



wwPDB X-ray Structure Validation Summary Report ⓘ

May 28, 2020 – 09:01 pm BST

PDB ID : 1YOV
Title : Insights into the Ubiquitin Transfer Cascade from the refined structure of the activating enzyme for NEDD8
Authors : Walden, H.; Podgorski, M.S.; Schulman, B.A.
Deposited on : 2005-01-28
Resolution : 2.60 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

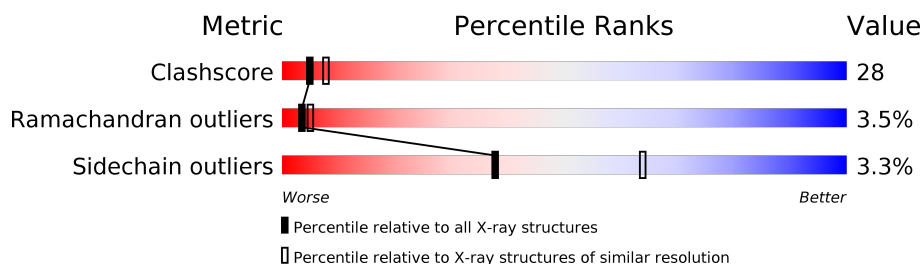
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	537	 64% 30% . .
1	C	537	 51% 42% 5% .
2	B	444	 57% 29% . 11%
2	D	444	 42% 39% 5% 14%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14604 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 Amyloid protein-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	529	Total	C	N	O	S	0	0	0
			4208	2662	718	812	16			
1	C	526	Total	C	N	O	S	0	0	0
			4183	2644	714	809	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	CLONING ARTIFACT	UNP Q13564
A	-1	LYS	-	CLONING ARTIFACT	UNP Q13564
A	0	LEU	-	CLONING ARTIFACT	UNP Q13564
C	-2	MET	-	CLONING ARTIFACT	UNP Q13564
C	-1	LYS	-	CLONING ARTIFACT	UNP Q13564
C	0	LEU	-	CLONING ARTIFACT	UNP Q13564

- Molecule 2 is a protein called Ubiquitin-activating enzyme E1C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	397	Total	C	N	O	S	0	0	0
			3089	1975	523	573	18			
2	D	382	Total	C	N	O	S	0	0	0
			2972	1901	502	551	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	CLONING ARTIFACT	UNP Q8TBC4
B	0	SER	-	CLONING ARTIFACT	UNP Q8TBC4
D	-1	GLY	-	CLONING ARTIFACT	UNP Q8TBC4
D	0	SER	-	CLONING ARTIFACT	UNP Q8TBC4

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Zn 1	0	0
3	D	1	Total 1	Zn 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	53	Total 53	O 53	0	0
4	B	62	Total 62	O 62	0	0
4	C	19	Total 19	O 19	0	0
4	D	16	Total 16	O 16	0	0

E401	GLU	ARG	THR	ARG	PRO	ASN	LEU	SER	LYS	THR	LEU	LYS	GLU	GLU	GLY	LEU	VAL	ASP	GLY	GLN	GLU	LEU	ALA	V425	A426	D427	V428	T429	T430	P431	Q432	T433	V434	L435	F436	LYS	LEU	HIS	PHE	THR	SER
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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.40 Å 123.60 Å 198.20 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.236 , 0.280	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14604	wwPDB-VP
Average B, all atoms (Å ²)	79.0	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:
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 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	0.41	0/4290	0.63	0/5802
1	C	0.33	0/4265	0.59	1/5769 (0.0%)
2	B	0.45	0/3158	0.70	2/4300 (0.0%)
2	D	0.35	0/3036	0.61	1/4130 (0.0%)
All	All	0.39	0/14749	0.63	4/20001 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	320	ASN	N-CA-C	7.71	131.82	111.00
2	B	319	ASN	C-N-CA	6.24	137.29	121.70
2	D	37	PRO	N-CA-C	-5.93	96.68	112.10
1	C	519	THR	N-CA-C	5.16	124.92	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	4208	0	4157	171	0
1	C	4183	0	4122	281	0
2	B	3089	0	3012	133	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2972	0	2914	240	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	53	0	0	7	0
4	B	62	0	0	9	0
4	C	19	0	0	6	0
4	D	16	0	0	1	0
All	All	14604	0	14205	789	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 28.

The worst 5 of 789 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:C:518:ASN:ND2	1:C:519:THR:H	1.49	1.10
2:D:380:ALA:HB3	2:D:426:ALA:HB3	1.34	1.06
1:C:298:THR:HG22	1:C:299:LYS:H	1.20	1.04
2:D:27:SER:HB3	2:D:37:PRO:HG3	1.38	1.01
1:A:489:GLU:H	2:B:19:HIS:HD2	1.10	1.00

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	527/537 (98%)	477 (90%)	39 (7%)	11 (2%)	7	13
1	C	524/537 (98%)	438 (84%)	65 (12%)	21 (4%)	3	3
2	B	387/444 (87%)	351 (91%)	24 (6%)	12 (3%)	4	6
2	D	372/444 (84%)	298 (80%)	54 (14%)	20 (5%)	2	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1810/1962 (92%)	1564 (86%)	182 (10%)	64 (4%)	3 5

5 of 64 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	518	ASN
2	B	320	ASN
2	B	395	GLN
1	C	229	THR
1	C	234	PRO

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	461/467 (99%)	442 (96%)	19 (4%)	30 56
1	C	458/467 (98%)	445 (97%)	13 (3%)	43 69
2	B	335/387 (87%)	323 (96%)	12 (4%)	35 61
2	D	325/387 (84%)	317 (98%)	8 (2%)	47 73
All	All	1579/1708 (92%)	1527 (97%)	52 (3%)	38 64

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	165	GLU
2	B	325	ASN
2	D	128	GLN
2	B	201	GLU
2	B	218	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	128	GLN
2	B	351	GLN
2	D	227	HIS
2	B	131	ASN
2	B	236	GLN

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

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.

5.7 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 ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.