



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 13, 2024 – 10:15 AM JST

PDB ID : 7EP0  
Title : Crystal structure of ZYG11B bound to GSTE degron  
Authors : Yan, X.; Li, Y.  
Deposited on : 2021-04-26  
Resolution : 2.16 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](mailto: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>.

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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 : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

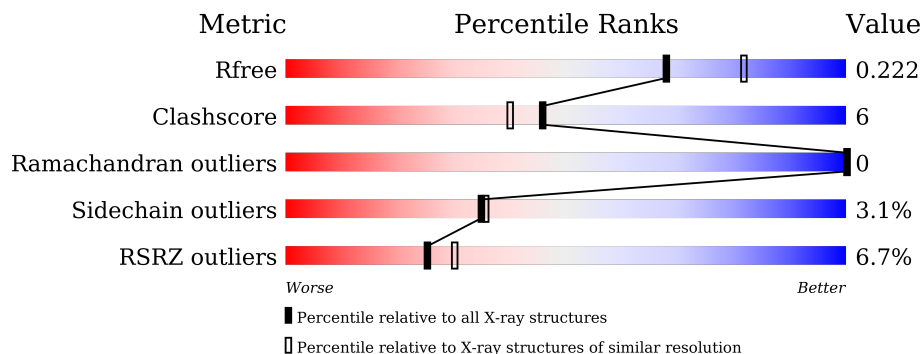
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.16 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))
$R_{free}$	164625	1881 (2.16-2.16)
Clashscore	180529	2047 (2.16-2.16)
Ramachandran outliers	177936	2027 (2.16-2.16)
Sidechain outliers	177891	2026 (2.16-2.16)
RSRZ outliers	164620	1882 (2.16-2.16)

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  $\geq 3$ , 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	250	<div> <div>3%</div> <div>87%</div> <div>13%</div> </div>
1	B	250	<div> <div>10%</div> <div>85%</div> <div>14%</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4198 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.

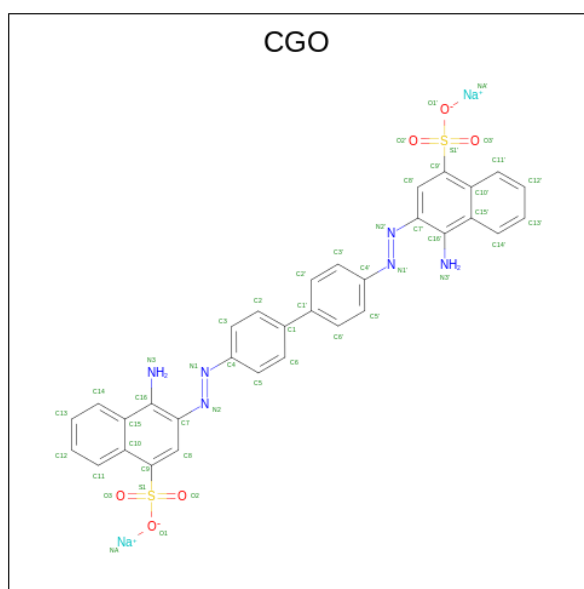
- Molecule 1 is a protein called Protein zyg-11 homolog B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	Se	0	0	0
			2007	1279	343	375	5	5			
1	B	250	Total	C	N	O	S	Se	0	0	0
			2007	1279	343	375	5	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	479	GLY	-	expression tag	UNP Q9C0D3
B	479	GLY	-	expression tag	UNP Q9C0D3

- Molecule 2 is sodium 3,3'-(1E,1'E)-biphenyl-4,4'-diylbis(diazene-2,1-diyl)bis(4-aminonaphthalene-1-sulfonate) (three-letter code: CGO) (formula: C<sub>32</sub>H<sub>22</sub>N<sub>6</sub>Na<sub>2</sub>O<sub>6</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	Na	O	S	0	0
			48	32	6	2	6	2		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	Na	O	S	0	0
			48	32	6	2	6	2		

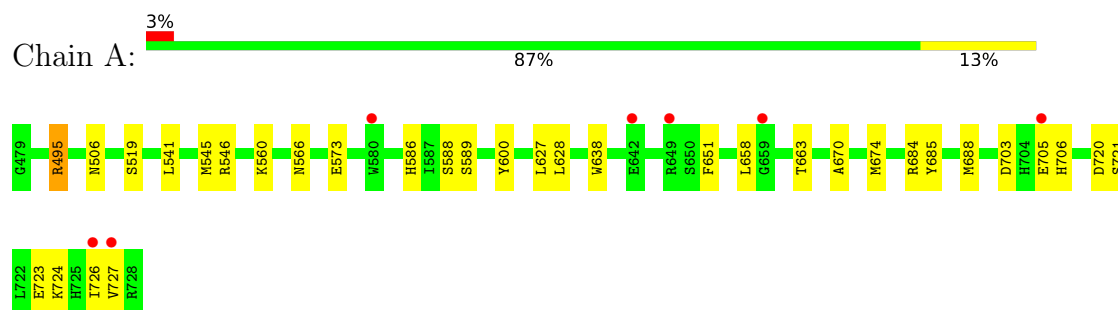
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	58	Total	O	0	0
			58	58		
3	B	30	Total	O	0	0
			30	30		

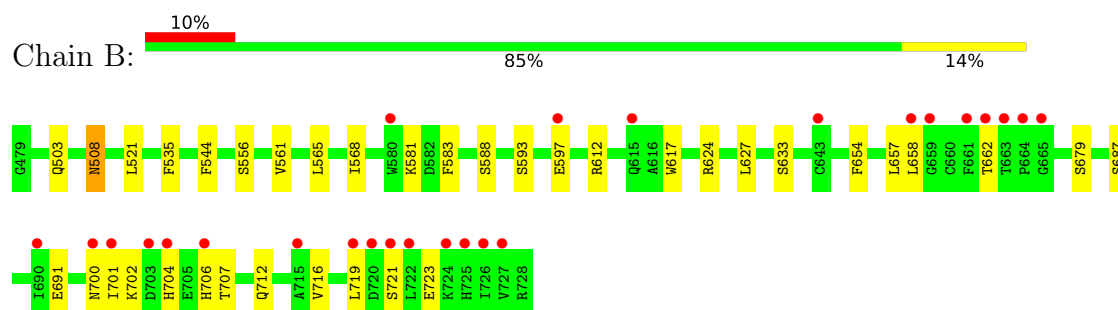
### 3 Residue-property plots

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: Protein zyg-11 homolog B



#### • Molecule 1: Protein zyg-11 homolog B



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	131.50Å 131.50Å 87.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.75 – 2.16 65.75 – 2.16	Depositor EDS
% Data completeness (in resolution range)	93.6 (65.75-2.16) 90.6 (65.75-2.16)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.48 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, $R_{free}$	0.190 , 0.222 0.190 , 0.222	Depositor DCC
$R_{free}$ test set	39446 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.4	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 39.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4198	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: CGO

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	0.43	0/2049	0.62	2/2777 (0.1%)
1	B	0.38	0/2049	0.53	0/2777
All	All	0.40	0/4098	0.57	2/5554 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	495	ARG	NE-CZ-NH2	-9.08	115.76	120.30
1	A	495	ARG	NE-CZ-NH1	5.85	123.22	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2007	0	1980	24	1
1	B	2007	0	1980	16	0
2	A	96	0	0	6	0
3	A	58	0	0	1	0
3	B	30	0	0	0	0
All	All	4198	0	3960	46	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (46) 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)
2:A:801:CGO:C9'	2:A:801:CGO:S1'	2.07	1.42
2:A:802:CGO:C9'	2:A:802:CGO:S1'	2.09	1.40
2:A:802:CGO:N2	2:A:802:CGO:C7	2.10	1.14
2:A:801:CGO:N2	2:A:801:CGO:C7	2.10	1.14
1:A:658:LEU:HD21	1:A:674:MSE:HE1	1.71	0.73
2:A:801:CGO:C7	2:A:801:CGO:N1	2.55	0.69
1:A:506:ASN:OD1	1:A:546:ARG:NH2	2.26	0.65
2:A:802:CGO:C7	2:A:802:CGO:N1	2.63	0.60
1:B:508:ASN:O	1:B:508:ASN:ND2	2.32	0.60
1:B:702:LYS:HD2	1:B:716:VAL:HG22	1.84	0.57
1:B:707:THR:OG1	1:B:712:GLN:OE1	2.25	0.54
1:A:588:SER:HB2	1:A:627:LEU:HD21	1.95	0.49
1:A:545:MSE:CE	1:A:586:HIS:ND1	2.75	0.49
1:B:588:SER:HB2	1:B:627:LEU:HD21	1.94	0.49
1:A:685:TYR:HD1	1:A:688:MSE:HE2	1.79	0.48
1:A:545:MSE:HE1	1:A:586:HIS:CG	2.49	0.48
1:A:545:MSE:HE1	1:A:586:HIS:ND1	2.29	0.48
1:A:600:TYR:HA	1:A:638:TRP:CH2	2.50	0.47
1:B:617:TRP:CE2	1:B:624:ARG:HB2	2.50	0.47
1:B:535:PHE:CD1	1:B:568:ILE:HD11	2.49	0.47
1:A:705:GLU:HG2	1:A:706:HIS:CE1	2.50	0.46
1:A:685:TYR:CD1	1:A:688:MSE:HE2	2.51	0.46
1:A:726:ILE:O	1:A:727:VAL:HG22	2.17	0.45
1:B:581:LYS:HB3	1:B:581:LYS:HE3	1.64	0.44
1:B:658:LEU:HB3	1:B:701:ILE:HD11	1.99	0.43
1:A:519:SER:OG	1:A:560:LYS:HE3	2.19	0.43
1:A:727:VAL:HG23	1:A:727:VAL:O	2.19	0.43
1:A:723:GLU:O	1:A:727:VAL:HG22	2.19	0.43
1:B:687:SER:O	1:B:691:GLU:HG3	2.18	0.43
1:A:720:ASP:OD2	1:A:724:LYS:HE2	2.18	0.43
1:A:545:MSE:HE1	1:A:586:HIS:HB2	2.00	0.43
1:B:719:LEU:O	1:B:723:GLU:HG2	2.18	0.43
1:A:627:LEU:HD23	1:A:627:LEU:HA	1.82	0.42
1:A:684:ARG:HH11	1:A:684:ARG:HG3	1.84	0.42
1:B:544:PHE:CD2	1:B:561:VAL:HG13	2.54	0.42
1:B:597:GLU:H	1:B:597:GLU:CD	2.21	0.42
1:B:654:PHE:O	1:B:657:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:586:HIS:HD2	3:A:955:HOH:O	2.02	0.42
1:A:628:LEU:HD11	1:A:663:THR:HB	2.01	0.42
1:A:573:GLU:H	1:A:573:GLU:CD	2.23	0.42
1:A:541:LEU:O	1:A:545:MSE:HG2	2.20	0.41
1:A:670:ALA:O	1:A:674:MSE:HG3	2.21	0.41
1:B:617:TRP:CG	1:B:624:ARG:HD2	2.55	0.41
1:B:565:LEU:HD13	1:B:583:PHE:HE1	1.85	0.41
1:A:651:PHE:CE2	1:A:688:MSE:HE2	2.56	0.40
1:B:700:ASN:O	1:B:704:HIS:HB2	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:ARG:NH2	1:A:703:ASP:OD2[4_555]	2.17	0.03

## 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	248/250 (99%)	244 (98%)	4 (2%)	0	100	100
1	B	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
All	All	496/500 (99%)	485 (98%)	11 (2%)	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	227/222 (102%)	224 (99%)	3 (1%)	65	71
1	B	227/222 (102%)	216 (95%)	11 (5%)	21	19
All	All	454/444 (102%)	440 (97%)	14 (3%)	35	36

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

Mol	Chain	Res	Type
1	A	566	ASN
1	A	589	SER
1	A	721	SER
1	B	503	GLN
1	B	508	ASN
1	B	521	LEU
1	B	556	SER
1	B	593	SER
1	B	612	ARG
1	B	633	SER
1	B	662	THR
1	B	679	SER
1	B	706	HIS
1	B	721	SER

Sometimes 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 oligosaccharides in this entry.

## 5.6 Ligand geometry

2 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	CGO	A	802	-	48,53,53	5.45	17 (35%)	64,78,78	2.93	30 (46%)
2	CGO	A	801	-	48,53,53	5.47	19 (39%)	64,78,78	3.23	26 (40%)

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	CGO	A	802	-	-	13/22/32/32	0/6/6/6
2	CGO	A	801	-	-	10/22/32/32	0/6/6/6

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	CGO	C7-N2	32.11	2.10	1.42
2	A	802	CGO	C7-N2	31.87	2.10	1.42
2	A	802	CGO	C9'-S1'	14.78	2.09	1.78
2	A	801	CGO	C9'-S1'	13.92	2.07	1.78
2	A	801	CGO	C16'-C15'	-6.17	1.36	1.44
2	A	802	CGO	C16'-C15'	-4.63	1.38	1.44
2	A	802	CGO	C15'-C10'	-4.35	1.35	1.43
2	A	802	CGO	C16-C15	-4.31	1.38	1.44
2	A	801	CGO	C7'-N2'	-4.14	1.33	1.42
2	A	801	CGO	C15'-C10'	-4.08	1.35	1.43
2	A	802	CGO	C7'-N2'	-3.87	1.34	1.42
2	A	801	CGO	C4'-N1'	-3.52	1.29	1.44
2	A	802	CGO	C4'-N1'	-3.28	1.30	1.44
2	A	801	CGO	C16-C15	-3.22	1.40	1.44
2	A	801	CGO	C16'-C7'	-3.15	1.37	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	CGO	C16-C7	-3.04	1.37	1.41
2	A	802	CGO	C16-C7	-3.03	1.37	1.41
2	A	801	CGO	C4-N1	-3.00	1.31	1.44
2	A	802	CGO	C9'-C10'	-2.98	1.38	1.43
2	A	801	CGO	C9'-C10'	-2.96	1.38	1.43
2	A	801	CGO	O2'-S1'	-2.92	1.37	1.43
2	A	802	CGO	C14'-C15'	-2.89	1.36	1.42
2	A	802	CGO	C16'-C7'	-2.75	1.37	1.41
2	A	801	CGO	C14'-C15'	-2.71	1.36	1.42
2	A	802	CGO	C10-C15	-2.66	1.38	1.43
2	A	801	CGO	C11'-C10'	-2.51	1.37	1.42
2	A	802	CGO	C4-N1	-2.50	1.33	1.44
2	A	802	CGO	C8-C7	-2.31	1.36	1.40
2	A	801	CGO	C10-C15	-2.30	1.39	1.43
2	A	801	CGO	C16'-N3'	-2.26	1.29	1.36
2	A	802	CGO	C11'-C10'	-2.25	1.37	1.42
2	A	801	CGO	C6'-C1'	-2.24	1.36	1.41
2	A	801	CGO	C14-C15	-2.16	1.37	1.42
2	A	802	CGO	C16'-N3'	-2.14	1.30	1.36
2	A	801	CGO	O3'-S1'	-2.02	1.39	1.43
2	A	802	CGO	C6'-C1'	-2.02	1.37	1.41

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	CGO	C8-C9-S1	-11.18	107.15	117.56
2	A	801	CGO	O1-S1-O3	-11.11	82.36	112.12
2	A	802	CGO	C8-C9-S1	-9.23	108.97	117.56
2	A	802	CGO	O1-S1-O3	-8.86	88.39	112.12
2	A	801	CGO	C10-C9-S1	7.88	130.91	121.21
2	A	801	CGO	C7-N2-N1	-7.60	97.03	114.56
2	A	802	CGO	C15-C16-N3	-6.89	95.37	119.60
2	A	802	CGO	C8'-C9'-S1'	5.82	122.98	117.56
2	A	801	CGO	C15-C16-N3	-5.76	99.33	119.60
2	A	802	CGO	C7-N2-N1	-5.73	101.34	114.56
2	A	802	CGO	C10-C9-S1	5.10	127.48	121.21
2	A	802	CGO	C7'-N2'-N1'	4.96	126.02	114.56
2	A	801	CGO	O3'-S1'-C9'	4.87	122.53	107.19
2	A	802	CGO	O3'-S1'-C9'	4.70	122.00	107.19
2	A	801	CGO	C7'-N2'-N1'	4.54	125.04	114.56
2	A	801	CGO	C8-C9-C10	-4.44	113.85	120.82
2	A	801	CGO	O2-S1-C9	4.37	120.95	107.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	802	CGO	C5-C4-C3	-4.31	112.30	119.22
2	A	801	CGO	C8'-C9'-S1'	4.15	121.43	117.56
2	A	801	CGO	C5-C4-C3	-3.88	112.98	119.22
2	A	801	CGO	O1-S1-O2	-3.86	101.79	112.12
2	A	802	CGO	C10'-C9'-S1'	-3.77	116.57	121.21
2	A	801	CGO	C10'-C9'-S1'	-3.66	116.70	121.21
2	A	802	CGO	C13'-C12'-C11'	-3.60	115.40	120.44
2	A	802	CGO	C8'-C9'-C10'	-3.60	115.17	120.82
2	A	801	CGO	C8'-C7'-C16'	-3.46	115.59	119.50
2	A	802	CGO	O1-S1-O2	-3.30	103.29	112.12
2	A	801	CGO	C13-C12-C11	-3.14	116.03	120.44
2	A	801	CGO	C14'-C15'-C16'	-3.06	116.41	123.08
2	A	801	CGO	C9-C10-C15	-2.97	114.19	117.94
2	A	801	CGO	C12-C13-C14	-2.91	116.36	120.44
2	A	802	CGO	O2-S1-C9	2.91	116.34	107.19
2	A	801	CGO	C12'-C13'-C14'	-2.85	116.45	120.44
2	A	802	CGO	O1'-S1'-O3'	-2.82	104.58	112.12
2	A	802	CGO	C8'-C7'-C16'	-2.76	116.38	119.50
2	A	801	CGO	O3-S1-C9	2.75	115.84	107.19
2	A	802	CGO	O1'-S1'-O2'	-2.71	104.87	112.12
2	A	802	CGO	C9-C10-C15	-2.66	114.59	117.94
2	A	802	CGO	C6-C1-C2	-2.51	116.42	118.65
2	A	801	CGO	O3'-S1'-O2'	-2.49	107.64	117.04
2	A	801	CGO	C8-C7-N2	2.47	130.58	119.60
2	A	801	CGO	C3-C2-C1	-2.41	117.09	120.82
2	A	801	CGO	C7-C16-N3	2.39	124.68	121.22
2	A	802	CGO	O3-S1-C9	2.33	114.52	107.19
2	A	802	CGO	C8-C7-N2	2.28	129.70	119.60
2	A	802	CGO	C2-C3-C4	2.23	121.78	119.38
2	A	802	CGO	O3'-S1'-O2'	-2.21	108.72	117.04
2	A	802	CGO	C3-C2-C1	-2.16	117.48	120.82
2	A	802	CGO	C12'-C13'-C14'	-2.16	117.42	120.44
2	A	801	CGO	C8'-C9'-C10'	-2.09	117.54	120.82
2	A	802	CGO	C11'-C10'-C9'	-2.08	120.87	123.60
2	A	802	CGO	C6'-C5'-C4'	2.08	121.62	119.38
2	A	802	CGO	C14'-C15'-C16'	-2.07	118.56	123.08
2	A	802	CGO	C4'-N1'-N2'	2.04	123.14	112.99
2	A	802	CGO	C13-C12-C11	-2.01	117.63	120.44
2	A	801	CGO	O1'-S1'-O3'	-2.00	106.77	112.12

There are no chirality outliers.

All (23) torsion outliers are listed below:

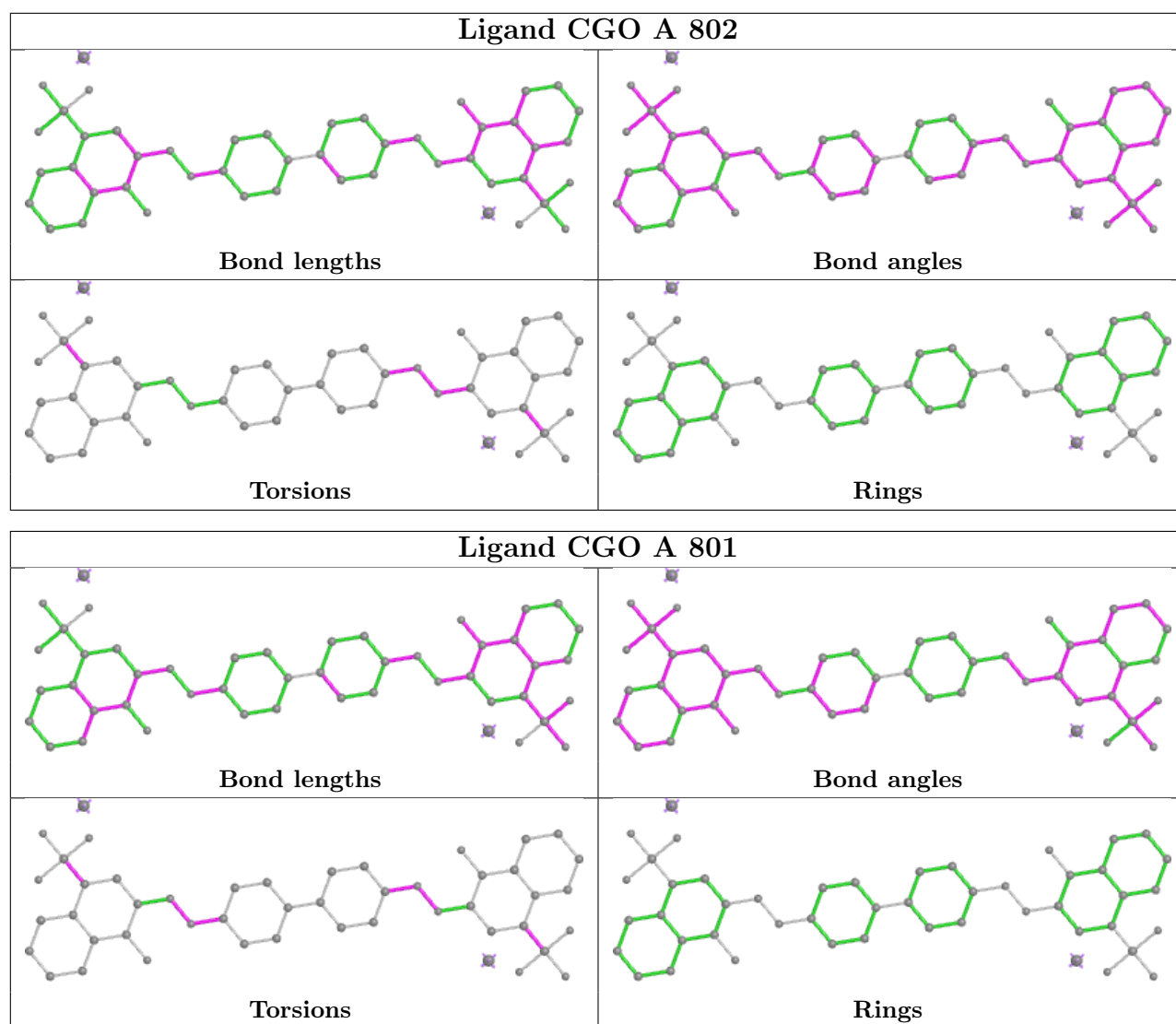
Mol	Chain	Res	Type	Atoms
2	A	801	CGO	C10'-C9'-S1'-O1'
2	A	802	CGO	C10'-C9'-S1'-O1'
2	A	802	CGO	C8'-C9'-S1'-O1'
2	A	802	CGO	C10'-C9'-S1'-O2'
2	A	802	CGO	C10'-C9'-S1'-O3'
2	A	802	CGO	C5'-C4'-N1'-N2'
2	A	802	CGO	C8'-C9'-S1'-O2'
2	A	801	CGO	C10-C9-S1-O3
2	A	801	CGO	C5-C4-N1-N2
2	A	801	CGO	C8-C9-S1-O2
2	A	802	CGO	C8'-C9'-S1'-O3'
2	A	802	CGO	C10-C9-S1-O3
2	A	802	CGO	C3'-C4'-N1'-N2'
2	A	801	CGO	C4-N1-N2-C7
2	A	801	CGO	C3'-C4'-N1'-N2'
2	A	802	CGO	C16'-C7'-N2'-N1'
2	A	801	CGO	C8-C9-S1-O1
2	A	802	CGO	C8'-C7'-N2'-N1'
2	A	802	CGO	C4'-N1'-N2'-C7'
2	A	801	CGO	C10'-C9'-S1'-O3'
2	A	802	CGO	C8-C9-S1-O2
2	A	801	CGO	C5'-C4'-N1'-N2'
2	A	801	CGO	C4'-N1'-N2'-C7'

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	802	CGO	3	0
2	A	801	CGO	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	245/250 (98%)	0.21	7 (2%) 54 59	31, 45, 59, 74	0
1	B	245/250 (98%)	0.64	26 (10%) 13 15	35, 53, 81, 106	0
All	All	490/500 (98%)	0.42	33 (6%) 25 30	31, 48, 73, 106	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	727	VAL	5.8
1	B	726	ILE	5.8
1	A	659	GLY	4.0
1	B	662	THR	3.7
1	B	706	HIS	3.6
1	B	580	TRP	3.5
1	B	703	ASP	3.1
1	B	690	ILE	3.0
1	B	663	THR	2.9
1	A	580	TRP	2.8
1	B	719	LEU	2.7
1	B	725	HIS	2.4
1	A	726	ILE	2.4
1	B	721	SER	2.4
1	A	642	GLU	2.3
1	B	665	GLY	2.3
1	B	615	GLN	2.2
1	B	658	LEU	2.2
1	B	724	LYS	2.2
1	A	727	VAL	2.2
1	B	700	ASN	2.2
1	B	661	PHE	2.2
1	B	701	ILE	2.1
1	B	664	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	705	GLU	2.1
1	B	720	ASP	2.1
1	B	704	HIS	2.1
1	B	722	LEU	2.1
1	B	715	ALA	2.0
1	B	597	GLU	2.0
1	B	659	GLY	2.0
1	A	649	ARG	2.0
1	B	643	CYS	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

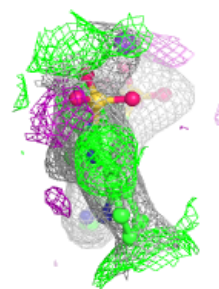
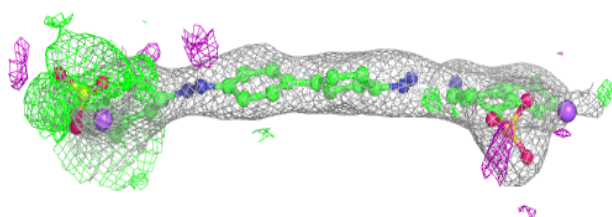
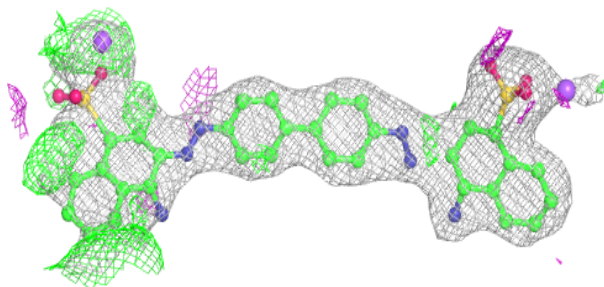
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CGO	A	801	48/48	0.87	0.14	32,46,70,75	7
2	CGO	A	802	48/48	0.88	0.13	34,47,65,79	7

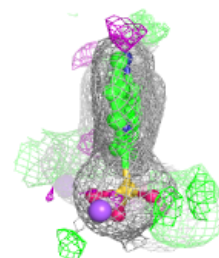
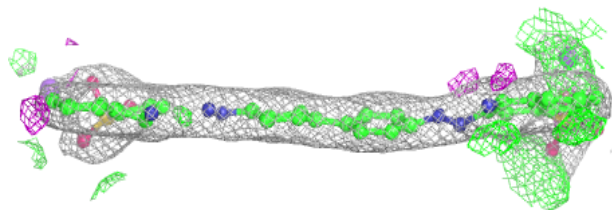
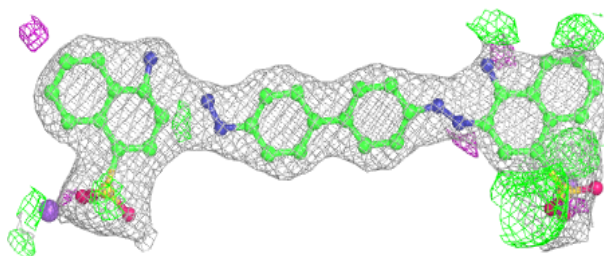
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around CGO A 801:**

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

**Electron density around CGO A 802:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.