wwPDB X-ray Structure Validation Summary Report (i)

Dec 24, 2024 – 06:11 PM EST

PDB ID	:	8W3D
Title	:	TAS-120 covalent structure with FGFR2 molecular brake mutant
Authors	:	Hoffman, I.D.; Nelson, K.J.; Bensen, D.C.; Bailey, J.B.
Deposited on	:	2024-02-22
Resolution	:	2.04 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 (i) 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 (i)) were used in the production of this report:

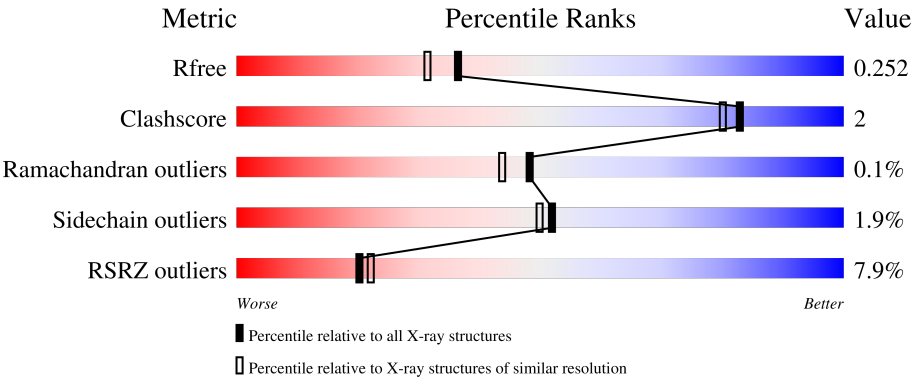
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	2096 (2.04-2.04)
Clashscore	180529	2229 (2.04-2.04)
Ramachandran outliers	177936	2217 (2.04-2.04)
Sidechain outliers	177891	2217 (2.04-2.04)
RSRZ outliers	164620	2096 (2.04-2.04)

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 <=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	324	8% 86% 6% 8%
1	B	324	7% 83% 5% 12%
1	C	324	5% 89% • • 7%
1	D	324	8% 83% 8% • 9%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10120 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 Fibroblast growth factor receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	1	0
			2393	1526	404	440	23			
1	B	286	Total	C	N	O	S	0	2	0
			2292	1464	389	417	22			
1	C	300	Total	C	N	O	S	0	4	0
			2416	1540	407	446	23			
1	D	296	Total	C	N	O	S	0	3	0
			2379	1518	401	438	22			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	445	MET	-	initiating methionine	UNP P21802
A	446	GLY	-	expression tag	UNP P21802
A	447	SER	-	expression tag	UNP P21802
A	448	SER	-	expression tag	UNP P21802
A	449	HIS	-	expression tag	UNP P21802
A	450	HIS	-	expression tag	UNP P21802
A	451	HIS	-	expression tag	UNP P21802
A	452	HIS	-	expression tag	UNP P21802
A	453	HIS	-	expression tag	UNP P21802
A	454	HIS	-	expression tag	UNP P21802
A	455	SER	-	expression tag	UNP P21802
A	456	GLN	-	expression tag	UNP P21802
A	457	ASP	-	expression tag	UNP P21802
A	549	LYS	ASN	engineered mutation	UNP P21802
A	650	VAL	ASP	engineered mutation	UNP P21802
B	445	MET	-	initiating methionine	UNP P21802
B	446	GLY	-	expression tag	UNP P21802
B	447	SER	-	expression tag	UNP P21802
B	448	SER	-	expression tag	UNP P21802
B	449	HIS	-	expression tag	UNP P21802
B	450	HIS	-	expression tag	UNP P21802

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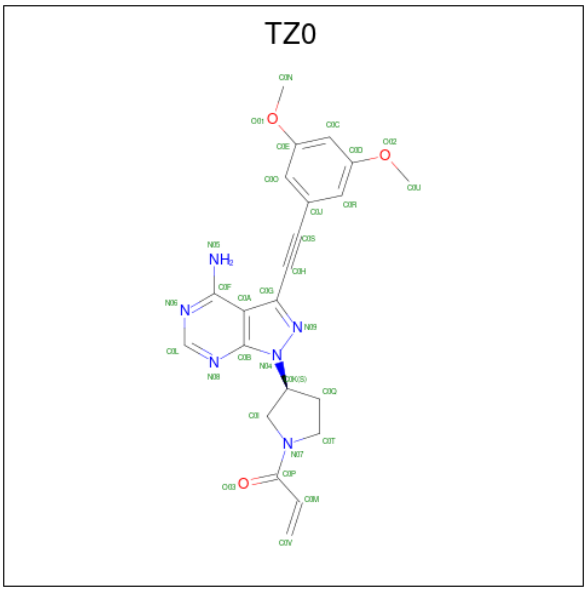
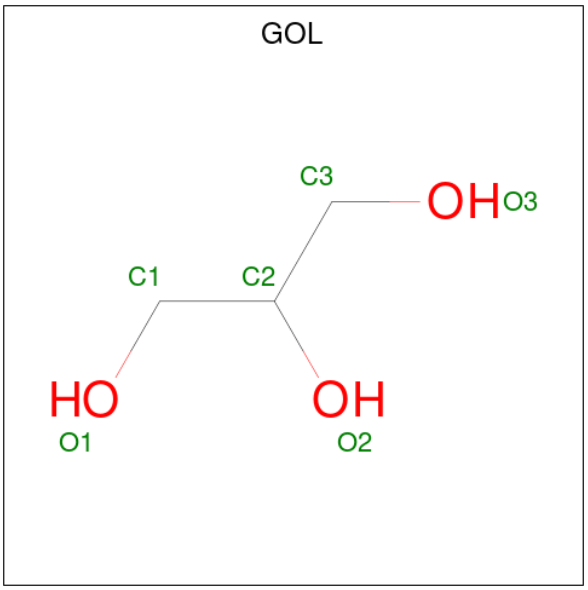
Chain	Residue	Modelled	Actual	Comment	Reference
B	451	HIS	-	expression tag	UNP P21802
B	452	HIS	-	expression tag	UNP P21802
B	453	HIS	-	expression tag	UNP P21802
B	454	HIS	-	expression tag	UNP P21802
B	455	SER	-	expression tag	UNP P21802
B	456	GLN	-	expression tag	UNP P21802
B	457	ASP	-	expression tag	UNP P21802
B	549	LYS	ASN	engineered mutation	UNP P21802
B	650	VAL	ASP	engineered mutation	UNP P21802
C	445	MET	-	initiating methionine	UNP P21802
C	446	GLY	-	expression tag	UNP P21802
C	447	SER	-	expression tag	UNP P21802
C	448	SER	-	expression tag	UNP P21802
C	449	HIS	-	expression tag	UNP P21802
C	450	HIS	-	expression tag	UNP P21802
C	451	HIS	-	expression tag	UNP P21802
C	452	HIS	-	expression tag	UNP P21802
C	453	HIS	-	expression tag	UNP P21802
C	454	HIS	-	expression tag	UNP P21802
C	455	SER	-	expression tag	UNP P21802
C	456	GLN	-	expression tag	UNP P21802
C	457	ASP	-	expression tag	UNP P21802
C	549	LYS	ASN	engineered mutation	UNP P21802
C	650	VAL	ASP	engineered mutation	UNP P21802
D	445	MET	-	initiating methionine	UNP P21802
D	446	GLY	-	expression tag	UNP P21802
D	447	SER	-	expression tag	UNP P21802
D	448	SER	-	expression tag	UNP P21802
D	449	HIS	-	expression tag	UNP P21802
D	450	HIS	-	expression tag	UNP P21802
D	451	HIS	-	expression tag	UNP P21802
D	452	HIS	-	expression tag	UNP P21802
D	453	HIS	-	expression tag	UNP P21802
D	454	HIS	-	expression tag	UNP P21802
D	455	SER	-	expression tag	UNP P21802
D	456	GLN	-	expression tag	UNP P21802
D	457	ASP	-	expression tag	UNP P21802
D	549	LYS	ASN	engineered mutation	UNP P21802
D	650	VAL	ASP	engineered mutation	UNP P21802

- Molecule 2 is 1-[(3S)-3-{4-amino-3-[(3,5-dimethoxyphenyl)ethynyl]-1H-pyrazolo[3,4-d]pyrimidin-1-yl}pyrrolidin-1-yl]prop-2-en-1-one (three-letter code: TZ0) (formula: $C_{22}H_{22}N_6O_3$) (labeled as "Ligand of Interest" by depositor).



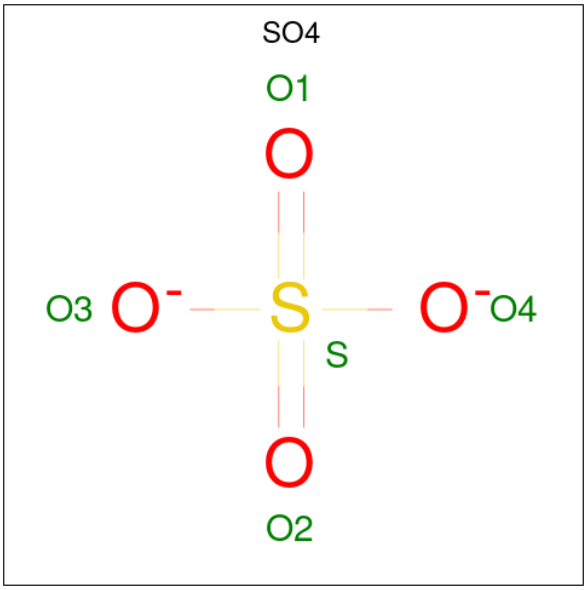
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			31	22	6	3		
2	B	1	Total	C	N	O	0	0
			31	22	6	3		
2	C	1	Total	C	N	O	0	0
			31	22	6	3		
2	D	1	Total	C	N	O	0	0
			31	22	6	3		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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

- Molecule 5 is water.

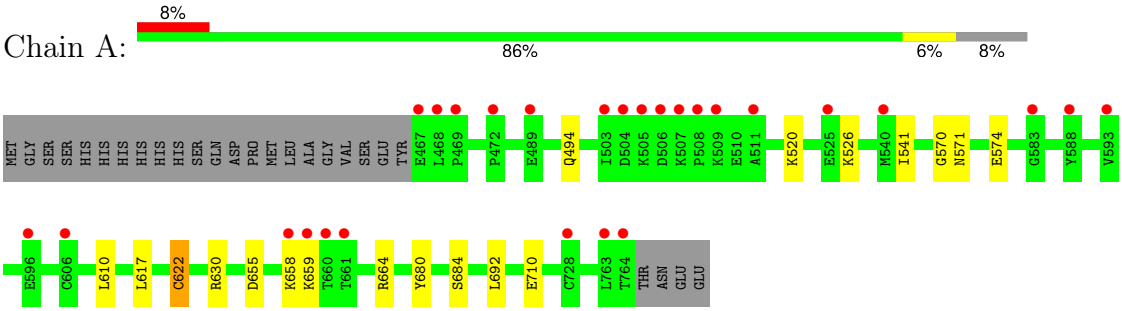
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	100	Total O 100 100	0	0
5	B	104	Total O 104 104	0	0
5	C	109	Total O 109 109	0	0
5	D	134	Total O 134 134	0	0

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.

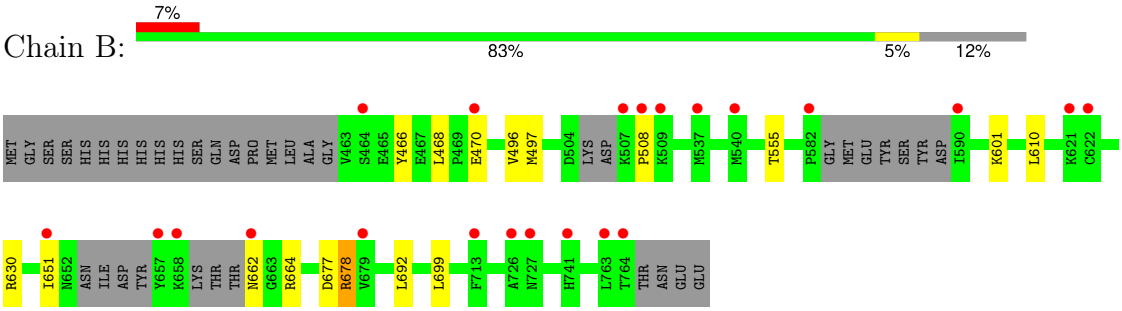
• Molecule 1: Fibroblast growth factor receptor 2

Chain A:



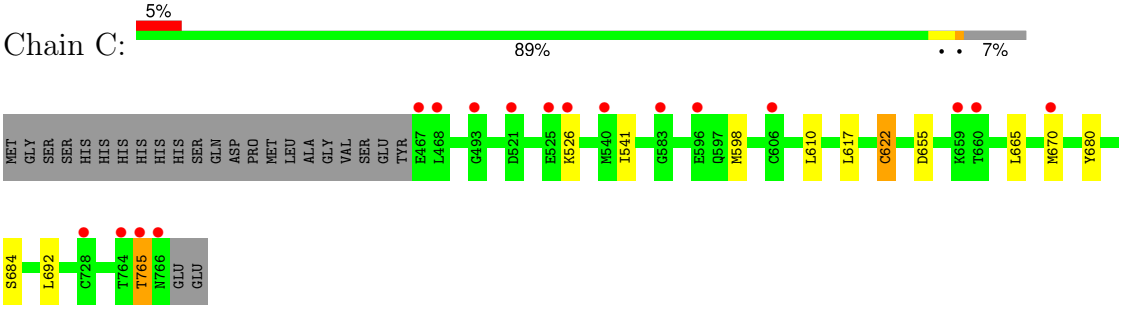
• Molecule 1: Fibroblast growth factor receptor 2

Chain B:



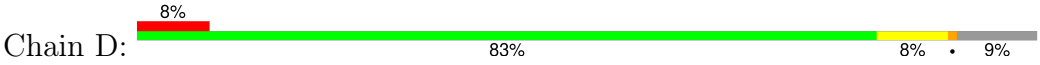
• Molecule 1: Fibroblast growth factor receptor 2

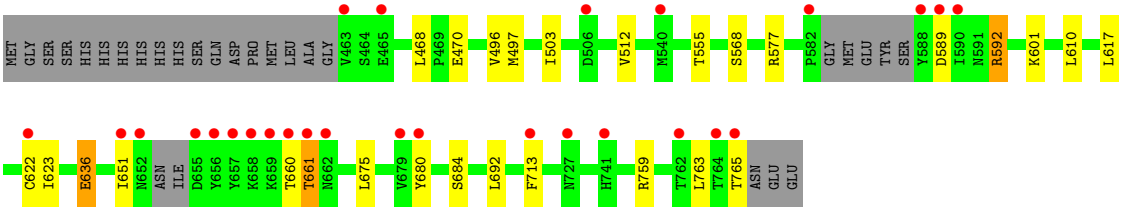
Chain C:



• Molecule 1: Fibroblast growth factor receptor 2

Chain D:




MET GLY SER SER HIS HIS HIS HIS HIS HIS SER GLN ASP PRO MET LEU ALA GLY V463 S464 E465 L468 P469 E470 V496 M497 I503 D506 V512 M540 T555 S568 R577 P582 GLY MET GLU TYR SER Y588 D589 I590 N591 R592 K601 L610 L617
C622 I623 E636 I651 N652 ASN ILE D655 Y656 Y657 K658 K659 T660 T661 M662 L675 V679 Y680 S684 L692 F713 N727 H741 R759 I762 L763 T764 T765 ASN GLU GLU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.13Å 129.87Å 132.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.00 – 2.04 33.00 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.7 (33.00-2.04) 99.7 (33.00-2.04)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.50 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.219 , 0.250 0.226 , 0.252	Depositor DCC
R_{free} test set	2002 reflections (2.23%)	wwPDB-VP
Wilson B-factor (Å^2)	33.3	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 43.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	10120	wwPDB-VP
Average B, all atoms (Å^2)	41.0	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 47.32 % 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 1.0097e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, TZ0, GOL

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.27	0/2448	0.53	0/3307
1	B	0.28	0/2341	0.52	0/3157
1	C	0.28	0/2474	0.55	0/3342
1	D	0.28	0/2432	0.54	0/3284
All	All	0.28	0/9695	0.53	0/13090

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

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	2393	0	2408	10	0
1	B	2292	0	2314	8	0
1	C	2416	0	2431	12	0
1	D	2379	0	2393	17	0
2	A	31	0	0	0	0
2	B	31	0	0	0	0
2	C	31	0	0	0	0
2	D	31	0	0	0	0
3	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	12	0	16	0	0
3	D	6	0	8	0	0
4	A	15	0	0	0	0
4	B	10	0	0	0	0
4	C	5	0	0	0	0
4	D	15	0	0	0	0
5	A	100	0	0	0	0
5	B	104	0	0	0	0
5	C	109	0	0	0	0
5	D	134	0	0	0	0
All	All	10120	0	9578	44	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 2.

The worst 5 of 44 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:D:589:ASP:HB2	1:D:592:ARG:HD2	1.73	0.68
1:D:503:ILE:HG22	1:D:512:VAL:CG2	2.24	0.67
1:D:759:ARG:O	1:D:763:LEU:HD23	1.94	0.67
1:B:468:LEU:HD23	1:B:555:THR:HB	1.80	0.64
1:C:665:LEU:HB3	1:C:670[A]:MET:CE	2.28	0.63

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	297/324 (92%)	292 (98%)	5 (2%)	0	100	100
1	B	277/324 (86%)	273 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	300/324 (93%)	297 (99%)	3 (1%)	0	100	100
1	D	291/324 (90%)	285 (98%)	5 (2%)	1 (0%)	37	30
All	All	1165/1296 (90%)	1147 (98%)	17 (2%)	1 (0%)	48	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	661	THR

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	263/285 (92%)	259 (98%)	4 (2%)	60	60
1	B	252/285 (88%)	246 (98%)	6 (2%)	44	40
1	C	266/285 (93%)	262 (98%)	4 (2%)	60	60
1	D	262/285 (92%)	256 (98%)	6 (2%)	45	41
All	All	1043/1140 (92%)	1023 (98%)	20 (2%)	52	50

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	470	GLU
1	D	636	GLU
1	D	765	THR
1	D	651	ILE
1	B	630	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	494	GLN

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Mol	Chain	Res	Type
1	A	597	GLN
1	B	727	ASN
1	C	597	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)

17 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GOL	B	802	-	5,5,5	0.10	0	5,5,5	0.28	0
2	TZ0	A	801	1	32,34,34	1.87	6 (18%)	34,48,48	2.18	9 (26%)
3	GOL	D	802	-	5,5,5	0.09	0	5,5,5	0.27	0
4	SO4	A	804	-	4,4,4	0.34	0	6,6,6	0.07	0
3	GOL	A	802	-	5,5,5	0.10	0	5,5,5	0.26	0
3	GOL	B	803	-	5,5,5	0.12	0	5,5,5	0.36	0
4	SO4	A	803	-	4,4,4	0.35	0	6,6,6	0.08	0
4	SO4	A	805	-	4,4,4	0.33	0	6,6,6	0.08	0
4	SO4	D	804	-	4,4,4	0.34	0	6,6,6	0.06	0
2	TZ0	D	801	1	32,34,34	1.96	7 (21%)	34,48,48	2.10	7 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	SO4	B	804	-	4,4,4	0.33	0	6,6,6	0.07	0
2	TZ0	B	801	1	32,34,34	1.90	7 (21%)	34,48,48	2.05	7 (20%)
4	SO4	D	803	-	4,4,4	0.34	0	6,6,6	0.08	0
4	SO4	C	802	-	4,4,4	0.34	0	6,6,6	0.08	0
4	SO4	B	805	-	4,4,4	0.33	0	6,6,6	0.07	0
2	TZ0	C	801	1	32,34,34	1.93	6 (18%)	34,48,48	2.13	8 (23%)
4	SO4	D	805	-	4,4,4	0.34	0	6,6,6	0.07	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
3	GOL	B	802	-	-	4/4/4/4	-
2	TZ0	A	801	1	-	0/12/28/28	0/4/4/4
3	GOL	D	802	-	-	2/4/4/4	-
3	GOL	A	802	-	-	1/4/4/4	-
3	GOL	B	803	-	-	2/4/4/4	-
2	TZ0	D	801	1	-	1/12/28/28	0/4/4/4
2	TZ0	B	801	1	-	1/12/28/28	0/4/4/4
2	TZ0	C	801	1	-	2/12/28/28	0/4/4/4

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	TZ0	C0L-N08	5.20	1.40	1.32
2	D	801	TZ0	C0G-C0A	-5.20	1.33	1.41
2	C	801	TZ0	C0L-N08	5.17	1.40	1.32
2	D	801	TZ0	C0V-C0M	4.96	1.54	1.30
2	B	801	TZ0	C0V-C0M	4.95	1.54	1.30

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	801	TZ0	N08-C0L-N06	-7.53	118.45	128.67
2	D	801	TZ0	N08-C0L-N06	-7.33	118.72	128.67
2	C	801	TZ0	N08-C0L-N06	-7.33	118.73	128.67
2	B	801	TZ0	N08-C0L-N06	-7.23	118.86	128.67
2	A	801	TZ0	C0V-C0M-C0P	-4.95	111.21	121.27

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

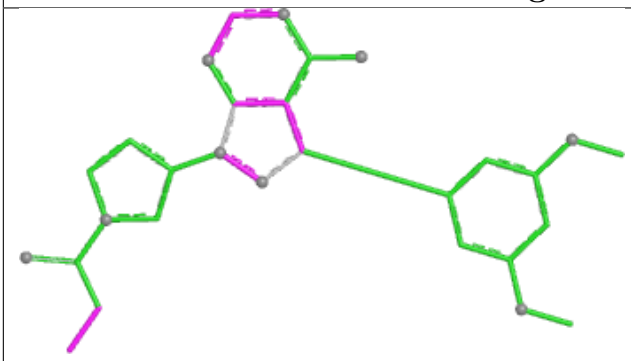
Mol	Chain	Res	Type	Atoms
3	B	802	GOL	O1-C1-C2-O2
3	B	802	GOL	O1-C1-C2-C3
3	B	802	GOL	C1-C2-C3-O3
3	B	802	GOL	O2-C2-C3-O3
3	D	802	GOL	O1-C1-C2-C3

There are no ring outliers.

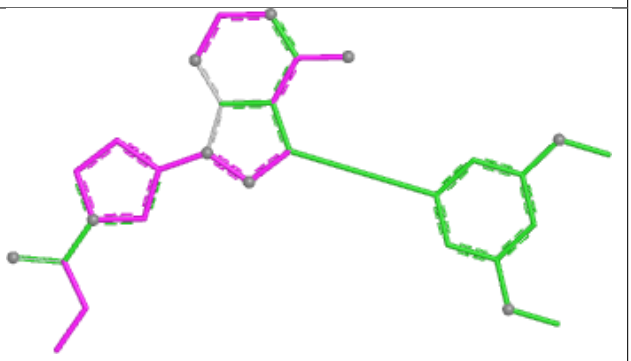
No monomer is involved in short contacts.

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 then 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.

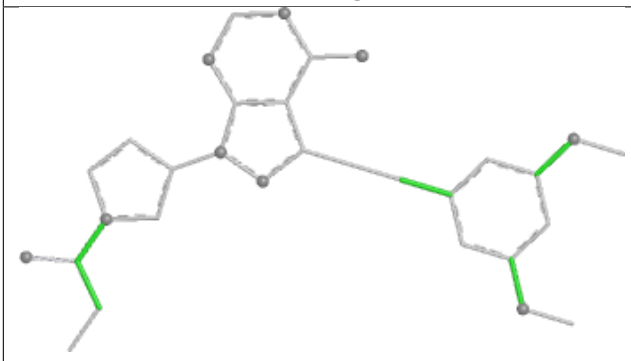
Ligand TZ0 A 801



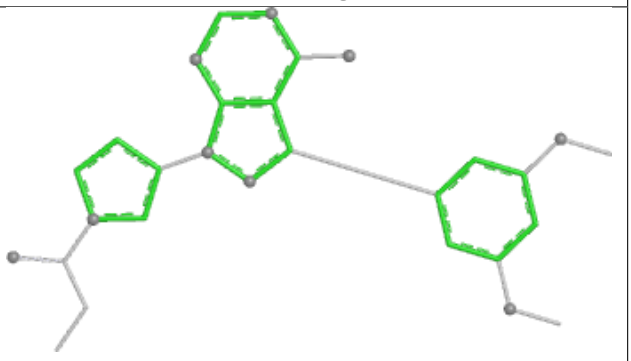
Bond lengths



Bond angles

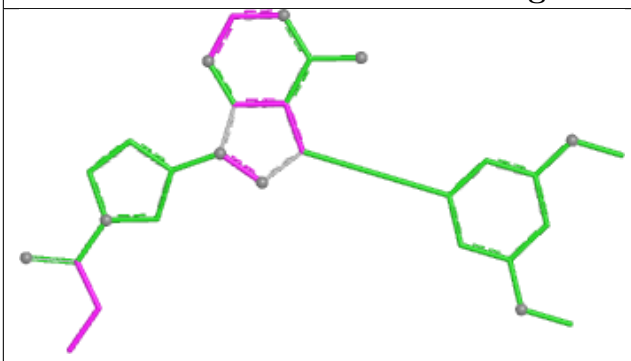


Torsions

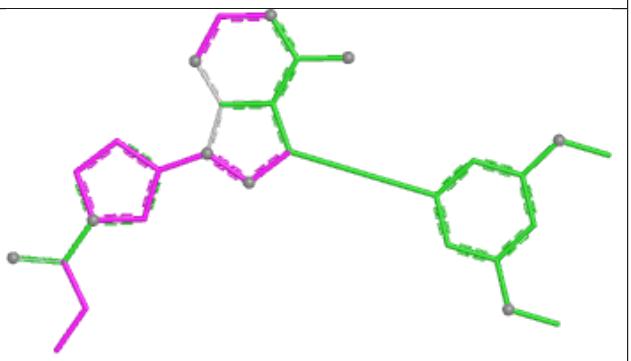


Rings

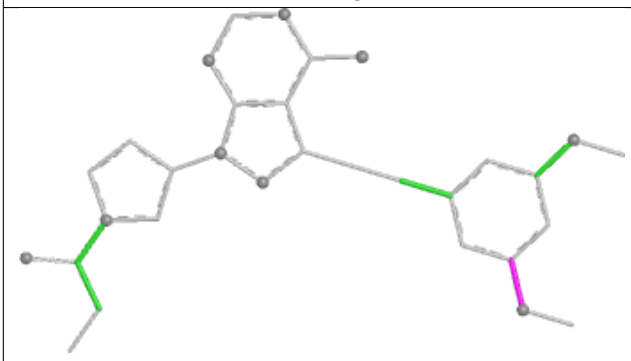
Ligand TZ0 D 801



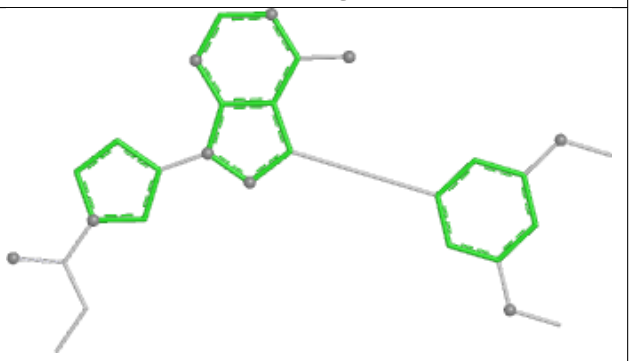
Bond lengths



Bond angles

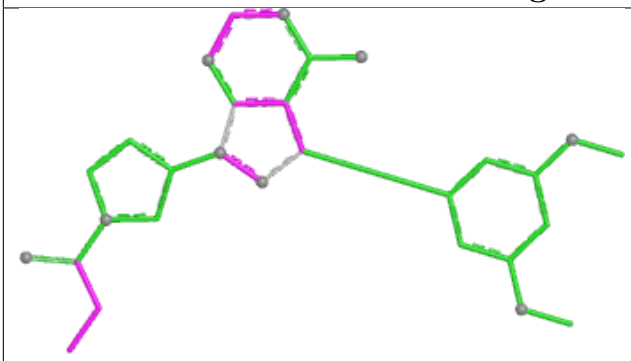


Torsions

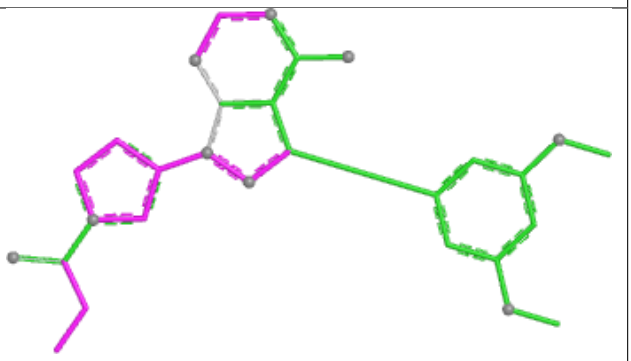


Rings

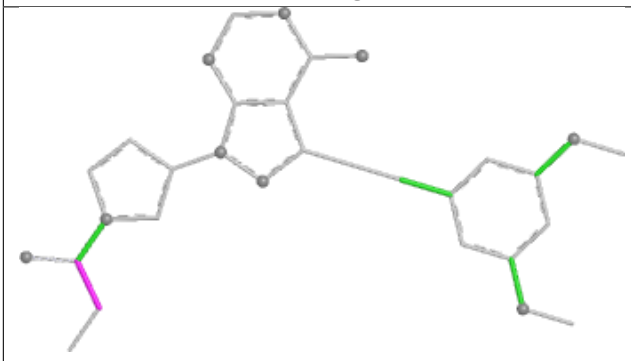
Ligand TZ0 B 801



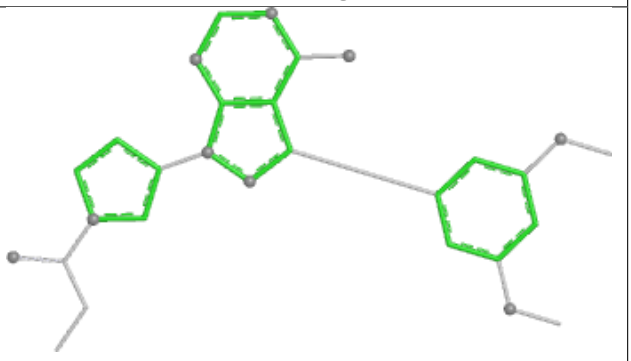
Bond lengths



Bond angles

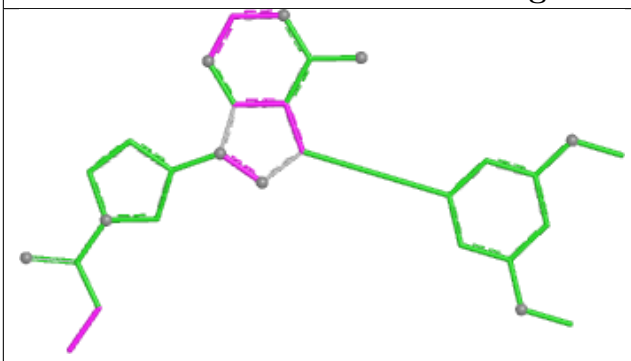


Torsions

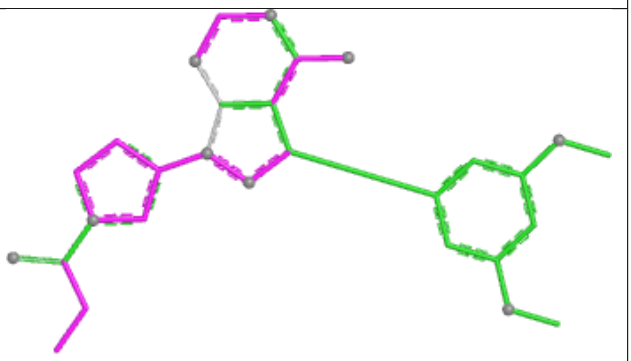


Rings

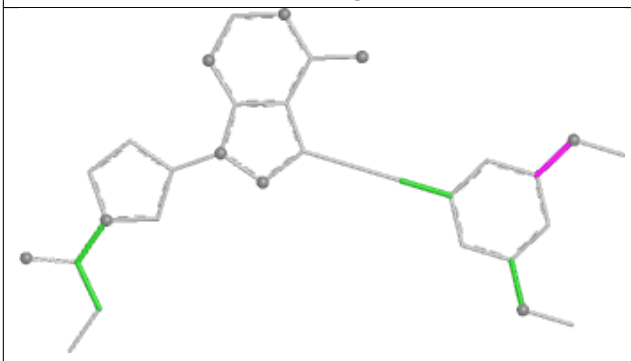
Ligand TZ0 C 801



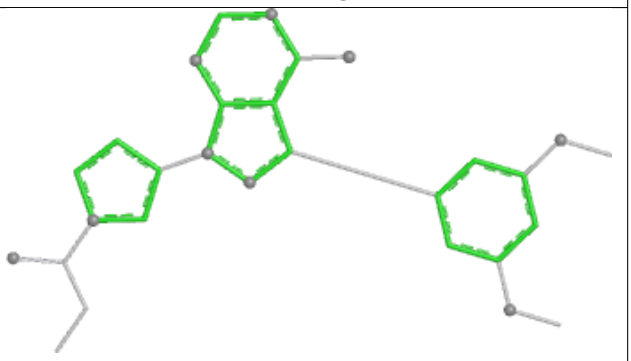
Bond lengths



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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	298/324 (91%)	0.61	27 (9%)	16	18	21, 39, 74, 117	1 (0%)
1	B	286/324 (88%)	0.62	22 (7%)	21	23	22, 38, 70, 93	1 (0%)
1	C	300/324 (92%)	0.42	17 (5%)	30	32	19, 37, 63, 91	2 (0%)
1	D	296/324 (91%)	0.62	27 (9%)	16	18	22, 37, 70, 101	1 (0%)
All	All	1180/1296 (91%)	0.57	93 (7%)	20	22	19, 37, 70, 117	5 (0%)

The worst 5 of 93 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	661	THR	5.9
1	D	657	TYR	5.6
1	A	468	LEU	5.0
1	B	657	TYR	4.9
1	B	590	ILE	4.4

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

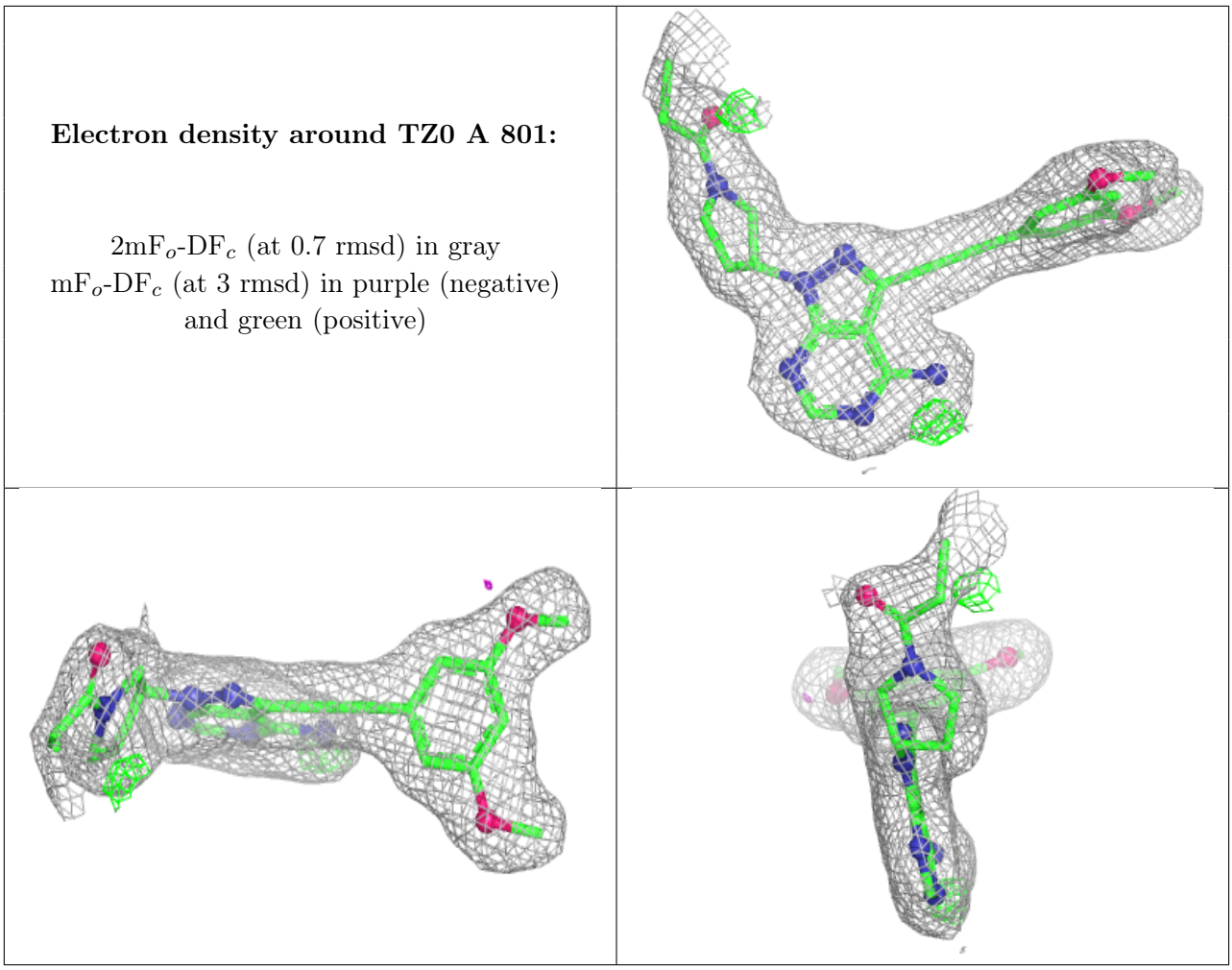
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
4	SO4	A	805	5/5	0.58	0.16	99,101,105,105	0
4	SO4	D	805	5/5	0.63	0.19	111,113,117,119	0
4	SO4	B	805	5/5	0.69	0.14	90,93,98,98	0
4	SO4	D	803	5/5	0.70	0.14	79,82,89,93	0
3	GOL	B	803	6/6	0.75	0.15	49,54,55,60	0
4	SO4	A	803	5/5	0.78	0.12	68,71,75,82	0
4	SO4	D	804	5/5	0.82	0.17	73,75,77,82	5
4	SO4	A	804	5/5	0.83	0.13	64,70,77,81	0
4	SO4	B	804	5/5	0.83	0.10	79,80,84,87	0
4	SO4	C	802	5/5	0.84	0.11	64,66,71,71	0
3	GOL	B	802	6/6	0.85	0.12	43,53,59,59	0
3	GOL	A	802	6/6	0.86	0.15	52,58,62,65	0
3	GOL	D	802	6/6	0.90	0.10	44,48,49,56	0
2	TZ0	A	801	31/31	0.94	0.08	25,29,44,48	0
2	TZ0	C	801	31/31	0.95	0.07	23,25,40,43	0
2	TZ0	D	801	31/31	0.95	0.07	20,25,35,36	0
2	TZ0	B	801	31/31	0.95	0.07	22,27,36,38	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.

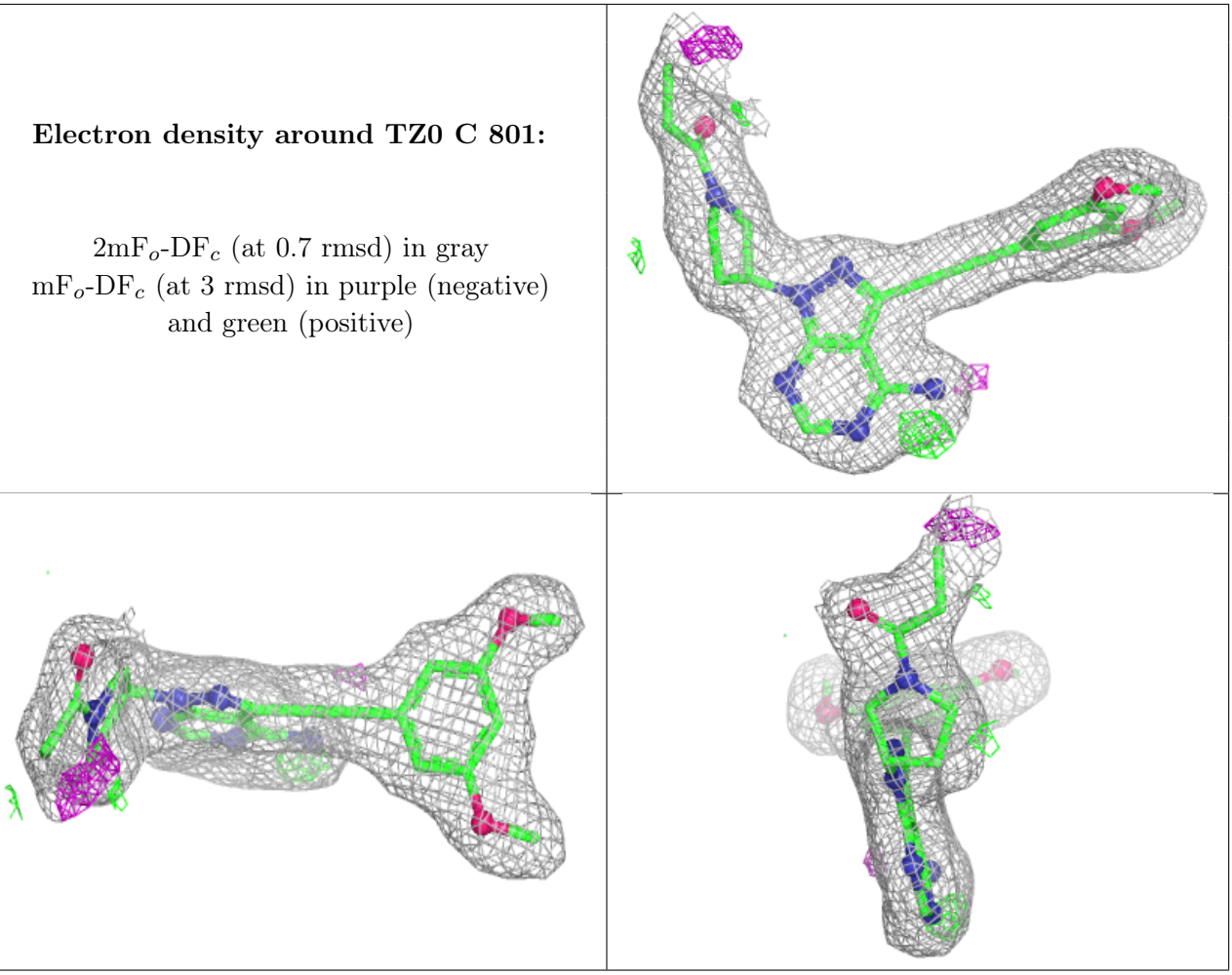
Electron density around TZ0 A 801:

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



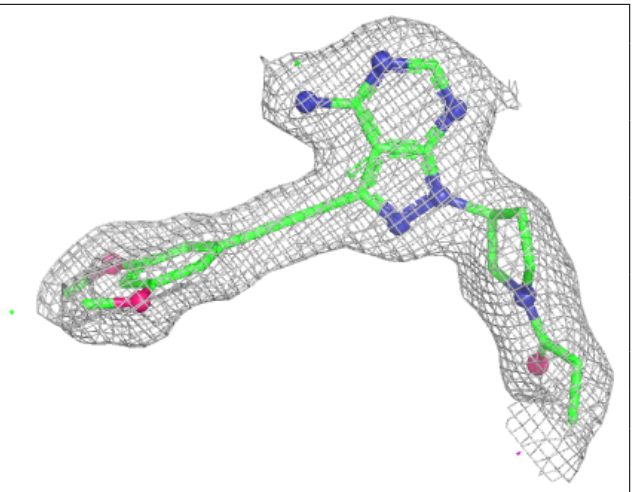
Electron density around TZ0 C 801:

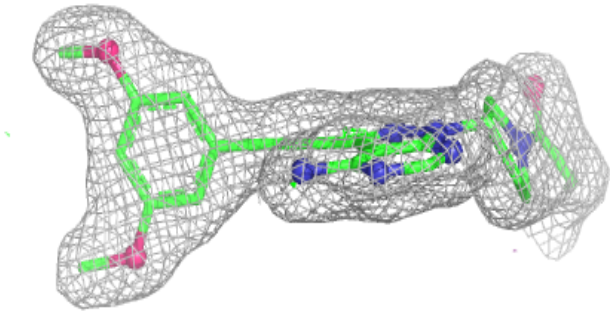
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

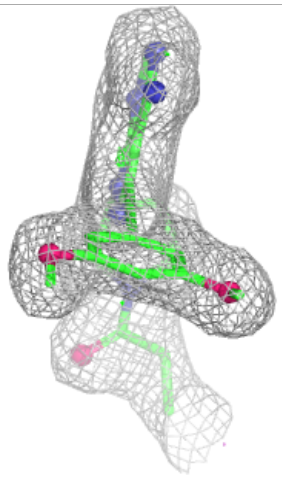


Electron density around TZ0 D 801:

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

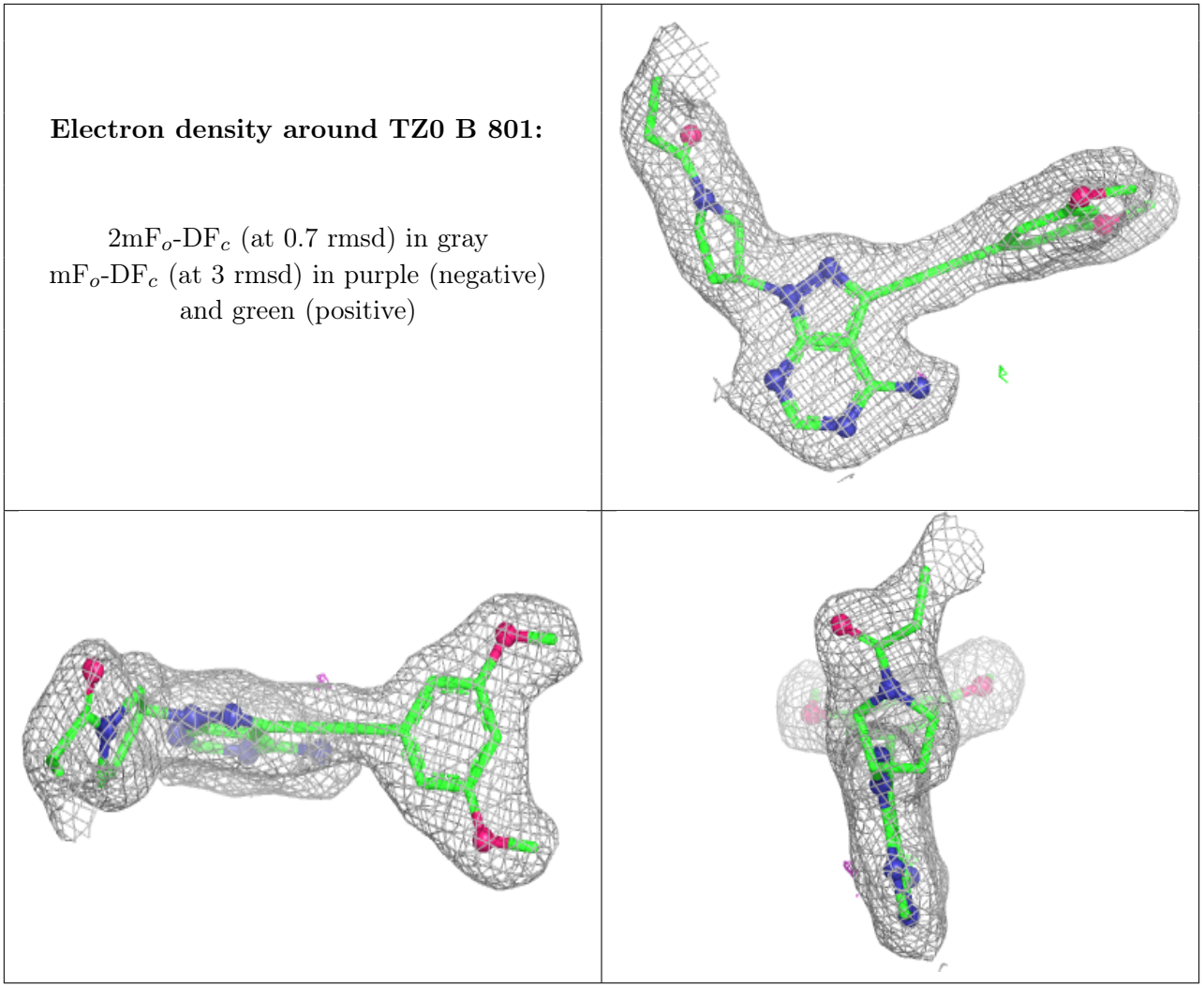






Electron density around TZ0 B 801:

$2mF_o$-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.