



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 11:39 PM BST

PDB ID : 3GOI
Title : Human glucokinase in complex with a synthetic activator
Authors : Kamata, K.; Mitsuya, M.
Deposited on : 2009-03-19
Resolution : 2.52 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 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

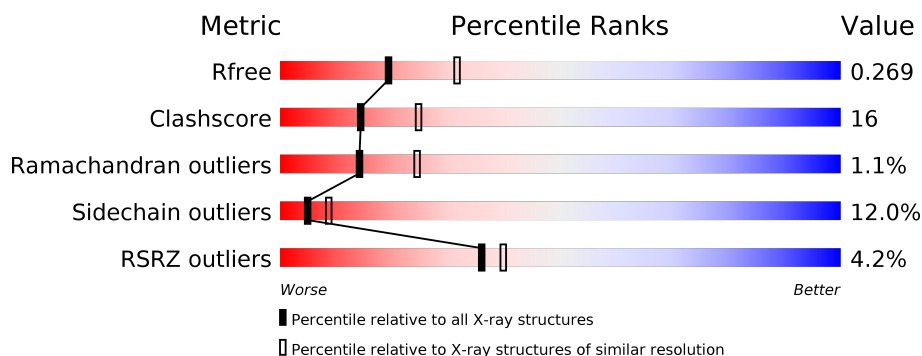
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

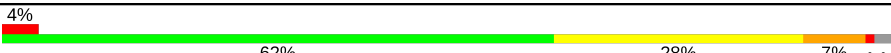
The reported resolution of this entry is 2.52 Å.

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	5743 (2.54-2.50)
Clashscore	141614	6463 (2.54-2.50)
Ramachandran outliers	138981	6335 (2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)
RSRZ outliers	127900	5630 (2.54-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	455	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3669 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 Glucokinase.

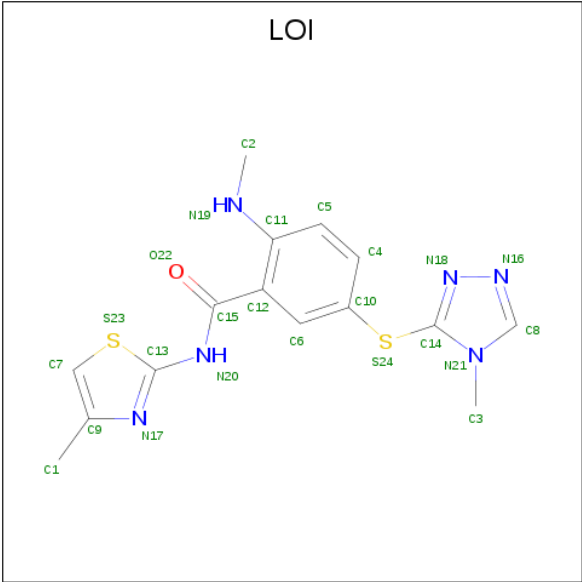
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	448	3505	2178	609	686	32	0	0	0

- Molecule 2 is alpha-D-glucopyranose (three-letter code: GLC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	12	6	6	0	0

- Molecule 3 is 2-(methylamino)-N-(4-methyl-1,3-thiazol-2-yl)-5-[(4-methyl-4H-1,2,4-triazol-3-yl)sulfanyl]benzamide (three-letter code: LOI) (formula: C₁₅H₁₆N₆OS₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			24	15	6	1	2		

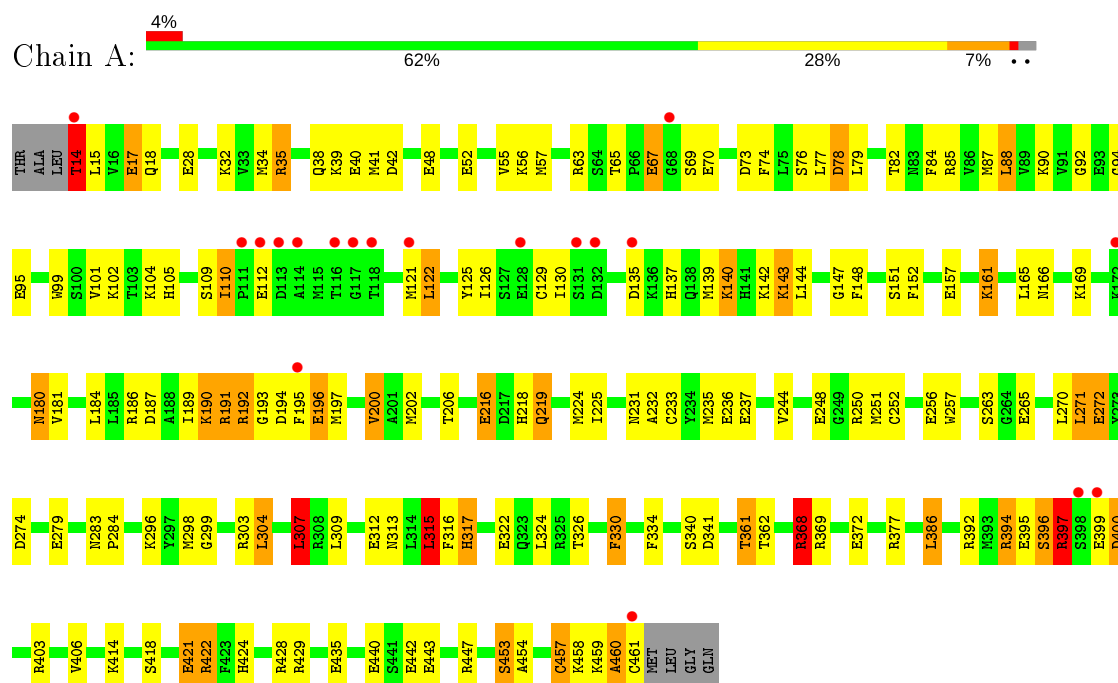
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	128	Total	O	0	0
			128	128		

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: Glucokinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	80.08 Å 80.08 Å 323.97 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.35 – 2.52 47.35 – 2.52	Depositor EDS
% Data completeness (in resolution range)	99.1 (47.35-2.52) 99.1 (47.35-2.52)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.26 (at 2.51 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.205 , 0.282 0.198 , 0.269	Depositor DCC
R_{free} test set	1103 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3669	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, LOI

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	1.44	22/3558 (0.6%)	1.27	25/4783 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	395	GLU	CG-CD	10.40	1.67	1.51
1	A	17	GLU	CB-CG	8.39	1.68	1.52
1	A	421	GLU	CG-CD	7.91	1.63	1.51
1	A	457	CYS	CB-SG	-7.79	1.69	1.82
1	A	14	THR	CA-CB	7.12	1.71	1.53
1	A	272	GLU	CG-CD	6.77	1.62	1.51
1	A	330	PHE	CE1-CZ	6.75	1.50	1.37
1	A	442	GLU	CG-CD	6.36	1.61	1.51
1	A	216	GLU	CG-CD	5.96	1.60	1.51
1	A	372	GLU	CG-CD	5.93	1.60	1.51
1	A	48	GLU	CB-CG	5.89	1.63	1.52
1	A	161	LYS	CE-NZ	5.87	1.63	1.49
1	A	17	GLU	CG-CD	5.73	1.60	1.51
1	A	334	PHE	CE1-CZ	5.58	1.48	1.37
1	A	78	ASP	N-CA	-5.53	1.35	1.46
1	A	28	GLU	CG-CD	5.52	1.60	1.51
1	A	435	GLU	CG-CD	5.24	1.59	1.51
1	A	236	GLU	CD-OE1	5.22	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	48	GLU	CD-OE1	5.13	1.31	1.25
1	A	279	GLU	CD-OE1	5.09	1.31	1.25
1	A	406	VAL	CB-CG1	5.09	1.63	1.52
1	A	28	GLU	CD-OE2	5.06	1.31	1.25

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	298	MET	CG-SD-CE	-8.29	86.94	100.20
1	A	35	ARG	NE-CZ-NH2	-7.85	116.38	120.30
1	A	403	ARG	NE-CZ-NH2	-7.16	116.72	120.30
1	A	429	ARG	NE-CZ-NH1	7.10	123.85	120.30
1	A	377	ARG	NE-CZ-NH1	-7.03	116.79	120.30
1	A	422	ARG	NE-CZ-NH1	6.73	123.67	120.30
1	A	35	ARG	NE-CZ-NH1	6.17	123.39	120.30
1	A	251	MET	CG-SD-CE	-6.09	90.46	100.20
1	A	233	CYS	CB-CA-C	-5.99	98.41	110.40
1	A	304	LEU	CB-CG-CD1	5.91	121.05	111.00
1	A	143	LYS	N-CA-C	-5.69	95.62	111.00
1	A	315	LEU	CA-CB-CG	5.59	128.15	115.30
1	A	369	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	88	LEU	CB-CG-CD2	5.58	120.48	111.00
1	A	442	GLU	C-N-CA	-5.57	107.78	121.70
1	A	122	LEU	CA-CB-CG	5.56	128.09	115.30
1	A	102	LYS	CD-CE-NZ	-5.55	98.92	111.70
1	A	386	LEU	CB-CG-CD2	5.51	120.36	111.00
1	A	422	ARG	NE-CZ-NH2	-5.48	117.56	120.30
1	A	270	LEU	CA-CB-CG	5.45	127.82	115.30
1	A	397	ARG	NE-CZ-NH1	5.37	122.99	120.30
1	A	368	ARG	CG-CD-NE	5.31	122.95	111.80
1	A	94	GLY	N-CA-C	-5.08	100.39	113.10
1	A	191	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	A	307	LEU	CB-CG-CD1	5.05	119.58	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	14	THR	Peptide
1	A	397	ARG	Peptide

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	3505	0	3443	108	0
2	A	12	0	12	1	0
3	A	24	0	16	2	0
4	A	128	0	0	7	0
All	All	3669	0	3471	109	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 16.

All (109) 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:263:SER:HB2	1:A:265:GLU:OE1	1.45	1.14
1:A:143:LYS:HG3	1:A:196:GLU:HB3	1.24	1.10
1:A:144:LEU:O	1:A:197:MET:CE	2.13	0.96
1:A:192:ARG:NH1	1:A:192:ARG:HB3	1.78	0.96
1:A:443:GLU:O	1:A:443:GLU:HG3	1.64	0.96
1:A:197:MET:HE3	1:A:197:MET:HA	1.54	0.90
1:A:144:LEU:O	1:A:197:MET:HE1	1.73	0.88
1:A:396:SER:O	1:A:397:ARG:HB2	1.73	0.87
1:A:67:GLU:HG2	1:A:67:GLU:O	1.76	0.84
1:A:192:ARG:O	1:A:194:ASP:N	2.11	0.83
1:A:192:ARG:HH11	1:A:192:ARG:HB3	1.44	0.80
1:A:144:LEU:O	1:A:197:MET:HE3	1.83	0.76
1:A:52:GLU:HB3	4:A:1108:HOH:O	1.87	0.75
1:A:135:ASP:OD1	1:A:140:LYS:HE2	1.85	0.74
1:A:192:ARG:HH11	1:A:192:ARG:CB	2.02	0.72
1:A:82:THR:O	1:A:110:ILE:HD11	1.89	0.72
1:A:312:GLU:O	1:A:313:ASN:HB2	1.91	0.71
1:A:73:ASP:HB3	1:A:88:LEU:HD11	1.71	0.70
1:A:84:PHE:CZ	1:A:126:ILE:HG23	2.28	0.69
1:A:180:ASN:HD22	1:A:180:ASN:C	1.95	0.68
1:A:197:MET:CE	1:A:197:MET:HA	2.22	0.68
1:A:195:PHE:HB2	4:A:1120:HOH:O	1.94	0.67
1:A:135:ASP:OD1	1:A:140:LYS:CE	2.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:GLU:CG	1:A:67:GLU:O	2.43	0.67
1:A:394:ARG:NH2	1:A:400:ASP:O	2.27	0.67
1:A:394:ARG:HH22	1:A:400:ASP:C	1.99	0.66
1:A:237:GLU:OE1	1:A:250:ARG:HD2	1.97	0.65
1:A:394:ARG:NH2	1:A:400:ASP:C	2.50	0.65
1:A:460:ALA:O	1:A:461:CYS:HB3	1.97	0.63
1:A:459:LYS:O	1:A:460:ALA:HB2	1.98	0.63
1:A:35:ARG:HA	1:A:38:GLN:HE21	1.64	0.62
1:A:443:GLU:CG	1:A:443:GLU:O	2.44	0.62
1:A:315:LEU:HD13	1:A:316:PHE:CD2	2.34	0.61
1:A:101:VAL:O	1:A:101:VAL:HG13	2.01	0.61
1:A:14:THR:HG21	1:A:17:GLU:HG2	1.82	0.61
1:A:126:ILE:O	1:A:130:ILE:HG13	2.00	0.60
1:A:231:ASN:HD21	1:A:256:GLU:N	2.00	0.59
1:A:418:SER:O	1:A:422:ARG:HG3	2.02	0.58
1:A:180:ASN:ND2	1:A:180:ASN:C	2.58	0.57
1:A:231:ASN:ND2	1:A:256:GLU:HA	2.20	0.57
1:A:197:MET:CA	1:A:197:MET:CE	2.81	0.56
1:A:397:ARG:NH1	4:A:1106:HOH:O	2.38	0.56
1:A:192:ARG:CZ	1:A:192:ARG:HB3	2.36	0.56
1:A:56:LYS:O	1:A:57:MET:HB2	2.06	0.56
1:A:303:ARG:NH1	1:A:307:LEU:HD21	2.21	0.55
1:A:143:LYS:HA	1:A:196:GLU:O	2.07	0.54
1:A:219:GLN:HG3	4:A:1104:HOH:O	2.08	0.54
1:A:271:LEU:HB2	1:A:274:ASP:OD2	2.08	0.53
1:A:368:ARG:CG	1:A:368:ARG:HH11	2.21	0.53
1:A:135:ASP:OD1	1:A:140:LYS:NZ	2.42	0.52
1:A:263:SER:HB2	1:A:265:GLU:CD	2.27	0.52
1:A:125:TYR:CE1	1:A:129:CYS:SG	3.05	0.50
1:A:70:GLU:HG3	1:A:457:CYS:HB3	1.94	0.50
1:A:87:MET:HB2	1:A:104:LYS:O	2.10	0.50
1:A:361:THR:HG22	1:A:362:THR:N	2.26	0.50
1:A:135:ASP:O	1:A:137:HIS:N	2.45	0.50
1:A:312:GLU:O	1:A:313:ASN:CB	2.55	0.49
1:A:443:GLU:HB3	1:A:447:ARG:HD3	1.94	0.49
1:A:197:MET:CA	1:A:197:MET:HE3	2.32	0.49
1:A:63:ARG:O	3:A:1:LOI:H6	2.13	0.49
1:A:41:MET:HE2	1:A:392:ARG:HD3	1.94	0.49
1:A:459:LYS:O	1:A:460:ALA:CB	2.61	0.49
1:A:283:ASN:N	1:A:284:PRO:HD3	2.28	0.49
1:A:187:ASP:O	1:A:191:ARG:NH1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:SER:HA	1:A:147:GLY:O	2.13	0.48
1:A:231:ASN:ND2	1:A:232:ALA:H	2.12	0.47
1:A:92:GLY:HA3	1:A:99:TRP:CZ2	2.50	0.47
1:A:414:LYS:HG2	1:A:440:GLU:OE2	2.15	0.47
1:A:144:LEU:C	1:A:197:MET:HE1	2.36	0.46
1:A:224:MET:HE2	1:A:224:MET:HB3	1.87	0.46
1:A:14:THR:HB	1:A:17:GLU:H	1.81	0.46
1:A:79:LEU:HD22	1:A:126:ILE:HD11	1.98	0.46
1:A:206:THR:HG22	1:A:225:ILE:HG12	1.97	0.46
1:A:169:LYS:HE2	2:A:2:GLC:H2	1.96	0.46
1:A:157:GLU:OE2	1:A:161:LYS:HD3	2.17	0.45
1:A:186:ARG:O	1:A:190:LYS:NZ	2.40	0.45
1:A:231:ASN:HD21	1:A:256:GLU:HA	1.82	0.45
1:A:231:ASN:HD21	1:A:256:GLU:CA	2.29	0.45
1:A:394:ARG:HD3	1:A:394:ARG:HA	1.80	0.44
1:A:85:ARG:HH11	1:A:105:HIS:CE1	2.35	0.44
1:A:69:SER:HB2	1:A:454:ALA:O	2.18	0.43
1:A:78:ASP:OD2	1:A:78:ASP:C	2.57	0.43
1:A:189:ILE:HG22	1:A:190:LYS:HE3	2.01	0.43
1:A:421:GLU:CD	1:A:421:GLU:H	2.21	0.43
3:A:1:LOI:S23	3:A:1:LOI:O22	2.76	0.43
1:A:244:VAL:O	4:A:1068:HOH:O	2.21	0.43
1:A:303:ARG:HH12	1:A:307:LEU:HD21	1.83	0.43
1:A:299:GLY:HA3	1:A:330:PHE:O	2.19	0.43
1:A:41:MET:CE	1:A:392:ARG:HD3	2.48	0.43
1:A:200:VAL:CG1	1:A:453:SER:HA	2.49	0.42
1:A:139:MET:O	1:A:140:LYS:C	2.58	0.42
1:A:152:PHE:O	4:A:1059:HOH:O	2.21	0.42
1:A:235:MET:SD	1:A:252:CYS:HB2	2.59	0.42
1:A:394:ARG:NH2	1:A:399:GLU:O	2.51	0.42
1:A:90:LYS:HB2	1:A:90:LYS:HE2	1.63	0.42
1:A:135:ASP:C	1:A:137:HIS:H	2.23	0.42
1:A:315:LEU:HD13	1:A:316:PHE:CE2	2.55	0.42
1:A:368:ARG:HG2	1:A:368:ARG:HH11	1.85	0.42
1:A:180:ASN:O	1:A:181:VAL:C	2.58	0.42
1:A:424:HIS:O	1:A:428:ARG:HG3	2.19	0.41
1:A:324:LEU:HA	1:A:324:LEU:HD12	1.91	0.41
1:A:322:GLU:O	1:A:326:THR:HG23	2.21	0.41
1:A:340:SER:O	1:A:341:ASP:C	2.59	0.41
1:A:55:VAL:HA	4:A:1004:HOH:O	2.21	0.41
1:A:135:ASP:C	1:A:137:HIS:N	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:PHE:O	1:A:88:LEU:HD12	2.21	0.41
1:A:184:LEU:HD23	1:A:184:LEU:HA	1.72	0.40
1:A:165:LEU:HA	1:A:165:LEU:HD23	1.90	0.40
1:A:77:LEU:HB2	1:A:148:PHE:CD2	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	446/455 (98%)	406 (91%)	35 (8%)	5 (1%)	14 24

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	GLY
1	A	460	ALA
1	A	317	HIS
1	A	397	ARG
1	A	453	SER

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	384/389 (99%)	338 (88%)	46 (12%)	5 9

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	A	18	GLN
1	A	32	LYS
1	A	34	MET
1	A	39	LYS
1	A	40	GLU
1	A	42	ASP
1	A	65	THR
1	A	67	GLU
1	A	95	GLU
1	A	109	SER
1	A	110	ILE
1	A	112	GLU
1	A	121	MET
1	A	122	LEU
1	A	140	LYS
1	A	142	LYS
1	A	151	SER
1	A	166	ASN
1	A	180	ASN
1	A	190	LYS
1	A	192	ARG
1	A	196	GLU
1	A	200	VAL
1	A	202	MET
1	A	216	GLU
1	A	218	HIS
1	A	219	GLN
1	A	248	GLU
1	A	257	TRP
1	A	271	LEU
1	A	272	GLU
1	A	296	LYS
1	A	304	LEU
1	A	307	LEU
1	A	309	LEU
1	A	315	LEU
1	A	317	HIS

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Mol	Chain	Res	Type
1	A	361	THR
1	A	368	ARG
1	A	386	LEU
1	A	394	ARG
1	A	396	SER
1	A	397	ARG
1	A	400	ASP
1	A	458	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	38	GLN
1	A	83	ASN
1	A	105	HIS
1	A	166	ASN
1	A	180	ASN
1	A	231	ASN
1	A	323	GLN
1	A	337	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](#)

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	GLC	A	2	-	12,12,12	1.37	1 (8%)	17,17,17	2.44	9 (52%)
3	LOI	A	1	-	18,26,26	1.05	1 (5%)	23,36,36	1.89	1 (4%)

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	GLC	A	2	-	-	0/2/22/22	0/1/1/1
3	LOI	A	1	-	-	2/10/14/14	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2	GLC	O2-C2	3.06	1.50	1.43
3	A	1	LOI	C12-C11	-2.67	1.36	1.41

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	LOI	C2-N19-C11	-7.60	110.52	122.44
2	A	2	GLC	C4-C3-C2	4.81	119.23	110.82
2	A	2	GLC	C1-O5-C5	3.80	120.82	113.66
2	A	2	GLC	O5-C1-C2	-3.27	104.45	110.28
2	A	2	GLC	C3-C4-C5	-3.05	104.80	110.24
2	A	2	GLC	O4-C4-C3	-2.88	103.69	110.35
2	A	2	GLC	O1-C1-C2	-2.71	101.41	109.03
2	A	2	GLC	O2-C2-C1	2.68	115.37	109.16
2	A	2	GLC	C1-C2-C3	-2.35	105.44	110.31
2	A	2	GLC	O6-C6-C5	-2.32	103.32	111.29

There are no chirality outliers.

All (2) torsion outliers are listed below:

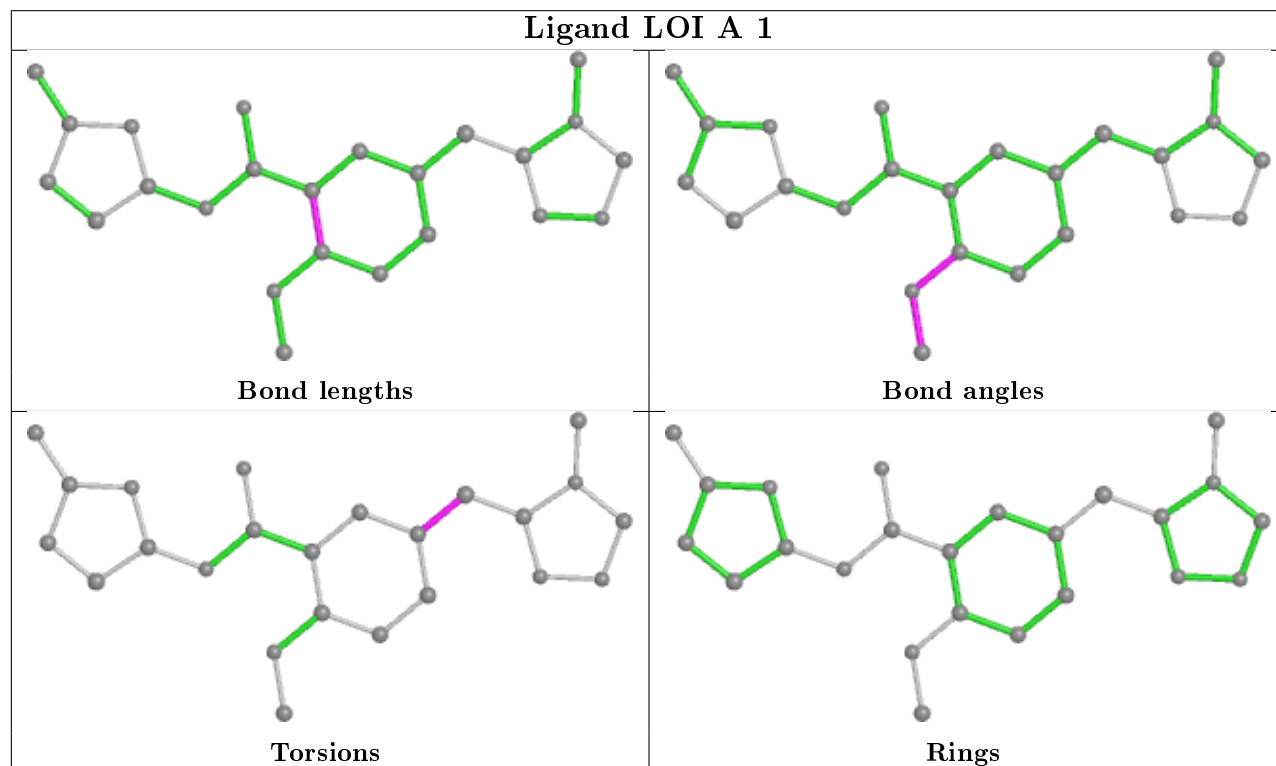
Mol	Chain	Res	Type	Atoms
3	A	1	LOI	C4-C10-S24-C14
3	A	1	LOI	C6-C10-S24-C14

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2	GLC	1	0
3	A	1	LOI	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

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, 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	448/455 (98%)	-0.09	19 (4%) 36 40	9, 28, 59, 78	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	14	THR	5.3
1	A	461	CYS	3.1
1	A	114	ALA	3.0
1	A	116	THR	2.9
1	A	112	GLU	2.9
1	A	128	GLU	2.6
1	A	131	SER	2.6
1	A	118	THR	2.6
1	A	132	ASP	2.6
1	A	135	ASP	2.6
1	A	172	LYS	2.4
1	A	113	ASP	2.4
1	A	121	MET	2.4
1	A	195	PHE	2.3
1	A	399	GLU	2.3
1	A	398	SER	2.2
1	A	68	GLY	2.1
1	A	117	GLY	2.1
1	A	111	PRO	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](#)

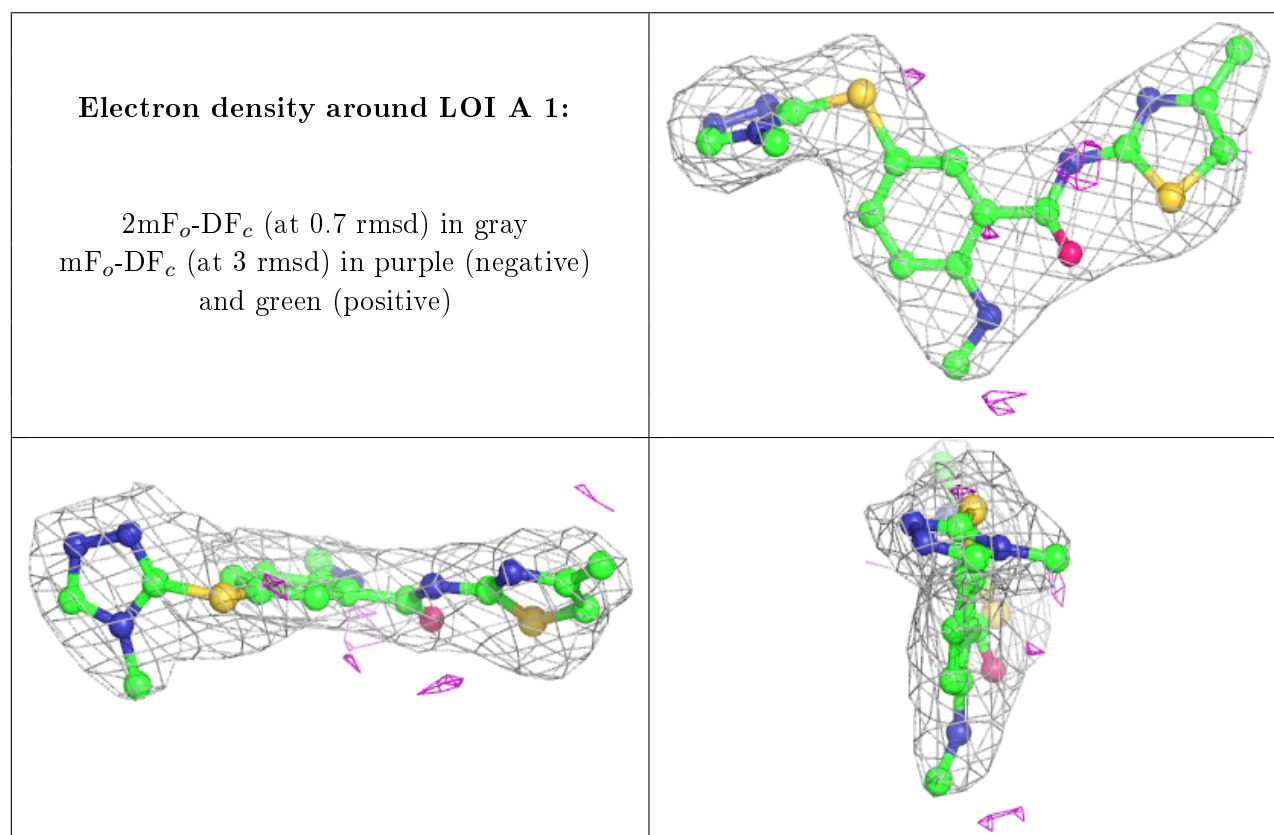
There are no monosaccharides in this entry.

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(\AA^2)	Q<0.9
2	GLC	A	2	12/12	0.98	0.10	7,12,15,19	0
3	LOI	A	1	24/24	0.98	0.13	23,26,34,38	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.



6.5 Other polymers ⓘ

There are no such residues in this entry.