



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 01:18 AM UTC

PDB ID : 7C0Z / pdb_00007c0z
Title : Crystal structure of a dinucleotide-binding protein (Y246A) of ABC transporter endogenously bound to uridylyl-3'-5'-phospho-guanosine (Form II)
Authors : Kanaujia, S.P.; Chandravanshi, M.; Samanta, R.
Deposited on : 2020-05-01
Resolution : 2.20 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

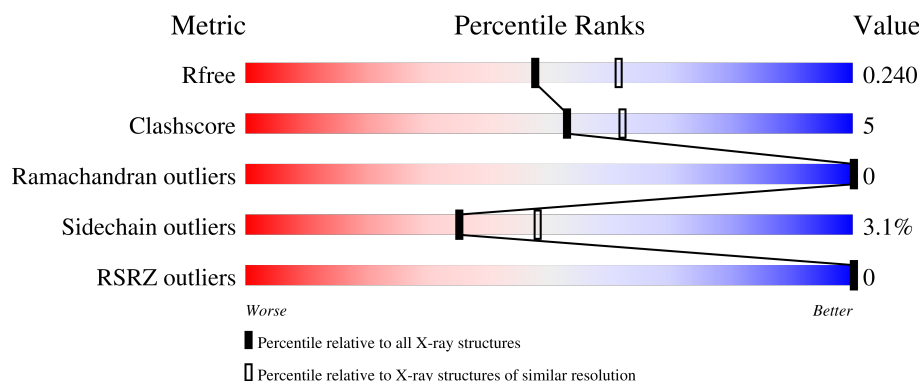
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	406	 78% 17% . .
1	B	406	 78% 17% . .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6268 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.

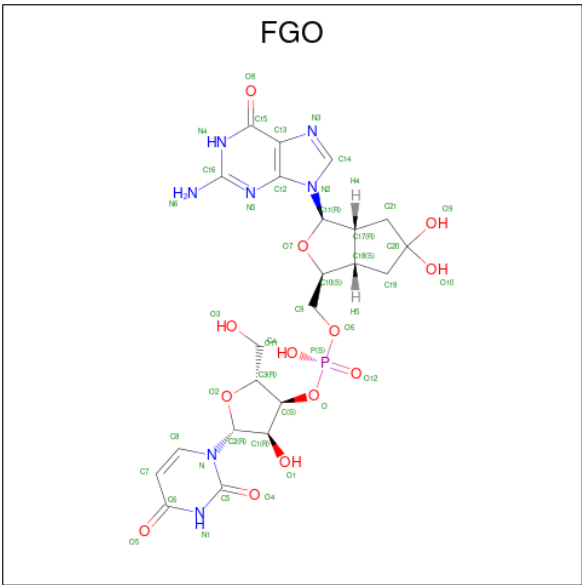
- Molecule 1 is a protein called Sugar ABC transporter, periplasmic sugar-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	3	0
			3045	1970	516	556	3			
1	B	392	Total	C	N	O	S	0	1	0
			3023	1955	512	553	3			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP Q5SLB4
A	0	MET	-	expression tag	UNP Q5SLB4
A	246	ALA	TYR	engineered mutation	UNP Q5SLB4
A	399	HIS	-	expression tag	UNP Q5SLB4
A	400	HIS	-	expression tag	UNP Q5SLB4
A	401	HIS	-	expression tag	UNP Q5SLB4
A	402	HIS	-	expression tag	UNP Q5SLB4
A	403	HIS	-	expression tag	UNP Q5SLB4
A	404	HIS	-	expression tag	UNP Q5SLB4
B	-1	MET	-	initiating methionine	UNP Q5SLB4
B	0	MET	-	expression tag	UNP Q5SLB4
B	246	ALA	TYR	engineered mutation	UNP Q5SLB4
B	399	HIS	-	expression tag	UNP Q5SLB4
B	400	HIS	-	expression tag	UNP Q5SLB4
B	401	HIS	-	expression tag	UNP Q5SLB4
B	402	HIS	-	expression tag	UNP Q5SLB4
B	403	HIS	-	expression tag	UNP Q5SLB4
B	404	HIS	-	expression tag	UNP Q5SLB4

- Molecule 2 is [(1S,3R,3aR,6aS)-3-(2-azanyl-6-oxidanylidene-1H-purin-9-yl)-5,5-bis(oxidanyl)-1,3,3a,4,6,6a-hexahydrocyclopenta[c]furan-1-yl)methyl [(2R,3S,4R,5R)-5-[2,4-bis(oxidanylidene)pyrimidin-1-yl]-2-(hydroxymethyl)-4-oxidanyl-oxolan-3-yl] hydrogen phosphate (CCD ID: FGO) (formula: C₂₂H₂₈N₇O₁₃P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 22	N 7	O 13	P 1	0	0
2	B	1	Total 43	C 22	N 7	O 13	P 1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

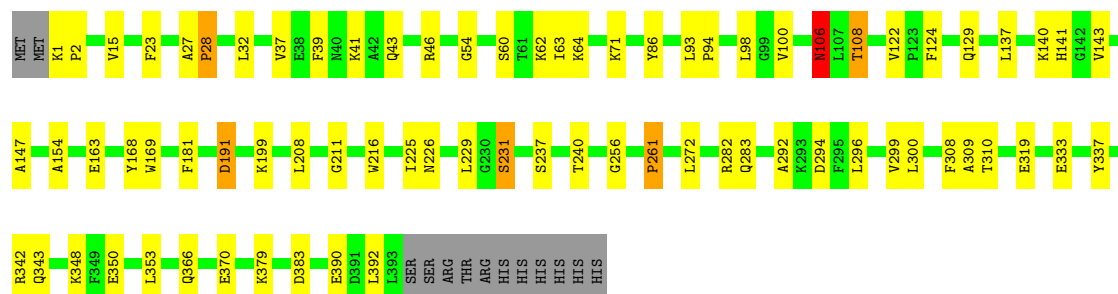
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	58	Total 58	O 58	0	0
4	B	52	Total 52	O 52	0	0

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.

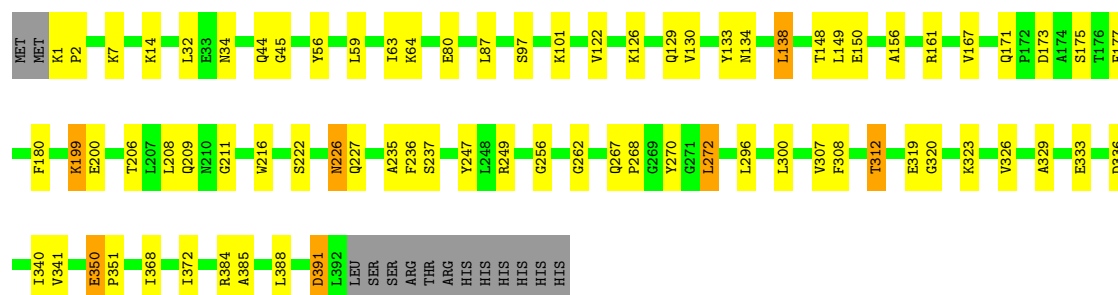
- Molecule 1: Sugar ABC transporter, periplasmic sugar-binding protein

Chain A: 



- Molecule 1: Sugar ABC transporter, periplasmic sugar-binding protein

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.80Å 104.39Å 65.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.74 – 2.20 65.74 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.6 (65.74-2.20) 97.6 (65.74-2.20)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.188 , 0.238 0.192 , 0.240	Depositor DCC
R_{free} test set	2011 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	19.9	Xtriage
Anisotropy	0.855	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 5.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.427 for h,-k,-l	Xtriage
Reported twinning fraction	0.441 for H, K, L 0.559 for -h,-k,l	Depositor
Outliers	0 of 39334 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6268	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	1.26	11/3123 (0.4%)	1.63	20/4236 (0.5%)
1	B	1.27	11/3095 (0.4%)	1.64	26/4199 (0.6%)
All	All	1.27	22/6218 (0.4%)	1.63	46/8435 (0.5%)

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	94	PRO	C-O	-6.85	1.15	1.23
1	A	181	PHE	C-O	6.83	1.31	1.24
1	B	312	THR	C-O	6.16	1.32	1.24
1	B	167	VAL	C-O	-6.01	1.18	1.24
1	B	351	PRO	C-O	-5.91	1.16	1.23
1	A	300	LEU	C-O	5.66	1.31	1.24
1	B	156	ALA	C-O	5.58	1.30	1.24
1	B	237	SER	C-O	5.53	1.30	1.23
1	A	143	VAL	N-CA	5.51	1.50	1.46
1	A	28	PRO	C-O	-5.48	1.17	1.24
1	A	23	PHE	C-O	5.44	1.30	1.24
1	B	130	VAL	C-O	5.44	1.29	1.23
1	A	299	VAL	C-O	-5.43	1.17	1.24
1	B	336	ASP	C-O	5.42	1.30	1.24
1	B	270	TYR	C-O	5.40	1.30	1.23
1	A	308	PHE	C-O	5.38	1.30	1.24
1	A	208	LEU	C-O	5.33	1.30	1.24
1	B	341	VAL	C-O	5.29	1.30	1.24
1	A	261	PRO	C-O	-5.27	1.17	1.23
1	B	138	LEU	C-O	5.23	1.30	1.24
1	A	129	GLN	C-O	-5.19	1.17	1.23
1	B	272	LEU	C-O	5.14	1.30	1.24

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	191	ASP	CA-CB-CG	8.05	120.65	112.60
1	B	150	GLU	CB-CG-CD	7.37	125.13	112.60
1	A	28	PRO	CB-CA-C	6.88	123.98	112.62
1	B	256	GLY	CA-C-O	-6.55	115.22	121.11
1	A	319	GLU	CB-CG-CD	6.48	123.62	112.60
1	B	101	LYS	CB-CA-C	6.42	120.13	109.53
1	A	225	ILE	CA-C-N	6.30	129.36	120.28
1	A	225	ILE	C-N-CA	6.30	129.36	120.28
1	A	106	ASN	CB-CA-C	6.21	119.58	109.90
1	A	60	SER	CA-C-N	6.09	128.36	120.44
1	A	60	SER	C-N-CA	6.09	128.36	120.44
1	B	307	VAL	N-CA-C	-5.87	105.02	110.53
1	B	226	ASN	CA-CB-CG	5.85	118.45	112.60
1	B	173	ASP	CA-C-N	5.81	128.86	120.38
1	B	173	ASP	C-N-CA	5.81	128.86	120.38
1	B	247	TYR	CA-C-N	5.74	128.54	120.28
1	B	247	TYR	C-N-CA	5.74	128.54	120.28
1	A	199	LYS	CB-CA-C	5.57	120.15	110.68
1	B	391	ASP	CA-CB-CG	5.53	118.13	112.60
1	B	350	GLU	N-CA-C	-5.50	103.80	110.13
1	A	294	ASP	CA-CB-CG	5.48	118.08	112.60
1	A	54	GLY	CA-C-O	-5.46	115.84	120.64
1	B	340	ILE	CA-C-O	-5.45	115.28	120.95
1	B	180	PHE	CA-C-N	5.38	128.26	120.79
1	B	180	PHE	C-N-CA	5.38	128.26	120.79
1	B	236	PHE	CB-CA-C	-5.34	99.10	109.68
1	A	154	ALA	CA-C-N	5.30	127.69	120.54
1	A	154	ALA	C-N-CA	5.30	127.69	120.54
1	B	161	ARG	N-CA-C	-5.28	105.60	111.36
1	B	320	GLY	CA-C-N	5.28	127.67	120.54
1	B	320	GLY	C-N-CA	5.28	127.67	120.54
1	B	171	GLN	CB-CA-C	5.26	117.94	109.41
1	B	34	ASN	CA-C-N	5.21	127.53	120.44
1	B	34	ASN	C-N-CA	5.21	127.53	120.44
1	A	108	THR	CB-CA-C	5.18	119.44	110.84
1	A	28	PRO	N-CA-C	-5.17	106.35	113.53
1	A	71	LYS	CB-CA-C	-5.15	104.72	112.09
1	A	309	ALA	O-C-N	5.15	127.58	122.12
1	B	351	PRO	CA-C-O	-5.09	115.60	121.36
1	B	227	GLN	N-CA-C	-5.09	107.46	113.97
1	B	391	ASP	CB-CA-C	-5.08	102.90	110.88
1	B	206	THR	CA-CB-OG1	-5.08	101.98	109.60
1	A	240	THR	CA-CB-OG1	-5.04	102.04	109.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	256	GLY	CA-C-O	-5.04	116.58	121.11
1	A	343	GLN	CA-C-O	-5.03	114.19	119.97
1	B	134	ASN	CA-C-O	-5.02	115.42	120.84

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	3045	0	3087	28	1
1	B	3023	0	3057	33	1
2	A	43	0	0	0	0
2	B	43	0	0	0	0
3	B	4	0	6	0	0
4	A	58	0	0	0	0
4	B	52	0	0	4	0
All	All	6268	0	6150	61	1

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 5.

All (61) 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:7:LYS:HD2	4:B:605:HOH:O	1.90	0.71
1:B:59:LEU:HD11	1:B:63:ILE:HD11	1.72	0.70
1:B:80:GLU:OE2	1:B:126:LYS:NZ	2.26	0.69
1:B:199:LYS:HE2	1:B:200:GLU:OE2	1.93	0.69
1:B:148:THR:HA	1:B:262:GLY:O	1.93	0.68
1:A:379:LYS:NZ	1:A:383:ASP:OD2	2.27	0.68
1:B:199:LYS:CE	1:B:200:GLU:OE2	2.48	0.62
1:A:342[A]:ARG:HH11	1:A:342[A]:ARG:HG3	1.65	0.61
1:A:93:LEU:CD2	1:A:282:ARG:HG2	2.32	0.59
1:B:129:GLN:NE2	1:B:175:SER:O	2.36	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:TYR:C	1:A:168:TYR:CD1	2.81	0.58
1:B:272:LEU:HD11	1:B:350:GLU:HG3	1.86	0.58
1:B:329:ALA:O	1:B:333:GLU:HG2	2.03	0.57
1:B:368:ILE:O	1:B:372:ILE:HG12	2.05	0.56
1:A:98:LEU:HB2	1:A:100:VAL:HG23	1.88	0.56
1:A:310:THR:HA	1:A:337:TYR:CE1	2.41	0.55
1:A:1:LYS:HB3	1:A:2:PRO:CD	2.36	0.55
1:B:267:GLN:HG2	1:B:268:PRO:O	2.07	0.54
1:B:59:LEU:CD1	1:B:63:ILE:HD11	2.36	0.54
1:B:211:GLY:HA2	1:B:216:TRP:CE2	2.43	0.54
1:A:15:VAL:CG1	1:A:46:ARG:HG2	2.36	0.54
1:B:319:GLU:HB2	4:B:635:HOH:O	2.08	0.54
1:A:366:GLN:O	1:A:370[B]:GLU:HG2	2.08	0.53
1:B:308:PHE:O	1:B:312:THR:HG23	2.10	0.52
1:A:39:PHE:O	1:A:43:GLN:HG2	2.10	0.51
1:A:392:LEU:HD12	1:A:392:LEU:O	2.11	0.50
1:A:140:LYS:HD3	1:A:141:HIS:NE2	2.26	0.50
1:B:14:LYS:HG2	1:B:45:GLY:O	2.13	0.48
1:B:388:LEU:O	1:B:391:ASP:HB2	2.13	0.48
1:A:226:ASN:HA	1:A:229:LEU:HD12	1.95	0.48
1:B:133:TYR:CD2	1:B:138:LEU:HD22	2.49	0.47
1:B:177:PHE:HB2	1:B:368:ILE:HD13	1.96	0.47
1:B:199:LYS:NZ	1:B:200:GLU:OE2	2.47	0.47
1:A:147:ALA:O	1:A:261:PRO:HA	2.15	0.47
1:B:32:LEU:HD12	1:B:32:LEU:O	2.15	0.47
1:A:272:LEU:HD11	1:A:350:GLU:HG3	1.97	0.46
1:A:211:GLY:HA2	1:A:216:TRP:CE2	2.51	0.46
1:B:122:VAL:HG21	1:B:296:LEU:HD22	1.98	0.46
1:A:37:VAL:HG12	1:A:41:LYS:HE3	1.98	0.46
1:A:169:TRP:CH2	1:A:231:SER:O	2.69	0.46
1:B:32:LEU:HD12	1:B:32:LEU:C	2.40	0.45
1:A:122:VAL:HG21	1:A:296:LEU:HD13	1.98	0.45
1:B:208:LEU:O	1:B:209:GLN:C	2.58	0.45
1:A:63:ILE:HD12	1:A:86:TYR:OH	2.17	0.45
1:A:106:ASN:OD1	1:A:108:THR:HB	2.17	0.45
1:A:27:ALA:HB3	1:A:28:PRO:HD3	1.99	0.45
1:B:1:LYS:O	1:B:2:PRO:C	2.58	0.44
1:B:7:LYS:HE3	4:B:605:HOH:O	2.17	0.44
1:B:384:ARG:O	1:B:385:ALA:C	2.61	0.43
1:A:292:ALA:O	1:A:296:LEU:HG	2.18	0.43
1:B:56:TYR:O	1:B:59:LEU:HB3	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:TYR:HA	1:B:235:ALA:O	2.19	0.43
1:A:1:LYS:HB3	1:A:2:PRO:HD2	2.01	0.42
1:B:122:VAL:CG1	1:B:300:LEU:HD21	2.49	0.42
1:B:384:ARG:NE	1:B:388:LEU:HD11	2.35	0.42
1:A:137:LEU:HD11	1:A:163:GLU:HG3	2.02	0.42
1:A:93:LEU:HD11	1:A:282:ARG:HA	2.02	0.41
1:A:32:LEU:HD13	1:A:124:PHE:CZ	2.55	0.41
1:B:87:LEU:HD23	1:B:87:LEU:HA	1.88	0.41
1:A:169:TRP:HH2	1:A:231:SER:O	2.04	0.41
1:B:7:LYS:CE	4:B:605:HOH:O	2.68	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:LYS:NZ	1:B:323:LYS:O[2_556]	2.10	0.10

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	394/406 (97%)	380 (96%)	14 (4%)	0	100	100
1	B	391/406 (96%)	375 (96%)	16 (4%)	0	100	100
All	All	785/812 (97%)	755 (96%)	30 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	308/318 (97%)	298 (97%)	10 (3%)	34	47
1	B	305/318 (96%)	296 (97%)	9 (3%)	36	49
All	All	613/636 (96%)	594 (97%)	19 (3%)	35	48

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

Mol	Chain	Res	Type
1	A	62	LYS
1	A	64	LYS
1	A	106	ASN
1	A	191	ASP
1	A	231	SER
1	A	237	SER
1	A	283	GLN
1	A	333	GLU
1	A	353	LEU
1	A	390	GLU
1	B	44	GLN
1	B	64	LYS
1	B	97	SER
1	B	149	LEU
1	B	199	LYS
1	B	222	SER
1	B	226	ASN
1	B	249	ARG
1	B	326	VAL

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

Mol	Chain	Res	Type
1	A	358	GLN
1	B	44	GLN
1	B	226	ASN

5.3.3 RNA ⓘ

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	FGO	A	501	-	48,48,48	1.32	6 (12%)	64,75,75	2.14	21 (32%)
2	FGO	B	502	-	48,48,48	1.47	6 (12%)	64,75,75	2.17	23 (35%)
3	EDO	B	501	-	3,3,3	0.15	0	2,2,2	0.19	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
2	FGO	A	501	-	-	1/21/63/63	0/6/6/6
2	FGO	B	502	-	-	2/21/63/63	0/6/6/6
3	EDO	B	501	-	-	1/1/1/1	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	FGO	C5-N	3.97	1.44	1.38
2	A	501	FGO	C5-N	3.41	1.43	1.38
2	B	502	FGO	C13-C12	3.25	1.47	1.38
2	A	501	FGO	C13-C12	2.95	1.46	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	FGO	C6-N1	-2.92	1.33	1.38
2	B	502	FGO	C15-N4	-2.84	1.33	1.38
2	B	502	FGO	C6-N1	-2.79	1.33	1.38
2	B	502	FGO	C12-N2	-2.66	1.31	1.38
2	A	501	FGO	O4-C5	2.41	1.27	1.23
2	A	501	FGO	C17-C11	2.26	1.55	1.52
2	B	502	FGO	C13-N3	-2.23	1.34	1.39
2	A	501	FGO	C12-N2	-2.09	1.32	1.38

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	FGO	O7-C11-N2	-6.15	94.42	108.36
2	B	502	FGO	C13-C12-N5	-5.44	119.72	128.39
2	B	502	FGO	C16-N5-C12	4.69	120.37	112.30
2	B	502	FGO	N1-C5-N	4.64	120.93	114.89
2	B	502	FGO	C6-N1-C5	-4.64	120.86	126.61
2	A	501	FGO	C13-C12-N5	-4.60	121.07	128.39
2	B	502	FGO	C15-C13-N3	4.40	138.29	130.29
2	A	501	FGO	C16-N5-C12	4.26	119.64	112.30
2	A	501	FGO	C6-N1-C5	-4.22	121.38	126.61
2	A	501	FGO	C15-C13-N3	4.00	137.57	130.29
2	B	502	FGO	C7-C6-N1	3.72	120.02	114.80
2	A	501	FGO	O10-C20-C21	3.71	122.83	110.56
2	A	501	FGO	C19-C18-C17	3.54	110.78	103.77
2	B	502	FGO	N2-C12-N5	3.54	133.03	125.95
2	A	501	FGO	C7-C6-N1	3.53	119.75	114.80
2	A	501	FGO	N1-C5-N	3.50	119.44	114.89
2	A	501	FGO	N2-C12-N5	3.49	132.93	125.95
2	B	502	FGO	C2-N-C5	3.31	123.53	117.59
2	B	502	FGO	C1-C2-N	3.27	122.36	113.25
2	A	501	FGO	O2-C2-C1	-3.24	99.69	106.62
2	B	502	FGO	O4-C5-N1	-3.14	115.70	121.49
2	A	501	FGO	C2-N-C5	3.00	122.98	117.59
2	A	501	FGO	O5-C6-C7	-3.00	119.98	125.16
2	B	502	FGO	C12-C13-N3	-2.88	106.10	110.67
2	B	502	FGO	O5-C6-C7	-2.86	120.23	125.16
2	B	502	FGO	O7-C11-N2	-2.83	101.94	108.36
2	B	502	FGO	C19-C18-C17	2.83	109.36	103.77
2	B	502	FGO	C10-O7-C11	-2.68	103.54	109.47
2	B	502	FGO	C8-N-C5	-2.68	117.73	121.00
2	A	501	FGO	O11-P-O6	-2.63	95.63	107.57

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	502	FGO	C13-C15-N4	2.62	119.93	113.25
2	A	501	FGO	O8-C15-C13	-2.50	119.92	126.53
2	B	502	FGO	C16-N4-C15	-2.46	120.64	125.11
2	A	501	FGO	C12-C13-N3	-2.38	106.89	110.67
2	B	502	FGO	C11-N2-C12	-2.37	119.49	126.49
2	A	501	FGO	O4-C5-N1	-2.37	117.12	121.49
2	A	501	FGO	C17-C18-C10	2.32	108.37	103.66
2	B	502	FGO	O7-C10-C18	2.31	109.15	104.88
2	A	501	FGO	C15-C13-C12	-2.19	115.54	118.83
2	A	501	FGO	C11-N2-C12	-2.15	120.14	126.49
2	B	502	FGO	C15-C13-C12	-2.14	115.61	118.83
2	A	501	FGO	C13-C15-N4	2.10	118.60	113.25
2	B	502	FGO	O8-C15-C13	-2.07	121.06	126.53
2	B	502	FGO	O6-C9-C10	-2.05	102.00	108.99

There are no chirality outliers.

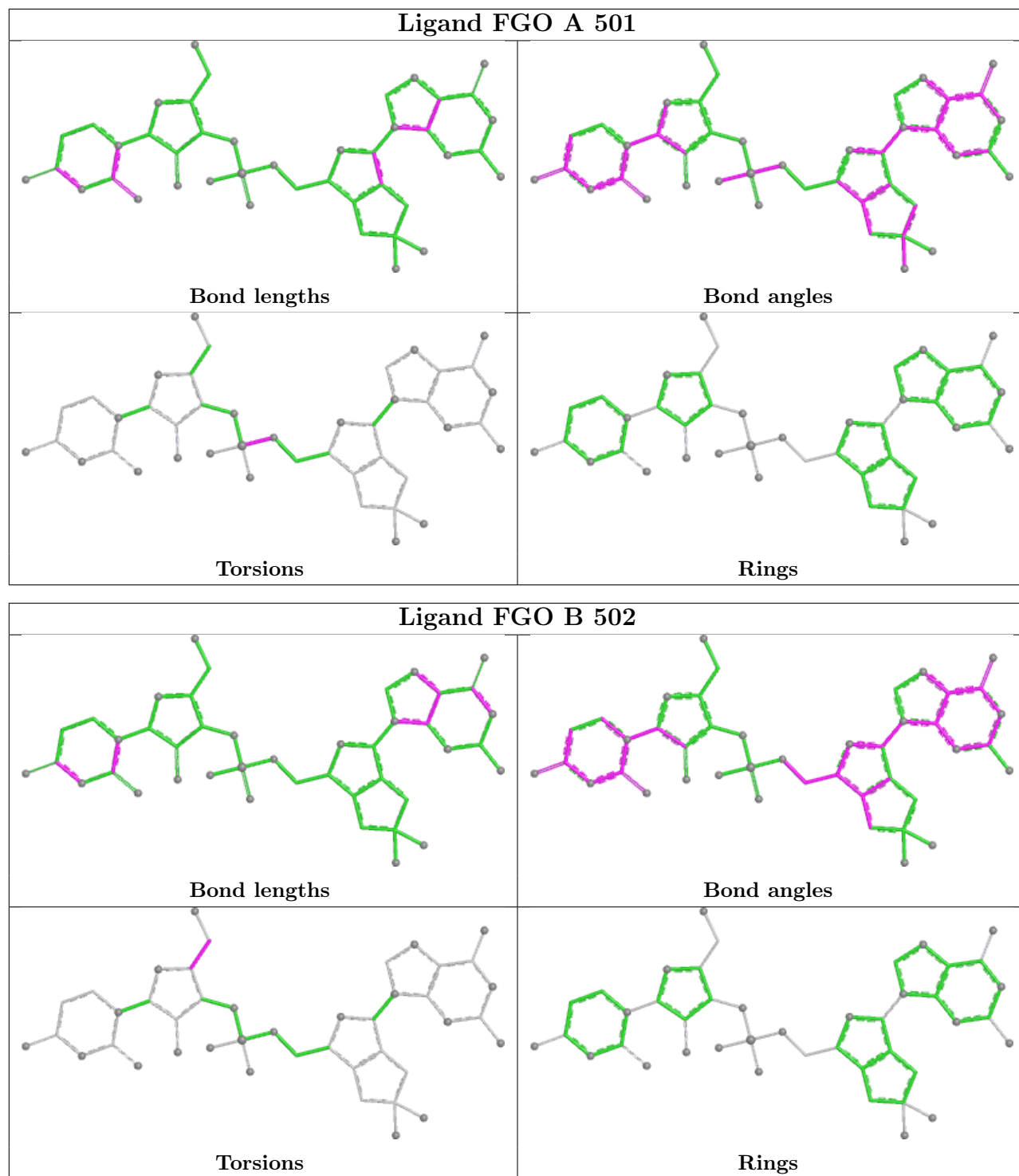
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	FGO	C9-O6-P-O
2	B	502	FGO	C-C3-C4-O3
3	B	501	EDO	O1-C1-C2-O2
2	B	502	FGO	O2-C3-C4-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 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	393/406 (96%)	-1.33	0 100 100	7, 19, 33, 42	3 (0%)
1	B	392/406 (96%)	-1.33	0 100 100	10, 19, 36, 46	1 (0%)
All	All	785/812 (96%)	-1.33	0 100 100	7, 19, 35, 46	4 (0%)

There are no RSRZ outliers to report.

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.

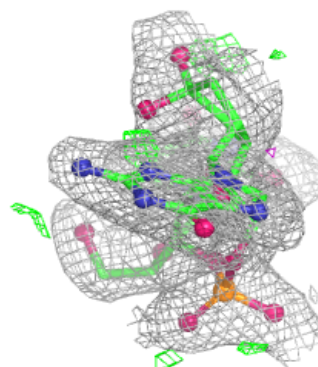
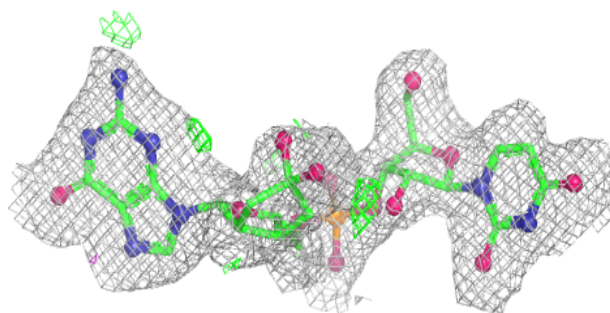
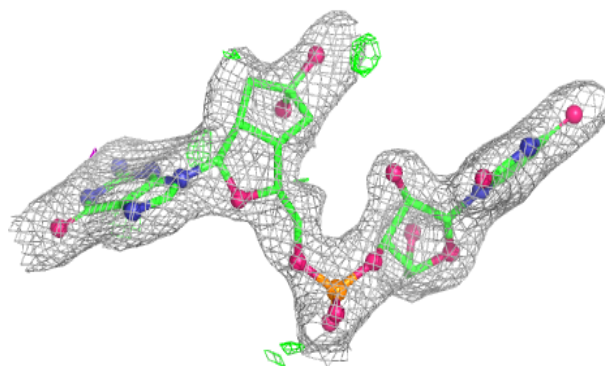
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FGO	A	501	43/43	0.99	0.03	17,21,27,28	0
2	FGO	B	502	43/43	0.99	0.04	17,24,37,44	0
3	EDO	B	501	4/4	1.00	0.03	18,18,19,21	0

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.

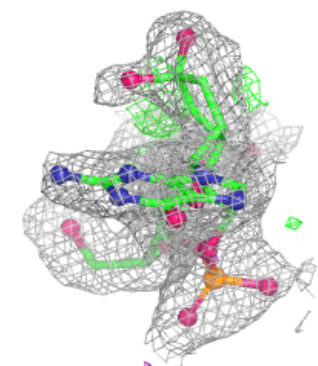
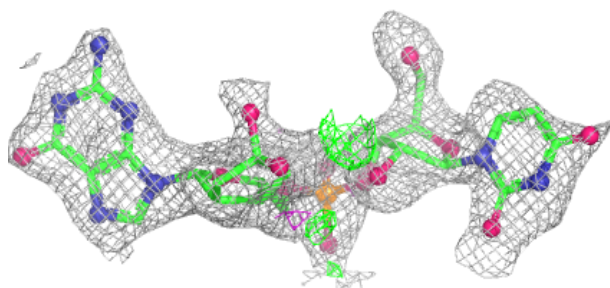
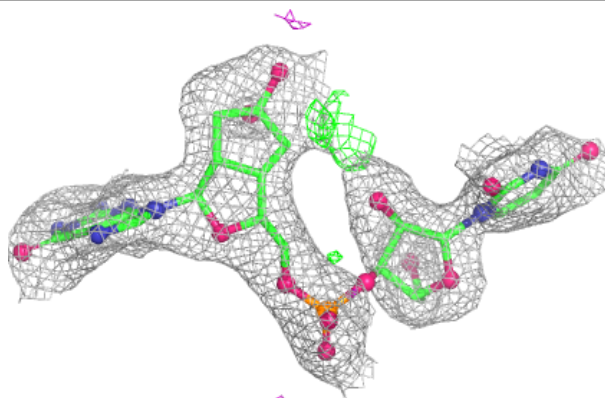
Electron density around FGO A 501:

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



Electron density around FGO B 502:

$2mF_o-DF_c$ (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.