Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2023 – 06:37 pm GMT

PDB ID	:	8PXN
Title	:	N-TERMINAL BROMODOMAIN OF HUMAN BRD4 WITH (1R,1'R)-7,7'-(ethane-1,2-diylbis(oxy))bis(1,3-dimethyl-1,3-dihydro-2H-benzo[d]azepin-2-one)
Authors	:	Chung, C.
Deposited on	:	2023-07-23
Resolution	:	1.95 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 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:

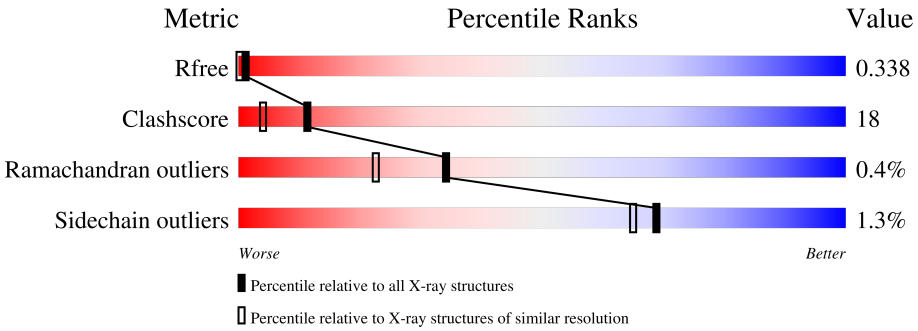
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)

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%

Mol	Chain	Length	Quality of chain
1	A	127	79% 20% .
1	B	127	65% 32% ..
1	C	127	74% 25% .
1	D	127	69% 31% .

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5068 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.

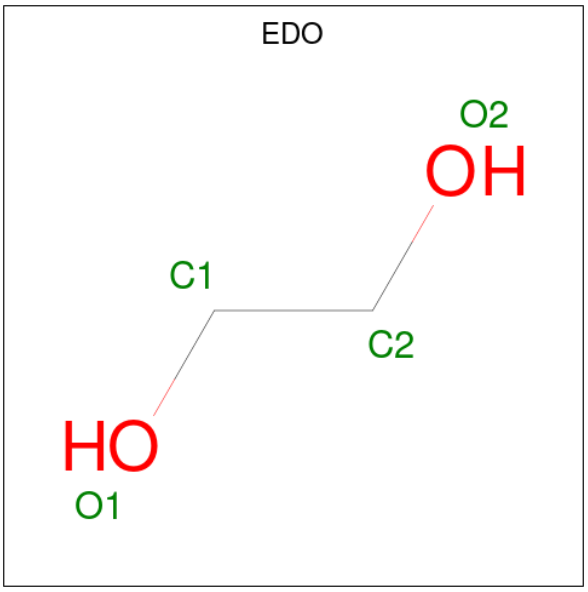
- Molecule 1 is a protein called Bromodomain-containing protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	127	Total	C	N	O	S	0	0	0
			1061	687	174	193	7			
1	B	126	Total	C	N	O	S	0	0	0
			1055	684	173	191	7			
1	C	126	Total	C	N	O	S	0	0	0
			1049	678	173	191	7			
1	D	127	Total	C	N	O	S	0	0	0
			1061	687	174	193	7			

There are 8 discrepancies between the modelled and reference sequences:

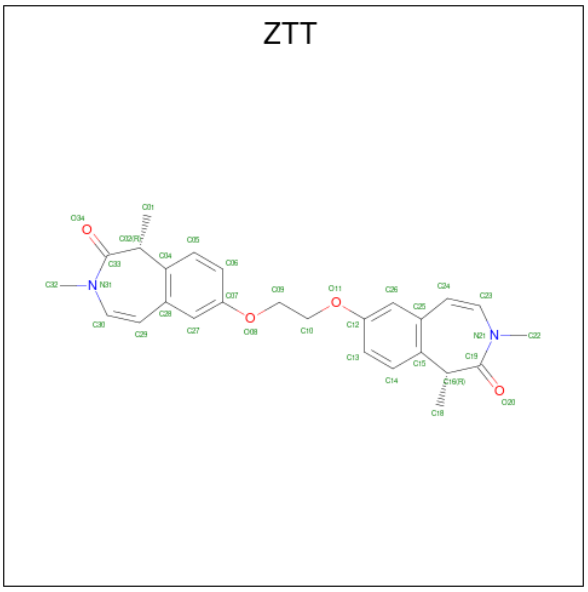
Chain	Residue	Modelled	Actual	Comment	Reference
A	42	SER	-	expression tag	UNP O60885
A	43	MET	-	expression tag	UNP O60885
B	42	SER	-	expression tag	UNP O60885
B	43	MET	-	expression tag	UNP O60885
C	42	SER	-	expression tag	UNP O60885
C	43	MET	-	expression tag	UNP O60885
D	42	SER	-	expression tag	UNP O60885
D	43	MET	-	expression tag	UNP O60885

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 3 is (1R)-7-[2-[[(1R)-1,3-dimethyl-2-oxidanylidene-1H-3-benzazepin-7-yl]oxy]ethoxy]-1,3-dimethyl-1H-3-benzazepin-2-one (three-letter code: ZTT) (formula: $C_{26}H_{28}N_2O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 32 26 2 4	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total C N O 32 26 2 4	0	0

- Molecule 4 is water.

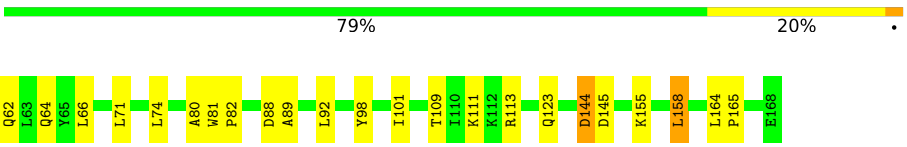
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	199	Total O 199 199	0	0
4	B	180	Total O 180 180	0	0
4	C	193	Total O 193 193	0	0
4	D	198	Total O 198 198	0	0

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. 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. 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.

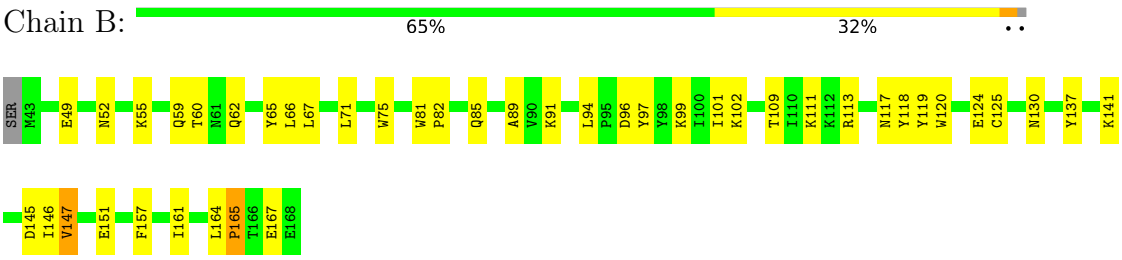
• Molecule 1: Bromodomain-containing protein 4

Chain A:



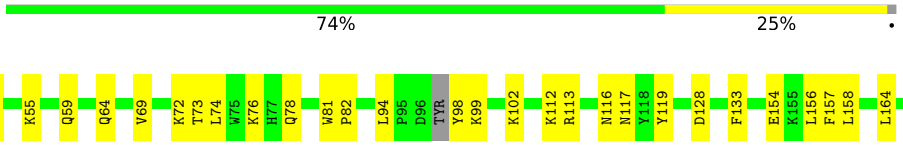
• Molecule 1: Bromodomain-containing protein 4

Chain B:



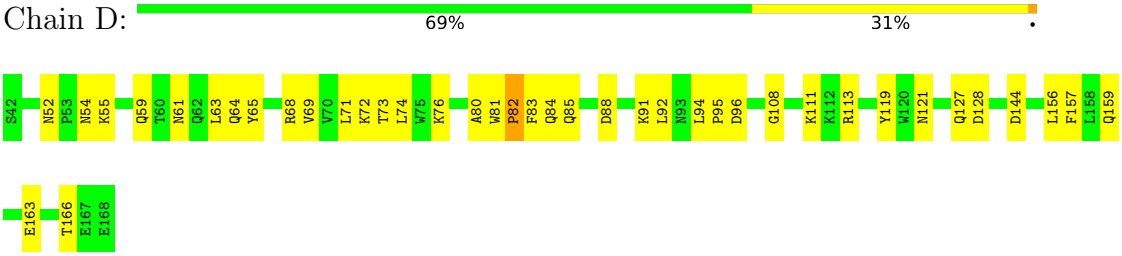
• Molecule 1: Bromodomain-containing protein 4

Chain C:



• Molecule 1: Bromodomain-containing protein 4

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	30.27Å 41.88Å 105.38Å 89.97° 89.95° 89.88°	Depositor
Resolution (Å)	35.13 – 1.95 35.13 – 1.95	Depositor EDS
% Data completeness (in resolution range)	90.4 (35.13-1.95) 99.1 (35.13-1.95)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.24 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.192 , 0.270 0.241 , 0.338	Depositor DCC
R_{free} test set	1770 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å^2)	12.8	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 46.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.53$, $< L^2 > = 0.37$	Xtriage
Estimated twinning fraction	0.137 for h,-k,-l 0.189 for -h,k,-l 0.125 for -h,-k,l	Xtriage
Reported twinning fraction	0.305 for H, K, L 0.277 for -h,-k,l 0.215 for -H, K, -L 0.203 for h,-k,-l	Depositor
Outliers	0 of 37311 reflections	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	5068	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.78% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: EDO, ZTT

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	0.33	0/1091	0.67	0/1484
1	B	0.33	0/1085	0.65	0/1476
1	C	0.33	0/1077	0.64	0/1463
1	D	0.31	0/1091	0.67	0/1484
All	All	0.33	0/4344	0.66	0/5907

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	1061	0	1056	29	0
1	B	1055	0	1051	37	0
1	C	1049	0	1046	40	0
1	D	1061	0	1056	52	0
2	A	4	0	6	2	0
2	D	4	0	6	0	0
3	A	32	0	0	1	0
3	D	32	0	0	0	0
4	A	199	0	0	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	180	0	0	15	0
4	C	193	0	0	14	0
4	D	198	0	0	15	0
All	All	5068	0	4221	152	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 18.

All (152) 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:81:TRP:CH2	1:D:81:TRP:CZ2	2.43	1.06
1:A:98:TYR:CD1	4:A:304:HOH:O	2.12	1.01
1:C:50:THR:O	4:C:201:HOH:O	1.87	0.92
1:C:81:TRP:CH2	1:D:81:TRP:CH2	2.59	0.91
1:C:73:THR:HG22	1:C:156:LEU:HD21	1.55	0.88
1:A:145:ASP:N	4:A:301:HOH:O	2.05	0.88
1:C:154:GLU:O	1:C:158:LEU:HG	1.74	0.87
1:C:81:TRP:CZ2	1:D:81:TRP:CH2	2.63	0.85
1:C:81:TRP:CZ2	1:D:81:TRP:CZ3	2.67	0.81
1:B:130:ASN:OD1	4:B:201:HOH:O	2.00	0.80
1:B:81:TRP:CD1	4:B:216:HOH:O	2.37	0.77
1:C:98:TYR:N	4:C:203:HOH:O	2.17	0.76
1:A:101:ILE:HB	4:A:304:HOH:O	1.85	0.76
4:A:353:HOH:O	1:B:146:ILE:HD11	1.86	0.73
1:D:92:LEU:HD23	1:D:94:LEU:HD12	1.71	0.73
1:B:52:ASN:HD22	1:B:55:LYS:HG3	1.55	0.72
1:D:113:ARG:NH1	1:D:128:ASP:OD2	2.23	0.71
1:A:144:ASP:C	4:A:301:HOH:O	2.28	0.71
1:A:123:GLN:NE2	1:C:49:GLU:OE2	2.25	0.69
1:C:72:LYS:O	4:C:202:HOH:O	2.10	0.69
1:D:95:PRO:HD2	4:D:420:HOH:O	1.94	0.68
2:A:201:EDO:O1	4:A:302:HOH:O	2.09	0.68
1:D:121:ASN:HB3	4:D:393:HOH:O	1.95	0.67
1:B:91:LYS:NZ	4:B:207:HOH:O	2.26	0.66
1:C:81:TRP:CD2	1:C:82:PRO:HD3	2.31	0.66
1:D:127:GLN:OE1	4:D:301:HOH:O	2.13	0.65
1:B:157:PHE:CE1	1:B:161:ILE:HD11	2.30	0.65
1:C:81:TRP:CZ3	1:D:81:TRP:CE2	2.85	0.65
1:C:81:TRP:CZ3	1:C:82:PRO:HB3	2.32	0.64
1:C:81:TRP:CH2	1:D:81:TRP:CE2	2.86	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:LYS:O	1:B:102:LYS:NZ	2.29	0.62
1:A:48:PRO:HG2	1:A:109:THR:HG21	1.82	0.62
1:C:51:SER:HB2	1:C:116:ASN:HD22	1.64	0.62
1:A:58:ARG:HA	4:A:378:HOH:O	2.00	0.62
1:D:64:GLN:O	1:D:68:ARG:HG2	2.00	0.61
1:A:98:TYR:HA	4:A:304:HOH:O	1.98	0.61
1:D:92:LEU:HD11	4:D:477:HOH:O	2.00	0.61
1:C:81:TRP:HH2	1:D:81:TRP:CZ2	2.13	0.61
1:A:48:PRO:HD2	4:A:308:HOH:O	2.01	0.60
1:D:61:ASN:ND2	1:D:166:THR:O	2.34	0.60
1:D:81:TRP:CD2	1:D:82:PRO:HD3	2.37	0.59
1:C:74:LEU:HD21	1:C:157:PHE:HB2	1.85	0.58
1:B:67:LEU:HD12	1:B:71:LEU:HD23	1.86	0.57
1:C:81:TRP:CG	1:C:82:PRO:HD3	2.40	0.57
1:D:81:TRP:CE3	1:D:82:PRO:N	2.73	0.57
1:B:96:ASP:OD2	4:B:202:HOH:O	2.17	0.56
1:B:65:TYR:HB2	4:B:229:HOH:O	2.05	0.56
1:C:59:GLN:NE2	1:C:64:GLN:NE2	2.54	0.56
1:B:62:GLN:NE2	4:B:208:HOH:O	2.26	0.56
1:D:108:GLY:HA3	4:D:391:HOH:O	2.05	0.56
1:B:120:TRP:HB3	4:B:245:HOH:O	2.06	0.55
1:C:112:LYS:O	4:C:201:HOH:O	2.18	0.55
1:D:80:ALA:O	1:D:84:GLN:HG3	2.07	0.55
1:B:52:ASN:ND2	1:B:55:LYS:HG3	2.20	0.55
1:B:59:GLN:NE2	4:B:213:HOH:O	2.39	0.55
4:A:353:HOH:O	1:B:82:PRO:HB2	2.07	0.54
1:D:71:LEU:N	4:D:307:HOH:O	2.39	0.54
1:C:164:LEU:O	4:C:204:HOH:O	2.18	0.54
1:B:164:LEU:HD12	1:B:165:PRO:HD2	1.89	0.53
1:C:113:ARG:HA	4:C:201:HOH:O	2.08	0.53
1:C:133:PHE:CD2	1:C:154:GLU:HG3	2.44	0.53
1:C:51:SER:HB2	1:C:116:ASN:ND2	2.24	0.53
1:D:81:TRP:CG	1:D:82:PRO:HD3	2.44	0.53
1:A:64:GLN:HG2	4:A:436:HOH:O	2.09	0.52
1:A:62:GLN:O	1:A:66:LEU:HG	2.09	0.52
1:B:89:ALA:HB1	1:B:94:LEU:O	2.09	0.52
1:D:52:ASN:HB3	1:D:55:LYS:HG2	1.90	0.52
1:B:167:GLU:N	4:B:206:HOH:O	2.25	0.52
1:D:80:ALA:C	1:D:82:PRO:HD2	2.30	0.52
4:A:353:HOH:O	1:B:82:PRO:CB	2.57	0.51
1:A:57:LYS:NZ	4:A:306:HOH:O	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:81:TRP:CD2	1:D:82:PRO:CD	2.93	0.51
1:D:74:LEU:HD21	1:D:157:PHE:HB2	1.93	0.51
1:D:81:TRP:CZ3	1:D:82:PRO:HB3	2.46	0.50
1:A:74:LEU:O	1:A:80:ALA:HB2	2.11	0.50
1:A:164:LEU:HD11	4:A:328:HOH:O	2.10	0.50
1:B:52:ASN:HD22	1:B:55:LYS:CG	2.24	0.50
1:C:81:TRP:CD2	1:C:82:PRO:CD	2.94	0.50
1:B:75:TRP:O	4:B:203:HOH:O	2.20	0.49
1:B:109:THR:O	1:B:113:ARG:HG3	2.11	0.49
1:D:81:TRP:N	1:D:82:PRO:CD	2.76	0.49
1:C:94:LEU:HD12	4:C:294:HOH:O	2.11	0.49
1:A:164:LEU:HD12	1:A:165:PRO:O	2.12	0.48
1:C:119:TYR:OH	1:C:128:ASP:OD2	2.16	0.48
1:C:99:LYS:O	1:C:102:LYS:NZ	2.47	0.48
1:D:166:THR:HG23	4:D:432:HOH:O	2.14	0.48
1:B:157:PHE:CZ	1:B:161:ILE:HD11	2.49	0.48
1:D:52:ASN:HD22	1:D:55:LYS:NZ	2.12	0.48
1:C:69:VAL:HG13	4:C:206:HOH:O	2.14	0.47
1:D:69:VAL:O	1:D:73:THR:OG1	2.28	0.47
1:C:52:ASN:HD22	1:C:55:LYS:NZ	2.13	0.47
1:B:81:TRP:NE1	4:B:216:HOH:O	2.42	0.47
2:A:201:EDO:O1	4:A:303:HOH:O	2.14	0.47
1:B:117:ASN:O	4:B:204:HOH:O	2.20	0.47
1:D:81:TRP:CZ2	1:D:82:PRO:HG3	2.50	0.47
1:C:76:LYS:HG3	4:C:202:HOH:O	2.15	0.47
1:C:78:GLN:HG3	1:D:91:LYS:HD2	1.96	0.47
1:C:73:THR:CG2	1:C:156:LEU:HD21	2.36	0.46
1:A:88:ASP:O	1:A:92:LEU:HG	2.16	0.46
1:A:71:LEU:C	1:A:71:LEU:HD23	2.36	0.46
1:C:78:GLN:HG2	4:C:329:HOH:O	2.15	0.46
1:D:81:TRP:CE3	1:D:82:PRO:CA	2.99	0.46
1:C:59:GLN:HG2	1:C:64:GLN:HE21	1.81	0.46
1:B:137:TYR:O	4:B:205:HOH:O	2.21	0.45
1:D:65:TYR:OH	1:D:163:GLU:CG	2.65	0.45
1:D:72:LYS:NZ	4:D:309:HOH:O	2.39	0.45
1:A:42:SER:O	1:A:42:SER:OG	2.31	0.44
1:A:89:ALA:HB3	4:A:404:HOH:O	2.17	0.44
1:A:111:LYS:HE2	4:A:401:HOH:O	2.17	0.44
1:C:117:ASN:ND2	4:C:211:HOH:O	2.42	0.44
1:A:62:GLN:NE2	1:A:164:LEU:HD11	2.32	0.44
1:D:63:LEU:CD1	4:D:346:HOH:O	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:TYR:CD1	1:B:124:GLU:HB3	2.53	0.43
1:D:63:LEU:HD12	4:D:346:HOH:O	2.18	0.43
1:A:42:SER:HB2	4:A:416:HOH:O	2.18	0.43
1:B:49:GLU:OE1	1:B:118:TYR:OH	2.28	0.43
1:C:43:MET:N	4:C:219:HOH:O	2.51	0.43
1:C:112:LYS:C	4:C:201:HOH:O	2.57	0.43
1:D:82:PRO:HG2	1:D:83:PHE:CE2	2.54	0.43
1:D:88:ASP:OD2	1:D:91:LYS:HD3	2.18	0.43
1:B:89:ALA:HB3	4:B:286:HOH:O	2.18	0.43
1:B:147:VAL:O	1:B:151:GLU:HG3	2.19	0.43
1:B:97:TYR:CZ	1:B:101:ILE:HG13	2.54	0.43
1:D:113:ARG:HD3	1:D:119:TYR:CE1	2.53	0.43
1:D:144:ASP:CG	4:D:304:HOH:O	2.57	0.43
1:D:54:ASN:HA	4:D:440:HOH:O	2.18	0.43
1:D:81:TRP:CH2	1:D:82:PRO:HG3	2.54	0.43
1:D:85:GLN:HA	4:D:391:HOH:O	2.18	0.43
1:D:71:LEU:HD21	1:D:111:LYS:HB2	2.00	0.42
1:D:73:THR:HG22	1:D:156:LEU:HD21	2.01	0.42
1:A:71:LEU:HD23	1:A:71:LEU:O	2.19	0.42
1:D:59:GLN:N	1:D:59:GLN:OE1	2.52	0.42
1:C:52:ASN:HD22	1:C:55:LYS:HZ3	1.66	0.42
1:B:67:LEU:CD1	1:B:71:LEU:HD23	2.50	0.42
1:D:76:LYS:O	4:D:302:HOH:O	2.21	0.42
1:A:144:ASP:N	4:A:301:HOH:O	2.53	0.41
1:A:158:LEU:HD21	4:A:314:HOH:O	2.20	0.41
1:A:155:LYS:CE	4:A:413:HOH:O	2.67	0.41
1:A:81:TRP:CG	1:A:82:PRO:HD3	2.56	0.41
1:B:66:LEU:HD13	1:B:125:CYS:HB3	2.02	0.41
1:B:71:LEU:HD21	1:B:111:LYS:HA	2.03	0.41
1:A:158:LEU:HD13	1:A:158:LEU:HA	1.89	0.41
1:D:159:GLN:HA	4:D:423:HOH:O	2.20	0.41
1:B:52:ASN:HD22	1:B:55:LYS:CB	2.34	0.41
1:C:116:ASN:HB2	4:C:201:HOH:O	2.20	0.41
1:D:80:ALA:C	1:D:82:PRO:CD	2.89	0.41
1:A:109:THR:O	1:A:113:ARG:HG3	2.21	0.41
3:A:202:ZTT:C22	4:A:353:HOH:O	2.69	0.40
1:B:60:THR:HA	4:B:290:HOH:O	2.21	0.40
1:B:81:TRP:O	1:B:85:GLN:NE2	2.52	0.40
1:D:52:ASN:HB3	1:D:55:LYS:CG	2.51	0.40
1:D:81:TRP:CZ3	1:D:82:PRO:CB	3.05	0.40

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	125/127 (98%)	119 (95%)	5 (4%)	1 (1%)	19 9
1	B	124/127 (98%)	120 (97%)	3 (2%)	1 (1%)	19 9
1	C	122/127 (96%)	117 (96%)	5 (4%)	0	100 100
1	D	125/127 (98%)	121 (97%)	4 (3%)	0	100 100
All	All	496/508 (98%)	477 (96%)	17 (3%)	2 (0%)	34 22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	ASP
1	B	165	PRO

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	120/120 (100%)	119 (99%)	1 (1%)	81 80
1	B	119/120 (99%)	116 (98%)	3 (2%)	47 38
1	C	119/120 (99%)	119 (100%)	0	100 100
1	D	120/120 (100%)	118 (98%)	2 (2%)	60 55
All	All	478/480 (100%)	472 (99%)	6 (1%)	69 65

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	LEU
1	B	141	LYS
1	B	145	ASP
1	B	147	VAL
1	D	82	PRO
1	D	96	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	52	ASN
1	B	59	GLN
1	B	117	ASN
1	B	130	ASN
1	C	52	ASN
1	C	59	GLN
1	C	64	GLN
1	C	78	GLN
1	C	116	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

4 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	ZTT	A	202	-	33,35,35	0.62	1 (3%)	34,50,50	0.92	2 (5%)
2	EDO	D	201	-	3,3,3	0.25	0	2,2,2	0.12	0
3	ZTT	D	202	-	33,35,35	0.56	0	34,50,50	1.48	6 (17%)
2	EDO	A	201	-	3,3,3	0.16	0	2,2,2	0.20	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	ZTT	A	202	-	-	1/7/41/41	0/2/4/4
2	EDO	D	201	-	-	1/1/1/1	-
3	ZTT	D	202	-	-	2/7/41/41	0/2/4/4
2	EDO	A	201	-	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	202	ZTT	O34-C33	2.06	1.26	1.22

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	202	ZTT	C16-C19-N21	4.44	118.10	115.73
3	D	202	ZTT	O08-C07-C27	3.69	137.53	119.86
3	D	202	ZTT	O08-C07-C06	-3.60	102.25	119.94
3	D	202	ZTT	O20-C19-C16	-2.80	120.21	122.22
3	A	202	ZTT	C16-C19-N21	2.63	117.14	115.73
3	D	202	ZTT	O11-C12-C26	-2.48	107.97	119.86
3	D	202	ZTT	O11-C12-C13	2.46	132.04	119.94
3	A	202	ZTT	C22-N21-C19	2.12	119.90	117.31

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	202	ZTT	O08-C09-C10-O11
3	D	202	ZTT	C27-C07-O08-C09
2	A	201	EDO	O1-C1-C2-O2
2	D	201	EDO	O1-C1-C2-O2
3	D	202	ZTT	O08-C09-C10-O11

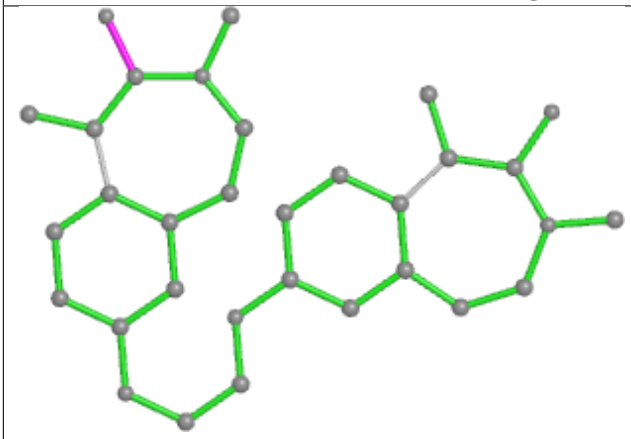
There are no ring outliers.

2 monomers are involved in 3 short contacts:

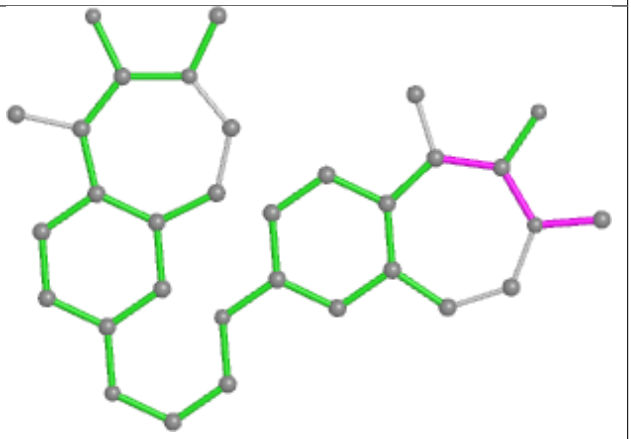
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	202	ZTT	1	0
2	A	201	EDO	2	0

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 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.

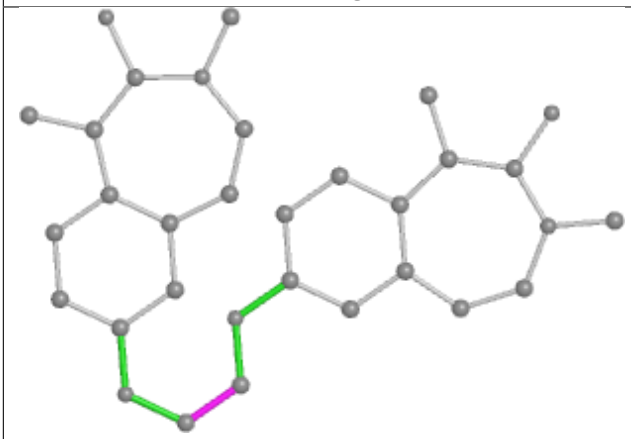
Ligand ZTT A 202



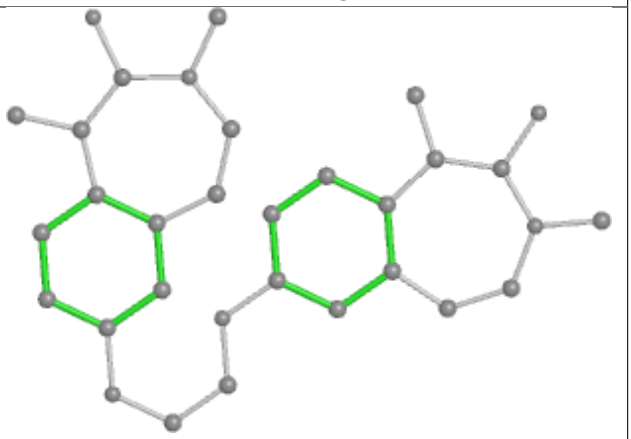
Bond lengths



Bond angles

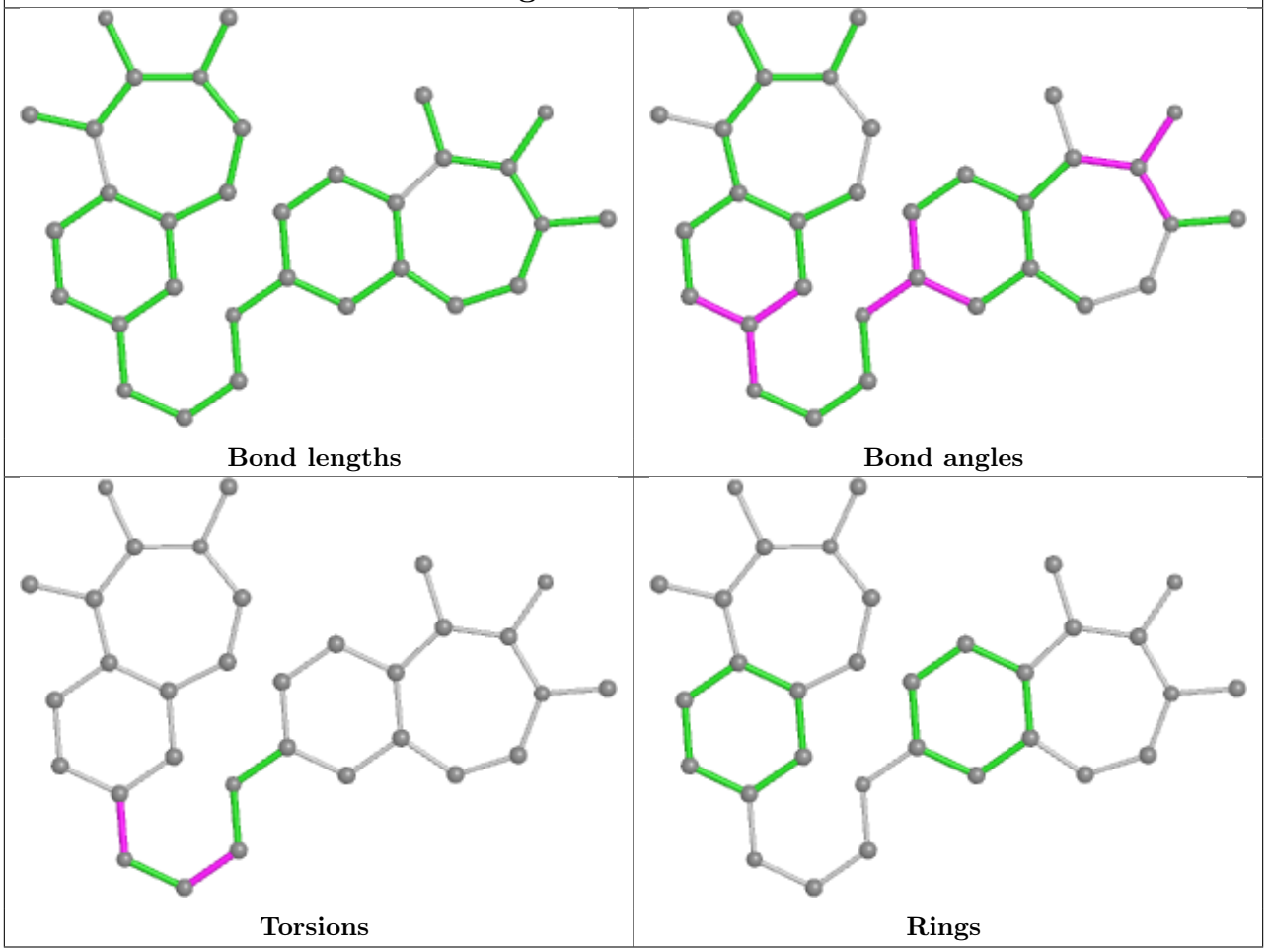


Torsions



Rings

Ligand ZTT D 202



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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

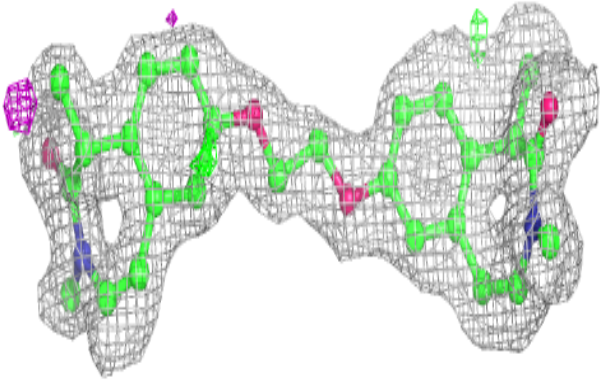
6.4 Ligands

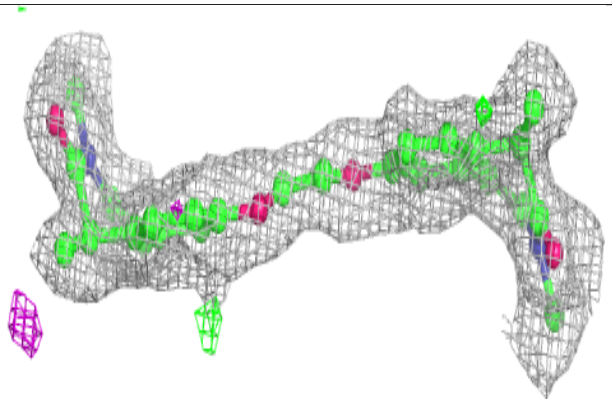
Unable to reproduce the depositors R factor - this section is therefore empty.

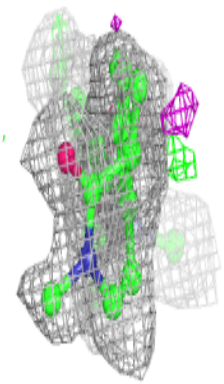
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ZTT A 202:

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

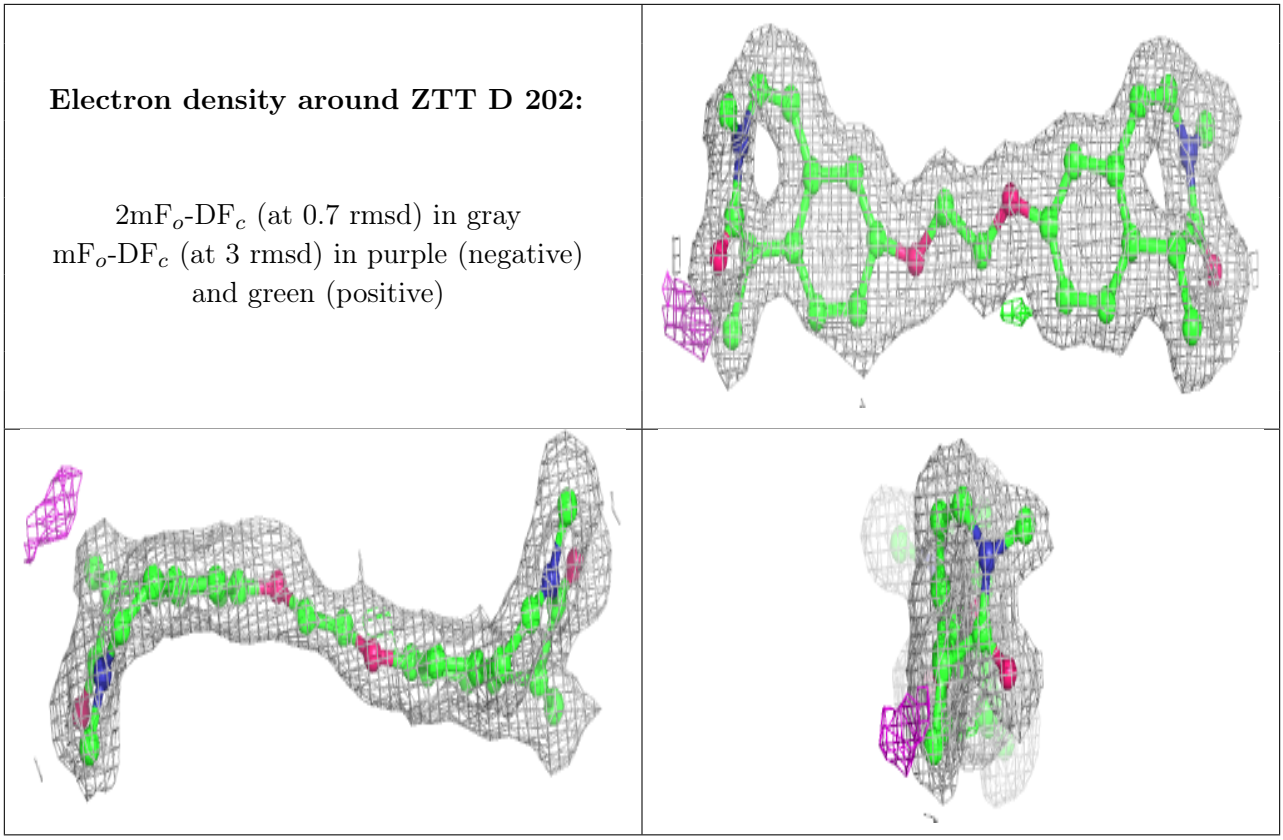






Electron density around ZTT D 202:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.