



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 11:21 PM UTC

PDB ID : 8PJ0 / pdb_00008pj0
Title : Pseudomonas aeruginosa FabF C164A mutant in complex with N-(1,5-dimethyl-3-oxo-2-phenyl-2,3-dihydro-1H-pyrazol-4-yl)-3-methylbutanamide
Authors : Georgiou, C.; Brenk, R.; Espeland, L.O.
Deposited on : 2023-06-22
Resolution : 1.70 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

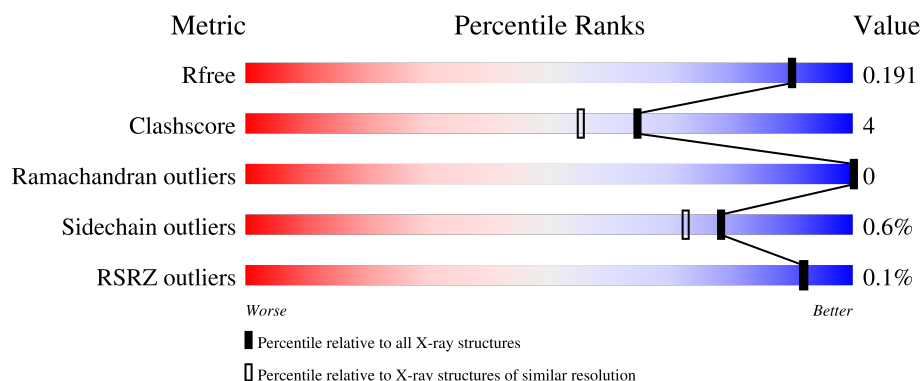
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

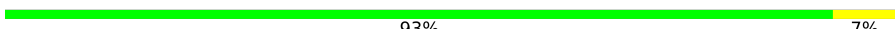
The reported resolution of this entry is 1.70 Å.

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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	412	 92% 8%
1	B	412	 92% 7%
1	C	412	 92% 8%
1	D	412	 93% 7%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13316 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.

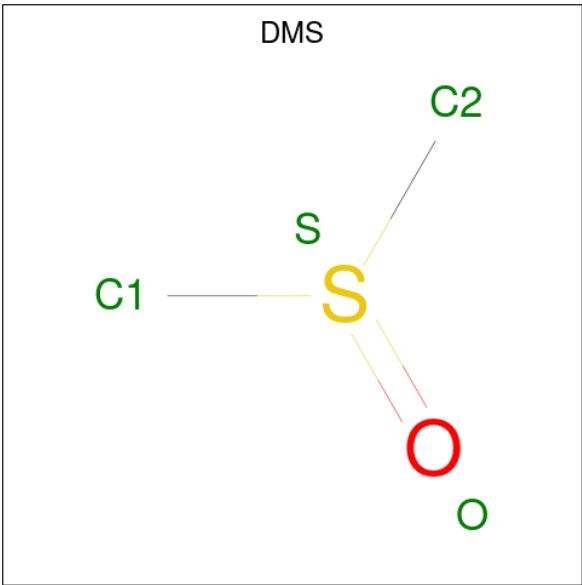
- Molecule 1 is a protein called 3-oxoacyl-[acyl-carrier-protein] synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	412	Total	C	N	O	S	0	8	0
			3075	1916	554	587	18			
1	B	412	Total	C	N	O	S	0	5	0
			3057	1901	551	587	18			
1	C	412	Total	C	N	O	S	0	8	0
			3075	1916	554	587	18			
1	D	412	Total	C	N	O	S	0	4	0
			3054	1899	551	586	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	164	ALA	CYS	engineered mutation	UNP G3XDA2
B	164	ALA	CYS	engineered mutation	UNP G3XDA2
C	164	ALA	CYS	engineered mutation	UNP G3XDA2
D	164	ALA	CYS	engineered mutation	UNP G3XDA2

- Molecule 2 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



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

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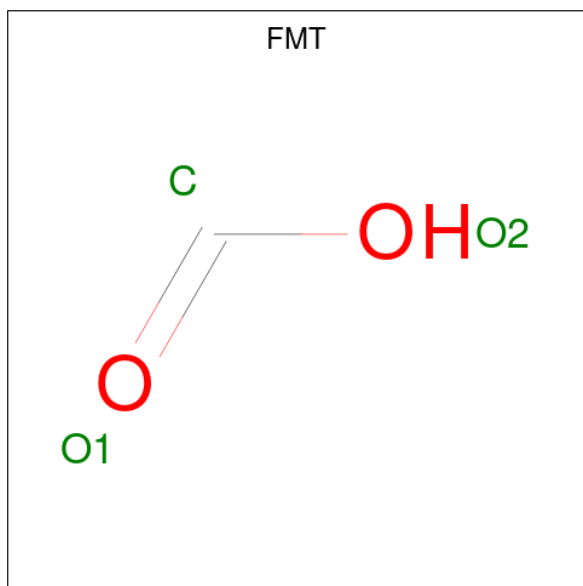
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total 4	C 2	O 1	S 1	0	0
2	B	1	Total 4	C 2	O 1	S 1	0	0
2	B	1	Total 4	C 2	O 1	S 1	0	0
2	B	1	Total 4	C 2	O 1	S 1	0	0
2	C	1	Total 4	C 2	O 1	S 1	0	0
2	C	1	Total 4	C 2	O 1	S 1	0	0
2	C	1	Total 4	C 2	O 1	S 1	0	0
2	C	1	Total 4	C 2	O 1	S 1	0	0
2	C	1	Total 4	C 2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

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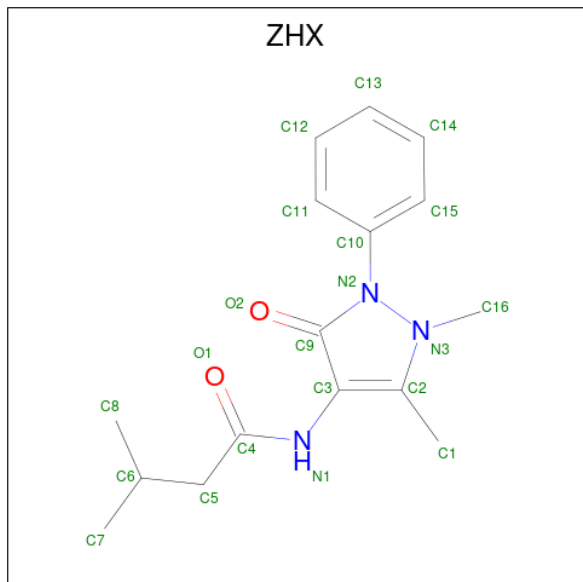
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	D	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		
2	D	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 3 is FORMIC ACID (CCD ID: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			3	1	2		
3	C	1	Total	C	O	0	0
			3	1	2		

- Molecule 4 is {N}-(1,5-dimethyl-3-oxidanylidene-2-phenyl-pyrazol-4-yl)-3-methyl-butanamide (CCD ID: ZHX) (formula: C₁₆H₂₁N₃O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			21	16	3	2		
4	B	1	Total	C	N	O	0	0
			21	16	3	2		
4	C	1	Total	C	N	O	0	0
			21	16	3	2		
4	D	1	Total	C	N	O	0	0
			21	16	3	2		

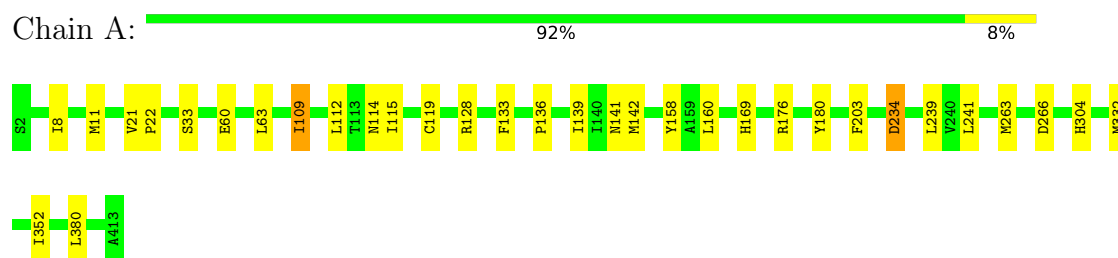
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	199	Total	O	0	0
			199	199		
5	B	197	Total	O	0	0
			197	197		
5	C	218	Total	O	0	0
			218	218		
5	D	175	Total	O	0	0
			175	175		

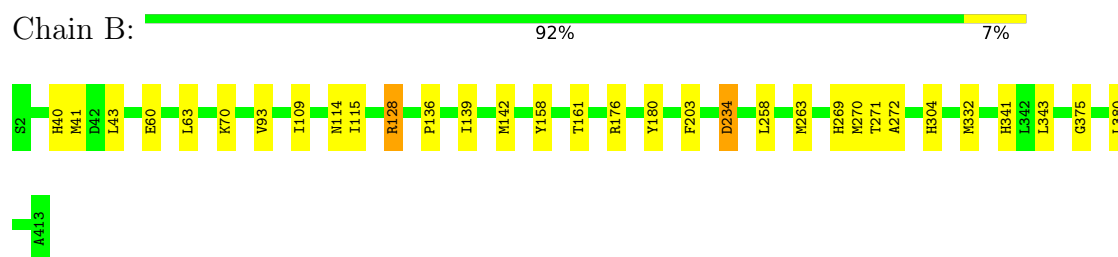
3 Residue-property plots [i](#)

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.

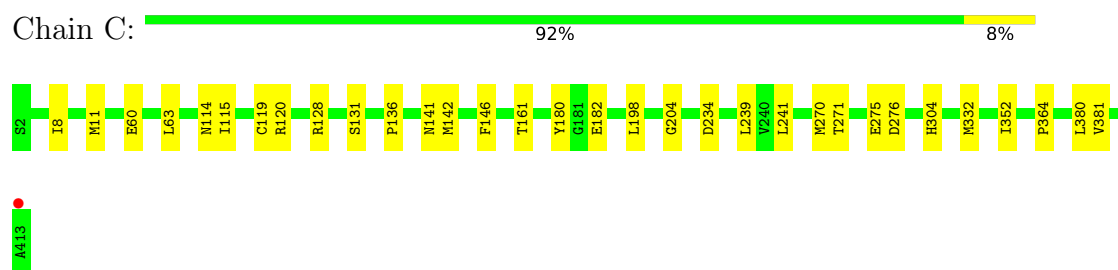
- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 2



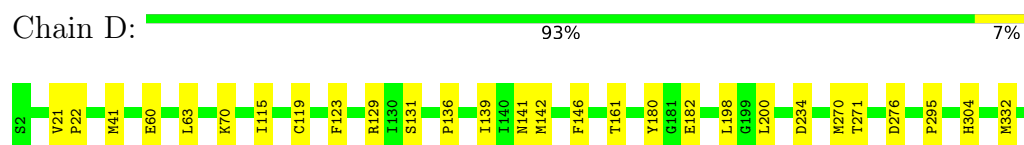
- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 2



- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 2



- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	72.46Å 141.34Å 72.48Å 90.00° 91.64° 90.00°	Depositor
Resolution (Å)	48.83 – 1.70 48.83 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.83-1.70) 98.9 (48.83-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.162 , 0.182 0.174 , 0.191	Depositor DCC
R_{free} test set	7819 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	23.0	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 26.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.040 for l,k,-h 0.043 for h,-k,-l 0.476 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13316	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.63% 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: ZHX, FMT, DMS

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	0.61	0/3152	0.83	3/4258 (0.1%)
1	B	0.61	0/3125	0.84	2/4222 (0.0%)
1	C	0.67	1/3152 (0.0%)	0.91	3/4258 (0.1%)
1	D	0.60	0/3119	0.84	3/4214 (0.1%)
All	All	0.62	1/12548 (0.0%)	0.86	11/16952 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	364	PRO	C-O	-5.86	1.20	1.25

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	234	ASP	CA-CB-CG	6.65	119.25	112.60
1	A	234	ASP	CA-CB-CG	6.45	119.05	112.60
1	D	234	ASP	CA-CB-CG	6.38	118.98	112.60
1	C	304	HIS	N-CA-C	-6.24	104.40	111.14
1	D	304	HIS	N-CA-C	-6.23	104.42	111.14
1	A	304	HIS	N-CA-C	-6.19	104.46	111.14
1	C	234	ASP	CA-CB-CG	6.12	118.72	112.60
1	B	304	HIS	N-CA-C	-5.91	104.76	111.14
1	C	276	ASP	CA-CB-CG	5.30	117.90	112.60
1	D	276	ASP	CA-CB-CG	5.21	117.81	112.60
1	A	266	ASP	CA-CB-CG	5.09	117.69	112.60

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	3075	0	3046	28	0
1	B	3057	0	3011	27	0
1	C	3075	0	3046	32	0
1	D	3054	0	3006	27	0
2	A	36	0	54	2	0
2	B	36	0	54	9	0
2	C	56	0	84	8	0
2	D	48	0	72	6	0
3	A	3	0	1	0	0
3	C	3	0	1	0	0
4	A	21	0	0	1	0
4	B	21	0	0	1	0
4	C	21	0	0	0	0
4	D	21	0	0	0	0
5	A	199	0	0	0	0
5	B	197	0	0	1	0
5	C	218	0	0	1	0
5	D	175	0	0	0	0
All	All	13316	0	12375	96	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 4.

All (96) 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:114:ASN:HD21	2:B:503:DMS:H12	1.15	1.05
1:B:114:ASN:ND2	2:B:503:DMS:H12	1.84	0.92
1:A:109:ILE:HD12	1:A:112:LEU:HD13	1.57	0.86
1:C:146:PHE:HZ	1:D:270:MET:HE3	1.45	0.81
1:C:270:MET:HE3	1:D:146:PHE:HZ	1.45	0.79
1:C:115:ILE:HG21	1:D:115:ILE:HG21	1.70	0.73
1:C:8:ILE:CD1	1:C:241[B]:LEU:HD22	2.24	0.68
1:A:109:ILE:HD13	1:A:109:ILE:O	1.93	0.66
1:B:375:GLY:HA3	2:B:508:DMS:H12	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:119:CYS:SG	1:D:198:LEU:HD11	2.37	0.64
1:D:270:MET:HG3	1:D:271:THR:HG23	1.80	0.63
1:C:136:PRO:O	1:C:142:MET:HG3	1.99	0.62
1:D:136:PRO:O	1:D:142:MET:HG3	1.99	0.62
1:C:270:MET:HE2	1:D:136:PRO:HB2	1.82	0.62
1:C:270:MET:HG3	1:C:271:THR:HG23	1.82	0.60
1:C:114:ASN:CG	2:C:514:DMS:H23	2.27	0.60
1:A:109:ILE:CD1	1:A:112:LEU:HD13	2.30	0.60
1:B:136:PRO:O	1:B:142:MET:HG3	2.02	0.59
1:D:180:TYR:HD1	1:D:182:GLU:HG3	1.68	0.58
1:A:136:PRO:O	1:A:142:MET:HG3	2.03	0.58
1:A:128:ARG:CZ	2:B:504:DMS:H23	2.33	0.58
1:B:332:MET:O	1:B:380:LEU:HA	2.04	0.58
1:C:180:TYR:HD1	1:C:182:GLU:HG3	1.69	0.58
1:A:332:MET:O	1:A:380:LEU:HA	2.04	0.57
1:B:93:VAL:HB	2:B:506:DMS:H11	1.85	0.57
1:C:332:MET:O	1:C:380:LEU:HA	2.05	0.57
1:C:136:PRO:HB2	1:D:270:MET:HE2	1.86	0.57
1:D:332:MET:O	1:D:380:LEU:HA	2.05	0.56
1:C:115:ILE:CD1	2:C:504:DMS:H21	2.36	0.56
1:C:270:MET:HE3	1:D:146:PHE:CZ	2.35	0.56
1:A:11:MET:HG2	1:A:239[B]:LEU:HD23	1.87	0.55
1:C:204:GLY:HA3	2:C:507:DMS:H23	1.86	0.55
1:A:239[B]:LEU:HD21	1:A:352:ILE:HG12	1.89	0.55
1:D:295:PRO:HD3	2:D:511:DMS:H21	1.88	0.54
1:B:269:HIS:HD2	1:B:272:ALA:H	1.54	0.54
1:B:341:HIS:CD2	1:B:343:LEU:H	2.25	0.54
1:C:198:LEU:HD11	1:D:119:CYS:SG	2.48	0.54
1:D:129:ARG:HD2	2:D:501:DMS:H11	1.91	0.52
1:B:203:PHE:CE1	4:B:507:ZHX:C16	2.92	0.51
1:C:131:SER:HB2	2:C:503:DMS:H13	1.93	0.51
1:B:269:HIS:HD2	1:B:271:THR:H	1.57	0.51
1:B:270:MET:HE3	5:B:743:HOH:O	2.11	0.51
1:B:40:HIS:HB3	2:B:510:DMS:H22	1.93	0.51
1:A:133:PHE:HE1	1:B:270:MET:HE1	1.76	0.50
1:C:239[B]:LEU:HD21	1:C:352:ILE:HG12	1.92	0.50
1:D:41:MET:HE1	1:D:200:LEU:HD23	1.93	0.50
1:C:146:PHE:CZ	1:D:270:MET:HE3	2.36	0.50
1:A:114:ASN:OD1	2:A:503:DMS:H22	2.12	0.49
1:B:269:HIS:CD2	1:B:271:THR:H	2.31	0.48
1:A:11:MET:HG2	1:A:239[B]:LEU:CD2	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:PHE:CE1	4:A:509:ZHX:C16	2.97	0.48
1:A:158:TYR:CD1	1:B:263:MET:HE1	2.49	0.48
1:B:269:HIS:CD2	1:B:272:ALA:H	2.32	0.48
1:A:8:ILE:CD1	1:A:241[B]:LEU:CD2	2.93	0.47
1:A:33:SER:O	2:A:507:DMS:H23	2.14	0.47
1:B:128:ARG:H	1:B:128:ARG:HG3	1.56	0.46
1:D:131:SER:OG	2:D:504:DMS:H13	2.15	0.46
1:A:8:ILE:CD1	1:A:241[B]:LEU:HD22	2.46	0.46
1:A:133:PHE:CE1	1:B:270:MET:HE1	2.50	0.46
1:A:139:ILE:HG13	1:A:142:MET:HG2	1.97	0.46
1:D:129:ARG:HH11	2:D:501:DMS:H11	1.81	0.46
1:A:115:ILE:HG21	1:B:115:ILE:HG21	1.97	0.45
1:A:239[B]:LEU:HD21	1:A:352:ILE:CG1	2.46	0.45
1:C:8:ILE:HD13	1:C:241[B]:LEU:HD22	1.97	0.45
2:C:504:DMS:H22	5:C:754:HOH:O	2.15	0.45
1:C:114:ASN:ND2	2:C:514:DMS:H23	2.31	0.45
1:A:60:GLU:HA	1:A:63:LEU:O	2.17	0.45
1:C:270:MET:HE2	1:D:136:PRO:CB	2.47	0.45
1:B:60:GLU:HA	1:B:63:LEU:O	2.17	0.44
1:B:70:LYS:C	2:B:503:DMS:H11	2.43	0.44
1:C:128:ARG:HG2	2:D:505:DMS:H22	2.00	0.43
1:C:60:GLU:HA	1:C:63:LEU:O	2.19	0.43
1:B:139:ILE:HG13	1:B:142:MET:HG2	2.00	0.43
1:C:115:ILE:HD11	2:C:504:DMS:H21	1.99	0.43
1:C:180:TYR:CD1	1:C:182:GLU:HG3	2.51	0.43
1:C:275:GLU:H	2:C:508:DMS:H12	1.83	0.43
1:D:70:LYS:O	2:D:504:DMS:H21	2.18	0.43
1:D:139:ILE:HG13	1:D:142:MET:HG2	2.00	0.42
1:A:160:LEU:CD1	1:A:169:HIS:HB3	2.49	0.42
1:A:263:MET:HE1	1:B:158:TYR:CD1	2.54	0.42
1:D:21:VAL:HB	1:D:22[B]:PRO:HD3	2.00	0.42
1:C:11:MET:HG2	1:C:239[B]:LEU:HD23	2.02	0.42
1:A:128:ARG:HD3	2:B:504:DMS:H21	2.01	0.42
1:D:60:GLU:HA	1:D:63:LEU:O	2.19	0.42
1:B:41:MET:HE3	1:B:43:LEU:HD21	2.02	0.42
1:B:176:ARG:HD2	1:B:180:TYR:HE2	1.85	0.41
1:A:141:ASN:HB3	1:B:161:THR:O	2.21	0.41
1:A:21:VAL:HB	1:A:22[B]:PRO:HD3	2.03	0.41
1:A:115:ILE:HD11	2:B:501:DMS:H21	2.03	0.41
1:D:180:TYR:CD1	1:D:182:GLU:HG3	2.51	0.40
1:C:141:ASN:HB3	1:D:161:THR:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:239[B]:LEU:HD21	1:C:352:ILE:CG1	2.50	0.40
1:A:176:ARG:HD2	1:A:180:TYR:HE2	1.86	0.40
1:C:120:ARG:NH2	1:D:123:PHE:CE1	2.90	0.40
1:C:161:THR:O	1:D:141:ASN:HB3	2.22	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	418/412 (102%)	406 (97%)	12 (3%)	0	100	100
1	B	415/412 (101%)	403 (97%)	12 (3%)	0	100	100
1	C	418/412 (102%)	406 (97%)	12 (3%)	0	100	100
1	D	414/412 (100%)	402 (97%)	12 (3%)	0	100	100
All	All	1665/1648 (101%)	1617 (97%)	48 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	316/308 (103%)	313 (99%)	3 (1%)	70	62
1	B	313/308 (102%)	310 (99%)	3 (1%)	68	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	316/308 (103%)	315 (100%)	1 (0%)	86	83
1	D	312/308 (101%)	312 (100%)	0	100	100
All	All	1257/1232 (102%)	1250 (99%)	7 (1%)	78	72

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	ILE
1	A	119	CYS
1	A	234	ASP
1	B	109	ILE
1	B	128	ARG
1	B	234	ASP
1	C	381	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	150	HIS
1	A	154	GLN
1	A	404	ASN
1	B	114	ASN
1	B	150	HIS
1	B	154	GLN
1	B	269	HIS
1	B	341	HIS
1	B	404	ASN
1	C	117	ASN
1	C	118	ASN
1	C	154	GLN
1	C	302	ASN
1	C	328	HIS
1	C	404	ASN
1	D	150	HIS
1	D	154	GLN
1	D	302	ASN
1	D	404	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

50 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	$\# Z > 2$
2	DMS	B	506	-	3,3,3	0.27	0	3,3,3	0.13	0
2	DMS	A	508	-	3,3,3	0.27	0	3,3,3	0.09	0
2	DMS	B	505	-	3,3,3	0.23	0	3,3,3	0.13	0
2	DMS	C	515	-	3,3,3	0.18	0	3,3,3	0.18	0
4	ZHX	C	512	-	22,22,22	0.67	0	31,31,31	1.36	6 (19%)
2	DMS	C	506	-	3,3,3	0.28	0	3,3,3	0.09	0
2	DMS	C	508	-	3,3,3	0.30	0	3,3,3	0.05	0
2	DMS	C	510	-	3,3,3	0.30	0	3,3,3	0.08	0
2	DMS	C	516	-	3,3,3	0.23	0	3,3,3	0.07	0
2	DMS	C	501	-	3,3,3	0.31	0	3,3,3	0.20	0
2	DMS	D	504	-	3,3,3	0.18	0	3,3,3	0.18	0
2	DMS	B	502	-	3,3,3	0.22	0	3,3,3	0.12	0
2	DMS	B	501	-	3,3,3	0.47	0	3,3,3	0.08	0
2	DMS	B	503	-	3,3,3	0.27	0	3,3,3	0.22	0
2	DMS	C	503	-	3,3,3	0.28	0	3,3,3	0.04	0
2	DMS	A	506	-	3,3,3	0.26	0	3,3,3	0.08	0
2	DMS	C	505	-	3,3,3	0.22	0	3,3,3	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DMS	A	504	-	3,3,3	0.27	0	3,3,3	0.11	0
4	ZHX	A	509	-	22,22,22	0.53	0	31,31,31	1.02	3 (9%)
2	DMS	A	507	-	3,3,3	0.37	0	3,3,3	0.14	0
2	DMS	A	511	-	3,3,3	0.23	0	3,3,3	0.08	0
2	DMS	B	504	-	3,3,3	0.19	0	3,3,3	0.18	0
2	DMS	D	506	-	3,3,3	0.30	0	3,3,3	0.22	0
2	DMS	D	511	-	3,3,3	0.25	0	3,3,3	0.19	0
2	DMS	C	509	-	3,3,3	0.32	0	3,3,3	0.08	0
2	DMS	D	503	-	3,3,3	0.23	0	3,3,3	0.08	0
2	DMS	A	505	-	3,3,3	0.25	0	3,3,3	0.06	0
2	DMS	C	513	-	3,3,3	0.24	0	3,3,3	0.12	0
2	DMS	C	511	-	3,3,3	0.22	0	3,3,3	0.08	0
2	DMS	D	505	-	3,3,3	0.28	0	3,3,3	0.11	0
2	DMS	A	510	-	3,3,3	0.22	0	3,3,3	0.18	0
2	DMS	C	507	-	3,3,3	0.22	0	3,3,3	0.17	0
3	FMT	A	502	-	2,2,2	0.85	0	1,1,1	0.33	0
2	DMS	B	509	-	3,3,3	0.21	0	3,3,3	0.11	0
2	DMS	D	510	-	3,3,3	0.23	0	3,3,3	0.12	0
2	DMS	C	504	-	3,3,3	0.59	0	3,3,3	0.22	0
2	DMS	A	503	-	3,3,3	0.23	0	3,3,3	0.08	0
4	ZHX	D	509	-	22,22,22	0.66	0	31,31,31	1.21	5 (16%)
2	DMS	D	512	-	3,3,3	0.25	0	3,3,3	0.11	0
2	DMS	B	510	-	3,3,3	0.33	0	3,3,3	0.08	0
4	ZHX	B	507	-	22,22,22	0.51	0	31,31,31	1.19	2 (6%)
2	DMS	A	501	-	3,3,3	0.25	0	3,3,3	0.21	0
2	DMS	D	502	-	3,3,3	0.30	0	3,3,3	0.04	0
2	DMS	D	507	-	3,3,3	0.25	0	3,3,3	0.06	0
2	DMS	D	508	-	3,3,3	0.25	0	3,3,3	0.20	0
2	DMS	D	513	-	3,3,3	0.26	0	3,3,3	0.14	0
3	FMT	C	502	-	2,2,2	0.97	0	1,1,1	0.27	0
2	DMS	B	508	-	3,3,3	0.28	0	3,3,3	0.12	0
2	DMS	D	501	-	3,3,3	0.23	0	3,3,3	0.23	0
2	DMS	C	514	-	3,3,3	0.24	0	3,3,3	0.23	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
4	ZHX	C	512	-	-	4/12/12/12	0/2/2/2
4	ZHX	D	509	-	-	4/12/12/12	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ZHX	B	507	-	-	4/12/12/12	0/2/2/2
4	ZHX	A	509	-	-	3/12/12/12	0/2/2/2

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	507	ZHX	C6-C5-C4	4.04	119.34	113.29
4	C	512	ZHX	C6-C5-C4	3.93	119.17	113.29
4	D	509	ZHX	C10-N2-N3	3.37	127.19	120.69
4	C	512	ZHX	C10-N2-N3	3.24	126.92	120.69
4	A	509	ZHX	C10-N2-N3	2.91	126.29	120.69
4	B	507	ZHX	C10-N2-N3	2.81	126.09	120.69
4	C	512	ZHX	C9-C3-C2	2.47	110.44	108.98
4	C	512	ZHX	C3-C2-N3	-2.41	107.95	109.49
4	D	509	ZHX	C1-C2-N3	2.21	123.69	121.01
4	C	512	ZHX	C16-N3-N2	2.13	123.64	117.99
4	D	509	ZHX	C16-N3-N2	2.13	123.64	117.99
4	D	509	ZHX	C3-C2-N3	-2.09	108.16	109.49
4	D	509	ZHX	C9-C3-C2	2.09	110.21	108.98
4	A	509	ZHX	C3-C2-N3	-2.08	108.16	109.49
4	C	512	ZHX	C1-C2-N3	2.05	123.49	121.01
4	A	509	ZHX	C16-N3-N2	2.00	123.31	117.99

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	507	ZHX	C4-C5-C6-C7
4	C	512	ZHX	C4-C5-C6-C7
4	B	507	ZHX	C4-C5-C6-C8
4	C	512	ZHX	C4-C5-C6-C8
4	B	507	ZHX	C11-C10-N2-N3
4	D	509	ZHX	C11-C10-N2-N3
4	C	512	ZHX	C11-C10-N2-N3
4	A	509	ZHX	C11-C10-N2-N3
4	D	509	ZHX	N1-C4-C5-C6
4	B	507	ZHX	C15-C10-N2-N3
4	D	509	ZHX	C15-C10-N2-N3
4	A	509	ZHX	C15-C10-N2-N3
4	A	509	ZHX	O1-C4-C5-C6

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Mol	Chain	Res	Type	Atoms
4	C	512	ZHX	C15-C10-N2-N3
4	D	509	ZHX	O1-C4-C5-C6

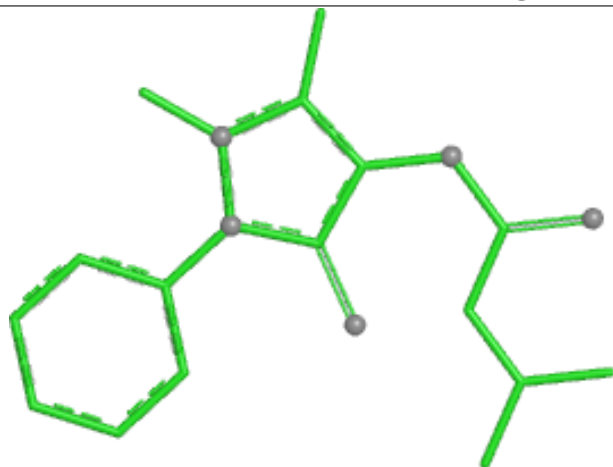
There are no ring outliers.

19 monomers are involved in 27 short contacts:

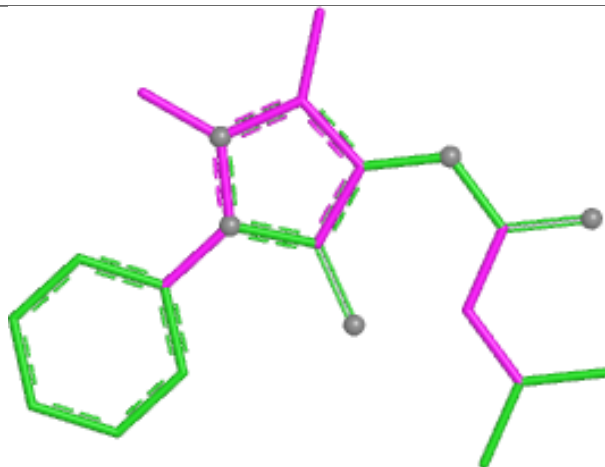
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	506	DMS	1	0
2	C	508	DMS	1	0
2	D	504	DMS	2	0
2	B	501	DMS	1	0
2	B	503	DMS	3	0
2	C	503	DMS	1	0
4	A	509	ZHX	1	0
2	A	507	DMS	1	0
2	B	504	DMS	2	0
2	D	511	DMS	1	0
2	D	505	DMS	1	0
2	C	507	DMS	1	0
2	C	504	DMS	3	0
2	A	503	DMS	1	0
2	B	510	DMS	1	0
4	B	507	ZHX	1	0
2	B	508	DMS	1	0
2	D	501	DMS	2	0
2	C	514	DMS	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 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.

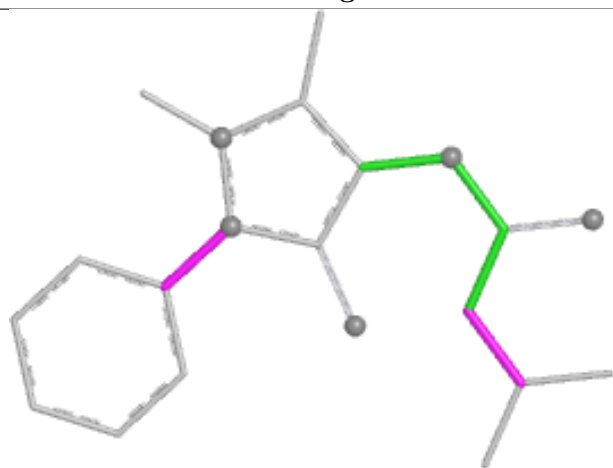
Ligand ZHX C 512



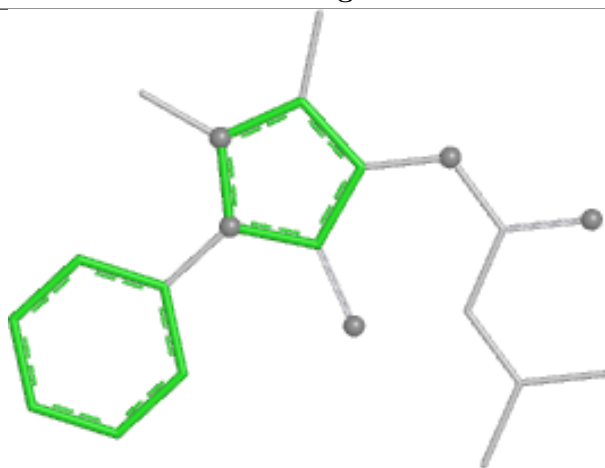
Bond lengths



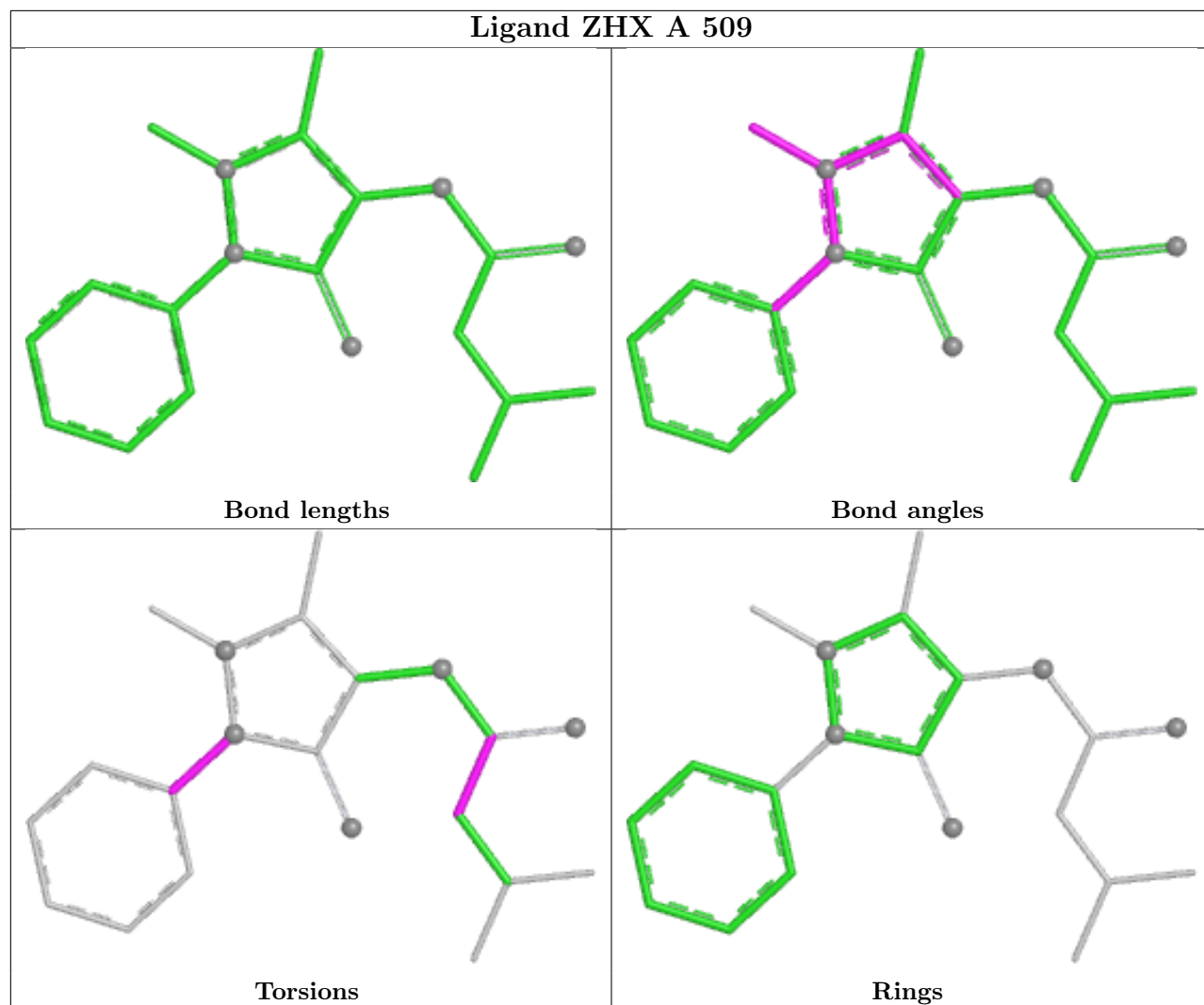
Bond angles

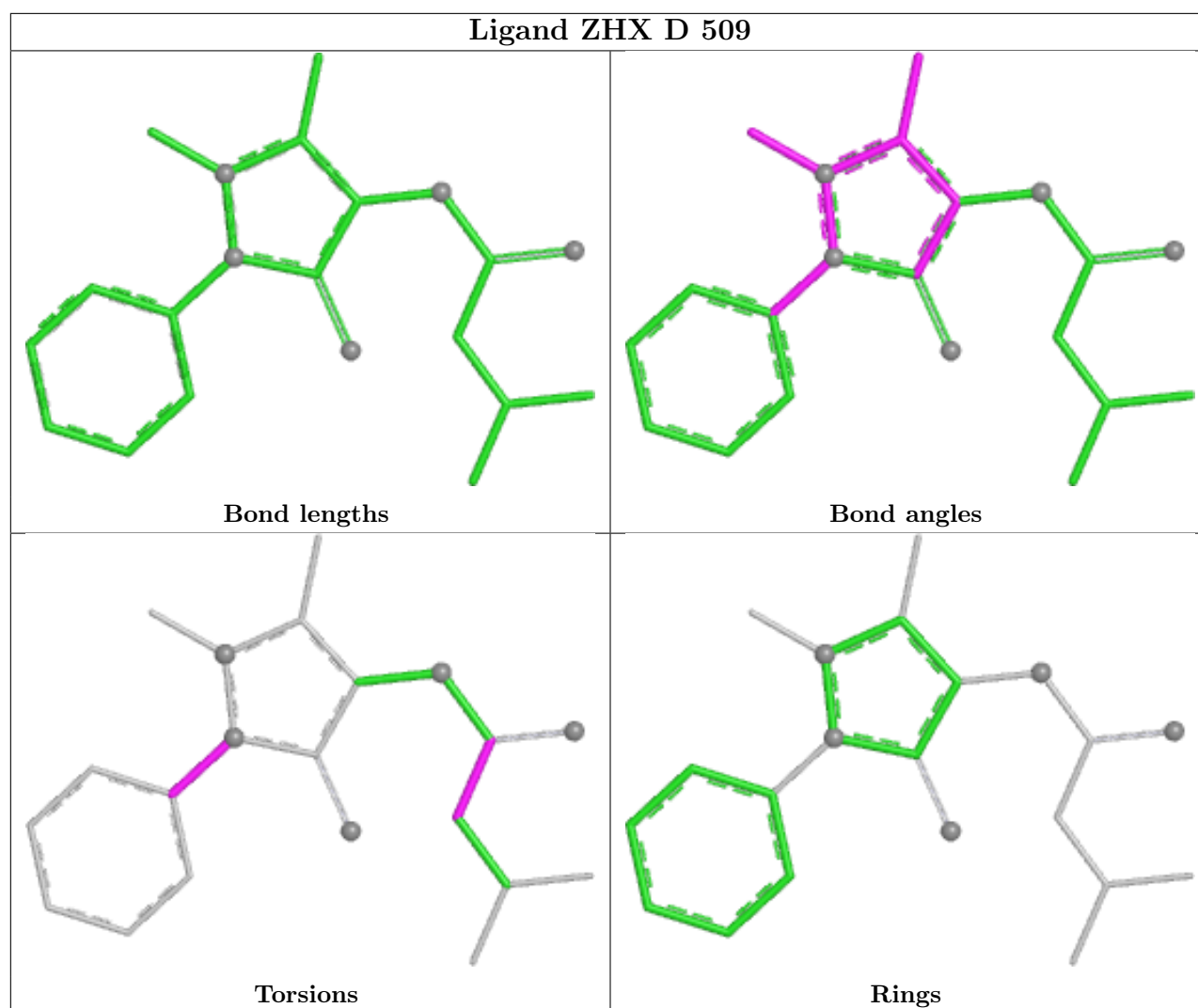


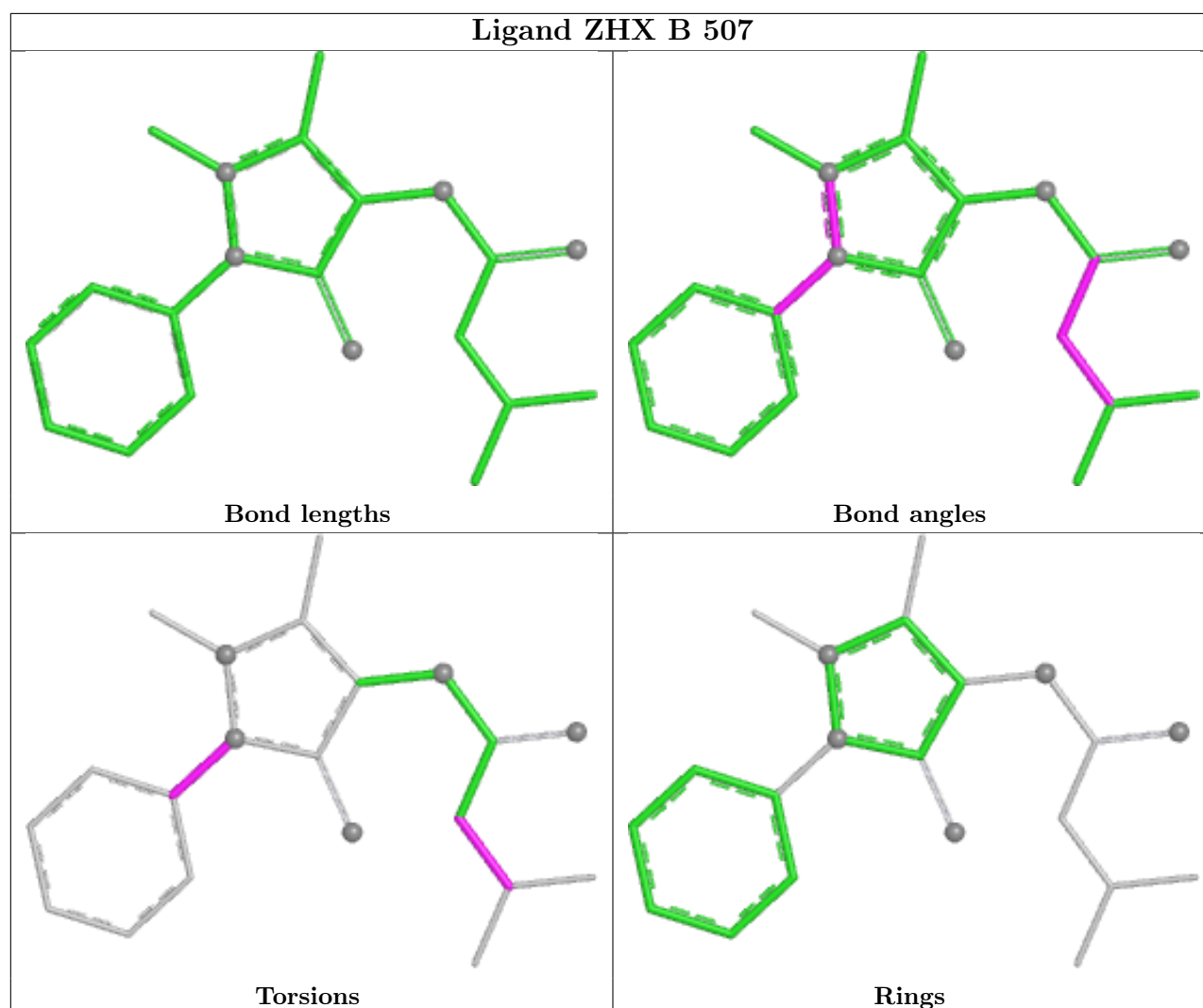
Torsions



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	412/412 (100%)	-1.11	0 100 100	13, 26, 48, 94	8 (1%)
1	B	412/412 (100%)	-1.12	0 100 100	13, 26, 48, 100	5 (1%)
1	C	412/412 (100%)	-1.17	1 (0%) 91 92	12, 24, 42, 84	8 (1%)
1	D	412/412 (100%)	-1.18	0 100 100	13, 24, 43, 95	4 (0%)
All	All	1648/1648 (100%)	-1.14	1 (0%) 92 92	12, 25, 46, 100	25 (1%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	413	ALA	2.4

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	DMS	A	505	4/4	0.94	0.10	74,76,76,86	0

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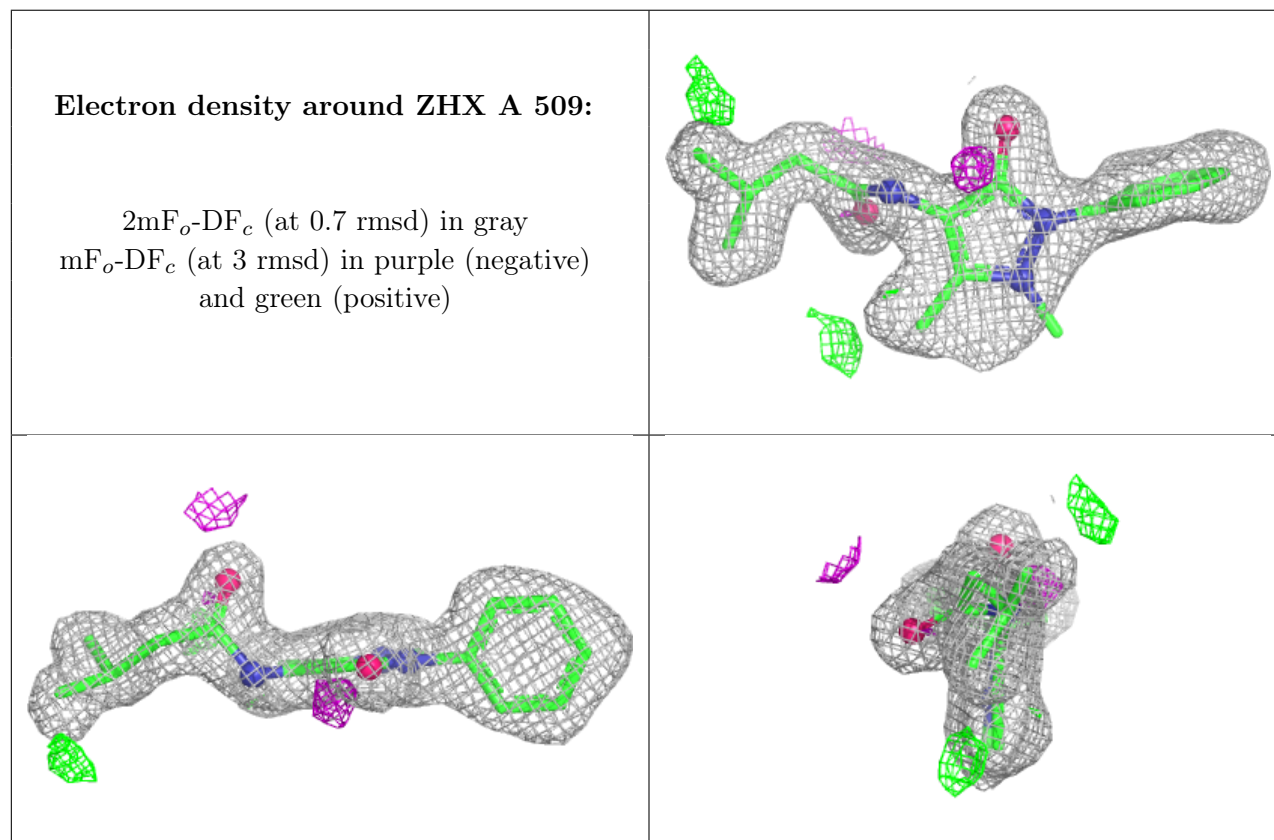
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	DMS	C	509	4/4	0.95	0.11	49,83,95,98	0
2	DMS	C	510	4/4	0.95	0.13	58,97,107,113	0
2	DMS	D	503	4/4	0.95	0.08	55,66,70,72	0
2	DMS	C	506	4/4	0.96	0.07	52,54,74,80	0
2	DMS	C	508	4/4	0.96	0.09	48,59,72,75	0
2	DMS	A	503	4/4	0.96	0.10	75,79,82,84	0
2	DMS	B	501	4/4	0.96	0.10	39,44,64,64	0
2	DMS	B	506	4/4	0.96	0.10	68,77,79,86	0
2	DMS	D	513	4/4	0.96	0.09	52,55,65,66	0
2	DMS	B	502	4/4	0.97	0.08	59,64,72,78	0
2	DMS	A	507	4/4	0.97	0.09	42,75,77,78	0
2	DMS	C	505	4/4	0.97	0.08	53,63,71,75	0
2	DMS	A	504	4/4	0.97	0.08	45,51,71,74	0
2	DMS	D	508	4/4	0.97	0.08	65,72,73,79	0
2	DMS	D	510	4/4	0.97	0.07	55,55,57,58	0
2	DMS	C	507	4/4	0.97	0.10	56,59,65,85	0
2	DMS	C	511	4/4	0.98	0.05	48,55,75,80	0
2	DMS	C	516	4/4	0.98	0.06	63,63,75,77	0
2	DMS	D	501	4/4	0.98	0.07	60,79,83,84	0
2	DMS	D	502	4/4	0.98	0.07	57,69,73,77	0
2	DMS	B	510	4/4	0.98	0.06	53,59,65,73	0
2	DMS	D	505	4/4	0.98	0.07	38,54,61,62	0
2	DMS	D	507	4/4	0.98	0.07	48,54,76,78	0
2	DMS	C	504	4/4	0.98	0.06	28,34,52,53	0
2	DMS	B	504	4/4	0.98	0.06	47,61,61,64	0
2	DMS	D	511	4/4	0.98	0.07	49,56,58,69	0
2	DMS	D	512	4/4	0.98	0.07	60,65,72,76	0
2	DMS	B	503	4/4	0.98	0.07	48,59,64,67	0
3	FMT	A	502	3/3	0.98	0.06	43,43,47,50	0
3	FMT	C	502	3/3	0.98	0.05	45,45,46,53	0
4	ZHX	A	509	21/21	0.98	0.05	21,27,38,57	0
4	ZHX	B	507	21/21	0.98	0.05	22,27,40,57	0
2	DMS	A	501	4/4	0.99	0.05	40,41,43,43	0
2	DMS	A	508	4/4	0.99	0.05	45,66,67,71	0
2	DMS	D	504	4/4	0.99	0.04	45,51,52,56	0
2	DMS	A	510	4/4	0.99	0.05	45,50,55,70	0
2	DMS	D	506	4/4	0.99	0.04	34,38,38,40	0
2	DMS	B	505	4/4	0.99	0.04	40,42,42,46	0
2	DMS	A	511	4/4	0.99	0.05	58,70,71,84	0
2	DMS	B	508	4/4	0.99	0.06	45,61,68,69	0
2	DMS	B	509	4/4	0.99	0.05	45,53,57,69	0
2	DMS	A	506	4/4	0.99	0.05	48,62,66,68	0

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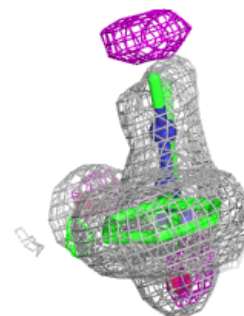
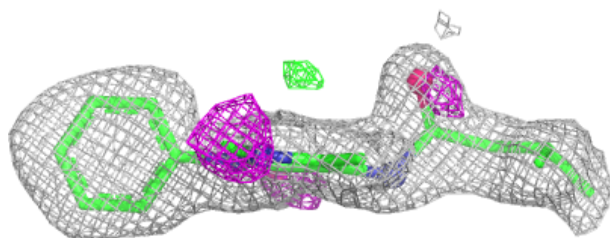
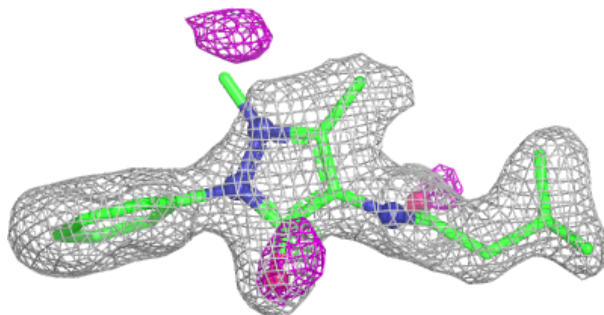
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	DMS	C	513	4/4	0.99	0.05	48,52,53,56	0
2	DMS	C	514	4/4	0.99	0.04	55,55,56,61	0
2	DMS	C	515	4/4	0.99	0.05	42,53,59,60	0
2	DMS	C	501	4/4	0.99	0.05	32,37,40,42	0
2	DMS	C	503	4/4	0.99	0.06	59,62,76,84	0
4	ZHX	C	512	21/21	0.99	0.04	19,23,35,46	0
4	ZHX	D	509	21/21	0.99	0.04	19,24,33,52	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.

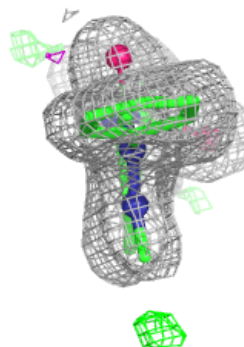
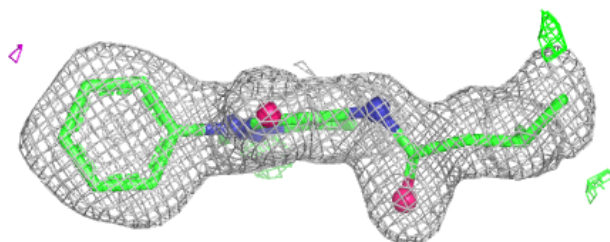
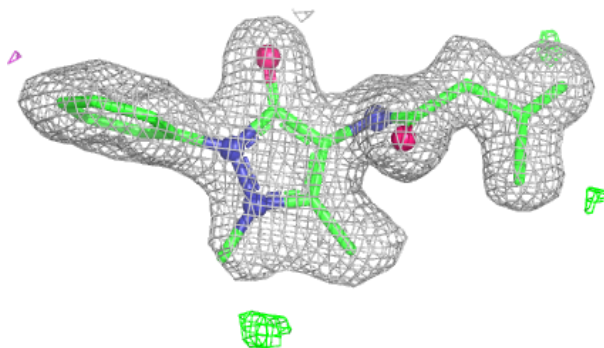


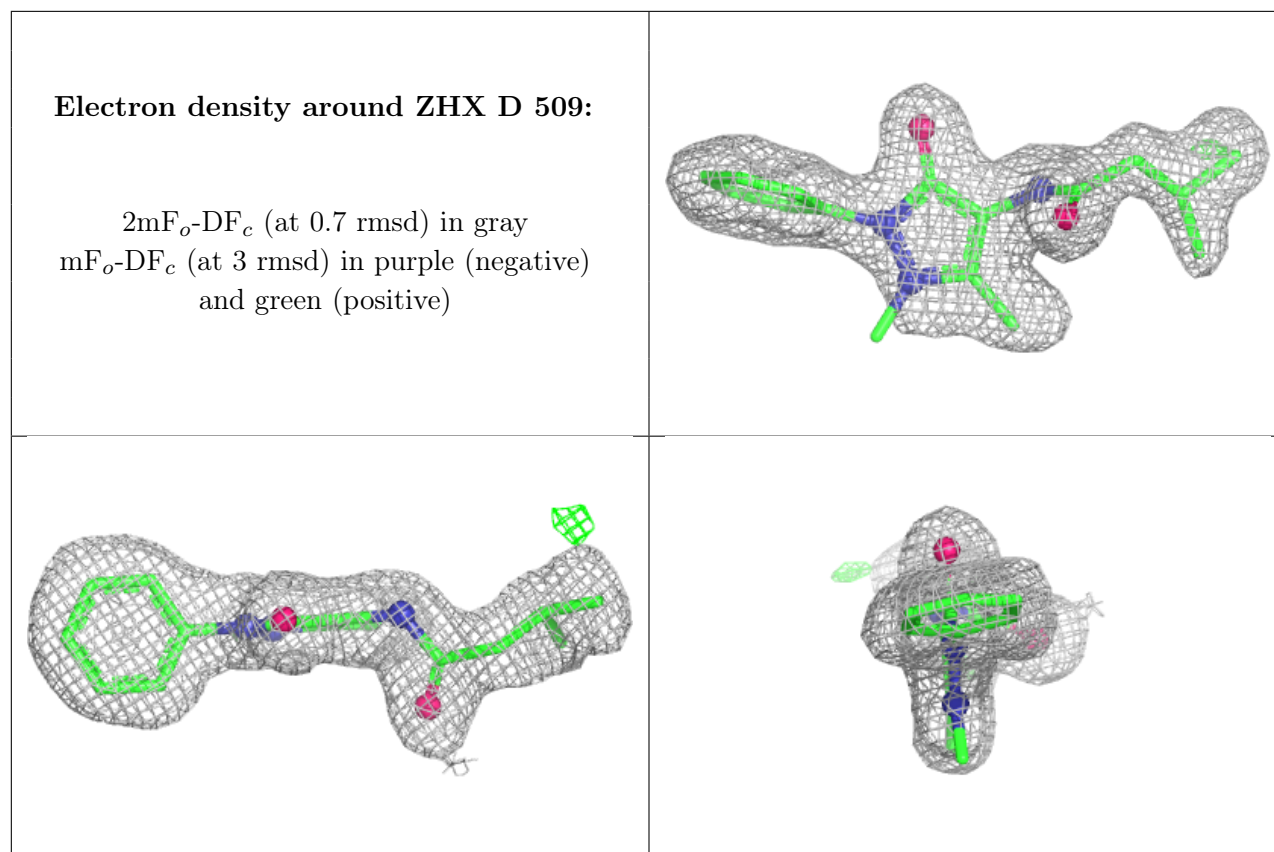
Electron density around ZHX B 507:

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

**Electron density around ZHX C 512:**

$2mF_o-DF_c$ (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.