



Full wwPDB X-ray Structure Validation Report

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PDB ID : 1G0S
Title : THE CRYSTAL STRUCTURE OF THE E.COLI ADP-RIBOSE PY-
ROPHOSPHATASE
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Deposited on : 2000-10-08
Resolution : 1.90 Å(reported)

This is a full wwPDB validation 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>

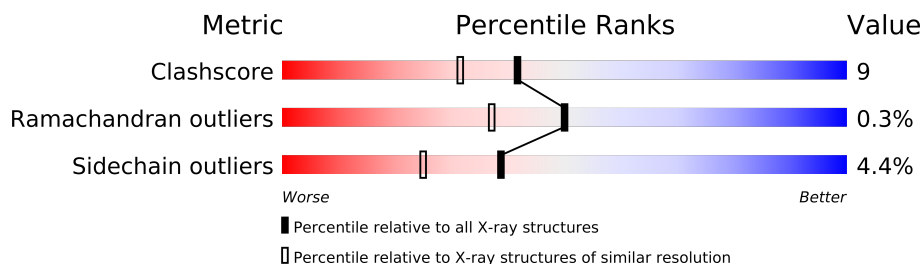
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
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 1.90 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	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	209	
1	B	209	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3618 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 HYPOTHETICAL 23.7 KDA PROTEIN IN ICC-TOLC INTERGENIC REGION.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	201	Total 1613	C 1019	N 284	O 305	S 5	0	0	0
1	B	202	Total 1613	C 1017	N 285	O 307	S 4	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	193	Total 193	O 193	0	0
2	B	199	Total 199	O 199	0	0

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	66.93Å 67.89Å 98.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.37 – 1.90	Depositor
% Data completeness (in resolution range)	89.1 (29.37-1.90)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.192 , 0.241	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3618	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

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	0.44	0/1644	0.74	1/2224 (0.0%)
1	B	0.43	0/1645	0.73	0/2226
All	All	0.44	0/3289	0.74	1/4450 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	128	LEU	CA-CB-CG	6.39	130.00	115.30

There are no chirality outliers.

There are no planarity outliers.

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	1613	0	1592	29	0
1	B	1613	0	1580	36	0
2	A	193	0	0	6	0
2	B	199	0	0	5	0
All	All	3618	0	3172	58	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 9.

All (58) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:101:GLU:CG	1:B:102:GLY:H	2.03	0.71
1:B:131:LEU:HD21	1:B:140:ARG:HH12	1.55	0.70
1:B:156:ILE:HD11	1:B:167:ARG:HG3	1.75	0.68
1:A:39:ARG:HG2	1:A:45:MET:HE1	1.75	0.68
1:A:26:ARG:HG3	2:A:262:HOH:O	1.94	0.68
1:A:53:ILE:HD12	1:B:81:ALA:HB2	1.74	0.67
1:B:103:GLU:OE1	1:B:111:ARG:NH1	2.29	0.65
1:B:131:LEU:HD21	1:B:140:ARG:NH1	2.11	0.65
1:B:101:GLU:HG2	1:B:102:GLY:H	1.63	0.64
1:A:85:THR:OG1	1:B:140:ARG:NH1	2.32	0.63
1:B:101:GLU:HG2	1:B:102:GLY:N	2.14	0.62
1:B:105:VAL:HG12	2:B:235:HOH:O	2.02	0.60
1:B:153:ALA:HB1	1:B:168:VAL:HG11	1.84	0.58
1:B:26:ARG:HD3	1:B:26:ARG:C	2.24	0.58
1:A:15:ASP:HB3	1:A:39:ARG:HG3	1.86	0.58
1:A:127:VAL:CG2	1:A:145:VAL:HG22	2.34	0.57
1:A:182:GLU:OE2	1:A:184:LYS:HE3	2.05	0.56
1:A:39:ARG:HG2	1:A:45:MET:CE	2.35	0.56
1:B:101:GLU:CG	1:B:102:GLY:N	2.68	0.55
1:B:127:VAL:HG12	1:B:128:LEU:N	2.21	0.55
1:A:42:ASN:C	1:A:42:ASN:HD22	2.12	0.52
1:A:191:VAL:O	1:A:195:GLN:HG3	2.10	0.52
1:B:140:ARG:HB2	1:B:140:ARG:HH11	1.76	0.51
1:B:122:LYS:NZ	1:B:149:ASP:HB2	2.27	0.50
1:A:9:VAL:HG11	1:B:90:TRP:HB2	1.93	0.50
1:A:9:VAL:HG13	1:B:76:GLU:OE2	2.12	0.50
1:A:114:ILE:HD11	2:A:391:HOH:O	2.11	0.49
1:A:17:GLU:HG3	1:A:17:GLU:O	2.12	0.49
1:A:100:GLU:HB2	1:A:103:GLU:OE2	2.13	0.49
1:A:99:ILE:HD11	1:A:105:VAL:HG22	1.95	0.48
1:A:35:ARG:HD2	1:A:50:ARG:HH12	1.77	0.48
1:B:69:ARG:HD3	1:B:71:GLU:OE1	2.14	0.47
1:B:23:THR:HG21	1:B:26:ARG:HB2	1.95	0.47
1:B:207:GLU:HG2	2:B:280:HOH:O	2.15	0.47
1:A:31:LEU:HD23	1:B:25:TYR:CD2	2.50	0.46
1:A:201:HIS:HE1	2:A:287:HOH:O	1.96	0.46
1:B:8:PRO:HA	2:B:281:HOH:O	2.15	0.46
1:B:173:ARG:HG3	1:B:197:LEU:HD21	1.96	0.46
1:A:111:ARG:NH2	2:A:246:HOH:O	2.49	0.46
1:B:111:ARG:NH2	2:B:408:HOH:O	2.48	0.46
1:B:156:ILE:CD1	1:B:167:ARG:HG3	2.44	0.46
1:B:51:ARG:HG3	2:B:347:HOH:O	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:392:HOH:O	1:B:8:PRO:HB3	2.16	0.45
1:A:62:LEU:HD11	1:A:146:GLY:HA3	1.99	0.44
1:A:129:SER:OG	1:A:140:ARG:HD2	2.17	0.43
1:A:9:VAL:HG22	1:B:76:GLU:HG3	1.99	0.43
1:B:64:PRO:HB2	1:B:73:VAL:HB	1.98	0.43
1:B:56:ARG:O	1:B:56:ARG:HD3	2.18	0.43
1:B:62:LEU:HB2	1:B:109:ALA:HB1	2.01	0.43
1:A:19:ILE:O	1:A:20:ALA:HB2	2.20	0.42
1:B:100:GLU:O	1:B:101:GLU:C	2.59	0.41
1:A:35:ARG:HD2	1:A:50:ARG:NH1	2.35	0.41
1:A:28:PHE:CZ	1:B:52:GLU:HG3	2.55	0.41
1:A:132:ALA:HB2	2:A:366:HOH:O	2.19	0.41
1:A:42:ASN:ND2	1:A:44:GLN:H	2.19	0.41
1:B:156:ILE:HD12	1:B:156:ILE:N	2.37	0.40
1:A:63:LEU:HD23	1:A:145:VAL:HG13	2.04	0.40
1:B:201:HIS:HD2	1:B:205:LYS:NZ	2.20	0.40

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	197/209 (94%)	191 (97%)	6 (3%)	0	100	100
1	B	200/209 (96%)	192 (96%)	7 (4%)	1 (0%)	38	23
All	All	397/418 (95%)	383 (96%)	13 (3%)	1 (0%)	50	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	101	GLU

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	172/177 (97%)	165 (96%)	7 (4%)	41	28
1	B	170/177 (96%)	162 (95%)	8 (5%)	36	22
All	All	342/354 (97%)	327 (96%)	15 (4%)	39	25

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	VAL
1	A	39	ARG
1	A	42	ASN
1	A	91	LEU
1	A	92	LEU
1	A	140	ARG
1	A	145	VAL
1	B	51	ARG
1	B	56	ARG
1	B	62	LEU
1	B	92	LEU
1	B	140	ARG
1	B	144	MET
1	B	148	VAL
1	B	178	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	44	GLN
1	A	175	GLN
1	A	201	HIS
1	A	202	GLN
1	B	44	GLN
1	B	201	HIS

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 ⓘ

There are no ligands in this entry.

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 ⓘ

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.