



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 21, 2021 – 04:24 pm BST

PDB ID : 7O2P
Title : Crystal structure of Danio rerio histone deacetylase 6 catalytic domain 2 in complex with ITF3756
Authors : Zrubek, K.; Sandrone, G.; Cukier, C.D.; Stevenazzi, A.
Deposited on : 2021-03-31
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

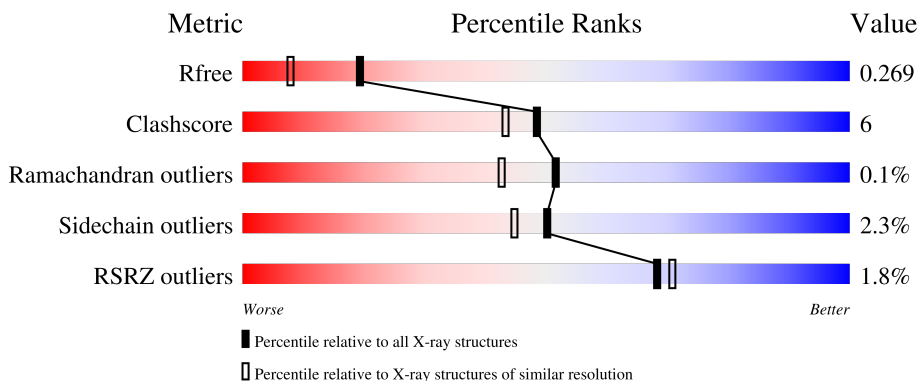
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	365	
1	B	365	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 5925 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.

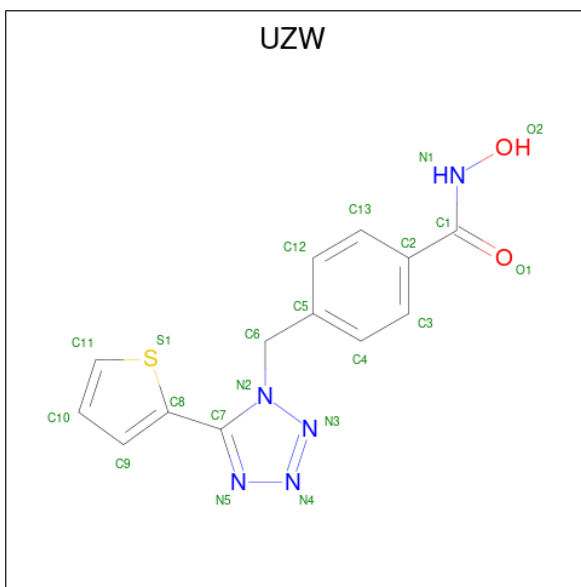
- Molecule 1 is a protein called Histone deacetylase 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	357	2790	1754	501	517	18	0	0	0
1	B	356	2783	1749	500	516	18	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	434	GLY	-	cloning artifact	UNP F8W4B7
A	435	SER	-	cloning artifact	UNP F8W4B7
A	436	ASN	-	cloning artifact	UNP F8W4B7
A	437	ALA	-	cloning artifact	UNP F8W4B7
A	438	GLY	-	cloning artifact	UNP F8W4B7
A	439	GLY	-	cloning artifact	UNP F8W4B7
B	434	GLY	-	cloning artifact	UNP F8W4B7
B	435	SER	-	cloning artifact	UNP F8W4B7
B	436	ASN	-	cloning artifact	UNP F8W4B7
B	437	ALA	-	cloning artifact	UNP F8W4B7
B	438	GLY	-	cloning artifact	UNP F8W4B7
B	439	GLY	-	cloning artifact	UNP F8W4B7

- Molecule 2 is {N}-oxidanyl-4-[(5-thiophen-2-yl-1,2,3,4-tetrazol-1-yl)methyl]benzamide (three-letter code: UZW) (formula: C₁₃H₁₁N₅O₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			21	13	5	2	1		
2	B	1	Total	C	N	O	S	0	0
			21	13	5	2	1		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	K	0	0
			2	2		
4	B	2	Total	K	0	0
			2	2		

- Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	I	0	0
			3	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total I 1 1	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



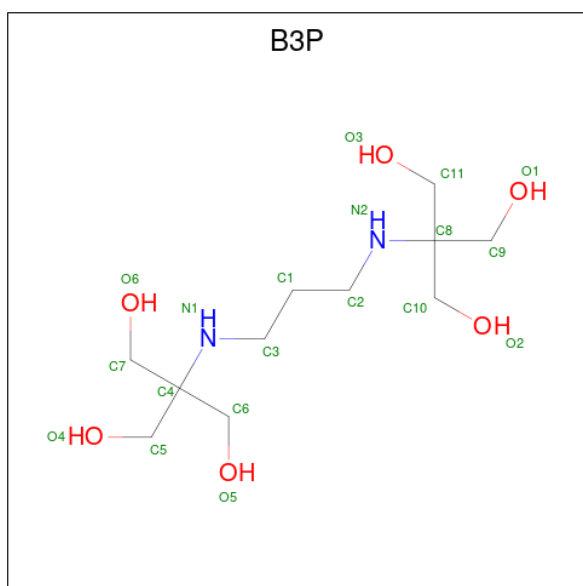
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			7	4	3		
7	B	1	Total	C	O	0	0
			7	4	3		
7	B	1	Total	C	O	0	0
			7	4	3		
7	B	1	Total	C	O	0	0
			5	3	2		

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

- Molecule 9 is 2-[3-(2-HYDROXY-1,1-DIHYDROXYMETHYL-ETHYLAMINO)-PROPYL AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: B3P) (formula: $C_{11}H_{26}N_2O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			19	11	2	6		

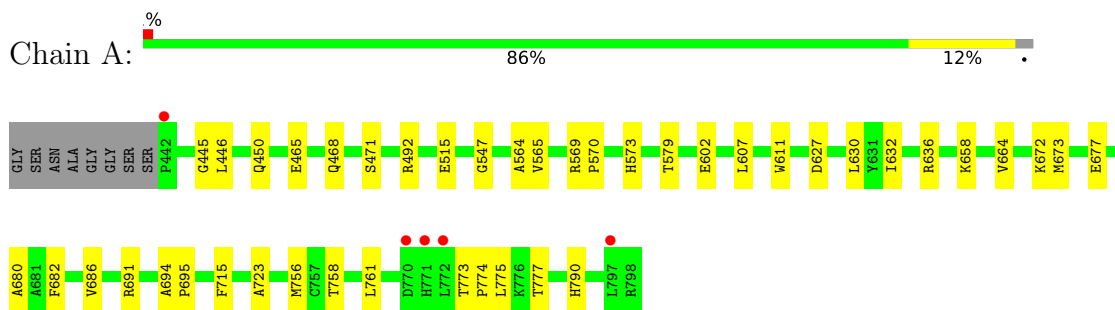
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	116	Total	O	0	0
			116	116		
10	B	97	Total	O	0	0
			97	97		

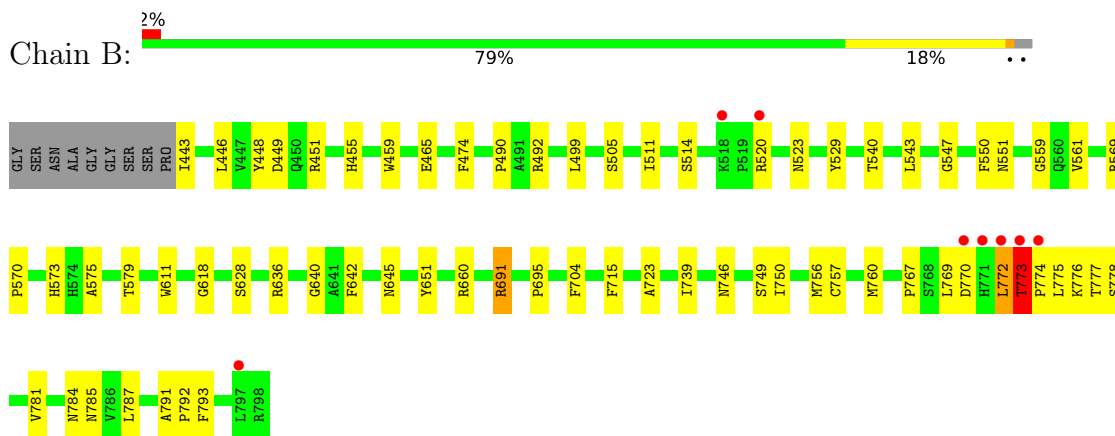
3 Residue-property plots [i](#)

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: Histone deacetylase 6



- Molecule 1: Histone deacetylase 6



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.48Å 90.75Å 71.96Å 90.00° 95.64° 90.00°	Depositor
Resolution (Å)	45.42 – 1.90 45.38 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (45.42-1.90) 100.0 (45.38-1.90)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.195 , 0.261 0.202 , 0.269	Depositor DCC
R_{free} test set	2406 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	25.7	Xtriage
Anisotropy	0.669	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	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	0.96	EDS
Total number of atoms	5925	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% of the height of the origin peak. No significant pseudotranslation is detected.*

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: UZW, GOL, IOD, EDO, B3P, ZN, PEG, K

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	0.70	0/2861	0.84	0/3880
1	B	0.75	0/2853	0.88	1/3869 (0.0%)
All	All	0.72	0/5714	0.86	1/7749 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	691	ARG	NE-CZ-NH1	-5.46	117.57	120.30

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	2790	0	2708	24	1
1	B	2783	0	2700	42	1
2	A	21	0	0	1	0
2	B	21	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	3	0	0	0	0
5	B	1	0	0	0	0
6	A	12	0	16	1	0
6	B	18	0	24	2	0
7	A	7	0	10	0	0
7	B	19	0	25	1	0
8	A	8	0	12	2	0
8	B	4	0	6	1	0
9	B	19	0	26	0	0
10	A	116	0	0	2	0
10	B	97	0	0	2	0
All	All	5925	0	5527	67	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 6.

All (67) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:773:THR:H	1:B:774:PRO:HD3	1.34	0.91
1:B:691:ARG:HD3	10:B:957:HOH:O	1.87	0.74
1:B:773:THR:N	1:B:774:PRO:HD3	2.01	0.74
1:B:781:VAL:O	1:B:785:ASN:OD1	2.10	0.69
1:B:443:ILE:HG23	1:B:561:VAL:HA	1.83	0.60
1:A:636:ARG:HD2	1:A:715:PHE:CE1	2.40	0.56
1:A:664:VAL:HG22	1:A:790:HIS:CE1	2.42	0.55
1:A:680:ALA:HB2	1:A:775:LEU:HD11	1.90	0.54
1:A:450:GLN:OE1	10:A:901:HOH:O	2.18	0.54
1:A:607:LEU:HD13	1:A:630:LEU:HD23	1.89	0.53
1:B:651:TYR:CE2	1:B:785:ASN:ND2	2.77	0.53
1:B:746:ASN:HB3	1:B:749:SER:HB2	1.91	0.53
2:A:801:UZW:N4	6:A:808:GOL:H2	2.25	0.51
1:A:694:ALA:HA	8:A:811:EDO:H11	1.92	0.51
1:B:559:GLY:O	6:B:806:GOL:O3	2.26	0.51
1:B:529:TYR:HE1	1:B:579:THR:HG1	1.59	0.51
1:A:695:PRO:HD2	8:A:811:EDO:H11	1.93	0.50
1:B:777:THR:O	1:B:781:VAL:HG23	2.12	0.49
1:B:446:LEU:C	1:B:446:LEU:HD23	2.33	0.49
1:B:499:LEU:HD11	1:B:543:LEU:HD21	1.95	0.48
1:B:704:PHE:HB2	1:B:750:ILE:HG22	1.95	0.48
1:A:723:ALA:HB2	1:A:756:MET:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:GLU:HG2	10:A:925:HOH:O	2.12	0.48
1:B:575:ALA:O	1:B:618:GLY:HA3	2.14	0.47
1:B:448:TYR:CD2	1:B:474:PHE:CD1	3.02	0.47
1:B:459:TRP:CZ2	1:B:523:ASN:HB2	2.50	0.47
1:B:499:LEU:HD11	1:B:543:LEU:CD2	2.45	0.47
1:B:640:GLY:O	1:B:645:ASN:HA	2.15	0.47
1:A:723:ALA:HB2	1:A:756:MET:CE	2.45	0.46
1:A:602:GLU:H	1:A:602:GLU:CD	2.18	0.46
1:B:770:ASP:O	1:B:772:LEU:HG	2.15	0.46
1:B:773:THR:N	1:B:774:PRO:CD	2.73	0.46
1:B:772:LEU:HA	10:B:977:HOH:O	2.14	0.46
1:A:682:PHE:HA	1:A:686:VAL:HB	1.97	0.46
1:B:776:LYS:HG2	1:B:778:SER:OG	2.16	0.46
1:B:636:ARG:HD2	1:B:715:PHE:CE1	2.51	0.45
1:A:673:MET:SD	1:A:677:GLU:HG2	2.57	0.45
1:A:569:ARG:HA	1:A:570:PRO:C	2.38	0.44
1:A:691:ARG:HG2	1:A:691:ARG:HH21	1.83	0.44
1:A:445:GLY:O	1:A:564:ALA:HA	2.17	0.44
1:B:723:ALA:O	1:B:760:MET:HG3	2.18	0.44
1:A:565:VAL:HG13	1:A:761:LEU:HD12	1.99	0.44
1:B:490:PRO:O	1:B:551:ASN:OD1	2.36	0.44
1:B:569:ARG:HA	1:B:570:PRO:C	2.38	0.44
1:A:632:ILE:HG21	1:A:686:VAL:HG22	1.99	0.44
1:B:540:THR:O	1:B:543:LEU:HB2	2.17	0.44
1:B:492:ARG:O	1:B:547:GLY:HA3	2.18	0.43
1:A:565:VAL:HG11	1:A:758:THR:OG1	2.18	0.43
1:B:511:ILE:O	1:B:514:SER:OG	2.34	0.43
1:B:651:TYR:CD2	1:B:785:ASN:HB3	2.54	0.42
1:B:449:ASP:OD2	1:B:451:ARG:NH2	2.53	0.42
1:B:547:GLY:O	1:B:550:PHE:HB2	2.19	0.42
1:A:773:THR:HB	1:A:774:PRO:HD2	2.01	0.42
1:B:455:HIS:HD2	1:B:569:ARG:NH2	2.18	0.42
1:B:642:PHE:CE1	6:B:808:GOL:H2	2.55	0.42
1:B:773:THR:H	1:B:774:PRO:CD	2.18	0.41
1:B:784:ASN:HA	1:B:787:LEU:HD12	2.02	0.41
1:A:446:LEU:C	1:A:446:LEU:HD23	2.41	0.41
1:A:468:GLN:HA	1:A:471:SER:OG	2.21	0.41
1:B:695:PRO:HD2	8:B:812:EDO:H22	2.01	0.41
1:A:492:ARG:O	1:A:547:GLY:HA3	2.21	0.40
1:A:627:ASP:HB3	1:A:658:LYS:O	2.20	0.40
1:B:739:ILE:HD13	1:B:757:CYS:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:791:ALA:N	1:B:792:PRO:CD	2.84	0.40
1:B:520:ARG:HG3	7:B:811:PEG:C4	2.51	0.40
1:B:660:ARG:HG2	1:B:793:PHE:CE1	2.57	0.40
1:B:756:MET:CE	1:B:767:PRO:HG3	2.51	0.40

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)
1:A:777:THR:OG1	1:B:773:THR:CG2[2_555]	1.81	0.39

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	355/365 (97%)	345 (97%)	10 (3%)	0	100	100
1	B	354/365 (97%)	335 (95%)	18 (5%)	1 (0%)	41	31
All	All	709/730 (97%)	680 (96%)	28 (4%)	1 (0%)	51	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	773	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	301/305 (99%)	296 (98%)	5 (2%)	60	57
1	B	300/305 (98%)	291 (97%)	9 (3%)	41	33
All	All	601/610 (98%)	587 (98%)	14 (2%)	50	45

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	465	GLU
1	A	573	HIS
1	A	579	THR
1	A	611	TRP
1	A	672	LYS
1	B	465	GLU
1	B	505	SER
1	B	573	HIS
1	B	611	TRP
1	B	628	SER
1	B	769	LEU
1	B	772	LEU
1	B	773	THR
1	B	775	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	450	GLN
1	A	462	HIS
1	A	536	ASN
1	A	784	ASN
1	B	551	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 25 ligands modelled in this entry, 10 are monoatomic - leaving 15 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
6	GOL	B	807	-	5,5,5	0.08	0	5,5,5	0.33	0
2	UZW	A	801	3	22,23,23	0.50	0	21,31,31	0.69	0
7	PEG	B	810	-	6,6,6	0.35	0	5,5,5	0.20	0
8	EDO	A	811	-	3,3,3	0.39	0	2,2,2	0.26	0
6	GOL	B	808	-	5,5,5	0.16	0	5,5,5	0.45	0
7	PEG	B	809	-	6,6,6	0.35	0	5,5,5	0.24	0
6	GOL	A	807	-	5,5,5	0.12	0	5,5,5	0.34	0
7	PEG	B	811	-	4,4,6	0.24	0	3,3,5	0.36	0
6	GOL	A	808	-	5,5,5	0.19	0	5,5,5	0.56	0
6	GOL	B	806	-	5,5,5	0.11	0	5,5,5	0.34	0
8	EDO	A	810	-	3,3,3	0.29	0	2,2,2	0.16	0
7	PEG	A	809	-	6,6,6	0.32	0	5,5,5	0.20	0
8	EDO	B	812	-	3,3,3	0.51	0	2,2,2	0.21	0
2	UZW	B	801	3	22,23,23	0.55	0	21,31,31	0.97	2 (9%)
9	B3P	B	813	-	18,18,18	0.28	0	21,23,23	0.72	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	GOL	B	807	-	-	4/4/4/4	-
2	UZW	A	801	3	-	0/10/14/14	0/3/3/3
7	PEG	B	810	-	-	2/4/4/4	-
8	EDO	A	811	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	B	808	-	-	1/4/4/4	-
7	PEG	B	809	-	-	2/4/4/4	-
6	GOL	A	807	-	-	0/4/4/4	-
7	PEG	B	811	-	-	1/2/2/4	-
6	GOL	A	808	-	-	2/4/4/4	-
6	GOL	B	806	-	-	4/4/4/4	-
8	EDO	A	810	-	-	0/1/1/1	-
7	PEG	A	809	-	-	2/4/4/4	-
8	EDO	B	812	-	-	0/1/1/1	-
2	UZW	B	801	3	-	0/10/14/14	0/3/3/3
9	B3P	B	813	-	-	5/28/28/28	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	UZW	O1-C1-N1	-2.14	118.95	122.94
2	B	801	UZW	C10-C11-S1	-2.03	111.33	112.98

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	807	GOL	O1-C1-C2-C3
6	B	807	GOL	C1-C2-C3-O3
6	B	806	GOL	O2-C2-C3-O3
7	B	809	PEG	O2-C3-C4-O4
6	B	806	GOL	O1-C1-C2-C3
6	B	806	GOL	C1-C2-C3-O3
7	B	810	PEG	O2-C3-C4-O4
6	B	807	GOL	O2-C2-C3-O3
6	B	807	GOL	O1-C1-C2-O2
8	A	811	EDO	O1-C1-C2-O2
6	B	808	GOL	O1-C1-C2-O2
6	A	808	GOL	O1-C1-C2-O2
7	A	809	PEG	O2-C3-C4-O4
9	B	813	B3P	C7-C4-C5-O4
9	B	813	B3P	O2-C10-C8-C11
7	B	809	PEG	O1-C1-C2-O2
7	B	811	PEG	O2-C3-C4-O4

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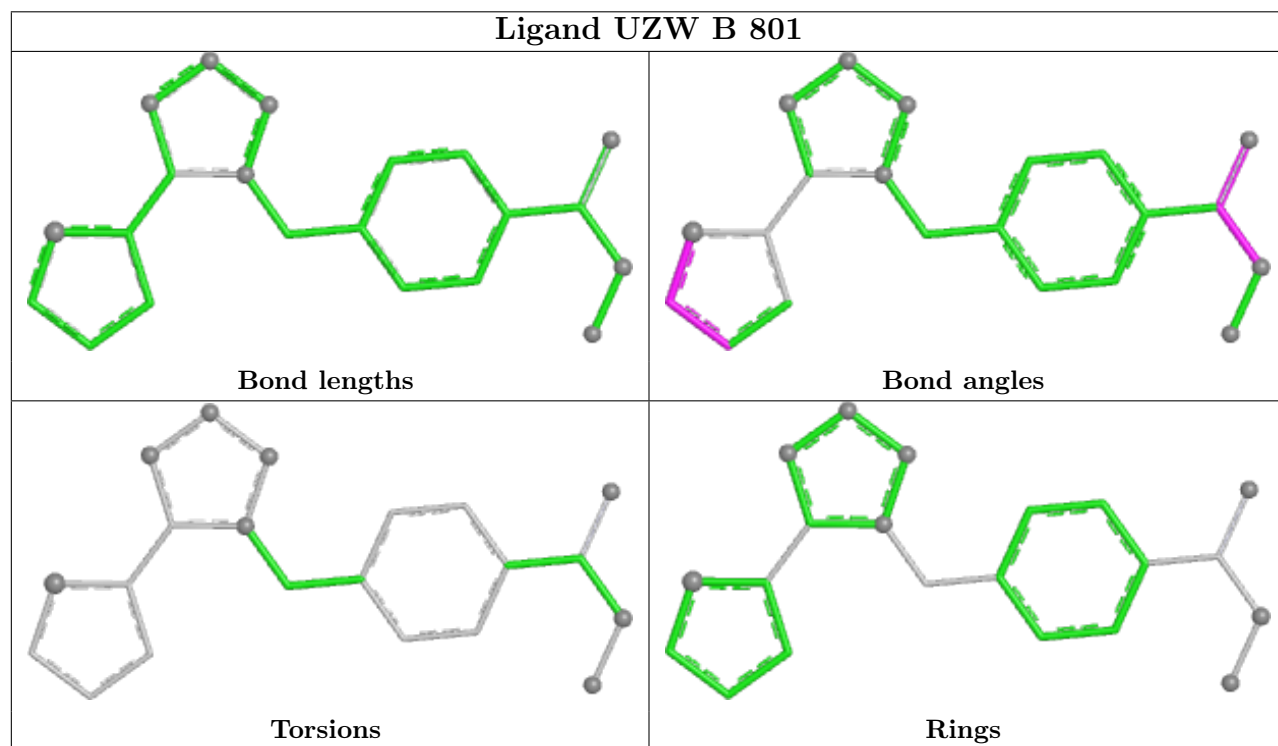
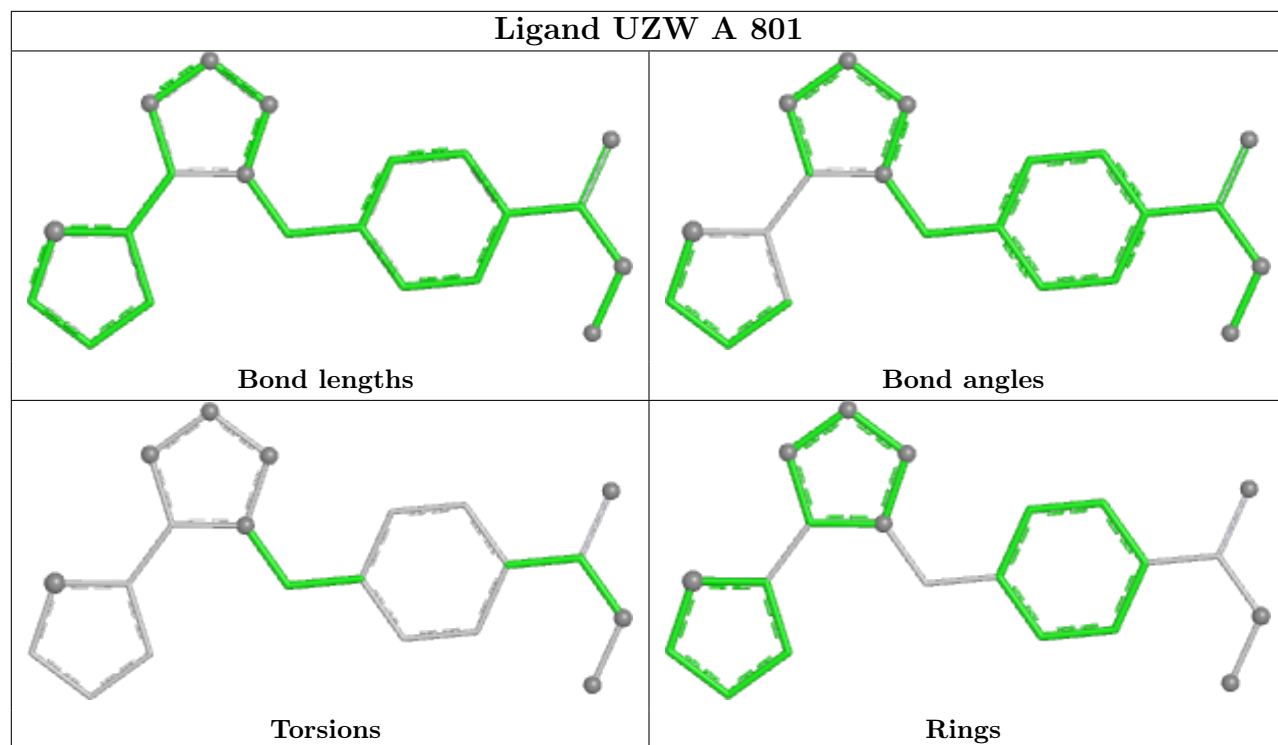
Mol	Chain	Res	Type	Atoms
6	B	806	GOL	O1-C1-C2-O2
7	A	809	PEG	O1-C1-C2-O2
9	B	813	B3P	N1-C4-C5-O4
6	A	808	GOL	O1-C1-C2-C3
7	B	810	PEG	C1-C2-O2-C3
9	B	813	B3P	C6-C4-N1-C3
9	B	813	B3P	C1-C2-N2-C8

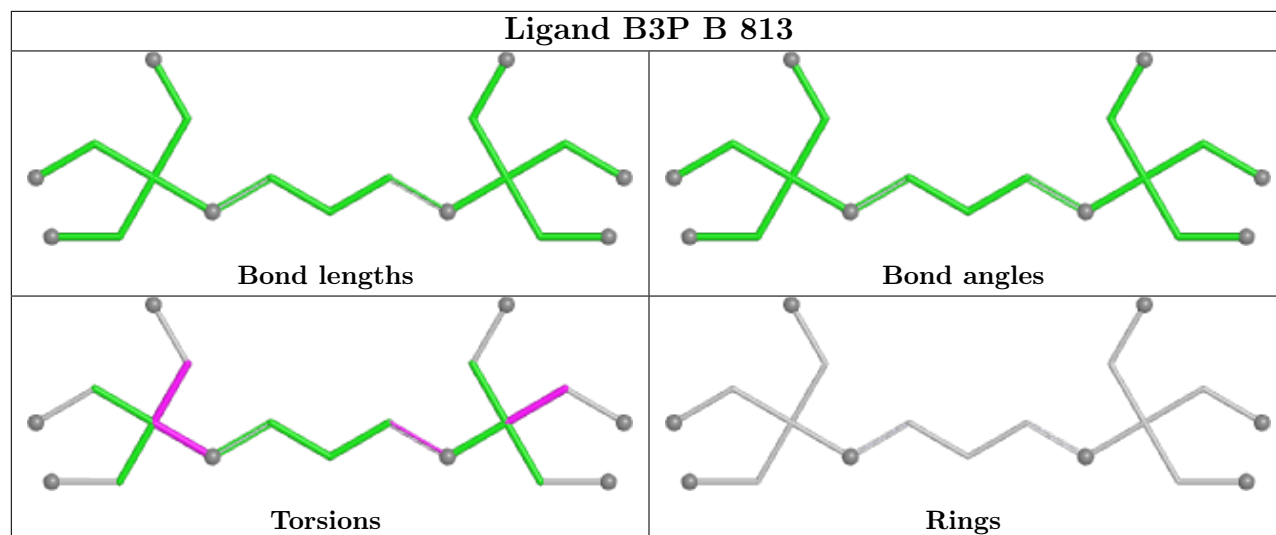
There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	UZW	1	0
8	A	811	EDO	2	0
6	B	808	GOL	1	0
7	B	811	PEG	1	0
6	A	808	GOL	1	0
6	B	806	GOL	1	0
8	B	812	EDO	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	357/365 (97%)	-0.19	5 (1%) 75 77	20, 30, 50, 84	0
1	B	356/365 (97%)	0.11	8 (2%) 62 64	19, 35, 52, 112	0
All	All	713/730 (97%)	-0.04	13 (1%) 68 71	19, 32, 52, 112	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	772	LEU	10.6
1	B	773	THR	6.9
1	B	771	HIS	6.4
1	B	774	PRO	3.1
1	A	797	LEU	2.8
1	B	520	ARG	2.5
1	A	442	PRO	2.5
1	A	771	HIS	2.5
1	A	770	ASP	2.5
1	B	770	ASP	2.3
1	A	772	LEU	2.1
1	B	797	LEU	2.1
1	B	518	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands

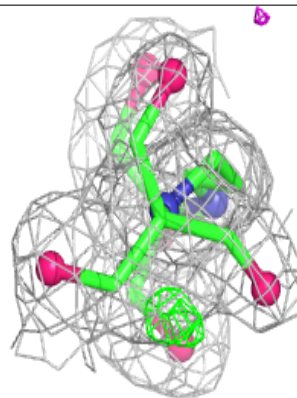
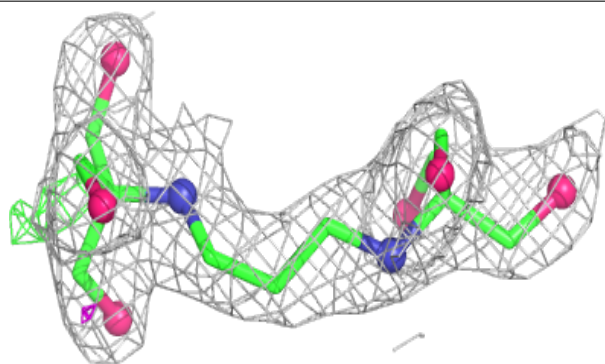
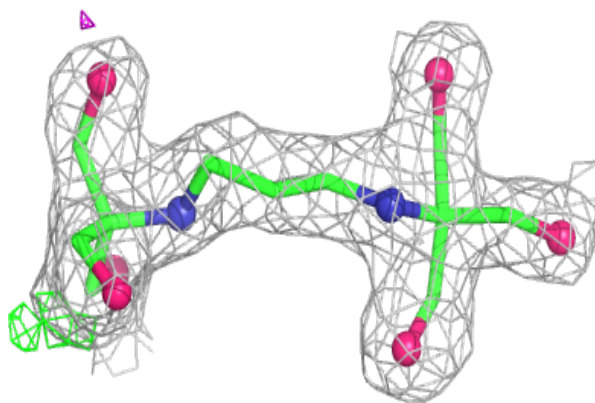
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	PEG	B	810	7/7	0.84	0.12	42,45,47,48	0
7	PEG	B	809	7/7	0.85	0.14	23,38,47,48	0
8	EDO	A	811	4/4	0.86	0.20	37,38,42,53	0
7	PEG	A	809	7/7	0.89	0.22	23,31,41,47	0
6	GOL	A	807	6/6	0.90	0.14	35,39,41,41	0
6	GOL	B	807	6/6	0.90	0.10	38,47,48,51	0
8	EDO	A	810	4/4	0.91	0.09	38,38,39,40	0
8	EDO	B	812	4/4	0.92	0.17	33,35,45,45	0
9	B3P	B	813	19/19	0.92	0.12	29,37,43,44	0
7	PEG	B	811	5/7	0.93	0.18	25,29,30,35	0
6	GOL	B	808	6/6	0.94	0.13	29,37,39,42	0
6	GOL	B	806	6/6	0.94	0.18	38,50,51,59	0
2	UZW	A	801	21/21	0.94	0.12	24,27,37,51	0
6	GOL	A	808	6/6	0.95	0.11	30,38,39,44	0
2	UZW	B	801	21/21	0.95	0.11	22,27,34,42	0
4	K	B	803	1/1	0.97	0.05	34,34,34,34	0
4	K	A	804	1/1	0.99	0.03	27,27,27,27	0
3	ZN	A	802	1/1	0.99	0.02	33,33,33,33	0
5	IOD	A	805	1/1	0.99	0.04	35,35,35,35	0
5	IOD	A	812	1/1	0.99	0.06	37,37,37,37	0
5	IOD	B	805	1/1	0.99	0.04	40,40,40,40	0
4	K	A	803	1/1	0.99	0.06	28,28,28,28	0
4	K	B	804	1/1	1.00	0.02	27,27,27,27	0
3	ZN	B	802	1/1	1.00	0.02	32,32,32,32	0
5	IOD	A	806	1/1	1.00	0.03	41,41,41,41	0

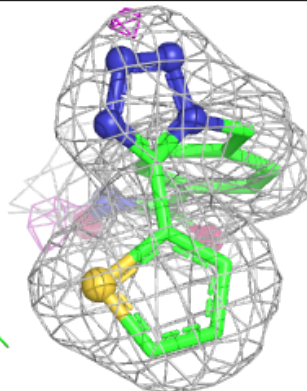
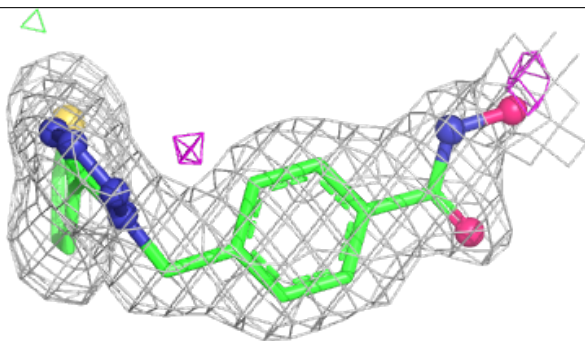
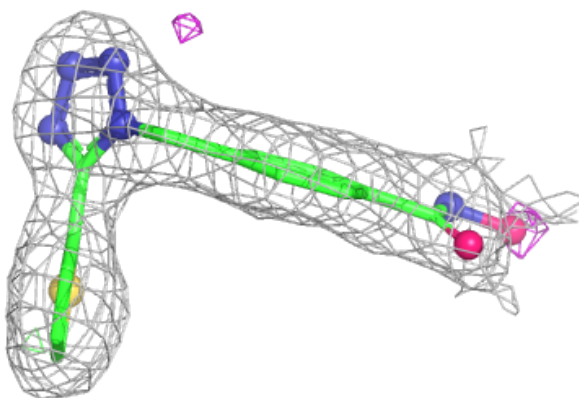
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

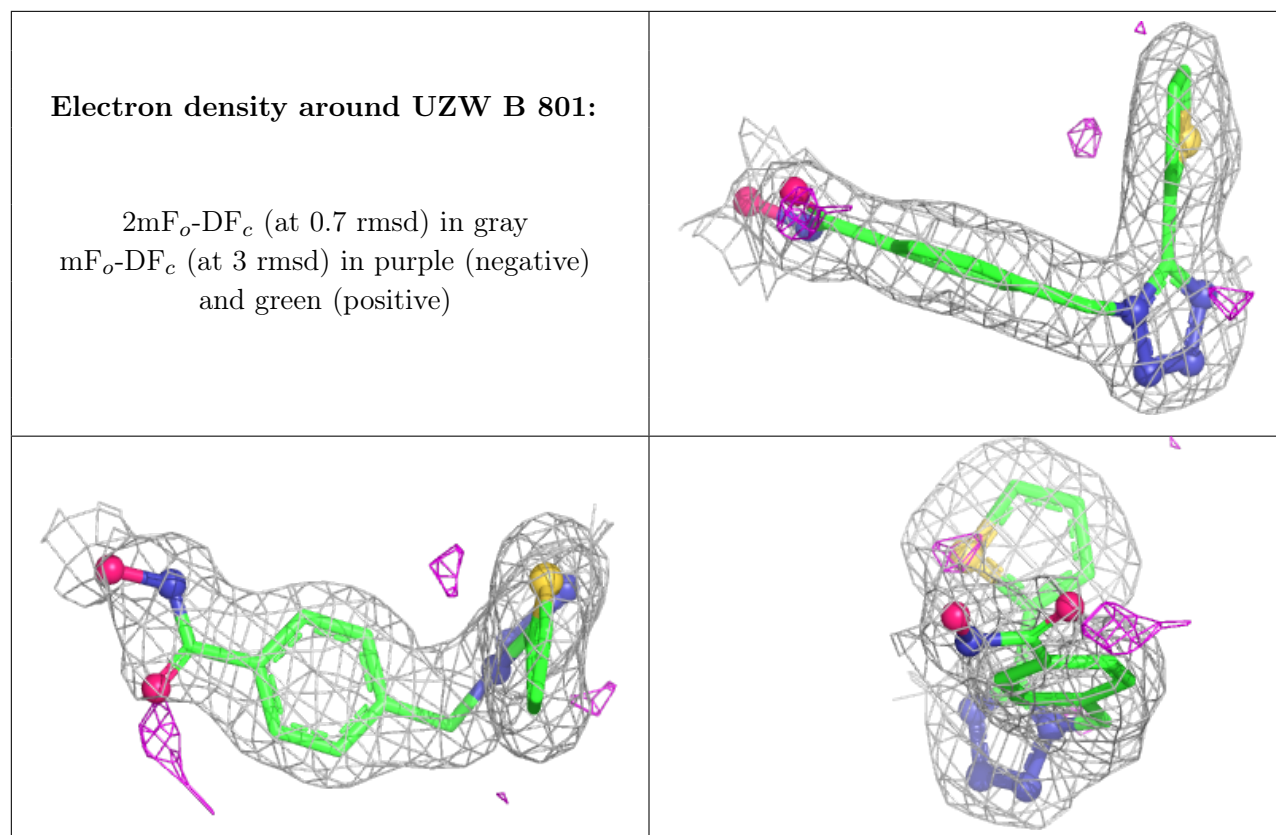
Electron density around B3P B 813:

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

**Electron density around UZW A 801:**

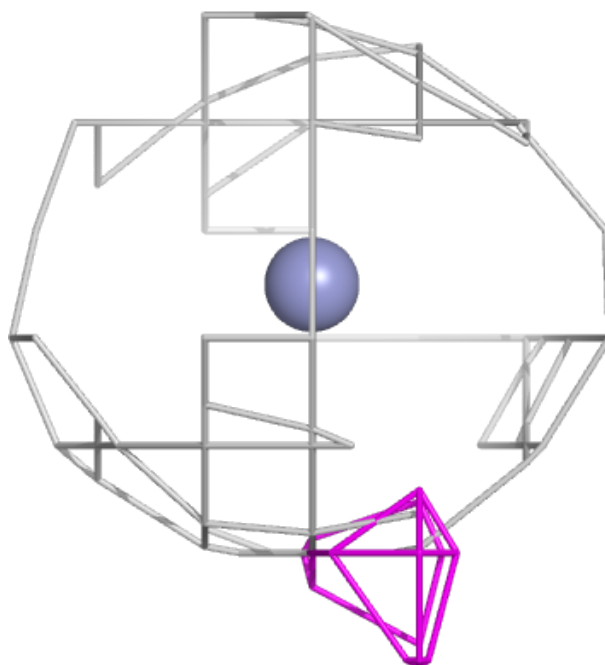
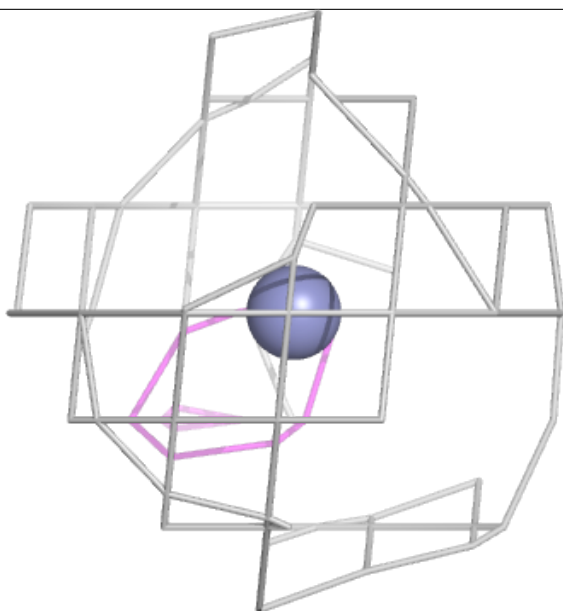
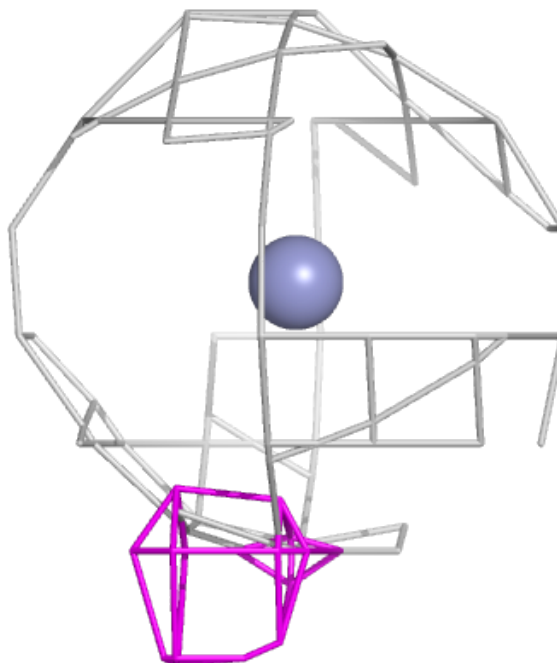
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

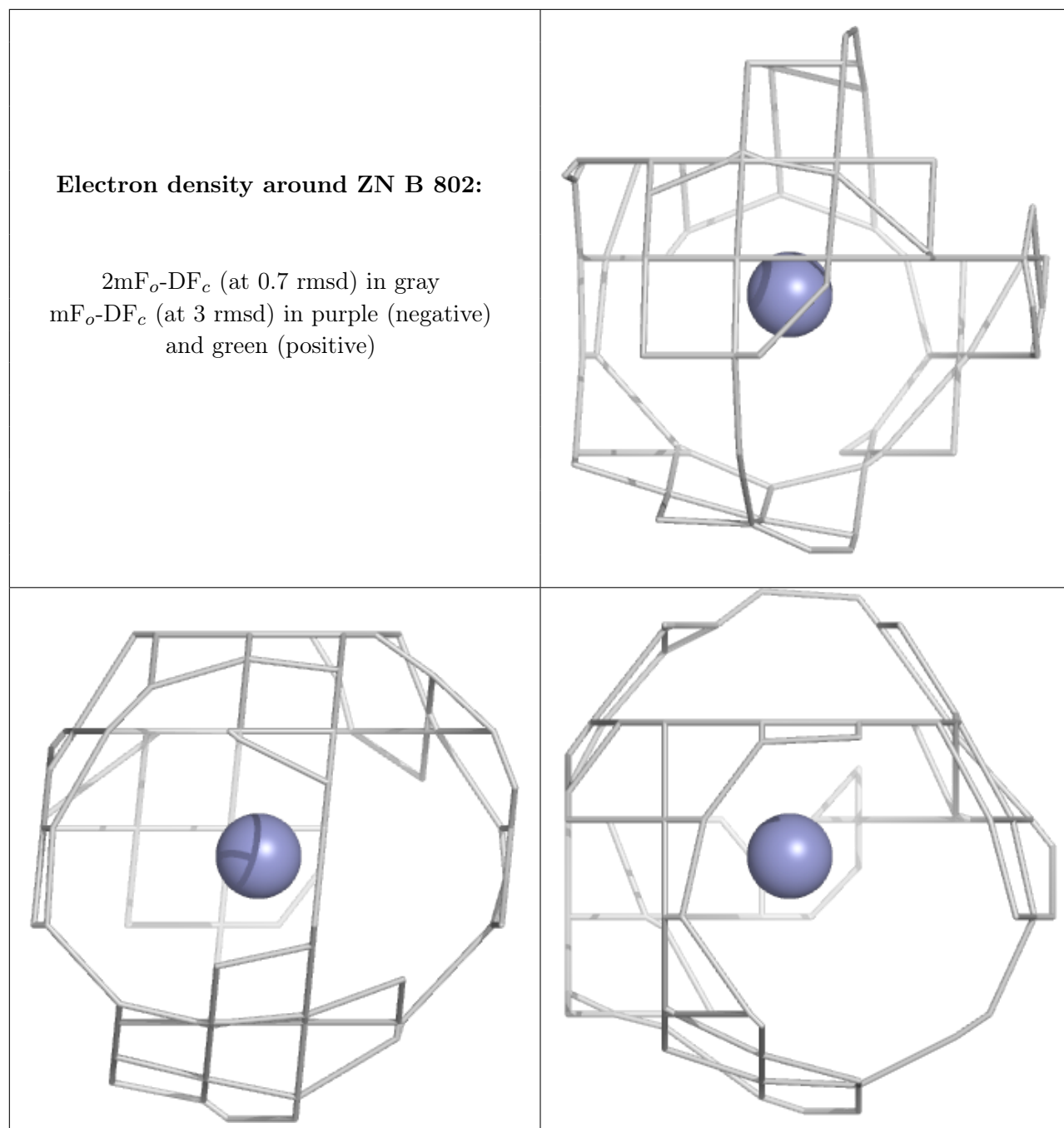




Electron density around ZN A 802:

$2mF_o-DF_c$ (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.