Full wwPDB X-ray Structure Validation Report (i)

Jun 22, 2024 – 09:06 PM EDT

PDB ID	:	5FOQ
Title	:	Acetylcholinesterase in complex with C7653
Authors	:	Berg, L.; Mishra, B.K.; Andersson, D.C.; Ekstrom, F.; Linusson, A.
Deposited on	:	2015-11-25
Resolution	:	2.30 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

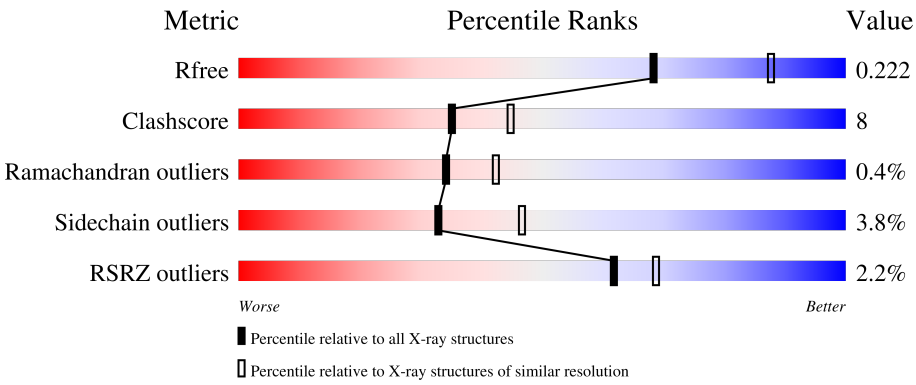
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	3% 79% 18% • •
1	B	548	2% 76% 20% • •

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
2	NAG	B	601	-	-	-	X

2 Entry composition (i)

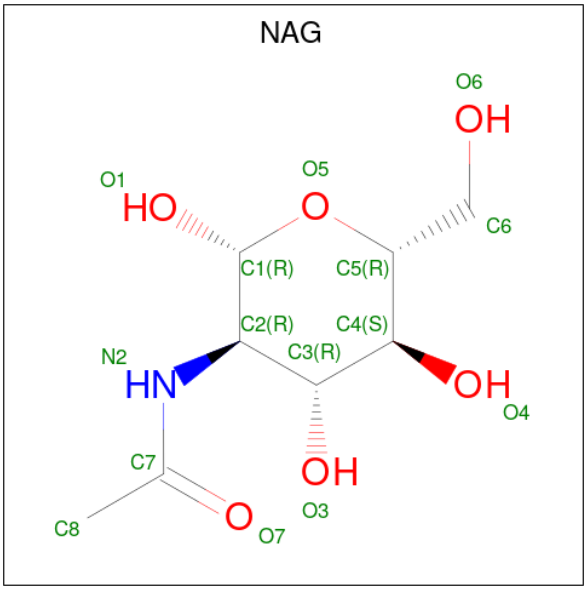
There are 6 unique types of molecules in this entry. The entry contains 8853 atoms, of which 76 are hydrogens and 0 are deuteriums.

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
			Total	C	N	O	S			
1	A	535	4176	2680	722	759	15	0	1	0
1	B	534	4160	2672	718	755	15	0	2	1

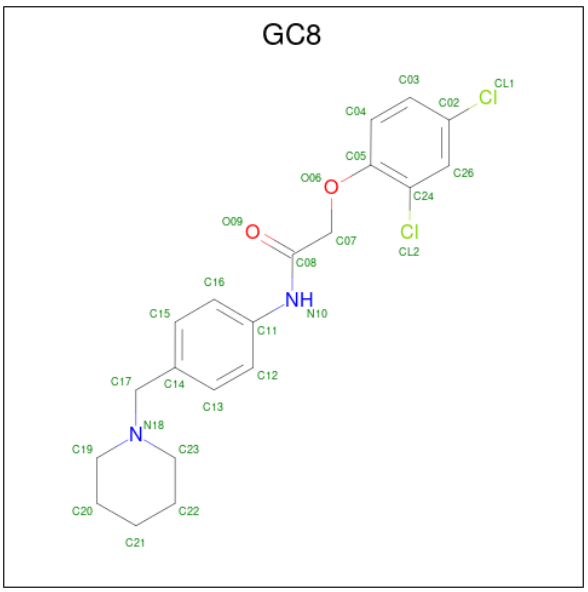
- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

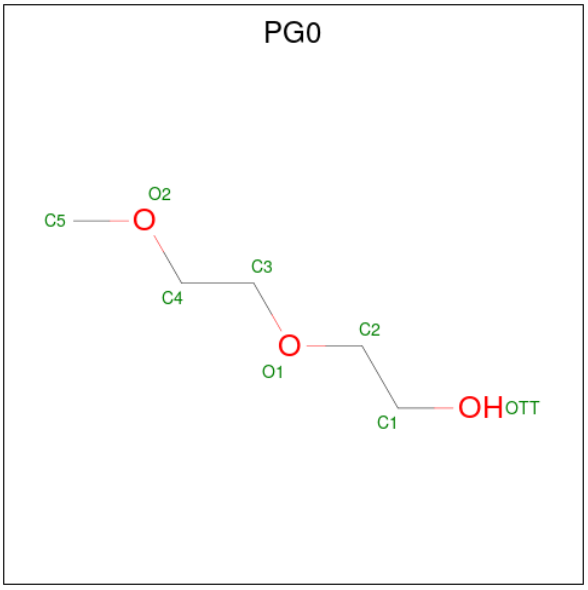
- Molecule 3 is 2-(2,4-dichlorophenoxy)-N-[4-(1-piperidinylmethyl)phenyl]acetamide

(three-letter code: GC8) (formula: $C_{20}H_{22}Cl_2N_2O_2$).



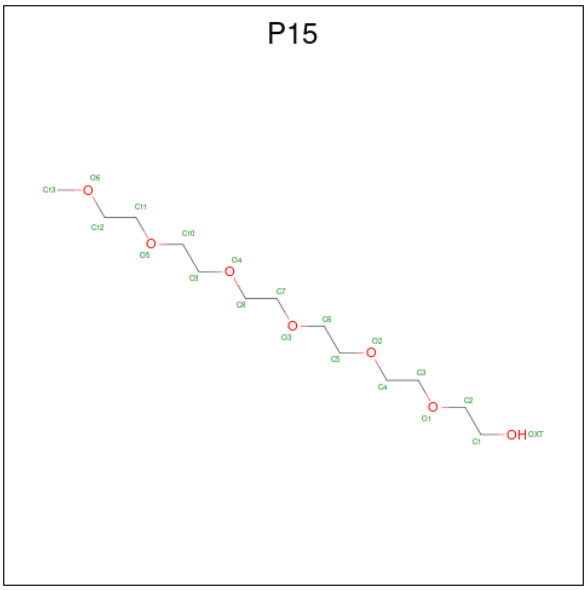
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
3	A	1	26	20	2	2	2	0	0
			Total	C	Cl	N	O		
3	B	1	26	20	2	2	2	0	0

- Molecule 4 is 2-(2-METHOXYETHOXY)ETHANOL (three-letter code: PG0) (formula: $C_5H_{12}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
4	A	1	20	5	12	3	0	0
			Total	C	H	O		
4	A	1	20	5	12	3	0	0
			Total	C	H	O		
4	B	1	20	5	12	3	0	0
			Total	C	H	O		
4	B	1	20	5	12	3	0	0

- Molecule 5 is 2,5,8,11,14,17-HEXAOXANONADECAN-19-OL (three-letter code: P15) (formula: $C_{13}H_{28}O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
5	B	1	48	13	28	7	0	0

- Molecule 6 is water.

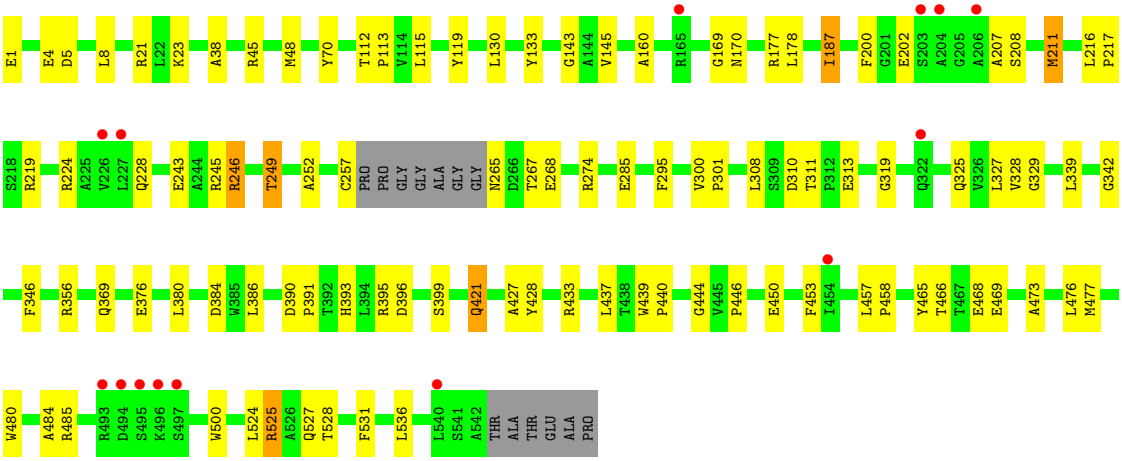
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	182	182	182	0	0
			Total	O		
6	B	113	113	113	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

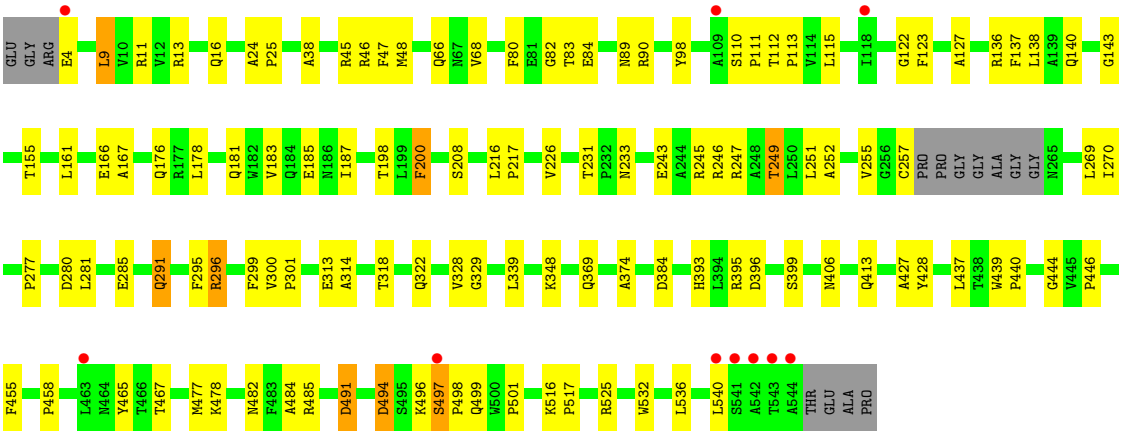
• Molecule 1: ACETYLCHOLINESTERASE

Chain A:



• Molecule 1: ACETYLCHOLINESTERASE

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	79.02Å 111.77Å 227.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.98 – 2.30 29.68 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.3 (28.98-2.30) 82.7 (29.68-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.99 (at 2.31Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.192 , 0.222 0.192 , 0.222	Depositor DCC
R_{free} test set	1761 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å^2)	38.2	Xtriage
Anisotropy	0.790	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 40.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8853	wwPDB-VP
Average B, all atoms (Å^2)	46.0	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.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: PG0, P15, GC8, NAG

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	0.42	1/4302 (0.0%)	0.54	0/5878
1	B	0.36	0/4287	0.53	0/5862
All	All	0.39	1/8589 (0.0%)	0.54	0/11740

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	119	TYR	CE1-CZ	5.78	1.46	1.38

There are no bond angle outliers.

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	4176	0	4061	65	0
1	B	4160	0	4035	71	0
2	A	28	0	26	0	0
2	B	14	0	13	1	0
3	A	26	0	0	0	0
3	B	26	0	0	0	0
4	A	16	24	24	2	0
4	B	16	24	24	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	20	28	28	2	0
6	A	182	0	0	4	0
6	B	113	0	0	4	0
All	All	8777	76	8211	137	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 8.

All (137) 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:374:ALA:HB2	1:B:540:LEU:HD21	1.47	0.96
1:B:161:LEU:HD12	1:B:270:ILE:HD11	1.60	0.84
1:B:13:ARG:HE	1:B:185:GLU:HB3	1.45	0.80
1:A:245:ARG:O	1:A:249:THR:HG23	1.84	0.77
1:A:211:MET:HE2	1:A:308:LEU:HD21	1.68	0.75
1:A:145:VAL:HG11	1:A:187:ILE:HD11	1.72	0.71
1:B:45:ARG:NH2	1:B:48:MET:SD	2.63	0.71
1:A:265:ASN:HD21	1:A:267:THR:HB	1.53	0.71
1:B:161:LEU:HD11	1:B:269:LEU:HD22	1.73	0.69
1:B:115:LEU:HD21	1:B:484:ALA:HB2	1.78	0.66
1:B:245:ARG:O	1:B:249:THR:HG23	1.96	0.66
1:B:374:ALA:CB	1:B:540:LEU:HD21	2.25	0.65
1:A:224:ARG:HG2	1:A:325:GLN:HB2	1.79	0.65
1:A:145:VAL:HG11	1:A:187:ILE:CD1	2.27	0.64
1:A:393:HIS:HB2	6:A:2147:HOH:O	1.96	0.64
1:B:233:ASN:HD22	1:B:413:GLN:HE21	1.45	0.64
1:B:161:LEU:HD12	1:B:270:ILE:CD1	2.28	0.64
1:B:369:GLN:HB2	6:B:2067:HOH:O	1.98	0.63
1:A:265:ASN:HD22	1:A:268:GLU:H	1.48	0.61
1:B:497:SER:HB2	1:B:498:PRO:C	2.22	0.60
1:B:348:LYS:O	1:B:440:PRO:HG3	1.99	0.60
1:A:531:PHE:HB2	5:B:1547:P15:H81	1.83	0.60
1:A:216:LEU:HB3	1:A:217:PRO:HD3	1.83	0.60
1:A:369:GLN:HB2	6:A:2122:HOH:O	2.03	0.59
1:B:24:ALA:HB3	1:B:140:GLN:HG3	1.84	0.59
1:A:376:GLU:O	1:A:380:LEU:HD23	2.03	0.58
1:A:207:ALA:O	1:A:211:MET:HG2	2.02	0.58
1:A:329:GLY:HA3	1:A:428:TYR:CE2	2.38	0.58
1:B:516:LYS:NZ	6:B:2104:HOH:O	2.37	0.58
1:B:112:THR:HG21	1:B:143:GLY:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:VAL:O	1:A:427:ALA:HA	2.05	0.56
1:B:200:PHE:CB	1:B:226:VAL:HB	2.34	0.56
1:B:384:ASP:HB2	1:B:393[B]:HIS:CE1	2.41	0.56
1:A:211:MET:CE	1:A:308:LEU:HD11	2.37	0.55
1:B:115:LEU:HD23	1:B:198:THR:HB	1.88	0.54
1:B:167:ALA:HB2	1:B:270:ILE:HD12	1.89	0.54
1:B:328:VAL:O	1:B:427:ALA:HA	2.07	0.54
1:B:532:TRP:CE3	1:B:536:LEU:HD12	2.43	0.53
1:B:296:ARG:NH2	1:B:406:ASN:OD1	2.42	0.53
1:B:24:ALA:HB1	1:B:25:PRO:HD2	1.90	0.52
1:B:110:SER:HB2	1:B:111:PRO:HD2	1.91	0.52
1:B:329:GLY:HA3	1:B:428:TYR:CZ	2.45	0.52
1:B:200:PHE:HB2	1:B:226:VAL:HB	1.92	0.51
1:B:491:ASP:HB3	1:B:494:ASP:HB3	1.93	0.51
1:A:145:VAL:CG1	1:A:187:ILE:HD11	2.40	0.51
1:A:395:ARG:HD2	1:A:396:ASP:OD1	2.10	0.51
1:A:211:MET:HE2	1:A:308:LEU:HD11	1.93	0.51
1:A:450:GLU:OE1	1:A:450:GLU:N	2.40	0.51
1:A:458:PRO:HA	1:A:465:TYR:CD1	2.46	0.51
1:B:167:ALA:CB	1:B:270:ILE:HD12	2.41	0.50
1:A:313:GLU:HB2	6:A:2092:HOH:O	2.11	0.50
1:B:231:THR:HB	1:B:233:ASN:OD1	2.12	0.49
1:B:252:ALA:HB1	1:B:257:CYS:HB2	1.94	0.49
1:B:313:GLU:HG3	6:B:2081:HOH:O	2.12	0.49
1:A:439:TRP:HB3	1:A:440:PRO:HD2	1.93	0.49
1:B:80:PHE:O	1:B:84:GLU:HG2	2.12	0.49
1:A:525:ARG:HD3	4:A:1545:PG0:H51	1.93	0.49
1:B:113:PRO:HG2	1:B:485:ARG:HG2	1.95	0.49
1:B:291:GLN:NE2	1:B:369:GLN:HE21	2.10	0.49
1:A:327:LEU:HD11	1:A:500:TRP:CH2	2.49	0.48
1:A:112:THR:HG21	1:A:143:GLY:O	2.12	0.48
1:A:384:ASP:HB2	1:A:393:HIS:CE1	2.49	0.48
1:A:252:ALA:HB1	1:A:257:CYS:HB2	1.96	0.48
1:B:300:VAL:HB	1:B:301:PRO:HD2	1.96	0.48
1:A:329:GLY:HA3	1:A:428:TYR:CZ	2.48	0.48
1:B:251:LEU:O	1:B:255:VAL:HG22	2.13	0.48
1:B:269:LEU:C	1:B:269:LEU:HD23	2.33	0.48
1:B:138:LEU:HD23	1:B:477:MET:HE3	1.96	0.47
1:B:46:ARG:HD3	1:B:47:PHE:CZ	2.49	0.47
1:B:329:GLY:HA3	1:B:428:TYR:CE2	2.50	0.47
1:A:433:ARG:CZ	1:A:437:LEU:HD23	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:314:ALA:O	1:B:318:THR:HG23	2.16	0.46
1:A:527:GLN:HG3	5:B:1547:P15:H61	1.98	0.46
1:A:457:LEU:N	1:A:458:PRO:CD	2.79	0.46
1:A:310:ASP:OD1	1:A:311:THR:N	2.40	0.46
1:A:528:THR:O	1:A:531:PHE:HB3	2.16	0.46
1:B:66:GLN:HG3	1:B:98:TYR:CD2	2.51	0.46
1:B:497:SER:HB2	1:B:498:PRO:O	2.16	0.45
1:A:224:ARG:HG2	1:A:325:GLN:HE21	1.82	0.45
1:A:444:GLY:O	1:A:446:PRO:HD3	2.16	0.45
1:B:277:PRO:HG2	1:B:280:ASP:OD2	2.16	0.45
1:B:516:LYS:HB3	1:B:517:PRO:HD2	1.98	0.45
1:B:444:GLY:O	1:B:446:PRO:HD3	2.17	0.45
1:B:478:LYS:O	1:B:482:ASN:HB2	2.16	0.45
1:B:499:GLN:O	1:B:501:PRO:HD3	2.17	0.45
1:A:1:GLU:HA	1:A:4:GLU:HG3	1.98	0.45
1:A:208:SER:HA	1:A:211:MET:HG3	1.99	0.44
1:B:243:GLU:O	1:B:247:ARG:HG3	2.18	0.44
1:B:80:PHE:CE2	1:B:82:GLY:HA3	2.52	0.44
1:B:339:LEU:HD11	1:B:399:SER:HA	2.00	0.44
1:A:130:LEU:HD12	1:A:133:TYR:CE2	2.53	0.44
1:B:291:GLN:HE21	1:B:291:GLN:HB2	1.56	0.44
1:B:395:ARG:HD2	1:B:396:ASP:OD1	2.18	0.43
1:A:160:ALA:HB2	1:A:169:GLY:HA3	2.00	0.43
1:A:525:ARG:HH11	1:A:525:ARG:CG	2.30	0.43
1:A:45:ARG:HA	1:A:48:MET:HG3	2.01	0.43
1:A:390:ASP:HA	1:A:391:PRO:HD3	1.84	0.43
1:A:219:ARG:HA	1:A:219:ARG:HD2	1.77	0.43
1:B:458:PRO:HA	1:B:465:TYR:CD2	2.53	0.43
1:A:536:LEU:HD12	1:A:536:LEU:HA	1.65	0.43
1:A:468:GLU:OE1	1:A:468:GLU:N	2.45	0.43
1:B:89:ASN:O	1:B:90:ARG:HD3	2.19	0.42
1:B:38:ALA:HB2	1:B:178:LEU:HD23	2.01	0.42
1:B:122:GLY:O	1:B:123:PHE:HB2	2.20	0.42
1:A:243:GLU:OE2	1:A:246:ARG:NH1	2.52	0.42
1:B:83:THR:HG23	1:B:439:TRP:CH2	2.54	0.42
1:B:536:LEU:HD23	1:B:536:LEU:HA	1.71	0.42
1:A:274:ARG:HD3	6:A:2019:HOH:O	2.19	0.42
1:A:38:ALA:HB2	1:A:178:LEU:HD23	2.02	0.42
1:A:319:GLY:O	1:A:421:GLN:HG2	2.20	0.42
1:A:466:THR:OG1	1:A:469:GLU:HG3	2.19	0.42
1:B:137:PHE:HB2	1:B:455:PHE:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:LEU:HB3	1:B:217:PRO:HD3	2.01	0.42
1:A:115:LEU:HD21	1:A:484:ALA:HB2	2.01	0.42
1:A:177:ARG:CZ	1:A:217:PRO:HB2	2.49	0.42
1:B:183:VAL:O	1:B:187:ILE:HB	2.19	0.42
1:B:291:GLN:HE22	1:B:369:GLN:HE21	1.66	0.42
1:A:300:VAL:HB	1:A:301:PRO:HD2	2.02	0.42
1:A:339:LEU:HD11	1:A:399:SER:HA	2.02	0.41
2:B:601:NAG:H61	6:B:2111:HOH:O	2.20	0.41
1:A:453:PHE:HB3	1:A:476:LEU:HD12	2.01	0.41
1:A:473:ALA:O	1:A:477:MET:HG3	2.20	0.41
1:B:176:GLN:OE1	1:B:208:SER:HB3	2.21	0.41
1:A:525:ARG:HD3	4:A:1545:PG0:C5	2.50	0.41
1:B:166:GLU:CD	1:B:166:GLU:H	2.21	0.41
1:A:224:ARG:HD3	1:A:325:GLN:NE2	2.35	0.41
1:A:339:LEU:HD13	1:A:346:PHE:CE2	2.56	0.41
1:B:155:THR:HG22	1:B:299:PHE:CE2	2.56	0.41
1:B:245:ARG:O	1:B:249:THR:CG2	2.66	0.41
1:A:5:ASP:HB3	1:A:8:LEU:HD12	2.01	0.41
1:A:23:LYS:HE3	1:A:23:LYS:HB3	1.83	0.41
1:A:113:PRO:HG3	1:A:485:ARG:HG2	2.02	0.41
1:A:170:ASN:OD1	1:A:301:PRO:HA	2.21	0.40
1:B:68:VAL:HG22	1:B:127:ALA:CB	2.51	0.40
1:B:9:LEU:HD22	1:B:16:GLN:NE2	2.37	0.40
1:A:202:GLU:HA	1:A:228:GLN:O	2.21	0.40
1:B:66:GLN:HG3	1:B:98:TYR:CG	2.56	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	532/548 (97%)	508 (96%)	23 (4%)	1 (0%)	47 58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	532/548 (97%)	507 (95%)	22 (4%)	3 (1%)	25	31
All	All	1064/1096 (97%)	1015 (95%)	45 (4%)	4 (0%)	34	42

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	322	GLN
1	B	497	SER
1	B	496	LYS
1	A	342	GLY

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%)	424 (97%)	15 (3%)	37	51
1	B	437/446 (98%)	419 (96%)	18 (4%)	30	43
All	All	876/892 (98%)	843 (96%)	33 (4%)	33	47

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	ARG
1	A	70	TYR
1	A	187	ILE
1	A	200	PHE
1	A	211	MET
1	A	246	ARG
1	A	249	THR
1	A	285	GLU
1	A	295	PHE
1	A	356	ARG
1	A	386	LEU
1	A	421	GLN

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Mol	Chain	Res	Type
1	A	480	TRP
1	A	524	LEU
1	A	525	ARG
1	B	4	GLU
1	B	9	LEU
1	B	11	ARG
1	B	136	ARG
1	B	181	GLN
1	B	200	PHE
1	B	246	ARG
1	B	249	THR
1	B	281	LEU
1	B	285	GLU
1	B	291	GLN
1	B	295	PHE
1	B	296	ARG
1	B	437	LEU
1	B	467	THR
1	B	491	ASP
1	B	494	ASP
1	B	525	ARG

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

Mol	Chain	Res	Type
1	A	265	ASN
1	A	325	GLN
1	B	16	GLN
1	B	291	GLN
1	B	413	GLN

5.3.3 RNA (i)

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)

10 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	GC8	A	1543	-	28,28,28	2.01	7 (25%)	37,37,37	1.69	9 (24%)
3	GC8	B	1544	-	28,28,28	2.04	5 (17%)	37,37,37	1.92	10 (27%)
4	PG0	B	1545	-	7,7,7	0.46	0	6,6,6	0.70	0
5	P15	B	1547	-	19,19,19	0.53	0	18,18,18	0.89	1 (5%)
2	NAG	A	701	1	14,14,15	0.57	0	17,19,21	0.58	0
2	NAG	B	601	1	14,14,15	0.69	0	17,19,21	0.54	0
4	PG0	A	1545	-	7,7,7	0.56	0	6,6,6	0.79	0
4	PG0	A	1544	-	7,7,7	0.58	0	6,6,6	0.83	0
4	PG0	B	1546	-	7,7,7	0.60	0	6,6,6	0.77	0
2	NAG	A	601	1	14,14,15	0.87	1 (7%)	17,19,21	0.58	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	GC8	A	1543	-	-	4/13/21/21	0/3/3/3
3	GC8	B	1544	-	-	4/13/21/21	0/3/3/3
4	PG0	B	1545	-	-	3/5/5/5	-
5	P15	B	1547	-	-	6/17/17/17	-
2	NAG	A	701	1	-	0/6/23/26	0/1/1/1
2	NAG	B	601	1	-	2/6/23/26	0/1/1/1
4	PG0	A	1545	-	-	3/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PG0	A	1544	-	-	2/5/5/5	-
4	PG0	B	1546	-	-	1/5/5/5	-
2	NAG	A	601	1	-	2/6/23/26	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1543	GC8	C17-N18	6.29	1.59	1.47
3	B	1544	GC8	C17-N18	5.58	1.58	1.47
3	B	1544	GC8	C19-N18	4.87	1.60	1.46
3	B	1544	GC8	C08-N10	4.43	1.45	1.35
3	A	1543	GC8	C08-N10	3.99	1.44	1.35
3	B	1544	GC8	C07-C08	3.08	1.57	1.51
3	A	1543	GC8	C19-N18	2.93	1.55	1.46
2	A	601	NAG	O5-C1	2.86	1.48	1.43
3	A	1543	GC8	C07-C08	2.68	1.56	1.51
3	A	1543	GC8	O06-C07	-2.61	1.36	1.42
3	A	1543	GC8	C17-C14	-2.53	1.46	1.51
3	A	1543	GC8	C16-C11	2.25	1.43	1.39
3	B	1544	GC8	O06-C07	-2.01	1.38	1.42

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1544	GC8	O06-C05-C24	5.53	123.23	116.40
3	A	1543	GC8	O06-C05-C24	4.35	121.77	116.40
3	B	1544	GC8	C17-C14-C15	3.82	127.95	120.77
3	A	1543	GC8	C17-C14-C15	3.72	127.77	120.77
3	A	1543	GC8	C17-C14-C13	-3.36	114.46	120.77
3	B	1544	GC8	C17-N18-C19	-3.19	103.97	111.06
3	B	1544	GC8	C17-C14-C13	-3.14	114.86	120.77
3	B	1544	GC8	C20-C19-N18	3.04	116.21	111.33
3	A	1543	GC8	C17-N18-C19	-3.00	104.38	111.06
3	B	1544	GC8	C14-C17-N18	2.73	118.41	113.12
3	A	1543	GC8	O09-C08-N10	-2.56	118.96	123.63
3	B	1544	GC8	O09-C08-N10	-2.55	118.98	123.63
3	B	1544	GC8	C04-C05-C24	-2.45	114.97	118.84
3	A	1543	GC8	C14-C17-N18	2.43	117.83	113.12
5	B	1547	P15	C10-O5-C11	2.33	123.36	113.29
3	A	1543	GC8	C26-C24-C05	2.18	123.94	121.02
3	B	1544	GC8	C26-C24-C05	2.18	123.93	121.02
3	A	1543	GC8	C16-C11-C12	-2.08	116.19	119.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1543	GC8	C04-C05-C24	-2.07	115.57	118.84
3	B	1544	GC8	C22-C23-N18	-2.03	108.06	111.33

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1547	P15	C12-C11-O5-C10
2	A	601	NAG	O5-C5-C6-O6
2	A	601	NAG	C4-C5-C6-O6
3	A	1543	GC8	C24-C05-O06-C07
3	B	1544	GC8	C24-C05-O06-C07
5	B	1547	P15	O1-C3-C4-O2
4	B	1545	PG0	O1-C3-C4-O2
4	B	1546	PG0	O1-C3-C4-O2
2	B	601	NAG	O5-C5-C6-O6
2	B	601	NAG	C4-C5-C6-O6
3	B	1544	GC8	O06-C07-C08-N10
3	B	1544	GC8	O06-C07-C08-O09
4	B	1545	PG0	OTT-C1-C2-O1
4	A	1545	PG0	OTT-C1-C2-O1
3	B	1544	GC8	C04-C05-O06-C07
5	B	1547	P15	C5-C6-O3-C7
3	A	1543	GC8	O06-C07-C08-O09
4	A	1544	PG0	C1-C2-O1-C3
3	A	1543	GC8	O06-C07-C08-N10
5	B	1547	P15	O5-C10-C9-O4
5	B	1547	P15	O2-C5-C6-O3
3	A	1543	GC8	C04-C05-O06-C07
4	A	1544	PG0	O1-C3-C4-O2
4	B	1545	PG0	C4-C3-O1-C2
4	A	1545	PG0	O1-C3-C4-O2
5	B	1547	P15	O5-C11-C12-O6
4	A	1545	PG0	C4-C3-O1-C2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1547	P15	2	0
2	B	601	NAG	1	0

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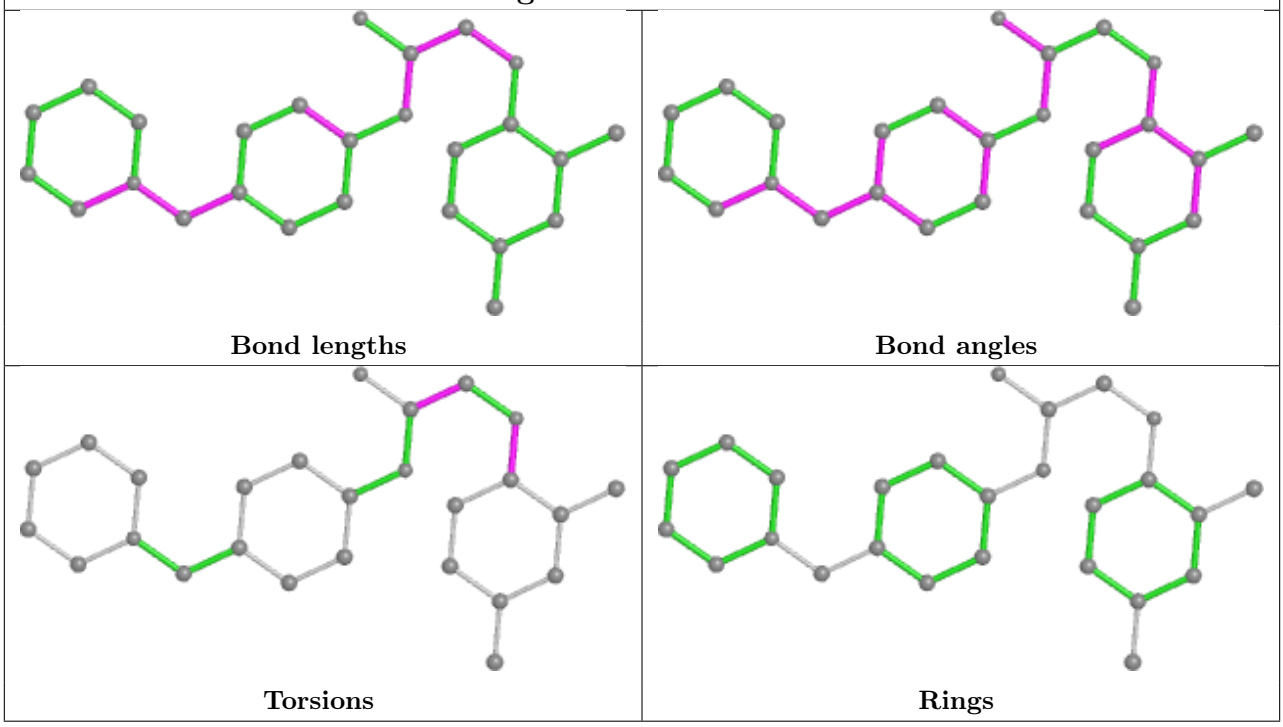
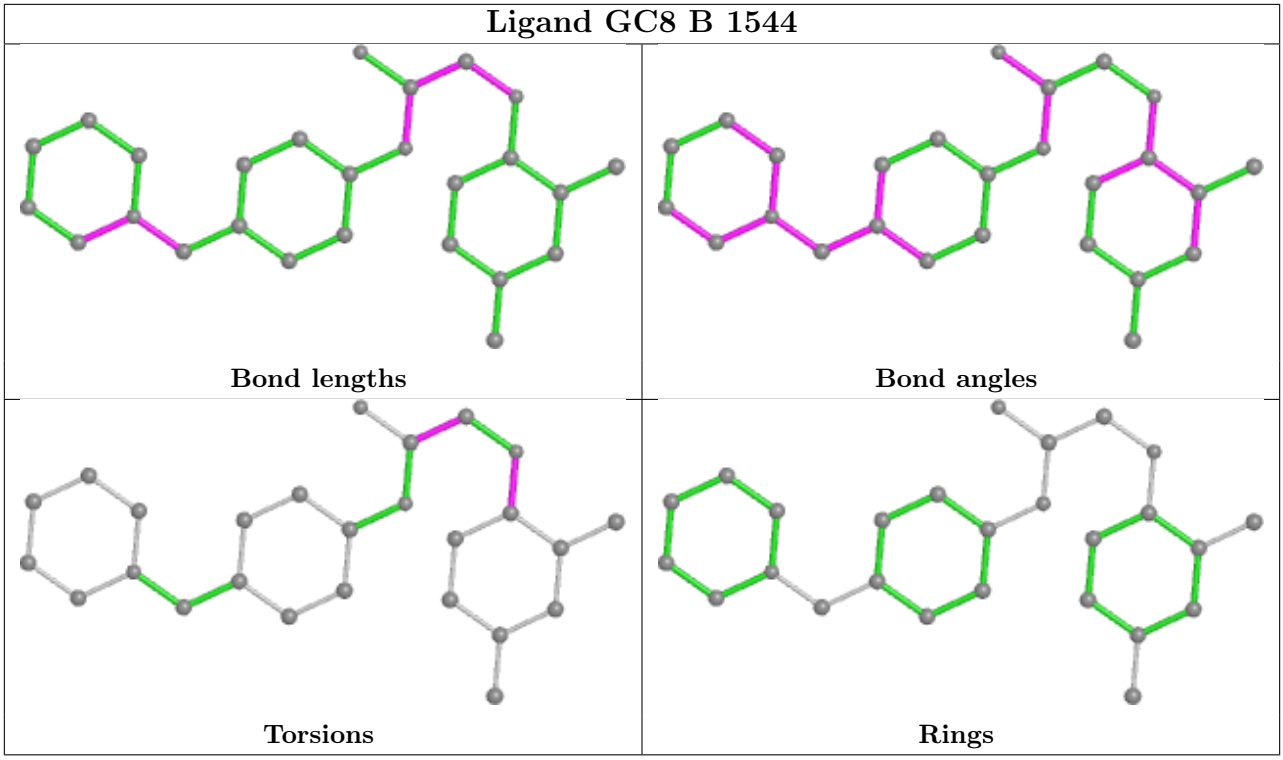
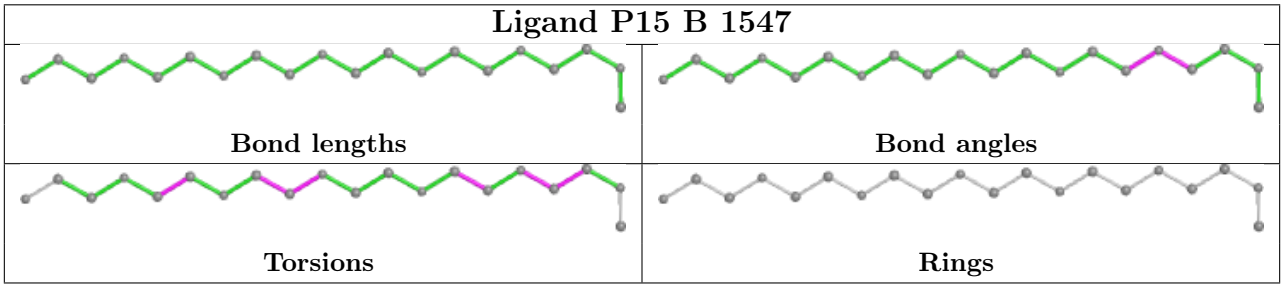
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1545	PG0	2	0

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 then 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 GC8 A 1543







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	535/548 (97%)	-0.22	14 (2%)	56	63	26, 39, 65, 120	0
1	B	534/548 (97%)	-0.09	10 (1%)	66	73	28, 46, 71, 151	0
All	All	1069/1096 (97%)	-0.15	24 (2%)	62	69	26, 42, 69, 151	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	544	ALA	20.3
1	B	543	THR	8.9
1	A	493	ARG	5.5
1	B	497	SER	4.6
1	A	495	SER	4.3
1	B	542	ALA	4.1
1	A	496	LYS	3.9
1	A	540	LEU	3.2
1	A	203	SER	3.0
1	A	322	GLN	2.8
1	A	494	ASP	2.8
1	B	541	SER	2.7
1	A	165	ARG	2.5
1	B	109	ALA	2.5
1	A	206	ALA	2.4
1	B	540	LEU	2.2
1	A	226	VAL	2.2
1	B	118	ILE	2.2
1	B	463	LEU	2.1
1	B	4	GLU	2.1
1	A	204	ALA	2.1
1	A	454	ILE	2.1
1	A	497	SER	2.1
1	A	227	LEU	2.1

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)

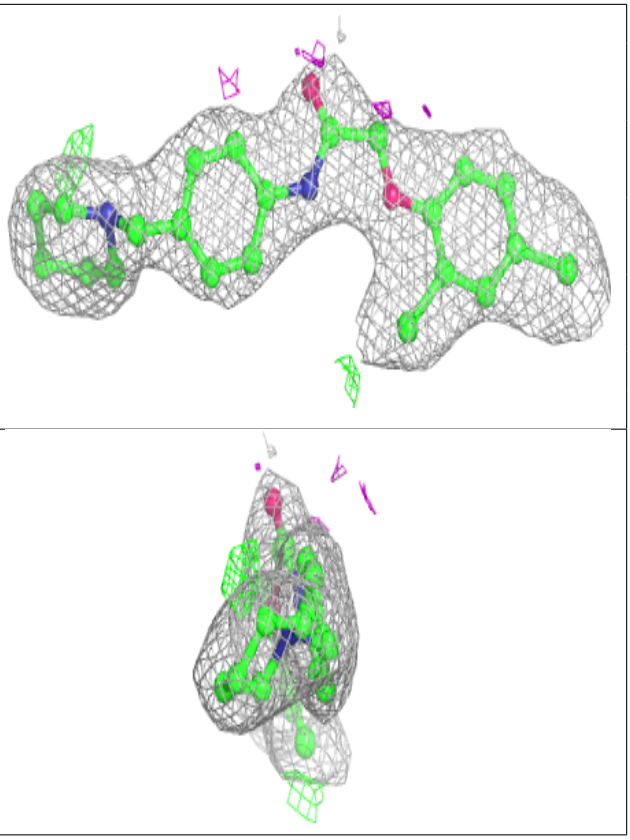
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	B	601	14/15	0.69	0.41	57,88,100,100	0
4	PG0	B	1545	8/8	0.73	0.16	53,70,84,84	0
2	NAG	A	601	14/15	0.80	0.29	65,77,83,88	0
4	PG0	B	1546	8/8	0.84	0.22	68,82,91,91	20
4	PG0	A	1545	8/8	0.85	0.22	48,81,109,109	0
2	NAG	A	701	14/15	0.86	0.27	77,87,96,99	0
3	GC8	A	1543	26/26	0.87	0.16	34,48,63,80	0
5	P15	B	1547	20/20	0.87	0.17	29,71,113,116	0
3	GC8	B	1544	26/26	0.90	0.15	27,47,97,110	0
4	PG0	A	1544	8/8	0.91	0.24	66,80,91,91	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.

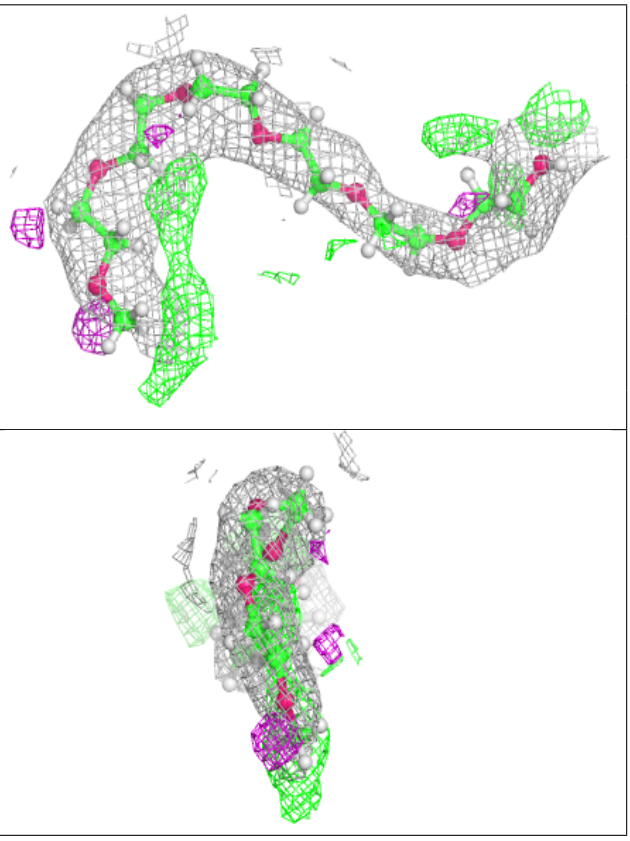
Electron density around GC8 A 1543:

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



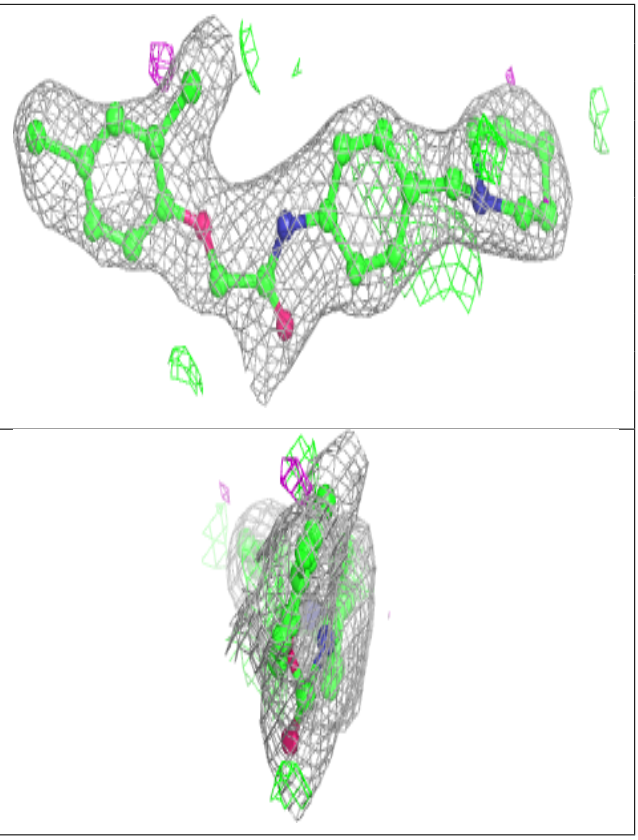
Electron density around P15 B 1547:

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



Electron density around GC8 B 1544:

$2mF_o$-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.