



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2014 – 09:50 PM EDT

PDB ID : 4PW5
Title : structure of UHRF2-SRA in complex with a 5hmC-containing DNA, complex I
Authors : ZHou, T.; Xiong, J.; Wang, M.; Yang, N.; Wong, J.; Zhu, B.; Xu, R.M.
Deposited on : 2014-03-18
Resolution : 2.20 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

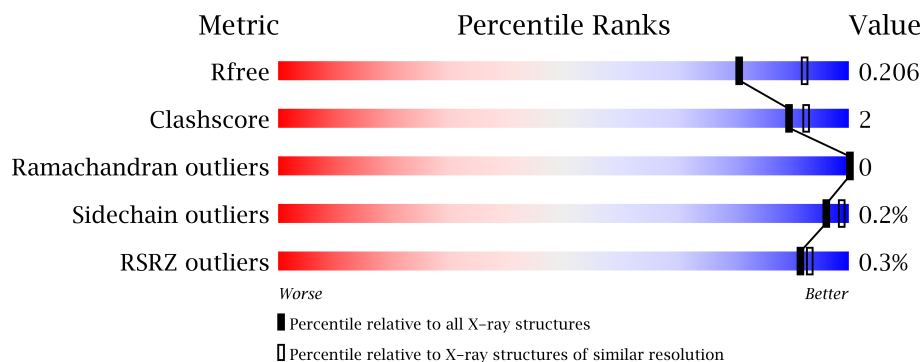
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : **FAILED**
Xtriage (Phenix) : dev-1439
EDS : stable23161
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23161

1 Overall quality at a glance

The reported resolution of this entry is 2.20 Å.

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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	230	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	B	230	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	E	230	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	F	230	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
2	C	12	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
2	G	12	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
3	D	12	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
3	H	12	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7619 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called E3 ubiquitin-protein ligase UHRF2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	189	Total	C	N	O	S	0	7	0
			1525	965	282	275	3			
1	B	188	Total	C	N	O	S	0	8	0
			1526	965	283	275	3			
1	E	188	Total	C	N	O	S	5	6	0
			1514	955	281	275	3			
1	F	187	Total	C	N	O	S	5	5	0
			1501	950	277	271	3			

- Molecule 2 is a DNA chain called 5hmC-containing DNA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	12	Total	C	N	O	P	0	0	0
			250	118	45	75	12			
2	G	12	Total	C	N	O	P	0	0	0
			250	118	45	75	12			

- Molecule 3 is a DNA chain called 5hmC-containing DNA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	11	Total	C	N	O	P	0	0	0
			222	105	42	64	11			
3	H	11	Total	C	N	O	P	0	0	0
			222	105	42	64	11			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	144	Total	O	0	0
			144	144		
4	B	110	Total	O	0	0
			110	110		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	35	Total 35	O 35	0	0
4	D	18	Total 18	O 18	0	0
4	E	106	Total 106	O 106	0	0
4	F	152	Total 152	O 152	0	0
4	G	31	Total 31	O 31	0	0
4	H	13	Total 13	O 13	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: E3 ubiquitin-protein ligase UHRF2

Chain A: 



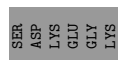
- Molecule 1: E3 ubiquitin-protein ligase UHRF2

Chain B: 



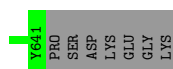
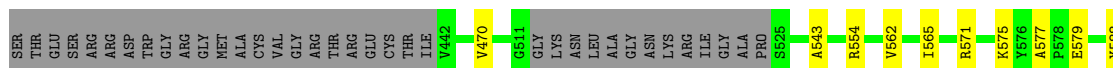
- Molecule 1: E3 ubiquitin-protein ligase UHRF2

Chain E: 



- Molecule 1: E3 ubiquitin-protein ligase UHRF2

Chain F: 



- Molecule 2: 5hmC-containing DNA1

Chain C: 



- Molecule 2: 5hmC-containing DNA1

Chain G: 

There are no outlier residues recorded for this chain.

- Molecule 3: 5hmC-containing DNA2

Chain D: 



- Molecule 3: 5hmC-containing DNA2

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.27Å 82.81Å 82.86Å 90.05° 90.00° 89.98°	Depositor
Resolution (Å)	41.43 – 2.20 42.27 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.2 (41.43-2.20) 96.2 (42.27-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4.1491)	Depositor
R, R_{free}	0.161 , 0.206 0.162 , 0.206	Depositor DCC
R_{free} test set	2740 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	28.8	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 33.4	EDS
Estimated twinning fraction	0.438 for h,l,-k 0.438 for h,-l,k 0.447 for h,-k,-l 0.037 for -h,k,-l 0.036 for -h,-k,l 0.037 for -h,l,k 0.037 for -h,-l,-k	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 54600 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7619	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5HC

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 root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.33	0/1586	0.48	0/2148
1	B	0.32	0/1591	0.48	0/2155
1	E	0.31	0/1570	0.48	0/2127
1	F	0.31	0/1556	0.47	0/2108
2	C	0.72	0/255	1.03	1/390 (0.3%)
2	G	0.70	0/255	0.99	0/390
3	D	0.70	0/248	0.89	0/379
3	H	0.66	0/248	0.86	0/379
All	All	0.39	0/7309	0.57	1/10076 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	12	DG	O4'-C1'-N9	5.63	111.94	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1525	0	1507	3	0
1	B	1526	0	1505	5	0
1	E	1514	0	1478	6	0
1	F	1501	0	1478	7	0
2	C	250	0	137	2	0
2	G	250	0	137	0	0
3	D	222	0	123	4	0
3	H	222	0	123	1	0
4	A	144	0	0	2	0
4	B	110	0	0	1	0
4	C	35	0	0	0	0
4	D	18	0	0	0	0
4	E	106	0	0	2	0
4	F	152	0	0	0	0
4	G	31	0	0	0	0
4	H	13	0	0	0	0
All	All	7619	0	6488	26	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (26) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:12:DG:O6	3:D:2:DC:N4	2.08	0.84
1:F:571:ARG:HD2	1:F:577:ALA:HB3	1.64	0.80
1:F:571:ARG:NH2	1:F:579:GLU:OE2	2.25	0.70
1:E:470:VAL:HG12	1:E:565:ILE:HD11	1.79	0.62
1:E:442:VAL:N	4:E:720:HOH:O	2.33	0.61
1:F:470:VAL:HG12	1:F:565:ILE:HD11	1.81	0.61
3:D:6:DC:H2''	3:D:7:DG:H5''	1.84	0.59
1:B:571:ARG:HD3	1:B:577:ALA:HB3	1.86	0.57
1:A:470:VAL:HG12	1:A:565:ILE:HD11	1.88	0.56
1:B:470:VAL:HG12	1:B:565:ILE:HD11	1.89	0.54
2:C:12:DG:N1	3:D:2:DC:N3	2.49	0.53
1:F:562[B]:VAL:HG22	1:F:588:TYR:O	2.13	0.48
1:E:466[A]:SER:OG	1:E:472:ARG:O	2.25	0.47
1:B:491[B]:LEU:HD11	4:B:714:HOH:O	2.15	0.47
1:E:504:GLU:OE2	1:E:611:ARG:NE	2.38	0.46
1:F:543:ALA:HA	1:F:554:ARG:HH21	1.79	0.46
3:H:6:DC:H2''	3:H:7:DG:O4'	2.16	0.45
1:A:511:GLY:HA3	4:A:717:HOH:O	2.16	0.44
1:B:638:PRO:HD2	1:B:641:TYR:HB3	2.00	0.43
1:A:472:ARG:HB2	1:A:473:PRO:HD3	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:704:HOH:O	1:F:575[A]:LYS:HG2	2.18	0.43
1:F:565:ILE:N	1:F:565:ILE:HD12	2.34	0.42
3:D:7:DG:H2'	3:D:8:DG:C8	2.55	0.41
1:E:477:GLY:O	1:E:489:LEU:HA	2.20	0.41
1:B:565:ILE:N	1:B:565:ILE:HD12	2.37	0.40
1:E:557:ARG:NH2	4:E:795:HOH:O	2.42	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. 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	192/230 (84%)	187 (97%)	5 (3%)	0	100	100
1	B	192/230 (84%)	188 (98%)	4 (2%)	0	100	100
1	E	190/230 (83%)	183 (96%)	7 (4%)	0	100	100
1	F	188/230 (82%)	183 (97%)	5 (3%)	0	100	100
All	All	762/920 (83%)	741 (97%)	21 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 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 X-ray entries followed by that with respect to entries of similar resolution. 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	161/186 (87%)	161 (100%)	0	100	100
1	B	162/186 (87%)	161 (99%)	1 (1%)	92	97
1	E	159/186 (86%)	159 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	158/186 (85%)	158 (100%)	0	100	100
All	All	640/744 (86%)	639 (100%)	1 (0%)	96	99

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	641	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	601	HIS
1	E	601	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

Mogul failed to run properly - this section will therefore be empty.

5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	189/230 (82%)	-0.56	0 100 100	18, 26, 44, 68	0
1	B	188/230 (81%)	-0.55	2 (1%) 77 78	18, 26, 46, 67	0
1	E	188/230 (81%)	-0.55	0 100 100	19, 26, 46, 63	1 (0%)
1	F	187/230 (81%)	-0.57	0 100 100	17, 27, 44, 69	1 (0%)
2	C	11/12 (91%)	-0.65	0 100 100	32, 35, 44, 44	0
2	G	11/12 (91%)	-0.69	0 100 100	33, 36, 45, 46	0
3	D	11/12 (91%)	-0.70	0 100 100	35, 42, 56, 68	0
3	H	11/12 (91%)	-0.61	0 100 100	37, 42, 58, 72	0
All	All	796/968 (82%)	-0.57	2 (0%) 91 93	17, 27, 47, 72	2 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	441	ILE	3.1
1	B	641	TYR	2.4

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	5HC	C	7	21/22	0.11	0.54	21,26,38,41	0
2	5HC	G	7	21/22	0.08	-1.02	21,29,39,41	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.