



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:33 AM UTC

PDB ID : 6RCA / pdb_00006rca
Title : X-ray structure uridine phosphorylase from *Vibrio cholerae* in complex with 2.2'-anhydrouridine at 1.34 Å
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Deposited on : 2019-04-11
Resolution : 1.34 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 Phenix2.0
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

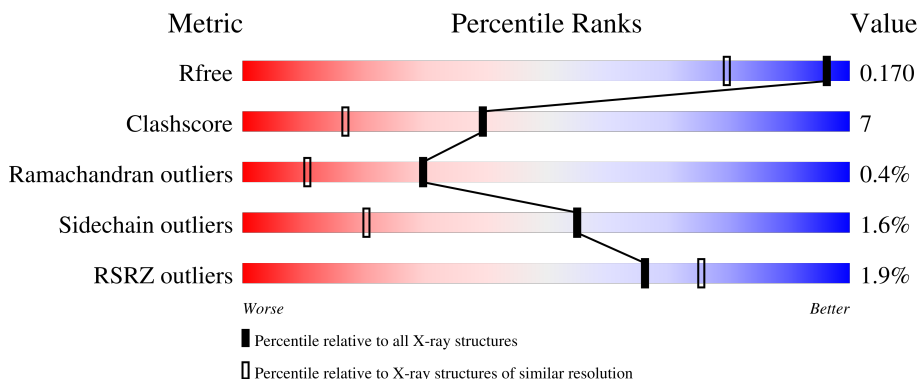
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.34 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.



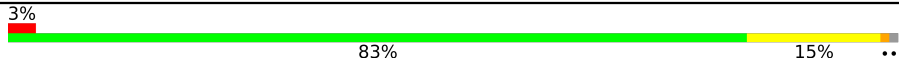
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2194 (1.36-1.32)
Clashscore	190562	2222 (1.36-1.32)
Ramachandran outliers	187476	2197 (1.36-1.32)
Sidechain outliers	187428	2197 (1.36-1.32)
RSRZ outliers	180081	2193 (1.36-1.32)

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	253	 88% 11%
1	B	253	 91% 8%
1	C	253	 83% 15%
1	D	253	 83% 16%
1	E	253	 84% 15%

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Mol	Chain	Length	Quality of chain
1	F	253	 3% 83% 15% **

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BJE	A	302	X	-	-	-
3	BJE	B	301	X	-	-	-
3	BJE	C	302	X	-	-	-
3	BJE	D	301	X	-	-	-
3	BJE	E	302	X	-	-	-
3	BJE	F	301	X	-	-	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14891 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.

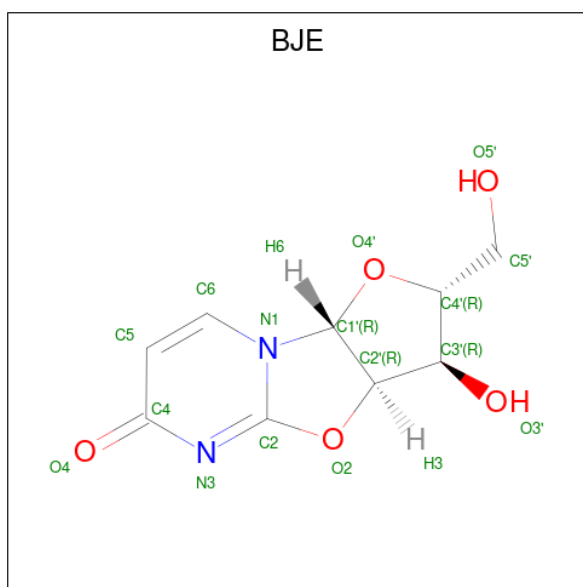
- Molecule 1 is a protein called Uridine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	251	2062	1287	365	392	18	0	22	0
1	B	252	2078	1294	368	399	17	0	22	0
1	C	251	2166	1351	388	409	18	0	35	0
1	D	252	2101	1310	371	403	17	0	27	0
1	E	251	2114	1325	371	400	18	0	32	0
1	F	251	2182	1363	388	413	18	0	37	0

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		
2	C	1	Total	Na	0	0
			1	1		
2	E	1	Total	Na	0	0
			1	1		

- Molecule 3 is 2,2'-Anhydro-(1-beta-D-ribofuranosyl)uracil (CCD ID: BJE) (formula: C₉H₁₀N₂O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	16	9	2	5	0	0
3	B	1	16	9	2	5	0	0
3	C	1	16	9	2	5	0	0
3	D	1	16	9	2	5	0	0
3	E	1	16	9	2	5	0	0
3	F	1	16	9	2	5	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 12 6 6	0	1
4	B	1	Total C O 6 3 3	0	0
4	D	1	Total C O 12 6 6	0	1
4	D	1	Total C O 12 6 6	0	1
4	D	1	Total C O 6 3 3	0	0
4	F	1	Total C O 12 6 6	0	1
4	F	1	Total C O 6 3 3	0	0
4	F	1	Total C O 12 6 6	0	1

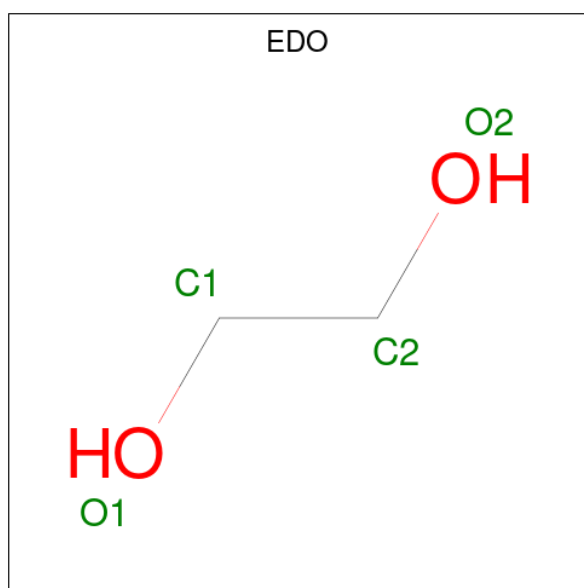
- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total Cl 1 1	0	0
5	F	1	Total Cl 1 1	0	0

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	1	Total Mg 1 1	0	0

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	F	1	Total C O 4 2 2	0	0

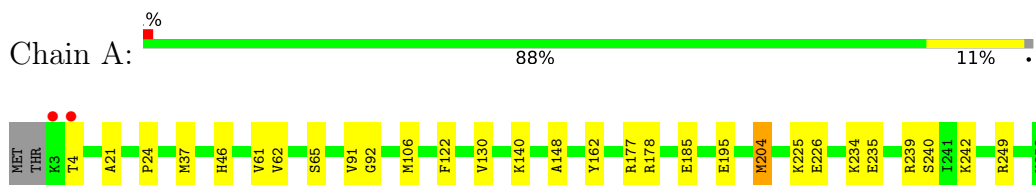
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	351	Total O 358 358	0	7
8	B	344	Total O 347 347	0	3
8	C	326	Total O 332 332	0	5
8	D	309	Total O 311 311	0	2
8	E	316	Total O 319 319	0	3
8	F	329	Total O 337 337	0	8

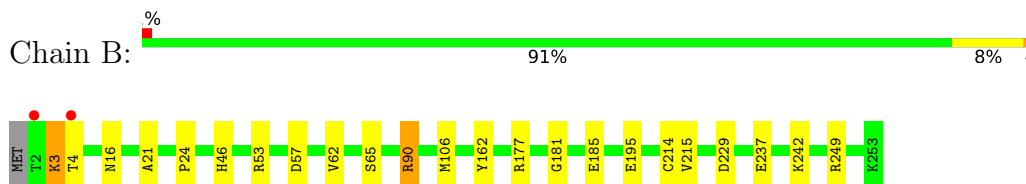
3 Residue-property plots [i](#)

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.

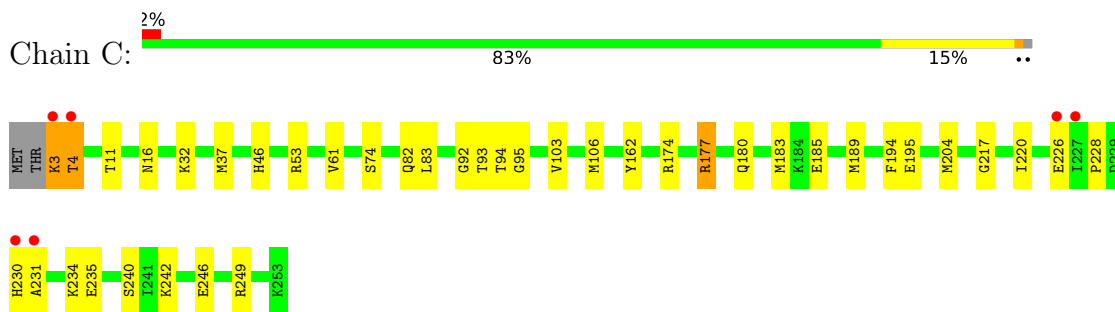
- Molecule 1: Uridine phosphorylase



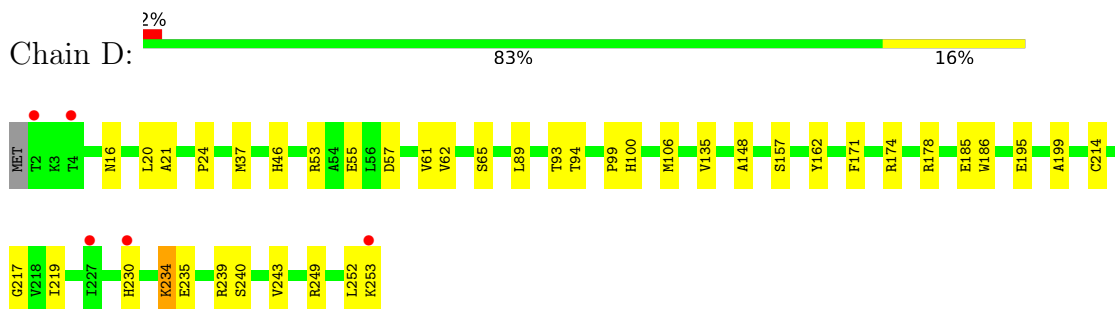
- Molecule 1: Uridine phosphorylase



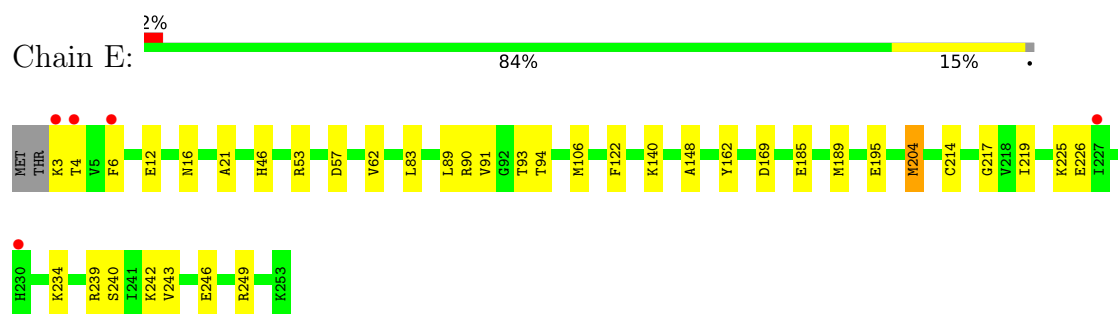
- Molecule 1: Uridine phosphorylase



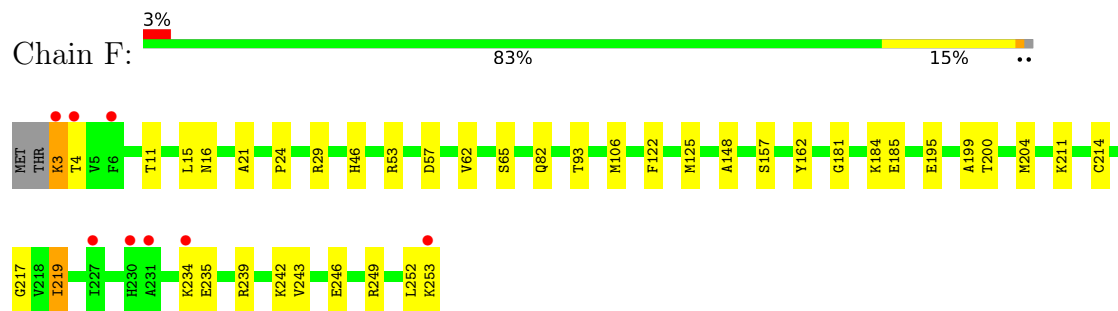
- Molecule 1: Uridine phosphorylase



- Molecule 1: Uridine phosphorylase



- Molecule 1: Uridine phosphorylase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	93.25Å 93.25Å 152.93Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.60 – 1.34 44.60 – 1.34	Depositor EDS
% Data completeness (in resolution range)	99.7 (44.60-1.34) 99.8 (44.60-1.34)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 1.34Å)	Xtrriage
Refinement program	PHENIX 2.6.1	Depositor
R, R_{free}	0.135 , 0.169 0.137 , 0.170	Depositor DCC
R_{free} test set	3463 reflections (1.05%)	wwPDB-VP
Wilson B-factor (Å ²)	9.4	Xtrriage
Anisotropy	0.590	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.55$, $\langle L^2 \rangle = 0.38$	Xtrriage
Estimated twinning fraction	0.000 for -h,-k,l 0.000 for h,-h-k,-l 0.000 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	14891	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.35 % 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 8.1136e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, MG, CL, NA, BJE, GOL

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	1.09	5/2109 (0.2%)	1.00	0/2849
1	B	1.00	1/2116 (0.0%)	1.02	0/2862
1	C	1.02	1/2206 (0.0%)	1.02	0/2978
1	D	1.09	5/2148 (0.2%)	1.02	2/2903 (0.1%)
1	E	1.07	2/2168 (0.1%)	1.02	0/2928
1	F	0.99	2/2233 (0.1%)	1.01	0/3012
All	All	1.04	16/12980 (0.1%)	1.02	2/17532 (0.0%)

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	174[A]	ARG	CA-C	8.94	1.63	1.52
1	D	174[B]	ARG	CA-C	8.94	1.63	1.52
1	A	91	VAL	C-O	-7.39	1.16	1.24
1	D	55	GLU	C-O	-7.19	1.15	1.23
1	F	219	ILE	C-O	6.24	1.31	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	235[A]	GLU	O-C-N	5.37	128.27	122.15
1	D	235[B]	GLU	O-C-N	5.37	128.27	122.15

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	2062	0	2072	19	0
1	B	2078	0	2073	19	0
1	C	2166	0	2171	41	0
1	D	2101	0	2106	32	0
1	E	2114	0	2141	27	0
1	F	2182	0	2200	35	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0
2	E	1	0	0	0	0
3	A	16	0	0	0	0
3	B	16	0	0	0	0
3	C	16	0	0	0	0
3	D	16	0	0	0	0
3	E	16	0	0	0	0
3	F	16	0	0	0	0
4	B	18	0	24	1	0
4	D	30	0	40	7	0
4	F	30	0	40	2	0
5	C	1	0	0	1	0
5	F	1	0	0	0	0
6	E	1	0	0	0	0
7	F	4	0	6	3	0
8	A	358	0	0	8	0
8	B	347	0	0	12	0
8	C	332	0	0	17	0
8	D	311	0	0	9	0
8	E	319	0	0	11	0
8	F	337	0	0	13	0
All	All	14891	0	12873	174	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 7.

The worst 5 of 174 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:C:93[B]:THR:CG2	8:C:402:HOH:O	1.67	1.22
1:C:93[B]:THR:HG23	8:C:402:HOH:O	1.24	1.16
1:F:3[A]:LYS:N	8:F:401[A]:HOH:O	1.90	1.05
1:B:214[A]:CYS:SG	8:B:644:HOH:O	2.30	0.90
1:E:93[B]:THR:HB	1:E:219:ILE:HG23	1.55	0.88

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	272/253 (108%)	269 (99%)	2 (1%)	1 (0%)	30	11
1	B	273/253 (108%)	267 (98%)	5 (2%)	1 (0%)	30	11
1	C	284/253 (112%)	278 (98%)	5 (2%)	1 (0%)	30	11
1	D	278/253 (110%)	274 (99%)	3 (1%)	1 (0%)	30	11
1	E	280/253 (111%)	276 (99%)	3 (1%)	1 (0%)	30	11
1	F	286/253 (113%)	280 (98%)	5 (2%)	1 (0%)	36	16
All	All	1673/1518 (110%)	1644 (98%)	23 (1%)	6 (0%)	30	11

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	162	TYR
1	E	162	TYR
1	A	162	TYR
1	B	162	TYR
1	C	162	TYR

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	224/203 (110%)	219 (98%)	5 (2%)	45	12
1	B	225/203 (111%)	222 (99%)	3 (1%)	61	26
1	C	233/203 (115%)	226 (97%)	7 (3%)	36	6
1	D	228/203 (112%)	227 (100%)	1 (0%)	84	67
1	E	230/203 (113%)	223 (97%)	7 (3%)	36	6
1	F	237/203 (117%)	232 (98%)	5 (2%)	47	13
All	All	1377/1218 (113%)	1349 (98%)	28 (2%)	55	14

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

Mol	Chain	Res	Type
1	C	226[B]	GLU
1	F	195	GLU
1	E	4[B]	THR
1	F	3[B]	LYS
1	E	4[A]	THR

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	144	GLN
1	C	193	ASN
1	D	82	GLN
1	E	16	ASN
1	E	144	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](#)

Of 26 ligands modelled in this entry, 6 are monoatomic - leaving 20 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
3	BJE	C	302	-	18,18,18	2.32	3 (16%)	23,27,27	2.48	9 (39%)
3	BJE	B	301	-	18,18,18	1.90	2 (11%)	23,27,27	2.51	6 (26%)
4	GOL	D	304	-	5,5,5	0.40	0	5,5,5	0.73	0
4	GOL	D	302[C]	-	5,5,5	0.21	0	5,5,5	0.45	0
3	BJE	D	301	-	18,18,18	2.16	4 (22%)	23,27,27	2.38	8 (34%)
3	BJE	F	301	-	18,18,18	1.86	2 (11%)	23,27,27	2.59	7 (30%)
4	GOL	D	302[B]	-	5,5,5	0.54	0	5,5,5	1.78	2 (40%)
4	GOL	B	302[B]	-	5,5,5	0.35	0	5,5,5	0.32	0
3	BJE	A	302	-	18,18,18	2.19	4 (22%)	23,27,27	2.32	11 (47%)
4	GOL	B	302[A]	-	5,5,5	0.31	0	5,5,5	0.59	0
3	BJE	E	302	-	18,18,18	1.77	2 (11%)	23,27,27	2.46	8 (34%)
7	EDO	F	302	-	3,3,3	0.18	0	2,2,2	0.44	0
4	GOL	F	305[A]	-	5,5,5	0.14	0	5,5,5	0.40	0
4	GOL	F	305[B]	-	5,5,5	0.21	0	5,5,5	0.40	0
4	GOL	F	304	-	5,5,5	0.18	0	5,5,5	0.76	0
4	GOL	F	303[B]	-	5,5,5	0.65	0	5,5,5	0.79	0
4	GOL	D	303[B]	-	5,5,5	0.25	0	5,5,5	0.82	0
4	GOL	F	303[A]	-	5,5,5	0.34	0	5,5,5	0.76	0
4	GOL	D	303[A]	-	5,5,5	0.38	0	5,5,5	1.04	0
4	GOL	B	303	-	5,5,5	0.31	0	5,5,5	0.40	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
3	BJE	C	302	-	1/1/4/4	0/2/26/26	0/3/3/3
3	BJE	B	301	-	1/1/4/4	0/2/26/26	0/3/3/3
4	GOL	D	304	-	-	2/4/4/4	-
4	GOL	D	302[C]	-	-	1/4/4/4	-
3	BJE	D	301	-	1/1/4/4	0/2/26/26	0/3/3/3
3	BJE	F	301	-	1/1/4/4	0/2/26/26	0/3/3/3
4	GOL	D	302[B]	-	-	2/4/4/4	-
4	GOL	B	302[B]	-	-	0/4/4/4	-
3	BJE	A	302	-	1/1/4/4	0/2/26/26	0/3/3/3
4	GOL	B	302[A]	-	-	3/4/4/4	-
3	BJE	E	302	-	1/1/4/4	0/2/26/26	0/3/3/3
7	EDO	F	302	-	-	0/1/1/1	-
4	GOL	F	305[A]	-	-	1/4/4/4	-
4	GOL	F	305[B]	-	-	2/4/4/4	-
4	GOL	F	304	-	-	3/4/4/4	-
4	GOL	F	303[B]	-	-	3/4/4/4	-
4	GOL	D	303[B]	-	-	3/4/4/4	-
4	GOL	F	303[A]	-	-	2/4/4/4	-
4	GOL	D	303[A]	-	-	4/4/4/4	-
4	GOL	B	303	-	-	3/4/4/4	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	302	BJE	C6-C5	7.60	1.52	1.35
3	A	302	BJE	C6-C5	6.91	1.51	1.35
3	B	301	BJE	C6-C5	6.87	1.51	1.35
3	D	301	BJE	C6-C5	6.73	1.50	1.35
3	F	301	BJE	C6-C5	6.41	1.49	1.35

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	301	BJE	N1-C2-N3	-6.12	121.74	127.09
3	D	301	BJE	N1-C2-N3	-5.94	121.90	127.09
3	E	302	BJE	C6-C5-C4	-5.71	115.88	120.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	301	BJE	C5-C6-N1	-5.70	112.57	121.84
3	B	301	BJE	N1-C2-N3	-5.48	122.30	127.09

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	302	BJE	C2'
3	B	301	BJE	C2'
3	C	302	BJE	C2'
3	D	301	BJE	C2'
3	E	302	BJE	C2'

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	302[B]	GOL	O1-C1-C2-C3
4	D	303[A]	GOL	O1-C1-C2-C3
4	D	303[B]	GOL	O1-C1-C2-C3
4	F	303[B]	GOL	O1-C1-C2-C3
4	F	304	GOL	O1-C1-C2-C3

There are no ring outliers.

7 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	304	GOL	3	0
4	D	302[B]	GOL	2	0
4	B	302[B]	GOL	1	0
7	F	302	EDO	3	0
4	F	305[A]	GOL	1	0
4	F	304	GOL	1	0
4	D	303[A]	GOL	2	0

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	251/253 (99%)	-0.63	2 (0%) 82 89	4, 10, 24, 63	24 (9%)
1	B	252/253 (99%)	-0.61	2 (0%) 82 89	3, 10, 23, 77	23 (9%)
1	C	251/253 (99%)	-0.47	6 (2%) 59 69	4, 10, 27, 69	38 (15%)
1	D	252/253 (99%)	-0.46	5 (1%) 65 74	4, 11, 30, 71	28 (11%)
1	E	251/253 (99%)	-0.51	5 (1%) 65 74	4, 10, 26, 70	34 (13%)
1	F	251/253 (99%)	-0.54	8 (3%) 50 61	3, 10, 22, 70	38 (15%)
All	All	1508/1518 (99%)	-0.54	28 (1%) 66 75	3, 10, 25, 77	185 (12%)

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	4[A]	THR	5.7
1	C	227	ILE	5.1
1	C	3[A]	LYS	4.2
1	E	6[A]	PHE	3.9
1	F	4[A]	THR	3.9

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

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
4	GOL	D	303[A]	6/6	0.80	0.22	59,61,63,67	6
4	GOL	D	303[B]	6/6	0.80	0.22	59,61,63,67	6
4	GOL	F	304	6/6	0.81	0.17	52,56,58,60	6
4	GOL	F	305[A]	6/6	0.84	0.16	40,42,43,44	6
4	GOL	F	305[B]	6/6	0.84	0.16	32,37,40,41	6
4	GOL	D	304	6/6	0.85	0.11	32,34,35,39	0
4	GOL	B	302[A]	6/6	0.86	0.15	22,27,29,30	6
4	GOL	B	302[B]	6/6	0.86	0.15	15,15,16,18	6
4	GOL	B	303	6/6	0.86	0.11	28,32,33,33	0
4	GOL	F	303[B]	6/6	0.89	0.12	13,14,17,17	6
4	GOL	F	303[A]	6/6	0.89	0.12	18,22,23,24	6
4	GOL	D	302[B]	6/6	0.90	0.11	14,15,18,18	6
4	GOL	D	302[C]	6/6	0.90	0.11	22,24,24,24	6
7	EDO	F	302	4/4	0.90	0.14	32,32,32,34	4
3	BJE	C	302	16/16	0.97	0.06	11,12,16,19	16
3	BJE	E	302	16/16	0.98	0.05	9,10,13,16	16
3	BJE	F	301	16/16	0.98	0.04	10,12,14,17	0
3	BJE	B	301	16/16	0.98	0.04	9,11,13,15	0
3	BJE	A	302	16/16	0.98	0.04	10,11,13,16	0
5	CL	C	301	1/1	0.99	0.10	26,26,26,26	0
5	CL	F	306	1/1	0.99	0.14	24,24,24,24	0
6	MG	E	303	1/1	0.99	0.09	21,21,21,21	1
3	BJE	D	301	16/16	0.99	0.04	11,12,15,17	0
2	NA	E	301	1/1	1.00	0.06	18,18,18,18	0
2	NA	A	301	1/1	1.00	0.05	18,18,18,18	0
2	NA	C	303	1/1	1.00	0.08	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.