



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 03:41 pm BST

PDB ID : 4OGB
Title : Crystal structure of the catalytic domain of PDE4D2 with compound 2
Authors : Feil, S.C.; Parker, M.W.
Deposited on : 2014-01-15
Resolution : 2.03 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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

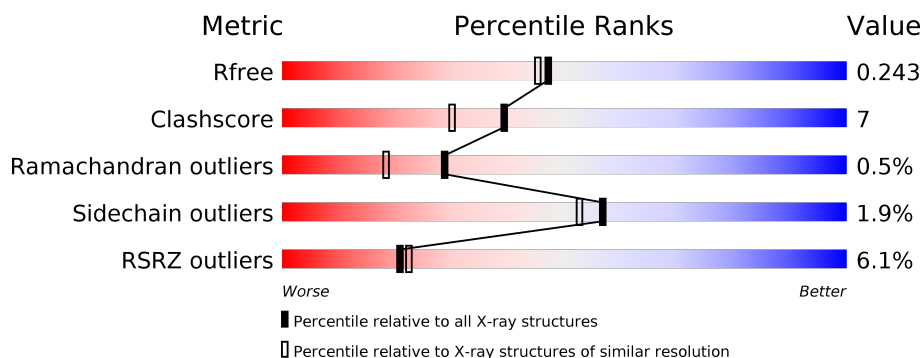
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	361	<div> <div>6%</div> <div> <div></div> <div>77%</div> <div>12%</div> <div>9%</div> </div> </div>
1	B	361	<div> <div>8%</div> <div> <div></div> <div>77%</div> <div>11%</div> <div>11%</div> </div> </div>
1	C	361	<div> <div>6%</div> <div> <div></div> <div>74%</div> <div>15%</div> <div>10%</div> </div> </div>
1	D	361	<div> <div>2%</div> <div> <div></div> <div>80%</div> <div>10%</div> <div>10%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	C	512	-	-	X	-
4	PEG	D	515	-	-	-	X
4	PEG	D	516	-	-	X	-
6	DMS	A	513	-	-	X	-

2 Entry composition [i](#)

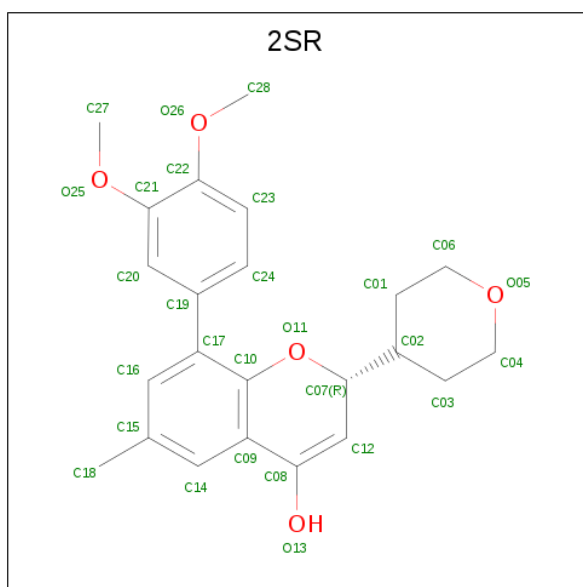
There are 8 unique types of molecules in this entry. The entry contains 11286 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	328	Total	C	N	O	S	0	0	0
			2651	1676	453	508	14			
1	B	321	Total	C	N	O	S	0	1	0
			2606	1649	447	496	14			
1	C	325	Total	C	N	O	S	0	1	0
			2642	1669	453	506	14			
1	D	324	Total	C	N	O	S	0	2	0
			2640	1669	452	505	14			

- Molecule 2 is (2R)-8-(3,4-dimethoxyphenyl)-6-methyl-2-(tetrahydro-2H-pyran-4-yl)-2H-chromen-4-ol (three-letter code: 2SR) (formula: C₂₃H₂₆O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			28	23	5		
2	B	1	Total	C	O	0	0
			28	23	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			28	23	5		
2	D	1	Total	C	O	0	0
			28	23	5		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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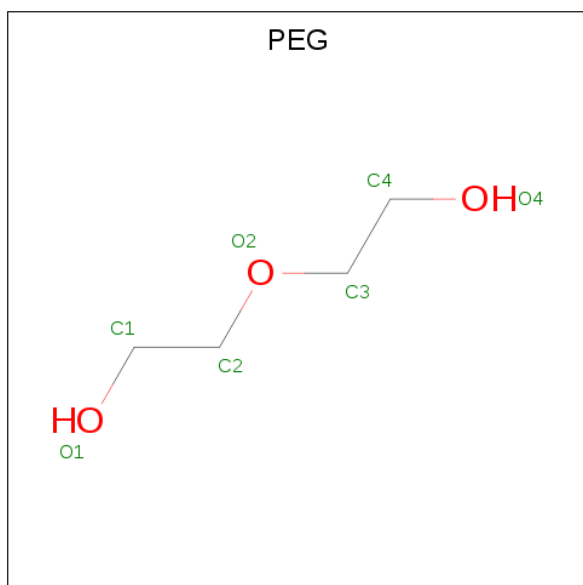
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0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

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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		

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

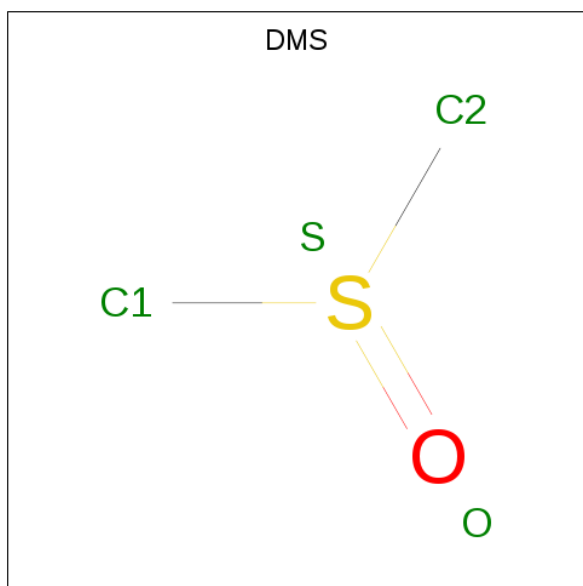
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Zn	0	0
			2	2		
5	A	2	Total	Zn	0	0
			2	2		
5	D	2	Total	Zn	0	0
			2	2		

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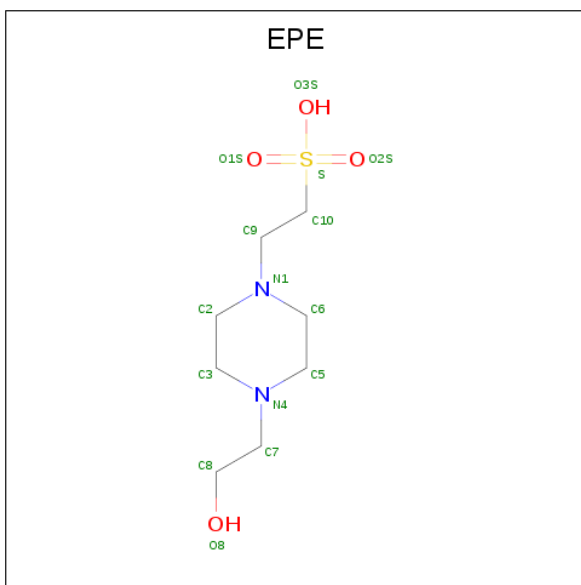
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total	Zn	0	0
			2	2		

- Molecule 6 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



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

- Molecule 7 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



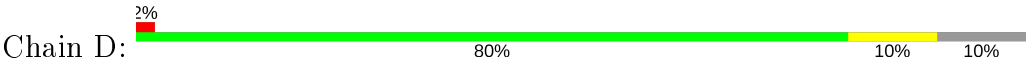
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	120	Total	O	0	0
			120	120		
8	B	104	Total	O	0	0
			104	104		
8	C	77	Total	O	0	0
			77	77		
8	D	131	Total	O	0	0
			131	131		

ALA
PRO
ASP
ASP
PRO
GLU
GLU
GLY
GLY
ARG
GLN
GLY
GLN
THR
GLU
LYS
PHE
GLN
PHE
GLU
LEU
THR
LEU
GLU

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



ILE
PRO
ARG
PHE
GLY
VAL
LYS
THR
GLU
Q88
E89
D90
W102
G103
L104
H105
V106
F107
V120
H123
D140
Q170
L219
A220
I221
M222
V228
L229
K262
A270
M273
L279
M286
N302
R306
I307
Q308
N321
P322
F340
F341
R342
R348

E349
R350
I354
D359
K360
R361
N362
A363
K367
Y375
I376
I410
P411
GLN
SER
PRO
SER
PRO
PRO
ALA
PRO
ASP
ASP
PRO
GLU
GLU
GLY
GLY
ARG
GLN
GLY
GLN
THR
GLU
LYS
PHE
GLN
PHE
GLU
LEU
THR
LEU
GLU

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	98.84Å 111.55Å 160.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.22 – 2.03 48.13 – 2.03	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.22-2.03) 99.9 (48.13-2.03)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.03Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.202 , 0.243 0.205 , 0.243	Depositor DCC
R_{free} test set	5713 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.9	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	0.95	EDS
Total number of atoms	11286	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% 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, EDO, DMS, PEG, 2SR

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	0.51	0/2704	0.55	0/3672
1	B	0.47	0/2660	0.57	1/3615 (0.0%)
1	C	0.57	0/2695	0.57	1/3660 (0.0%)
1	D	0.54	0/2695	0.59	2/3662 (0.1%)
All	All	0.52	0/10754	0.57	4/14609 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	410	ILE	C-N-CD	5.92	140.84	128.40
1	C	178	THR	C-N-CD	5.55	140.06	128.40
1	B	355	SER	C-N-CD	5.36	139.66	128.40
1	D	367	LYS	CB-CA-C	-5.17	100.05	110.40

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	2651	0	2609	47	0
1	B	2606	0	2565	34	0
1	C	2642	0	2596	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2640	0	2587	34	0
2	A	28	0	26	4	0
2	B	28	0	26	2	0
2	C	28	0	26	1	0
2	D	28	0	26	3	0
3	A	32	0	48	6	0
3	B	28	0	42	5	0
3	C	36	0	54	9	0
3	D	32	0	48	2	0
4	A	7	0	10	0	0
4	D	21	0	30	7	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	8	0	12	5	0
6	B	8	0	12	3	0
6	D	8	0	12	0	0
7	C	15	0	17	0	0
8	A	120	0	0	2	0
8	B	104	0	0	5	0
8	C	77	0	0	1	0
8	D	131	0	0	2	0
All	All	11286	0	10746	159	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 7.

The worst 5 of 159 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:222:MET:CE	1:D:222:MET:SD	2.25	1.25
1:C:222:MET:HE1	1:D:222:MET:SD	1.80	1.22
1:C:222:MET:HG3	3:C:512:EDO:H21	1.18	1.17
1:C:222:MET:HG3	3:C:512:EDO:C2	1.85	1.05
1:C:222:MET:HE2	1:D:222:MET:SD	2.04	0.98

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	326/361 (90%)	312 (96%)	10 (3%)	4 (1%)	13	5
1	B	320/361 (89%)	310 (97%)	10 (3%)	0	100	100
1	C	324/361 (90%)	313 (97%)	9 (3%)	2 (1%)	25	15
1	D	324/361 (90%)	318 (98%)	6 (2%)	0	100	100
All	All	1294/1444 (90%)	1253 (97%)	35 (3%)	6 (0%)	29	18

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	297	VAL
1	C	294	SER
1	A	295	SER
1	A	292	VAL
1	A	294	SER

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	299/329 (91%)	291 (97%)	8 (3%)	44	38
1	B	294/329 (89%)	287 (98%)	7 (2%)	49	42
1	C	298/329 (91%)	290 (97%)	8 (3%)	44	38
1	D	298/329 (91%)	297 (100%)	1 (0%)	92	93
All	All	1189/1316 (90%)	1165 (98%)	24 (2%)	57	50

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	222	MET
1	B	321[A]	ASN
1	C	301	ASP
1	B	259	SER
1	B	286	MET

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

Mol	Chain	Res	Type
1	B	210	GLN
1	C	308	GLN
1	C	362	ASN
1	C	389	HIS
1	D	308	GLN

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 55 ligands modelled in this entry, 8 are monoatomic - leaving 47 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
3	EDO	B	505	-	3,3,3	0.50	0	2,2,2	0.32	0
7	EPE	C	506	-	15,15,15	0.82	1 (6%)	18,20,20	2.11	6 (33%)
3	EDO	B	511	-	3,3,3	0.46	0	2,2,2	0.40	0
3	EDO	D	511	-	3,3,3	0.52	0	2,2,2	0.26	0
4	PEG	D	515	-	6,6,6	0.31	0	5,5,5	0.33	0
3	EDO	C	512	-	3,3,3	0.53	0	2,2,2	0.26	0
3	EDO	D	514	-	3,3,3	0.57	0	2,2,2	0.12	0
3	EDO	A	505	-	3,3,3	0.42	0	2,2,2	0.50	0
3	EDO	D	503	-	3,3,3	0.35	0	2,2,2	0.42	0
4	PEG	D	516	-	6,6,6	0.34	0	5,5,5	0.57	0
2	2SR	B	501	-	28,31,31	3.09	10 (35%)	36,44,44	1.64	6 (16%)
3	EDO	D	505	-	3,3,3	0.53	0	2,2,2	0.24	0
3	EDO	A	503	-	3,3,3	0.54	0	2,2,2	0.36	0
3	EDO	C	503	-	3,3,3	0.41	0	2,2,2	0.52	0
3	EDO	C	508	-	3,3,3	0.45	0	2,2,2	0.41	0
3	EDO	A	502	-	3,3,3	0.48	0	2,2,2	0.54	0
3	EDO	B	504	-	3,3,3	0.49	0	2,2,2	0.51	0
3	EDO	C	504	-	3,3,3	0.46	0	2,2,2	0.58	0
3	EDO	C	509	-	3,3,3	0.49	0	2,2,2	0.41	0
6	DMS	B	512	-	3,3,3	0.62	0	3,3,3	0.50	0
3	EDO	B	509	-	3,3,3	0.49	0	2,2,2	0.27	0
3	EDO	A	508	-	3,3,3	0.47	0	2,2,2	0.30	0
2	2SR	C	502	-	28,31,31	3.08	11 (39%)	36,44,44	1.78	9 (25%)
3	EDO	B	506	-	3,3,3	0.51	0	2,2,2	0.10	0
6	DMS	A	513	-	3,3,3	0.52	0	3,3,3	0.57	0
3	EDO	D	506	-	3,3,3	0.56	0	2,2,2	0.13	0
3	EDO	B	507	-	3,3,3	0.52	0	2,2,2	0.15	0
3	EDO	C	505	-	3,3,3	0.49	0	2,2,2	0.45	0
3	EDO	A	512	-	3,3,3	0.48	0	2,2,2	0.39	0
4	PEG	A	504	-	6,6,6	0.26	0	5,5,5	0.53	0
6	DMS	A	511	-	3,3,3	0.66	0	3,3,3	0.73	0
6	DMS	D	504	-	3,3,3	0.69	0	3,3,3	0.62	0
3	EDO	D	501	-	3,3,3	0.48	0	2,2,2	0.63	0
6	DMS	D	508	-	3,3,3	0.65	0	3,3,3	0.71	0
3	EDO	C	507	-	3,3,3	0.54	0	2,2,2	0.25	0
3	EDO	A	514	-	3,3,3	0.64	0	2,2,2	0.33	0
3	EDO	B	508	-	3,3,3	0.46	0	2,2,2	0.32	0
2	2SR	D	502	-	28,31,31	2.98	11 (39%)	36,44,44	1.75	9 (25%)
3	EDO	A	506	-	3,3,3	0.37	0	2,2,2	0.63	0
4	PEG	D	507	-	6,6,6	0.40	0	5,5,5	0.39	0
6	DMS	B	510	-	3,3,3	0.65	0	3,3,3	0.62	0
3	EDO	C	501	-	3,3,3	0.69	0	2,2,2	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	D	509	-	3,3,3	0.50	0	2,2,2	0.25	0
3	EDO	D	510	-	3,3,3	0.49	0	2,2,2	0.45	0
3	EDO	C	513	-	3,3,3	0.48	0	2,2,2	0.21	0
2	2SR	A	501	-	28,31,31	3.02	9 (32%)	36,44,44	1.58	5 (13%)
3	EDO	A	507	-	3,3,3	0.54	0	2,2,2	0.25	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	EDO	B	505	-	-	1/1/1/1	-
7	EPE	C	506	-	-	6/9/19/19	0/1/1/1
3	EDO	B	511	-	-	0/1/1/1	-
3	EDO	D	511	-	-	0/1/1/1	-
4	PEG	D	515	-	-	2/4/4/4	-
3	EDO	C	512	-	-	1/1/1/1	-
3	EDO	A	505	-	-	1/1/1/1	-
3	EDO	D	503	-	-	1/1/1/1	-
4	PEG	D	516	-	-	3/4/4/4	-
2	2SR	B	501	-	-	8/12/32/32	1/4/4/4
3	EDO	D	505	-	-	1/1/1/1	-
3	EDO	A	503	-	-	1/1/1/1	-
3	EDO	C	503	-	-	1/1/1/1	-
3	EDO	C	508	-	-	0/1/1/1	-
3	EDO	A	502	-	-	1/1/1/1	-
3	EDO	B	504	-	-	0/1/1/1	-
3	EDO	C	504	-	-	1/1/1/1	-
3	EDO	C	509	-	-	0/1/1/1	-
3	EDO	B	509	-	-	1/1/1/1	-
3	EDO	A	508	-	-	1/1/1/1	-
2	2SR	C	502	-	-	7/12/32/32	0/4/4/4
3	EDO	B	506	-	-	0/1/1/1	-
3	EDO	D	506	-	-	1/1/1/1	-
3	EDO	B	507	-	-	0/1/1/1	-
3	EDO	C	505	-	-	0/1/1/1	-
3	EDO	A	512	-	-	0/1/1/1	-
4	PEG	A	504	-	-	3/4/4/4	-
3	EDO	D	509	-	-	0/1/1/1	-
3	EDO	D	501	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	507	-	-	1/1/1/1	-
3	EDO	A	514	-	-	0/1/1/1	-
3	EDO	B	508	-	-	0/1/1/1	-
2	2SR	D	502	-	-	4/12/32/32	1/4/4/4
3	EDO	A	506	-	-	0/1/1/1	-
4	PEG	D	507	-	-	3/4/4/4	-
3	EDO	C	501	-	-	0/1/1/1	-
3	EDO	D	514	-	-	0/1/1/1	-
3	EDO	D	510	-	-	0/1/1/1	-
3	EDO	C	513	-	-	0/1/1/1	-
2	2SR	A	501	-	-	8/12/32/32	0/4/4/4
3	EDO	A	507	-	-	0/1/1/1	-

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	2SR	O11-C10	11.15	1.54	1.37
2	C	502	2SR	O11-C10	11.13	1.54	1.37
2	B	501	2SR	O11-C10	10.67	1.53	1.37
2	D	502	2SR	O11-C10	10.38	1.53	1.37
2	B	501	2SR	C14-C09	6.65	1.50	1.39

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	2SR	O25-C21-C22	4.77	122.05	115.41
2	B	501	2SR	O26-C22-C21	4.50	121.68	115.41
7	C	506	EPE	C7-N4-C5	4.30	122.23	111.23
7	C	506	EPE	C5-N4-C3	4.23	118.35	108.83
2	A	501	2SR	O26-C22-C21	4.14	121.18	115.41

There are no chirality outliers.

5 of 57 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	505	EDO	O1-C1-C2-O2
2	B	501	2SR	C01-C02-C07-O11
2	B	501	2SR	C01-C02-C07-C12
2	B	501	2SR	C03-C02-C07-O11
2	B	501	2SR	C03-C02-C07-C12

All (2) ring outliers are listed below:

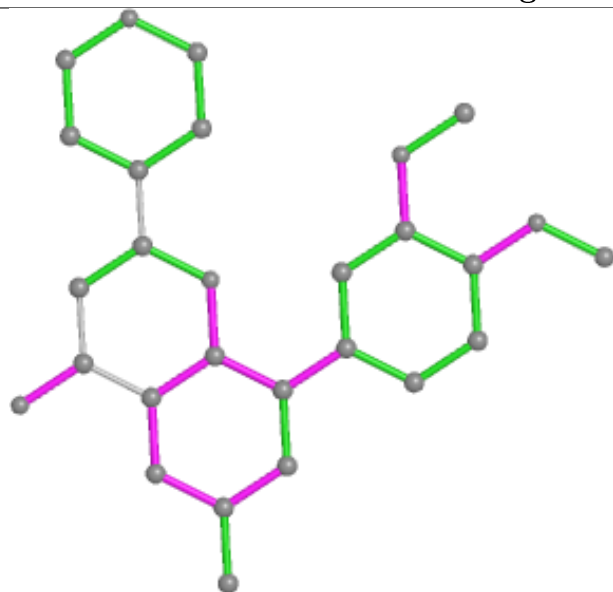
Mol	Chain	Res	Type	Atoms
2	B	501	2SR	C01-C02-C03-C04-C06-O05
2	D	502	2SR	C01-C02-C03-C04-C06-O05

20 monomers are involved in 47 short contacts:

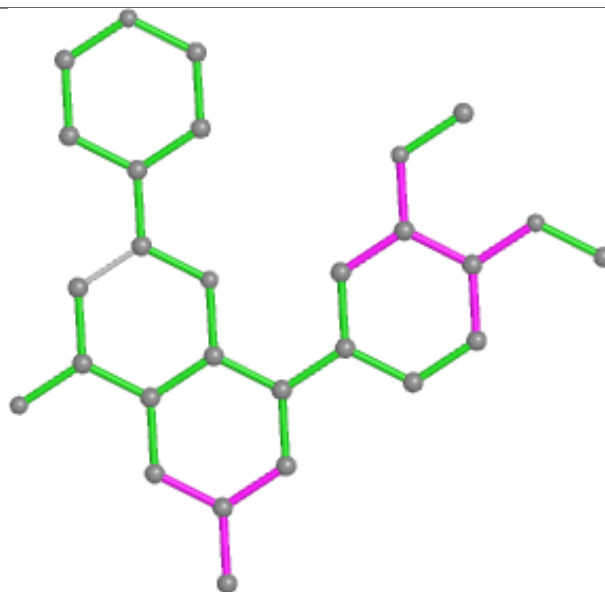
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	512	EDO	5	0
4	D	516	PEG	4	0
2	B	501	2SR	2	0
3	D	505	EDO	2	0
3	A	503	EDO	1	0
3	C	504	EDO	1	0
3	C	509	EDO	2	0
6	B	512	DMS	1	0
3	B	509	EDO	2	0
3	A	508	EDO	3	0
2	C	502	2SR	1	0
6	A	513	DMS	5	0
3	B	507	EDO	3	0
3	C	505	EDO	1	0
2	D	502	2SR	3	0
3	A	506	EDO	1	0
4	D	507	PEG	3	0
6	B	510	DMS	2	0
2	A	501	2SR	4	0
3	A	507	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.

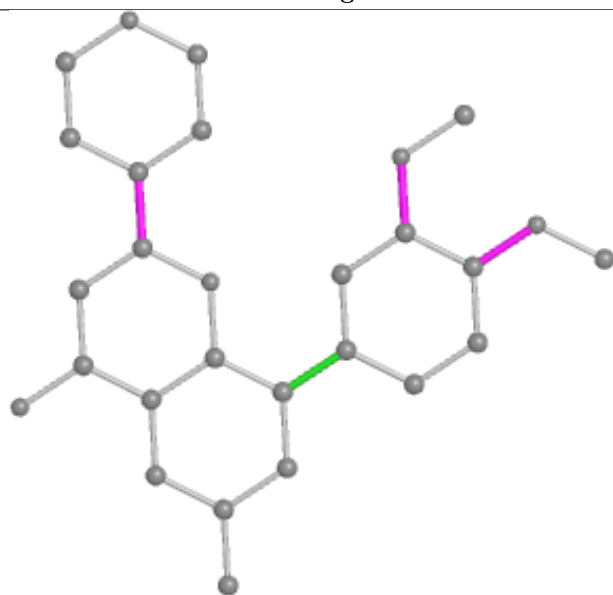
Ligand 2SR B 501



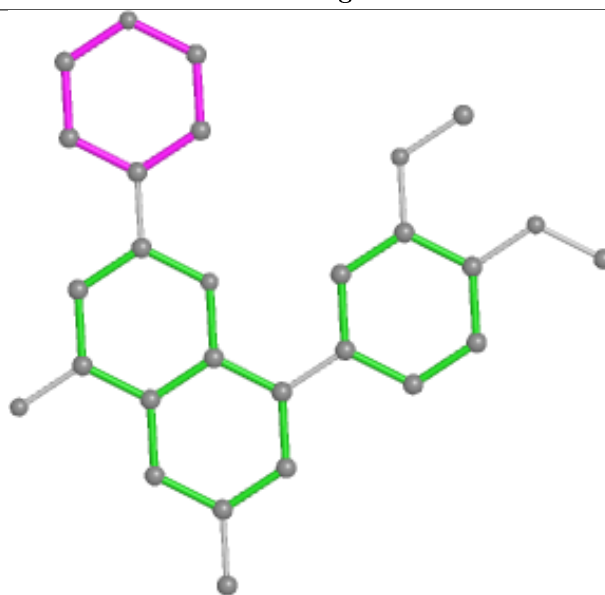
Bond lengths



Bond angles

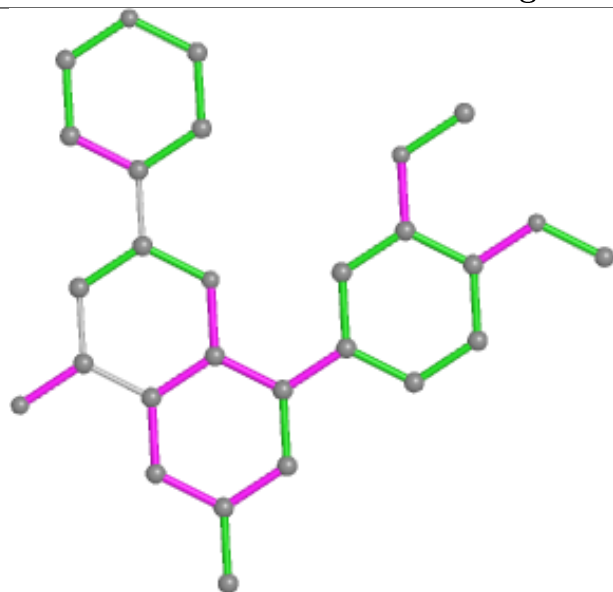


Torsions

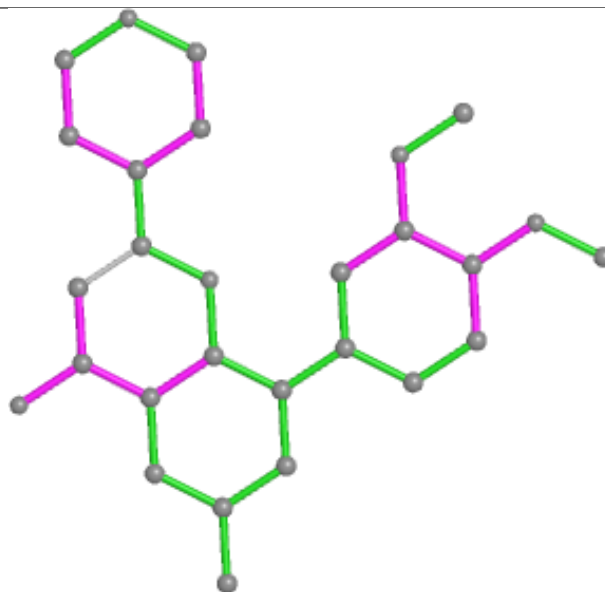


Rings

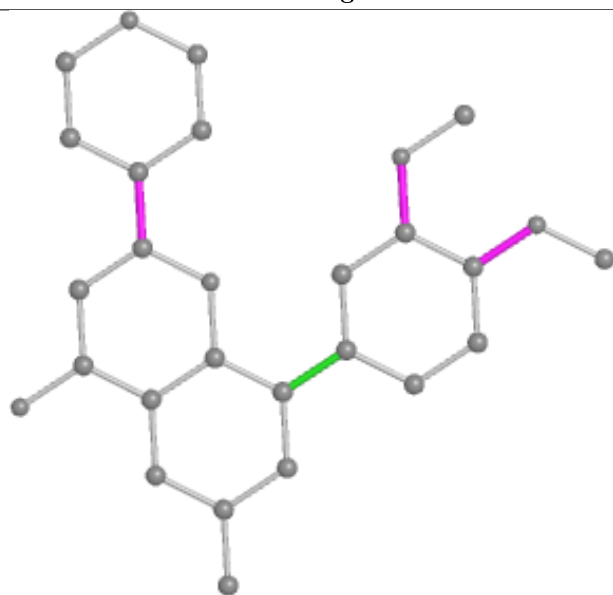
Ligand 2SR C 502



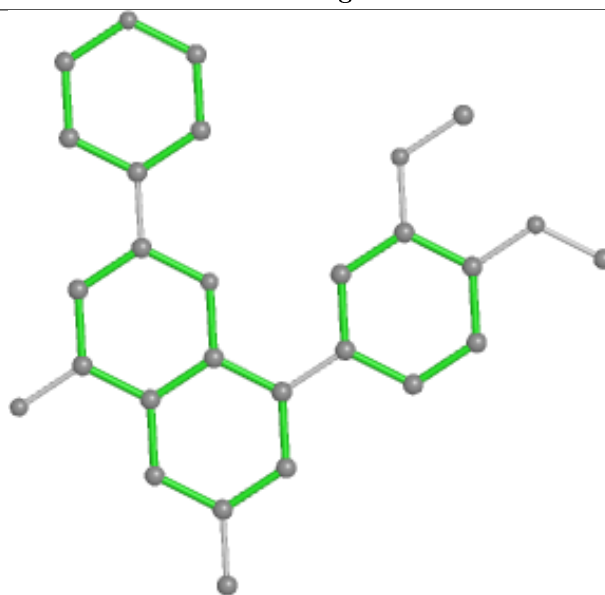
Bond lengths



Bond angles

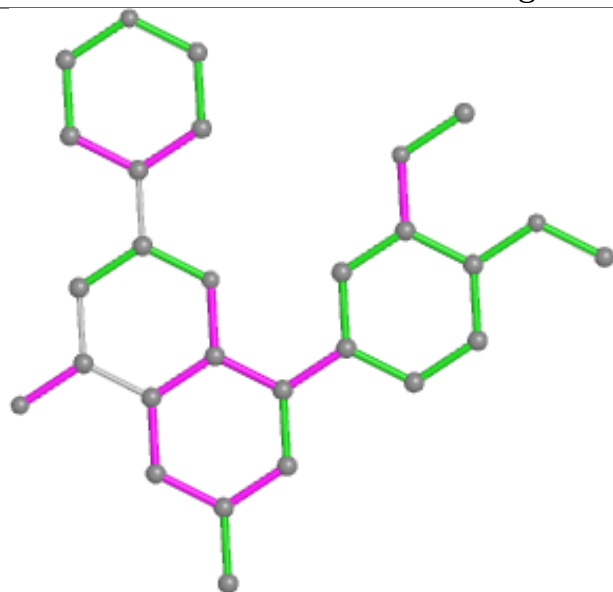


Torsions

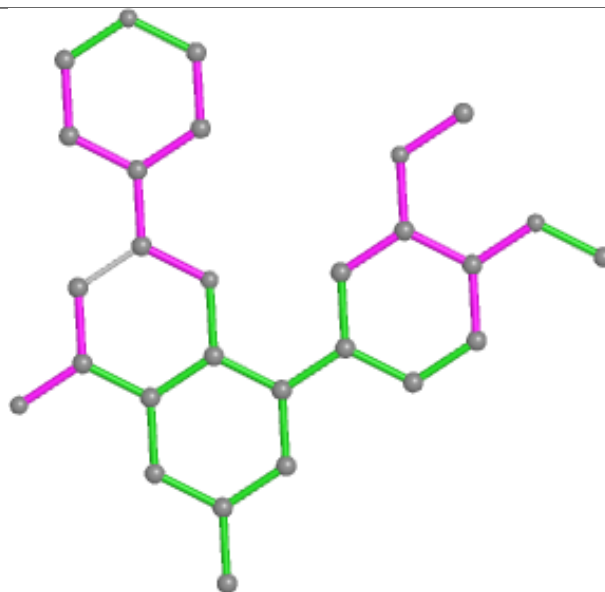


Rings

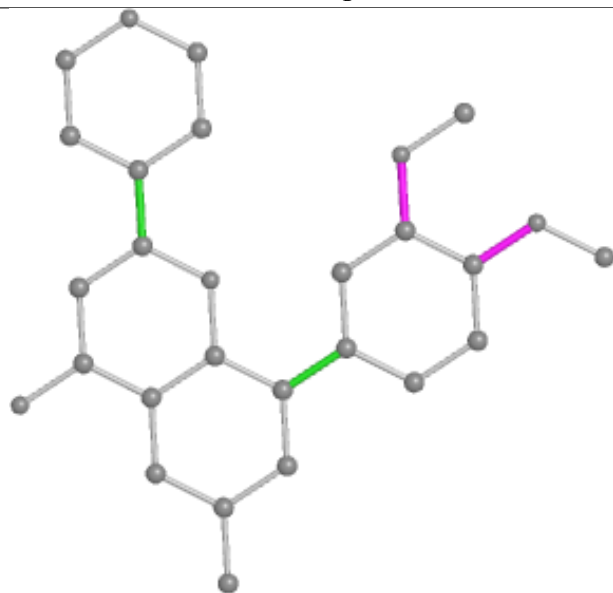
Ligand 2SR D 502



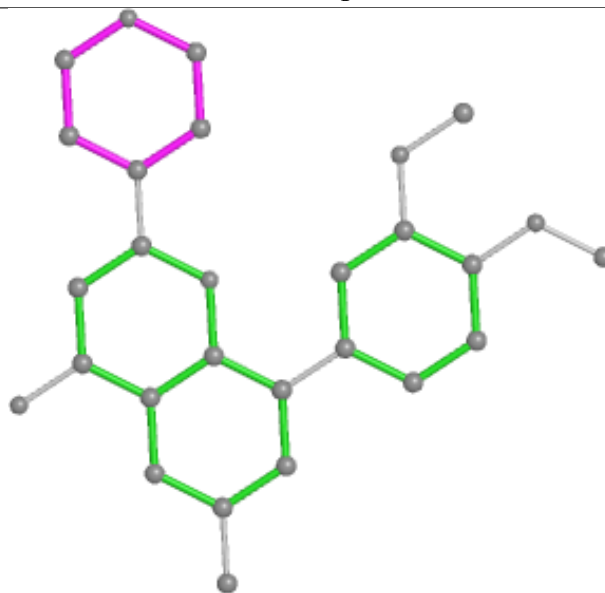
Bond lengths



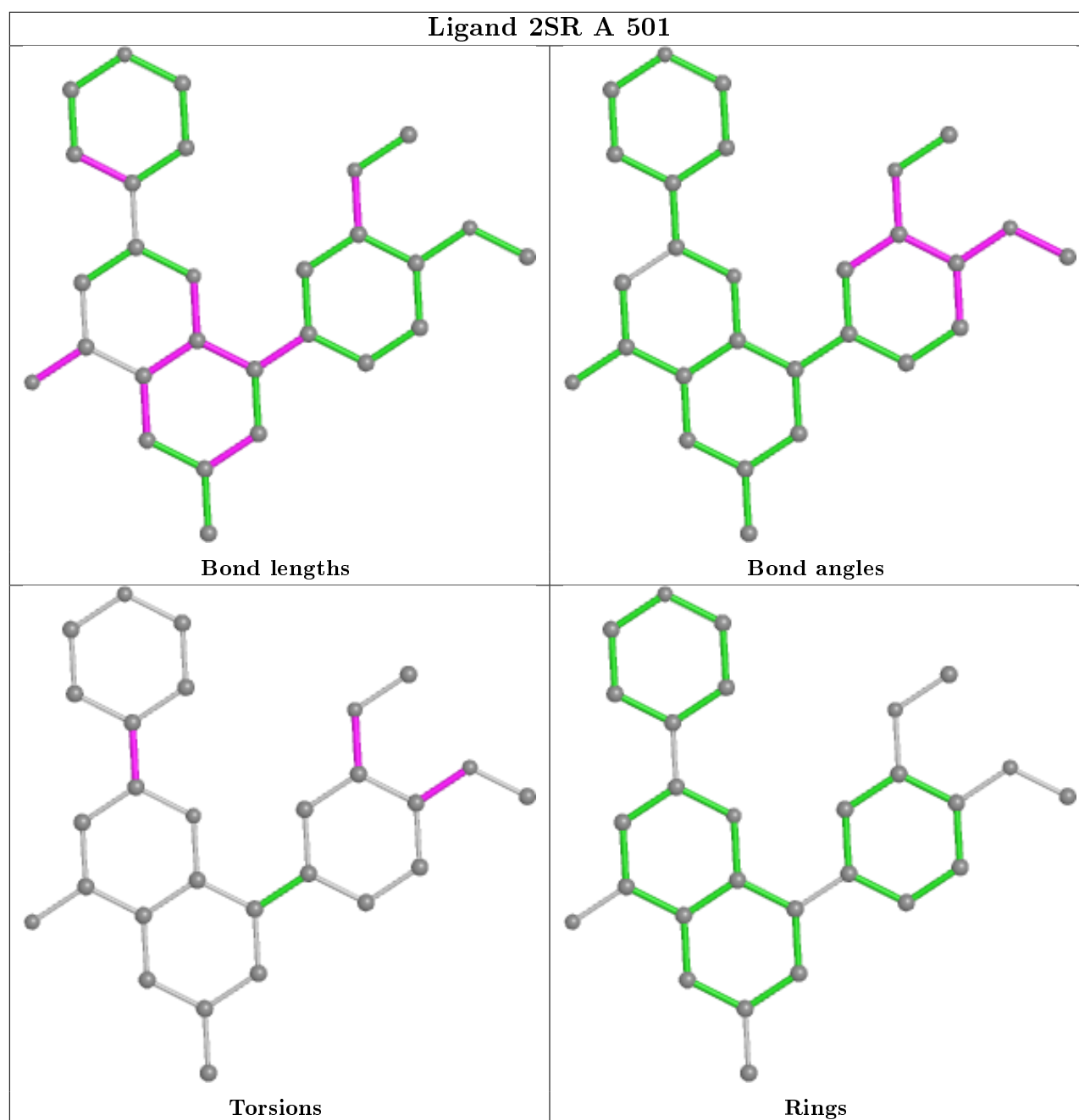
Bond angles



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	328/361 (90%)	0.49	21 (6%) 19 21	17, 32, 59, 115	0
1	B	321/361 (88%)	0.58	29 (9%) 9 10	21, 43, 61, 77	0
1	C	325/361 (90%)	0.48	22 (6%) 17 18	22, 39, 66, 106	0
1	D	324/361 (89%)	0.19	7 (2%) 62 66	16, 29, 56, 75	0
All	All	1298/1444 (89%)	0.44	79 (6%) 21 22	16, 36, 61, 115	0

The worst 5 of 79 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	295	SER	6.6
1	C	294	SER	6.2
1	A	293	THR	5.9
1	C	292	VAL	5.6
1	A	296	GLY	5.6

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 carbohydrates 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(\AA^2)	Q<0.9
3	EDO	A	503	4/4	0.60	0.34	40,40,48,51	0
4	PEG	D	515	7/7	0.65	0.47	53,67,90,105	0
2	2SR	B	501	28/28	0.70	0.27	45,56,68,76	0
3	EDO	B	511	4/4	0.73	0.17	58,58,58,66	0
3	EDO	C	512	4/4	0.74	0.35	43,45,52,54	0
3	EDO	C	508	4/4	0.76	0.22	57,57,60,60	0
3	EDO	A	507	4/4	0.76	0.21	46,49,53,54	0
2	2SR	A	501	28/28	0.77	0.35	51,62,70,72	0
2	2SR	C	502	28/28	0.78	0.26	46,58,63,67	0
3	EDO	D	505	4/4	0.80	0.16	41,50,51,52	0
2	2SR	D	502	28/28	0.81	0.23	47,54,58,59	0
3	EDO	D	506	4/4	0.84	0.22	41,42,43,48	0
3	EDO	C	509	4/4	0.84	0.18	34,41,43,47	0
3	EDO	C	507	4/4	0.84	0.29	45,46,47,48	0
3	EDO	B	509	4/4	0.84	0.40	40,46,48,54	0
3	EDO	B	505	4/4	0.84	0.33	45,46,49,54	0
3	EDO	D	509	4/4	0.85	0.18	38,47,49,52	0
3	EDO	D	511	4/4	0.85	0.18	49,49,50,55	0
4	PEG	D	516	7/7	0.86	0.27	36,44,59,69	0
3	EDO	A	514	4/4	0.86	0.23	27,38,38,45	0
4	PEG	D	507	7/7	0.87	0.18	29,33,37,42	0
6	DMS	A	513	4/4	0.88	0.19	29,46,51,55	0
6	DMS	D	508	4/4	0.89	0.19	38,42,53,61	0
3	EDO	C	501	4/4	0.89	0.16	35,38,41,43	0
4	PEG	A	504	7/7	0.89	0.20	33,36,46,51	0
3	EDO	C	503	4/4	0.89	0.24	39,41,44,55	0
3	EDO	A	502	4/4	0.90	0.29	52,52,53,54	0
3	EDO	B	507	4/4	0.90	0.32	30,30,38,41	0
6	DMS	A	511	4/4	0.90	0.23	45,59,63,71	0
3	EDO	A	505	4/4	0.91	0.14	27,32,36,39	0
3	EDO	A	512	4/4	0.91	0.20	28,30,30,31	0
3	EDO	C	513	4/4	0.91	0.12	41,53,55,58	0
3	EDO	C	504	4/4	0.91	0.29	45,45,50,53	0
3	EDO	A	508	4/4	0.91	0.21	30,31,36,51	0
6	DMS	D	504	4/4	0.92	0.29	41,42,55,63	0
3	EDO	C	505	4/4	0.92	0.12	44,44,52,54	0
3	EDO	D	510	4/4	0.92	0.24	38,40,45,52	0
3	EDO	B	504	4/4	0.92	0.13	35,40,40,50	0
6	DMS	B	512	4/4	0.92	0.29	33,45,52,66	0
3	EDO	A	506	4/4	0.94	0.18	31,31,32,34	0
3	EDO	B	506	4/4	0.94	0.11	40,41,42,43	0
3	EDO	B	508	4/4	0.94	0.14	55,57,63,64	0
3	EDO	D	503	4/4	0.94	0.16	34,35,36,43	0

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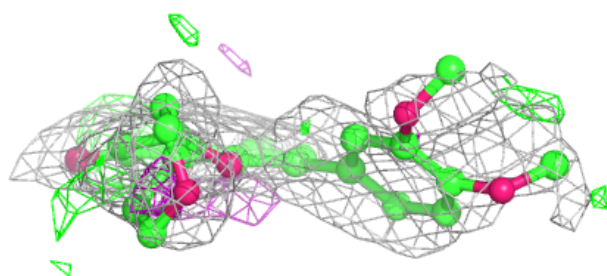
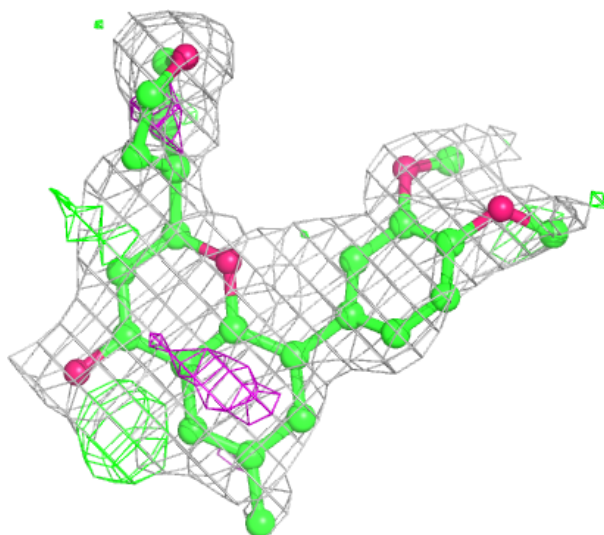
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	DMS	B	510	4/4	0.95	0.38	59,64,73,74	0
7	EPE	C	506	15/15	0.96	0.24	41,52,71,74	0
3	EDO	D	501	4/4	0.97	0.12	30,31,33,37	0
3	EDO	D	514	4/4	0.97	0.12	25,28,29,30	0
5	ZN	B	503	1/1	0.98	0.08	35,35,35,35	1
5	ZN	A	509	1/1	0.99	0.14	28,28,28,28	0
5	ZN	C	511	1/1	0.99	0.10	32,32,32,32	1
5	ZN	D	513	1/1	0.99	0.10	33,33,33,33	1
5	ZN	A	510	1/1	0.99	0.10	30,30,30,30	1
5	ZN	C	510	1/1	0.99	0.12	33,33,33,33	0
5	ZN	B	502	1/1	0.99	0.08	34,34,34,34	0
5	ZN	D	512	1/1	1.00	0.12	27,27,27,27	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.

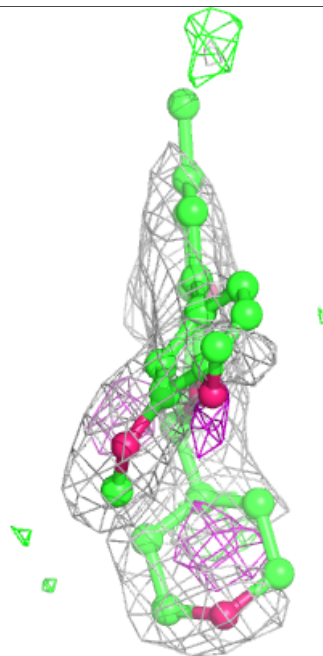
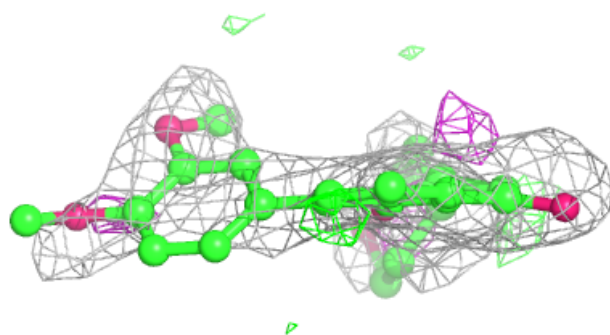
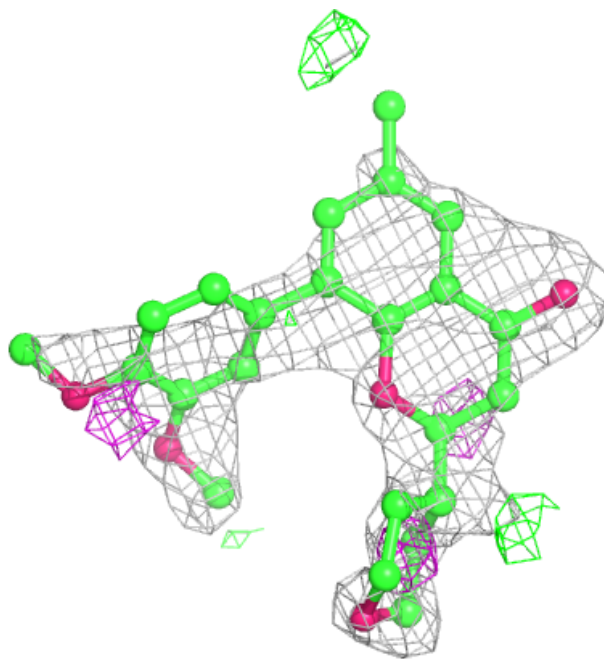
Electron density around 2SR B 501:

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



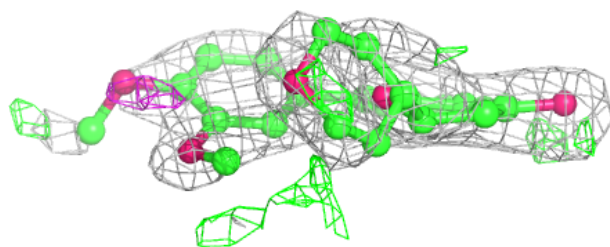
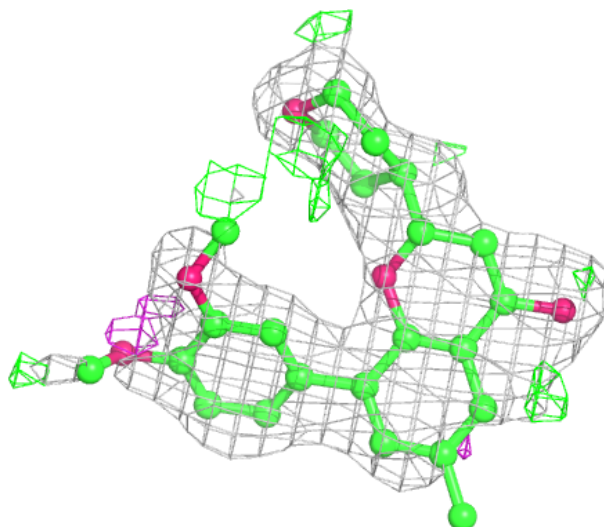
Electron density around 2SR A 501:

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



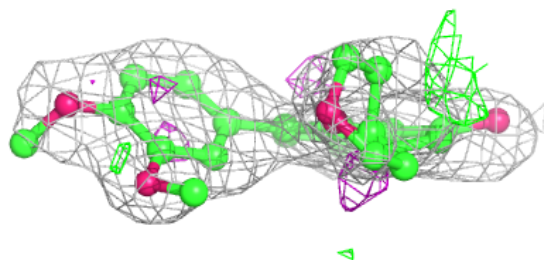
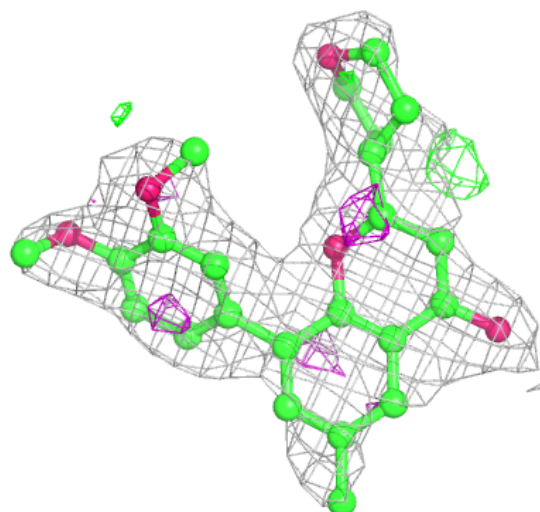
Electron density around 2SR C 502:

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 2SR D 502:

$2mF_o-DF_c$ (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.