



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2021 – 06:44 PM EDT

PDB ID : 3G42
Title : Crystal Structure of TACE with Tryptophan Sulfonamide Derivative Inhibitor
Authors : Xu, W.; Park, K.; Gopalsamy, A.; Aplasca, A.; Zhang, Y.H.; Levin, J.I.
Deposited on : 2009-02-03
Resolution : 2.10 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 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 : 2.23.2
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) : 2.23.2

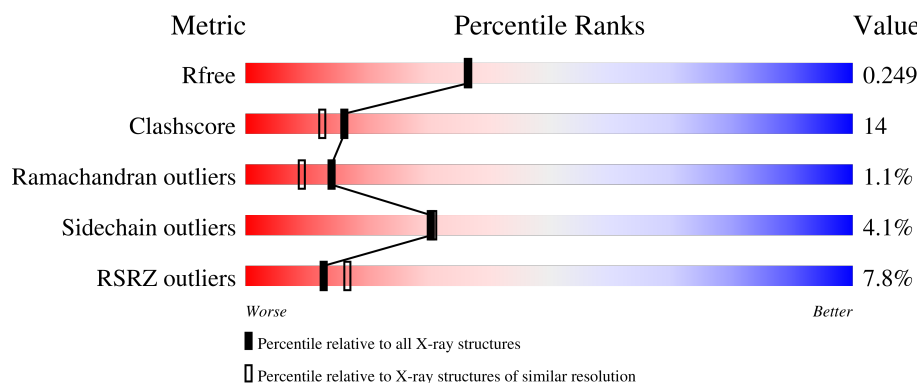
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	288	<div> <div>7%</div> <div> <div></div> <div>67%</div> <div>19%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	288	<div> <div>11%</div> <div> <div></div> <div>62%</div> <div>24%</div> <div>•</div> <div>12%</div> </div> </div>
1	C	288	<div> <div>4%</div> <div> <div></div> <div>69%</div> <div>18%</div> <div>•</div> <div>11%</div> </div> </div>
1	D	288	<div> <div>5%</div> <div> <div></div> <div>66%</div> <div>18%</div> <div>•</div> <div>12%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8642 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 ADAM 17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total 2016	C 1268	N 341	O 394	S 13	0	0	0
1	B	254	Total 2016	C 1268	N 341	O 394	S 13	0	0	0
1	C	256	Total 2031	C 1277	N 343	O 398	S 13	0	0	0
1	D	254	Total 2017	C 1270	N 341	O 393	S 13	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

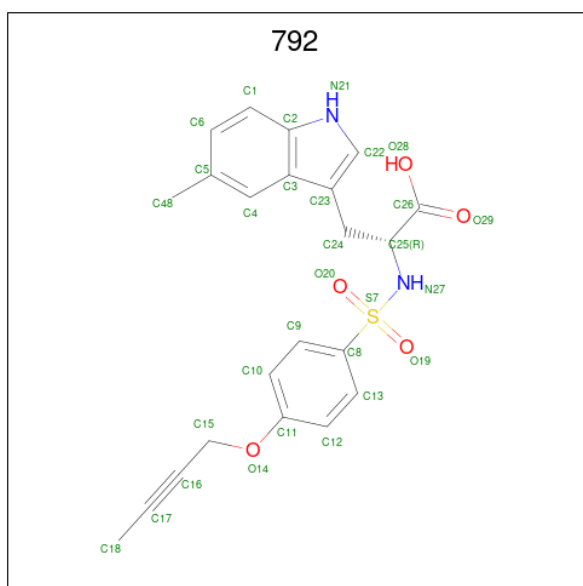
Chain	Residue	Modelled	Actual	Comment	Reference
A	266	ALA	SER	engineered mutation	UNP P78536
A	452	GLN	ASN	acetylation	UNP P78536
A	493	SER	-	expression tag	UNP P78536
A	494	HIS	-	expression tag	UNP P78536
A	495	HIS	-	expression tag	UNP P78536
A	496	HIS	-	expression tag	UNP P78536
A	497	HIS	-	expression tag	UNP P78536
A	498	HIS	-	expression tag	UNP P78536
A	499	HIS	-	expression tag	UNP P78536
B	266	ALA	SER	engineered mutation	UNP P78536
B	452	GLN	ASN	engineered mutation	UNP P78536
B	493	SER	-	expression tag	UNP P78536
B	494	HIS	-	expression tag	UNP P78536
B	495	HIS	-	expression tag	UNP P78536
B	496	HIS	-	expression tag	UNP P78536
B	497	HIS	-	expression tag	UNP P78536
B	498	HIS	-	expression tag	UNP P78536
B	499	HIS	-	expression tag	UNP P78536
C	266	ALA	SER	engineered mutation	UNP P78536
C	452	GLN	ASN	engineered mutation	UNP P78536
C	493	SER	-	expression tag	UNP P78536

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Chain	Residue	Modelled	Actual	Comment	Reference
C	494	HIS	-	expression tag	UNP P78536
C	495	HIS	-	expression tag	UNP P78536
C	496	HIS	-	expression tag	UNP P78536
C	497	HIS	-	expression tag	UNP P78536
C	498	HIS	-	expression tag	UNP P78536
C	499	HIS	-	expression tag	UNP P78536
D	266	ALA	SER	engineered mutation	UNP P78536
D	452	GLN	ASN	engineered mutation	UNP P78536
D	493	SER	-	expression tag	UNP P78536
D	494	HIS	-	expression tag	UNP P78536
D	495	HIS	-	expression tag	UNP P78536
D	496	HIS	-	expression tag	UNP P78536
D	497	HIS	-	expression tag	UNP P78536
D	498	HIS	-	expression tag	UNP P78536
D	499	HIS	-	expression tag	UNP P78536

- Molecule 2 is N-[[4-(but-2-yn-1-yloxy)phenyl]sulfonyl]-5-methyl-D-tryptophan (three-letter code: 792) (formula: C₂₂H₂₂N₂O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			29	21	2	5	1		
2	B	1	Total	C	N	O	S	0	0
			30	22	2	5	1		
2	C	1	Total	C	N	O	S	0	0
			30	22	2	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	S	0	0
			30	22	2	5	1		

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

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

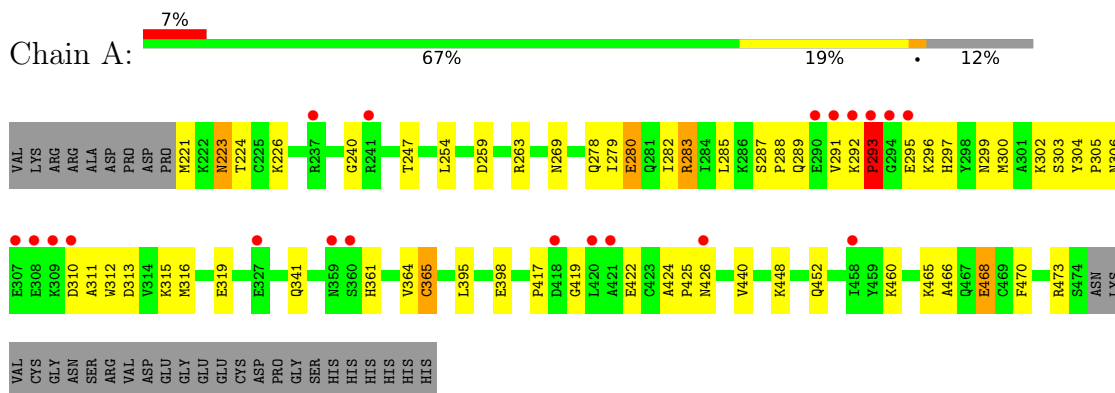
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	105	Total	O	0	0
			105	105		
4	B	97	Total	O	0	0
			97	97		
4	C	122	Total	O	0	0
			122	122		
4	D	115	Total	O	0	0
			115	115		

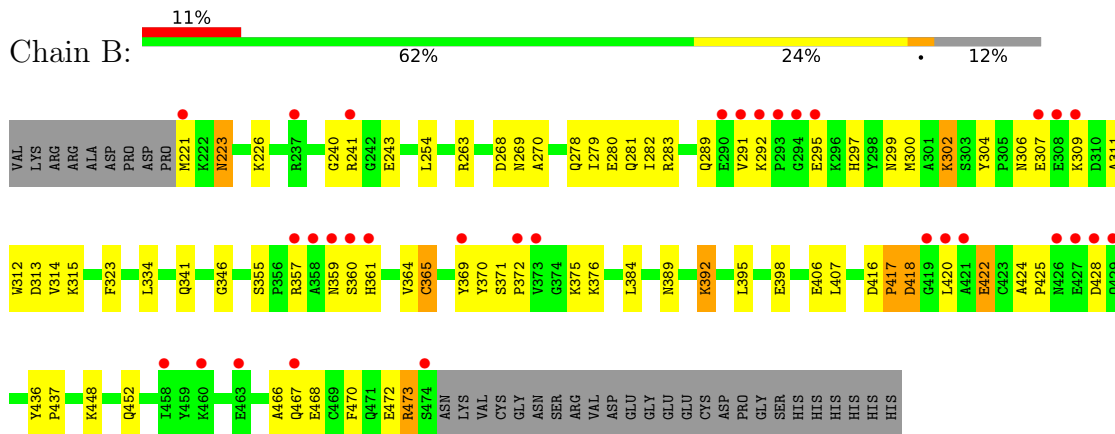
3 Residue-property plots [i](#)

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.

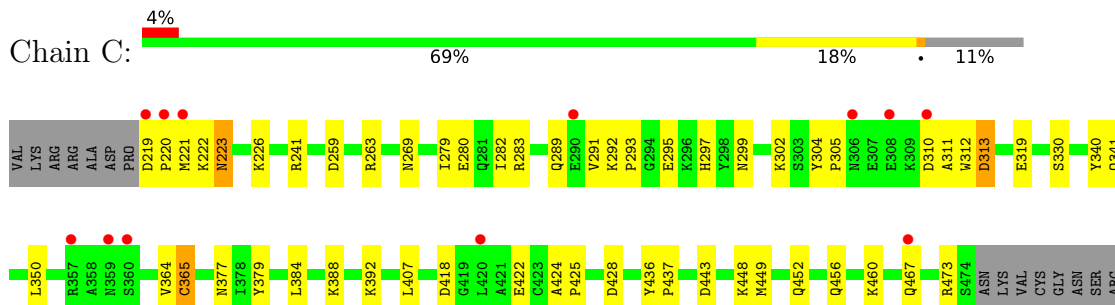
• Molecule 1: ADAM 17



• Molecule 1: ADAM 17



• Molecule 1: ADAM 17



VAL
ASP
GLU
GLY
GLU
GLU
CYS
ASP
PRO
GLY
SER
HIS
HIS
HIS
HIS
HIS

● Molecule 1: ADAM 17



VAL	LYS	ARG	ARG	ALA	ASP	PRO	ASP	P220	K221	K222	N223	K226	G240	T247	L254	N269	K273	I279	E280	Q281	I282	R283	I284	V291	K292	E295	K296	H297	T298	N299	M300	A301	K302	S303	Y304	A311	W312	D313	F323	E327	S330	Q341	A358	N359
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S360	H361	Y364	C365	P366	K367	A368	T369	P372	V373	G374	K375	Y379	L380	L395	T396	K397	E398	L401	V402	T403	L407	P417	D418	E422	C423	A424	P425	N426	E427	D428	Q429	Y436	P437	N449	Q452	K465	E472	R473	SER	ASN	LYS	VAL	CYS	GLY	ASN	SER
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ARG
VAL
ASP
GLU
GLY
GLU
GLU
CYS
ASP
PRO
GLY
SER
HIS
HIS
HIS
HIS

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	163.85Å 51.33Å 132.74Å 90.00° 102.64° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 19.98 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.5 (20.00-2.10) 98.4 (19.98-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.22 (at 2.09Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.218 , 0.257 0.211 , 0.249	Depositor DCC
R_{free} test set	3153 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	27.1	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 49.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8642	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 61.98 % 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 1.2067e-05. 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: 792, 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	0.34	0/2061	0.62	1/2780 (0.0%)
1	B	0.32	0/2061	0.58	0/2780
1	C	0.34	0/2077	0.62	1/2803 (0.0%)
1	D	0.34	0/2063	0.61	1/2783 (0.0%)
All	All	0.33	0/8262	0.61	3/11146 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	313	ASP	N-CA-C	-5.95	94.94	111.00
1	C	313	ASP	N-CA-C	-5.53	96.07	111.00
1	D	313	ASP	N-CA-C	-5.50	96.14	111.00

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	2016	0	1932	54	0
1	B	2016	0	1932	74	0
1	C	2031	0	1943	51	0
1	D	2017	0	1935	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	29	0	18	0	0
2	B	30	0	21	0	0
2	C	30	0	21	0	0
2	D	30	0	21	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	105	0	0	6	0
4	B	97	0	0	5	0
4	C	122	0	0	8	0
4	D	115	0	0	2	0
All	All	8642	0	7823	231	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 14.

The worst 5 of 231 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:C:291:VAL:HG22	1:C:295:GLU:HG3	1.29	1.11
1:B:311:ALA:HB2	1:B:341:GLN:HB2	1.46	0.98
1:D:291:VAL:HG13	1:D:295:GLU:HG3	1.46	0.98
1:B:263:ARG:HD3	1:B:473:ARG:HH21	1.35	0.89
1:A:263:ARG:HE	1:A:473:ARG:HH21	1.22	0.87

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	252/288 (88%)	237 (94%)	13 (5%)	2 (1%)	19	15
1	B	252/288 (88%)	240 (95%)	9 (4%)	3 (1%)	13	8
1	C	254/288 (88%)	244 (96%)	8 (3%)	2 (1%)	19	15
1	D	252/288 (88%)	244 (97%)	4 (2%)	4 (2%)	9	5
All	All	1010/1152 (88%)	965 (96%)	34 (3%)	11 (1%)	14	9

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	293	PRO
1	B	417	PRO
1	D	417	PRO
1	B	418	ASP
1	D	418	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	217/247 (88%)	209 (96%)	8 (4%)	34	35
1	B	217/247 (88%)	206 (95%)	11 (5%)	24	22
1	C	219/247 (89%)	212 (97%)	7 (3%)	39	41
1	D	217/247 (88%)	207 (95%)	10 (5%)	27	26
All	All	870/988 (88%)	834 (96%)	36 (4%)	30	31

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	281	GLN
1	D	429	GLN
1	D	283	ARG
1	D	359	ASN
1	B	392	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	361	HIS
1	D	429	GLN
1	D	471	GLN
1	B	297	HIS
1	B	281	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\# Z > 2$
2	792	C	3	3	28,32,32	1.96	10 (35%)	33,45,45	1.22	3 (9%)
2	792	B	2	3	28,32,32	1.96	11 (39%)	33,45,45	1.02	2 (6%)
2	792	A	1	3	27,31,32	2.06	10 (37%)	33,44,45	1.12	3 (9%)
2	792	D	4	3	28,32,32	1.93	9 (32%)	33,45,45	1.01	3 (9%)

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
2	792	C	3	3	-	3/18/24/24	0/3/3/3
2	792	B	2	3	-	3/18/24/24	0/3/3/3
2	792	A	1	3	-	3/18/23/24	0/3/3/3
2	792	D	4	3	-	3/18/24/24	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	792	C13-C8	3.73	1.44	1.38
2	B	2	792	C12-C11	3.54	1.45	1.38
2	D	4	792	C12-C11	3.53	1.45	1.38
2	C	3	792	C12-C11	3.50	1.45	1.38
2	B	2	792	C1-C6	3.49	1.44	1.36

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3	792	C8-S7-N27	3.77	113.00	107.78
2	A	1	792	O20-S7-O19	-3.49	115.26	119.55
2	C	3	792	O20-S7-O19	-3.42	115.34	119.55
2	D	4	792	O20-S7-O19	-3.29	115.50	119.55
2	B	2	792	O20-S7-O19	-3.18	115.64	119.55

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

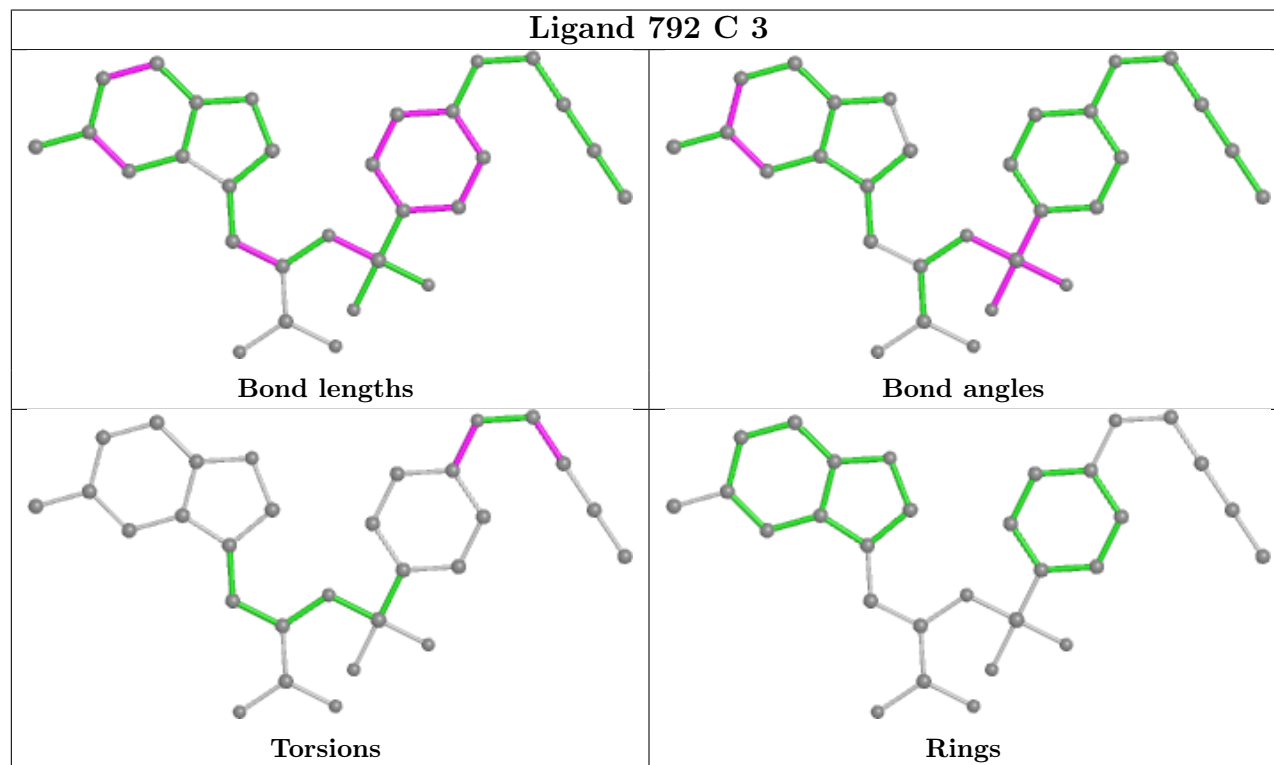
Mol	Chain	Res	Type	Atoms
2	A	1	792	C10-C11-O14-C15
2	A	1	792	C12-C11-O14-C15
2	C	3	792	C10-C11-O14-C15
2	C	3	792	C12-C11-O14-C15
2	B	2	792	C10-C11-O14-C15

There are no ring outliers.

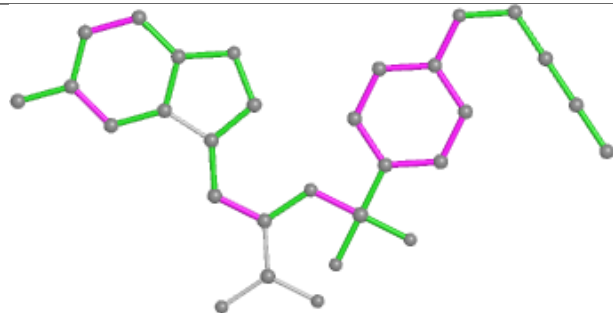
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

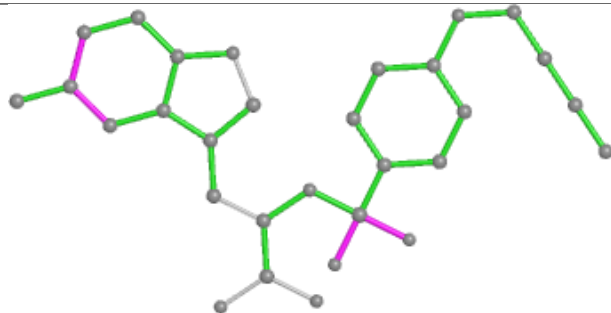
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



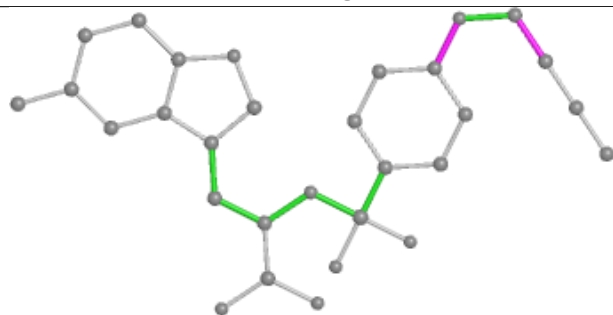
Ligand 792 B 2



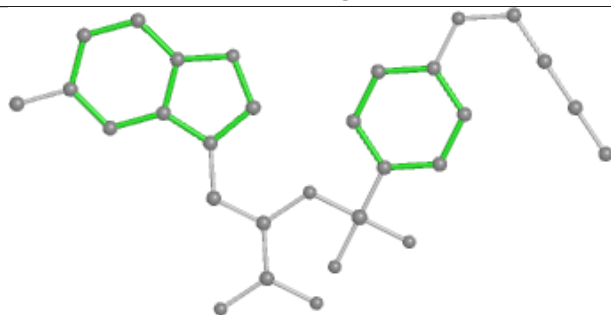
Bond lengths



Bond angles

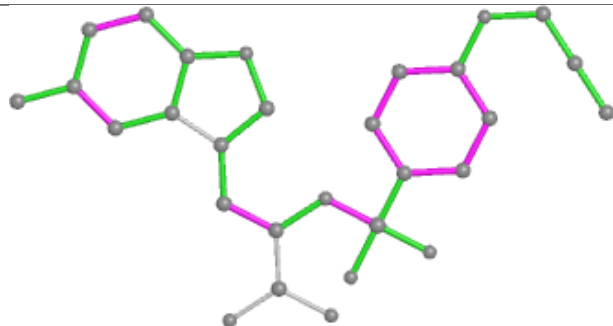


Torsions

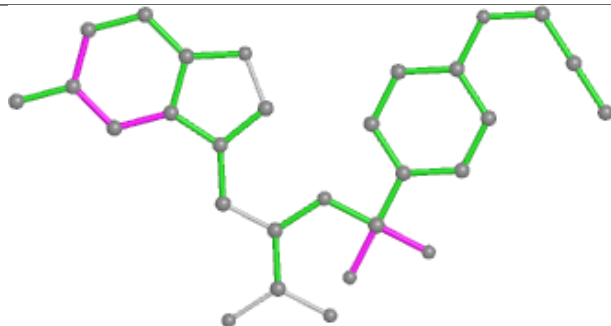


Rings

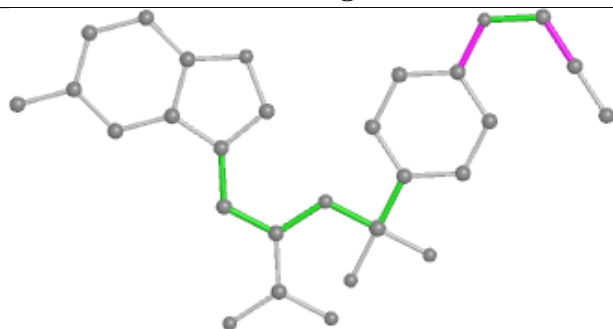
Ligand 792 A 1



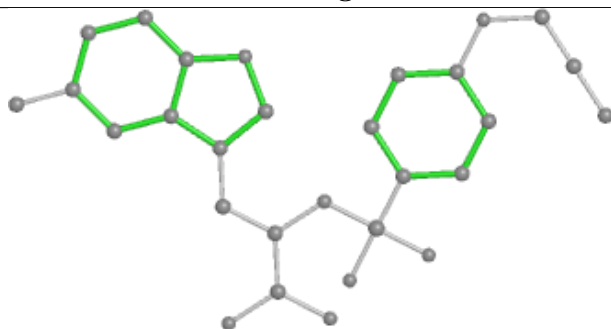
Bond lengths



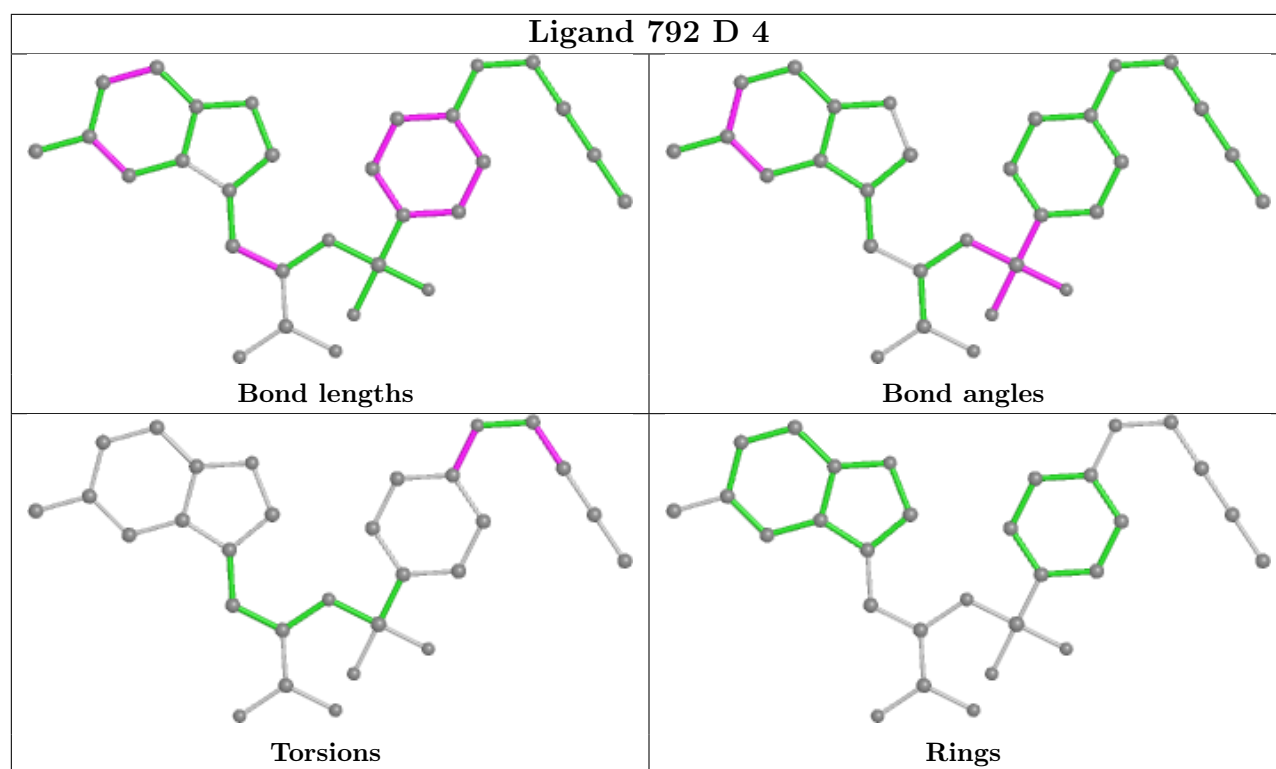
Bond angles



Torsions



Rings



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	254/288 (88%)	0.41	20 (7%) 12 16	17, 29, 50, 56	0
1	B	254/288 (88%)	0.59	32 (12%) 3 5	19, 34, 53, 59	0
1	C	256/288 (88%)	0.32	12 (4%) 31 37	17, 27, 47, 61	0
1	D	254/288 (88%)	0.35	15 (5%) 22 27	17, 29, 49, 56	0
All	All	1018/1152 (88%)	0.42	79 (7%) 13 17	17, 29, 50, 61	0

The worst 5 of 79 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	219	ASP	8.4
1	C	221	MET	5.4
1	B	359	ASN	5.0
1	D	221	MET	5.0
1	C	310	ASP	4.8

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](#)

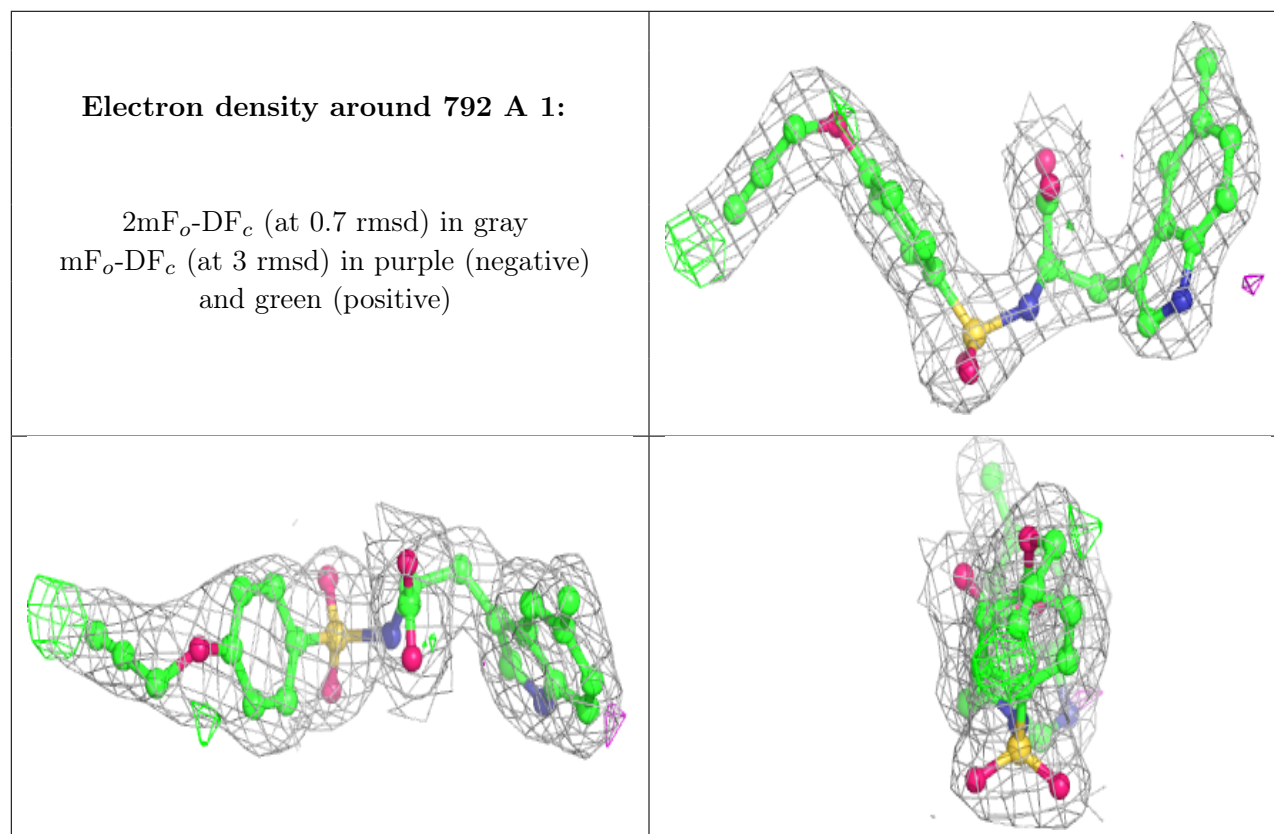
There are no monosaccharides in this entry.

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.

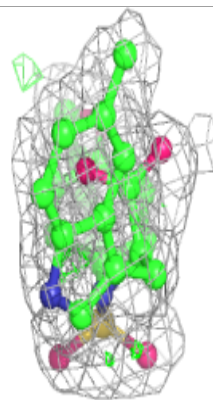
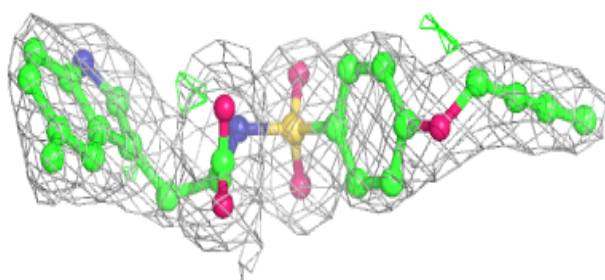
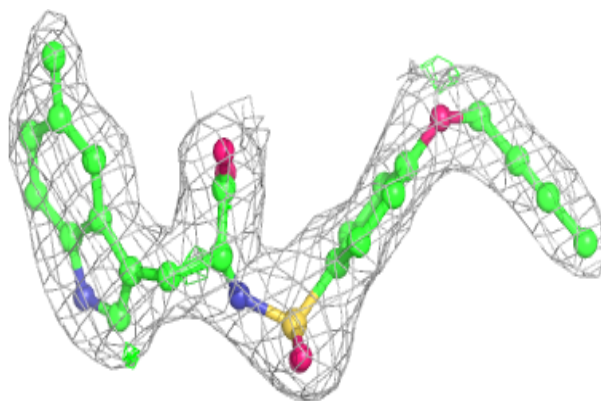
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	792	A	1	29/30	0.94	0.13	20,28,33,36	0
2	792	B	2	30/30	0.94	0.11	26,32,37,38	0
2	792	C	3	30/30	0.94	0.13	26,29,33,35	0
2	792	D	4	30/30	0.95	0.12	22,30,35,39	0
3	ZN	B	500	1/1	0.99	0.04	31,31,31,31	0
3	ZN	C	500	1/1	0.99	0.06	24,24,24,24	0
3	ZN	A	500	1/1	1.00	0.04	23,23,23,23	0
3	ZN	D	500	1/1	1.00	0.06	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.

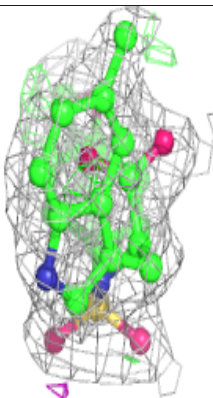
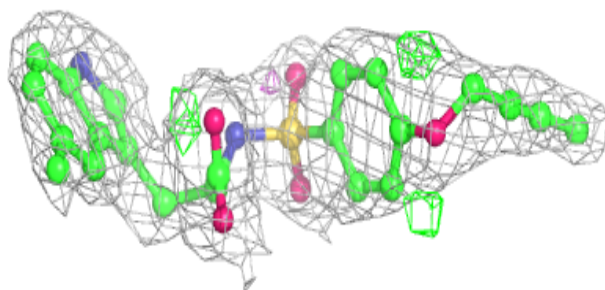
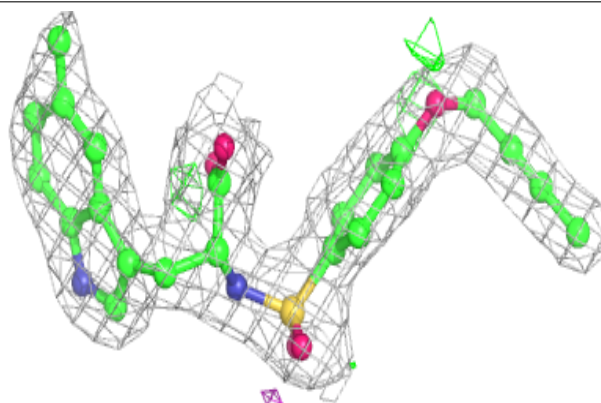


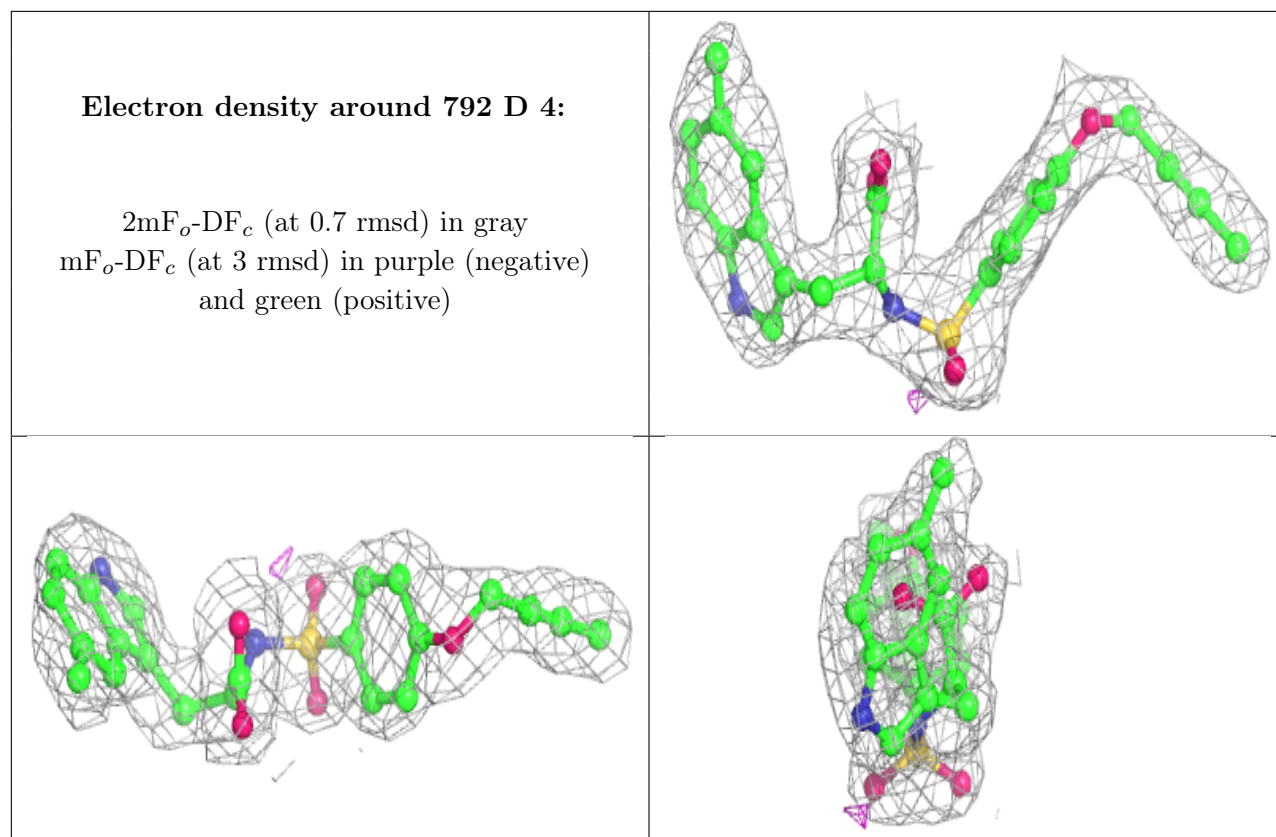
Electron density around 792 B 2:

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

**Electron density around 792 C 3:**

$2mF_o-DF_c$ (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.