



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:34 AM UTC

PDB ID : 5SG2 / pdb_00005sg2
Title : CRYSTAL STRUCTURE OF HUMAN PHOSPHODIESTERASE 10 IN COMPLEX WITH n1c(N)n(c3c1c2c(nccc2)cc3)C, micromolar IC₅₀=32.68161
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Deposited on : 2022-02-01
Resolution : 2.15 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

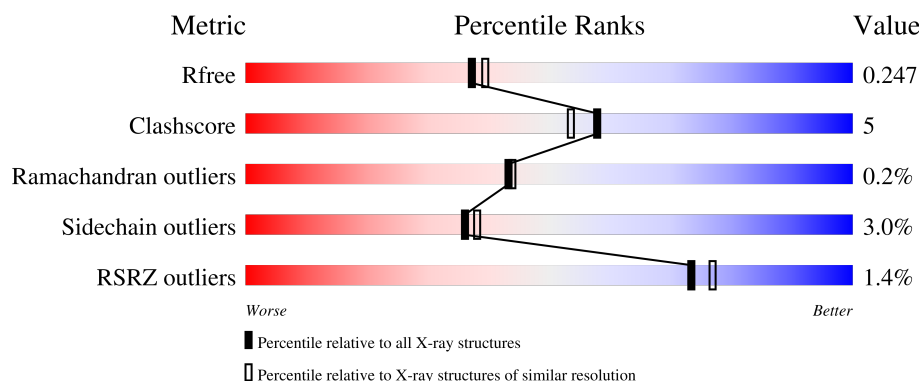
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (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 ≥ 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	343	
1	B	343	
1	C	343	
1	D	343	

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	GIQ	C	803	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10602 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 and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	313	Total	C	N	O	S	0	0	0
			2541	1624	432	461	24			
1	B	315	Total	C	N	O	S	0	0	0
			2551	1630	434	463	24			
1	C	313	Total	C	N	O	S	0	0	0
			2541	1624	432	461	24			
1	D	310	Total	C	N	O	S	0	0	0
			2519	1612	429	454	24			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	447	GLY	-	expression tag	UNP Q9Y233
A	448	SER	-	expression tag	UNP Q9Y233
B	447	GLY	-	expression tag	UNP Q9Y233
B	448	SER	-	expression tag	UNP Q9Y233
C	447	GLY	-	expression tag	UNP Q9Y233
C	448	SER	-	expression tag	UNP Q9Y233
D	447	GLY	-	expression tag	UNP Q9Y233
D	448	SER	-	expression tag	UNP Q9Y233

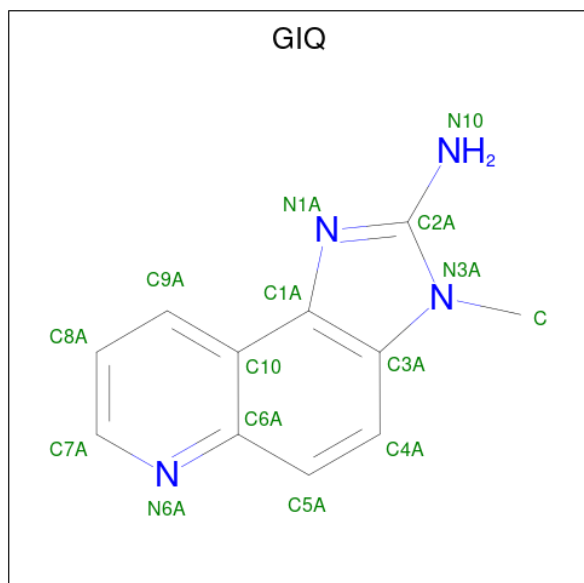
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 3-METHYL-3H-IMIDAZO[4,5-F]QUINOLIN-2-AMINE (CCD ID: GIQ) (formula: C₁₁H₁₀N₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	1
			30	22	8		
4	C	1	Total	C	N	0	0
			15	11	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	107	Total	O	0	0
			107	107		
5	B	103	Total	O	0	0
			103	103		

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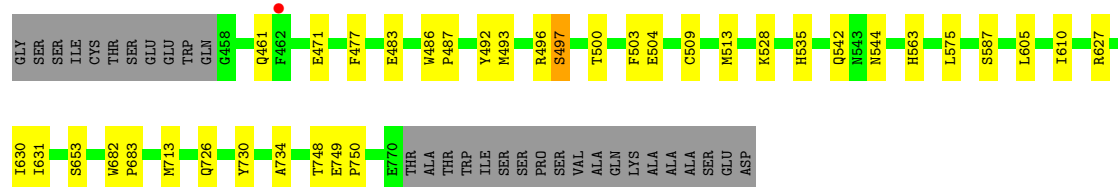
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	131	Total 131	O 131	0	0
5	D	56	Total 56	O 56	0	0

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.

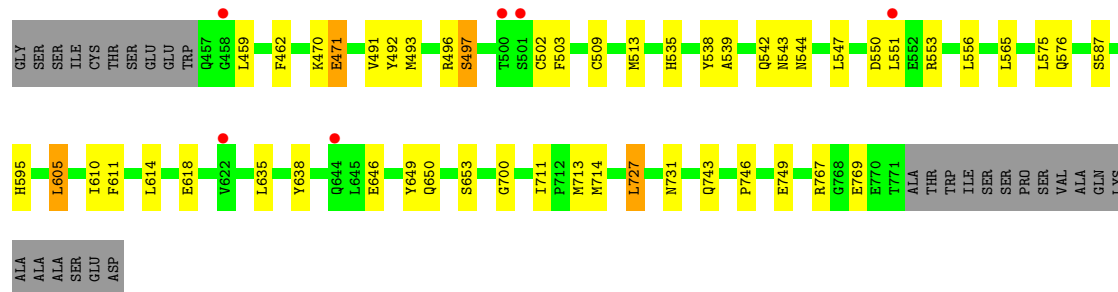
- Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

Chain A: 



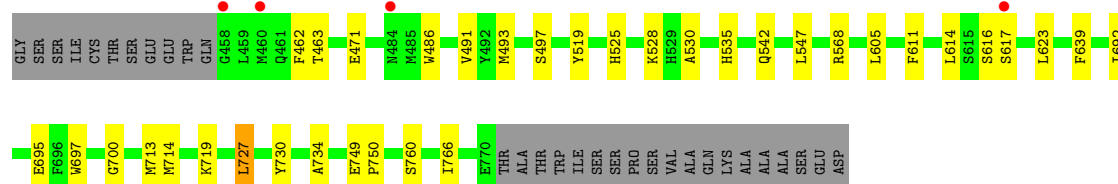
- Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

Chain B: 



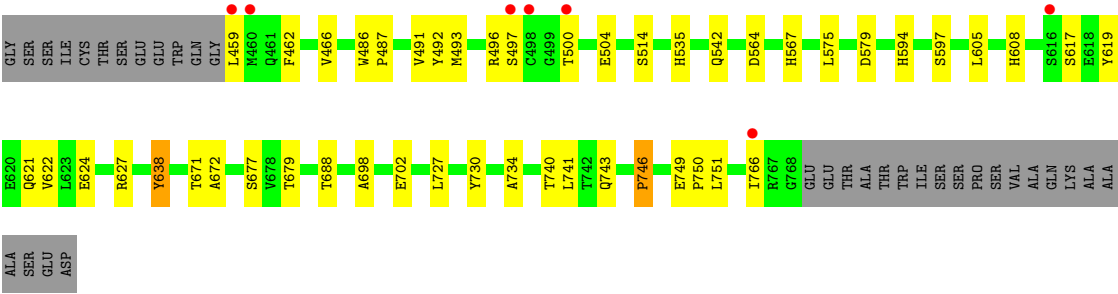
- Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

Chain C: 



- Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	134.82Å 134.82Å 234.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.37 – 2.15 41.37 – 2.15	Depositor EDS
% Data completeness (in resolution range)	70.6 (41.37-2.15) 70.6 (41.37-2.15)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.185 , 0.243 0.192 , 0.247	Depositor DCC
R_{free} test set	3322 reflections (3.85%)	wwPDB-VP
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.034 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10602	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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: GIQ, ZN, MG, CME

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	0.99	0/2592	1.40	2/3507 (0.1%)
1	B	0.97	0/2602	1.42	1/3521 (0.0%)
1	C	1.00	0/2592	1.41	2/3507 (0.1%)
1	D	1.03	0/2570	1.47	1/3478 (0.0%)
All	All	1.00	0/10356	1.43	6/14013 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	639	PHE	CA-C-N	5.33	125.90	119.98
1	C	639	PHE	C-N-CA	5.33	125.90	119.98
1	A	544	ASN	CA-C-N	5.33	127.73	120.54
1	A	544	ASN	C-N-CA	5.33	127.73	120.54
1	B	746	PRO	N-CA-C	5.30	117.16	110.70
1	D	746	PRO	N-CA-C	5.19	117.03	110.70

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	2541	0	2511	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2551	0	2515	28	0
1	C	2541	0	2511	20	0
1	D	2519	0	2496	26	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	30	0	20	2	0
4	C	15	0	10	6	0
5	A	107	0	0	0	0
5	B	103	0	0	0	0
5	C	131	0	0	1	0
5	D	56	0	0	0	0
All	All	10602	0	10063	92	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 5.

All (92) 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:A:726:GLN:HE22	4:A:803[A]:GIQ:H5A	1.44	0.83
1:B:470:LYS:HE2	1:D:746:PRO:HG3	1.63	0.78
1:D:492:TYR:CZ	1:D:496:ARG:HD2	2.28	0.68
1:C:692:ILE:CD1	4:C:803:GIQ:H2	2.25	0.66
1:C:700:GLY:HA3	1:C:714:MET:O	1.95	0.66
1:C:568:ARG:NH1	5:C:901:HOH:O	2.29	0.65
1:D:677:SER:HB2	1:D:688:THR:HG21	1.79	0.64
1:C:713:MET:SD	4:C:803:GIQ:H8A	2.39	0.62
1:D:766:ILE:HG22	1:D:766:ILE:O	1.98	0.62
1:B:711:ILE:HD11	1:B:713:MET:HE2	1.83	0.61
1:D:497:SER:HA	1:D:542:GLN:NE2	2.16	0.61
1:D:462:PHE:CE1	1:D:491:VAL:HG11	2.35	0.60
1:A:509:CME:O	1:A:513:MET:HG2	2.03	0.59
1:B:493:MET:O	1:B:497:SER:HB2	2.03	0.58
1:C:692:ILE:HD11	4:C:803:GIQ:H2	1.84	0.58
1:B:496:ARG:NH1	1:B:538:TYR:OH	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:539:ALA:O	1:B:543:ASN:ND2	2.33	0.56
1:D:493:MET:SD	1:D:535:HIS:HA	2.46	0.56
1:B:727:LEU:HD22	1:B:731:ASN:HD21	1.70	0.56
1:B:497:SER:HA	1:B:542:GLN:NE2	2.20	0.55
1:A:503:PHE:CE1	1:A:610:ILE:HD12	2.41	0.55
1:C:749:GLU:HB3	1:C:750:PRO:HD3	1.87	0.55
1:B:611:PHE:HB3	1:B:614:LEU:HD22	1.88	0.55
1:D:727:LEU:C	1:D:727:LEU:HD23	2.32	0.55
1:A:461:GLN:HE22	1:A:500:THR:HG21	1.72	0.54
1:D:564:ASP:O	1:D:567:HIS:HB2	2.08	0.54
1:A:713:MET:SD	4:A:803[A]:GIQ:H2	2.48	0.53
1:A:483:GLU:HG2	1:A:486:TRP:CH2	2.44	0.53
1:B:646:GLU:OE2	1:B:650:GLN:OE1	2.26	0.52
1:A:749:GLU:N	1:A:750:PRO:CD	2.72	0.52
1:B:635:LEU:O	1:B:638:TYR:HB3	2.10	0.51
1:C:497:SER:HA	1:C:542:GLN:HE22	1.75	0.51
1:B:551:LEU:HD11	1:B:618:GLU:HB3	1.93	0.51
1:A:492:TYR:CZ	1:A:496:ARG:HD2	2.45	0.50
1:B:509:CME:O	1:B:513:MET:HG2	2.11	0.50
1:C:727:LEU:HG	1:C:766:ILE:CD1	2.42	0.50
1:A:486:TRP:CH2	1:A:528:LYS:HB2	2.48	0.49
1:C:493:MET:SD	1:C:535:HIS:HA	2.53	0.48
1:D:766:ILE:O	1:D:766:ILE:CG2	2.61	0.48
1:B:492:TYR:CZ	1:B:496:ARG:HD2	2.49	0.48
1:D:514:SER:OG	1:D:608:HIS:NE2	2.38	0.48
1:D:672:ALA:CB	1:D:741:LEU:HD22	2.44	0.48
1:D:740:THR:HA	1:D:743:GLN:HE21	1.79	0.48
1:C:497:SER:HA	1:C:542:GLN:NE2	2.29	0.47
1:B:470:LYS:HE2	1:D:746:PRO:CG	2.39	0.47
1:D:730:TYR:HA	1:D:734:ALA:HB3	1.96	0.47
1:B:462:PHE:CE1	1:B:491:VAL:HG11	2.50	0.47
1:D:594:HIS:O	1:D:597:SER:HB3	2.14	0.47
1:B:497:SER:HA	1:B:542:GLN:HE22	1.80	0.46
1:B:565:LEU:O	1:B:595:HIS:ND1	2.43	0.46
1:C:486:TRP:CH2	1:C:528:LYS:HB2	2.50	0.46
1:C:697:TRP:CZ2	1:C:719:LYS:HG2	2.50	0.46
1:A:748:THR:C	1:A:750:PRO:HD2	2.41	0.46
1:B:649:TYR:CE2	1:B:743:GLN:HB3	2.51	0.46
1:D:619:TYR:O	1:D:622:VAL:HG12	2.16	0.45
1:B:470:LYS:HG3	1:B:471:GLU:N	2.30	0.45
1:C:462:PHE:CE1	1:C:491:VAL:HG11	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:730:TYR:HA	1:C:734:ALA:HB3	1.99	0.45
1:A:542:GLN:NE2	1:A:542:GLN:HA	2.30	0.45
1:A:563:HIS:HA	1:A:630:ILE:HG12	1.98	0.45
1:D:679:THR:HG21	1:D:751:LEU:HD22	2.00	0.44
1:A:493:MET:O	1:A:497:SER:HB2	2.17	0.43
1:D:638:TYR:CD1	1:D:671:THR:HG21	2.53	0.43
1:A:627:ARG:O	1:A:631:ILE:HG12	2.18	0.43
1:C:692:ILE:CD1	4:C:803:GIQ:C	2.96	0.43
1:D:486:TRP:N	1:D:487:PRO:CD	2.81	0.43
1:A:461:GLN:NE2	1:A:500:THR:HG21	2.33	0.43
1:A:730:TYR:HA	1:A:734:ALA:HB3	2.01	0.43
1:C:713:MET:SD	4:C:803:GIQ:C8A	3.07	0.43
1:A:493:MET:SD	1:A:535:HIS:HA	2.58	0.43
1:D:493:MET:O	1:D:497:SER:HB3	2.18	0.43
1:D:624:GLU:OE2	1:D:627:ARG:NH2	2.48	0.43
1:C:525:HIS:ND1	1:C:695:GLU:OE1	2.37	0.43
1:B:544:ASN:HB3	1:B:547:LEU:HD22	2.01	0.42
1:D:621:GLN:HE21	1:D:621:GLN:HB2	1.69	0.42
1:B:550:ASP:OD1	1:B:553:ARG:NH2	2.53	0.42
1:B:700:GLY:HA3	1:B:714:MET:O	2.19	0.42
1:B:551:LEU:HD23	1:B:551:LEU:HA	1.90	0.42
1:D:698:ALA:O	1:D:702:GLU:HG2	2.20	0.42
1:B:503:PHE:CE1	1:B:610:ILE:HD12	2.55	0.41
1:B:605:LEU:HD12	1:B:605:LEU:HA	1.90	0.41
1:B:767:ARG:NH2	1:B:769:GLU:OE1	2.53	0.41
1:C:519:TYR:CZ	1:C:530:ALA:HB2	2.55	0.41
1:D:493:MET:O	1:D:497:SER:CB	2.69	0.41
1:A:477:PHE:HB3	1:A:535:HIS:CE1	2.56	0.41
1:D:749:GLU:N	1:D:750:PRO:CD	2.83	0.41
1:C:692:ILE:HD13	4:C:803:GIQ:H2	2.00	0.41
1:A:486:TRP:N	1:A:487:PRO:CD	2.84	0.40
1:A:682:TRP:N	1:A:683:PRO:CD	2.84	0.40
1:B:493:MET:SD	1:B:535:HIS:HA	2.61	0.40
1:B:556:LEU:HD23	1:B:556:LEU:HA	1.95	0.40
1:C:611:PHE:HB3	1:C:614:LEU:HD22	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	310/343 (90%)	298 (96%)	12 (4%)	0	100	100
1	B	312/343 (91%)	300 (96%)	12 (4%)	0	100	100
1	C	310/343 (90%)	302 (97%)	8 (3%)	0	100	100
1	D	307/343 (90%)	296 (96%)	9 (3%)	2 (1%)	18	13
All	All	1239/1372 (90%)	1196 (96%)	41 (3%)	2 (0%)	43	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	579	ASP
1	D	466	VAL

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	281/305 (92%)	274 (98%)	7 (2%)	42	45
1	B	281/305 (92%)	270 (96%)	11 (4%)	28	28
1	C	281/305 (92%)	272 (97%)	9 (3%)	34	36
1	D	279/305 (92%)	272 (98%)	7 (2%)	42	45
All	All	1122/1220 (92%)	1088 (97%)	34 (3%)	36	38

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	471	GLU
1	A	497	SER
1	A	504	GLU
1	A	575	LEU
1	A	587	SER
1	A	605	LEU
1	A	653	SER
1	B	459	LEU
1	B	471	GLU
1	B	497	SER
1	B	502	CYS
1	B	575	LEU
1	B	576	GLN
1	B	587	SER
1	B	605	LEU
1	B	653	SER
1	B	727	LEU
1	B	749	GLU
1	C	463	THR
1	C	471	GLU
1	C	547	LEU
1	C	605	LEU
1	C	616	SER
1	C	617	SER
1	C	623	LEU
1	C	727	LEU
1	C	760	SER
1	D	459	LEU
1	D	500	THR
1	D	504	GLU
1	D	575	LEU
1	D	605	LEU
1	D	617	SER
1	D	638	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	461	GLN
1	A	542	GLN
1	A	545	HIS
1	A	604	GLN
1	A	609	ASN

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Mol	Chain	Res	Type
1	A	644	GLN
1	A	726	GLN
1	A	743	GLN
1	B	484	ASN
1	B	576	GLN
1	B	604	GLN
1	B	726	GLN
1	B	731	ASN
1	C	542	GLN
1	C	593	GLN
1	C	743	GLN
1	D	484	ASN
1	D	542	GLN
1	D	543	ASN
1	D	598	GLN
1	D	604	GLN
1	D	621	GLN
1	D	644	GLN
1	D	726	GLN
1	D	743	GLN
1	D	761	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CME	D	509	1	8,9,10	0.49	0	6,9,11	0.46	0
1	CME	B	509	1	8,9,10	0.29	0	6,9,11	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CME	A	509	1	8,9,10	0.49	0	6,9,11	0.86	0
1	CME	C	509	1	8,9,10	0.39	0	6,9,11	0.99	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
1	CME	D	509	1	-	2/5/8/10	-
1	CME	B	509	1	-	1/5/8/10	-
1	CME	A	509	1	-	1/5/8/10	-
1	CME	C	509	1	-	2/5/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	509	CME	SD-CE-CZ-OH
1	C	509	CME	CE-SD-SG-CB
1	D	509	CME	SD-CE-CZ-OH
1	C	509	CME	CZ-CE-SD-SG
1	D	509	CME	N-CA-CB-SG
1	A	509	CME	CZ-CE-SD-SG

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	509	CME	1	0
1	A	509	CME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 11 ligands modelled in this entry, 8 are monoatomic - leaving 3 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$
4	GIQ	A	803[A]	-	16,17,17	1.07	2 (12%)	20,25,25	2.13	7 (35%)
4	GIQ	A	803[B]	-	16,17,17	1.05	1 (6%)	20,25,25	1.97	5 (25%)
4	GIQ	C	803	-	16,17,17	1.25	2 (12%)	20,25,25	1.69	4 (20%)

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
4	GIQ	A	803[A]	-	-	-	0/3/3/3
4	GIQ	A	803[B]	-	-	-	0/3/3/3
4	GIQ	C	803	-	-	-	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	803	GIQ	C2A-N10	3.28	1.39	1.34
4	A	803[B]	GIQ	C2A-N10	2.87	1.39	1.34
4	A	803[A]	GIQ	C2A-N10	2.65	1.38	1.34
4	C	803	GIQ	C6A-N6A	-2.22	1.33	1.37
4	A	803[A]	GIQ	C6A-N6A	-2.00	1.34	1.37

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	803[A]	GIQ	C10-C6A-N6A	-5.42	117.08	122.82
4	A	803[B]	GIQ	C10-C6A-N6A	-4.50	118.05	122.82
4	C	803	GIQ	C10-C1A-N1A	3.81	133.97	127.92
4	A	803[A]	GIQ	C7A-N6A-C6A	3.64	122.43	116.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	803[B]	GIQ	C10-C1A-N1A	3.53	133.52	127.92
4	A	803[B]	GIQ	C7A-N6A-C6A	3.29	121.92	116.93
4	C	803	GIQ	C8A-C9A-C10	-3.05	116.80	120.91
4	A	803[A]	GIQ	C10-C1A-N1A	2.77	132.31	127.92
4	A	803[A]	GIQ	C1A-N1A-C2A	2.54	108.61	104.96
4	A	803[B]	GIQ	C1A-N1A-C2A	2.40	108.41	104.96
4	A	803[A]	GIQ	C5A-C6A-N6A	2.36	122.34	118.55
4	C	803	GIQ	C10-C6A-N6A	-2.35	120.33	122.82
4	C	803	GIQ	C1A-N1A-C2A	2.26	108.21	104.96
4	A	803[A]	GIQ	C9A-C10-C6A	2.23	120.84	118.36
4	A	803[B]	GIQ	N10-C2A-N3A	2.23	126.10	122.38
4	A	803[A]	GIQ	C4A-C3A-N3A	2.11	134.24	129.88

There are no chirality outliers.

There are no torsion outliers.

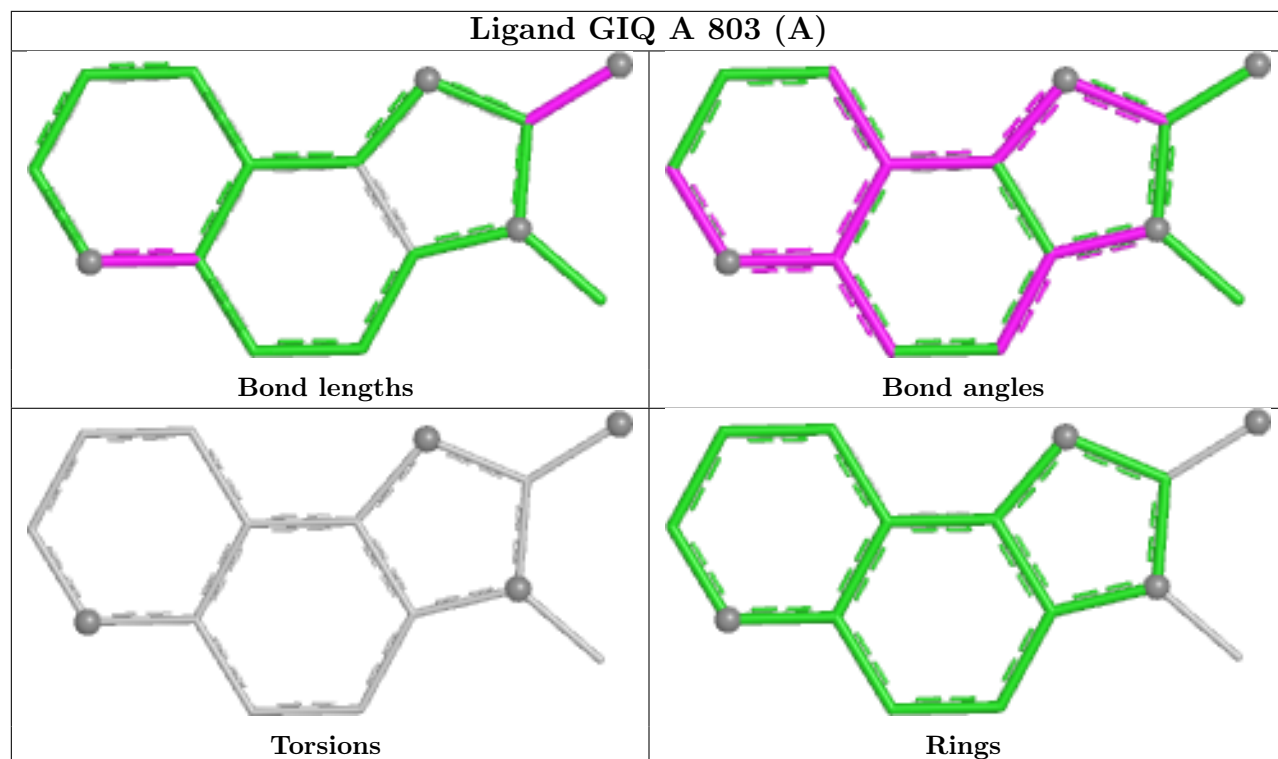
There are no ring outliers.

2 monomers are involved in 8 short contacts:

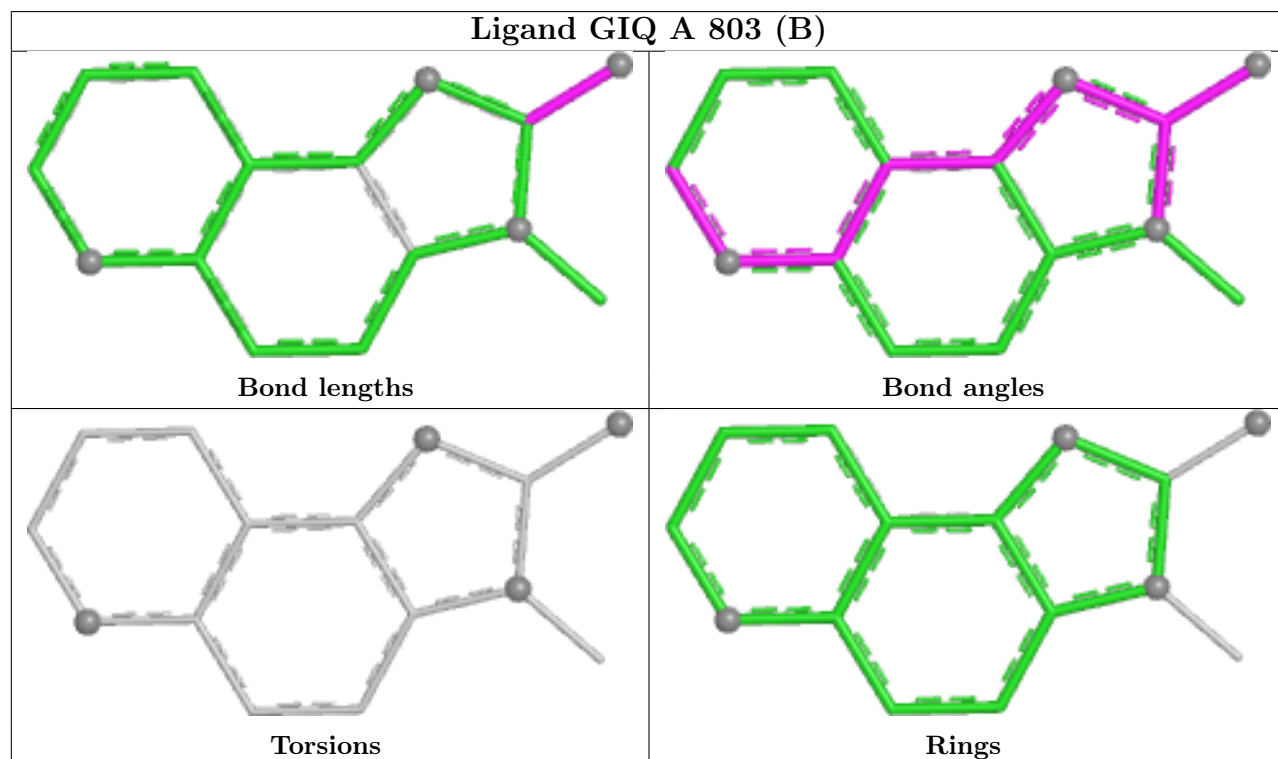
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	803[A]	GIQ	2	0
4	C	803	GIQ	6	0

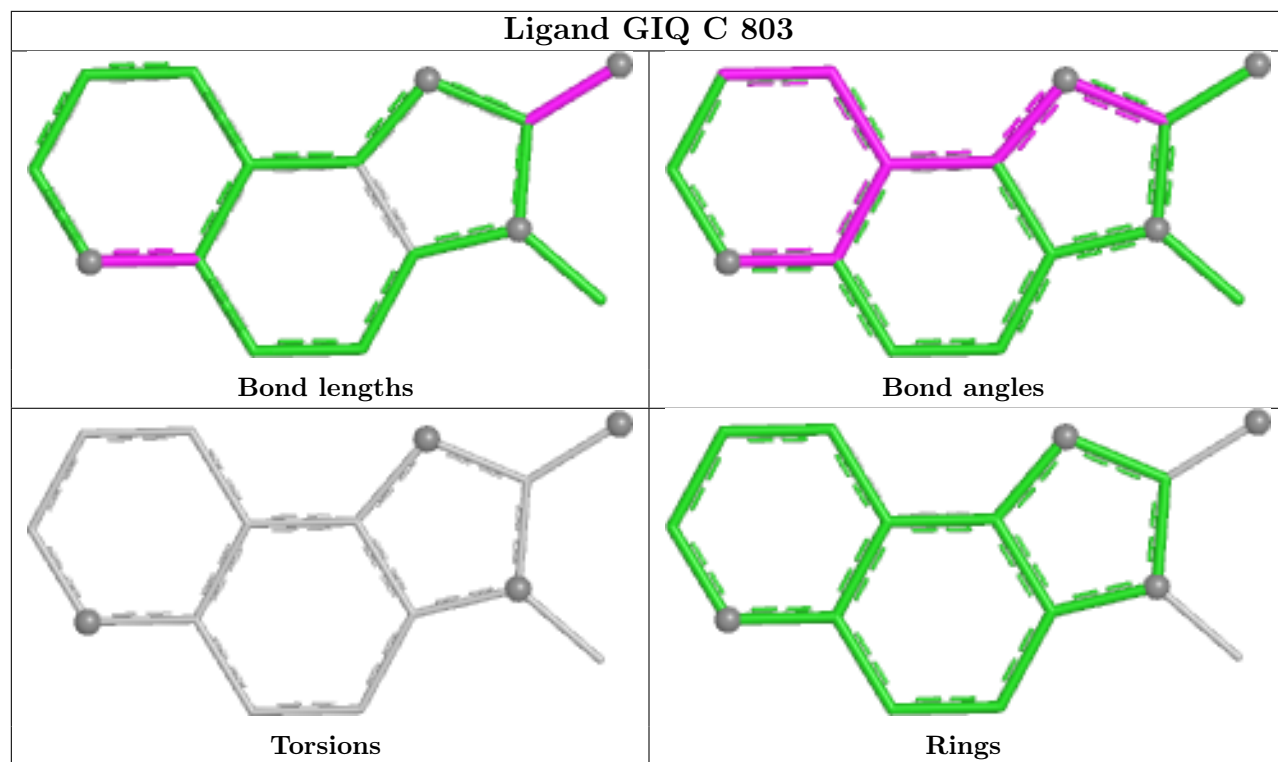
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 GIQ A 803 (A)



Ligand GIQ A 803 (B)





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	312/343 (90%)	0.03	1 (0%) 90 91	30, 42, 67, 106	0
1	B	314/343 (91%)	0.11	6 (1%) 66 70	29, 44, 72, 94	0
1	C	312/343 (90%)	-0.05	4 (1%) 75 78	29, 41, 65, 88	0
1	D	309/343 (90%)	0.34	7 (2%) 61 64	40, 58, 76, 98	0
All	All	1247/1372 (90%)	0.11	18 (1%) 73 77	29, 47, 73, 106	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	459	LEU	4.2
1	D	460	MET	3.8
1	A	462	PHE	3.7
1	C	484	ASN	2.9
1	B	458	GLY	2.9
1	B	500	THR	2.8
1	C	460	MET	2.7
1	D	766	ILE	2.7
1	C	617	SER	2.6
1	B	501	SER	2.6
1	D	498	CYS	2.4
1	C	458	GLY	2.4
1	B	551	LEU	2.4
1	D	616	SER	2.3
1	D	500	THR	2.2
1	B	644	GLN	2.1
1	D	497	SER	2.1
1	B	622	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CME	B	509	10/11	0.85	0.16	46,61,73,79	0
1	CME	C	509	10/11	0.91	0.10	42,48,68,72	0
1	CME	D	509	10/11	0.92	0.10	60,72,88,89	0
1	CME	A	509	10/11	0.95	0.08	49,57,78,78	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

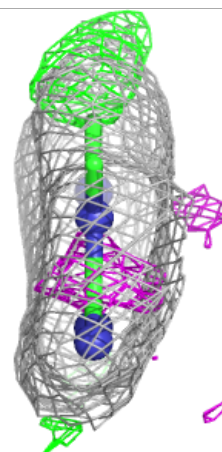
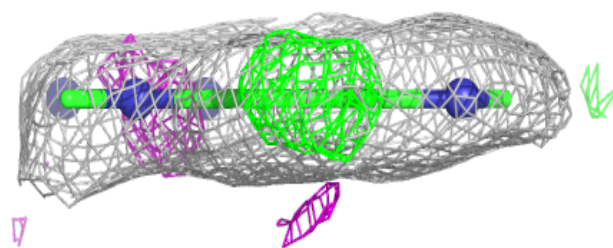
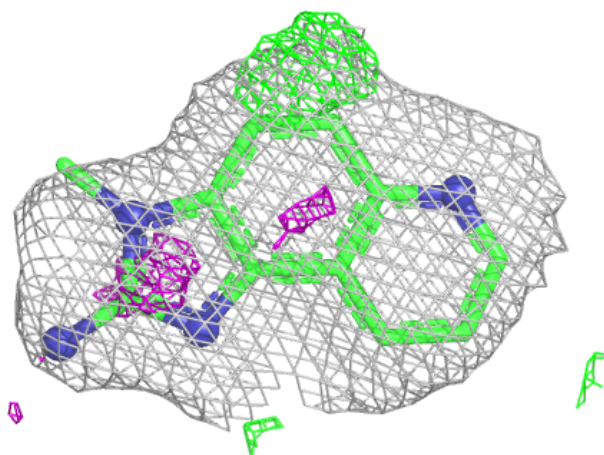
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GIQ	A	803[A]	15/15	0.83	0.13	44,49,54,55	15
4	GIQ	A	803[B]	15/15	0.83	0.13	52,55,58,58	15
4	GIQ	C	803	15/15	0.91	0.10	48,56,61,64	0
3	MG	C	802	1/1	0.98	0.04	28,28,28,28	0
3	MG	B	802	1/1	0.99	0.02	26,26,26,26	0
2	ZN	D	801	1/1	0.99	0.04	52,52,52,52	0
3	MG	D	802	1/1	0.99	0.03	42,42,42,42	0
2	ZN	A	801	1/1	1.00	0.01	36,36,36,36	0
3	MG	A	802	1/1	1.00	0.01	33,33,33,33	0
2	ZN	B	801	1/1	1.00	0.02	36,36,36,36	0
2	ZN	C	801	1/1	1.00	0.01	34,34,34,34	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.

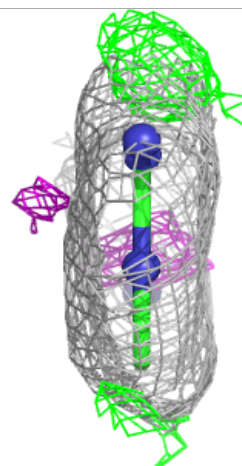
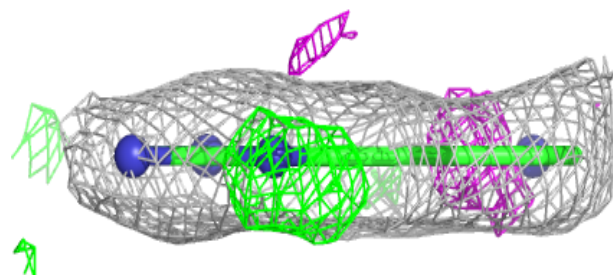
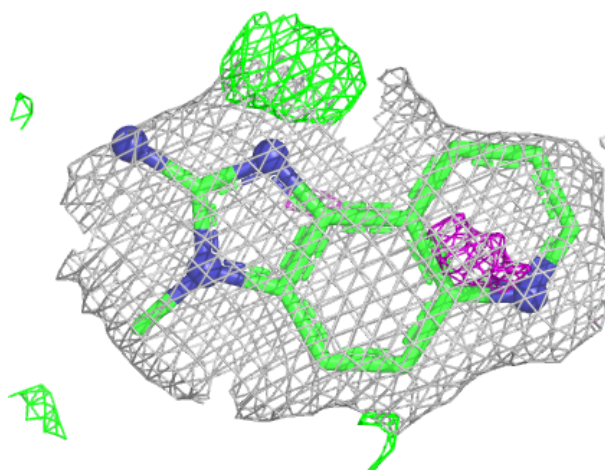
Electron density around GIQ A 803 (A):

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



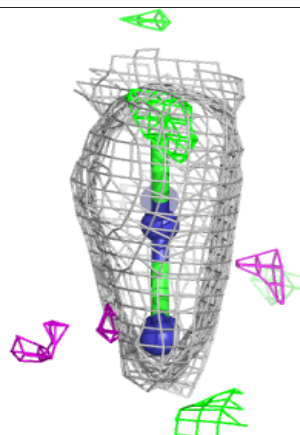
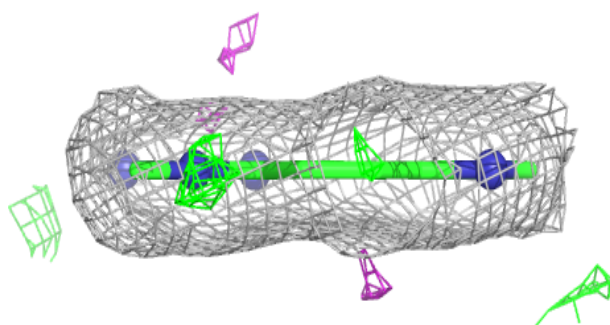
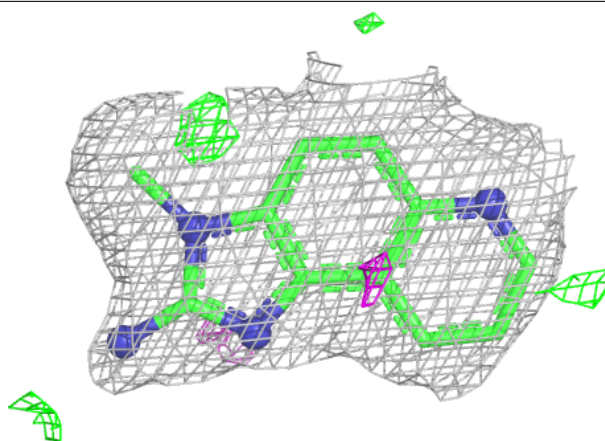
Electron density around GIQ A 803 (B):

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



Electron density around GIQ C 803:

$2mF_o-DF_c$ (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.