



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:52 PM GMT

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
<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)
Xtrriage (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

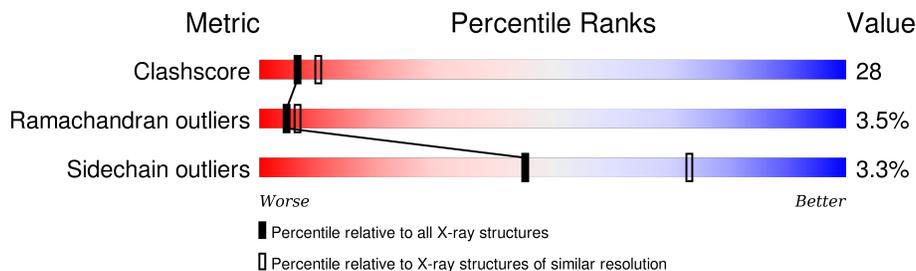
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (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. 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	537	
1	C	537	
2	B	444	
2	D	444	

2 Entry composition [i](#)

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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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.

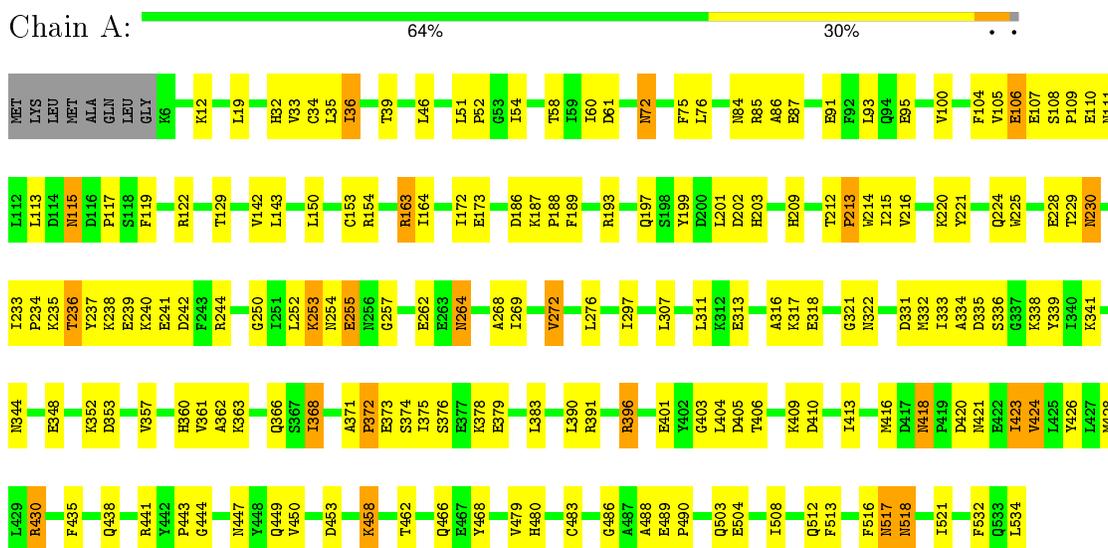
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	53	Total 53	O 53	0	0
4	B	62	Total 62	O 62	0	0
4	C	19	Total 19	O 19	0	0
4	D	16	Total 16	O 16	0	0

3 Residue-property plots

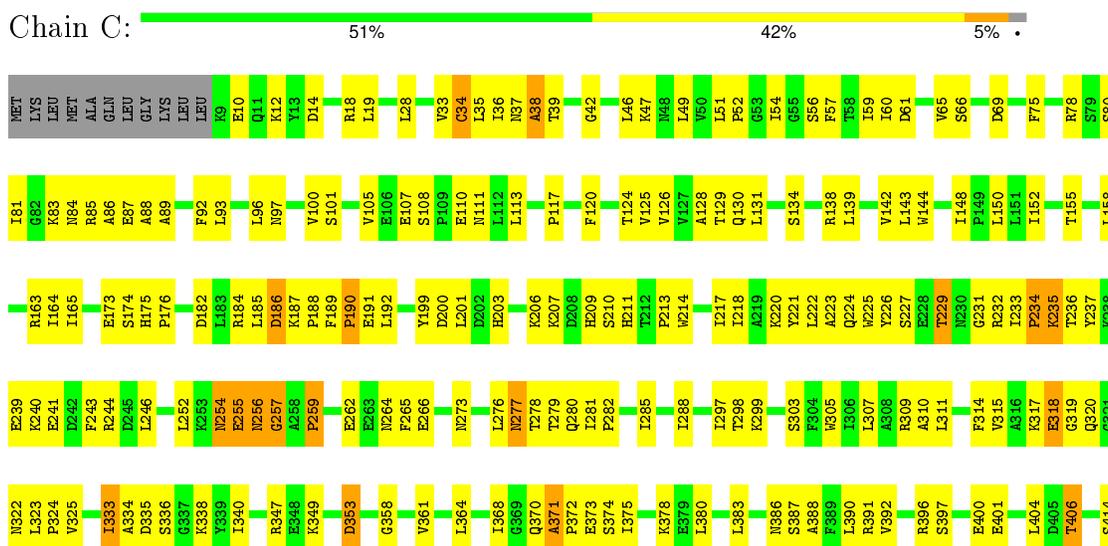
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

- Molecule 1: Amyloid protein-binding protein 1



- Molecule 1: Amyloid protein-binding protein 1



4 Data and refinement statistics

Xtrriage (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	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.	Xtrriage
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%)	9	16
1	C	524/537 (98%)	438 (84%)	65 (12%)	21 (4%)	4	4
2	B	387/444 (87%)	351 (91%)	24 (6%)	12 (3%)	5	8
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%)	4 6

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 [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	461/467 (99%)	442 (96%)	19 (4%)	37 66
1	C	458/467 (98%)	445 (97%)	13 (3%)	51 78
2	B	335/387 (87%)	323 (96%)	12 (4%)	42 71
2	D	325/387 (84%)	317 (98%)	8 (2%)	55 81
All	All	1579/1708 (92%)	1527 (97%)	52 (3%)	45 73

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 will therefore be empty.

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

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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