



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 18, 2023 – 01:51 AM EDT

PDB ID : 4ZWE
Title : Crystal structure of the dGTP-bound catalytic core of SAMHD1 T592V mutant
Authors : Tang, C.; Ji, X.; Xiong, Y.
Deposited on : 2015-05-19
Resolution : 2.81 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

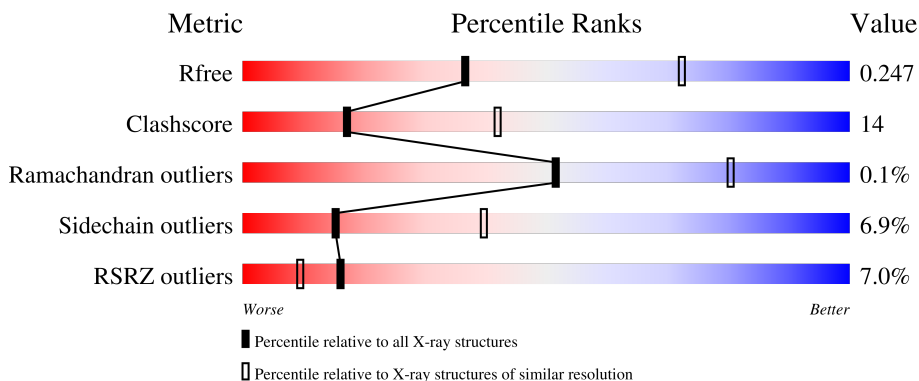
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 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	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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	514	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 68%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 23%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="margin-left: 40px;">4% 68% 23% • 7%</p>
1	B	514	<div style="display: flex; align-items: center;"> <div style="width: 14%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 63%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 27%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="margin-left: 40px;">14% 63% 27% • 7%</p>
1	C	514	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 66%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 25%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="margin-left: 40px;">4% 66% 25% • 7%</p>
1	D	514	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 68%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 23%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="margin-left: 40px;">4% 68% 23% • 7%</p>

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
2	DGT	B	701	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 16098 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 Deoxynucleoside triphosphate triphosphohydrolase SAMHD1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	480	3925	2514	684	707	20	0	0	0
1	B	480	3934	2519	686	709	20	0	1	0
1	C	480	3925	2514	684	707	20	0	0	0
1	D	480	3934	2519	685	710	20	0	1	0

There are 12 discrepancies between the modelled and reference sequences:

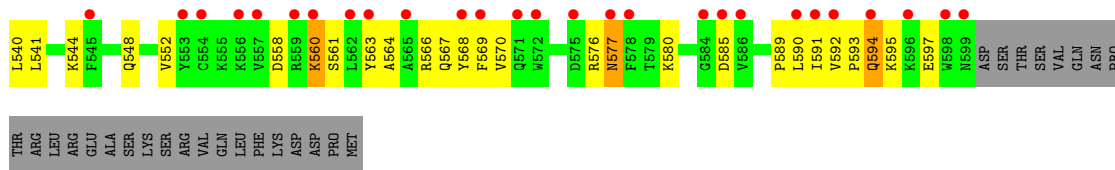
Chain	Residue	Modelled	Actual	Comment	Reference
A	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
A	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
A	592	VAL	THR	engineered mutation	UNP Q9Y3Z3
B	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
B	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
B	592	VAL	THR	engineered mutation	UNP Q9Y3Z3
C	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
C	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
C	592	VAL	THR	engineered mutation	UNP Q9Y3Z3
D	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
D	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
D	592	VAL	THR	engineered mutation	UNP Q9Y3Z3

- Molecule 2 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (three-letter code: DGT) (formula: C₁₀H₁₆N₅O₁₃P₃).

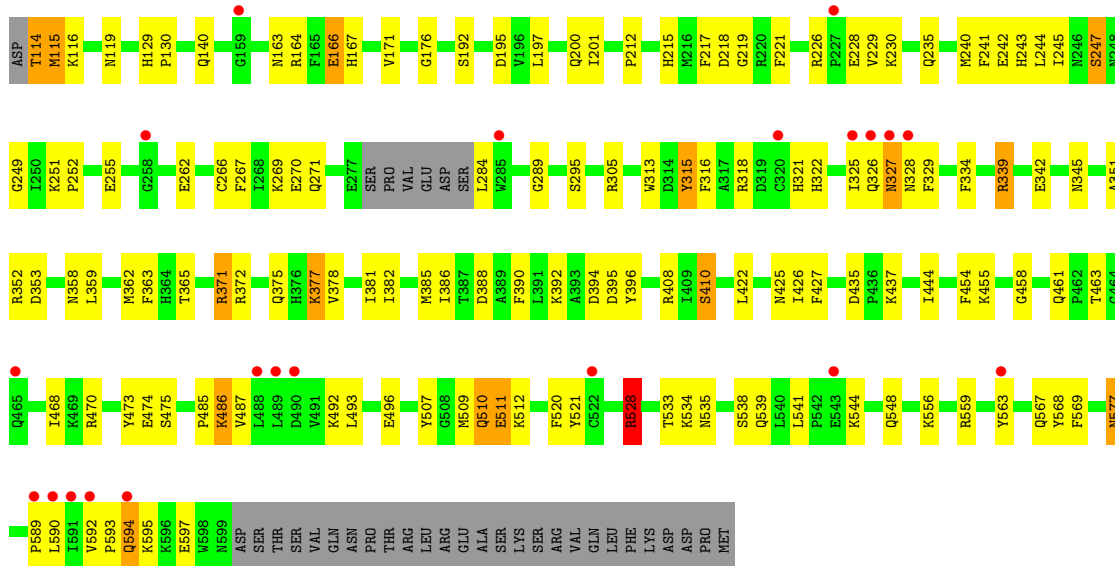
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	2	Total Mg 2 2	0	0
3	C	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0

- Molecule 4 is water.

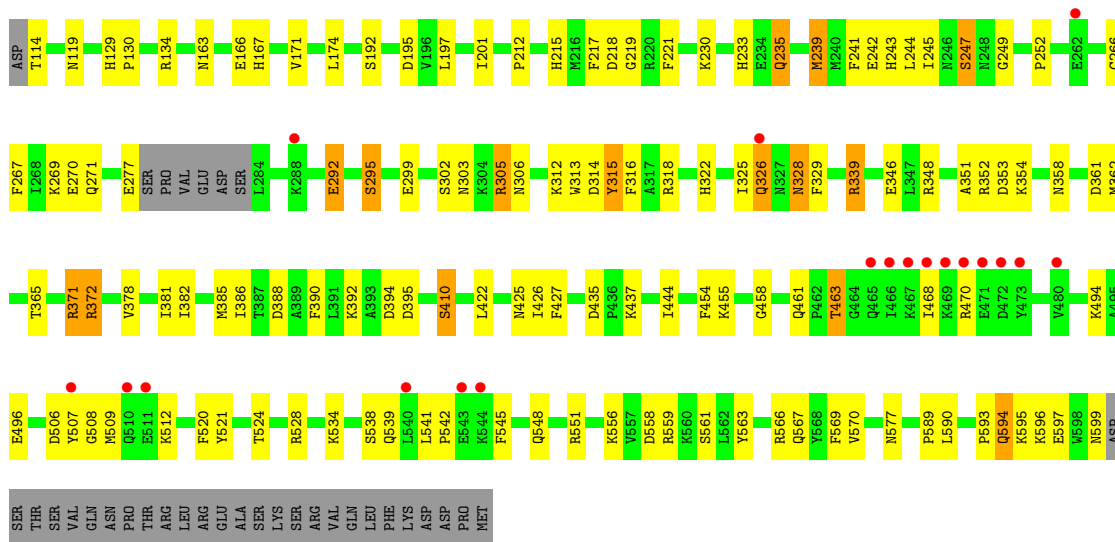
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	3	Total O 3 3	0	0



• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.08Å 146.09Å 98.46Å 90.00° 115.03° 90.00°	Depositor
Resolution (Å)	50.00 – 2.81 48.74 – 2.81	Depositor EDS
% Data completeness (in resolution range)	98.1 (50.00-2.81) 98.1 (48.74-2.81)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.81Å)	Xtrriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.208 , 0.248 0.211 , 0.247	Depositor DCC
R_{free} test set	2789 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	59.7	Xtrriage
Anisotropy	0.255	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 66.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.018 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16098	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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: MG, DGT

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	0.57	0/4017	0.72	1/5422 (0.0%)
1	B	0.54	0/4026	0.71	5/5434 (0.1%)
1	C	0.55	0/4017	0.70	3/5422 (0.1%)
1	D	0.59	0/4026	0.71	2/5434 (0.0%)
All	All	0.56	0/16086	0.71	11/21712 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	218	ASP	CB-CG-OD2	-8.96	110.23	118.30
1	B	371	ARG	NE-CZ-NH2	-8.36	116.12	120.30
1	B	371	ARG	NE-CZ-NH1	7.98	124.29	120.30
1	C	528	ARG	NE-CZ-NH2	6.42	123.51	120.30
1	B	395	ASP	CB-CG-OD1	6.35	124.01	118.30
1	A	408	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	D	239	MET	CG-SD-CE	-5.39	91.57	100.20
1	C	218	ASP	CB-CG-OD1	5.30	123.07	118.30
1	D	305	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	B	359	LEU	CB-CG-CD1	5.13	119.72	111.00
1	B	354	LYS	CB-CG-CD	-5.08	98.38	111.60

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	3925	0	3919	100	0
1	B	3934	0	3922	152	0
1	C	3925	0	3919	117	0
1	D	3934	0	3923	90	0
2	A	124	0	48	4	0
2	B	93	0	36	23	0
2	C	62	0	24	9	0
2	D	93	0	36	7	0
3	A	1	0	0	0	0
3	B	2	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	3	0	0	0	0
All	All	16098	0	15827	445	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 14.

All (445) 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:D:303:ASN:ND2	1:D:306:ASN:OD1	1.56	1.37
1:B:329:PHE:CD2	1:B:362:MET:HB2	1.62	1.35
1:B:328:ASN:CB	1:B:365:THR:OG1	1.82	1.28
1:D:303:ASN:CG	1:D:306:ASN:OD1	1.71	1.25
1:B:354:LYS:HZ1	2:B:705:DGT:PA	1.58	1.24
1:D:242:GLU:OE1	1:D:269:LYS:NZ	1.74	1.21
1:C:242:GLU:OE1	1:C:269:LYS:NZ	1.75	1.20
1:B:469:LYS:N	1:B:472:ASP:OD2	1.74	1.18
1:B:354:LYS:NZ	2:B:705:DGT:PA	2.16	1.18
1:B:470:ARG:HA	1:B:473:TYR:CE2	1.80	1.15
1:B:577:ASN:ND2	1:B:595:LYS:HZ1	1.48	1.11
1:A:558:ASP:CG	1:A:561:SER:OG	1.92	1.07
1:A:329:PHE:CD2	1:A:362:MET:HG3	1.92	1.04
1:B:215:HIS:CE1	2:B:701:DGT:O2B	2.11	1.04
1:B:242:GLU:OE1	1:B:269:LYS:NZ	1.89	1.04
1:B:328:ASN:HB3	1:B:365:THR:OG1	1.49	1.04
1:A:558:ASP:OD1	1:A:561:SER:OG	1.75	1.04
1:B:328:ASN:HB2	1:B:365:THR:OG1	1.54	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:ASP:OD1	1:A:408:ARG:NH1	1.91	1.03
1:B:375:GLN:NE2	2:B:701:DGT:O6	1.92	1.02
1:A:242:GLU:OE1	1:A:269:LYS:NZ	1.92	1.01
1:A:558:ASP:OD2	1:A:561:SER:OG	1.77	1.01
1:C:533:THR:OG1	1:C:535:ASN:OD1	1.80	1.00
1:B:577:ASN:ND2	1:B:595:LYS:NZ	2.10	0.99
1:D:315:TYR:OH	2:D:703:DGT:O3G	1.82	0.96
1:C:394:ASP:OD2	1:C:410:SER:OG	1.83	0.96
1:D:394:ASP:OD2	1:D:410:SER:OG	1.83	0.96
1:B:597:GLU:OE1	1:B:597:GLU:N	1.99	0.96
1:B:394:ASP:OD2	1:B:410:SER:OG	1.82	0.95
1:A:314:ASP:OD1	1:A:318:ARG:NH2	2.00	0.94
1:D:597:GLU:N	1:D:597:GLU:OE1	2.00	0.94
1:B:425:ASN:ND2	1:C:425:ASN:OD1	2.01	0.94
1:A:425:ASN:OD1	1:D:425:ASN:ND2	2.01	0.94
1:B:329:PHE:CD2	1:B:362:MET:CB	2.49	0.93
1:A:597:GLU:N	1:A:597:GLU:OE1	2.00	0.93
1:C:328:ASN:OD1	1:C:365:THR:OG1	1.85	0.92
1:B:329:PHE:HD2	1:B:362:MET:HB2	1.22	0.91
1:A:558:ASP:CG	1:A:561:SER:HG	1.67	0.90
1:B:328:ASN:HB3	1:B:365:THR:HG1	1.30	0.90
1:A:354:LYS:NZ	2:A:704:DGT:O1A	2.04	0.89
1:B:354:LYS:NZ	2:B:705:DGT:O2A	2.01	0.89
1:A:328:ASN:HB3	1:A:365:THR:OG1	1.74	0.88
1:B:372:ARG:NH2	1:D:358:ASN:OD1	2.07	0.87
1:A:479:GLU:OE1	1:A:576:ARG:NH2	2.11	0.84
1:C:266:CYS:O	1:C:270:GLU:HG3	1.79	0.82
1:B:577:ASN:HD22	1:B:595:LYS:NZ	1.76	0.82
1:C:228:GLU:OE2	1:C:228:GLU:N	2.10	0.81
1:B:577:ASN:HD21	1:B:595:LYS:HZ1	1.28	0.81
1:D:266:CYS:O	1:D:270:GLU:HG3	1.81	0.80
1:D:312:LYS:NZ	2:D:703:DGT:O1G	2.12	0.80
1:A:372:ARG:NH1	1:C:358:ASN:OD1	2.14	0.80
1:C:192:SER:OG	1:C:195:ASP:OD2	2.00	0.80
1:A:465:GLN:H	1:A:465:GLN:HE21	1.27	0.80
1:B:266:CYS:O	1:B:270:GLU:HG3	1.81	0.79
1:D:243:HIS:O	1:D:247:SER:OG	2.01	0.79
1:D:506:ASP:OD1	1:D:508:GLY:N	2.15	0.79
1:B:375:GLN:NE2	2:B:701:DGT:C6	2.46	0.79
1:B:329:PHE:CE2	1:B:362:MET:HB2	2.17	0.79
1:B:469:LYS:N	1:B:472:ASP:CG	2.33	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:CYS:O	1:A:270:GLU:HG3	1.84	0.78
1:B:315:TYR:OH	2:B:701:DGT:O2G	2.00	0.78
1:D:558:ASP:OD1	1:D:561:SER:OG	2.03	0.77
1:A:486:LYS:HE2	1:A:594:GLN:NE2	1.99	0.76
1:B:157:PHE:CD2	1:B:323:LEU:HD22	2.21	0.76
1:B:375:GLN:HE22	2:B:701:DGT:C6	1.99	0.76
1:B:325:ILE:HG22	1:B:326:GLN:N	2.02	0.75
1:C:371:ARG:NH1	1:C:372:ARG:HE	1.85	0.75
1:B:479:GLU:OE2	1:B:576:ARG:NH2	2.19	0.74
1:C:342:GLU:OE2	1:C:345:ASN:N	2.19	0.73
1:A:329:PHE:HD2	1:A:362:MET:HG3	1.48	0.73
1:B:215:HIS:NE2	2:B:701:DGT:O2B	2.22	0.73
1:C:487:VAL:HG23	1:C:590:LEU:HD12	1.70	0.72
1:B:215:HIS:CD2	2:B:701:DGT:O4'	2.42	0.72
1:A:558:ASP:OD1	1:A:561:SER:N	2.20	0.72
1:D:534:LYS:NZ	1:D:541:LEU:O	2.22	0.71
1:C:243:HIS:O	1:C:247:SER:OG	2.08	0.70
1:D:303:ASN:ND2	1:D:306:ASN:CG	2.43	0.70
1:C:485:PRO:O	1:C:486:LYS:HB2	1.92	0.69
1:C:509:MET:HE3	1:C:512:LYS:HD2	1.75	0.69
1:B:487:VAL:HG23	1:B:590:LEU:HD12	1.74	0.69
1:B:361:ASP:OD2	1:D:372:ARG:NH2	2.27	0.68
1:B:215:HIS:HE1	2:B:701:DGT:O2B	1.69	0.68
1:A:329:PHE:CD2	1:A:362:MET:CG	2.75	0.67
1:C:378:VAL:O	1:C:381:ILE:HG22	1.95	0.67
1:B:469:LYS:CA	1:B:472:ASP:OD2	2.43	0.67
1:B:592:VAL:HG13	1:B:593:PRO:HD3	1.77	0.66
1:B:378:VAL:O	1:B:381:ILE:HG22	1.95	0.66
1:A:378:VAL:O	1:A:381:ILE:HG22	1.95	0.66
1:A:328:ASN:HB3	1:A:365:THR:HG1	1.60	0.65
1:B:243:HIS:O	1:B:247:SER:OG	2.13	0.65
1:D:378:VAL:O	1:D:381:ILE:HG22	1.96	0.65
2:B:705:DGT:O6	1:D:372:ARG:HG2	1.96	0.65
1:B:506:ASP:OD1	1:B:508:GLY:N	2.25	0.65
1:B:487:VAL:CG2	1:B:590:LEU:HD12	2.28	0.64
1:C:408:ARG:HH11	1:C:408:ARG:HG2	1.62	0.64
1:B:325:ILE:HG22	1:B:326:GLN:H	1.62	0.64
1:C:487:VAL:CG2	1:C:590:LEU:HD12	2.28	0.64
1:A:328:ASN:CB	1:A:365:THR:OG1	2.46	0.63
1:B:140:GLN:HG3	1:B:240:MET:CE	2.28	0.63
1:D:339:ARG:HB2	1:D:521:TYR:CE1	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:ARG:HB3	1:C:229:VAL:HG12	1.81	0.63
1:A:140:GLN:HG3	1:A:240:MET:CE	2.28	0.62
1:A:339:ARG:HB2	1:A:521:TYR:CE2	2.33	0.62
1:A:243:HIS:O	1:A:247:SER:OG	2.16	0.62
1:D:594:GLN:HG3	1:D:595:LYS:N	2.12	0.62
1:C:140:GLN:HG3	1:C:240:MET:CE	2.29	0.62
1:C:528:ARG:HH21	1:C:528:ARG:HG3	1.65	0.62
1:B:558:ASP:OD1	1:B:561:SER:N	2.30	0.62
1:B:592:VAL:CG1	1:B:593:PRO:HD3	2.29	0.61
1:B:352:ARG:NE	1:B:353:ASP:OD1	2.30	0.61
1:A:325:ILE:HG22	1:A:326:GLN:N	2.16	0.61
1:B:377:LYS:HG2	1:B:378:VAL:N	2.15	0.61
1:C:226:ARG:CB	1:C:229:VAL:HG12	2.30	0.61
1:B:470:ARG:O	1:B:473:TYR:CD2	2.55	0.60
1:D:463:THR:OG1	1:D:577:ASN:O	2.18	0.60
1:B:140:GLN:CG	1:B:240:MET:HE2	2.32	0.59
1:B:385:MET:HG2	1:B:454:PHE:CE2	2.37	0.59
1:D:235:GLN:HG3	1:D:239:MET:HE3	1.84	0.59
1:C:509:MET:HB3	1:C:512:LYS:HB2	1.84	0.59
1:B:215:HIS:CD2	2:B:701:DGT:C1'	2.86	0.59
2:B:704:DGT:O3G	1:C:455:LYS:NZ	2.35	0.59
1:D:352:ARG:NE	1:D:353:ASP:OD1	2.34	0.59
1:B:470:ARG:CA	1:B:473:TYR:CE2	2.73	0.58
1:C:352:ARG:NE	1:C:353:ASP:OD1	2.32	0.58
1:A:115:MET:HB2	1:A:128:LEU:O	2.04	0.58
1:C:315:TYR:CE1	1:C:316:PHE:CE1	2.90	0.58
1:D:292:GLU:O	1:D:295:SER:OG	2.15	0.58
1:D:315:TYR:CZ	2:D:703:DGT:O3G	2.55	0.58
1:B:339:ARG:HB2	1:B:521:TYR:CE2	2.38	0.58
1:A:465:GLN:HE21	1:A:465:GLN:N	2.01	0.58
1:B:306:ASN:OD1	1:B:308:ILE:HG13	2.04	0.58
1:B:315:TYR:CE1	1:B:316:PHE:CE1	2.91	0.58
1:A:486:LYS:HE2	1:A:594:GLN:HE22	1.68	0.58
1:A:377:LYS:HG2	1:A:378:VAL:N	2.19	0.57
1:C:119:ASN:ND2	2:D:702:DGT:HN2A	2.01	0.57
1:A:315:TYR:CE1	1:A:316:PHE:CE1	2.92	0.57
1:B:215:HIS:HD2	2:B:701:DGT:C1'	2.18	0.57
1:C:377:LYS:HG2	1:C:378:VAL:N	2.18	0.57
1:D:303:ASN:OD1	1:D:306:ASN:OD1	2.18	0.57
1:A:352:ARG:NE	1:A:353:ASP:OD1	2.35	0.57
1:B:577:ASN:HD22	1:B:595:LYS:HZ1	1.31	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:351:ALA:O	1:D:520:PHE:HA	2.05	0.57
1:C:509:MET:CE	1:C:512:LYS:HD2	2.35	0.57
1:C:327:ASN:HB2	1:C:365:THR:HG21	1.86	0.56
1:D:461:GLN:HG2	1:D:548:GLN:O	2.05	0.56
1:B:371:ARG:HH12	1:B:372:ARG:HE	1.52	0.56
1:B:351:ALA:O	1:B:520:PHE:HA	2.05	0.56
1:C:251:LYS:O	1:C:255:GLU:HG3	2.05	0.56
1:B:157:PHE:CG	1:B:323:LEU:HD22	2.40	0.56
1:B:435:ASP:OD2	1:B:437:LYS:HE3	2.06	0.56
1:C:226:ARG:O	1:C:229:VAL:HG12	2.05	0.55
1:A:509:MET:HB3	1:A:512:LYS:HB2	1.89	0.55
1:D:325:ILE:HG22	1:D:326:GLN:N	2.22	0.55
1:D:315:TYR:CE1	1:D:316:PHE:CE1	2.94	0.55
1:A:351:ALA:O	1:A:520:PHE:HA	2.06	0.55
1:C:493:LEU:HD12	1:C:568:TYR:CD2	2.42	0.55
1:B:461:GLN:HG2	1:B:548:GLN:O	2.07	0.54
1:C:315:TYR:CE1	1:C:316:PHE:CD1	2.94	0.54
1:A:354:LYS:HZ3	2:A:704:DGT:PA	2.30	0.54
1:B:215:HIS:NE2	2:B:701:DGT:O4'	2.40	0.54
1:B:470:ARG:HA	1:B:473:TYR:CD2	2.40	0.54
1:B:469:LYS:CB	1:B:472:ASP:OD2	2.56	0.54
2:B:701:DGT:H5'A	2:B:701:DGT:O3B	2.07	0.54
1:B:363:PHE:HB3	1:B:507:TYR:CE2	2.43	0.54
1:C:140:GLN:CG	1:C:240:MET:HE3	2.37	0.54
1:C:339:ARG:HB2	1:C:521:TYR:CE2	2.43	0.54
1:D:244:LEU:C	1:D:244:LEU:HD23	2.28	0.54
1:A:218:ASP:OD2	1:A:233:HIS:HD2	1.91	0.53
1:B:354:LYS:NZ	2:B:705:DGT:O1A	2.27	0.53
1:C:351:ALA:O	1:C:520:PHE:HA	2.08	0.53
1:B:244:LEU:HD23	1:B:244:LEU:C	2.28	0.53
1:B:164:ARG:HH22	2:B:701:DGT:H4'	1.73	0.53
1:C:325:ILE:HG22	1:C:326:GLN:N	2.24	0.53
1:C:244:LEU:C	1:C:244:LEU:HD23	2.29	0.53
1:B:311:ASP:OD1	2:B:701:DGT:O1A	2.26	0.53
1:B:315:TYR:CE1	1:B:316:PHE:CD1	2.96	0.53
1:A:140:GLN:CG	1:A:240:MET:HE3	2.38	0.53
1:A:315:TYR:CE1	1:A:316:PHE:CD1	2.97	0.53
1:A:486:LYS:CE	1:A:594:GLN:NE2	2.71	0.53
1:B:589:PRO:O	1:B:593:PRO:HD3	2.08	0.53
1:C:461:GLN:HG2	1:C:548:GLN:O	2.07	0.53
1:A:385:MET:HG2	1:A:454:PHE:CE2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:GLN:HG2	1:A:548:GLN:O	2.09	0.53
1:B:325:ILE:CG2	1:B:326:GLN:N	2.69	0.53
1:D:235:GLN:HG3	1:D:239:MET:CE	2.39	0.52
1:B:485:PRO:O	1:B:486:LYS:HB2	2.09	0.52
1:D:422:LEU:CD1	1:D:426:ILE:HG13	2.40	0.52
1:C:590:LEU:O	1:C:593:PRO:HD2	2.09	0.52
1:C:595:LYS:HE3	1:C:597:GLU:OE1	2.09	0.52
1:A:244:LEU:C	1:A:244:LEU:HD23	2.30	0.52
1:B:465:GLN:HG3	1:B:465:GLN:O	2.10	0.52
1:D:299:GLU:OE2	1:D:305:ARG:NH1	2.43	0.52
1:D:329:PHE:CD1	1:D:362:MET:HB2	2.45	0.52
1:D:167:HIS:ND1	1:D:314:ASP:OD2	2.36	0.51
1:D:218:ASP:OD2	1:D:233:HIS:HD2	1.93	0.51
1:B:594:GLN:N	1:B:594:GLN:OE1	2.44	0.51
1:A:478:LYS:HD2	1:A:495:ALA:HB2	1.92	0.51
1:C:363:PHE:HB3	1:C:507:TYR:CE2	2.45	0.51
1:A:395:ASP:CG	1:A:408:ARG:NH1	2.63	0.51
1:A:598:TRP:O	1:A:599:ASN:HB3	2.11	0.51
1:C:329:PHE:HB2	1:C:362:MET:HA	1.92	0.51
1:B:534:LYS:NZ	1:B:541:LEU:O	2.37	0.51
1:A:167:HIS:ND1	1:A:314:ASP:OD2	2.39	0.51
1:C:270:GLU:OE1	1:C:289:GLY:N	2.43	0.51
1:B:590:LEU:O	1:B:593:PRO:HD2	2.11	0.51
1:C:385:MET:HG2	1:C:454:PHE:CE2	2.46	0.51
1:B:329:PHE:HB2	1:B:362:MET:HA	1.91	0.51
1:D:385:MET:HG2	1:D:454:PHE:CE2	2.45	0.51
1:A:589:PRO:O	1:A:593:PRO:HD3	2.10	0.51
1:B:215:HIS:CD2	2:B:701:DGT:N9	2.79	0.51
1:D:589:PRO:O	1:D:593:PRO:HD3	2.11	0.51
1:B:218:ASP:OD2	1:B:233:HIS:HD2	1.94	0.50
1:B:392:LYS:HE2	1:B:444:ILE:HD11	1.93	0.50
1:C:589:PRO:O	1:C:593:PRO:HD3	2.10	0.50
1:A:463:THR:HG22	1:A:464:GLY:N	2.26	0.50
1:D:329:PHE:HB2	1:D:362:MET:HA	1.92	0.50
1:C:392:LYS:HE2	1:C:444:ILE:HD11	1.94	0.50
1:A:486:LYS:CD	1:A:594:GLN:NE2	2.75	0.50
1:A:435:ASP:OD1	1:A:437:LYS:HG3	2.12	0.50
1:C:119:ASN:HD21	2:D:702:DGT:HN2A	1.58	0.50
1:D:435:ASP:OD1	1:D:437:LYS:HG3	2.11	0.50
1:D:509:MET:HB3	1:D:512:LYS:HB2	1.94	0.50
1:B:504:ASN:OD1	1:B:548:GLN:NE2	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:318:ARG:O	1:D:322:HIS:HD2	1.95	0.49
1:B:325:ILE:CG2	1:B:326:GLN:H	2.24	0.49
1:C:470:ARG:NH1	1:C:470:ARG:HB2	2.27	0.49
1:C:318:ARG:O	1:C:322:HIS:HD2	1.96	0.49
1:C:422:LEU:CD1	1:C:426:ILE:HG13	2.42	0.49
1:D:315:TYR:CE1	1:D:316:PHE:CD1	3.00	0.49
1:D:534:LYS:HZ3	1:D:541:LEU:C	2.14	0.49
1:A:267:PHE:O	1:A:271:GLN:HG3	2.13	0.49
1:A:326:GLN:HB3	1:C:327:ASN:O	2.13	0.49
1:B:206:ARG:HD3	1:B:311:ASP:OD2	2.13	0.49
1:B:315:TYR:CZ	2:B:701:DGT:O2G	2.66	0.49
1:B:329:PHE:HD2	1:B:362:MET:CB	2.05	0.49
1:C:396:TYR:CD2	1:C:437:LYS:HB3	2.48	0.49
1:A:422:LEU:CD1	1:A:426:ILE:HG13	2.43	0.49
1:B:267:PHE:O	1:B:271:GLN:HG3	2.13	0.49
1:C:371:ARG:HH11	1:C:372:ARG:HE	1.56	0.49
1:C:221:PHE:CE1	1:C:390:PHE:HB3	2.48	0.48
1:C:493:LEU:HD12	1:C:568:TYR:CE2	2.48	0.48
1:A:518:VAL:O	1:A:531:ARG:NH1	2.46	0.48
1:B:577:ASN:ND2	1:B:595:LYS:CE	2.76	0.48
1:D:458:GLY:HA3	1:D:569:PHE:CE2	2.48	0.48
1:C:242:GLU:OE1	1:C:269:LYS:CE	2.59	0.48
1:A:455:LYS:HG2	1:A:557:VAL:HG12	1.95	0.48
1:D:242:GLU:OE1	1:D:269:LYS:CE	2.59	0.48
1:B:509:MET:HB3	1:B:512:LYS:HB2	1.96	0.48
1:A:221:PHE:CE1	1:A:390:PHE:HB3	2.49	0.48
1:A:463:THR:OG1	1:A:577:ASN:O	2.15	0.48
1:C:328:ASN:OD1	1:C:328:ASN:N	2.45	0.48
1:C:267:PHE:O	1:C:271:GLN:HG3	2.13	0.48
1:D:392:LYS:HE2	1:D:444:ILE:HD11	1.95	0.48
1:A:358:ASN:OD1	1:C:372:ARG:NH1	2.46	0.48
1:D:590:LEU:O	1:D:593:PRO:HD2	2.13	0.48
1:A:315:TYR:CD1	1:A:315:TYR:C	2.88	0.48
1:A:590:LEU:O	1:A:593:PRO:HD2	2.13	0.48
1:B:577:ASN:HD22	1:B:595:LYS:HZ3	1.58	0.48
1:A:323:LEU:O	1:D:119:ASN:ND2	2.47	0.47
1:B:519:SER:OG	1:B:531:ARG:NH1	2.47	0.47
1:C:116:LYS:NZ	2:C:702:DGT:O1G	2.47	0.47
1:C:215:HIS:CD2	2:C:703:DGT:N9	2.82	0.47
1:A:354:LYS:NZ	2:A:704:DGT:PA	2.87	0.47
1:B:120:ASP:CG	1:B:318:ARG:HH22	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:580:LYS:NZ	1:B:585:ASP:OD2	2.46	0.47
1:C:241:PHE:O	1:C:245:ILE:HG12	2.15	0.47
1:B:234:GLU:O	1:B:235[B]:GLN:C	2.47	0.47
1:C:197:LEU:O	1:C:201:ILE:HG13	2.15	0.47
1:C:594:GLN:HG3	1:C:595:LYS:N	2.29	0.47
1:C:329:PHE:CD1	1:C:362:MET:HB2	2.49	0.47
1:D:267:PHE:O	1:D:271:GLN:HG3	2.14	0.47
1:D:422:LEU:HD12	1:D:426:ILE:HG13	1.97	0.47
1:C:539:GLN:HA	1:C:539:GLN:OE1	2.15	0.47
1:D:313:TRP:CD1	1:D:329:PHE:HE2	2.32	0.47
1:D:427:PHE:CD1	1:D:427:PHE:C	2.88	0.47
1:A:212:PRO:HD2	1:A:217:PHE:CD1	2.50	0.47
1:A:325:ILE:CG2	1:A:326:GLN:N	2.78	0.47
1:C:249:GLY:O	1:C:252:PRO:HD2	2.15	0.47
1:D:197:LEU:O	1:D:201:ILE:HG13	2.15	0.47
1:B:363:PHE:CB	1:B:507:TYR:CE2	2.97	0.47
1:C:375:GLN:HE22	2:C:703:DGT:C6	2.28	0.46
1:B:234:GLU:O	1:B:235[A]:GLN:C	2.48	0.46
1:C:212:PRO:HD2	1:C:217:PHE:CD1	2.49	0.46
1:D:539:GLN:OE1	1:D:539:GLN:HA	2.15	0.46
1:B:249:GLY:O	1:B:252:PRO:HD2	2.15	0.46
1:B:563:TYR:O	1:B:567:GLN:HG2	2.15	0.46
1:C:226:ARG:CB	1:C:229:VAL:CG1	2.92	0.46
1:A:140:GLN:HG3	1:A:240:MET:HE3	1.98	0.46
1:A:594:GLN:HG3	1:A:595:LYS:N	2.29	0.46
1:C:163:ASN:O	1:C:166:GLU:HG2	2.16	0.46
1:D:534:LYS:HZ2	1:D:541:LEU:HB2	1.81	0.46
1:A:458:GLY:HA3	1:A:569:PHE:CE2	2.50	0.46
1:A:496:GLU:O	1:A:555:LYS:HE3	2.16	0.46
1:B:241:PHE:O	1:B:245:ILE:HG12	2.16	0.46
1:D:241:PHE:O	1:D:245:ILE:HG12	2.15	0.46
1:B:157:PHE:CG	1:B:323:LEU:CD2	2.99	0.46
1:B:334:PHE:CE2	1:B:359:LEU:HD21	2.51	0.46
1:B:115:MET:HG3	1:B:128:LEU:O	2.16	0.46
1:B:197:LEU:O	1:B:201:ILE:HG13	2.16	0.46
1:A:241:PHE:O	1:A:245:ILE:HG12	2.16	0.46
2:A:703:DGT:H3'	2:A:703:DGT:O2A	2.16	0.46
1:B:326:GLN:OE1	1:D:326:GLN:HG2	2.15	0.46
1:B:552:VAL:HG21	1:B:569:PHE:CD1	2.51	0.46
1:B:435:ASP:OD1	1:B:437:LYS:HE3	2.16	0.45
1:D:394:ASP:CG	1:D:410:SER:OG	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:LEU:O	1:A:201:ILE:HG13	2.16	0.45
1:B:140:GLN:HG3	1:B:240:MET:HE2	1.93	0.45
1:C:563:TYR:O	1:C:567:GLN:HG2	2.16	0.45
1:D:212:PRO:HD2	1:D:217:PHE:CD1	2.51	0.45
1:B:558:ASP:OD2	1:B:561:SER:OG	2.34	0.45
1:A:119:ASN:ND2	2:B:705:DGT:HN2A	2.14	0.45
1:B:372:ARG:CZ	1:D:358:ASN:OD1	2.64	0.45
1:A:563:TYR:O	1:A:567:GLN:HG2	2.16	0.45
1:D:221:PHE:CE1	1:D:390:PHE:HB3	2.52	0.45
1:B:564:ALA:O	1:B:568:TYR:HD1	1.98	0.45
1:C:129:HIS:CG	1:C:130:PRO:HD2	2.52	0.45
1:C:327:ASN:H	1:C:327:ASN:HD22	1.65	0.45
1:B:163:ASN:O	1:B:166:GLU:HG2	2.17	0.45
1:D:249:GLY:O	1:D:252:PRO:HD2	2.17	0.45
1:D:563:TYR:O	1:D:567:GLN:HG2	2.16	0.45
1:B:470:ARG:HG3	1:B:473:TYR:CE2	2.52	0.44
1:B:558:ASP:HB2	1:B:560:LYS:HD2	1.99	0.44
1:A:334:PHE:CE2	1:A:359:LEU:HD11	2.52	0.44
1:B:591:ILE:O	1:B:594:GLN:HG2	2.17	0.44
1:C:382:ILE:O	1:C:386:ILE:HG13	2.17	0.44
1:C:394:ASP:CG	1:C:410:SER:OG	2.53	0.44
1:A:372:ARG:NE	1:C:358:ASN:OD1	2.50	0.44
1:C:427:PHE:CD1	1:C:427:PHE:C	2.90	0.44
1:A:167:HIS:O	1:A:171:VAL:HG23	2.17	0.44
1:A:329:PHE:HB2	1:A:362:MET:HA	1.99	0.44
1:A:382:ILE:O	1:A:386:ILE:HG13	2.18	0.44
1:B:315:TYR:CE1	1:B:316:PHE:HE1	2.36	0.44
1:B:315:TYR:CD1	1:B:315:TYR:C	2.91	0.44
1:B:329:PHE:CD2	1:B:362:MET:CG	3.01	0.44
1:D:134:ARG:HD2	1:D:134:ARG:HA	1.86	0.44
1:D:167:HIS:O	1:D:171:VAL:HG23	2.17	0.44
1:C:538:SER:HB3	1:C:541:LEU:HG	1.99	0.44
1:B:363:PHE:HB3	1:B:507:TYR:CD2	2.52	0.44
1:B:382:ILE:O	1:B:386:ILE:HG13	2.18	0.44
1:B:129:HIS:CG	1:B:130:PRO:HD2	2.53	0.43
1:B:167:HIS:O	1:B:171:VAL:HG23	2.17	0.43
1:C:167:HIS:O	1:C:171:VAL:HG23	2.17	0.43
1:A:465:GLN:H	1:A:465:GLN:NE2	2.05	0.43
1:B:371:ARG:NH2	1:D:361:ASP:OD2	2.44	0.43
1:B:394:ASP:CG	1:B:410:SER:OG	2.52	0.43
1:C:315:TYR:CD1	1:C:315:TYR:C	2.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:315:TYR:OH	2:C:703:DGT:O2G	2.30	0.43
1:C:463:THR:OG1	1:C:577:ASN:O	2.35	0.43
1:A:163:ASN:O	1:A:166:GLU:HG2	2.18	0.43
1:A:315:TYR:CE1	1:A:316:PHE:HE1	2.37	0.43
1:A:422:LEU:HD12	1:A:426:ILE:HG13	2.00	0.43
1:B:212:PRO:HD2	1:B:217:PHE:CD1	2.54	0.43
1:D:163:ASN:O	1:D:166:GLU:HG2	2.18	0.43
1:C:313:TRP:CD1	1:C:329:PHE:HE2	2.36	0.43
1:C:334:PHE:CE2	1:C:359:LEU:HD11	2.54	0.43
1:D:346:GLU:OE1	1:D:348:ARG:NH2	2.50	0.43
1:B:293:ASN:OD1	1:B:293:ASN:N	2.52	0.43
1:C:325:ILE:O	1:C:326:GLN:OE1	2.36	0.43
1:A:372:ARG:CZ	1:C:358:ASN:OD1	2.66	0.43
1:B:134:ARG:HA	1:B:134:ARG:HD2	1.83	0.43
1:C:226:ARG:HB2	1:C:229:VAL:CG1	2.48	0.43
1:C:363:PHE:HB3	1:C:507:TYR:CD2	2.54	0.43
1:C:377:LYS:HG2	1:C:378:VAL:H	1.84	0.43
1:B:427:PHE:CD1	1:B:427:PHE:C	2.92	0.43
1:B:468:ILE:CG2	1:B:472:ASP:HB2	2.49	0.43
1:C:116:LYS:HZ1	2:C:702:DGT:PG	2.42	0.43
1:C:535:ASN:OD1	1:C:535:ASN:N	2.52	0.43
1:D:593:PRO:HA	1:D:599:ASN:ND2	2.34	0.43
1:A:504:ASN:OD1	1:A:548:GLN:NE2	2.29	0.42
1:B:377:LYS:HG2	1:B:378:VAL:H	1.82	0.42
1:B:469:LYS:HB2	1:B:472:ASP:CG	2.38	0.42
1:C:226:ARG:HB3	1:C:229:VAL:CG1	2.47	0.42
1:C:363:PHE:CB	1:C:507:TYR:CE2	3.02	0.42
1:A:114:THR:N	1:A:115:MET:HA	2.32	0.42
1:C:192:SER:O	1:C:195:ASP:HB2	2.19	0.42
1:C:244:LEU:HD23	1:C:244:LEU:O	2.19	0.42
1:B:566:ARG:O	1:B:570:VAL:HG23	2.20	0.42
1:A:192:SER:O	1:A:195:ASP:HB2	2.20	0.42
1:C:215:HIS:O	1:C:219:GLY:N	2.50	0.42
1:D:174:LEU:HD23	1:D:174:LEU:HA	1.89	0.42
1:D:129:HIS:CG	1:D:130:PRO:HD2	2.54	0.42
1:B:192:SER:O	1:B:195:ASP:HB2	2.19	0.42
1:D:382:ILE:O	1:D:386:ILE:HG13	2.20	0.42
1:D:538:SER:HB3	1:D:541:LEU:HG	2.02	0.42
1:A:226:ARG:NH1	1:A:229:VAL:HG21	2.35	0.42
1:A:249:GLY:O	1:A:252:PRO:HD2	2.20	0.42
1:B:320:CYS:HB3	1:B:325:ILE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:315:TYR:CE1	1:D:316:PHE:HE1	2.38	0.42
1:D:315:TYR:CE2	2:D:703:DGT:O3G	2.73	0.42
1:A:307:GLY:O	1:A:312:LYS:NZ	2.50	0.42
1:C:164:ARG:HH22	2:C:703:DGT:H4'	1.84	0.42
1:D:192:SER:O	1:D:195:ASP:HB2	2.19	0.42
1:D:244:LEU:HD23	1:D:244:LEU:O	2.19	0.42
1:D:315:TYR:CD1	1:D:315:TYR:C	2.93	0.42
1:A:134:ARG:HA	1:A:134:ARG:HD2	1.84	0.42
1:A:244:LEU:HD23	1:A:244:LEU:O	2.19	0.42
1:A:285:TRP:CG	1:A:292:GLU:HG3	2.54	0.42
1:B:244:LEU:HD23	1:B:244:LEU:O	2.20	0.42
1:B:537:VAL:O	1:D:371:ARG:NH1	2.53	0.42
1:C:114:THR:HB	1:C:115:MET:H	1.72	0.42
1:B:228:GLU:N	1:B:228:GLU:OE1	2.53	0.42
1:B:381:ILE:HD12	1:B:381:ILE:HA	1.87	0.42
1:B:435:ASP:CG	1:B:437:LYS:HE3	2.41	0.42
1:C:315:TYR:CE1	1:C:316:PHE:HE1	2.35	0.42
1:D:303:ASN:HD21	1:D:306:ASN:ND2	2.18	0.42
1:C:470:ARG:HB2	1:C:470:ARG:HH11	1.84	0.41
1:C:534:LYS:HE3	1:C:534:LYS:HB3	1.78	0.41
1:D:507:TYR:CD2	1:D:545:PHE:HD2	2.38	0.41
1:B:346:GLU:OE2	1:B:348:ARG:NH2	2.48	0.41
1:C:422:LEU:HD12	1:C:426:ILE:HG13	2.01	0.41
1:D:215:HIS:HD2	2:D:703:DGT:C4	2.33	0.41
1:B:215:HIS:O	1:B:219:GLY:N	2.48	0.41
1:A:304:LYS:HA	1:A:304:LYS:HD3	1.91	0.41
1:B:245:ILE:HG23	1:B:250:ILE:HB	2.02	0.41
1:C:176:GLY:HA3	1:C:200:GLN:HE21	1.86	0.41
1:A:486:LYS:CE	1:A:594:GLN:HE22	2.31	0.41
1:B:304:LYS:HA	1:B:304:LYS:HD3	1.94	0.41
1:C:116:LYS:NZ	2:C:702:DGT:O1A	2.45	0.41
1:C:381:ILE:HD12	1:C:381:ILE:HA	1.84	0.41
1:A:486:LYS:HD2	1:A:594:GLN:NE2	2.35	0.41
1:C:215:HIS:NE2	2:C:703:DGT:O4'	2.54	0.41
1:A:129:HIS:CG	1:A:130:PRO:HD2	2.56	0.41
1:B:458:GLY:HA3	1:B:569:PHE:CE2	2.54	0.41
1:A:245:ILE:HG23	1:A:250:ILE:HB	2.03	0.41
1:A:427:PHE:CD1	1:A:427:PHE:C	2.94	0.41
1:A:509:MET:SD	1:A:514:PRO:HA	2.61	0.41
1:B:321:HIS:NE2	1:C:321:HIS:NE2	2.69	0.41
1:C:327:ASN:HB2	1:C:365:THR:CG2	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:435:ASP:OD1	1:C:437:LYS:N	2.38	0.41
1:C:470:ARG:HA	1:C:473:TYR:CE1	2.56	0.41
1:C:510:GLN:HB3	1:C:511:GLU:H	1.75	0.41
1:A:226:ARG:HB3	1:A:229:VAL:HG23	2.03	0.41
1:B:115:MET:HG2	1:B:127:GLU:HB3	2.03	0.41
1:B:470:ARG:HG3	1:B:473:TYR:HE2	1.84	0.41
1:C:592:VAL:N	1:C:593:PRO:CD	2.84	0.41
1:B:469:LYS:CB	1:B:472:ASP:CG	2.89	0.40
1:C:458:GLY:HA3	1:C:569:PHE:CE2	2.56	0.40
1:D:328:ASN:HB2	1:D:365:THR:OG1	2.21	0.40
1:D:566:ARG:O	1:D:570:VAL:HG23	2.21	0.40
1:B:540:LEU:O	1:D:542:PRO:HB3	2.20	0.40
1:C:215:HIS:CD2	2:C:703:DGT:C8	3.05	0.40
1:D:325:ILE:CG2	1:D:326:GLN:N	2.83	0.40
1:D:506:ASP:HA	1:D:545:PHE:O	2.21	0.40
1:B:534:LYS:O	1:B:537:VAL:HG23	2.21	0.40
1:D:215:HIS:O	1:D:219:GLY:N	2.49	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	476/514 (93%)	472 (99%)	4 (1%)	0	100	100
1	B	477/514 (93%)	471 (99%)	6 (1%)	0	100	100
1	C	476/514 (93%)	468 (98%)	7 (2%)	1 (0%)	47	76
1	D	477/514 (93%)	470 (98%)	7 (2%)	0	100	100
All	All	1906/2056 (93%)	1881 (99%)	24 (1%)	1 (0%)	51	80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	486	LYS

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	426/459 (93%)	401 (94%)	25 (6%)	19	47
1	B	427/459 (93%)	396 (93%)	31 (7%)	14	37
1	C	426/459 (93%)	395 (93%)	31 (7%)	14	37
1	D	427/459 (93%)	396 (93%)	31 (7%)	14	37
All	All	1706/1836 (93%)	1588 (93%)	118 (7%)	15	40

All (118) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	230	LYS
1	A	247	SER
1	A	277	GLU
1	A	284	LEU
1	A	315	TYR
1	A	339	ARG
1	A	354	LYS
1	A	371	ARG
1	A	377	LYS
1	A	388	ASP
1	A	465	GLN
1	A	468	ILE
1	A	478	LYS
1	A	484	LYS
1	A	488	LEU
1	A	511	GLU
1	A	524	THR
1	A	539	GLN
1	A	544	LYS
1	A	551	ARG
1	A	556	LYS

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Mol	Chain	Res	Type
1	A	561	SER
1	A	594	GLN
1	A	596	LYS
1	A	599	ASN
1	B	114	THR
1	B	115	MET
1	B	166	GLU
1	B	230	LYS
1	B	247	SER
1	B	277	GLU
1	B	284	LEU
1	B	302	SER
1	B	305	ARG
1	B	315	TYR
1	B	326	GLN
1	B	328	ASN
1	B	339	ARG
1	B	354	LYS
1	B	371	ARG
1	B	388	ASP
1	B	410	SER
1	B	455	LYS
1	B	468	ILE
1	B	471	GLU
1	B	472	ASP
1	B	474	GLU
1	B	494	LYS
1	B	496	GLU
1	B	511	GLU
1	B	524	THR
1	B	537	VAL
1	B	544	LYS
1	B	560	LYS
1	B	577	ASN
1	B	594	GLN
1	C	114	THR
1	C	115	MET
1	C	166	GLU
1	C	230	LYS
1	C	235	GLN
1	C	247	SER
1	C	262	GLU

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Mol	Chain	Res	Type
1	C	284	LEU
1	C	295	SER
1	C	305	ARG
1	C	315	TYR
1	C	327	ASN
1	C	339	ARG
1	C	371	ARG
1	C	377	LYS
1	C	388	ASP
1	C	395	ASP
1	C	410	SER
1	C	468	ILE
1	C	474	GLU
1	C	475	SER
1	C	492	LYS
1	C	496	GLU
1	C	510	GLN
1	C	511	GLU
1	C	528	ARG
1	C	544	LYS
1	C	556	LYS
1	C	559	ARG
1	C	577	ASN
1	C	594	GLN
1	D	114	THR
1	D	230	LYS
1	D	235	GLN
1	D	247	SER
1	D	277	GLU
1	D	292	GLU
1	D	295	SER
1	D	302	SER
1	D	315	TYR
1	D	326	GLN
1	D	328	ASN
1	D	339	ARG
1	D	354	LYS
1	D	371	ARG
1	D	372	ARG
1	D	388	ASP
1	D	395	ASP
1	D	410	SER

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Mol	Chain	Res	Type
1	D	455	LYS
1	D	463	THR
1	D	468	ILE
1	D	470	ARG
1	D	494	LYS
1	D	496	GLU
1	D	524	THR
1	D	528	ARG
1	D	551	ARG
1	D	556	LYS
1	D	559	ARG
1	D	594	GLN
1	D	596	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	233	HIS
1	A	243	HIS
1	A	328	ASN
1	A	425	ASN
1	A	465	GLN
1	A	594	GLN
1	A	599	ASN
1	B	180	HIS
1	B	215	HIS
1	B	233	HIS
1	B	243	HIS
1	B	322	HIS
1	B	370	HIS
1	B	425	ASN
1	B	527	ASN
1	B	577	ASN
1	C	119	ASN
1	C	200	GLN
1	C	243	HIS
1	C	322	HIS
1	C	327	ASN
1	C	364	HIS
1	C	425	ASN
1	C	594	GLN
1	D	119	ASN

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Mol	Chain	Res	Type
1	D	233	HIS
1	D	322	HIS
1	D	326	GLN
1	D	425	ASN
1	D	599	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 5 are monoatomic - leaving 12 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
2	DGT	A	702	3	26,33,33	0.99	2 (7%)	32,52,52	1.25	2 (6%)
2	DGT	A	703	3	26,33,33	1.11	1 (3%)	32,52,52	1.52	7 (21%)
2	DGT	B	705	3	26,33,33	0.94	1 (3%)	32,52,52	1.28	3 (9%)
2	DGT	C	702	3	26,33,33	0.86	1 (3%)	32,52,52	1.57	5 (15%)
2	DGT	B	704	3	26,33,33	0.95	1 (3%)	32,52,52	1.49	5 (15%)
2	DGT	D	702	3	26,33,33	1.00	1 (3%)	32,52,52	1.12	3 (9%)
2	DGT	D	704	3	26,33,33	1.02	1 (3%)	32,52,52	1.41	4 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DGT	B	701	3	26,33,33	0.85	1 (3%)	32,52,52	1.41	4 (12%)
2	DGT	A	704	3	26,33,33	1.03	1 (3%)	32,52,52	1.31	4 (12%)
2	DGT	C	703	-	26,33,33	0.87	0	32,52,52	1.35	5 (15%)
2	DGT	D	703	-	26,33,33	0.96	0	32,52,52	1.28	4 (12%)
2	DGT	A	701	-	26,33,33	0.95	1 (3%)	32,52,52	1.58	8 (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
2	DGT	A	702	3	-	3/18/34/34	0/3/3/3
2	DGT	A	703	3	-	2/18/34/34	0/3/3/3
2	DGT	B	705	3	-	5/18/34/34	0/3/3/3
2	DGT	C	702	3	-	2/18/34/34	0/3/3/3
2	DGT	B	704	3	-	5/18/34/34	0/3/3/3
2	DGT	D	702	3	-	1/18/34/34	0/3/3/3
2	DGT	D	704	3	-	1/18/34/34	0/3/3/3
2	DGT	B	701	3	-	1/18/34/34	0/3/3/3
2	DGT	A	704	3	-	4/18/34/34	0/3/3/3
2	DGT	C	703	-	-	4/18/34/34	0/3/3/3
2	DGT	D	703	-	-	3/18/34/34	0/3/3/3
2	DGT	A	701	-	-	4/18/34/34	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	704	DGT	C6-N1	-3.94	1.32	1.37
2	A	703	DGT	C6-N1	-3.82	1.32	1.37
2	A	704	DGT	C6-N1	-3.12	1.33	1.37
2	D	702	DGT	C6-N1	-2.93	1.33	1.37
2	B	704	DGT	C6-N1	-2.76	1.33	1.37
2	B	705	DGT	C6-N1	-2.76	1.33	1.37
2	A	702	DGT	C6-N1	-2.59	1.34	1.37
2	C	702	DGT	C6-N1	-2.53	1.34	1.37
2	B	701	DGT	C6-N1	-2.35	1.34	1.37
2	A	702	DGT	C5-C4	2.13	1.48	1.43
2	A	701	DGT	C6-N1	-2.01	1.34	1.37

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	702	DGT	PA-O3A-PB	-4.70	116.69	132.83
2	B	704	DGT	PA-O3A-PB	-4.36	117.86	132.83
2	C	702	DGT	O2G-PG-O1G	4.03	123.03	107.64
2	A	703	DGT	PA-O3A-PB	-3.99	119.12	132.83
2	B	705	DGT	O6-C6-N1	3.85	125.20	120.65
2	A	701	DGT	PB-O3B-PG	-3.76	119.92	132.83
2	D	704	DGT	PA-O3A-PB	-3.75	119.95	132.83
2	B	701	DGT	PA-O3A-PB	-3.53	120.71	132.83
2	B	701	DGT	PB-O3B-PG	-3.38	121.24	132.83
2	C	703	DGT	PB-O3B-PG	-3.35	121.32	132.83
2	C	703	DGT	PA-O3A-PB	-3.32	121.44	132.83
2	D	703	DGT	PA-O3A-PB	-3.14	122.06	132.83
2	A	701	DGT	O6-C6-C5	-2.96	118.60	124.37
2	D	703	DGT	C8-N7-C5	2.85	108.42	102.99
2	B	705	DGT	O6-C6-C5	-2.82	118.86	124.37
2	D	702	DGT	O1A-PA-O2A	2.77	125.93	112.24
2	B	704	DGT	O1G-PG-O3G	2.75	121.44	110.68
2	A	704	DGT	O6-C6-C5	-2.73	119.05	124.37
2	B	704	DGT	O3B-PG-O3G	-2.70	96.24	111.19
2	C	703	DGT	C5-C6-N1	2.66	118.65	113.95
2	D	704	DGT	C8-N7-C5	2.60	107.94	102.99
2	A	703	DGT	PB-O3B-PG	-2.59	123.92	132.83
2	B	704	DGT	PB-O3B-PG	-2.57	124.02	132.83
2	D	704	DGT	O1A-PA-O5'	-2.54	95.95	107.75
2	A	701	DGT	N2-C2-N1	2.53	122.10	116.71
2	A	703	DGT	C5-C6-N1	2.51	118.39	113.95
2	C	702	DGT	C8-N7-C5	2.51	107.77	102.99
2	D	703	DGT	PB-O3B-PG	-2.48	124.33	132.83
2	C	703	DGT	O2G-PG-O1G	2.46	117.03	107.64
2	C	702	DGT	PB-O3B-PG	-2.42	124.51	132.83
2	A	704	DGT	C5-C6-N1	2.42	118.22	113.95
2	D	703	DGT	O2G-PG-O1G	2.42	116.87	107.64
2	A	704	DGT	PB-O3B-PG	-2.41	124.57	132.83
2	A	701	DGT	C5-C6-N1	2.40	118.19	113.95
2	B	701	DGT	C5-C6-N1	2.39	118.18	113.95
2	A	702	DGT	N2-C2-N3	-2.34	115.19	119.74
2	A	703	DGT	N2-C2-N3	-2.34	115.19	119.74
2	A	701	DGT	N2-C2-N3	-2.31	115.25	119.74
2	B	704	DGT	C5-C6-N1	2.22	117.87	113.95
2	B	705	DGT	PB-O3B-PG	-2.21	125.23	132.83
2	A	703	DGT	O6-C6-C5	-2.21	120.06	124.37
2	A	701	DGT	O6-C6-N1	2.17	123.21	120.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	702	DGT	C5-C6-N1	2.15	117.76	113.95
2	D	702	DGT	C8-N7-C5	2.13	107.05	102.99
2	A	703	DGT	O2G-PG-O1G	2.13	115.78	107.64
2	B	701	DGT	C8-N7-C5	2.13	107.04	102.99
2	A	701	DGT	C8-N7-C5	2.11	107.01	102.99
2	A	704	DGT	PA-O3A-PB	-2.11	125.59	132.83
2	A	703	DGT	N2-C2-N1	2.11	121.20	116.71
2	A	701	DGT	O3B-PG-O3G	-2.10	99.55	111.19
2	D	704	DGT	O1A-PA-O2A	2.07	122.49	112.24
2	C	703	DGT	C8-N7-C5	2.06	106.92	102.99
2	C	702	DGT	O2G-PG-O3B	-2.04	97.78	104.64
2	A	702	DGT	C8-N7-C5	2.01	106.82	102.99

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	703	DGT	C3'-C4'-C5'-O5'
2	D	702	DGT	PB-O3B-PG-O2G
2	A	701	DGT	O4'-C4'-C5'-O5'
2	A	701	DGT	C3'-C4'-C5'-O5'
2	C	703	DGT	O4'-C4'-C5'-O5'
2	D	703	DGT	PB-O3B-PG-O3G
2	A	701	DGT	PA-O3A-PB-O2B
2	A	702	DGT	PG-O3B-PB-O2B
2	D	703	DGT	PA-O3A-PB-O2B
2	A	703	DGT	C4'-C5'-O5'-PA
2	B	701	DGT	PB-O3A-PA-O5'
2	B	704	DGT	PB-O3B-PG-O1G
2	B	705	DGT	PB-O3B-PG-O1G
2	A	702	DGT	PB-O3A-PA-O1A
2	A	704	DGT	PG-O3B-PB-O2B
2	B	705	DGT	PG-O3B-PB-O2B
2	C	703	DGT	PG-O3B-PB-O1B
2	B	704	DGT	C4'-C5'-O5'-PA
2	B	704	DGT	PG-O3B-PB-O1B
2	D	703	DGT	PA-O3A-PB-O1B
2	C	702	DGT	C4'-C5'-O5'-PA
2	B	704	DGT	PB-O3A-PA-O1A
2	C	703	DGT	PG-O3B-PB-O2B
2	B	705	DGT	PB-O3B-PG-O2G
2	A	703	DGT	C5'-O5'-PA-O3A

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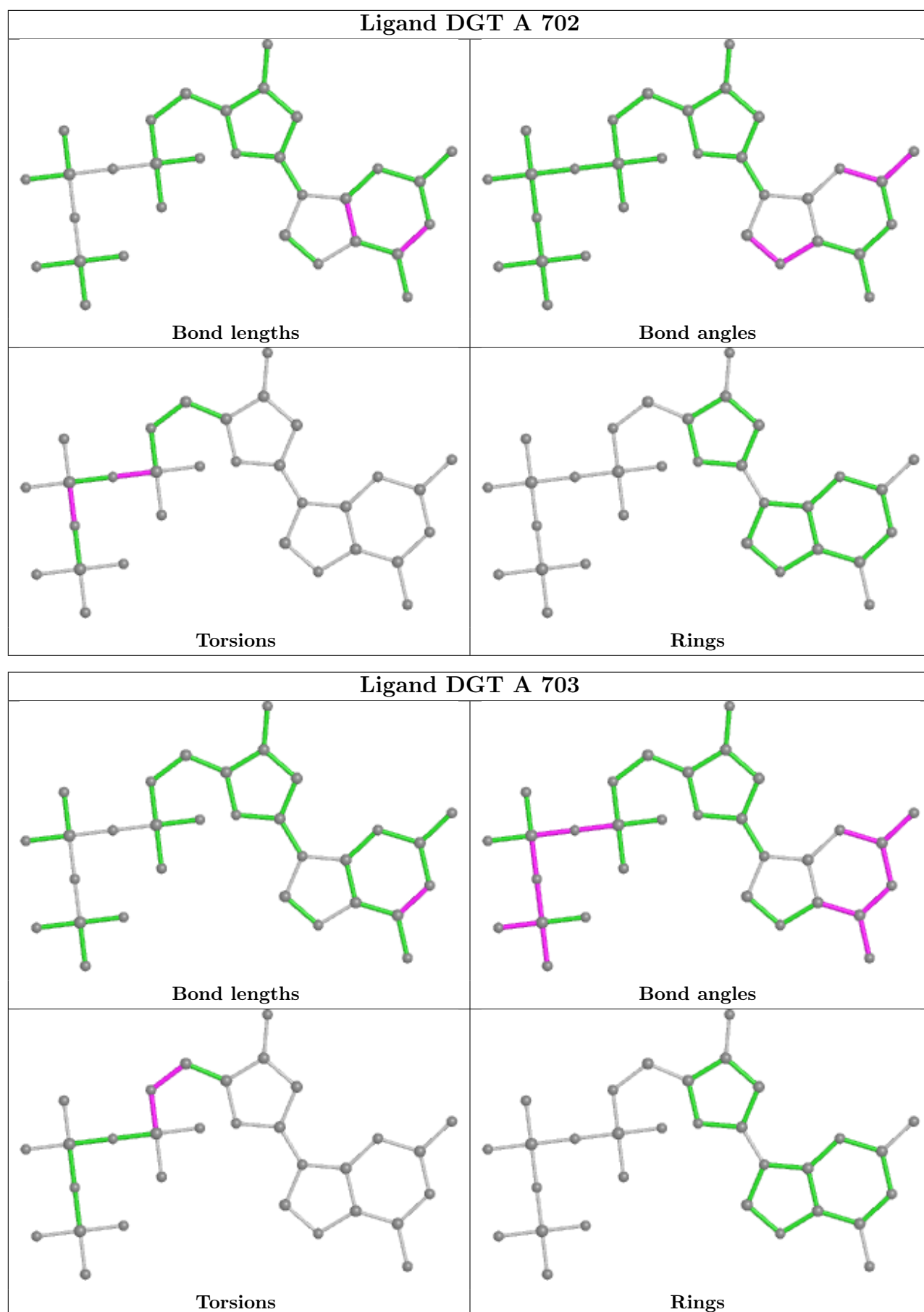
Mol	Chain	Res	Type	Atoms
2	A	701	DGT	PA-O3A-PB-O1B
2	A	702	DGT	PG-O3B-PB-O1B
2	A	704	DGT	PG-O3B-PB-O1B
2	A	704	DGT	PA-O3A-PB-O1B
2	A	704	DGT	PB-O3A-PA-O1A
2	B	704	DGT	PG-O3B-PB-O2B
2	B	705	DGT	PG-O3B-PB-O1B
2	B	705	DGT	PB-O3A-PA-O1A
2	C	702	DGT	PG-O3B-PB-O1B
2	D	704	DGT	PB-O3A-PA-O1A

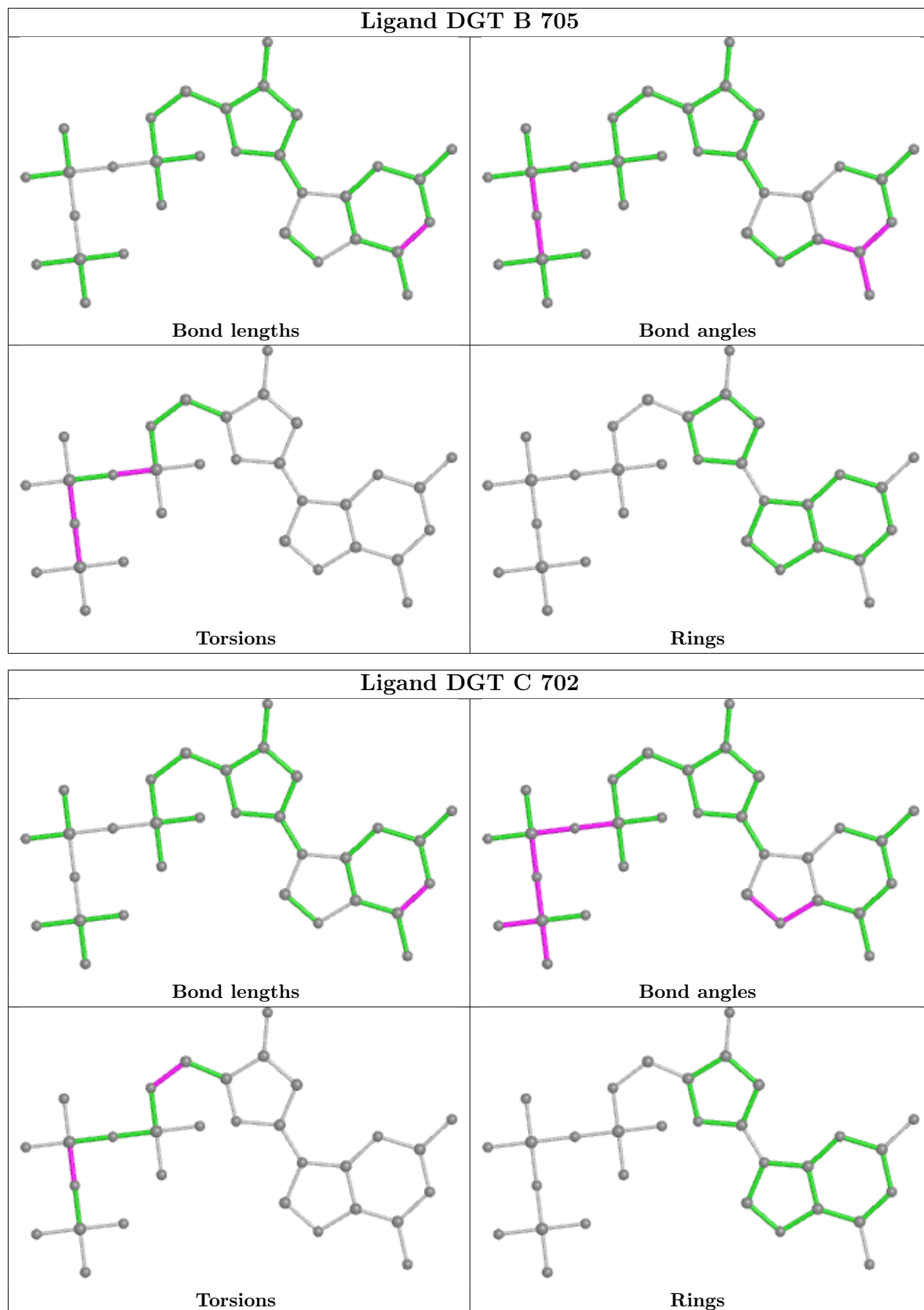
There are no ring outliers.

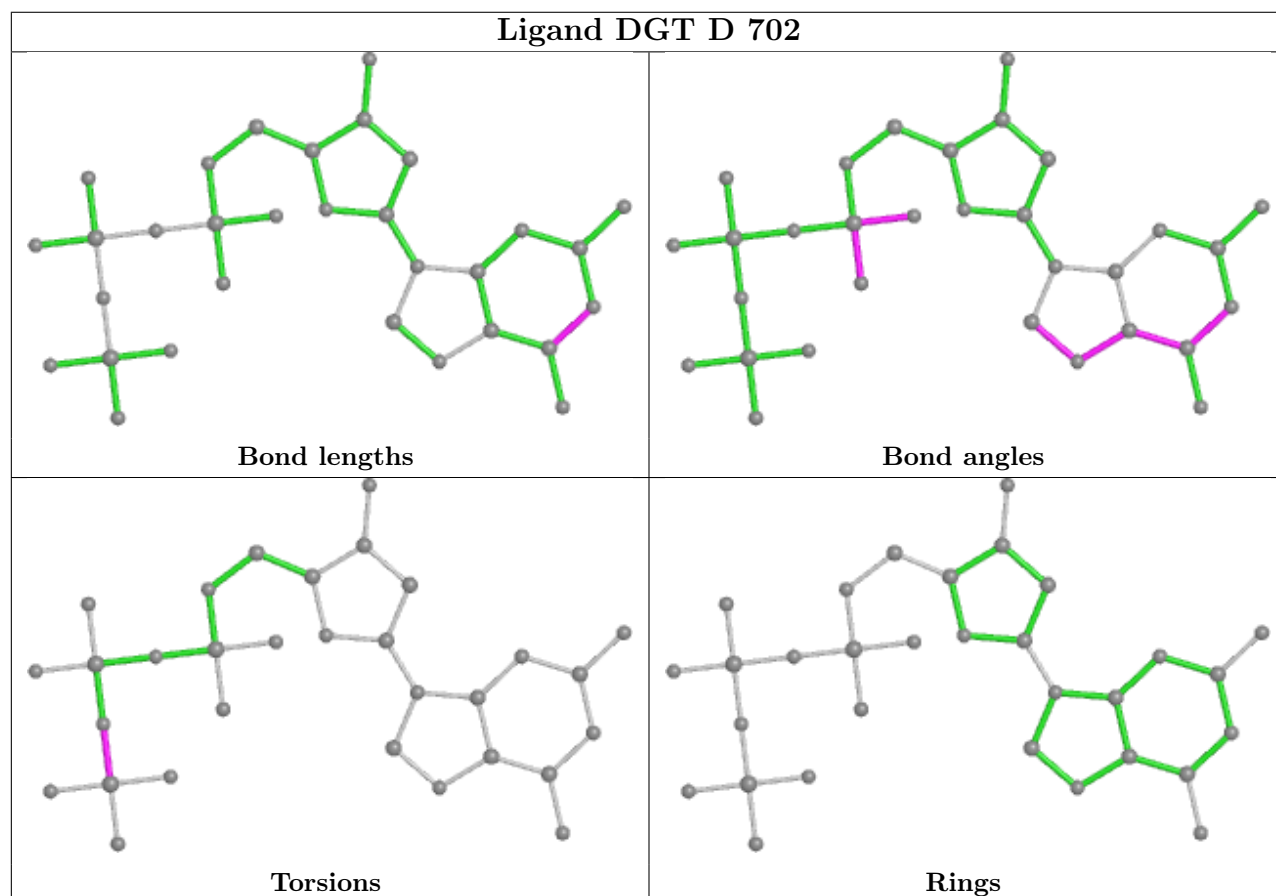
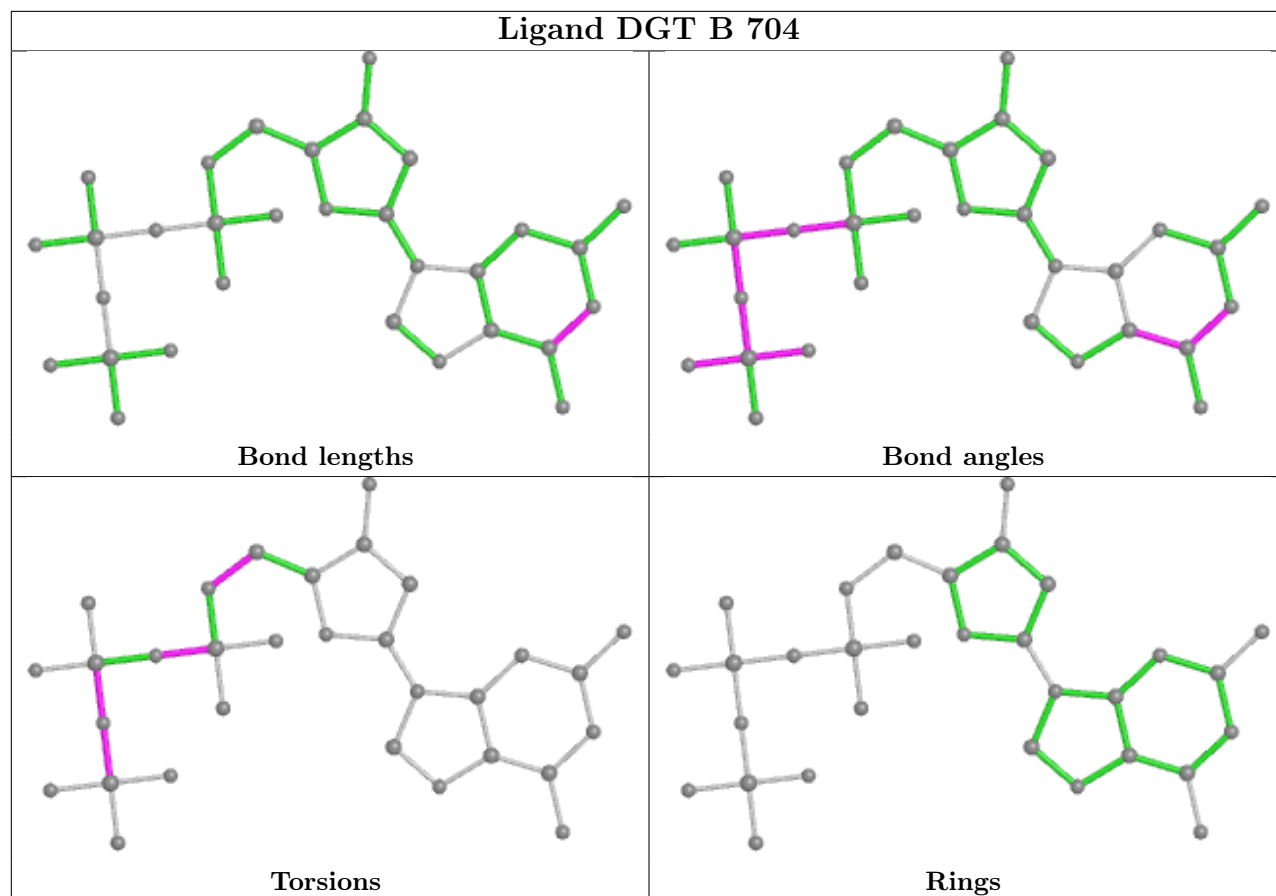
9 monomers are involved in 43 short contacts:

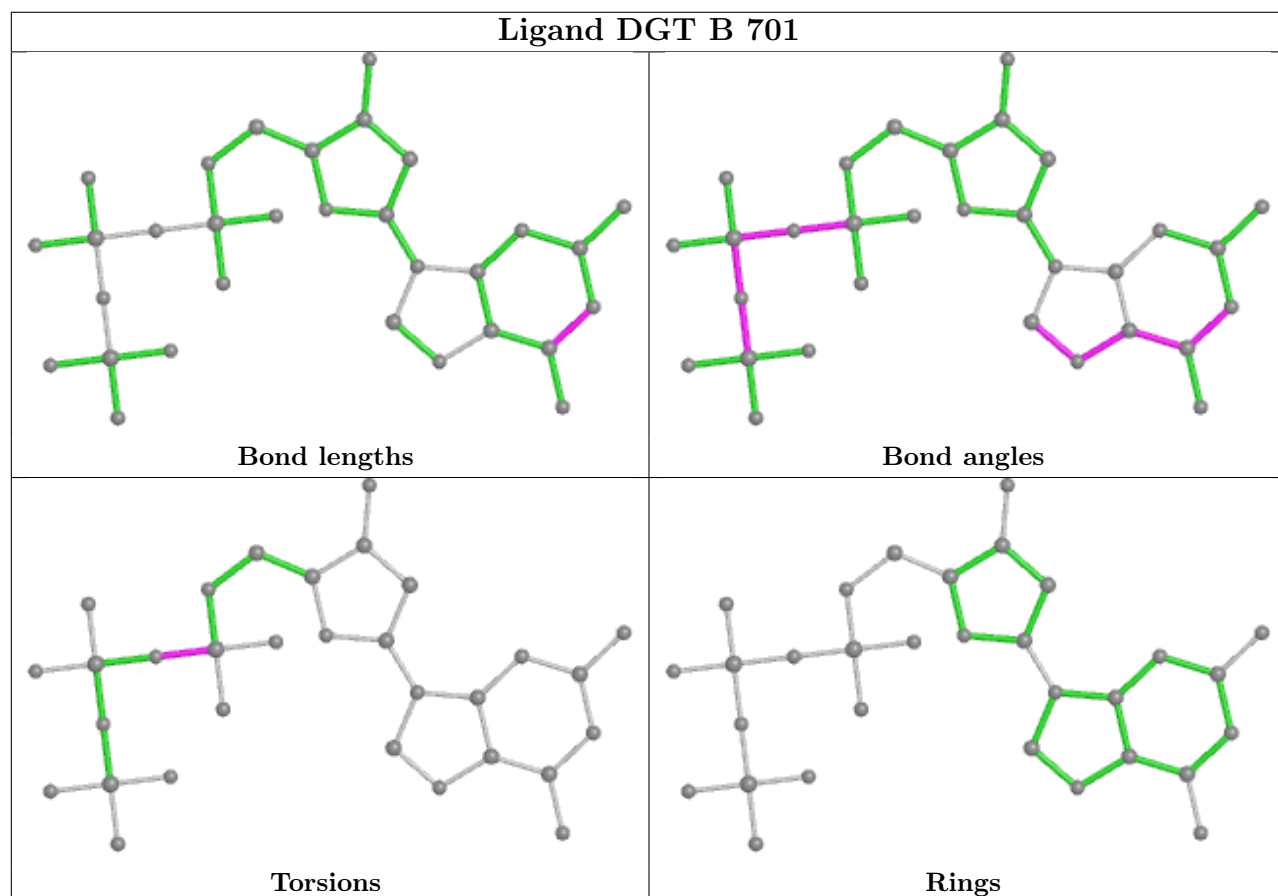
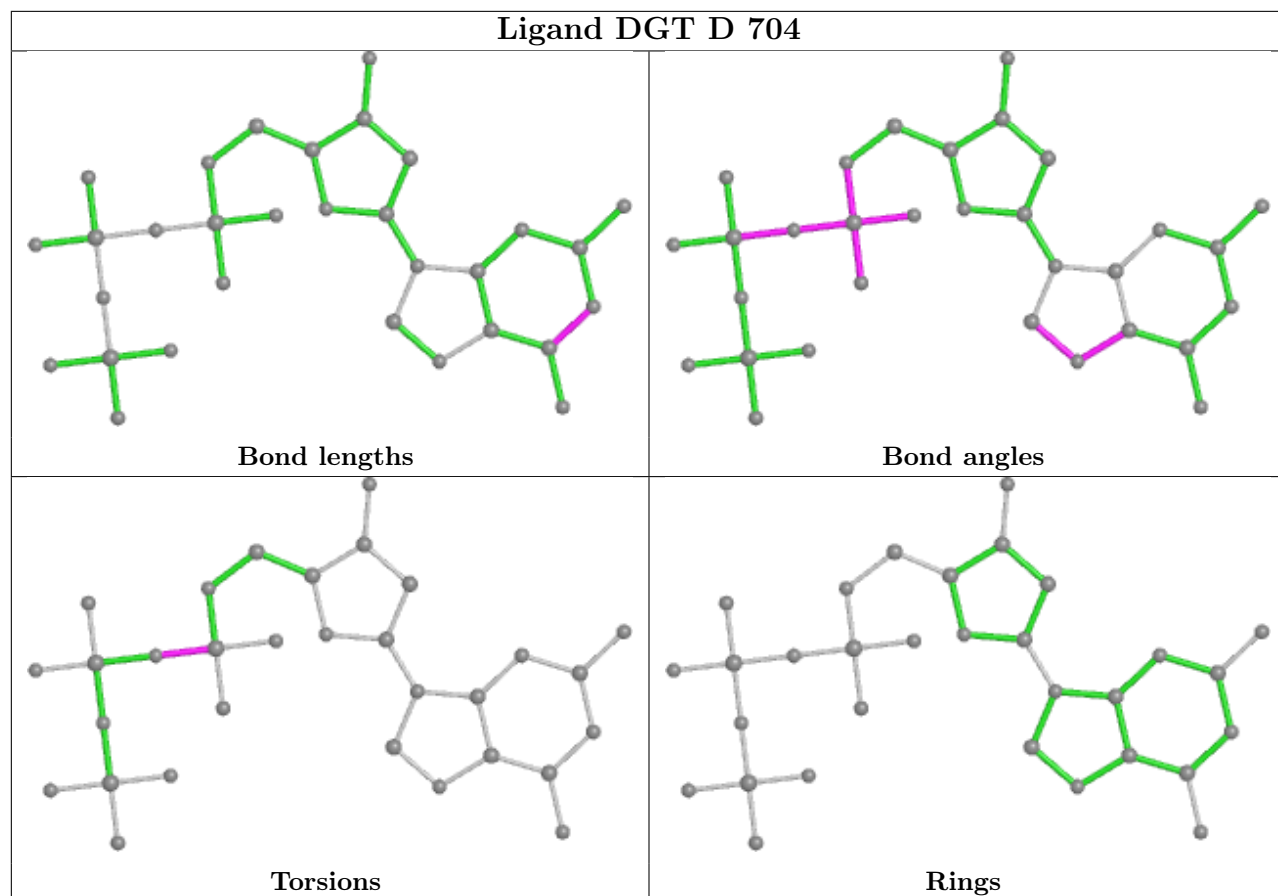
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	703	DGT	1	0
2	B	705	DGT	6	0
2	C	702	DGT	3	0
2	B	704	DGT	1	0
2	D	702	DGT	2	0
2	B	701	DGT	16	0
2	A	704	DGT	3	0
2	C	703	DGT	6	0
2	D	703	DGT	5	0

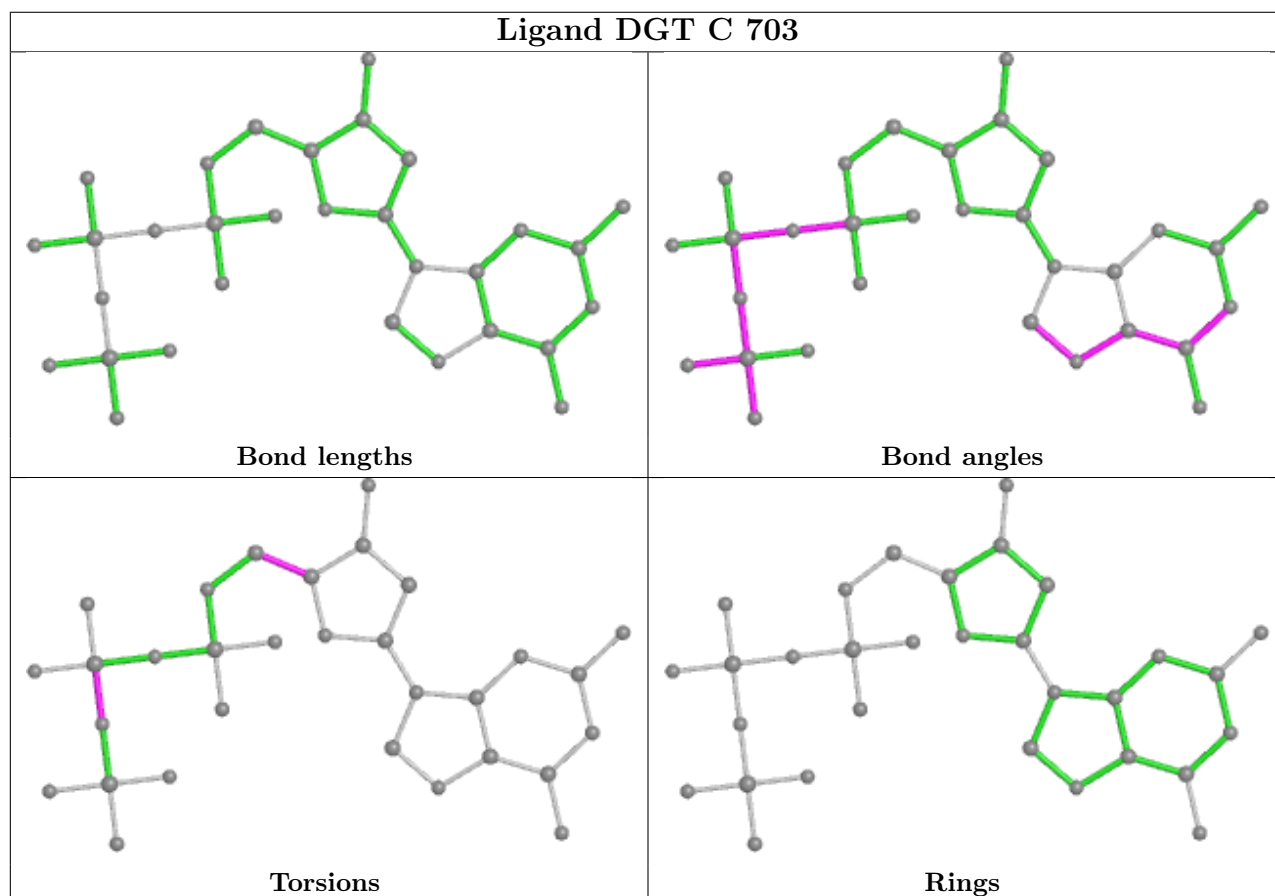
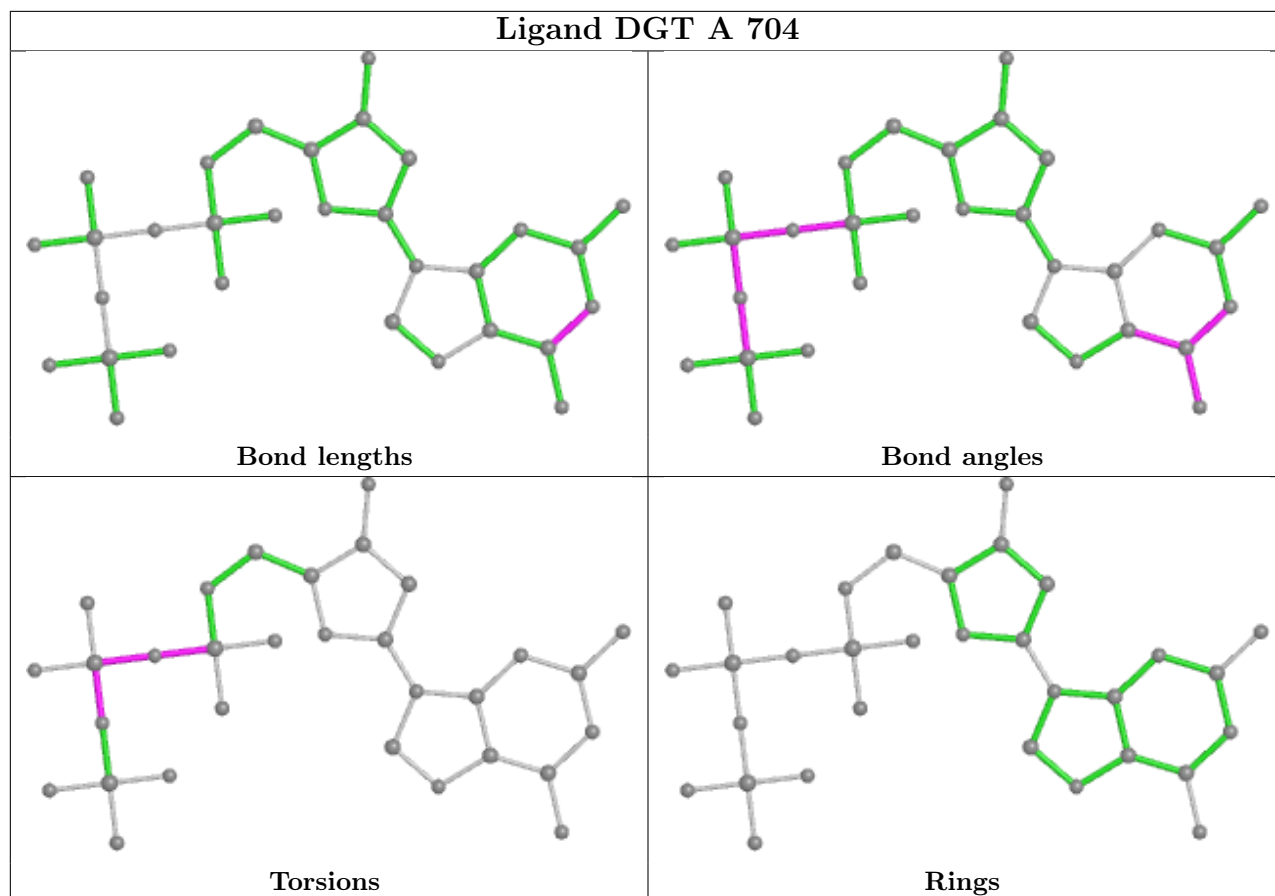
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

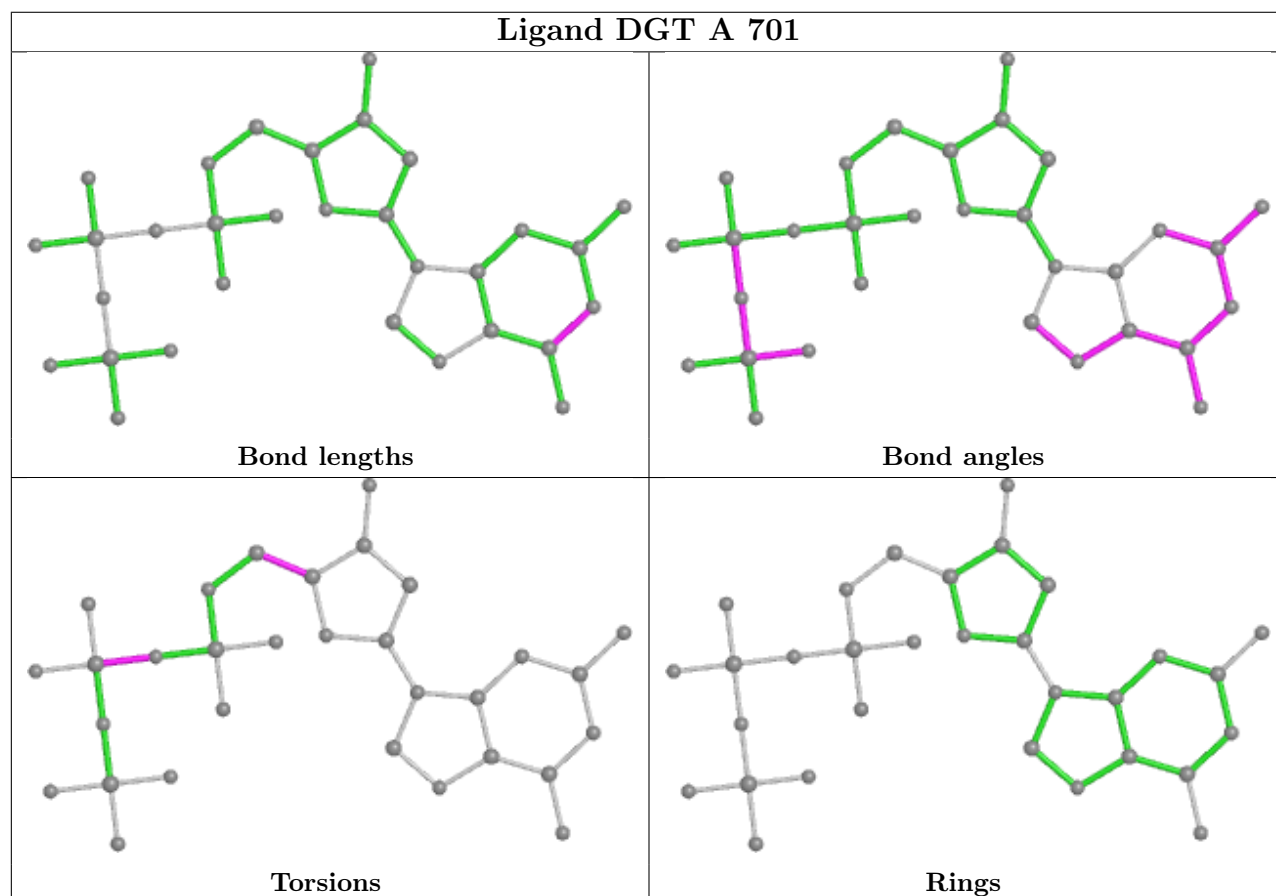
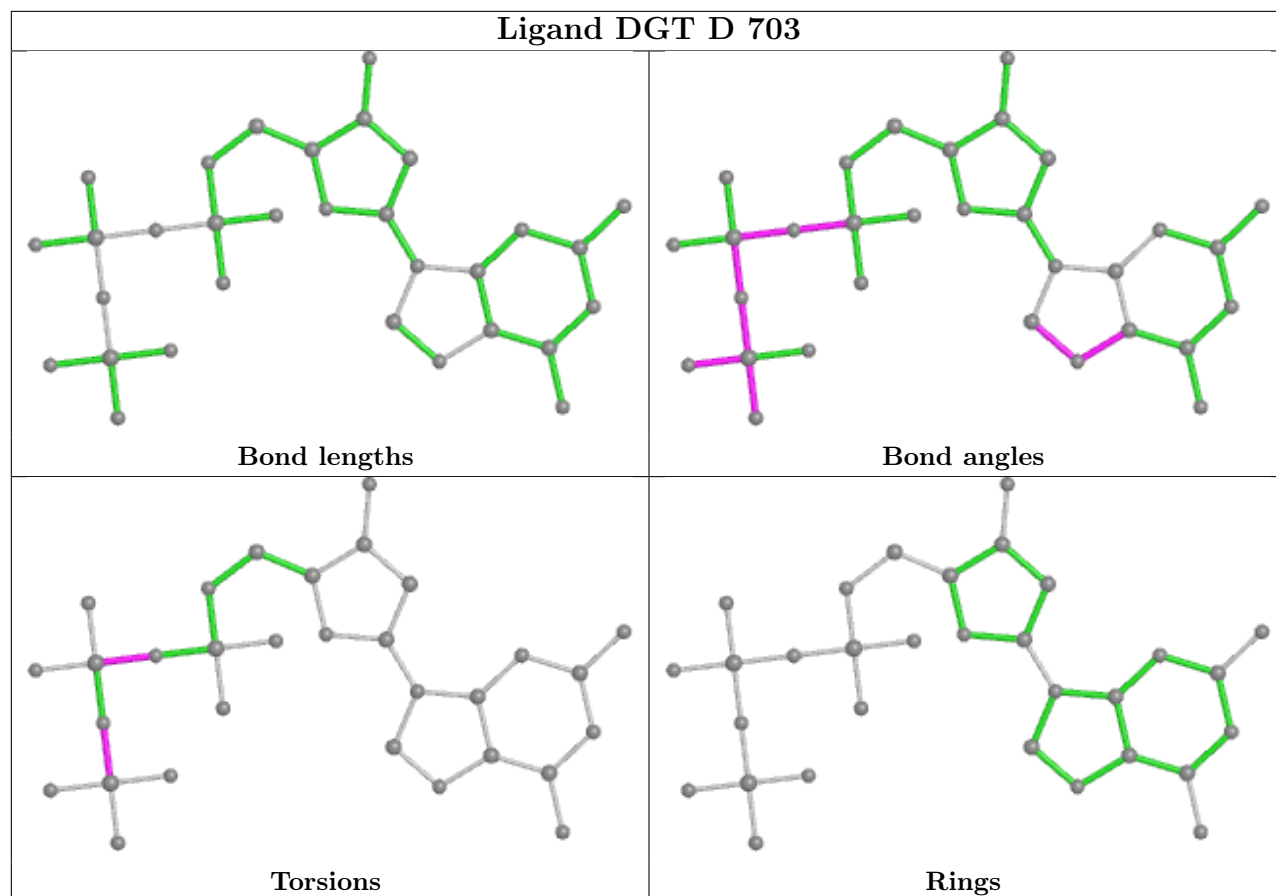












5.7 Other polymers [i](#)

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 [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	480/514 (93%)	0.31	23 (4%) 30 21	39, 60, 95, 109	0
1	B	480/514 (93%)	0.76	71 (14%) 2 1	48, 73, 113, 143	0
1	C	480/514 (93%)	0.45	21 (4%) 34 24	48, 70, 98, 119	0
1	D	480/514 (93%)	0.31	19 (3%) 38 28	39, 62, 100, 140	0
All	All	1920/2056 (93%)	0.46	134 (6%) 16 9	39, 66, 104, 143	0

All (134) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	486	LYS	8.2
1	B	488	LEU	7.5
1	B	491	VAL	6.9
1	B	489	LEU	6.9
1	D	544	LYS	6.3
1	B	492	LYS	6.2
1	B	326	GLN	6.0
1	B	487	VAL	5.7
1	B	599	ASN	5.7
1	C	490	ASP	5.6
1	B	498	PHE	5.4
1	C	326	GLN	5.1
1	B	490	ASP	5.0
1	B	560	LYS	5.0
1	C	590	LEU	5.0
1	B	493	LEU	4.8
1	A	326	GLN	4.5
1	B	481	ALA	4.5
1	B	559	ARG	4.4
1	B	562	LEU	4.4
1	B	557	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	B	554	CYS	4.2
1	B	465	GLN	4.2
1	D	326	GLN	4.1
1	B	284	LEU	4.1
1	B	285	TRP	4.0
1	B	482	SER	4.0
1	B	345	ASN	4.0
1	D	510	GLN	3.9
1	D	511[A]	GLU	3.8
1	D	466	ILE	3.8
1	B	485	PRO	3.8
1	D	543	GLU	3.7
1	D	467	LYS	3.6
1	B	563	TYR	3.6
1	B	586	VAL	3.6
1	A	498	PHE	3.6
1	D	473	TYR	3.5
1	B	590	LEU	3.5
1	B	277	GLU	3.5
1	D	465	GLN	3.5
1	A	488	LEU	3.4
1	B	327	ASN	3.4
1	B	571	GLN	3.4
1	B	556	LYS	3.4
1	B	577	ASN	3.4
1	B	305	ARG	3.3
1	A	465	GLN	3.3
1	B	569	PHE	3.2
1	B	468	ILE	3.2
1	A	491	VAL	3.1
1	B	475	SER	3.1
1	C	285	TRP	3.1
1	B	477	PRO	3.1
1	B	585	ASP	3.1
1	C	327	ASN	3.1
1	A	484	LYS	3.1
1	C	488	LEU	3.1
1	D	468	ILE	3.0
1	B	565	ALA	3.0
1	B	346	GLU	3.0
1	C	320	CYS	3.0
1	D	507	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	345	ASN	3.0
1	A	327	ASN	2.9
1	B	496	GLU	2.9
1	D	469	LYS	2.9
1	A	594	GLN	2.9
1	B	286	PRO	2.8
1	B	568	TYR	2.8
1	B	575	ASP	2.8
1	A	489	LEU	2.8
1	B	497	ASP	2.7
1	B	553	TYR	2.7
1	B	329	PHE	2.7
1	A	347	LEU	2.7
1	B	287	TYR	2.7
1	B	476	LEU	2.7
1	B	483	ALA	2.7
1	B	507	TYR	2.7
1	B	484	LYS	2.7
1	C	325	ILE	2.6
1	B	495	ALA	2.6
1	D	262	GLU	2.6
1	B	478	LYS	2.6
1	A	473	TYR	2.6
1	B	592	VAL	2.6
1	D	288	LYS	2.6
1	C	489	LEU	2.5
1	C	328	ASN	2.5
1	C	543	GLU	2.5
1	B	572	TRP	2.5
1	B	293	ASN	2.4
1	C	563	TYR	2.4
1	D	471	GLU	2.4
1	B	313	TRP	2.4
1	A	528	ARG	2.4
1	B	578	PHE	2.4
1	B	494	LYS	2.4
1	B	598	TRP	2.3
1	B	341	CYS	2.3
1	B	545	PHE	2.3
1	B	275	PRO	2.3
1	B	324	GLY	2.3
1	C	592	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	591	ILE	2.2
1	C	589	PRO	2.2
1	C	591	ILE	2.2
1	B	457	VAL	2.2
1	C	465	GLN	2.2
1	C	522	CYS	2.1
1	B	596	LYS	2.1
1	B	584	GLY	2.1
1	B	594	GLN	2.1
1	D	470	ARG	2.1
1	D	540	LEU	2.1
1	A	482	SER	2.1
1	A	490	ASP	2.1
1	C	594	GLN	2.1
1	D	480	VAL	2.1
1	A	476	LEU	2.1
1	A	466	ILE	2.1
1	D	472	ASP	2.1
1	C	227	PRO	2.1
1	B	296	PHE	2.1
1	A	486	LYS	2.1
1	A	284	LEU	2.0
1	C	159	GLY	2.0
1	A	471	GLU	2.0
1	B	288	LYS	2.0
1	A	483	ALA	2.0
1	C	258	GLY	2.0
1	A	472	ASP	2.0
1	A	468	ILE	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 monosaccharides in this entry.

6.4 Ligands

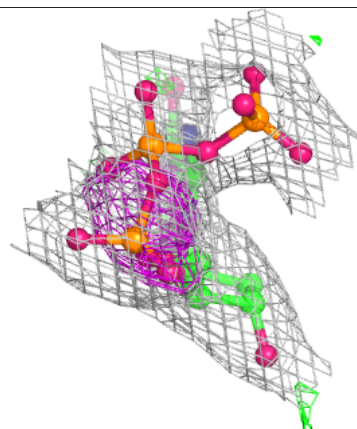
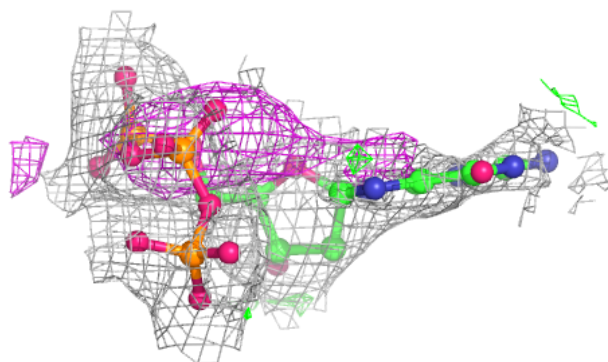
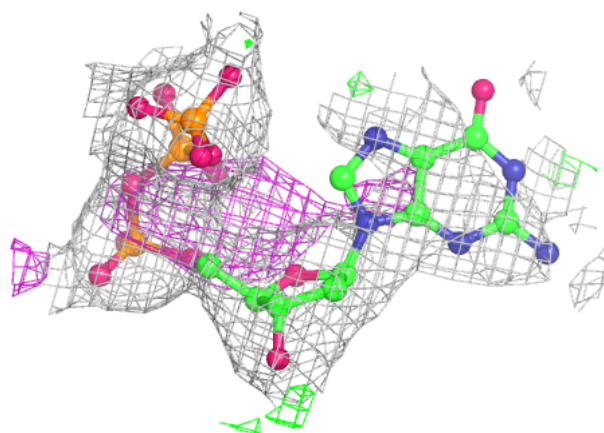
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	DGT	B	701	31/31	0.72	0.28	79,121,143,148	0
2	DGT	D	703	31/31	0.73	0.36	82,124,149,155	0
2	DGT	C	703	31/31	0.77	0.27	80,113,136,141	0
2	DGT	A	701	31/31	0.85	0.22	54,92,113,116	0
3	MG	B	702	1/1	0.88	0.13	100,100,100,100	0
3	MG	C	701	1/1	0.92	0.21	60,60,60,60	0
3	MG	D	701	1/1	0.95	0.17	39,39,39,39	0
3	MG	A	705	1/1	0.96	0.20	46,46,46,46	0
3	MG	B	703	1/1	0.96	0.20	48,48,48,48	0
2	DGT	C	702	31/31	0.97	0.14	51,55,59,60	0
2	DGT	A	702	31/31	0.98	0.17	38,42,54,60	0
2	DGT	D	704	31/31	0.98	0.17	38,45,48,49	0
2	DGT	B	704	31/31	0.98	0.17	46,52,61,65	0
2	DGT	B	705	31/31	0.98	0.18	40,44,48,53	0
2	DGT	A	703	31/31	0.98	0.16	41,44,51,51	0
2	DGT	A	704	31/31	0.98	0.19	47,51,60,62	0
2	DGT	D	702	31/31	0.98	0.16	52,55,60,62	0

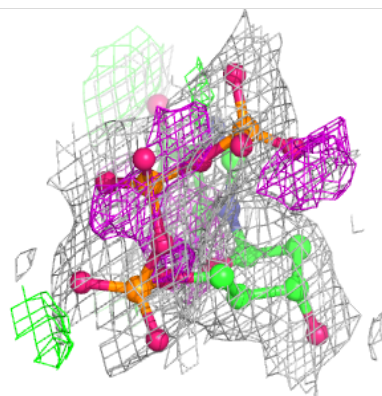
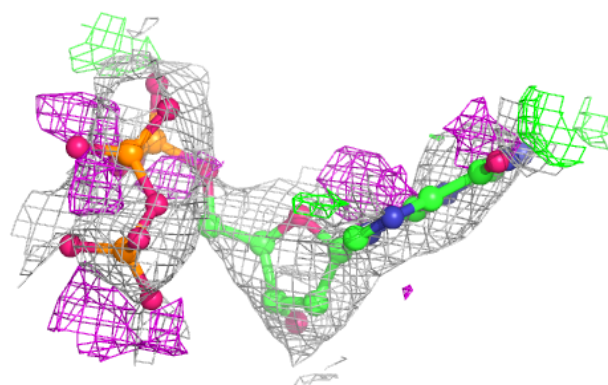
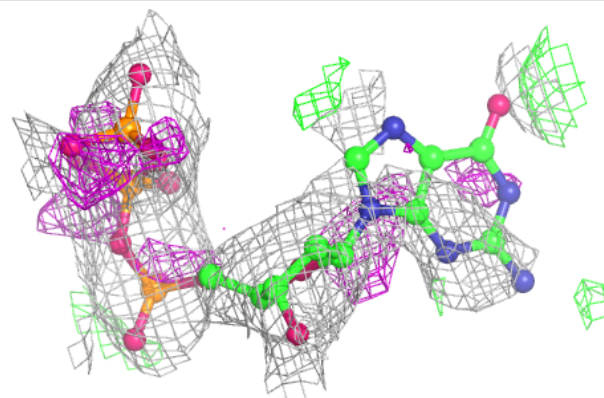
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DGT 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)

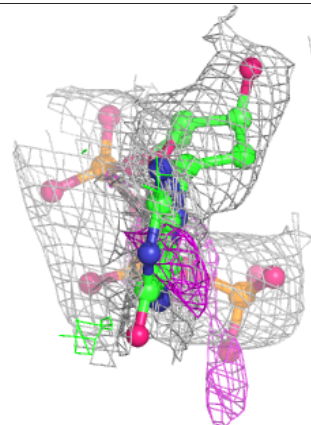
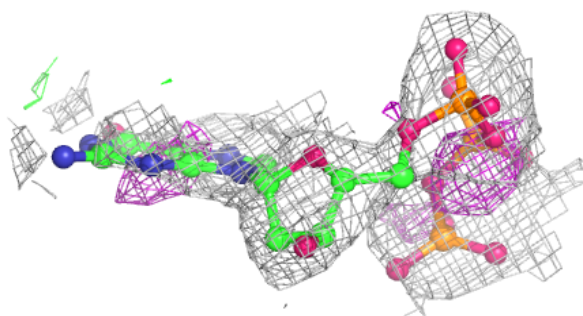
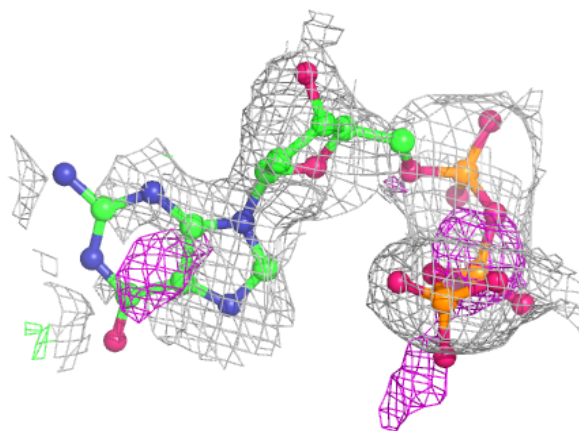
**Electron density around DGT D 703:**

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



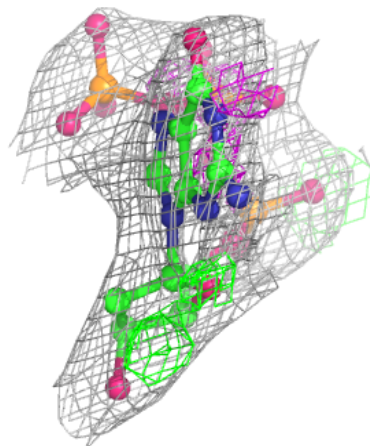
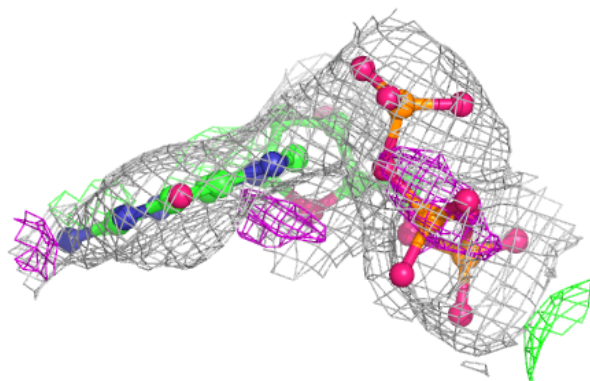
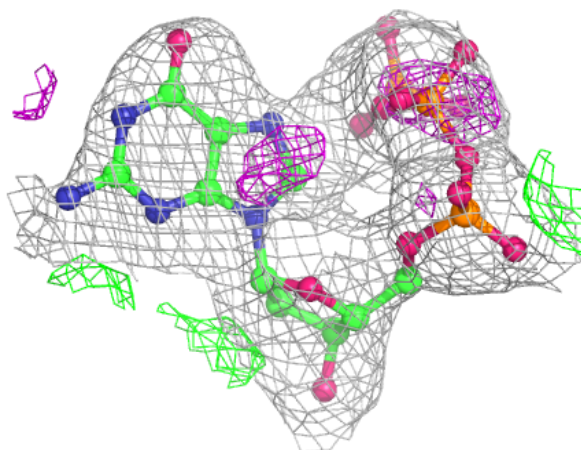
Electron density around DGT C 703:

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



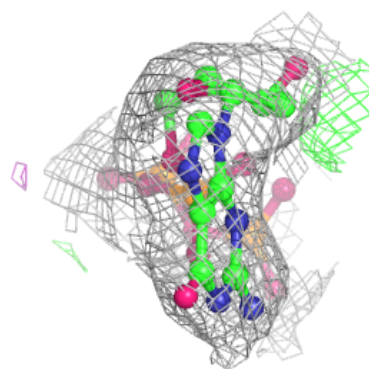
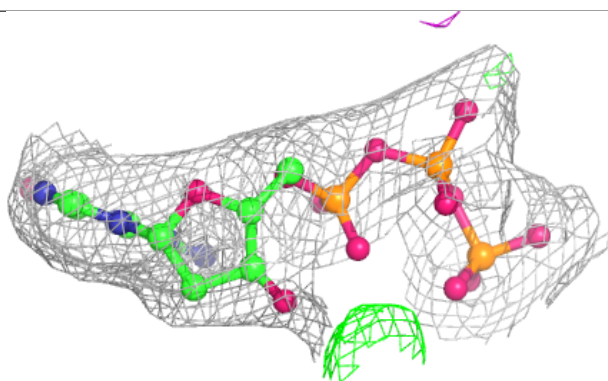
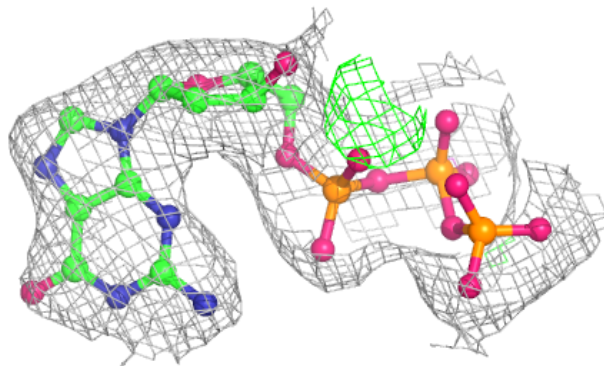
Electron density around DGT A 701:

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

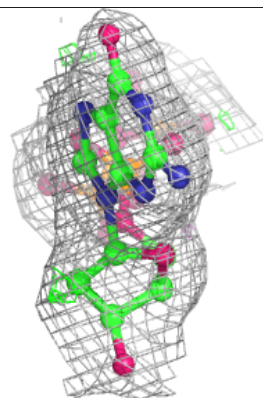
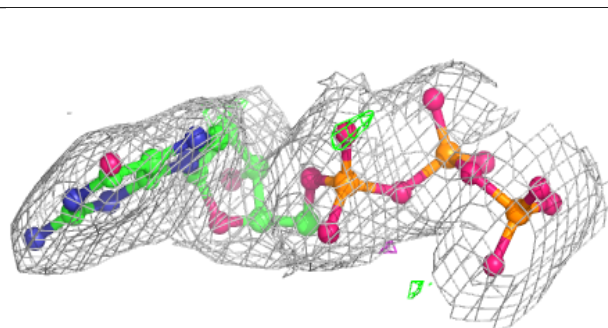
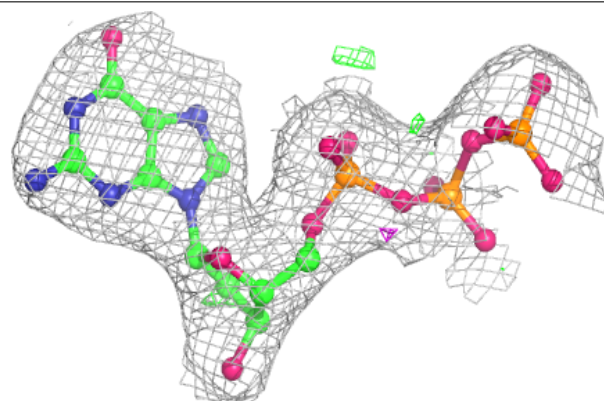


Electron density around DGT C 702:

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

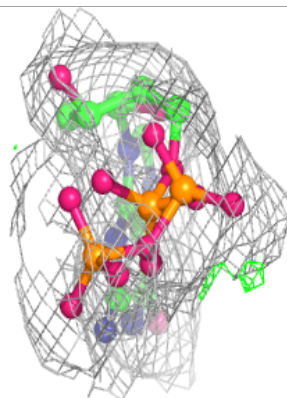
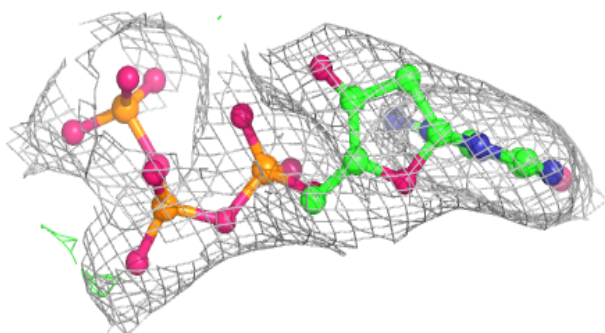
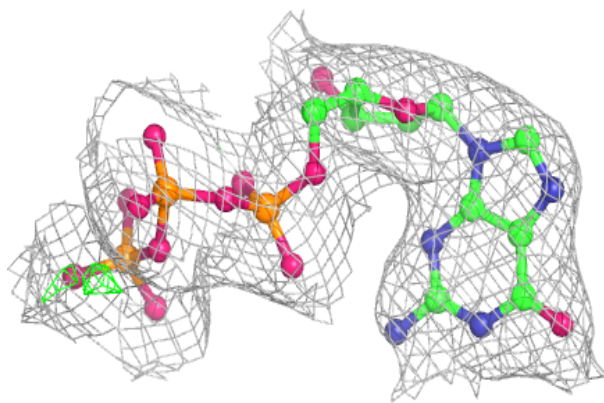
**Electron density around DGT A 702:**

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

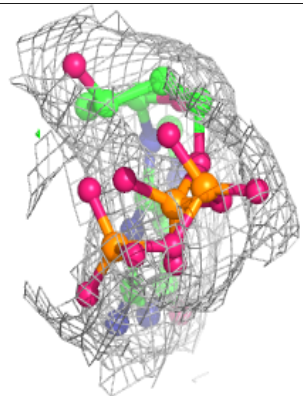
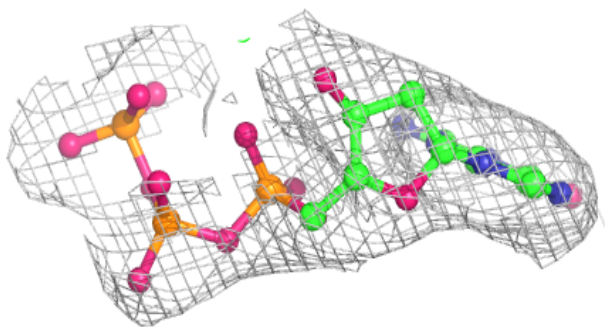
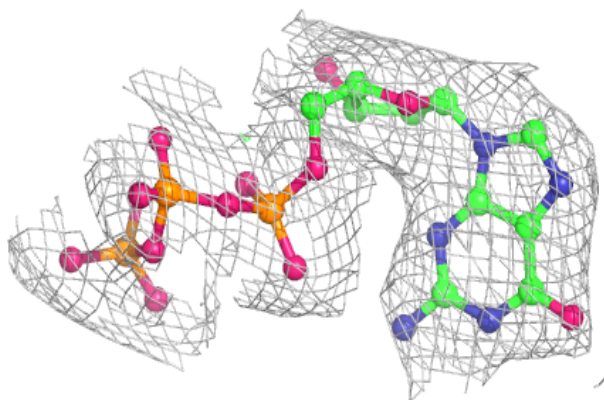


Electron density around DGT D 704:

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

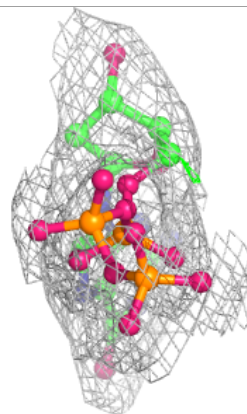
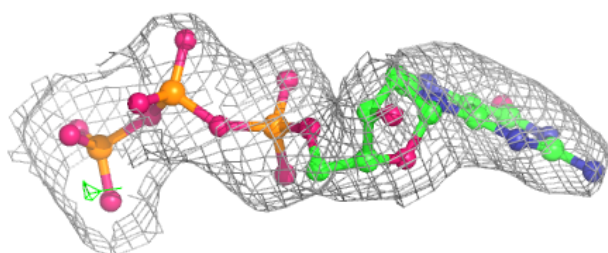
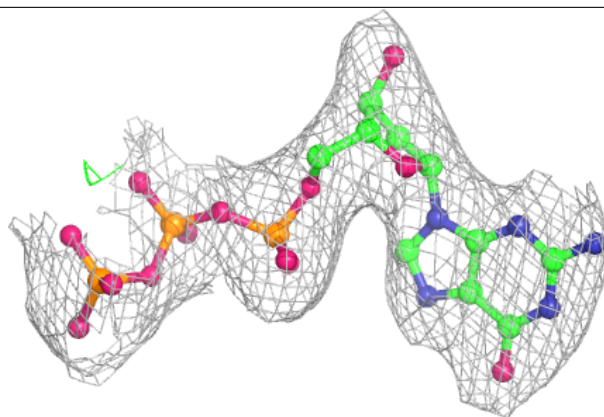
**Electron density around DGT B 704:**

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

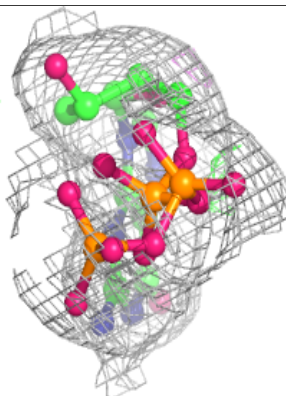
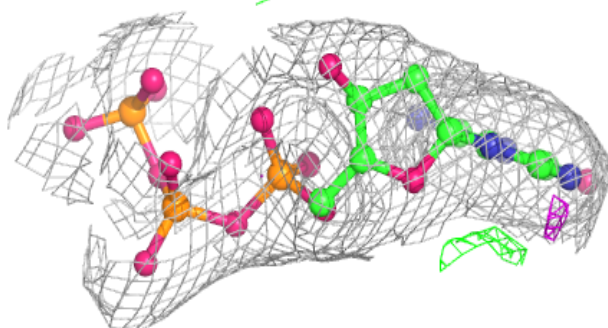
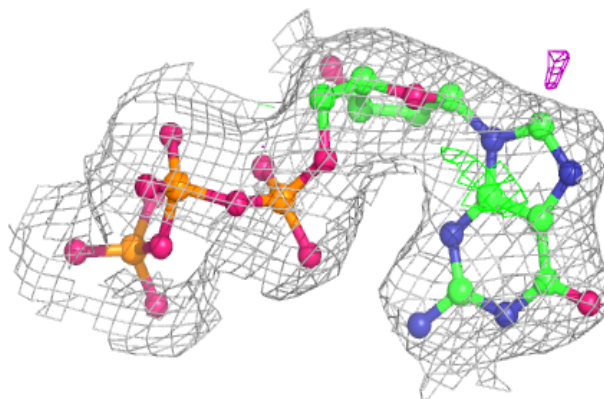


Electron density around DGT B 705:

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

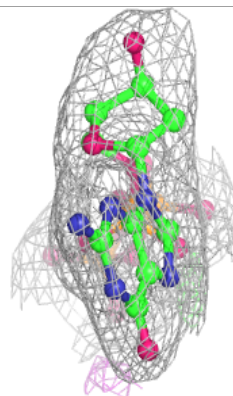
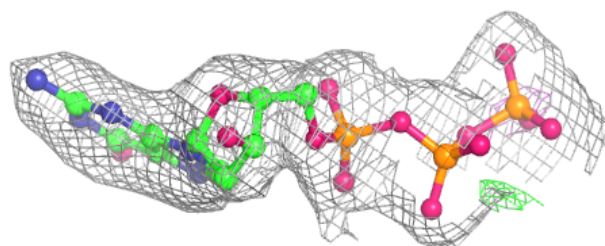
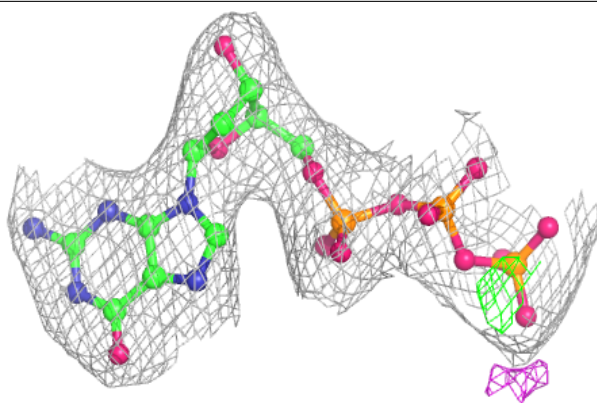
**Electron density around DGT A 703:**

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

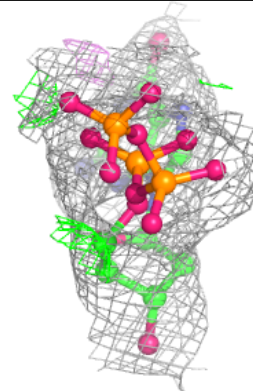
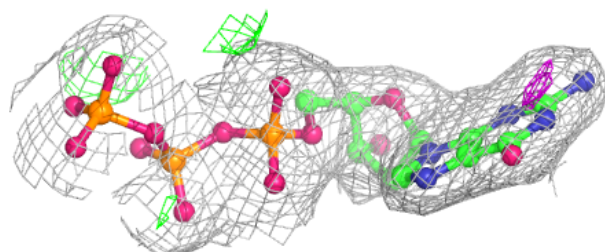
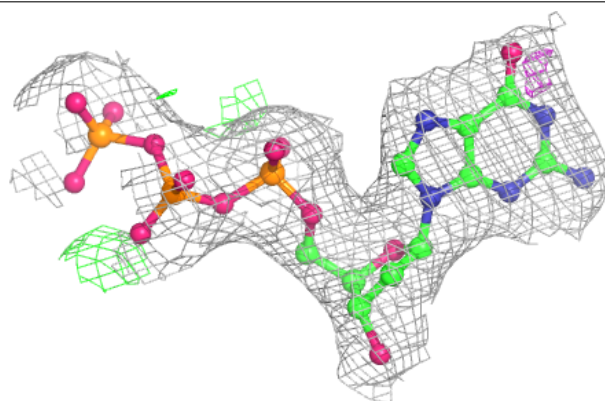


Electron density around DGT A 704:

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

**Electron density around DGT D 702:**

$2mF_o-DF_c$ (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.