



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:50 PM UTC

PDB ID : 9BIY / pdb_00009biy
Title : Crystal structure of the periplasmic domain of IgaA from Escherichia coli
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Deposited on : 2024-04-24
Resolution : 1.80 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)	:	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

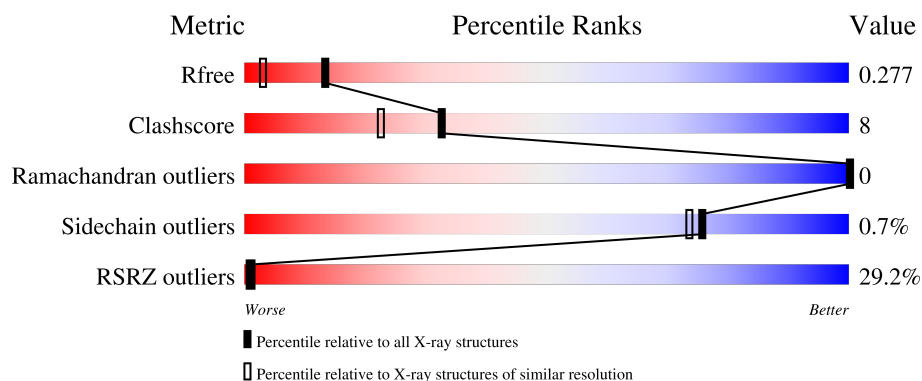
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	275	15% 88% 8% .
2	B	88	66% 65% 28% .. 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2868 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 Intracellular growth attenuator protein igaA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	Se	0	0	0
			1992	1249	345	390	4	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	373	SER	-	expression tag	UNP A0A8T5ZEU4

- Molecule 2 is a protein called Outer membrane lipoprotein RcsF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	84	Total	C	N	O	S	0	0	0
			622	379	114	123	6			

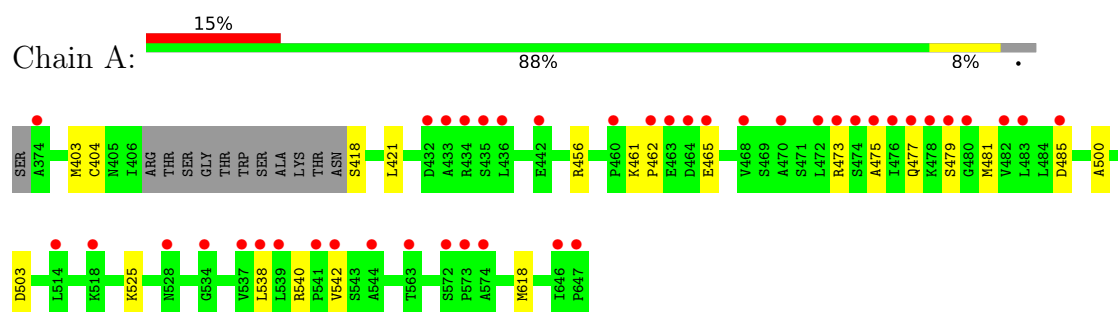
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	235	Total	O	0	0
			235	235		
3	B	19	Total	O	0	0
			19	19		

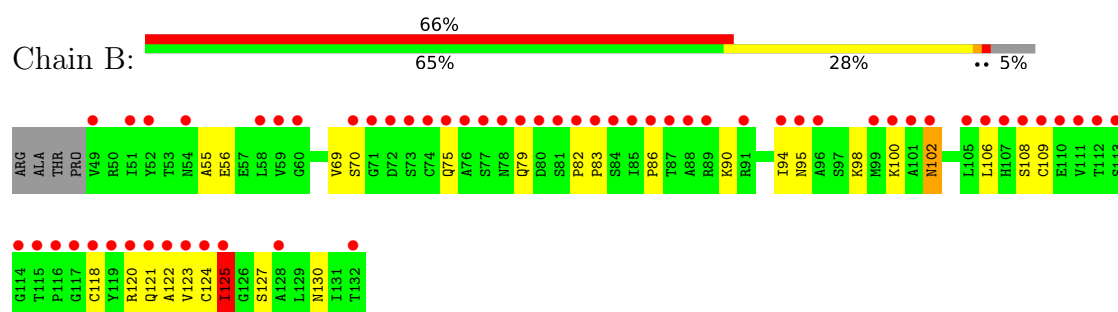
3 Residue-property plots [i](#)

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: Intracellular growth attenuator protein igaA



- Molecule 2: Outer membrane lipoprotein RcsF



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	78.38Å 38.27Å 120.07Å 90.00° 94.97° 90.00°	Depositor
Resolution (Å)	39.87 – 1.80 39.87 – 1.80	Depositor EDS
% Data completeness (in resolution range)	92.0 (39.87-1.80) 86.9 (39.87-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 1.81Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.240 , 0.276 0.241 , 0.277	Depositor DCC
R_{free} test set	1583 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.382	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2868	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.72% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.33	0/2027	0.53	0/2755
2	B	0.30	0/630	0.63	2/852 (0.2%)
All	All	0.32	0/2657	0.56	2/3607 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	102	ASN	N-CA-C	-6.16	106.40	114.04
2	B	125	ILE	N-CA-C	5.05	116.87	108.99

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	1992	0	1968	14	0
2	B	622	0	619	29	0
3	A	235	0	0	2	0
3	B	19	0	0	1	0
All	All	2868	0	2587	41	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 8.

All (41) 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)
2:B:70:SER:CB	2:B:125:ILE:HG13	2.15	0.76
2:B:69:VAL:O	2:B:125:ILE:HG12	1.87	0.74
2:B:70:SER:HB3	2:B:125:ILE:HG13	1.68	0.74
2:B:127:SER:OG	3:B:201:HOH:O	2.14	0.66
2:B:75:GLN:OE1	2:B:82:PRO:HA	1.96	0.66
2:B:75:GLN:O	2:B:75:GLN:HG3	1.96	0.64
2:B:83:PRO:HD2	2:B:120:ARG:HH21	1.63	0.64
1:A:461:LYS:HB3	1:A:462:PRO:HD2	1.81	0.62
2:B:69:VAL:O	2:B:125:ILE:CG1	2.49	0.60
1:A:540:ARG:HG3	1:A:542:VAL:HG22	1.88	0.54
1:A:403:MSE:HG3	1:A:618:MSE:HA	1.90	0.53
1:A:538:LEU:HD21	2:B:55:ALA:HB1	1.90	0.52
1:A:418:SER:HB3	1:A:421:LEU:CD1	2.39	0.52
1:A:456:ARG:NH2	1:A:465:GLU:O	2.32	0.51
2:B:86:PRO:O	2:B:90:LYS:HD3	2.10	0.51
1:A:475:ALA:O	1:A:479:SER:OG	2.17	0.51
1:A:473:ARG:NH2	1:A:485:ASP:OD1	2.44	0.51
2:B:94:ILE:HG13	2:B:98:LYS:NZ	2.26	0.50
2:B:90:LYS:HD3	2:B:90:LYS:N	2.28	0.49
2:B:75:GLN:O	2:B:118:CYS:HB2	2.14	0.47
2:B:90:LYS:O	2:B:94:ILE:HG22	2.14	0.47
2:B:121:GLN:OE1	2:B:122:ALA:N	2.49	0.46
2:B:75:GLN:NE2	2:B:120:ARG:NH1	2.64	0.46
1:A:540:ARG:NH2	2:B:56:GLU:OE1	2.50	0.45
2:B:95:ASN:HA	2:B:98:LYS:HG2	1.99	0.45
2:B:75:GLN:HE22	2:B:120:ARG:NH1	2.15	0.45
2:B:102:ASN:HB3	2:B:130:ASN:HA	1.99	0.44
2:B:109:CYS:HA	2:B:124:CYS:HA	2.00	0.43
1:A:403:MSE:HG2	1:A:404:CYS:O	2.19	0.42
2:B:70:SER:CA	2:B:125:ILE:HG13	2.50	0.42
1:A:500:ALA:HB1	3:A:864:HOH:O	2.19	0.42
1:A:477:GLN:NE2	3:A:728:HOH:O	2.52	0.42
1:A:525:LYS:HB2	1:A:525:LYS:HE3	1.96	0.42
1:A:500:ALA:HB3	1:A:503:ASP:OD2	2.21	0.41
2:B:98:LYS:HA	2:B:98:LYS:HD3	1.78	0.41
2:B:79:GLN:O	2:B:79:GLN:HG2	2.20	0.41
2:B:118:CYS:SG	2:B:121:GLN:HB2	2.61	0.41
2:B:106:LEU:HD13	2:B:108:SER:N	2.36	0.40
2:B:109:CYS:HA	2:B:123:VAL:O	2.21	0.40
2:B:100:LYS:O	2:B:100:LYS:HD3	2.21	0.40
2:B:90:LYS:HD3	2:B:90:LYS:H	1.86	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	259/275 (94%)	254 (98%)	5 (2%)	0	100	100
2	B	82/88 (93%)	78 (95%)	4 (5%)	0	100	100
All	All	341/363 (94%)	332 (97%)	9 (3%)	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	220/226 (97%)	219 (100%)	1 (0%)	81	80
2	B	70/73 (96%)	69 (99%)	1 (1%)	59	52
All	All	290/299 (97%)	288 (99%)	2 (1%)	76	73

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

Mol	Chain	Res	Type
1	A	481	MSE
2	B	125	ILE

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	375	GLN
1	A	459	HIS
1	A	536	ASN
1	A	619	HIS
2	B	107	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

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	259/275 (94%)	0.78	42 (16%) 4 3	20, 32, 67, 114	0
2	B	84/88 (95%)	2.66	58 (69%) 0 0	35, 68, 110, 129	0
All	All	343/363 (94%)	1.24	100 (29%) 1 1	20, 37, 95, 129	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	111	VAL	5.6
2	B	123	VAL	5.5
2	B	76	ALA	5.4
2	B	74	CYS	5.2
1	A	480	GLY	5.1
2	B	85	ILE	5.1
2	B	109	CYS	4.9
2	B	122	ALA	4.8
2	B	83	PRO	4.5
2	B	88	ALA	4.4
1	A	563	THR	4.2
2	B	119	TYR	4.2
2	B	77	SER	4.1
2	B	81	SER	4.0
1	A	462	PRO	4.0
2	B	71	GLY	3.9
1	A	433	ALA	3.7
2	B	112	THR	3.7
2	B	115	THR	3.7
1	A	476	ILE	3.6
2	B	73	SER	3.5
1	A	477	GLN	3.5
1	A	647	PRO	3.4
2	B	124	CYS	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	72	ASP	3.4
2	B	117	GLY	3.4
2	B	118	CYS	3.4
1	A	432	ASP	3.3
2	B	120	ARG	3.3
1	A	473	ARG	3.3
2	B	125	ILE	3.2
2	B	113	SER	3.2
1	A	538	LEU	3.2
1	A	534	GLY	3.2
2	B	110	GLU	3.2
2	B	114	GLY	3.1
1	A	478	LYS	3.0
2	B	101	ALA	3.0
2	B	51	ILE	3.0
1	A	435	SER	3.0
1	A	460	PRO	3.0
2	B	116	PRO	2.9
2	B	87	THR	2.9
2	B	96	ALA	2.9
1	A	479	SER	2.9
2	B	80	ASP	2.9
2	B	82	PRO	2.8
2	B	121	GLN	2.8
2	B	86	PRO	2.8
1	A	518	LYS	2.7
1	A	482	VAL	2.7
2	B	59	VAL	2.7
2	B	79	GLN	2.7
1	A	573	PRO	2.6
1	A	483	LEU	2.6
1	A	542	VAL	2.6
2	B	100	LYS	2.6
2	B	91	ARG	2.6
2	B	106	LEU	2.6
2	B	94	ILE	2.6
2	B	89	ARG	2.5
1	A	463	GLU	2.5
1	A	434	ARG	2.5
2	B	84	SER	2.5
1	A	442	GLU	2.5
1	A	468	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	132	THR	2.5
1	A	464	ASP	2.5
2	B	54	ASN	2.5
2	B	70	SER	2.4
1	A	646	ILE	2.4
1	A	475	ALA	2.4
2	B	128	ALA	2.4
2	B	60	GLY	2.4
1	A	436	LEU	2.3
2	B	58	LEU	2.3
2	B	99	MET	2.3
2	B	108	SER	2.3
1	A	544	ALA	2.3
2	B	78	ASN	2.3
2	B	95	ASN	2.3
2	B	102	ASN	2.3
1	A	514	LEU	2.3
1	A	541	PRO	2.2
1	A	539	LEU	2.2
2	B	105	LEU	2.2
2	B	52	TYR	2.2
1	A	474	SER	2.2
1	A	472	LEU	2.2
2	B	49	VAL	2.1
2	B	75	GLN	2.1
1	A	537	VAL	2.1
1	A	465	GLU	2.1
1	A	572	SER	2.1
2	B	107	HIS	2.1
1	A	528	ASN	2.1
1	A	374	ALA	2.0
1	A	470	ALA	2.0
1	A	574	ALA	2.0
1	A	485	ASP	2.0

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

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.