



Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 08:07 am BST

PDB ID : 5MCS
Title : Solution structure and dynamics of the outer membrane cytochrome OmcF from *Geobacter sulfurreducens*
Authors : Dantas, J.M.; Silva, M.A.; Morgado, L.; Pantoja-Uceda, D.; Turner, D.L.; Bruix, M.; Salgueiro, C.A.
Deposited on : 2016-11-10

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 ⓘ symbol.

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

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
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

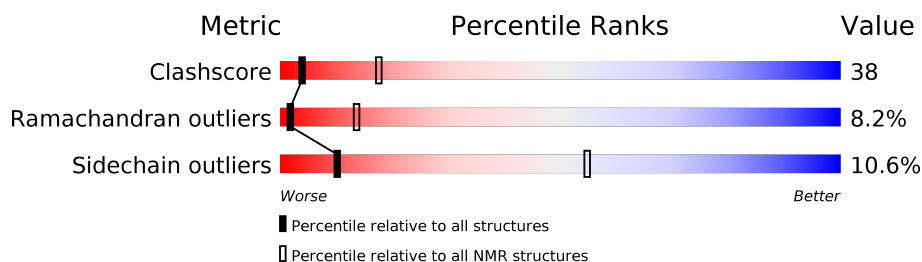
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 52%.

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	80	 55% 36% 6% ..

2 Ensemble composition and analysis

This entry contains 20 models. Model 18 is the overall representative, medoid model (most similar to other models). The authors have identified model 20 as representative, based on the following criterion: *target function*.

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:26-A:104 (79)	0.16	18

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

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

The models can be grouped into 4 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 3, 4, 6, 8, 9, 16, 18
2	5, 11, 13, 14, 15
3	2, 12, 20
4	7, 10
Single-model clusters	17; 19

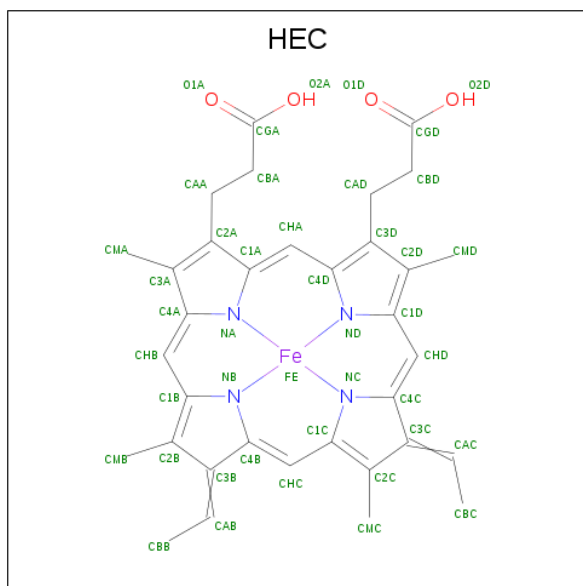
3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1176 atoms, of which 550 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Lipoprotein cytochrome c, 1 heme-binding site.

Mol	Chain	Residues	Atoms						Trace
1	A	80	Total	C	H	N	O	S	0
			1133	364	550	110	105	4	

- Molecule 2 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



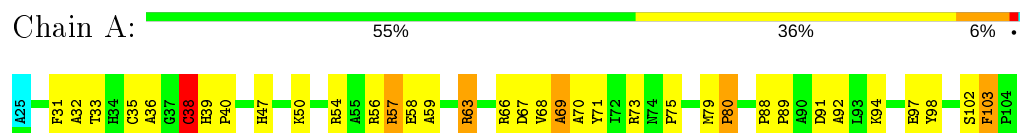
Mol	Chain	Residues	Atoms				
2	A	1	Total	C	Fe	N	O
			43	34	1	4	4

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

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: Lipoprotein cytochrome c, 1 heme-binding site

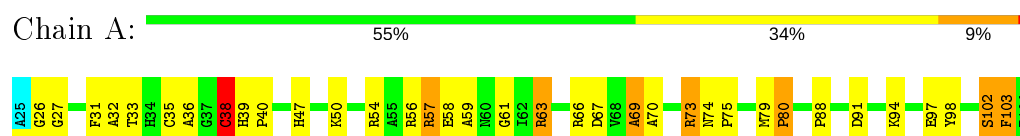


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

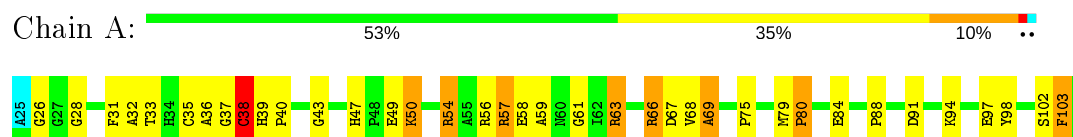
4.2.1 Score per residue for model 1

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



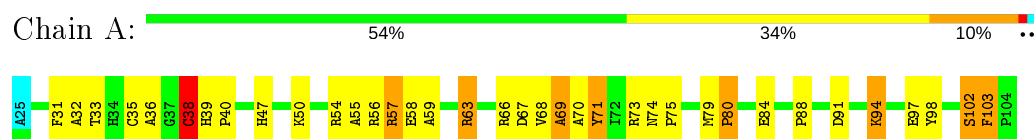
4.2.2 Score per residue for model 2

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



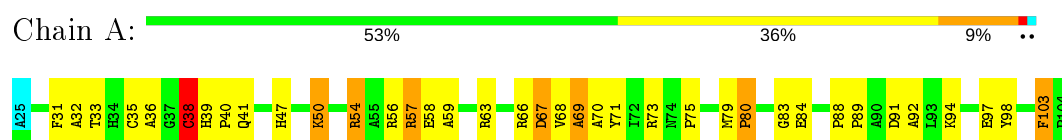
4.2.3 Score per residue for model 3

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



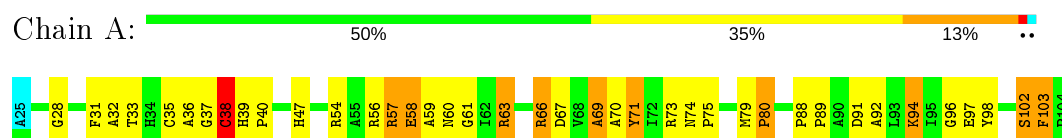
4.2.4 Score per residue for model 4

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



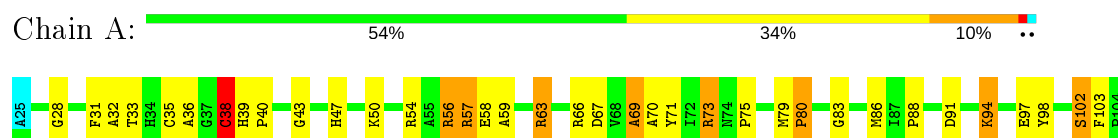
4.2.5 Score per residue for model 5

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



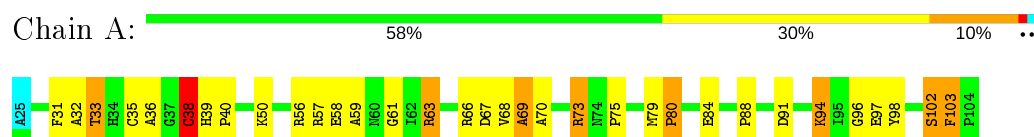
4.2.6 Score per residue for model 6

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



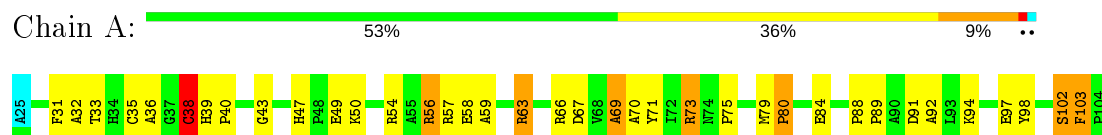
4.2.7 Score per residue for model 7

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



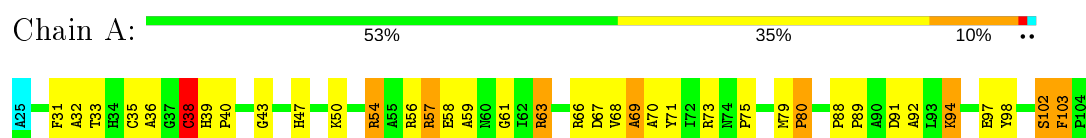
4.2.8 Score per residue for model 8

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



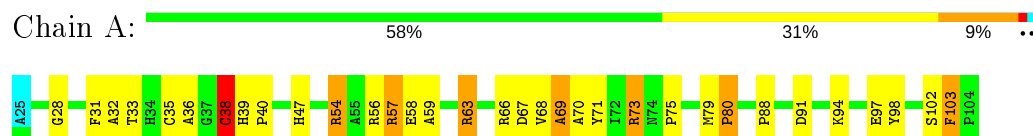
4.2.9 Score per residue for model 9

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



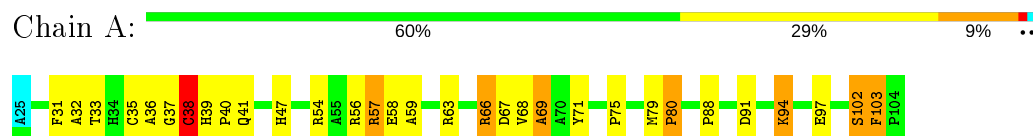
4.2.10 Score per residue for model 10

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



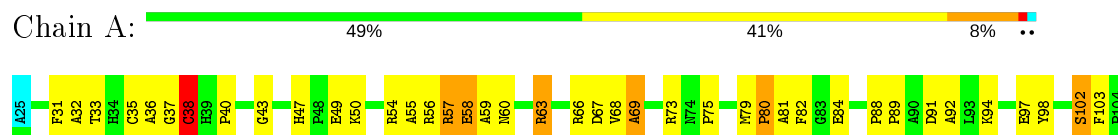
4.2.11 Score per residue for model 11

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



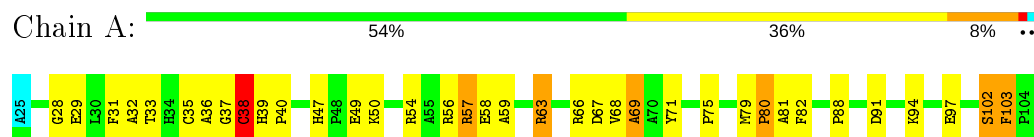
4.2.12 Score per residue for model 12

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



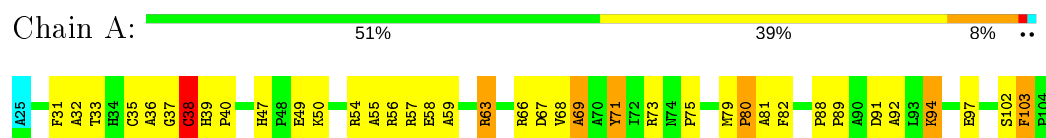
4.2.13 Score per residue for model 13

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



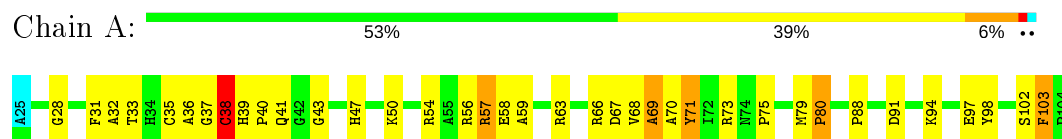
4.2.14 Score per residue for model 14

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



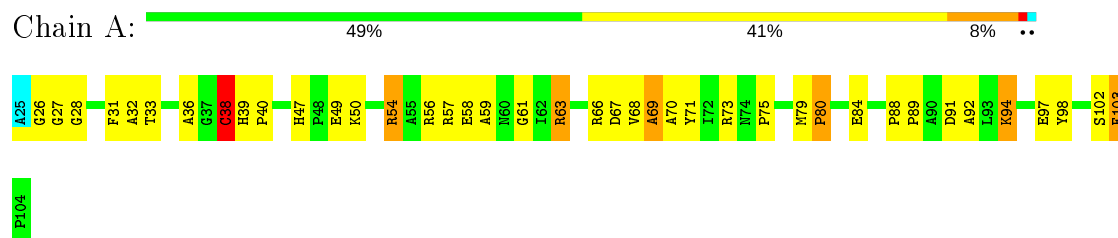
4.2.15 Score per residue for model 15

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



4.2.16 Score per residue for model 16

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site



4.2.17 Score per residue for model 17

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site





4.2.18 Score per residue for model 18 (medoid)

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site

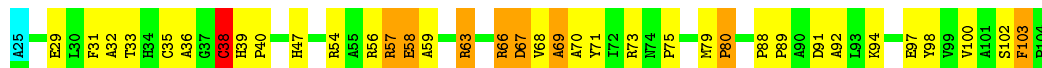
Chain A: 54% 36% 8% ..



4.2.19 Score per residue for model 19

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site

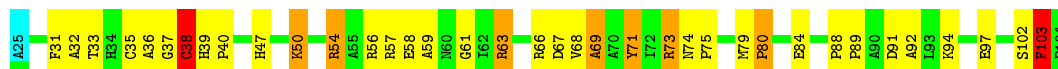
Chain A: 54% 34% 10% ..



4.2.20 Score per residue for model 20

- Molecule 1: Lipoprotein cytochrome c, 1 heme-binding site

Chain A: 53% 35% 9% ..



5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
DYANA	refinement	
DYANA	structure calculation	

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	592
Number of shifts mapped to atoms	572
Number of unparsed shifts	0
Number of shifts with mapping errors	20
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	52%

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

6 Model quality

6.1 Standard geometry

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

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

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	578	545	388	35±4
2	A	43	0	30	6±2
All	All	12420	10900	8360	780

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 38.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:32:ALA:HA	1:A:36:ALA:HB2	0.78	1.55	3	20
1:A:88:PRO:HG2	1:A:91:ASP:CG	0.74	2.03	9	20
1:A:31:PHE:CG	1:A:98:TYR:CE1	0.70	2.79	19	4
1:A:88:PRO:HG2	1:A:91:ASP:OD1	0.67	1.89	5	8
1:A:61:GLY:C	1:A:63:ARG:HH11	0.66	1.93	17	4
2:A:201:HEC:CHA	2:A:201:HEC:CGA	0.65	2.74	13	5
1:A:57:ARG:HE	2:A:201:HEC:HMA3	0.63	1.52	6	1
1:A:88:PRO:HG2	1:A:91:ASP:OD2	0.62	1.94	7	6
2:A:201:HEC:CGA	2:A:201:HEC:CHA	0.62	2.77	2	3
1:A:73:ARG:NH2	1:A:89:PRO:HG3	0.60	2.11	8	4
1:A:102:SER:OG	1:A:103:PHE:CE1	0.60	2.54	16	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:PHE:CD1	1:A:31:PHE:O	0.59	2.55	17	4
1:A:75:PRO:HG2	1:A:80:PRO:O	0.59	1.98	17	20
1:A:79:MET:O	1:A:80:PRO:O	0.58	2.21	8	20
1:A:31:PHE:CD1	1:A:98:TYR:CE1	0.58	2.91	19	5
1:A:89:PRO:O	1:A:92:ALA:HB3	0.58	1.98	8	11
1:A:31:PHE:CD2	1:A:31:PHE:O	0.57	2.58	6	7
1:A:31:PHE:O	1:A:31:PHE:CD2	0.56	2.59	18	3
1:A:57:ARG:NH2	2:A:201:HEC:CBA	0.56	2.69	4	1
1:A:31:PHE:CD2	1:A:98:TYR:CE1	0.56	2.94	6	6
2:A:201:HEC:O1A	2:A:201:HEC:C3A	0.56	2.54	18	1
1:A:47:HIS:CE1	2:A:201:HEC:O1D	0.55	2.59	11	1
1:A:47:HIS:CE1	2:A:201:HEC:O2D	0.55	2.60	5	1
1:A:58:GLU:CG	1:A:59:ALA:N	0.55	2.70	17	20
1:A:31:PHE:CD2	1:A:98:TYR:CE2	0.55	2.95	16	3
2:A:201:HEC:HBC3	2:A:201:HEC:HMC1	0.54	1.78	1	10
1:A:31:PHE:CD1	1:A:31:PHE:C	0.54	2.81	10	6
1:A:102:SER:C	1:A:103:PHE:CG	0.54	2.79	20	1
1:A:47:HIS:CE1	2:A:201:HEC:CGD	0.54	2.91	11	1
1:A:57:ARG:CZ	2:A:201:HEC:CBA	0.53	2.86	20	1
2:A:201:HEC:O2A	2:A:201:HEC:C2A	0.53	2.56	10	1
1:A:31:PHE:CG	1:A:98:TYR:CE2	0.53	2.96	16	4
1:A:31:PHE:CD2	1:A:31:PHE:C	0.53	2.82	14	7
1:A:31:PHE:C	1:A:31:PHE:CD2	0.52	2.83	18	5
2:A:201:HEC:C1A	2:A:201:HEC:CGA	0.52	2.88	20	3
1:A:31:PHE:C	1:A:31:PHE:CD1	0.52	2.83	17	2
2:A:201:HEC:HMC1	2:A:201:HEC:HBC3	0.52	1.81	15	10
1:A:81:ALA:C	1:A:82:PHE:CD1	0.52	2.83	13	3
1:A:61:GLY:CA	1:A:63:ARG:NH1	0.51	2.74	2	5
1:A:88:PRO:CG	1:A:91:ASP:CG	0.51	2.79	7	15
1:A:103:PHE:N	1:A:103:PHE:CD1	0.51	2.78	14	7
1:A:57:ARG:NE	2:A:201:HEC:HMA3	0.51	2.21	6	1
2:A:201:HEC:O1A	2:A:201:HEC:HMA2	0.50	2.05	18	1
2:A:201:HEC:CGA	2:A:201:HEC:C1A	0.50	2.89	13	1
1:A:47:HIS:ND1	2:A:201:HEC:CGD	0.49	2.75	11	1
1:A:103:PHE:CD1	1:A:103:PHE:N	0.49	2.80	4	9
1:A:54:ARG:O	1:A:58:GLU:N	0.49	2.44	14	18
2:A:201:HEC:C3D	2:A:201:HEC:O1D	0.49	2.60	4	1
2:A:201:HEC:O1A	2:A:201:HEC:C2A	0.49	2.57	18	2
2:A:201:HEC:HBB3	2:A:201:HEC:HMB1	0.49	1.82	17	11
2:A:201:HEC:HMB1	2:A:201:HEC:HBB3	0.49	1.83	9	9
1:A:57:ARG:NH1	1:A:103:PHE:CD1	0.49	2.81	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:201:HEC:C3D	2:A:201:HEC:O2D	0.49	2.61	17	1
2:A:201:HEC:O2A	2:A:201:HEC:C3A	0.48	2.61	10	2
2:A:201:HEC:C2A	2:A:201:HEC:O1A	0.48	2.61	4	1
1:A:58:GLU:C	1:A:58:GLU:CD	0.48	2.72	12	2
1:A:91:ASP:O	1:A:94:LYS:CG	0.48	2.61	7	8
1:A:88:PRO:O	1:A:91:ASP:N	0.48	2.47	16	11
1:A:31:PHE:CD1	1:A:98:TYR:CE2	0.47	3.02	15	2
1:A:66:ARG:O	1:A:67:ASP:C	0.47	2.53	11	20
1:A:57:ARG:NH2	2:A:201:HEC:CAA	0.47	2.78	4	1
1:A:63:ARG:CG	1:A:63:ARG:O	0.47	2.63	13	1
1:A:70:ALA:O	1:A:73:ARG:CB	0.46	2.63	4	14
2:A:201:HEC:C2A	2:A:201:HEC:O2A	0.46	2.62	17	2
1:A:57:ARG:CZ	2:A:201:HEC:HBA2	0.46	2.40	20	1
1:A:56:ARG:CB	1:A:57:ARG:NH1	0.46	2.78	4	1
1:A:57:ARG:NH1	1:A:103:PHE:O	0.46	2.49	16	1
1:A:66:ARG:O	1:A:69:ALA:N	0.46	2.49	14	20
1:A:49:GLU:O	1:A:56:ARG:NH2	0.46	2.49	16	5
2:A:201:HEC:HHA	2:A:201:HEC:CGA	0.46	2.41	14	3
1:A:54:ARG:NH1	1:A:58:GLU:OE1	0.45	2.49	9	1
2:A:201:HEC:CGA	2:A:201:HEC:HHA	0.45	2.42	15	2
1:A:88:PRO:HG2	1:A:91:ASP:CB	0.45	2.41	9	12
1:A:31:PHE:O	1:A:31:PHE:CD1	0.45	2.69	5	2
1:A:28:GLY:O	1:A:32:ALA:N	0.45	2.49	2	6
1:A:31:PHE:CG	1:A:98:TYR:CD1	0.45	3.05	6	1
1:A:35:CYS:C	1:A:37:GLY:N	0.45	2.70	14	8
1:A:28:GLY:CA	1:A:98:TYR:CD1	0.45	3.00	10	1
2:A:201:HEC:HMD1	2:A:201:HEC:O1D	0.45	2.12	11	1
1:A:31:PHE:O	1:A:36:ALA:N	0.44	2.50	14	4
1:A:38:CYS:CB	2:A:201:HEC:C2C	0.44	2.95	20	19
1:A:58:GLU:HG3	1:A:59:ALA:N	0.44	2.28	12	3
1:A:70:ALA:O	1:A:73:ARG:N	0.44	2.49	15	3
1:A:35:CYS:O	1:A:36:ALA:C	0.44	2.56	15	19
1:A:102:SER:OG	1:A:103:PHE:CD1	0.43	2.71	16	1
1:A:38:CYS:C	1:A:40:PRO:HD3	0.43	2.34	14	20
1:A:50:LYS:O	2:A:201:HEC:CGA	0.43	2.66	15	1
1:A:38:CYS:C	1:A:40:PRO:CD	0.43	2.86	14	20
2:A:201:HEC:CHA	2:A:201:HEC:O2A	0.43	2.66	20	1
1:A:35:CYS:O	1:A:37:GLY:N	0.43	2.51	13	6
1:A:39:HIS:N	1:A:40:PRO:CD	0.43	2.82	14	19
1:A:58:GLU:O	1:A:61:GLY:N	0.43	2.52	9	1
1:A:57:ARG:HH21	2:A:201:HEC:HMA3	0.42	1.74	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:79:MET:HG3	2:A:201:HEC:C4C	0.42	2.44	17	9
1:A:61:GLY:C	1:A:63:ARG:NH1	0.42	2.70	17	1
2:A:201:HEC:HMA2	2:A:201:HEC:O1A	0.42	2.14	1	1
2:A:201:HEC:O1A	2:A:201:HEC:CMA	0.42	2.68	18	1
1:A:31:PHE:CG	1:A:98:TYR:CD2	0.41	3.08	3	2
1:A:54:ARG:C	1:A:56:ARG:N	0.41	2.71	8	1
1:A:54:ARG:O	1:A:55:ALA:C	0.41	2.59	12	3
1:A:57:ARG:O	1:A:61:GLY:CA	0.41	2.69	7	1
1:A:61:GLY:CA	1:A:63:ARG:HH11	0.41	2.29	2	1
1:A:50:LYS:O	2:A:201:HEC:O2A	0.40	2.39	15	1
1:A:40:PRO:O	1:A:43:GLY:N	0.40	2.52	9	1

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	114/80 (142%)	79±2 (69±1%)	26±2 (23±2%)	9±1 (8±1%)	2	13
All	All	2280/1600 (142%)	1579 (69%)	514 (23%)	187 (8%)	2	13

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

Mol	Chain	Res	Type	Models (Total)
1	A	33[1]	THR	20
1	A	33[2]	THR	20
1	A	80	PRO	20
1	A	33[3]	THR	20
1	A	69	ALA	20
1	A	38	CYS	20
1	A	68[1]	VAL	15
1	A	68[2]	VAL	15
1	A	68[3]	VAL	15
1	A	102	SER	14
1	A	26	GLY	4

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Mol	Chain	Res	Type	Models (Total)
1	A	100[2]	VAL	1
1	A	100[3]	VAL	1
1	A	103	PHE	1
1	A	100[1]	VAL	1

6.3.2 Protein sidechains ⓘ

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	92/56 (164%)	82±2 (89±2%)	10±2 (11±2%)	10	55
All	All	1840/1120 (164%)	1645 (89%)	195 (11%)	10	55

All 27 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	103	PHE	20
1	A	94	LYS	20
1	A	38	CYS	20
1	A	63	ARG	18
1	A	57	ARG	14
1	A	56	ARG	14
1	A	102	SER	9
1	A	71	TYR	9
1	A	73	ARG	9
1	A	84	GLU	9
1	A	54	ARG	6
1	A	41[1]	GLN	5
1	A	41[2]	GLN	5
1	A	50	LYS	5
1	A	74[2]	ASN	5
1	A	74[1]	ASN	5
1	A	66	ARG	4
1	A	58	GLU	3
1	A	29	GLU	2
1	A	67	ASP	2
1	A	60[1]	ASN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	86	MET	2
1	A	60[2]	ASN	2
1	A	49	GLU	2
1	A	33[1]	THR	1
1	A	33[2]	THR	1
1	A	33[3]	THR	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

LIGAND-GEOMETRY INFOmissingINFO

6.6 Other polymers ⓘ

There are no such molecules in this entry.

6.7 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 52% for the well-defined parts and 52% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *OmcF_pH7.str*

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	592
Number of shifts mapped to atoms	572
Number of unparsed shifts	0
Number of shifts with mapping errors	20
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	19

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. All 20 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	238	HEC	QT2	1.141	0.003	1
A	238	HEC	QM8	3.024	0.004	1
A	238	HEC	HT2A	5.479	0.003	1
A	238	HEC	HB62	2.887	0.01	1
A	238	HEC	HB72	2.014	0.004	1
A	238	HEC	HB73	3.119	0.002	1
A	238	HEC	QM3	4.074	0.003	1
A	238	HEC	QM5	3.197	0.004	1
A	238	HEC	HA72	2.693	0.002	1
A	238	HEC	HB63	3.241	0.004	1
A	238	HEC	HA73	4.114	0.003	1
A	238	HEC	HDM	9.334	0.003	1
A	238	HEC	QT4	2.5	0.002	1
A	238	HEC	HAM	10.097	0.003	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	238	HEC	HA63	4.446	0.002	1
A	238	HEC	HBM	9.417	0.002	1
A	238	HEC	HA62	4.152	0.004	1
A	238	HEC	HGM	9.588	0.002	1
A	238	HEC	QM1	3.638	0.002	1
A	238	HEC	HT4A	6.195	0.003	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	69	1.29 ± 0.18	Should be applied

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 52%, i.e. 467 atoms were assigned a chemical shift out of a possible 905. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	217/379 (57%)	149/150 (99%)	0/158 (0%)	68/71 (96%)
Sidechain	230/462 (50%)	226/274 (82%)	0/164 (0%)	4/24 (17%)
Aromatic	20/64 (31%)	20/35 (57%)	0/26 (0%)	0/3 (0%)
Overall	467/905 (52%)	395/459 (86%)	0/348 (0%)	72/98 (73%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 52%, i.e. 471 atoms were assigned a chemical shift out of a possible 912. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	220/384 (57%)	151/152 (99%)	0/160 (0%)	69/72 (96%)
Sidechain	231/464 (50%)	227/275 (83%)	0/165 (0%)	4/24 (17%)
Aromatic	20/64 (31%)	20/35 (57%)	0/26 (0%)	0/3 (0%)
Overall	471/912 (52%)	398/462 (86%)	0/351 (0%)	73/99 (74%)

7.1.4 Statistically unusual chemical shifts ⓘ

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, <i>ppm</i>	Expected range, <i>ppm</i>	Z-score
1	A	79	MET	HG3	-3.29	4.30 – 0.50	-15.0
1	A	79	MET	HB2	-2.99	3.73 – 0.33	-14.8
1	A	39	HIS	HD2	0.52	9.28 – 4.78	-14.5
1	A	39	HIS	HE1	1.15	10.53 – 5.43	-13.4
1	A	79	MET	HG2	-1.25	4.23 – 0.63	-10.2
1	A	79	MET	HE2	-2.85	4.28 – -0.52	-9.8
1	A	79	MET	HE3	-2.85	4.28 – -0.52	-9.8
1	A	79	MET	HE1	-2.85	4.28 – -0.52	-9.8
1	A	102	SER	HB3	1.59	5.25 – 2.45	-8.1
1	A	79	MET	HB3	-0.52	3.70 – 0.30	-7.4
1	A	52	LEU	HD22	-1.07	2.14 – -0.66	-6.5
1	A	52	LEU	HD21	-1.07	2.14 – -0.66	-6.5
1	A	52	LEU	HD23	-1.07	2.14 – -0.66	-6.5
1	A	75	PRO	HB3	-0.28	3.81 – 0.21	-6.4
1	A	102	SER	HB2	2.27	5.18 – 2.58	-6.2
1	A	39	HIS	HB2	1.00	4.91 – 1.31	-5.9
1	A	75	PRO	HB2	0.04	3.82 – 0.32	-5.8
1	A	42	GLY	HA3	1.76	5.80 – 2.00	-5.6
1	A	38	CYS	HB2	0.63	5.20 – 0.70	-5.2

7.1.5 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 A:

