



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:16 AM UTC

PDB ID : 1LUC / pdb_00001luc
Title : BACTERIAL LUCIFERASE
Authors : Fisher, A.J.; Rayment, I.
Deposited on : 1996-05-10
Resolution : 1.50 Å(reported)

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 ⓘ 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

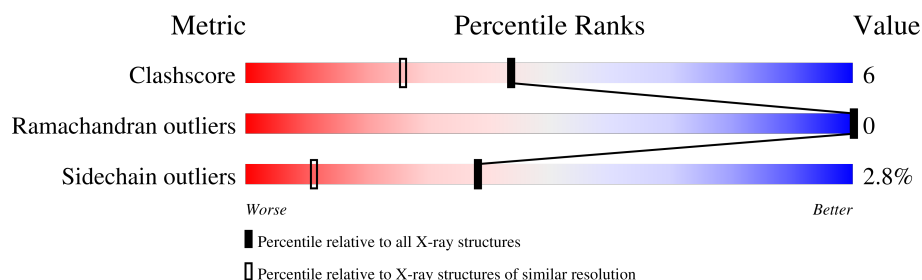
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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))
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	355	
2	B	324	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5754 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 BACTERIAL LUCIFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	3	0
			2577	1633	428	498	18			

- Molecule 2 is a protein called BACTERIAL LUCIFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	320	Total	C	N	O	S	0	0	0
			2516	1584	430	487	15			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	305	Total	O	0	0
			305	305		
5	B	333	Total	O	0	0
			333	333		

3 Residue-property plots

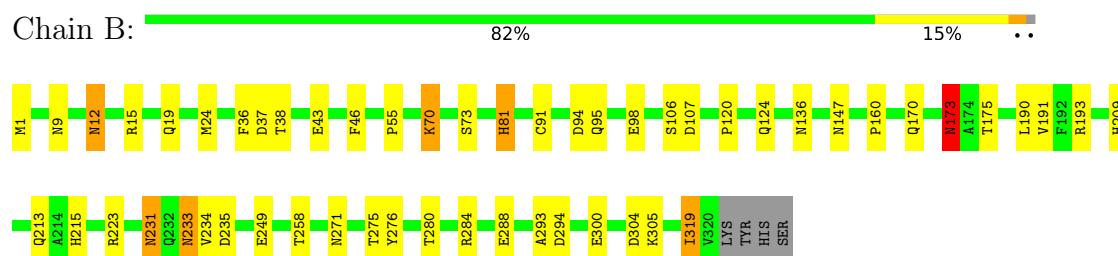
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

Note EDS was not executed.

• Molecule 1: BACTERIAL LUCIFERASE



• Molecule 2: BACTERIAL LUCIFERASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	150.50Å 59.00Å 76.50Å 90.00° 93.86° 90.00°	Depositor
Resolution (Å)	30.00 – 1.50	Depositor
% Data completeness (in resolution range)	98.0 (30.00-1.50)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5754	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, 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	2.07	3/2651 (0.1%)	1.53	29/3593 (0.8%)
2	B	1.24	0/2570	1.56	23/3479 (0.7%)
All	All	1.71	3/5221 (0.1%)	1.55	52/7072 (0.7%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	355	GLN	C-OXT	85.47	2.94	1.23
1	A	168	ALA	CA-C	-5.03	1.48	1.53
1	A	48	GLU	CD-OE1	5.03	1.34	1.25

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	249	HIS	CA-CB-CG	11.03	124.83	113.80
2	B	191	VAL	N-CA-CB	9.60	124.00	111.90
2	B	319	ILE	N-CA-C	-8.77	102.28	111.58
1	A	330	ASN	N-CA-C	8.24	122.44	112.38
2	B	70	LYS	N-CA-C	-7.97	98.68	110.48
2	B	73	SER	N-CA-C	-7.71	98.03	110.20
2	B	46	PHE	N-CA-C	7.55	121.90	112.24
1	A	299	ASN	O-C-N	7.20	127.17	121.55
1	A	31	SER	N-CA-C	7.01	118.57	111.07
1	A	355	GLN	CB-CA-C	-6.95	96.89	110.10
1	A	110	TYR	N-CA-C	6.91	119.99	108.73
1	A	36	PHE	CA-CB-CG	-6.86	106.94	113.80
2	B	173	ASN	CA-CB-CG	-6.79	105.81	112.60
2	B	319	ILE	CB-CA-C	-6.60	103.62	111.94
2	B	294	ASP	CA-CB-CG	-6.26	106.34	112.60
1	A	150	HIS	CA-CB-CG	-6.08	107.72	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	ASP	CA-CB-CG	-6.08	106.52	112.60
1	A	229	ILE	N-CA-C	-6.05	98.97	108.23
1	A	292	ILE	N-CA-C	-6.05	103.33	111.44
1	A	80	THR	N-CA-C	6.03	120.33	113.15
2	B	193	ARG	N-CA-C	6.01	119.43	109.46
1	A	78	LEU	N-CA-C	5.99	121.04	113.25
1	A	199	HIS	CA-CB-CG	-5.99	107.81	113.80
1	A	292	ILE	CA-C-O	5.96	126.68	120.25
2	B	271	ASN	CA-CB-CG	-5.79	106.81	112.60
2	B	36	PHE	CA-CB-CG	-5.72	108.08	113.80
2	B	12	ASN	CA-CB-CG	-5.69	106.91	112.60
1	A	94	ASP	CA-CB-CG	5.69	118.29	112.60
2	B	304	ASP	CA-CB-CG	-5.67	106.93	112.60
2	B	300	GLU	N-CA-C	5.61	119.22	112.38
1	A	109	LEU	CB-CA-C	-5.59	99.12	109.29
1	A	293	ASP	N-CA-C	5.59	117.05	111.07
2	B	147	ASN	N-CA-CB	5.51	119.81	110.49
1	A	6	PHE	CA-CB-CG	5.47	119.27	113.80
2	B	190	LEU	CB-CA-C	-5.42	99.95	109.71
1	A	256	ASN	CA-CB-CG	5.41	118.01	112.60
2	B	107	ASP	N-CA-C	-5.39	102.78	110.59
2	B	106	SER	N-CA-CB	-5.38	103.22	111.56
2	B	94	ASP	CA-CB-CG	5.36	117.96	112.60
1	A	133	ASP	CA-CB-CG	5.35	117.95	112.60
1	A	305	GLU	CB-CG-CD	5.32	121.65	112.60
1	A	114	PHE	CA-CB-CG	-5.30	108.50	113.80
2	B	249	GLU	CB-CG-CD	-5.30	103.59	112.60
2	B	81	HIS	N-CA-CB	-5.29	102.63	111.20
1	A	79	PRO	N-CA-C	5.24	120.72	113.65
1	A	295	SER	CB-CA-C	5.21	119.39	110.74
2	B	37	ASP	N-CA-C	5.17	120.23	113.30
2	B	124	GLN	N-CA-C	5.15	117.31	111.02
1	A	6	PHE	CB-CA-C	-5.15	101.35	109.80
1	A	122	ASP	CA-CB-CG	-5.10	107.50	112.60
1	A	46	PHE	N-CA-C	5.07	121.60	110.80
1	A	123	ASN	CB-CA-C	-5.00	102.96	111.02

There are no chirality outliers.

There are no planarity outliers.

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	2577	0	2478	37	0
2	B	2516	0	2395	25	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
4	A	8	0	12	0	0
4	B	12	0	18	0	0
5	A	305	0	0	6	0
5	B	333	0	0	5	0
All	All	5754	0	4903	61	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 6.

All (61) 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:291:ARG:HG3	1:A:292:ILE:H	1.29	0.95
1:A:197:ASN:OD1	1:A:200:GLU:HG3	1.88	0.74
1:A:291:ARG:HG3	1:A:292:ILE:N	2.03	0.74
1:A:341:LYS:HE2	5:A:3169:HOH:O	1.91	0.71
1:A:255:VAL:O	1:A:259:LYS:HG3	1.94	0.68
1:A:352:LYS:HG3	5:A:3590:HOH:O	1.92	0.68
1:A:355:GLN:H	1:A:355:GLN:CD	2.03	0.66
2:B:209:HIS:O	2:B:213:GLN:HG2	1.97	0.65
1:A:316:ASP:OD1	1:A:355:GLN:NE2	2.29	0.63
1:A:109:LEU:C	1:A:121:MET:HE1	2.25	0.62
2:B:233:ASN:HD22	2:B:235:ASP:H	1.48	0.61
2:B:284:ARG:O	2:B:288:GLU:HG3	2.02	0.59
2:B:276:TYR:CZ	2:B:280:THR:HG21	2.38	0.58
2:B:233:ASN:ND2	2:B:235:ASP:H	2.02	0.57
1:A:123:ASN:ND2	5:A:3211:HOH:O	2.35	0.57
2:B:19:GLN:NE2	5:B:3423:HOH:O	2.29	0.55
1:A:107:ARG:HD3	1:A:125:ARG:HG2	1.89	0.54
1:A:14:GLU:H	1:A:14:GLU:CD	2.16	0.54
1:A:109:LEU:O	1:A:121:MET:HE1	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:258:THR:HG23	5:B:3625:HOH:O	2.10	0.52
1:A:74:ALA:N	1:A:75:ALA:HA	2.25	0.52
2:B:231:ASN:C	2:B:231:ASN:HD22	2.18	0.51
1:A:246:PHE:CD1	1:A:249:HIS:CE1	2.99	0.50
2:B:284:ARG:NH2	5:B:3347:HOH:O	2.44	0.50
1:A:22:LYS:HE3	2:B:98:GLU:OE2	2.12	0.50
1:A:143:TYR:CD2	1:A:157:GLN:HA	2.46	0.50
1:A:231:SER:HB2	1:A:243[B]:CYS:SG	2.52	0.49
1:A:261:PHE:HD2	5:A:3570:HOH:O	1.95	0.49
1:A:6:PHE:CE2	1:A:227[A]:SER:HB3	2.47	0.49
2:B:12:ASN:HD22	2:B:15:ARG:NH2	2.11	0.49
2:B:136:ASN:HD22	2:B:170:GLN:HE22	1.61	0.48
2:B:120:PRO:HD2	5:B:3490:HOH:O	2.12	0.48
1:A:165:GLN:HG2	5:A:3442:HOH:O	2.15	0.47
1:A:299:ASN:O	1:A:310:ILE:HD13	2.14	0.47
2:B:173:ASN:HB3	2:B:175:THR:HG23	1.94	0.47
1:A:107:ARG:HH11	1:A:125:ARG:HE	1.62	0.47
1:A:291:ARG:CG	1:A:292:ILE:H	2.13	0.47
1:A:177:ALA:O	1:A:181:GLU:HG3	2.15	0.46
1:A:6:PHE:CE2	1:A:227[B]:SER:HB2	2.50	0.46
2:B:12:ASN:ND2	2:B:15:ARG:CZ	2.78	0.46
2:B:9:ASN:HD21	2:B:24:MET:HB2	1.81	0.46
2:B:43:GLU:HB2	2:B:55:PRO:HG3	1.97	0.45
1:A:246:PHE:CD1	1:A:249:HIS:HE1	2.35	0.44
1:A:229:ILE:HG22	1:A:299:ASN:CG	2.42	0.44
2:B:319:ILE:HG21	2:B:319:ILE:HD13	1.77	0.44
2:B:233:ASN:HD22	2:B:234:VAL:N	2.16	0.44
2:B:38:THR:OG1	2:B:70:LYS:HE3	2.18	0.43
1:A:43:GLU:HB2	1:A:55:PRO:CG	2.48	0.43
2:B:233:ASN:O	2:B:275:THR:HA	2.18	0.43
2:B:223:ARG:HB3	2:B:293:ALA:HB3	2.01	0.43
1:A:181:GLU:O	1:A:185:GLU:HG3	2.19	0.43
1:A:73:THR:O	1:A:104:GLY:HA3	2.19	0.43
1:A:194:TRP:CD1	1:A:194:TRP:H	2.37	0.42
2:B:276:TYR:O	2:B:280:THR:HG23	2.20	0.42
1:A:231:SER:CB	1:A:243[B]:CYS:SG	3.08	0.41
1:A:1:MET:HE2	1:A:1:MET:HB2	1.83	0.41
1:A:29:LYS:HE2	1:A:65:ALA:HB1	2.02	0.41
2:B:215:HIS:HE1	5:B:3579:HOH:O	2.02	0.41
1:A:134:LEU:HD23	5:A:3218:HOH:O	2.21	0.41
1:A:156:ILE:O	1:A:156:ILE:HD12	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:91:CYS:HB3	2:B:160:PRO:O	2.22	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	325/355 (92%)	318 (98%)	7 (2%)	0	100	100
2	B	318/324 (98%)	311 (98%)	7 (2%)	0	100	100
All	All	643/679 (95%)	629 (98%)	14 (2%)	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	279/303 (92%)	271 (97%)	8 (3%)	37	10
2	B	269/274 (98%)	262 (97%)	7 (3%)	40	13
All	All	548/577 (95%)	533 (97%)	15 (3%)	38	12

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

Mol	Chain	Res	Type
1	A	42	LEU
1	A	54	ASN
1	A	67	GLU
1	A	107	ARG
1	A	131	TRP
1	A	175	GLU
1	A	291	ARG
1	A	355	GLN
2	B	1	MET
2	B	81	HIS
2	B	95	GLN
2	B	173	ASN
2	B	231	ASN
2	B	233	ASN
2	B	305	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	95	GLN
1	A	140	ASN
1	A	204	GLN
1	A	237	ASN
1	A	245	ASN
1	A	256	ASN
1	A	344	GLN
2	B	9	ASN
2	B	49	ASN
2	B	124	GLN
2	B	136	ASN
2	B	209	HIS
2	B	221	GLN
2	B	231	ASN
2	B	233	ASN
2	B	318	ASN

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](#)

Of 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 for Mogul analysis.

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	$\# Z > 2$
4	EDO	A	2500	-	3,3,3	0.41	0	2,2,2	0.40	0
4	EDO	A	2502	-	3,3,3	0.36	0	2,2,2	0.21	0
4	EDO	B	2503	-	3,3,3	0.63	0	2,2,2	0.06	0
4	EDO	B	2504	-	3,3,3	0.31	0	2,2,2	0.45	0
4	EDO	B	2501	-	3,3,3	0.62	0	2,2,2	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	2500	-	-	0/1/1/1	-
4	EDO	A	2502	-	-	1/1/1/1	-
4	EDO	B	2503	-	-	0/1/1/1	-
4	EDO	B	2504	-	-	1/1/1/1	-
4	EDO	B	2501	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	2504	EDO	O1-C1-C2-O2
4	A	2502	EDO	O1-C1-C2-O2

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.