



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 01:14 PM EDT

PDB ID : 6HB7 / pdb_00006hb7
Title : Crystal structure of E. coli tyrRS in complex with 5'-O-(N-L-tyrosyl)sulfamoyl-N3-methyluridine
Authors : De Graef, S.; Pang, L.; Strelkov, S.V.; Weeks, S.D.
Deposited on : 2018-08-09
Resolution : 1.90 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

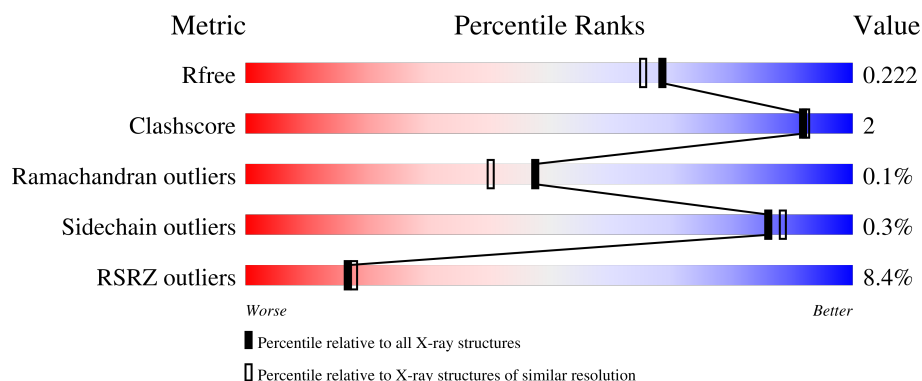
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	424	 3% 91% 5% •
1	B	424	 14% 92% 5% •

2 Entry composition [i](#)

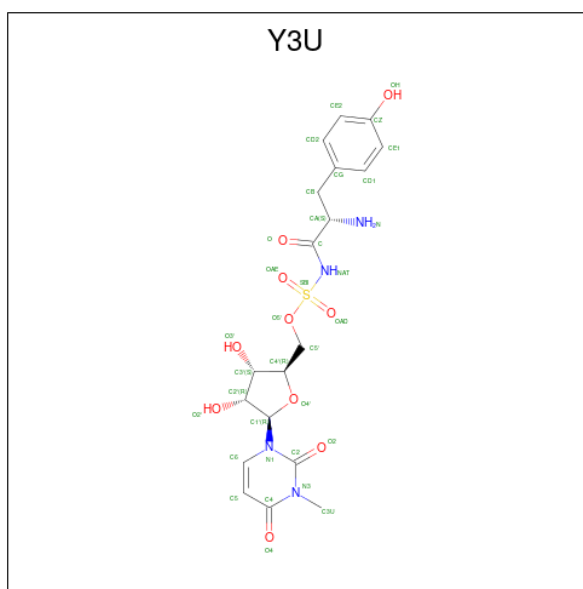
There are 5 unique types of molecules in this entry. The entry contains 7096 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Tyrosine-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total	C	N	O	S	0	1	0
			3219	2048	554	604	13			
1	B	413	Total	C	N	O	S	0	2	0
			3188	2022	550	603	13			

- Molecule 2 is [(2 {R},3 {S},4 {R},5 {R})-5-[3-methyl-2,4-bis(oxidanylidene)pyrimidin-1-yl]-3,4-bis(oxidanyl)oxolan-2-yl]methyl {N}-[(2 {S})-2-azanyl-3-(4-hydroxyphenyl)propano yl]sulfamate (CCD ID: Y3U) (formula: C₁₉H₂₄N₄O₁₀S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			34	19	4	10	1		
2	B	1	Total	C	N	O	S	0	0
			34	19	4	10	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

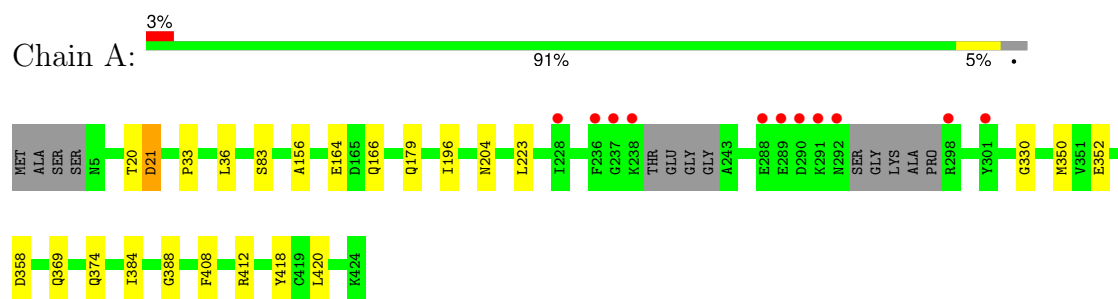
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	380	Total	O	0	0
			380	380		
5	B	228	Total	O	0	0
			228	228		

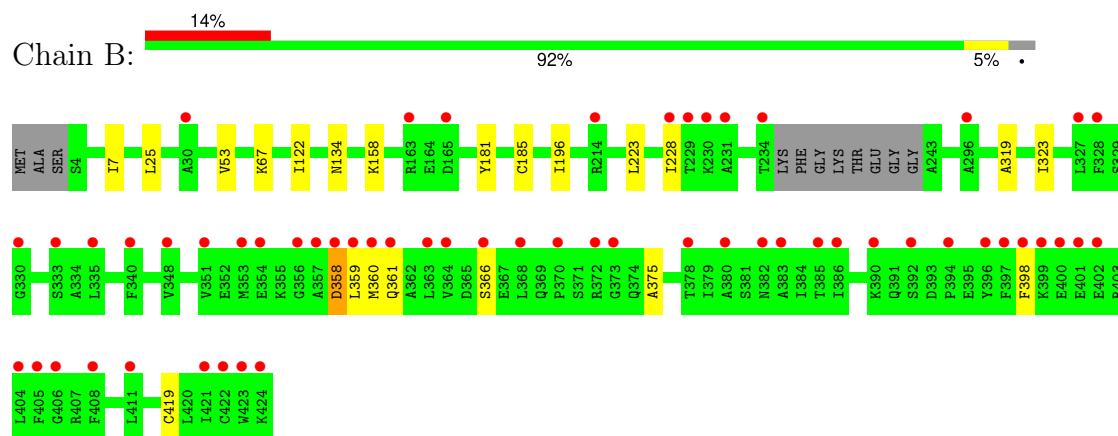
3 Residue-property plots [i](#)

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: Tyrosine-tRNA ligase



• Molecule 1: Tyrosine-tRNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.62Å 64.61Å 89.67Å 90.00° 100.98° 90.00°	Depositor
Resolution (Å)	27.85 – 1.90 27.85 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.5 (27.85-1.90) 98.5 (27.85-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 1.86Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.200 , 0.234 0.193 , 0.222	Depositor DCC
R_{free} test set	2270 reflections (2.94%)	wwPDB-VP
Wilson B-factor (Å ²)	29.2	Xtriage
Anisotropy	0.332	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7096	wwPDB-VP
Average B, all atoms (Å ²)	39.0	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 34.49 % 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 6.7698e-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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, Y3U, CL

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	0.85	0/3285	1.15	7/4441 (0.2%)
1	B	0.81	0/3256	1.23	4/4414 (0.1%)
All	All	0.83	0/6541	1.19	11/8855 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	21	ASP	CA-C-N	6.36	129.13	120.54
1	A	21	ASP	C-N-CA	6.36	129.13	120.54
1	B	359	LEU	CA-C-N	6.11	128.79	120.54
1	B	359	LEU	C-N-CA	6.11	128.79	120.54
1	A	358	ASP	CA-CB-CG	5.65	118.25	112.60
1	B	358	ASP	CA-CB-CG	5.43	118.03	112.60
1	A	164	GLU	CA-C-N	5.26	127.85	120.28
1	A	164	GLU	C-N-CA	5.26	127.85	120.28
1	A	384	ILE	N-CA-C	5.26	115.53	108.17
1	B	134	ASN	CA-CB-CG	5.22	117.83	112.60
1	A	166	GLN	N-CA-C	-5.18	104.22	110.44

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	3219	0	3128	10	0
1	B	3188	0	3066	10	0
2	A	34	0	0	0	0
2	B	34	0	0	0	0
3	A	12	0	18	1	0
4	A	1	0	0	0	0
5	A	380	0	0	0	0
5	B	228	0	0	0	0
All	All	7096	0	6212	20	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 2.

All (20) 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:B:53:VAL:HG21	1:B:228:ILE:HD11	1.75	0.69
1:A:33:PRO:HB2	3:A:502:EDO:H22	1.87	0.56
1:B:319:ALA:O	1:B:323:ILE:HG13	2.11	0.51
1:B:181:TYR:CE2	1:B:185:CYS:SG	3.05	0.50
1:A:412:ARG:HD3	1:A:418:TYR:CZ	2.47	0.48
1:B:67:LYS:HE3	1:B:122:ILE:CD1	2.44	0.48
1:A:350:MET:HE1	1:A:352:GLU:HG3	1.96	0.47
1:A:196:ILE:HA	1:A:223:LEU:O	2.14	0.47
1:A:179:GLN:CD	1:A:204:ASN:HB3	2.39	0.47
1:B:196:ILE:HA	1:B:223:LEU:O	2.15	0.46
1:A:83:SER:HA	1:A:156:ALA:HB1	1.98	0.46
1:A:408:PHE:HB3	1:A:420:LEU:HD11	1.98	0.45
1:B:366:SER:HB2	1:B:419:CYS:SG	2.56	0.45
1:A:20:THR:O	1:A:21:ASP:C	2.61	0.44
1:B:7:ILE:HD11	1:B:25:LEU:HG	1.99	0.44
1:B:67:LYS:HE3	1:B:122:ILE:HD11	2.01	0.43
1:B:358:ASP:HB3	1:B:361[A]:GLN:HB2	2.02	0.42
1:A:330:GLY:O	1:A:388:GLY:HA3	2.20	0.41
1:A:369:GLN:OE1	1:A:374:GLN:HG3	2.21	0.41
1:B:360:MET:HG3	1:B:375:ALA:HB3	2.02	0.41

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	406/424 (96%)	398 (98%)	8 (2%)	0	100	100
1	B	411/424 (97%)	400 (97%)	10 (2%)	1 (0%)	43	36
All	All	817/848 (96%)	798 (98%)	18 (2%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	398	PHE

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	333/354 (94%)	332 (100%)	1 (0%)	86	88
1	B	326/354 (92%)	325 (100%)	1 (0%)	86	88
All	All	659/708 (93%)	657 (100%)	2 (0%)	86	88

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

Mol	Chain	Res	Type
1	A	36	LEU
1	B	158	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	262	ASN
1	A	292	ASN
1	B	189	GLN
1	B	216	HIS
1	B	292	ASN
1	B	382	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	EDO	A	503	-	3,3,3	0.49	0	2,2,2	0.24	0
3	EDO	A	504	-	3,3,3	0.56	0	2,2,2	0.43	0
2	Y3U	B	501	-	36,36,36	0.29	0	49,53,53	0.77	2 (4%)
3	EDO	A	502	-	3,3,3	0.46	0	2,2,2	0.37	0
2	Y3U	A	501	-	36,36,36	0.29	0	49,53,53	0.82	1 (2%)

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	EDO	A	503	-	-	0/1/1/1	-
3	EDO	A	504	-	-	0/1/1/1	-
2	Y3U	B	501	-	-	1/22/39/39	0/3/3/3
3	EDO	A	502	-	-	1/1/1/1	-
2	Y3U	A	501	-	-	1/22/39/39	0/3/3/3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	Y3U	CB-CA-C	-3.82	100.04	108.97
2	B	501	Y3U	CB-CA-C	-3.34	101.15	108.97
2	B	501	Y3U	O-C-CA	2.07	124.63	120.28

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	Y3U	C-NAT-SBI-OAE
2	B	501	Y3U	C-NAT-SBI-OAE
3	A	502	EDO	O1-C1-C2-O2

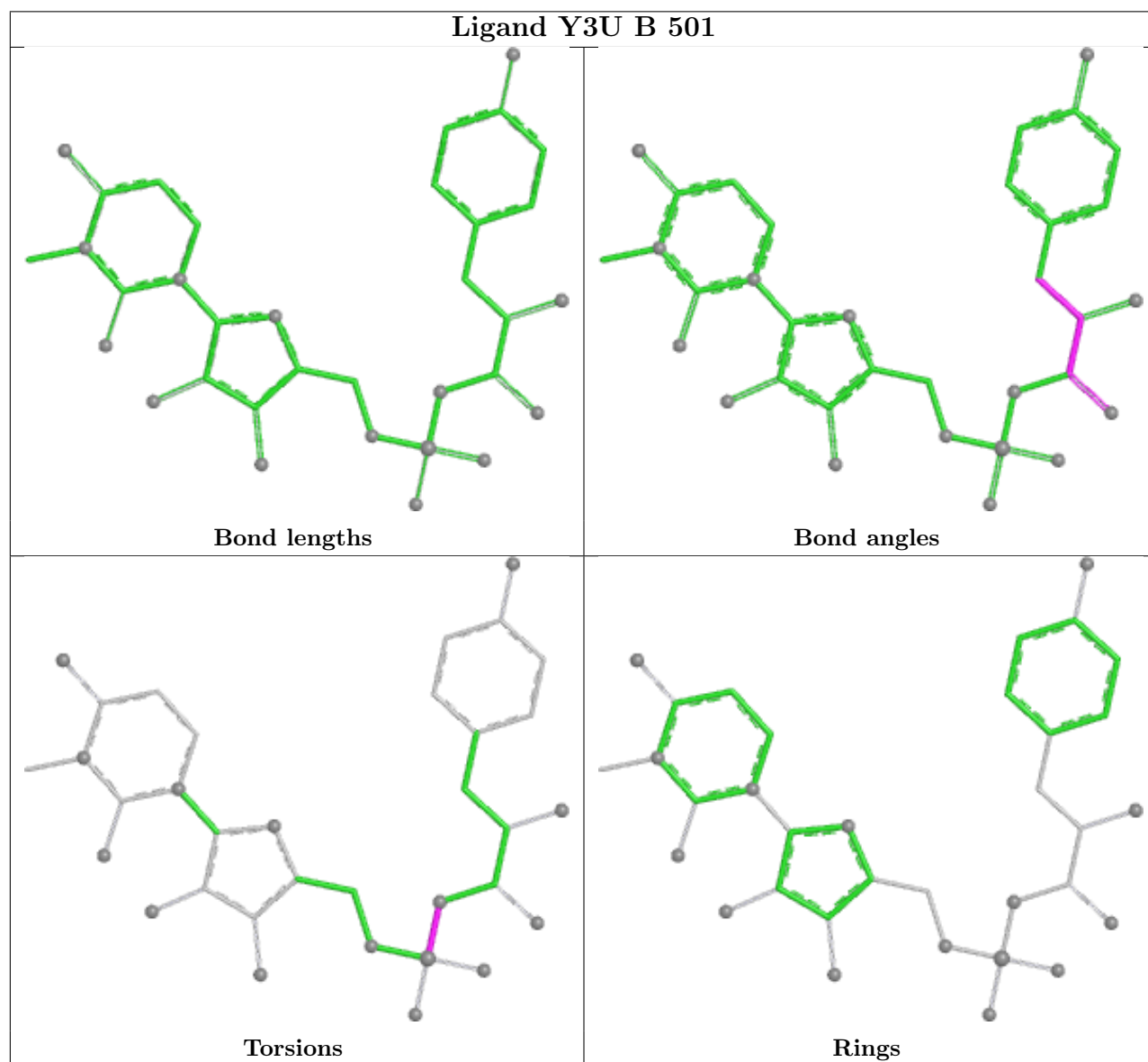
There are no ring outliers.

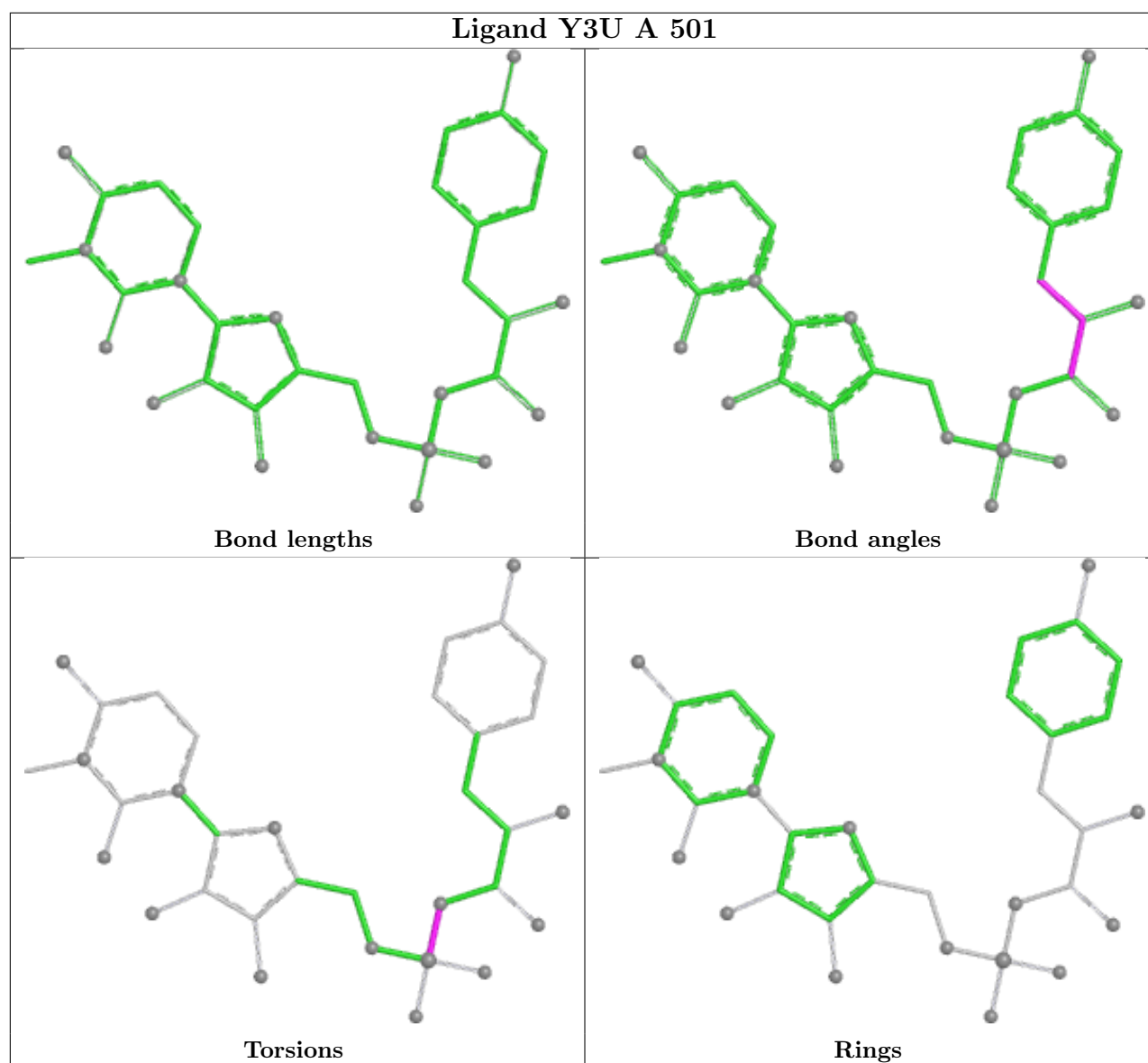
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	EDO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	411/424 (96%)	0.05	11 (2%) 56 60	19, 29, 55, 99	1 (0%)
1	B	413/424 (97%)	0.80	58 (14%) 6 6	22, 42, 73, 98	2 (0%)
All	All	824/848 (97%)	0.42	69 (8%) 17 18	19, 34, 71, 99	3 (0%)

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	359	LEU	5.3
1	A	228	ILE	4.8
1	B	361[A]	GLN	4.6
1	B	234	THR	4.5
1	B	423	TRP	4.3
1	B	398	PHE	4.1
1	B	357	ALA	4.1
1	B	397	PHE	4.0
1	B	424	LYS	3.9
1	A	238	LYS	3.8
1	B	404	LEU	3.8
1	B	296	ALA	3.8
1	B	399	LYS	3.8
1	A	290	ASP	3.7
1	B	228	ILE	3.5
1	B	372	ARG	3.5
1	B	370	PRO	3.3
1	B	358	ASP	3.3
1	A	292	ASN	3.3
1	B	356	GLY	3.2
1	B	373	GLY	3.2
1	B	405	PHE	3.2
1	A	301	TYR	3.1
1	A	236	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	289	GLU	3.0
1	B	330	GLY	3.0
1	B	340	PHE	2.9
1	B	363	LEU	2.9
1	B	383	ALA	2.9
1	A	288	GLU	2.9
1	A	291	LYS	2.9
1	B	421	ILE	2.8
1	B	328	PHE	2.8
1	B	366	SER	2.8
1	A	298	ARG	2.8
1	B	364	VAL	2.8
1	B	214	ARG	2.8
1	B	392	SER	2.7
1	B	396	TYR	2.7
1	B	353	MET	2.7
1	B	386	ILE	2.7
1	B	406	GLY	2.6
1	B	390	LYS	2.6
1	B	368	LEU	2.6
1	B	402	GLU	2.6
1	A	237	GLY	2.5
1	B	335	LEU	2.5
1	B	230	LYS	2.5
1	B	351	VAL	2.4
1	B	400	GLU	2.4
1	B	382	ASN	2.4
1	B	385	THR	2.4
1	B	394	PRO	2.4
1	B	333	SER	2.4
1	B	231	ALA	2.3
1	B	360	MET	2.3
1	B	229	THR	2.3
1	B	165	ASP	2.3
1	B	378	THR	2.3
1	B	354	GLU	2.2
1	B	408	PHE	2.2
1	B	163	ARG	2.2
1	B	348	VAL	2.2
1	B	380	ALA	2.2
1	B	422	CYS	2.2
1	B	327	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	411	LEU	2.2
1	B	401	GLU	2.1
1	B	30	ALA	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](#)

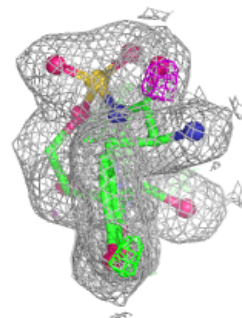
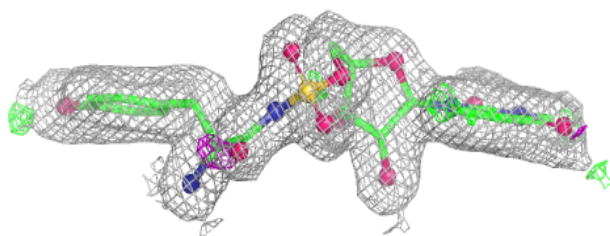
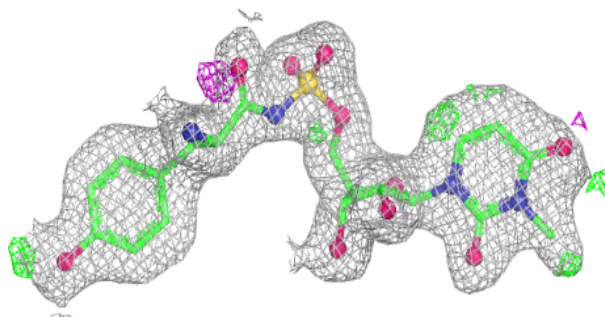
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	EDO	A	502	4/4	0.90	0.14	54,54,55,57	0
3	EDO	A	503	4/4	0.90	0.12	45,47,47,48	0
2	Y3U	A	501	34/34	0.95	0.08	15,23,38,43	0
3	EDO	A	504	4/4	0.95	0.07	27,30,34,36	0
2	Y3U	B	501	34/34	0.97	0.06	23,26,38,44	0
4	CL	A	505	1/1	0.98	0.14	41,41,41,41	0

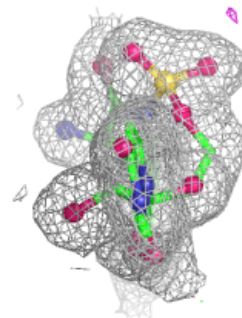
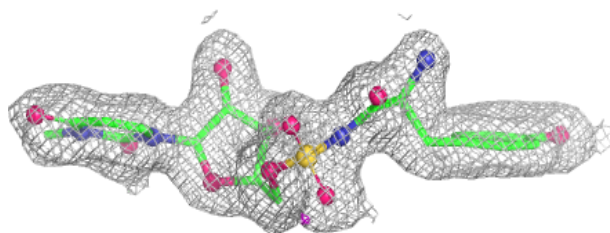
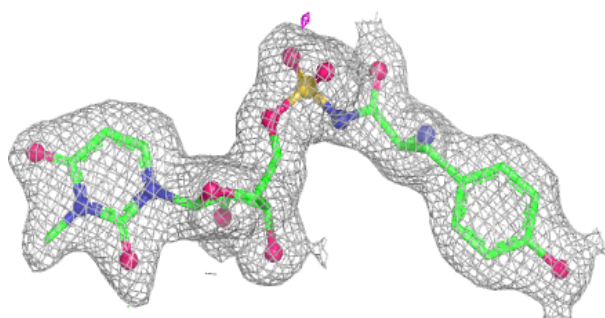
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Y3U A 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around Y3U B 501:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.