



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1J9A / pdb_00001j9a
Title : OLIGORIBONUCLEASE
Authors : Bonander, N.; Tordova, M.; Ladner, J.E.; Eisenstein, E.; Gilliland, G.L.; Structure 2 Function Project (S2F)
Deposited on : 2001-05-24
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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A user guide is available at

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

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
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
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

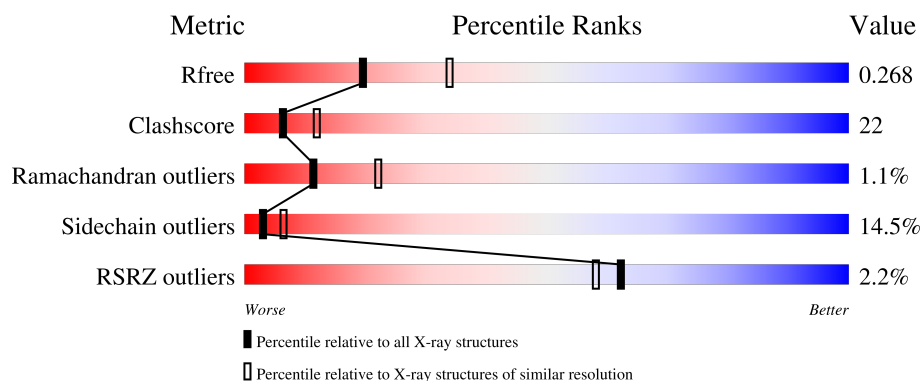
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 of 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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	184	2% 49% 39% 12%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1656 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 OLIGORIBONUCLEASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	184	1507	962	257	281	2	5	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	SER	-	cloning artifact	UNP P45340
A	3	HIS	-	cloning artifact	UNP P45340
A	4	MSE	MET	modified residue	UNP P45340
A	18	MSE	MET	modified residue	UNP P45340
A	61	MSE	MET	modified residue	UNP P45340
A	123	MSE	MET	modified residue	UNP P45340
A	182	MSE	MET	modified residue	UNP P45340

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

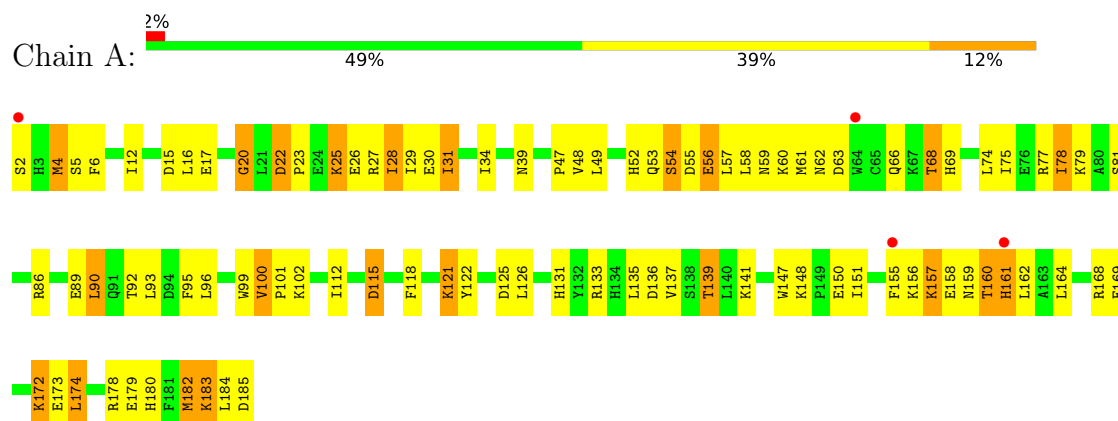
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	139	Total	O	0	0
			139	139		

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 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: OLIGORIBONUCLEASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	55.11Å 55.11Å 144.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.50) 98.9 (20.00-2.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.01Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.192 , 0.299 0.177 , 0.268	Depositor DCC
R_{free} test set	2308 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.576	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 121.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1656	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% 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: SO4

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	0.45	0/1533	1.62	15/2059 (0.7%)

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

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	LEU	O-C-N	7.98	130.71	122.09
1	A	78	ILE	O-C-N	7.85	129.91	121.83
1	A	22	ASP	O-C-N	7.35	128.10	121.19
1	A	6	PHE	CA-CB-CG	6.90	120.70	113.80
1	A	55	ASP	CA-CB-CG	-6.71	105.89	112.60
1	A	131	HIS	CA-CB-CG	-6.39	107.41	113.80
1	A	161	HIS	CA-C-N	6.24	131.52	122.85
1	A	161	HIS	C-N-CA	6.24	131.52	122.85
1	A	115	ASP	CA-CB-CG	-5.93	106.67	112.60
1	A	20	GLY	CA-C-O	-5.74	116.18	121.63
1	A	39	ASN	CA-CB-CG	-5.61	107.00	112.60
1	A	15	ASP	CA-CB-CG	5.60	118.20	112.60
1	A	4	MSE	CG-SE-CE	-5.13	87.63	98.92
1	A	68	THR	O-C-N	5.03	127.52	122.09
1	A	174	LEU	N-CA-C	-5.01	105.73	111.14

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	182	MSE	Mainchain

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	1507	0	1513	67	0
2	A	10	0	0	1	0
3	A	139	0	0	3	0
All	All	1656	0	1513	67	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 22.

All (67) 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:A:52:HIS:HB2	1:A:81:SER:HB3	1.56	0.87
1:A:16:LEU:HD13	1:A:28:ILE:HD13	1.72	0.72
1:A:47:PRO:HG2	3:A:1014:HOH:O	1.94	0.67
1:A:27:ARG:HB3	1:A:53:GLN:NE2	2.13	0.64
1:A:56:GLU:HG2	3:A:1042:HOH:O	1.97	0.64
1:A:178:ARG:HA	1:A:182:MSE:HE2	1.80	0.63
1:A:22:ASP:HB3	1:A:25:LYS:HE2	1.81	0.63
1:A:54:SER:O	1:A:58:LEU:HG	2.00	0.61
1:A:47:PRO:HB2	1:A:49:LEU:HD11	1.84	0.60
1:A:56:GLU:O	1:A:60:LYS:HG3	2.03	0.59
1:A:100:VAL:HG12	1:A:101:PRO:HD2	1.86	0.58
1:A:17:GLU:HB2	1:A:30:GLU:HB3	1.86	0.58
1:A:148:LYS:HD3	1:A:151:ILE:HG21	1.86	0.58
1:A:86:ARG:HG3	1:A:90:LEU:HD22	1.88	0.56
1:A:183:LYS:O	1:A:183:LYS:HG2	2.06	0.55
1:A:75:ILE:HG22	1:A:79:LYS:HE3	1.91	0.53
1:A:164:LEU:O	1:A:168:ARG:HD2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:THR:HG22	1:A:162:LEU:H	1.73	0.52
1:A:23:PRO:HA	1:A:118:PHE:CE2	2.46	0.51
1:A:16:LEU:CD2	1:A:31:ILE:HG13	2.41	0.50
1:A:29:ILE:CG2	1:A:78:ILE:HD13	2.41	0.50
1:A:57:LEU:HA	1:A:60:LYS:HZ2	1.76	0.50
1:A:16:LEU:HD13	1:A:28:ILE:CD1	2.40	0.49
1:A:148:LYS:O	1:A:148:LYS:HG2	2.13	0.49
1:A:169:GLU:HA	1:A:172:LYS:HB2	1.94	0.49
1:A:12:ILE:HD13	1:A:96:LEU:HD13	1.96	0.47
1:A:56:GLU:O	1:A:60:LYS:HE3	2.14	0.47
1:A:169:GLU:OE1	1:A:172:LYS:HE3	2.14	0.47
1:A:184:LEU:O	1:A:185:ASP:HB2	2.14	0.47
1:A:58:LEU:O	1:A:61:MSE:HB2	2.14	0.47
1:A:95:PHE:CE2	1:A:96:LEU:HD23	2.50	0.47
1:A:95:PHE:CD2	1:A:96:LEU:HD23	2.49	0.47
1:A:89:GLU:OE1	1:A:125:ASP:HB2	2.15	0.46
1:A:121:LYS:HD3	1:A:122:TYR:CZ	2.51	0.46
1:A:59:ASN:HD22	1:A:59:ASN:HA	1.47	0.46
1:A:158:GLU:N	1:A:158:GLU:OE1	2.50	0.45
1:A:115:ASP:OD2	1:A:115:ASP:N	2.50	0.45
1:A:179:GLU:HG2	1:A:180:HIS:NE2	2.31	0.45
1:A:62:ASN:OD1	1:A:63:ASP:N	2.49	0.45
1:A:77:ARG:NH2	2:A:200:SO4:O1	2.50	0.45
1:A:47:PRO:HB2	1:A:49:LEU:CD1	2.45	0.45
1:A:157:LYS:HE2	1:A:169:GLU:HB3	1.98	0.45
1:A:86:ARG:NH1	3:A:1061:HOH:O	2.50	0.44
1:A:27:ARG:HD3	1:A:53:GLN:CD	2.43	0.44
1:A:136:ASP:O	1:A:139:THR:HB	2.17	0.44
1:A:182:MSE:HB3	1:A:184:LEU:HD13	1.99	0.44
1:A:92:THR:O	1:A:95:PHE:HB3	2.17	0.44
1:A:22:ASP:O	1:A:26:GLU:HG2	2.18	0.43
1:A:148:LYS:HG2	1:A:151:ILE:HG23	1.99	0.43
1:A:16:LEU:HG	1:A:115:ASP:HB3	2.00	0.43
1:A:20:GLY:C	1:A:26:GLU:HG3	2.43	0.43
1:A:93:LEU:HA	1:A:93:LEU:HD23	1.73	0.43
1:A:48:VAL:O	1:A:49:LEU:HD23	2.19	0.43
1:A:179:GLU:HB3	1:A:180:HIS:CD2	2.54	0.43
1:A:30:GLU:OE2	1:A:77:ARG:NH1	2.50	0.42
1:A:133:ARG:HH11	1:A:133:ARG:HD2	1.64	0.42
1:A:27:ARG:HD3	1:A:53:GLN:OE1	2.19	0.42
1:A:52:HIS:HB2	1:A:81:SER:CB	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:PHE:CE2	1:A:173:GLU:HB2	2.54	0.42
1:A:57:LEU:HA	1:A:60:LYS:NZ	2.35	0.42
1:A:161:HIS:C	1:A:162:LEU:HD23	2.44	0.42
1:A:147:TRP:O	1:A:148:LYS:HB2	2.19	0.41
1:A:74:LEU:O	1:A:78:ILE:HG13	2.20	0.41
1:A:69:HIS:HB2	1:A:75:ILE:HD11	2.03	0.41
1:A:4:MSE:H	1:A:4:MSE:HG2	1.48	0.41
1:A:5:SER:OG	1:A:99:TRP:HZ3	2.03	0.40
1:A:137:VAL:CG1	1:A:173:GLU:HG2	2.52	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 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	182/184 (99%)	168 (92%)	12 (7%)	2 (1%)	11	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	160	THR
1	A	54	SER

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	165/160 (103%)	141 (86%)	24 (14%)	3 6

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	25	LYS
1	A	28	ILE
1	A	31	ILE
1	A	34	ILE
1	A	56	GLU
1	A	66	GLN
1	A	68	THR
1	A	90	LEU
1	A	100	VAL
1	A	102	LYS
1	A	112	ILE
1	A	121	LYS
1	A	126	LEU
1	A	135	LEU
1	A	139	THR
1	A	141	LYS
1	A	150	GLU
1	A	156	LYS
1	A	157	LYS
1	A	159	ASN
1	A	172	LYS
1	A	174	LEU
1	A	183	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	ASN
1	A	72	ASN
1	A	134	HIS

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	A	190	-	4,4,4	0.38	0	6,6,6	0.16	0
2	SO4	A	200	-	4,4,4	0.37	0	6,6,6	0.25	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	200	SO4	1	0

5.7 Other polymers [i](#)

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 [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, 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	179/184 (97%)	-0.15	4 (2%) 62 58	8, 30, 67, 106	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	161	HIS	3.1
1	A	2	SER	2.9
1	A	155	PHE	2.8
1	A	64	TRP	2.2

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 oligosaccharides 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, 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SO4	A	200	5/5	0.91	0.11	39,46,72,79	0
2	SO4	A	190	5/5	0.99	0.03	24,27,31,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.