

Full wwPDB NMR Structure Validation Report (i)

Apr 16, 2023 – 07:45 AM EDT

PDB ID : 7XGA BMRB ID : 36483

Title: NMR strucutre of chimeric protein for model of PHD-Stella complex

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Deposited on : 2022-04-04

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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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)

wwPDB-RCI : v 1n 11 5 13 A (Berjanski et al., 2005)

PANAV : Wang et al. (2010)

wwPDB-ShiftChecker : v1.2

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

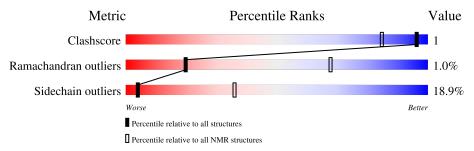
Validation Pipeline (wwPDB-VP) : 2.32.2

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 83%.

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 $(\# \mathrm{Entries})$	$egin{array}{c} { m NMR \ archive} \ (\#{ m Entries}) \end{array}$	
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	126	55%	13%	•	30%	



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 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 mod					
1	A:11-A:71, A:87-A:113 (88)	0.34	13		

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 3 clusters. No single-model clusters were found.

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



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2015 atoms, of which 999 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-associated protein 3.

Mol	Chain	Residues		Atoms			Trace		
1	Λ	196	Total	С	Н	N	О	S	0
1	A	126	2012	625	999	191	184	13	U

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q8VDF2
A	2	PRO	-	expression tag	_
A	3	LEU	-	expression tag	UNP Q8VDF2
A	4	GLY	-	expression tag	UNP Q8VDF2
A	5	SER	-	expression tag	UNP Q8VDF2

• Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms
9	Λ	9	Total Zn
2	A	9	3 3



4 Residue-property plots (i)

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.

• Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3

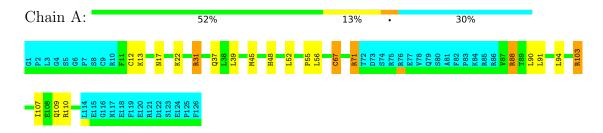


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

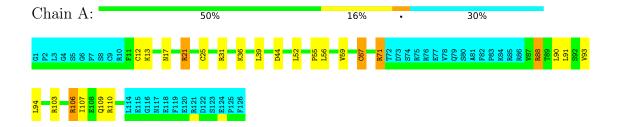
4.2.1 Score per residue for model 1

• Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3



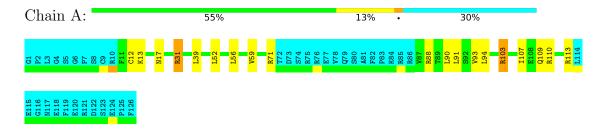
4.2.2 Score per residue for model 2





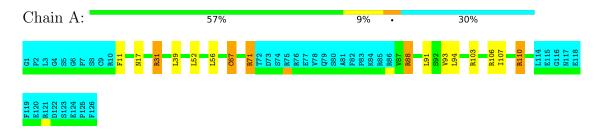
4.2.3 Score per residue for model 3

 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3

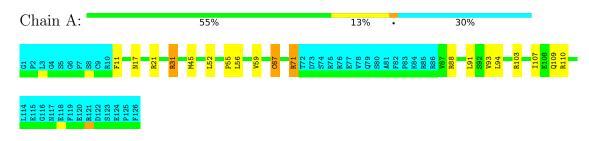


4.2.4 Score per residue for model 4

 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3



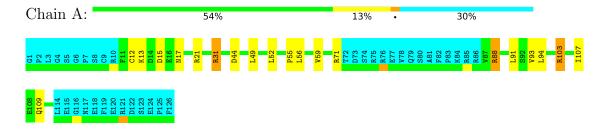
4.2.5 Score per residue for model 5





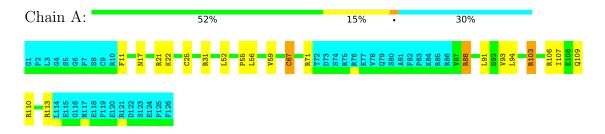
4.2.6 Score per residue for model 6

• Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3



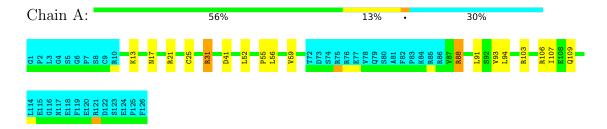
4.2.7 Score per residue for model 7

 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3



4.2.8 Score per residue for model 8

 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3



4.2.9 Score per residue for model 9

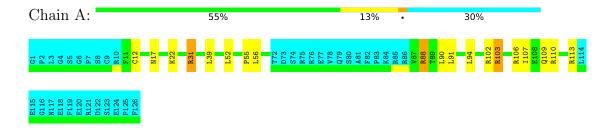






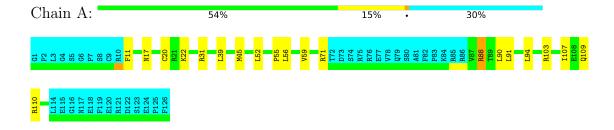
4.2.10 Score per residue for model 10

 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3

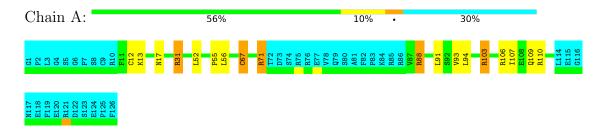


4.2.11 Score per residue for model 11

 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3



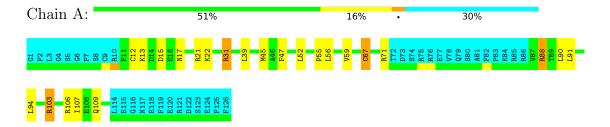
4.2.12 Score per residue for model 12





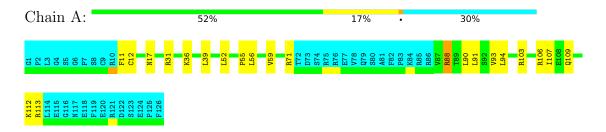
4.2.13 Score per residue for model 13 (medoid)

 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3



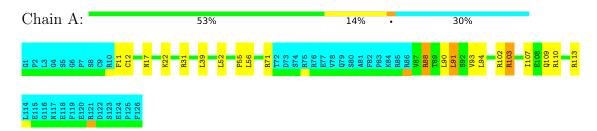
4.2.14 Score per residue for model 14

• Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3



4.2.15 Score per residue for model 15

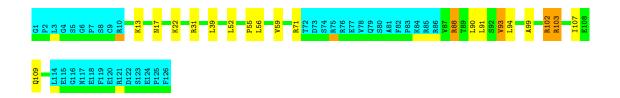
 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3



4.2.16 Score per residue for model 16

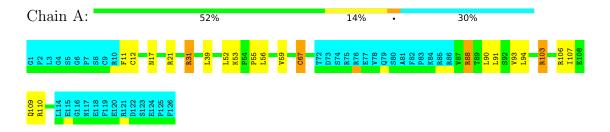






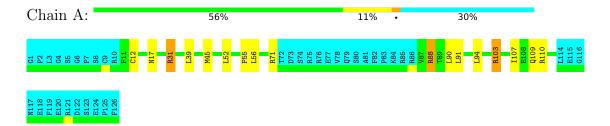
4.2.17 Score per residue for model 17

 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3

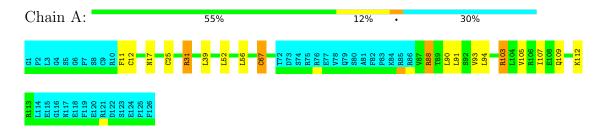


4.2.18 Score per residue for model 18

 \bullet Molecule 1: Chimera of E3 ubiquitin-protein ligase UHRF1 and Developmental pluripotency-as sociated protein 3

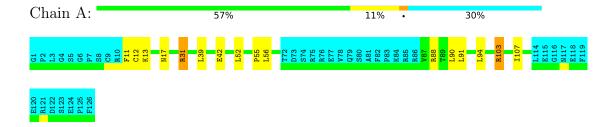


4.2.19 Score per residue for model 19





4.2.20 Score per residue for model 20





Refinement protocol and experimental data overview (i) 5



The models were refined using the following method: molecular dynamics.

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
CYANA	structure calculation	3.98
Amber	refinement	12

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	1
Total number of shifts	1361
Number of shifts mapped to atoms	1361
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%



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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain Dag I		Sond lengths	Bond angles	
MIOI	Chain	RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.71 ± 0.01	$0\pm0/728~(~0.0\pm~0.0\%)$	1.16 ± 0.02	$5\pm1/982~(~0.5\pm~0.1\%)$
All	All	0.71	0/14560 (0.0%)	1.16	99/19640 (0.5%)

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Mol Chain R		Type	Atoma	\mathbf{z}	Observed(0)	Ideal(0)	Models	
MIOI	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}(^{o})$	Worst	Total
1	A	88	ARG	NE-CZ-NH1	9.37	124.99	120.30	19	17
1	A	71	ARG	NE-CZ-NH1	8.79	124.70	120.30	3	12
1	A	110	ARG	NE-CZ-NH1	8.44	124.52	120.30	4	12
1	A	113	ARG	NE-CZ-NH1	7.42	124.01	120.30	14	6
1	A	103	ARG	NE-CZ-NH1	7.16	123.88	120.30	18	15
1	A	67	CYS	CA-CB-SG	7.03	126.65	114.00	13	9
1	A	88	ARG	CD-NE-CZ	6.72	133.01	123.60	19	1
1	A	21	ARG	NE-CZ-NH1	5.83	123.22	120.30	17	6
1	A	102	ARG	NE-CZ-NH1	5.82	123.21	120.30	10	2
1	A	106	ARG	NE-CZ-NH1	5.67	123.13	120.30	10	2
1	A	31	ARG	NE-CZ-NH1	5.37	122.99	120.30	6	14
1	A	12	CYS	N-CA-CB	-5.35	100.96	110.60	18	1
1	A	113	ARG	NE-CZ-NH2	-5.18	117.71	120.30	14	1
1	A	103	ARG	NE-CZ-NH2	-5.18	117.71	120.30	16	1

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.

Mo	l Chain	Non-H	H(model)	H(added)	Clashes
1	A	711	715	715	1±1
All	All	14280	14300	14300	24

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 1.

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

Atom-1	Atom-2	Clash(Å)	$Distance(\mathring{A})$	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:39:LEU:HD21	1:A:90:LEU:HD12	0.68	1.63	2	9
1:A:39:LEU:HD21	1:A:90:LEU:HD11	0.47	1.85	16	5
1:A:105:VAL:HG12	1:A:109:GLN:NE2	0.45	2.26	19	1
1:A:39:LEU:HD21	1:A:90:LEU:CD1	0.45	2.42	19	5
1:A:22:LYS:HE3	1:A:45:MET:SD	0.43	2.54	11	1
1:A:37:GLN:CG	1:A:48:HIS:CD2	0.41	3.03	1	1
1:A:91:LEU:H	1:A:91:LEU:HD23	0.40	1.76	15	1
1:A:93:VAL:HG22	1:A:99:ALA:HB1	0.40	1.92	16	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	Perce	ntiles
1	A	88/126 (70%)	78±1 (88±2%)	9±1 (11±2%)	1±0 (1±0%)	20	68
All	All	1760/2520 (70%)	1556 (88%)	187 (11%)	17 (1%)	20	68

All 2 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	55	PRO	16
1	A	56	LEU	1

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	82/115 (71%)	66±3 (81±3%)	16±3 (19±3%)	4 36
All	All	1640/2300 (71%)	1330 (81%)	310 (19%)	4 36

All 35 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	17	ASN	20
1	A	31	ARG	20
1	A	52	LEU	20
1	A	88	ARG	20
1	A	91	LEU	20
1	A	94	LEU	20
1	A	107	ILE	20
1	A	56	LEU	19
1	A	103	ARG	19
1	A	109	GLN	17
1	A	12	CYS	13
1	A	93	VAL	13
1	A	59	VAL	11
1	A	11	PHE	10
1	A	13	LYS	9
1	A	67	CYS	9
1	A	106	ARG	8
1	A	71	ARG	7
1	A	22	LYS	6
1	A	45	MET	4
1	A	25	CYS	4
1	A	21	ARG	3
1	A	36	LYS	2
1	A	44	ASP	2

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Mol	Chain	Res	Type	Models (Total)
1	A	15	ASP	2
1	A	112	LYS	2
1	A	102	ARG	2
1	A	39	LEU	1
1	A	110	ARG	1
1	A	49	LEU	1
1	A	41	ASP	1
1	A	20	CYS	1
1	A	47	PHE	1
1	A	53	LYS	1
1	A	42	GLU	1

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 3 ligands modelled in this entry, 3 are 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 83% for the well-defined parts and 78% for the entire structure.

7.1 Chemical shift list 1

File name: working cs.cif

Chemical shift list name: PHD_Ste_stereo2.str

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	1361
Number of shifts mapped to atoms	1361
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	${\rm Correction} \pm {\rm precision}, ppm$	Suggested action
$^{13}\mathrm{C}_{\alpha}$	124	-0.13 ± 0.17	None needed ($< 0.5 \text{ ppm}$)
$^{13}C_{\beta}$	119	0.20 ± 0.17	None needed ($< 0.5 \text{ ppm}$)
¹³ C′	120	0.05 ± 0.08	None needed ($< 0.5 \text{ ppm}$)
^{15}N	112	-0.72 ± 0.32	Should be applied

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 83%, i.e. 1025 atoms were assigned a chemical shift out of a possible 1242. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}{ m H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Backbone	$419/424 \ (99\%)$	168/169 (99%)	172/176 (98%)	79/79 (100%)
Sidechain	554/754 (73%)	364/485 (75%)	182/230 (79%)	8/39 (21%)

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	Total	$^{1}{ m H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Aromatic	52/64 (81%)	25/32~(78%)	25/29~(86%)	2/3~(67%)
Overall	1025/1242 (83%)	557/686 (81%)	379/435 (87%)	89/121 (74%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 1360 atoms were assigned a chemical shift out of a possible 1748. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}{ m H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Backbone	596/610 (98%)	240/245 (98%)	$244/252 \ (97\%)$	112/113 (99%)
Sidechain	704/1044 (67%)	458/667 (69%)	237/317 (75%)	9/60 (15%)
Aromatic	60/94 (64%)	29/47 (62%)	29/44~(66%)	2/3 (67%)
Overall	1360/1748 (78%)	727/959 (76%)	510/613 (83%)	123/176 (70%)

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

