Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	6Q2Z
Title	:	NMR solution structure of the HVO_2922 protein from Haloferax volcanii
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Deposited on	:	2018-12-03

This is a Full wwPDB NMR Structure Validation 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

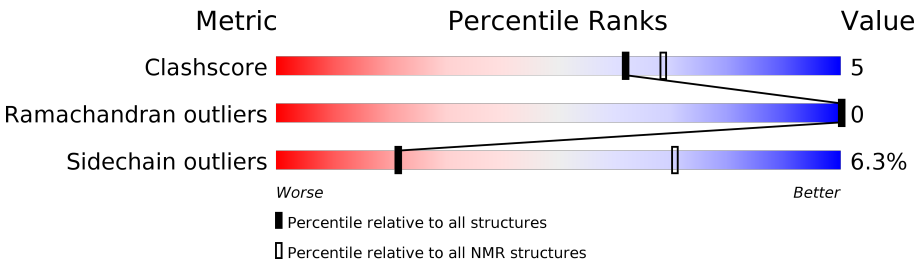
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 43%.

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
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	60	87% 7% • 5%
1	B	60	90% 7% • •

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	A:102-A:158, B:202-B:260 (116)	0.18	1

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: Failed to create NmrClust input

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1856 atoms, of which 914 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called UPF0339 family protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	60	928	292	457	86	92	1	0
1	B	60	928	292	457	86	92	1	0

SEQUENCE-PLOTS INFOmissingINFO

4 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *simulated annealing with torsion angle dynamics, cartesian angle dynamics, molecular dynamics.*

Of the 200 calculated structures, 20 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
CYANA	structure calculation	3.97
CNS	structure calculation	1.1
ARIA	refinement	1.2 HJ

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	697
Number of shifts mapped to atoms	697
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	43%

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

5 Model quality (i)

5.1 Standard geometry (i)

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.

5.2 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	448	435	433	4±2
1	B	463	446	444	4±2
All	All	18220	17620	15786	154

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 5.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:220:LEU:HG	1:B:228:LEU:HD12	0.54	1.79	16	18
1:A:120:LEU:HG	1:A:128:LEU:HD12	0.53	1.80	16	18
1:A:122:HIS:CB	1:A:126:ASN:HD21	0.53	2.16	4	18
1:B:222:HIS:CB	1:B:226:ASN:HD21	0.51	2.18	13	17
1:A:117:ARG:HD3	1:A:134:GLY:HA2	0.47	1.86	4	1
1:B:217:ARG:HD3	1:B:234:GLY:HA2	0.47	1.87	20	4
1:A:117:ARG:CD	1:A:134:GLY:HA2	0.45	2.41	4	1
1:B:217:ARG:CD	1:B:234:GLY:HA2	0.45	2.41	20	4
1:A:157:VAL:HA	1:B:206:PHE:HB2	0.44	1.90	13	7
1:B:230:ASP:OD1	1:B:231:SER:N	0.44	2.51	12	1
1:B:240:LYS:HA	1:B:240:LYS:HE3	0.44	1.90	8	2
1:A:122:HIS:HB2	1:A:126:ASN:HD21	0.43	1.71	1	5
1:A:140:LYS:HE3	1:A:140:LYS:HA	0.43	1.89	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:210:VAL:HA	1:B:215:LYS:O	0.43	2.13	18	5
1:A:106:PHE:HB2	1:B:257:VAL:HA	0.43	1.89	9	4
1:B:222:HIS:HB2	1:B:226:ASN:HD21	0.43	1.71	9	2
1:A:117:ARG:NH2	1:A:131:SER:HB2	0.43	2.29	4	1
1:B:252:ALA:N	1:B:253:PRO:HD2	0.43	2.29	7	7
1:B:240:LYS:HE3	1:B:240:LYS:HA	0.43	1.89	3	2
1:A:122:HIS:CB	1:A:126:ASN:ND2	0.43	2.82	4	4
1:A:152:ALA:N	1:A:153:PRO:HD2	0.43	2.29	3	8
1:A:140:LYS:HA	1:A:140:LYS:HE2	0.43	1.91	15	1
1:A:117:ARG:NH2	1:A:133:GLU:HB2	0.43	2.29	4	1
1:B:217:ARG:NH2	1:B:231:SER:HB2	0.42	2.30	5	2
1:B:248:VAL:HG22	1:B:252:ALA:HB2	0.41	1.91	1	1
1:A:145:ILE:O	1:A:148:VAL:HG12	0.41	2.15	8	3
1:A:110:VAL:HA	1:A:115:LYS:O	0.41	2.15	6	4
1:A:108:VAL:HG22	1:A:118:TRP:HB3	0.41	1.93	6	1
1:B:245:ILE:O	1:B:248:VAL:HG12	0.41	2.15	18	3
1:B:210:VAL:HG13	1:B:214:ASP:HA	0.41	1.93	8	1
1:A:140:LYS:HA	1:A:140:LYS:HE3	0.41	1.91	19	1
1:B:216:TYR:O	1:B:217:ARG:NH1	0.40	2.55	18	1
1:B:240:LYS:HE2	1:B:240:LYS:HA	0.40	1.93	6	1
1:B:222:HIS:CB	1:B:226:ASN:ND2	0.40	2.84	13	1
1:B:222:HIS:HB2	1:B:226:ASN:ND2	0.40	2.32	9	1
1:A:122:HIS:HB2	1:A:126:ASN:ND2	0.40	2.32	5	1
1:A:148:VAL:HG22	1:A:152:ALA:HB2	0.40	1.93	14	1

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 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	57/60 (95%)	47±20 (82±34%)	2±1 (3±2%)	0±0 (0±0%)	100	100
1	B	58/60 (97%)	48±20 (82±35%)	1±1 (2±2%)	0±0 (0±0%)	100	100
All	All	1955/2400 (81%)	1888 (97%)	67 (3%)	0 (0%)	100	100

There are no Ramachandran outliers.

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 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	45/47 (96%)	36±15 (80±33%)	2±1 (5±3%)	26 75
1	B	46/47 (98%)	37±15 (80±34%)	2±1 (5±3%)	27 76
All	All	1547/1880 (82%)	1450 (94%)	97 (6%)	21 70

All 15 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	126	ASN	17
1	B	226	ASN	17
1	B	248	VAL	15
1	A	148	VAL	15
1	A	124	ASN	8
1	A	140	LYS	6
1	B	224	ASN	5
1	B	240	LYS	4
1	B	254	ASP	3
1	A	154	ASP	2
1	B	250	ARG	1
1	A	150	ARG	1
1	B	222	HIS	1
1	B	257	VAL	1
1	B	258	ILE	1

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such molecules in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 43% for the well-defined parts and 43% for the entire structure.

6.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *NinaP17-bmrb.tbl*

6.1.1 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	697
Number of shifts mapped to atoms	697
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

6.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	60	-0.58 ± 0.25	Should be applied
$^{13}C_{\beta}$	55	-0.05 ± 0.20	None needed (< 0.5 ppm)
$^{13}C'$	55	-0.18 ± 0.17	None needed (< 0.5 ppm)
^{15}N	56	0.62 ± 0.40	None needed (imprecise)

6.1.3 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 43%, i.e. 607 atoms were assigned a chemical shift out of a possible 1419. 7 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	276/576 (48%)	111/230 (48%)	111/232 (48%)	54/114 (47%)
Sidechain	307/719 (43%)	192/419 (46%)	109/258 (42%)	6/42 (14%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	24/124 (19%)	17/64 (27%)	6/50 (12%)	1/10 (10%)
Overall	607/1419 (43%)	320/713 (45%)	226/540 (42%)	61/166 (37%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 43%, i.e. 633 atoms were assigned a chemical shift out of a possible 1464. 7 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	287/596 (48%)	116/238 (49%)	115/240 (48%)	56/118 (47%)
Sidechain	322/744 (43%)	202/434 (47%)	114/268 (43%)	6/42 (14%)
Aromatic	24/124 (19%)	17/64 (27%)	6/50 (12%)	1/10 (10%)
Overall	633/1464 (43%)	335/736 (46%)	235/558 (42%)	63/170 (37%)

6.1.4 Statistically unusual chemical shifts (i)

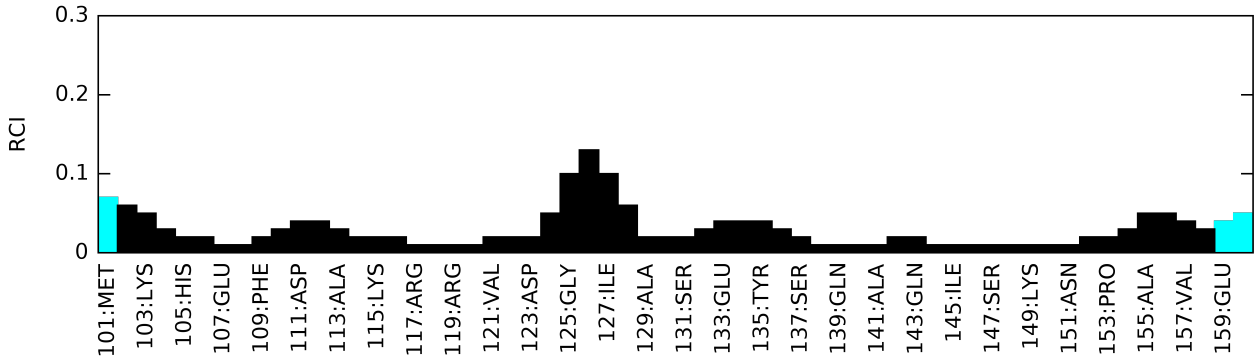
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	145	ILE	HG22	-0.78	2.13 – -0.57	-5.8
1	A	145	ILE	HG23	-0.78	2.13 – -0.57	-5.8
1	A	145	ILE	HG21	-0.78	2.13 – -0.57	-5.8
1	A	117	ARG	HB3	0.35	3.17 – 0.37	-5.1

6.1.5 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:


RCI
0.3
0.2
0.1
0
101:MET
103:LYS
105:HIS
107:GLU
109:PHE
111:ASP
113:ALA
115:LYS
117:ARG
119:ARG
121:VAL
123:ASP
125:GLY
127:ILE
129:ALA
131:SER
133:GLU
135:TYR
137:SER
139:GLN
141:ALA
143:GLN
145:ILE
147:SER
149:LYS
151:ASN
153:PRO
155:ALA
157:VAL
159:GLU