



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 04:51 PM UTC

PDB ID : 1GPJ / pdb_00001gpj
Title : Glutamyl-tRNA Reductase from Methanopyrus kandleri
Authors : Moser, J.; Schubert, W.-D.; Beier, V.; Bringemeier, I.; Jahn, D.; Heinz, D.W.
Deposited on : 2001-11-05
Resolution : 1.95 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

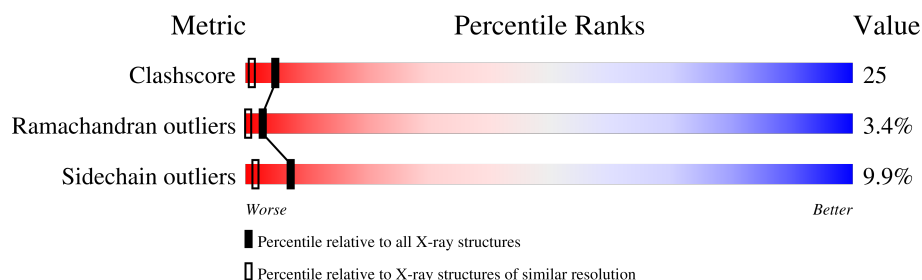
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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))
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	404	 67% 23% 5% ..

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	CIT	A	1407	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3695 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.

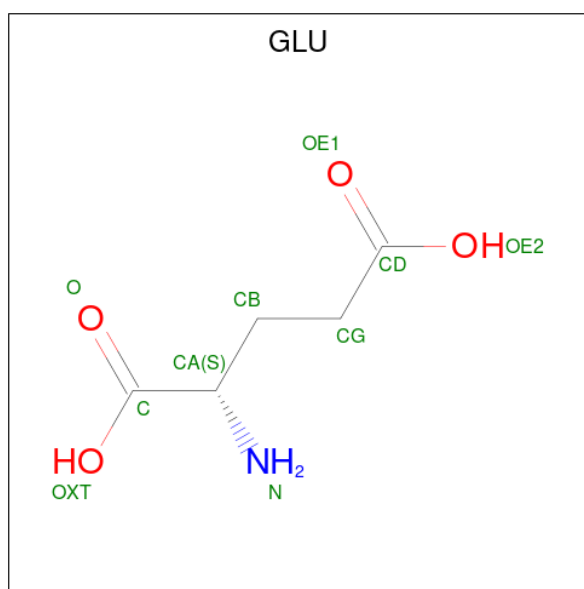
- Molecule 1 is a protein called Glutamyl-tRNA reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	399	3299	2028	623	643	5	0	17	0

There are 5 discrepancies between the modelled and reference sequences:

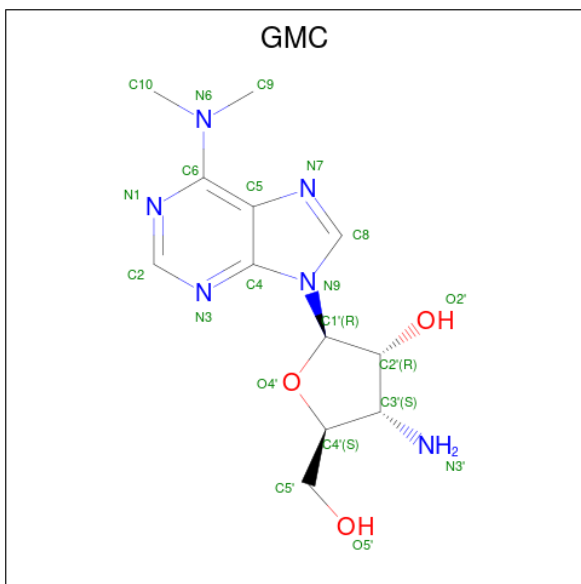
Chain	Residue	Modelled	Actual	Comment	Reference
A	6	SER	CYS	engineered mutation	UNP Q9UXR8
A	42	SER	CYS	engineered mutation	UNP Q9UXR8
A	48	SER	CYS	engineered mutation	UNP Q9UXR8
A	90	SER	CYS	engineered mutation	UNP Q9UXR8
A	393	SER	CYS	engineered mutation	UNP Q9UXR8

- Molecule 2 is GLUTAMIC ACID (CCD ID: GLU) (formula: C₅H₉NO₄).



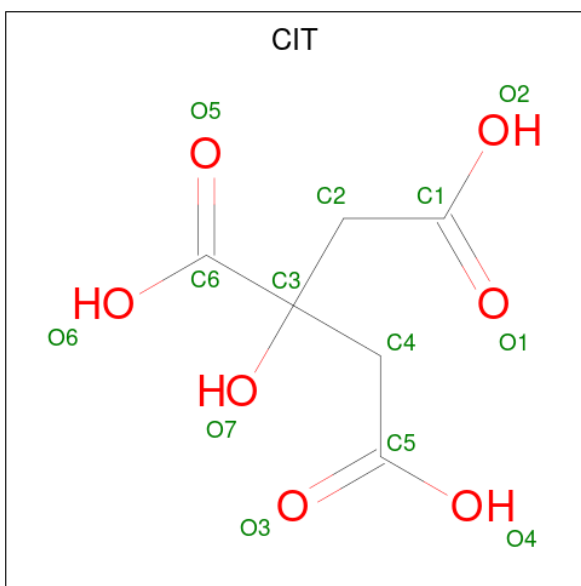
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	9	5	1	3	0	0

- Molecule 3 is (2R,3R,4S,5S)-4-AMINO-2-[6-(DIMETHYLAMINO)-9H-PURIN-9-YL]-5-(HYDROXYMETHYL)TETRAHYDRO-3-FURANOL (CCD ID: GMC) (formula: $C_{12}H_{18}N_6O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			21	12	6	3		

- Molecule 4 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 5 is water.

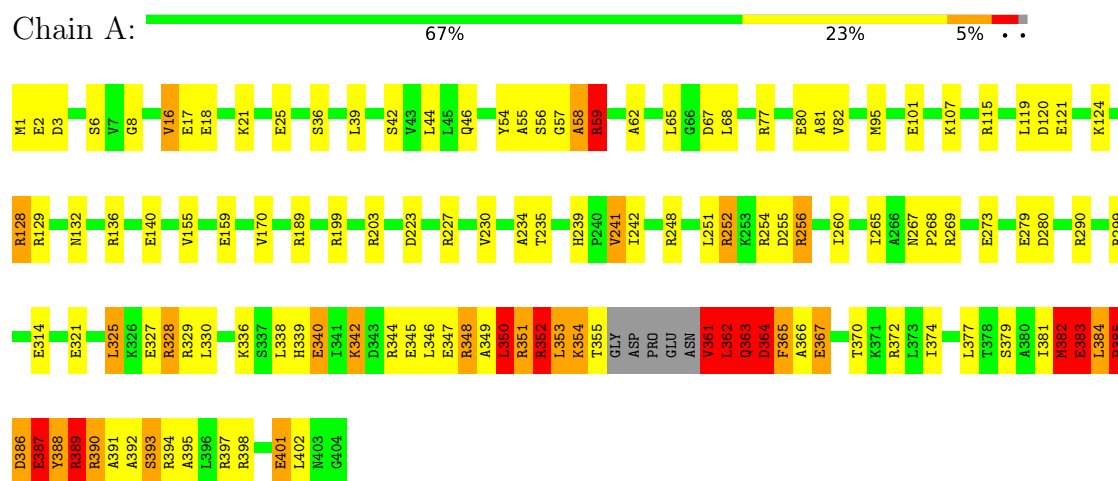
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	353	Total	O	0	3
			353	353		

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. 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. 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.

Note EDS was not executed.

• Molecule 1: Glutamyl-tRNA reductase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	78.27Å 98.65Å 68.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.00 – 1.95	Depositor
% Data completeness (in resolution range)	91.1 (69.00-1.95)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.212 , 0.262	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3695	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.03	7/3324 (0.2%)	1.35	35/4463 (0.8%)

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	5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	362	LEU	CA-C	7.13	1.62	1.52
1	A	352	ARG	CA-C	6.51	1.60	1.53
1	A	352	ARG	N-CA	6.15	1.52	1.46
1	A	374	ILE	CA-CB	-6.09	1.47	1.54
1	A	234	ALA	CA-CB	5.62	1.59	1.53
1	A	362	LEU	N-CA	5.36	1.53	1.46
1	A	95	MET	SD-CE	-5.34	1.66	1.79

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	385	PRO	N-CA-C	14.84	143.03	112.47
1	A	59	ARG	N-CA-C	13.56	129.28	113.01
1	A	382	MET	CA-C-N	11.88	143.08	121.70
1	A	382	MET	C-N-CA	11.88	143.08	121.70
1	A	382	MET	N-CA-C	11.86	125.86	111.40
1	A	363	GLN	N-CA-C	11.65	135.61	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	353	LEU	N-CA-C	-11.14	94.66	111.81
1	A	361	VAL	CA-C-O	-10.70	102.62	120.80
1	A	361	VAL	O-C-N	-10.24	106.61	123.00
1	A	367	GLU	N-CA-C	-9.04	101.50	111.36
1	A	388	TYR	CB-CA-C	-8.98	92.55	110.42
1	A	365	PHE	N-CA-C	-8.88	101.68	111.36
1	A	383	GLU	N-CA-CB	8.64	125.18	110.50
1	A	352	ARG	N-CA-C	8.60	121.52	109.31
1	A	362	LEU	CA-C-N	7.46	135.78	121.54
1	A	362	LEU	C-N-CA	7.46	135.78	121.54
1	A	383	GLU	CB-CA-C	6.99	123.38	110.10
1	A	361	VAL	CB-CA-C	-6.96	98.17	111.40
1	A	389	ARG	N-CA-C	-6.93	96.04	110.80
1	A	382	MET	CA-C-O	-6.45	113.64	120.55
1	A	350	LEU	CB-CA-C	6.33	120.81	110.88
1	A	67	ASP	N-CA-C	6.32	118.98	111.71
1	A	382	MET	O-C-N	-6.23	114.63	122.17
1	A	392	ALA	N-CA-C	-6.14	104.58	111.28
1	A	364	ASP	N-CA-CB	5.66	120.12	110.50
1	A	350	LEU	CA-CB-CG	5.57	135.78	116.30
1	A	354	LYS	CA-C-N	5.42	131.46	121.70
1	A	354	LYS	C-N-CA	5.42	131.46	121.70
1	A	8	GLY	N-CA-C	5.42	118.49	110.42
1	A	354	LYS	N-CA-C	-5.39	100.91	109.76
1	A	364	ASP	N-CA-C	-5.33	96.08	111.00
1	A	385	PRO	CA-N-CD	-5.21	104.70	112.00
1	A	372	ARG	CG-CD-NE	-5.19	100.58	112.00
1	A	377	LEU	N-CA-C	5.16	116.98	111.36
1	A	241	VAL	CB-CA-C	-5.04	105.71	110.65

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	361	VAL	Mainchain
1	A	362	LEU	Peptide
1	A	363	GLN	Peptide
1	A	383	GLU	Peptide
1	A	58	ALA	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	3299	0	3355	169	5
2	A	9	0	5	1	0
3	A	21	0	17	1	0
4	A	13	0	5	1	0
5	A	353	0	0	19	0
All	All	3695	0	3382	171	5

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 25.

All (171) 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:384[B]:LEU:HD23	1:A:385:PRO:CD	1.33	1.51
1:A:384[B]:LEU:CD2	1:A:385:PRO:CD	2.23	1.17
1:A:384[B]:LEU:HD23	1:A:385:PRO:HD3	1.18	1.13
1:A:254:ARG:HB2	1:A:256[B]:ARG:HH21	1.02	1.11
1:A:384[B]:LEU:HD23	1:A:385:PRO:HD2	1.28	1.07
1:A:329[A]:ARG:NH2	5:A:2312:HOH:O	1.87	1.04
1:A:384[B]:LEU:CD2	1:A:385:PRO:HD2	1.87	1.02
1:A:347:GLU:O	1:A:350:LEU:HG	1.61	0.99
1:A:254:ARG:HB2	1:A:256[B]:ARG:NH2	1.79	0.98
1:A:388:TYR:O	1:A:389:ARG:C	2.05	0.98
1:A:223[B]:ASP:OD1	5:A:2210:HOH:O	1.84	0.94
1:A:379:SER:O	1:A:383:GLU:HB2	1.68	0.94
1:A:254:ARG:CB	1:A:256[B]:ARG:HH21	1.83	0.92
1:A:384[B]:LEU:CD2	1:A:385:PRO:HD3	1.96	0.91
1:A:362:LEU:C	1:A:364:ASP:HB2	1.97	0.90
1:A:385:PRO:O	1:A:388:TYR:HB2	1.72	0.89
1:A:362:LEU:C	1:A:364:ASP:CB	2.46	0.88
1:A:132[B]:ASN:HD22	1:A:132[B]:ASN:C	1.83	0.86
1:A:18:GLU:OE1	1:A:21:LYS:NZ	2.08	0.86
1:A:388:TYR:C	1:A:389:ARG:O	2.17	0.85
1:A:394:ARG:HD3	5:A:2337:HOH:O	1.75	0.84
1:A:124[B]:LYS:NZ	5:A:2132:HOH:O	2.11	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:TYR:O	1:A:389:ARG:O	1.96	0.83
1:A:384[A]:LEU:HG	1:A:385:PRO:CD	2.07	0.82
1:A:363:GLN:N	1:A:364:ASP:HB2	1.93	0.82
1:A:386:ASP:HA	1:A:389:ARG:HB2	1.61	0.82
1:A:336:LYS:NZ	1:A:340[A]:GLU:OE2	2.13	0.81
1:A:390:ARG:N	1:A:393[A]:SER:OG	2.15	0.79
1:A:362:LEU:HD12	1:A:364:ASP:OD2	1.82	0.79
1:A:361:VAL:O	1:A:361:VAL:HG23	1.80	0.79
1:A:391:ALA:HA	1:A:394:ARG:HB2	1.66	0.77
1:A:339:HIS:HD2	1:A:342:LYS:NZ	1.83	0.76
1:A:384[B]:LEU:HD23	1:A:385:PRO:N	2.00	0.75
1:A:347:GLU:O	1:A:350:LEU:CG	2.34	0.74
1:A:339:HIS:CD2	1:A:342:LYS:NZ	2.57	0.73
1:A:362:LEU:C	1:A:364:ASP:HB3	2.11	0.73
1:A:18:GLU:OE1	1:A:21:LYS:CE	2.38	0.72
1:A:390:ARG:HB3	1:A:390:ARG:HH11	1.55	0.72
1:A:391:ALA:O	1:A:395:ALA:N	2.19	0.72
1:A:386:ASP:C	1:A:388:TYR:N	2.48	0.72
1:A:390:ARG:HB3	1:A:390:ARG:NH1	2.03	0.72
1:A:159:GLU:OE2	1:A:189[B]:ARG:NE	2.23	0.71
1:A:394:ARG:HG2	1:A:394:ARG:HH11	1.56	0.70
1:A:336:LYS:CG	1:A:397:ARG:HH22	2.05	0.70
1:A:381:ILE:O	1:A:389:ARG:HG2	1.93	0.68
1:A:107[B]:LYS:NZ	5:A:2119:HOH:O	2.28	0.67
1:A:402:LEU:O	5:A:2343:HOH:O	2.13	0.67
1:A:344:ARG:NH1	1:A:401:GLU:O	2.28	0.66
1:A:362:LEU:HA	1:A:364:ASP:CB	2.25	0.66
1:A:381:ILE:O	1:A:389:ARG:CG	2.43	0.65
1:A:389:ARG:O	1:A:390:ARG:CB	2.45	0.65
1:A:330:LEU:HD11	1:A:381:ILE:HG21	1.80	0.64
1:A:132[B]:ASN:C	1:A:132[B]:ASN:ND2	2.49	0.64
1:A:129:ARG:NH2	1:A:321:GLU:OE2	2.29	0.63
1:A:328:ARG:HG3	1:A:328:ARG:HH11	1.63	0.63
1:A:386:ASP:C	1:A:388:TYR:H	2.05	0.63
1:A:251:LEU:HD21	1:A:260:ILE:HD12	1.80	0.62
1:A:339:HIS:CD2	1:A:342:LYS:HZ1	2.18	0.61
1:A:59:ARG:HG2	1:A:59:ARG:O	2.00	0.61
1:A:119:LEU:HD13	1:A:124[B]:LYS:HG2	1.82	0.61
1:A:361:VAL:O	1:A:363:GLN:N	2.33	0.60
1:A:397:ARG:NH1	5:A:2339:HOH:O	2.33	0.60
1:A:119:LEU:HD13	1:A:124[A]:LYS:HG2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:LEU:HD21	1:A:260:ILE:CD1	2.32	0.59
1:A:339:HIS:HE1	5:A:2314:HOH:O	1.84	0.59
1:A:352:ARG:C	1:A:354:LYS:H	2.07	0.59
1:A:384[A]:LEU:HG	1:A:385:PRO:HD3	1.83	0.58
1:A:115:ARG:HD2	5:A:2127[A]:HOH:O	2.03	0.58
1:A:390:ARG:H	1:A:393[A]:SER:HG	1.48	0.57
1:A:252:ARG:NH2	5:A:2233:HOH:O	2.36	0.57
1:A:398:ARG:NH2	5:A:2342:HOH:O	2.37	0.57
1:A:16[B]:VAL:HG23	5:A:2020:HOH:O	2.05	0.56
1:A:136:ARG:HD2	1:A:140:GLU:OE2	2.04	0.56
1:A:267:ASN:HA	1:A:268:PRO:C	2.29	0.56
1:A:325:LEU:HD21	1:A:329[B]:ARG:HD2	1.87	0.56
1:A:279[A]:GLU:O	1:A:280:ASP:HB2	2.06	0.56
1:A:39:LEU:HD13	1:A:55:ALA:HB1	1.88	0.56
1:A:299:ARG:HD2	5:A:2274:HOH:O	2.07	0.55
1:A:279[A]:GLU:H	1:A:279[A]:GLU:CD	2.15	0.55
1:A:386:ASP:O	1:A:387:GLU:C	2.49	0.55
1:A:115:ARG:O	1:A:115:ARG:HG2	2.04	0.55
1:A:345[B]:GLU:OE1	5:A:2320:HOH:O	2.18	0.55
1:A:347:GLU:C	1:A:350:LEU:HG	2.32	0.55
1:A:339:HIS:CD2	1:A:342:LYS:HZ3	2.25	0.55
1:A:336:LYS:HG3	1:A:397:ARG:HH22	1.71	0.54
1:A:59:ARG:HD2	5:A:2007:HOH:O	2.07	0.54
1:A:339:HIS:HD2	1:A:342:LYS:HZ3	1.53	0.54
1:A:362:LEU:HA	1:A:364:ASP:HB2	1.89	0.54
1:A:6:SER:HB2	1:A:81:ALA:HB1	1.90	0.53
1:A:390:ARG:CA	1:A:393[A]:SER:OG	2.57	0.53
1:A:279[B]:GLU:O	1:A:280:ASP:HB2	2.09	0.53
1:A:385:PRO:O	1:A:388:TYR:CB	2.49	0.53
1:A:199:ARG:HH12	1:A:239:HIS:HD2	1.58	0.52
1:A:327:GLU:HA	1:A:382:MET:HE3	1.92	0.52
1:A:248:ARG:O	1:A:252:ARG:HG2	2.09	0.52
1:A:391:ALA:O	1:A:394:ARG:HB2	2.09	0.52
1:A:390:ARG:O	1:A:394:ARG:N	2.43	0.52
1:A:330:LEU:HD22	1:A:382:MET:HE2	1.93	0.51
1:A:362:LEU:CD1	1:A:364:ASP:OD2	2.58	0.51
1:A:386:ASP:O	1:A:388:TYR:N	2.43	0.51
1:A:361:VAL:CG2	1:A:363:GLN:HB2	2.41	0.50
1:A:330:LEU:CD2	1:A:382:MET:HE2	2.41	0.50
1:A:349:ALA:HA	5:A:2322:HOH:O	2.11	0.50
1:A:394:ARG:HG2	1:A:394:ARG:NH1	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:ARG:HH22	1:A:239:HIS:HB2	1.76	0.50
1:A:354:LYS:HA	1:A:355:THR:C	2.37	0.50
1:A:391:ALA:CA	1:A:394:ARG:HB2	2.39	0.50
1:A:136:ARG:NH1	1:A:140:GLU:OE1	2.45	0.50
1:A:325:LEU:CD2	1:A:329[B]:ARG:HD2	2.42	0.50
1:A:39:LEU:CD2	1:A:58:ALA:HA	2.42	0.49
1:A:361:VAL:O	1:A:361:VAL:CG2	2.35	0.49
3:A:1405:GMC:HC1	3:A:1405:GMC:N7	2.27	0.49
1:A:383:GLU:HB2	5:A:2333:HOH:O	2.12	0.49
1:A:170:VAL:HG22	1:A:230:VAL:CG1	2.42	0.49
1:A:363:GLN:CA	1:A:364:ASP:HB2	2.43	0.48
1:A:199:ARG:HH21	1:A:241:VAL:HG12	1.79	0.48
1:A:328:ARG:HH11	1:A:328:ARG:CG	2.25	0.48
1:A:362:LEU:HA	1:A:364:ASP:CG	2.39	0.47
1:A:56:SER:OG	1:A:120:ASP:OD2	2.22	0.47
1:A:364:ASP:HB3	1:A:365:PHE:H	1.48	0.47
1:A:121:GLU:OE2	1:A:328:ARG:NH2	2.43	0.47
1:A:362:LEU:HA	1:A:364:ASP:OD2	2.16	0.47
1:A:290:ARG:HH11	1:A:290:ARG:HG2	1.81	0.46
1:A:348:ARG:C	1:A:350:LEU:N	2.71	0.46
1:A:389:ARG:O	1:A:390:ARG:HB2	2.15	0.46
1:A:256[A]:ARG:HB3	1:A:256[A]:ARG:NH1	2.31	0.46
1:A:362:LEU:CA	1:A:364:ASP:HB2	2.45	0.46
1:A:223[A]:ASP:O	1:A:227:ARG:HG2	2.16	0.45
1:A:362:LEU:CA	1:A:364:ASP:CB	2.92	0.45
1:A:155:VAL:HG11	1:A:189[B]:ARG:HD3	1.97	0.45
1:A:189[A]:ARG:NH2	5:A:2181:HOH:O	2.49	0.45
1:A:254:ARG:CA	1:A:256[B]:ARG:HH21	2.29	0.45
1:A:256[B]:ARG:CZ	1:A:256[B]:ARG:H	2.29	0.45
1:A:361:VAL:HG23	1:A:363:GLN:HB2	1.97	0.45
1:A:18:GLU:OE1	1:A:21:LYS:HE3	2.16	0.45
1:A:235:THR:HG21	1:A:241:VAL:HG11	1.98	0.45
4:A:1407:CIT:C1	4:A:1407:CIT:C5	2.95	0.44
1:A:101:GLU:OE1	2:A:1406:GLU:N	2.50	0.44
1:A:330:LEU:HD21	1:A:381:ILE:HB	2.00	0.44
1:A:223[B]:ASP:O	1:A:227:ARG:HG2	2.18	0.44
1:A:124[B]:LYS:O	1:A:128:ARG:HB2	2.17	0.43
1:A:364:ASP:H	1:A:367:GLU:H	1.66	0.43
1:A:385:PRO:HB2	1:A:386:ASP:H	1.24	0.43
1:A:42:SER:HA	1:A:54:TYR:O	2.18	0.43
1:A:255:ASP:N	1:A:256[B]:ARG:NH2	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:ALA:O	1:A:394:ARG:N	2.51	0.43
1:A:124[A]:LYS:O	1:A:128:ARG:HB2	2.18	0.43
1:A:170:VAL:HG22	1:A:230:VAL:HG13	2.00	0.43
1:A:256[A]:ARG:HB3	1:A:256[A]:ARG:HH11	1.83	0.42
1:A:203:ARG:NE	1:A:203:ARG:HA	2.35	0.42
1:A:366:ALA:O	1:A:370:THR:CB	2.68	0.42
1:A:241:VAL:HG23	1:A:242:ILE:HG12	2.02	0.42
1:A:394:ARG:HB3	5:A:2338:HOH:O	2.20	0.42
1:A:342:LYS:HE2	1:A:342:LYS:HB3	1.64	0.41
1:A:62:ALA:HB3	1:A:77:ARG:HH22	1.84	0.41
1:A:3:ASP:OD1	1:A:57:GLY:N	2.53	0.41
1:A:18:GLU:OE1	1:A:18:GLU:HA	2.19	0.41
1:A:325:LEU:CD2	1:A:325:LEU:C	2.93	0.41
1:A:379:SER:O	1:A:383:GLU:CB	2.53	0.41
1:A:346:LEU:O	1:A:347:GLU:C	2.63	0.41
1:A:330:LEU:HD23	1:A:382:MET:HG2	2.03	0.41
1:A:361:VAL:O	1:A:363:GLN:HB2	2.21	0.41
1:A:1:MET:SD	1:A:82:VAL:HG21	2.61	0.41
1:A:119:LEU:HA	1:A:119:LEU:HD23	1.74	0.41
1:A:267:ASN:CA	1:A:268:PRO:C	2.92	0.41
1:A:129:ARG:CG	1:A:314:GLU:OE2	2.69	0.40
1:A:279[B]:GLU:H	1:A:279[B]:GLU:HG3	1.53	0.40
1:A:388:TYR:HB2	1:A:389:ARG:H	1.14	0.40
1:A:25:GLU:CD	1:A:25:GLU:C	2.89	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:ARG:NH2	1:A:362:LEU:CD2[2_665]	1.55	0.65
1:A:352:ARG:NH2	1:A:362:LEU:CG[2_665]	1.63	0.57
1:A:352:ARG:NH2	1:A:362:LEU:CD1[2_665]	1.95	0.25
1:A:352:ARG:CZ	1:A:362:LEU:CD2[2_665]	2.09	0.11
1:A:352:ARG:NH1	1:A:362:LEU:CD2[2_665]	2.16	0.04

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	275/404 (68%)	251 (91%)	14 (5%)	10 (4%)	2 0

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	363	GLN
1	A	364	ASP
1	A	387	GLU
1	A	389	ARG
1	A	390	ARG
1	A	383	GLU
1	A	351	ARG
1	A	16[A]	VAL
1	A	16[B]	VAL

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	350/339 (103%)	312 (89%)	38 (11%)	6 1

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	GLU

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Mol	Chain	Res	Type
1	A	36	SER
1	A	44	LEU
1	A	46	GLN
1	A	59	ARG
1	A	65	LEU
1	A	68	LEU
1	A	80[A]	GLU
1	A	80[B]	GLU
1	A	128	ARG
1	A	252	ARG
1	A	256[A]	ARG
1	A	256[B]	ARG
1	A	265	ILE
1	A	269	ARG
1	A	273	GLU
1	A	325	LEU
1	A	328	ARG
1	A	338	LEU
1	A	340[A]	GLU
1	A	340[B]	GLU
1	A	342	LYS
1	A	348	ARG
1	A	350	LEU
1	A	351	ARG
1	A	352	ARG
1	A	353	LEU
1	A	363	GLN
1	A	382	MET
1	A	384[A]	LEU
1	A	384[B]	LEU
1	A	385	PRO
1	A	386	ASP
1	A	387	GLU
1	A	389	ARG
1	A	393[A]	SER
1	A	393[B]	SER
1	A	401	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	239	HIS

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Mol	Chain	Res	Type
1	A	339	HIS
1	A	363	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 ⓘ

3 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
4	CIT	A	1407	-	12,12,12	2.04	2 (16%)	17,17,17	3.00	11 (64%)
3	GMC	A	1405	2	23,23,23	1.53	4 (17%)	31,34,34	3.01	14 (45%)
2	GLU	A	1406	3	7,8,9	1.31	0	4,9,11	0.86	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
4	CIT	A	1407	-	-	5/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GMC	A	1405	2	-	0/10/26/26	0/3/3/3
2	GLU	A	1406	3	-	0/6/7/9	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1407	CIT	C2-C3	-5.08	1.47	1.54
3	A	1405	GMC	C5-C4	4.41	1.46	1.39
4	A	1407	CIT	C3-C6	3.71	1.57	1.53
3	A	1405	GMC	C5-C6	2.81	1.48	1.41
3	A	1405	GMC	C5-N7	-2.33	1.34	1.39
3	A	1405	GMC	C8-N7	2.03	1.35	1.31

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1405	GMC	C2'-C1'-N9	8.02	133.24	113.30
4	A	1407	CIT	O6-C6-C3	6.48	125.56	113.14
3	A	1405	GMC	C5-C4-N3	-6.31	118.03	126.72
4	A	1407	CIT	O4-C5-C4	5.53	131.88	114.35
3	A	1405	GMC	O4'-C1'-N9	-5.43	97.66	108.09
3	A	1405	GMC	N3-C4-N9	4.94	135.57	127.17
3	A	1405	GMC	C2-N1-C6	4.30	122.33	111.83
3	A	1405	GMC	C2-N3-C4	4.16	122.00	111.83
3	A	1405	GMC	N1-C2-N3	-3.97	122.57	128.58
4	A	1407	CIT	O7-C3-C6	3.67	114.17	108.96
3	A	1405	GMC	C4-C5-N7	-3.52	106.56	110.58
4	A	1407	CIT	O4-C5-O3	-3.40	114.60	123.33
4	A	1407	CIT	O3-C5-C4	-3.34	113.49	122.95
4	A	1407	CIT	C4-C3-C6	3.11	116.91	110.03
4	A	1407	CIT	C3-C2-C1	-2.87	106.06	113.92
3	A	1405	GMC	C1'-N9-C8	-2.85	120.76	127.09
4	A	1407	CIT	C2-C3-C6	-2.85	103.74	110.03
3	A	1405	GMC	O4'-C4'-C5'	2.59	114.69	109.22
3	A	1405	GMC	C4-N9-C8	2.49	108.35	105.74
3	A	1405	GMC	C5-N7-C8	2.47	107.34	103.45
4	A	1407	CIT	O5-C6-C3	-2.40	117.44	122.09
3	A	1405	GMC	O4'-C4'-C3'	-2.38	100.75	104.22
4	A	1407	CIT	O7-C3-C2	-2.32	104.08	109.38
3	A	1405	GMC	O2'-C2'-C1'	2.18	117.62	110.10
4	A	1407	CIT	O6-C6-O5	-2.14	117.00	123.86

There are no chirality outliers.

All (5) torsion outliers are listed below:

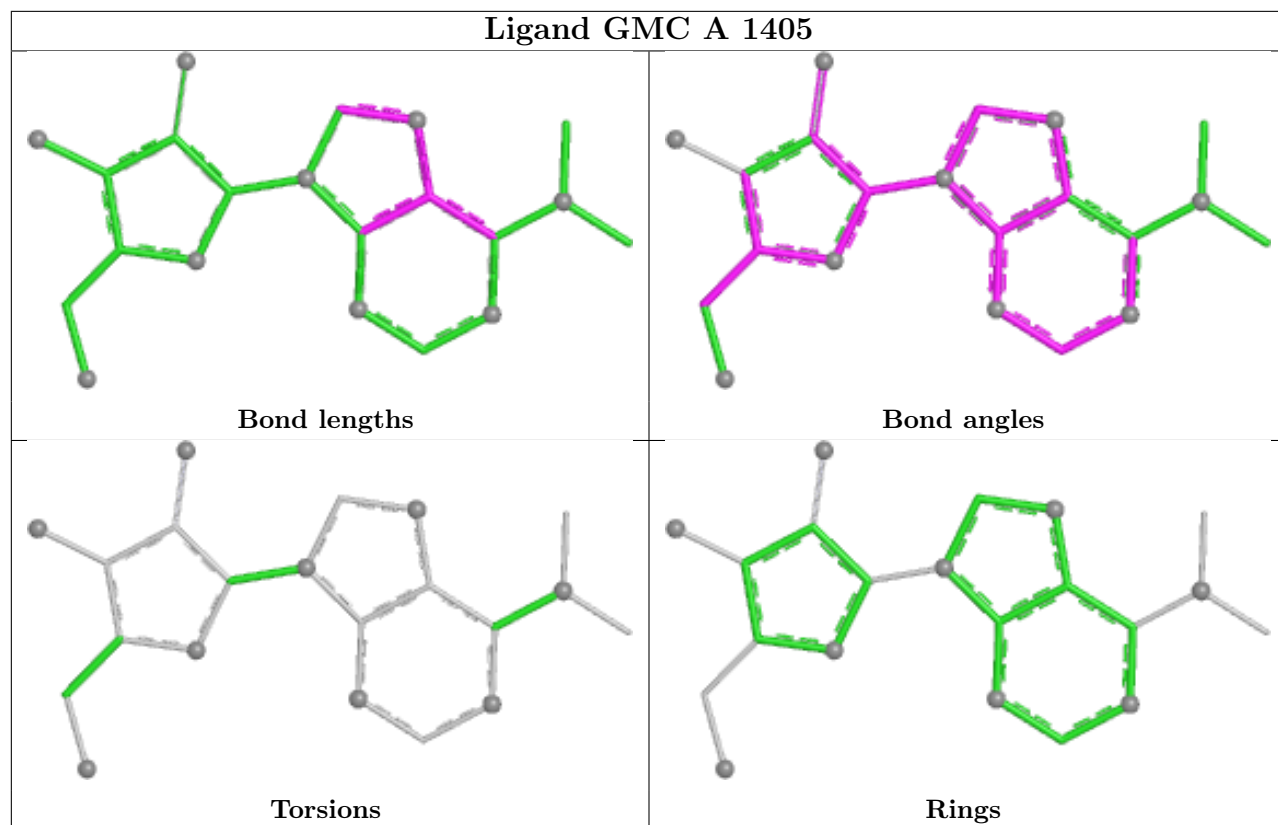
Mol	Chain	Res	Type	Atoms
4	A	1407	CIT	O7-C3-C4-C5
4	A	1407	CIT	C2-C3-C4-C5
4	A	1407	CIT	C6-C3-C4-C5
4	A	1407	CIT	C3-C4-C5-O4
4	A	1407	CIT	C3-C4-C5-O3

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1407	CIT	1	0
3	A	1405	GMC	1	0
2	A	1406	GLU	1	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.