	A	597	ASP

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	243/252 (96%)	210 (86%)	33 (14%)	9 49
2	B	204/221 (92%)	186 (91%)	18 (9%)	17 62
All	All	447/473 (95%)	396 (89%)	51 (11%)	11 54

5 of 51 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
2	B	127	SER
1	A	681	SER

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Mol	Chain	Res	Type
1	A	636	ARG
1	A	649	SER
1	A	678	VAL

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 carbohydrates 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 (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

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: 2mzw_cs.str

Chemical shift list name: *C3_assigned_chem_shift_list*

7.1.1 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	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 (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	129	0.34 ± 0.11	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	0	—	—
$^{13}C'$	117	0.11 ± 0.15	None needed (< 0.5 ppm)
^{15}N	157	-0.33 ± 0.22	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments (i)

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	^{1}H	^{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%)

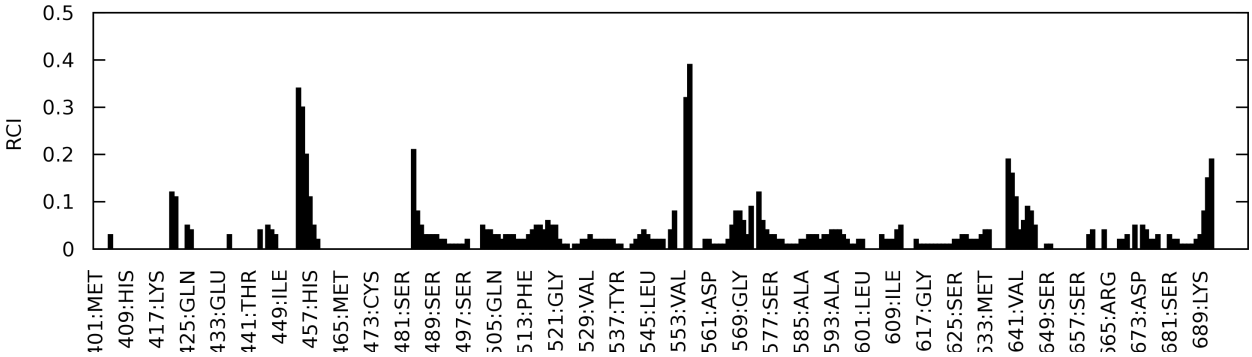
7.1.4 Statistically unusual chemical shifts (i)

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: 2mzw_cs.str

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 (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	0	—	—
$^{13}C_{\beta}$	0	—	—
$^{13}C'$	0	—	—
^{15}N	126	-0.24 ± 0.18	None needed (< 0.5 ppm)

7.2.3 Completeness of resonance assignments (i)

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	^{1}H	^{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%)

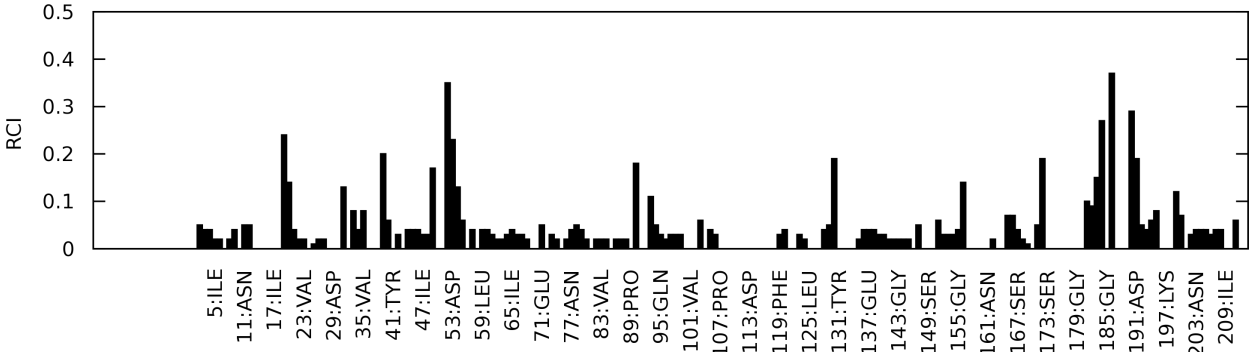
7.2.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.2.5 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 B:


RCI
0.5
0.4
0.3
0.2
0.1
0
5:ILE
11:ASN
17:ILE
23:VAL
29:ASP
35:VAL
41:TYR
47:ILE
53:ASP
59:LEU
65:ILE
71:GLU
77:ASN
83:VAL
89:PRO
95:GLN
101:VAL
107:PRO
113:ASP
119:PHE
125:LEU
131:TYR
137:GLU
143:GLY
149:SER
155:GLY
161:ASN
167:SER
173:SER
179:GLY
185:GLY
191:ASP
197:LYS
203:ASN
209:ILE