

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

#### Nov 14, 2021 – 07:06 pm GMT

PDB ID : 707K

Title : Crystal structure of the human DYRK1A kinase domain bound to abemaciclib

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Deposited on : 2021-04-13

Resolution : 1.82 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 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 (270009), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.23.2buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0267$ 

CCP4 : 7.1.010 (Gargrove)

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

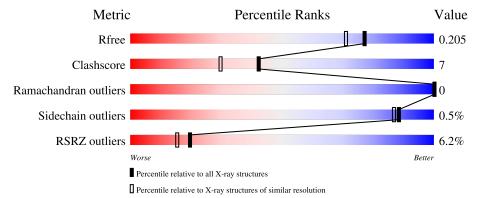
Validation Pipeline (wwPDB-VP) : 2.23.2

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.82 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	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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	Quality of chain				
1	A	361	86%	10%	<del>.</del>			
1	В	361	6% 83%	12%				

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
4	EDO	В	509	-	-	X	-
4	EDO	В	512	-	-	=	X
4	EDO	В	515	-	-	X	-
5	PEG	A	811	-	-	-	X



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 6444 atoms, of which 152 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.

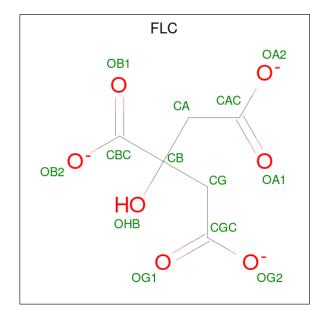
• Molecule 1 is a protein called Dual specificity tyrosine-phosphorylation-regulated kinase 1A.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	345	Total C N O P S 2849 1831 493 507 1 17	6	2	0
1	В	345	Total C H N O P S 2996 1833 143 494 508 1 17	10	2	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	125	SER	-	expression tag	UNP Q13627
A	126	MET	-	expression tag	UNP Q13627
В	125	SER	-	expression tag	UNP Q13627
В	126	MET	-	expression tag	UNP Q13627

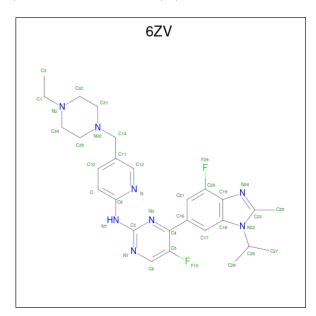
• Molecule 2 is CITRATE ANION (three-letter code: FLC) (formula: C<sub>6</sub>H<sub>5</sub>O<sub>7</sub>).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 13 6 7	0	0
2	A	1	Total C O 13 6 7	0	0
2	В	1	Total C H O 17 6 4 7	0	0
2	В	1	Total C H O 18 6 5 7	0	0

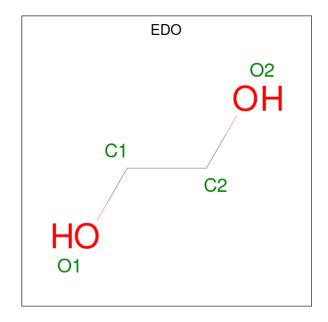
• Molecule 3 is N-{5-[(4-ethylpiperazin-1-yl)methyl]pyridin-2-yl}-5-fluoro-4-[4-fluoro-2-methyl-1-(propan-2-yl)-1H-benzimidazol-6-yl]py rimidin-2-amine (three-letter code: 6ZV) (formula:  $C_{27}H_{32}F_2N_8$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	A	ton	ıs	ZeroOcc	AltConf
3	A	1	Total 37			0	0
3	В	1	Total 37			0	0

• Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).





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	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
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
4	В	1	Total C O 4 2 2	0	0

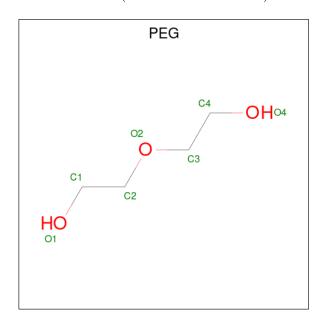
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total C O 4 2 2	0	0
4	В	1	Total C O 4 2 2	0	0
4	В	1	Total C O 4 2 2	0	0
4	В	1	Total C O 4 2 2	0	0
4	В	1	Total C O 4 2 2	0	0
4	В	1	Total C O 4 2 2	0	0

 $\bullet \ \ Molecule \ 5 \ is \ DI(HYDROXYETHYL)ETHER \ (three-letter \ code: \ PEG) \ (formula: \ C_4H_{10}O_3).$ 



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total C C 7 4 3	) 3	0	0

• Molecule 6 is LITHIUM ION (three-letter code: LI) (formula: Li).

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



#### • Molecule 7 is water.

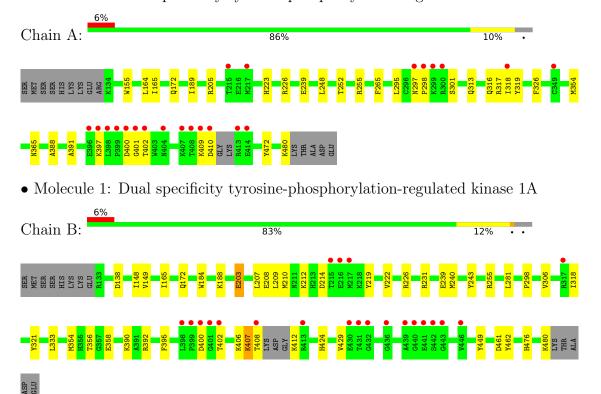
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	196	Total O 196 196	0	0
7	В	179	Total O 179 179	0	0



# 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: Dual specificity tyrosine-phosphorylation-regulated kinase 1A





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	76.70Å 109.98Å 112.50Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	41.93 - 1.82	Depositor
Resolution (A)	44.69 - 1.82	EDS
% Data completeness	99.5 (41.93-1.82)	Depositor
(in resolution range)	99.6 (44.69-1.82)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.72 (at 1.82Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
D D	0.177 , 0.205	Depositor
$R, R_{free}$	0.178 , $0.205$	DCC
$R_{free}$ test set	4286 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.4	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning <sup>2</sup>	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.011 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6444	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.88% of the height of the origin peak. No significant pseudotranslation is detected.

<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: LI, 6ZV, PEG, FLC, PTR, EDO

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		nd lengths	Bond angles		
Mol Chain		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.71	$2/2900 \ (0.1\%)$	0.92	5/3905 (0.1%)	
1	В	0.63	$2/2901 \ (0.1\%)$	0.71	2/3906 (0.1%)	
All	All	0.67	4/5801 (0.1%)	0.82	7/7811 (0.1%)	

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	$\operatorname{Ideal}( ext{\AA})$
1	A	239	GLU	CD-OE2	12.07	1.39	1.25
1	В	203	GLU	CG-CD	6.09	1.61	1.51
1	A	239	GLU	CB-CG	5.64	1.62	1.52
1	В	203	GLU	CB-CG	5.17	1.61	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	410	ASP	CB-CG-OD1	27.51	143.06	118.30
1	A	410	ASP	CB-CG-OD2	-14.74	105.04	118.30
1	A	409	LYS	CD-CE-NZ	-11.02	86.35	111.70
1	A	239	GLU	OE1-CD-OE2	-9.76	111.59	123.30
1	A	410	ASP	OD1-CG-OD2	-7.33	109.36	123.30

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



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the ass	zmmetric	11n1f	whereas S	Symm-	Liashes	LISTS ST	vmmetry	v-related	clashes
UIIC COD	y IIIIII OUI IO	aiii o,	WITCICOD	$\cup$ y IIIIII	CIUDIICO	110000	y IIIIIIC UI	y iciauca	CIGOTICO.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2849	0	2864	30	1
1	В	2853	143	2865	49	0
2	A	26	0	8	1	0
2	В	26	9	8	0	0
3	A	37	0	0	0	0
3	В	37	0	0	0	0
4	A	32	0	48	2	0
4	В	48	0	72	24	0
5	A	7	0	10	0	0
6	A	1	0	0	1	0
6	В	1	0	0	0	0
7	A	196	0	0	5	0
7	В	179	0	0	9	1
All	All	6292	152	5875	81	1

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 81 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:184:TRP:HB3	1:B:240:MET:HE3	1.30	1.06
1:B:184:TRP:HB3	1:B:240:MET:CE	2.07	0.85
4:B:505:EDO:H11	7:B:735:HOH:O	1.79	0.82
1:B:212:LYS:HD3	7:B:671:HOH:O	1.83	0.79
1:B:149:VAL:H	4:B:509:EDO:H11	1.47	0.78

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	1200111 2		$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$
1:A:472:TYR:OH	7:B:756:HOH:O[3_655]	2.17	0.03



#### 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	Perce	$\mathbf{ntiles}$	
1	A	342/361 (95%)	330 (96%)	12 (4%)	0	100	100
1	В	342/361~(95%)	330 (96%)	12 (4%)	0	100	100
All	All	$684/722 \ (95\%)$	660 (96%)	24 (4%)	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	308/320 (96%)	308 (100%)	0	100	100	
1	В	308/320 (96%)	305 (99%)	3 (1%)	76	70	
All	All	616/640 (96%)	613 (100%)	3 (0%)	88	87	

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	318	ILE
1	В	407	LYS
1	В	412	LYS

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

#### 5.6 Ligand geometry (i)

Of 29 ligands modelled in this entry, 2 are monoatomic - leaving 27 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

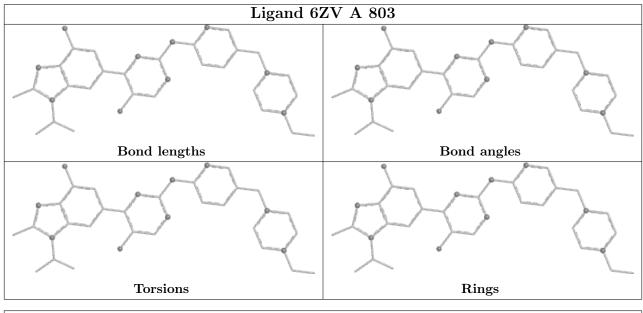
There are no ring outliers.

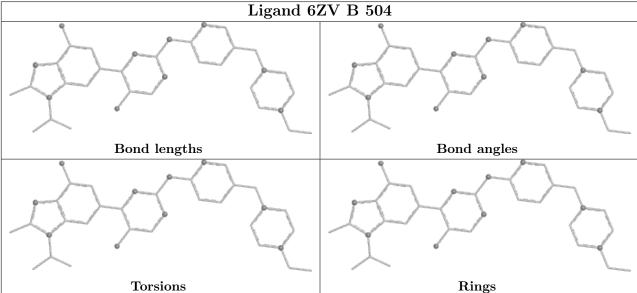
No monomer is involved in short contacts.

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 $>$	$\#\mathrm{RSRZ}{>}2$		$OWAB(A^2)$	Q<0.9	
1	A	344/361~(95%)	0.32	22 (6%)	19	15	29, 43, 70, 102	2 (0%)
1	В	$344/361 \ (95\%)$	0.34	21 (6%)	21	16	30, 46, 71, 95	4 (1%)
All	All	$688/722 \ (95\%)$	0.33	43 (6%)	20	15	29, 44, 73, 102	6 (0%)

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	413	ARG	8.1
1	A	408	THR	7.8
1	В	440	GLY	6.9
1	В	408	THR	6.7
1	A	410	ASP	6.3

#### 6.2 Non-standard residues in protein, DNA, RNA chains (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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	PTR	A	321	16/17	0.98	0.14	36,43,50,51	0
1	PTR	В	321	16/17	0.98	0.14	35,40,48,51	0

#### 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.

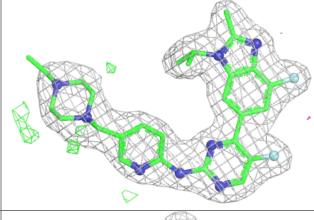
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q < 0.9
4	EDO	A	805	4/4	0.61	0.22	67,68,74,77	0
4	EDO	В	508	4/4	0.62	0.29	61,64,67,73	0
4	EDO	В	506	4/4	0.65	0.35	60,62,62,65	0
5	PEG	A	811	7/7	0.72	0.43	62,68,75,76	0
4	EDO	В	512	4/4	0.74	0.44	62,63,67,67	0
4	EDO	A	809	4/4	0.76	0.21	52,53,61,62	0
4	EDO	В	507	4/4	0.80	0.19	80,81,86,88	0
4	EDO	В	513	4/4	0.81	0.35	47,54,54,58	0
4	EDO	В	510	4/4	0.82	0.27	65,67,72,83	0
4	EDO	В	514	4/4	0.89	0.45	47,51,57,59	0
4	EDO	A	808	4/4	0.90	0.13	52,53,63,66	0
4	EDO	В	515	4/4	0.90	0.45	46,47,55,61	0
4	EDO	A	807	4/4	0.90	0.17	40,51,58,65	0
3	6ZV	В	504	37/37	0.91	0.15	30,35,65,67	0
4	EDO	В	509	4/4	0.91	0.32	37,55,59,66	0
4	EDO	В	511	4/4	0.92	0.11	52,58,59,64	0
4	EDO	A	810	4/4	0.92	0.17	49,52,57,63	0
4	EDO	A	806	4/4	0.92	0.20	48,52,53,62	0
4	EDO	В	505	4/4	0.93	0.16	42,47,51,65	0
4	EDO	A	812	4/4	0.94	0.08	49,51,52,52	0
6	LI	A	813	1/1	0.94	0.25	28,28,28,28	0
6	LI	В	516	1/1	0.94	0.22	32,32,32,32	0
3	6ZV	A	803	37/37	0.95	0.13	29,35,62,68	0
2	FLC	В	502	13/13	0.95	0.10	33,38,46,48	0
4	EDO	A	804	4/4	0.95	0.12	51,53,55,56	0
2	FLC	A	801	13/13	0.96	0.10	30,33,38,39	0
4	EDO	В	501	4/4	0.96	0.11	45,46,49,54	0
2	FLC	В	503	13/13	0.97	0.11	31,38,45,45	0
2	FLC	A	802	13/13	0.97	0.11	27,33,38,43	0

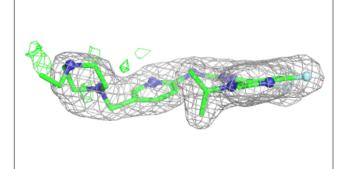
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

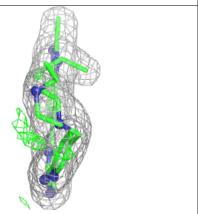


# Electron density around 6ZV B 504: $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray ${ m mF}_o{ m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive) Electron density around 6ZV A 803:

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









# 6.5 Other polymers (i)

There are no such residues in this entry.

