

# wwPDB X-ray Structure Validation Summary Report (i)

#### Sep 27, 2023 – 12:53 PM EDT

PDB ID	:	8EH1
Title	:	Engineered tyrosine synthase (TmTyrS1) derived from T. maritima TrpB
		with Ser bound as the amino-acrylate intermediate and complexed with 4-
		hydroxyquinoline
Authors	:	Porter, N.J.; Almhjell, P.J.; Arnold, F.H.
Deposited on	:	2022-09-13
Resolution	:	2.00  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 (i) 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 (i)) were used in the production of this report:

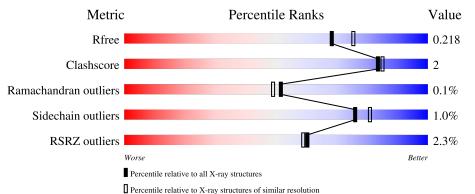
MolProbity		4 021 467
MOIFIODILY	•	4.020-407
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 2.00 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	А	397	% 90% 6%					
1	В	397	90%	6%	•			



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6040 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	٨	383	Total	С	Ν	0	S	0	1	0
	A	303	2907	1854	499	546	8	0	1	0
1	D	384	Total	С	Ν	0	S	0	1	0
	D	304	2895	1848	496	544	7	0		0

• Molecule 1 is a protein called Engineered tyrosine synthase (TmTyrS1).

Chain	Residue	Modelled	Actual	Comment	Reference
А	4	ASN	TYR	engineered mutation	UNP P50909
А	12	ASN	TYR	engineered mutation	UNP P50909
А	19	GLY	PRO	engineered mutation	UNP P50909
А	30	GLY	GLU	engineered mutation	UNP P50909
А	41	TYR	PHE	engineered mutation	UNP P50909
А	69	VAL	ILE	engineered mutation	UNP P50909
А	96	LEU	LYS	engineered mutation	UNP P50909
А	103	THR	ILE	engineered mutation	UNP P50909
А	105	GLY	GLU	engineered mutation	UNP P50909
А	140	LEU	PRO	engineered mutation	UNP P50909
А	167	ASP	ASN	engineered mutation	UNP P50909
А	184	PRO	ILE	engineered mutation	UNP P50909
А	213	PRO	LEU	engineered mutation	UNP P50909
А	228	SER	GLY	engineered mutation	UNP P50909
А	291	ALA	VAL	engineered mutation	UNP P50909
А	292	SER	THR	engineered mutation	UNP P50909
А	302	PRO	SER	engineered mutation	UNP P50909
А	389	HIS	ARG	engineered mutation	UNP P50909
А	390	LEU	-	expression tag	UNP P50909
А	391	GLU	-	expression tag	UNP P50909
А	392	HIS	-	expression tag	UNP P50909
А	393	HIS	-	expression tag	UNP P50909
А	394	HIS	-	expression tag	UNP P50909
А	395	HIS	-	expression tag	UNP P50909
А	396	HIS	-	expression tag	UNP P50909

There are 52 discrepancies between the modelled and reference sequences:

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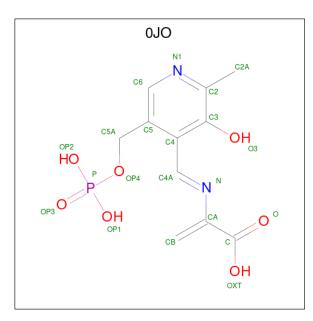


Chain	Residue	Modelled	Actual	Comment	Reference
А	397	HIS	-	expression tag	UNP P50909
В	4	ASN	TYR	engineered mutation	UNP P50909
В	12	ASN	TYR	engineered mutation	UNP P50909
В	19	GLY	PRO	engineered mutation	UNP P50909
В	30	GLY	GLU	engineered mutation	UNP P50909
В	41	TYR	PHE	engineered mutation	UNP P50909
В	69	VAL	ILE	engineered mutation	UNP P50909
В	96	LEU	LYS	engineered mutation	UNP P50909
В	103	THR	ILE	engineered mutation	UNP P50909
В	105	GLY	GLU	engineered mutation	UNP P50909
В	140	LEU	PRO	engineered mutation	UNP P50909
В	167	ASP	ASN	engineered mutation	UNP P50909
В	184	PRO	ILE	engineered mutation	UNP P50909
В	213	PRO	LEU	engineered mutation	UNP P50909
В	228	SER	GLY	engineered mutation	UNP P50909
В	291	ALA	VAL	engineered mutation	UNP P50909
В	292	SER	THR	engineered mutation	UNP P50909
В	302	PRO	SER	engineered mutation	UNP P50909
В	389	HIS	ARG	engineered mutation	UNP P50909
В	390	LEU	-	expression tag	UNP P50909
В	391	GLU	-	expression tag	UNP P50909
В	392	HIS	-	expression tag	UNP P50909
В	393	HIS	-	expression tag	UNP P50909
В	394	HIS	-	expression tag	UNP P50909
В	395	HIS	-	expression tag	UNP P50909
В	396	HIS	-	expression tag	UNP P50909
В	397	HIS	-	expression tag	UNP P50909

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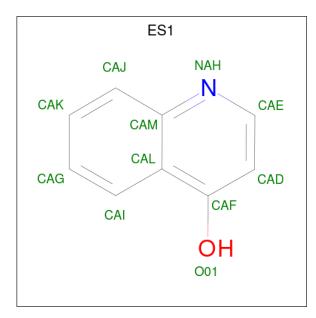
• Molecule 2 is 2-{[(E)-{3-hydroxy-2-methyl-5-[(phosphonooxy)methyl]pyridin-4-yl}methylid ene]amino}prop-2-enoic acid (three-letter code: 0JO) (formula:  $C_{11}H_{13}N_2O_7P$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
0	Λ	1	Total	С	Ν	0	Р	0	0
	A	1	21	11	2	7	1	0	0
0	р	1	Total	С	Ν	0	Р	0	0
	D	1	21	11	2	7	1	U	U

• Molecule 3 is quinolin-4-ol (three-letter code: ES1) (formula: C<sub>9</sub>H<sub>7</sub>NO) (labeled as "Ligand of Interest" by depositor).



Mo	l Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total         C         N         O           11         9         1         1	0	0

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Mol	Chain	Residues	A	tor	ns		ZeroOcc	AltConf
3	В	1	Total 11	C 9	N 1	0 1	0	0

• Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total K 1 1	0	0
4	В	1	Total K 1 1	0	0

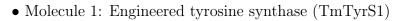
• Molecule 5 is water.

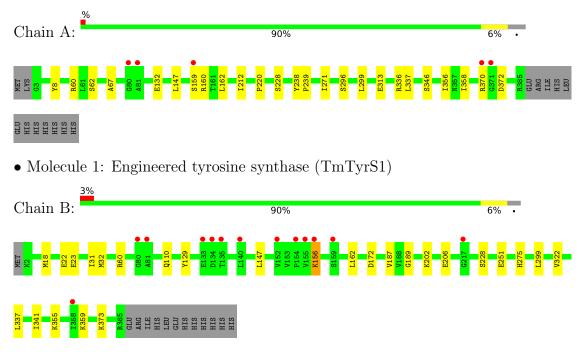
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	109	Total O 109 109	0	0
5	В	63	Total         O           63         63	0	0



# 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.







# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4	Depositor
Cell constants	164.86Å 164.86Å 84.06Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.86 - 2.00	Depositor
Resolution (A)	38.86 - 2.00	EDS
% Data completeness	99.7 (38.86-2.00)	Depositor
(in resolution range)	99.7 (38.86 - 2.00)	EDS
R <sub>merge</sub>	0.11	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.17 (at 2.00 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
D D	0.188 , $0.219$	Depositor
$R, R_{free}$	0.187 , $0.218$	DCC
$R_{free}$ test set	3846 reflections $(5.07%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	38.8	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35 , $46.0$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.021 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6040	wwPDB-VP
Average B, all atoms $(Å^2)$	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.47% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: ES1, 0JO, K

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
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.26	0/2971	0.51	0/4029
1	В	0.26	0/2959	0.50	0/4016
All	All	0.26	0/5930	0.50	0/8045

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

#### 5.2 Too-close contacts (i)

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	А	2907	0	2870	15	0
1	В	2895	0	2844	15	0
2	А	21	0	9	0	0
2	В	21	0	9	1	0
3	А	11	0	6	1	0
3	В	11	0	6	1	0
4	А	1	0	0	0	0
4	В	1	0	0	0	0
5	А	109	0	0	1	0
5	В	63	0	0	1	0
All	All	6040	0	5744	28	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.

The worst 5 of 28 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:18:MET:O	1:B:22:GLU:HG3	1.93	0.67
1:B:110:GLN:HE21	1:B:373:LYS:HD3	1.65	0.61
1:A:132:GLU:HB3	1:A:160:ARG:HH11	1.69	0.58
1:A:132:GLU:HB3	1:A:160:ARG:NH1	2.19	0.56
1:B:156:LYS:HG3	1:B:156:LYS:O	2.09	0.52

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	Analysed Favoured A		Outliers	Perce	entiles
1	А	382/397~(96%)	374~(98%)	8 (2%)	0	100	100
1	В	383/397~(96%)	375~(98%)	7 (2%)	1 (0%)	41	37
All	All	765/794~(96%)	749~(98%)	15~(2%)	1 (0%)	51	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
1	В	187	VAL	

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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



Mol	Chain	Analysed	Rotameric	Outliers	Percer	ntiles
1	А	294/319~(92%)	291~(99%)	3 (1%)	76	81
1	В	290/319~(91%)	287~(99%)	3 (1%)	76	81
All	All	584/638~(92%)	578~(99%)	6 (1%)	76	81

analysed, and the total number of residues.

5 of 6 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	В	23	GLU
1	В	156	LYS
1	В	359	LYS
1	А	296	SER
1	А	159	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	293	HIS
1	В	110	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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	Bo	ond leng	ths	В	ond ang	les
IVIOI	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	ES1	А	402	-	12,12,12	1.15	1 (8%)	16, 16, 16	0.63	0
3	ES1	В	402	-	12,12,12	1.14	1 (8%)	16, 16, 16	0.65	0
2	0JO	В	401	-	20,21,21	1.35	2 (10%)	23,30,30	0.59	0
2	0JO	А	401	-	20,21,21	1.44	2 (10%)	23,30,30	0.54	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	$\mathbf{Res}$	Link	Chirals	Torsions	Rings
3	ES1	А	402	-	-	-	0/2/2/2
3	ES1	В	402	-	-	-	0/2/2/2
2	0JO	В	401	-	-	1/10/15/15	0/1/1/1
2	0JO	А	401	-	-	0/10/15/15	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	401	0JO	CA-C	-4.50	1.41	1.50
2	В	401	0JO	CA-C	-4.18	1.41	1.50
2	А	401	0JO	OXT-C	-4.13	1.18	1.30
2	В	401	0JO	OXT-C	-3.33	1.20	1.30
3	В	402	ES1	CAD-CAE	2.81	1.44	1.38

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	401	0JO	C3-C4-C4A-N

There are no ring outliers.

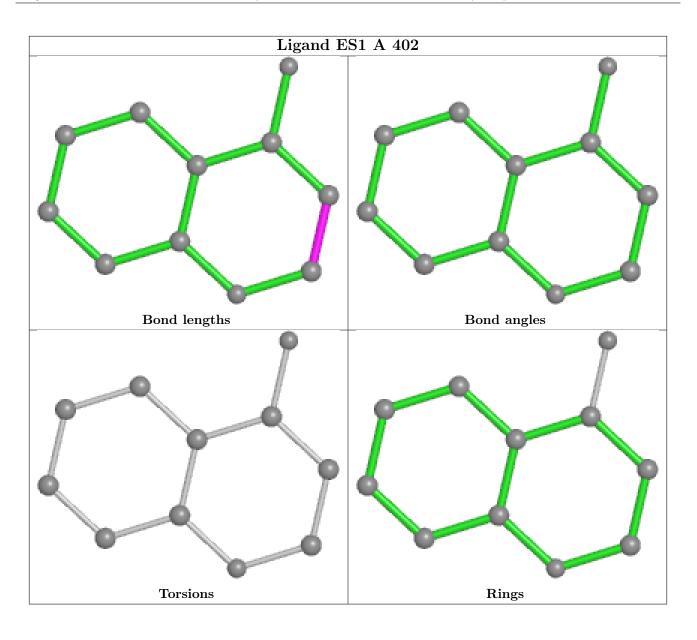
3 monomers are involved in 3 short contacts:



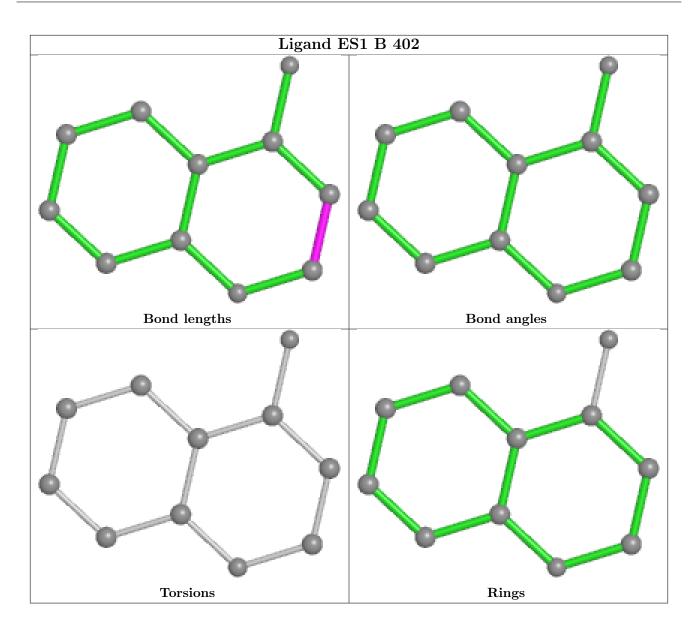
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	402	ES1	1	0
3	В	402	ES1	1	0
2	В	401	0JO	1	0

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

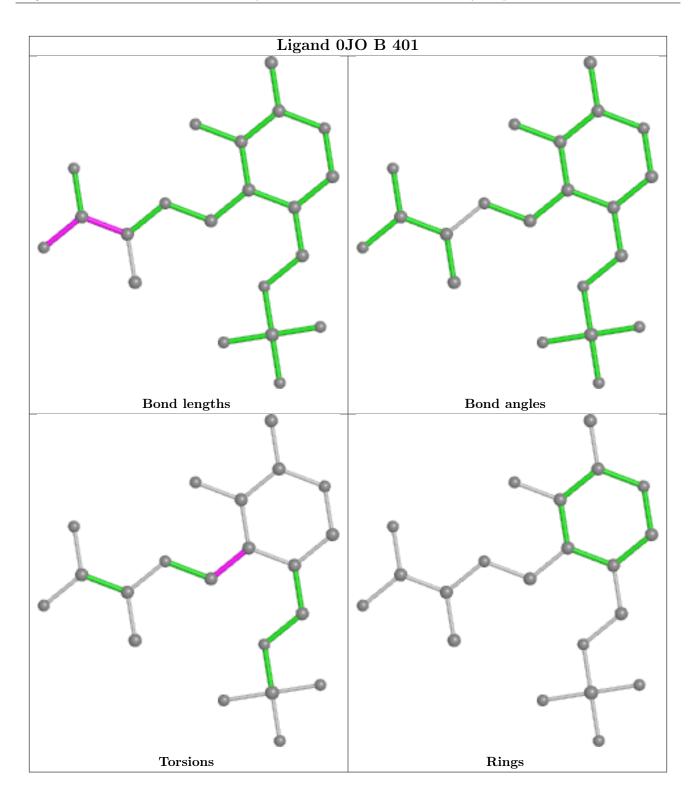




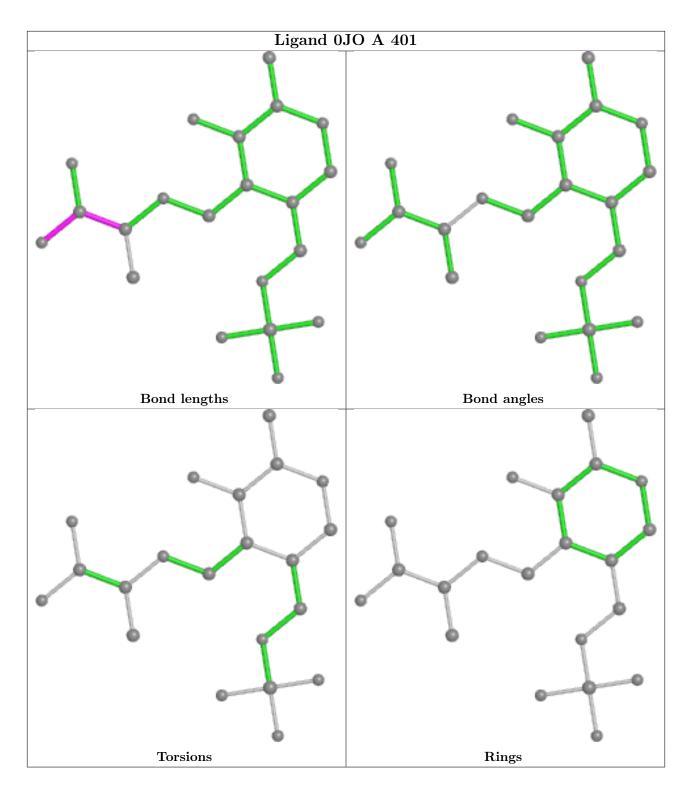












## 5.7 Other polymers (i)

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 (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,  $95^{th}$  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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	383/397~(96%)	-0.35	5 (1%) 77 76	27, 36, 57, 75	0
1	В	384/397~(96%)	-0.05	13 (3%) 45 44	31, 42, 65, 79	0
All	All	767/794~(96%)	-0.20	18 (2%) 60 59	27, 39, 62, 79	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	159	SER	4.7
1	В	140	LEU	4.5
1	В	133	GLU	4.0
1	В	154	PRO	3.7
1	В	156	LYS	3.6

#### 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 monosaccharides in this entry.

#### 6.4 Ligands (i)

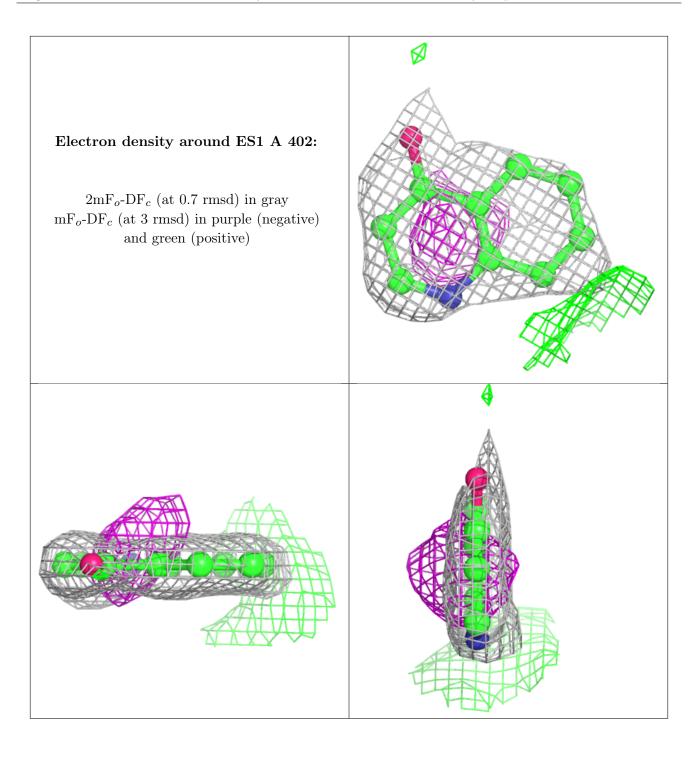
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.



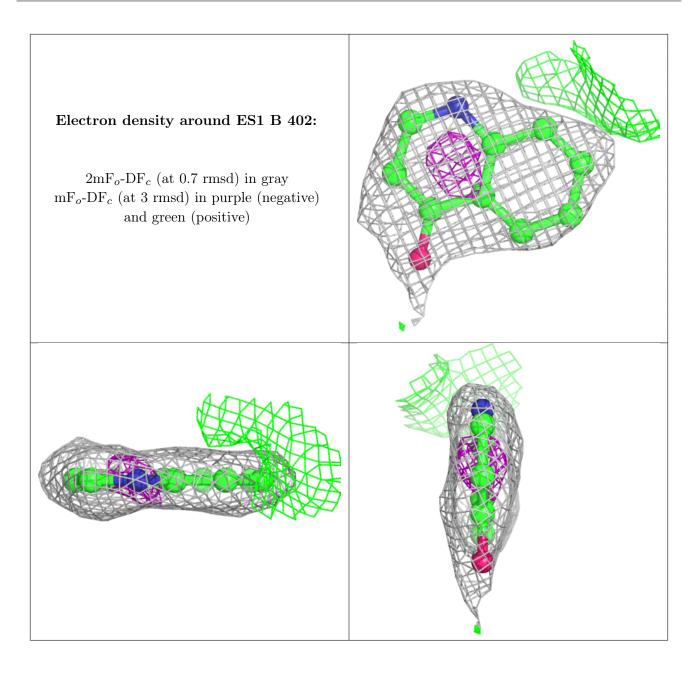
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
3	ES1	А	402	11/11	0.87	0.19	42,53,64,66	0
3	ES1	В	402	11/11	0.88	0.13	49,55,64,69	0
2	0JO	В	401	21/21	0.95	0.17	38,42,55,63	0
2	0JO	А	401	21/21	0.96	0.17	30,39,51,52	0
4	Κ	В	403	1/1	0.99	0.04	39,39,39,39	0
4	К	А	403	1/1	1.00	0.10	36,36,36,36	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.

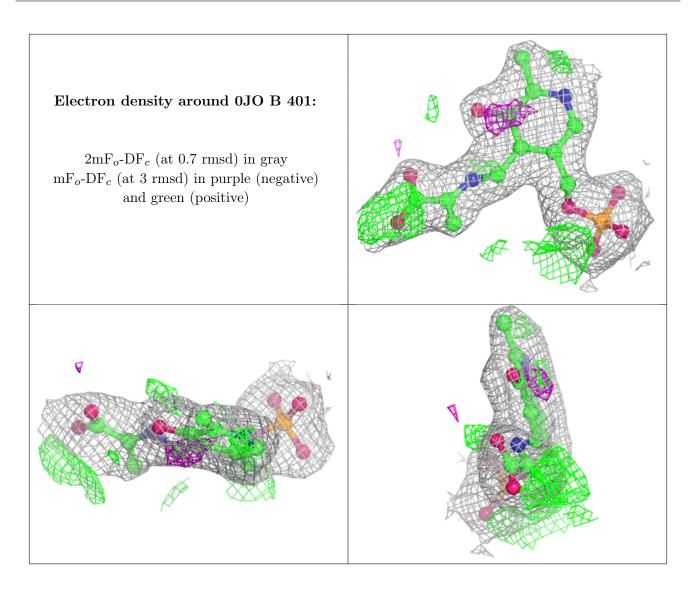




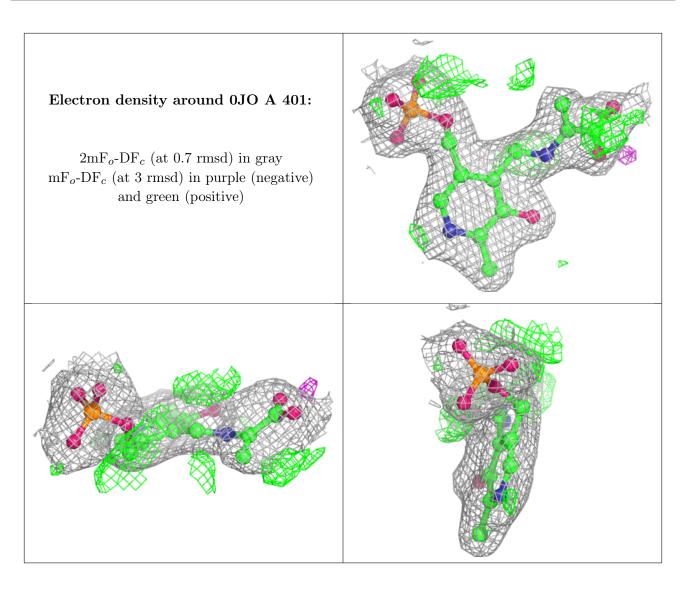












## 6.5 Other polymers (i)

There are no such residues in this entry.

