



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 09:06 AM GMT

PDB ID : 2FP0
Title : human ADP-ribosylhydrolase 3
Authors : Mueller-Dieckmann, C.; Weiss, M.S.; Koch-Nolte, F.
Deposited on : 2006-01-15
Resolution : 2.05 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

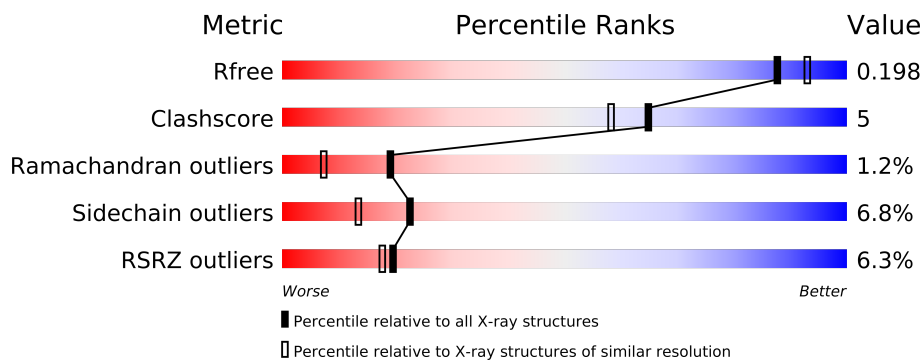
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
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)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.05 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	1380 (2.06-2.02)
Clashscore	79885	1577 (2.06-2.02)
Ramachandran outliers	78287	1565 (2.06-2.02)
Sidechain outliers	78261	1565 (2.06-2.02)
RSRZ outliers	66119	1381 (2.06-2.02)

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	347	
1	B	347	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5337 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 ADP-ribosylhydrolase like 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	0	0
			2593	1622	443	513	15			
1	B	339	Total	C	N	O	S	0	0	0
			2593	1622	443	513	15			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Mg	0	0
			2	2		
2	A	2	Total	Mg	0	0
			2	2		

- Molecule 3 is water.

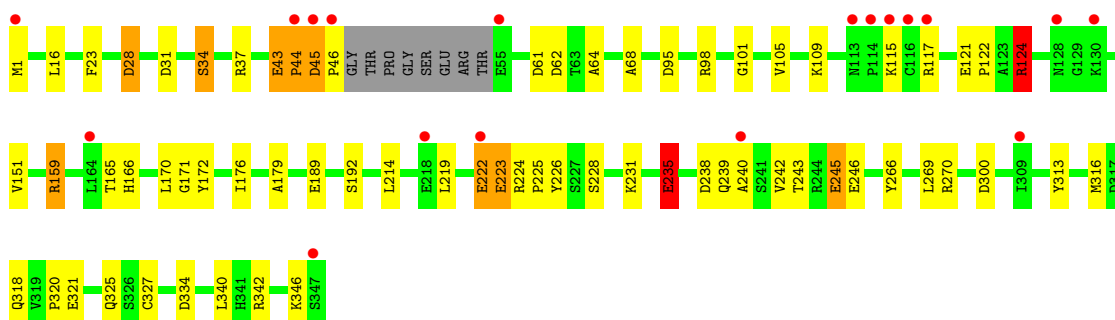
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	96	Total	O	0	0
			96	96		
3	B	51	Total	O	0	0
			51	51		

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.

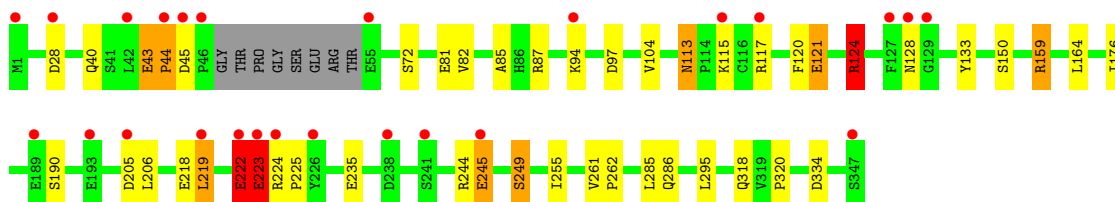
- Molecule 1: ADP-ribosylhydrolase like 2

Chain A: 



- Molecule 1: ADP-ribosylhydrolase like 2

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.33Å 60.63Å 102.88Å 90.00° 96.43° 90.00°	Depositor
Resolution (Å)	30.00 – 2.05 24.42 – 2.05	Depositor EDS
% Data completeness (in resolution range)	98.8 (30.00-2.05) 98.8 (24.42-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.04Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.188 , 0.231 0.195 , 0.198	Depositor DCC
R_{free} test set	896 reflections (2.09%)	DCC
Wilson B-factor (Å ²)	38.7	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 74.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 43737 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5337	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.06% 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: MG

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	1.20	9/2639 (0.3%)	1.11	16/3564 (0.4%)
1	B	0.99	1/2639 (0.0%)	0.89	6/3564 (0.2%)
All	All	1.10	10/5278 (0.2%)	1.00	22/7128 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
All	All	0	4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	313	TYR	CD1-CE1	8.12	1.51	1.39
1	B	121	GLU	CG-CD	6.92	1.62	1.51
1	A	64	ALA	CA-CB	-6.36	1.39	1.52
1	A	68	ALA	CA-CB	-6.21	1.39	1.52
1	A	240	ALA	CA-CB	5.54	1.64	1.52

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	342	ARG	NE-CZ-NH2	-13.50	113.55	120.30
1	A	61	ASP	CB-CG-OD2	-11.07	108.34	118.30
1	A	61	ASP	CB-CG-OD1	9.36	126.72	118.30
1	A	316	MET	CG-SD-CE	8.72	114.16	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	ARG	NE-CZ-NH1	7.72	124.16	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	222	GLU	Peptide
1	A	43	GLU	Peptide
1	B	222	GLU	Peptide
1	B	43	GLU	Peptide

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	2593	0	2521	35	0
1	B	2593	0	2521	20	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	96	0	0	1	0
3	B	51	0	0	1	0
All	All	5337	0	5042	54	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 5.

The worst 5 of 54 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:45:ASP:HB3	1:A:46:PRO:HA	1.41	1.02
1:A:45:ASP:HB3	1:A:46:PRO:CA	2.03	0.88
1:A:45:ASP:CB	1:A:46:PRO:HA	2.10	0.80
1:A:44:PRO:HB2	1:A:45:ASP:HA	1.64	0.80
1:A:235:GLU:O	1:A:235:GLU:OE2	2.02	0.77

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	335/347 (96%)	323 (96%)	8 (2%)	4 (1%)	19	7
1	B	335/347 (96%)	320 (96%)	11 (3%)	4 (1%)	19	7
All	All	670/694 (96%)	643 (96%)	19 (3%)	8 (1%)	19	7

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	ASP
1	A	45	ASP
1	A	223	GLU
1	B	28	ASP
1	B	44	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	273/279 (98%)	255 (93%)	18 (7%)	24	14
1	B	273/279 (98%)	254 (93%)	19 (7%)	21	12
All	All	546/558 (98%)	509 (93%)	37 (7%)	22	13

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	334	ASP
1	B	104	VAL
1	B	245	GLU
1	A	346	LYS

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Mol	Chain	Res	Type
1	B	40	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	27	HIS
1	B	38	HIS
1	B	318	GLN
1	A	198	GLN
1	B	211	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

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	339/347 (97%)	0.22	18 (5%) 25 24	39, 47, 60, 69	0
1	B	339/347 (97%)	0.45	25 (7%) 14 13	41, 47, 59, 71	0
All	All	678/694 (97%)	0.33	43 (6%) 19 18	39, 47, 60, 71	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	46	PRO	9.4
1	B	45	ASP	8.1
1	B	44	PRO	7.3
1	B	222	GLU	6.8
1	B	219	LEU	5.0

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 ⓘ

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(\AA^2)	Q<0.9
2	MG	A	401	1/1	0.20	1.77	19,19,19,19	0
2	MG	A	402	1/1	0.18	1.53	29,29,29,29	0
2	MG	B	502	1/1	0.11	0.73	37,37,37,37	0
2	MG	B	501	1/1	0.12	0.67	27,27,27,27	0

6.5 Other polymers ⓘ

There are no such residues in this entry.