Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2KQL
Title	:	Maurocalcine in D configuration from Scorpio maurus palmatus
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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 (i)) were used in the production of this report:

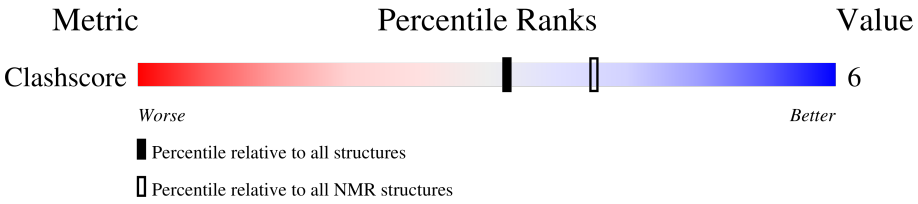
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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 was not calculated.

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

WHATHAPPENED The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
1	A	DIL	28	20	-
1	A	DTH	26	20	-

2 Ensemble composition and analysis (i)

This entry contains 20 models. This entry does not contain polypeptide chains, therefore identification of well-defined residues and clustering analysis are not possible. All residues are included in the validation scores.

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 542 atoms, of which 278 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein (with D amino acids) called D-MAUROCALCINE.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	33	542	156	278	56	46	6	0

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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.

4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.2 Score per residue for model 2

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.3 Score per residue for model 3

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.4 Score per residue for model 4

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.5 Score per residue for model 5

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.6 Score per residue for model 6

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.7 Score per residue for model 7

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.8 Score per residue for model 8

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.9 Score per residue for model 9

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.10 Score per residue for model 10

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.11 Score per residue for model 11

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.12 Score per residue for model 12

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.13 Score per residue for model 13

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.14 Score per residue for model 14

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.15 Score per residue for model 15

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.16 Score per residue for model 16

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.17 Score per residue for model 17

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.18 Score per residue for model 18

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.19 Score per residue for model 19

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.20 Score per residue for model 20

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
CYANA	structure solution	2.1
X-PLOR NIH	refinement	2.21

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DSG, DHI, DIL, DAS, DLY, DLE, DPR, DTH, DCY, DAR, DGL, DSN

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

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	2.0±0.0	0.0±0.0
All	All	40	0

There are no bond-length outliers.

There are no bond-angle outliers.

All unique chiral outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	26	DTH	CB	20
1	A	28	DIL	CB	20

There are no planarity outliers.

6.2 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 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	264	278	245	3±2
All	All	5280	5560	4909	57

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:DCY:HB3	1:A:32:DCY:SG	0.76	2.20	2	2
1:A:10:DCY:SG	1:A:32:DCY:HB2	0.74	2.22	20	1
1:A:13:DSG:O	1:A:19:DLY:HA	0.63	1.92	10	18
1:A:4:DLE:HB2	1:A:16:DCY:SG	0.59	2.38	5	1
1:A:3:DCY:HA	1:A:15:DAS:O	0.59	1.98	10	1
1:A:20:DLY:O	1:A:32:DCY:HA	0.55	2.01	2	4
1:A:13:DSG:HA	1:A:21:DCY:SG	0.55	2.41	14	3
1:A:10:DCY:HA	1:A:32:DCY:SG	0.52	2.45	5	3
1:A:23:DAR:HA	1:A:29:DGL:O	0.49	2.08	2	2
1:A:7:DLE:C	1:A:8:DLY:HD2	0.48	2.38	20	4
1:A:14:DLY:HD3	1:A:14:DLY:O	0.48	2.08	10	2
1:A:21:DCY:SG	1:A:30:DLY:HE3	0.48	2.49	16	1
1:A:21:DCY:SG	1:A:32:DCY:SG	0.47	3.12	5	1
1:A:21:DCY:SG	1:A:30:DLY:HE2	0.46	2.51	8	1
1:A:8:DLY:O	1:A:31:DAR:HB3	0.45	2.12	7	1
1:A:10:DCY:SG	1:A:30:DLY:HG3	0.44	2.53	10	1
1:A:13:DSG:OD1	1:A:21:DCY:HB3	0.43	2.13	19	2
1:A:23:DAR:HB2	1:A:28:DIL:O	0.43	2.14	8	1
1:A:16:DCY:SG	1:A:21:DCY:HB2	0.43	2.54	8	1
1:A:16:DCY:SG	1:A:21:DCY:SG	0.42	3.18	15	1
1:A:5:DPR:O	1:A:8:DLY:HB2	0.42	2.14	16	1
1:A:4:DLE:HD13	1:A:9:DLE:O	0.41	2.15	4	1
1:A:6:DHI:HB2	1:A:33:DAR:O	0.41	2.16	12	1
1:A:21:DCY:SG	1:A:30:DLY:HD2	0.40	2.56	2	1
1:A:22:DLY:HB2	1:A:33:DAR:NH2	0.40	2.32	4	1
1:A:4:DLE:HD23	1:A:10:DCY:HA	0.40	1.94	14	1

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

There are no protein molecules in this entry.

6.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

31 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	DTH	A	26	1	1±0,1,2,3	-	-
1	DIL	A	28	1	1±0,1,2,3	-	-

There are no bond-length outliers.

There are no bond-angle outliers.

All unique chiral outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	26	DTH	CB	20
1	A	28	DIL	CB	20

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

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

No chemical shift data were provided