

Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2020 – 01:27 PM BST

PDB ID : 6QO7

> Title Crystal structure of ribonucleotide reductase NrdF from Bacillus anthracis

> > aerobically soaked with ferrous ions (photo-reduced)

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Deposited on 2019-02-12

1.63 Å(reported) Resolution

This is a Full wwPDB X-ray Structure Validation 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

4.02b-467MolProbity Xtriage (Phenix) 1.13

EDS 2.13.1

Percentile statistics 20191225.v01 (using entries in the PDB archive December 25th 2019)

> Refmac 5.8.0158

7.0.044 (Gargrove) CCP4

Ideal geometry (proteins) Engh & Huber (2001) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

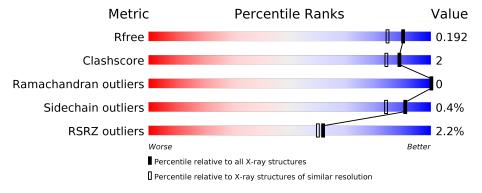
Validation Pipeline (wwPDB-VP) 2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.63 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
R_{free}	130704	4693 (1.64-1.60)
Clashscore	141614	5002 (1.64-1.60)
Ramachandran outliers	138981	4888 (1.64-1.60)
Sidechain outliers	138945	4887 (1.64-1.60)
RSRZ outliers	127900	4609 (1.64-1.60)

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 <=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.

Mol	Chain	Length	Quality of chain		
1	A	322	2% 	5%	10%
1	В	322	84%	5%	11%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9779 atoms, of which 4710 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 Ribonucleoside-diphosphate reductase subunit beta.

Mol	Chain	Residues			Atom	ıs			ZeroOcc	AltConf	Trace
1	A	291	Total 4737	C 1539	H 2356	N 378	O 454	S 10	0	4	0
1	В	288	Total 4720	C 1527		N 375	O 454	S 10	0	9	0

• Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	2	Total Fe 2 2	0	0
2	A	2	Total Fe 2 2	0	0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0

• Molecule 4 is water.

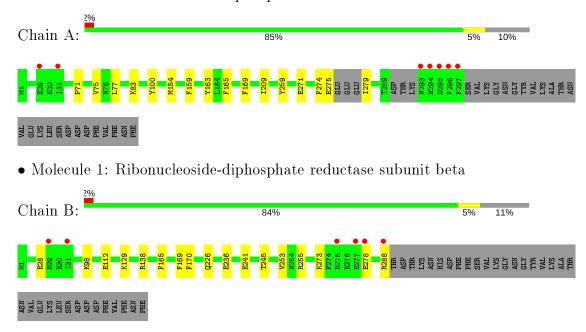
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	167	Total O 167 167	0	0
4	В	150	Total O 150 150	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Ribonucleoside-diphosphate reductase subunit beta





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	$57.29 { $	Danagitan
a, b, c, α , β , γ	90.00° 107.11° 90.00°	Depositor
Resolution (Å)	41.82 - 1.63	Depositor
Resolution (A)	45.57 - 1.63	EDS
% Data completeness	99.6 (41.82-1.63)	Depositor
(in resolution range)	99.7 (45.57-1.63)	EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.09 \; ({\rm at} \; 1.63 {\rm \AA})$	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
D D.	0.159 , 0.192	Depositor
R, R_{free}	0.159 , 0.192	DCC
R_{free} test set	3862 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.46 , 45.4	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	9779	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 77.80 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.9067e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: FE2, CL

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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.64	0/2445	0.72	0/3303	
1	В	0.63	0/2457	0.69	0/3321	
All	All	0.63	0/4902	0.71	0/6624	

There are no bond length outliers.

There are no bond angle outliers.

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	2381	2356	2345	9	0
1	В	2366	2354	2315	9	0
2	A	2	0	0	0	0
2	В	2	0	0	0	0
3	A	1	0	0	0	0
4	A	167	0	0	1	1
4	В	150	0	0	2	2
All	All	5069	4710	4660	18	2

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 2.



All (18) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
		${\rm distance} \; ({\rm \AA})$	overlap (Å)
1:B:112:GLU:OE1	4:B:501:HOH:O	2.01	0.78
1:B:241:GLU:O	1:B:245:THR:HG23	1.98	0.64
1:A:100:TYR:OH	4:A:501:HOH:O	2.11	0.62
1:B:255:ARG:NH2	1:B:278:GLU:O	2.33	0.62
1:A:271[B]:GLU:CD	1:A:271[B]:GLU:H	2.07	0.58
1:A:154:MET:SD	1:A:209:ILE:HD12	2.49	0.52
1:B:129:LYS:NZ	1:B:236:GLU:OE2	2.38	0.52
1:A:77:LEU:O	1:A:83:LYS:NZ	2.38	0.51
1:A:259:TYR:CE1	1:A:279:ILE:HD11	2.51	0.46
1:B:138:ARG:HB3	1:B:138:ARG:CZ	2.47	0.45
1:A:159:PHE:O	1:A:163:TYR:HB3	2.17	0.44
1:A:165:PHE:HB3	1:A:169:PHE:CE2	2.53	0.44
1:A:71:PRO:O	1:A:75:VAL:HG13	2.17	0.44
1:B:170:PHE:CD2	1:B:253[A]:VAL:HG22	2.53	0.43
1:B:165:PHE:HB3	1:B:169:PHE:CE2	2.54	0.43
1:B:226:GLN:OE1	1:B:273:LYS:HE2	2.19	0.43
1:B:288:ARG:NH1	4:B:508:HOH:O	2.51	0.42
1:A:274:PHE:O	1:A:275:GLU:C	2.58	0.42

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} ({\rm \AA}) \end{array}$	$egin{array}{c} { m Clash} \\ { m overlap} \ ({ m \AA}) \end{array}$
4:A:625:HOH:O	4:B:593:HOH:O[2_846]	1.98	0.22
4:B:531:HOH:O	4:B:636:HOH:O[2_856]	2.19	0.01

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	Perce	\mathbf{ntiles}
1	A	$289/322 \ (90\%)$	286 (99%)	3 (1%)	0	100	100
1	В	$295/322 \ (92\%)$	293 (99%)	2 (1%)	0	100	100
All	All	584/644 (91%)	579 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	$259/283 \ (92\%)$	259 (100%)	0	100 100	
1	В	261/283 (92%)	259 (99%)	2 (1%)	81 69	
All	All	520/566~(92%)	518 (100%)	2 (0%)	91 84	

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	28	GLU
1	В	98	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 5 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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95^{th} 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q < 0.9
1	A	$291/322 \ (90\%)$	-0.15	7 (2%) 59 56	12, 22, 42, 62	2 (0%)
1	В	$288/322 \ (89\%)$	-0.17	6 (2%) 63 62	12, 22, 43, 66	1 (0%)
All	All	579/644 (89%)	-0.16	13 (2%) 62 60	12, 22, 43, 66	3 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ
1	A	296	PHE	5.5
1	В	29	GLU	3.7
1	A	294	HIS	3.5
1	В	31	ILE	3.0
1	A	31	ILE	2.9
1	A	295	ASP	2.8
1	В	275	GLU	2.6
1	A	293	ASN	2.6
1	A	29	GLU	2.4
1	В	278	GLU	2.4
1	A	297	PHE	2.3
1	В	277	GLU	2.3
1	В	288	ARG	2.1

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.



6.4 Ligands (i)

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. The B-factors column lists the minimum, median, 95^{th} 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	RSCC	RSR	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
3	CL	A	403	1/1	0.96	0.06	31,31,31,31	0
2	FE2	В	401	1/1	1.00	0.12	16,16,16,16	0
2	FE2	A	402	1/1	1.00	0.13	17,17,17,17	0
2	FE2	A	401	1/1	1.00	0.11	15,15,15,15	0
2	FE2	В	402	1/1	1.00	0.10	14,14,14,14	0

6.5 Other polymers (i)

There are no such residues in this entry.

