



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:38 AM UTC

PDB ID : 6JT9 / pdb_00006jt9
Title : Crystal Structure of D464A mutant of FGAM Synthetase
Authors : Sharma, N.; Ahalawat, N.; Sandhu, P.; Mondal, J.; Anand, R.
Deposited on : 2019-04-10
Resolution : 2.10 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

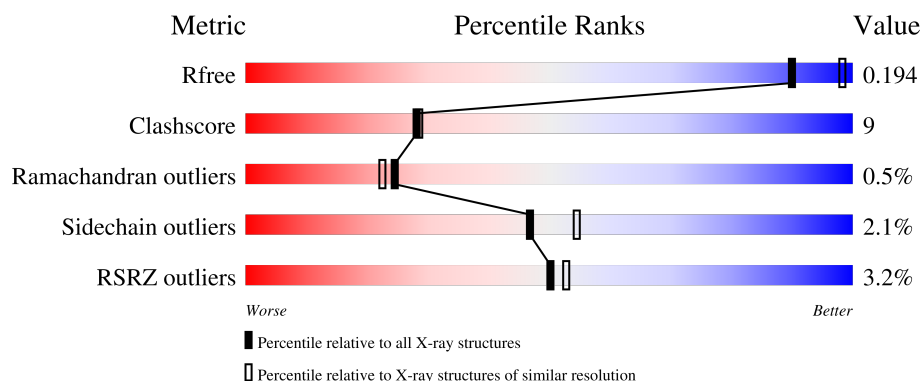
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

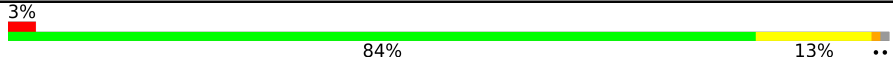
The reported resolution of this entry is 2.10 Å.

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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	1305	

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
5	GOL	A	1320	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	A	1321	-	X	-	-
5	GOL	A	1322	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11047 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 Phosphoribosylformylglycinamide synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1286	Total	C	N	O	S	0	26	0
			10051	6316	1785	1899	51			

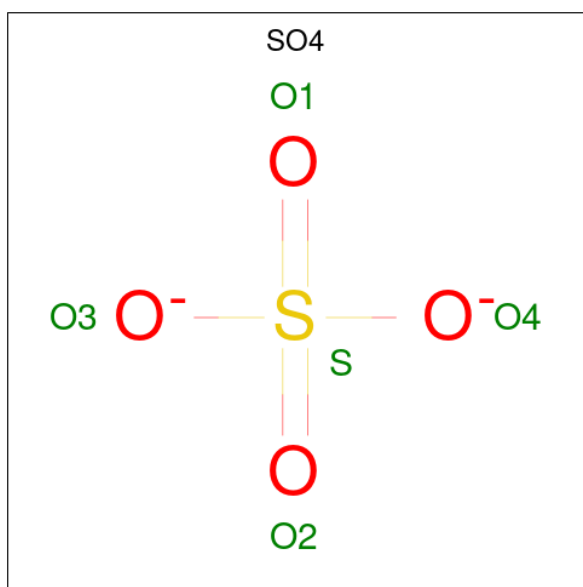
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	GLY	-	expression tag	UNP A0A0D6F9Y3
A	-8	SER	-	expression tag	UNP A0A0D6F9Y3
A	-7	GLY	-	expression tag	UNP A0A0D6F9Y3
A	-6	LEU	-	expression tag	UNP A0A0D6F9Y3
A	-5	VAL	-	expression tag	UNP A0A0D6F9Y3
A	-4	PRO	-	expression tag	UNP A0A0D6F9Y3
A	-3	ARG	-	expression tag	UNP A0A0D6F9Y3
A	-2	GLY	-	expression tag	UNP A0A0D6F9Y3
A	-1	SER	-	expression tag	UNP A0A0D6F9Y3
A	0	HIS	-	expression tag	UNP A0A0D6F9Y3
A	464	ALA	ASP	engineered mutation	UNP A0A0D6F9Y3

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

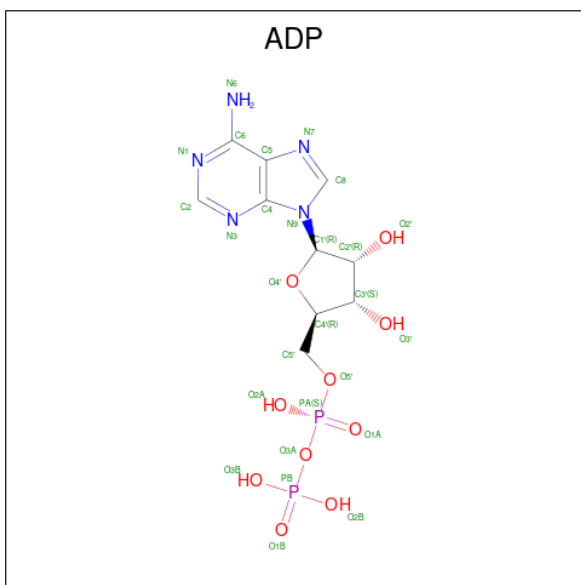
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Mg	0	0
			3	3		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



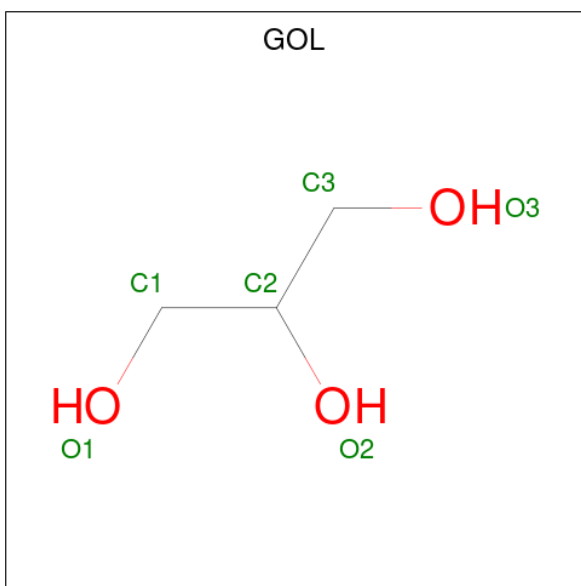
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	Cl	0	0
			3	3		

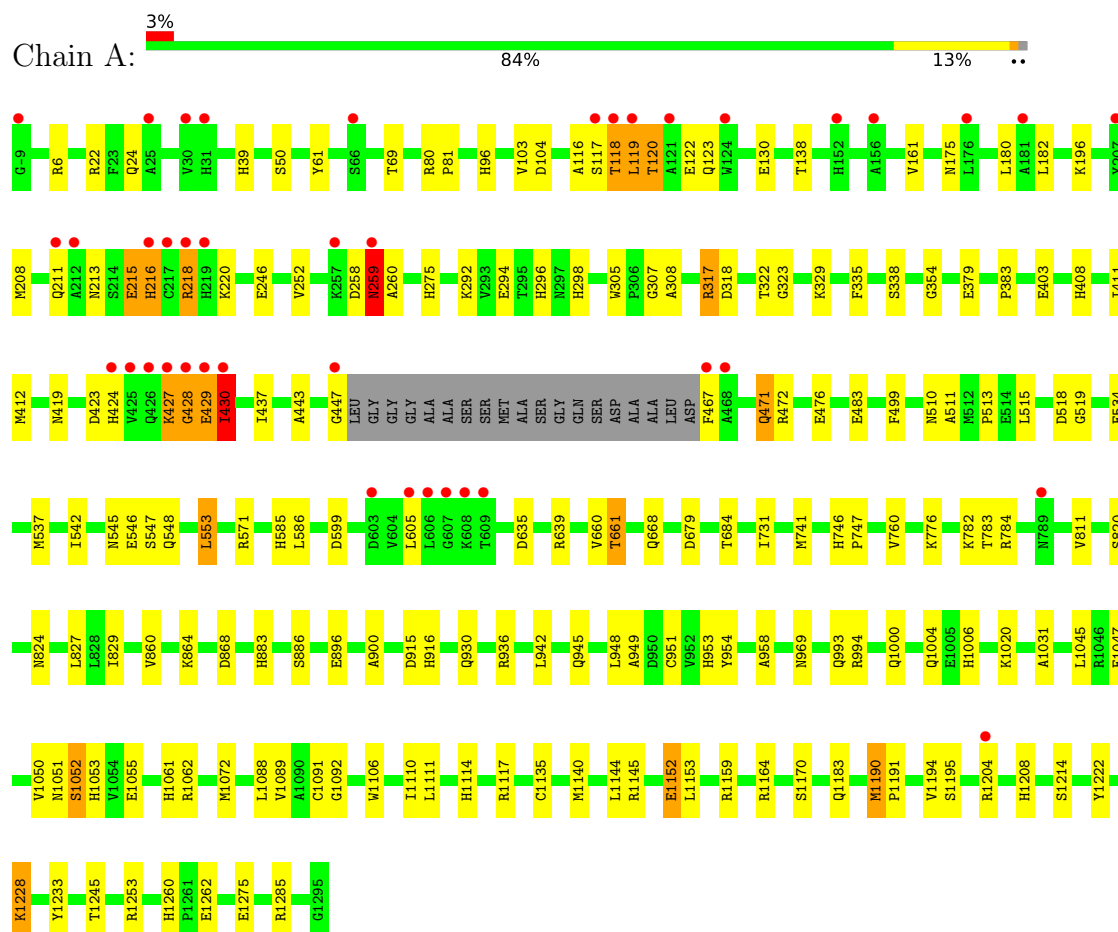
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	855	Total	O	0	0
			855	855		

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: Phosphoribosylformylglycinamide synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	146.46Å 146.46Å 141.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.52 – 2.10 32.52 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (32.52-2.10) 99.9 (32.52-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.99 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.145 , 0.189 0.158 , 0.194	Depositor DCC
R_{free} test set	5004 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	22.9	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11047	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.36% 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: CYG, MG, GOL, SO4, CL, ADP

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	1.24	20/10300 (0.2%)	1.07	19/13978 (0.1%)

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	660	VAL	C-O	-7.54	1.16	1.24
1	A	868	ASP	C-O	-6.71	1.16	1.24
1	A	246	GLU	C-O	-6.47	1.16	1.24
1	A	639	ARG	C-O	-6.23	1.17	1.24
1	A	259	ASN	N-CA	-6.05	1.40	1.46
1	A	1214	SER	C-O	-5.88	1.16	1.24
1	A	635	ASP	C-O	-5.79	1.17	1.24
1	A	1152	GLU	C-O	-5.78	1.16	1.24
1	A	1190	MET	C-O	-5.77	1.17	1.24
1	A	1253	ARG	C-O	-5.72	1.16	1.24
1	A	661	THR	C-N	-5.70	1.25	1.33
1	A	668	GLN	C-O	-5.57	1.17	1.24
1	A	994	ARG	C-O	-5.53	1.17	1.24
1	A	50	SER	CA-C	5.37	1.59	1.52
1	A	69	THR	CA-C	5.33	1.58	1.52
1	A	993	GLN	C-O	-5.32	1.17	1.24
1	A	317	ARG	C-O	-5.29	1.18	1.24
1	A	1228	LYS	C-O	-5.27	1.17	1.23
1	A	252	VAL	C-O	-5.20	1.18	1.24
1	A	1031	ALA	C-O	-5.18	1.19	1.24

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	215	GLU	N-CA-C	-9.06	96.27	109.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	HIS	N-CA-C	-7.91	93.96	110.80
1	A	1091	CYS	N-CA-C	7.00	119.02	110.41
1	A	660	VAL	CA-C-N	6.95	134.81	121.54
1	A	660	VAL	C-N-CA	6.95	134.81	121.54
1	A	119	LEU	N-CA-C	6.90	125.50	110.80
1	A	430	ILE	N-CA-C	6.37	122.60	109.34
1	A	161	VAL	N-CA-C	-6.30	98.66	107.80
1	A	259	ASN	N-CA-C	-6.00	101.75	111.04
1	A	122	GLU	N-CA-C	-5.74	104.94	111.14
1	A	900	ALA	N-CA-C	5.64	117.43	111.28
1	A	511	ALA	N-CA-C	5.63	117.41	111.28
1	A	760	VAL	N-CA-C	5.25	117.14	111.58
1	A	1275	GLU	N-CA-C	5.20	117.69	111.71
1	A	1114	HIS	N-CA-C	5.14	116.89	111.28
1	A	69	THR	CB-CA-C	5.05	118.00	109.67
1	A	534	GLU	CA-C-N	5.03	124.81	119.28
1	A	534	GLU	C-N-CA	5.03	124.81	119.28
1	A	118	THR	N-CA-C	-5.02	100.10	110.80

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	10051	0	9843	176	0
2	A	3	0	0	0	0
3	A	60	0	0	1	0
4	A	27	0	12	0	0
5	A	48	0	64	19	0
6	A	3	0	0	0	0
7	A	855	0	0	49	0
All	All	11047	0	9919	179	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 9.

All (179) 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:424:HIS:HB3	7:A:1414:HOH:O	1.32	1.23
5:A:1322:GOL:H31	7:A:1973:HOH:O	1.48	1.13
1:A:1045[B]:LEU:HD11	1:A:1072[B]:MET:CE	1.79	1.12
1:A:1159:ARG:HH22	5:A:1320:GOL:H2	1.16	1.07
1:A:1045[A]:LEU:HD12	1:A:1088[A]:LEU:HD21	1.33	1.05
1:A:1045[A]:LEU:CD1	1:A:1088[A]:LEU:HD21	1.92	0.98
1:A:215:GLU:HB2	1:A:220:LYS:HE3	1.46	0.97
1:A:1204[B]:ARG:H	1:A:1208[B]:HIS:HD2	1.03	0.97
1:A:120:THR:HG22	1:A:123:GLN:HE21	1.29	0.95
1:A:1204[B]:ARG:H	1:A:1208[B]:HIS:CD2	1.85	0.95
1:A:747:PRO:HD3	5:A:1324:GOL:H2	1.52	0.92
1:A:1052:SER:HB3	7:A:1412:HOH:O	1.67	0.91
1:A:1045[B]:LEU:HD11	1:A:1072[B]:MET:HE1	1.52	0.90
1:A:1062:ARG:HA	5:A:1322:GOL:H32	1.54	0.89
1:A:942:LEU:HG	7:A:2015:HOH:O	1.74	0.86
1:A:824:ASN:HD21	1:A:958:ALA:H	1.24	0.84
1:A:820:SER:H	1:A:930:GLN:HE22	1.27	0.83
1:A:120:THR:HG23	1:A:123:GLN:H	1.47	0.80
1:A:81:PRO:HD3	1:A:138[A]:THR:HG21	1.63	0.79
1:A:1045[B]:LEU:HD21	7:A:1427:HOH:O	1.83	0.77
1:A:437:ILE:HB	1:A:553:LEU:HD12	1.66	0.77
1:A:305:TRP:CD1	7:A:1401:HOH:O	2.39	0.75
1:A:215:GLU:HG2	1:A:220:LYS:HB2	1.69	0.74
1:A:412[B]:MET:SD	7:A:2064:HOH:O	2.47	0.73
1:A:215:GLU:HB2	1:A:220:LYS:CE	2.18	0.73
1:A:96:HIS:HE1	1:A:103:VAL:O	1.71	0.72
1:A:1055:GLU:HB2	7:A:1571:HOH:O	1.89	0.72
1:A:437:ILE:HB	1:A:553:LEU:CD1	2.20	0.71
1:A:1045[B]:LEU:HD11	1:A:1072[B]:MET:HE2	1.72	0.70
1:A:80:ARG:HA	1:A:138[B]:THR:HG23	1.73	0.70
1:A:259:ASN:ND2	1:A:259:ASN:H	1.90	0.70
1:A:218:ARG:HG2	1:A:220:LYS:HG3	1.74	0.69
1:A:1045[A]:LEU:HD12	1:A:1088[A]:LEU:CD2	2.18	0.69
1:A:784:ARG:NH2	5:A:1324:GOL:H31	2.09	0.68
1:A:499[B]:PHE:CD2	1:A:515:LEU:HD12	2.29	0.68
1:A:585:HIS:HE1	1:A:599:ASP:OD1	1.75	0.67
1:A:208[B]:MET:HE1	1:A:586:LEU:HD21	1.74	0.67
1:A:1045[A]:LEU:CD1	1:A:1088[A]:LEU:CD2	2.70	0.67
1:A:829:ILE:HG23	7:A:2115:HOH:O	1.95	0.67
1:A:39:HIS:HE1	1:A:61:TYR:OH	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1045[A]:LEU:HD11	1:A:1088[A]:LEU:CG	2.26	0.65
1:A:1204[B]:ARG:N	1:A:1208[B]:HIS:HD2	1.86	0.65
1:A:335:PHE:CE1	1:A:412[A]:MET:SD	2.90	0.64
1:A:954:TYR:CD2	5:A:1323:GOL:H2	2.32	0.64
1:A:429:GLU:N	1:A:499[A]:PHE:HE1	1.95	0.64
1:A:429:GLU:OE2	1:A:429:GLU:HA	1.96	0.64
1:A:467:PHE:N	7:A:1404:HOH:O	2.31	0.64
1:A:208[B]:MET:HE1	1:A:586:LEU:CD2	2.27	0.63
1:A:545:ASN:HD22	1:A:547:SER:H	1.46	0.63
1:A:1260:HIS:HD2	1:A:1262:GLU:OE2	1.81	0.63
1:A:936:ARG:HH22	5:A:1323:GOL:H11	1.64	0.62
1:A:292:LYS:HE3	7:A:1799:HOH:O	2.00	0.62
1:A:215:GLU:CG	1:A:220:LYS:HB2	2.30	0.61
1:A:429:GLU:N	1:A:499[A]:PHE:CE1	2.68	0.61
1:A:1088[A]:LEU:HD23	1:A:1089:VAL:N	2.16	0.61
1:A:215:GLU:CB	1:A:220:LYS:HE3	2.26	0.61
1:A:208[B]:MET:HE2	1:A:605:LEU:HD21	1.81	0.61
1:A:428:GLY:C	1:A:499[A]:PHE:CZ	2.80	0.60
1:A:305:TRP:HD1	7:A:1401:HOH:O	1.79	0.59
1:A:208[B]:MET:HE2	1:A:605:LEU:CD2	2.32	0.59
1:A:1045[A]:LEU:HD11	1:A:1088[A]:LEU:HD11	1.84	0.59
1:A:1159:ARG:NH2	5:A:1320:GOL:H2	2.02	0.58
1:A:175:ASN:HD22	1:A:180:LEU:HB2	1.68	0.58
1:A:275:HIS:HD2	7:A:2202:HOH:O	1.86	0.58
1:A:259:ASN:HD22	1:A:260:ALA:H	1.50	0.58
1:A:218:ARG:CG	1:A:220:LYS:HG3	2.34	0.58
1:A:258:ASP:OD2	1:A:259:ASN:ND2	2.37	0.58
1:A:1183:GLN:HE22	1:A:1285:ARG:HH21	1.51	0.57
1:A:679:ASP:OD2	1:A:883:HIS:HD2	1.87	0.57
1:A:1062:ARG:HB2	5:A:1322:GOL:H12	1.87	0.57
1:A:1110:ILE:HD11	7:A:1427:HOH:O	2.05	0.57
1:A:1045[A]:LEU:HD11	1:A:1088[A]:LEU:HD21	1.83	0.56
1:A:1204[B]:ARG:N	1:A:1208[B]:HIS:CD2	2.66	0.55
1:A:208[B]:MET:HE3	1:A:513:PRO:HG2	1.89	0.54
1:A:81:PRO:CD	1:A:138[A]:THR:HG21	2.36	0.54
1:A:883:HIS:HE1	1:A:896:GLU:OE1	1.91	0.53
1:A:949:ALA:N	7:A:1416:HOH:O	2.42	0.53
1:A:969:ASN:HA	7:A:1418:HOH:O	2.07	0.53
1:A:1051:ASN:HB3	7:A:1408:HOH:O	2.09	0.53
1:A:1061:HIS:ND1	5:A:1322:GOL:H11	2.24	0.52
1:A:427:LYS:HB2	1:A:499[A]:PHE:CE2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:ASN:HB2	7:A:2080:HOH:O	2.09	0.52
1:A:1072[B]:MET:HE2	1:A:1072[B]:MET:HA	1.91	0.52
1:A:39:HIS:CE1	1:A:61:TYR:OH	2.61	0.52
1:A:429:GLU:C	7:A:1469:HOH:O	2.53	0.52
1:A:81:PRO:HD3	1:A:138[A]:THR:CG2	2.38	0.52
1:A:471:GLN:HE21	1:A:472:ARG:H	1.58	0.51
1:A:1164:ARG:HD3	5:A:1320:GOL:O3	2.09	0.51
1:A:215:GLU:HG2	1:A:220:LYS:H	1.75	0.51
1:A:951:CYS:HB2	7:A:2115:HOH:O	2.11	0.51
1:A:1045[A]:LEU:HD11	1:A:1088[A]:LEU:CD1	2.40	0.51
1:A:1051:ASN:ND2	7:A:1408:HOH:O	2.43	0.51
1:A:96:HIS:CE1	1:A:103:VAL:O	2.58	0.50
1:A:954:TYR:HD2	5:A:1323:GOL:H2	1.73	0.50
1:A:827:LEU:HD23	1:A:954:TYR:HA	1.93	0.50
1:A:969:ASN:ND2	7:A:1418:HOH:O	2.43	0.50
1:A:354:GLY:O	1:A:408:HIS:HE1	1.94	0.50
1:A:428:GLY:C	1:A:499[A]:PHE:CE1	2.90	0.50
1:A:499[B]:PHE:HD2	1:A:515:LEU:HD12	1.75	0.50
1:A:1228:LYS:HB3	7:A:2136:HOH:O	2.12	0.50
1:A:403:GLU:OE1	1:A:746:HIS:HE1	1.95	0.49
1:A:1020:LYS:HE2	7:A:2191:HOH:O	2.12	0.49
1:A:39:HIS:HD2	7:A:1524:HOH:O	1.95	0.49
1:A:294:GLU:OE2	1:A:318:ASP:OD1	2.31	0.49
1:A:969:ASN:CA	7:A:1418:HOH:O	2.61	0.49
1:A:80:ARG:HA	1:A:138[A]:THR:HG22	1.95	0.49
1:A:296:HIS:HD2	1:A:307:GLY:O	1.95	0.49
1:A:175:ASN:HD21	1:A:182:LEU:H	1.60	0.48
1:A:731:ILE:HG21	1:A:864[B]:LYS:HE2	1.94	0.48
1:A:259:ASN:HD21	1:A:322:THR:HA	1.77	0.48
1:A:1153:LEU:O	1:A:1208[B]:HIS:HE1	1.97	0.48
1:A:218:ARG:HG2	1:A:220:LYS:CG	2.42	0.48
1:A:1045[A]:LEU:HD11	1:A:1088[A]:LEU:CD2	2.40	0.48
1:A:329:LYS:HE3	1:A:419:ASN:ND2	2.28	0.48
1:A:1106:TRP:NE1	7:A:1427:HOH:O	2.47	0.47
1:A:1006:HIS:HE1	7:A:1456:HOH:O	1.98	0.47
1:A:953:HIS:ND1	3:A:1311:SO4:O4	2.33	0.47
1:A:120:THR:HG22	1:A:123:GLN:NE2	2.13	0.47
1:A:1050:VAL:HG13	1:A:1092:GLY:O	2.14	0.47
1:A:1062:ARG:CA	5:A:1322:GOL:H12	2.45	0.46
1:A:215:GLU:HG2	1:A:220:LYS:CB	2.43	0.46
1:A:1000:GLN:NE2	7:A:1428:HOH:O	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:GLU:HG3	7:A:1725:HOH:O	2.14	0.46
1:A:447:GLY:HA2	1:A:546:GLU:HB2	1.97	0.45
1:A:427:LYS:HG3	1:A:499[B]:PHE:CE1	2.52	0.45
1:A:1004:GLN:NE2	1:A:1233:TYR:H	2.15	0.45
1:A:80:ARG:HA	1:A:138[B]:THR:CG2	2.44	0.45
1:A:1006:HIS:HD2	7:A:1771:HOH:O	1.99	0.45
1:A:323:GLY:HA3	1:A:424:HIS:O	2.17	0.45
1:A:1020:LYS:CE	7:A:2191:HOH:O	2.64	0.45
1:A:1045[A]:LEU:HD11	1:A:1088[A]:LEU:HG	1.97	0.45
1:A:298:HIS:HD2	7:A:2192:HOH:O	1.98	0.44
1:A:948:LEU:C	7:A:1416:HOH:O	2.59	0.44
1:A:305:TRP:CD1	1:A:305:TRP:C	2.96	0.44
1:A:1111:LEU:HA	1:A:1117:ARG:HG3	1.99	0.44
1:A:1159:ARG:HH22	5:A:1320:GOL:C2	2.07	0.44
1:A:116:ALA:C	1:A:118:THR:H	2.25	0.44
1:A:329:LYS:O	1:A:383:PRO:HD2	2.17	0.44
1:A:915:ASP:HB3	5:A:1317:GOL:H31	1.99	0.44
1:A:6:ARG:CB	7:A:2082:HOH:O	2.64	0.44
1:A:942:LEU:CG	7:A:2015:HOH:O	2.46	0.44
1:A:430:ILE:HG12	1:A:499[A]:PHE:CD1	2.53	0.44
1:A:860:VAL:HB	5:A:1319:GOL:H2	2.00	0.43
1:A:684:THR:HG22	1:A:811:VAL:HG21	2.00	0.43
1:A:338:SER:OG	1:A:408:HIS:HD2	2.01	0.43
1:A:571[A]:ARG:NH1	1:A:1047:GLU:OE2	2.49	0.43
1:A:427:LYS:CE	7:A:1840:HOH:O	2.66	0.43
1:A:483:GLU:OE2	1:A:1053:HIS:HE1	2.01	0.43
1:A:427:LYS:HB3	7:A:1840:HOH:O	2.18	0.42
1:A:218:ARG:CG	1:A:220:LYS:CG	2.97	0.42
1:A:427:LYS:HE3	7:A:1840:HOH:O	2.20	0.42
1:A:864[A]:LYS:HD3	7:A:1421:HOH:O	2.18	0.42
1:A:1062:ARG:N	5:A:1322:GOL:H12	2.34	0.42
1:A:1140:MET:HE2	7:A:1427:HOH:O	2.19	0.42
5:A:1319:GOL:C3	7:A:1518:HOH:O	2.68	0.42
1:A:499[B]:PHE:CE1	1:A:518:ASP:HB3	2.55	0.41
1:A:916:HIS:HD2	7:A:1494:HOH:O	2.03	0.41
1:A:1222:TYR:CE2	1:A:1245:THR:HB	2.55	0.41
1:A:537:MET:HE3	1:A:542:ILE:HG12	2.02	0.41
1:A:80:ARG:HG2	1:A:138[B]:THR:CG2	2.50	0.41
1:A:945[B]:GLN:NE2	7:A:1423:HOH:O	2.54	0.41
1:A:430:ILE:HG13	1:A:519:GLY:HA3	2.03	0.41
1:A:317:ARG:HH22	1:A:548:GLN:HE22	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:ARG:HG2	1:A:130:GLU:CD	2.45	0.41
1:A:275:HIS:CD2	7:A:2202:HOH:O	2.68	0.41
1:A:443:ALA:HB3	7:A:1829:HOH:O	2.20	0.41
1:A:1145:ARG:HH11	1:A:1145:ARG:HD2	1.72	0.41
1:A:411:ILE:HG12	1:A:741:MET:HG2	2.01	0.41
1:A:864[A]:LYS:CD	7:A:1421:HOH:O	2.68	0.41
1:A:1260:HIS:CD2	1:A:1262:GLU:OE2	2.68	0.41
1:A:308:ALA:HA	1:A:412[B]:MET:HE3	2.02	0.40
1:A:259:ASN:ND2	1:A:259:ASN:N	2.59	0.40
1:A:476:GLU:HB2	7:A:1725:HOH:O	2.22	0.40
1:A:1170:SER:O	1:A:1191:PRO:HA	2.21	0.40
1:A:408:HIS:CB	1:A:783[B]:THR:HG21	2.52	0.40
1:A:942:LEU:C	1:A:942:LEU:HD23	2.46	0.40
5:A:1319:GOL:H31	7:A:1518:HOH:O	2.20	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	1307/1305 (100%)	1260 (96%)	40 (3%)	7 (0%)	24	22

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	117	SER
1	A	119	LEU
1	A	216	HIS
1	A	661	THR
1	A	886	SER
1	A	428	GLY
1	A	430	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1047/1040 (101%)	1026 (98%)	21 (2%)	48 56

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	104	ASP
1	A	120	THR
1	A	196	LYS
1	A	211	GLN
1	A	213	ASN
1	A	218	ARG
1	A	259	ASN
1	A	423	ASP
1	A	427	LYS
1	A	429	GLU
1	A	471	GLN
1	A	553	LEU
1	A	776	LYS
1	A	782	LYS
1	A	1052	SER
1	A	1144	LEU
1	A	1152	GLU
1	A	1190	MET
1	A	1194	VAL
1	A	1195	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	HIS
1	A	96	HIS
1	A	123	GLN
1	A	175	ASN

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Mol	Chain	Res	Type
1	A	191	GLN
1	A	243	ASN
1	A	259	ASN
1	A	275	HIS
1	A	276	ASN
1	A	296	HIS
1	A	298	HIS
1	A	339	ASN
1	A	408	HIS
1	A	419	ASN
1	A	471	GLN
1	A	545	ASN
1	A	548	GLN
1	A	559	GLN
1	A	585	HIS
1	A	739	ASN
1	A	746	HIS
1	A	824	ASN
1	A	862	GLN
1	A	883	HIS
1	A	916	HIS
1	A	930	GLN
1	A	993	GLN
1	A	1004	GLN
1	A	1006	HIS
1	A	1053	HIS
1	A	1125	HIS
1	A	1183	GLN
1	A	1189	GLN
1	A	1260	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	CYG	A	1135	1	12,14,15	3.00	5 (41%)	10,17,19	2.72	4 (40%)

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	CYG	A	1135	1	-	3/14/16/18	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1135	CYG	CD1-SG	-8.61	1.55	1.76
1	A	1135	CYG	O2-C1	-3.40	1.19	1.30
1	A	1135	CYG	CG1-CD1	2.82	1.53	1.50
1	A	1135	CYG	OE2-CD1	-2.61	1.17	1.21
1	A	1135	CYG	CB-SG	-2.42	1.75	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1135	CYG	CG1-CD1-SG	6.17	120.76	113.40
1	A	1135	CYG	OE2-CD1-SG	-4.47	117.00	122.68
1	A	1135	CYG	CB-SG-CD1	2.29	103.91	100.76
1	A	1135	CYG	CB1-CG1-CD1	-2.16	107.49	112.27

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1135	CYG	SG-CD1-CG1-CB1
1	A	1135	CYG	OE2-CD1-CG1-CB1
1	A	1135	CYG	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 27 ligands modelled in this entry, 6 are monoatomic - leaving 21 for Mogul analysis.

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	$\# Z > 2$
5	GOL	A	1318	-	5,5,5	1.18	0	5,5,5	0.95	0
3	SO4	A	1315	-	4,4,4	0.40	0	6,6,6	0.41	0
3	SO4	A	1311	-	4,4,4	1.10	0	6,6,6	1.75	2 (33%)
5	GOL	A	1321	-	5,5,5	1.42	1 (20%)	5,5,5	1.80	2 (40%)
5	GOL	A	1317	-	5,5,5	1.14	0	5,5,5	2.76	2 (40%)
5	GOL	A	1324	-	5,5,5	0.33	0	5,5,5	1.13	0
5	GOL	A	1320	-	5,5,5	0.75	0	5,5,5	0.95	0
3	SO4	A	1308	-	4,4,4	0.68	0	6,6,6	0.89	0
3	SO4	A	1304	-	4,4,4	0.25	0	6,6,6	0.49	0
3	SO4	A	1309	-	4,4,4	0.67	0	6,6,6	0.58	0
4	ADP	A	1316	2	28,29,29	1.32	3 (10%)	43,45,45	1.68	8 (18%)
5	GOL	A	1322	-	5,5,5	0.54	0	5,5,5	1.06	0
3	SO4	A	1313	-	4,4,4	0.63	0	6,6,6	0.86	0
5	GOL	A	1323	-	5,5,5	0.29	0	5,5,5	1.25	0
5	GOL	A	1319	-	5,5,5	1.40	0	5,5,5	2.37	2 (40%)
3	SO4	A	1306	-	4,4,4	0.36	0	6,6,6	0.83	0
3	SO4	A	1314	-	4,4,4	1.60	1 (25%)	6,6,6	2.71	2 (33%)
3	SO4	A	1307	-	4,4,4	0.65	0	6,6,6	0.67	0
3	SO4	A	1310	-	4,4,4	0.69	0	6,6,6	0.74	0
3	SO4	A	1312	-	4,4,4	1.12	0	6,6,6	0.58	0
3	SO4	A	1305	-	4,4,4	0.62	0	6,6,6	0.71	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
5	GOL	A	1318	-	-	4/4/4/4	-
5	GOL	A	1317	-	-	2/4/4/4	-
4	ADP	A	1316	2	-	1/16/32/32	0/3/3/3
5	GOL	A	1322	-	-	4/4/4/4	-
5	GOL	A	1324	-	-	0/4/4/4	-
5	GOL	A	1323	-	-	1/4/4/4	-
5	GOL	A	1321	-	-	4/4/4/4	-
5	GOL	A	1320	-	-	0/4/4/4	-
5	GOL	A	1319	-	-	2/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1316	ADP	C4-N9	-3.22	1.31	1.37
3	A	1314	SO4	O2-S	3.04	1.62	1.44
4	A	1316	ADP	PA-O3A	2.97	1.62	1.59
4	A	1316	ADP	C5-C4	2.43	1.43	1.39
5	A	1321	GOL	O3-C3	2.28	1.52	1.42

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1314	SO4	O3-S-O1	-5.50	80.80	109.56
4	A	1316	ADP	C5-C4-N3	-5.32	119.39	126.72
5	A	1317	GOL	O3-C3-C2	4.79	131.94	110.38
4	A	1316	ADP	N3-C4-N9	4.31	134.49	127.17
5	A	1319	GOL	O1-C1-C2	-4.21	91.43	110.38
4	A	1316	ADP	C2-N3-C4	3.53	120.45	111.83
3	A	1311	SO4	O3-S-O1	3.26	126.61	109.56
5	A	1317	GOL	O2-C2-C3	3.12	122.11	109.18
3	A	1314	SO4	O2-S-O1	3.02	130.36	109.06
5	A	1319	GOL	O3-C3-C2	-2.61	98.62	110.38
5	A	1321	GOL	O3-C3-C2	2.51	121.69	110.38
4	A	1316	ADP	O2A-PA-O1A	2.48	123.99	112.44
4	A	1316	ADP	N3-C2-N1	-2.47	124.84	128.58
4	A	1316	ADP	O4'-C1'-N9	2.40	112.70	108.09
4	A	1316	ADP	C5-C6-N6	-2.36	117.45	123.29
5	A	1321	GOL	C3-C2-C1	2.16	119.72	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1311	SO4	O4-S-O1	-2.15	98.31	109.56
4	A	1316	ADP	O2A-PA-O3A	2.12	113.00	107.27

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1317	GOL	O1-C1-C2-C3
5	A	1318	GOL	O1-C1-C2-C3
5	A	1319	GOL	O1-C1-C2-C3
5	A	1321	GOL	O1-C1-C2-O2
5	A	1321	GOL	O1-C1-C2-C3
5	A	1321	GOL	C1-C2-C3-O3
5	A	1322	GOL	O1-C1-C2-C3
5	A	1322	GOL	C1-C2-C3-O3
5	A	1318	GOL	O2-C2-C3-O3
5	A	1317	GOL	C1-C2-C3-O3
5	A	1318	GOL	C1-C2-C3-O3
5	A	1323	GOL	C1-C2-C3-O3
5	A	1318	GOL	O1-C1-C2-O2
5	A	1319	GOL	O1-C1-C2-O2
5	A	1321	GOL	O2-C2-C3-O3
5	A	1322	GOL	O2-C2-C3-O3
5	A	1322	GOL	O1-C1-C2-O2
4	A	1316	ADP	PA-O3A-PB-O3B

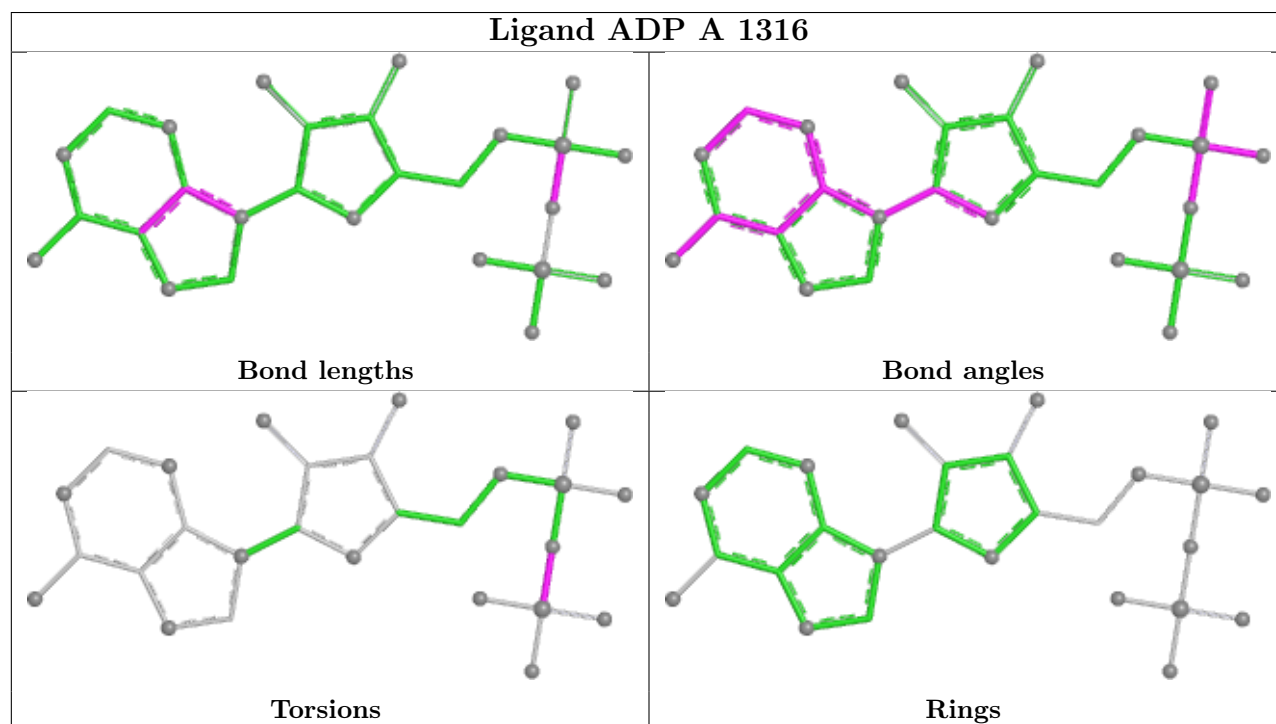
There are no ring outliers.

7 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1311	SO4	1	0
5	A	1317	GOL	1	0
5	A	1324	GOL	2	0
5	A	1320	GOL	4	0
5	A	1322	GOL	6	0
5	A	1323	GOL	3	0
5	A	1319	GOL	3	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 ⓘ

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	1285/1305 (98%)	-0.24	41 (3%) 50 53	8, 23, 55, 93	26 (2%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	216	HIS	6.2
1	A	428	GLY	5.6
1	A	447	GLY	4.1
1	A	1204[A]	ARG	3.9
1	A	429	GLU	3.8
1	A	606	LEU	3.7
1	A	425	VAL	3.7
1	A	31	HIS	3.6
1	A	-9	GLY	3.6
1	A	426	GLN	3.6
1	A	66	SER	3.6
1	A	259	ASN	3.5
1	A	427	LYS	3.4
1	A	217	CYS	3.2
1	A	176	LEU	3.1
1	A	605	LEU	3.1
1	A	257	LYS	2.9
1	A	218	ARG	2.9
1	A	468	ALA	2.9
1	A	609	THR	2.7
1	A	212	ALA	2.7
1	A	608	LYS	2.6
1	A	124	TRP	2.6
1	A	118	THR	2.5
1	A	181	ALA	2.5
1	A	207	TYR	2.5
1	A	424	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	607	GLY	2.5
1	A	219	HIS	2.4
1	A	211	GLN	2.4
1	A	25	ALA	2.4
1	A	119	LEU	2.3
1	A	603	ASP	2.3
1	A	117	SER	2.2
1	A	121	ALA	2.2
1	A	467	PHE	2.2
1	A	30	VAL	2.1
1	A	430	ILE	2.1
1	A	156	ALA	2.1
1	A	152	HIS	2.0
1	A	789	ASN	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	CYG	A	1135	15/16	0.95	0.12	17,26,38,48	2

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.

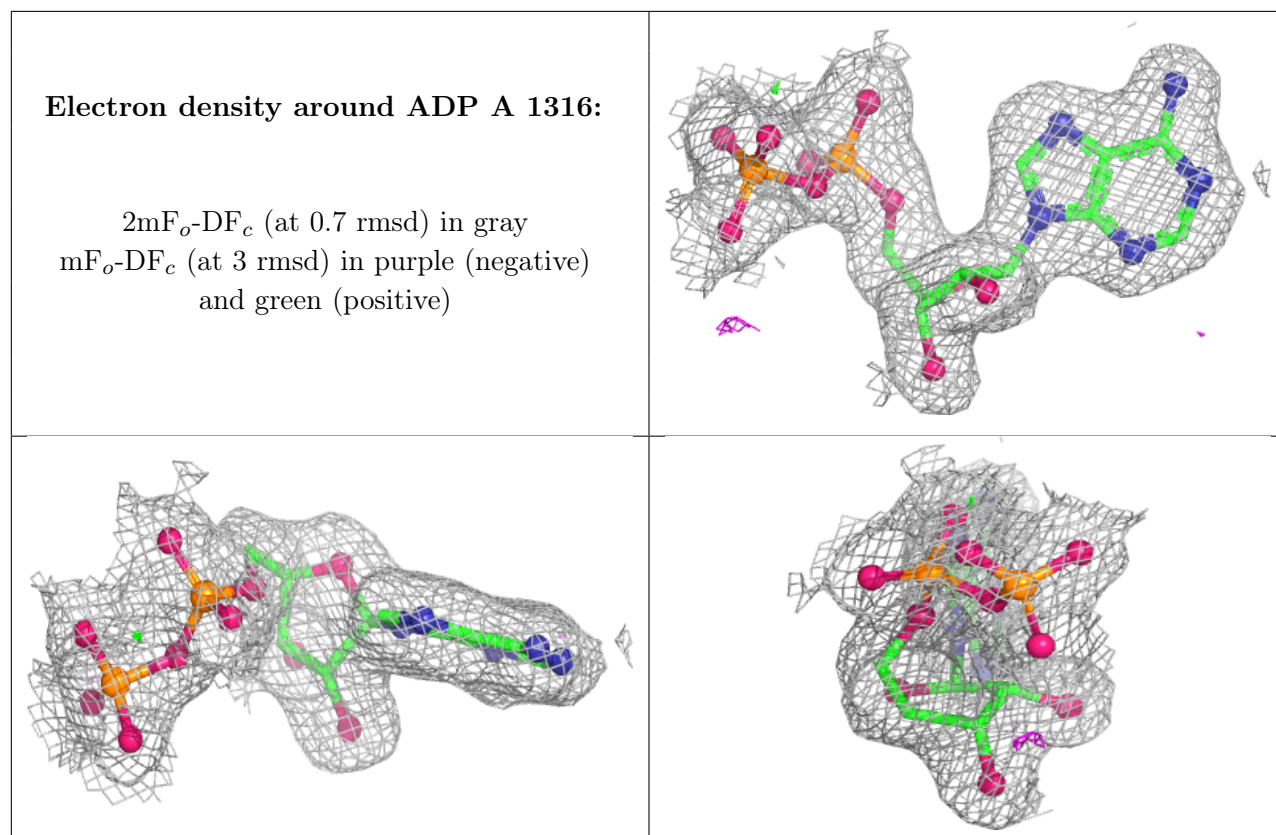
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	A	1311	5/5	0.59	0.18	49,52,57,73	0
5	GOL	A	1323	6/6	0.65	0.23	50,51,55,57	0
5	GOL	A	1324	6/6	0.69	0.24	22,45,48,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	A	1314	5/5	0.73	0.20	38,47,64,73	0
5	GOL	A	1317	6/6	0.77	0.17	27,41,43,55	0
3	SO4	A	1315	5/5	0.78	0.10	70,75,80,84	0
5	GOL	A	1320	6/6	0.79	0.18	30,42,47,48	0
5	GOL	A	1318	6/6	0.81	0.17	43,57,58,63	0
3	SO4	A	1310	5/5	0.81	0.11	55,58,63,81	0
3	SO4	A	1312	5/5	0.85	0.19	37,50,60,67	0
5	GOL	A	1322	6/6	0.85	0.21	28,42,43,63	0
5	GOL	A	1319	6/6	0.88	0.13	26,33,40,49	0
5	GOL	A	1321	6/6	0.90	0.15	29,40,46,51	0
6	CL	A	1326	1/1	0.91	0.17	66,66,66,66	0
6	CL	A	1327	1/1	0.92	0.11	54,54,54,54	0
3	SO4	A	1309	5/5	0.93	0.16	41,48,49,50	0
3	SO4	A	1313	5/5	0.93	0.11	41,42,54,60	0
3	SO4	A	1308	5/5	0.94	0.15	42,49,59,65	0
3	SO4	A	1306	5/5	0.96	0.13	32,34,45,51	0
3	SO4	A	1305	5/5	0.98	0.10	24,34,37,38	0
3	SO4	A	1304	5/5	0.98	0.07	33,37,40,45	0
2	MG	A	1301	1/1	0.99	0.01	13,13,13,13	0
2	MG	A	1302	1/1	0.99	0.02	17,17,17,17	0
2	MG	A	1303	1/1	0.99	0.01	16,16,16,16	0
6	CL	A	1325	1/1	0.99	0.06	27,27,27,27	0
3	SO4	A	1307	5/5	0.99	0.04	24,28,29,30	0
4	ADP	A	1316	27/27	0.99	0.03	13,16,19,20	0

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



6.5 Other polymers [i](#)

There are no such residues in this entry.