

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

#### Nov 19, 2024 – 12:34 pm GMT

PDB ID : 8RBA

Title: p53-Y220C Core Domain Covalently Bound to 2,5,6-trifluoropyridine-3-carbo

nitrile Soaked at 5 mM

Authors: Stahlecker, J.; Klett, T.; Stehle, T.; Boeckler, F.M.

Deposited on : 2023-12-04

Resolution : 1.57 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 3.0

buster-report : 1.1.7 (2018)

Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)

CCP4 : 9.0.003 (Gargrove)

Density-Fitness : 1.0.11

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

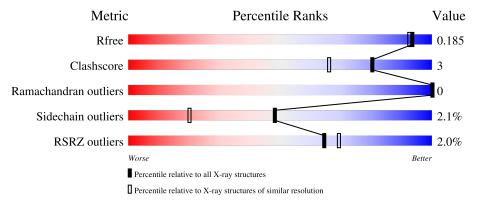
Validation Pipeline (wwPDB-VP) : 2.39

## 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 1.57 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	164625	7165 (1.60-1.56)
Clashscore	180529	1026 (1.58-1.58)
Ramachandran outliers	177936	1005 (1.58-1.58)
Sidechain outliers	177891	1004 (1.58-1.58)
RSRZ outliers	164620	7163 (1.60-1.56)

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	219	84%	6%	10%	
1	В	219	83%	6%	10%	

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
5	EPE	A	407	-	X	-	-



# 2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 3620 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 Cellular tumor antigen p53.

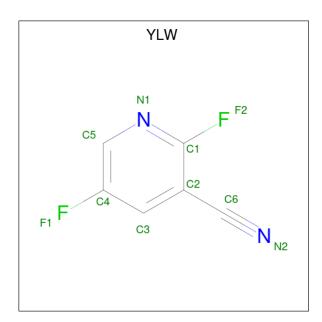
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	198	Total	С	N	О	S	0	7	0
1	A	190	1549	957	276	299	17	0	·	U
1	B	197	Total	С	N	О	S	0	6	0
1	ъ	191	1548	958	277	296	17		U	U

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	133	LEU	MET	engineered mutation	UNP P04637
A	203	ALA	VAL	engineered mutation	UNP P04637
A	220	CYS	TYR	engineered mutation	UNP P04637
A	239	TYR	ASN	engineered mutation	UNP P04637
A	268	ASP	ASN	engineered mutation	UNP P04637
В	133	LEU	MET	engineered mutation	UNP P04637
В	203	ALA	VAL	engineered mutation	UNP P04637
В	220	CYS	TYR	engineered mutation	UNP P04637
В	239	TYR	ASN	engineered mutation	UNP P04637
В	268	ASP	ASN	engineered mutation	UNP P04637

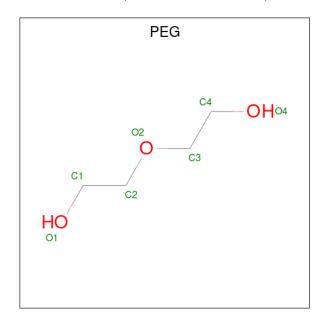
• Molecule 2 is 2,5-bis(fluoranyl)pyridine-3-carbonitrile (three-letter code: YLW) (formula:  $C_6H_2F_2N_2$ ) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 10				0	0
2	В	1	Total 10	C 6	F 2	N 2	0	0

 $\bullet \ \ Molecule \ 3 \ is \ DI(HYDROXYETHYL)ETHER \ (three-letter \ code: \ PEG) \ (formula: \ C_4H_{10}O_3).$ 



]	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	3	A	1	Total C O 7 4 3	0	0
	3	A	1	Total C O 7 4 3	0	0

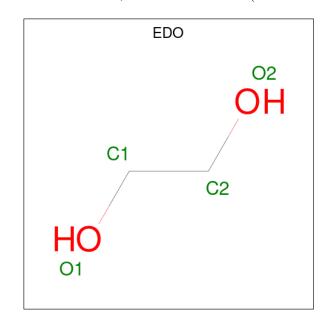
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total C O 7 4 3	0	0
3	В	1	Total C O 5 3 2	0	0

 $\bullet$  Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $\mathrm{C_2H_6O_2}).$ 



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

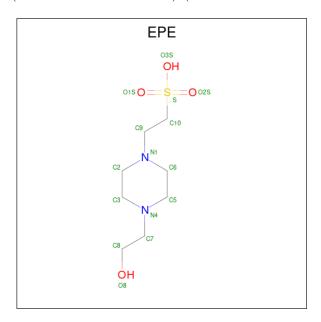
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total C O 4 2 2	0	0
4	В	1	Total C O 4 2 2	0	0
4	В	1	Total C O 4 2 2	0	0

• Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula:  $C_8H_{18}N_2O_4S$ ).



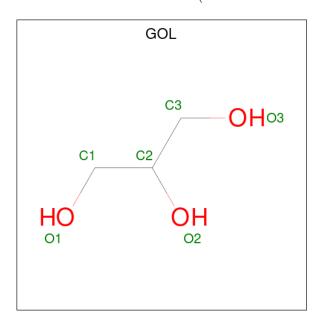
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O S 6 2 3 1	0	0
5	В	1	Total C N O S 9 4 1 3 1	0	0
5	В	1	Total C O S 6 2 3 1	0	0

• Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Zn 1 1	0	0
6	В	1	Total Zn 1 1	0	0



• Molecule 7 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	В	1	Total 6	C 3	O 3	0	0

• Molecule 8 is water.

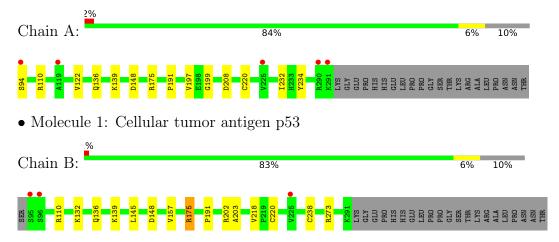
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	202	Total O 202 202	0	0
8	В	198	Total O 198 198	0	0



# 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.

• Molecule 1: Cellular tumor antigen p53





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	64.91Å 70.70Å 105.33Å	Donositon
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.82 - 1.57	Depositor
Resolution (A)	47.82 - 1.57	EDS
% Data completeness	97.1 (47.82-1.57)	Depositor
(in resolution range)	97.1 (47.82-1.57)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.17 (at 1.57Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
D D.	0.150 , 0.183	Depositor
$R, R_{free}$	0.151 , $0.185$	DCC
$R_{free}$ test set	1501 reflections (2.26%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.7	Xtriage
Anisotropy	0.484	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.35, 47.0	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.54, < L^2> = 0.38$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	3620	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	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 45.98 % 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 1.2225e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

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



<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: ZN, PEG, EPE, YLW, EDO, 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		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.46	0/1584	0.65	0/2156	
1	В	0.47	0/1583	0.68	0/2153	
All	All	0.47	0/3167	0.66	0/4309	

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 maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	В	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	175	ARG	Sidechain

## 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	A	1549	0	1451	7	0
1	В	1548	0	1471	9	0
2	A	10	0	0	0	0
2	В	10	0	0	0	0
3	A	14	0	20	0	0
3	В	12	0	15	0	0
4	A	28	0	42	2	0
4	В	20	0	30	2	0
5	A	6	0	2	0	0
5	В	15	0	6	0	0
6	A	1	0	0	0	0
6	В	1	0	0	0	0
7	В	6	0	8	3	0
8	A	202	0	0	0	0
8	В	198	0	0	1	0
All	All	3620	0	3045	16	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 3.

The worst 5 of 16 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:273:ARG:HH11	7:B:410:GOL:H31	1.65	0.62
1:B:132:LYS:HZ1	7:B:410:GOL:H32	1.69	0.57
1:B:202:ARG:NE	8:B:502:HOH:O	2.38	0.56
1:B:136:GLN:HB2	1:B:139:LYS:HG3	1.91	0.53
1:A:148:ASP:HA	4:A:406:EDO:H22	1.91	0.51

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 Allowed		Outliers	Perce	$_{ m ntiles}$
1	A	203/219 (93%)	202 (100%)	1 (0%)	0	100	100
1	В	201/219 (92%)	201 (100%)	0	0	100	100
All	All	404/438 (92%)	403 (100%)	1 (0%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	171/195 (88%)	167 (98%)	4 (2%)	45 17		
1	В	173/195 (89%)	170 (98%)	3 (2%)	56 29		
All	All	344/390 (88%)	337 (98%)	7 (2%)	48 22		

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	220	CYS
1	В	110	ARG
1	В	238	CYS
1	В	220	CYS
1	A	122	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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 24 ligands modelled in this entry, 2 are monoatomic - leaving 22 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	Trino	Chain Res Link		Link	В	Bond lengths			Bond angles		
MIOI	Type	Chain	Res	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
5	EPE	В	404	-	8,8,15	1.22	1 (12%)	10,11,20	1.41	3 (30%)	
2	YLW	A	401	1	9,10,10	0.36	0	12,13,13	2.49	2 (16%)	
4	EDO	A	405	-	3,3,3	0.43	0	2,2,2	0.47	0	
4	EDO	В	408	-	3,3,3	0.48	0	2,2,2	0.17	0	
4	EDO	A	410	-	3,3,3	0.51	0	2,2,2	0.37	0	
3	PEG	В	403	-	6,6,6	0.14	0	5,5,5	0.06	0	
4	EDO	A	411	-	3,3,3	0.43	0	2,2,2	0.37	0	
4	EDO	A	409	-	3,3,3	0.40	0	2,2,2	0.50	0	
5	EPE	A	407	-	5,5,15	0.73	0	7,7,20	1.79	3 (42%)	
4	EDO	В	405	-	3,3,3	0.50	0	2,2,2	0.21	0	
2	YLW	В	401	1	9,10,10	0.32	0	12,13,13	2.09	3 (25%)	
4	EDO	A	404	-	3,3,3	0.52	0	2,2,2	0.22	0	
4	EDO	A	408	-	3,3,3	0.38	0	2,2,2	0.77	0	
3	PEG	A	403	-	6,6,6	0.12	0	5,5,5	0.20	0	
5	EPE	В	407	-	5,5,15	0.62	0	7,7,20	1.82	3 (42%)	
4	EDO	В	406	-	3,3,3	0.43	0	2,2,2	0.49	0	
7	GOL	В	410	-	5,5,5	0.65	0	5,5,5	1.25	0	
3	PEG	В	409	-	4,4,6	0.22	0	3,3,5	0.19	0	
4	EDO	A	406	-	3,3,3	0.45	0	2,2,2	0.40	0	
3	PEG	A	402	-	6,6,6	0.14	0	5,5,5	0.08	0	
4	EDO	В	411	-	3,3,3	0.47	0	2,2,2	0.67	0	
4	EDO	В	402	-	3,3,3	0.48	0	2,2,2	0.29	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.



, ,		. 1.	C 1	. 1 . 1		· 1 / · C 1
- means	no	outliers	of tha	t kind	were	identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EPE	В	404	-	-	2/6/6/19	-
2	YLW	A	401	1	-	0/1/2/2	0/1/1/1
4	EDO	A	405	-	-	1/1/1/1	-
4	EDO	В	408	-	-	0/1/1/1	-
4	EDO	A	410	_	-	0/1/1/1	-
3	PEG	В	403	_	-	3/4/4/4	-
4	EDO	A	411	-	-	1/1/1/1	-
4	EDO	A	409	-	-	0/1/1/1	-
5	EPE	A	407	_	-	3/3/3/19	-
4	EDO	В	405	-	-	0/1/1/1	-
2	YLW	В	401	1	-	0/1/2/2	0/1/1/1
4	EDO	A	404	_	-	1/1/1/1	-
4	EDO	A	408	-	-	0/1/1/1	-
3	PEG	A	403	_	-	2/4/4/4	-
5	EPE	В	407	-	-	0/3/3/19	-
4	EDO	В	406	_	-	0/1/1/1	-
7	GOL	В	410	_	-	2/4/4/4	-
3	PEG	В	409	-	-	1/2/2/4	-
4	EDO	A	406	-	-	1/1/1/1	-
3	PEG	A	402	-	-	3/4/4/4	-
4	EDO	В	411	-	-	1/1/1/1	-
4	EDO	В	402	_	-	0/1/1/1	-

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
5	В	404	EPE	C10-S	3.19	1.82	1.77

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
2	A	401	YLW	C5-N1-C1	7.82	118.57	115.79
2	В	401	YLW	C5-N1-C1	5.50	117.75	115.79
5	В	407	EPE	O2S-S-C10	3.26	110.83	106.92
2	В	401	YLW	C4-C5-N1	2.75	123.11	121.46
5	A	407	EPE	O1S-S-C10	2.70	110.16	106.92

There are no chirality outliers.

5 of 21 torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
5	A	407	EPE	C9-C10-S-O1S
5	A	407	EPE	C9-C10-S-O3S
3	В	403	PEG	O2-C3-C4-O4
3	A	403	PEG	O2-C3-C4-O4
3	В	409	PEG	O2-C3-C4-O4

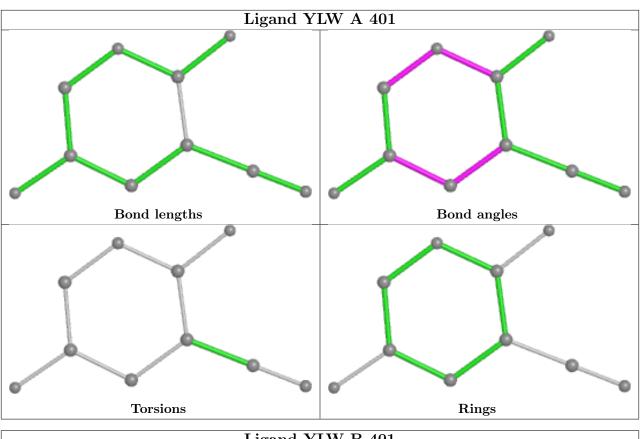
There are no ring outliers.

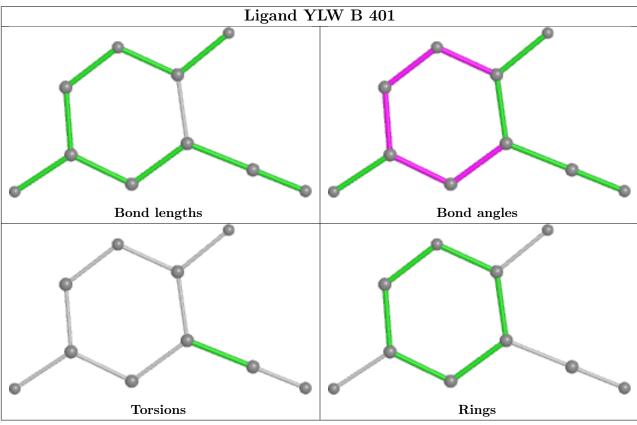
5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	409	EDO	1	0
7	В	410	GOL	3	0
4	A	406	EDO	1	0
4	В	411	EDO	1	0
4	В	402	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 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 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 (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	<RSRZ $>$	# RSRZ > 2		$OWAB(A^2)$	Q < 0.9
1	A	198/219 (90%)	-0.16	5 (2%) 58	63	9, 24, 46, 59	7 (3%)
1	В	197/219 (89%)	-0.20	3 (1%) 71	76	10, 23, 43, 57	6 (3%)
All	All	395/438 (90%)	-0.18	8 (2%) 64	69	9, 24, 44, 59	13 (3%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	225	VAL	2.8
1	В	95	SER	2.6
1	В	225	VAL	2.6
1	A	291	LYS	2.5
1	A	290	ARG	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 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.



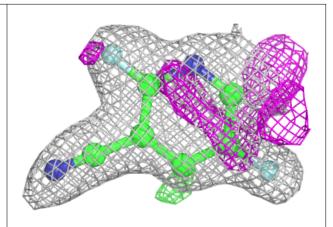
Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B\text{-}factors}({f \AA}^2)$	Q < 0.9
5	EPE	A	407	6/15	0.69	0.20	75,76,77,78	0
3	PEG	В	409	5/7	0.74	0.19	56,57,58,59	0
7	GOL	В	410	6/6	0.75	0.18	57,61,62,64	0
5	EPE	В	407	6/15	0.81	0.18	64,66,67,68	0
4	EDO	A	411	4/4	0.82	0.17	57,57,58,59	0
3	PEG	В	403	7/7	0.82	0.15	57,58,60,60	0
5	EPE	В	404	9/15	0.83	0.17	68,69,70,71	0
4	EDO	A	409	4/4	0.84	0.13	50,52,53,54	0
3	PEG	A	403	7/7	0.85	0.15	57,57,58,59	0
4	EDO	A	410	4/4	0.86	0.16	58,59,60,60	0
4	EDO	A	408	4/4	0.87	0.15	45,46,47,47	0
4	EDO	В	405	4/4	0.87	0.13	63,63,63,64	0
2	YLW	В	401	10/10	0.88	0.11	38,40,42,44	0
3	PEG	A	402	7/7	0.88	0.13	52,52,54,54	0
4	EDO	A	404	4/4	0.89	0.13	51,53,53,54	0
4	EDO	В	406	4/4	0.89	0.14	58,58,59,60	0
4	EDO	A	406	4/4	0.89	0.15	48,49,50,53	0
4	EDO	В	408	4/4	0.90	0.13	40,43,45,45	0
4	EDO	A	405	4/4	0.91	0.12	58,58,59,59	0
4	EDO	В	411	4/4	0.91	0.14	43,49,49,49	0
2	YLW	A	401	10/10	0.91	0.10	35,37,40,43	0
4	EDO	В	402	4/4	0.92	0.12	49,51,52,52	0
6	ZN	В	412	1/1	1.00	0.02	22,22,22,22	0
6	ZN	A	412	1/1	1.00	0.01	24,24,24,24	0

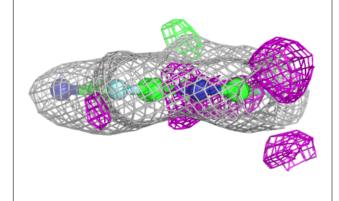
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

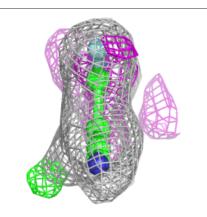


#### Electron density around YLW B 401:

 $2 {\rm mF}_o\text{-}{\rm DF}_c$  (at 0.7 rmsd) in gray  ${\rm mF}_o\text{-}{\rm DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)

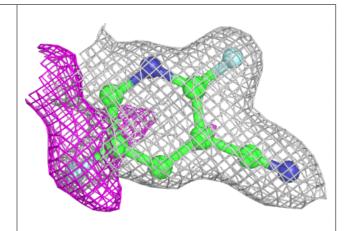


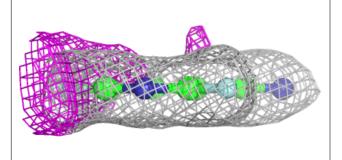


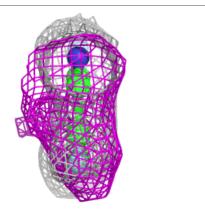


#### Electron density around YLW A 401:

 $2 \text{mF}_o\text{-DF}_c$  (at 0.7 rmsd) in gray  $\text{mF}_o\text{-DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)









# 6.5 Other polymers (i)

There are no such residues in this entry.

