W O R L D W I D E

wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Sep 13, 2023 – 09:58 AM EDT

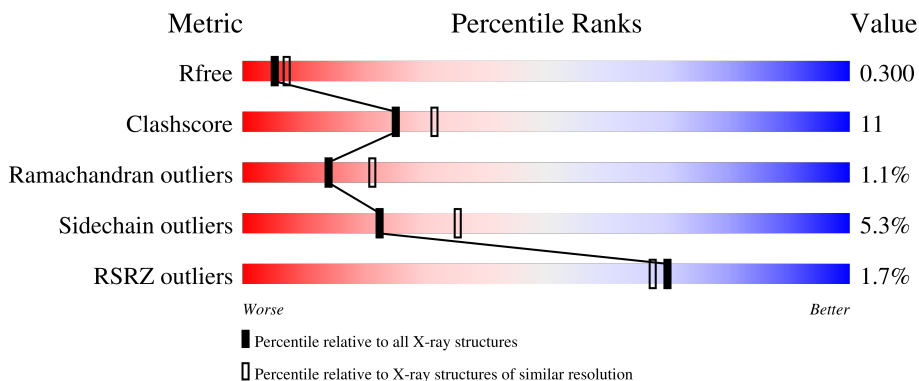|		
PDB ID	:	4OUD
Title	:	Engineered tyrosyl-tRNA synthetase with the nonstandard amino acid L-4,4-biphenylalanine
Authors	:	Takeuchi, R.; Mandell, D.J.; Lajoie, M.J.; Church, G.M.; Stoddard, B.L.
Deposited on	:	2014-02-16
Resolution	:	2.65 Å(reported)

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 2.65 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	Percentile Ranks	Value
Rfree		0.300
Clashscore		11
Ramachandran outliers		1.1%
Sidechain outliers		5.3%
RSRZ outliers		1.7%

Worse ... *Better*

▮ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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 <=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	425	% 80% 16% · ·
2	B	394	2% 64% 22% · · 9%

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 6108 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 Tyrosyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total 3249	C 2060	N 562	O 614	S 13	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP U6N9P2
A	1	PRO	-	expression tag	UNP U6N9P2
A	49	ALA	LEU	engineered mutation	UNP U6N9P2
A	236	ALA	PHE	engineered mutation	UNP U6N9P2
A	260	ALA	TRP	engineered mutation	UNP U6N9P2
A	263	ALA	THR	engineered mutation	UNP U6N9P2
A	271	TRP	PHE	engineered mutation	UNP U6N9P2
A	275	GLY	PHE	engineered mutation	UNP U6N9P2
A	303	BIF	LEU	engineered mutation	UNP U6N9P2

- Molecule 2 is a protein called Tyrosyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	359	Total 2789	C 1778	N 479	O 520	S 12	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP U6N9P2
B	1	PRO	-	expression tag	UNP U6N9P2
B	49	ALA	LEU	engineered mutation	UNP U6N9P2
B	236	ALA	PHE	engineered mutation	UNP U6N9P2
B	260	ALA	TRP	engineered mutation	UNP U6N9P2
B	263	ALA	THR	engineered mutation	UNP U6N9P2
B	271	TRP	PHE	engineered mutation	UNP U6N9P2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	275	GLY	PHE	engineered mutation	UNP U6N9P2
B	303	BIF	LEU	engineered mutation	UNP U6N9P2

- Molecule 3 is TYROSINE (three-letter code: TYR) (formula: $C_9H_{11}NO_3$).
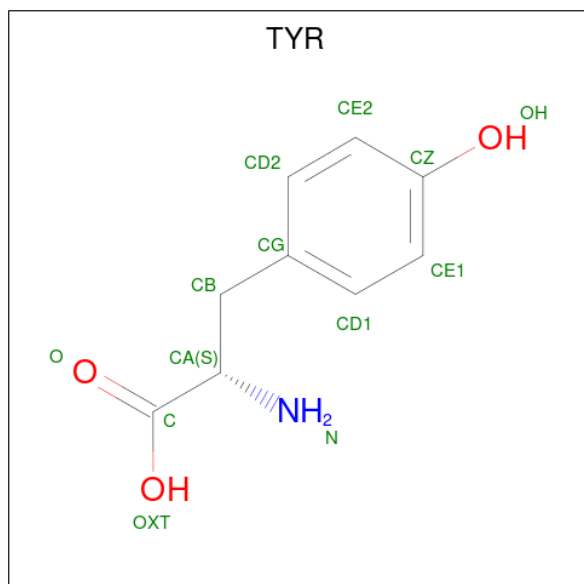
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 13	C 9	N 1	O 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	37	Total 37	O 37	0	0
4	B	20	Total 20	O 20	0	0

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 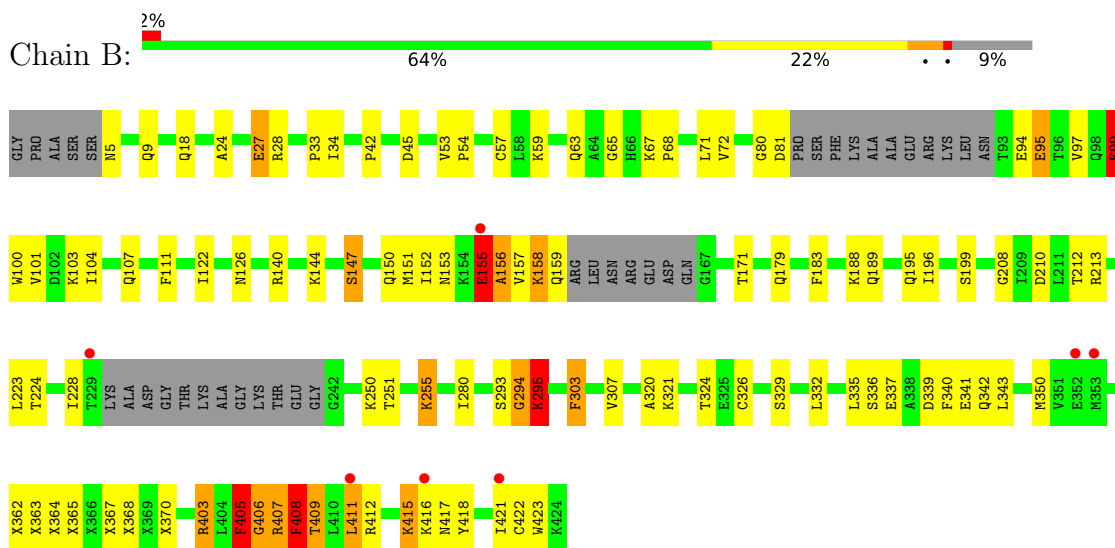= 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Tyrosyl-tRNA synthetase

Chain A:
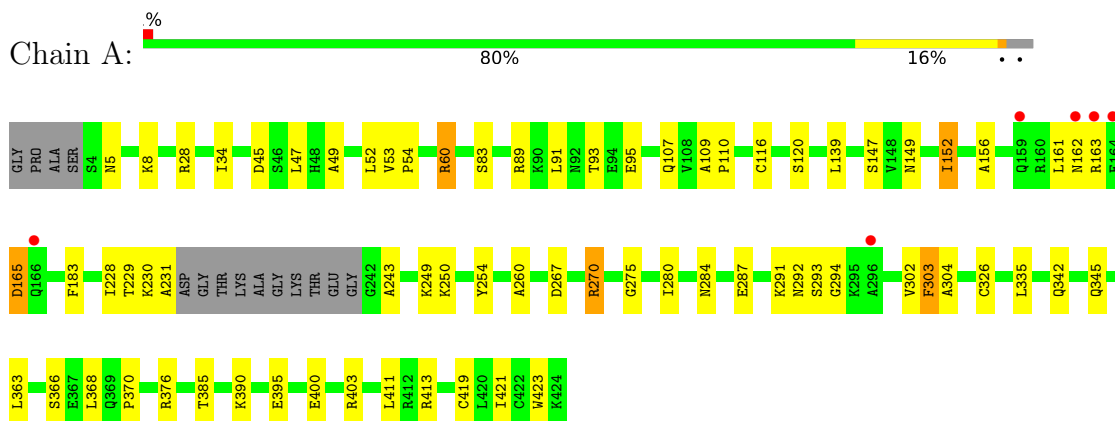
- Molecule 2: Tyrosyl-tRNA synthetase

Chain B:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	81.34Å 67.20Å 90.68Å 90.00° 102.65° 90.00°	Depositor
Resolution (Å)	45.00 – 2.65 44.24 – 2.65	Depositor EDS
% Data completeness (in resolution range)	98.9 (45.00-2.65) 98.9 (44.24-2.65)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.54 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.222 , 0.306 0.226 , 0.300	Depositor DCC
R_{free} test set	1398 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	46.7	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 33.5	EDS
L-test for twinning[2]	$< |L| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6108	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.55 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0057e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: BIF

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	0.61	0/3293	0.75	2/4442 (0.0%)
2	B	0.62	0/2738	0.81	1/3694 (0.0%)
All	All	0.61	0/6031	0.78	3/8136 (0.0%)

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
2	B	0	5
All	All	0	6

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	413	ARG	NE-CZ-NH1	7.09	123.84	120.30
2	B	408	PHE	N-CA-C	-5.76	95.44	111.00
1	A	163	ARG	N-CA-C	5.03	124.57	111.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	162	ASN	Peptide
2	B	155	GLU	Peptide
2	B	329	SER	Peptide

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Mol	Chain	Res	Type	Group
2	B	403	ARG	Peptide
2	B	405	PHE	Peptide

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	3249	0	3196	44	0
2	B	2789	0	2674	88	0
3	A	13	0	8	0	0
4	A	37	0	0	2	0
4	B	20	0	0	3	0
All	All	6108	0	5878	128	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.

The worst 5 of 128 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:407:ARG:CZ	2:B:407:ARG:HA	1.99	0.92
2:B:408:PHE:HB2	2:B:422:CYS:HA	1.51	0.88
2:B:320:ALA:O	2:B:324:THR:HG22	1.78	0.83
2:B:251:THR:HG23	2:B:255:LYS:HD2	1.62	0.81
1:A:45:ASP:OD1	1:A:250:LYS:HE3	1.82	0.79

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	406/425 (96%)	388 (96%)	15 (4%)	3 (1%)	22	33
2	B	331/394 (84%)	309 (93%)	17 (5%)	5 (2%)	10	15
All	All	737/819 (90%)	697 (95%)	32 (4%)	8 (1%)	14	21

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	293	SER
2	B	156	ALA
2	B	294	GLY
1	A	229	THR
2	B	295	LYS

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	340/348 (98%)	334 (98%)	6 (2%)	59	75
2	B	282/308 (92%)	255 (90%)	27 (10%)	8	12
All	All	622/656 (95%)	589 (95%)	33 (5%)	22	35

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	408	PHE
2	B	409	THR
2	B	416	LYS
2	B	147	SER
2	B	140	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	417	ASN
2	B	179	GLN
2	B	176	ASN
2	B	187	ASN
1	A	179	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	BIF	B	303	2	16,18,19	0.90	0	16,23,25	0.81	1 (6%)
1	BIF	A	303	1	16,18,19	0.95	0	16,23,25	0.99	1 (6%)

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
2	BIF	B	303	2	-	0/5/10/12	0/2/2/2
1	BIF	A	303	1	-	1/5/10/12	0/2/2/2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	303	BIF	CG-CB-CA	-3.14	107.75	114.10
2	B	303	BIF	CG-CB-CA	-2.17	109.71	114.10

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	303	BIF	CA-CB-CG-CD1

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	303	BIF	2	0
1	A	303	BIF	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	$\#|Z| > 2$
3	TYR	A	501	-	12,13,13	0.79	0	16,17,17	1.10	2 (12%)

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
3	TYR	A	501	-	-	0/8/8/8	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	501	TYR	OXT-C-O	-2.89	117.52	124.09
3	A	501	TYR	OXT-C-CA	2.59	122.21	113.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	354:GLU	C	361:UNK	N	19.35
1	B	377:UNK	C	403:ARG	N	12.46

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(Å²)	Q<0.9
1	A	410/425 (96%)	-0.36	6 (1%)	73	71	32, 50, 82, 150	0
2	B	341/394 (86%)	-0.21	7 (2%)	63	59	36, 57, 102, 123	0
All	All	751/819 (91%)	-0.29	13 (1%)	70	67	32, 53, 101, 150	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	163	ARG	3.8
2	B	421	ILE	3.6
1	A	162	ASN	3.3
2	B	411	LEU	2.9
1	A	166	GLN	2.7

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

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(Å²)	Q<0.9
1	BIF	A	303	17/18	0.97	0.13	40,42,44,44	0
2	BIF	B	303	17/18	0.97	0.13	41,45,46,47	0

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4   Ligands ⓘ

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
3	TYR	A	501	13/13	0.94	0.13	38,51,59,61	0

6.5   Other polymers ⓘ

There are no such residues in this entry.