



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:33 PM UTC

PDB ID : 3CM2 / pdb\_00003cm2  
Title : Crystal Structure of XIAP BIR3 domain in complex with a Smac-mimetic compound, Smac010  
Authors : Cossu, F.; Mastrangelo, E.; Milani, M.  
Deposited on : 2008-03-20  
Resolution : 2.50 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)  
Xtrriage (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

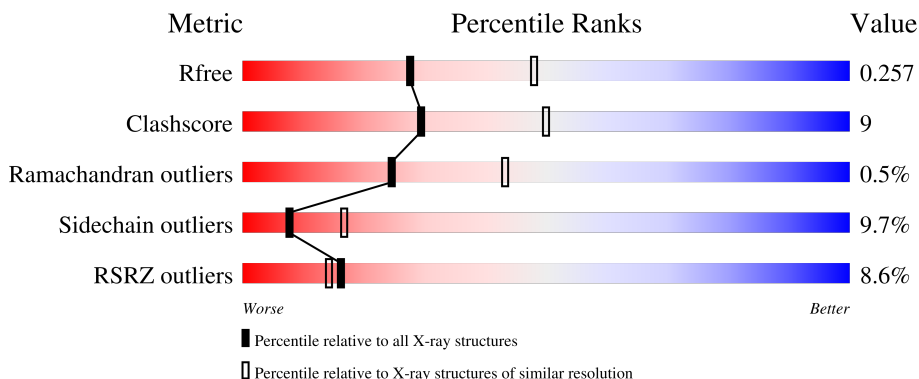
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	130	 6% 62% 15% • 21%
1	B	130	 11% 58% 19% •• 21%
1	C	130	 5% 62% 15% • 22%
1	D	130	 4% 62% 14% •• 22%
1	E	130	 8% 68% 8% • 22%

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Mol	Chain	Length	Quality of chain
1	F	130	<p>7% 59% 16% •• 21%</p>
1	G	130	<p>9% 64% 12% • 22%</p>
1	H	130	<p>6% 56% 19% • 22%</p>
1	I	130	<p>4% 64% 12% •• 22%</p>
1	J	130	<p>7% 60% 17% • 21%</p>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8952 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 Baculoviral IAP repeat-containing protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	D	102	832	532	142	153	5	0	0	0
1	A	103	838	535	143	155	5	0	0	0
1	B	103	838	535	143	155	5	0	0	0
1	C	102	831	531	142	153	5	0	0	0
1	E	102	832	532	142	153	5	0	0	0
1	F	103	838	535	143	155	5	0	0	0
1	G	102	832	532	142	153	5	0	0	0
1	H	102	832	532	142	153	5	0	0	0
1	I	102	832	532	142	153	5	0	0	0
1	J	103	839	536	143	155	5	0	0	0

There are 140 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	227	MET	-	expression tag	UNP P98170
D	228	ALA	-	expression tag	UNP P98170
D	229	SER	-	expression tag	UNP P98170
D	230	MET	-	expression tag	UNP P98170
D	231	THR	-	expression tag	UNP P98170
D	232	GLY	-	expression tag	UNP P98170
D	233	GLY	-	expression tag	UNP P98170
D	234	GLN	-	expression tag	UNP P98170
D	235	GLN	-	expression tag	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
D	236	MET	-	expression tag	UNP P98170
D	237	GLY	-	expression tag	UNP P98170
D	238	ARG	-	expression tag	UNP P98170
D	239	GLY	-	expression tag	UNP P98170
D	240	SER	-	expression tag	UNP P98170
A	227	MET	-	expression tag	UNP P98170
A	228	ALA	-	expression tag	UNP P98170
A	229	SER	-	expression tag	UNP P98170
A	230	MET	-	expression tag	UNP P98170
A	231	THR	-	expression tag	UNP P98170
A	232	GLY	-	expression tag	UNP P98170
A	233	GLY	-	expression tag	UNP P98170
A	234	GLN	-	expression tag	UNP P98170
A	235	GLN	-	expression tag	UNP P98170
A	236	MET	-	expression tag	UNP P98170
A	237	GLY	-	expression tag	UNP P98170
A	238	ARG	-	expression tag	UNP P98170
A	239	GLY	-	expression tag	UNP P98170
A	240	SER	-	expression tag	UNP P98170
B	227	MET	-	expression tag	UNP P98170
B	228	ALA	-	expression tag	UNP P98170
B	229	SER	-	expression tag	UNP P98170
B	230	MET	-	expression tag	UNP P98170
B	231	THR	-	expression tag	UNP P98170
B	232	GLY	-	expression tag	UNP P98170
B	233	GLY	-	expression tag	UNP P98170
B	234	GLN	-	expression tag	UNP P98170
B	235	GLN	-	expression tag	UNP P98170
B	236	MET	-	expression tag	UNP P98170
B	237	GLY	-	expression tag	UNP P98170
B	238	ARG	-	expression tag	UNP P98170
B	239	GLY	-	expression tag	UNP P98170
B	240	SER	-	expression tag	UNP P98170
C	227	MET	-	expression tag	UNP P98170
C	228	ALA	-	expression tag	UNP P98170
C	229	SER	-	expression tag	UNP P98170
C	230	MET	-	expression tag	UNP P98170
C	231	THR	-	expression tag	UNP P98170
C	232	GLY	-	expression tag	UNP P98170
C	233	GLY	-	expression tag	UNP P98170
C	234	GLN	-	expression tag	UNP P98170
C	235	GLN	-	expression tag	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
C	236	MET	-	expression tag	UNP P98170
C	237	GLY	-	expression tag	UNP P98170
C	238	ARG	-	expression tag	UNP P98170
C	239	GLY	-	expression tag	UNP P98170
C	240	SER	-	expression tag	UNP P98170
E	227	MET	-	expression tag	UNP P98170
E	228	ALA	-	expression tag	UNP P98170
E	229	SER	-	expression tag	UNP P98170
E	230	MET	-	expression tag	UNP P98170
E	231	THR	-	expression tag	UNP P98170
E	232	GLY	-	expression tag	UNP P98170
E	233	GLY	-	expression tag	UNP P98170
E	234	GLN	-	expression tag	UNP P98170
E	235	GLN	-	expression tag	UNP P98170
E	236	MET	-	expression tag	UNP P98170
E	237	GLY	-	expression tag	UNP P98170
E	238	ARG	-	expression tag	UNP P98170
E	239	GLY	-	expression tag	UNP P98170
E	240	SER	-	expression tag	UNP P98170
F	227	MET	-	expression tag	UNP P98170
F	228	ALA	-	expression tag	UNP P98170
F	229	SER	-	expression tag	UNP P98170
F	230	MET	-	expression tag	UNP P98170
F	231	THR	-	expression tag	UNP P98170
F	232	GLY	-	expression tag	UNP P98170
F	233	GLY	-	expression tag	UNP P98170
F	234	GLN	-	expression tag	UNP P98170
F	235	GLN	-	expression tag	UNP P98170
F	236	MET	-	expression tag	UNP P98170
F	237	GLY	-	expression tag	UNP P98170
F	238	ARG	-	expression tag	UNP P98170
F	239	GLY	-	expression tag	UNP P98170
F	240	SER	-	expression tag	UNP P98170
G	227	MET	-	expression tag	UNP P98170
G	228	ALA	-	expression tag	UNP P98170
G	229	SER	-	expression tag	UNP P98170
G	230	MET	-	expression tag	UNP P98170
G	231	THR	-	expression tag	UNP P98170
G	232	GLY	-	expression tag	UNP P98170
G	233	GLY	-	expression tag	UNP P98170
G	234	GLN	-	expression tag	UNP P98170
G	235	GLN	-	expression tag	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
G	236	MET	-	expression tag	UNP P98170
G	237	GLY	-	expression tag	UNP P98170
G	238	ARG	-	expression tag	UNP P98170
G	239	GLY	-	expression tag	UNP P98170
G	240	SER	-	expression tag	UNP P98170
H	227	MET	-	expression tag	UNP P98170
H	228	ALA	-	expression tag	UNP P98170
H	229	SER	-	expression tag	UNP P98170
H	230	MET	-	expression tag	UNP P98170
H	231	THR	-	expression tag	UNP P98170
H	232	GLY	-	expression tag	UNP P98170
H	233	GLY	-	expression tag	UNP P98170
H	234	GLN	-	expression tag	UNP P98170
H	235	GLN	-	expression tag	UNP P98170
H	236	MET	-	expression tag	UNP P98170
H	237	GLY	-	expression tag	UNP P98170
H	238	ARG	-	expression tag	UNP P98170
H	239	GLY	-	expression tag	UNP P98170
H	240	SER	-	expression tag	UNP P98170
I	227	MET	-	expression tag	UNP P98170
I	228	ALA	-	expression tag	UNP P98170
I	229	SER	-	expression tag	UNP P98170
I	230	MET	-	expression tag	UNP P98170
I	231	THR	-	expression tag	UNP P98170
I	232	GLY	-	expression tag	UNP P98170
I	233	GLY	-	expression tag	UNP P98170
I	234	GLN	-	expression tag	UNP P98170
I	235	GLN	-	expression tag	UNP P98170
I	236	MET	-	expression tag	UNP P98170
I	237	GLY	-	expression tag	UNP P98170
I	238	ARG	-	expression tag	UNP P98170
I	239	GLY	-	expression tag	UNP P98170
I	240	SER	-	expression tag	UNP P98170
J	227	MET	-	expression tag	UNP P98170
J	228	ALA	-	expression tag	UNP P98170
J	229	SER	-	expression tag	UNP P98170
J	230	MET	-	expression tag	UNP P98170
J	231	THR	-	expression tag	UNP P98170
J	232	GLY	-	expression tag	UNP P98170
J	233	GLY	-	expression tag	UNP P98170
J	234	GLN	-	expression tag	UNP P98170
J	235	GLN	-	expression tag	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
J	236	MET	-	expression tag	UNP P98170
J	237	GLY	-	expression tag	UNP P98170
J	238	ARG	-	expression tag	UNP P98170
J	239	GLY	-	expression tag	UNP P98170
J	240	SER	-	expression tag	UNP P98170

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0
2	G	1	Total Zn 1 1	0	0
2	H	1	Total Zn 1 1	0	0
2	I	1	Total Zn 1 1	0	0
2	J	1	Total Zn 1 1	0	0

- Molecule 3 is (3S,6S,7R,9aS)-6-([(2S)-2-aminobutanoyl]amino)-7-(aminomethyl)-N-(di phenylmethyl)-5-oxooctahydro-1H-pyrrolo[1,2-a]azepine-3-carboxamide (CCD ID: X23) (formula: C<sub>28</sub>H<sub>37</sub>N<sub>5</sub>O<sub>3</sub>).



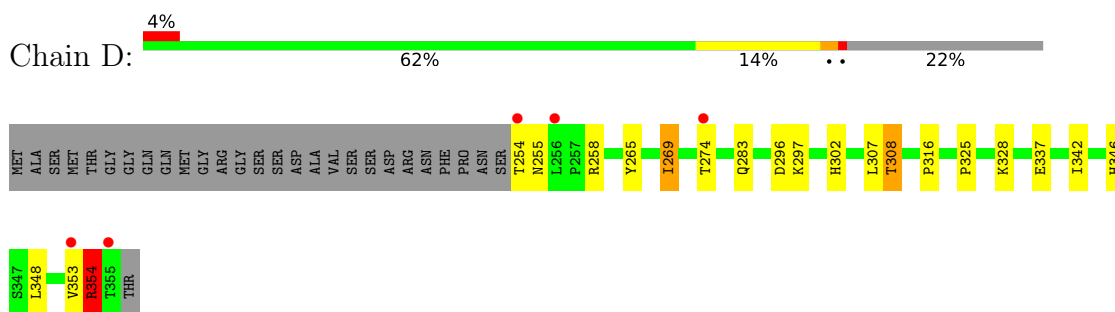
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
4	B	23	Total O 23 23	0	0
4	C	22	Total O 22 22	0	0
4	E	33	Total O 33 33	0	0
4	F	24	Total O 24 24	0	0
4	G	18	Total O 18 18	0	0
4	H	27	Total O 27 27	0	0
4	I	29	Total O 29 29	0	0
4	J	19	Total O 19 19	0	0

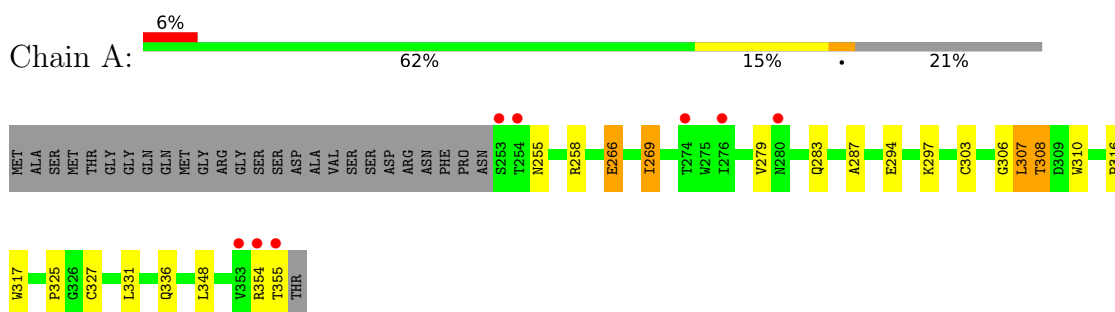
### 3 Residue-property plots [i](#)

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.

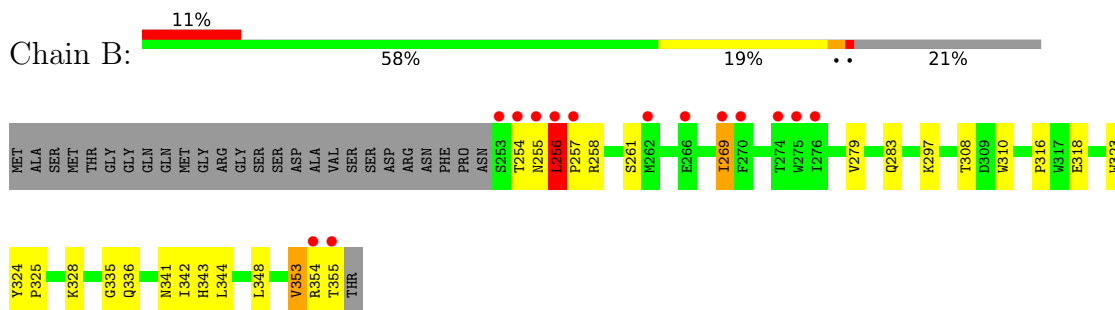
- Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4

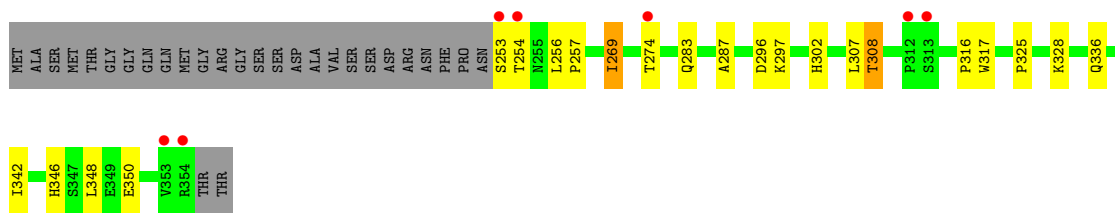


- Molecule 1: Baculoviral IAP repeat-containing protein 4

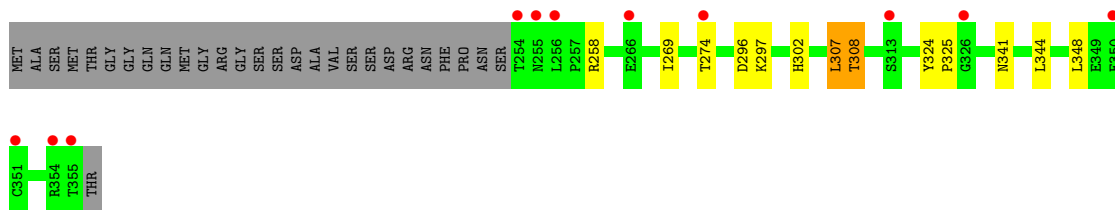


- Molecule 1: Baculoviral IAP repeat-containing protein 4

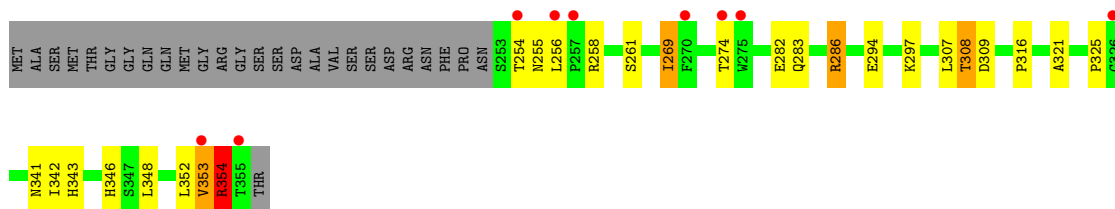




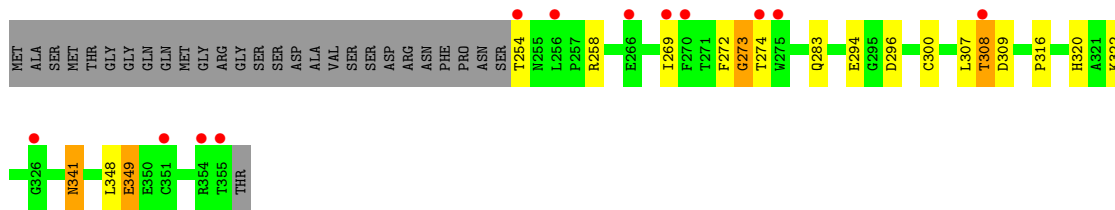
● Molecule 1: Baculoviral IAP repeat-containing protein 4



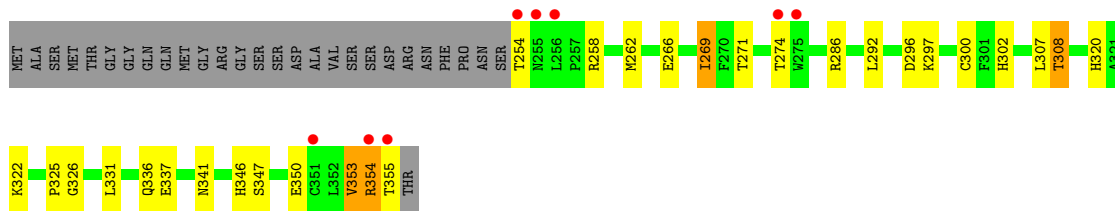
● Molecule 1: Baculoviral IAP repeat-containing protein 4



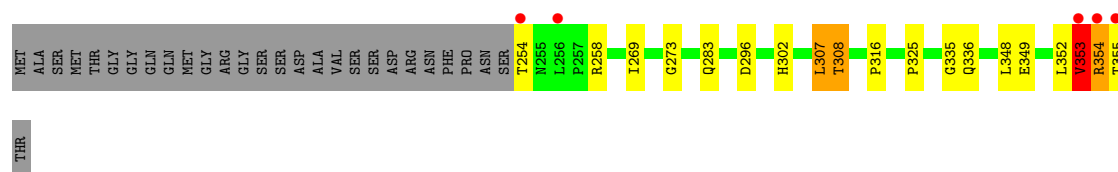
● Molecule 1: Baculoviral IAP repeat-containing protein 4



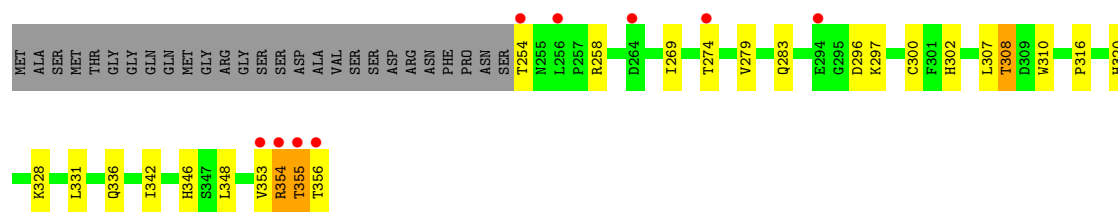
● Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.53Å 108.35Å 225.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.50 40.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.00-2.50) 99.9 (40.00-2.50)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.27 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.221 , 0.264 (Not available) , 0.257	Depositor DCC
$R_{free}$ test set	3376 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	50.0	Xtrriage
Anisotropy	0.215	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 48.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8952	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.57% 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: ZN, X23

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	0.50	0/864	0.85	0/1171
1	B	0.49	0/864	0.87	3/1171 (0.3%)
1	C	0.49	0/857	0.86	0/1161
1	D	0.51	0/858	0.82	1/1163 (0.1%)
1	E	0.49	0/858	0.83	0/1163
1	F	0.47	0/864	0.87	0/1171
1	G	0.49	0/858	0.81	0/1163
1	H	0.51	0/858	0.87	0/1163
1	I	0.48	0/858	0.83	0/1163
1	J	0.48	0/865	0.81	0/1173
All	All	0.49	0/8604	0.84	4/11662 (0.0%)

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
1	C	0	1
1	F	0	1
1	I	0	1
1	J	1	1
All	All	1	5

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	353	VAL	N-CA-C	6.03	112.67	106.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	324	TYR	CA-C-N	5.53	125.36	119.28
1	B	324	TYR	C-N-CA	5.53	125.36	119.28
1	D	354	ARG	CB-CA-C	-5.17	100.49	110.35

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	J	355	THR	CB

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	255	ASN	Peptide
1	C	253	SER	Peptide
1	F	354	ARG	Peptide
1	I	353	VAL	Peptide
1	J	354	ARG	Peptide

## 5.2 Too-close contacts

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	838	0	787	18	0
1	B	838	0	786	35	0
1	C	831	0	779	15	0
1	D	832	0	782	19	0
1	E	832	0	781	8	0
1	F	838	0	787	13	0
1	G	832	0	781	7	0
1	H	832	0	781	24	0
1	I	832	0	781	12	0
1	J	839	0	789	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	36	0	37	0	0
3	B	36	0	37	0	0
3	C	36	0	36	3	0
3	D	36	0	36	0	0
3	E	36	0	37	0	0
3	F	36	0	37	0	0
3	G	36	0	37	1	0
3	H	36	0	37	2	0
3	I	36	0	37	1	0
3	J	36	0	37	0	0
4	A	20	0	0	0	0
4	B	23	0	0	0	0
4	C	22	0	0	0	0
4	D	23	0	0	1	0
4	E	33	0	0	0	0
4	F	24	0	0	0	0
4	G	18	0	0	0	0
4	H	27	0	0	0	0
4	I	29	0	0	1	0
4	J	19	0	0	0	0
All	All	8952	0	8202	145	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 9.

The worst 5 of 145 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:256:LEU:CB	1:B:257:PRO:HD3	1.59	1.29
1:B:256:LEU:HB3	1:B:257:PRO:HD3	1.15	1.11
1:D:354:ARG:HG2	1:D:354:ARG:O	1.48	1.04
1:B:297:LYS:HG2	1:B:308:THR:CG2	1.94	0.96
1:B:354:ARG:H	1:B:355:THR:HA	1.31	0.95

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	101/130 (78%)	97 (96%)	4 (4%)	0	100	100
1	B	101/130 (78%)	90 (89%)	10 (10%)	1 (1%)	12	24
1	C	100/130 (77%)	97 (97%)	3 (3%)	0	100	100
1	D	100/130 (77%)	96 (96%)	4 (4%)	0	100	100
1	E	100/130 (77%)	99 (99%)	1 (1%)	0	100	100
1	F	101/130 (78%)	94 (93%)	7 (7%)	0	100	100
1	G	100/130 (77%)	95 (95%)	4 (4%)	1 (1%)	12	24
1	H	100/130 (77%)	94 (94%)	5 (5%)	1 (1%)	12	24
1	I	100/130 (77%)	95 (95%)	3 (3%)	2 (2%)	6	10
1	J	101/130 (78%)	98 (97%)	3 (3%)	0	100	100
All	All	1004/1300 (77%)	955 (95%)	44 (4%)	5 (0%)	24	43

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	273	GLY
1	I	353	VAL
1	B	256	LEU
1	H	353	VAL
1	I	273	GLY

### 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	88/109 (81%)	82 (93%)	6 (7%)	14	31
1	B	88/109 (81%)	82 (93%)	6 (7%)	14	31
1	C	87/109 (80%)	81 (93%)	6 (7%)	14	30
1	D	87/109 (80%)	78 (90%)	9 (10%)	7	14
1	E	87/109 (80%)	80 (92%)	7 (8%)	11	24
1	F	88/109 (81%)	73 (83%)	15 (17%)	2	4
1	G	87/109 (80%)	76 (87%)	11 (13%)	4	9
1	H	87/109 (80%)	78 (90%)	9 (10%)	7	14
1	I	87/109 (80%)	79 (91%)	8 (9%)	8	19
1	J	88/109 (81%)	80 (91%)	8 (9%)	9	19
All	All	874/1090 (80%)	789 (90%)	85 (10%)	8	17

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	341	ASN
1	I	269	ILE
1	G	349	GLU
1	H	307	LEU
1	I	353	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	343	HIS
1	J	343	HIS
1	H	346	HIS
1	J	302	HIS
1	C	319	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 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
3	X23	D	600	-	37,39,39	1.10	2 (5%)	45,54,54	2.43	11 (24%)
3	X23	F	600	-	37,39,39	0.78	1 (2%)	45,54,54	2.04	9 (20%)
3	X23	C	600	-	37,39,39	0.68	0	45,54,54	2.48	12 (26%)
3	X23	H	600	-	37,39,39	0.90	2 (5%)	45,54,54	2.30	9 (20%)
3	X23	G	600	-	37,39,39	0.73	1 (2%)	45,54,54	2.05	8 (17%)
3	X23	B	600	-	37,39,39	0.78	1 (2%)	45,54,54	2.15	10 (22%)
3	X23	E	600	-	37,39,39	0.74	1 (2%)	45,54,54	2.23	13 (28%)
3	X23	I	600	-	37,39,39	0.95	3 (8%)	45,54,54	2.14	9 (20%)
3	X23	A	600	-	37,39,39	0.68	0	45,54,54	2.17	9 (20%)
3	X23	J	600	-	37,39,39	0.78	0	45,54,54	2.17	8 (17%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	X23	D	600	-	-	3/28/58/58	0/4/4/4
3	X23	F	600	-	-	6/28/58/58	0/4/4/4
3	X23	C	600	-	-	3/28/58/58	0/4/4/4
3	X23	H	600	-	-	5/28/58/58	0/4/4/4
3	X23	G	600	-	-	7/28/58/58	0/4/4/4
3	X23	B	600	-	-	5/28/58/58	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	X23	E	600	-	-	6/28/58/58	0/4/4/4
3	X23	I	600	-	-	10/28/58/58	0/4/4/4
3	X23	A	600	-	-	8/28/58/58	0/4/4/4
3	X23	J	600	-	-	8/28/58/58	0/4/4/4

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	600	X23	CBC-CBG	4.74	1.58	1.52
3	D	600	X23	CBA-NBJ	-3.09	1.32	1.35
3	H	600	X23	CBC-CBG	2.81	1.56	1.52
3	H	600	X23	CBA-NBJ	-2.56	1.32	1.35
3	I	600	X23	CBC-CBG	2.50	1.55	1.52

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	600	X23	CBG-NAW-CAZ	11.52	135.37	122.50
3	D	600	X23	CBG-NAW-CAZ	10.94	134.73	122.50
3	H	600	X23	CBG-NAW-CAZ	10.40	134.13	122.50
3	J	600	X23	CBG-NAW-CAZ	10.26	133.96	122.50
3	E	600	X23	CBG-NAW-CAZ	9.91	133.58	122.50

There are no chirality outliers.

5 of 61 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	600	X23	NAB-CAR-CBE-CAS
3	D	600	X23	CBC-CBG-NAW-CAZ
3	A	600	X23	C-CA-CB-CAA
3	A	600	X23	CBC-CBG-NAW-CAZ
3	B	600	X23	N-CA-CB-CAA

There are no ring outliers.

4 monomers are involved in 7 short contacts:

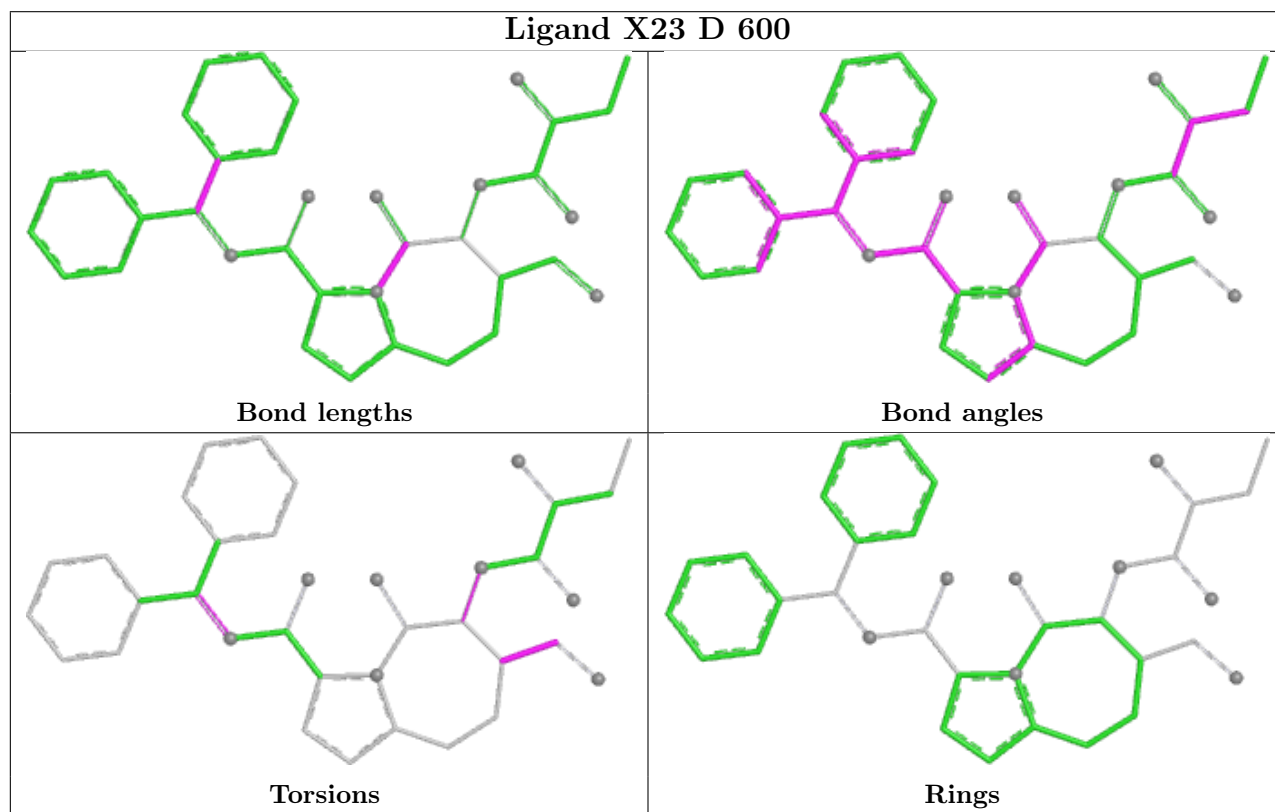
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	600	X23	3	0
3	H	600	X23	2	0
3	G	600	X23	1	0

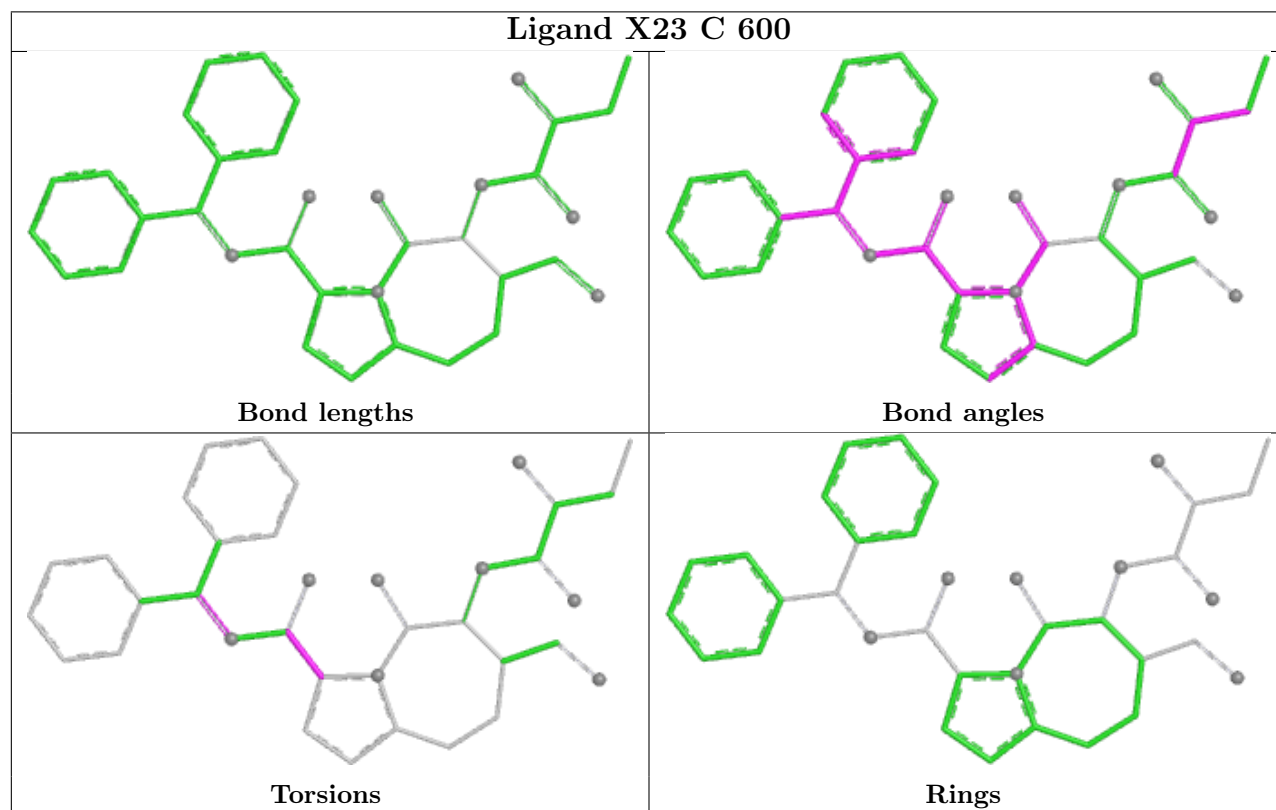
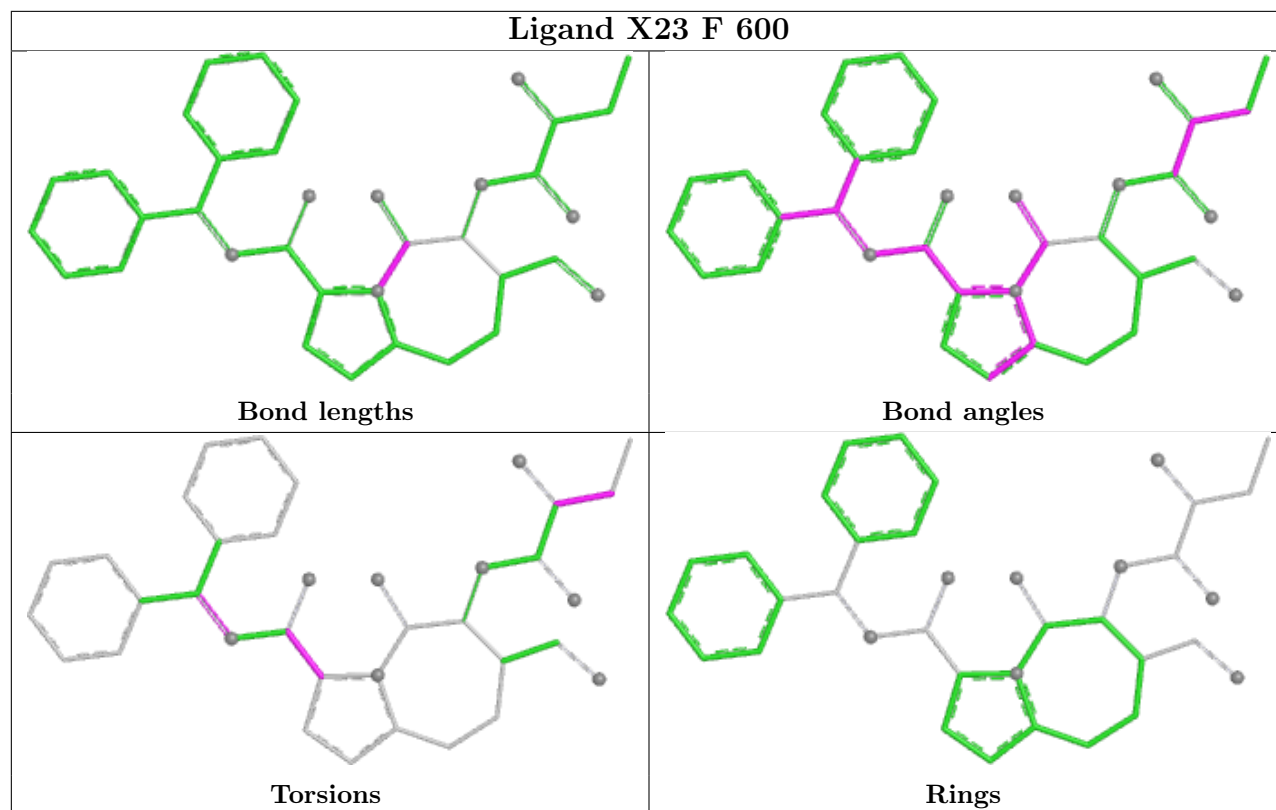
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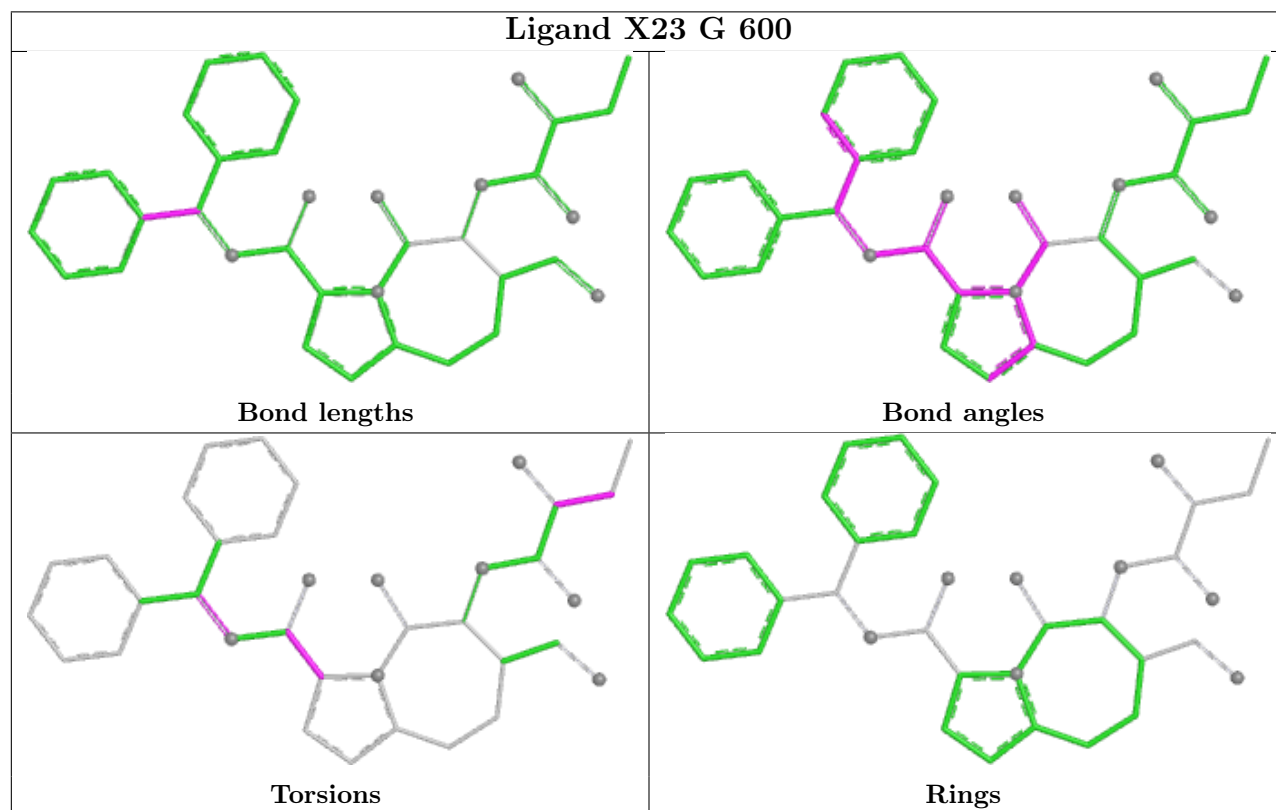
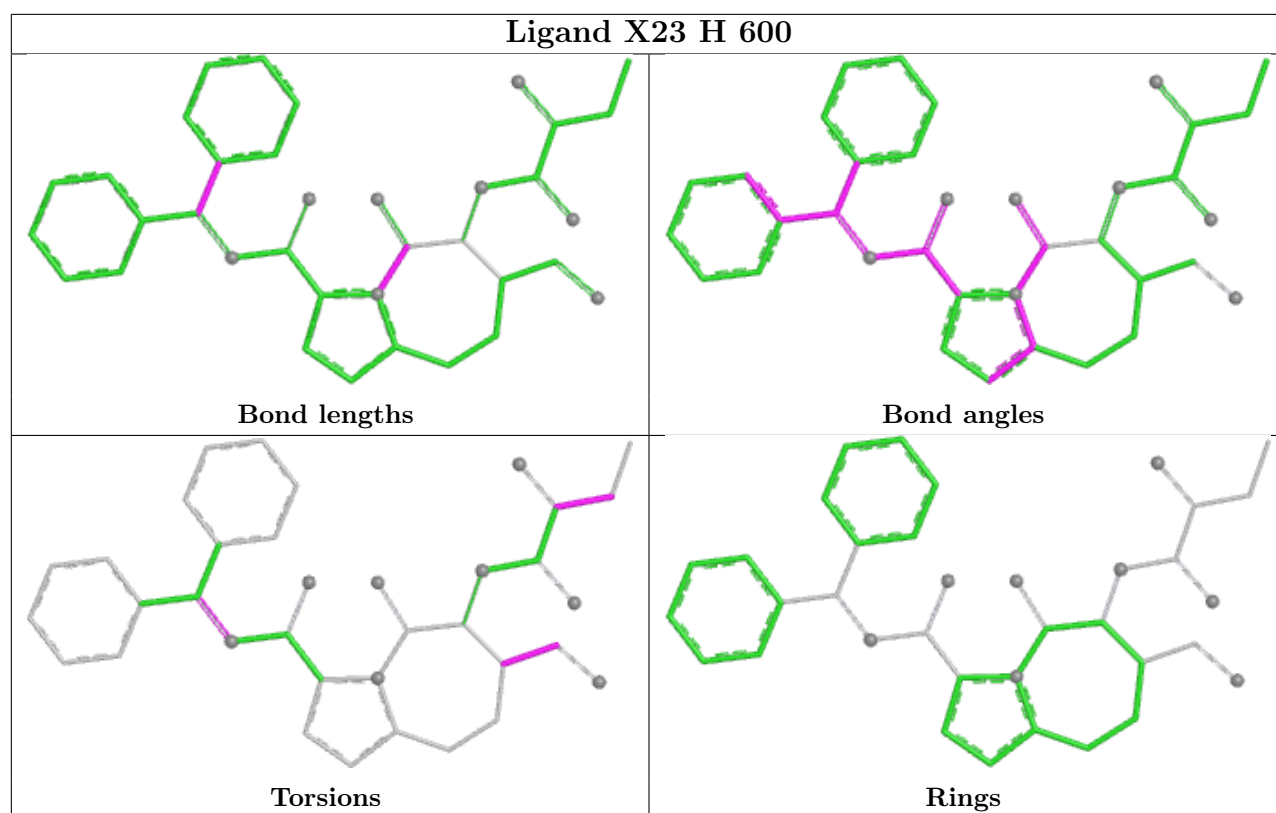
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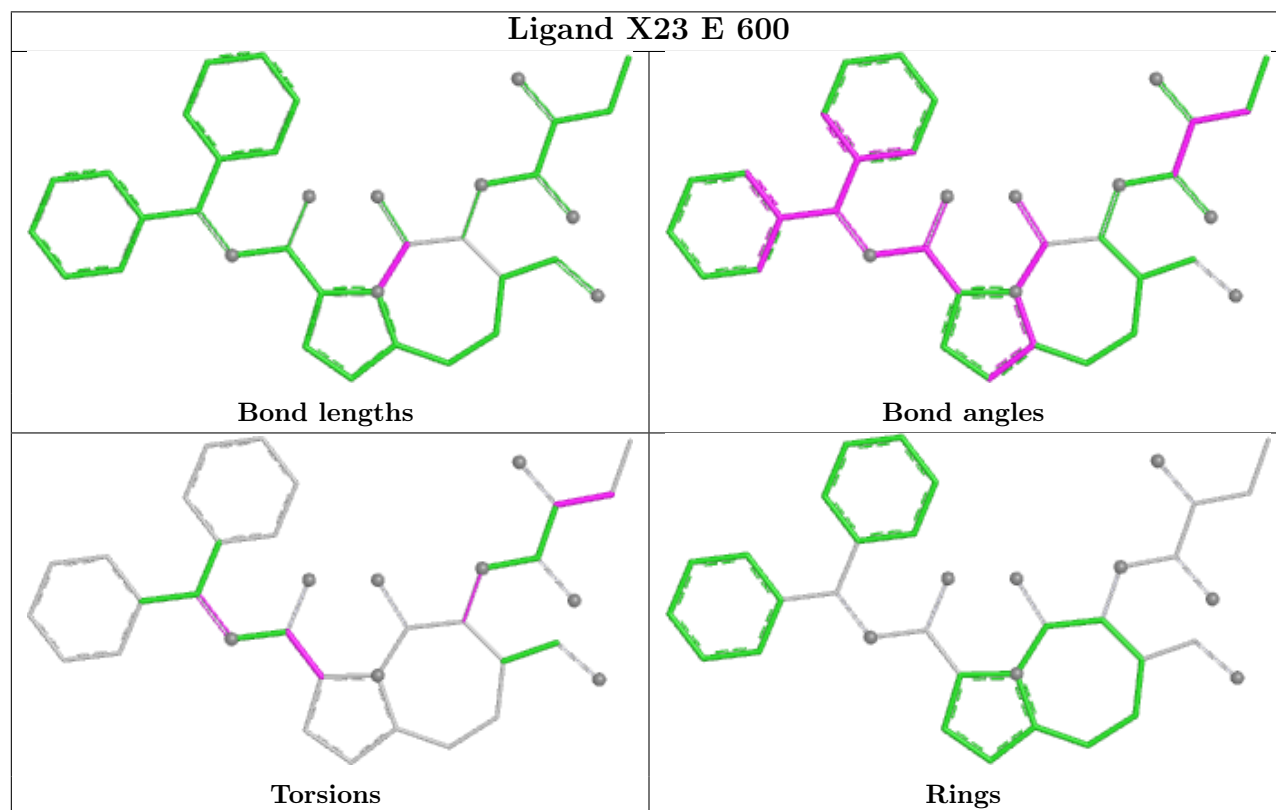
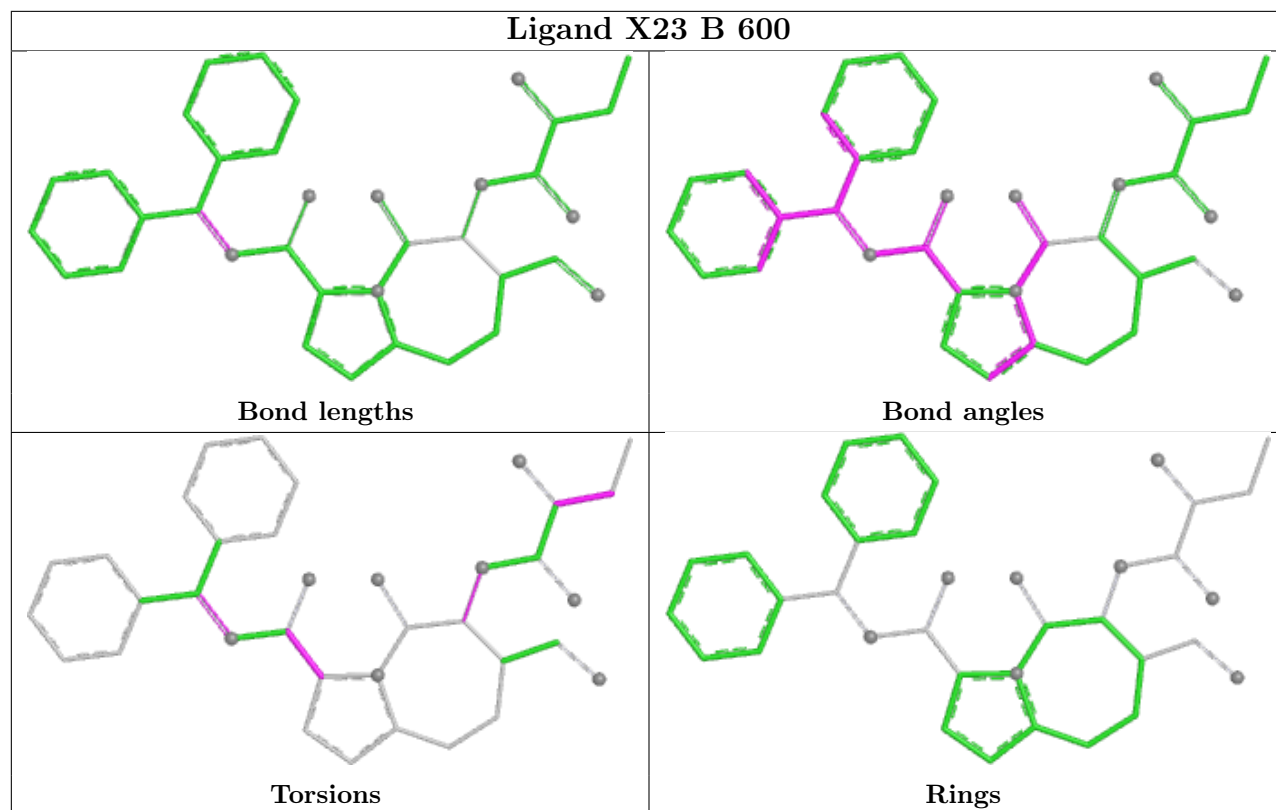
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	600	X23	1	0

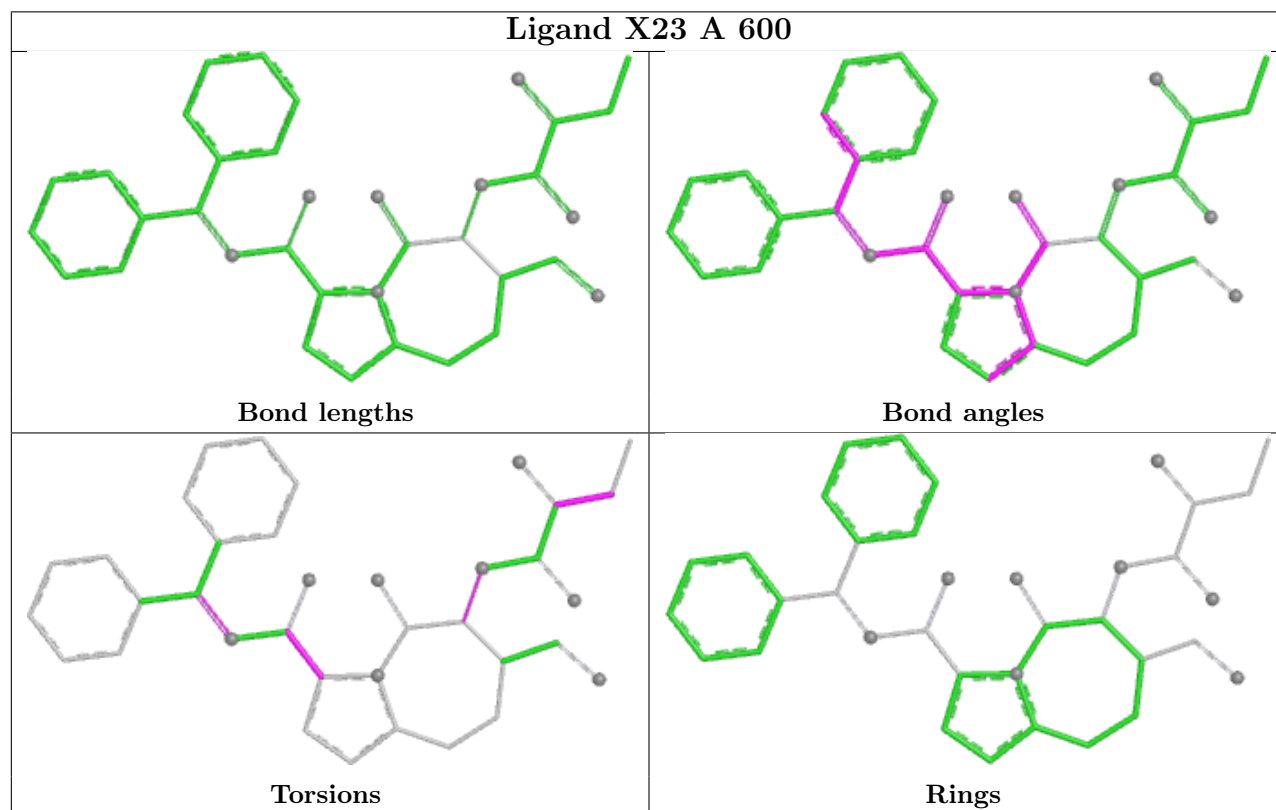
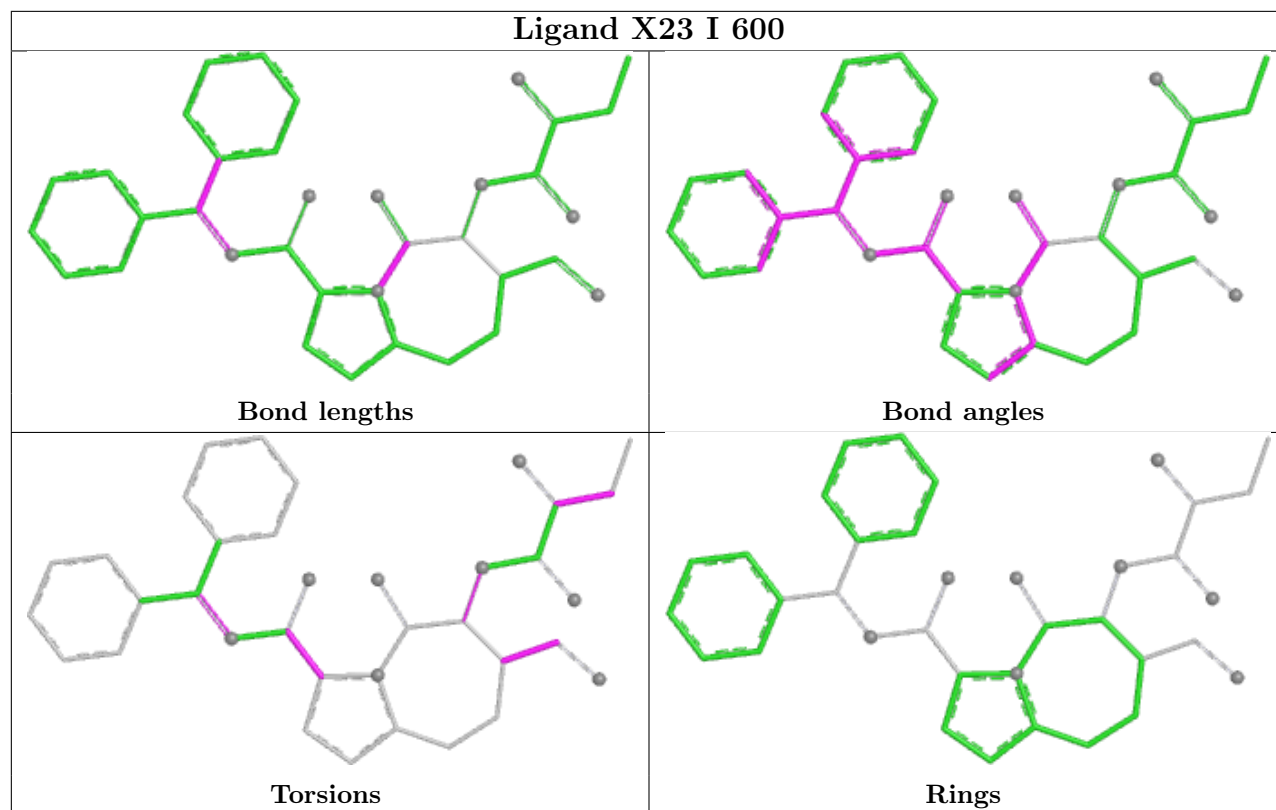
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

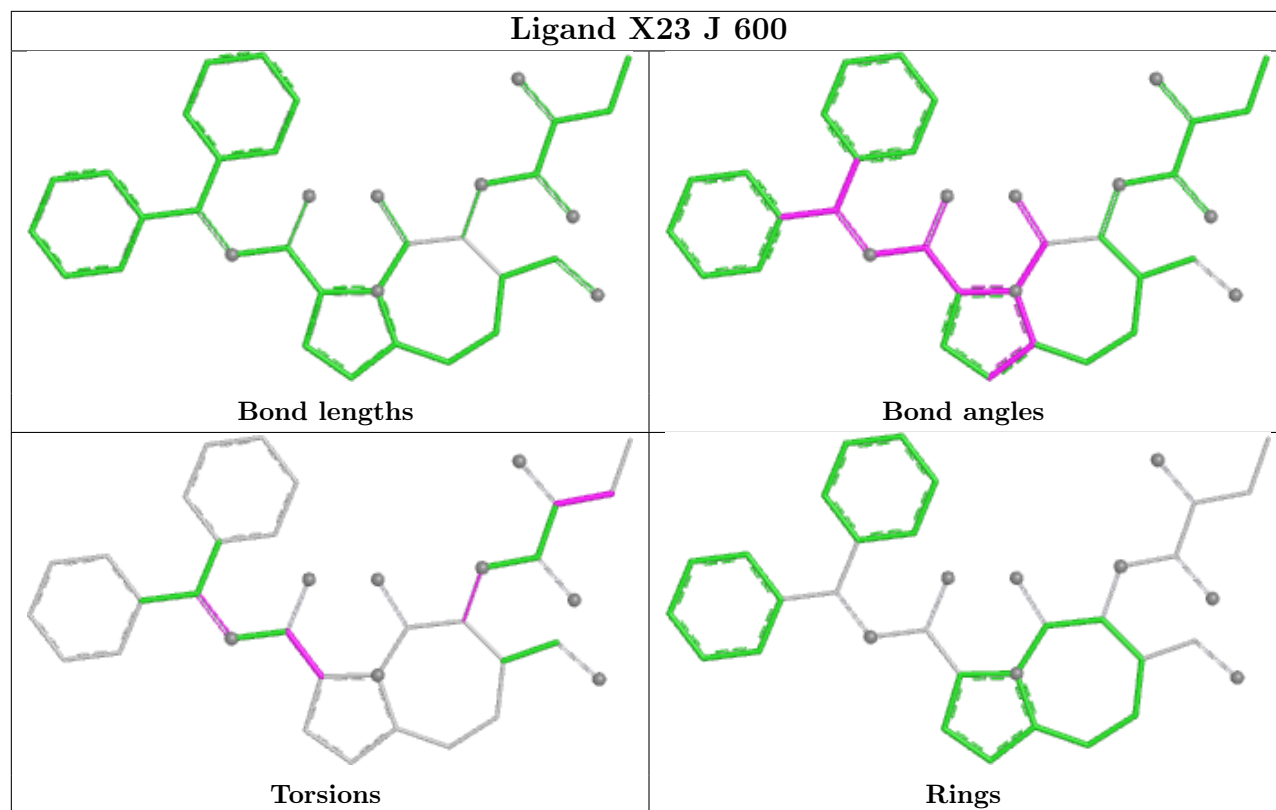












## 5.7 Other polymers [i](#)

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 [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	103/130 (79%)	0.50	8 (7%) 19 17	28, 48, 71, 90	1 (0%)
1	B	103/130 (79%)	0.83	14 (13%) 7 5	28, 54, 86, 97	1 (0%)
1	C	102/130 (78%)	0.28	7 (6%) 23 20	28, 44, 69, 92	1 (0%)
1	D	102/130 (78%)	0.20	5 (4%) 35 31	25, 42, 66, 89	1 (0%)
1	E	102/130 (78%)	0.20	11 (10%) 11 9	26, 42, 66, 94	1 (0%)
1	F	103/130 (79%)	0.59	9 (8%) 16 14	29, 54, 78, 94	1 (0%)
1	G	102/130 (78%)	0.55	12 (11%) 9 7	31, 50, 74, 88	1 (0%)
1	H	102/130 (78%)	0.37	8 (7%) 19 17	28, 46, 70, 88	1 (0%)
1	I	102/130 (78%)	0.44	5 (4%) 35 31	30, 48, 70, 93	1 (0%)
1	J	103/130 (79%)	0.65	9 (8%) 16 14	34, 53, 76, 105	1 (0%)
All	All	1024/1300 (78%)	0.46	88 (8%) 16 14	25, 49, 77, 105	10 (0%)

The worst 5 of 88 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	253	SER	6.0
1	B	274	THR	5.7
1	B	256	LEU	5.5
1	C	254	THR	5.1
1	I	355	THR	5.0

### 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](#)

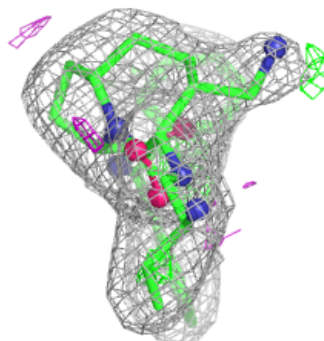
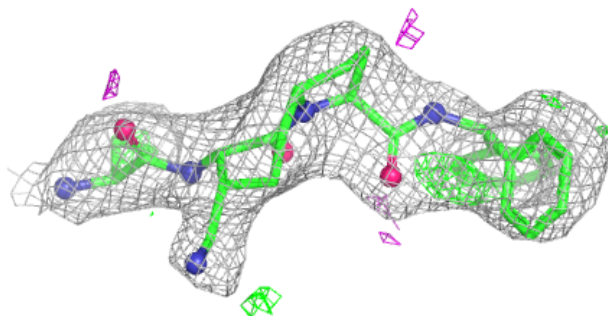
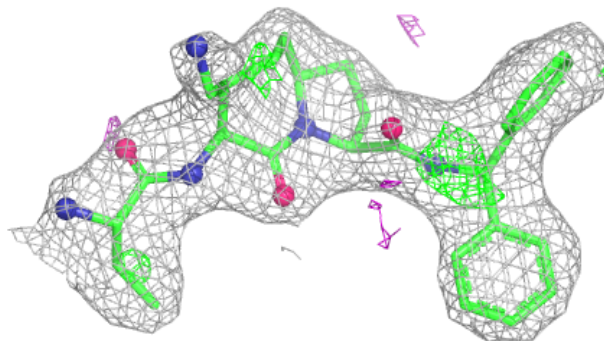
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	X23	A	600	36/36	0.92	0.13	46,53,61,62	0
3	X23	E	600	36/36	0.92	0.12	38,49,53,55	0
3	X23	I	600	36/36	0.92	0.12	40,51,54,55	0
3	X23	J	600	36/36	0.92	0.13	48,55,62,62	0
3	X23	D	600	36/36	0.93	0.11	35,42,47,51	0
3	X23	F	600	36/36	0.93	0.11	45,55,61,61	0
3	X23	G	600	36/36	0.93	0.12	47,53,62,63	0
3	X23	H	600	36/36	0.93	0.11	38,49,55,58	0
3	X23	B	600	36/36	0.93	0.12	45,49,55,58	0
3	X23	C	600	36/36	0.93	0.12	39,47,52,63	0
2	ZN	A	502	1/1	0.99	0.02	33,33,33,33	0
2	ZN	I	502	1/1	0.99	0.02	38,38,38,38	0
2	ZN	E	502	1/1	1.00	0.02	32,32,32,32	0
2	ZN	F	502	1/1	1.00	0.01	39,39,39,39	0
2	ZN	G	502	1/1	1.00	0.02	36,36,36,36	0
2	ZN	H	502	1/1	1.00	0.02	38,38,38,38	0
2	ZN	D	502	1/1	1.00	0.02	30,30,30,30	0
2	ZN	J	502	1/1	1.00	0.01	38,38,38,38	0
2	ZN	B	502	1/1	1.00	0.02	38,38,38,38	0
2	ZN	C	502	1/1	1.00	0.02	30,30,30,30	0

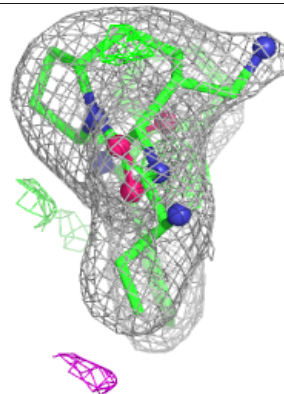
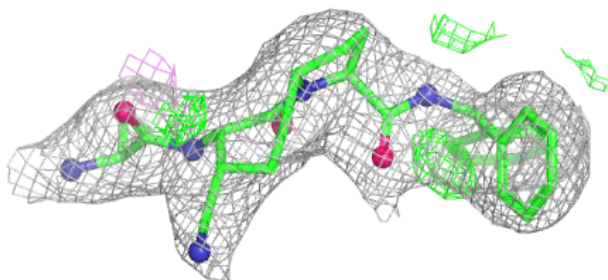
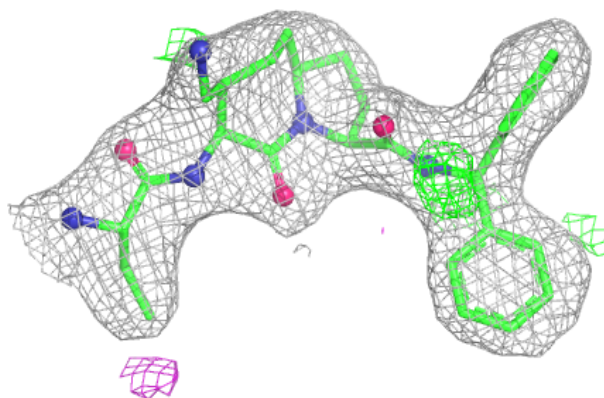
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around X23 A 600:**

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

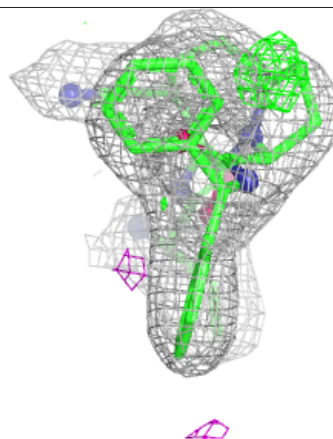
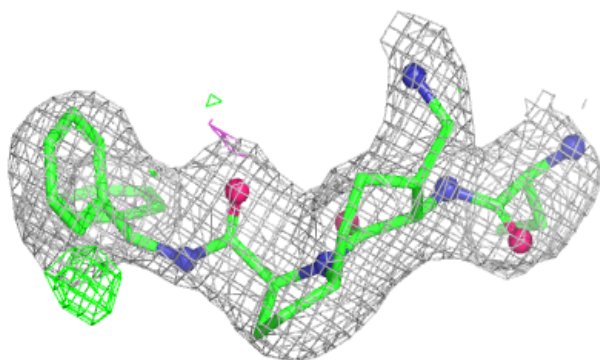
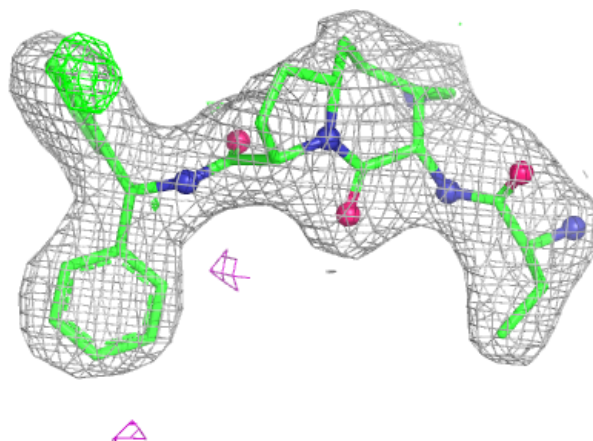
**Electron density around X23 E 600:**

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and green (positive)

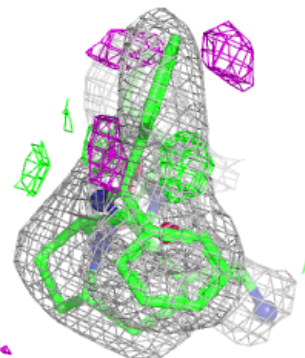
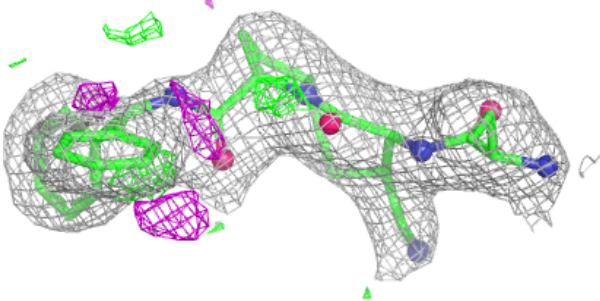
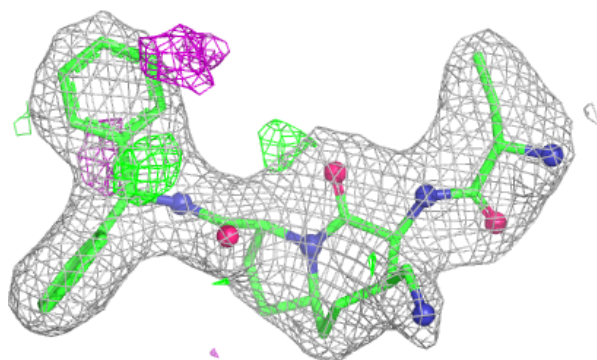


**Electron density around X23 I 600:**

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

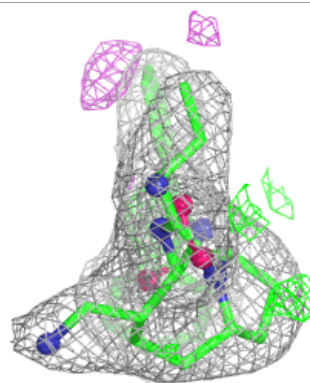
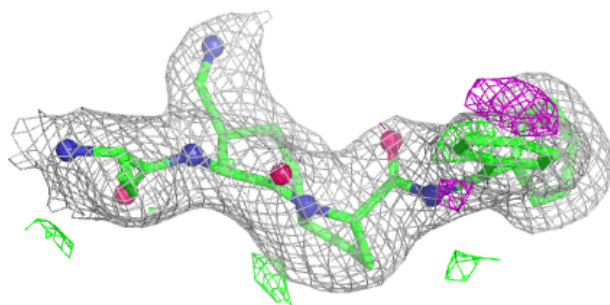
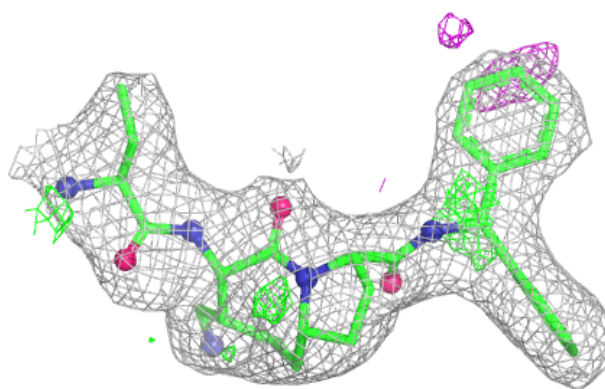
**Electron density around X23 J 600:**

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

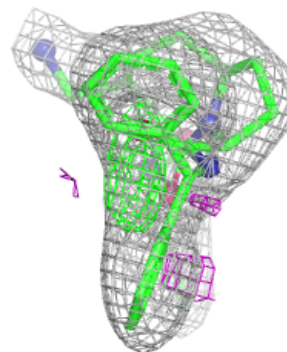
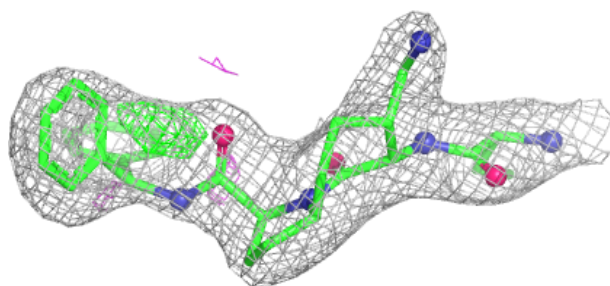
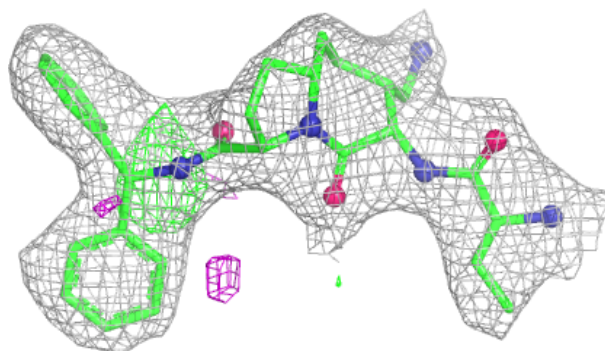


**Electron density around X23 D 600:**

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and green (positive)

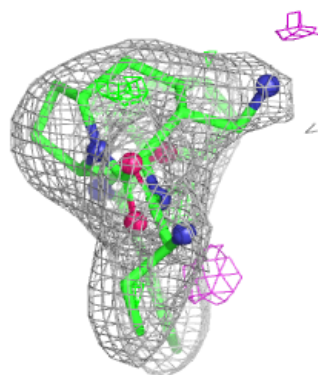
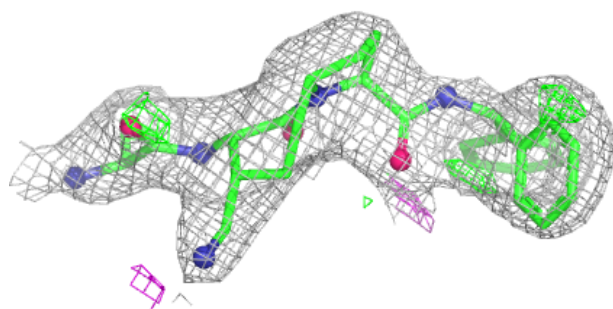
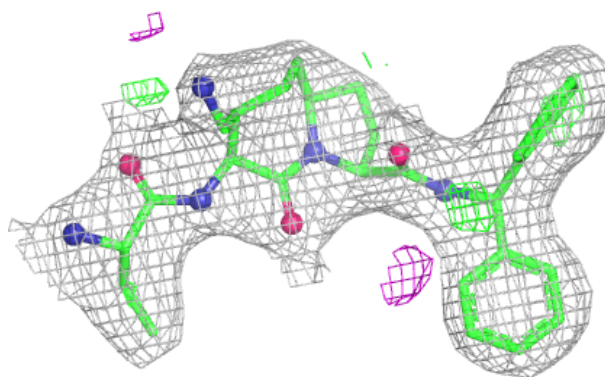
**Electron density around X23 F 600:**

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

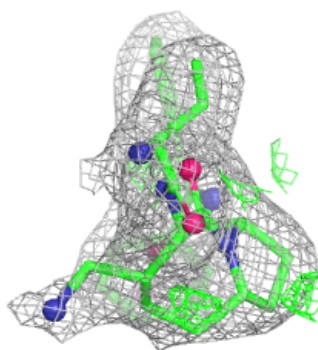
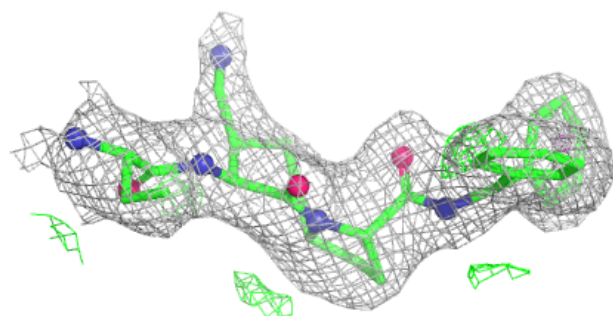
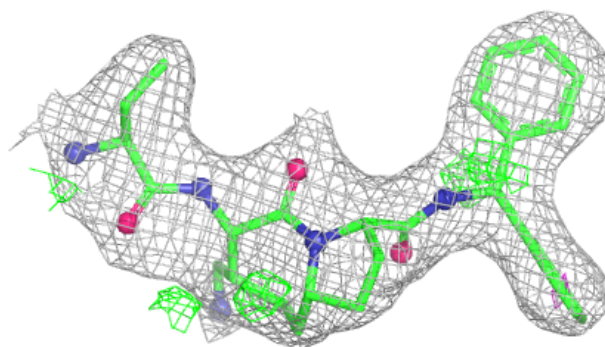


**Electron density around X23 G 600:**

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

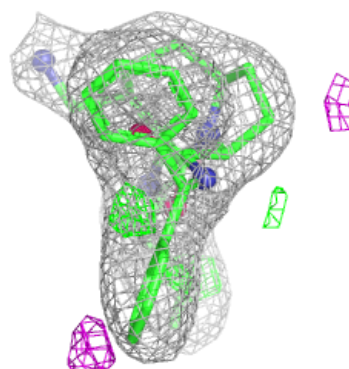
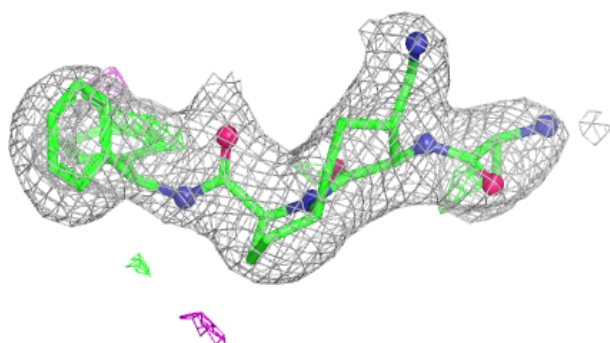
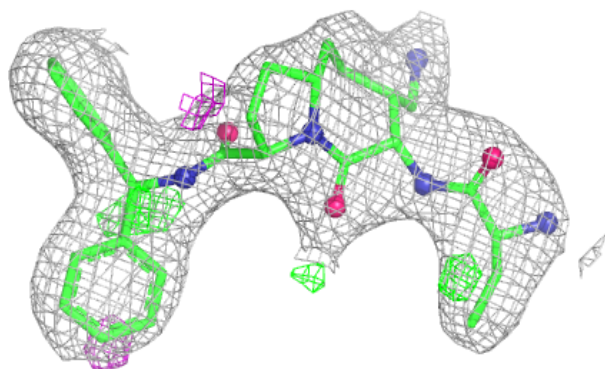
**Electron density around X23 H 600:**

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

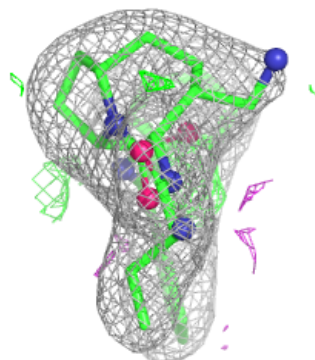
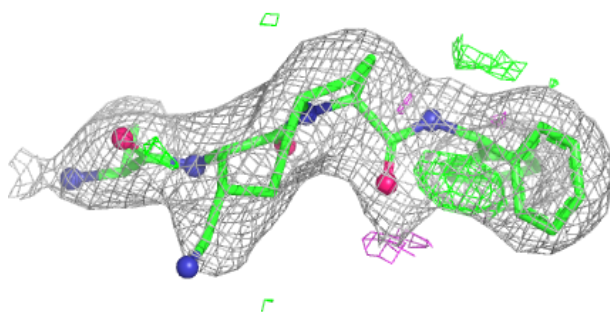
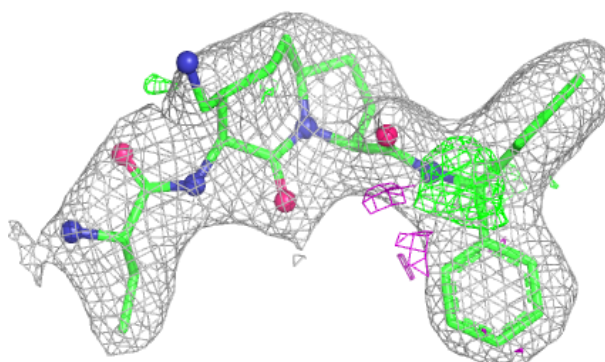


**Electron density around X23 B 600:**

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

**Electron density around X23 C 600:**

$2mF_o-DF_c$  (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.