Full wwPDB X-ray Structure Validation Report (i)

Jun 26, 2024 – 03:29 AM EDT

PDB ID	:	6SVO
Title	:	Crystal structure of human GFAT-1 in complex with Glucosamine-6-Phosphate and L-Glu
Authors	:	Ruegenberg, S.; Horn, M.; Pichlo, C.; Allmeroth, K.; Baumann, U.; Denzel, M.S.
Deposited on	:	2019-09-18
Resolution	:	2.33 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 (i) 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 (i)) were used in the production of this report:

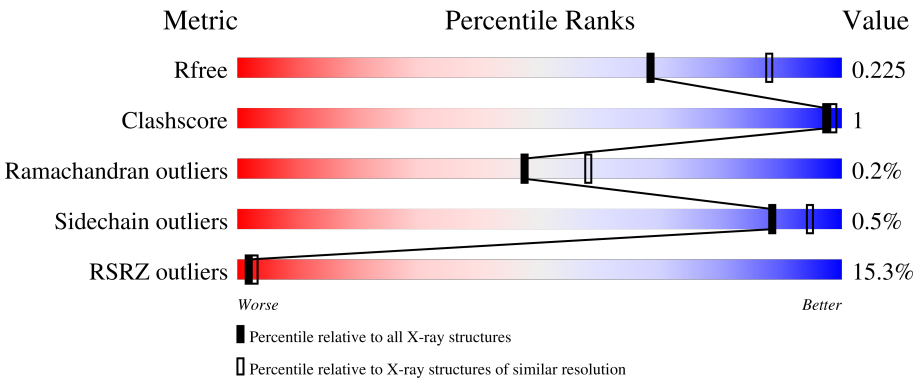
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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 <=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	3% 93%
1	B	687	26% 93%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 21050 atoms, of which 10476 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.

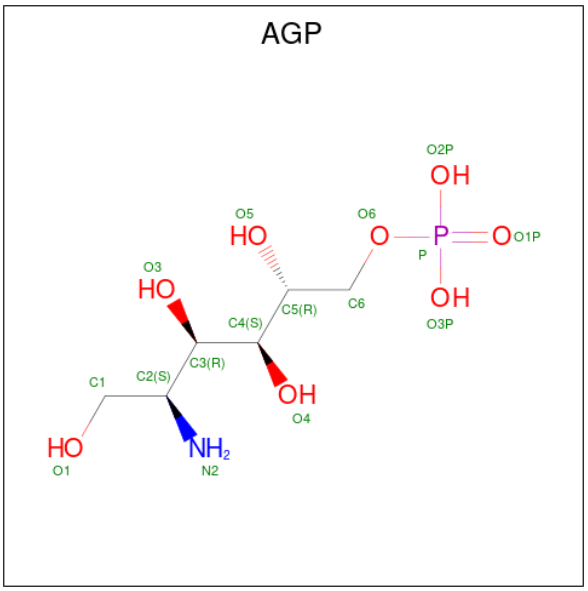
- Molecule 1 is a protein called Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
			Total	C	H	N	O	P	S			
1	A	663	10459	3297	5228	910	991	1	32	0	0	0
1	B	657	10411	3279	5212	902	985	1	32	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

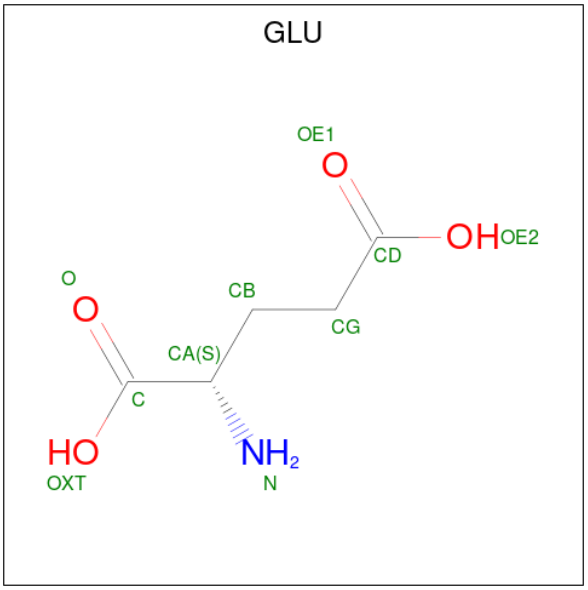
Chain	Residue	Modelled	Actual	Comment	Reference
A	299A	HIS	-	insertion	UNP Q06210
A	299B	HIS	-	insertion	UNP Q06210
A	299C	HIS	-	insertion	UNP Q06210
A	299D	HIS	-	insertion	UNP Q06210
A	299E	HIS	-	insertion	UNP Q06210
A	299F	HIS	-	insertion	UNP Q06210
B	299A	HIS	-	insertion	UNP Q06210
B	299B	HIS	-	insertion	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

- Molecule 2 is 2-DEOXY-2-AMINO GLUCITOL-6-PHOSPHATE (three-letter code: AGP) (formula: $C_6H_{16}NO_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	P		
2	A	1	30	6	14	1	8	1	0	0
			Total	C	H	N	O	P		
2	B	1	30	6	14	1	8	1	0	0

- Molecule 3 is GLUTAMIC ACID (three-letter code: GLU) (formula: $C_5H_9NO_4$).



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

- Molecule 4 is water.

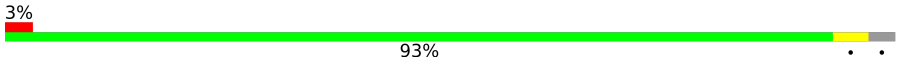
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	62	62	62	0	0
			Total	O		
4	B	40	40	40	0	0

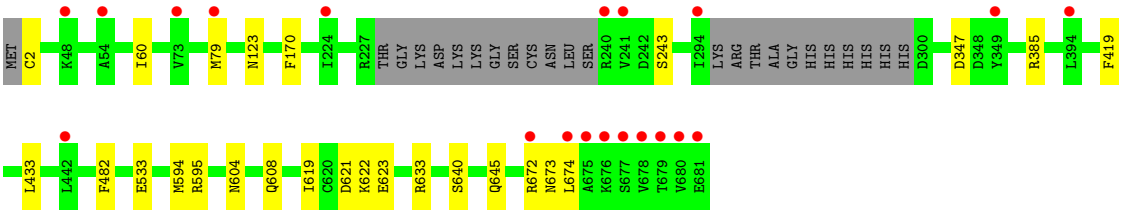
3 Residue-property plots (i)

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

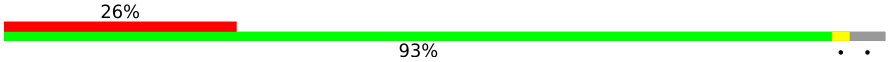
Chain A:

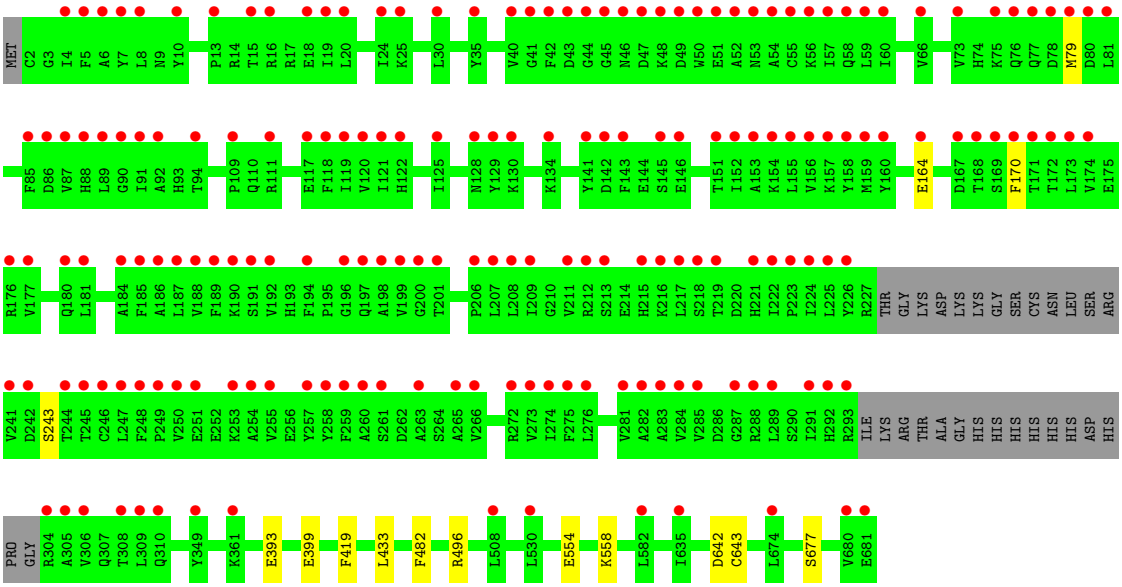




• Molecule 1: Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	152.85Å 152.85Å 165.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.34 – 2.33 112.26 – 2.33	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.34-2.33) 96.0 (112.26-2.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.89 (at 2.32Å)	Xtriage
Refinement program	PHENIX dev_2499	Depositor
R, R_{free}	0.190 , 0.224 0.190 , 0.225	Depositor DCC
R_{free} test set	1927 reflections (2.29%)	wwPDB-VP
Wilson B-factor (Å^2)	55.8	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 53.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	21050	wwPDB-VP
Average B, all atoms (Å^2)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.52% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: SEP, AGP

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	0.24	0/5309	0.42	0/7167
1	B	0.24	0/5276	0.42	0/7120
All	All	0.24	0/10585	0.42	0/14287

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	A	5231	5228	5227	11	0
1	B	5199	5212	5211	6	0
2	A	16	14	14	0	0
2	B	16	14	14	0	0
3	A	10	8	5	0	0
4	A	62	0	0	0	0
4	B	40	0	0	0	0
All	All	10574	10476	10471	16	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 (16) 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:604:ASN:OD1	1:A:608:GLN:NE2	2.29	0.66
1:A:640:SER:N	1:A:645:GLN:OE1	2.32	0.61
1:A:621:ASP:OD1	1:A:622:LYS:N	2.43	0.52
1:B:642:ASP:OD1	1:B:643:CYS:N	2.43	0.51
1:A:533:GLU:OE1	1:A:633:ARG:NE	2.45	0.49
1:A:595:ARG:NH2	1:A:623:GLU:O	2.46	0.49
1:A:385:ARG:NH2	1:B:399:GLU:OE2	2.44	0.48
1:A:419:PHE:CZ	1:A:433:LEU:HA	2.51	0.45
1:B:393:GLU:OE2	1:B:496:ARG:NH1	2.45	0.43
1:A:2:CYS:N	1:A:123:ASN:OD1	2.51	0.43
1:B:419:PHE:CZ	1:B:433:LEU:HA	2.54	0.42
1:B:164:GLU:OE1	1:B:164:GLU:N	2.48	0.42
1:A:594:MET:HE1	1:A:619:ILE:HG22	2.01	0.42
1:B:554:GLU:OE1	1:B:558:LYS:NZ	2.50	0.41
1:A:672:ARG:O	1:A:674:LEU:N	2.54	0.41
1:A:60:ILE:HD11	1:A:79:MET:HE1	2.02	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	656/687 (96%)	639 (97%)	16 (2%)	1 (0%)	47	58
1	B	650/687 (95%)	619 (95%)	30 (5%)	1 (0%)	47	58
All	All	1306/1374 (95%)	1258 (96%)	46 (4%)	2 (0%)	47	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	673	ASN
1	B	677	SER

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	574/600 (96%)	571 (100%)	3 (0%)	88 95
1	B	573/600 (96%)	570 (100%)	3 (0%)	88 95
All	All	1147/1200 (96%)	1141 (100%)	6 (0%)	88 95

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	170	PHE
1	A	347	ASP
1	A	482	PHE
1	B	79	MET
1	B	170	PHE
1	B	482	PHE

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)

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	SEP	A	243	1	8,9,10	1.55	1 (12%)	8,12,14	1.56	2 (25%)
1	SEP	B	243	1	8,9,10	1.55	1 (12%)	8,12,14	1.53	2 (25%)

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
1	SEP	A	243	1	-	0/5/8/10	-
1	SEP	B	243	1	-	0/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243	SEP	P-O1P	3.39	1.61	1.50
1	B	243	SEP	P-O1P	3.37	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	243	SEP	P-OG-CB	-2.81	110.55	118.30
1	A	243	SEP	OG-CB-CA	2.80	110.87	108.14
1	B	243	SEP	P-OG-CB	-2.76	110.69	118.30
1	B	243	SEP	OG-CB-CA	2.70	110.78	108.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides 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	$\#\|Z\| > 2$
3	GLU	A	702	-	8,9,9	1.04	1 (12%)	10,11,11	1.26	2 (20%)
2	AGP	A	701	-	15,15,15	0.84	0	17,21,21	1.06	1 (5%)
2	AGP	B	701	-	15,15,15	0.87	0	17,21,21	0.92	1 (5%)

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	A	702	-	-	3/9/9/9	-
2	AGP	A	701	-	-	6/20/20/20	-
2	AGP	B	701	-	-	4/20/20/20	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	GLU	OXT-C	-2.14	1.23	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	701	AGP	C5-C4-C3	-3.33	107.25	112.47
2	B	701	AGP	C5-C4-C3	-2.89	107.94	112.47
3	A	702	GLU	OXT-C-O	-2.66	118.04	124.09
3	A	702	GLU	OXT-C-CA	2.22	120.96	113.38

There are no chirality outliers.

All (13) torsion outliers are listed below:

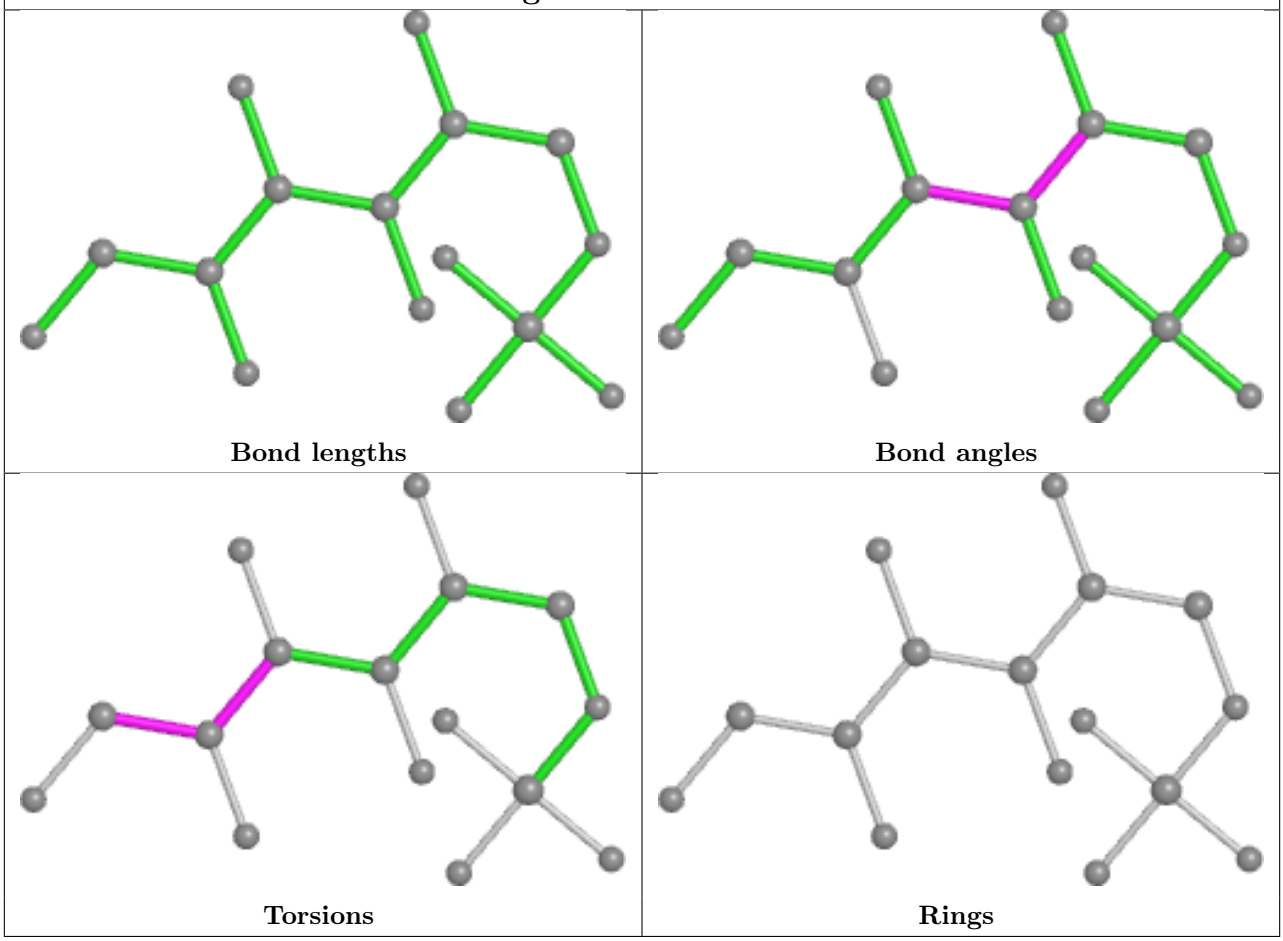
Mol	Chain	Res	Type	Atoms
2	A	701	AGP	O1-C1-C2-N2
2	A	701	AGP	O1-C1-C2-C3
2	A	701	AGP	N2-C2-C3-C4
2	B	701	AGP	C1-C2-C3-O3
2	B	701	AGP	C1-C2-C3-C4
2	B	701	AGP	N2-C2-C3-O3
2	B	701	AGP	N2-C2-C3-C4
2	A	701	AGP	N2-C2-C3-O3
3	A	702	GLU	OE1-CD-CG-CB
3	A	702	GLU	OE2-CD-CG-CB
3	A	702	GLU	OXT-C-CA-N
2	A	701	AGP	C1-C2-C3-C4
2	A	701	AGP	C1-C2-C3-O3

There are no ring outliers.

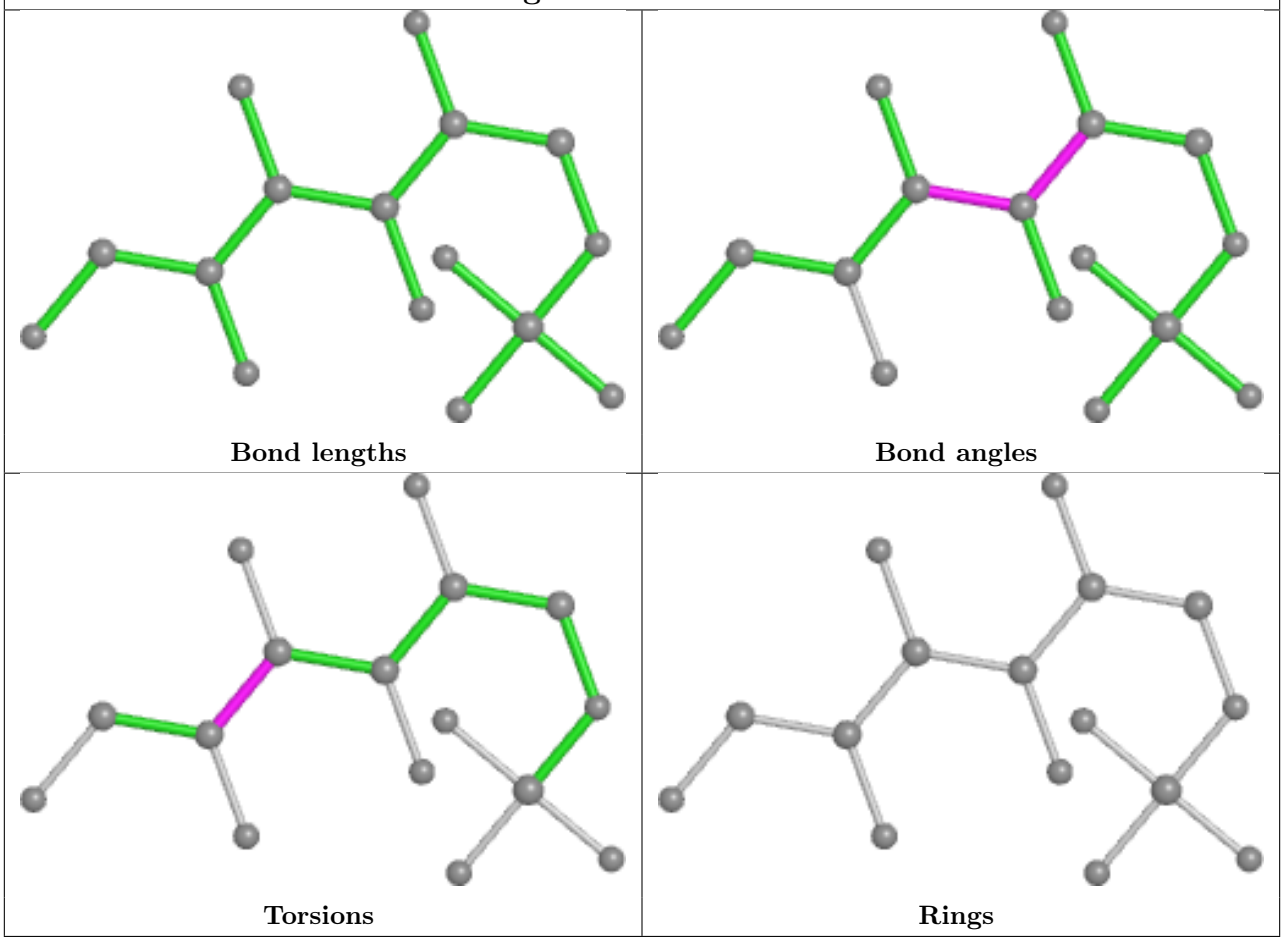
No monomer is involved in short contacts.

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 then 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 AGP A 701



Ligand AGP B 701



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	662/687 (96%)	0.71	20 (3%)	50	57	43, 65, 120, 176	0
1	B	656/687 (95%)	1.83	182 (27%)	0	0	47, 88, 188, 253	0
All	All	1318/1374 (95%)	1.26	202 (15%)	2	3	43, 73, 172, 253	0

All (202) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	241	VAL	19.5
1	B	247	LEU	12.8
1	B	217	LEU	11.0
1	B	170	PHE	10.7
1	B	222	ILE	9.8
1	B	225	LEU	9.7
1	B	79	MET	9.5
1	B	118	PHE	9.4
1	B	41	GLY	9.2
1	B	75	LYS	9.2
1	B	259	PHE	9.1
1	B	73	VAL	9.1
1	B	50	TRP	8.9
1	B	54	ALA	8.5
1	B	257	TYR	8.5
1	B	57	ILE	8.4
1	B	254	ALA	8.4
1	A	680	VAL	8.3
1	B	223	PRO	8.2
1	B	51	GLU	8.1
1	B	281	VAL	8.0
1	B	53	ASN	8.0
1	B	255	VAL	7.8
1	B	45	GLY	7.8

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Mol	Chain	Res	Type	RSRZ
1	B	153	ALA	7.7
1	B	198	ALA	7.6
1	B	78	ASP	7.6
1	B	20	LEU	7.6
1	B	284	VAL	7.3
1	B	189	PHE	7.2
1	B	199	VAL	7.2
1	B	6	ALA	7.2
1	B	245	THR	7.2
1	B	155	LEU	7.0
1	B	77	GLN	6.9
1	B	177	VAL	6.8
1	B	55	CYS	6.8
1	B	7	TYR	6.8
1	B	42	PHE	6.7
1	A	675	ALA	6.6
1	B	258	TYR	6.5
1	B	156	VAL	6.4
1	B	209	ILE	6.2
1	A	241	VAL	6.2
1	B	304	ARG	6.2
1	B	291	ILE	6.1
1	B	174	VAL	6.1
1	B	120	VAL	6.1
1	B	246	CYS	6.0
1	B	201	THR	5.9
1	B	81	LEU	5.9
1	B	143	PHE	5.9
1	B	160	TYR	5.8
1	B	52	ALA	5.8
1	B	173	LEU	5.8
1	B	129	TYR	5.7
1	B	19	ILE	5.7
1	B	211	VAL	5.7
1	B	306	VAL	5.7
1	B	274	ILE	5.7
1	B	309	LEU	5.6
1	B	91	ILE	5.6
1	B	8	LEU	5.5
1	B	200	GLY	5.4
1	B	176	ARG	5.4
1	B	226	TYR	5.4

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Mol	Chain	Res	Type	RSRZ
1	B	44	GLY	5.4
1	B	49	ASP	5.2
1	B	47	ASP	5.2
1	B	152	ILE	5.2
1	B	46	ASN	5.1
1	B	292	HIS	5.1
1	B	224	ILE	5.1
1	B	218	SER	4.8
1	B	90	GLY	4.8
1	B	273	VAL	4.8
1	B	261	SER	4.8
1	B	283	ALA	4.7
1	B	185	PHE	4.7
1	B	197	GLN	4.6
1	B	289	LEU	4.6
1	B	250	VAL	4.5
1	B	89	LEU	4.4
1	B	80	ASP	4.4
1	B	249	PRO	4.4
1	B	56	LYS	4.4
1	B	85	PHE	4.3
1	B	119	ILE	4.3
1	B	66	VAL	4.2
1	A	677	SER	4.2
1	B	154	LYS	4.2
1	B	158	TYR	4.2
1	B	24	ILE	4.1
1	B	125	ILE	4.1
1	B	10	TYR	4.1
1	B	13	PRO	4.1
1	B	168	THR	4.0
1	B	159	MET	3.9
1	A	678	VAL	3.9
1	A	294	ILE	3.9
1	B	171	THR	3.9
1	B	141	TYR	3.9
1	B	111	ARG	3.8
1	B	58	GLN	3.8
1	B	88	HIS	3.7
1	B	272	ARG	3.7
1	B	244	THR	3.7
1	B	48	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	190	LYS	3.7
1	B	248	PHE	3.7
1	B	59	LEU	3.6
1	B	187	LEU	3.6
1	B	216	LYS	3.6
1	A	681	GLU	3.6
1	B	157	LYS	3.6
1	B	260	ALA	3.6
1	B	194	PHE	3.5
1	A	674	LEU	3.5
1	B	275	PHE	3.5
1	B	208	LEU	3.5
1	B	142	ASP	3.4
1	B	76	GLN	3.4
1	B	681	GLU	3.4
1	B	215	HIS	3.4
1	B	251	GLU	3.4
1	B	121	ILE	3.4
1	B	188	VAL	3.3
1	B	169	SER	3.3
1	B	680	VAL	3.3
1	B	305	ALA	3.2
1	B	213	SER	3.2
1	B	5	PHE	3.2
1	B	192	VAL	3.2
1	B	242	ASP	3.2
1	A	240	ARG	3.2
1	B	92	ALA	3.1
1	B	282	ALA	3.1
1	B	151	THR	3.1
1	A	676	LYS	3.1
1	B	191	SER	3.1
1	B	276	LEU	3.0
1	B	15	THR	3.0
1	B	266	VAL	3.0
1	B	40	VAL	3.0
1	B	212	ARG	2.9
1	B	221	HIS	2.9
1	A	73	VAL	2.9
1	A	54	ALA	2.9
1	B	117	GLU	2.8
1	A	672	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	167	ASP	2.8
1	B	287	GLY	2.8
1	B	35	TYR	2.8
1	A	349	TYR	2.8
1	B	207	LEU	2.8
1	B	94	THR	2.7
1	B	186	ALA	2.7
1	B	265	ALA	2.7
1	B	180	GLN	2.7
1	B	109	PRO	2.6
1	B	308	THR	2.6
1	A	79	MET	2.6
1	B	86	ASP	2.6
1	B	196	GLY	2.6
1	B	4	ILE	2.6
1	B	164	GLU	2.6
1	A	679	THR	2.6
1	B	60	ILE	2.6
1	B	361	LYS	2.5
1	B	145	SER	2.5
1	B	349	TYR	2.4
1	A	394	LEU	2.4
1	B	130	LYS	2.4
1	B	18	GLU	2.4
1	B	25	LYS	2.4
1	A	48	LYS	2.3
1	B	122	HIS	2.3
1	B	310	GLN	2.3
1	B	16	ARG	2.3
1	B	288	ARG	2.3
1	B	184	ALA	2.2
1	B	146	GLU	2.2
1	B	285	VAL	2.2
1	B	43	ASP	2.2
1	A	442	LEU	2.2
1	B	508	LEU	2.2
1	B	674	LEU	2.2
1	B	253	LYS	2.2
1	B	172	THR	2.1
1	B	87	VAL	2.1
1	B	635	ILE	2.1
1	B	530	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	219	THR	2.1
1	B	206	PRO	2.1
1	B	128	ASN	2.1
1	A	224	ILE	2.1
1	B	181	LEU	2.1
1	B	582	LEU	2.1
1	B	134	LYS	2.1
1	B	263	ALA	2.1
1	B	293	ARG	2.0
1	B	30	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	SEP	B	243	10/11	0.48	0.31	217,232,270,270	0
1	SEP	A	243	10/11	0.85	0.17	144,169,191,191	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

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

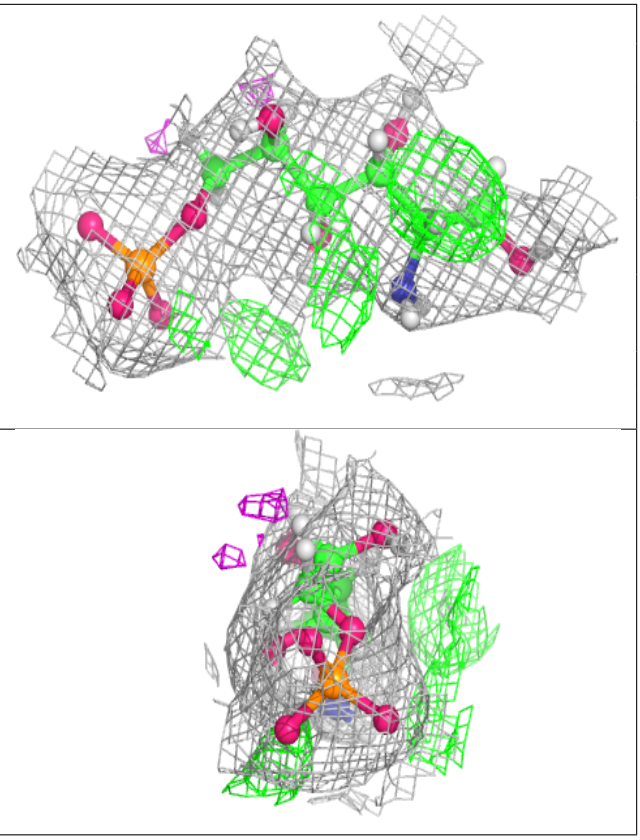
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	AGP	B	701	16/16	0.97	0.19	53,61,74,76	0
3	GLU	A	702	10/10	0.97	0.15	81,82,86,87	0
2	AGP	A	701	16/16	0.98	0.19	46,59,70,74	0

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.

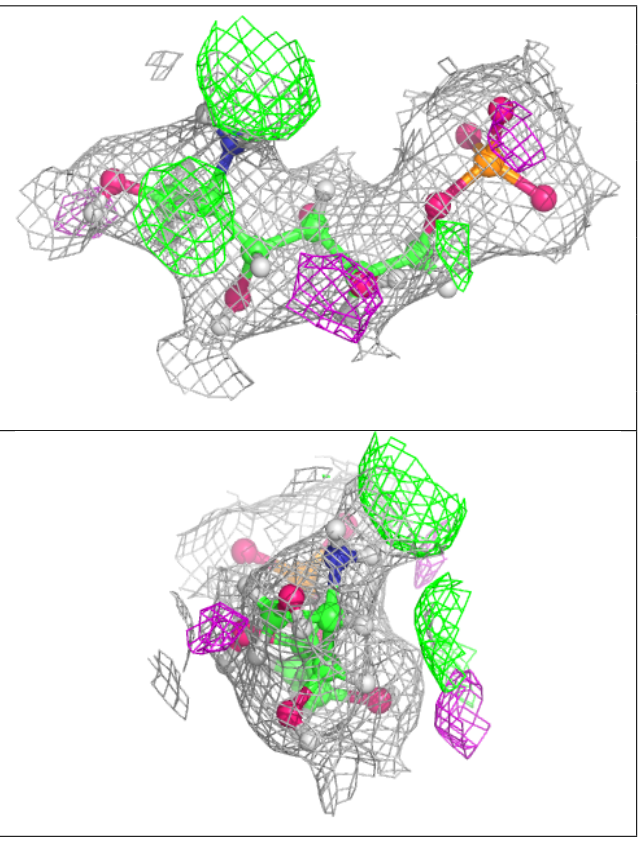
Electron density around AGP B 701:

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



Electron density around AGP 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 (i)

There are no such residues in this entry.