



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 9, 2026 – 10:27 PM UTC

PDB ID : 9RDF / pdb\_00009rdf  
Title : Liver Pyruvate kinase in complex with a phthalazine-based fluorescent probe IV  
Authors : Nilsson, O.; Brear, P.; Grotli, M.; Hyvonen, M.  
Deposited on : 2025-06-02  
Resolution : 1.62 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](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 Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

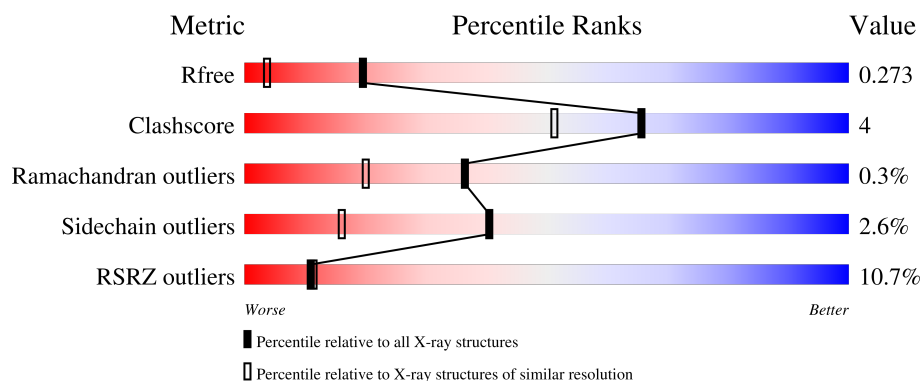
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.62 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	6728 (1.64-1.60)
Clashscore	190562	7023 (1.64-1.60)
Ramachandran outliers	187476	6898 (1.64-1.60)
Sidechain outliers	187428	6896 (1.64-1.60)
RSRZ outliers	180081	6727 (1.64-1.60)

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	545	
1	B	545	
1	C	545	
1	D	545	

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	OXL	A	604	-	X	-	-

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 17309 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 Isoform L-type of Pyruvate kinase PKLR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	521	Total	C	N	O	S	0	5	0
			3979	2502	718	740	19			
1	B	521	Total	C	N	O	S	0	6	0
			3977	2502	716	740	19			
1	C	521	Total	C	N	O	S	0	5	0
			3979	2502	718	740	19			
1	D	521	Total	C	N	O	S	0	6	0
			3977	2502	716	740	19			

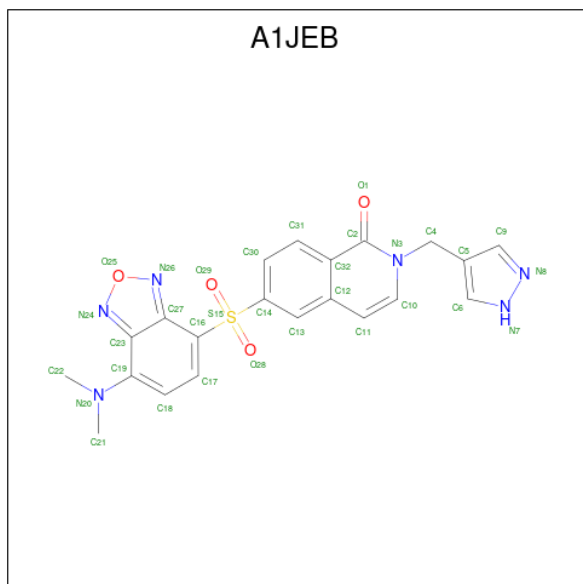
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P30613
A	0	SER	-	expression tag	UNP P30613
B	-1	GLY	-	expression tag	UNP P30613
B	0	SER	-	expression tag	UNP P30613
C	-1	GLY	-	expression tag	UNP P30613
C	0	SER	-	expression tag	UNP P30613
D	-1	GLY	-	expression tag	UNP P30613
D	0	SER	-	expression tag	UNP P30613

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

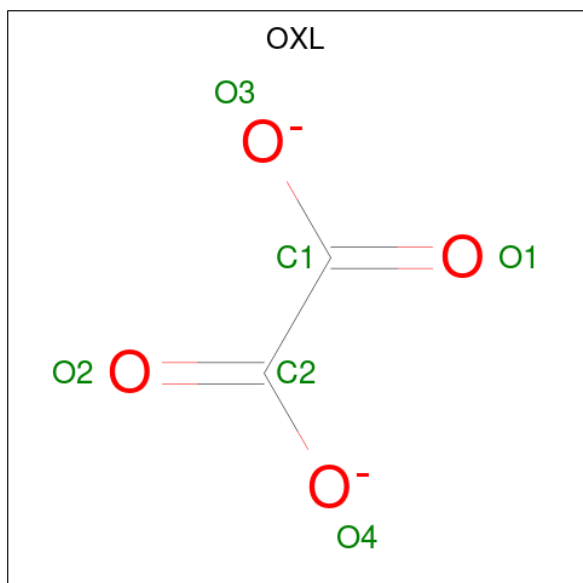
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		
2	C	3	Total	Mg	0	0
			3	3		
2	D	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 6-[[7-(dimethylamino)-2,1,3-benzoxadiazol-4-yl]sulfonyl]-2-(1 {H}-pyrazol-4-ylmethyl)isoquinolin-1-one (CCD ID: A1JEB) (formula:  $C_{21}H_{18}N_6O_4S$ ) (labeled as "Ligand of Interest" by depositor).



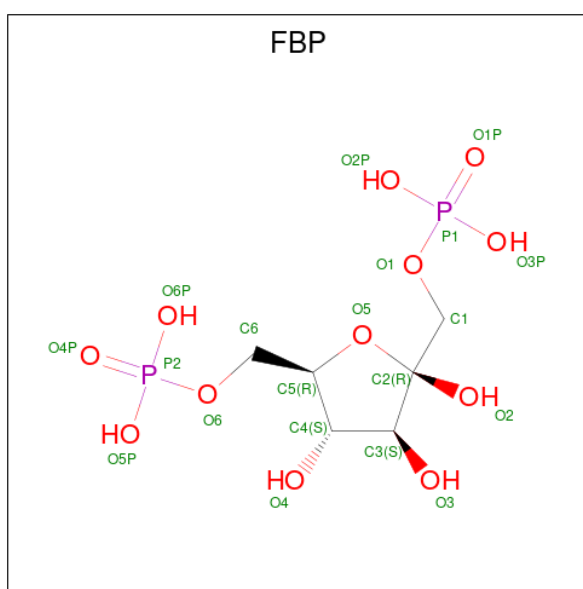
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	1
			64	42	12	8	2		
3	B	1	Total	C	N	O	S	0	1
			64	42	12	8	2		

- Molecule 4 is OXALATE ION (CCD ID: OXL) (formula:  $C_2O_4$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 2 4	0	0
4	B	1	Total C O 6 2 4	0	0
4	C	1	Total C O 6 2 4	0	0
4	D	1	Total C O 6 2 4	0	0

- Molecule 5 is 1,6-di-O-phosphono-beta-D-fructofuranose (CCD ID: FBP) (formula:  $C_6H_{14}O_{12}P_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O P 20 6 12 2	0	0
5	B	1	Total C O P 20 6 12 2	0	0
5	C	1	Total C O P 20 6 12 2	0	0
5	D	1	Total C O P 20 6 12 2	0	0

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula:  $C_4H_{10}O_3$ ).



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

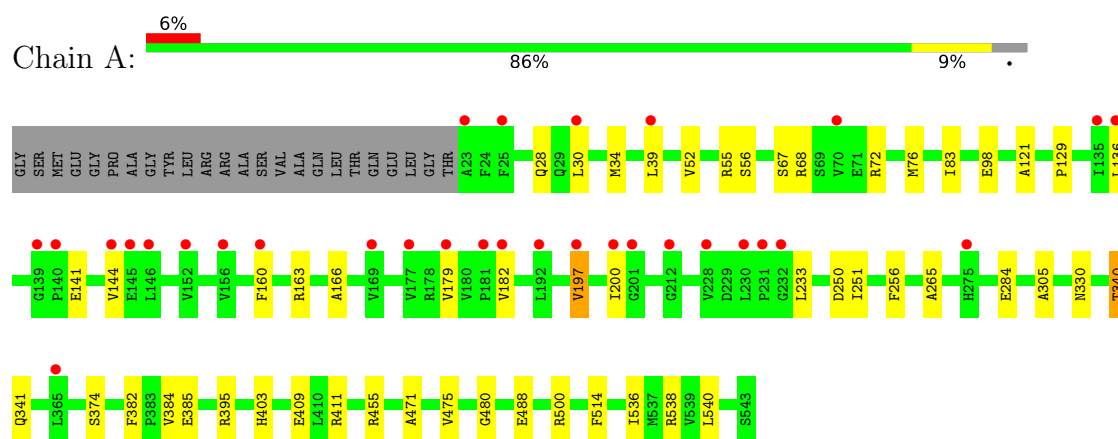
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	348	Total	O	0	0
			348	348		
7	B	315	Total	O	0	1
			316	316		
7	C	268	Total	O	0	0
			268	268		
7	D	214	Total	O	0	4
			218	218		

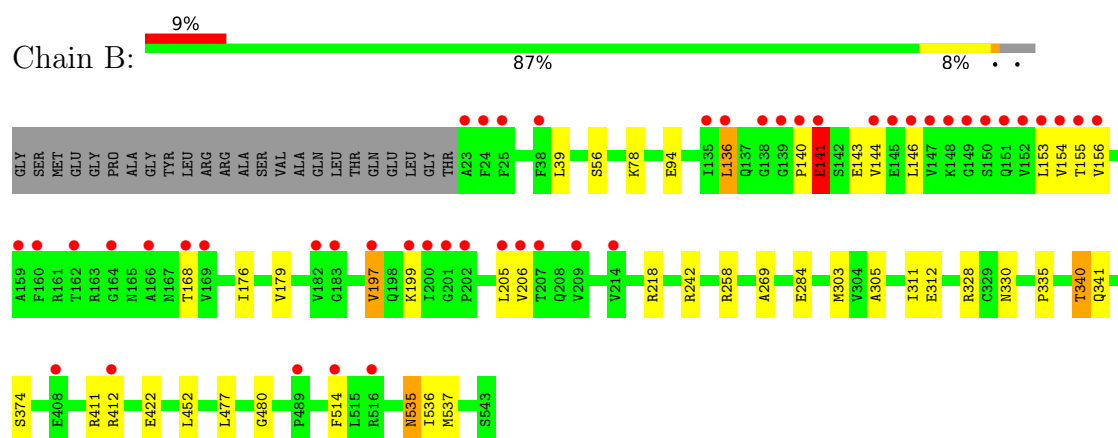
### 3 Residue-property plots [i](#)

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.

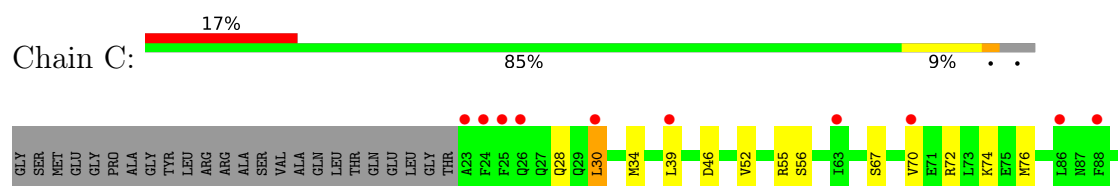
- Molecule 1: Isoform L-type of Pyruvate kinase PKLR



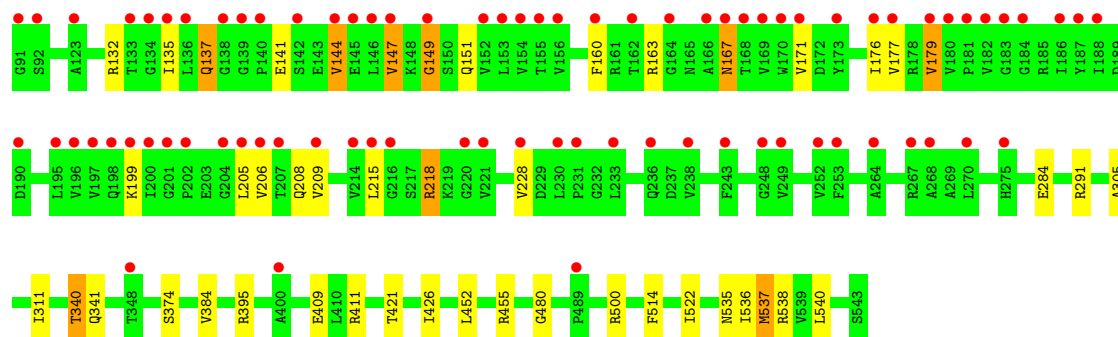
- Molecule 1: Isoform L-type of Pyruvate kinase PKLR



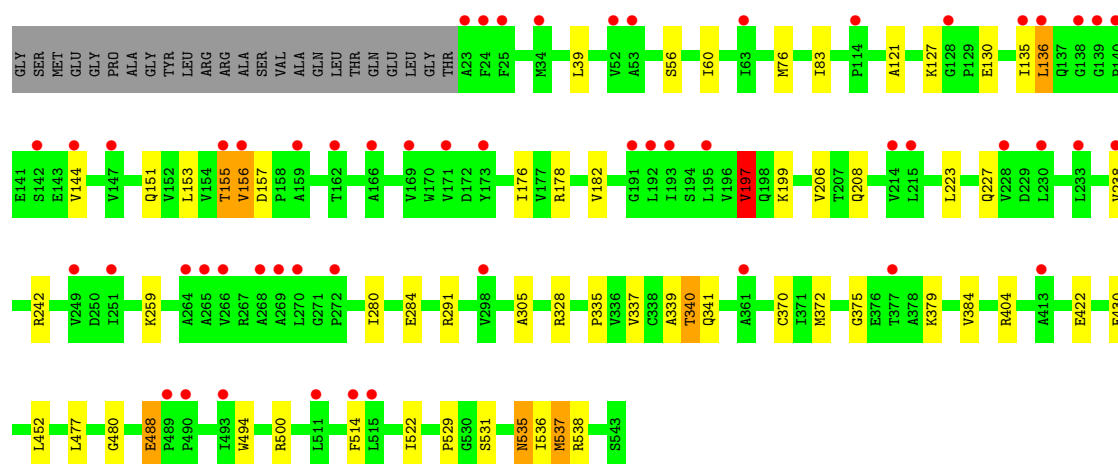
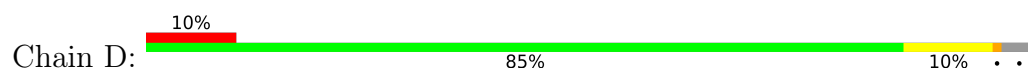
- Molecule 1: Isoform L-type of Pyruvate kinase PKLR







● Molecule 1: Isoform L-type of Pyruvate kinase PKLR



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	200.18Å 97.58Å 136.40Å 90.00° 118.53° 90.00°	Depositor
Resolution (Å)	78.65 – 1.62 78.65 – 1.62	Depositor EDS
% Data completeness (in resolution range)	98.4 (78.65-1.62) 98.5 (78.65-1.62)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.99 (at 1.62Å)	Xtriage
Refinement program	BUSTER 2.10.4 (10-JUL-2024)	Depositor
R, $R_{free}$	0.238 , 0.277 0.229 , 0.273	Depositor DCC
$R_{free}$ test set	1919 reflections (0.66%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.6	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	17309	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 4.07% 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: FBP, PEG, MG, OXL, A1JEB

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.88	1/4055 (0.0%)	1.02	2/5494 (0.0%)
1	B	0.89	2/4061 (0.0%)	1.03	7/5501 (0.1%)
1	C	0.84	1/4055 (0.0%)	1.02	4/5494 (0.1%)
1	D	0.83	1/4061 (0.0%)	1.03	3/5501 (0.1%)
All	All	0.86	5/16232 (0.0%)	1.03	16/21990 (0.1%)

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

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

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	374	SER	CA-C	8.87	1.56	1.52
1	C	374	SER	CA-C	7.35	1.55	1.52
1	B	374	SER	CA-C	6.56	1.55	1.52
1	B	303	MET	SD-CE	-6.13	1.64	1.79
1	D	156	VAL	CA-C	5.92	1.58	1.52

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	46	ASP	CA-CB-CG	7.31	119.91	112.60
1	B	94	GLU	CB-CG-CD	7.25	124.92	112.60
1	C	514	PHE	CA-CB-CG	6.56	120.36	113.80
1	C	167	ASN	CA-CB-CG	6.19	118.79	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	156	VAL	CB-CA-C	6.14	116.78	110.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	258	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	3979	0	4053	34	0
1	B	3977	0	4064	21	0
1	C	3979	0	4053	36	0
1	D	3977	0	4064	39	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	3	0	0	0	0
2	D	1	0	0	0	0
3	A	64	0	0	4	0
3	B	64	0	0	3	0
4	A	6	0	0	0	0
4	B	6	0	0	0	0
4	C	6	0	0	0	0
4	D	6	0	0	0	0
5	A	20	0	10	0	0
5	B	20	0	10	0	0
5	C	20	0	10	0	0
5	D	20	0	10	1	0
6	A	7	0	10	1	0
7	A	348	0	0	2	0
7	B	316	0	0	0	0
7	C	268	0	0	0	0
7	D	218	0	0	2	0
All	All	17309	0	16284	122	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 4.

The worst 5 of 122 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)
3:B:605[B]:A1JEB:C22	1:C:39:LEU:HD13	2.14	0.77
1:A:536:ILE:HG12	1:C:538:ARG:HG2	1.69	0.72
1:B:56:SER:HB2	1:B:480:GLY:HA2	1.73	0.71
1:A:68:ARG:NH2	1:A:98:GLU:HB2	2.04	0.71
1:A:136:LEU:HD13	1:A:144:VAL:HG23	1.77	0.67

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	524/545 (96%)	519 (99%)	4 (1%)	1 (0%)	43	25
1	B	525/545 (96%)	514 (98%)	9 (2%)	2 (0%)	30	14
1	C	524/545 (96%)	508 (97%)	13 (2%)	3 (1%)	21	7
1	D	525/545 (96%)	515 (98%)	9 (2%)	1 (0%)	43	25
All	All	2098/2180 (96%)	2056 (98%)	35 (2%)	7 (0%)	36	20

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	141	GLU
1	C	149	GLY
1	A	340	THR
1	B	340	THR
1	C	144	VAL

### 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	422/434 (97%)	415 (98%)	7 (2%)	53	29
1	B	423/434 (98%)	411 (97%)	12 (3%)	38	14
1	C	422/434 (97%)	408 (97%)	14 (3%)	33	11
1	D	423/434 (98%)	412 (97%)	11 (3%)	40	16
All	All	1690/1736 (97%)	1646 (97%)	44 (3%)	40	16

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	291	ARG
1	D	153	LEU
1	C	455	ARG
1	C	540	LEU
1	D	156	VAL

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

Mol	Chain	Res	Type
1	C	211	ASN
1	D	137	GLN
1	D	535	ASN
1	D	208	GLN
1	B	535	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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 21 ligands modelled in this entry, 8 are monoatomic - leaving 13 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	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	OXL	D	602	2	5,5,5	1.81	1 (20%)	6,6,6	2.11	3 (50%)
3	A1JEB	A	603[B]	-	36,36,36	0.81	2 (5%)	45,54,54	1.60	7 (15%)
4	OXL	B	601	2	5,5,5	1.55	1 (20%)	6,6,6	1.79	2 (33%)
3	A1JEB	B	605[B]	-	36,36,36	0.88	2 (5%)	45,54,54	1.59	6 (13%)
5	FBP	C	605	-	18,20,20	0.52	0	21,32,32	0.90	1 (4%)
5	FBP	B	602	-	18,20,20	0.49	0	21,32,32	0.69	0
4	OXL	C	604	2	5,5,5	1.80	1 (20%)	6,6,6	1.88	2 (33%)
5	FBP	D	603	-	18,20,20	0.49	0	21,32,32	0.92	0
6	PEG	A	606	-	6,6,6	0.22	0	5,5,5	0.23	0
3	A1JEB	A	603[A]	-	36,36,36	0.80	2 (5%)	45,54,54	1.54	7 (15%)
5	FBP	A	605	-	18,20,20	0.48	0	21,32,32	0.92	1 (4%)
4	OXL	A	604	2	5,5,5	2.11	2 (40%)	6,6,6	1.69	2 (33%)
3	A1JEB	B	605[A]	-	36,36,36	0.86	2 (5%)	45,54,54	1.57	7 (15%)

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
4	OXL	D	602	2	-	0/4/4/4	-
3	A1JEB	A	603[B]	-	-	1/20/20/20	0/5/5/5
4	OXL	B	601	2	-	1/4/4/4	-
3	A1JEB	B	605[B]	-	-	1/20/20/20	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FBP	C	605	-	-	2/13/32/32	0/1/1/1
5	FBP	B	602	-	-	2/13/32/32	0/1/1/1
4	OXL	C	604	2	-	0/4/4/4	-
5	FBP	D	603	-	-	2/13/32/32	0/1/1/1
6	PEG	A	606	-	-	0/4/4/4	-
3	A1JEB	A	603[A]	-	-	1/20/20/20	0/5/5/5
5	FBP	A	605	-	-	2/13/32/32	0/1/1/1
4	OXL	A	604	2	-	3/4/4/4	-
3	A1JEB	B	605[A]	-	-	1/20/20/20	0/5/5/5

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	602	OXL	C2-C1	-3.16	1.49	1.54
3	B	605[A]	A1JEB	C17-C16	-3.13	1.35	1.39
4	A	604	OXL	C2-C1	-3.12	1.49	1.54
4	C	604	OXL	C2-C1	-3.10	1.49	1.54
3	B	605[B]	A1JEB	C17-C16	-3.03	1.35	1.39

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	605[B]	A1JEB	C17-C18-C19	6.92	122.89	116.82
3	B	605[A]	A1JEB	C17-C18-C19	6.91	122.89	116.82
3	A	603[B]	A1JEB	C17-C18-C19	6.83	122.82	116.82
3	A	603[A]	A1JEB	C17-C18-C19	6.67	122.67	116.82
3	A	603[B]	A1JEB	C17-C16-C27	-5.04	117.16	121.07

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	603	FBP	C4-C5-C6-O6
5	C	605	FBP	C4-C5-C6-O6
5	A	605	FBP	C4-C5-C6-O6
5	B	602	FBP	C4-C5-C6-O6
5	C	605	FBP	O5-C5-C6-O6

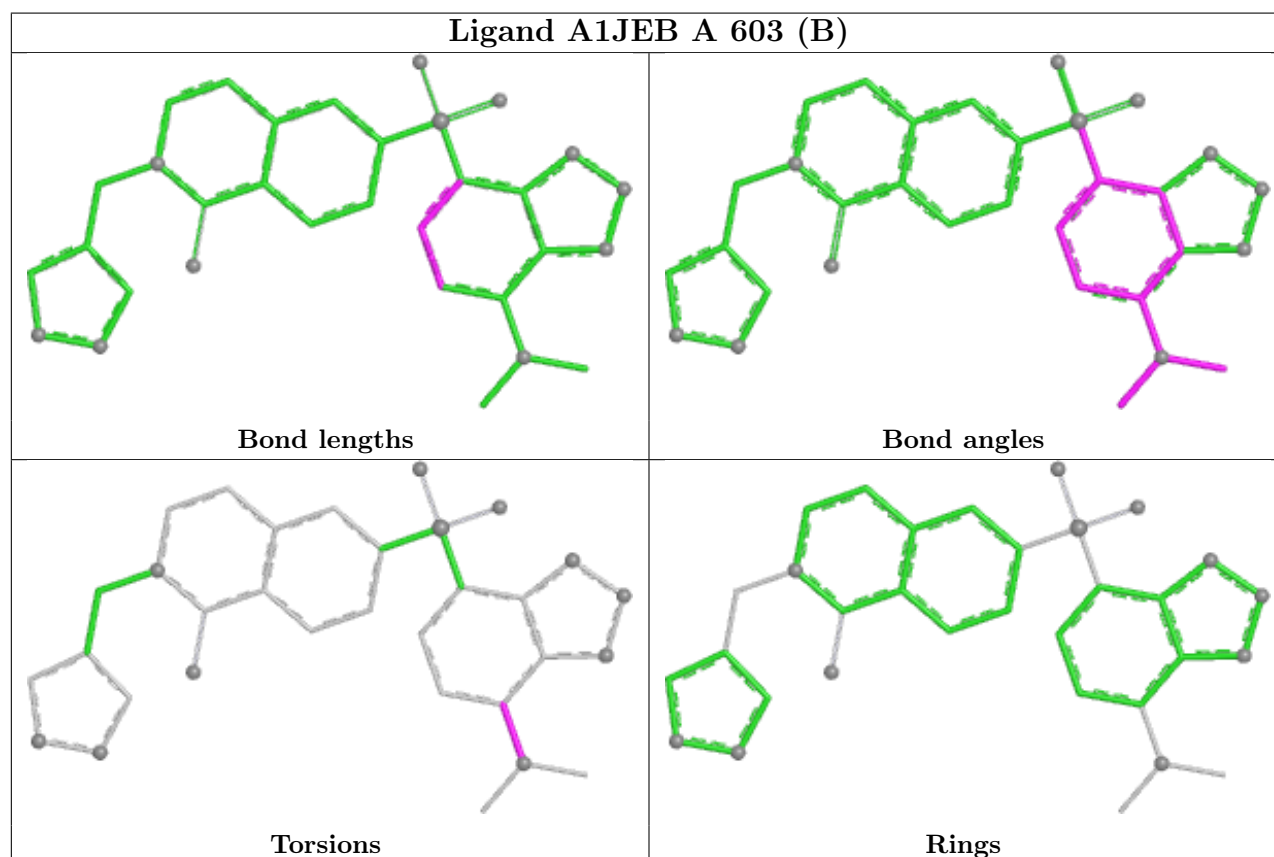
There are no ring outliers.

6 monomers are involved in 9 short contacts:

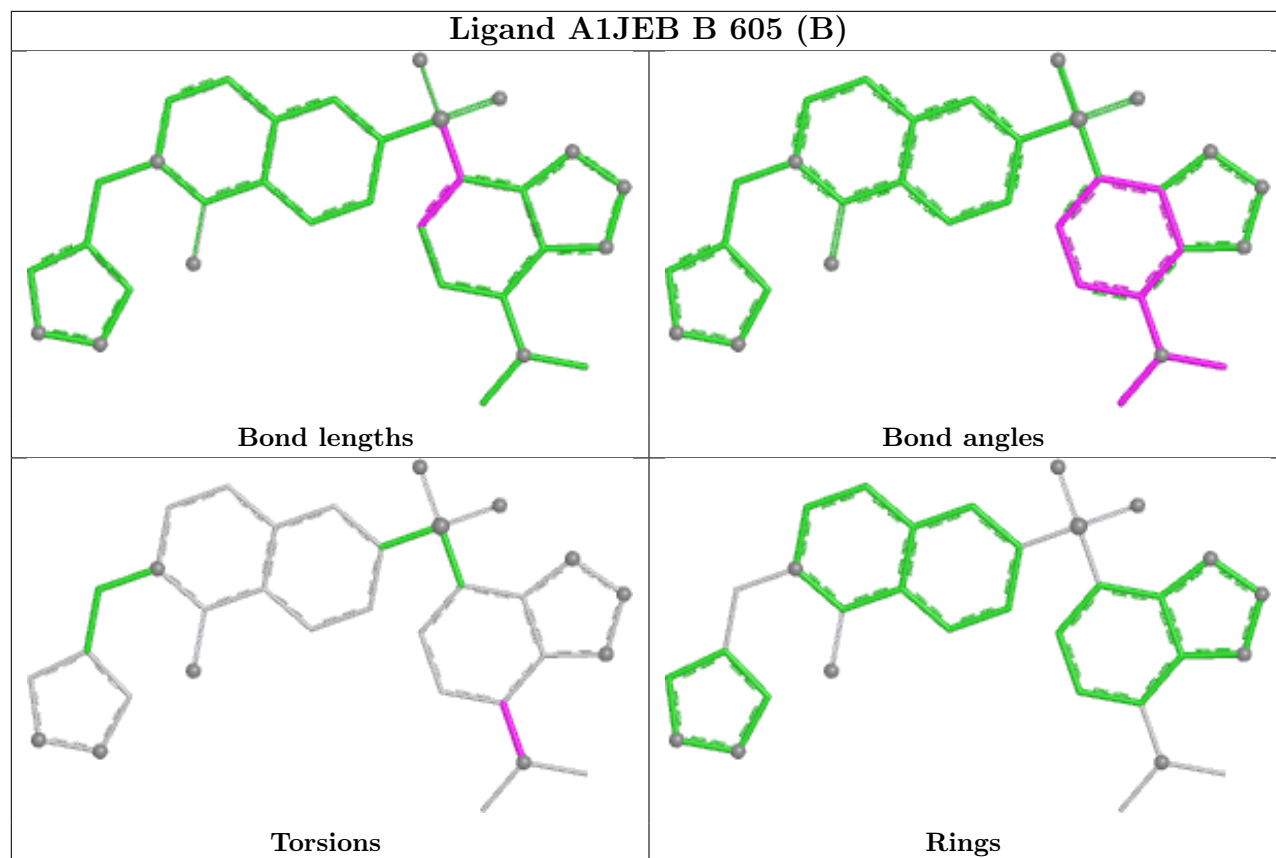


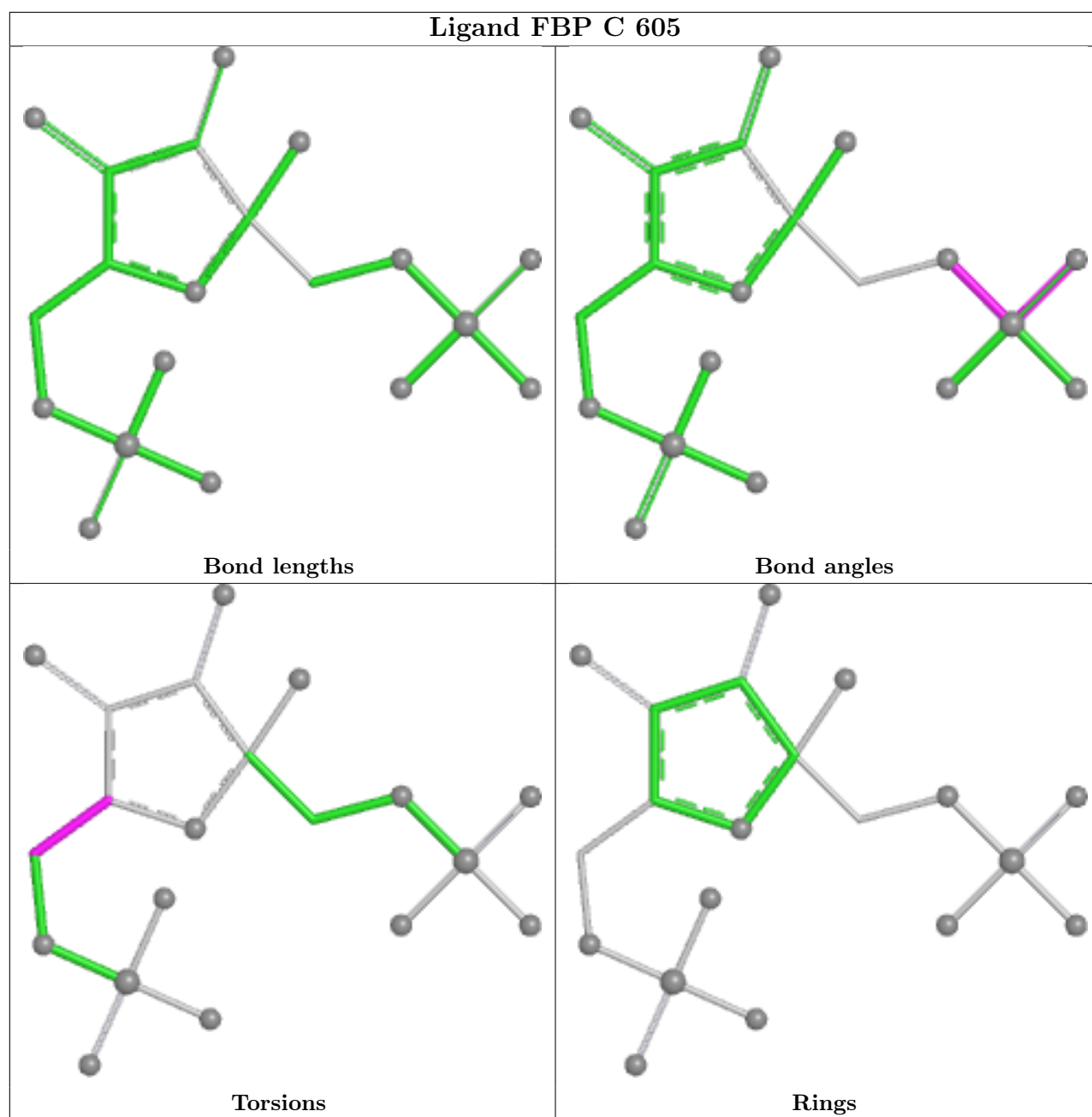
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	603[B]	A1JEB	2	0
3	B	605[B]	A1JEB	1	0
5	D	603	FBP	1	0
6	A	606	PEG	1	0
3	A	603[A]	A1JEB	2	0
3	B	605[A]	A1JEB	2	0

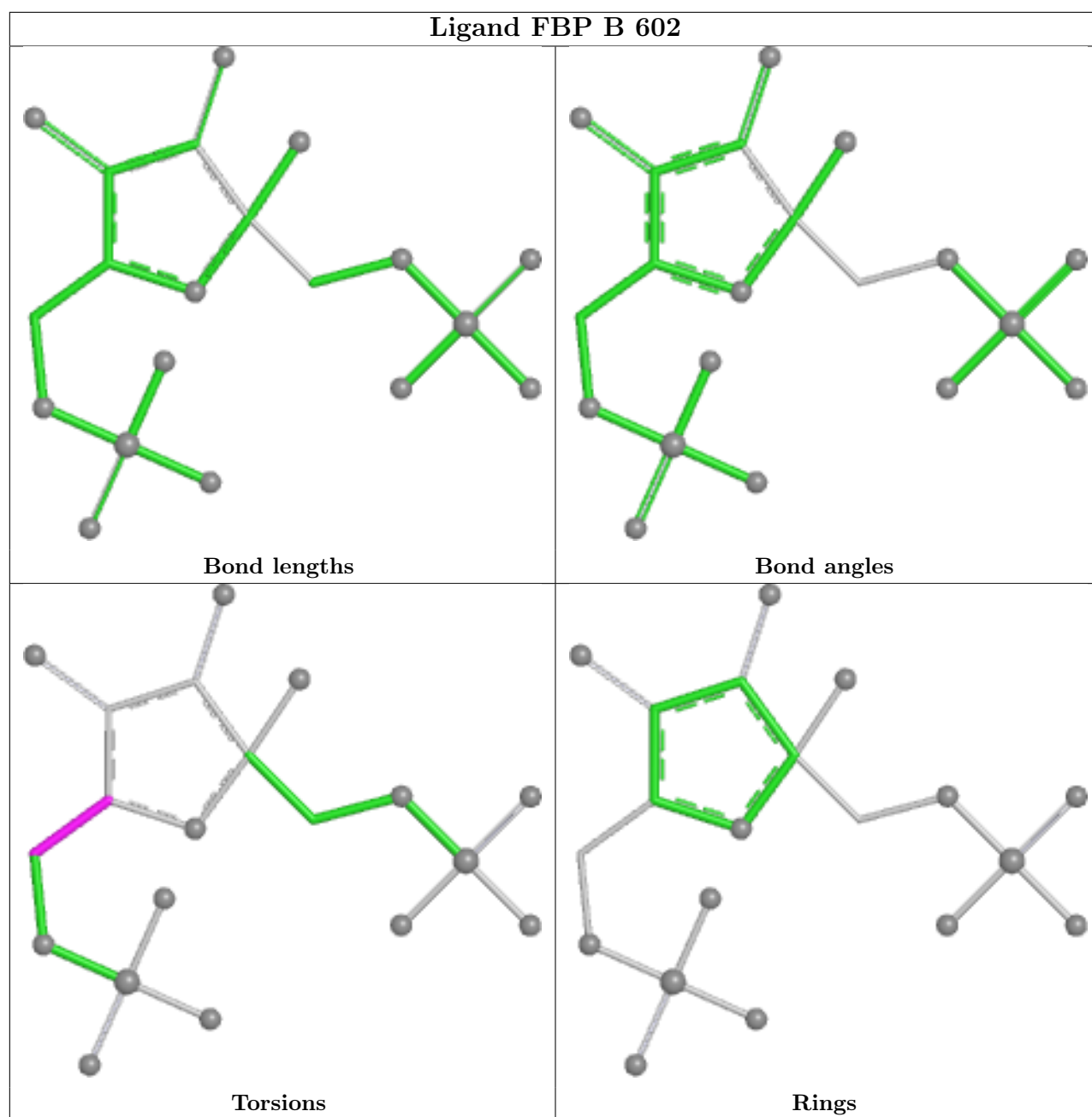
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

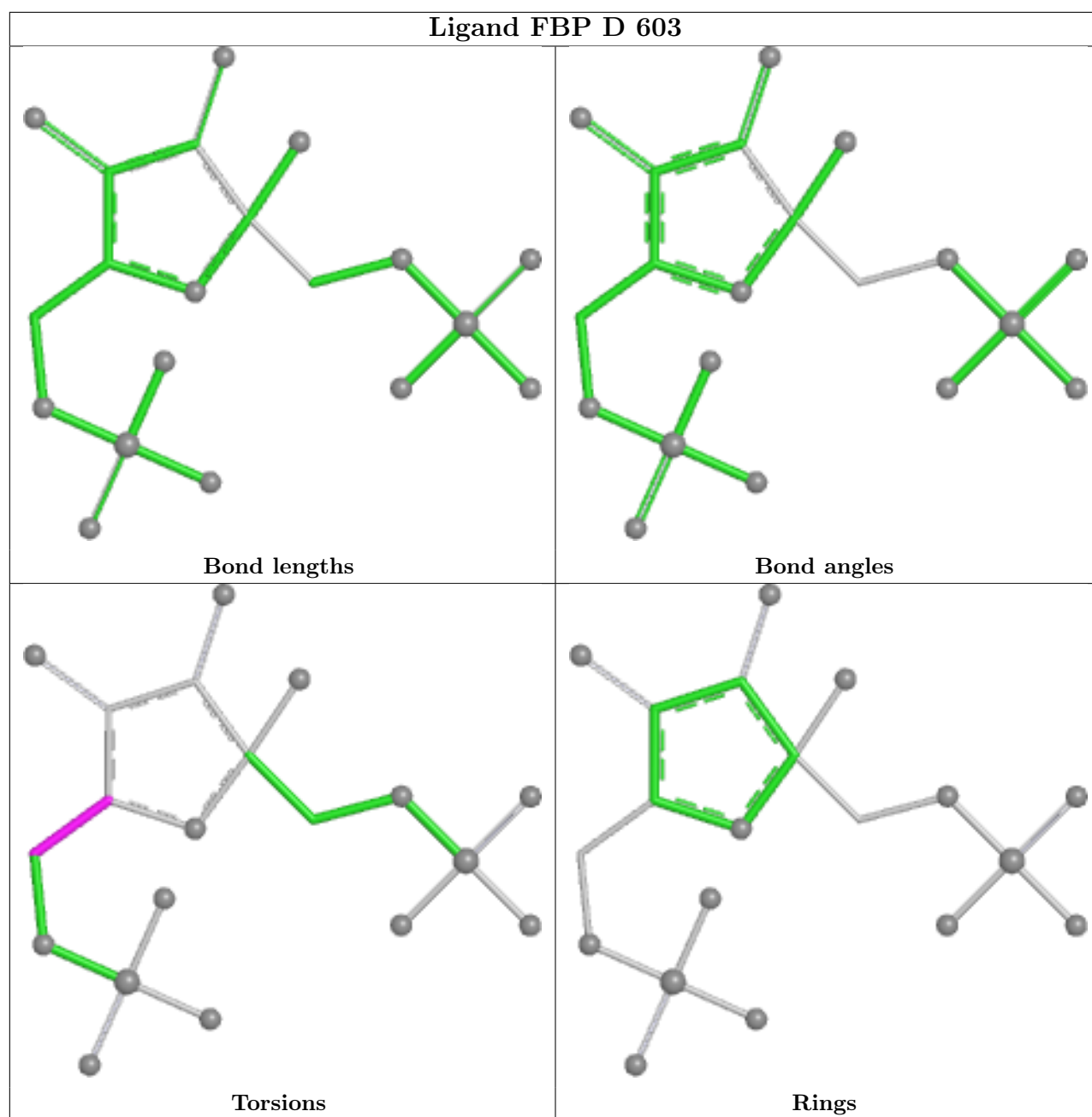


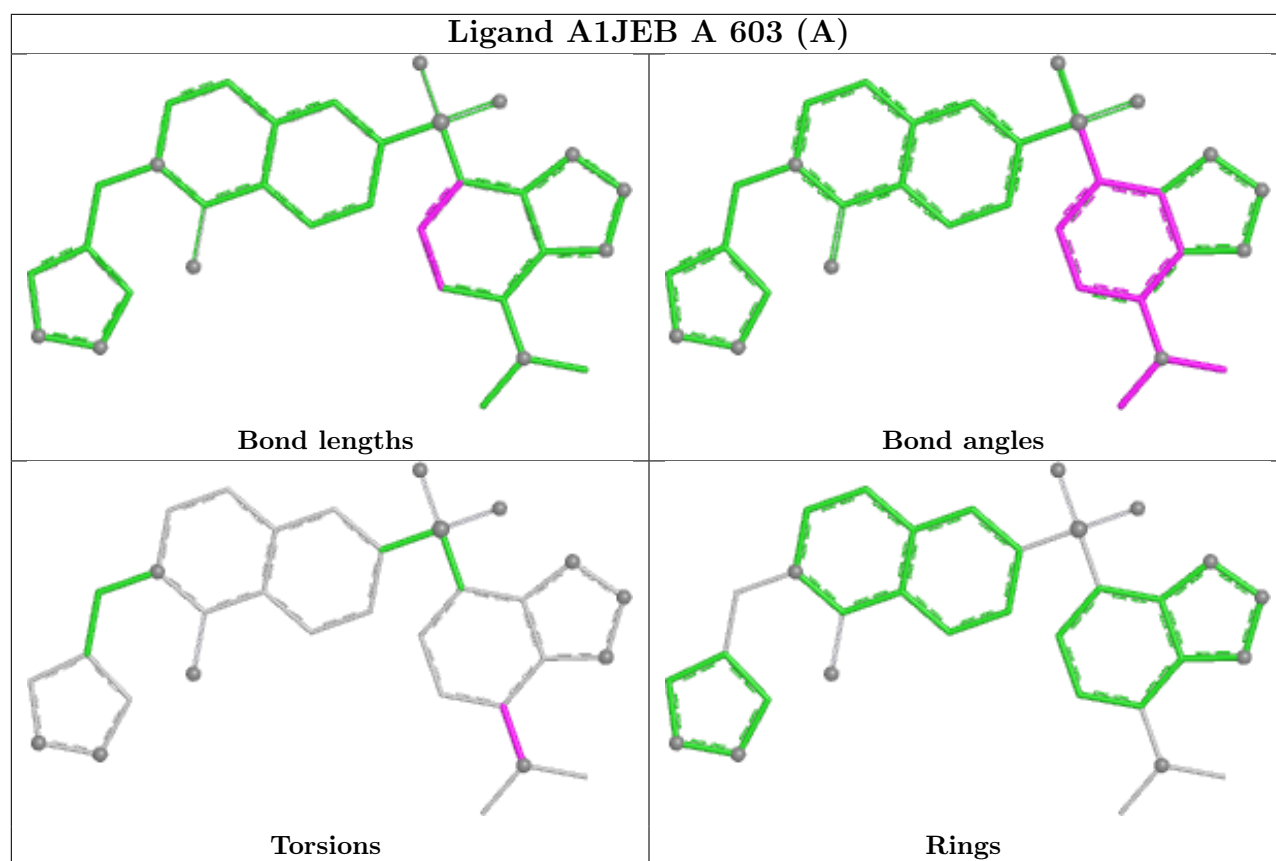
## Ligand A1JEB B 605 (B)

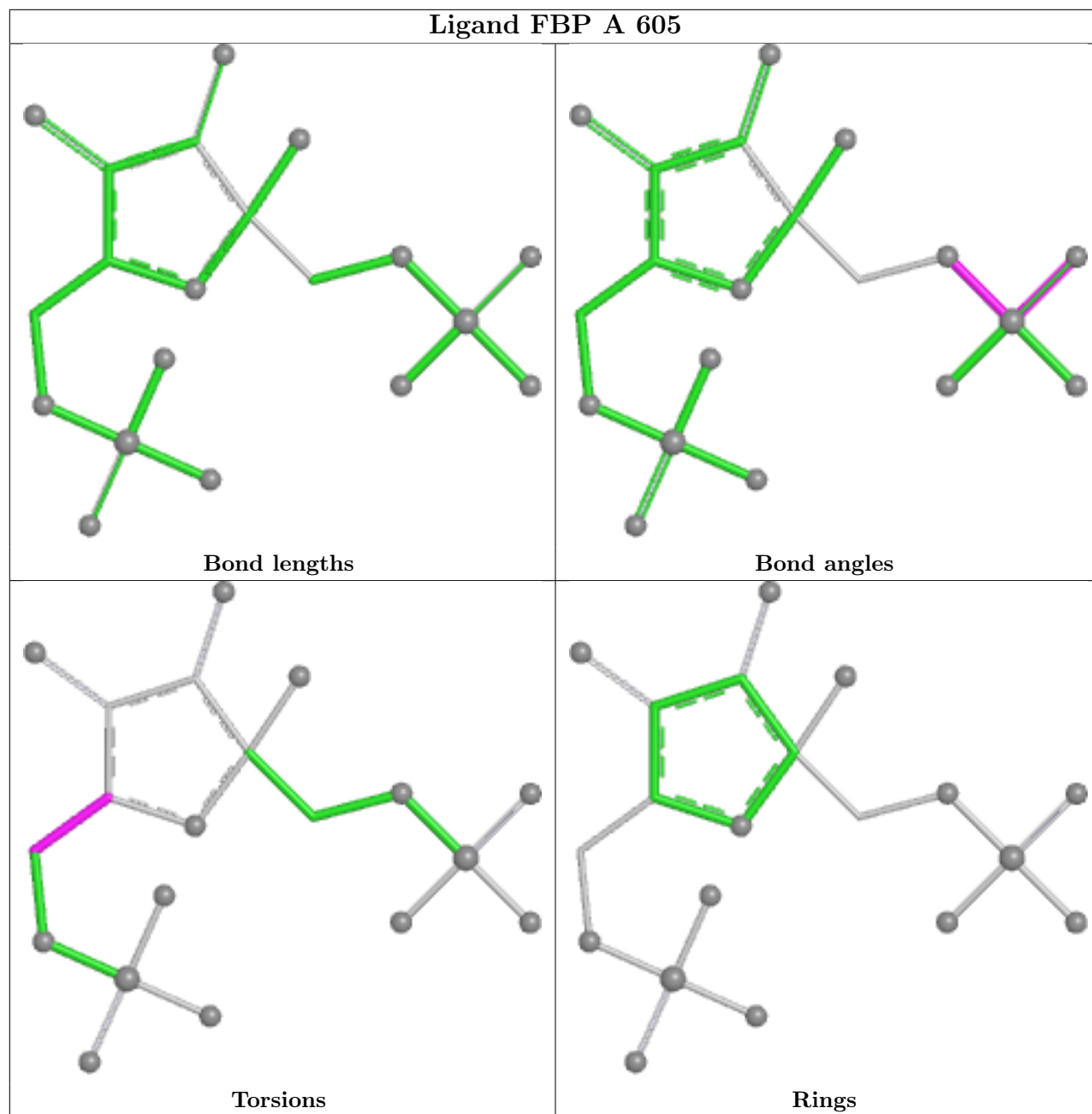


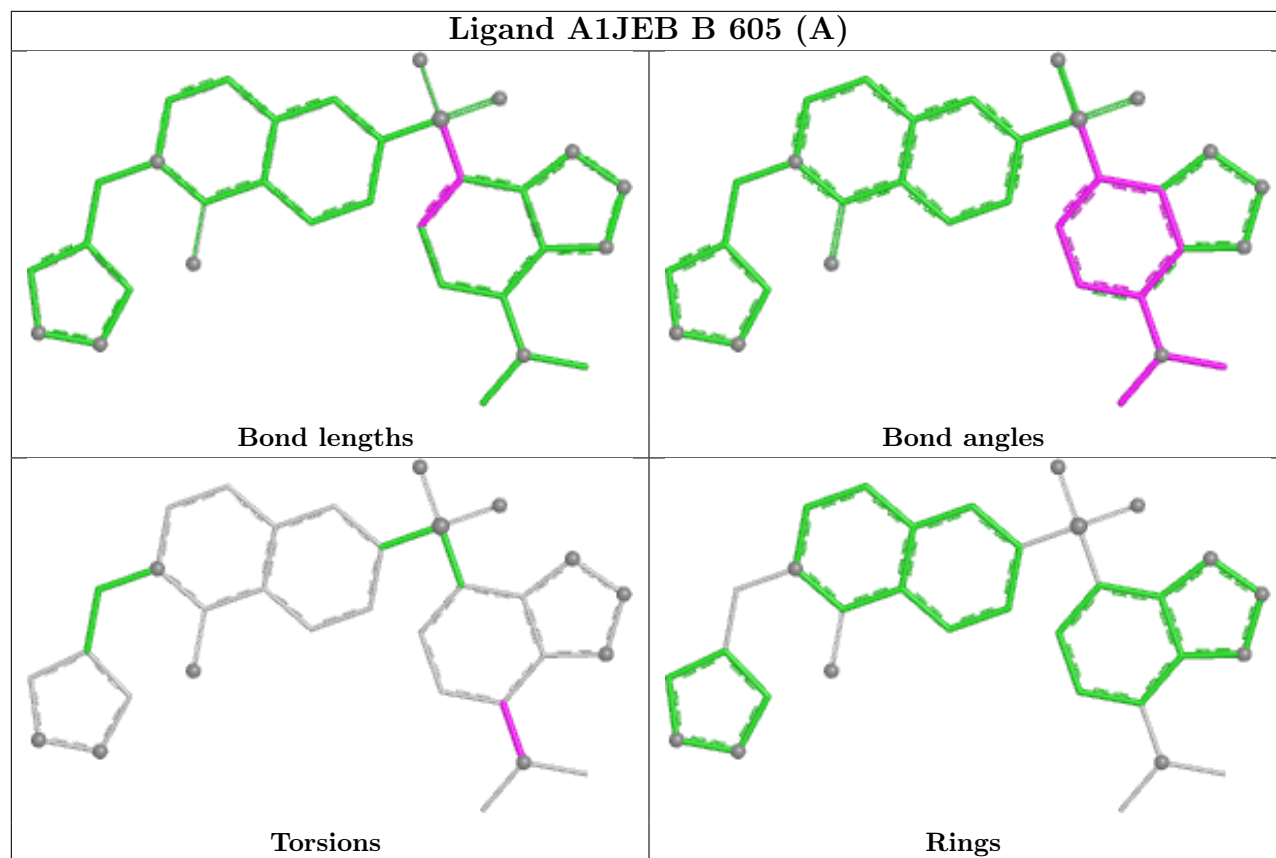












## 5.7 Other polymers [i](#)

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<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	521/545 (95%)	0.34	31 (5%)	27 29	20, 38, 64, 81	5 (0%)
1	B	521/545 (95%)	0.51	47 (9%)	15 15	19, 37, 90, 114	6 (1%)
1	C	521/545 (95%)	0.93	90 (17%)	4 4	19, 43, 102, 116	5 (0%)
1	D	521/545 (95%)	0.94	54 (10%)	11 12	22, 47, 75, 97	6 (1%)
All	All	2084/2180 (95%)	0.68	222 (10%)	11 11	19, 41, 86, 116	22 (1%)

The worst 5 of 222 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	140	PRO	7.6
1	C	146	LEU	7.1
1	C	147	VAL	6.6
1	C	154	VAL	6.5
1	C	200	ILE	6.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

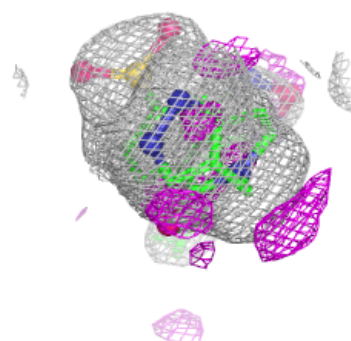
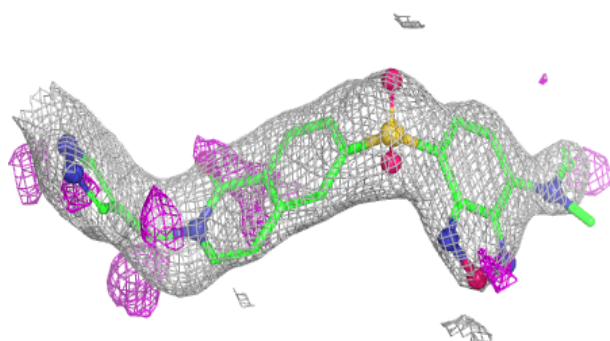
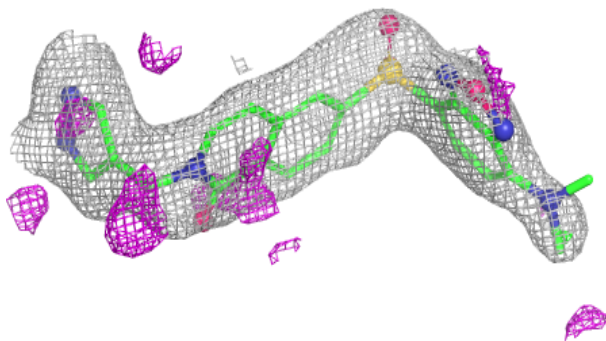
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	PEG	A	606	7/7	0.76	0.14	55,56,56,56	0
4	OXL	C	604	6/6	0.92	0.07	41,43,43,44	0
2	MG	C	601	1/1	0.92	0.13	67,67,67,67	0
3	A1JEB	B	605[A]	32/32	0.93	0.09	28,33,35,35	32
4	OXL	D	602	6/6	0.93	0.07	42,43,43,43	0
3	A1JEB	B	605[B]	32/32	0.93	0.09	29,31,33,33	32
4	OXL	B	601	6/6	0.94	0.06	37,37,37,38	0
2	MG	C	602	1/1	0.95	0.12	39,39,39,39	0
3	A1JEB	A	603[B]	32/32	0.96	0.07	36,38,42,42	32
4	OXL	A	604	6/6	0.96	0.05	31,33,34,34	0
5	FBP	D	603	20/20	0.96	0.06	38,40,42,43	0
3	A1JEB	A	603[A]	32/32	0.96	0.07	33,34,35,35	32
5	FBP	A	605	20/20	0.97	0.05	34,35,38,38	0
5	FBP	C	605	20/20	0.98	0.04	31,33,35,36	0
2	MG	C	603	1/1	0.98	0.09	43,43,43,43	0
5	FBP	B	602	20/20	0.98	0.04	30,32,34,34	0
2	MG	B	603	1/1	0.99	0.14	31,31,31,31	0
2	MG	D	601	1/1	0.99	0.07	46,46,46,46	0
2	MG	B	604	1/1	0.99	0.08	39,39,39,39	0
2	MG	A	601	1/1	0.99	0.04	32,32,32,32	0
2	MG	A	602	1/1	0.99	0.17	26,26,26,26	0

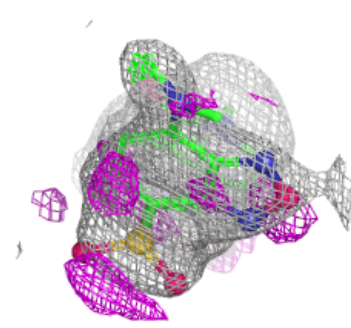
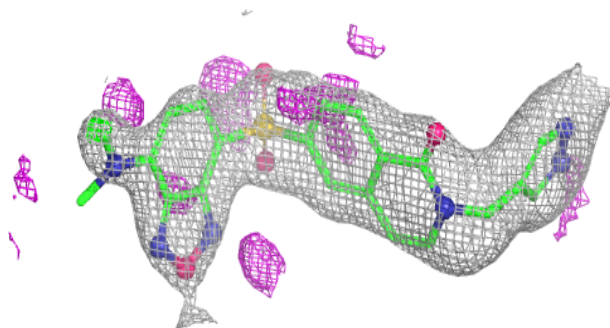
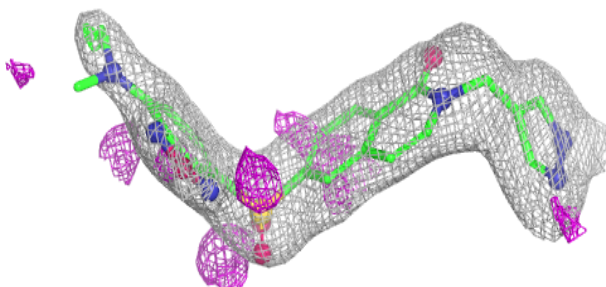
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around A1JEB B 605 (A):**

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

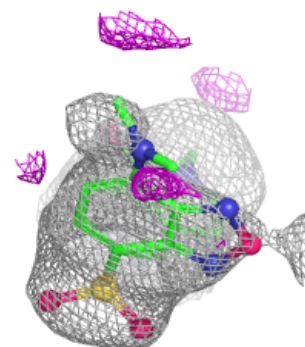
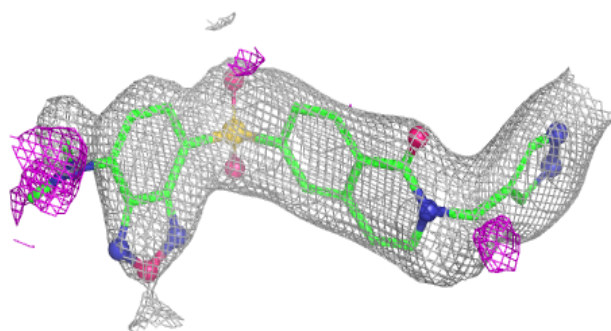
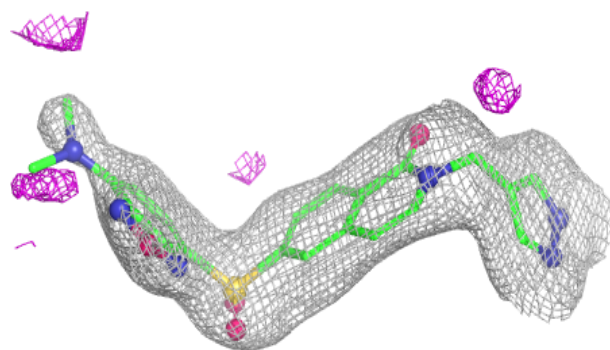
**Electron density around A1JEB B 605 (B):**

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

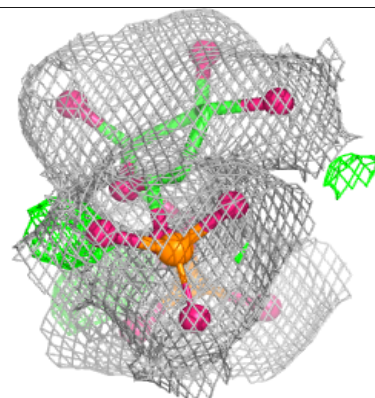
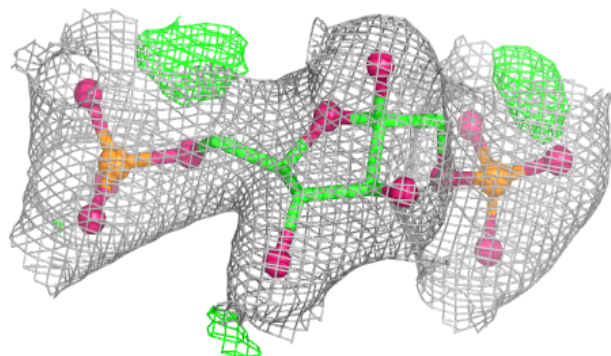
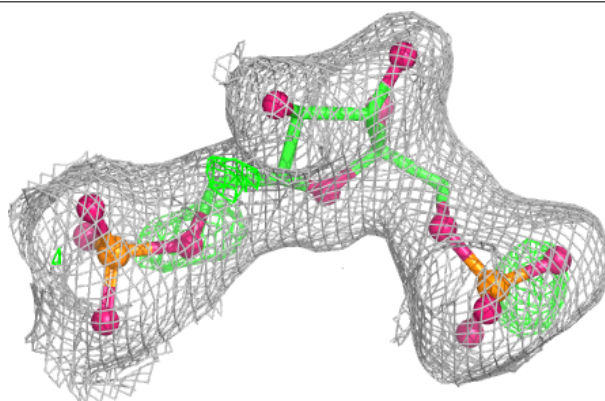


**Electron density around A1JEB A 603 (B):**

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

**Electron density around FBP D 603:**

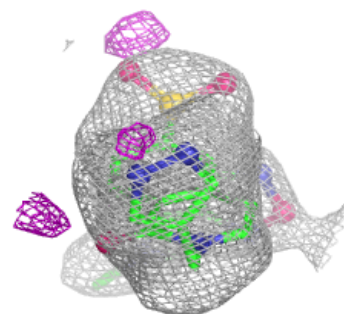
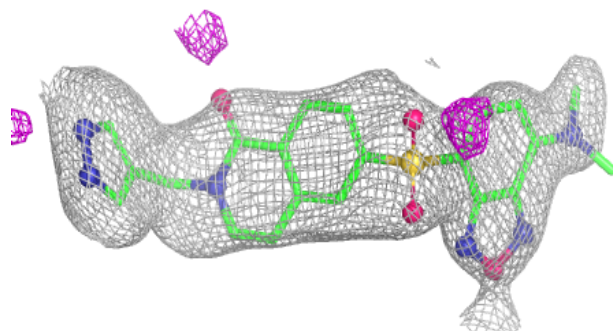
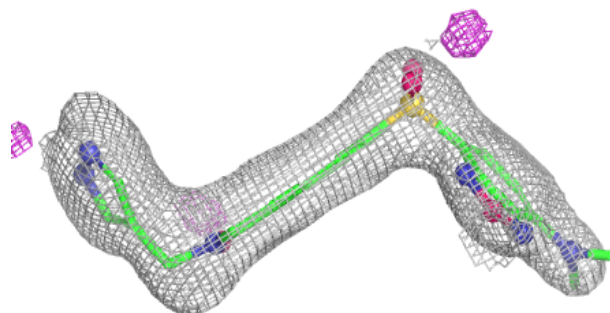
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



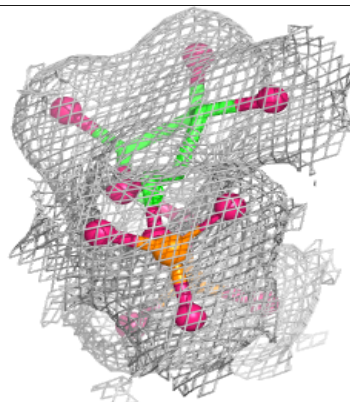
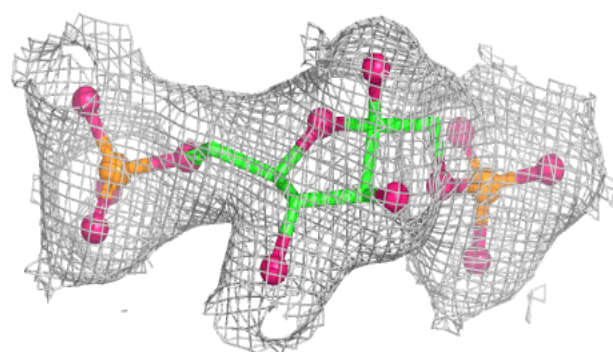
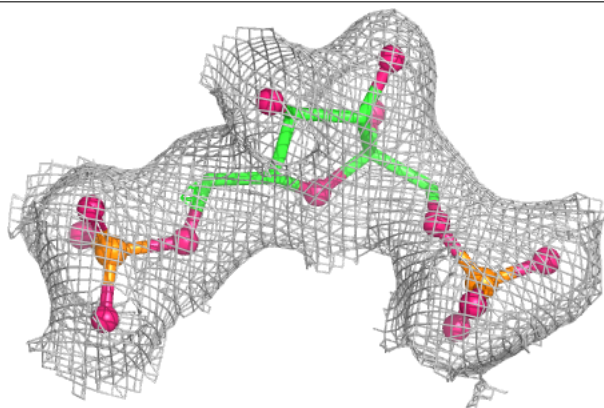


**Electron density around A1JEB A 603 (A):**

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

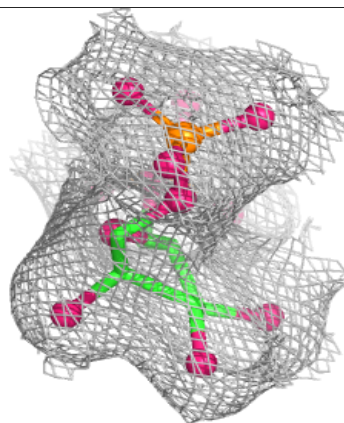
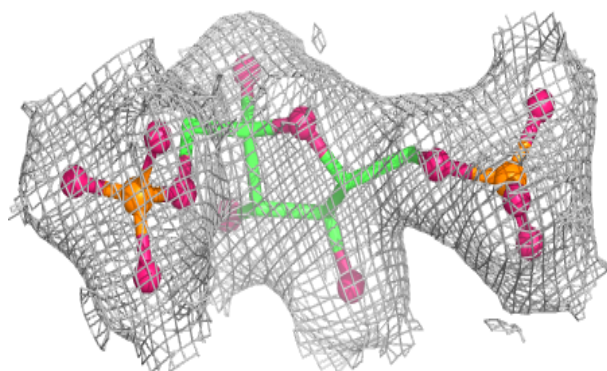
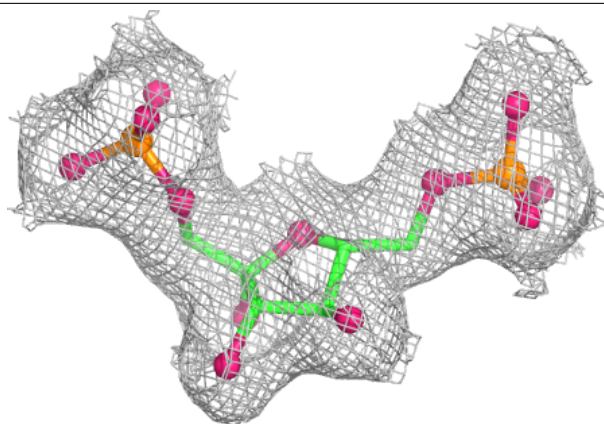
**Electron density around FBP A 605:**

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



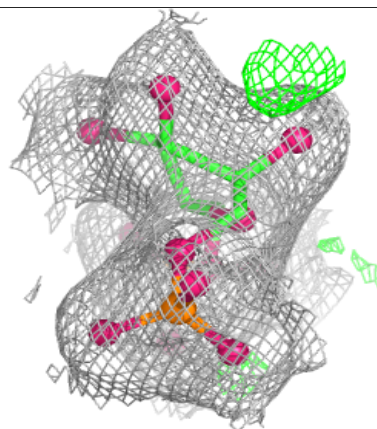
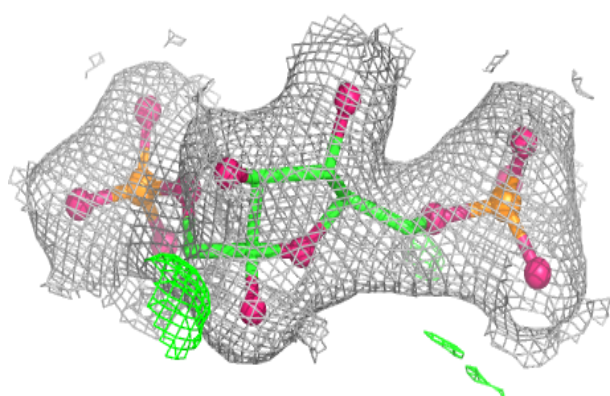
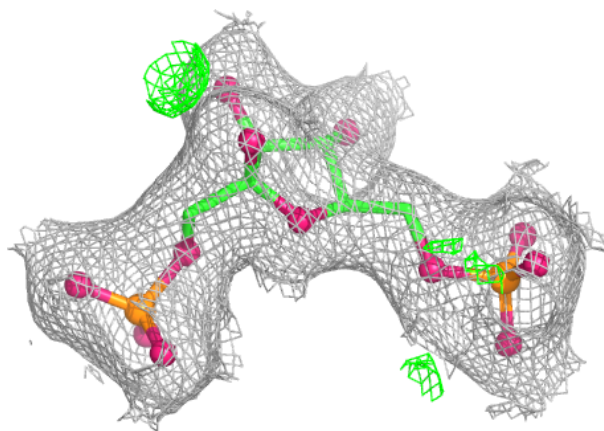
**Electron density around FBP C 605:**

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



**Electron density around FBP B 602:**

$2mF_o-DF_c$  (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.