



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 06:20 am BST

PDB ID : 6FEB
Title : Crystal structure of human phosphodiesterase 4D2 catalytic domain with inhibitor NPD-1086
Authors : Singh, A.K.; Brown, D.G.
Deposited on : 2017-12-31
Resolution : 1.93 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 : 2.11
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) : 2.11

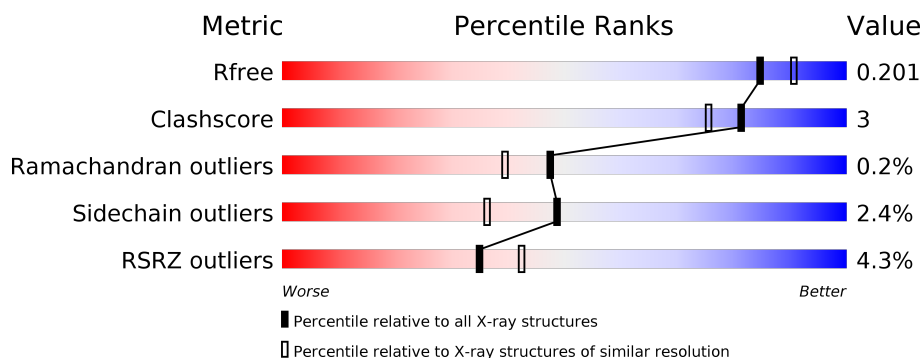
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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 on 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	364	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>•</div> <div>11%</div> </div> </div>
1	B	364	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>5%</div> <div>•</div> <div>11%</div> </div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5772 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 cAMP-specific 3',5'-cyclic phosphodiesterase 4D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total	C	N	O	S	0	0	0
			2631	1664	450	503	14			
1	B	323	Total	C	N	O	S	0	0	0
			2615	1654	447	500	14			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	GLY	-	expression tag	UNP Q08499
A	76	SER	-	expression tag	UNP Q08499
A	77	HIS	-	expression tag	UNP Q08499
A	78	MET	-	expression tag	UNP Q08499
B	75	GLY	-	expression tag	UNP Q08499
B	76	SER	-	expression tag	UNP Q08499
B	77	HIS	-	expression tag	UNP Q08499
B	78	MET	-	expression tag	UNP Q08499

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



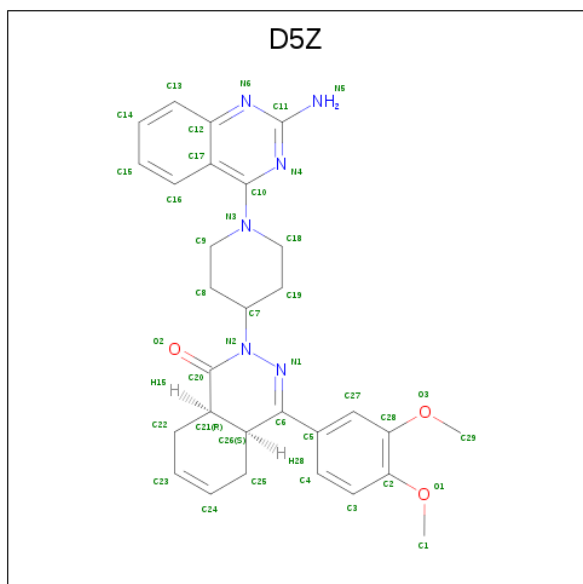
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total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

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

- Molecule 3 is (4aS,8aR)-2-[1-(2-aminoquinazolin-4-yl)piperidin-4-yl]-4-(3,4-dimethoxyphenyl)-1,2,4a,5,8,8a-hexahydrophthalazin-1-one (three-letter code: D5Z) (formula: C₂₉H₃₂N₆O₃) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			38	29	6	3		
3	A	1	Total	C	N	O	0	0
			38	29	6	3		
3	B	1	Total	C	N	O	0	0
			38	29	6	3		

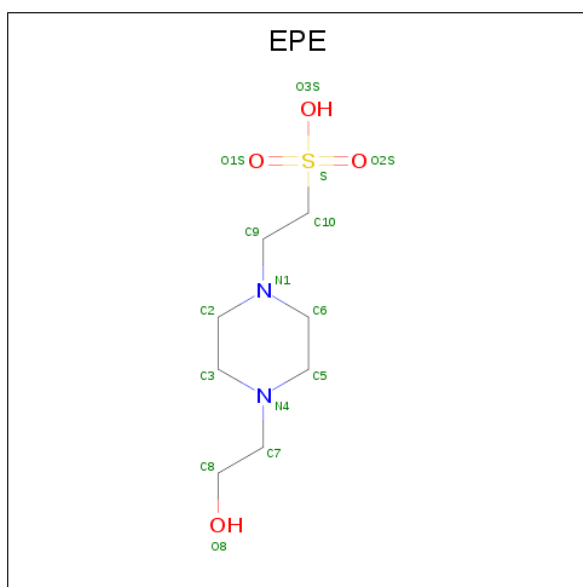
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 6 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C N O S 15 8 2 4 1	0	0
6	B	1	Total C N O S 15 8 2 4 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	179	Total O 179 179	0	0

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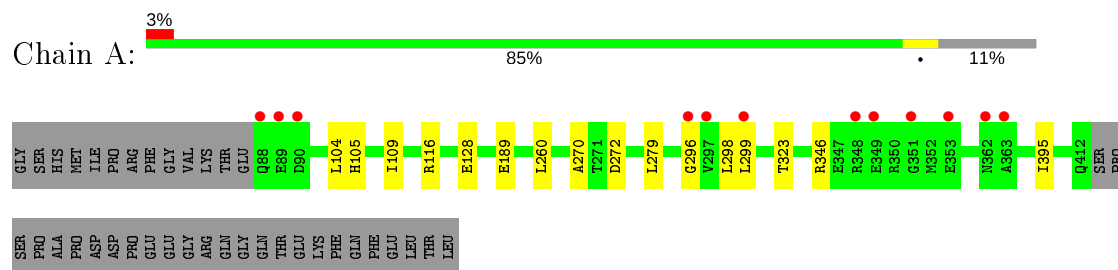
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	123	Total 123	O 123	0	0

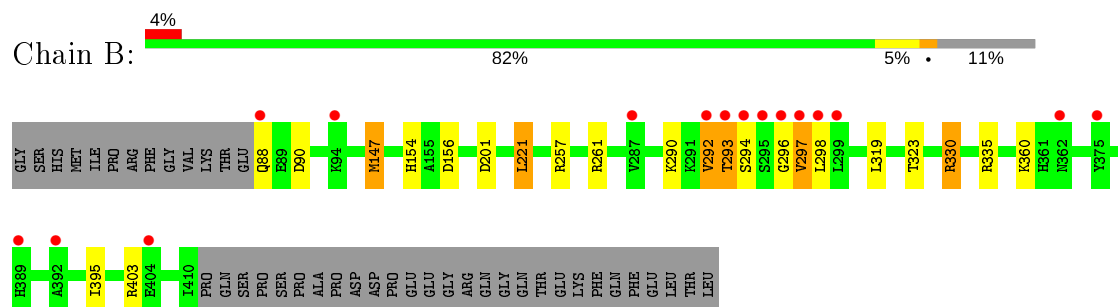
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	95.07Å 158.23Å 111.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	81.49 – 1.93 65.77 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.1 (81.49-1.93) 99.1 (65.77-1.93)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.160 , 0.196 0.172 , 0.201	Depositor DCC
R_{free} test set	3200 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	32.0	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.020 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5772	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% 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: ZN, EPE, D5Z, MG, EDO

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	0.96	1/2685 (0.0%)	0.82	2/3648 (0.1%)
1	B	0.80	0/2668	0.79	9/3624 (0.2%)
All	All	0.89	1/5353 (0.0%)	0.80	11/7272 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	189	GLU	CD-OE2	-5.16	1.20	1.25

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	335	ARG	NE-CZ-NH1	6.56	123.58	120.30
1	A	272	ASP	CB-CG-OD1	6.48	124.13	118.30
1	B	257	ARG	NE-CZ-NH1	6.20	123.40	120.30
1	B	296	GLY	N-CA-C	-5.94	98.25	113.10
1	B	297	VAL	N-CA-C	5.52	125.89	111.00
1	B	403	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	B	335	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	B	147	MET	CG-SD-CE	-5.22	91.84	100.20
1	A	346	ARG	NE-CZ-NH1	5.17	122.89	120.30
1	B	261	ARG	CG-CD-NE	-5.11	101.06	111.80
1	B	201	ASP	CB-CG-OD1	5.10	122.89	118.30

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	2631	0	2586	4	0
1	B	2615	0	2571	24	0
2	A	44	0	66	0	0
2	B	32	0	48	0	0
3	A	76	0	0	0	0
3	B	38	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	15	0	17	1	0
6	B	15	0	18	0	0
7	A	179	0	0	0	0
7	B	123	0	0	1	0
All	All	5772	0	5306	28	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 3.

All (28) 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:293:THR:O	1:B:297:VAL:HG12	1.12	1.24
1:B:292:VAL:CG2	1:B:297:VAL:HB	1.71	1.19
1:B:293:THR:O	1:B:297:VAL:CG1	1.96	1.11
1:B:292:VAL:HG23	1:B:297:VAL:HB	1.07	1.03
1:B:292:VAL:HG23	1:B:297:VAL:CB	2.00	0.86
1:B:330:ARG:HG3	1:B:330:ARG:HH11	1.51	0.76
1:B:221:LEU:HD13	1:B:221:LEU:O	1.86	0.75
1:B:293:THR:OG1	1:B:294:SER:N	2.19	0.74
1:B:292:VAL:CG2	1:B:293:THR:N	2.59	0.66
1:B:88:GLN:O	1:B:88:GLN:HG2	1.97	0.65
1:B:292:VAL:HG21	1:B:297:VAL:HB	1.77	0.65
1:B:293:THR:O	1:B:297:VAL:CB	2.44	0.65
1:A:323:THR:HB	1:A:395:ILE:HG23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:ALA:HB1	1:A:279:LEU:HD11	1.89	0.55
1:B:330:ARG:CG	1:B:330:ARG:HH11	2.13	0.53
1:B:330:ARG:NH1	1:B:330:ARG:CG	2.71	0.53
1:B:292:VAL:HG23	1:B:293:THR:N	2.26	0.50
1:B:154:HIS:HB3	1:B:156:ASP:OD1	2.12	0.49
1:B:221:LEU:HD13	1:B:221:LEU:C	2.32	0.49
1:A:105:HIS:HB3	6:A:515:EPE:O2S	2.13	0.49
1:A:104:LEU:HD11	1:A:109:ILE:HD11	1.94	0.48
1:B:360:LYS:HG2	7:B:647:HOH:O	2.14	0.47
1:B:293:THR:O	1:B:297:VAL:CA	2.63	0.47
1:B:292:VAL:HG22	1:B:293:THR:N	2.32	0.45
1:B:292:VAL:HG23	1:B:293:THR:H	1.81	0.44
1:B:221:LEU:CD1	1:B:221:LEU:C	2.86	0.44
1:B:323:THR:HB	1:B:395:ILE:HG23	2.00	0.42
1:B:330:ARG:NH1	1:B:330:ARG:HG3	2.26	0.41

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	323/364 (89%)	316 (98%)	6 (2%)	1 (0%)	41	32
1	B	321/364 (88%)	315 (98%)	6 (2%)	0	100	100
All	All	644/728 (88%)	631 (98%)	12 (2%)	1 (0%)	47	39

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	296	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	297/331 (90%)	292 (98%)	5 (2%)	60	49
1	B	295/331 (89%)	286 (97%)	9 (3%)	40	26
All	All	592/662 (89%)	578 (98%)	14 (2%)	49	36

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

Mol	Chain	Res	Type
1	A	116	ARG
1	A	128	GLU
1	A	260	LEU
1	A	298	LEU
1	A	299	LEU
1	B	90	ASP
1	B	147	MET
1	B	221	LEU
1	B	290	LYS
1	B	292	VAL
1	B	293	THR
1	B	298	LEU
1	B	319	LEU
1	B	330	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 28 ligands modelled in this entry, 4 are monoatomic - leaving 24 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	A	506	-	3,3,3	0.51	0	2,2,2	0.39	0
6	EPE	B	511	-	15,15,15	1.96	1 (6%)	18,20,20	1.98	5 (27%)
2	EDO	B	501	-	3,3,3	0.33	0	2,2,2	0.17	0
2	EDO	B	512	-	3,3,3	0.28	0	2,2,2	1.05	0
2	EDO	A	507	-	3,3,3	0.32	0	2,2,2	0.41	0
2	EDO	A	508	-	3,3,3	0.45	0	2,2,2	0.23	0
2	EDO	A	516	-	3,3,3	0.48	0	2,2,2	0.21	0
2	EDO	B	503	-	3,3,3	0.24	0	2,2,2	1.07	0
2	EDO	B	506	-	3,3,3	0.35	0	2,2,2	1.12	0
2	EDO	A	509	-	3,3,3	0.57	0	2,2,2	0.13	0
3	D5Z	B	508	-	43,43,43	0.52	0	51,62,62	1.18	8 (15%)
2	EDO	B	504	-	3,3,3	0.66	0	2,2,2	0.60	0
2	EDO	A	505	-	3,3,3	0.50	0	2,2,2	0.44	0
2	EDO	A	503	-	3,3,3	0.27	0	2,2,2	1.58	1 (50%)
2	EDO	B	505	-	3,3,3	0.54	0	2,2,2	0.20	0
2	EDO	A	510	-	3,3,3	0.53	0	2,2,2	0.20	0
2	EDO	A	501	-	3,3,3	0.52	0	2,2,2	0.31	0
2	EDO	B	502	-	3,3,3	0.54	0	2,2,2	0.54	0
2	EDO	B	507	-	3,3,3	0.53	0	2,2,2	0.26	0
2	EDO	A	502	-	3,3,3	0.62	0	2,2,2	0.64	0
6	EPE	A	515	-	15,15,15	2.16	1 (6%)	18,20,20	1.71	3 (16%)
3	D5Z	A	511	-	43,43,43	0.50	0	51,62,62	1.21	6 (11%)
2	EDO	A	504	-	3,3,3	0.47	0	2,2,2	0.45	0
3	D5Z	A	512	-	43,43,43	0.63	1 (2%)	51,62,62	1.31	7 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	A	506	-	-	0/1/1/1	-
6	EPE	B	511	-	-	5/9/19/19	0/1/1/1
2	EDO	B	501	-	-	0/1/1/1	-
2	EDO	B	512	-	-	1/1/1/1	-
2	EDO	A	507	-	-	1/1/1/1	-
2	EDO	A	508	-	-	1/1/1/1	-
2	EDO	A	516	-	-	1/1/1/1	-
2	EDO	B	503	-	-	1/1/1/1	-
2	EDO	B	506	-	-	1/1/1/1	-
2	EDO	A	509	-	-	1/1/1/1	-
3	D5Z	B	508	-	-	2/16/53/53	0/6/6/6
2	EDO	B	504	-	-	0/1/1/1	-
2	EDO	A	505	-	-	0/1/1/1	-
2	EDO	A	503	-	-	1/1/1/1	-
2	EDO	B	505	-	-	1/1/1/1	-
2	EDO	A	510	-	-	1/1/1/1	-
2	EDO	A	501	-	-	1/1/1/1	-
2	EDO	B	502	-	-	1/1/1/1	-
2	EDO	B	507	-	-	1/1/1/1	-
2	EDO	A	502	-	-	0/1/1/1	-
6	EPE	A	515	-	-	1/9/19/19	0/1/1/1
3	D5Z	A	511	-	-	2/16/53/53	0/6/6/6
2	EDO	A	504	-	-	1/1/1/1	-
3	D5Z	A	512	-	-	4/16/53/53	0/6/6/6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	515	EPE	C10-S	-7.81	1.66	1.77
6	B	511	EPE	C10-S	-7.18	1.67	1.77
3	A	512	D5Z	C7-N2	2.04	1.50	1.47

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	511	EPE	O1S-S-C10	4.90	112.81	106.92
3	A	512	D5Z	C17-C10-N3	4.59	129.90	120.97
6	A	515	EPE	O3S-S-C10	4.28	112.70	105.77
3	A	511	D5Z	C17-C10-N3	4.16	129.06	120.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	508	D5Z	C17-C10-N3	3.96	128.68	120.97
6	B	511	EPE	O2S-S-C10	3.65	111.31	106.92
3	A	512	D5Z	C18-N3-C10	3.21	127.90	118.73
6	B	511	EPE	C5-N4-C3	2.89	115.33	108.83
6	A	515	EPE	C6-N1-C2	2.87	115.29	108.83
6	A	515	EPE	O2S-S-C10	2.78	110.26	106.92
3	A	511	D5Z	N6-C11-N4	-2.77	123.53	127.22
3	B	508	D5Z	N6-C11-N4	-2.75	123.55	127.22
3	A	512	D5Z	C19-C7-N2	2.71	113.87	110.86
3	A	512	D5Z	C11-N4-C10	2.64	121.23	113.91
3	A	511	D5Z	C6-N1-N2	-2.62	116.23	118.97
3	A	512	D5Z	N6-C11-N4	-2.61	123.74	127.22
3	A	511	D5Z	C11-N4-C10	2.54	120.94	113.91
3	B	508	D5Z	C4-C5-C6	2.52	123.74	120.75
3	A	511	D5Z	C9-N3-C18	2.35	116.71	111.52
3	B	508	D5Z	C11-N4-C10	2.33	120.38	113.91
6	B	511	EPE	C9-N1-C2	-2.29	105.38	111.23
2	A	503	EDO	O2-C2-C1	-2.22	95.95	111.91
6	B	511	EPE	C3-C2-N1	2.20	115.16	110.64
3	B	508	D5Z	C5-C6-N1	2.19	118.68	115.95
3	A	512	D5Z	O2-C20-N2	2.16	124.27	121.64
3	B	508	D5Z	C9-N3-C18	2.15	116.26	111.52
3	B	508	D5Z	C19-C7-N2	-2.13	108.50	110.86
3	B	508	D5Z	C17-C12-N6	-2.08	120.60	122.81
3	A	511	D5Z	C4-C5-C6	2.08	123.21	120.75
3	A	512	D5Z	C5-C6-N1	2.04	118.49	115.95

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	508	D5Z	C17-C10-N3-C18
3	B	508	D5Z	N4-C10-N3-C18
6	B	511	EPE	C9-C10-S-O2S
3	A	511	D5Z	C17-C10-N3-C18
3	A	511	D5Z	N4-C10-N3-C18
3	A	512	D5Z	C17-C10-N3-C9
3	A	512	D5Z	N4-C10-N3-C9
2	A	508	EDO	O1-C1-C2-O2
2	A	516	EDO	O1-C1-C2-O2
6	B	511	EPE	C9-C10-S-O3S
2	B	507	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
3	A	512	D5Z	N4-C10-N3-C18
2	B	505	EDO	O1-C1-C2-O2
2	A	504	EDO	O1-C1-C2-O2
2	B	506	EDO	O1-C1-C2-O2
2	A	509	EDO	O1-C1-C2-O2
6	B	511	EPE	C9-C10-S-O1S
2	A	507	EDO	O1-C1-C2-O2
2	B	503	EDO	O1-C1-C2-O2
2	A	510	EDO	O1-C1-C2-O2
2	B	502	EDO	O1-C1-C2-O2
6	A	515	EPE	N4-C7-C8-O8
2	B	512	EDO	O1-C1-C2-O2
2	A	503	EDO	O1-C1-C2-O2
3	A	512	D5Z	C17-C10-N3-C18
6	B	511	EPE	S-C10-C9-N1
2	A	501	EDO	O1-C1-C2-O2
6	B	511	EPE	C8-C7-N4-C3

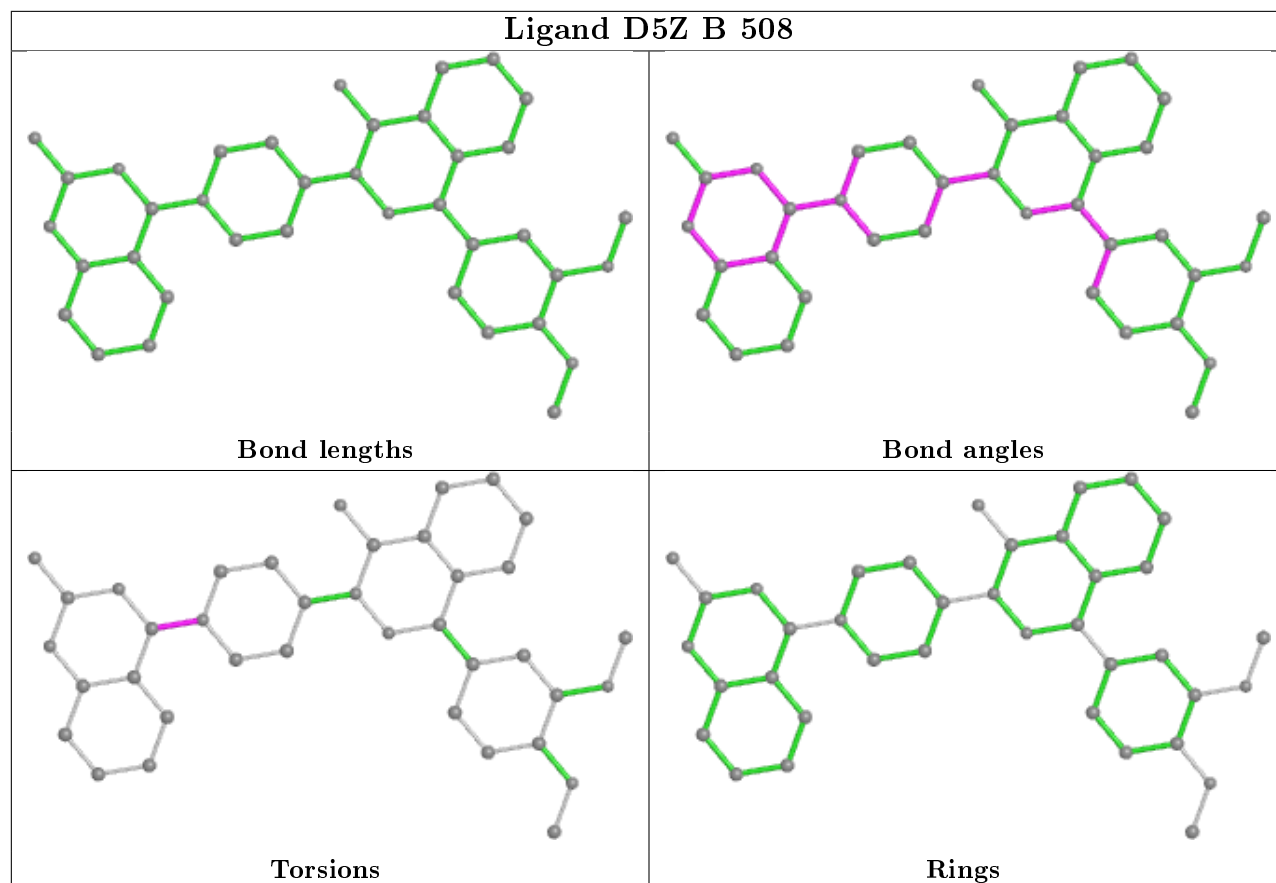
There are no ring outliers.

1 monomer is involved in 1 short contact:

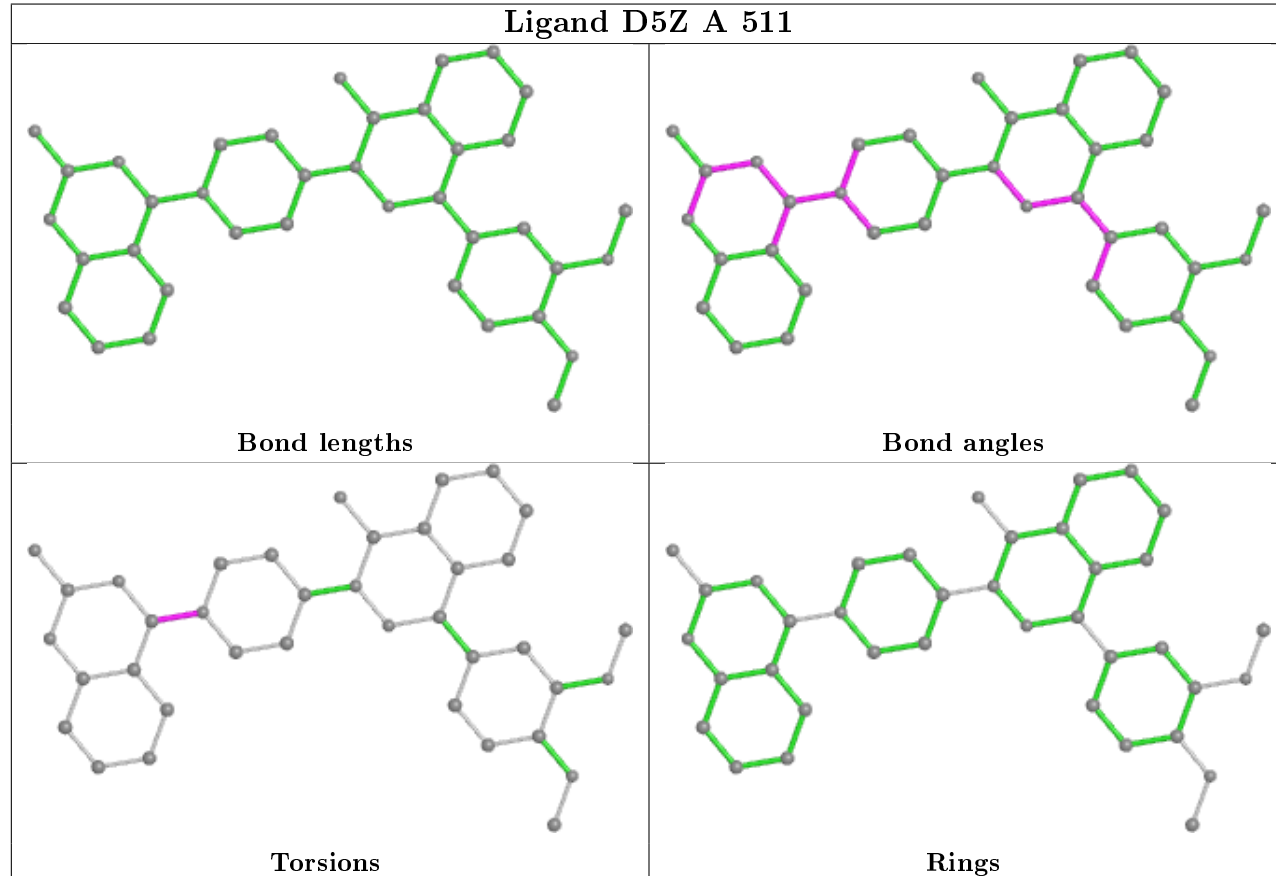
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	515	EPE	1	0

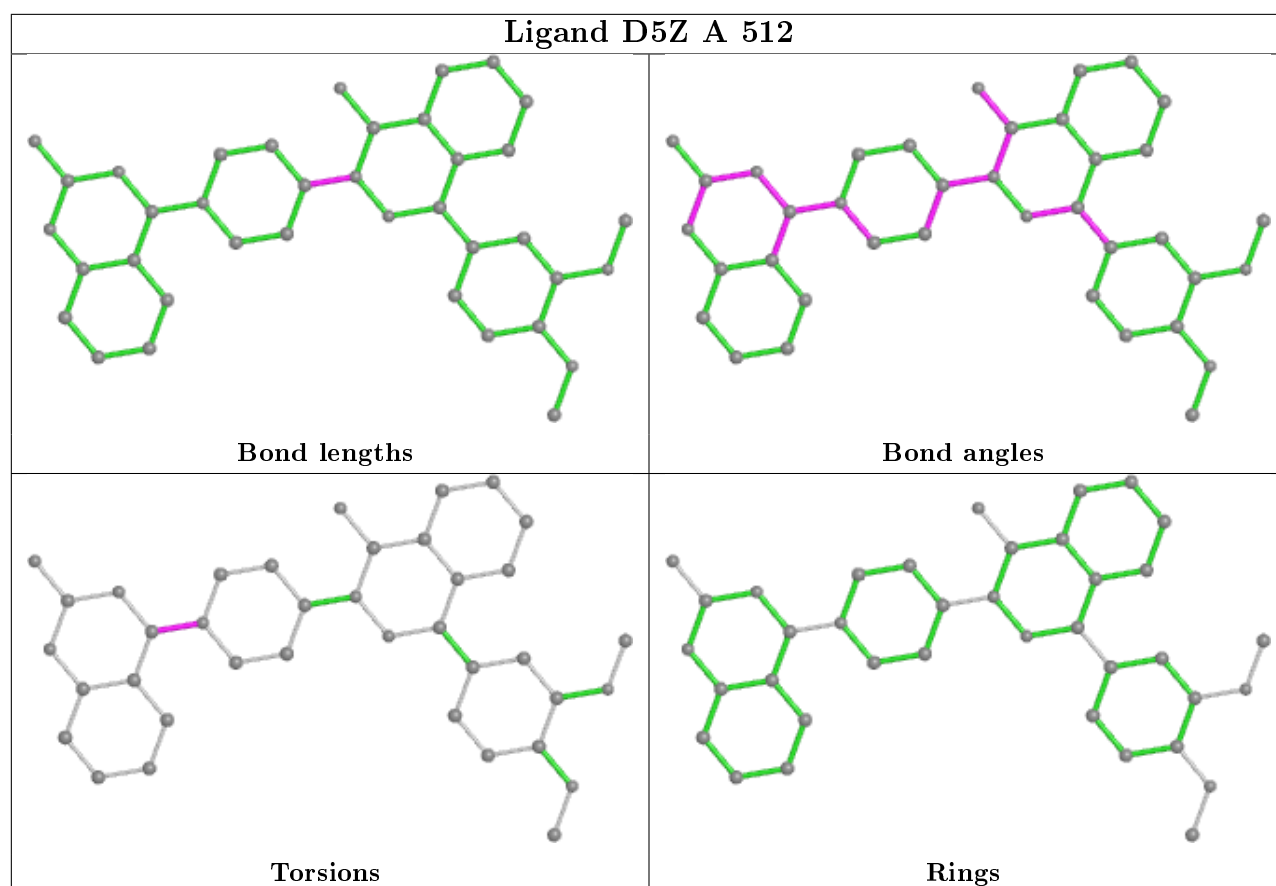
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand D5Z B 508



Ligand D5Z A 511





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, 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	325/364 (89%)	0.19	12 (3%) 41 49	19, 31, 62, 93	0
1	B	323/364 (88%)	0.32	16 (4%) 28 36	21, 38, 75, 134	0
All	All	648/728 (89%)	0.25	28 (4%) 35 42	19, 35, 68, 134	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	295	SER	15.7
1	B	296	GLY	9.6
1	A	363	ALA	6.5
1	B	297	VAL	6.1
1	B	294	SER	5.2
1	A	297	VAL	4.3
1	B	293	THR	4.2
1	B	88	GLN	4.0
1	A	90	ASP	3.9
1	B	375	TYR	3.6
1	A	88	GLN	3.0
1	B	389	HIS	2.9
1	B	287	VAL	2.9
1	B	292	VAL	2.9
1	A	362	ASN	2.8
1	B	362	ASN	2.7
1	B	404	GLU	2.6
1	B	299	LEU	2.5
1	A	351	GLY	2.4
1	B	392	ALA	2.4
1	A	349	GLU	2.4
1	A	89	GLU	2.4
1	A	299	LEU	2.4
1	B	298	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	94	LYS	2.2
1	A	353	GLU	2.2
1	A	296	GLY	2.2
1	A	348	ARG	2.2

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 carbohydrates 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(\AA^2)	Q<0.9
2	EDO	A	509	4/4	0.60	0.29	76,84,87,91	0
2	EDO	A	516	4/4	0.64	0.26	50,50,53,54	0
2	EDO	B	504	4/4	0.66	0.23	53,59,63,66	0
2	EDO	A	510	4/4	0.73	0.17	69,70,71,71	0
2	EDO	B	505	4/4	0.77	0.32	53,65,66,68	0
2	EDO	A	508	4/4	0.84	0.17	52,55,55,57	0
2	EDO	B	512	4/4	0.87	0.22	56,58,61,63	0
2	EDO	B	507	4/4	0.88	0.10	55,59,60,64	0
2	EDO	A	503	4/4	0.89	0.20	44,49,52,59	0
2	EDO	A	501	4/4	0.89	0.13	36,36,37,40	0
2	EDO	B	502	4/4	0.89	0.13	47,49,50,56	0
2	EDO	B	506	4/4	0.89	0.28	68,68,68,70	0
2	EDO	A	507	4/4	0.91	0.20	61,65,67,73	0
3	D5Z	B	508	38/38	0.92	0.15	30,36,82,87	0
2	EDO	A	506	4/4	0.92	0.22	53,58,63,65	0
2	EDO	A	502	4/4	0.92	0.12	42,44,46,52	0
2	EDO	A	504	4/4	0.92	0.15	37,47,53,58	0
2	EDO	A	505	4/4	0.93	0.15	46,48,49,50	0
3	D5Z	A	511	38/38	0.94	0.12	22,27,72,80	0

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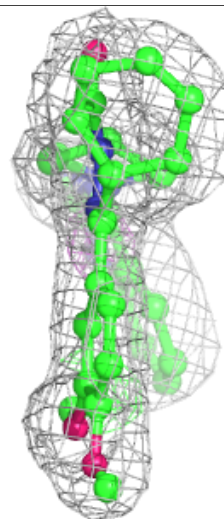
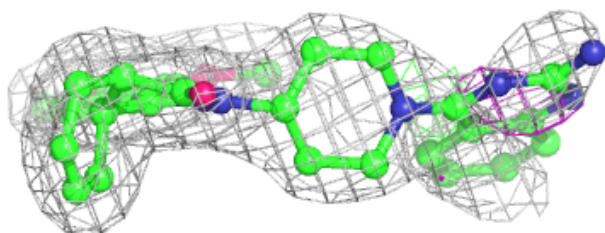
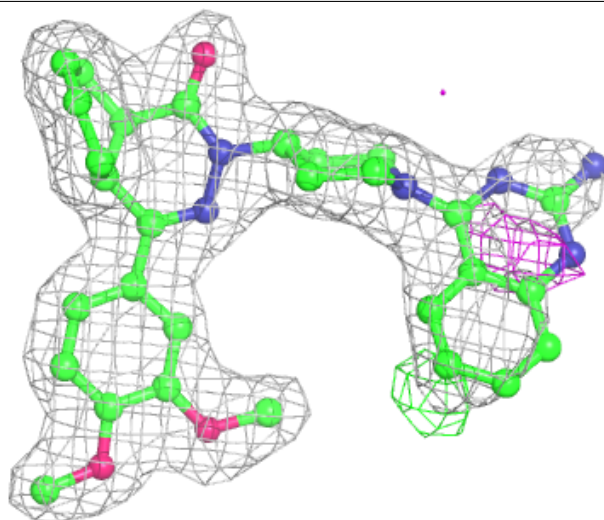
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	EPE	A	515	15/15	0.94	0.34	46,89,103,103	0
3	D5Z	A	512	38/38	0.94	0.12	42,47,55,60	0
2	EDO	B	501	4/4	0.95	0.12	34,35,35,37	0
2	EDO	B	503	4/4	0.95	0.14	37,42,43,52	0
6	EPE	B	511	15/15	0.96	0.14	48,64,79,86	0
4	MG	A	513	1/1	0.99	0.14	15,15,15,15	0
5	ZN	A	514	1/1	1.00	0.12	26,26,26,26	0
5	ZN	B	510	1/1	1.00	0.11	31,31,31,31	0
4	MG	B	509	1/1	1.00	0.14	19,19,19,19	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.

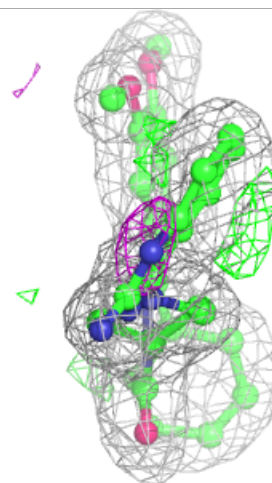
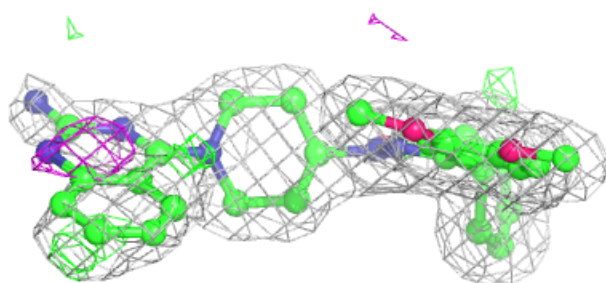
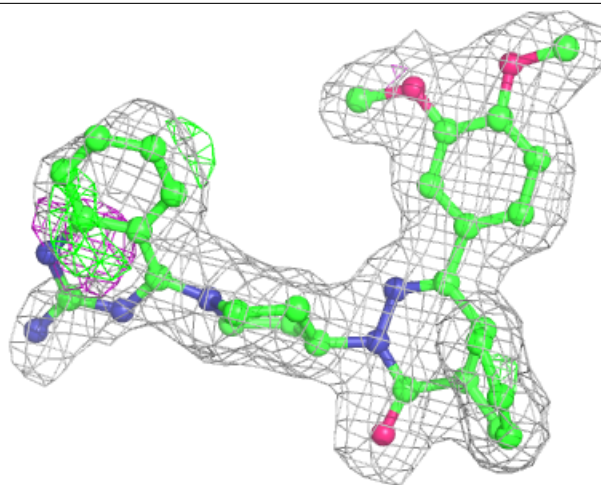
Electron density around D5Z B 508:

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



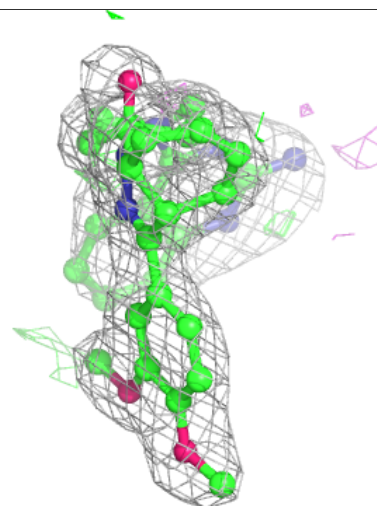
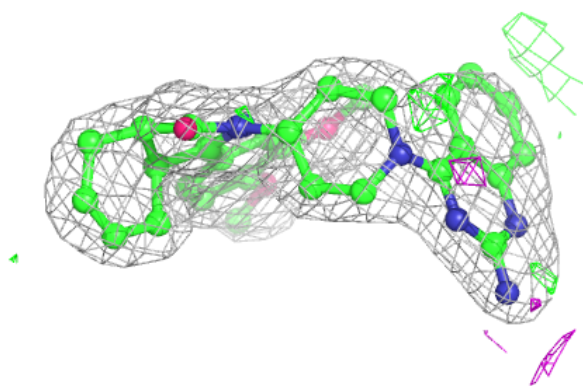
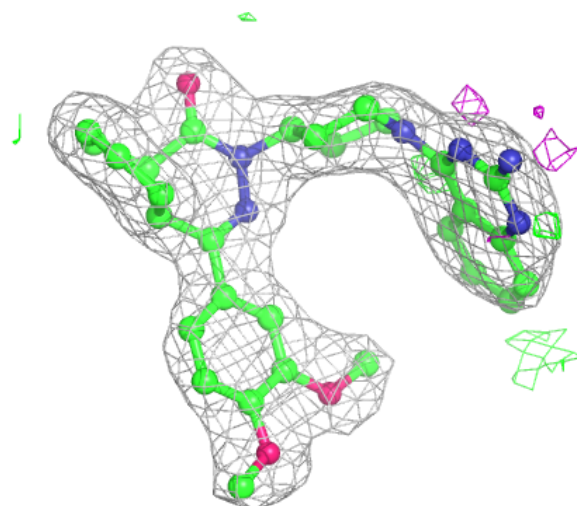
Electron density around D5Z A 511:

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



Electron density around D5Z A 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.