



wwPDB X-ray Structure Validation Summary Report ⓘ

May 27, 2025 – 10:32 am BST

PDB ID : 9HYJ / pdb_00009hyj
Title : AlfB fucosidase in complex with Fucose
Authors : Marina, A.; Gallego del Sol, F.
Deposited on : 2025-01-10
Resolution : 2.25 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 Phenix2.0rc1
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

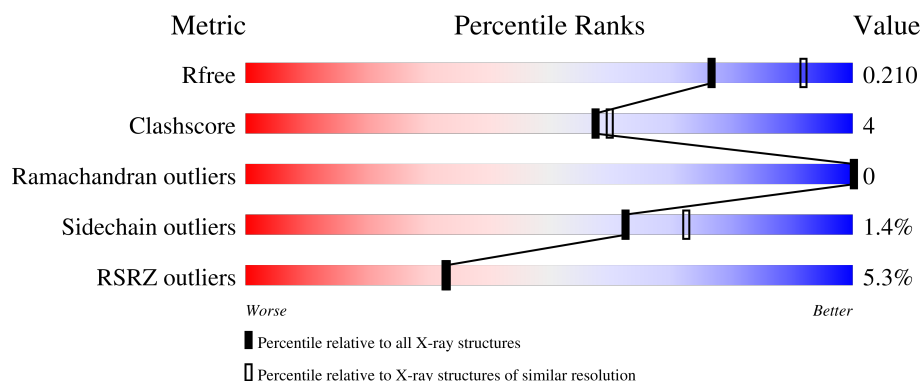
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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}	164625	1763 (2.26-2.26)
Clashscore	180529	1919 (2.26-2.26)
Ramachandran outliers	177936	1884 (2.26-2.26)
Sidechain outliers	177891	1885 (2.26-2.26)
RSRZ outliers	164620	1763 (2.26-2.26)

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	414	<div> <div>5%</div> <div> <div></div> <div>87%</div> <div>11%</div> <div>.</div> </div> </div>
1	B	414	<div> <div>6%</div> <div> <div></div> <div>86%</div> <div>12%</div> <div>..</div> </div> </div>
1	C	414	<div> <div>5%</div> <div> <div></div> <div>86%</div> <div>12%</div> <div>..</div> </div> </div>
1	D	414	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>11%</div> <div>..</div> </div> </div>
1	E	414	<div> <div>5%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>..</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	414	<div><div></div><div>7%</div><div></div><div>87%</div><div></div><div>10%</div><div>..</div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 20742 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 Alpha-L-fucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	412	Total	C	N	O	S	0	0	0
			3293	2119	559	604	11			
1	B	410	Total	C	N	O	S	0	1	0
			3282	2112	558	601	11			
1	C	407	Total	C	N	O	S	0	0	0
			3257	2097	553	597	10			
1	D	409	Total	C	N	O	S	0	0	0
			3271	2104	556	601	10			
1	E	407	Total	C	N	O	S	0	1	0
			3266	2103	555	598	10			
1	F	410	Total	C	N	O	S	0	0	0
			3276	2109	556	601	10			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	196	SER	ASN	conflict	UNP A0A806EKD1
A	261	MET	VAL	conflict	UNP A0A806EKD1
A	346	LYS	ASN	conflict	UNP A0A806EKD1
B	196	SER	ASN	conflict	UNP A0A806EKD1
B	261	MET	VAL	conflict	UNP A0A806EKD1
B	346	LYS	ASN	conflict	UNP A0A806EKD1
C	196	SER	ASN	conflict	UNP A0A806EKD1
C	261	MET	VAL	conflict	UNP A0A806EKD1
C	346	LYS	ASN	conflict	UNP A0A806EKD1
D	196	SER	ASN	conflict	UNP A0A806EKD1
D	261	MET	VAL	conflict	UNP A0A806EKD1
D	346	LYS	ASN	conflict	UNP A0A806EKD1
E	196	SER	ASN	conflict	UNP A0A806EKD1
E	261	MET	VAL	conflict	UNP A0A806EKD1
E	346	LYS	ASN	conflict	UNP A0A806EKD1
F	196	SER	ASN	conflict	UNP A0A806EKD1
F	261	MET	VAL	conflict	UNP A0A806EKD1

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Chain	Residue	Modelled	Actual	Comment	Reference
F	346	LYS	ASN	conflict	UNP A0A806EKD1

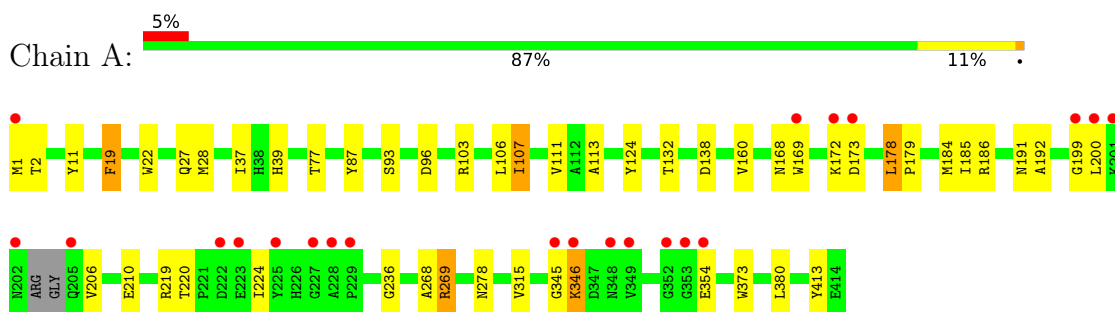
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	203	Total 203	O 203	0	0
2	B	197	Total 197	O 197	0	0
2	C	155	Total 155	O 155	0	0
2	D	225	Total 225	O 225	0	0
2	E	153	Total 153	O 153	0	0
2	F	164	Total 164	O 164	0	0

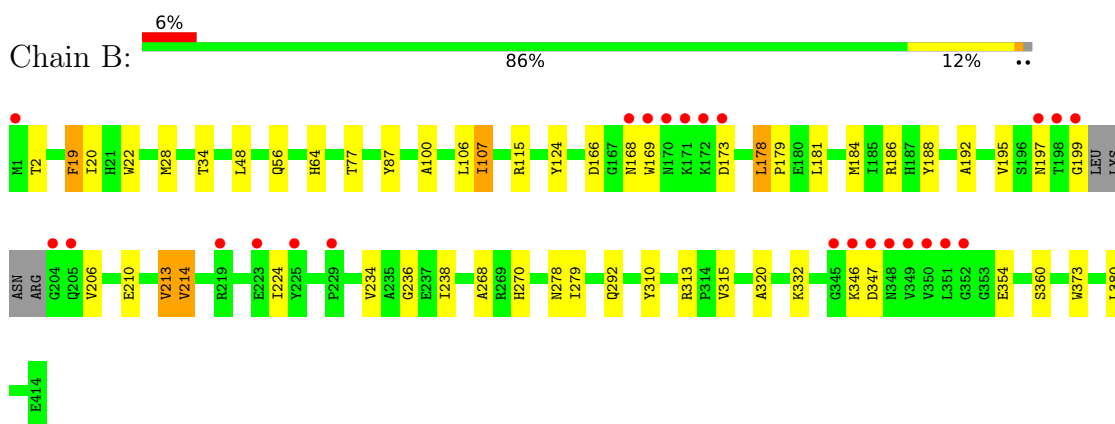
3 Residue-property plots [i](#)

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.

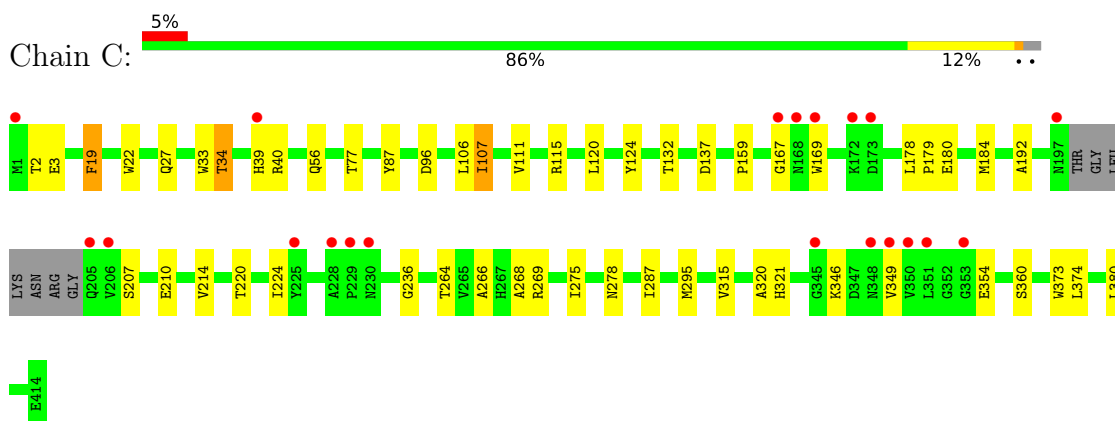
• Molecule 1: Alpha-L-fucosidase



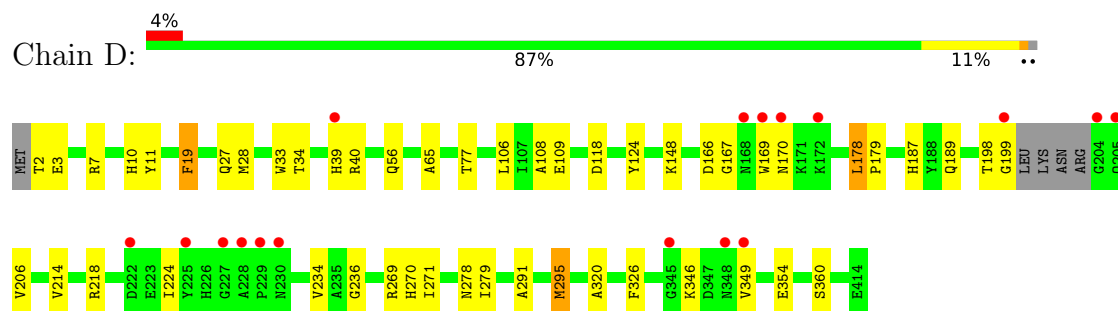
• Molecule 1: Alpha-L-fucosidase



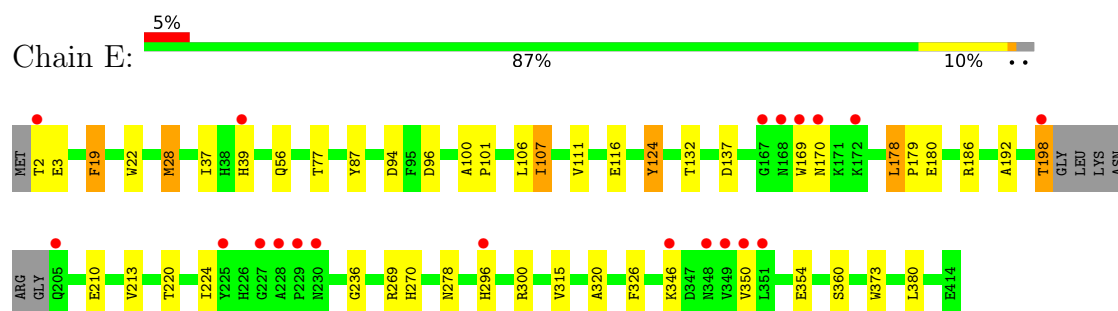
• Molecule 1: Alpha-L-fucosidase



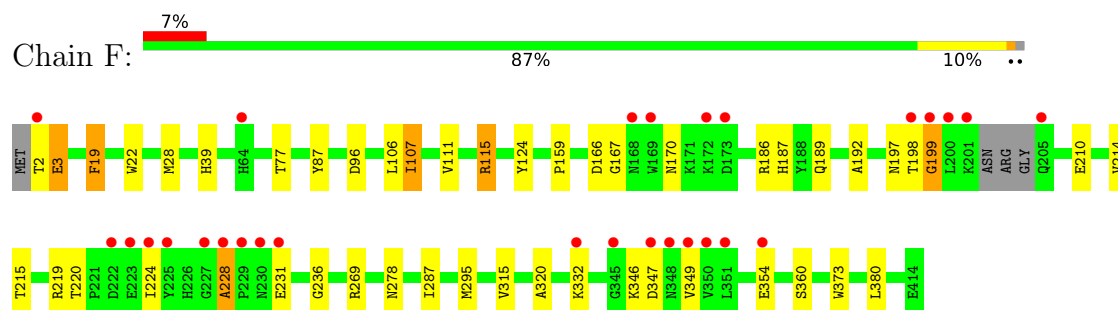
- Molecule 1: Alpha-L-fucosidase



- Molecule 1: Alpha-L-fucosidase



- Molecule 1: Alpha-L-fucosidase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	167.16Å 308.29Å 173.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.03 – 2.25 49.03 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.03-2.25) 99.9 (49.03-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.8.0430	Depositor
R, R_{free}	0.180 , 0.209 0.181 , 0.210	Depositor DCC
R_{free} test set	10595 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	34.3	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 35.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20742	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.52% 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

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	1.00	9/3390 (0.3%)	1.09	9/4622 (0.2%)
1	B	0.93	6/3383 (0.2%)	1.11	8/4612 (0.2%)
1	C	0.95	4/3354 (0.1%)	1.10	10/4574 (0.2%)
1	D	1.03	12/3368 (0.4%)	1.12	5/4592 (0.1%)
1	E	0.85	2/3367 (0.1%)	1.11	12/4592 (0.3%)
1	F	0.83	2/3373 (0.1%)	1.11	11/4600 (0.2%)
All	All	0.93	35/20235 (0.2%)	1.11	55/27592 (0.2%)

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	271	ILE	C-O	-6.84	1.16	1.24
1	D	189	GLN	C-O	-6.39	1.16	1.24
1	C	268	ALA	C-O	-6.14	1.17	1.24
1	C	27	GLN	C-O	-5.97	1.17	1.24
1	D	109	GLU	C-O	-5.89	1.17	1.24

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	220	THR	CA-C-N	8.85	128.50	118.85
1	E	220	THR	C-N-CA	8.85	128.50	118.85
1	C	220	THR	CA-C-N	8.71	128.35	118.85
1	C	220	THR	C-N-CA	8.71	128.35	118.85
1	F	215	THR	CA-CB-OG1	-7.57	98.25	109.60

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	3293	0	3166	24	0
1	B	3282	0	3155	31	0
1	C	3257	0	3128	29	0
1	D	3271	0	3142	36	0
1	E	3266	0	3137	34	0
1	F	3276	0	3146	38	0
2	A	203	0	0	3	0
2	B	197	0	0	2	0
2	C	155	0	0	0	0
2	D	225	0	0	4	0
2	E	153	0	0	0	0
2	F	164	0	0	0	0
All	All	20742	0	18874	169	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 4.

The worst 5 of 169 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:39:HIS:NE2	1:B:346:LYS:HD3	1.83	0.94
1:E:39:HIS:CE1	1:F:346:LYS:HE3	2.03	0.93
1:E:39:HIS:CE1	1:F:346:LYS:HG3	2.05	0.91
1:E:186:ARG:HD2	1:E:210:GLU:OE1	1.70	0.90
1:D:279:ILE:HD11	1:D:295:MET:CE	2.03	0.88

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	408/414 (99%)	396 (97%)	12 (3%)	0	100	100
1	B	407/414 (98%)	397 (98%)	10 (2%)	0	100	100
1	C	403/414 (97%)	391 (97%)	12 (3%)	0	100	100
1	D	405/414 (98%)	394 (97%)	11 (3%)	0	100	100
1	E	404/414 (98%)	395 (98%)	9 (2%)	0	100	100
1	F	406/414 (98%)	396 (98%)	10 (2%)	0	100	100
All	All	2433/2484 (98%)	2369 (97%)	64 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	343/346 (99%)	337 (98%)	6 (2%)	56	66
1	B	342/346 (99%)	338 (99%)	4 (1%)	67	76
1	C	339/346 (98%)	333 (98%)	6 (2%)	54	64
1	D	341/346 (99%)	339 (99%)	2 (1%)	84	89
1	E	341/346 (99%)	333 (98%)	8 (2%)	45	54
1	F	341/346 (99%)	339 (99%)	2 (1%)	84	89
All	All	2047/2076 (99%)	2019 (99%)	28 (1%)	62	72

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	214	VAL
1	F	354	GLU
1	D	354	GLU
1	E	198	THR
1	D	56	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	187	HIS
1	E	366	GLN
1	F	27	GLN
1	C	168	ASN
1	B	410	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	412/414 (99%)	-0.29	22 (5%)	33 33	19, 30, 76, 116	0
1	B	410/414 (99%)	-0.32	24 (5%)	29 29	19, 30, 74, 135	1 (0%)
1	C	407/414 (98%)	-0.19	20 (4%)	36 35	21, 34, 71, 134	0
1	D	409/414 (98%)	-0.44	17 (4%)	41 41	19, 28, 67, 112	0
1	E	407/414 (98%)	-0.11	20 (4%)	36 35	18, 35, 77, 123	1 (0%)
1	F	410/414 (99%)	-0.14	28 (6%)	25 24	23, 33, 82, 150	0
All	All	2455/2484 (98%)	-0.25	131 (5%)	33 33	18, 32, 75, 150	2 (0%)

The worst 5 of 131 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	169	TRP	9.4
1	F	228	ALA	8.2
1	A	202	ASN	7.8
1	F	169	TRP	7.1
1	F	225	TYR	6.9

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 monosaccharides 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.