



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2025 – 08:18 PM JST

PDB ID : 6LIL / pdb\_00006lil  
Title : Crystal structure of human PDK2 complexed with an allosteric inhibitor compound 8c  
Authors : Kang, J.; Kim, J.  
Deposited on : 2019-12-12  
Resolution : 1.93 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

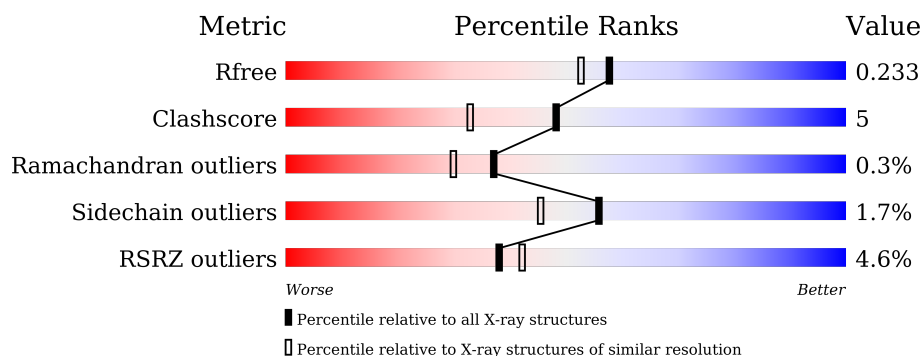
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.93 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))
$R_{free}$	164625	1306 (1.94-1.94)
Clashscore	180529	1400 (1.94-1.94)
Ramachandran outliers	177936	1387 (1.94-1.94)
Sidechain outliers	177891	1387 (1.94-1.94)
RSRZ outliers	164620	1306 (1.94-1.94)

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  $\geq 3$ , 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	411	<div> <div>4%</div> <div> <div></div> <div>74%</div> <div>10%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	411	<div> <div>4%</div> <div> <div></div> <div>76%</div> <div>8%</div> <div>16%</div> </div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5812 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 [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	346	Total	C	N	O	S	0	1	0
			2724	1747	452	508	17			
1	B	344	Total	C	N	O	S	0	1	0
			2730	1753	450	510	17			

There are 60 discrepancies between the modelled and reference sequences:

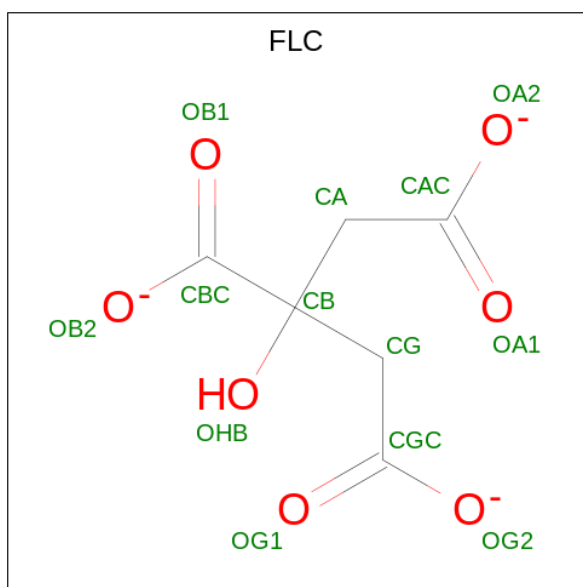
Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	expression tag	UNP Q15119
A	-23	ALA	-	expression tag	UNP Q15119
A	-22	GLY	-	expression tag	UNP Q15119
A	-21	SER	-	expression tag	UNP Q15119
A	-20	HIS	-	expression tag	UNP Q15119
A	-19	HIS	-	expression tag	UNP Q15119
A	-18	HIS	-	expression tag	UNP Q15119
A	-17	HIS	-	expression tag	UNP Q15119
A	-16	HIS	-	expression tag	UNP Q15119
A	-15	HIS	-	expression tag	UNP Q15119
A	-14	GLY	-	expression tag	UNP Q15119
A	-13	MET	-	expression tag	UNP Q15119
A	-12	ALA	-	expression tag	UNP Q15119
A	-11	SER	-	expression tag	UNP Q15119
A	-10	MET	-	expression tag	UNP Q15119
A	-9	THR	-	expression tag	UNP Q15119
A	-8	GLY	-	expression tag	UNP Q15119
A	-7	GLY	-	expression tag	UNP Q15119
A	-6	GLN	-	expression tag	UNP Q15119
A	-5	GLN	-	expression tag	UNP Q15119
A	-4	MET	-	expression tag	UNP Q15119
A	-3	GLY	-	expression tag	UNP Q15119
A	-2	ARG	-	expression tag	UNP Q15119
A	-1	SER	-	expression tag	UNP Q15119

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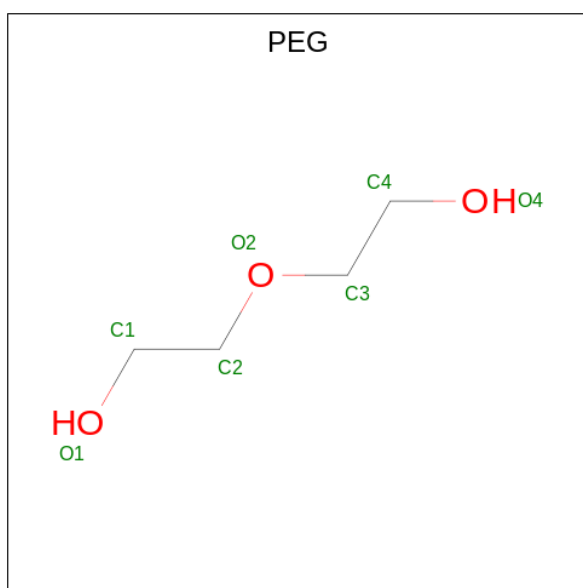
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q15119
A	1	ASP	-	expression tag	UNP Q15119
A	2	ASP	-	expression tag	UNP Q15119
A	3	ASP	-	expression tag	UNP Q15119
A	4	ASP	-	expression tag	UNP Q15119
A	5	LYS	-	expression tag	UNP Q15119
B	-24	MET	-	expression tag	UNP Q15119
B	-23	ALA	-	expression tag	UNP Q15119
B	-22	GLY	-	expression tag	UNP Q15119
B	-21	SER	-	expression tag	UNP Q15119
B	-20	HIS	-	expression tag	UNP Q15119
B	-19	HIS	-	expression tag	UNP Q15119
B	-18	HIS	-	expression tag	UNP Q15119
B	-17	HIS	-	expression tag	UNP Q15119
B	-16	HIS	-	expression tag	UNP Q15119
B	-15	HIS	-	expression tag	UNP Q15119
B	-14	GLY	-	expression tag	UNP Q15119
B	-13	MET	-	expression tag	UNP Q15119
B	-12	ALA	-	expression tag	UNP Q15119
B	-11	SER	-	expression tag	UNP Q15119
B	-10	MET	-	expression tag	UNP Q15119
B	-9	THR	-	expression tag	UNP Q15119
B	-8	GLY	-	expression tag	UNP Q15119
B	-7	GLY	-	expression tag	UNP Q15119
B	-6	GLN	-	expression tag	UNP Q15119
B	-5	GLN	-	expression tag	UNP Q15119
B	-4	MET	-	expression tag	UNP Q15119
B	-3	GLY	-	expression tag	UNP Q15119
B	-2	ARG	-	expression tag	UNP Q15119
B	-1	SER	-	expression tag	UNP Q15119
B	0	GLY	-	expression tag	UNP Q15119
B	1	ASP	-	expression tag	UNP Q15119
B	2	ASP	-	expression tag	UNP Q15119
B	3	ASP	-	expression tag	UNP Q15119
B	4	ASP	-	expression tag	UNP Q15119
B	5	LYS	-	expression tag	UNP Q15119

- Molecule 2 is CITRATE ANION (CCD ID: FLC) (formula:  $C_6H_5O_7$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula:  $C_4H_{10}O_3$ ).



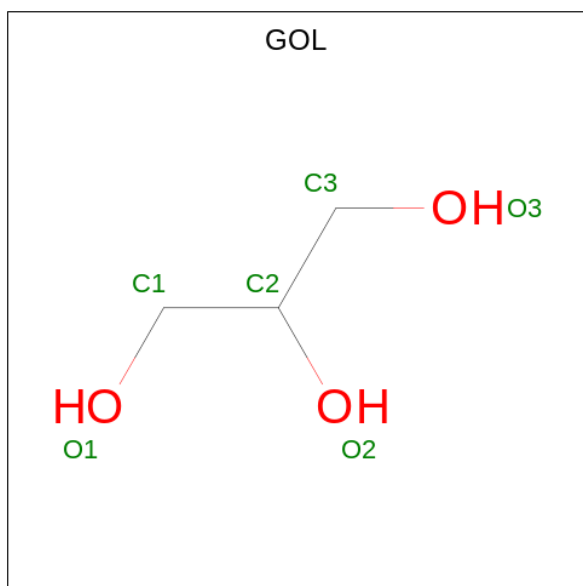
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		

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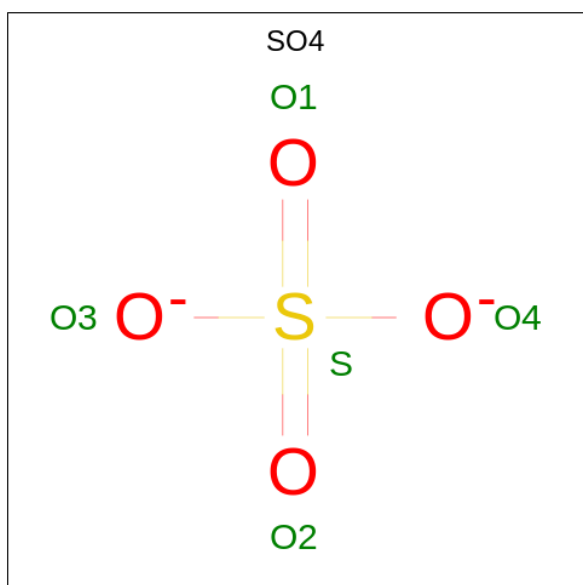
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula:  $C_3H_8O_3$ ).



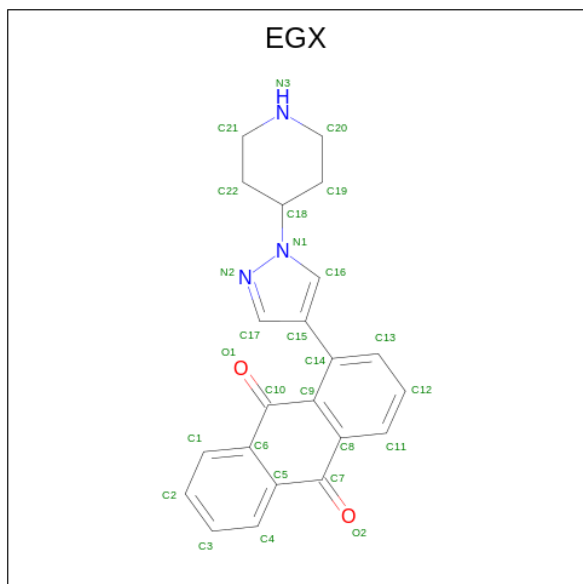
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is 1-(1-piperidin-4-ylpyrazol-4-yl)anthracene-9,10-dione (CCD ID: EGX) (formula: C<sub>22</sub>H<sub>19</sub>N<sub>3</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			27	22	3	2		
6	B	1	Total	C	N	O	0	0
			27	22	3	2		

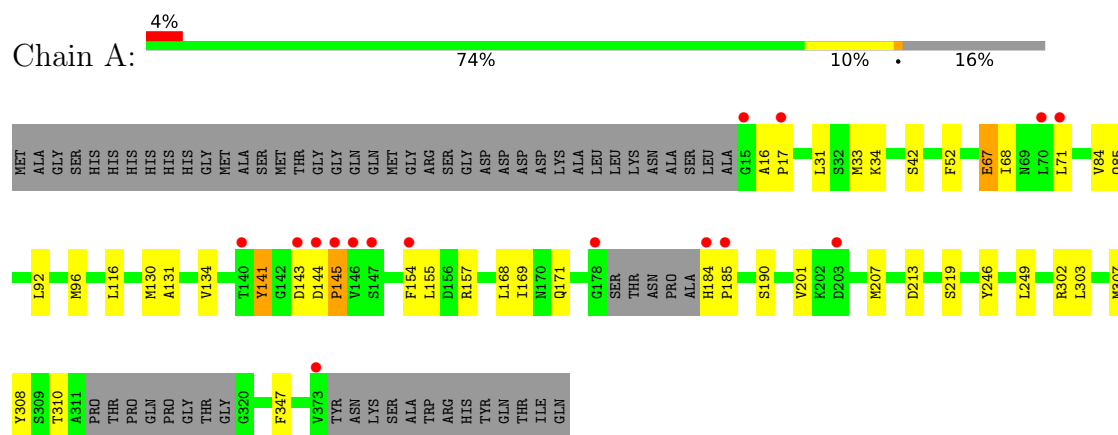
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	123	Total	O	0	0
			123	123		
7	B	123	Total	O	0	0
			123	123		

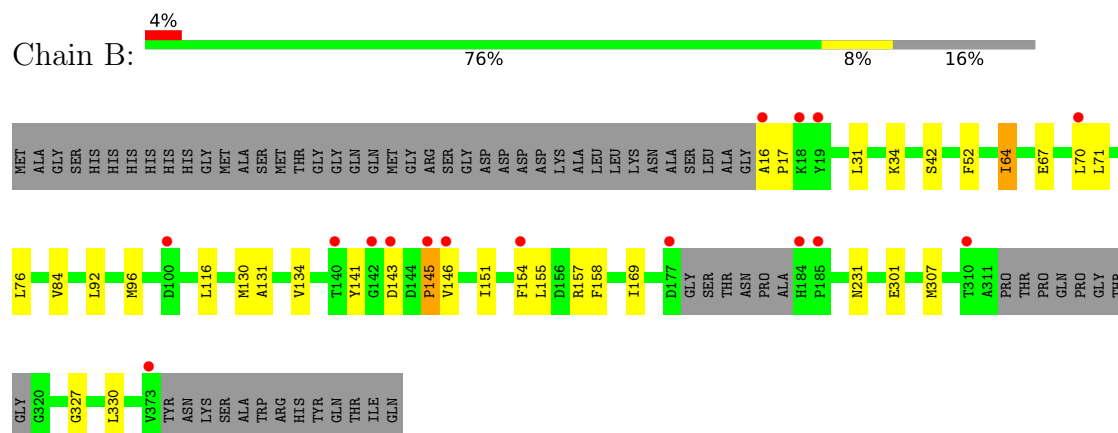
### 3 Residue-property plots

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: [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial



- Molecule 1: [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.78Å 52.84Å 92.14Å 88.20° 78.00° 60.93°	Depositor
Resolution (Å)	29.80 – 1.93 29.80 – 1.93	Depositor EDS
% Data completeness (in resolution range)	97.5 (29.80-1.93) 97.5 (29.80-1.93)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.50 (at 1.93Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, $R_{free}$	0.191 , 0.231 0.199 , 0.233	Depositor DCC
$R_{free}$ test set	3038 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.7	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 34.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for -h+k,k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5812	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.13% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 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: EGX, FLC, PEG, SO4, 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	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	1.02	0/2786	1.31	2/3776 (0.1%)
1	B	1.03	0/2793	1.32	6/3788 (0.2%)
All	All	1.02	0/5579	1.32	8/7564 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	347	PHE	CA-CB-CG	7.49	121.29	113.80
1	B	301	GLU	CA-C-N	6.07	128.41	120.28
1	B	301	GLU	C-N-CA	6.07	128.41	120.28
1	B	141	TYR	CB-CA-C	5.90	118.98	109.07
1	B	231	ASN	CA-C-N	5.40	127.78	120.38
1	B	231	ASN	C-N-CA	5.40	127.78	120.38
1	B	151	ILE	CA-C-O	-5.35	115.11	121.05
1	A	141	TYR	CB-CA-C	5.19	117.79	109.07

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	A	2724	0	2668	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2730	0	2680	25	0
2	A	13	0	5	0	0
2	B	13	0	5	1	0
3	A	7	0	10	3	0
3	B	14	0	20	3	0
4	A	6	0	8	0	0
5	A	5	0	0	0	0
6	A	27	0	0	1	0
6	B	27	0	0	4	0
7	A	123	0	0	0	0
7	B	123	0	0	0	0
All	All	5812	0	5396	59	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 5.

All (59) 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:64:ILE:HD11	1:B:158:PHE:HA	1.62	0.80
1:A:171:GLN:HE22	1:A:190:SER:H	1.34	0.75
1:A:144:ASP:N	1:A:145:PRO:HD3	2.06	0.70
1:B:96:MET:HA	1:B:96:MET:HE2	1.81	0.62
1:B:67:GLU:OE2	1:B:157:ARG:NH2	2.30	0.62
1:A:96:MET:HA	1:A:96:MET:HE2	1.80	0.62
1:A:171:GLN:NE2	1:A:190:SER:H	1.98	0.61
1:A:143:ASP:C	1:A:145:PRO:HD3	2.27	0.59
1:A:303:LEU:HD22	3:A:402:PEG:H21	1.86	0.57
1:B:84:VAL:HG11	1:B:130:MET:HE3	1.87	0.56
1:B:330:LEU:H	3:B:402:PEG:C1	2.18	0.55
1:A:154:PHE:CE2	1:A:155:LEU:HD23	2.43	0.54
1:A:310:THR:OG1	3:A:402:PEG:H22	2.07	0.54
1:B:154:PHE:CE2	1:B:155:LEU:HD23	2.43	0.53
1:A:67:GLU:OE2	1:A:157:ARG:NH2	2.37	0.53
1:B:327:GLY:HA2	3:B:402:PEG:H22	1.90	0.53
1:A:68:ILE:HG22	1:A:85:GLN:HE21	1.75	0.52
1:B:143:ASP:N	1:B:143:ASP:OD1	2.42	0.52
1:B:64:ILE:HD12	1:B:67:GLU:HB2	1.92	0.52
1:A:84:VAL:HG11	1:A:130:MET:HE3	1.91	0.51
1:B:52:PHE:HB2	6:B:404:EGX:C11	2.41	0.50
1:A:131:ALA:O	1:A:307:MET:HE1	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:ALA:O	1:B:307:MET:HE1	2.12	0.50
1:A:302:ARG:HG3	1:A:308:TYR:CE2	2.48	0.49
1:B:130:MET:HA	1:B:130:MET:HE2	1.95	0.48
1:A:303:LEU:CD2	3:A:402:PEG:H21	2.45	0.47
1:A:130:MET:HA	1:A:130:MET:HE2	1.97	0.46
1:A:96:MET:HE2	1:A:96:MET:CA	2.46	0.46
1:A:141:TYR:HB3	1:A:143:ASP:OD1	2.15	0.45
1:B:330:LEU:H	3:B:402:PEG:H12	1.82	0.45
1:B:134:VAL:HB	1:B:307:MET:CE	2.47	0.45
1:A:52:PHE:HB2	6:A:405:EGX:C11	2.46	0.45
1:A:134:VAL:HB	1:A:307:MET:CE	2.47	0.45
1:A:184:HIS:CB	1:A:185:PRO:HD3	2.47	0.44
1:A:31:LEU:HD12	1:A:168:LEU:HD21	1.99	0.44
6:B:404:EGX:C15	6:B:404:EGX:O1	2.66	0.44
1:B:64:ILE:HD12	1:B:64:ILE:HA	1.80	0.44
1:B:96:MET:HE2	1:B:96:MET:CA	2.48	0.44
2:B:401:FLC:OA1	2:B:401:FLC:CBC	2.65	0.43
1:A:116:LEU:HB3	1:A:169:ILE:HG23	2.00	0.43
1:A:84:VAL:HG21	1:A:130:MET:CE	2.48	0.43
1:B:154:PHE:CD2	1:B:154:PHE:C	2.95	0.43
1:B:92:LEU:O	1:B:96:MET:HG2	2.18	0.43
1:A:213:ASP:OD1	1:A:219:SER:OG	2.33	0.42
1:B:31:LEU:HD13	6:B:404:EGX:C2	2.49	0.42
1:A:84:VAL:HG21	1:A:130:MET:HE2	1.99	0.42
1:B:71:LEU:HD21	1:B:154:PHE:CD2	2.54	0.42
1:A:71:LEU:HD21	1:A:154:PHE:CD2	2.54	0.42
1:B:84:VAL:HG21	1:B:130:MET:CE	2.50	0.42
1:A:92:LEU:O	1:A:96:MET:HG2	2.20	0.41
1:A:16:ALA:N	1:A:17:PRO:HD2	2.35	0.41
1:B:16:ALA:N	1:B:17:PRO:HD2	2.35	0.41
1:B:31:LEU:HD13	6:B:404:EGX:C1	2.51	0.41
1:B:116:LEU:HB3	1:B:169:ILE:HG23	2.02	0.41
1:B:143:ASP:HB2	1:B:145:PRO:HD3	2.03	0.41
1:A:154:PHE:CD2	1:A:154:PHE:C	2.95	0.41
1:A:207:MET:HG2	1:A:246:TYR:OH	2.21	0.40
1:A:144:ASP:N	1:A:145:PRO:CD	2.81	0.40
1:A:201:VAL:HA	1:A:249:LEU:HD13	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	341/411 (83%)	333 (98%)	7 (2%)	1 (0%)	37	30
1	B	339/411 (82%)	331 (98%)	7 (2%)	1 (0%)	37	30
All	All	680/822 (83%)	664 (98%)	14 (2%)	2 (0%)	37	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	145	PRO
1	B	145	PRO

### 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	299/361 (83%)	295 (99%)	4 (1%)	65	58
1	B	303/361 (84%)	297 (98%)	6 (2%)	50	38
All	All	602/722 (83%)	592 (98%)	10 (2%)	56	45

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	MET
1	A	34	LYS
1	A	42	SER
1	A	67	GLU

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Mol	Chain	Res	Type
1	B	34	LYS
1	B	42	SER
1	B	64	ILE
1	B	70	LEU
1	B	76	LEU
1	B	146	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	85	GLN
1	A	171	GLN
1	A	237	HIS
1	B	234	GLN
1	B	237	HIS

### 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](#)

9 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
3	PEG	B	402	-	6,6,6	0.46	0	5,5,5	0.55	0
3	PEG	A	402	-	6,6,6	0.33	0	5,5,5	0.33	0
5	SO4	A	404	-	4,4,4	0.27	0	6,6,6	0.11	0
2	FLC	B	401	-	12,12,12	1.14	1 (8%)	17,17,17	1.62	2 (11%)
3	PEG	B	403	-	6,6,6	0.38	0	5,5,5	0.23	0
6	EGX	A	405	-	29,31,31	0.78	1 (3%)	36,45,45	1.00	1 (2%)
4	GOL	A	403	-	5,5,5	0.15	0	5,5,5	0.33	0
6	EGX	B	404	-	29,31,31	0.73	1 (3%)	36,45,45	2.61	2 (5%)
2	FLC	A	401	-	12,12,12	1.29	1 (8%)	17,17,17	1.37	2 (11%)

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	PEG	B	402	-	-	4/4/4/4	-
3	PEG	A	402	-	-	3/4/4/4	-
2	FLC	B	401	-	-	0/16/16/16	-
3	PEG	B	403	-	-	3/4/4/4	-
6	EGX	A	405	-	-	2/4/32/32	0/5/5/5
4	GOL	A	403	-	-	1/4/4/4	-
6	EGX	B	404	-	-	2/4/32/32	0/5/5/5
2	FLC	A	401	-	-	9/16/16/16	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	404	EGX	C16-N1	2.87	1.38	1.35
2	A	401	FLC	CB-CBC	2.58	1.56	1.53
6	A	405	EGX	C16-N1	2.35	1.38	1.35
2	B	401	FLC	CB-CBC	2.34	1.55	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	404	EGX	C16-N1-C18	15.16	138.91	125.48
2	B	401	FLC	OB1-CBC-CB	-4.35	116.10	122.25
6	A	405	EGX	C16-N1-C18	4.25	129.25	125.48
2	B	401	FLC	OB2-CBC-CB	3.17	118.56	113.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	FLC	OB1-CBC-CB	-2.93	118.10	122.25
6	B	404	EGX	C20-C19-C18	-2.33	108.62	110.44
2	A	401	FLC	OB2-CBC-CB	2.17	116.81	113.05

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	405	EGX	C13-C14-C15-C17
6	A	405	EGX	C13-C14-C15-C16
6	B	404	EGX	C13-C14-C15-C17
6	B	404	EGX	C13-C14-C15-C16
3	B	402	PEG	O2-C3-C4-O4
3	B	403	PEG	O1-C1-C2-O2
3	B	402	PEG	O1-C1-C2-O2
3	B	403	PEG	O2-C3-C4-O4
3	A	402	PEG	O2-C3-C4-O4
2	A	401	FLC	CA-CB-CBC-OB1
2	A	401	FLC	CA-CB-CBC-OB2
2	A	401	FLC	CG-CB-CBC-OB2
3	A	402	PEG	C4-C3-O2-C2
3	B	403	PEG	C4-C3-O2-C2
3	A	402	PEG	C1-C2-O2-C3
2	A	401	FLC	CB-CG-CGC-OG2
2	A	401	FLC	OHB-CB-CBC-OB2
2	A	401	FLC	CG-CB-CBC-OB1
3	B	402	PEG	C4-C3-O2-C2
2	A	401	FLC	CB-CG-CGC-OG1
4	A	403	GOL	O1-C1-C2-C3
2	A	401	FLC	CB-CA-CAC-OA1
2	A	401	FLC	CB-CA-CAC-OA2
3	B	402	PEG	C1-C2-O2-C3

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	402	PEG	3	0
3	A	402	PEG	3	0
2	B	401	FLC	1	0
6	A	405	EGX	1	0

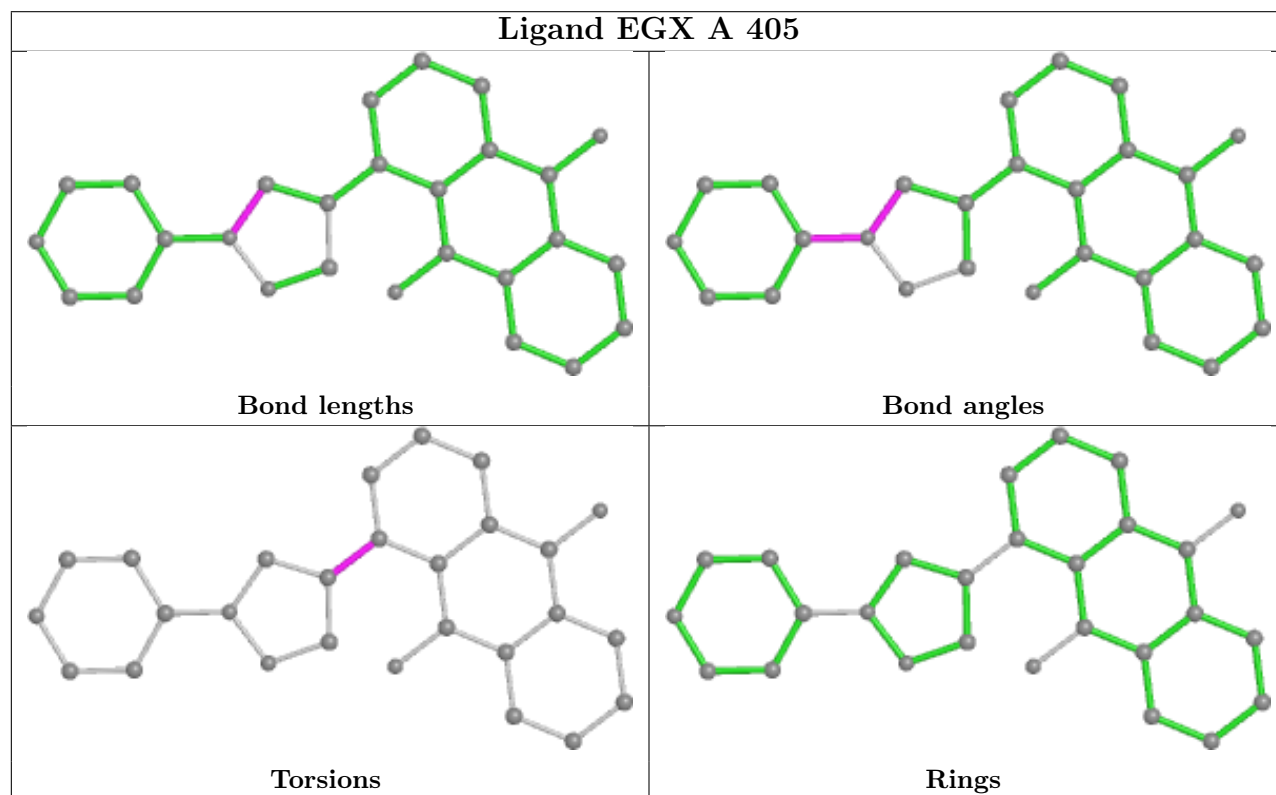
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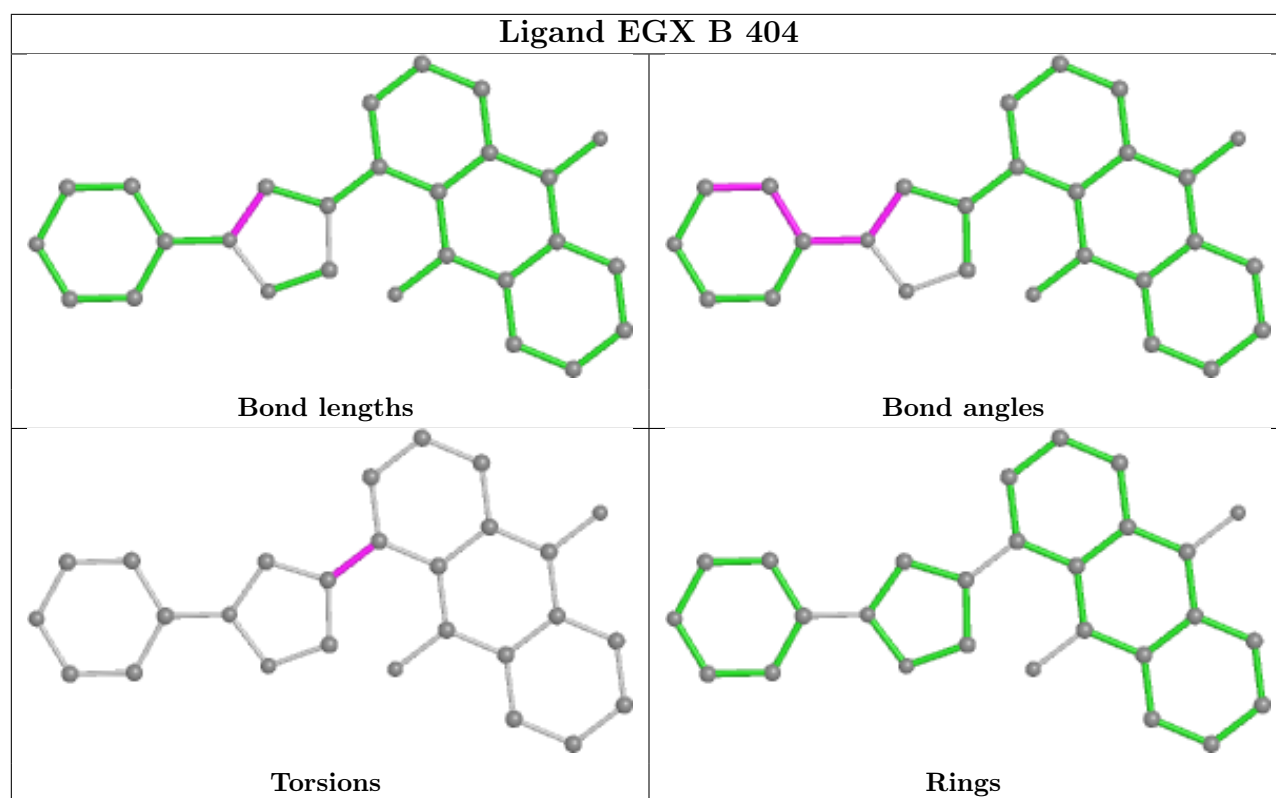


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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	404	EGX	4	0

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	346/411 (84%)	0.09	16 (4%) 38 42	18, 37, 67, 103	1 (0%)
1	B	344/411 (83%)	0.06	16 (4%) 37 41	17, 35, 66, 114	1 (0%)
All	All	690/822 (83%)	0.08	32 (4%) 38 42	17, 36, 67, 114	2 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	146	VAL	5.5
1	A	145	PRO	4.7
1	B	142	GLY	4.4
1	B	143	ASP	4.2
1	B	154	PHE	3.6
1	B	184	HIS	3.5
1	A	184	HIS	3.4
1	A	146	VAL	3.3
1	B	70	LEU	3.3
1	B	140	THR	3.3
1	A	143	ASP	3.2
1	A	178	GLY	3.2
1	B	145	PRO	3.2
1	A	70	LEU	3.1
1	A	373	VAL	3.0
1	B	177	ASP	2.9
1	B	19	TYR	2.9
1	A	185	PRO	2.9
1	A	15	GLY	2.7
1	A	144	ASP	2.7
1	B	16	ALA	2.4
1	A	71	LEU	2.3
1	B	373	VAL	2.3
1	B	185	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	203	ASP	2.3
1	A	17	PRO	2.2
1	A	147	SER	2.1
1	A	140	THR	2.1
1	B	310	THR	2.1
1	B	100	ASP	2.1
1	A	154	PHE	2.1
1	B	18	LYS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

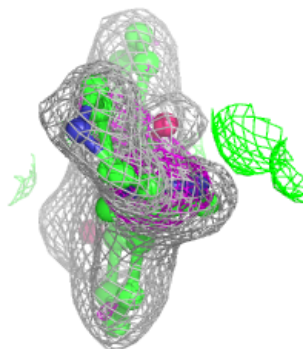
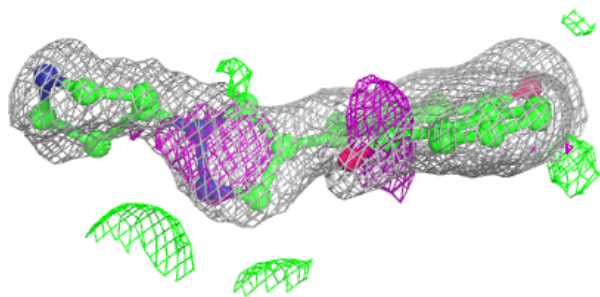
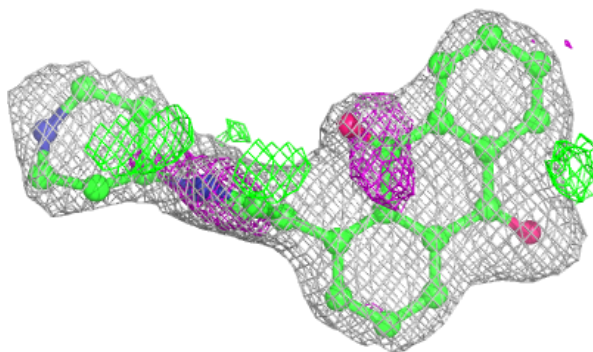
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	PEG	A	402	7/7	0.70	0.19	52,59,65,66	0
5	SO4	A	404	5/5	0.70	0.14	81,86,95,103	0
3	PEG	B	402	7/7	0.86	0.16	36,43,50,50	0
6	EGX	A	405	27/27	0.86	0.11	39,43,52,54	0
3	PEG	B	403	7/7	0.87	0.12	54,63,72,74	0
4	GOL	A	403	6/6	0.88	0.10	55,64,68,70	0
2	FLC	B	401	13/13	0.90	0.07	43,47,51,55	0
2	FLC	A	401	13/13	0.92	0.07	44,51,60,60	0
6	EGX	B	404	27/27	0.93	0.08	32,36,44,46	0

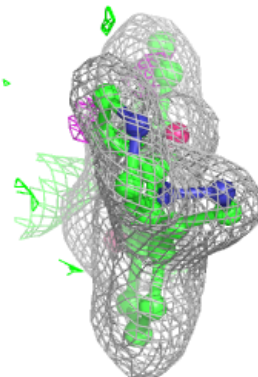
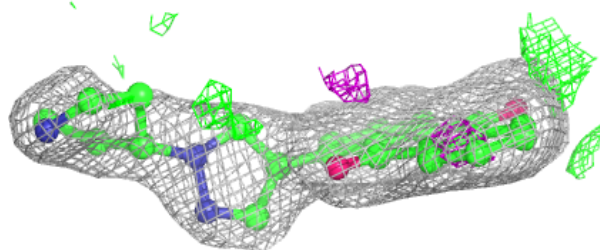
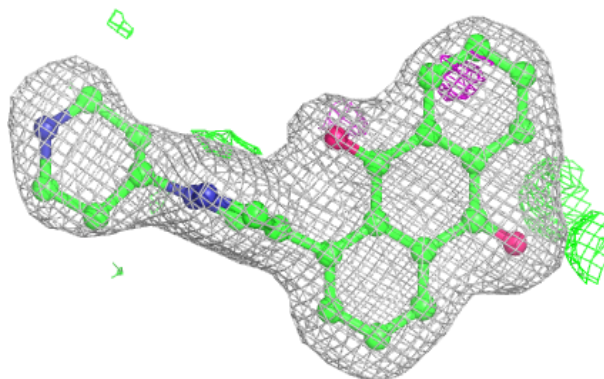
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around EGX A 405:**

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

**Electron density around EGX B 404:**

$2mF_o-DF_c$  (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.