



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 10:49 AM UTC

PDB ID : 4J40 / pdb_00004j40
Title : Crystal structure of the dual-domain GGDEF-EAL module of FimX from *Pseudomonas aeruginosa*
Authors : Navarro, M.V.; De, N.; Bae, N.; Wang, Q.; Sondermann, H.
Deposited on : 2013-02-06
Resolution : 2.99 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
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

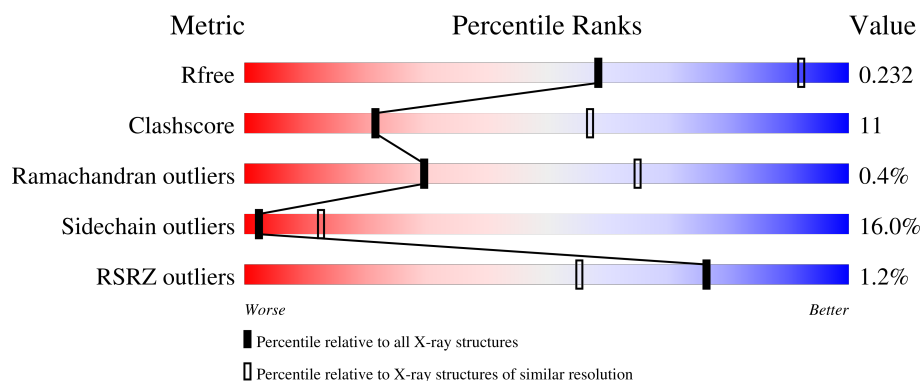
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	437	
1	B	437	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3916 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 FimX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	0	0
			1958	1257	335	363	3			
1	B	251	Total	C	N	O	S	0	0	0
			1958	1257	335	363	3			

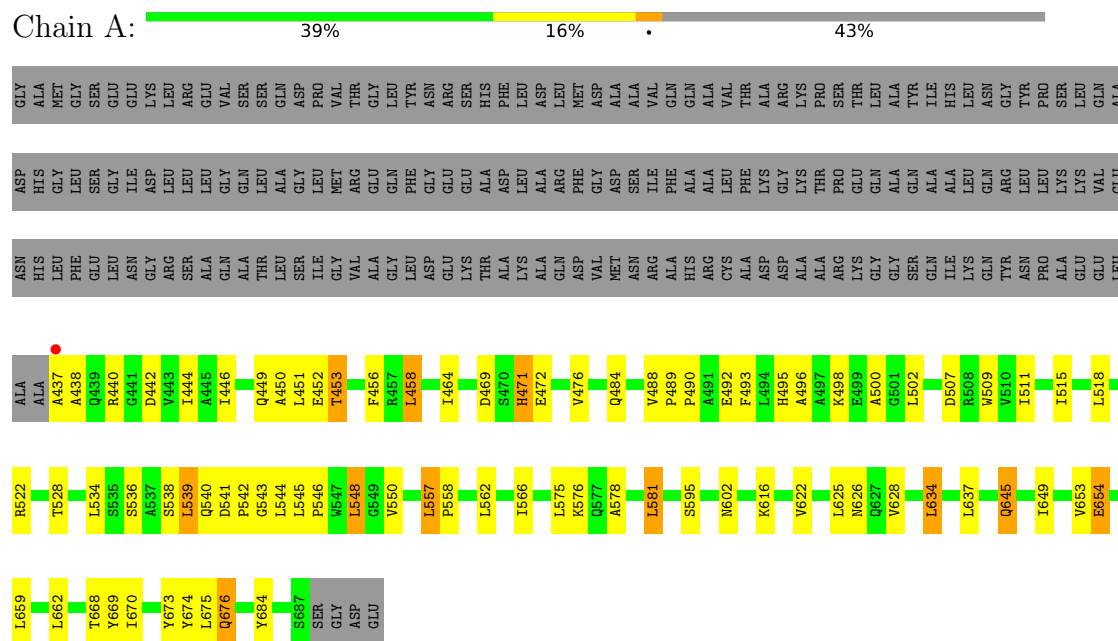
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	255	GLY	-	expression tag	UNP Q9HUK6
A	256	ALA	-	expression tag	UNP Q9HUK6
A	257	MET	-	expression tag	UNP Q9HUK6
A	258	GLY	-	expression tag	UNP Q9HUK6
A	259	SER	-	expression tag	UNP Q9HUK6
B	255	GLY	-	expression tag	UNP Q9HUK6
B	256	ALA	-	expression tag	UNP Q9HUK6
B	257	MET	-	expression tag	UNP Q9HUK6
B	258	GLY	-	expression tag	UNP Q9HUK6
B	259	SER	-	expression tag	UNP Q9HUK6

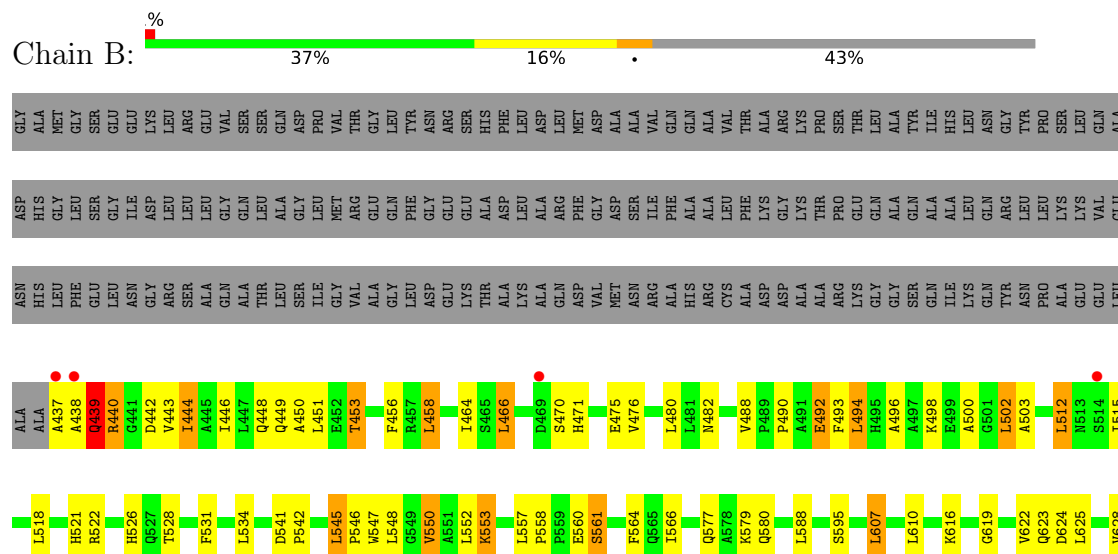
3 Residue-property plots

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: FimX



• Molecule 1: FimX





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	106.25Å 106.25Å 193.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.36 – 2.99 25.36 – 2.99	Depositor EDS
% Data completeness (in resolution range)	90.0 (25.36-2.99) 89.8 (25.36-2.99)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.31 (at 3.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.208 , 0.232 0.207 , 0.232	Depositor DCC
R_{free} test set	2000 reflections (9.65%)	wwPDB-VP
Wilson B-factor (Å ²)	79.4	Xtriage
Anisotropy	0.371	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 39.1	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	0.95	EDS
Total number of atoms	3916	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% 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

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	0/1999	0.80	2/2715 (0.1%)
1	B	0.32	0/1999	0.81	1/2715 (0.0%)
All	All	0.33	0/3998	0.80	3/5430 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	439	GLN	N-CA-C	5.97	115.97	108.45
1	A	602	ASN	CA-C-N	5.94	126.36	119.47
1	A	602	ASN	C-N-CA	5.94	126.36	119.47

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	1958	0	1973	44	0
1	B	1958	0	1973	54	0
All	All	3916	0	3946	85	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 11.

All (85) 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:496:ALA:HB2	1:B:654:GLU:HG2	1.63	0.81
1:A:674:TYR:O	1:B:440:ARG:NH2	2.17	0.78
1:A:440:ARG:NH2	1:B:674:TYR:O	2.22	0.72
1:A:449:GLN:O	1:A:453:THR:OG1	2.08	0.71
1:B:439:GLN:OE1	1:B:482:ASN:ND2	2.25	0.69
1:A:673:TYR:HB2	1:B:492:GLU:HG2	1.73	0.69
1:B:522:ARG:HD2	1:B:558:PRO:HG2	1.74	0.68
1:B:653:VAL:HG21	1:B:670:ILE:HG23	1.78	0.65
1:B:518:LEU:HD23	1:B:557:LEU:HD21	1.79	0.65
1:A:654:GLU:HG3	1:B:443:VAL:HB	1.80	0.63
1:B:552:LEU:HB2	1:B:553:LYS:HZ2	1.64	0.62
1:B:515:ILE:HG23	1:B:557:LEU:HD22	1.82	0.62
1:B:444:ILE:HD13	1:B:500:ALA:HB2	1.82	0.61
1:B:534:LEU:HB2	1:B:566:ILE:HG22	1.83	0.59
1:B:545:LEU:HG	1:B:546:PRO:HD3	1.84	0.57
1:B:545:LEU:HD23	1:B:545:LEU:H	1.69	0.57
1:A:464:ILE:HD13	1:A:675:LEU:HD23	1.88	0.56
1:B:670:ILE:HG22	1:B:675:LEU:HD21	1.86	0.56
1:B:475:GLU:HA	1:B:531:PHE:HB2	1.88	0.55
1:A:676:GLN:HG3	1:A:684:TYR:CD2	2.43	0.54
1:A:595:SER:HA	1:A:616:LYS:HB3	1.90	0.53
1:A:539:LEU:HD21	1:A:578:ALA:HA	1.89	0.53
1:A:489:PRO:HB2	1:A:492:GLU:HB2	1.91	0.51
1:B:466:LEU:HD11	1:B:670:ILE:HD12	1.93	0.51
1:A:511:ILE:O	1:A:515:ILE:HG12	2.11	0.51
1:A:676:GLN:HA	1:B:440:ARG:HB3	1.93	0.51
1:B:629:GLU:O	1:B:633:ILE:HG12	2.11	0.51
1:A:654:GLU:HG2	1:B:496:ALA:HB2	1.93	0.50
1:A:495:HIS:HE1	1:B:619:GLY:HA3	1.76	0.50
1:A:534:LEU:HB2	1:A:566:ILE:HG22	1.94	0.50
1:A:659:LEU:HD12	1:A:675:LEU:HD11	1.94	0.49
1:B:490:PRO:HA	1:B:493:PHE:CD2	2.48	0.49
1:B:595:SER:HA	1:B:616:LYS:HB3	1.94	0.49
1:A:653:VAL:HG22	1:A:662:LEU:HD12	1.94	0.48
1:B:522:ARG:HA	1:B:526:HIS:O	2.13	0.48
1:A:536:SER:O	1:A:540:GLN:HG3	2.14	0.48
1:B:466:LEU:HD13	1:B:663:TRP:HD1	1.79	0.47
1:A:492:GLU:HG2	1:B:673:TYR:HB2	1.95	0.47
1:A:437:ALA:HA	1:A:438:ALA:HA	1.60	0.47
1:B:670:ILE:CG2	1:B:675:LEU:HD21	2.45	0.47
1:A:472:GLU:HB2	1:A:528:THR:HG22	1.97	0.46
1:B:450:ALA:HA	1:B:453:THR:HG23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:466:LEU:HD13	1:B:663:TRP:CD1	2.50	0.46
1:A:490:PRO:HA	1:A:493:PHE:CE2	2.50	0.46
1:A:545:LEU:HD21	1:A:581:LEU:HD23	1.98	0.46
1:A:625:LEU:HD21	1:A:634:LEU:HD12	1.97	0.46
1:B:448:GLN:HG3	1:B:502:LEU:HD21	1.97	0.45
1:B:558:PRO:O	1:B:561:SER:HB3	2.17	0.45
1:B:458:LEU:HD12	1:B:458:LEU:HA	1.83	0.45
1:A:498:LYS:HB3	1:B:623:GLN:HG3	1.98	0.44
1:A:444:ILE:HD13	1:A:500:ALA:HB2	2.00	0.44
1:A:458:LEU:HD13	1:A:509:TRP:HZ3	1.81	0.44
1:B:649:ILE:HG12	1:B:669:TYR:HB2	1.99	0.44
1:A:653:VAL:HG21	1:A:670:ILE:HB	1.99	0.44
1:A:492:GLU:CG	1:B:673:TYR:HB2	2.47	0.44
1:B:490:PRO:O	1:B:494:LEU:HB2	2.18	0.44
1:B:512:LEU:HD12	1:B:512:LEU:HA	1.79	0.43
1:A:557:LEU:HA	1:A:558:PRO:HD3	1.89	0.42
1:B:502:LEU:HD12	1:B:502:LEU:HA	1.88	0.42
1:B:442:ASP:O	1:B:446:ILE:HG13	2.19	0.42
1:A:442:ASP:O	1:A:446:ILE:HG13	2.18	0.42
1:A:492:GLU:HG3	1:B:654:GLU:OE2	2.19	0.42
1:B:653:VAL:HG22	1:B:662:LEU:HD12	2.00	0.42
1:A:541:ASP:HA	1:A:542:PRO:HD3	1.72	0.42
1:A:676:GLN:HG3	1:A:684:TYR:HD2	1.82	0.42
1:A:446:ILE:O	1:A:450:ALA:N	2.53	0.42
1:A:469:ASP:CG	1:A:471:HIS:HB2	2.45	0.42
1:B:548:LEU:HD11	1:B:564:PHE:CZ	2.55	0.42
1:A:507:ASP:OD2	1:A:538:SER:OG	2.32	0.41
1:A:544:LEU:O	1:A:548:LEU:HB2	2.20	0.41
1:B:437:ALA:HA	1:B:438:ALA:HA	1.55	0.41
1:A:649:ILE:HG12	1:A:669:TYR:HB2	2.03	0.41
1:B:547:TRP:O	1:B:550:VAL:HG22	2.20	0.41
1:A:518:LEU:O	1:A:522:ARG:HB2	2.20	0.41
1:A:543:GLY:C	1:A:546:PRO:HD2	2.46	0.41
1:B:625:LEU:HD23	1:B:625:LEU:HA	1.90	0.41
1:A:495:HIS:CE1	1:B:619:GLY:HA3	2.56	0.41
1:B:662:LEU:HB2	1:B:670:ILE:HD11	2.03	0.41
1:A:456:PHE:HB2	1:A:509:TRP:CH2	2.55	0.41
1:B:494:LEU:HD13	1:B:494:LEU:HA	1.85	0.41
1:B:541:ASP:HA	1:B:542:PRO:HD3	1.81	0.41
1:B:607:LEU:HD13	1:B:607:LEU:HA	1.92	0.41
1:B:456:PHE:CE1	1:B:480:LEU:HD13	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:464:ILE:HG12	1:B:675:LEU:HD23	2.02	0.40
1:B:553:LYS:H	1:B:553:LYS:CE	2.35	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	249/437 (57%)	235 (94%)	13 (5%)	1 (0%)	30	65
1	B	249/437 (57%)	231 (93%)	17 (7%)	1 (0%)	30	65
All	All	498/874 (57%)	466 (94%)	30 (6%)	2 (0%)	30	65

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	645	GLN
1	B	503	ALA

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	209/351 (60%)	183 (88%)	26 (12%)	4	20
1	B	209/351 (60%)	168 (80%)	41 (20%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	418/702 (60%)	351 (84%)	67 (16%)	2 12

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	451	LEU
1	A	452	GLU
1	A	453	THR
1	A	458	LEU
1	A	471	HIS
1	A	476	VAL
1	A	484	GLN
1	A	488	VAL
1	A	502	LEU
1	A	539	LEU
1	A	548	LEU
1	A	550	VAL
1	A	557	LEU
1	A	562	LEU
1	A	575	LEU
1	A	576	LYS
1	A	581	LEU
1	A	622	VAL
1	A	626	ASN
1	A	628	VAL
1	A	634	LEU
1	A	637	LEU
1	A	645	GLN
1	A	654	GLU
1	A	668	THR
1	A	676	GLN
1	B	439	GLN
1	B	440	ARG
1	B	444	ILE
1	B	449	GLN
1	B	451	LEU
1	B	453	THR
1	B	458	LEU
1	B	466	LEU
1	B	470	SER
1	B	471	HIS
1	B	476	VAL

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Mol	Chain	Res	Type
1	B	488	VAL
1	B	492	GLU
1	B	494	LEU
1	B	498	LYS
1	B	502	LEU
1	B	512	LEU
1	B	521	HIS
1	B	528	THR
1	B	545	LEU
1	B	550	VAL
1	B	553	LYS
1	B	560	GLU
1	B	561	SER
1	B	577	GLN
1	B	579	LYS
1	B	580	GLN
1	B	588	LEU
1	B	607	LEU
1	B	610	LEU
1	B	622	VAL
1	B	624	ASP
1	B	628	VAL
1	B	634	LEU
1	B	637	LEU
1	B	643	GLU
1	B	645	GLN
1	B	648	SER
1	B	668	THR
1	B	670	ILE
1	B	675	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	644	GLN
1	B	565	GLN
1	B	630	ASN
1	B	631	GLN

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 [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	251/437 (57%)	-0.06	1 (0%) 88 76	52, 76, 121, 180	0
1	B	251/437 (57%)	0.17	5 (1%) 65 41	58, 93, 136, 191	0
All	All	502/874 (57%)	0.05	6 (1%) 76 55	52, 86, 129, 191	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	629	GLU	3.1
1	B	438	ALA	2.8
1	B	437	ALA	2.6
1	A	437	ALA	2.6
1	B	514	SER	2.4
1	B	469	ASP	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 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.