



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:42 PM UTC

PDB ID : 6SVQ / pdb_00006svq
Title : Crystal structure of human GFAT-1 G461E after UDP-GlcNAc soaking
Authors : Ruegenberg, S.; Horn, M.; Pichlo, C.; Allmeroth, K.; Baumann, U.; Denzel, M.S.
Deposited on : 2019-09-18
Resolution : 2.72 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

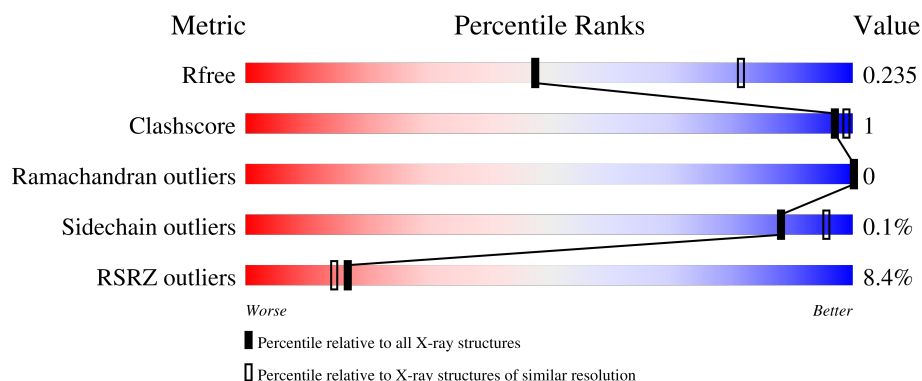
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.72 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	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)

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	687	2% 93% • 5%
1	B	687	13% 90% • 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20533 atoms, of which 10263 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.

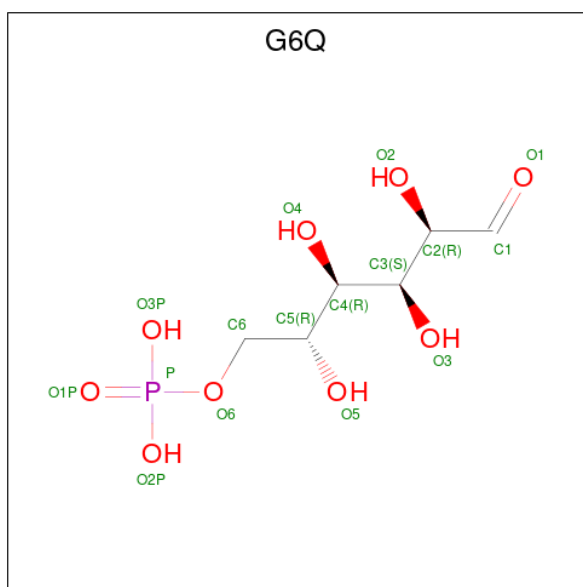
- Molecule 1 is a protein called Glutamine--fructose-6-phosphate-aminotransferase [isomerizing] 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	651	Total	C	H	N	O	S	0	0	0
			10302	3251	5153	896	970	32			
1	B	640	Total	C	H	N	O	S	0	0	0
			10145	3201	5076	882	955	31			

There are 14 discrepancies between the modelled and reference sequences:

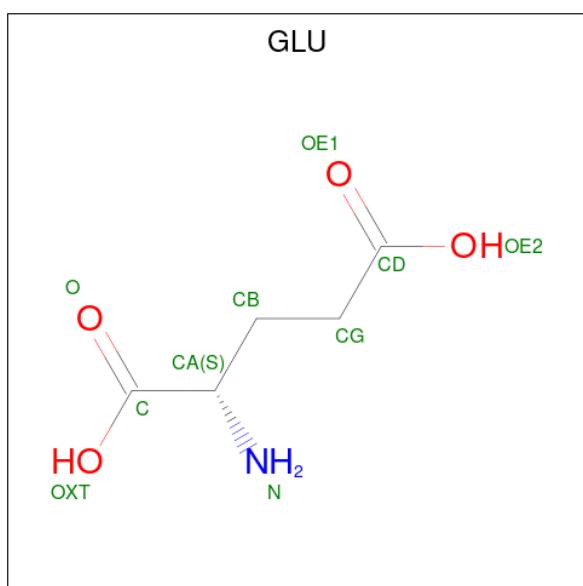
Chain	Residue	Modelled	Actual	Comment	Reference
A	299A	HIS	-	insertion	UNP Q06210
A	299B	HIS	-	insertion	UNP Q06210
A	299C	HIS	-	insertion	UNP Q06210
A	299D	HIS	-	insertion	UNP Q06210
A	299E	HIS	-	insertion	UNP Q06210
A	299F	HIS	-	insertion	UNP Q06210
A	461	GLU	GLY	engineered mutation	UNP Q06210
B	299A	HIS	-	insertion	UNP Q06210
B	299B	HIS	-	insertion	UNP Q06210
B	299C	HIS	-	insertion	UNP Q06210
B	299D	HIS	-	insertion	UNP Q06210
B	299E	HIS	-	insertion	UNP Q06210
B	299F	HIS	-	insertion	UNP Q06210
B	461	GLU	GLY	engineered mutation	UNP Q06210

- Molecule 2 is GLUCOSE-6-PHOSPHATE (CCD ID: G6Q) (formula: C₆H₁₃O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			29	6	13	9	1		
2	B	1	Total	C	H	O	P	0	0
			29	6	13	9	1		

- Molecule 3 is GLUTAMIC ACID (CCD ID: GLU) (formula: $C_5H_9NO_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			18	5	8	1	4		

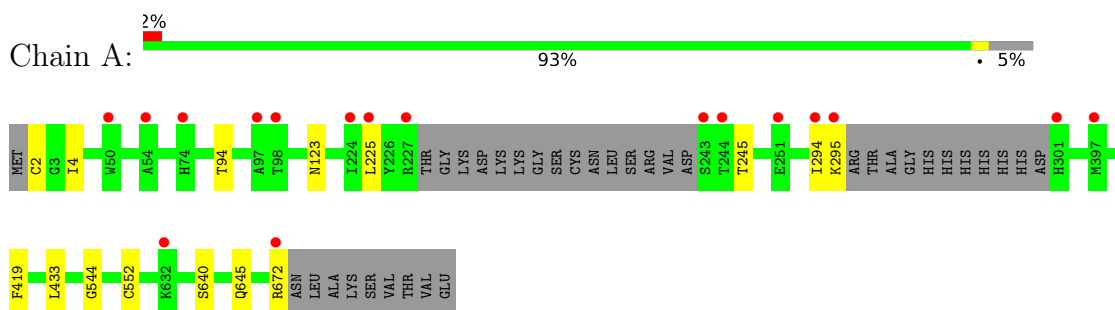
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	9	Total 9	O 9	0	0
4	B	1	Total 1	O 1	0	0

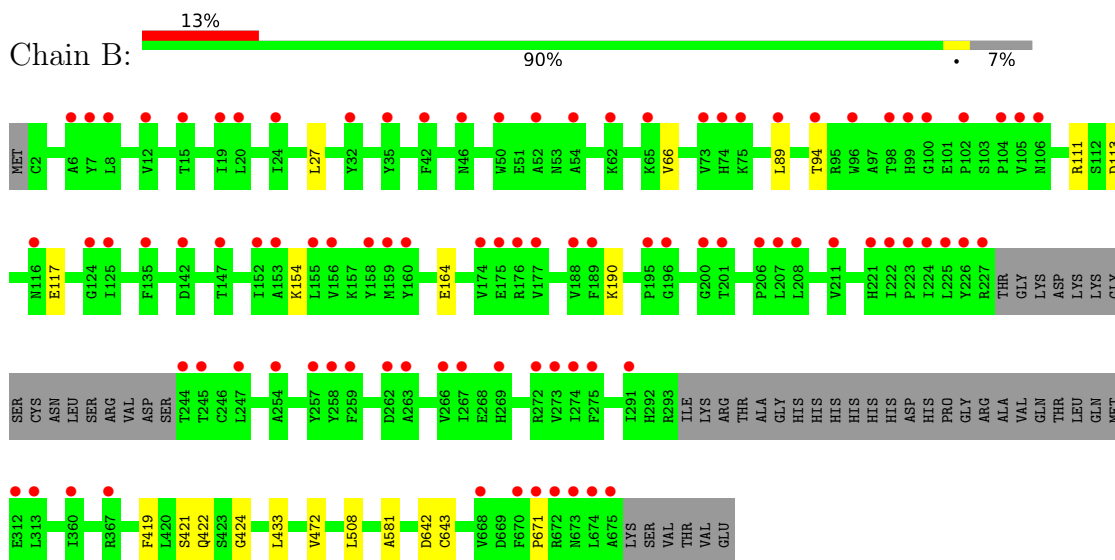
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Glutamine--fructose-6-phosphate-aminotransferase [isomerizing] 1



- Molecule 1: Glutamine--fructose-6-phosphate-aminotransferase [isomerizing] 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	152.45Å 152.45Å 164.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.97 – 2.72 48.97 – 2.72	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.97-2.72) 96.3 (48.97-2.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 2.73Å)	Xtriage
Refinement program	PHENIX dev_2499	Depositor
R, R_{free}	0.205 , 0.234 0.207 , 0.235	Depositor DCC
R_{free} test set	1940 reflections (3.68%)	wwPDB-VP
Wilson B-factor (Å ²)	66.3	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 59.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20533	wwPDB-VP
Average B, all atoms (Å ²)	125.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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: G6Q

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.13	0/5238	0.27	0/7071
1	B	0.10	0/5157	0.25	0/6960
All	All	0.11	0/10395	0.26	0/14031

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

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	5149	5153	5153	8	0
1	B	5069	5076	5076	12	0
2	A	16	13	11	0	0
2	B	16	13	11	1	0
3	A	10	8	5	0	0
4	A	9	0	0	0	0
4	B	1	0	0	0	0
All	All	10270	10263	10256	19	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 1.

All (19) 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:B:422:GLN:N	2:B:701:G6Q:O1P	2.28	0.66
1:A:640:SER:N	1:A:645:GLN:OE1	2.44	0.51
1:B:89:LEU:O	1:B:190:LYS:NZ	2.44	0.49
1:B:642:ASP:OD1	1:B:643:CYS:N	2.46	0.48
1:A:544:GLY:N	1:A:552:CYS:SG	2.87	0.48
1:B:111:ARG:O	1:B:154:LYS:NZ	2.47	0.47
1:B:27:LEU:HD22	1:B:94:THR:HG23	1.96	0.46
1:B:164:GLU:OE1	1:B:164:GLU:N	2.49	0.45
1:A:2:CYS:N	1:A:94:THR:O	2.49	0.45
1:B:113:ASP:OD2	1:B:117:GLU:HB2	2.17	0.44
1:A:225:LEU:HD21	1:A:245:THR:HB	2.00	0.43
1:B:421:SER:OG	1:B:424:GLY:N	2.51	0.42
1:A:4:ILE:HG12	1:A:123:ASN:ND2	2.35	0.42
1:B:419:PHE:CZ	1:B:433:LEU:HA	2.55	0.41
1:A:419:PHE:CZ	1:A:433:LEU:HA	2.54	0.41
1:A:294:ILE:O	1:A:295:LYS:C	2.63	0.41
1:B:472:VAL:HG21	1:B:671:PRO:HD2	2.02	0.41
1:B:66:VAL:HG22	1:B:94:THR:HG21	2.03	0.41
1:A:672:ARG:NH1	1:B:581:ALA:O	2.54	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	645/687 (94%)	627 (97%)	18 (3%)	0	100	100
1	B	634/687 (92%)	599 (94%)	35 (6%)	0	100	100
All	All	1279/1374 (93%)	1226 (96%)	53 (4%)	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 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	566/602 (94%)	566 (100%)	0	100	100
1	B	558/602 (93%)	557 (100%)	1 (0%)	87	95
All	All	1124/1204 (93%)	1123 (100%)	1 (0%)	88	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	508	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	HIS
1	A	193	HIS
1	A	359	HIS
1	A	422	GLN
1	A	448	ASN
1	A	463	HIS
1	A	604	ASN
1	A	608	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
2	G6Q	B	701	-	14,15,15	0.40	0	19,21,21	0.82	0
2	G6Q	A	701	-	14,15,15	0.34	0	19,21,21	0.68	1 (5%)
3	GLU	A	702	-	8,9,9	1.09	1 (12%)	8,11,11	1.18	1 (12%)

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	G6Q	B	701	-	-	10/19/20/20	-
2	G6Q	A	701	-	-	5/19/20/20	-
3	GLU	A	702	-	-	3/9/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	GLU	OXT-C	-2.24	1.23	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	GLU	OXT-C-O	-2.62	118.14	124.08
2	A	701	G6Q	O2-C2-C3	2.05	114.27	109.46

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	G6Q	O1-C1-C2-C3
2	A	701	G6Q	C1-C2-C3-C4
2	A	701	G6Q	C1-C2-C3-O3
2	A	701	G6Q	O2-C2-C3-C4
2	A	701	G6Q	O2-C2-C3-O3
2	B	701	G6Q	O1-C1-C2-C3
2	B	701	G6Q	C1-C2-C3-C4
2	B	701	G6Q	C1-C2-C3-O3
2	B	701	G6Q	O2-C2-C3-C4
2	B	701	G6Q	O2-C2-C3-O3
2	B	701	G6Q	C4-C5-C6-O6
2	B	701	G6Q	O5-C5-C6-O6
2	B	701	G6Q	C2-C3-C4-C5
3	A	702	GLU	OE1-CD-CG-CB
2	B	701	G6Q	C2-C3-C4-O4
3	A	702	GLU	OE2-CD-CG-CB
2	B	701	G6Q	C6-O6-P-O3P
3	A	702	GLU	OXT-C-CA-N

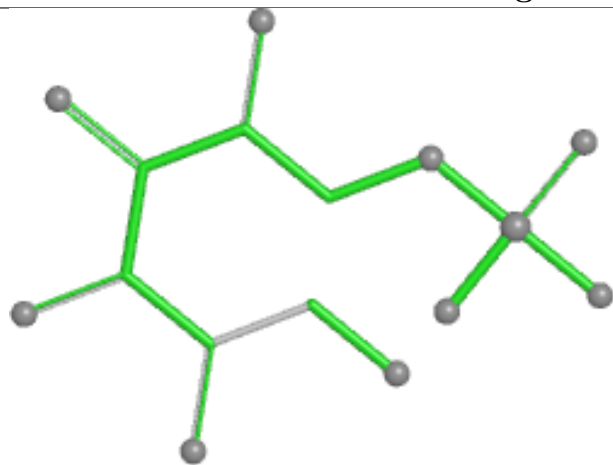
There are no ring outliers.

1 monomer is involved in 1 short contact:

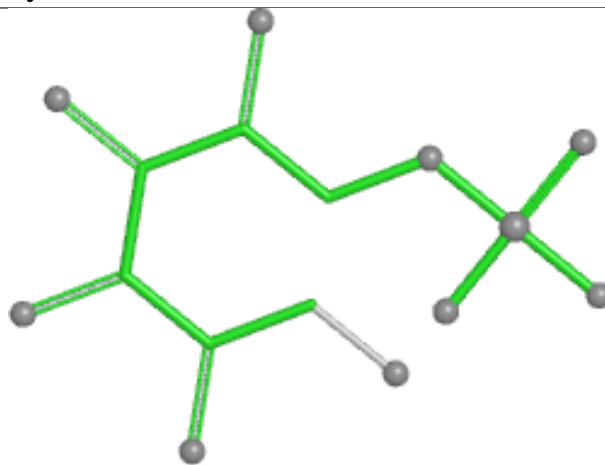
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	G6Q	1	0

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.

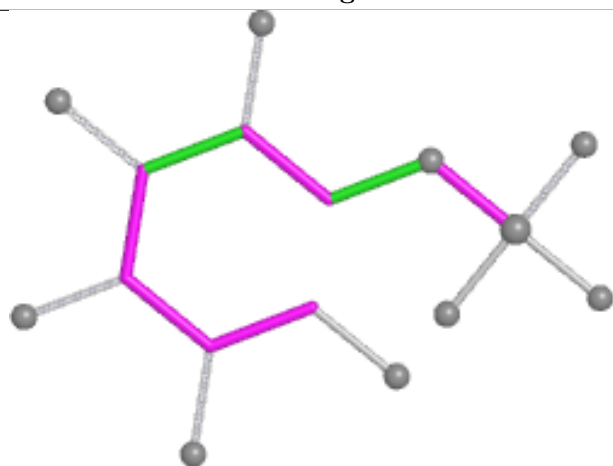
Ligand G6Q B 701



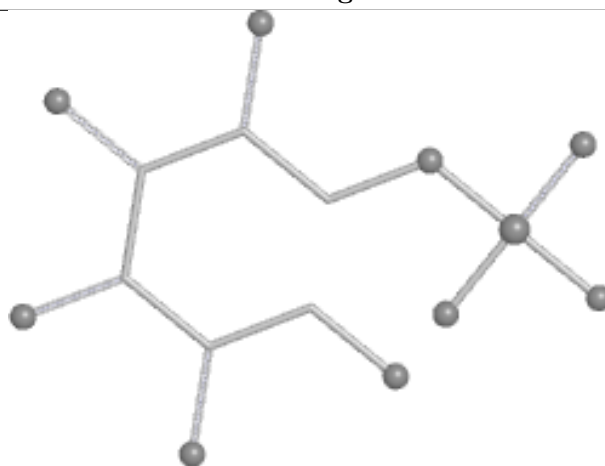
Bond lengths



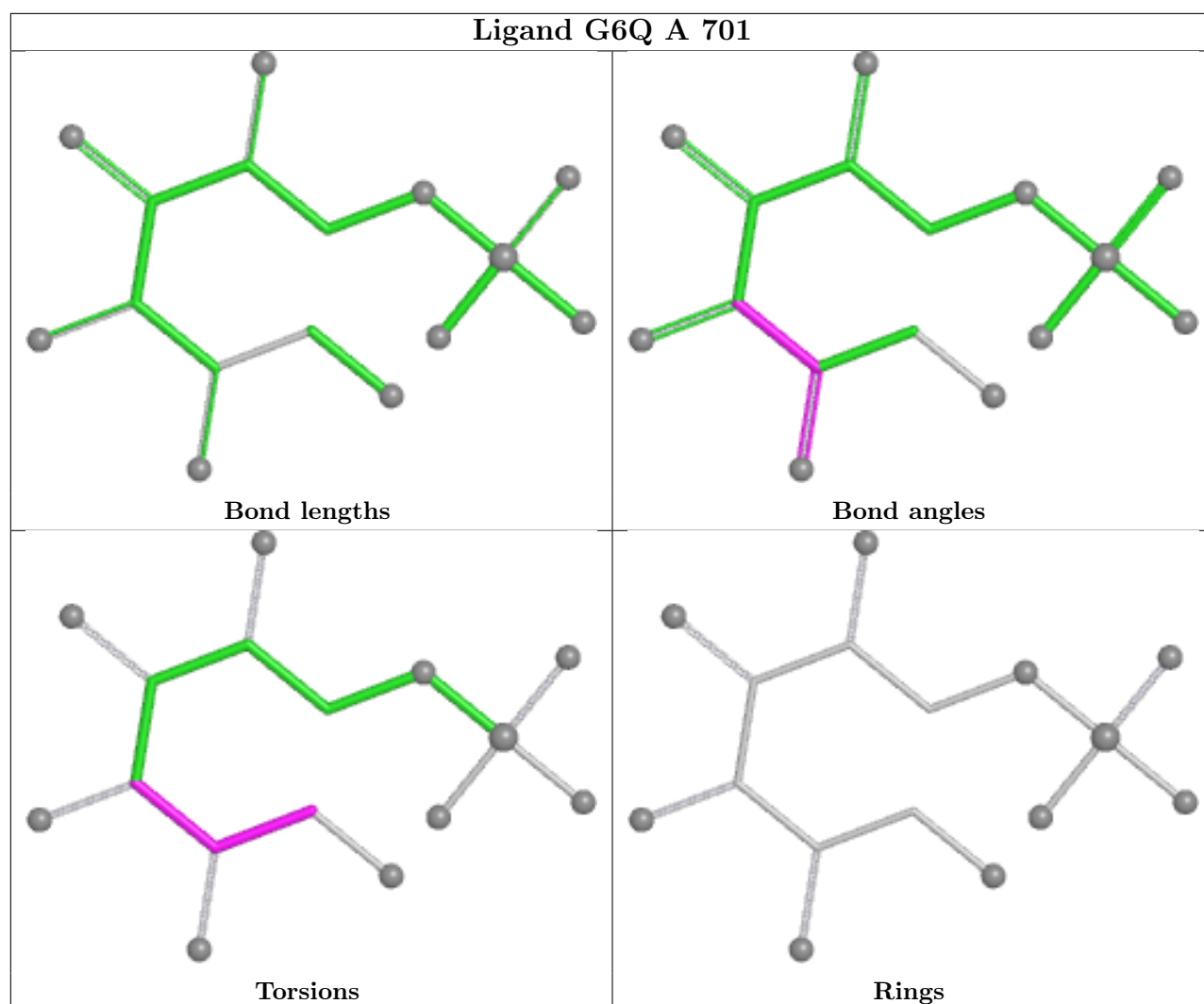
Bond angles



Torsions



Rings



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	651/687 (94%)	0.07	17 (2%) 57 54	50, 77, 138, 206	0
1	B	640/687 (93%)	0.74	92 (14%) 6 5	52, 112, 336, 505	0
All	All	1291/1374 (93%)	0.40	109 (8%) 17 14	50, 87, 307, 505	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	243	SER	6.3
1	B	20	LEU	5.3
1	B	155	LEU	4.5
1	B	275	PHE	4.4
1	B	312	GLU	4.2
1	A	301	HIS	4.1
1	B	675	ALA	4.1
1	B	124	GLY	3.8
1	B	360	ILE	3.7
1	B	189	PHE	3.7
1	B	156	VAL	3.7
1	B	206	PRO	3.7
1	B	224	ILE	3.6
1	B	259	PHE	3.6
1	B	100	GLY	3.6
1	B	135	PHE	3.5
1	B	15	THR	3.5
1	B	32	TYR	3.4
1	B	24	ILE	3.3
1	A	227	ARG	3.3
1	B	105	VAL	3.2
1	B	125	ILE	3.2
1	B	158	TYR	3.2
1	A	294	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	201	THR	3.2
1	B	263	ALA	3.2
1	B	367	ARG	3.1
1	B	225	LEU	3.1
1	B	177	VAL	3.1
1	A	54	ALA	3.1
1	B	73	VAL	3.1
1	B	670	PHE	3.0
1	B	254	ALA	3.0
1	B	274	ILE	3.0
1	B	674	LEU	2.9
1	B	174	VAL	2.8
1	B	50	TRP	2.8
1	A	244	THR	2.8
1	B	244	THR	2.8
1	B	74	HIS	2.8
1	B	19	ILE	2.7
1	B	98	THR	2.7
1	B	104	PRO	2.7
1	B	46	ASN	2.7
1	A	295	LYS	2.7
1	B	313	LEU	2.7
1	B	227	ARG	2.7
1	B	116	ASN	2.7
1	B	54	ALA	2.7
1	B	159	MET	2.6
1	B	247	LEU	2.6
1	A	97	ALA	2.6
1	B	35	TYR	2.6
1	B	291	ILE	2.6
1	A	225	LEU	2.6
1	A	632	LYS	2.6
1	B	99	HIS	2.6
1	A	74	HIS	2.5
1	B	273	VAL	2.5
1	B	221	HIS	2.5
1	B	196	GLY	2.5
1	B	102	PRO	2.5
1	B	188	VAL	2.5
1	B	96	TRP	2.5
1	B	200	GLY	2.4
1	A	672	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	176	ARG	2.4
1	B	262	ASP	2.4
1	A	224	ILE	2.4
1	B	6	ALA	2.4
1	B	42	PHE	2.4
1	B	153	ALA	2.4
1	B	8	LEU	2.3
1	B	208	LEU	2.3
1	B	160	TYR	2.3
1	B	226	TYR	2.3
1	B	147	THR	2.3
1	A	50	TRP	2.3
1	B	207	LEU	2.3
1	B	257	TYR	2.3
1	B	672	ARG	2.3
1	B	89	LEU	2.3
1	A	98	THR	2.3
1	A	397	MET	2.2
1	B	94	THR	2.2
1	B	175	GLU	2.2
1	B	673	ASN	2.2
1	B	152	ILE	2.2
1	A	251	GLU	2.2
1	B	223	PRO	2.2
1	B	65	LYS	2.2
1	B	668	VAL	2.2
1	B	52	ALA	2.2
1	B	266	VAL	2.2
1	B	142	ASP	2.2
1	B	222	ILE	2.2
1	B	269	HIS	2.2
1	B	7	TYR	2.1
1	B	272	ARG	2.1
1	B	195	PRO	2.1
1	B	106	ASN	2.1
1	B	267	ILE	2.1
1	B	62	LYS	2.1
1	B	258	TYR	2.1
1	B	12	VAL	2.1
1	B	245	THR	2.0
1	B	75	LYS	2.0
1	B	671	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	211	VAL	2.0

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](#)

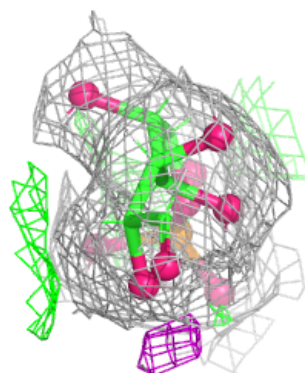
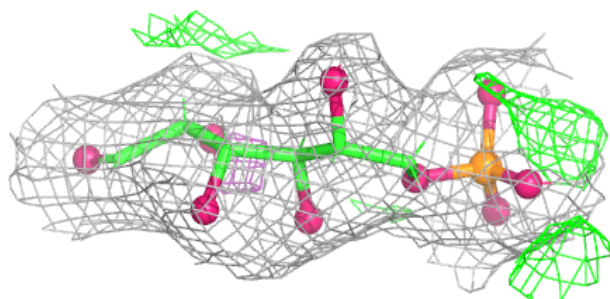
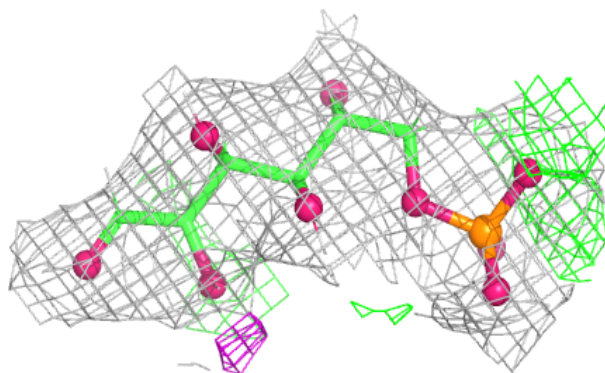
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GLU	A	702	10/10	0.91	0.13	90,93,110,110	0
2	G6Q	B	701	16/16	0.93	0.10	61,67,81,89	0
2	G6Q	A	701	16/16	0.95	0.09	54,60,71,81	0

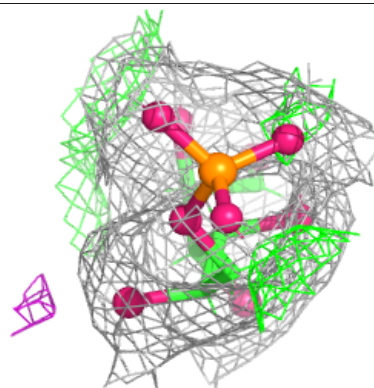
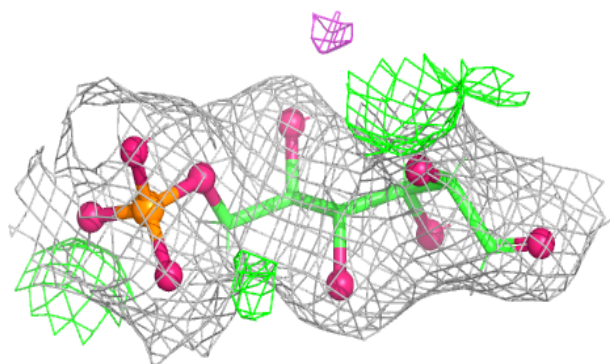
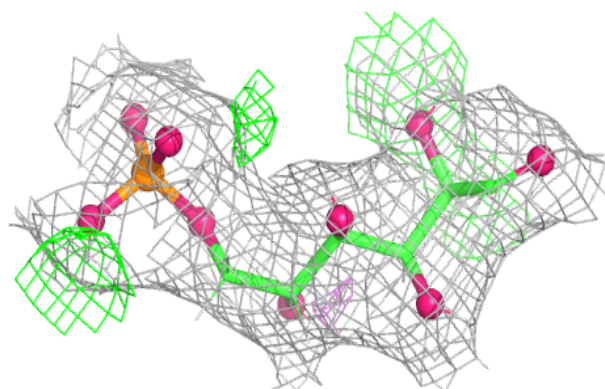
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around G6Q B 701:

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

**Electron density around G6Q A 701:**

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



6.5 Other polymers ⓘ

There are no such residues in this entry.