



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:04 PM GMT

PDB ID : 1NBF
Title : Crystal structure of a UBP-family deubiquitinating enzyme in isolation and in complex with ubiquitin aldehyde
Authors : Hu, M.; Li, P.; Li, M.; Li, W.; Yao, T.; Wu, J.-W.; Gu, W.; Cohen, R.E.; Shi, Y.
Deposited on : 2002-12-02
Resolution : 2.30 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
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:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

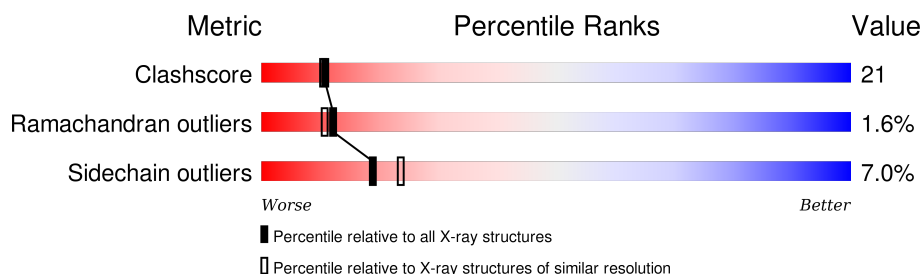
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)

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. 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 $\leq 5\%$. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	353	 66% 27% 5% ••
1	B	353	 69% 25% ••
1	E	353	 43% 47% 6% •
2	C	76	 76% 21% •
2	D	76	 72% 25% •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9976 atoms, of which 0 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 Ubiquitin carboxyl-terminal hydrolase 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	347	Total	C	N	O	S	0	0	0
			2820	1781	482	541	16			
1	B	347	Total	C	N	O	S	0	0	0
			2820	1781	482	541	16			
1	E	340	Total	C	N	O	S	0	0	0
			2760	1745	473	526	16			

- Molecule 2 is a protein called Ubiquitin aldehyde.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	76	Total	C	N	O	S	10	0	0
			601	378	105	117	1			
2	D	76	Total	C	N	O	S	10	0	0
			601	378	105	117	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	376	GLZ	GLY	MODIFIED RESIDUE	UNP P62988
D	376	GLZ	GLY	MODIFIED RESIDUE	UNP P62988

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	142	Total	O	0	0
			142	142		
3	B	139	Total	O	0	0
			139	139		
3	C	31	Total	O	0	0
			31	31		
3	D	22	Total	O	0	0
			22	22		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	40	Total	O	0	0
			40	40		



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.73 Å 101.17 Å 141.13 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.218 , 0.262	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9976	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.42	0/2880	0.71	4/3885 (0.1%)
1	B	0.42	0/2880	0.70	4/3885 (0.1%)
1	E	0.34	0/2817	0.61	2/3796 (0.1%)
2	C	0.39	0/603	0.67	0/811
2	D	0.37	0/603	0.67	0/811
All	All	0.39	0/9783	0.67	10/13188 (0.1%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	554	LYS	N-CA-C	-8.61	87.74	111.00
1	B	384	HIS	N-CA-C	-7.53	90.67	111.00
1	A	505	LEU	CA-CB-CG	6.55	130.37	115.30
1	B	382	GLY	N-CA-C	-6.51	96.83	113.10
1	E	419	ILE	N-CA-C	5.99	127.17	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 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	2820	0	2753	104	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2820	0	2753	83	0
1	E	2760	0	2706	202	0
2	C	601	0	626	15	0
2	D	601	0	626	16	0
3	A	142	0	0	7	0
3	B	139	0	0	8	0
3	C	31	0	0	2	0
3	D	22	0	0	2	0
3	E	40	0	0	13	0
All	All	9976	0	9464	402	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 21.

The worst 5 of 402 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:E:332:ILE:HB	1:E:341:SER:HB3	1.38	1.05
1:E:451:HIS:HA	1:E:470:ASN:HD21	1.27	0.96
1:A:417:GLN:HE22	1:A:461:HIS:CE1	1.83	0.95
1:E:449:ILE:HD12	1:E:524:LEU:HD11	1.45	0.95
1:A:552:ALA:C	1:A:554:LYS:H	1.70	0.94

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	345/353 (98%)	323 (94%)	18 (5%)	4 (1%)	16	16
1	B	345/353 (98%)	322 (93%)	20 (6%)	3 (1%)	21	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	336/353 (95%)	278 (83%)	46 (14%)	12 (4%)	4	2
2	C	74/76 (97%)	72 (97%)	2 (3%)	0	100	100
2	D	74/76 (97%)	73 (99%)	1 (1%)	0	100	100
All	All	1174/1211 (97%)	1068 (91%)	87 (7%)	19 (2%)	12	11

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	375	GLY
1	A	415	THR
1	B	211	THR
1	E	252	SER
1	B	375	GLY

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	314/320 (98%)	287 (91%)	27 (9%)	13	15
1	B	314/320 (98%)	290 (92%)	24 (8%)	16	20
1	E	307/320 (96%)	290 (94%)	17 (6%)	27	36
2	C	68/68 (100%)	64 (94%)	4 (6%)	24	32
2	D	68/68 (100%)	65 (96%)	3 (4%)	35	46
All	All	1071/1096 (98%)	996 (93%)	75 (7%)	19	23

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	306	ASN
1	B	402	LEU
1	E	470	ASN
1	B	316	VAL
1	B	353	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	387	GLN
2	C	360	ASN
1	E	501	HIS
1	B	529	GLN
2	D	340	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GLZ	C	376	1,2	3,3,3	2.08	1 (33%)	0,2,2	0.00	-
2	GLZ	D	376	1,2	3,3,3	2.15	1 (33%)	0,2,2	0.00	-

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
2	GLZ	C	376	1,2	-	0/0/1/1	0/0/0/0
2	GLZ	D	376	1,2	-	0/0/1/1	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	376	GLZ	O-C	3.55	1.42	1.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	376	GLZ	O-C	3.69	1.43	1.19

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.