



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 10:53 PM BST

PDB ID : 4B81  
Title : Mus musculus Acetylcholinesterase in complex with 1-(4-Chloro-phenyl)- N-(2-diethylamino-ethyl)-methanesulfonamide  
Authors : Andersson, C.D.; Forsgren, N.; Akfur, C.; Allgardsson, A.; Berg, L.; Qian, W.; Ekstrom, F.; Linusson, A.  
Deposited on : 2012-08-24  
Resolution : 2.80 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.

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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 : 2.13.1  
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) : 2.13.1

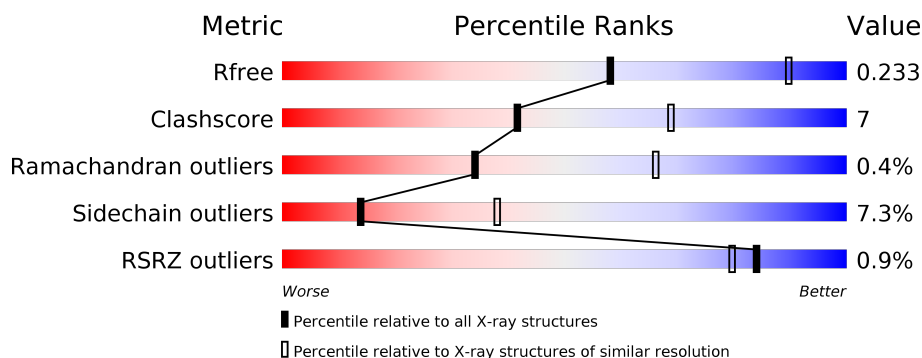
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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  $\geq 3$ , 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	548	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 82%, yellow 15%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>82%</span> <span>15%</span> <span>..</span> </div> </div>
1	B	548	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 71%, yellow 23%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>71%</span> <span>23%</span> <span>..</span> </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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	NAG	A	1546	X	-	-	-
4	NAG	B	1549	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8680 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.

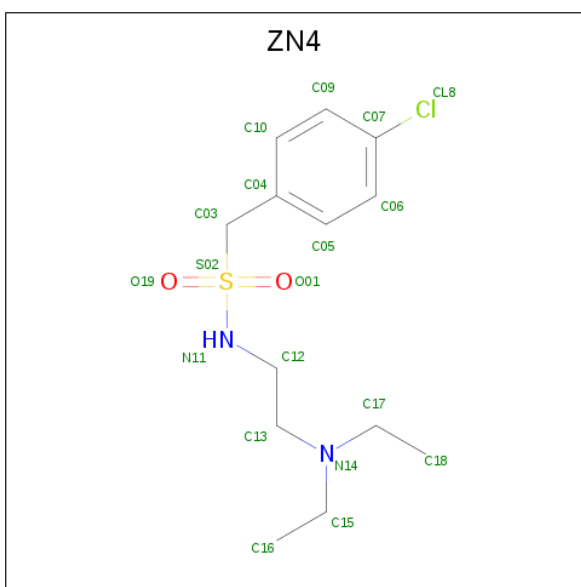
- Molecule 1 is a protein called ACETYLCHOLINESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	535	Total	C	N	O	S	0	0	0
			4177	2679	725	759	14			
1	B	533	Total	C	N	O	S	0	0	0
			4158	2670	718	756	14			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	544	ALA	-	expression tag	UNP P21836
A	545	THR	-	expression tag	UNP P21836
A	546	GLU	-	expression tag	UNP P21836
A	547	ALA	-	expression tag	UNP P21836
A	548	PRO	-	expression tag	UNP P21836
B	544	ALA	-	expression tag	UNP P21836
B	545	THR	-	expression tag	UNP P21836
B	546	GLU	-	expression tag	UNP P21836
B	547	ALA	-	expression tag	UNP P21836
B	548	PRO	-	expression tag	UNP P21836

- Molecule 2 is 1-(4-chlorophenyl)-N-[2-(diethylamino)ethyl]methanesulfonamide (three-letter code: ZN4) (formula: C<sub>13</sub>H<sub>21</sub>ClN<sub>2</sub>O<sub>2</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	S	0	0
			19	13	1	2	2	1		
2	B	1	Total	C	Cl	N	O	S	0	0
			19	13	1	2	2	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



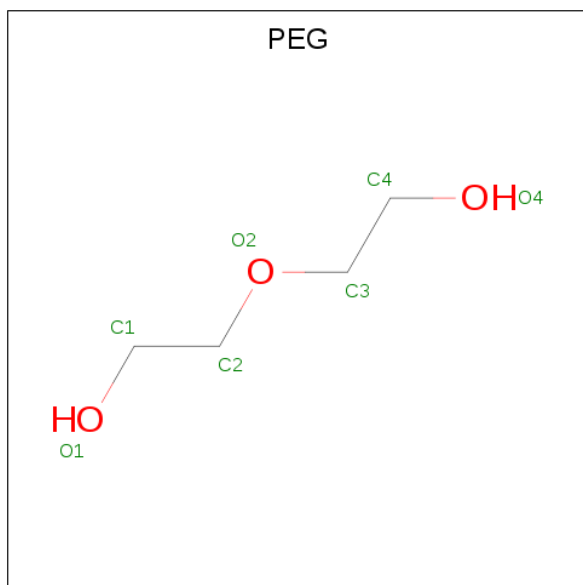
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



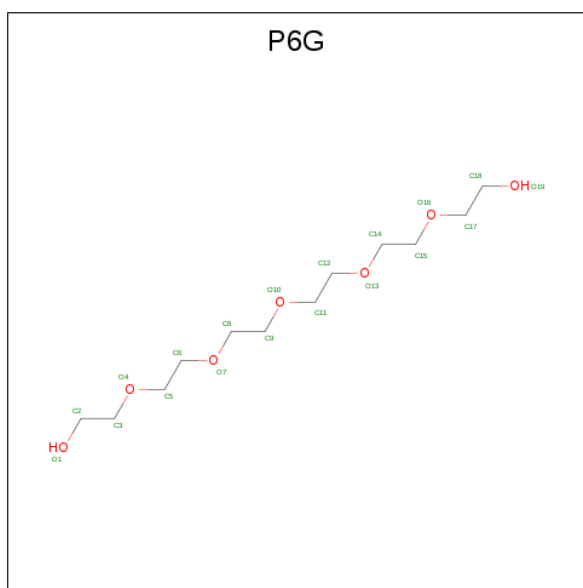
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



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

- Molecule 6 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula:  $C_{12}H_{26}O_7$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C O 19 12 7	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	104	Total O 104 104	0	0

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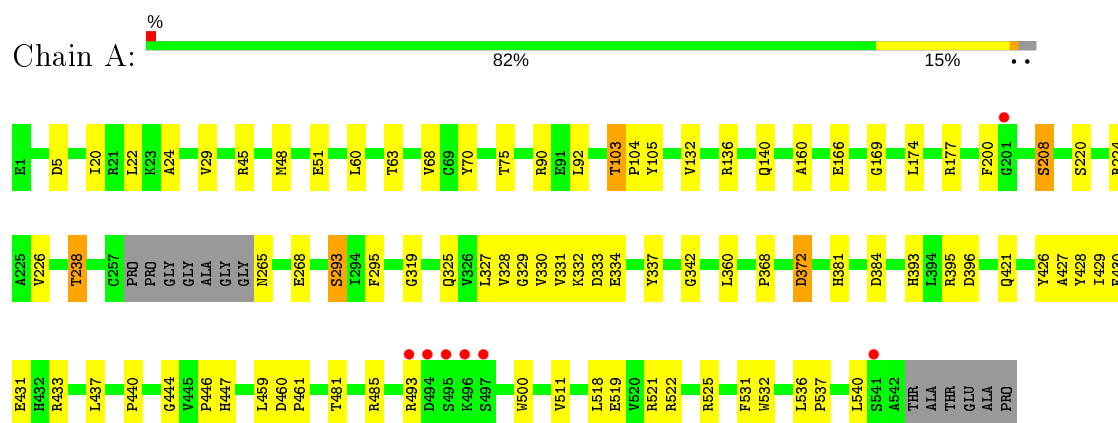
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	76	Total	O	0	0
			76	76		



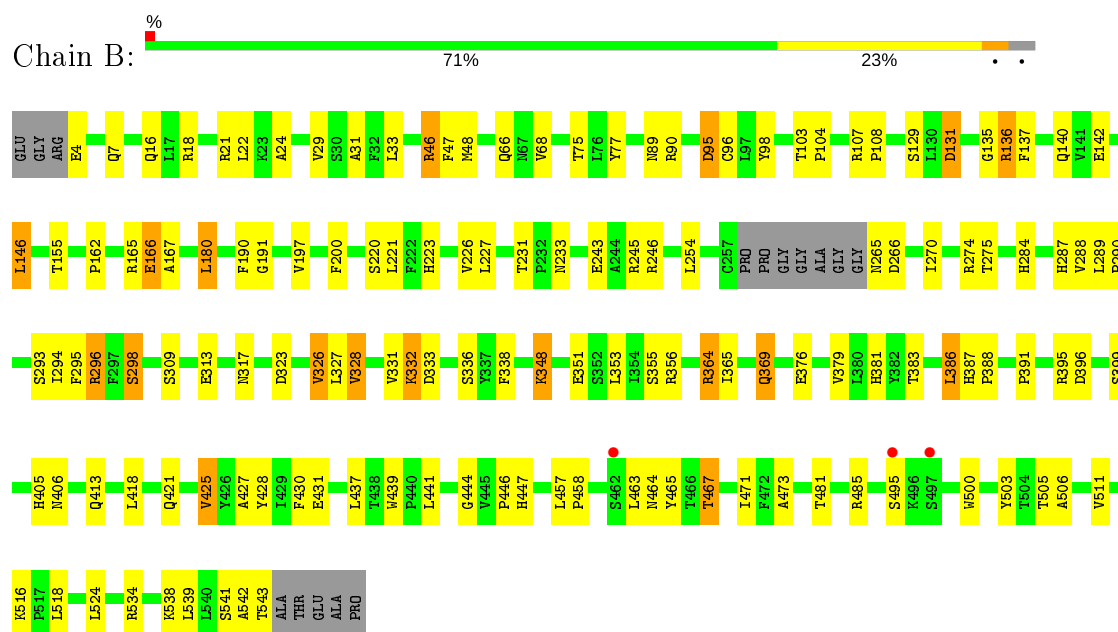
### 3 Residue-property plots

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: ACETYLCHOLINESTERASE



#### • Molecule 1: ACETYLCHOLINESTERASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.96Å 109.88Å 227.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.00 – 2.80 29.33 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.00-2.80) 99.9 (29.33-2.80)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.26 (at 2.80Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.3_928)	Depositor
R, $R_{free}$	0.197 , 0.239 0.194 , 0.233	Depositor DCC
$R_{free}$ test set	965 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	53.0	Xtriage
Anisotropy	0.834	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 43.8	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	0.95	EDS
Total number of atoms	8680	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, ZN4, NAG, P6G, SO4

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	0.31	0/4300	0.46	0/5875
1	B	0.31	0/4281	0.48	0/5851
All	All	0.31	0/8581	0.47	0/11726

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4177	0	4063	43	0
1	B	4158	0	4046	75	0
2	A	19	0	21	1	0
2	B	19	0	21	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	28	0	26	0	0
4	B	14	0	13	0	0
5	A	21	0	30	0	0
5	B	35	0	50	1	0
6	B	19	0	26	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	104	0	0	4	0
7	B	76	0	0	5	0
All	All	8680	0	8296	118	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.

All (118) 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:166:GLU:HB2	1:B:274:ARG:HH22	1.49	0.77
1:B:142:GLU:OE1	1:B:485:ARG:NH2	2.21	0.74
1:B:166:GLU:HG2	1:B:270:ILE:HD13	1.73	0.70
1:B:516:LYS:NZ	7:B:2069:HOH:O	2.24	0.70
1:B:326:VAL:HG21	1:B:418:LEU:HD13	1.73	0.70
1:B:68:VAL:HG23	1:B:90:ARG:HB2	1.76	0.68
1:B:162:PRO:O	1:B:245:ARG:NH2	2.27	0.67
1:B:395:ARG:NH1	1:B:396:ASP:OD1	2.28	0.66
1:B:369:GLN:OE1	1:B:405:HIS:NE2	2.24	0.64
1:A:45:ARG:NH1	1:A:51:GLU:OE1	2.31	0.64
1:B:296:ARG:NH2	1:B:406:ASN:OD1	2.31	0.63
1:B:135:GLY:HA3	1:B:146:LEU:HD22	1.80	0.63
1:B:46:ARG:O	1:B:274:ARG:NH1	2.31	0.63
1:A:327:LEU:HD12	1:A:426:TYR:HB2	1.82	0.61
1:A:226:VAL:HG22	1:A:327:LEU:HB3	1.82	0.60
1:A:381:HIS:HA	6:B:1546:P6G:H31	1.82	0.60
1:A:319:GLY:O	1:A:421:GLN:NE2	2.35	0.60
1:B:166:GLU:HB2	1:B:274:ARG:NH2	2.16	0.60
1:A:166:GLU:N	1:A:166:GLU:OE1	2.33	0.59
1:A:433:ARG:NH2	1:A:440:PRO:O	2.34	0.59
1:A:224:ARG:HG2	1:A:325:GLN:HB2	1.84	0.59
1:B:108:PRO:HG2	1:B:191:GLY:HA3	1.85	0.59
1:B:226:VAL:HG22	1:B:327:LEU:HB3	1.85	0.59
1:A:532:TRP:HA	1:A:536:LEU:HD13	1.85	0.58
1:B:331:VAL:HG12	1:B:430:PHE:HB3	1.84	0.58
1:B:317:ASN:ND2	7:B:2049:HOH:O	2.36	0.58
1:A:68:VAL:HG23	1:A:90:ARG:HB2	1.86	0.57
1:B:131:ASP:N	1:B:131:ASP:OD1	2.37	0.56
1:B:7:GLN:O	1:B:107:ARG:NH2	2.37	0.56
1:B:425:VAL:HG22	1:B:503:TYR:HB3	1.88	0.55
1:A:395:ARG:NH1	1:A:396:ASP:OD1	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:ILE:HB	1:A:63:THR:HG22	1.88	0.54
1:B:332:LYS:NZ	7:B:2051:HOH:O	2.41	0.53
1:B:200:PHE:HB2	1:B:226:VAL:HB	1.90	0.53
1:A:332:LYS:NZ	1:A:333:ASP:OD1	2.41	0.53
1:A:331:VAL:HG12	1:A:430:PHE:HB3	1.91	0.53
1:B:464:ASN:ND2	7:B:2060:HOH:O	2.42	0.53
1:A:265:ASN:ND2	7:A:2059:HOH:O	2.43	0.52
1:B:458:PRO:HG2	1:B:473:ALA:HB2	1.91	0.52
1:B:77:TYR:CE2	1:B:348:LYS:HG2	2.44	0.52
1:B:104:PRO:HG2	1:B:108:PRO:HD3	1.91	0.52
1:A:431:GLU:OE2	1:A:521:ARG:NH1	2.39	0.51
1:A:22:LEU:HB2	1:A:29:VAL:HG23	1.91	0.51
1:B:180:LEU:HB3	1:B:221:LEU:HD13	1.92	0.51
1:A:24:ALA:HB3	1:A:140:GLN:HG3	1.93	0.51
1:B:458:PRO:HA	1:B:465:TYR:CD2	2.46	0.51
1:B:539:LEU:O	1:B:543:THR:HG23	2.11	0.50
1:A:531:PHE:CZ	1:A:536:LEU:HD11	2.46	0.50
1:A:238:THR:OG1	7:A:2050:HOH:O	2.19	0.50
1:A:531:PHE:CE2	1:A:536:LEU:HD11	2.48	0.49
1:B:243:GLU:OE2	1:B:246:ARG:NH1	2.46	0.49
1:B:200:PHE:CB	1:B:226:VAL:HB	2.42	0.49
1:B:166:GLU:N	1:B:166:GLU:OE1	2.44	0.48
1:B:381:HIS:HA	6:B:1546:P6G:H141	1.95	0.48
1:B:294:ILE:HG12	1:B:365:ILE:HG22	1.95	0.48
1:B:4:GLU:OE2	1:B:18:ARG:NH1	2.46	0.48
1:B:197:VAL:H	1:B:223:HIS:CE1	2.32	0.47
1:B:511:VAL:HB	1:B:518:LEU:HD22	1.95	0.47
1:B:227:LEU:HB2	1:B:328:VAL:HG12	1.97	0.47
1:B:332:LYS:HG3	1:B:431:GLU:HG2	1.95	0.47
1:B:89:ASN:ND2	1:B:129:SER:O	2.39	0.47
1:B:333:ASP:OD2	5:B:1544:PEG:H41	2.14	0.47
1:A:328:VAL:O	1:A:427:ALA:HA	2.15	0.46
1:A:444:GLY:O	1:A:446:PRO:HD3	2.15	0.46
1:B:266:ASP:O	1:B:270:ILE:HD12	2.15	0.46
1:B:31:ALA:HB1	1:B:33:LEU:HD21	1.98	0.46
1:B:444:GLY:O	1:B:446:PRO:HD3	2.16	0.46
1:A:208:SER:OG	7:A:2038:HOH:O	2.20	0.45
1:B:386:LEU:HB3	1:B:387:HIS:CE1	2.51	0.45
1:A:103:THR:HG22	1:A:104:PRO:HD2	1.97	0.45
1:B:428:TYR:HB3	1:B:500:TRP:CZ2	2.50	0.45
1:B:338:PHE:HZ	1:B:447:HIS:HD1	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:ALA:HB2	1:A:169:GLY:HA3	1.97	0.45
1:B:353:LEU:HB3	1:B:391:PRO:HB2	1.99	0.45
1:A:293:SER:HB3	1:A:368:PRO:HG3	1.98	0.45
1:A:5:ASP:OD2	1:A:105:TYR:OH	2.28	0.45
1:B:481:THR:O	1:B:485:ARG:HG3	2.17	0.45
1:B:265:ASN:N	7:B:2043:HOH:O	2.50	0.45
1:B:66:GLN:HG3	1:B:98:TYR:CD1	2.52	0.44
1:A:329:GLY:HA3	1:A:428:TYR:CE2	2.52	0.44
1:A:511:VAL:HG11	1:A:518:LEU:HD13	2.00	0.44
1:B:369:GLN:HG3	1:B:369:GLN:H	1.35	0.44
1:B:46:ARG:HD3	1:B:47:PHE:CZ	2.53	0.44
1:A:29:VAL:HG21	1:A:136:ARG:HB2	2.00	0.44
1:B:289:LEU:HA	1:B:290:PRO:HD3	1.79	0.43
1:B:254:LEU:HB3	1:B:284:HIS:ND1	2.33	0.43
1:A:372:ASP:N	1:A:372:ASP:OD1	2.52	0.43
1:A:330:VAL:HG23	1:A:429:ILE:HD12	2.00	0.43
1:B:136:ARG:HG2	1:B:137:PHE:N	2.33	0.43
1:A:177:ARG:NH1	7:A:2044:HOH:O	2.37	0.43
1:B:457:LEU:O	1:B:463:LEU:HD12	2.19	0.42
1:B:538:LYS:HA	1:B:541:SER:HB3	2.00	0.42
1:A:481:THR:O	1:A:485:ARG:HG2	2.19	0.42
1:B:364:ARG:HA	1:B:364:ARG:HD2	1.75	0.42
1:B:22:LEU:HB2	1:B:29:VAL:HG23	2.02	0.42
1:B:167:ALA:HB2	1:B:270:ILE:HG12	2.02	0.42
1:A:334:GLU:OE1	1:A:447:HIS:ND1	2.50	0.42
1:B:437:LEU:HD11	1:B:439:TRP:HD1	1.84	0.42
1:B:518:LEU:HA	1:B:518:LEU:HD23	1.76	0.42
1:B:95:ASP:OD1	1:B:98:TYR:OH	2.14	0.42
1:B:356:ARG:NH1	1:B:388:PRO:O	2.53	0.42
1:B:66:GLN:HG3	1:B:98:TYR:CG	2.54	0.42
1:A:536:LEU:N	1:A:537:PRO:HD2	2.35	0.41
1:B:21:ARG:HE	1:B:21:ARG:HB3	1.60	0.41
1:A:519:GLU:OE1	1:A:521:ARG:NE	2.36	0.41
1:B:467:THR:O	1:B:471:ILE:HG13	2.20	0.41
1:A:522:ARG:HE	1:A:522:ARG:HB3	1.61	0.41
1:B:534:ARG:O	1:B:538:LYS:HG3	2.21	0.41
1:A:460:ASP:HA	1:A:461:PRO:HD3	1.89	0.41
1:B:288:VAL:HG23	1:B:298:SER:HB3	2.02	0.41
1:B:24:ALA:HB3	1:B:140:GLN:HG3	2.02	0.41
1:B:103:THR:HG21	1:B:190:PHE:HB3	2.03	0.41
1:A:337:TYR:HE1	2:A:600:ZN4:H031	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:328:VAL:O	1:B:427:ALA:HA	2.21	0.40
1:A:327:LEU:HD11	1:A:500:TRP:CH2	2.56	0.40
1:B:231:THR:HB	1:B:233:ASN:OD1	2.21	0.40
1:B:379:VAL:O	1:B:383:THR:OG1	2.26	0.40
1:A:384:ASP:HB2	1:A:393:HIS:CE1	2.57	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	531/548 (97%)	503 (95%)	27 (5%)	1 (0%)	47	78
1	B	529/548 (96%)	496 (94%)	30 (6%)	3 (1%)	25	56
All	All	1060/1096 (97%)	999 (94%)	57 (5%)	4 (0%)	34	66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	342	GLY
1	B	355	SER
1	B	506	ALA
1	B	542	ALA

### 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	439/446 (98%)	417 (95%)	22 (5%)	24	56
1	B	438/446 (98%)	396 (90%)	42 (10%)	8	24
All	All	877/892 (98%)	813 (93%)	64 (7%)	14	38

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	MET
1	A	60	LEU
1	A	70	TYR
1	A	75	THR
1	A	92	LEU
1	A	103	THR
1	A	132	VAL
1	A	174	LEU
1	A	200	PHE
1	A	208	SER
1	A	220	SER
1	A	238	THR
1	A	268	GLU
1	A	293	SER
1	A	295	PHE
1	A	360	LEU
1	A	372	ASP
1	A	437	LEU
1	A	459	LEU
1	A	493	ARG
1	A	525	ARG
1	A	540	LEU
1	B	16	GLN
1	B	46	ARG
1	B	48	MET
1	B	75	THR
1	B	95	ASP
1	B	96	CYS
1	B	131	ASP
1	B	136	ARG
1	B	146	LEU
1	B	155	THR
1	B	165	ARG
1	B	166	GLU
1	B	180	LEU

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Mol	Chain	Res	Type
1	B	220	SER
1	B	275	THR
1	B	287	HIS
1	B	293	SER
1	B	295	PHE
1	B	296	ARG
1	B	298	SER
1	B	309	SER
1	B	313	GLU
1	B	323	ASP
1	B	326	VAL
1	B	328	VAL
1	B	332	LYS
1	B	336	SER
1	B	348	LYS
1	B	351	GLU
1	B	364	ARG
1	B	369	GLN
1	B	376	GLU
1	B	386	LEU
1	B	399	SER
1	B	413	GLN
1	B	421	GLN
1	B	425	VAL
1	B	441	LEU
1	B	467	THR
1	B	495	SER
1	B	505	THR
1	B	524	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	421	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

16 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	SO4	B	1545	-	4,4,4	0.18	0	6,6,6	0.12	0
5	PEG	A	1547	-	6,6,6	0.66	0	5,5,5	1.44	0
2	ZN4	B	600	-	18,19,19	1.21	2 (11%)	24,25,25	1.06	3 (12%)
4	NAG	A	1546	1	14,14,15	0.45	0	17,19,21	1.06	2 (11%)
5	PEG	B	1547	-	6,6,6	0.65	0	5,5,5	1.45	0
5	PEG	B	1550	-	6,6,6	0.63	0	5,5,5	1.48	0
2	ZN4	A	600	-	18,19,19	1.31	3 (16%)	24,25,25	1.66	2 (8%)
5	PEG	B	1551	-	6,6,6	0.60	0	5,5,5	1.64	2 (40%)
4	NAG	A	1544	1	14,14,15	0.44	0	17,19,21	1.37	1 (5%)
5	PEG	A	1548	-	6,6,6	0.65	0	5,5,5	1.47	0
5	PEG	B	1544	-	6,6,6	0.65	0	5,5,5	1.47	0
5	PEG	A	1545	-	6,6,6	0.68	0	5,5,5	1.42	0
4	NAG	B	1549	1	14,14,15	0.50	0	17,19,21	1.29	2 (11%)
5	PEG	B	1548	-	6,6,6	0.64	0	5,5,5	1.43	0
6	P6G	B	1546	-	18,18,18	0.52	0	17,17,17	1.78	4 (23%)
3	SO4	A	1543	-	4,4,4	0.16	0	6,6,6	0.14	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
5	PEG	A	1547	-	-	3/4/4/4	-
2	ZN4	B	600	-	-	9/16/16/16	0/1/1/1
4	NAG	A	1546	1	1/1/5/7	3/6/23/26	0/1/1/1
5	PEG	B	1547	-	-	2/4/4/4	-
5	PEG	B	1550	-	-	3/4/4/4	-
2	ZN4	A	600	-	-	3/16/16/16	0/1/1/1
5	PEG	B	1551	-	-	2/4/4/4	-
4	NAG	A	1544	1	-	0/6/23/26	0/1/1/1
5	PEG	A	1548	-	-	2/4/4/4	-
5	PEG	B	1544	-	-	3/4/4/4	-
5	PEG	A	1545	-	-	2/4/4/4	-
4	NAG	B	1549	1	-	2/6/23/26	0/1/1/1
5	PEG	B	1548	-	-	2/4/4/4	-
6	P6G	B	1546	-	-	8/16/16/16	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	ZN4	S02-N11	2.86	1.68	1.61
2	B	600	ZN4	C13-N14	2.73	1.53	1.47
2	B	600	ZN4	S02-N11	2.70	1.68	1.61
2	A	600	ZN4	C13-N14	2.66	1.53	1.47
2	A	600	ZN4	C13-C12	2.22	1.58	1.51

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600	ZN4	C13-C12-N11	6.41	122.42	110.20
4	A	1544	NAG	C1-O5-C5	4.78	118.66	112.19
2	A	600	ZN4	C04-C03-S02	3.46	119.73	112.34
4	B	1549	NAG	C1-O5-C5	3.43	116.84	112.19
4	A	1546	NAG	C1-O5-C5	2.94	116.18	112.19
2	B	600	ZN4	C13-C12-N11	2.64	115.24	110.20
2	B	600	ZN4	C12-C13-N14	-2.56	106.52	112.88
4	B	1549	NAG	C4-C3-C2	2.52	114.71	111.02
4	A	1546	NAG	O5-C5-C6	2.47	111.07	107.20
6	B	1546	P6G	O13-C14-C15	2.40	121.21	110.39
6	B	1546	P6G	O7-C8-C9	2.24	120.49	110.39
2	B	600	ZN4	C04-C03-S02	2.20	117.05	112.34
6	B	1546	P6G	O10-C9-C8	2.15	120.08	110.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1551	PEG	O2-C2-C1	2.14	119.45	110.07
5	B	1551	PEG	O2-C3-C4	2.03	119.00	110.07
6	B	1546	P6G	O13-C12-C11	2.01	119.47	110.39

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1546	NAG	C1

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	600	ZN4	C12-N11-S02-O01
2	B	600	ZN4	C12-N11-S02-C03
2	B	600	ZN4	C04-C03-S02-O01
2	B	600	ZN4	C04-C03-S02-O19
2	B	600	ZN4	N11-C12-C13-N14
4	B	1549	NAG	C8-C7-N2-C2
4	B	1549	NAG	O7-C7-N2-C2
4	A	1546	NAG	C8-C7-N2-C2
4	A	1546	NAG	O7-C7-N2-C2
5	A	1547	PEG	O1-C1-C2-O2
6	B	1546	P6G	O13-C14-C15-O16
5	B	1550	PEG	O2-C3-C4-O4
5	B	1544	PEG	O1-C1-C2-O2
5	B	1548	PEG	O2-C3-C4-O4
5	B	1544	PEG	O2-C3-C4-O4
5	A	1545	PEG	O2-C3-C4-O4
6	B	1546	P6G	O7-C8-C9-O10
5	B	1547	PEG	O2-C3-C4-O4
5	B	1551	PEG	O1-C1-C2-O2
2	B	600	ZN4	C18-C17-N14-C13
2	A	600	ZN4	C18-C17-N14-C13
6	B	1546	P6G	O4-C5-C6-O7
4	A	1546	NAG	O5-C5-C6-O6
6	B	1546	P6G	O1-C2-C3-O4
2	A	600	ZN4	C16-C15-N14-C13
2	A	600	ZN4	C16-C15-N14-C17
2	B	600	ZN4	S02-C03-C04-C10
5	A	1547	PEG	O2-C3-C4-O4
2	B	600	ZN4	C12-C13-N14-C17
6	B	1546	P6G	C8-C9-O10-C11

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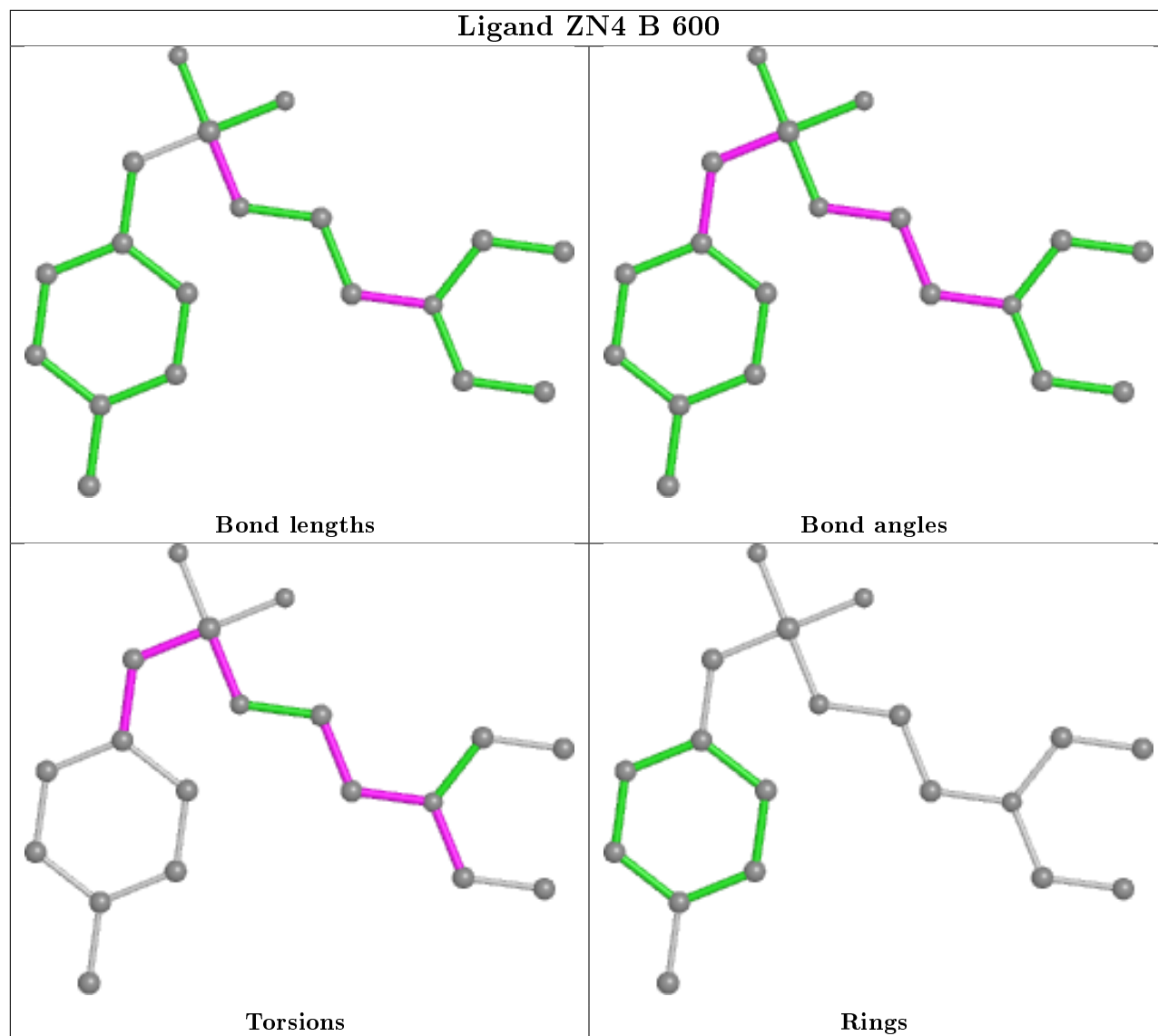
Mol	Chain	Res	Type	Atoms
5	A	1548	PEG	C4-C3-O2-C2
5	B	1544	PEG	C4-C3-O2-C2
5	A	1548	PEG	O1-C1-C2-O2
6	B	1546	P6G	O16-C17-C18-O19
5	A	1547	PEG	C1-C2-O2-C3
6	B	1546	P6G	C15-C14-O13-C12
5	B	1550	PEG	C1-C2-O2-C3
6	B	1546	P6G	O10-C11-C12-O13
5	B	1547	PEG	C4-C3-O2-C2
5	A	1545	PEG	C1-C2-O2-C3
5	B	1550	PEG	C4-C3-O2-C2
5	B	1551	PEG	O2-C3-C4-O4
5	B	1548	PEG	O1-C1-C2-O2
2	B	600	ZN4	C12-C13-N14-C15

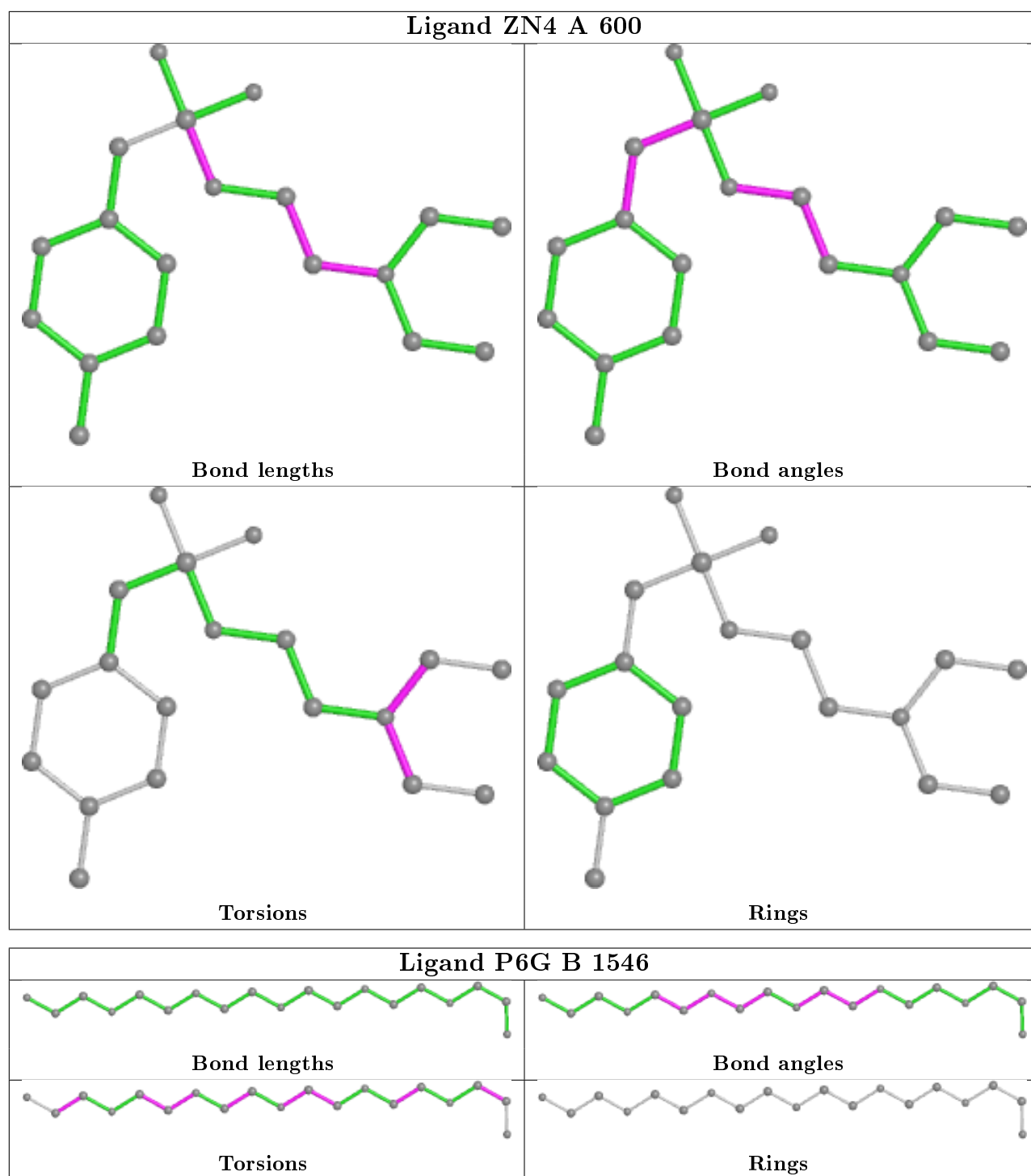
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	ZN4	1	0
5	B	1544	PEG	1	0
6	B	1546	P6G	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.





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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, 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	535/548 (97%)	-0.34	7 (1%) 77 72	36, 58, 84, 132	0
1	B	533/548 (97%)	-0.26	3 (0%) 89 86	37, 62, 88, 129	0
All	All	1068/1096 (97%)	-0.30	10 (0%) 84 80	36, 60, 88, 132	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	493	ARG	3.8
1	A	495	SER	3.7
1	A	497	SER	3.4
1	A	496	LYS	3.3
1	B	497	SER	2.9
1	B	495	SER	2.6
1	B	462	SER	2.6
1	A	541	SER	2.6
1	A	201	GLY	2.1
1	A	494	ASP	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 ⓘ

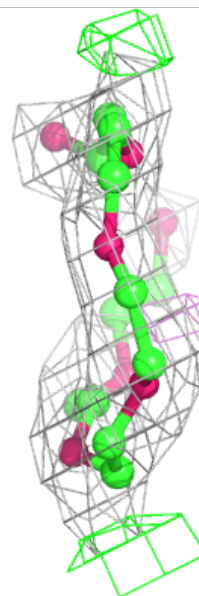
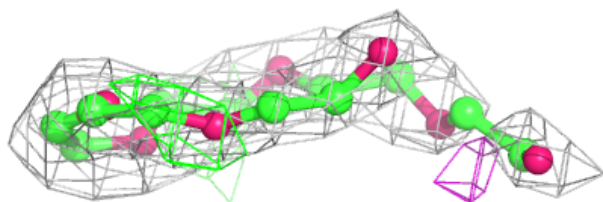
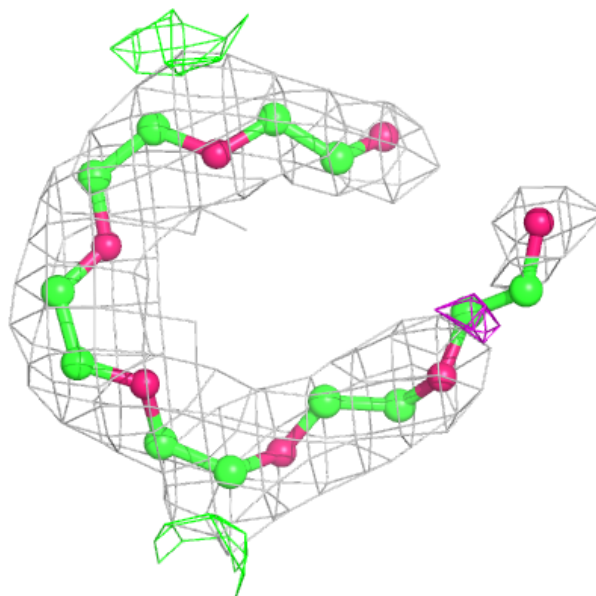
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	NAG	B	1549	14/15	0.76	0.42	89,100,103,104	0
4	NAG	A	1546	14/15	0.79	0.36	99,103,107,108	0
5	PEG	B	1544	7/7	0.82	0.25	81,83,87,88	0
5	PEG	A	1547	7/7	0.82	0.24	90,90,92,93	0
5	PEG	B	1547	7/7	0.83	0.20	82,84,87,88	0
6	P6G	B	1546	19/19	0.83	0.27	72,83,88,89	0
5	PEG	B	1548	7/7	0.85	0.25	80,86,93,94	0
4	NAG	A	1544	14/15	0.85	0.38	88,97,101,102	0
5	PEG	B	1550	7/7	0.86	0.41	73,83,88,88	0
5	PEG	B	1551	7/7	0.87	0.18	53,66,70,70	0
5	PEG	A	1548	7/7	0.87	0.19	55,59,68,70	0
3	SO4	A	1543	5/5	0.87	0.22	95,101,101,104	0
5	PEG	A	1545	7/7	0.88	0.33	77,78,85,85	0
2	ZN4	A	600	19/19	0.89	0.29	54,60,69,128	19
2	ZN4	B	600	19/19	0.92	0.23	48,81,98,101	0
3	SO4	B	1545	5/5	0.93	0.27	105,107,110,111	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.

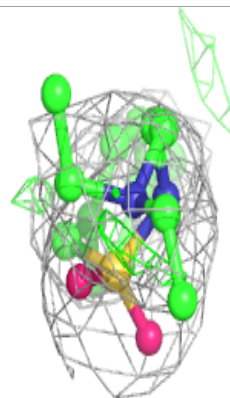
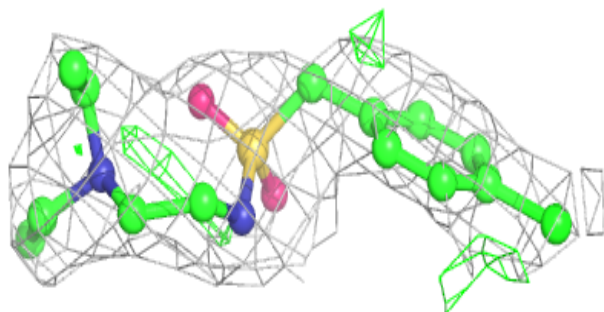
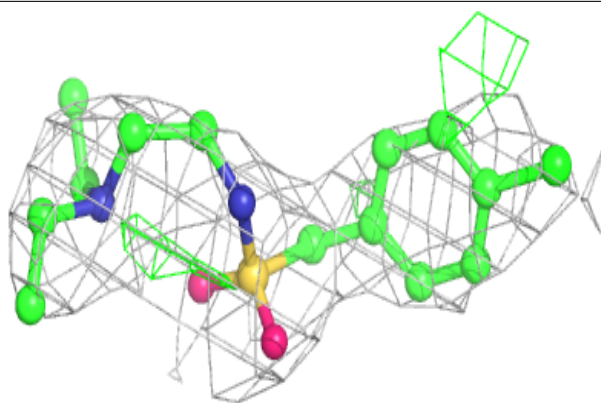
**Electron density around P6G B 1546:**

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

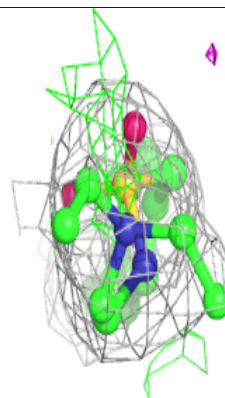
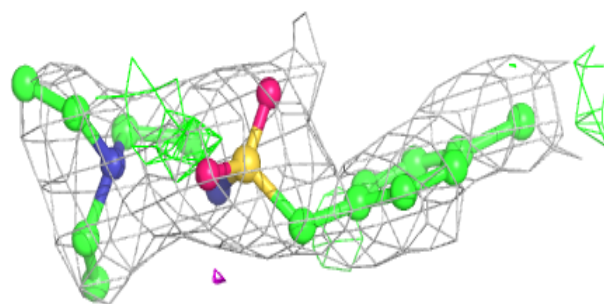
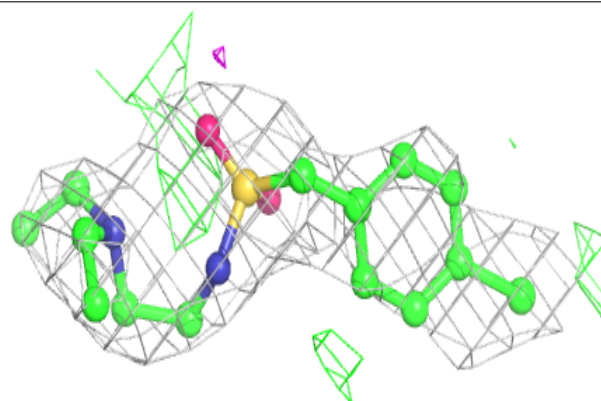


**Electron density around ZN4 A 600:**

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

**Electron density around ZN4 B 600:**

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



## 6.5 Other polymers

There are no such residues in this entry.