



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 4LEI / pdb_00004lei
Title : Spinosyn Forosaminyltransferase SpnP
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Deposited on : 2013-06-25
Resolution : 3.15 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
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

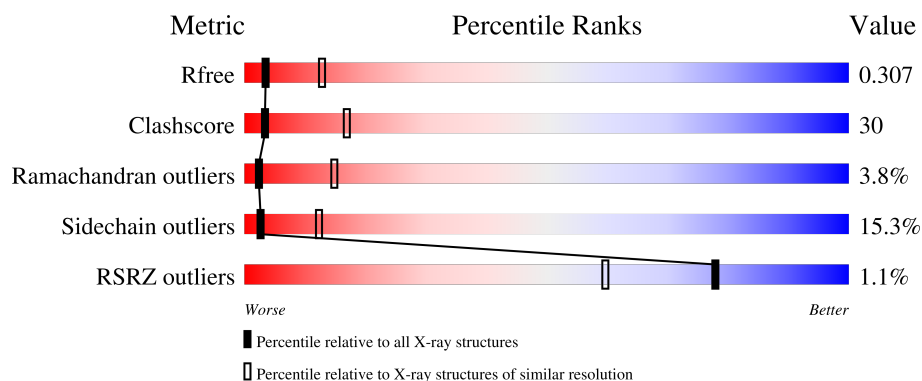
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	455	42% 31% 9% • 18%
1	B	455	39% 33% 9% • 18%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5958 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 NDP-forosamyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	375	Total	C	N	O	S	0	0	0
			2922	1852	514	543	13			
1	B	373	Total	C	N	O	S	0	0	0
			2905	1840	511	541	13			

There are 32 discrepancies between the modelled and reference sequences:

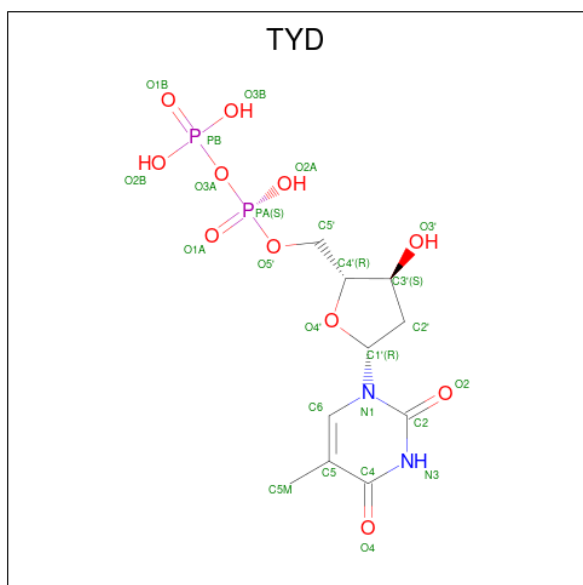
Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	HIS	-	expression tag	UNP Q9ALN7
A	-14	HIS	-	expression tag	UNP Q9ALN7
A	-13	HIS	-	expression tag	UNP Q9ALN7
A	-12	HIS	-	expression tag	UNP Q9ALN7
A	-11	HIS	-	expression tag	UNP Q9ALN7
A	-10	HIS	-	expression tag	UNP Q9ALN7
A	-9	SER	-	expression tag	UNP Q9ALN7
A	-8	SER	-	expression tag	UNP Q9ALN7
A	-7	GLY	-	expression tag	UNP Q9ALN7
A	-6	LEU	-	expression tag	UNP Q9ALN7
A	-5	VAL	-	expression tag	UNP Q9ALN7
A	-4	PRO	-	expression tag	UNP Q9ALN7
A	-3	ARG	-	expression tag	UNP Q9ALN7
A	-2	GLY	-	expression tag	UNP Q9ALN7
A	-1	SER	-	expression tag	UNP Q9ALN7
A	0	HIS	-	expression tag	UNP Q9ALN7
B	-15	HIS	-	expression tag	UNP Q9ALN7
B	-14	HIS	-	expression tag	UNP Q9ALN7
B	-13	HIS	-	expression tag	UNP Q9ALN7
B	-12	HIS	-	expression tag	UNP Q9ALN7
B	-11	HIS	-	expression tag	UNP Q9ALN7
B	-10	HIS	-	expression tag	UNP Q9ALN7
B	-9	SER	-	expression tag	UNP Q9ALN7
B	-8	SER	-	expression tag	UNP Q9ALN7
B	-7	GLY	-	expression tag	UNP Q9ALN7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	LEU	-	expression tag	UNP Q9ALN7
B	-5	VAL	-	expression tag	UNP Q9ALN7
B	-4	PRO	-	expression tag	UNP Q9ALN7
B	-3	ARG	-	expression tag	UNP Q9ALN7
B	-2	GLY	-	expression tag	UNP Q9ALN7
B	-1	SER	-	expression tag	UNP Q9ALN7
B	0	HIS	-	expression tag	UNP Q9ALN7

- Molecule 2 is THYMIDINE-5'-DIPHOSPHATE (CCD ID: TYD) (formula: $C_{10}H_{16}N_2O_{11}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
2	B	1	Total	C	N	O	P	0	0
			25	10	2	11	2		

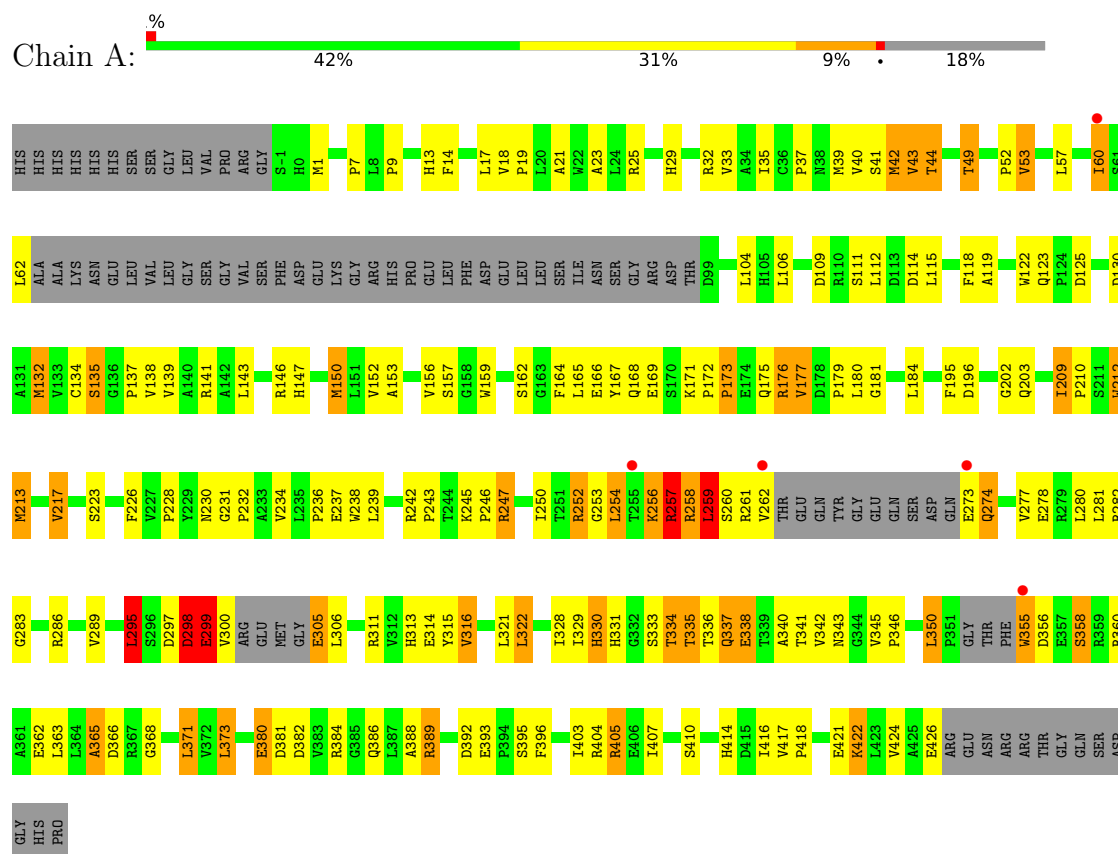
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	40	Total	O	0	0
			40	40		
3	B	41	Total	O	0	0
			41	41		

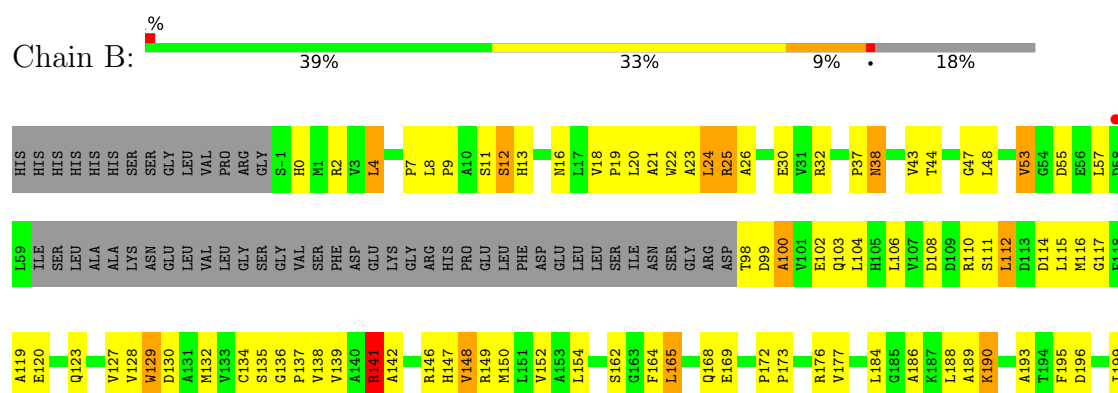
3 Residue-property plots

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: NDP-forosamyltransferase



• Molecule 1: NDP-forosamyltransferase



H355	D282	R282	T205
D356	G283	G285	M213
R360	A284	A285	V217
L363	R286	L287	D218
A369	D288	D289	L219
L373	E290	V291	S223
D374	I292	I292	Y229
P375	T294	A293	N230
A376	L295	L295	V234
T377	S296	D297	L235
F378	D298	D298	P236
T379	E299	E299	E237
E380	V300	R301	W238
D381	R301	E302	L239
D382	M303	G304	E240
V383	E305	G304	E241
R384	L306	E305	R242
R385	P307	P307	P243
Q386	V310	V310	T244
I387	R311	R311	K245
A388	H313	H313	F246
R389	E314	E314	R247
D392	Y315	V316	T251
E393	V316	E320	R252
I403	L321	L321	G253
E406	S324	S324	L254
P411	V327	V327	T255
S412	I328	I328	K256
P413	H331	H331	R257
H414	G332	G332	R258
D415	S333	S333	L259
I416	T334	T334	S260
V417	Q337	Q337	ARG
P418	E338	E338	VAL
R419	T339	T339	THR
L420	V345	V345	GLU
E421	I349	I349	GLN
E426	L350	L350	TYR
ARG	P351	P351	GLY
GLU	G352	G352	GLU
ASN	T353	T353	GLN
ASN	F354	F354	ASP
ARG			GLN
ARG			ALA
THR			MET
GLN			VAL
SER			E276
GLY			R279
SER			L280
ASP			L281
GLY			
HIS			
PRO			

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	162.37Å 162.37Å 81.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	114.81 – 3.15 114.81 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.0 (114.81-3.15) 99.1 (114.81-3.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.13 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.209 , 0.314 0.210 , 0.307	Depositor DCC
R_{free} test set	990 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	67.6	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5958	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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

Bond lengths and bond angles in the following residue types are not validated in this section: TYD

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	0.96	2/2983 (0.1%)	1.22	11/4065 (0.3%)
1	B	0.94	0/2969	1.21	20/4048 (0.5%)
All	All	0.95	2/5952 (0.0%)	1.22	31/8113 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	212	TRP	CD2-CE2	5.30	1.50	1.41
1	A	299	GLU	CA-C	5.01	1.59	1.52

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	245	LYS	CA-C-N	-10.92	108.84	119.76
1	A	245	LYS	C-N-CA	-10.92	108.84	119.76
1	B	297	ASP	CB-CA-C	-9.28	102.88	116.53
1	B	129	TRP	N-CA-C	7.44	121.03	108.90
1	A	42	MET	N-CA-C	-7.24	103.08	110.97

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	2922	0	2933	164	0
1	B	2905	0	2906	194	0
2	A	25	0	13	5	0
2	B	25	0	13	8	0
3	A	40	0	0	6	0
3	B	41	0	0	4	0
All	All	5958	0	5865	354	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 30.

The worst 5 of 354 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:273:GLU:HA	1:A:274:GLN:HB3	1.23	1.18
1:B:287:LEU:HD23	1:B:384:ARG:HB2	1.28	1.09
1:A:316:VAL:HG21	1:A:321:LEU:HD22	1.38	1.06
1:B:287:LEU:CD2	1:B:384:ARG:HB2	1.87	1.05
1:A:273:GLU:CA	1:A:274:GLN:HB3	1.89	1.03

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	365/455 (80%)	308 (84%)	42 (12%)	15 (4%)	2	14
1	B	367/455 (81%)	298 (81%)	56 (15%)	13 (4%)	3	16
All	All	732/910 (80%)	606 (83%)	98 (13%)	28 (4%)	2	15

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	SER
1	A	257	ARG
1	A	258	ARG
1	A	259	LEU
1	A	261	ARG

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	319/386 (83%)	267 (84%)	52 (16%)	2	10
1	B	316/386 (82%)	271 (86%)	45 (14%)	3	15
All	All	635/772 (82%)	538 (85%)	97 (15%)	3	12

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	104	LEU
1	B	254	LEU
1	B	112	LEU
1	B	217	VAL
1	B	287	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	103	GLN
1	B	147	HIS
1	B	399	ASN
1	B	230	ASN
1	A	337	GLN

5.3.3 RNA ⓘ

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](#)

2 ligands 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	TYD	A	501	-	25,26,26	1.34	5 (20%)	38,40,40	1.83	10 (26%)
2	TYD	B	501	-	25,26,26	1.54	6 (24%)	38,40,40	2.17	12 (31%)

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	TYD	A	501	-	-	1/16/28/28	0/2/2/2
2	TYD	B	501	-	-	7/16/28/28	0/2/2/2

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	TYD	C6-C5	3.62	1.40	1.34
2	B	501	TYD	C2-N1	3.53	1.44	1.38
2	B	501	TYD	C4-C5	3.02	1.49	1.44
2	A	501	TYD	PA-O3A	3.00	1.62	1.59
2	A	501	TYD	C4-C5	2.60	1.49	1.44

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	TYD	N3-C2-N1	6.52	123.37	114.89
2	B	501	TYD	C4-N3-C2	-5.26	120.44	127.34
2	A	501	TYD	C5M-C5-C4	4.34	123.41	118.78
2	B	501	TYD	O4'-C1'-N1	3.88	114.75	107.86
2	A	501	TYD	C5-C4-N3	3.77	118.60	115.32

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

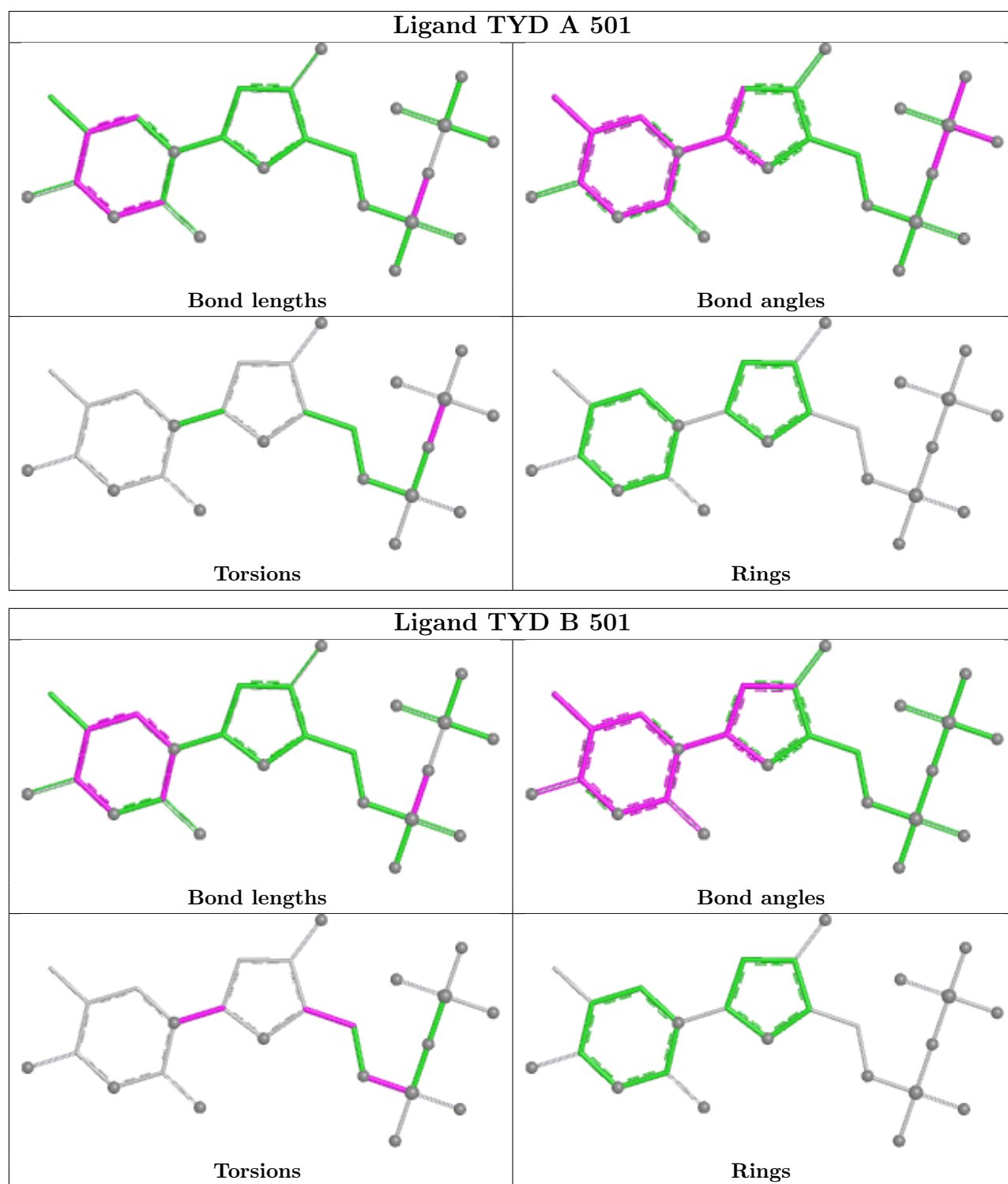
Mol	Chain	Res	Type	Atoms
2	B	501	TYD	C5'-O5'-PA-O1A
2	B	501	TYD	C5'-O5'-PA-O2A
2	B	501	TYD	C5'-O5'-PA-O3A
2	B	501	TYD	C3'-C4'-C5'-O5'
2	B	501	TYD	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	TYD	5	0
2	B	501	TYD	8	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 ⓘ

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	375/455 (82%)	-0.26	5 (1%)	75 55	32, 59, 91, 119	0
1	B	373/455 (81%)	-0.28	3 (0%)	82 66	29, 53, 95, 116	0
All	All	748/910 (82%)	-0.27	8 (1%)	78 60	29, 56, 94, 119	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	262	VAL	2.9
1	A	255	THR	2.8
1	A	355	TRP	2.6
1	A	60	ILE	2.6
1	B	58	ASP	2.6

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](#)

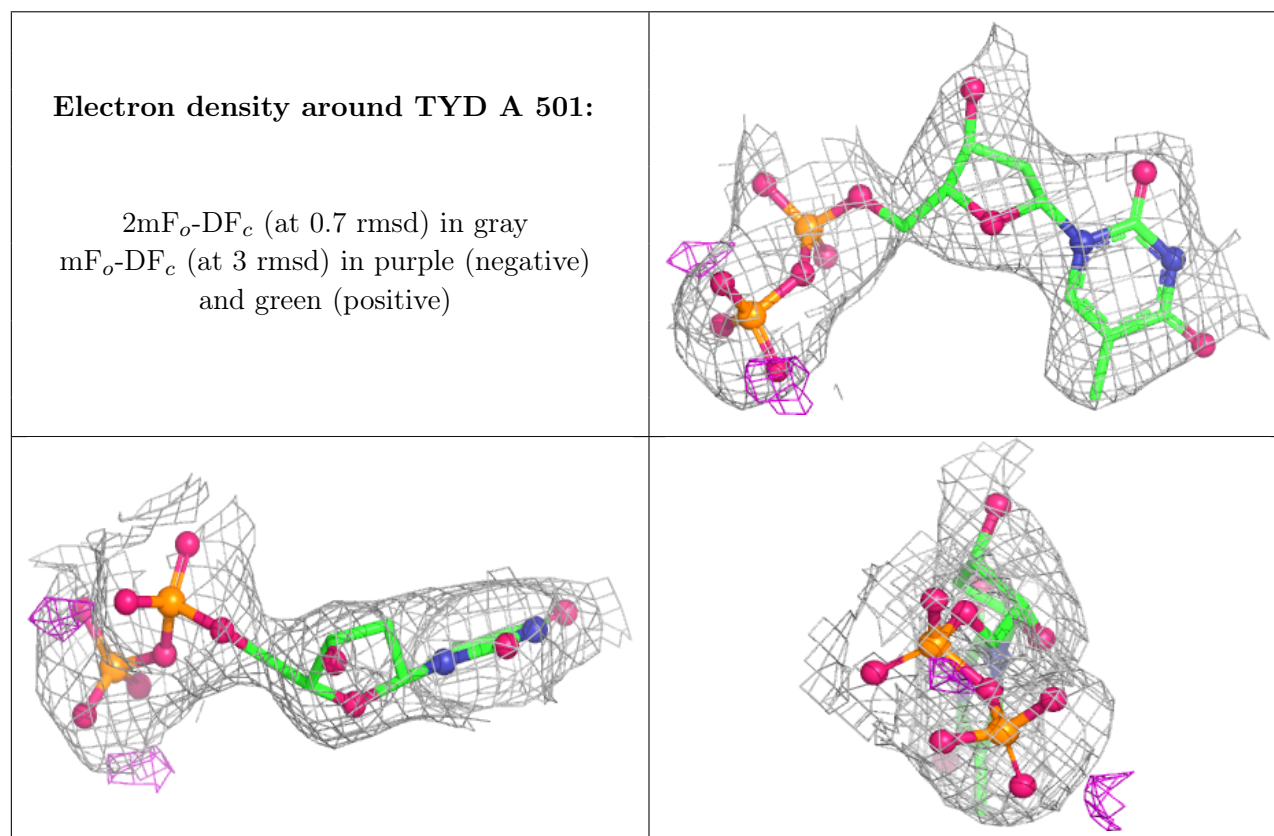
There are no oligosaccharides in this entry.

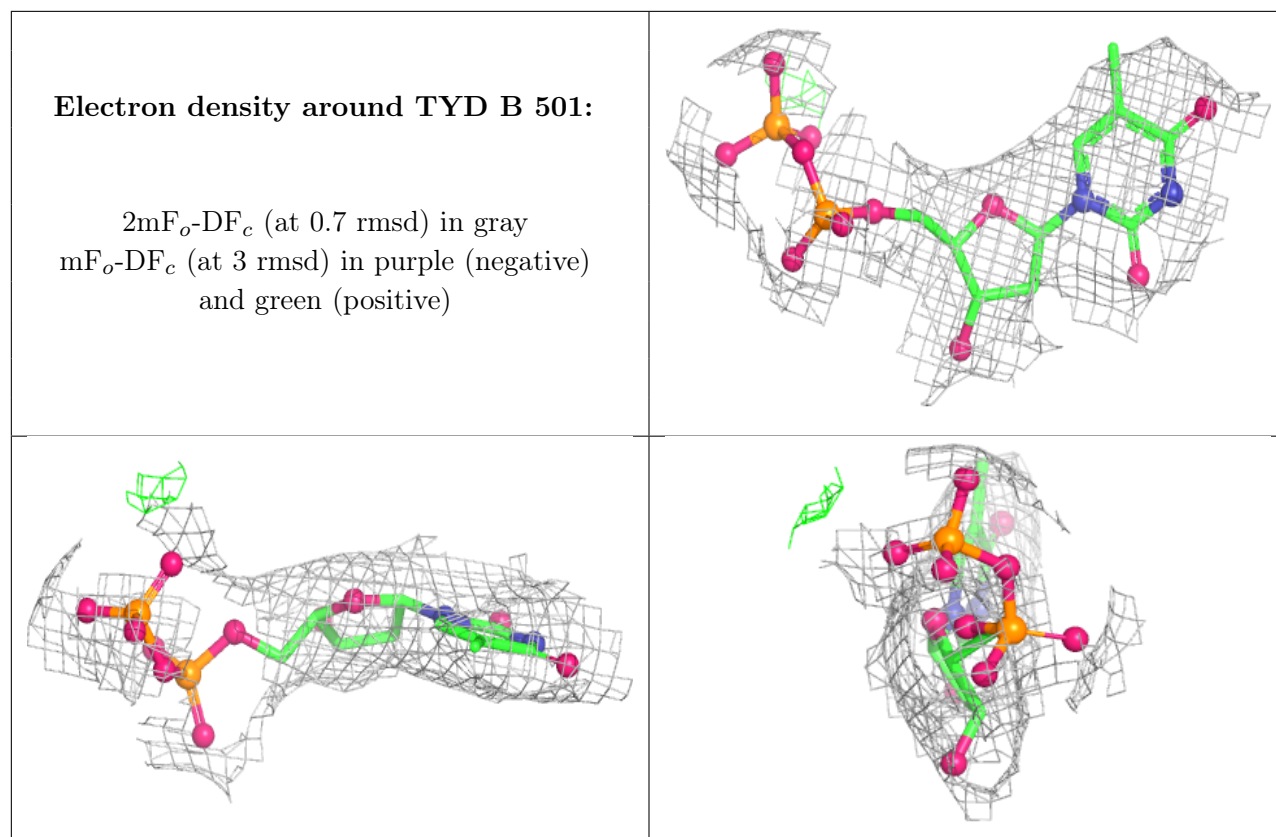
6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
2	TYD	A	501	25/25	0.95	0.08	50,65,71,77	0
2	TYD	B	501	25/25	0.95	0.08	59,72,78,80	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.