



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 18, 2023 – 04:40 PM EDT

PDB ID : 4ZY1
Title : X-ray crystal structure of PfA-M17 in complex with hydroxamic acid-based inhibitor 10r
Authors : Drinkwater, N.; McGowan, S.
Deposited on : 2015-05-21
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

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>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

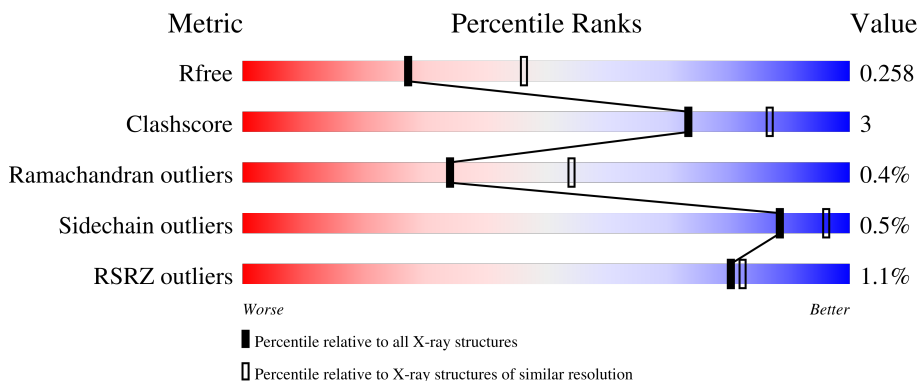
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 ≥ 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	522	92% 7% ..
1	B	522	3% 87% 11% ..
1	C	522	91% 8% .
1	D	522	% 88% 10% ..
1	E	522	92% 6% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	522	 89% 9%
1	G	522	 93% 6%
1	H	522	 88% 11%
1	I	522	 91% 8%
1	J	522	 93% 6%
1	K	522	 87% 10%
1	L	522	 86% 12%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	SO4	A	1007	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 49124 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 Probable M17 family aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	518	Total 3970	C 2549	N 638	O 764	S 19	0	0	0
1	B	516	Total 3909	C 2513	N 634	O 743	S 19	0	0	0
1	C	516	Total 3946	C 2535	N 635	O 756	S 20	0	0	0
1	D	514	Total 3934	C 2532	N 635	O 747	S 20	0	0	0
1	E	508	Total 3890	C 2505	N 626	O 740	S 19	0	0	0
1	F	511	Total 3837	C 2468	N 620	O 730	S 19	0	0	0
1	G	519	Total 3971	C 2548	N 639	O 765	S 19	0	0	0
1	H	517	Total 3904	C 2507	N 634	O 744	S 19	0	0	0
1	I	517	Total 3944	C 2535	N 635	O 754	S 20	0	0	0
1	J	514	Total 3914	C 2517	N 633	O 744	S 20	0	0	0
1	K	509	Total 3890	C 2504	N 624	O 743	S 19	0	0	0
1	L	510	Total 3840	C 2468	N 618	O 735	S 19	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

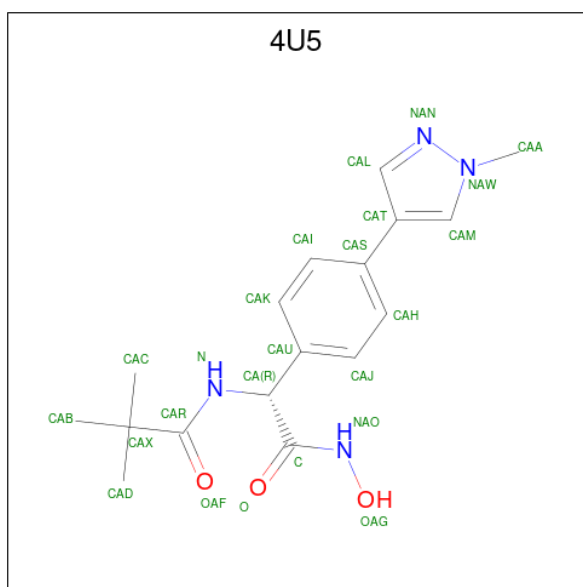
Chain	Residue	Modelled	Actual	Comment	Reference
A	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
A	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
A	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
B	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
B	515	GLN	ASN	engineered mutation	UNP A0A024V0B1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
C	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
C	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
C	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
D	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
D	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
D	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
E	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
E	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
E	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
F	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
F	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
F	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
G	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
G	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
G	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
H	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
H	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
H	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
I	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
I	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
I	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
J	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
J	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
J	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
K	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
K	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
K	546	GLN	ASN	engineered mutation	UNP A0A024V0B1
L	152	GLN	ASN	engineered mutation	UNP A0A024V0B1
L	515	GLN	ASN	engineered mutation	UNP A0A024V0B1
L	546	GLN	ASN	engineered mutation	UNP A0A024V0B1

- Molecule 2 is N-{(1R)-2-(hydroxyamino)-1-[4-(1-methyl-1H-pyrazol-4-yl)phenyl]-2-oxoethyl}-2,2-dimethylpropanamide (three-letter code: 4U5) (formula: C₁₇H₂₂N₄O₃).

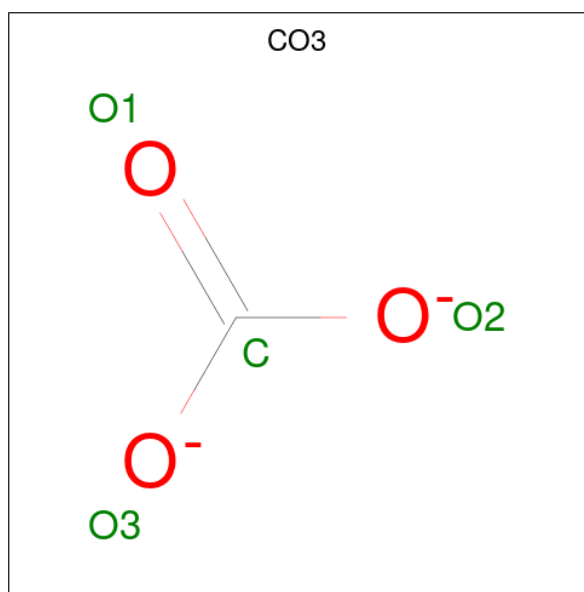


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	24	17	4	3	0	0
2	B	1	24	17	4	3	0	0
2	C	1	24	17	4	3	0	0
2	D	1	24	17	4	3	0	0
2	E	1	24	17	4	3	0	0
2	F	1	24	17	4	3	0	0
2	G	1	24	17	4	3	0	0
2	H	1	24	17	4	3	0	0
2	I	1	24	17	4	3	0	0
2	J	1	24	17	4	3	0	0
2	K	1	24	17	4	3	0	0
2	L	1	24	17	4	3	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

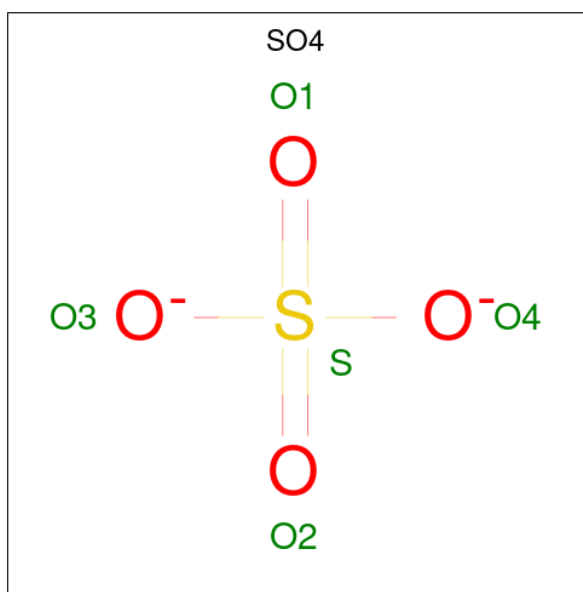
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Zn 2 2	0	0
3	B	2	Total Zn 2 2	0	0
3	C	2	Total Zn 2 2	0	0
3	D	2	Total Zn 2 2	0	0
3	E	2	Total Zn 2 2	0	0
3	F	2	Total Zn 2 2	0	0
3	G	2	Total Zn 2 2	0	0
3	H	2	Total Zn 2 2	0	0
3	I	2	Total Zn 2 2	0	0
3	J	2	Total Zn 2 2	0	0
3	K	2	Total Zn 2 2	0	0
3	L	2	Total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

- Molecule 4 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 1 3	0	0
4	B	1	Total C O 4 1 3	0	0
4	C	1	Total C O 4 1 3	0	0
4	D	1	Total C O 4 1 3	0	0
4	E	1	Total C O 4 1 3	0	0
4	F	1	Total C O 4 1 3	0	0
4	G	1	Total C O 4 1 3	0	0
4	H	1	Total C O 4 1 3	0	0
4	I	1	Total C O 4 1 3	0	0
4	J	1	Total C O 4 1 3	0	0
4	K	1	Total C O 4 1 3	0	0
4	L	1	Total C O 4 1 3	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



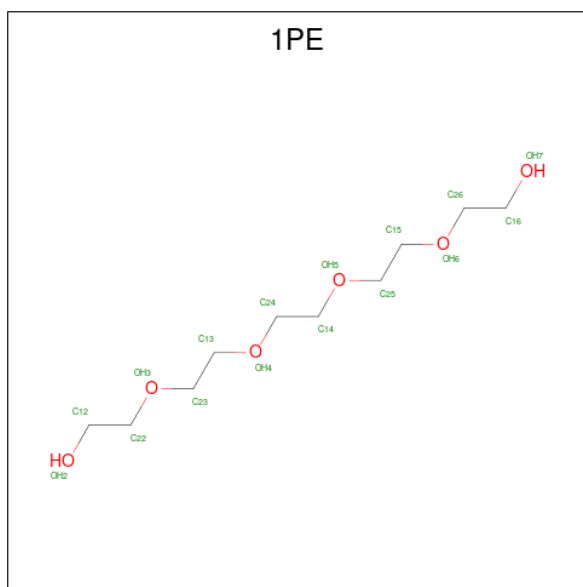
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		
5	I	1	Total	O	S	0	0
			5	4	1		
5	I	1	Total	O	S	0	0
			5	4	1		
5	J	1	Total	O	S	0	0
			5	4	1		
5	J	1	Total	O	S	0	0
			5	4	1		
5	K	1	Total	O	S	0	0
			5	4	1		
5	K	1	Total	O	S	0	0
			5	4	1		
5	K	1	Total	O	S	0	0
			5	4	1		
5	K	1	Total	O	S	0	0
			5	4	1		
5	L	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

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

- Molecule 6 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 9 6 3	0	0
6	A	1	Total C O 12 8 4	0	0
6	B	1	Total C O 10 7 3	0	0
6	B	1	Total C O 10 7 3	0	0
6	C	1	Total C O 13 9 4	0	0
6	C	1	Total C O 9 6 3	0	0
6	D	1	Total C O 10 7 3	0	0
6	D	1	Total C O 10 7 3	0	0
6	E	1	Total C O 12 8 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	C	O	0	0
			12	8	4		
6	F	1	Total	C	O	0	0
			10	6	4		
6	G	1	Total	C	O	0	0
			9	6	3		
6	G	1	Total	C	O	0	0
			6	4	2		
6	G	1	Total	C	O	0	0
			6	4	2		
6	H	1	Total	C	O	0	0
			10	7	3		
6	I	1	Total	C	O	0	0
			12	8	4		
6	I	1	Total	C	O	0	0
			11	8	3		
6	J	1	Total	C	O	0	0
			11	7	4		
6	J	1	Total	C	O	0	0
			10	6	4		
6	K	1	Total	C	O	0	0
			12	8	4		
6	K	1	Total	C	O	0	0
			12	8	4		
6	L	1	Total	C	O	0	0
			7	4	3		
6	L	1	Total	C	O	0	0
			10	6	4		
6	L	1	Total	C	O	0	0
			11	7	4		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	110	Total	O	0	0
			110	110		
8	B	114	Total	O	0	0
			114	114		
8	C	121	Total	O	0	0
			121	121		
8	D	138	Total	O	0	0
			138	138		
8	E	129	Total	O	0	0
			129	129		
8	F	106	Total	O	0	0
			106	106		
8	G	116	Total	O	0	0
			116	116		
8	H	125	Total	O	0	0
			125	125		
8	I	138	Total	O	0	0
			138	138		
8	J	106	Total	O	0	0
			106	106		
8	K	140	Total	O	0	0
			140	140		

Continued on next page...

Continued from previous page...

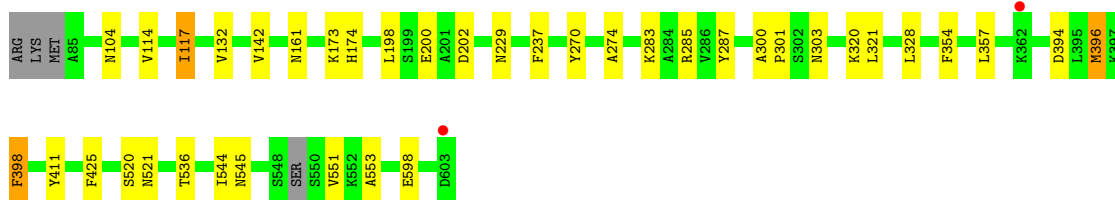
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	L	102	Total 102	O 102	0	0

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.

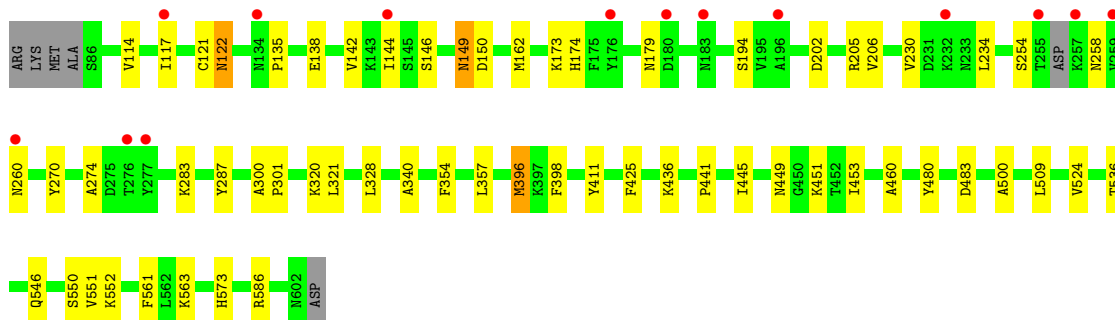
- Molecule 1: Probable M17 family aminopeptidase

Chain A: 




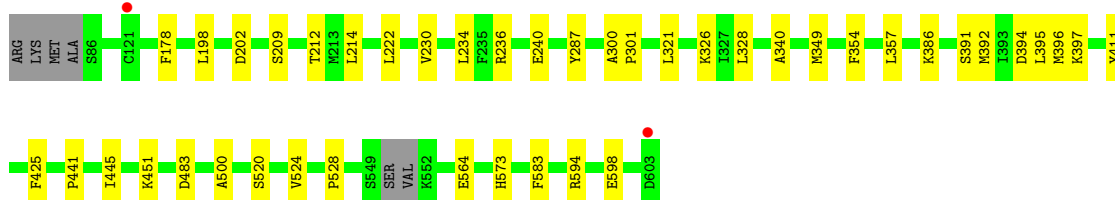
- Molecule 1: Probable M17 family aminopeptidase

Chain B: 

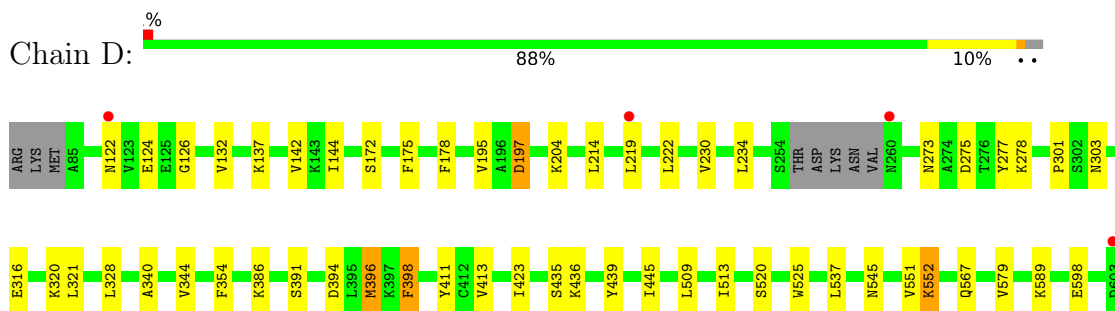


- Molecule 1: Probable M17 family aminopeptidase

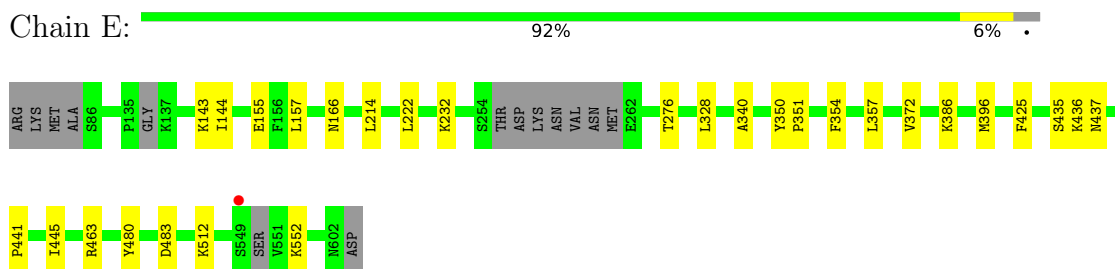
Chain C: 



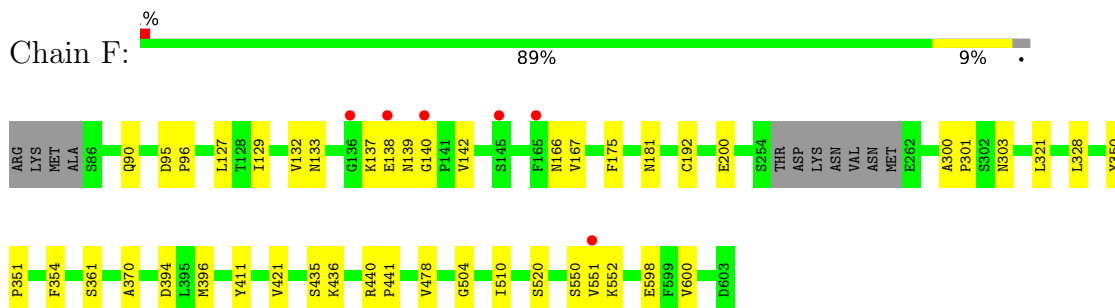
- Molecule 1: Probable M17 family aminopeptidase



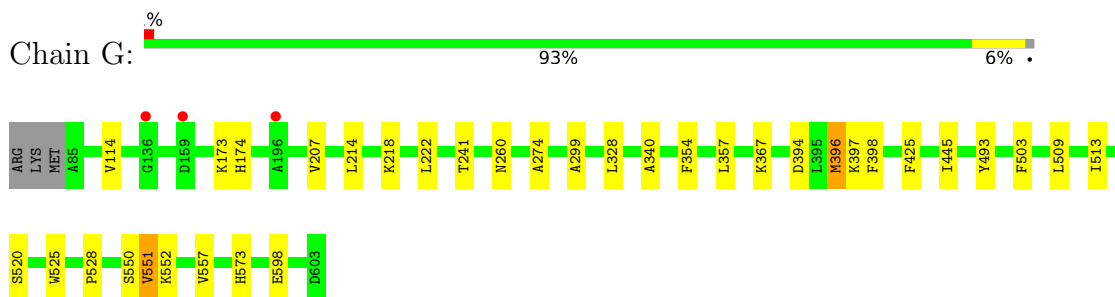
- Molecule 1: Probable M17 family aminopeptidase



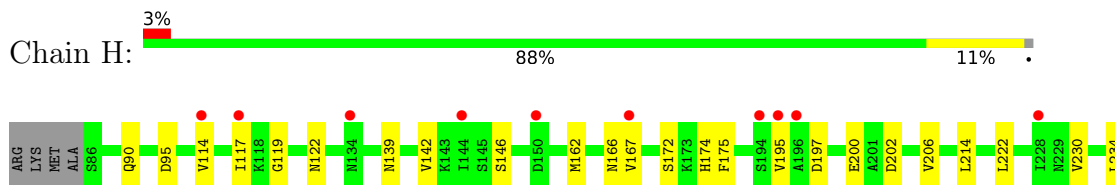
- Molecule 1: Probable M17 family aminopeptidase

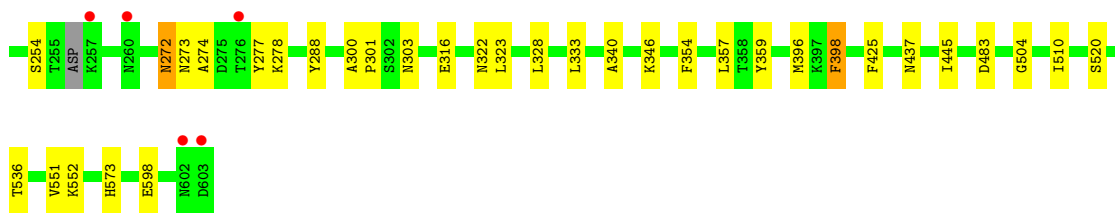


- Molecule 1: Probable M17 family aminopeptidase

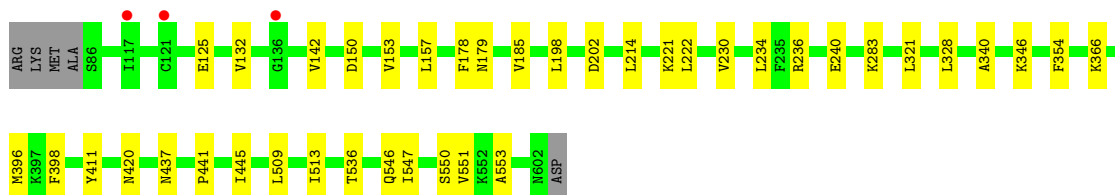
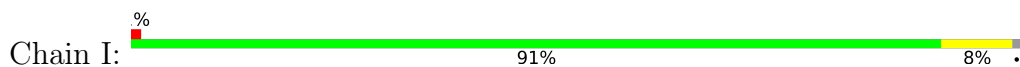


- Molecule 1: Probable M17 family aminopeptidase

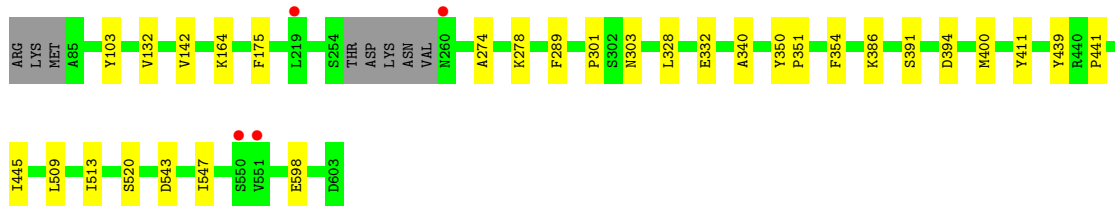
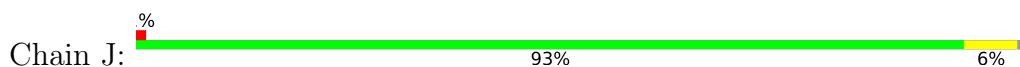




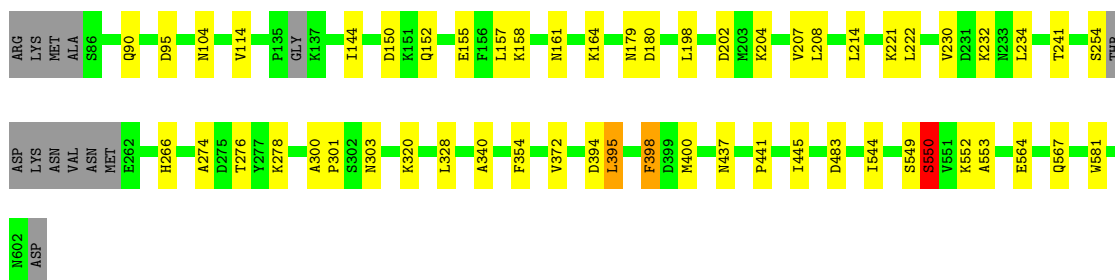
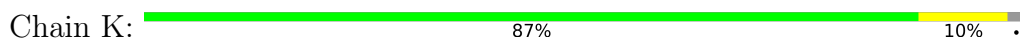
- Molecule 1: Probable M17 family aminopeptidase



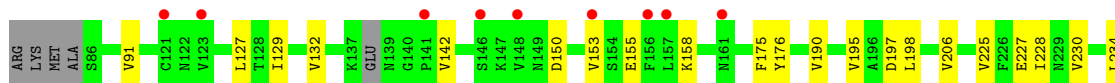
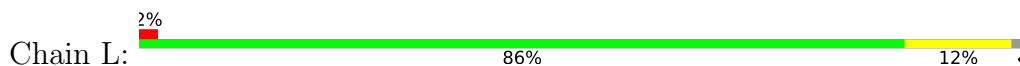
- Molecule 1: Probable M17 family aminopeptidase

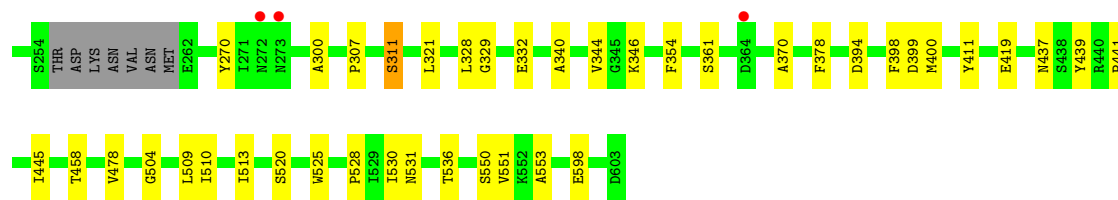


- Molecule 1: Probable M17 family aminopeptidase



- Molecule 1: Probable M17 family aminopeptidase





4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	174.10Å 177.32Å 229.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.90 – 2.50 48.90 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.0 (48.90-2.50) 82.3 (48.90-2.50)	Depositor EDS
R_{merge}	0.30	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.95 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.203 , 0.257 0.205 , 0.258	Depositor DCC
R_{free} test set	11527 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtrriage
Anisotropy	0.365	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	49124	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.83 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4421e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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: CO3, 1PE, GOL, 4U5, SO4, ZN

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	0.22	0/4047	0.38	0/5491
1	B	0.23	0/3986	0.40	0/5414
1	C	0.22	0/4023	0.37	0/5458
1	D	0.22	0/4011	0.38	0/5439
1	E	0.21	0/3965	0.38	0/5376
1	F	0.23	0/3914	0.40	0/5323
1	G	0.22	0/4049	0.39	0/5497
1	H	0.24	0/3981	0.39	0/5411
1	I	0.22	0/4022	0.38	0/5459
1	J	0.22	0/3991	0.39	0/5416
1	K	0.22	0/3966	0.39	0/5381
1	L	0.23	0/3916	0.40	0/5327
All	All	0.22	0/47871	0.39	0/64992

There are no bond length outliers.

There are no bond angle outliers.

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	3970	0	3881	26	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3909	0	3794	37	0
1	C	3946	0	3853	24	0
1	D	3934	0	3873	34	0
1	E	3890	0	3817	16	0
1	F	3837	0	3692	23	0
1	G	3971	0	3876	24	0
1	H	3904	0	3773	33	0
1	I	3944	0	3857	21	0
1	J	3914	0	3833	17	0
1	K	3890	0	3807	39	0
1	L	3840	0	3699	39	0
2	A	24	0	0	0	0
2	B	24	0	0	0	0
2	C	24	0	0	0	0
2	D	24	0	0	1	0
2	E	24	0	0	0	0
2	F	24	0	0	0	0
2	G	24	0	0	0	0
2	H	24	0	0	0	0
2	I	24	0	0	0	0
2	J	24	0	0	0	0
2	K	24	0	0	0	0
2	L	24	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
3	G	2	0	0	0	0
3	H	2	0	0	0	0
3	I	2	0	0	0	0
3	J	2	0	0	0	0
3	K	2	0	0	0	0
3	L	2	0	0	0	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
4	D	4	0	0	1	0
4	E	4	0	0	1	0
4	F	4	0	0	0	0
4	G	4	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	4	0	0	0	0
4	I	4	0	0	0	0
4	J	4	0	0	0	0
4	K	4	0	0	0	0
4	L	4	0	0	0	0
5	A	15	0	0	3	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	D	10	0	0	0	0
5	E	10	0	0	0	0
5	F	5	0	0	0	0
5	G	5	0	0	0	0
5	H	10	0	0	0	0
5	I	10	0	0	0	0
5	J	10	0	0	0	0
5	K	20	0	0	1	0
5	L	15	0	0	0	0
6	A	21	0	22	1	0
6	B	20	0	20	2	0
6	C	22	0	24	0	0
6	D	20	0	20	2	0
6	E	24	0	28	0	0
6	F	10	0	13	0	0
6	G	21	0	20	1	0
6	H	10	0	10	1	0
6	I	23	0	26	0	0
6	J	21	0	26	1	0
6	K	24	0	28	2	0
6	L	28	0	34	3	0
7	G	6	0	8	0	0
8	A	110	0	0	3	1
8	B	114	0	0	2	0
8	C	121	0	0	0	0
8	D	138	0	0	1	0
8	E	129	0	0	1	0
8	F	106	0	0	2	0
8	G	116	0	0	2	1
8	H	125	0	0	3	0
8	I	138	0	0	0	0
8	J	106	0	0	0	0
8	K	140	0	0	1	0
8	L	102	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	49124	0	46034	307	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 307 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:K:328:LEU:HB2	1:K:354:PHE:HB3	1.62	0.80
1:G:551:VAL:HG21	1:G:557:VAL:HG21	1.65	0.79
1:F:328:LEU:HB2	1:F:354:PHE:HB3	1.70	0.73
1:L:531:ASN:H	6:L:1008:1PE:H251	1.55	0.72
1:H:117:ILE:HD11	1:H:146:SER:OG	1.90	0.71

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1106:HOH:O	8:G:1104:HOH:O[2_685]	2.18	0.02

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	514/522 (98%)	499 (97%)	14 (3%)	1 (0%)	47 68
1	B	512/522 (98%)	493 (96%)	13 (2%)	6 (1%)	13 24
1	C	512/522 (98%)	498 (97%)	13 (2%)	1 (0%)	47 68
1	D	510/522 (98%)	490 (96%)	18 (4%)	2 (0%)	34 54
1	E	500/522 (96%)	486 (97%)	13 (3%)	1 (0%)	47 68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	507/522 (97%)	488 (96%)	15 (3%)	4 (1%)	19	35
1	G	517/522 (99%)	500 (97%)	15 (3%)	2 (0%)	34	54
1	H	513/522 (98%)	495 (96%)	14 (3%)	4 (1%)	19	35
1	I	515/522 (99%)	498 (97%)	16 (3%)	1 (0%)	47	68
1	J	510/522 (98%)	495 (97%)	15 (3%)	0	100	100
1	K	503/522 (96%)	486 (97%)	16 (3%)	1 (0%)	47	68
1	L	504/522 (97%)	480 (95%)	22 (4%)	2 (0%)	34	54
All	All	6117/6264 (98%)	5908 (97%)	184 (3%)	25 (0%)	34	54

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	550	SER
1	G	551	VAL
1	K	550	SER
1	B	550	SER
1	B	552	LYS

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	422/450 (94%)	420 (100%)	2 (0%)	88	96
1	B	408/450 (91%)	407 (100%)	1 (0%)	93	98
1	C	418/450 (93%)	418 (100%)	0	100	100
1	D	418/450 (93%)	415 (99%)	3 (1%)	84	94
1	E	413/450 (92%)	412 (100%)	1 (0%)	93	98
1	F	396/450 (88%)	394 (100%)	2 (0%)	88	96
1	G	422/450 (94%)	422 (100%)	0	100	100
1	H	407/450 (90%)	402 (99%)	5 (1%)	71	88
1	I	418/450 (93%)	417 (100%)	1 (0%)	93	98

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	414/450 (92%)	411 (99%)	3 (1%)	84	94
1	K	413/450 (92%)	409 (99%)	4 (1%)	76	90
1	L	401/450 (89%)	400 (100%)	1 (0%)	93	98
All	All	4950/5400 (92%)	4927 (100%)	23 (0%)	88	96

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	185	VAL
1	J	439	TYR
1	J	400	MET
1	K	395	LEU
1	E	143	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	272	ASN
1	K	161	ASN
1	K	437	ASN
1	F	104	ASN
1	B	122	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 97 ligands modelled in this entry, 24 are monoatomic - leaving 73 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
5	SO4	A	1007	-	4,4,4	0.14	0	6,6,6	0.05	0
5	SO4	E	1006	-	4,4,4	0.14	0	6,6,6	0.06	0
4	CO3	C	1004	-	2,3,3	0.40	0	2,3,3	0.20	0
4	CO3	F	1004	-	2,3,3	0.41	0	2,3,3	0.14	0
5	SO4	K	1005	-	4,4,4	0.15	0	6,6,6	0.07	0
6	1PE	G	1009	-	5,5,15	0.68	0	4,4,14	0.45	0
6	1PE	A	1009	-	11,11,15	0.63	0	10,10,14	0.41	0
5	SO4	G	1005	-	4,4,4	0.14	0	6,6,6	0.04	0
5	SO4	L	1006	-	4,4,4	0.14	0	6,6,6	0.04	0
2	4U5	K	1001	3	22,25,25	2.27	3 (13%)	32,36,36	1.54	3 (9%)
6	1PE	I	1007	-	11,11,15	0.58	0	10,10,14	0.43	0
4	CO3	L	1004	-	2,3,3	0.40	0	2,3,3	0.19	0
5	SO4	A	1006	-	4,4,4	0.14	0	6,6,6	0.06	0
4	CO3	D	1004	-	2,3,3	0.41	0	2,3,3	0.21	0
5	SO4	E	1005	-	4,4,4	0.14	0	6,6,6	0.07	0
2	4U5	L	1001	3	22,25,25	2.28	3 (13%)	32,36,36	1.46	2 (6%)
6	1PE	L	1008	-	6,6,15	0.60	0	5,5,14	0.50	0
6	1PE	K	1010	-	11,11,15	0.59	0	10,10,14	0.38	0
6	1PE	F	1006	-	9,9,15	0.89	0	8,8,14	0.41	0
2	4U5	D	1001	3	22,25,25	2.29	3 (13%)	32,36,36	1.52	3 (9%)
2	4U5	I	1001	3	22,25,25	2.28	3 (13%)	32,36,36	1.49	4 (12%)
6	1PE	J	1007	-	10,10,15	0.87	0	9,9,14	0.34	0
4	CO3	G	1004	-	2,3,3	0.39	0	2,3,3	0.15	0
5	SO4	K	1006	-	4,4,4	0.14	0	6,6,6	0.05	0
5	SO4	L	1005	-	4,4,4	0.15	0	6,6,6	0.05	0
6	1PE	E	1007	-	11,11,15	0.59	0	10,10,14	0.43	0
6	1PE	G	1008	-	5,5,15	0.67	0	4,4,14	0.53	0
5	SO4	I	1005	-	4,4,4	0.13	0	6,6,6	0.05	0
2	4U5	B	1001	3	22,25,25	2.23	3 (13%)	32,36,36	1.56	4 (12%)
6	1PE	H	1007	-	9,9,15	0.54	0	8,8,14	0.42	0
6	1PE	C	1006	-	12,12,15	0.64	0	11,11,14	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	1PE	G	1007	-	8,8,15	0.53	0	7,7,14	0.31	0
6	1PE	K	1009	-	11,11,15	0.59	0	10,10,14	0.46	0
5	SO4	D	1005	-	4,4,4	0.14	0	6,6,6	0.05	0
2	4U5	E	1001	3	22,25,25	2.26	3 (13%)	32,36,36	1.56	4 (12%)
5	SO4	A	1005	-	4,4,4	0.14	0	6,6,6	0.04	0
4	CO3	B	1004	-	2,3,3	0.41	0	2,3,3	0.20	0
2	4U5	H	1001	3	22,25,25	2.25	3 (13%)	32,36,36	1.59	3 (9%)
6	1PE	B	1007	-	9,9,15	0.55	0	8,8,14	0.33	0
5	SO4	J	1005	-	4,4,4	0.15	0	6,6,6	0.04	0
5	SO4	H	1005	-	4,4,4	0.14	0	6,6,6	0.07	0
5	SO4	H	1006	-	4,4,4	0.14	0	6,6,6	0.05	0
5	SO4	I	1006	-	4,4,4	0.14	0	6,6,6	0.04	0
6	1PE	L	1010	-	10,10,15	0.85	0	9,9,14	0.41	0
4	CO3	A	1004	-	2,3,3	0.41	0	2,3,3	0.19	0
5	SO4	L	1007	-	4,4,4	0.14	0	6,6,6	0.07	0
7	GOL	G	1006	-	5,5,5	0.34	0	5,5,5	0.35	0
4	CO3	I	1004	-	2,3,3	0.39	0	2,3,3	0.21	0
2	4U5	F	1001	3	22,25,25	2.28	3 (13%)	32,36,36	1.49	3 (9%)
2	4U5	C	1001	3	22,25,25	2.25	3 (13%)	32,36,36	1.51	4 (12%)
5	SO4	B	1005	-	4,4,4	0.14	0	6,6,6	0.07	0
5	SO4	F	1005	-	4,4,4	0.14	0	6,6,6	0.07	0
5	SO4	K	1007	-	4,4,4	0.14	0	6,6,6	0.05	0
5	SO4	K	1008	-	4,4,4	0.14	0	6,6,6	0.04	0
6	1PE	A	1008	-	8,8,15	0.52	0	7,7,14	0.40	0
5	SO4	C	1005	-	4,4,4	0.15	0	6,6,6	0.04	0
6	1PE	B	1006	-	9,9,15	0.53	0	8,8,14	0.38	0
5	SO4	D	1006	-	4,4,4	0.15	0	6,6,6	0.04	0
6	1PE	D	1007	-	9,9,15	0.55	0	8,8,14	0.37	0
4	CO3	J	1004	-	2,3,3	0.40	0	2,3,3	0.19	0
6	1PE	D	1008	-	9,9,15	0.54	0	8,8,14	0.36	0
6	1PE	I	1008	-	10,10,15	0.56	0	9,9,14	0.38	0
4	CO3	E	1004	-	2,3,3	0.40	0	2,3,3	0.19	0
4	CO3	K	1004	-	2,3,3	0.40	0	2,3,3	0.15	0
6	1PE	L	1009	-	9,9,15	0.89	0	8,8,14	0.41	0
6	1PE	E	1008	-	11,11,15	0.58	0	10,10,14	0.51	0
2	4U5	A	1001	3	22,25,25	2.22	3 (13%)	32,36,36	1.50	4 (12%)
4	CO3	H	1004	-	2,3,3	0.40	0	2,3,3	0.18	0
6	1PE	J	1008	-	9,9,15	0.88	0	8,8,14	0.43	0
5	SO4	J	1006	-	4,4,4	0.14	0	6,6,6	0.07	0
2	4U5	G	1001	3	22,25,25	2.26	3 (13%)	32,36,36	1.54	3 (9%)
2	4U5	J	1001	3	22,25,25	2.25	3 (13%)	32,36,36	1.52	3 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	1PE	C	1007	-	8,8,15	0.53	0	7,7,14	0.39	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	1PE	G	1009	-	-	2/3/3/13	-
6	1PE	A	1009	-	-	5/9/9/13	-
2	4U5	K	1001	3	-	2/24/24/24	0/2/2/2
6	1PE	I	1007	-	-	6/9/9/13	-
2	4U5	L	1001	3	-	0/24/24/24	0/2/2/2
6	1PE	L	1008	-	-	2/4/4/13	-
6	1PE	K	1010	-	-	5/9/9/13	-
6	1PE	F	1006	-	-	6/7/7/13	-
2	4U5	D	1001	3	-	3/24/24/24	0/2/2/2
2	4U5	I	1001	3	-	0/24/24/24	0/2/2/2
6	1PE	J	1007	-	-	5/8/8/13	-
6	1PE	E	1007	-	-	3/9/9/13	-
6	1PE	G	1008	-	-	0/3/3/13	-
2	4U5	B	1001	3	-	0/24/24/24	0/2/2/2
6	1PE	H	1007	-	-	3/7/7/13	-
6	1PE	C	1006	-	-	4/10/10/13	-
6	1PE	G	1007	-	-	4/6/6/13	-
2	4U5	E	1001	3	-	1/24/24/24	0/2/2/2
2	4U5	H	1001	3	-	2/24/24/24	0/2/2/2
6	1PE	B	1007	-	-	4/7/7/13	-
6	1PE	L	1010	-	-	2/8/8/13	-
7	GOL	G	1006	-	-	2/4/4/4	-
2	4U5	F	1001	3	-	3/24/24/24	0/2/2/2
2	4U5	C	1001	3	-	0/24/24/24	0/2/2/2
6	1PE	B	1006	-	-	4/7/7/13	-
6	1PE	D	1008	-	-	6/7/7/13	-
6	1PE	I	1008	-	-	3/8/8/13	-
6	1PE	A	1008	-	-	5/6/6/13	-
6	1PE	K	1009	-	-	4/9/9/13	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	1PE	D	1007	-	-	2/7/7/13	-
6	1PE	L	1009	-	-	3/7/7/13	-
6	1PE	E	1008	-	-	3/9/9/13	-
2	4U5	A	1001	3	-	0/24/24/24	0/2/2/2
6	1PE	J	1008	-	-	3/7/7/13	-
2	4U5	G	1001	3	-	0/24/24/24	0/2/2/2
2	4U5	J	1001	3	-	0/24/24/24	0/2/2/2
6	1PE	C	1007	-	-	4/6/6/13	-

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1001	4U5	CAU-CA	-7.68	1.40	1.52
2	D	1001	4U5	CAU-CA	-7.68	1.40	1.52
2	L	1001	4U5	CAU-CA	-7.66	1.40	1.52
2	K	1001	4U5	CAU-CA	-7.65	1.40	1.52
2	E	1001	4U5	CAU-CA	-7.65	1.40	1.52

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1001	4U5	CAL-NAN-NAW	5.79	110.26	104.23
2	A	1001	4U5	CAL-NAN-NAW	5.68	110.15	104.23
2	B	1001	4U5	CAL-NAN-NAW	5.63	110.09	104.23
2	H	1001	4U5	CAL-NAN-NAW	5.62	110.08	104.23
2	I	1001	4U5	CAL-NAN-NAW	5.57	110.03	104.23

There are no chirality outliers.

5 of 101 torsion outliers are listed below:

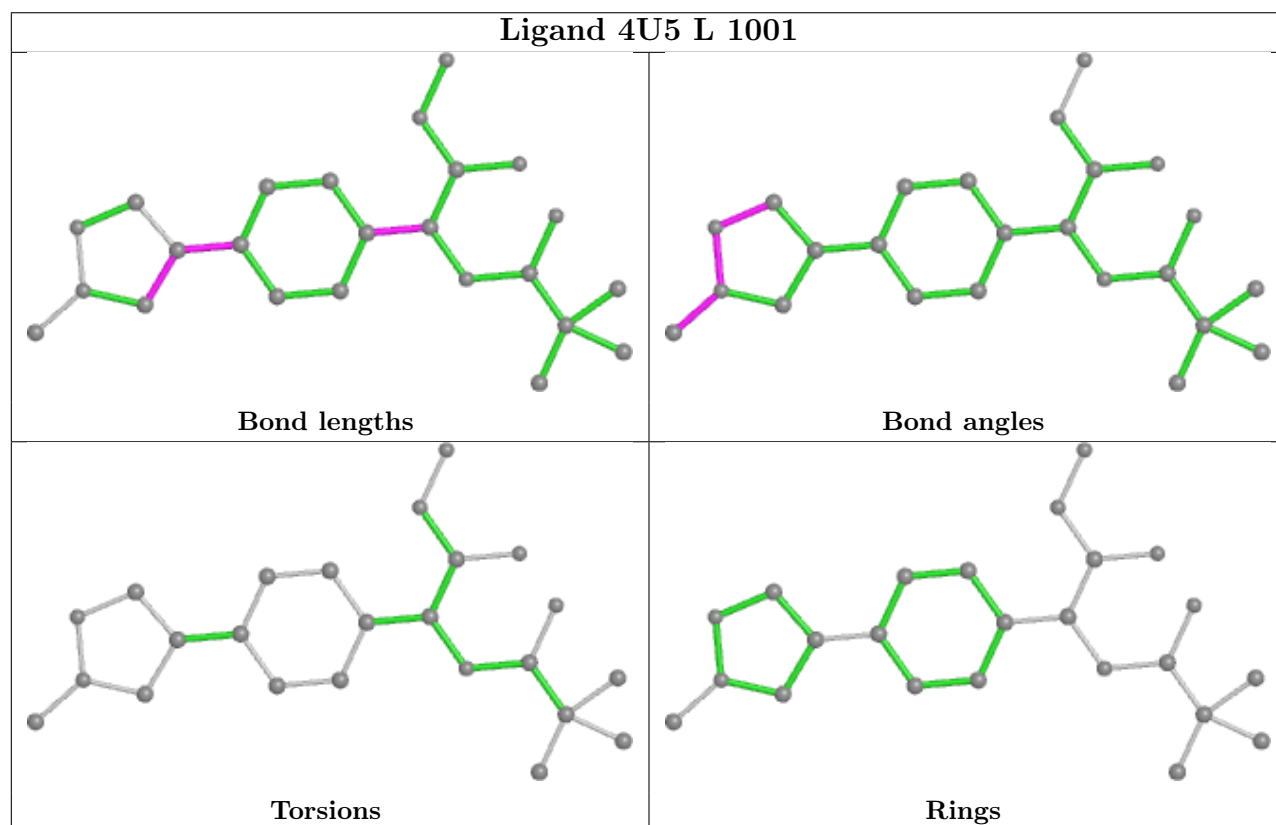
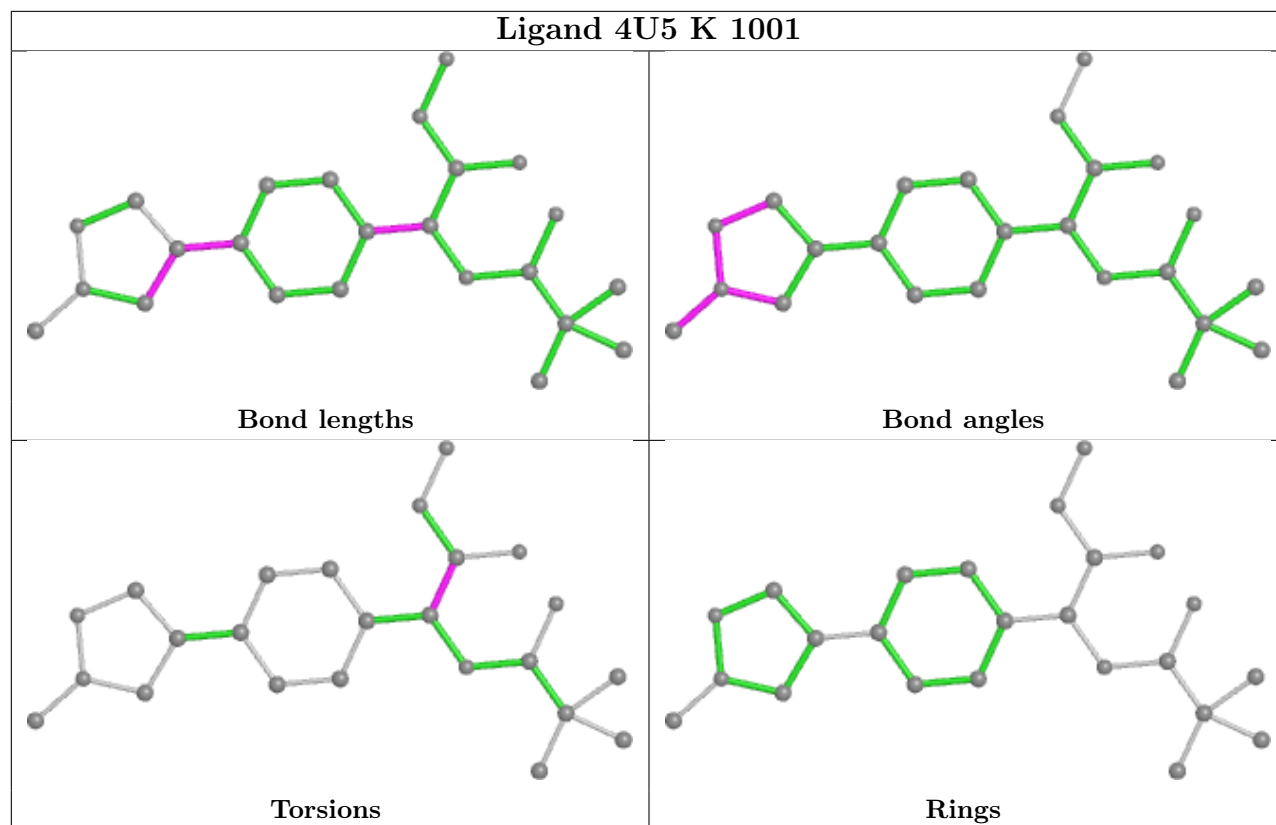
Mol	Chain	Res	Type	Atoms
6	E	1007	1PE	OH5-C14-C24-OH4
6	A	1008	1PE	OH4-C13-C23-OH3
6	G	1007	1PE	OH4-C13-C23-OH3
6	J	1007	1PE	OH5-C14-C24-OH4
6	L	1010	1PE	OH5-C14-C24-OH4

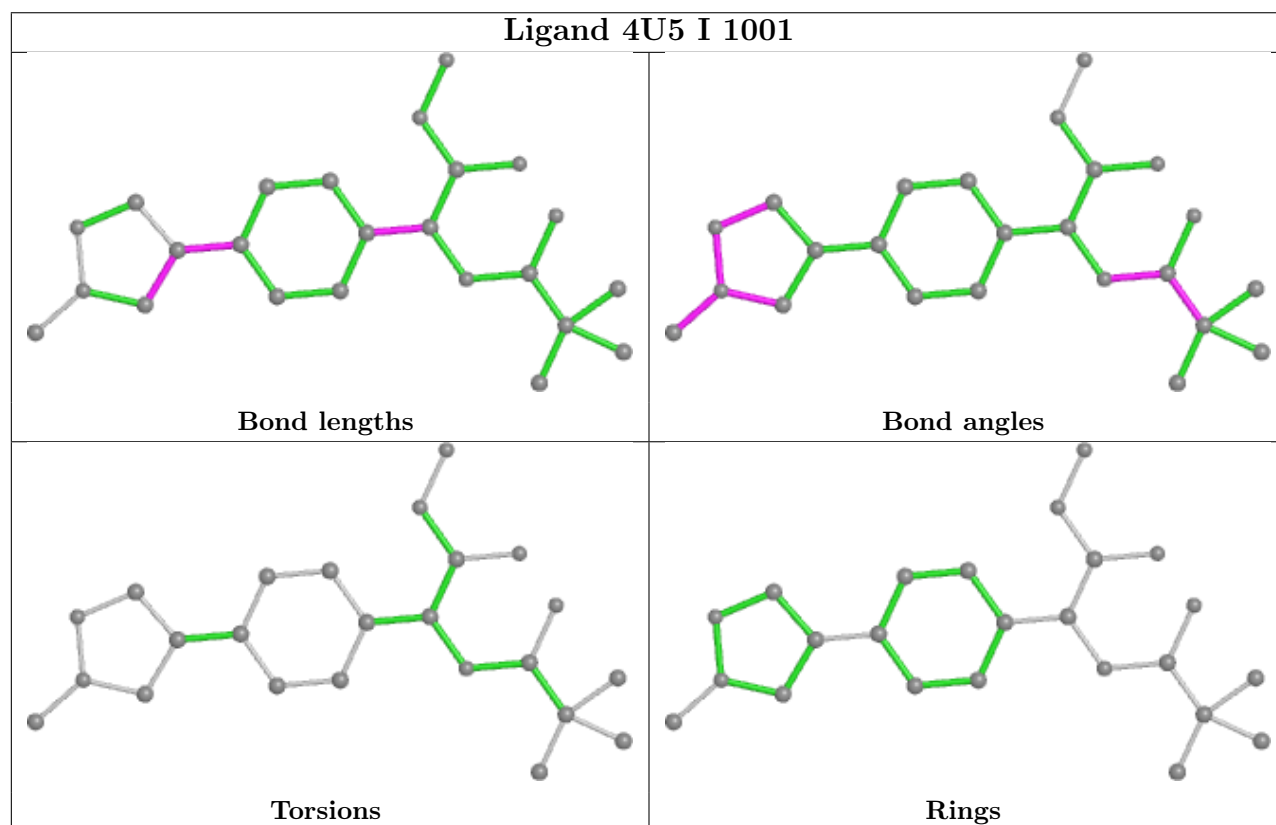
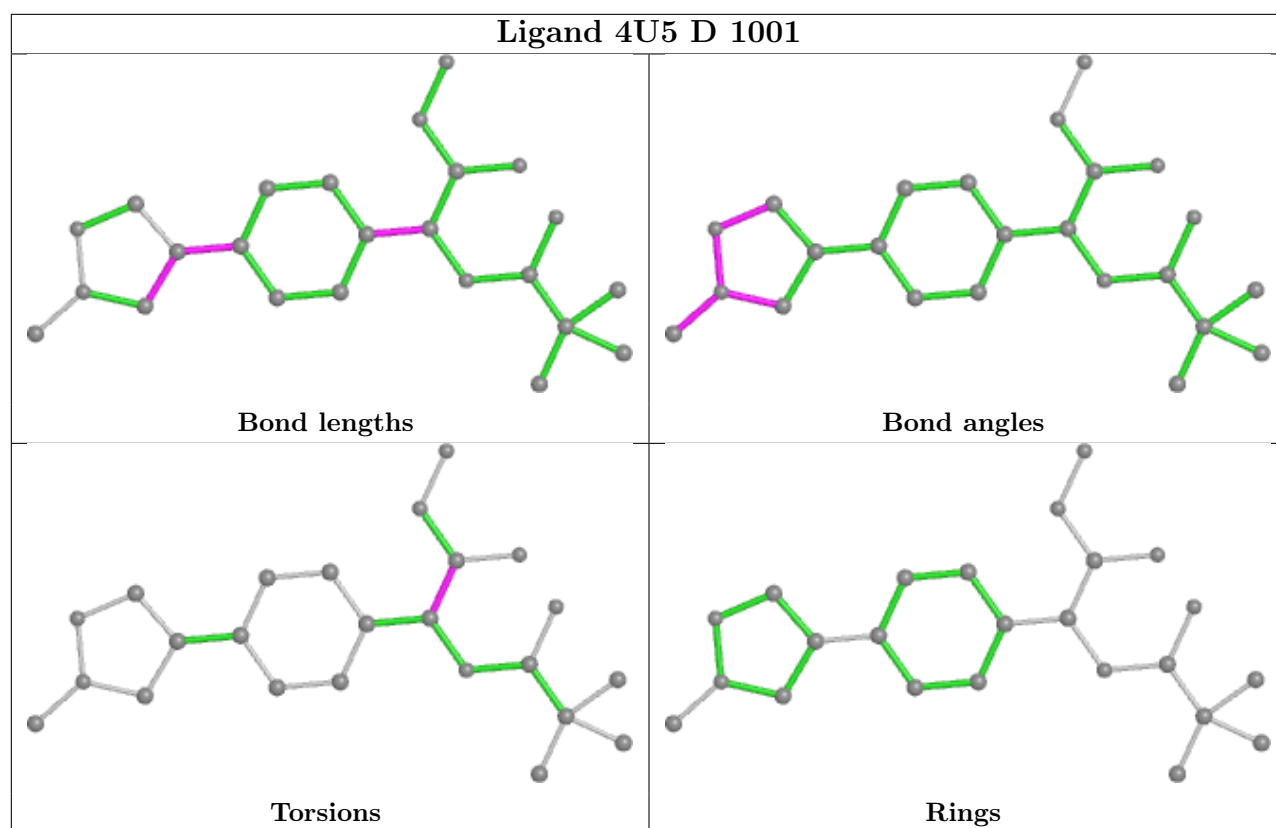
There are no ring outliers.

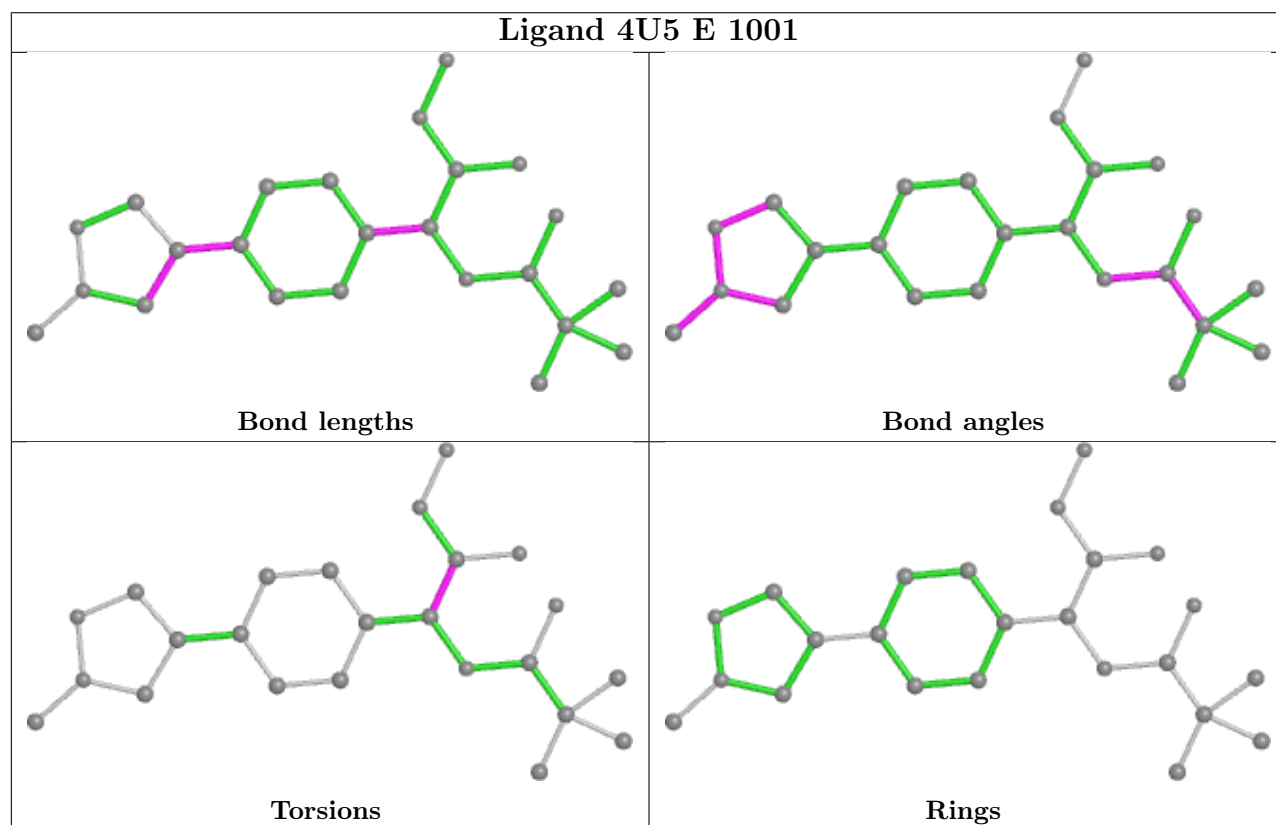
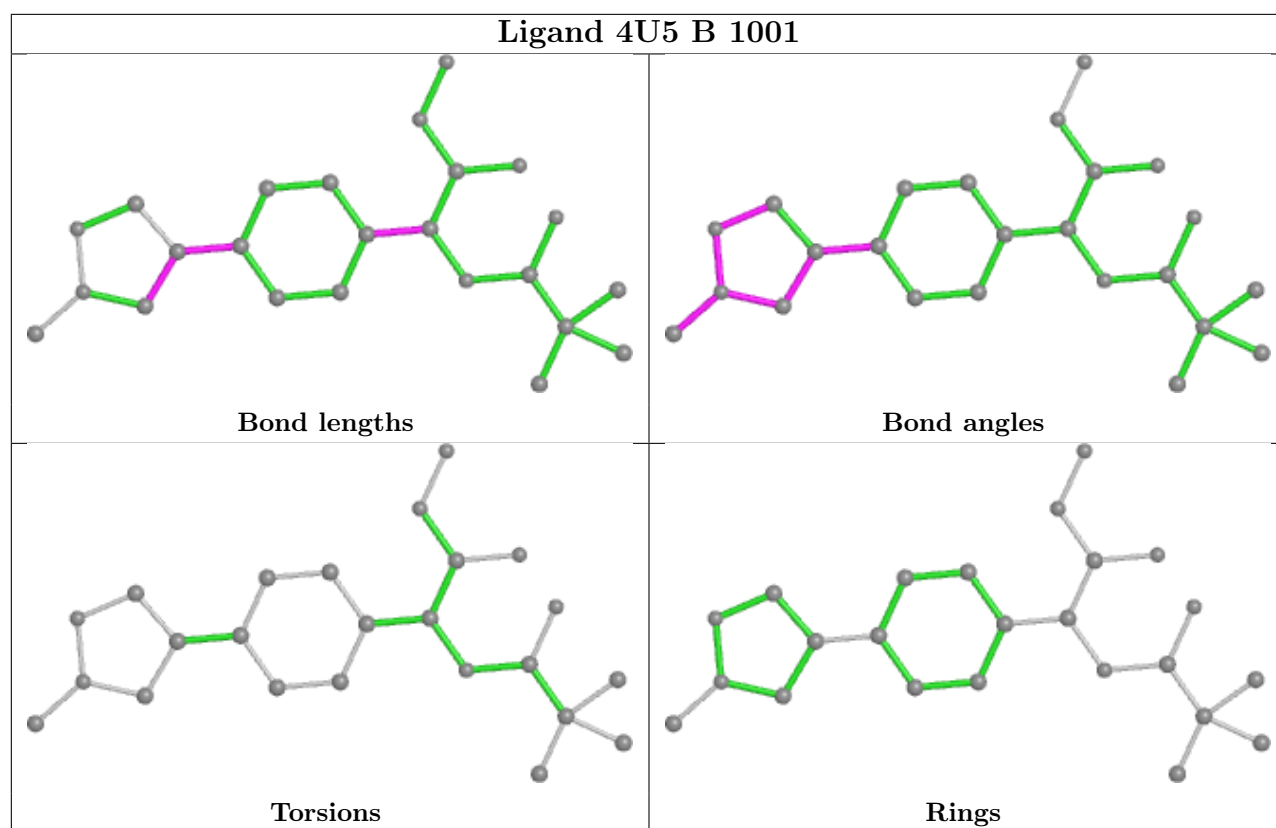
17 monomers are involved in 19 short contacts:

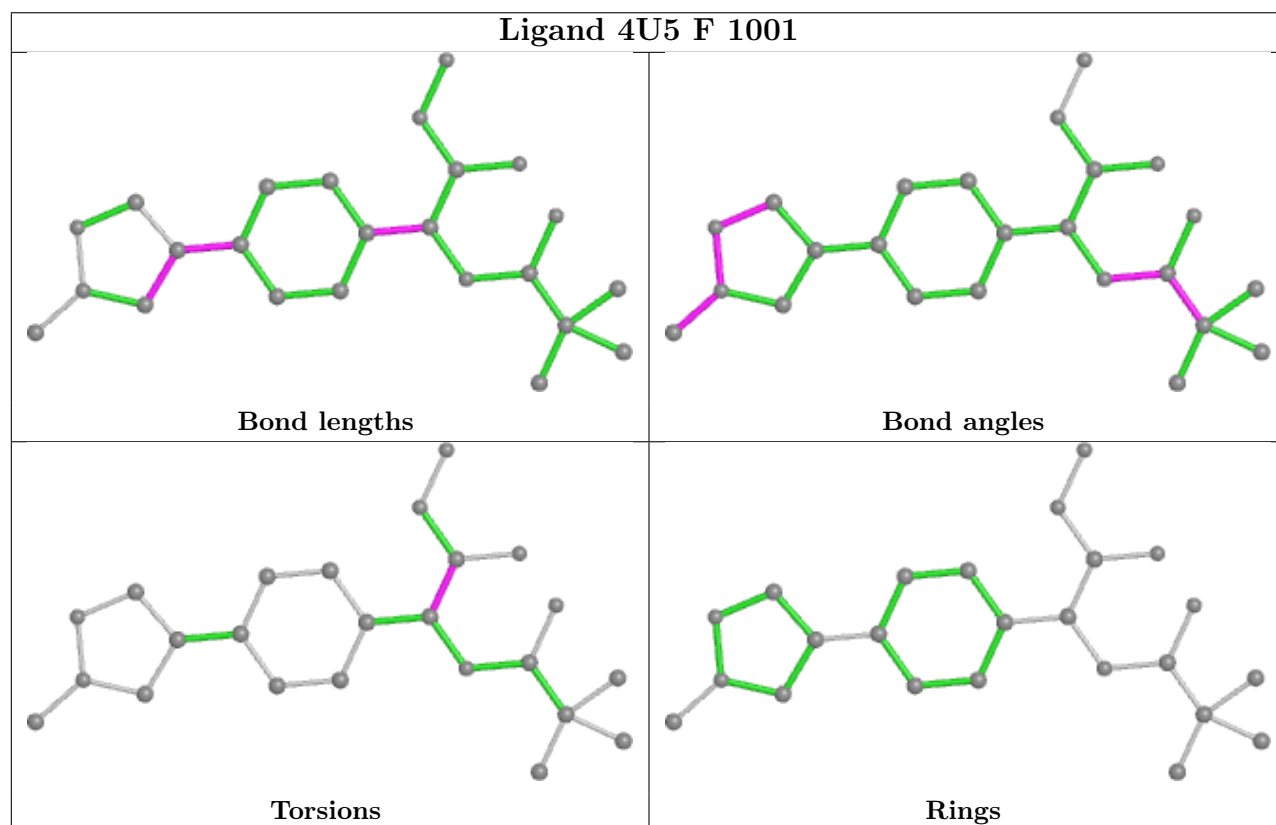
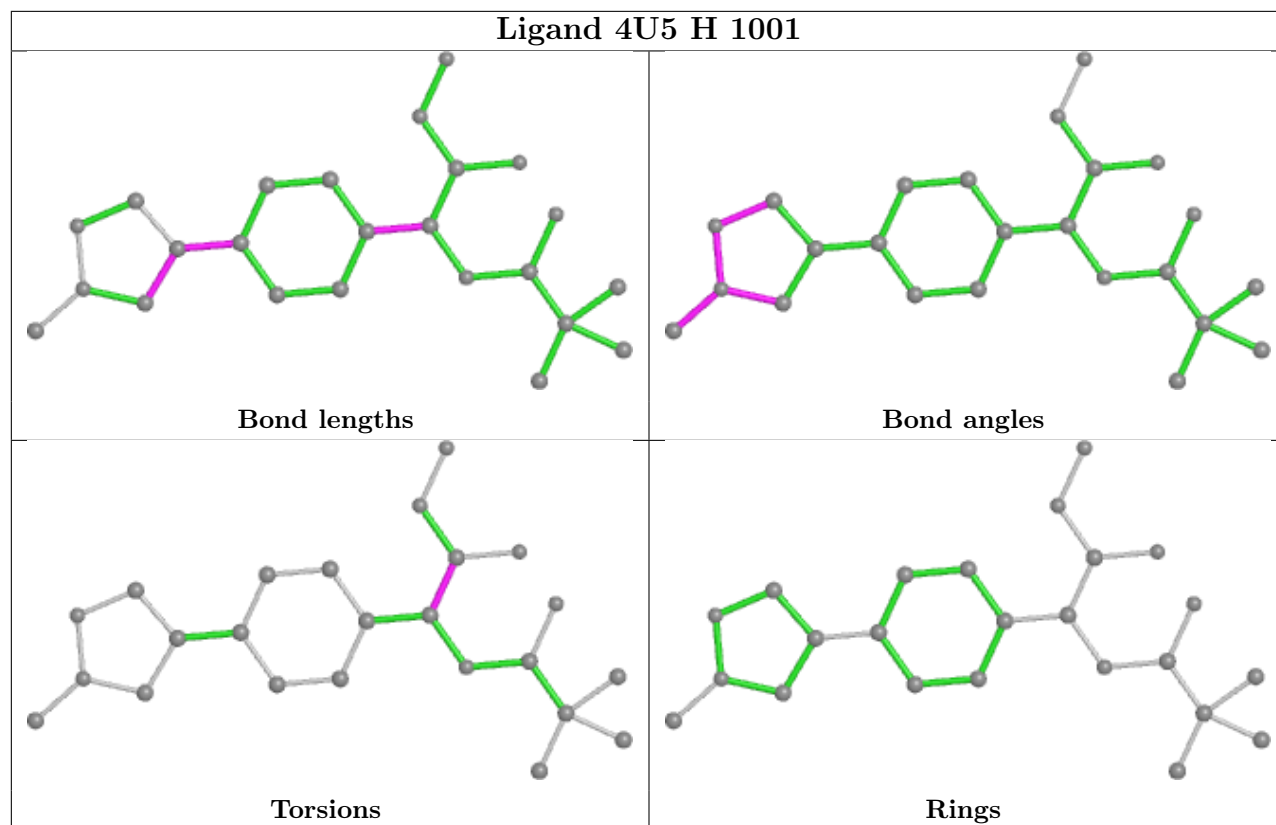
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1007	SO4	2	0
6	A	1009	1PE	1	0
4	D	1004	CO3	1	0
6	L	1008	1PE	2	0
6	K	1010	1PE	1	0
2	D	1001	4U5	1	0
6	H	1007	1PE	1	0
6	G	1007	1PE	1	0
6	K	1009	1PE	1	0
5	A	1005	SO4	1	0
6	B	1007	1PE	1	0
5	K	1007	SO4	1	0
6	B	1006	1PE	1	0
6	D	1007	1PE	2	0
4	E	1004	CO3	1	0
6	L	1009	1PE	1	0
6	J	1008	1PE	1	0

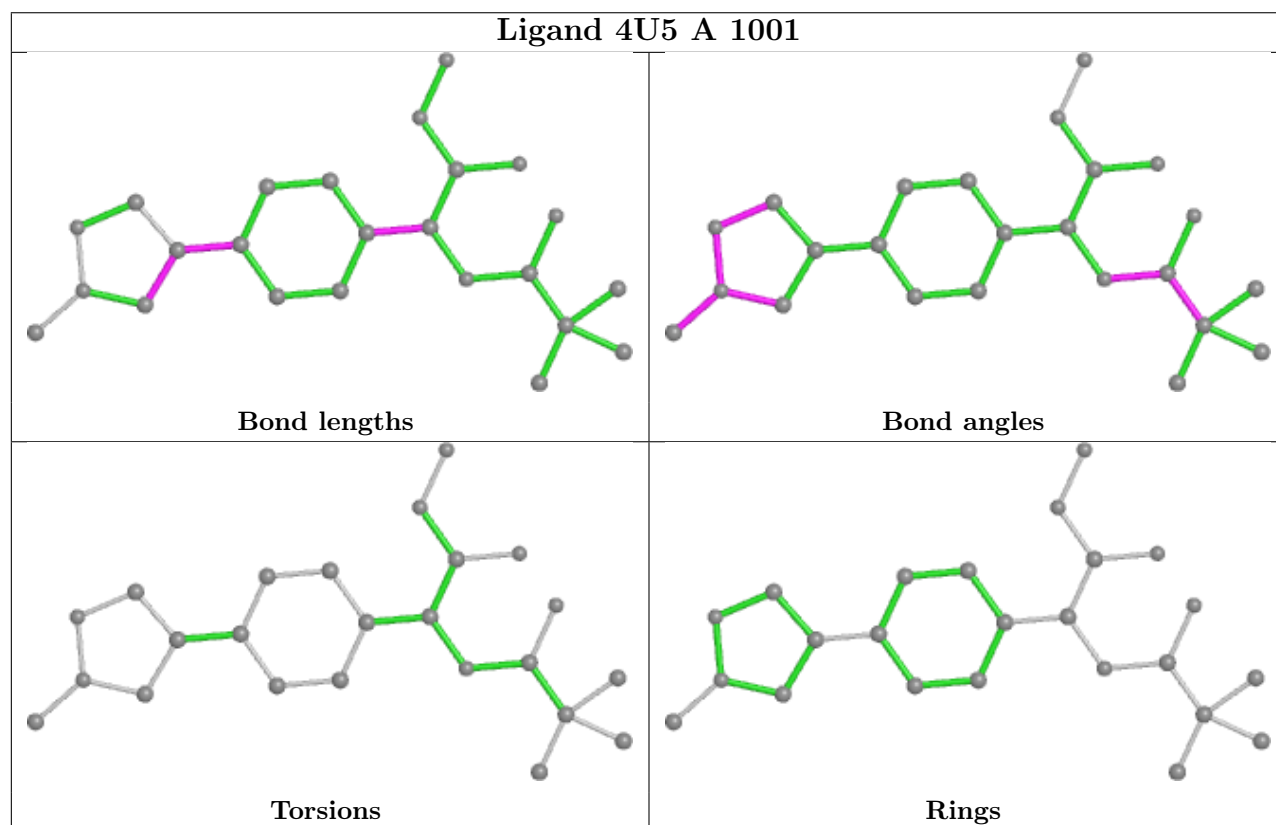
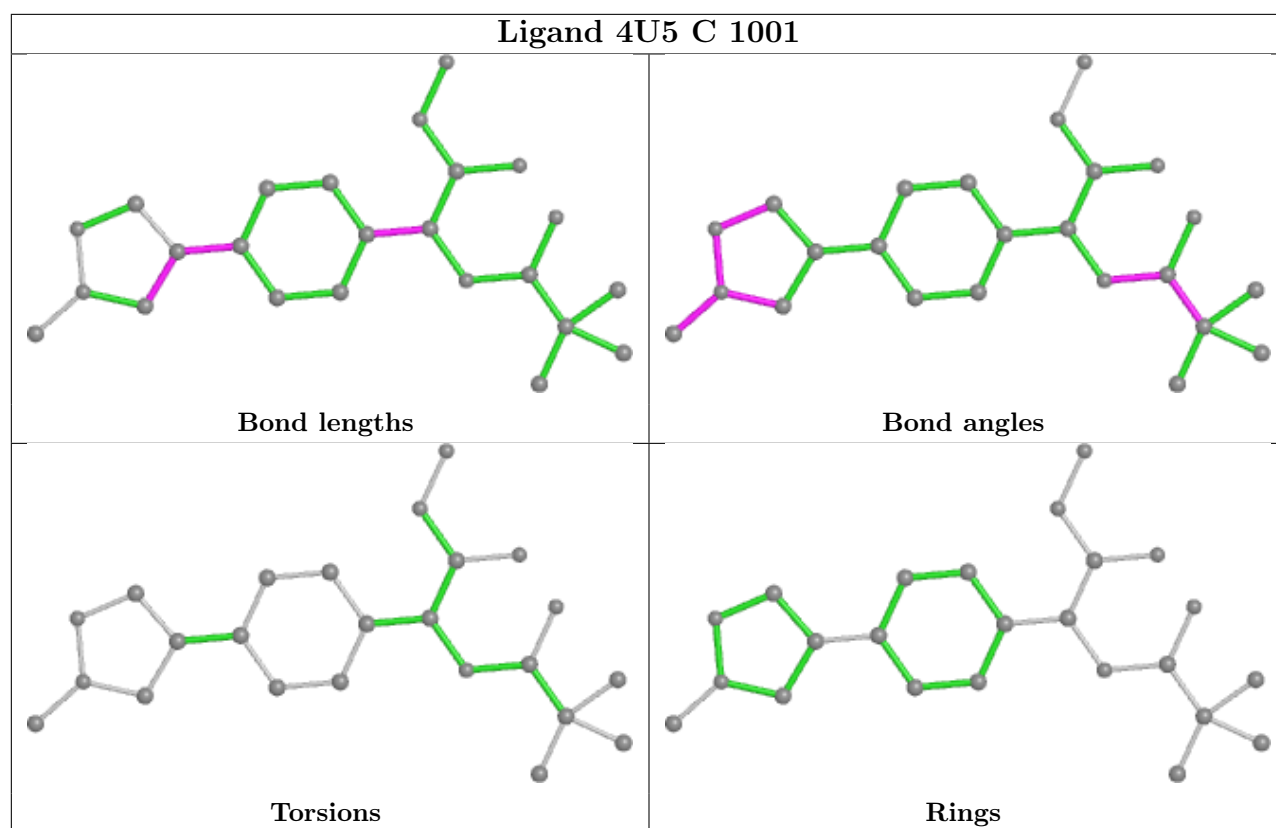
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

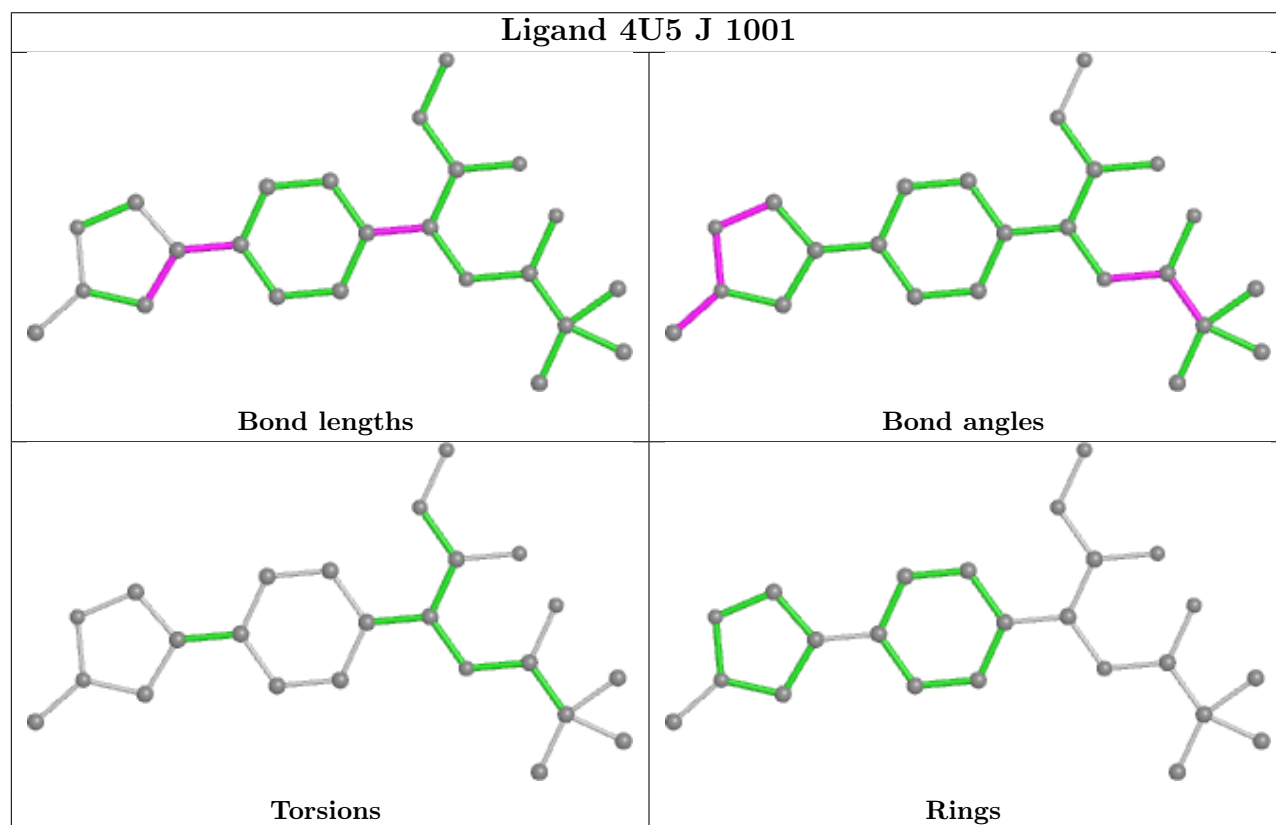
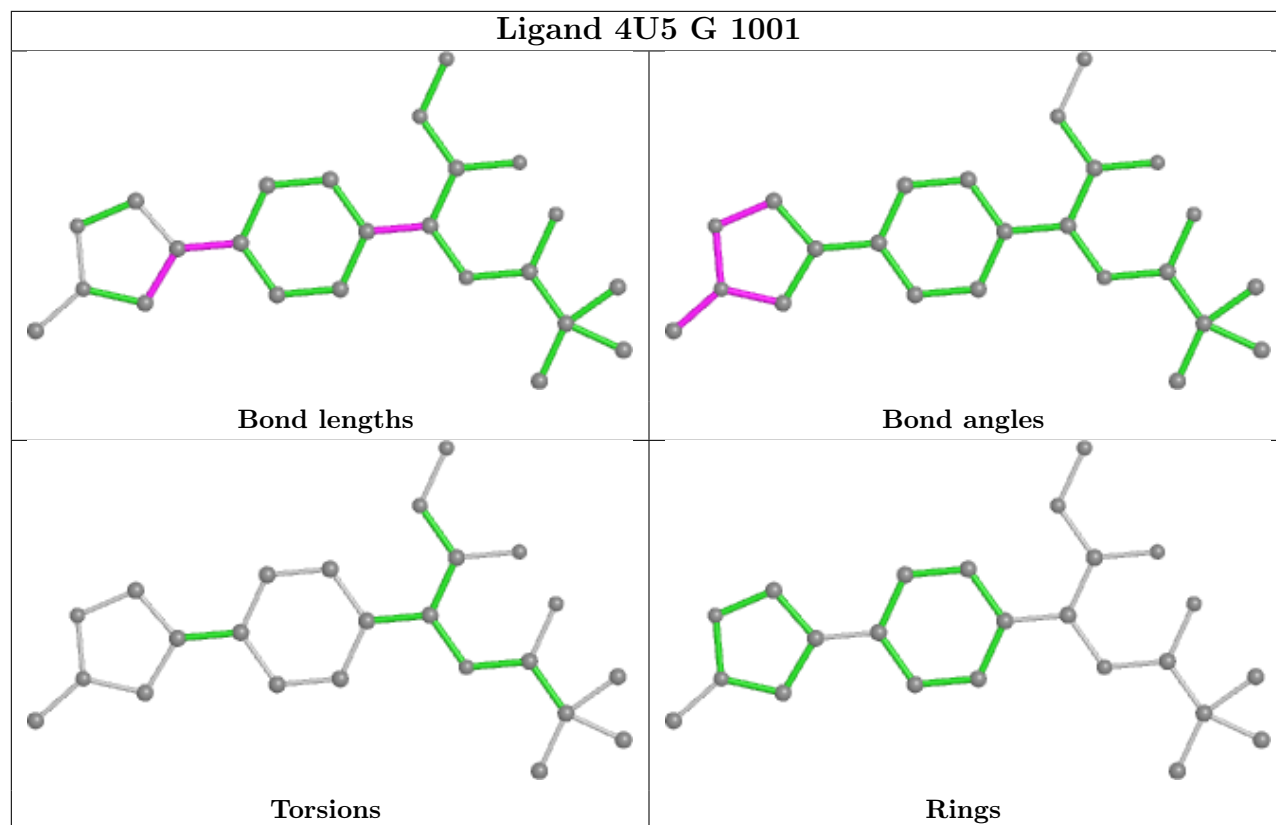












5.7 Other polymers [i](#)

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, 95th 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 ²)	Q<0.9
1	A	518/522 (99%)	-0.31	2 (0%) 92 93	16, 32, 57, 96	1 (0%)
1	B	516/522 (98%)	-0.12	14 (2%) 54 58	20, 35, 71, 104	0
1	C	516/522 (98%)	-0.30	2 (0%) 92 93	18, 33, 65, 106	4 (0%)
1	D	514/522 (98%)	-0.41	4 (0%) 86 87	19, 31, 54, 88	5 (0%)
1	E	508/522 (97%)	-0.46	1 (0%) 95 95	19, 32, 47, 80	2 (0%)
1	F	511/522 (97%)	-0.26	6 (1%) 79 80	21, 35, 65, 97	3 (0%)
1	G	519/522 (99%)	-0.31	3 (0%) 89 90	19, 32, 61, 113	3 (0%)
1	H	517/522 (99%)	-0.12	15 (2%) 51 55	18, 34, 75, 98	3 (0%)
1	I	517/522 (99%)	-0.29	3 (0%) 89 90	19, 32, 61, 77	2 (0%)
1	J	514/522 (98%)	-0.43	4 (0%) 86 87	17, 31, 52, 86	6 (1%)
1	K	509/522 (97%)	-0.45	0 100 100	20, 31, 46, 88	3 (0%)
1	L	510/522 (97%)	-0.18	12 (2%) 59 62	22, 39, 70, 88	5 (0%)
All	All	6169/6264 (98%)	-0.30	66 (1%) 80 82	16, 33, 64, 113	37 (0%)

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	260	ASN	4.9
1	F	551	VAL	4.5
1	B	255	THR	4.0
1	L	121	CYS	3.8
1	L	148	VAL	3.6

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th 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 ²)	Q<0.9
6	1PE	L	1008	7/16	0.77	0.35	64,70,83,86	0
6	1PE	L	1009	10/16	0.81	0.23	50,56,73,75	0
6	1PE	A	1009	12/16	0.82	0.19	52,56,62,62	0
7	GOL	G	1006	6/6	0.82	0.33	58,61,64,66	0
6	1PE	J	1007	11/16	0.83	0.20	41,55,63,63	0
6	1PE	L	1010	11/16	0.84	0.24	59,62,79,79	0
6	1PE	G	1007	9/16	0.84	0.24	51,56,62,62	0
5	SO4	J	1006	5/5	0.85	0.30	103,106,107,107	0
6	1PE	C	1006	13/16	0.86	0.19	51,55,58,58	0
6	1PE	I	1008	11/16	0.87	0.20	41,43,53,54	0
6	1PE	D	1007	10/16	0.87	0.17	36,49,56,58	0
6	1PE	H	1007	10/16	0.87	0.20	37,50,61,62	0
6	1PE	B	1007	10/16	0.88	0.23	55,70,76,76	0
6	1PE	J	1008	10/16	0.88	0.17	43,49,57,60	0
5	SO4	L	1006	5/5	0.89	0.27	104,104,105,107	0
5	SO4	A	1007	5/5	0.89	0.19	81,82,83,87	0
6	1PE	C	1007	9/16	0.89	0.17	42,45,49,50	0
6	1PE	K	1009	12/16	0.89	0.13	47,49,52,52	0
6	1PE	E	1007	12/16	0.90	0.14	45,50,57,59	0
6	1PE	I	1007	12/16	0.90	0.20	37,53,55,61	0
5	SO4	K	1008	5/5	0.90	0.18	93,96,97,97	0
6	1PE	G	1008	6/16	0.90	0.20	40,49,58,61	0
6	1PE	G	1009	6/16	0.90	0.18	45,48,49,53	0
5	SO4	K	1006	5/5	0.91	0.21	87,89,90,90	0
6	1PE	A	1008	9/16	0.91	0.20	42,45,49,51	0
5	SO4	H	1006	5/5	0.91	0.17	89,91,93,93	0
6	1PE	B	1006	10/16	0.91	0.22	41,51,68,69	0
6	1PE	E	1008	12/16	0.91	0.14	24,39,58,58	0
5	SO4	L	1005	5/5	0.91	0.16	100,101,101,102	0
5	SO4	D	1006	5/5	0.92	0.24	93,94,94,95	0
5	SO4	D	1005	5/5	0.92	0.19	91,93,93,94	0
6	1PE	D	1008	10/16	0.92	0.17	38,47,59,59	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	SO4	I	1005	5/5	0.93	0.14	103,104,105,105	0
5	SO4	A	1006	5/5	0.93	0.18	71,75,78,79	0
6	1PE	F	1006	10/16	0.93	0.13	42,44,57,59	0
6	1PE	K	1010	12/16	0.93	0.15	33,38,58,60	0
2	4U5	D	1001	24/24	0.94	0.18	25,37,44,47	0
2	4U5	H	1001	24/24	0.94	0.15	25,37,42,45	0
5	SO4	I	1006	5/5	0.94	0.23	92,92,93,93	0
5	SO4	C	1005	5/5	0.95	0.24	71,71,72,74	0
2	4U5	K	1001	24/24	0.95	0.14	25,34,38,44	0
5	SO4	L	1007	5/5	0.95	0.14	72,72,73,78	0
5	SO4	J	1005	5/5	0.95	0.22	84,84,85,87	0
2	4U5	B	1001	24/24	0.95	0.14	28,38,43,48	0
5	SO4	G	1005	5/5	0.95	0.14	79,83,84,85	0
2	4U5	J	1001	24/24	0.95	0.14	24,36,46,48	0
4	CO3	L	1004	4/4	0.96	0.15	27,32,34,34	0
5	SO4	A	1005	5/5	0.96	0.15	69,71,74,74	0
2	4U5	G	1001	24/24	0.96	0.14	25,36,39,41	0
2	4U5	C	1001	24/24	0.96	0.13	22,30,35,39	0
2	4U5	I	1001	24/24	0.96	0.13	22,34,40,45	0
2	4U5	E	1001	24/24	0.96	0.16	31,38,50,54	0
2	4U5	F	1001	24/24	0.96	0.14	30,36,45,52	0
5	SO4	E	1006	5/5	0.96	0.15	69,70,72,74	0
4	CO3	D	1004	4/4	0.96	0.13	33,37,38,40	0
4	CO3	E	1004	4/4	0.96	0.14	33,35,36,39	0
4	CO3	K	1004	4/4	0.96	0.17	32,34,34,34	0
5	SO4	K	1007	5/5	0.97	0.16	68,70,72,73	0
5	SO4	F	1005	5/5	0.97	0.16	69,70,71,72	0
2	4U5	A	1001	24/24	0.97	0.13	26,33,42,46	0
2	4U5	L	1001	24/24	0.97	0.13	29,38,45,48	0
4	CO3	J	1004	4/4	0.97	0.16	32,32,33,36	0
4	CO3	I	1004	4/4	0.98	0.09	29,35,36,37	0
3	ZN	J	1002	1/1	0.98	0.10	31,31,31,31	0
4	CO3	A	1004	4/4	0.98	0.13	32,35,37,37	0
4	CO3	B	1004	4/4	0.98	0.12	23,26,26,29	0
4	CO3	C	1004	4/4	0.98	0.14	30,31,31,36	0
3	ZN	B	1002	1/1	0.98	0.08	30,30,30,30	0
3	ZN	H	1002	1/1	0.98	0.07	30,30,30,30	0
5	SO4	B	1005	5/5	0.98	0.10	24,25,30,33	0
4	CO3	F	1004	4/4	0.98	0.17	21,24,26,27	0
4	CO3	G	1004	4/4	0.98	0.16	31,33,33,35	0
3	ZN	D	1002	1/1	0.99	0.11	32,32,32,32	0
3	ZN	E	1003	1/1	0.99	0.11	30,30,30,30	0

Continued on next page...

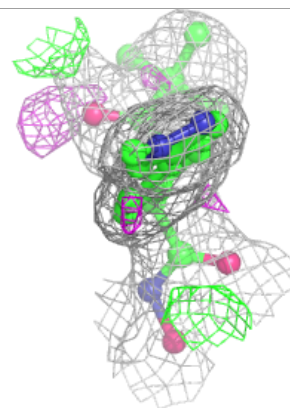
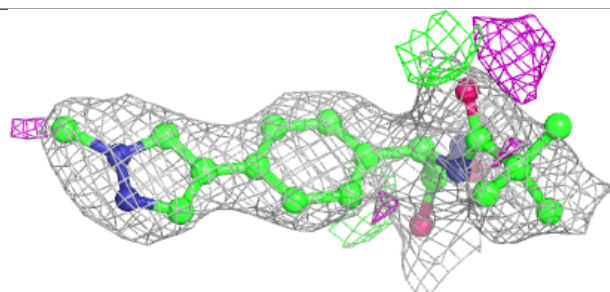
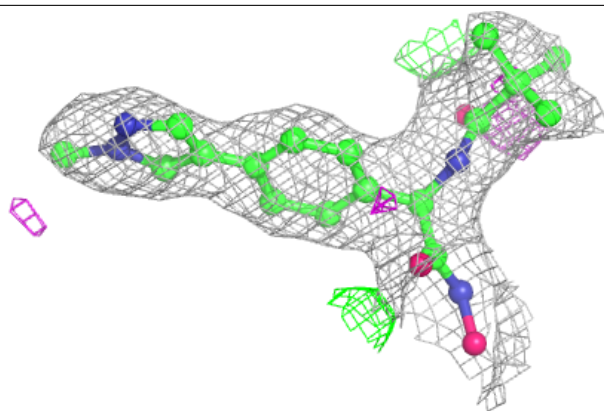
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	SO4	H	1005	5/5	0.99	0.09	24,27,29,30	0
3	ZN	F	1002	1/1	0.99	0.10	27,27,27,27	0
3	ZN	F	1003	1/1	0.99	0.07	30,30,30,30	0
4	CO3	H	1004	4/4	0.99	0.12	24,26,27,27	0
3	ZN	G	1002	1/1	0.99	0.09	32,32,32,32	0
3	ZN	G	1003	1/1	0.99	0.12	27,27,27,27	0
5	SO4	K	1005	5/5	0.99	0.12	31,32,33,33	0
3	ZN	A	1003	1/1	0.99	0.11	26,26,26,26	0
3	ZN	H	1003	1/1	0.99	0.08	23,23,23,23	0
3	ZN	I	1002	1/1	0.99	0.09	30,30,30,30	0
3	ZN	A	1002	1/1	0.99	0.09	31,31,31,31	0
3	ZN	K	1002	1/1	0.99	0.09	30,30,30,30	0
3	ZN	K	1003	1/1	0.99	0.10	31,31,31,31	0
3	ZN	L	1003	1/1	0.99	0.09	33,33,33,33	0
3	ZN	B	1003	1/1	0.99	0.08	22,22,22,22	0
3	ZN	C	1002	1/1	0.99	0.09	23,23,23,23	0
5	SO4	E	1005	5/5	0.99	0.13	30,30,32,32	0
3	ZN	C	1003	1/1	0.99	0.09	28,28,28,28	0
3	ZN	E	1002	1/1	1.00	0.10	32,32,32,32	0
3	ZN	I	1003	1/1	1.00	0.09	25,25,25,25	0
3	ZN	L	1002	1/1	1.00	0.10	30,30,30,30	0
3	ZN	D	1003	1/1	1.00	0.07	25,25,25,25	0
3	ZN	J	1003	1/1	1.00	0.08	25,25,25,25	0

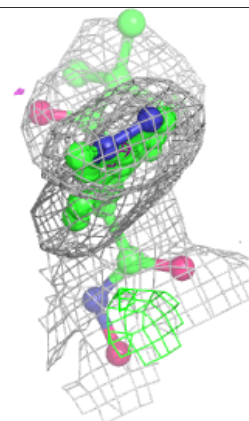
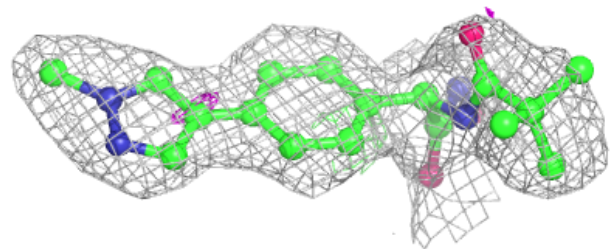
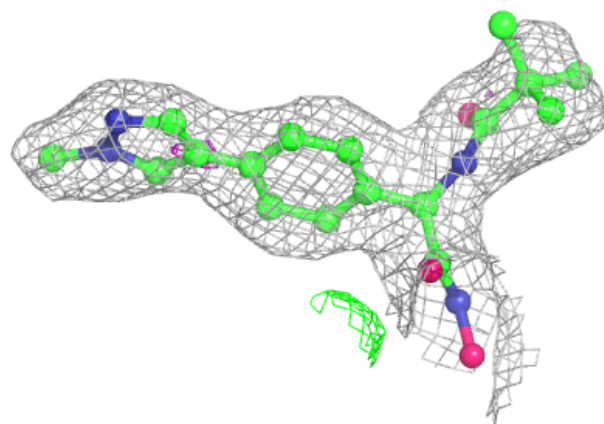
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 4U5 D 1001:

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

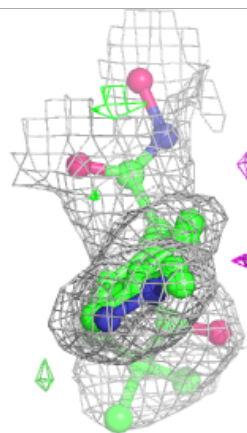
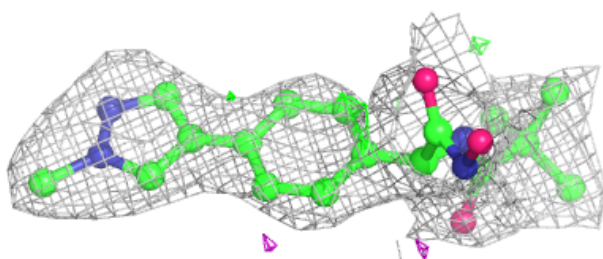
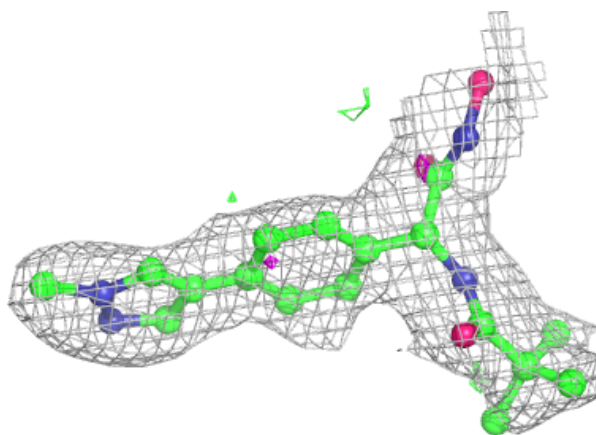
**Electron density around 4U5 H 1001:**

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



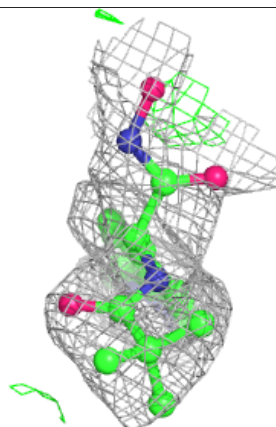
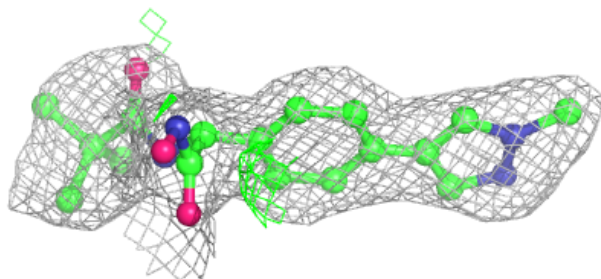
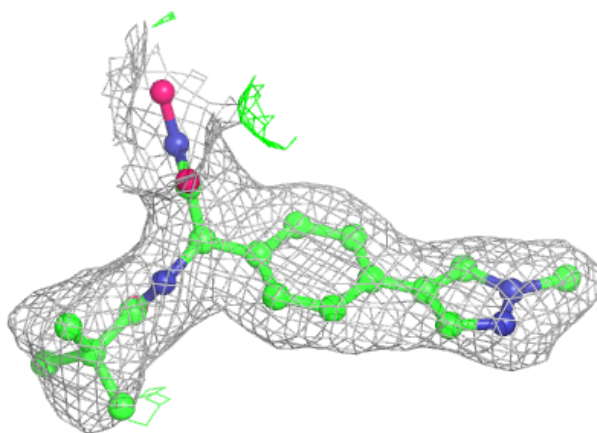
Electron density around 4U5 K 1001:

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



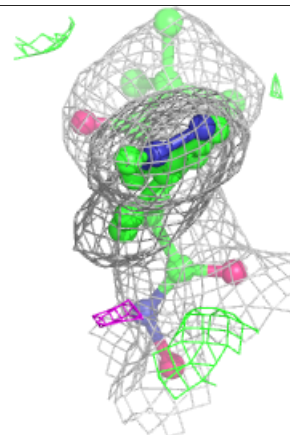
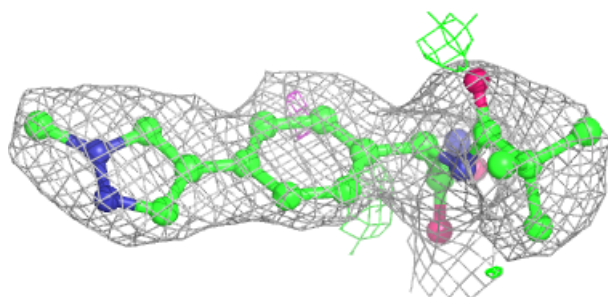
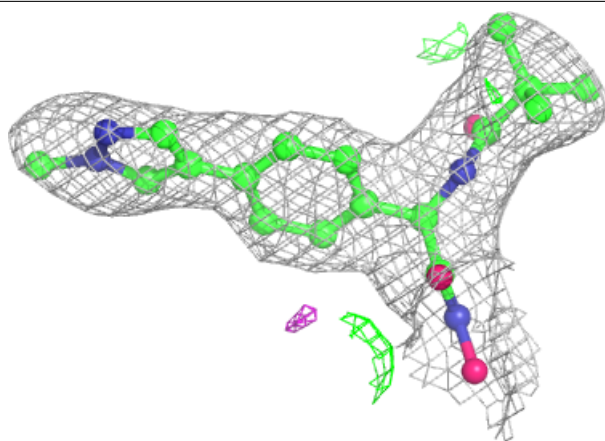
Electron density around 4U5 B 1001:

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



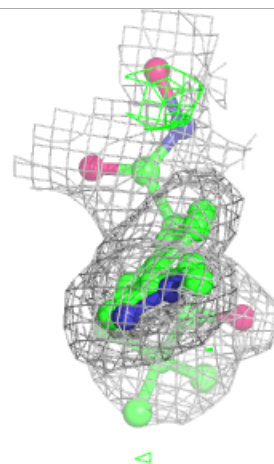
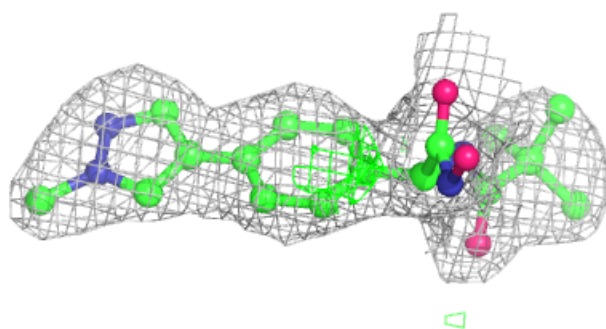
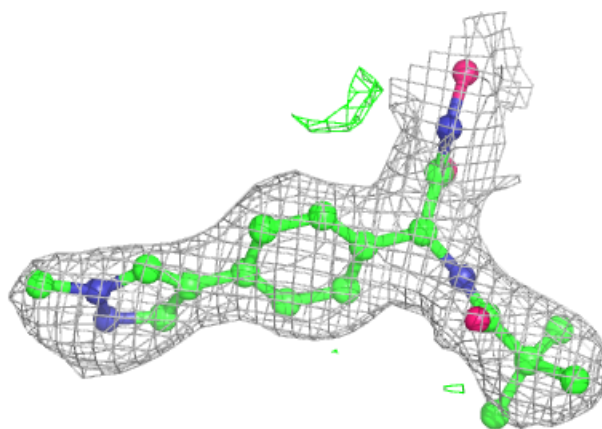
Electron density around 4U5 J 1001:

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



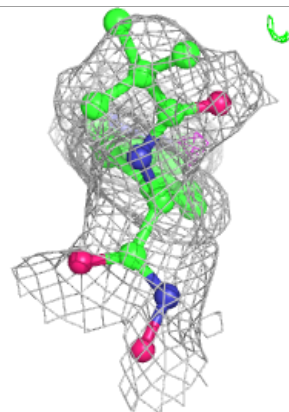
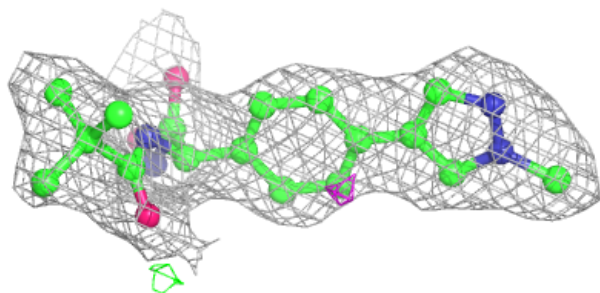
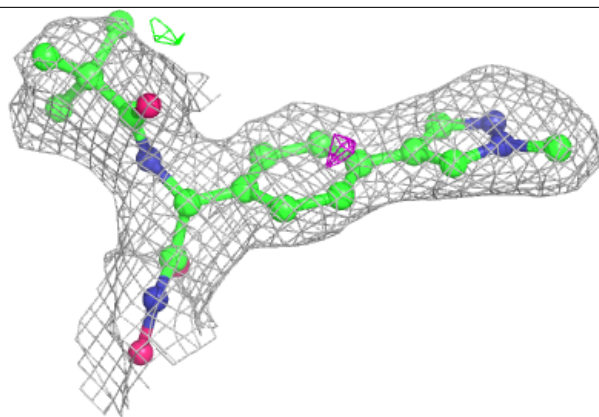
Electron density around 4U5 G 1001:

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

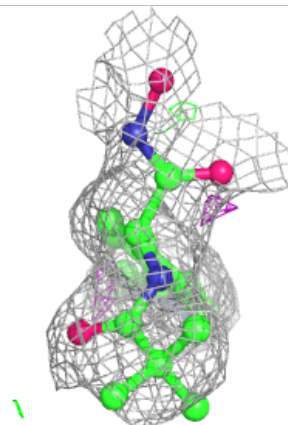
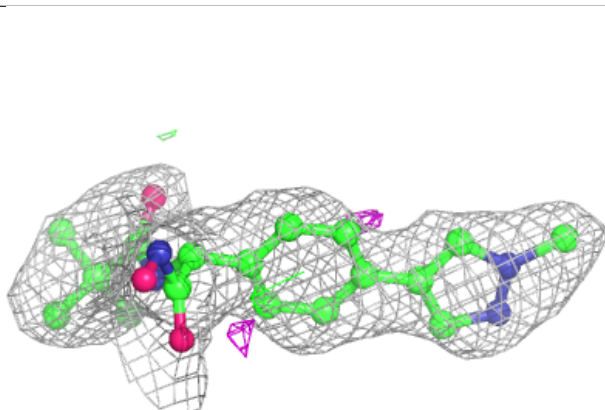
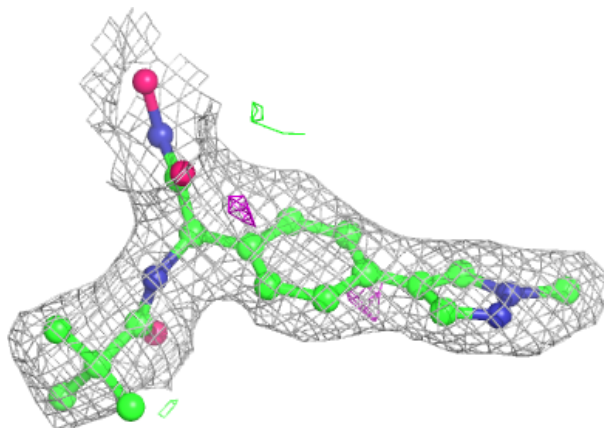


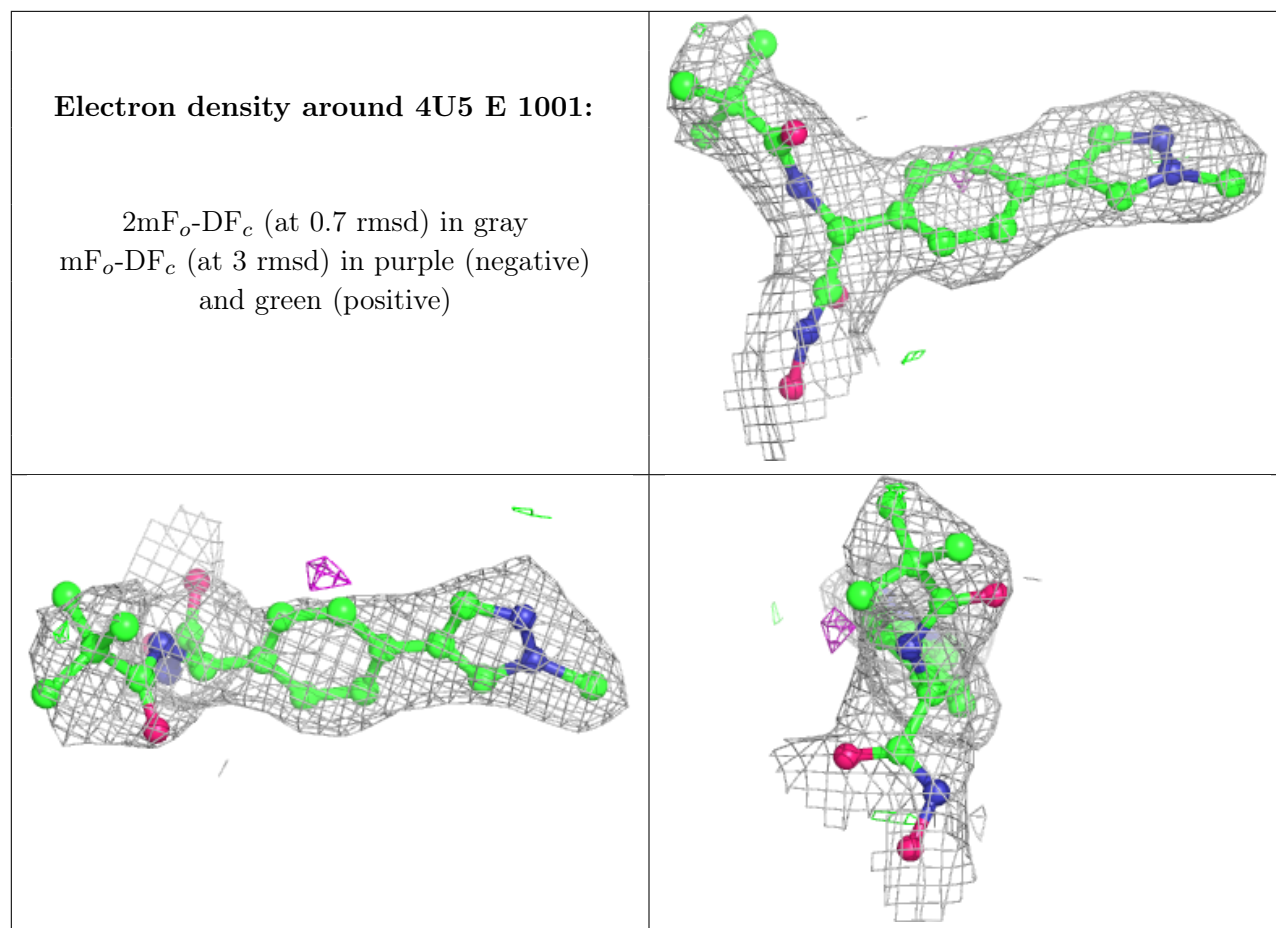
Electron density around 4U5 C 1001:

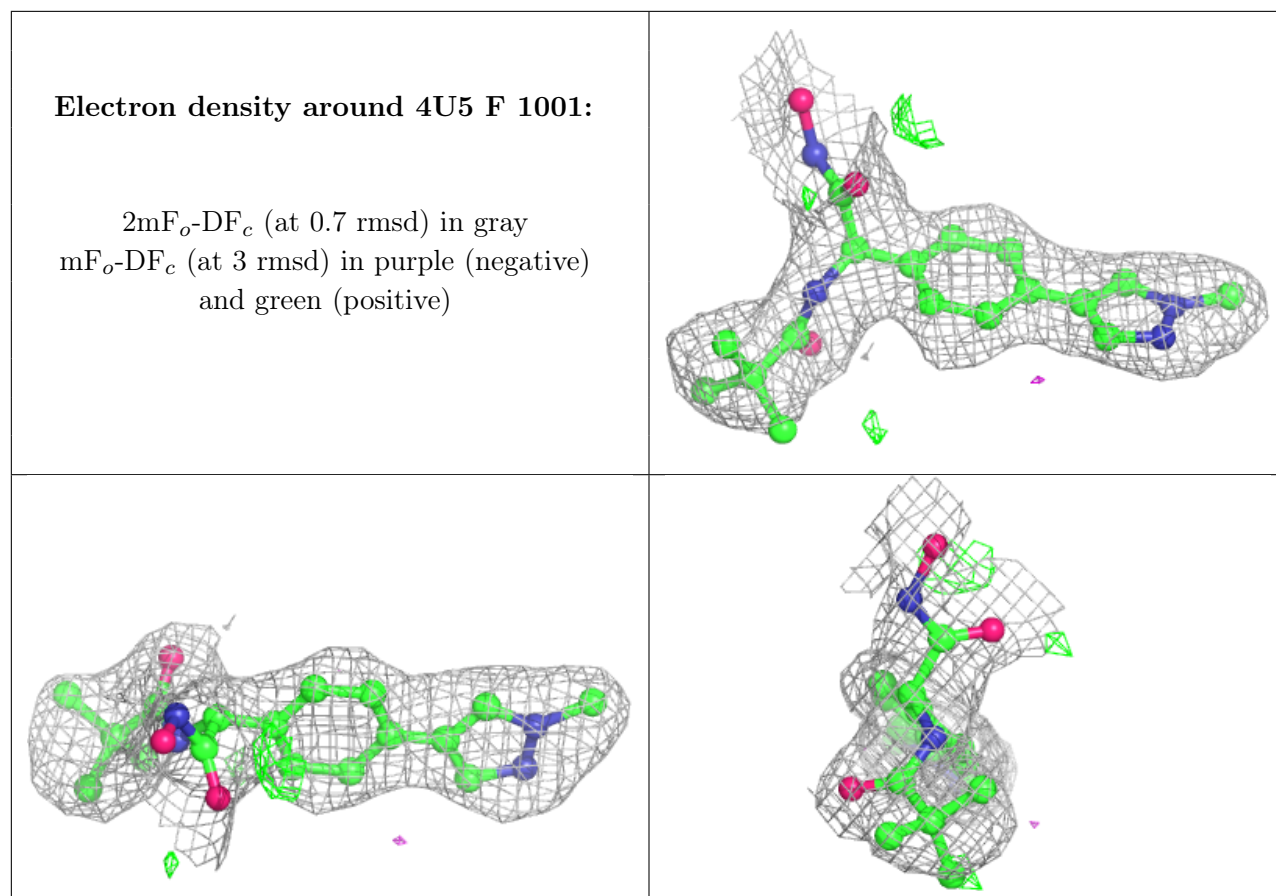
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around 4U5 I 1001:**

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

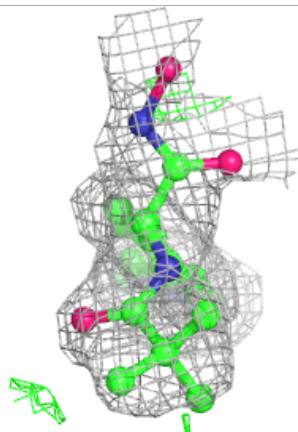
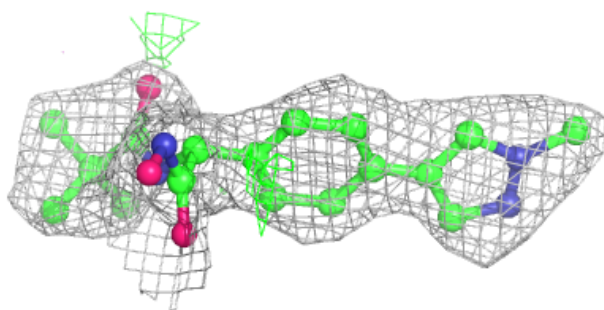
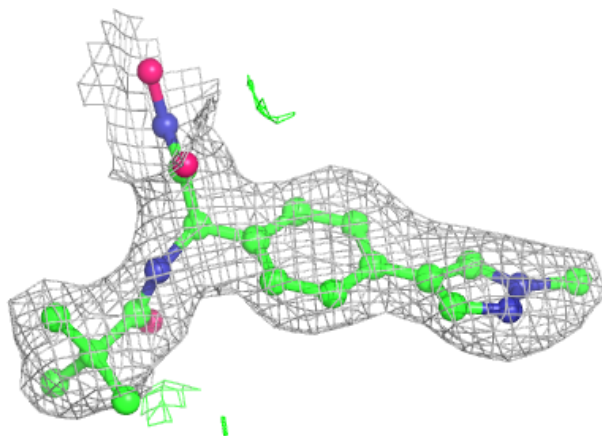


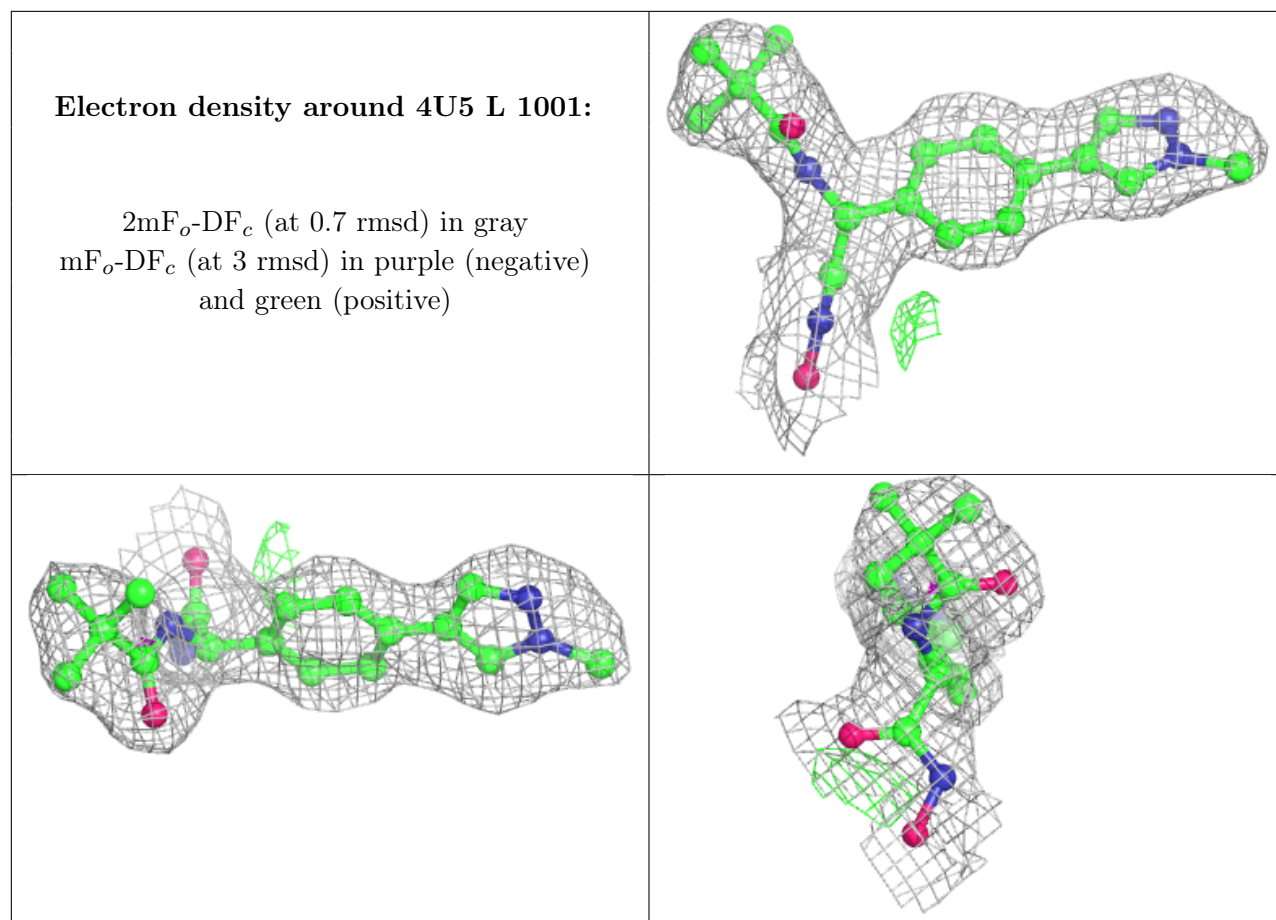




Electron density around 4U5 A 1001:

$2mF_o-DF_c$ (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.