



Full wwPDB EM Validation Report ⓘ

Apr 16, 2026 – 10:11 am BST

PDB ID : 9SJY / pdb_00009sjy
Title : Serial electron diffraction (SerialED) structure of Ribonucleotide reductase R2 from E. coli in its oxidised (met) form
Authors : Pacoste, L.; Kumar, R.; Hongyi, X.; Hofer, G.; Hogbom, M.; Zou, X.
Deposited on : 2025-09-01
Resolution : 1.80 Å (reported)
Based on initial model : 9SJW

This is a Full wwPDB EM Validation Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

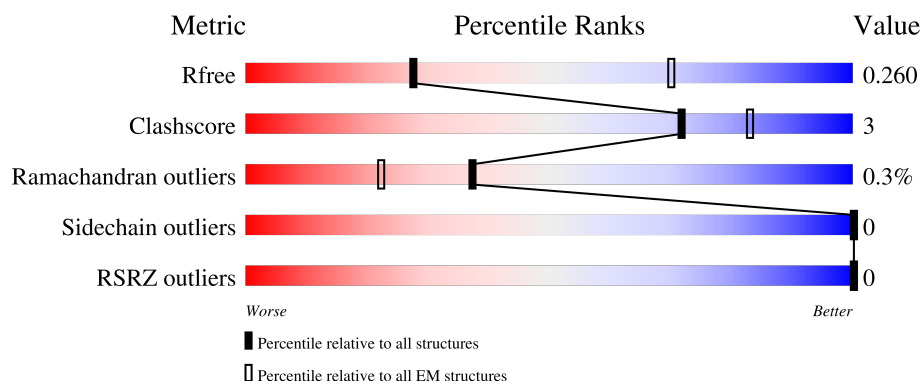
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON CRYSTALLOGRAPHY

The reported resolution of this entry is 1.80 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)	EM structures (#Entries)
R_{free}	180332	208
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RSRZ outliers	180361	209

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	375	
1	B	375	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11683 atoms, of which 5635 are hydrogens and 0 are deuteriums.

In the tables below, 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 1 subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	341	Total	C	H	N	O	S	12	0
			5636	1815	2791	478	538	14		
1	B	340	Total	C	H	N	O	S	26	0
			5735	1844	2844	481	550	16		

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	A	2	Total	Fe	0
			2	2	
2	B	2	Total	Fe	0
			2	2	

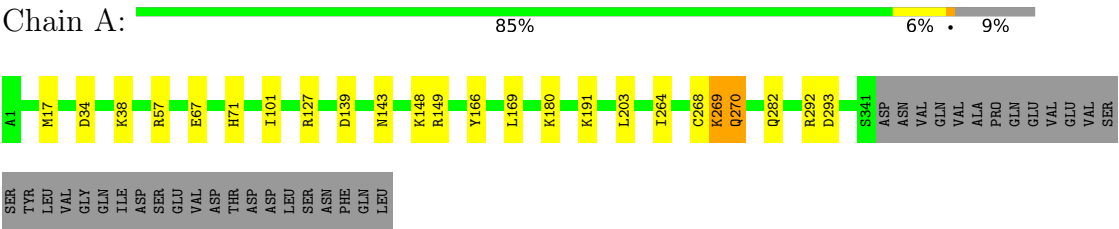
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	A	171	Total	O	0
			171	171	
3	B	137	Total	O	0
			137	137	

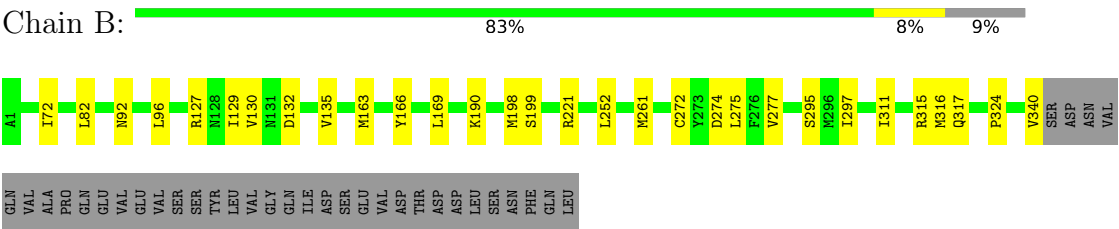
3 Residue-property plots

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. 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. 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 1 subunit beta



- Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.95Å 76.54Å 145.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.93 – 1.80 19.93 – 1.80	Depositor EDS
% Data completeness (in resolution range)	88.2 (19.93-1.80) 71.7 (19.93-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.84 (at 1.38Å)	Xtriage
Refinement program	unknown	Depositor
R, R_{free}	0.210 , 0.253 0.230 , 0.260	Depositor DCC
R_{free} test set	2270 reflections (2.33%)	wwPDB-VP
Wilson B-factor (Å ²)	9.7	Xtriage
Anisotropy	0.395	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 21.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.082 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11683	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE

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	0.31	0/2953	0.55	0/4004
1	B	0.31	0/3064	0.52	0/4151
All	All	0.31	0/6017	0.54	0/8155

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	127	ARG	Sidechain
1	B	127	ARG	Sidechain

5.2 Too-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 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	2845	2791	2747	20	0
1	B	2891	2844	2725	23	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	171	0	0	1	0
3	B	137	0	0	2	0
All	All	6048	5635	5472	38	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 3.

All (38) 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:B:132:ASP:O	1:B:135:VAL:HG22	1.97	0.65
1:A:292:ARG:HG3	1:A:293:ASP:OD1	2.01	0.61
1:B:221[A]:ARG:NH2	1:B:297:ILE:HG22	2.19	0.57
1:B:72:ILE:HD11	1:B:295:SER:CB	2.35	0.56
1:B:317:GLN:NE2	3:B:505:HOH:O	2.39	0.56
1:A:169:LEU:HD12	1:B:169:LEU:HD12	1.92	0.51
1:B:72:ILE:HD11	1:B:295:SER:HB2	1.92	0.51
1:B:129:ILE:HG13	1:B:130:VAL:HG13	1.93	0.50
1:B:82:LEU:C	1:B:82:LEU:HD23	2.38	0.48
1:A:203:LEU:C	1:A:203:LEU:HD23	2.38	0.48
1:A:169:LEU:CD1	1:B:169:LEU:HD12	2.44	0.48
1:A:169:LEU:HD22	1:B:166:TYR:CZ	2.49	0.48
1:A:269:LYS:O	1:A:270[A]:GLN:HB2	2.15	0.46
1:A:148:LYS:HB2	3:A:544:HOH:O	2.17	0.45
1:B:199:SER:HA	1:B:275:LEU:HD21	2.00	0.44
1:A:57:ARG:O	1:A:57:ARG:HG3	2.18	0.43
1:B:277[A]:VAL:HG23	3:B:583:HOH:O	2.18	0.43
1:A:191:LYS:HG2	1:A:264:ILE:HG23	2.01	0.43
1:A:166:TYR:CE1	1:B:169:LEU:HD22	2.54	0.43
1:A:139:ASP:CG	1:A:139:ASP:O	2.61	0.42
1:A:180:LYS:HB2	1:A:180:LYS:HE2	1.79	0.42
1:A:149:ARG:HD3	1:A:282:GLN:HB3	2.01	0.42
1:A:268:CYS:O	1:A:270[B]:GLN:N	2.53	0.42
1:A:169:LEU:HD12	1:B:169:LEU:CD1	2.50	0.42
1:B:190:LYS:HB3	1:B:261:MET:SD	2.60	0.42
1:A:17:MET:HG2	1:A:101:ILE:HD11	2.02	0.42
1:A:67:GLU:OE2	1:A:71[A]:HIS:NE2	2.52	0.42
1:B:198:MET:HG3	1:B:272:CYS:SG	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:ASP:O	1:A:38:LYS:HG3	2.20	0.41
1:B:274:ASP:HA	1:B:277[A]:VAL:HG22	2.01	0.41
1:B:92:ASN:O	1:B:96:LEU:HB2	2.21	0.41
1:B:311[A]:ILE:O	1:B:315:ARG:HG2	2.21	0.41
1:A:268:CYS:O	1:A:270[A]:GLN:N	2.54	0.41
1:A:139:ASP:O	1:A:143:ASN:HB2	2.21	0.40
1:B:252:LEU:HD22	1:B:261:MET:HG3	2.03	0.40
1:B:316:MET:HE1	1:B:324:PRO:HG3	2.02	0.40
1:B:340:VAL:O	1:B:340:VAL:HG13	2.21	0.40

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 PDB entries followed by that with respect to all EM entries.

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	351/375 (94%)	342 (97%)	6 (2%)	3 (1%)	14	5
1	B	364/375 (97%)	356 (98%)	8 (2%)	0	100	100
All	All	715/750 (95%)	698 (98%)	14 (2%)	3 (0%)	37	19

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	270[A]	GLN
1	A	270[B]	GLN
1	A	269	LYS

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 PDB entries followed by that with respect to all EM entries.

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	319/340 (94%)	319 (100%)	0	100	100
1	B	333/340 (98%)	333 (100%)	0	100	100
All	All	652/680 (96%)	652 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	143	ASN
1	A	168	HIS
1	A	306	GLN
1	B	246	GLN
1	B	317	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides 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.

No monomer is involved in short contacts.

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.