wwPDB X-ray Structure Validation Summary Report (i)

May 25, 2020 – 11:06 pm BST

PDB ID	:	5LP8
Title	:	Crystal structure of an asymmetric dimer of the ubiquitin ligase HUWE1
Authors	:	Sander, B.; Lorenz, S.G.
Deposited on	:	2016-08-12
Resolution	:	2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/XrayValidationReportHelp
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:

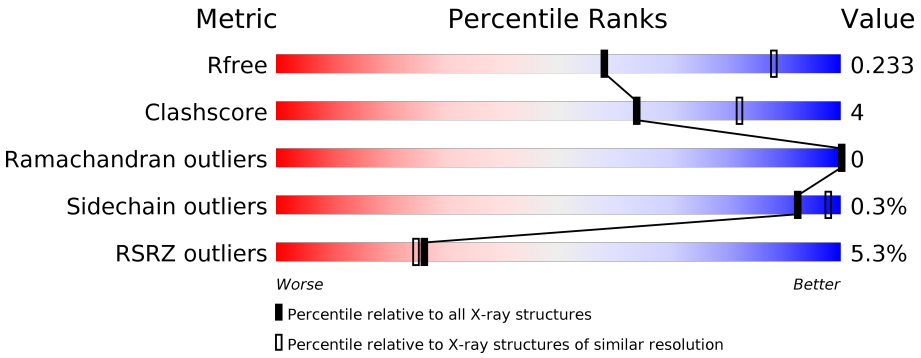
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

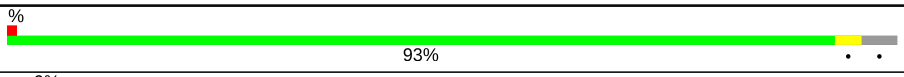
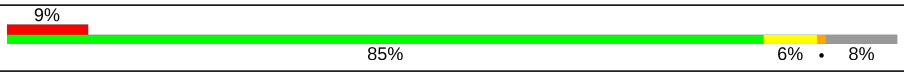
The reported resolution of this entry is 2.70 Å.

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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 respectively. 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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	450	
1	B	450	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 13785 atoms, of which 6770 are hydrogens and 0 are deuteriums.

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 HUWE1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	416	Total	C	H	N	O	S	0	0	0
			6693	2170	3285	593	629	16			
1	A	432	Total	C	H	N	O	S	0	0	0
			7060	2280	3485	616	663	16			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	3925	MET	-	initiating methionine	UNP Q7Z6Z7
B	3926	LYS	-	expression tag	UNP Q7Z6Z7
B	3927	HIS	-	expression tag	UNP Q7Z6Z7
B	3928	HIS	-	expression tag	UNP Q7Z6Z7
B	3929	HIS	-	expression tag	UNP Q7Z6Z7
B	3930	HIS	-	expression tag	UNP Q7Z6Z7
B	3931	HIS	-	expression tag	UNP Q7Z6Z7
B	3932	HIS	-	expression tag	UNP Q7Z6Z7
B	3933	PRO	-	expression tag	UNP Q7Z6Z7
B	3934	MET	-	expression tag	UNP Q7Z6Z7
B	3935	SER	-	expression tag	UNP Q7Z6Z7
B	3936	ASP	-	expression tag	UNP Q7Z6Z7
B	3937	TYR	-	expression tag	UNP Q7Z6Z7
B	3938	ASP	-	expression tag	UNP Q7Z6Z7
B	3939	ILE	-	expression tag	UNP Q7Z6Z7
B	3940	PRO	-	expression tag	UNP Q7Z6Z7
B	3941	THR	-	expression tag	UNP Q7Z6Z7
B	3942	THR	-	expression tag	UNP Q7Z6Z7
B	3943	GLU	-	expression tag	UNP Q7Z6Z7
B	3944	ASN	-	expression tag	UNP Q7Z6Z7
B	3945	LEU	-	expression tag	UNP Q7Z6Z7
B	3946	TYR	-	expression tag	UNP Q7Z6Z7
B	3947	PHE	-	expression tag	UNP Q7Z6Z7
B	3948	GLN	-	expression tag	UNP Q7Z6Z7
B	3949	GLY	-	expression tag	UNP Q7Z6Z7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	3950	ALA	-	expression tag	UNP Q7Z6Z7
A	3925	MET	-	initiating methionine	UNP Q7Z6Z7
A	3926	LYS	-	expression tag	UNP Q7Z6Z7
A	3927	HIS	-	expression tag	UNP Q7Z6Z7
A	3928	HIS	-	expression tag	UNP Q7Z6Z7
A	3929	HIS	-	expression tag	UNP Q7Z6Z7
A	3930	HIS	-	expression tag	UNP Q7Z6Z7
A	3931	HIS	-	expression tag	UNP Q7Z6Z7
A	3932	HIS	-	expression tag	UNP Q7Z6Z7
A	3933	PRO	-	expression tag	UNP Q7Z6Z7
A	3934	MET	-	expression tag	UNP Q7Z6Z7
A	3935	SER	-	expression tag	UNP Q7Z6Z7
A	3936	ASP	-	expression tag	UNP Q7Z6Z7
A	3937	TYR	-	expression tag	UNP Q7Z6Z7
A	3938	ASP	-	expression tag	UNP Q7Z6Z7
A	3939	ILE	-	expression tag	UNP Q7Z6Z7
A	3940	PRO	-	expression tag	UNP Q7Z6Z7
A	3941	THR	-	expression tag	UNP Q7Z6Z7
A	3942	THR	-	expression tag	UNP Q7Z6Z7
A	3943	GLU	-	expression tag	UNP Q7Z6Z7
A	3944	ASN	-	expression tag	UNP Q7Z6Z7
A	3945	LEU	-	expression tag	UNP Q7Z6Z7
A	3946	TYR	-	expression tag	UNP Q7Z6Z7
A	3947	PHE	-	expression tag	UNP Q7Z6Z7
A	3948	GLN	-	expression tag	UNP Q7Z6Z7
A	3949	GLY	-	expression tag	UNP Q7Z6Z7
A	3950	ALA	-	expression tag	UNP Q7Z6Z7

- Molecule 2 is water.

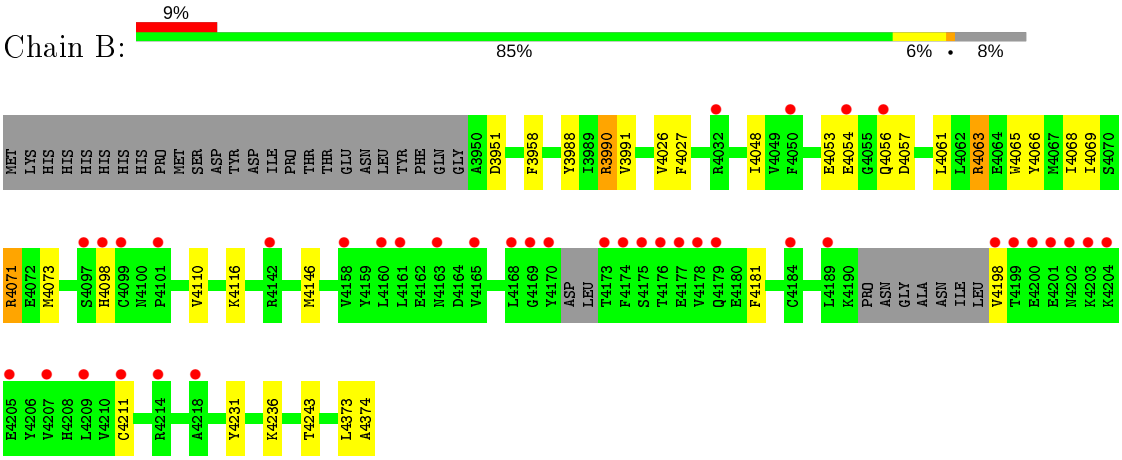
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total O 2 2	0	0
2	A	30	Total O 30 30	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

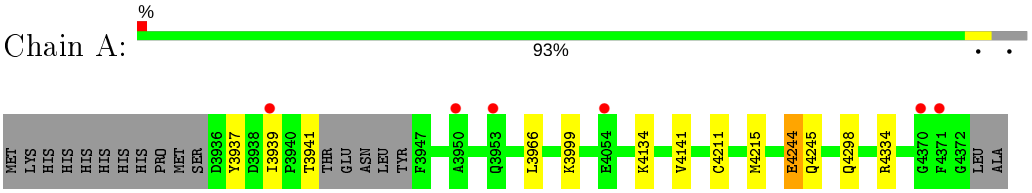
- Molecule 1: E3 ubiquitin-protein ligase HUWE1

Chain B:



- Molecule 1: E3 ubiquitin-protein ligase HUWE1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α, β, γ	177.46Å 177.46Å 106.26Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.15 – 2.70 46.15 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (46.15-2.70) 99.3 (46.15-2.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.25 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.194 , 0.225 0.206 , 0.233	Depositor DCC
R_{free} test set	2551 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	55.3	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 41.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.035 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	13785	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.34	0/3657	0.48	0/4933
1	B	0.50	6/3483 (0.2%)	0.53	0/4695
All	All	0.42	6/7140 (0.1%)	0.50	0/9628

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	3990	ARG	CZ-NH2	7.13	1.42	1.33
1	B	4063	ARG	CZ-NH2	7.05	1.42	1.33
1	B	4071	ARG	CZ-NH2	6.97	1.42	1.33
1	B	3990	ARG	CZ-NH1	6.95	1.42	1.33
1	B	4071	ARG	CZ-NH1	6.85	1.42	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3575	3485	3484	14	0
1	B	3408	3285	3296	47	0
2	A	30	0	0	0	0
2	B	2	0	0	0	0
All	All	7015	6770	6780	58	0

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 4.

The worst 5 of 58 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4027:PHE:HD1	1:B:4069:ILE:CD1	1.45	1.29
1:B:4027:PHE:CD1	1:B:4069:ILE:HD11	1.77	1.17
1:A:3939:ILE:HD11	1:A:3966:LEU:HD23	1.28	1.14
1:B:4073:MET:CE	1:B:4110:VAL:CG2	2.26	1.13
1:B:4027:PHE:HD1	1:B:4069:ILE:HD11	1.07	1.11

There are no symmetry-related clashes.

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 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	428/450 (95%)	421 (98%)	7 (2%)	0	100	100
1	B	410/450 (91%)	398 (97%)	12 (3%)	0	100	100
All	All	838/900 (93%)	819 (98%)	19 (2%)	0	100	100

There are no Ramachandran outliers to report.

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 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	388/405 (96%)	386 (100%)	2 (0%)	88 96
1	B	362/405 (89%)	362 (100%)	0	100 100
All	All	750/810 (93%)	748 (100%)	2 (0%)	92 98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4244	GLU
1	A	4334	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 residues in this entry.

5.8 Polymer linkage issues (i)

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, 95^{th} 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	432/450 (96%)	0.16	6 (1%) 75 77	27, 52, 97, 149	0
1	B	416/450 (92%)	0.52	39 (9%) 8 6	30, 74, 133, 166	0
All	All	848/900 (94%)	0.34	45 (5%) 26 25	27, 61, 124, 166	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	4173	THR	5.4
1	B	4204	LYS	5.2
1	B	4203	LYS	5.0
1	B	4209	LEU	4.9
1	B	4168	LEU	4.8

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

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

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.