



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 05:14 PM EDT

PDB ID : 3GOI / pdb_00003goi
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 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

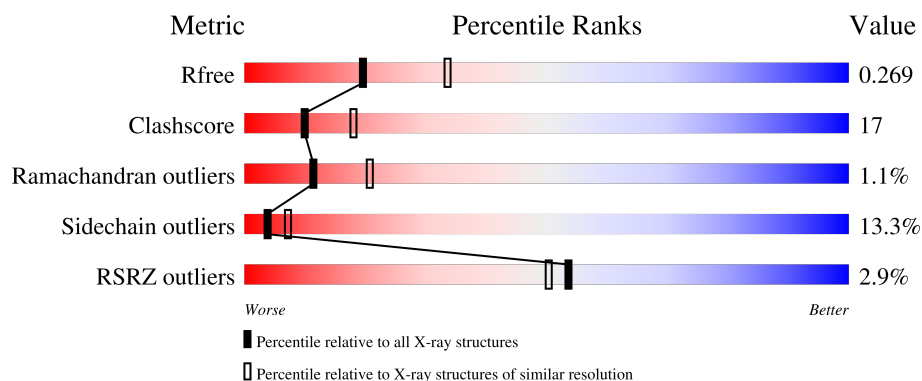
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.52 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}	180053	7383 (2.54-2.50)
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (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 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	455	3% 53% 33% 12% ..

2 Entry composition [i](#)

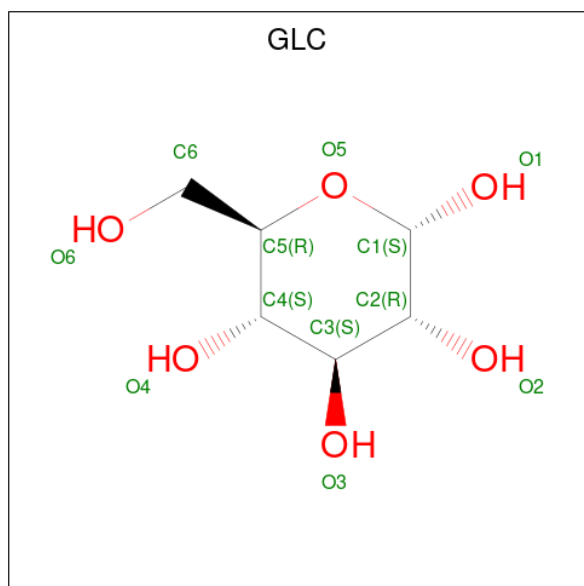
There are 4 unique types of molecules in this entry. The entry contains 3669 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

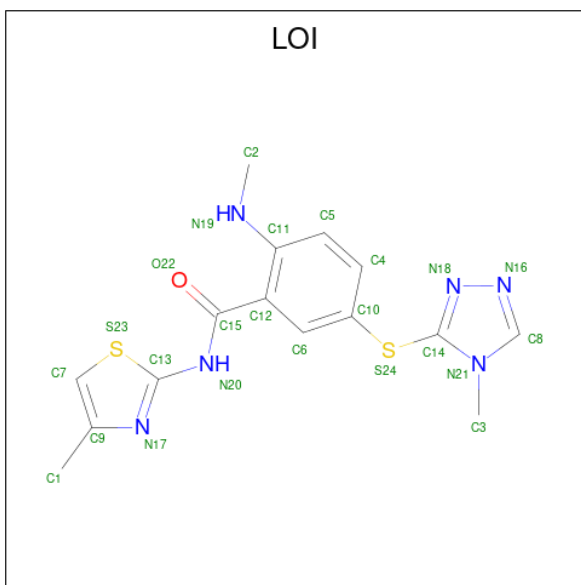
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	448	3505	2178	609	686	32	0	0	0

- Molecule 2 is alpha-D-glucopyranose (CCD ID: 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 (CCD ID: LOI) (formula: C₁₅H₁₆N₆OS₂).



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

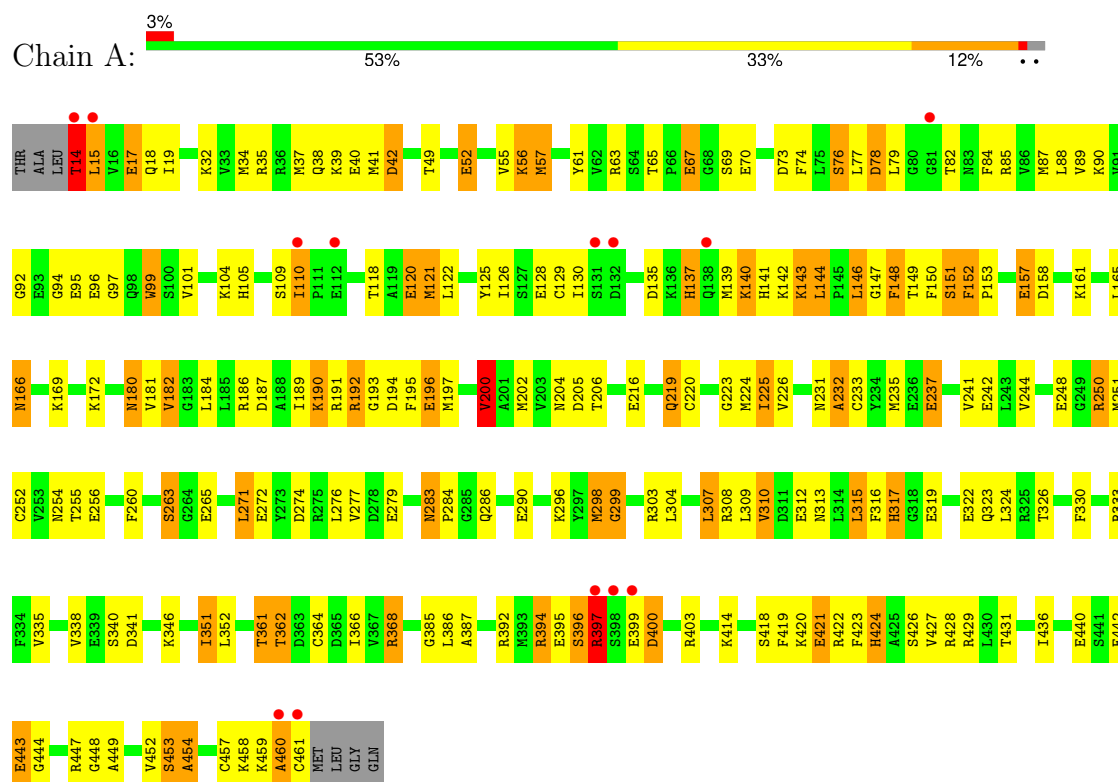
- Molecule 4 is water.

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	80.08Å 80.08Å 323.97Å 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) 99.0 (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 2.51Å)	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 , 45.3	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: LOI, GLC

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	1.71	36/3558 (1.0%)	1.62	58/4783 (1.2%)

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 (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	78	ASP	N-CA	-9.55	1.35	1.46
1	A	148	PHE	CA-C	7.11	1.60	1.52
1	A	76	SER	CA-C	-7.05	1.43	1.52
1	A	89	VAL	C-O	-6.99	1.17	1.24
1	A	436	ILE	CA-CB	-6.92	1.46	1.54
1	A	200	VAL	CA-C	6.86	1.61	1.52
1	A	149	THR	CA-C	-6.71	1.44	1.52
1	A	444	GLY	C-O	-6.71	1.15	1.23
1	A	220	CYS	C-O	-6.45	1.16	1.23
1	A	431	THR	CA-CB	6.45	1.60	1.53
1	A	14	THR	CA-CB	6.45	1.71	1.54
1	A	152	PHE	N-CA	6.35	1.51	1.45
1	A	237	GLU	CA-C	-6.29	1.44	1.52
1	A	395	GLU	CG-CD	6.20	1.67	1.52
1	A	452	VAL	CA-CB	6.14	1.62	1.54
1	A	204	ASN	CA-C	6.11	1.60	1.52
1	A	49	THR	CA-CB	6.01	1.63	1.54
1	A	397	ARG	CA-C	5.80	1.60	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	232	ALA	C-O	5.70	1.30	1.23
1	A	426	SER	CA-C	5.66	1.60	1.52
1	A	366	ILE	N-CA	-5.64	1.39	1.46
1	A	424	HIS	N-CA	5.54	1.53	1.46
1	A	57	MET	CA-C	5.52	1.59	1.53
1	A	143	LYS	C-O	5.51	1.30	1.24
1	A	362	THR	N-CA	-5.51	1.39	1.46
1	A	364	CYS	N-CA	-5.46	1.39	1.46
1	A	223	GLY	C-O	5.41	1.30	1.23
1	A	286	GLN	CA-C	5.37	1.59	1.52
1	A	226	VAL	CA-CB	5.34	1.59	1.53
1	A	241	VAL	CA-CB	5.32	1.61	1.54
1	A	403	ARG	C-O	-5.27	1.17	1.24
1	A	17	GLU	CB-CG	5.21	1.68	1.52
1	A	290	GLU	C-O	5.18	1.30	1.24
1	A	37	MET	C-O	5.15	1.30	1.24
1	A	99	TRP	CA-C	-5.08	1.46	1.53
1	A	158	ASP	N-CA	-5.06	1.40	1.46

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	442	GLU	CA-C-N	-11.38	107.78	123.03
1	A	442	GLU	C-N-CA	-11.38	107.78	123.03
1	A	152	PHE	CA-C-N	-9.26	109.83	119.83
1	A	152	PHE	C-N-CA	-9.26	109.83	119.83
1	A	255	THR	N-CA-C	-8.97	101.41	111.82
1	A	143	LYS	N-CA-C	-8.04	95.62	108.73
1	A	319	GLU	N-CA-C	7.50	121.44	108.76
1	A	308	ARG	N-CA-C	-7.46	103.12	112.90
1	A	94	GLY	N-CA-C	-7.03	100.39	112.06
1	A	157	GLU	N-CA-C	-7.00	105.00	113.97
1	A	56	LYS	CA-C-N	-6.94	112.64	122.63
1	A	56	LYS	C-N-CA	-6.94	112.64	122.63
1	A	442	GLU	N-CA-CB	6.66	119.56	110.10
1	A	144	LEU	CA-C-N	-6.61	112.96	119.90
1	A	144	LEU	C-N-CA	-6.61	112.96	119.90
1	A	15	LEU	N-CA-C	-6.54	103.80	113.61
1	A	242	GLU	N-CA-C	6.37	120.31	112.54
1	A	298	MET	CG-SD-CE	-6.35	86.94	100.90
1	A	151	SER	CB-CA-C	-6.28	103.02	111.88
1	A	121	MET	N-CA-C	-6.25	104.09	111.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	338	VAL	CB-CA-C	-6.22	103.89	112.04
1	A	436	ILE	N-CA-C	6.02	116.60	108.17
1	A	263	SER	N-CA-C	-6.00	105.27	112.59
1	A	385	GLY	N-CA-C	-5.92	105.63	112.50
1	A	346	LYS	CA-C-N	-5.74	111.55	121.66
1	A	346	LYS	C-N-CA	-5.74	111.55	121.66
1	A	97	GLY	N-CA-C	-5.70	102.81	111.42
1	A	276	LEU	N-CA-C	5.67	117.54	111.36
1	A	233	CYS	CB-CA-C	-5.60	98.41	110.45
1	A	182	VAL	CB-CA-C	-5.59	104.59	112.14
1	A	279	GLU	CB-CA-C	-5.58	101.20	110.68
1	A	137	HIS	N-CA-C	5.53	120.73	112.94
1	A	277	VAL	CB-CA-C	-5.49	104.73	112.14
1	A	260	PHE	N-CA-C	-5.47	102.30	110.23
1	A	172	LYS	N-CA-C	5.42	122.19	114.16
1	A	351	ILE	CA-C-N	-5.37	113.09	120.28
1	A	351	ILE	C-N-CA	-5.37	113.09	120.28
1	A	141	HIS	CA-C-N	-5.35	115.17	122.93
1	A	141	HIS	C-N-CA	-5.35	115.17	122.93
1	A	118	THR	N-CA-C	-5.35	102.54	110.46
1	A	225	ILE	CB-CA-C	-5.30	102.79	110.63
1	A	42	ASP	N-CA-C	5.25	117.00	111.28
1	A	387	ALA	N-CA-C	-5.23	105.64	112.23
1	A	42	ASP	CA-C-N	5.20	127.25	120.28
1	A	42	ASP	C-N-CA	5.20	127.25	120.28
1	A	299	GLY	N-CA-C	-5.19	106.36	112.64
1	A	427	VAL	N-CA-C	-5.19	105.33	110.62
1	A	310	VAL	N-CA-CB	5.17	117.56	110.54
1	A	454	ALA	N-CA-C	5.16	118.36	111.75
1	A	150	PHE	N-CA-C	-5.16	98.83	108.02
1	A	283	ASN	CA-C-N	5.14	125.94	119.98
1	A	283	ASN	C-N-CA	5.14	125.94	119.98
1	A	19	ILE	N-CA-C	5.10	115.31	110.42
1	A	96	GLU	CA-C-N	5.07	128.56	120.55
1	A	96	GLU	C-N-CA	5.07	128.56	120.55
1	A	420	LYS	CA-C-N	-5.02	113.17	120.29
1	A	420	LYS	C-N-CA	-5.02	113.17	120.29
1	A	333	ARG	N-CA-C	-5.00	106.69	112.89

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 [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	3505	0	3443	121	0
2	A	12	0	12	2	0
3	A	24	0	16	2	0
4	A	128	0	0	7	0
All	All	3669	0	3471	122	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 17.

All (122) 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:144:LEU:O	1:A:197:MET:HE1	1.45	1.17
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:197:MET:HA	1:A:197:MET:HE3	1.35	1.03
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:144:LEU:O	1:A:197:MET:CE	2.13	0.95
1:A:197:MET:HE3	1:A:197:MET:CA	1.96	0.94
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:HB3	1:A:192:ARG:HH11	1.44	0.80
1:A:144:LEU:C	1:A:197:MET:HE1	2.08	0.78
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:180:ASN:HD22	1:A:180:ASN:C	1.95	0.73
1:A:82:THR:O	1:A:110:ILE:HD11	1.89	0.72
1:A:192:ARG:HH11	1:A:192:ARG:CB	2.02	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:GLU:O	1:A:313:ASN:HB2	1.91	0.71
1:A:394:ARG:HH22	1:A:400:ASP:C	1.99	0.71
1:A:73:ASP:HB3	1:A:88:LEU:HD11	1.71	0.70
1:A:394:ARG:NH2	1:A:400:ASP:C	2.50	0.69
1:A:84:PHE:CZ	1:A:126:ILE:HG23	2.28	0.69
1:A:195:PHE:HB2	4:A:1120:HOH:O	1.94	0.67
1:A:67:GLU:O	1:A:67:GLU:CG	2.43	0.67
1:A:135:ASP:OD1	1:A:140:LYS:CE	2.43	0.67
1:A:394:ARG:NH2	1:A:400:ASP:O	2.27	0.67
1:A:224:MET:HE1	1:A:423:PHE:CZ	2.31	0.65
1:A:237:GLU:OE1	1:A:250:ARG:HD2	1.97	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:O	1:A:443:GLU:CG	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:298:MET:HE3	1:A:335:VAL:HG11	1.83	0.59
1:A:197:MET:HA	1:A:197:MET:CE	2.22	0.59
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:231:ASN:ND2	1:A:256:GLU:HA	2.20	0.57
1:A:180:ASN:C	1:A:180:ASN:ND2	2.58	0.56
1:A:263:SER:HB2	1:A:265:GLU:CD	2.27	0.56
1:A:397:ARG:NH1	4:A:1106:HOH:O	2.38	0.56
1:A:192:ARG:HB3	1:A:192:ARG:CZ	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:61:TYR:HA	1:A:251:MET:HE2	1.88	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:HH11	1:A:368:ARG:CG	2.21	0.53
1:A:135:ASP:OD1	1:A:140:LYS:NZ	2.42	0.52
1:A:41:MET:HE2	1:A:392:ARG:HD3	1.92	0.51
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:125:TYR:CE1	1:A:129:CYS:SG	3.05	0.50
1:A:361:THR:HG22	1:A:362:THR:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:63:ARG:O	3:A:1:LOI:H6	2.13	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
1:A:76:SER:HA	1:A:147:GLY:O	2.13	0.48
1:A:78:ASP:C	1:A:78:ASP:OD2	2.57	0.48
1:A:421:GLU:H	1:A:421:GLU:CD	2.21	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:135:ASP:C	1:A:137:HIS:H	2.23	0.47
1:A:414:LYS:HG2	1:A:440:GLU:OE2	2.15	0.47
1:A:180:ASN:O	1:A:181:VAL:C	2.58	0.46
1:A:224:MET:HE1	1:A:423:PHE:CE1	2.50	0.46
1:A:139:MET:O	1:A:140:LYS:C	2.58	0.46
1:A:340:SER:O	1:A:341:ASP:C	2.59	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:169:LYS:HE2	2:A:2:GLC:H2	1.96	0.46
1:A:206:THR:HG22	1:A:225:ILE:HG12	1.97	0.46
1:A:135:ASP:C	1:A:137:HIS:N	2.74	0.45
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:HA	1:A:394:ARG:HD3	1.80	0.44
1:A:85:ARG:HH11	1:A:105:HIS:CE1	2.35	0.44
1:A:120:GLU:CD	1:A:120:GLU:H	2.24	0.44
1:A:152:PHE:O	1:A:153:PRO:C	2.57	0.44
1:A:69:SER:HB2	1:A:454:ALA:O	2.18	0.43
1:A:192:ARG:C	1:A:194:ASP:H	2.18	0.43
1:A:189:ILE:HG22	1:A:190:LYS:HE3	2.01	0.43
1:A:205:ASP:OD1	2:A:2:GLC:O6	2.31	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:419:PHE:C	1:A:419:PHE:CD2	2.96	0.43
1:A:254:ASN:OD1	1:A:254:ASN:C	2.62	0.43
1:A:299:GLY:HA3	1:A:330:PHE:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:GLN:O	1:A:324:LEU:C	2.59	0.43
1:A:41:MET:CE	1:A:392:ARG:HD3	2.48	0.43
1:A:166:ASN:HD22	1:A:166:ASN:C	2.27	0.43
1:A:428:ARG:O	1:A:429:ARG:C	2.62	0.43
1:A:200:VAL:CG1	1:A:453:SER:HA	2.49	0.42
1:A:152:PHE:O	4:A:1059:HOH:O	2.21	0.42
1:A:90:LYS:HE2	1:A:90:LYS:HB2	1.63	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:315:LEU:HD13	1:A:316:PHE:CE2	2.55	0.42
1:A:368:ARG:HH11	1:A:368:ARG:HG2	1.85	0.42
1:A:424:HIS:O	1:A:428:ARG:HG3	2.19	0.41
1:A:322:GLU:O	1:A:326:THR:HG23	2.21	0.41
1:A:324:LEU:HD12	1:A:324:LEU:HA	1.91	0.41
1:A:55:VAL:HA	4:A:1004:HOH:O	2.21	0.41
1:A:351:ILE:O	1:A:352:LEU:C	2.62	0.41
1:A:74:PHE:O	1:A:88:LEU:HD12	2.21	0.41
1:A:448:GLY:O	1:A:449:ALA:C	2.64	0.41
1:A:146:LEU:HD23	1:A:146:LEU:C	2.46	0.40
1:A:184:LEU:HD23	1:A:184:LEU:HA	1.72	0.40
1:A:165:LEU:HD23	1:A:165:LEU:HA	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%)	11 21

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 ⓘ

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%)	333 (87%)	51 (13%)	4 7

All (51) 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	52	GLU
1	A	65	THR
1	A	67	GLU
1	A	95	GLU
1	A	109	SER
1	A	110	ILE
1	A	120	GLU
1	A	121	MET
1	A	122	LEU
1	A	128	GLU
1	A	140	LYS
1	A	142	LYS
1	A	146	LEU
1	A	151	SER
1	A	166	ASN

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Mol	Chain	Res	Type
1	A	180	ASN
1	A	182	VAL
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	219	GLN
1	A	248	GLU
1	A	250	ARG
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	310	VAL
1	A	315	LEU
1	A	317	HIS
1	A	361	THR
1	A	368	ARG
1	A	386	LEU
1	A	394	ARG
1	A	396	SER
1	A	400	ASP
1	A	421	GLU
1	A	443	GLU
1	A	458	LYS

Sometimes 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	137	HIS
1	A	166	ASN
1	A	180	ASN
1	A	231	ASN
1	A	337	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	GLC	A	2	-	12,12,12	1.34	1 (8%)	17,17,17	2.42	9 (52%)
3	LOI	A	1	-	26,26,26	1.18	2 (7%)	33,36,36	1.95	2 (6%)

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	-	-	0/14/14/14	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2	GLC	O2-C2	2.92	1.50	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	LOI	C12-C11	-2.69	1.36	1.41
3	A	1	LOI	C13-S23	-2.50	1.70	1.74

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	LOI	C2-N19-C11	-7.51	110.52	122.37
3	A	1	LOI	N21-C8-N16	-5.10	106.73	111.39
2	A	2	GLC	C4-C3-C2	4.78	119.23	110.83
2	A	2	GLC	C1-O5-C5	3.71	120.82	113.65
2	A	2	GLC	O5-C1-C2	-3.32	104.45	110.30
2	A	2	GLC	C3-C4-C5	-2.99	104.80	110.23
2	A	2	GLC	O4-C4-C3	-2.84	103.69	110.38
2	A	2	GLC	O2-C2-C1	2.65	115.37	109.25
2	A	2	GLC	O1-C1-C2	-2.61	101.41	108.98
2	A	2	GLC	C1-C2-C3	-2.41	105.44	110.36
2	A	2	GLC	O6-C6-C5	-2.35	103.32	111.33

There are no chirality outliers.

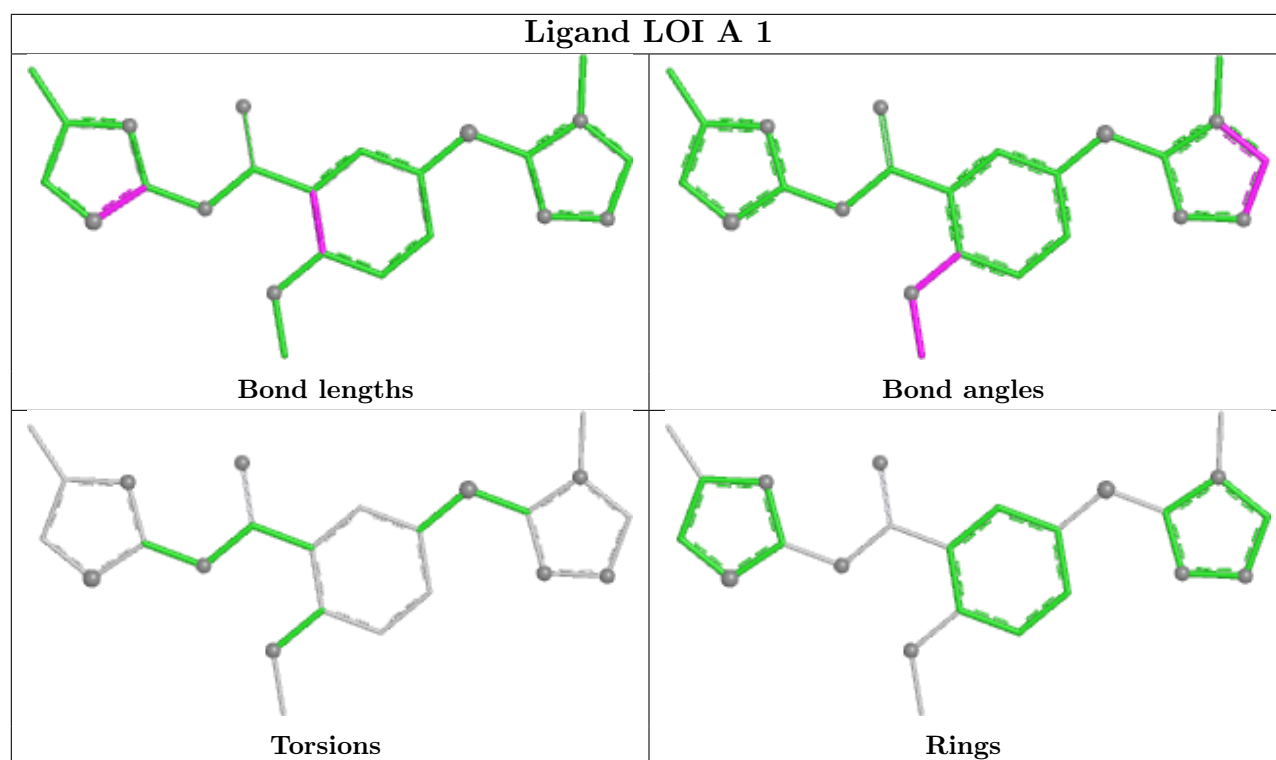
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2	GLC	2	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 [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	448/455 (98%)	-0.03	13 (2%) 53 50	9, 28, 59, 78	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	14	THR	5.6
1	A	461	CYS	3.1
1	A	399	GLU	2.9
1	A	110	ILE	2.8
1	A	81	GLY	2.5
1	A	398	SER	2.5
1	A	460	ALA	2.3
1	A	131	SER	2.2
1	A	132	ASP	2.2
1	A	138	GLN	2.1
1	A	15	LEU	2.1
1	A	397	ARG	2.1
1	A	112	GLU	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](#)

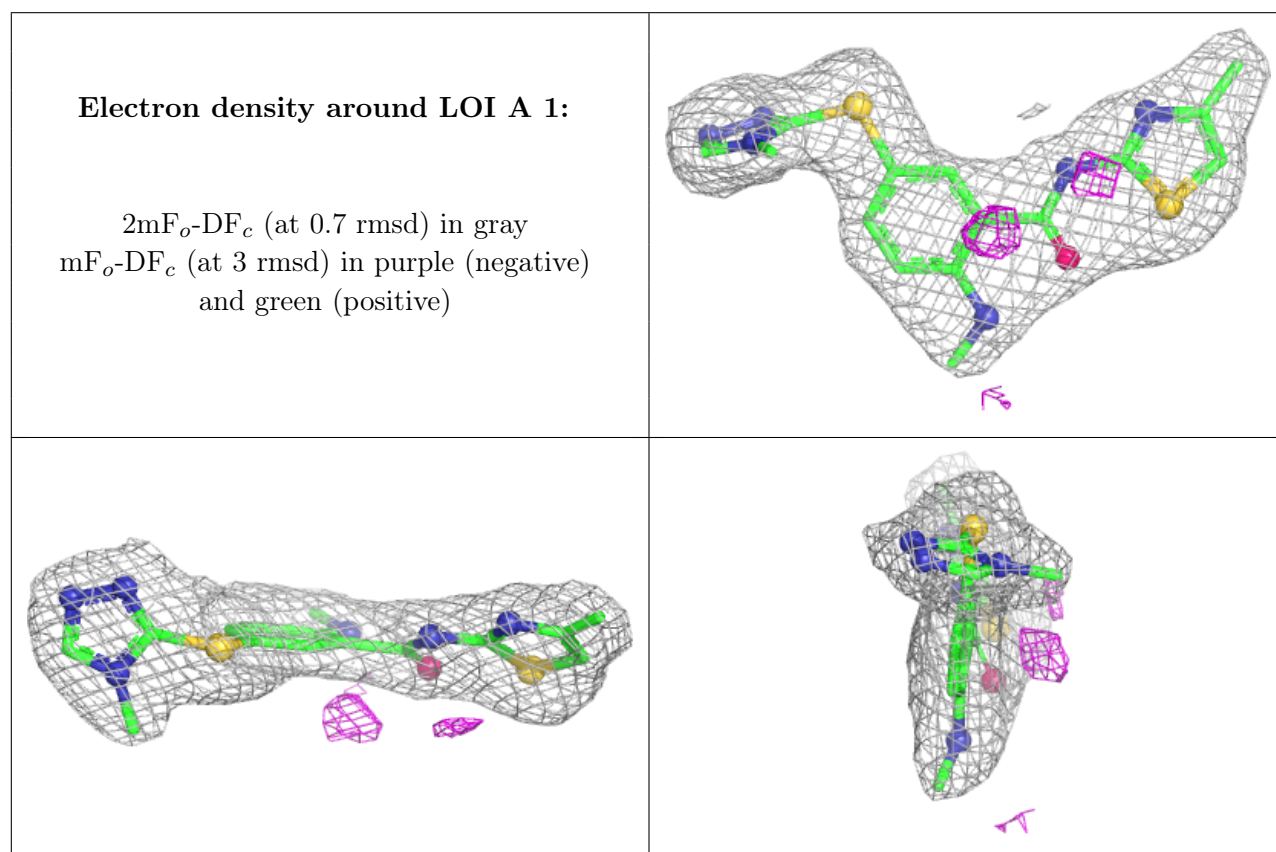
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
3	LOI	A	1	24/24	0.97	0.07	23,26,34,38	0
2	GLC	A	2	12/12	0.98	0.04	7,12,15,19	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 [i](#)

There are no such residues in this entry.