



Full wwPDB EM Validation Report ⓘ

Oct 8, 2023 – 12:44 AM JST

PDB ID : 8JD2
EMDB ID : EMD-36173
Title : Cryo-EM structure of G protein-free mGlu2-mGlu3 heterodimer in Acc state
Authors : Wang, X.; Wang, M.; Xu, T.; Feng, Y.; Han, S.; Lin, S.; Zhao, Q.; Wu, B.
Deposited on : 2023-05-12
Resolution : 2.80 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

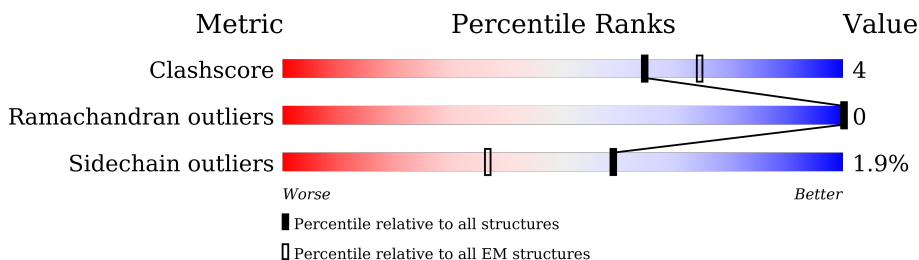
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	2	993	68% (green), 7% (yellow), 24% (grey)
2	3	993	67% (green), 8% (yellow), 25% (grey)

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10730 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Metabotropic glutamate receptor 2,Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	2	750	5258	3306	940	978	34	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	9	ASP	-	expression tag	UNP Q14416
2	10	TYR	-	expression tag	UNP Q14416
2	11	LYS	-	expression tag	UNP Q14416
2	12	ASP	-	expression tag	UNP Q14416
2	13	ASP	-	expression tag	UNP Q14416
2	14	ASP	-	expression tag	UNP Q14416
2	15	ASP	-	expression tag	UNP Q14416
2	16	GLY	-	expression tag	UNP Q14416
2	17	ALA	-	expression tag	UNP Q14416
2	18	PRO	-	expression tag	UNP Q14416
2	873	LEU	-	linker	UNP Q14416
2	874	GLU	-	linker	UNP Q14416
2	875	VAL	-	linker	UNP Q14416
2	876	LEU	-	linker	UNP Q14416
2	877	PHE	-	linker	UNP Q14416
2	878	GLN	-	linker	UNP Q14416
2	879	GLY	-	linker	UNP Q14416
2	880	PRO	-	linker	UNP Q14416
2	988	PHE	-	expression tag	UNP P62942
2	989	ALA	-	expression tag	UNP P62942
2	990	ALA	-	expression tag	UNP P62942
2	991	ALA	-	expression tag	UNP P62942
2	992	HIS	-	expression tag	UNP P62942
2	993	HIS	-	expression tag	UNP P62942
2	994	HIS	-	expression tag	UNP P62942
2	995	HIS	-	expression tag	UNP P62942
2	996	HIS	-	expression tag	UNP P62942

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Chain	Residue	Modelled	Actual	Comment	Reference
2	997	HIS	-	expression tag	UNP P62942
2	998	HIS	-	expression tag	UNP P62942
2	999	HIS	-	expression tag	UNP P62942
2	1000	HIS	-	expression tag	UNP P62942
2	1001	HIS	-	expression tag	UNP P62942

- Molecule 2 is a protein called Metabotropic glutamate receptor 3, Serine/threonine-protein kinase mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	3	749	5424	3417	941	1030	36	0	0

There are 41 discrepancies between the modelled and reference sequences:

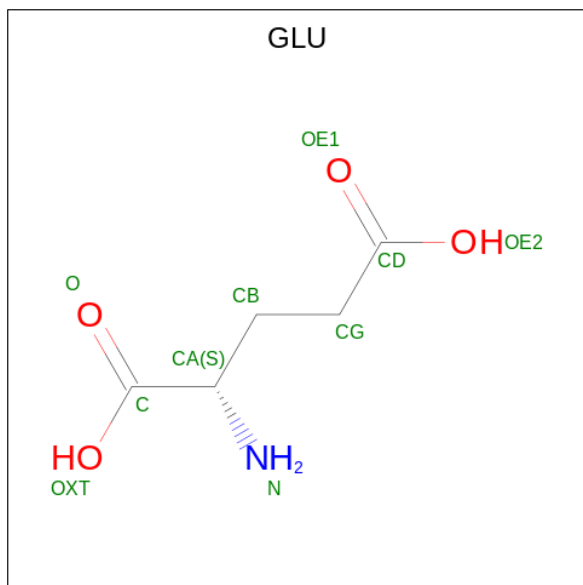
Chain	Residue	Modelled	Actual	Comment	Reference
3	-8	ASP	-	expression tag	UNP Q14832
3	-7	TYR	-	expression tag	UNP Q14832
3	-6	LYS	-	expression tag	UNP Q14832
3	-5	ASP	-	expression tag	UNP Q14832
3	-4	ASP	-	expression tag	UNP Q14832
3	-3	ASP	-	expression tag	UNP Q14832
3	-2	ASP	-	expression tag	UNP Q14832
3	-1	LYS	-	expression tag	UNP Q14832
3	0	GLY	-	expression tag	UNP Q14832
3	1	ALA	-	expression tag	UNP Q14832
3	2	PRO	-	expression tag	UNP Q14832
3	3	TRP	-	expression tag	UNP Q14832
3	4	SER	-	expression tag	UNP Q14832
3	5	HIS	-	expression tag	UNP Q14832
3	6	PRO	-	expression tag	UNP Q14832
3	7	GLN	-	expression tag	UNP Q14832
3	8	PHE	-	expression tag	UNP Q14832
3	9	GLU	-	expression tag	UNP Q14832
3	10	LYS	-	expression tag	UNP Q14832
3	11	GLY	-	expression tag	UNP Q14832
3	12	SER	-	expression tag	UNP Q14832
3	13	GLY	-	expression tag	UNP Q14832
3	14	SER	-	expression tag	UNP Q14832
3	15	TRP	-	expression tag	UNP Q14832
3	16	SER	-	expression tag	UNP Q14832
3	17	HIS	-	expression tag	UNP Q14832

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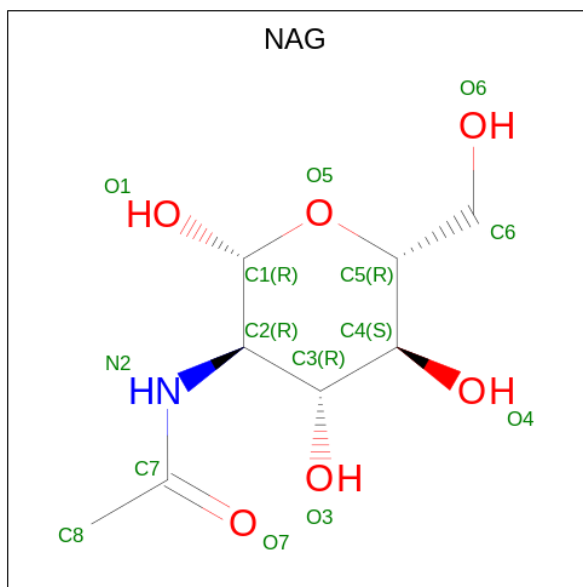
Chain	Residue	Modelled	Actual	Comment	Reference
3	18	PRO	-	expression tag	UNP Q14832
3	19	GLN	-	expression tag	UNP Q14832
3	20	PHE	-	expression tag	UNP Q14832
3	21	GLU	-	expression tag	UNP Q14832
3	22	LYS	-	expression tag	UNP Q14832
3	880	LEU	-	linker	UNP Q14832
3	881	GLU	-	linker	UNP Q14832
3	882	VAL	-	linker	UNP Q14832
3	883	LEU	-	linker	UNP Q14832
3	884	PHE	-	linker	UNP Q14832
3	885	GLN	-	linker	UNP Q14832
3	886	GLY	-	linker	UNP Q14832
3	887	PRO	-	linker	UNP Q14832
3	983	GLU	-	expression tag	UNP A0A8V8TRG9
3	984	PHE	-	expression tag	UNP A0A8V8TRG9

- Molecule 3 is GLUTAMIC ACID (three-letter code: GLU) (formula: C₅H₉NO₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
3	2	1	10	5	1	4	0
3	3	1	10	5	1	4	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

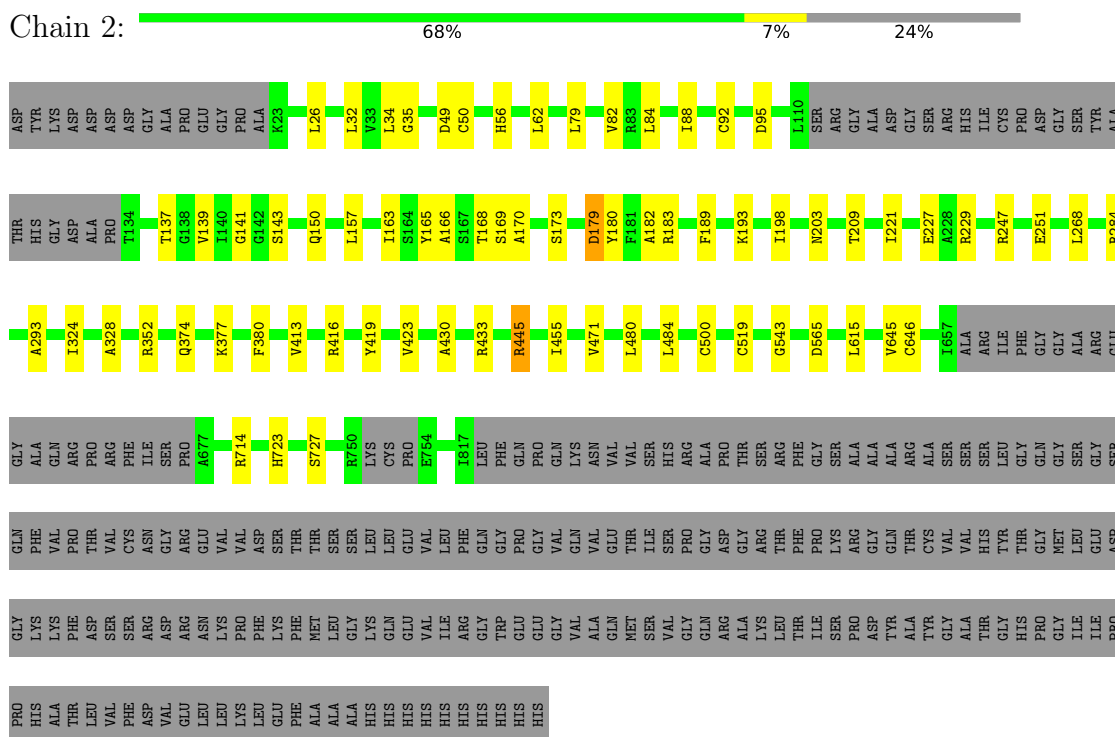


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	2	1	Total	C	N	O	0
			14	8	1	5	
4	3	1	Total	C	N	O	0
			14	8	1	5	

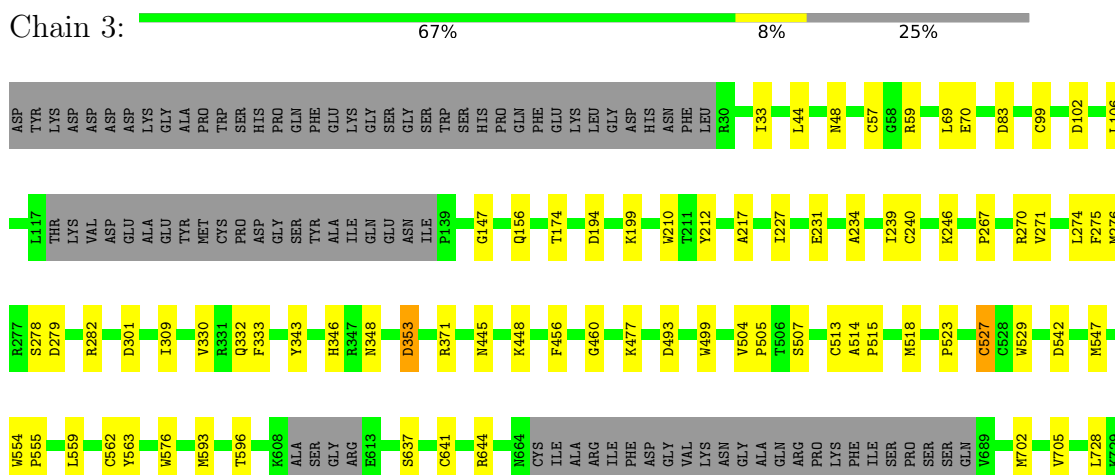
3 Residue-property plots [i](#)

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. 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.

- Molecule 1: Metabotropic glutamate receptor 2, Peptidyl-prolyl cis-trans isomerase FKBP1A



- Molecule 2: Metabotropic glutamate receptor 3, Serine/threonine-protein kinase mTOR



C730	LEU	ASP	LEU
T774	SER	LYS	GLU
M775	THR	THR	THR
T778	SER	SER	PHE
L786	LEU	ASN	GLN
P787	LEU	GLN	ALA
T801	VAL	TYR	TYR
C817	LEU	GLY	GLY
L827	PHE	ASP	ASP

PHE	THR	THR	THR
GLN	PRO	GLU	GLU
PRO	GLN	LEU	LEU
LYS	ASN	GLY	GLY
ASN	VAL	HIS	HIS
VAL	VAL	MET	MET
THR	THR	LYS	LYS
HIS	HIS	TYR	TYR
ARG	ARG	MET	MET
LEU	LEU	GLY	GLY
HIS	HIS	LEU	LEU
LEU	LEU	GLY	GLY
LEU	LEU	ASN	ASN
ASN	ASN	VAL	VAL
ARG	ARG	LYS	LYS
PHE	PHE	ASP	ASP
SER	SER	LEU	LEU
VAL	VAL	THR	THR
GLY	GLY	GLN	GLN
THR	THR	ALA	ALA
THR	THR	TRP	TRP
GLY	GLY	ASP	ASP
THR	THR	LEU	LEU
THR	THR	TYR	TYR
TYR	TYR	TYR	TYR
SER	SER	HIS	HIS
GLN	GLN	VAL	VAL
SER	SER	ARG	ARG
SER	SER	ARG	ARG
ALA	ALA	ILE	ILE
SER	SER	SER	SER
THR	THR	LYS	LYS
TYR	TYR	GLN	GLN
VAL	VAL	GLU	GLU
PRO	PRO	PHE	PHE
THR	THR	THR	THR
VAL	VAL	THR	THR
CYS	CYS	MET	MET
ASN	ASN	GLU	GLU
ARG	ARG	GLY	GLY
PRO	PRO	GLN	GLN
GLU	GLU	THR	THR
VAL	VAL	LEU	LEU

LEU	LEU	LEU	LEU
LYS	LYS	LYS	LYS
THR	THR	THR	THR
SER	SER	SER	SER
PHE	PHE	PHE	PHE
ASN	ASN	ASN	ASN
GLN	GLN	GLN	GLN
ALA	ALA	ALA	ALA
TYR	TYR	TYR	TYR
GLY	GLY	GLY	GLY
ARG	ARG	ARG	ARG
ASP	ASP	ASP	ASP
LEU	LEU	LEU	LEU
MET	MET	MET	MET
GLU	GLU	GLU	GLU
ALA	ALA	ALA	ALA
GLN	GLN	GLN	GLN
GLY	GLY	GLY	GLY
TRP	TRP	TRP	TRP
CYS	CYS	CYS	CYS
GLU	GLU	GLU	GLU
ARG	ARG	ARG	ARG
LYS	LYS	LYS	LYS
TYR	TYR	TYR	TYR
HIS	HIS	HIS	HIS
GLY	GLY	GLY	GLY
LEU	LEU	LEU	LEU
ASN	ASN	ASN	ASN
VAL	VAL	VAL	VAL
LYS	LYS	LYS	LYS
ASP	ASP	ASP	ASP
LEU	LEU	LEU	LEU
THR	THR	THR	THR
GLN	GLN	GLN	GLN
ALA	ALA	ALA	ALA
TRP	TRP	TRP	TRP
ASP	ASP	ASP	ASP
LEU	LEU	LEU	LEU
TYR	TYR	TYR	TYR
TYR	TYR	TYR	TYR
HIS	HIS	HIS	HIS
VAL	VAL	VAL	VAL
PHE	PHE	PHE	PHE
ARG	ARG	ARG	ARG
ARG	ARG	ARG	ARG
ILE	ILE	ILE	ILE
SER	SER	SER	SER
LYS	LYS	LYS	LYS
GLN	GLN	GLN	GLN
GLU	GLU	GLU	GLU
PHE	PHE	PHE	PHE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	890025	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

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: NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2	0.24	0/5367	0.46	0/7336
2	3	0.24	0/5529	0.46	0/7541
All	All	0.24	0/10896	0.46	0/14877

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	5258	0	4689	42	0
2	3	5424	0	4934	45	0
3	2	10	0	5	2	0
3	3	10	0	5	1	0
4	2	14	0	13	1	0
4	3	14	0	13	0	0
All	All	10730	0	9659	86	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 4.

All (86) 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)
1:2:445:ARG:HD3	1:2:445:ARG:H	1.55	0.71
1:2:328:ALA:HB2	1:2:374:GLN:HE21	1.62	0.65
1:2:430:ALA:HB3	1:2:433:ARG:HB3	1.79	0.64
1:2:35:GLY:HA3	1:2:139:VAL:HG12	1.78	0.63
1:2:198:ILE:HD11	1:2:455:ILE:HD12	1.83	0.61
2:3:343:TYR:O	2:3:346:HIS:NE2	2.34	0.61
2:3:641:CYS:HA	2:3:644:ARG:HE	1.65	0.61
1:2:26:LEU:HD22	1:2:88:ILE:HD12	1.82	0.59
1:2:251:GLU:OE2	1:2:284:ARG:NH1	2.33	0.58
1:2:163:ILE:HG12	1:2:182:ALA:HB3	1.87	0.57
1:2:209:THR:HB	1:2:221:ILE:HD11	1.89	0.55
1:2:157:LEU:HD11	2:3:106:LEU:HG	1.88	0.55
2:3:523:PRO:HD3	2:3:529:TRP:HA	1.89	0.54
1:2:324:ILE:O	1:2:374:GLN:NE2	2.38	0.54
1:2:32:LEU:HD22	1:2:137:THR:HG21	1.90	0.54
1:2:168:THR:HG1	3:2:1101:GLU:N	2.06	0.54
2:3:70:GLU:OE2	2:3:348:ASN:ND2	2.43	0.52
2:3:48:ASN:HB3	2:3:57:CYS:HB2	1.92	0.52
2:3:274:LEU:HD22	2:3:276:MET:HE2	1.92	0.52
1:2:169:SER:O	1:2:183:ARG:NH2	2.34	0.51
2:3:301:ASP:OD2	3:3:1001:GLU:N	2.43	0.51
1:2:543:GLY:O	1:2:714:ARG:NH2	2.41	0.51
1:2:419:TYR:HA	1:2:423:VAL:HB	1.93	0.50
1:2:170:ALA:O	1:2:173:SER:OG	2.29	0.50
2:3:554:TRP:O	2:3:563:TYR:N	2.44	0.49
1:2:615:LEU:HD21	1:2:645:VAL:HG11	1.94	0.49
1:2:95:ASP:HB2	1:2:150:GLN:HG3	1.95	0.48
2:3:282:ARG:HA	2:3:309:ILE:HG23	1.94	0.48
2:3:593:MET:O	2:3:596:THR:OG1	2.29	0.48
2:3:102:ASP:OD1	2:3:102:ASP:N	2.44	0.48
1:2:247:ARG:O	1:2:251:GLU:HG2	2.14	0.47
2:3:445:ASN:HD21	2:3:448:LYS:HD2	1.78	0.47
1:2:180:TYR:HE1	1:2:416:ARG:HA	1.79	0.47
2:3:637:SER:HB3	2:3:641:CYS:HB3	1.97	0.47
1:2:143:SER:HA	1:2:166:ALA:HB3	1.97	0.47
2:3:330:VAL:HG12	2:3:333:PHE:H	1.80	0.47
2:3:774:THR:HG21	2:3:817:CYS:HB2	1.96	0.47
1:2:79:LEU:HD22	1:2:82:VAL:HB	1.97	0.47
1:2:723:HIS:O	1:2:727:SER:N	2.49	0.46
1:2:193:LYS:NZ	1:2:227:GLU:OE2	2.37	0.46
1:2:50:CYS:HB3	1:2:92:CYS:HB3	1.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:353:ASP:OD1	2:3:353:ASP:N	2.49	0.46
1:2:189:PHE:CZ	1:2:193:LYS:HE2	2.51	0.46
2:3:174:THR:O	2:3:194:ASP:N	2.48	0.46
2:3:212:TYR:O	2:3:507:SER:OG	2.27	0.45
2:3:57:CYS:HB3	2:3:99:CYS:HB3	1.49	0.45
2:3:240:CYS:HB2	2:3:527:CYS:HB3	1.66	0.45
2:3:775:MET:O	2:3:778:THR:OG1	2.31	0.45
1:2:166:ALA:O	3:2:1101:GLU:N	2.50	0.45
2:3:217:ALA:HB3	2:3:246:LYS:HZ3	1.82	0.44
2:3:234:ALA:HB1	2:3:239:ILE:HB	1.99	0.44
1:2:62:LEU:HD13	1:2:88:ILE:HG21	1.99	0.44
2:3:542:ASP:OD1	2:3:542:ASP:N	2.51	0.43
2:3:210:TRP:HZ2	2:3:505:PRO:HD2	1.82	0.43
1:2:471:VAL:HG12	1:2:484:LEU:HB3	2.00	0.43
2:3:199:LYS:HB3	2:3:199:LYS:HE2	1.86	0.43
2:3:210:TRP:CD2	2:3:271:VAL:HG21	2.54	0.43
2:3:499:TRP:NE1	2:3:504:VAL:HG22	2.34	0.43
2:3:513:CYS:HB3	2:3:518:MET:SD	2.58	0.43
2:3:555:PRO:HA	2:3:562:CYS:HA	2.00	0.43
2:3:576:TRP:HE3	2:3:801:THR:HG21	1.84	0.43
2:3:786:LEU:HB3	2:3:787:PRO:HD3	2.00	0.43
1:2:95:ASP:OD2	1:2:95:ASP:N	2.39	0.42
1:2:455:ILE:HG21	1:2:480:LEU:HD21	2.01	0.42
2:3:279:ASP:N	2:3:279:ASP:OD1	2.52	0.42
2:3:702:MET:HA	2:3:705:VAL:HG23	2.01	0.42
2:3:33:ILE:HD12	2:3:69:LEU:HD11	2.01	0.42
2:3:102:ASP:HB2	2:3:156:GLN:HG3	2.00	0.42
1:2:141:GLY:HA2	1:2:165:TYR:HE2	1.83	0.42
1:2:203:ASN:OD1	4:2:1102:NAG:N2	2.52	0.42
2:3:44:LEU:H	2:3:147:GLY:HA3	1.84	0.42
1:2:137:THR:HB	1:2:413:VAL:HG11	2.02	0.42
2:3:246:LYS:HB2	2:3:246:LYS:HE2	1.79	0.42
2:3:728:LEU:HD12	2:3:730:CYS:H	1.85	0.42
1:2:49:ASP:OD1	1:2:49:ASP:N	2.52	0.41
1:2:268:LEU:HD12	1:2:293:ALA:HB2	2.02	0.41
2:3:456:PHE:HB3	2:3:460:GLY:HA2	2.03	0.41
1:2:179:ASP:OD2	1:2:179:ASP:N	2.54	0.41
1:2:377:LYS:HA	1:2:380:PHE:HD2	1.84	0.41
2:3:227:ILE:O	2:3:231:GLU:HG2	2.20	0.41
2:3:332:GLN:OE1	2:3:332:GLN:N	2.45	0.41
2:3:514:ALA:HA	2:3:515:PRO:HD3	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:44:LEU:HB2	2:3:147:GLY:HA3	2.03	0.40
1:2:34:LEU:HG	1:2:84:LEU:HD22	2.04	0.40
1:2:500:CYS:HB3	1:2:519:CYS:HB3	1.47	0.40
1:2:565:ASP:OD1	1:2:565:ASP:N	2.55	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 PDB entries followed by that with respect to all EM entries.

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	2	742/993 (75%)	712 (96%)	30 (4%)	0	100	100
2	3	741/993 (75%)	698 (94%)	43 (6%)	0	100	100
All	All	1483/1986 (75%)	1410 (95%)	73 (5%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	2	465/813 (57%)	459 (99%)	6 (1%)	69	91
2	3	523/867 (60%)	510 (98%)	13 (2%)	47	80
All	All	988/1680 (59%)	969 (98%)	19 (2%)	59	85

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	2	56	HIS
1	2	179	ASP
1	2	229	ARG
1	2	352	ARG
1	2	445	ARG
1	2	646	CYS
2	3	59	ARG
2	3	83	ASP
2	3	267	PRO
2	3	270	ARG
2	3	275	PHE
2	3	278	SER
2	3	353	ASP
2	3	371	ARG
2	3	477	LYS
2	3	493	ASP
2	3	527	CYS
2	3	547	MET
2	3	559	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GLU	2	1101	-	8,9,9	1.03	0	10,11,11	1.19	0
4	NAG	3	1002	2	14,14,15	0.63	1 (7%)	17,19,21	0.78	0
3	GLU	3	1001	-	8,9,9	1.03	0	10,11,11	1.19	0
4	NAG	2	1102	1	14,14,15	0.58	0	17,19,21	0.76	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLU	2	1101	-	-	2/9/9/9	-
4	NAG	3	1002	2	-	4/6/23/26	0/1/1/1
3	GLU	3	1001	-	-	2/9/9/9	-
4	NAG	2	1102	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	3	1002	NAG	O5-C1	-2.15	1.40	1.43

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	3	1002	NAG	C4-C5-C6-O6
4	3	1002	NAG	O5-C5-C6-O6
4	2	1102	NAG	C3-C2-N2-C7
4	3	1002	NAG	C3-C2-N2-C7
3	2	1101	GLU	OE2-CD-CG-CB
3	2	1101	GLU	OE1-CD-CG-CB

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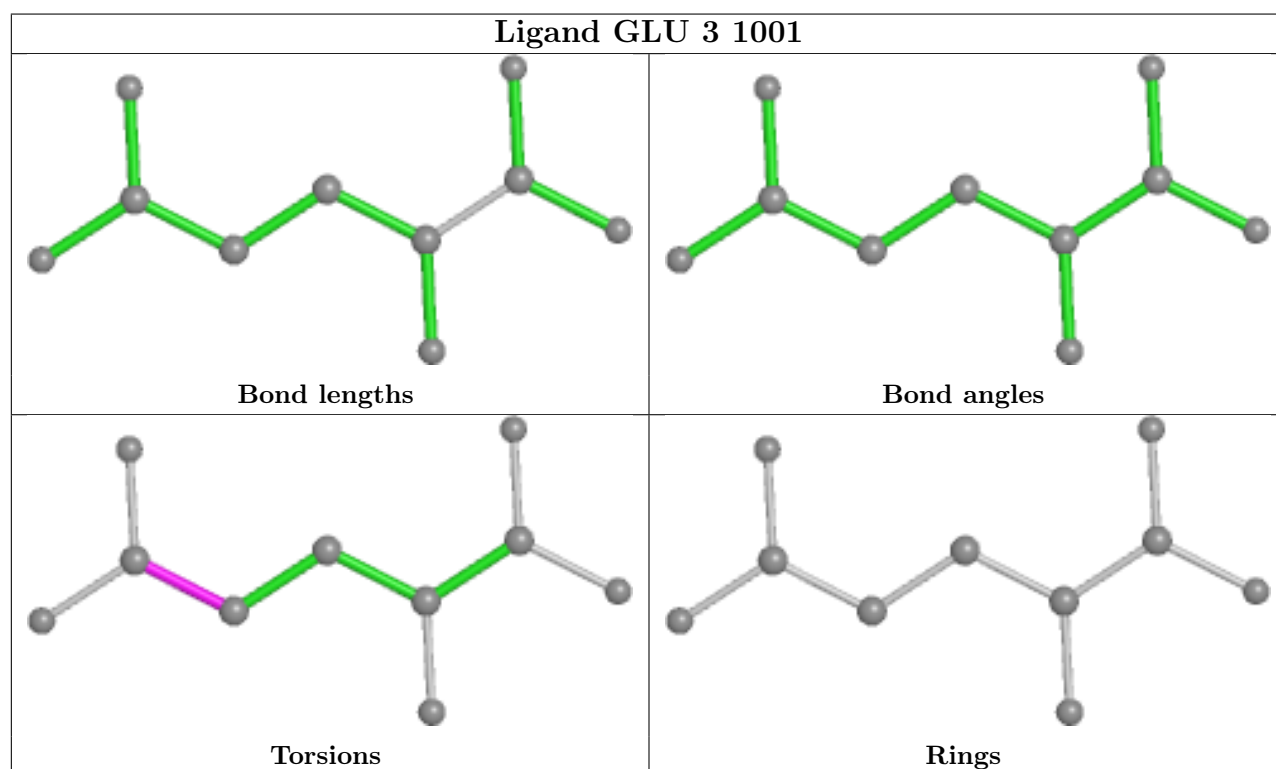
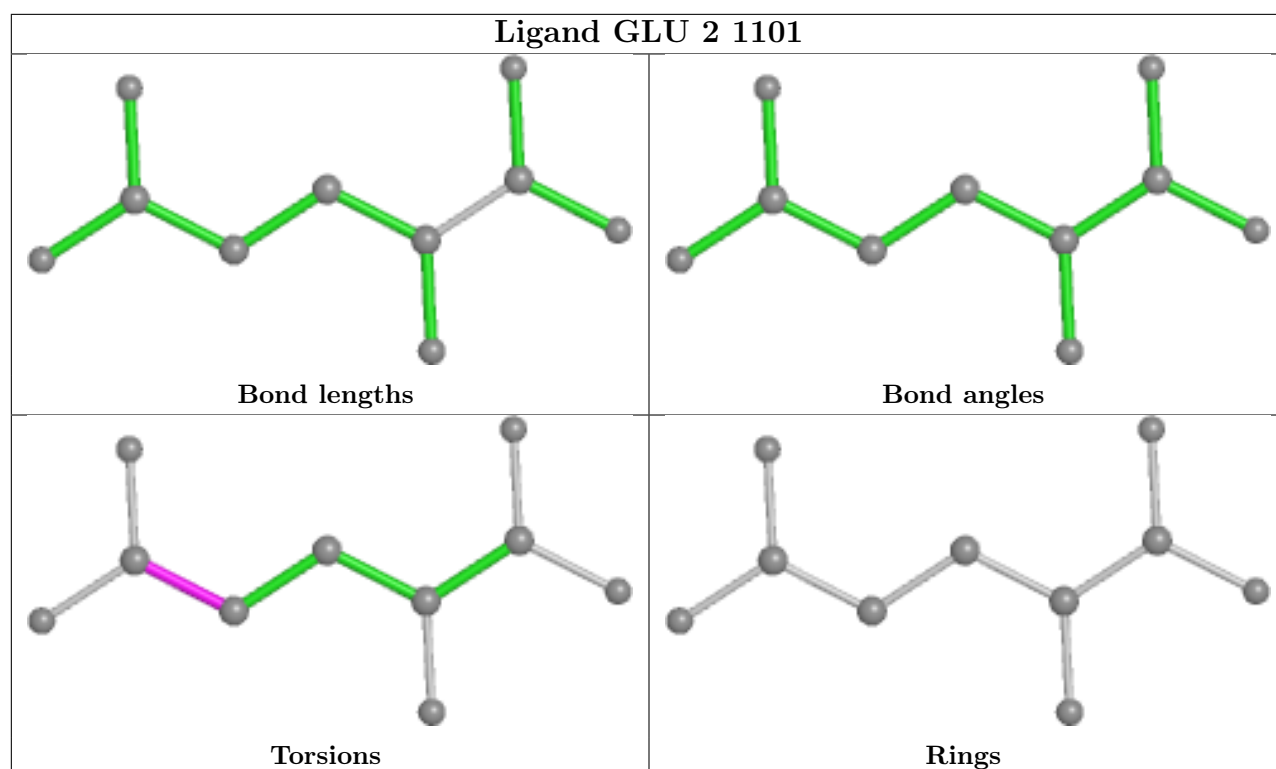
Mol	Chain	Res	Type	Atoms
4	2	1102	NAG	C1-C2-N2-C7
3	3	1001	GLU	OE1-CD-CG-CB
3	3	1001	GLU	OE2-CD-CG-CB
4	3	1002	NAG	C1-C2-N2-C7

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	2	1101	GLU	2	0
3	3	1001	GLU	1	0
4	2	1102	NAG	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

There are no chain breaks in this entry.