Full wwPDB X-ray Structure Validation Report (i)

Nov 1, 2023 – 01:57 PM JST

PDB ID	:	5KD0
Title	:	Crystal structure of the aromatic prenyltransferase AtaPT(E91A) mutant from Aspergillus terreus A8-4 in complex with geranyl S-thiolodiphosphate and (+)-butyrolactone II
Authors	:	Sun, F.; Gao, B.
Deposited on	:	2016-06-07
Resolution	:	2.82 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

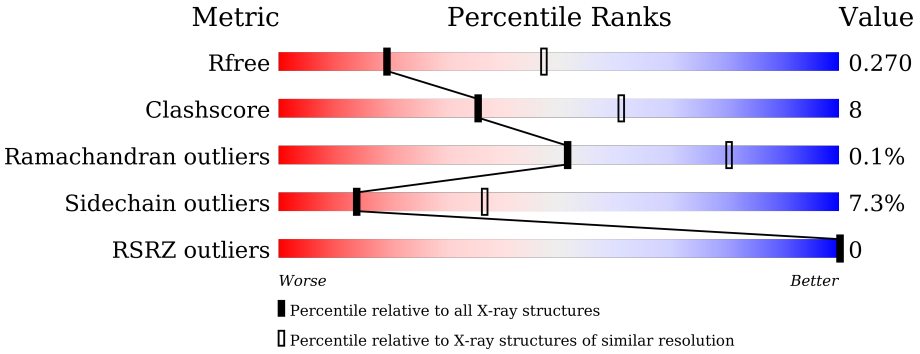
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.82 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 <=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	416	72% 20% • •
1	B	416	76% 15% • 5%

2 Entry composition (i)

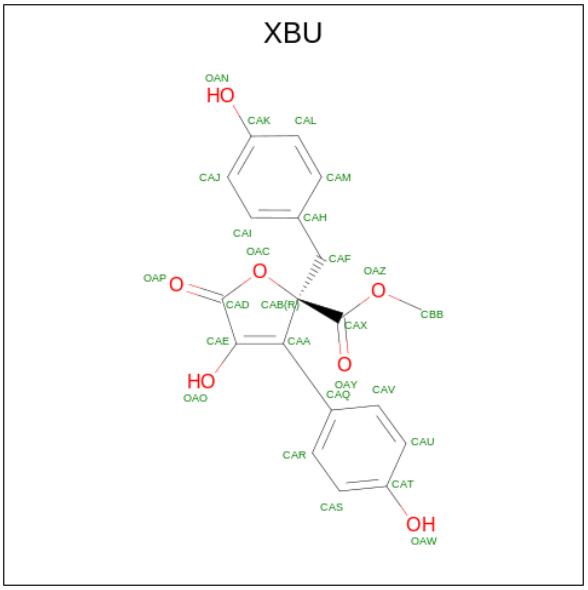
There are 4 unique types of molecules in this entry. The entry contains 6366 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 aromatic prenyltransferase.

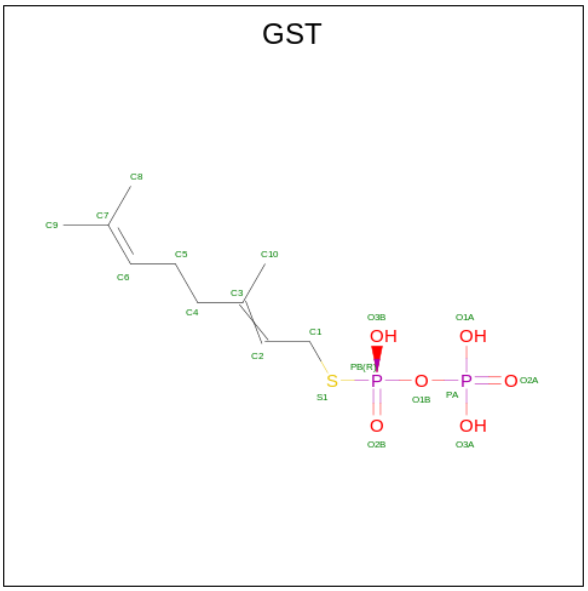
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	398	3152	2039	526	574	13	0	0	0
1	B	397	3141	2033	522	573	13	0	0	0

- Molecule 2 is methyl (2 {R})-3-(4-hydroxyphenyl)-2-[(4-hydroxyphenyl)methyl]-4-oxidanyl-5-oxidanylidene-furan-2-carboxylate (three-letter code: XBU) (formula: $C_{19}H_{16}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	26	19	7	0	0

- Molecule 3 is GERANYL S-THIOLODIPHOSPHATE (three-letter code: GST) (formula: $C_{10}H_{20}O_6P_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	O	P	S		
3	A	1	19	10	6	2	1	0	0
			Total	C	O	P	S		
3	B	1	19	10	6	2	1	0	0

- Molecule 4 is water.

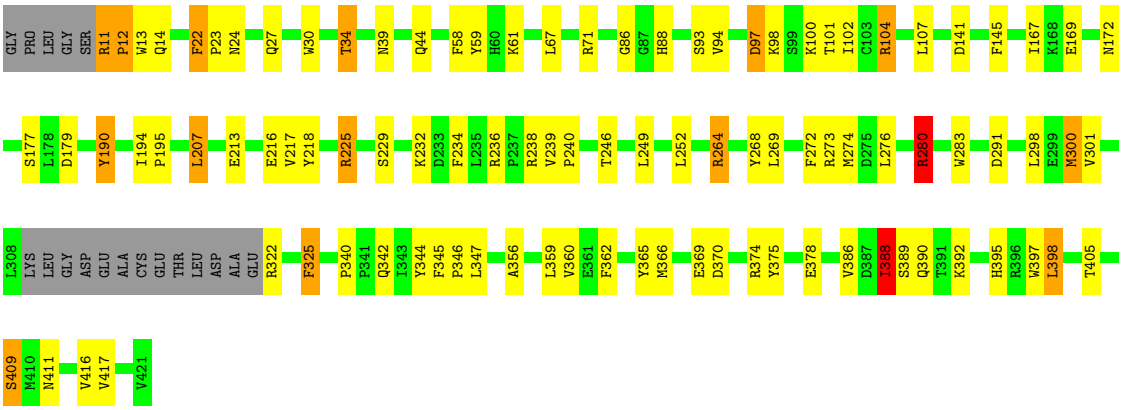
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	4	4	4	0	0
			Total	O		
4	B	5	5	5	0	0

3 Residue-property plots (i)

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

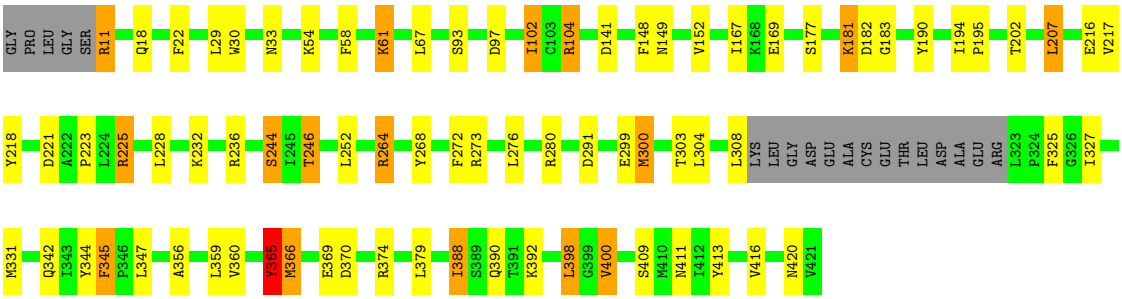
- Molecule 1: aromatic prenyltransferase

Chain A:



- Molecule 1: aromatic prenyltransferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	96.69Å 139.24Å 68.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	139.24 – 2.82 56.06 – 2.82	Depositor EDS
% Data completeness (in resolution range)	98.5 (139.24-2.82) 98.5 (56.06-2.82)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	4.16 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.205 , 0.268 0.207 , 0.270	Depositor DCC
R_{free} test set	1144 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	44.3	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 26.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	6366	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

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

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.90	18/3232 (0.6%)	0.98	15/4397 (0.3%)
1	B	0.88	17/3221 (0.5%)	1.00	15/4383 (0.3%)
All	All	0.89	35/6453 (0.5%)	0.99	30/8780 (0.3%)

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	236	ARG	CZ-NH1	-9.97	1.20	1.33
1	B	236	ARG	CZ-NH1	-9.52	1.20	1.33
1	B	365	TYR	CE1-CZ	-9.14	1.26	1.38
1	A	365	TYR	CE1-CZ	-8.25	1.27	1.38
1	A	365	TYR	CG-CD2	-7.13	1.29	1.39
1	A	58	PHE	CG-CD1	-6.70	1.28	1.38
1	B	272	PHE	CG-CD2	-6.48	1.29	1.38
1	B	22	PHE	CG-CD1	-6.45	1.29	1.38
1	A	22	PHE	CG-CD2	-6.28	1.29	1.38
1	B	365	TYR	CG-CD2	-6.25	1.31	1.39
1	B	58	PHE	CG-CD1	-6.18	1.29	1.38
1	B	365	TYR	CG-CD1	-6.17	1.31	1.39
1	B	345	PHE	CG-CD1	-6.16	1.29	1.38
1	A	272	PHE	CG-CD1	-6.06	1.29	1.38
1	B	409	SER	CB-OG	-6.00	1.34	1.42
1	A	272	PHE	CG-CD2	-5.86	1.29	1.38
1	A	409	SER	CB-OG	-5.85	1.34	1.42
1	B	22	PHE	CG-CD2	-5.80	1.30	1.38
1	A	58	PHE	CG-CD2	-5.80	1.30	1.38
1	A	365	TYR	CG-CD1	-5.80	1.31	1.39
1	B	272	PHE	CG-CD1	-5.69	1.30	1.38
1	B	365	TYR	CE2-CZ	-5.66	1.31	1.38
1	A	365	TYR	CE2-CZ	-5.64	1.31	1.38
1	A	325	PHE	CG-CD2	-5.63	1.30	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	216	GLU	CD-OE1	-5.62	1.19	1.25
1	A	22	PHE	CG-CD1	-5.59	1.30	1.38
1	B	325	PHE	CG-CD2	-5.58	1.30	1.38
1	B	420	ASN	CG-ND2	-5.53	1.19	1.32
1	A	345	PHE	CG-CD1	-5.37	1.30	1.38
1	B	325	PHE	CG-CD1	-5.32	1.30	1.38
1	B	216	GLU	CD-OE1	-5.32	1.19	1.25
1	A	325	PHE	CG-CD1	-5.29	1.30	1.38
1	A	27	GLN	CD-NE2	-5.28	1.19	1.32
1	A	12	PRO	N-CD	5.11	1.55	1.47
1	B	149	ASN	CG-ND2	-5.02	1.20	1.32

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	225	ARG	NE-CZ-NH1	-18.30	111.15	120.30
1	B	225	ARG	NE-CZ-NH2	-17.46	111.57	120.30
1	B	225	ARG	NE-CZ-NH1	15.39	128.00	120.30
1	A	225	ARG	NE-CZ-NH2	15.02	127.81	120.30
1	B	236	ARG	NE-CZ-NH2	13.25	126.92	120.30
1	A	236	ARG	NE-CZ-NH2	12.51	126.55	120.30
1	B	102	ILE	CG1-CB-CG2	-9.97	89.47	111.40
1	A	280	ARG	NE-CZ-NH2	-8.51	116.05	120.30
1	B	280	ARG	NE-CZ-NH1	-8.38	116.11	120.30
1	B	207	LEU	CA-CB-CG	8.23	134.24	115.30
1	A	207	LEU	CA-CB-CG	7.89	133.45	115.30
1	A	236	ARG	NE-CZ-NH1	-7.75	116.43	120.30
1	B	236	ARG	NE-CZ-NH1	-7.09	116.75	120.30
1	B	141	ASP	CB-CG-OD1	6.64	124.28	118.30
1	A	264	ARG	NE-CZ-NH2	6.46	123.53	120.30
1	B	369	GLU	OE1-CD-OE2	-6.33	115.70	123.30
1	B	264	ARG	NE-CZ-NH2	6.22	123.41	120.30
1	A	207	LEU	CB-CG-CD2	-6.16	100.53	111.00
1	B	225	ARG	CD-NE-CZ	6.15	132.21	123.60
1	A	225	ARG	CD-NE-CZ	6.07	132.10	123.60
1	B	273	ARG	NE-CZ-NH2	-6.07	117.26	120.30
1	A	388	ILE	CB-CA-C	-5.84	99.92	111.60
1	A	280	ARG	NH1-CZ-NH2	5.60	125.56	119.40
1	A	213	GLU	OE1-CD-OE2	-5.47	116.73	123.30
1	B	327	ILE	CG1-CB-CG2	-5.37	99.60	111.40
1	B	61	LYS	CD-CE-NZ	5.32	123.93	111.70
1	B	366	MET	CB-CG-SD	-5.27	96.59	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	291	ASP	CB-CG-OD2	5.25	123.02	118.30
1	A	369	GLU	OE1-CD-OE2	-5.21	117.05	123.30
1	A	141	ASP	CB-CG-OD1	5.10	122.89	118.30

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	3152	0	3167	53	1
1	B	3141	0	3154	44	1
2	A	26	0	0	6	0
3	A	19	0	17	6	0
3	B	19	0	17	2	0
4	A	4	0	0	1	0
4	B	5	0	0	1	0
All	All	6366	0	6355	103	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 8.

All (103) 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:12:PRO:HD2	1:A:39:ASN:ND2	1.64	1.11
1:A:11:ARG:NH1	1:A:14:GLN:OE1	1.89	1.04
1:A:12:PRO:CD	1:A:39:ASN:HD21	1.73	1.01
1:A:12:PRO:HD2	1:A:39:ASN:HD21	0.79	0.94
1:B:300:MET:HG2	1:B:366:MET:HE1	1.54	0.87
1:B:300:MET:CG	1:B:366:MET:HE1	2.07	0.84
1:B:308:LEU:C	4:B:603:HOH:O	2.19	0.80
1:B:11:ARG:HH12	1:B:18:GLN:HE22	1.31	0.78
1:B:300:MET:HG2	1:B:366:MET:CE	2.13	0.78
1:B:228:LEU:CD2	1:B:331:MET:HE1	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:THR:HG1	1:A:59:TYR:HH	1.29	0.77
1:A:61:LYS:HE3	4:A:604:HOH:O	1.88	0.73
1:B:29:LEU:O	1:B:33:ASN:ND2	2.21	0.73
2:A:501:XBU:CBB	3:A:502:GST:H42	2.25	0.67
2:A:501:XBU:CBB	3:A:502:GST:C4	2.74	0.65
1:A:13:TRP:NE1	1:A:14:GLN:HG3	2.13	0.64
1:A:94:VAL:HG22	1:A:101:THR:HG22	1.80	0.63
1:A:13:TRP:CE2	1:A:14:GLN:HG3	2.34	0.61
1:B:370:ASP:O	1:B:374:ARG:HG2	2.00	0.61
1:B:342:GLN:OE1	1:B:411:ASN:ND2	2.33	0.61
1:A:370:ASP:O	1:A:374:ARG:HG3	2.00	0.61
1:B:194:ILE:HB	1:B:195:PRO:HD3	1.83	0.61
1:B:228:LEU:HD23	1:B:331:MET:HE1	1.82	0.59
1:B:300:MET:SD	1:B:366:MET:CE	2.90	0.59
1:B:303:THR:HG21	1:B:365:TYR:CD2	2.38	0.59
1:B:356:ALA:O	1:B:360:VAL:HG23	2.02	0.59
1:A:359:LEU:HD21	1:A:398:LEU:HD22	1.83	0.59
1:A:356:ALA:O	1:A:360:VAL:HG23	2.03	0.59
1:B:347:LEU:HD11	1:B:398:LEU:HB3	1.84	0.57
1:B:365:TYR:C	1:B:365:TYR:CD1	2.77	0.57
1:A:280:ARG:HG3	1:A:298:LEU:HD21	1.85	0.57
1:B:300:MET:SD	1:B:366:MET:HE1	2.45	0.57
1:A:94:VAL:HG22	1:A:101:THR:CG2	2.33	0.57
1:A:30:TRP:CE3	1:A:67:LEU:HD13	2.40	0.56
2:A:501:XBU:OAY	3:A:502:GST:C2	2.53	0.56
1:A:398:LEU:C	1:A:398:LEU:HD12	2.26	0.56
1:B:303:THR:HG21	1:B:365:TYR:CE2	2.41	0.55
1:B:30:TRP:CE3	1:B:67:LEU:HD13	2.42	0.55
1:B:300:MET:CG	1:B:366:MET:CE	2.79	0.54
1:B:300:MET:SD	1:B:366:MET:HE3	2.49	0.53
1:A:218:TYR:CE1	1:A:225:ARG:HD3	2.44	0.53
2:A:501:XBU:OAY	3:A:502:GST:C3	2.57	0.53
1:A:274:MET:HB3	1:A:325:PHE:CE2	2.44	0.52
1:B:202:THR:HG21	1:B:207:LEU:HD23	1.91	0.52
1:B:342:GLN:HG3	1:B:400:VAL:O	2.09	0.52
1:A:347:LEU:HD11	1:A:398:LEU:HB3	1.91	0.52
1:A:375:TYR:OH	1:A:395:HIS:NE2	2.37	0.50
1:B:228:LEU:HD21	1:B:331:MET:HE1	1.91	0.50
1:B:304:LEU:HD22	1:B:400:VAL:HG11	1.94	0.49
1:B:359:LEU:HD21	1:B:398:LEU:HD22	1.94	0.49
1:B:181:LYS:O	1:B:182:ASP:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:TYR:CE1	1:B:225:ARG:HG2	2.48	0.49
2:A:501:XBU:CBB	3:A:502:GST:H41	2.43	0.48
1:B:221:ASP:OD1	1:B:223:PRO:HD2	2.13	0.48
1:A:194:ILE:O	1:A:195:PRO:C	2.52	0.48
1:B:344:TYR:CZ	3:B:501:GST:H2	2.49	0.48
1:A:397:TRP:CH2	3:A:502:GST:H82	2.48	0.48
1:A:13:TRP:CD1	1:A:14:GLN:HG3	2.49	0.47
1:A:252:LEU:HB2	1:A:268:TYR:HB2	1.95	0.47
1:A:342:GLN:NE2	1:A:344:TYR:OH	2.47	0.47
1:A:194:ILE:HB	1:A:195:PRO:HD3	1.96	0.47
1:A:24:ASN:OD1	1:A:24:ASN:C	2.53	0.46
1:B:244:SER:HB2	1:B:246:THR:OG1	2.15	0.46
1:A:274:MET:HB2	1:A:325:PHE:CD2	2.50	0.46
1:A:11:ARG:CB	1:A:11:ARG:HH11	2.29	0.45
1:A:325:PHE:CE1	1:A:346:PRO:HD2	2.51	0.45
1:A:167:ILE:HD12	1:A:169:GLU:HB2	1.97	0.45
1:B:148:PHE:O	1:B:152:VAL:HG22	2.17	0.44
1:A:97:ASP:HB2	1:A:100:LYS:O	2.18	0.44
1:B:413:TYR:OH	3:B:501:GST:S1	2.75	0.44
1:A:300:MET:SD	1:A:366:MET:HE2	2.58	0.44
1:B:102:ILE:HD13	1:B:102:ILE:HG23	1.45	0.44
1:A:145:PHE:C	1:A:145:PHE:CD1	2.92	0.43
1:A:342:GLN:OE1	1:A:411:ASN:ND2	2.51	0.43
1:A:13:TRP:CE2	1:A:14:GLN:CG	3.00	0.43
1:A:283:TRP:CZ3	1:A:301:VAL:HG21	2.54	0.43
1:A:374:ARG:O	1:A:375:TYR:C	2.57	0.43
1:B:228:LEU:O	1:B:232:LYS:HG3	2.18	0.43
1:B:102:ILE:HD12	1:B:181:LYS:HG2	2.00	0.42
1:A:388:ILE:HG21	1:A:388:ILE:HD12	1.72	0.42
1:A:234:PHE:CE1	1:A:238:ARG:CZ	3.02	0.42
1:A:234:PHE:CE1	1:A:238:ARG:NE	2.88	0.42
1:B:93:SER:OG	1:B:104:ARG:NH1	2.53	0.42
1:A:88:HIS:CE1	1:A:417:VAL:HG11	2.55	0.42
1:B:252:LEU:HB2	1:B:268:TYR:HB2	2.01	0.41
1:B:167:ILE:HD12	1:B:169:GLU:HB2	2.01	0.41
1:A:22:PHE:HA	1:A:23:PRO:HD3	1.91	0.41
2:A:501:XBU:CAM	2:A:501:XBU:OAC	2.68	0.41
1:B:190:TYR:CD1	1:B:190:TYR:N	2.87	0.41
1:A:190:TYR:CD1	1:A:190:TYR:N	2.88	0.41
1:A:388:ILE:HD13	1:A:388:ILE:HG23	1.74	0.41
1:B:398:LEU:C	1:B:398:LEU:HD12	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:SER:OG	1:A:104:ARG:NH1	2.54	0.41
1:A:249:LEU:O	1:A:269:LEU:HA	2.21	0.41
1:B:379:LEU:HD23	1:B:388:ILE:HD12	2.03	0.41
1:A:44:GLN:NE2	1:A:378:GLU:HB3	2.36	0.41
1:B:54:LYS:HE2	1:B:183:GLY:O	2.21	0.41
1:A:362:PHE:O	1:A:366:MET:HG2	2.21	0.40
1:A:239:VAL:HB	1:A:240:PRO:HD2	2.03	0.40
1:A:388:ILE:H	1:A:388:ILE:HG12	1.61	0.40
1:B:345:PHE:CD1	1:B:345:PHE:N	2.89	0.40
1:A:71:ARG:HD3	1:A:86:GLY:O	2.22	0.40
1:A:239:VAL:HB	1:A:240:PRO:CD	2.52	0.40

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:273:ARG:NH1	1:B:299:GLU:OE1[4_556]	1.98	0.22

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	394/416 (95%)	376 (95%)	18 (5%)	0	100 100
1	B	393/416 (94%)	377 (96%)	15 (4%)	1 (0%)	41 70
All	All	787/832 (95%)	753 (96%)	33 (4%)	1 (0%)	51 80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	291	ASP

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	342/355 (96%)	311 (91%)	31 (9%)	9 26
1	B	341/355 (96%)	322 (94%)	19 (6%)	21 49
All	All	683/710 (96%)	633 (93%)	50 (7%)	14 37

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ARG
1	A	34	THR
1	A	97	ASP
1	A	98	LYS
1	A	102	ILE
1	A	104	ARG
1	A	107	LEU
1	A	172	ASN
1	A	177	SER
1	A	179	ASP
1	A	190	TYR
1	A	207	LEU
1	A	217	VAL
1	A	229	SER
1	A	232	LYS
1	A	246	THR
1	A	264	ARG
1	A	276	LEU
1	A	280	ARG
1	A	300	MET
1	A	322	ARG
1	A	340	PRO
1	A	386	VAL
1	A	388	ILE
1	A	389	SER
1	A	390	GLN
1	A	392	LYS

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Mol	Chain	Res	Type
1	A	398	LEU
1	A	405	THR
1	A	409	SER
1	A	416	VAL
1	B	11	ARG
1	B	61	LYS
1	B	97	ASP
1	B	104	ARG
1	B	177	SER
1	B	181	LYS
1	B	217	VAL
1	B	244	SER
1	B	246	THR
1	B	264	ARG
1	B	276	LEU
1	B	300	MET
1	B	365	TYR
1	B	388	ILE
1	B	390	GLN
1	B	392	LYS
1	B	398	LEU
1	B	400	VAL
1	B	416	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	44	GLN
1	A	151	GLN
1	A	214	GLN
1	A	342	GLN
1	A	390	GLN
1	A	411	ASN
1	B	18	GLN
1	B	108	GLN
1	B	149	ASN
1	B	214	GLN
1	B	342	GLN
1	B	411	ASN
1	B	420	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)

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	XBU	A	501	-	27,28,28	3.01	6 (22%)	29,41,41	2.01	9 (31%)
3	GST	B	501	-	14,18,18	3.46	5 (35%)	17,25,25	1.85	4 (23%)
3	GST	A	502	-	14,18,18	3.65	6 (42%)	17,25,25	1.98	6 (35%)

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	XBU	A	501	-	-	1/17/36/36	0/3/3/3
3	GST	B	501	-	-	5/13/19/19	-
3	GST	A	502	-	-	1/13/19/19	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	GST	C2-C3	8.85	1.54	1.33
3	B	501	GST	C2-C3	8.83	1.54	1.33
2	A	501	XBU	CAB-CAX	-8.66	1.41	1.53
3	B	501	GST	C6-C7	7.35	1.53	1.32
2	A	501	XBU	CAQ-CAA	-7.11	1.34	1.48
2	A	501	XBU	CAF-CAH	-6.99	1.39	1.51
3	A	502	GST	C6-C7	6.73	1.51	1.32
2	A	501	XBU	CAE-CAD	-5.83	1.31	1.45
3	A	502	GST	C1-S1	-5.27	1.78	1.84
3	A	502	GST	PA-O2A	3.99	1.63	1.50
2	A	501	XBU	CAB-CAA	-3.91	1.44	1.53
3	B	501	GST	PA-O2A	3.31	1.61	1.50
3	A	502	GST	PB-O3B	2.75	1.64	1.56
3	B	501	GST	PB-O3B	-2.68	1.49	1.56
2	A	501	XBU	OAZ-CAX	2.60	1.38	1.33
3	B	501	GST	C1-S1	-2.31	1.81	1.84
3	A	502	GST	PA-O1A	2.07	1.62	1.54

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	XBU	OAP-CAD-CAE	-5.40	120.91	129.37
3	B	501	GST	O3A-PA-O1B	4.41	119.42	104.64
3	A	502	GST	O3A-PA-O1B	4.05	118.22	104.64
2	A	501	XBU	CAV-CAQ-CAA	-4.03	115.16	120.89
2	A	501	XBU	OAZ-CAX-CAB	3.70	114.98	111.04
3	A	502	GST	C4-C5-C6	-3.65	99.87	111.88
2	A	501	XBU	CAR-CAQ-CAA	3.59	126.00	120.89
2	A	501	XBU	OAC-CAD-OAP	3.38	125.97	121.12
3	A	502	GST	C10-C3-C4	3.22	120.69	115.27
3	B	501	GST	C10-C3-C4	2.75	119.89	115.27
3	B	501	GST	C4-C5-C6	-2.61	103.32	111.88
3	A	502	GST	C4-C3-C2	-2.55	115.96	121.12
2	A	501	XBU	CAB-CAA-CAQ	2.38	127.44	122.45
2	A	501	XBU	OAY-CAX-CAB	-2.37	119.81	123.79
2	A	501	XBU	CAS-CAR-CAQ	-2.30	118.10	120.78
3	A	502	GST	C8-C7-C9	2.25	119.57	114.60
3	A	502	GST	C2-C1-S1	-2.09	101.50	112.00
2	A	501	XBU	CBB-OAZ-CAX	2.04	119.38	115.94
3	B	501	GST	C8-C7-C9	2.00	119.02	114.60

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	XBU	CAA-CAB-CAF-CAH
3	B	501	GST	PB-O1B-PA-O1A
3	B	501	GST	PA-O1B-PB-O3B
3	B	501	GST	PB-O1B-PA-O2A
3	B	501	GST	PB-O1B-PA-O3A
3	B	501	GST	PA-O1B-PB-O2B
3	A	502	GST	PA-O1B-PB-O3B

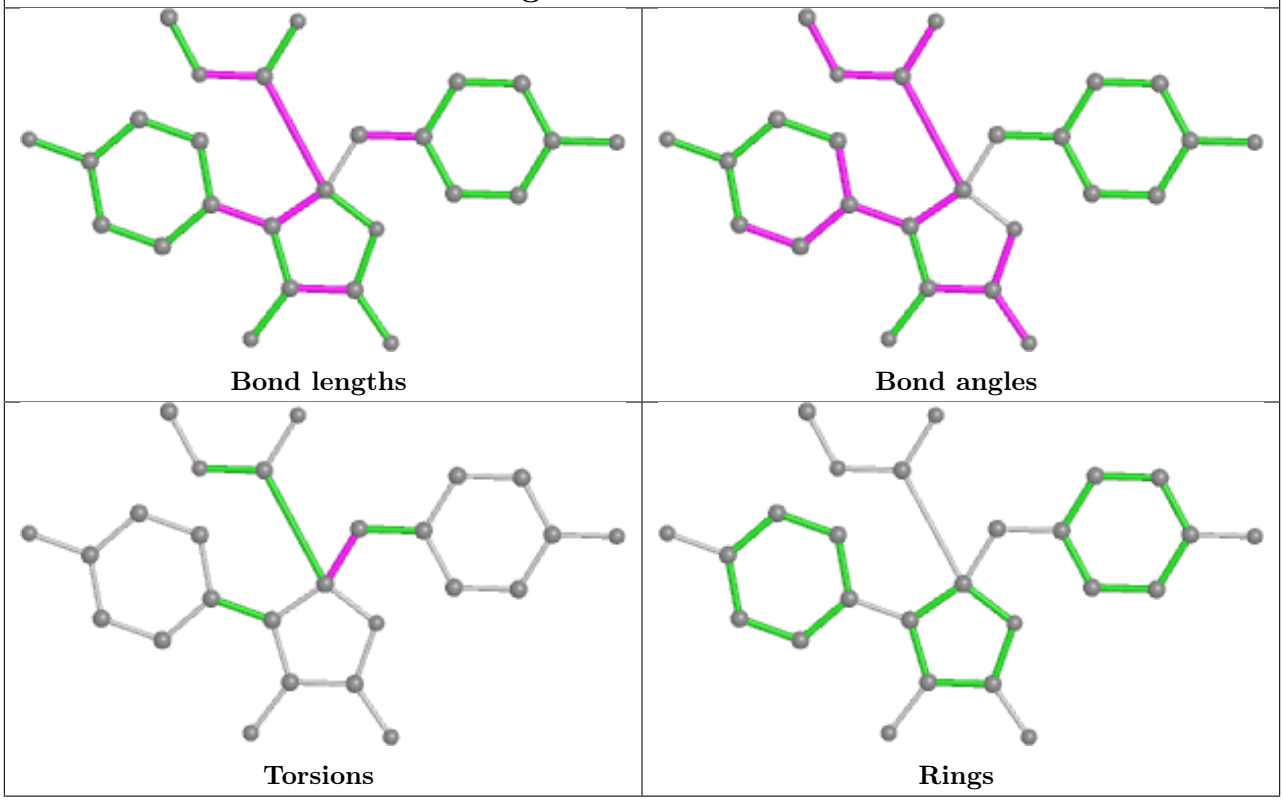
There are no ring outliers.

3 monomers are involved in 9 short contacts:

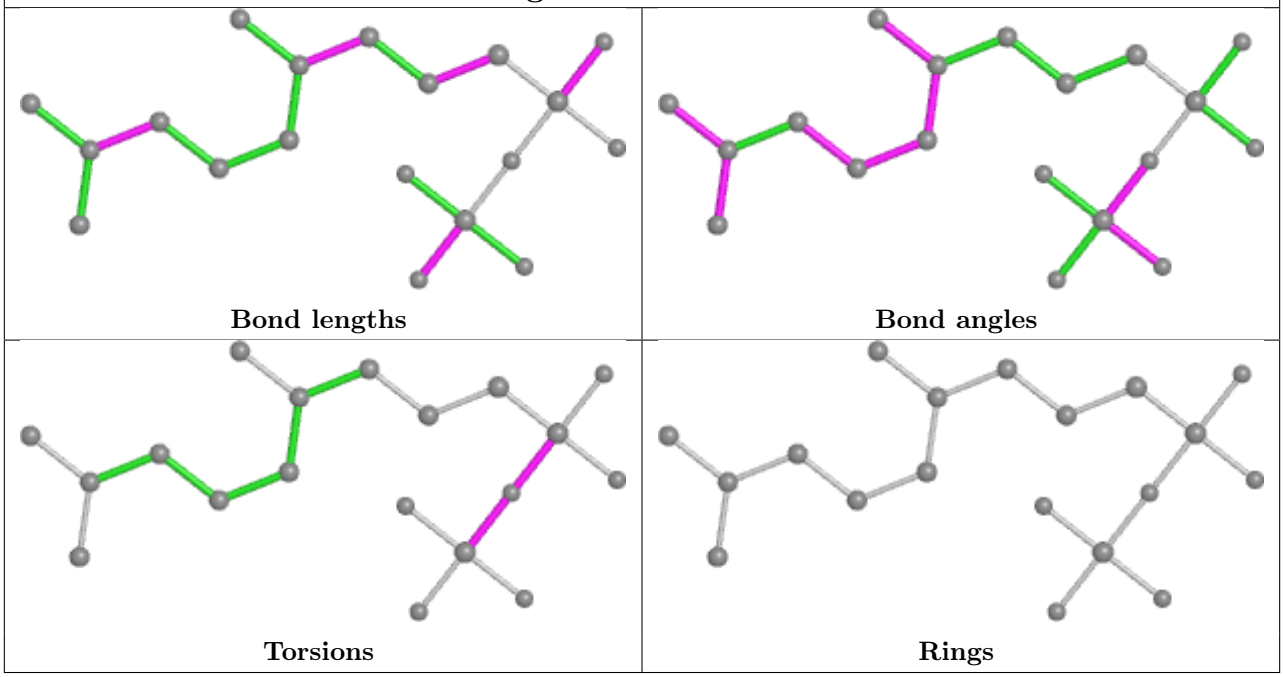
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	XBU	6	0
3	B	501	GST	2	0
3	A	502	GST	6	0

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

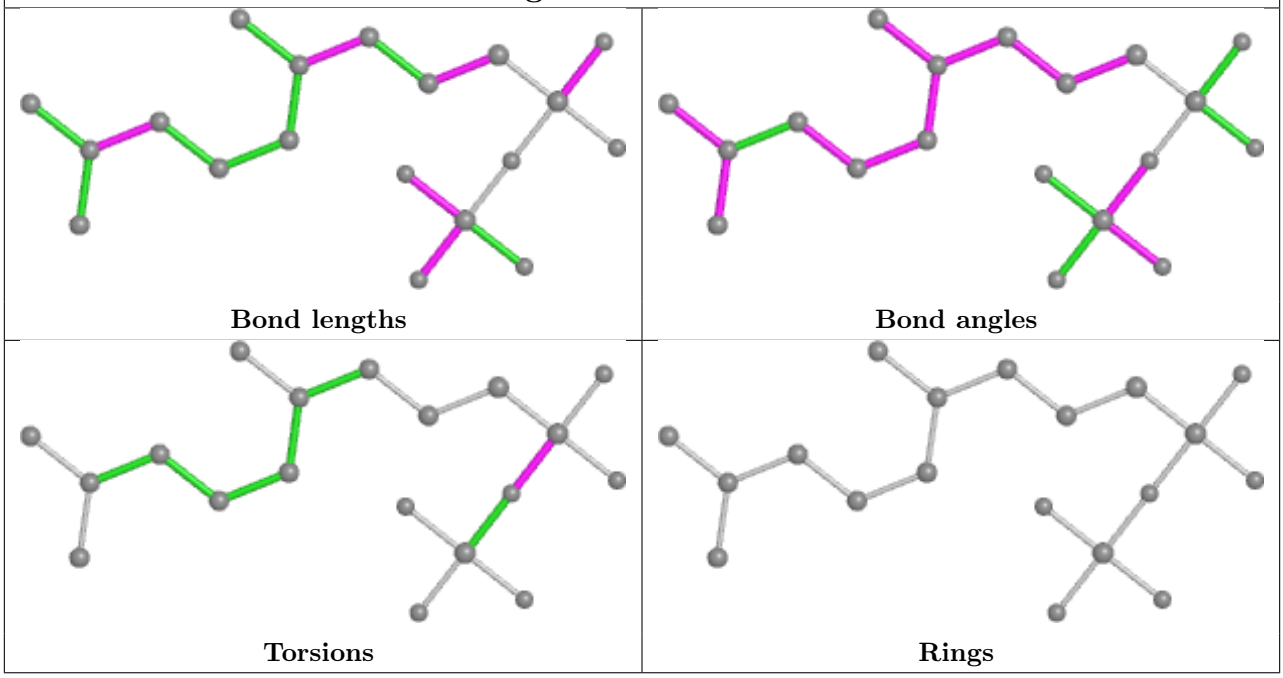
Ligand XBU A 501



Ligand GST B 501



Ligand GST A 502



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	398/416 (95%)	-0.24	0	100	100	18, 39, 66, 88	0
1	B	397/416 (95%)	-0.29	0	100	100	17, 41, 64, 92	0
All	All	795/832 (95%)	-0.26	0	100	100	17, 40, 65, 92	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 monosaccharides in this entry.

6.4 Ligands (i)

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

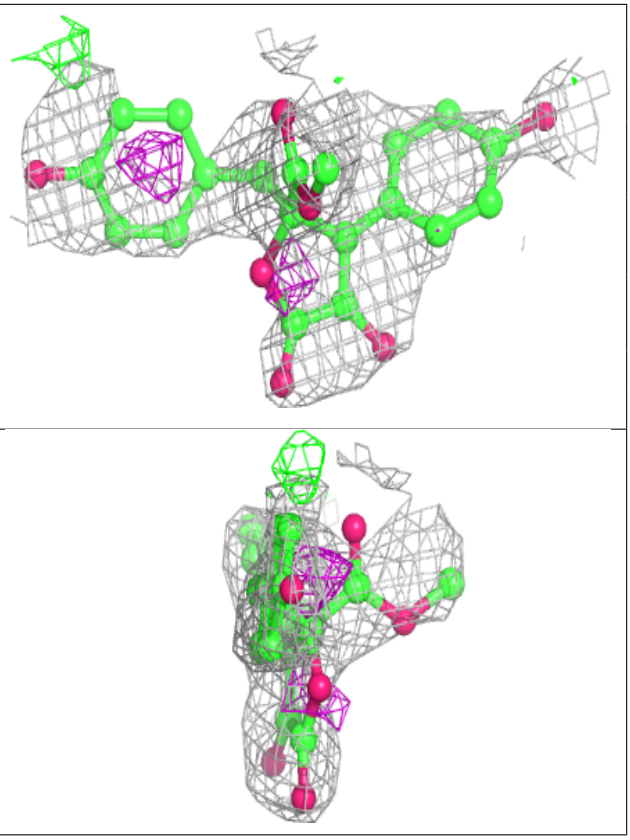
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	XBU	A	501	26/26	0.80	0.46	67,78,86,86	0
3	GST	A	502	19/19	0.94	0.22	43,49,55,55	0
3	GST	B	501	19/19	0.95	0.17	58,66,79,81	0

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

orientation to approximate a three-dimensional view.

Electron density around XBU 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 GST A 502:

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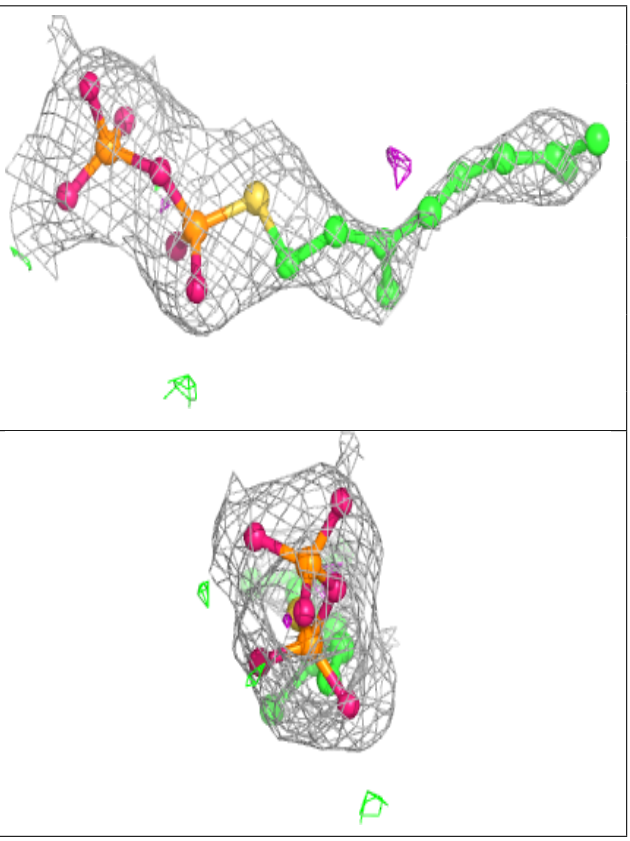
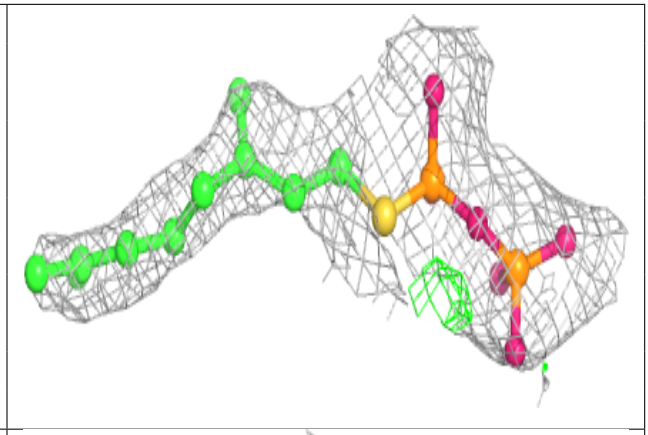
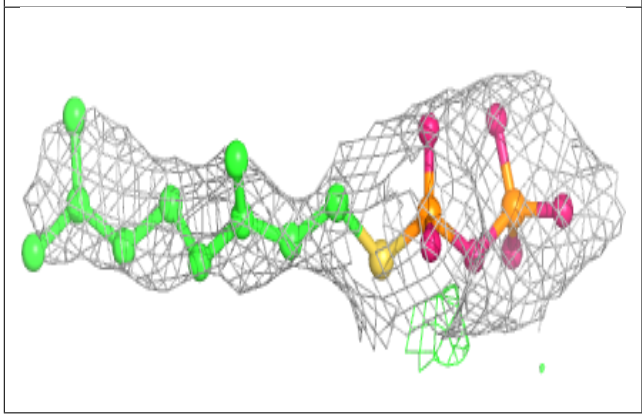
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

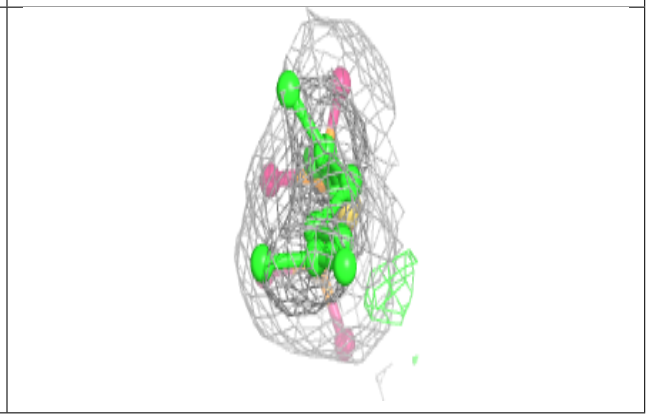


Electron density around GST B 501:

$2mF_o$-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.