Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 12:14 AM EDT

PDB ID	:	1Z6J
Title	:	Crystal Structure of a ternary complex of Factor VIIa/Tissue Factor/Pyrazinone Inhibitor
Authors	:	Schweitzer, B.A.; Neumann, W.L.; Rahman, H.K.; Kusturin, C.L.; Sample, K.R.; Poda, G.I.; Kurumbail, R.G.; Stevens, A.M.; Stegeman, R.A.; Stallings, W.C.
Deposited on	:	2005-03-22
Resolution	:	2.00 Å(reported)

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

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

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

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

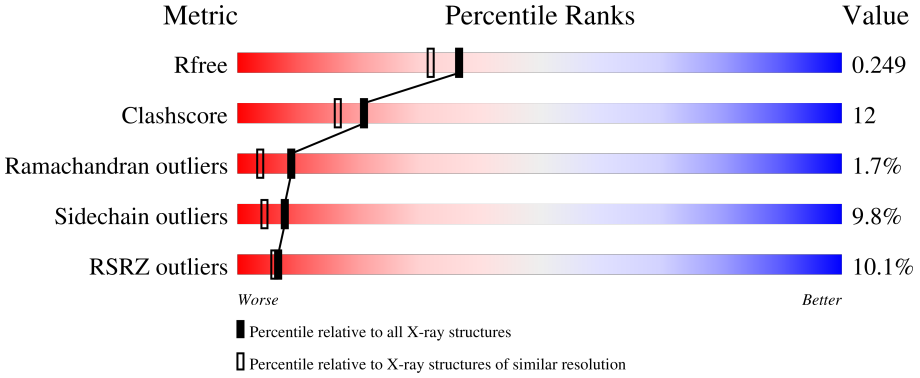
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	L	142	18% 71% 22% 6% •
2	H	254	2% 81% 17% •
3	T	211	13% 66% 24% 7% • •

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
1	CGU	L	19	-	-	-	X
1	CGU	L	20	-	-	-	X
1	CGU	L	35	-	-	-	X

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5207 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 Coagulation factor VII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	142	1135	683	189	248	15	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	6	CGU	GLU	MODIFIED RESIDUE	UNP P08709
L	7	CGU	GLU	MODIFIED RESIDUE	UNP P08709
L	14	CGU	GLU	MODIFIED RESIDUE	UNP P08709
L	16	CGU	GLU	MODIFIED RESIDUE	UNP P08709
L	19	CGU	GLU	MODIFIED RESIDUE	UNP P08709
L	20	CGU	GLU	MODIFIED RESIDUE	UNP P08709
L	25	CGU	GLU	MODIFIED RESIDUE	UNP P08709
L	26	CGU	GLU	MODIFIED RESIDUE	UNP P08709
L	29	CGU	GLU	MODIFIED RESIDUE	UNP P08709
L	35	CGU	GLU	MODIFIED RESIDUE	UNP P08709

- Molecule 2 is a protein called Coagulation factor VII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	254	1974	1253	351	357	13	0	0	0

- Molecule 3 is a protein called Tissue factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	T	207	1658	1047	269	337	5	0	0	0

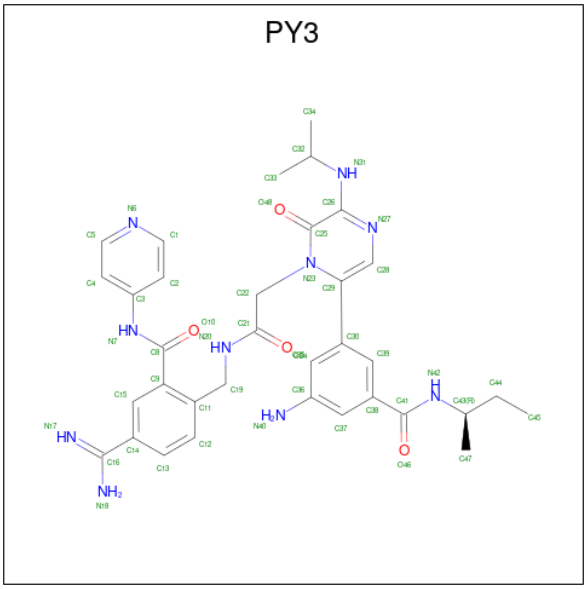
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	L	1	Total Ca 1 1	0	0
4	H	1	Total Ca 1 1	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	L	1	Total Mg 1 1	0	0

- Molecule 6 is 5-[AMINO(IMINO)METHYL]-2-[({[6-[3-AMINO-5-({[(1R)-1-METHYLPROPYL]AMINO}CARBONYL)PHENYL]-3-(ISOPROPYLAMINO)-2-OXOPYRAZIN-1(2H)-YL]ACETYL}AMINO)METHYL]-N-PYRIDIN-4-YLBENZAMIDE (three-letter code: PY3) (formula: $C_{34}H_{40}N_{10}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	1	Total C N O 48 34 10 4	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	L	91	Total O 91 91	0	0
7	H	181	Total O 181 181	0	0

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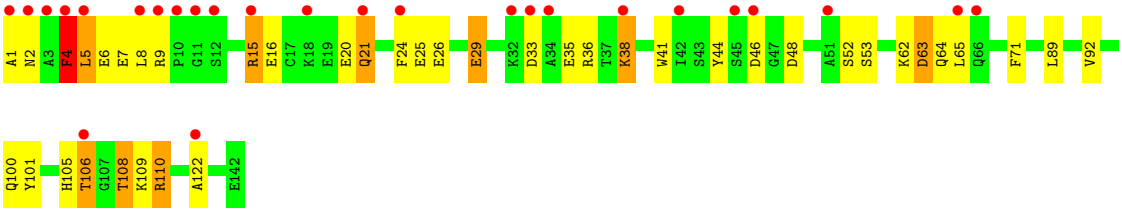
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	T	117	117	117	0	0

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.

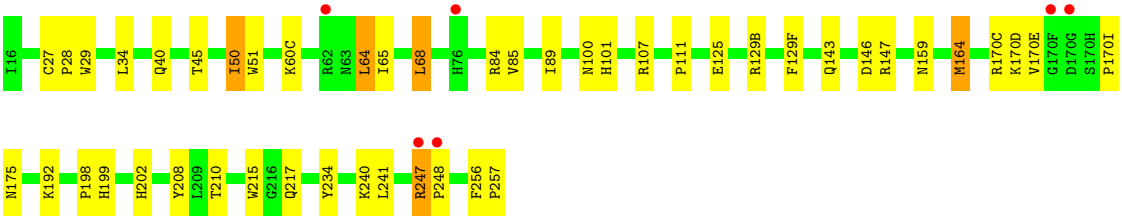
• Molecule 1: Coagulation factor VII

Chain L:



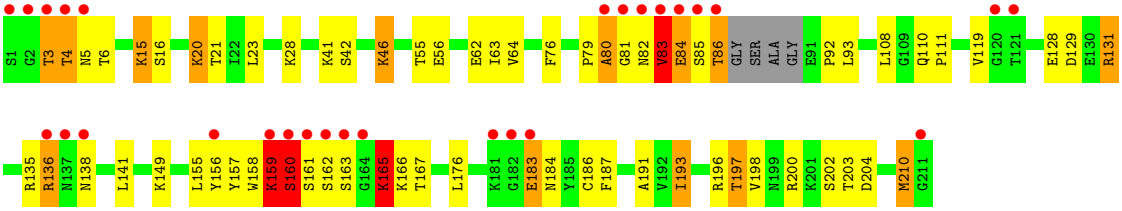
• Molecule 2: Coagulation factor VII

Chain H:



• Molecule 3: Tissue factor

Chain T:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	69.65Å 81.14Å 125.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 19.90 – 2.00	Depositor EDS
% Data completeness (in resolution range)	90.1 (20.00-2.00) 90.7 (19.90-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	3.54 (at 2.01Å)	Xtriage
Refinement program	X-PLOR 98.1, CNS	Depositor
R, R_{free}	0.209 , 0.258 0.200 , 0.249	Depositor DCC
R_{free} test set	4402 reflections (9.96%)	wwPDB-VP
Wilson B-factor (Å^2)	19.0	Xtriage
Anisotropy	0.370	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 54.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5207	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.85% 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: MG, CA, CGU, PY3

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	L	0.44	0/1029	0.67	0/1374
2	H	0.54	0/2024	0.82	2/2755 (0.1%)
3	T	0.49	0/1693	0.79	3/2302 (0.1%)
All	All	0.50	0/4746	0.78	5/6431 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	199	HIS	N-CA-C	-7.87	89.74	111.00
2	H	68	LEU	CA-CB-CG	-7.76	97.45	115.30
3	T	20	LYS	N-CA-C	-5.38	96.48	111.00
3	T	193	ILE	N-CA-C	-5.05	97.37	111.00
3	T	129	ASP	CB-CG-OD1	5.01	122.81	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	L	1135	0	989	42	0
2	H	1974	0	1950	28	0
3	T	1658	0	1609	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	1	0	0	0	0
4	L	1	0	0	0	0
5	L	1	0	0	0	0
6	H	48	0	40	0	0
7	H	181	0	0	3	0
7	L	91	0	0	3	0
7	T	117	0	0	0	0
All	All	5207	0	4588	115	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 12.

All (115) 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:L:35:CGU:HA	1:L:38:LYS:HD3	1.47	0.96
1:L:122:ALA:HA	7:L:469:HOH:O	1.70	0.91
2:H:247:ARG:HG3	2:H:248:PRO:HD2	1.52	0.89
3:T:3:THR:HB	3:T:85:SER:HB2	1.53	0.89
3:T:159:LYS:HD3	3:T:183:GLU:CD	1.96	0.86
3:T:197:THR:HG22	3:T:198:VAL:HG13	1.61	0.80
1:L:4:PHE:O	1:L:5:LEU:HB2	1.80	0.80
3:T:135:ARG:HH22	3:T:138:ASN:HA	1.48	0.78
3:T:3:THR:HB	3:T:85:SER:CB	2.13	0.78
3:T:136:ARG:HB2	3:T:141:LEU:HD21	1.69	0.75
3:T:4:THR:N	3:T:85:SER:HB3	2.02	0.74
2:H:50:ILE:HG22	2:H:111:PRO:HB3	1.70	0.74
3:T:184:ASN:HA	3:T:210:MET:HE2	1.69	0.73
1:L:33:ASP:HB3	1:L:36:ARG:HB2	1.72	0.71
1:L:21:GLN:HA	1:L:44:TYR:OH	1.91	0.70
3:T:155:LEU:HD11	3:T:187:PHE:HB3	1.75	0.68
2:H:247:ARG:HG3	2:H:248:PRO:CD	2.24	0.67
1:L:16:CGU:HG	1:L:26:CGU:OE22	1.95	0.66
3:T:108:LEU:HD11	3:T:193:ILE:HG12	1.77	0.66
1:L:24:PHE:O	1:L:25:CGU:HB3	1.95	0.65
2:H:50:ILE:HD12	2:H:50:ILE:O	1.97	0.65
2:H:129(F):PHE:HE1	2:H:164:MET:HE2	1.63	0.63
1:L:6:CGU:CD2	1:L:9:ARG:HH21	2.12	0.62
1:L:62:LYS:NZ	1:L:64:GLN:HE22	1.98	0.62
3:T:80:ALA:O	3:T:83:VAL:HG23	2.00	0.62
3:T:110:GLN:HG3	3:T:203:THR:HG23	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:170(I):PRO:HG2	2:H:215:TRP:CZ3	2.37	0.60
3:T:136:ARG:HB2	3:T:141:LEU:CD2	2.31	0.60
1:L:2:ASN:HA	1:L:7:CGU:OE22	2.03	0.59
3:T:135:ARG:HH22	3:T:138:ASN:CA	2.17	0.58
3:T:159:LYS:HB2	3:T:162:SER:HB2	1.85	0.58
2:H:34:LEU:HD23	2:H:40:GLN:HA	1.85	0.58
1:L:36:ARG:HD3	3:T:158:TRP:CD1	2.39	0.57
2:H:143:GLN:NE2	2:H:147:ARG:H	2.02	0.57
2:H:50:ILE:CD1	2:H:107:ARG:HG3	2.36	0.56
2:H:143:GLN:HE22	2:H:147:ARG:H	1.54	0.55
3:T:63:ILE:HD12	3:T:64:VAL:N	2.21	0.55
1:L:5:LEU:HA	1:L:8:LEU:HD13	1.88	0.55
3:T:136:ARG:CB	3:T:141:LEU:HD21	2.36	0.55
3:T:4:THR:HB	3:T:85:SER:HA	1.88	0.54
2:H:50:ILE:HG13	2:H:51:TRP:CD1	2.42	0.54
1:L:108:THR:HG23	1:L:109:LYS:N	2.23	0.53
3:T:4:THR:HG22	3:T:5:ASN:N	2.24	0.52
3:T:159:LYS:HD3	3:T:183:GLU:OE1	2.09	0.52
1:L:110:ARG:HD2	1:L:110:ARG:C	2.30	0.52
1:L:101:TYR:CZ	2:H:125:GLU:HG3	2.45	0.52
1:L:4:PHE:O	1:L:5:LEU:CB	2.56	0.51
1:L:105:HIS:O	1:L:108:THR:O	2.29	0.51
1:L:92:VAL:HG22	1:L:92:VAL:O	2.10	0.50
1:L:62:LYS:HD3	1:L:63:ASP:O	2.11	0.50
2:H:170(I):PRO:HG2	2:H:215:TRP:CH2	2.47	0.50
1:L:6:CGU:OE22	1:L:9:ARG:NH2	2.44	0.50
1:L:1:ALA:HB3	1:L:20:CGU:OE22	2.13	0.49
2:H:129(F):PHE:HE1	2:H:164:MET:CE	2.26	0.49
2:H:247:ARG:CG	2:H:248:PRO:HD2	2.35	0.48
3:T:76:PHE:CD1	3:T:92:PRO:HG2	2.48	0.48
1:L:48:ASP:OD2	1:L:63:ASP:OD1	2.31	0.48
2:H:64:LEU:HB3	2:H:85:VAL:HB	1.94	0.48
2:H:101:HIS:HA	2:H:234:TYR:OH	2.15	0.47
1:L:71:PHE:CE2	3:T:131:ARG:HB3	2.49	0.47
3:T:136:ARG:CG	3:T:141:LEU:HD21	2.44	0.47
3:T:157:TYR:HA	3:T:186:CYS:O	2.15	0.47
1:L:35:CGU:N	1:L:35:CGU:CD2	2.78	0.47
2:H:27:CYS:N	2:H:28:PRO:CD	2.77	0.47
3:T:155:LEU:O	3:T:167:THR:HA	2.15	0.47
1:L:100:GLN:HG2	2:H:208:TYR:OH	2.16	0.46
3:T:3:THR:HB	3:T:85:SER:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:T:63:ILE:HD12	3:T:63:ILE:C	2.35	0.46
2:H:170(E):VAL:HB	7:H:575:HOH:O	2.15	0.46
3:T:191:ALA:HB3	3:T:202:SER:HB3	1.97	0.45
7:L:417:HOH:O	3:T:20:LYS:HE2	2.15	0.45
1:L:46:ASP:OD2	1:L:65:LEU:HD22	2.16	0.45
1:L:16:CGU:OE21	1:L:26:CGU:OE11	2.35	0.45
2:H:89:ILE:HG21	2:H:241:LEU:HD13	1.98	0.45
3:T:165:LYS:HG2	3:T:165:LYS:O	2.17	0.45
3:T:5:ASN:C	3:T:6:THR:HG23	2.37	0.45
3:T:136:ARG:HG3	3:T:141:LEU:HD21	1.99	0.44
1:L:62:LYS:HD2	1:L:64:GLN:HE21	1.82	0.44
3:T:46:LYS:HD3	3:T:62:GLU:OE1	2.17	0.44
3:T:16:SER:HB2	3:T:21:THR:HG23	1.99	0.44
3:T:79:PRO:O	3:T:81:GLY:N	2.51	0.44
3:T:156:TYR:CD1	3:T:165:LYS:HE2	2.53	0.44
1:L:92:VAL:HG23	7:H:509:HOH:O	2.18	0.43
1:L:38:LYS:O	1:L:41:TRP:N	2.52	0.43
2:H:256:PHE:HA	2:H:257:PRO:C	2.39	0.43
3:T:83:VAL:O	3:T:85:SER:N	2.51	0.43
3:T:110:GLN:HA	3:T:111:PRO:HD3	1.87	0.43
1:L:52:SER:O	1:L:53:SER:C	2.57	0.43
1:L:62:LYS:HZ3	1:L:64:GLN:HE22	1.64	0.43
1:L:101:TYR:CE2	2:H:125:GLU:HG3	2.54	0.43
3:T:15:LYS:N	3:T:15:LYS:HD2	2.29	0.43
1:L:29:CGU:OE11	1:L:29:CGU:OE21	2.37	0.42
3:T:183:GLU:H	3:T:183:GLU:HG2	1.42	0.42
3:T:3:THR:HG22	3:T:86:THR:O	2.20	0.42
3:T:82:ASN:C	3:T:84:GLU:H	2.22	0.42
3:T:3:THR:HG22	3:T:85:SER:O	2.19	0.42
1:L:25:CGU:O	1:L:29:CGU:HB3	2.20	0.42
1:L:106:THR:N	7:L:488:HOH:O	2.53	0.42
2:H:129(F):PHE:CE1	2:H:164:MET:HE2	2.50	0.42
2:H:45:THR:OG1	2:H:198:PRO:HB3	2.20	0.42
3:T:28:LYS:HD3	3:T:55:THR:HG21	2.01	0.42
1:L:15:ARG:HB3	1:L:15:ARG:NH1	2.35	0.41
1:L:62:LYS:CD	1:L:64:GLN:NE2	2.84	0.41
3:T:196:ARG:HB2	3:T:200:ARG:HB3	2.02	0.41
1:L:25:CGU:O	1:L:29:CGU:N	2.54	0.41
2:H:175:ASN:ND2	7:H:529:HOH:O	2.54	0.41
3:T:135:ARG:NH2	3:T:138:ASN:H	2.19	0.41
3:T:159:LYS:HB3	3:T:160:SER:H	1.66	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:T:184:ASN:HA	3:T:210:MET:CE	2.43	0.41
2:H:50:ILE:HD11	2:H:107:ARG:HG3	2.03	0.40
2:H:146:ASP:O	2:H:147:ARG:HB2	2.21	0.40
3:T:23:LEU:O	3:T:56:GLU:HA	2.21	0.40
1:L:21:GLN:HA	1:L:44:TYR:HH	1.85	0.40
1:L:21:GLN:O	1:L:21:GLN:HG3	2.19	0.40
1:L:38:LYS:HB3	1:L:38:LYS:HE2	1.96	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	L	130/142 (92%)	119 (92%)	8 (6%)	3 (2%)	6 2
2	H	252/254 (99%)	240 (95%)	12 (5%)	0	100 100
3	T	203/211 (96%)	179 (88%)	17 (8%)	7 (3%)	3 1
All	All	585/607 (96%)	538 (92%)	37 (6%)	10 (2%)	9 4

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	T	4	THR
3	T	160	SER
1	L	4	PHE
1	L	5	LEU
3	T	80	ALA
3	T	83	VAL
3	T	84	GLU
1	L	21	GLN
3	T	165	LYS
3	T	159	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	L	114/114 (100%)	106 (93%)	8 (7%)	15 10
2	H	216/216 (100%)	197 (91%)	19 (9%)	10 6
3	T	192/193 (100%)	168 (88%)	24 (12%)	4 2
All	All	522/523 (100%)	471 (90%)	51 (10%)	8 4

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	4	PHE
1	L	15	ARG
1	L	38	LYS
1	L	63	ASP
1	L	89	LEU
1	L	106	THR
1	L	108	THR
1	L	110	ARG
2	H	29	TRP
2	H	50	ILE
2	H	60(C)	LYS
2	H	64	LEU
2	H	65	ILE
2	H	68	LEU
2	H	84	ARG
2	H	100	ASN
2	H	129(B)	ARG
2	H	159	ASN
2	H	164	MET
2	H	170(C)	ARG
2	H	170(D)	LYS
2	H	192	LYS
2	H	202	HIS
2	H	210	THR
2	H	217	GLN
2	H	240	LYS

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Mol	Chain	Res	Type
2	H	247	ARG
3	T	3	THR
3	T	15	LYS
3	T	41	LYS
3	T	42	SER
3	T	46	LYS
3	T	83	VAL
3	T	86	THR
3	T	93	LEU
3	T	119	VAL
3	T	128	GLU
3	T	131	ARG
3	T	136	ARG
3	T	149	LYS
3	T	159	LYS
3	T	160	SER
3	T	161	SER
3	T	163	SER
3	T	165	LYS
3	T	166	LYS
3	T	176	LEU
3	T	183	GLU
3	T	197	THR
3	T	204	ASP
3	T	210	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	64	GLN
1	L	84	HIS
2	H	100	ASN
2	H	109	HIS
2	H	110	GLN
2	H	143	GLN
2	H	159	ASN
3	T	110	GLN
3	T	138	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)

10 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	CGU	L	35	1	9,11,12	1.16	0	10,14,16	0.80	0
1	CGU	L	7	1	9,11,12	1.09	0	10,14,16	0.79	0
1	CGU	L	25	1	9,11,12	1.12	0	10,14,16	0.68	0
1	CGU	L	26	1	9,11,12	1.20	0	10,14,16	0.66	0
1	CGU	L	29	1	9,11,12	1.22	0	10,14,16	0.82	1 (10%)
1	CGU	L	6	1	9,11,12	1.13	0	10,14,16	0.86	0
1	CGU	L	14	1,5	9,11,12	1.08	0	10,14,16	0.97	0
1	CGU	L	20	1	9,11,12	1.08	0	10,14,16	0.91	0
1	CGU	L	16	1	9,11,12	1.03	0	10,14,16	0.83	0
1	CGU	L	19	1,5	9,11,12	1.12	0	10,14,16	0.91	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
1	CGU	L	35	1	-	6/13/14/16	-
1	CGU	L	7	1	-	1/13/14/16	-
1	CGU	L	25	1	-	8/13/14/16	-
1	CGU	L	26	1	-	2/13/14/16	-
1	CGU	L	29	1	-	8/13/14/16	-
1	CGU	L	6	1	-	2/13/14/16	-
1	CGU	L	14	1,5	-	9/13/14/16	-
1	CGU	L	20	1	-	2/13/14/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CGU	L	16	1	-	3/13/14/16	-
1	CGU	L	19	1,5	-	4/13/14/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	29	CGU	CB-CG-CD2	-2.42	108.20	113.11

There are no chirality outliers.

All (45) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	L	6	CGU	OE11-CD1-CG-CD2
1	L	6	CGU	OE12-CD1-CG-CD2
1	L	7	CGU	N-CA-CB-CG
1	L	14	CGU	C-CA-CB-CG
1	L	14	CGU	CA-CB-CG-CD2
1	L	14	CGU	OE11-CD1-CG-CD2
1	L	14	CGU	OE12-CD1-CG-CD2
1	L	16	CGU	C-CA-CB-CG
1	L	16	CGU	CA-CB-CG-CD1
1	L	25	CGU	C-CA-CB-CG
1	L	25	CGU	CA-CB-CG-CD1
1	L	25	CGU	CA-CB-CG-CD2
1	L	29	CGU	N-CA-CB-CG
1	L	29	CGU	C-CA-CB-CG
1	L	29	CGU	CA-CB-CG-CD1
1	L	29	CGU	CA-CB-CG-CD2
1	L	35	CGU	O-C-CA-CB
1	L	35	CGU	N-CA-CB-CG
1	L	35	CGU	C-CA-CB-CG
1	L	35	CGU	CA-CB-CG-CD2
1	L	16	CGU	N-CA-CB-CG
1	L	14	CGU	OE21-CD2-CG-CB
1	L	14	CGU	OE22-CD2-CG-CB
1	L	20	CGU	OE11-CD1-CG-CB
1	L	25	CGU	OE21-CD2-CG-CB
1	L	25	CGU	OE22-CD2-CG-CB
1	L	29	CGU	OE21-CD2-CG-CB
1	L	19	CGU	OE21-CD2-CG-CD1

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Mol	Chain	Res	Type	Atoms
1	L	19	CGU	OE22-CD2-CG-CD1
1	L	25	CGU	OE11-CD1-CG-CD2
1	L	25	CGU	OE12-CD1-CG-CD2
1	L	29	CGU	OE21-CD2-CG-CD1
1	L	29	CGU	OE22-CD2-CG-CD1
1	L	14	CGU	CA-CB-CG-CD1
1	L	14	CGU	N-CA-CB-CG
1	L	25	CGU	N-CA-CB-CG
1	L	19	CGU	OE11-CD1-CG-CB
1	L	19	CGU	OE12-CD1-CG-CB
1	L	20	CGU	OE12-CD1-CG-CB
1	L	26	CGU	OE21-CD2-CG-CB
1	L	26	CGU	OE22-CD2-CG-CB
1	L	29	CGU	OE22-CD2-CG-CB
1	L	14	CGU	OE22-CD2-CG-CD1
1	L	35	CGU	OE11-CD1-CG-CD2
1	L	35	CGU	OE12-CD1-CG-CD2

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L	35	CGU	2	0
1	L	7	CGU	1	0
1	L	25	CGU	3	0
1	L	26	CGU	2	0
1	L	29	CGU	3	0
1	L	6	CGU	2	0
1	L	20	CGU	1	0
1	L	16	CGU	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
6	PY3	H	403	-	47,51,51	1.59	11 (23%)	54,71,71	1.74	13 (24%)

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
6	PY3	H	403	-	-	7/35/39/39	0/4/4/4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	403	PY3	C28-N27	4.34	1.40	1.32
6	H	403	PY3	C39-C38	3.16	1.43	1.37
6	H	403	PY3	C26-C25	2.97	1.48	1.43
6	H	403	PY3	C13-C12	2.74	1.43	1.38
6	H	403	PY3	C12-C11	2.64	1.43	1.39
6	H	403	PY3	C35-C36	2.43	1.43	1.39
6	H	403	PY3	C19-N20	2.33	1.50	1.46
6	H	403	PY3	C15-C9	2.25	1.43	1.39
6	H	403	PY3	C25-N23	2.10	1.41	1.38
6	H	403	PY3	C16-N17	2.10	1.36	1.27
6	H	403	PY3	C13-C14	2.02	1.42	1.39

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	H	403	PY3	C19-C11-C9	5.07	127.11	121.99
6	H	403	PY3	C22-N23-C29	4.38	126.11	120.14
6	H	403	PY3	O10-C8-C9	-4.03	113.64	121.03
6	H	403	PY3	C29-N23-C25	-3.73	117.92	121.72
6	H	403	PY3	C28-N27-C26	3.49	123.03	116.19
6	H	403	PY3	C9-C8-N7	2.56	121.34	116.03
6	H	403	PY3	C11-C19-N20	-2.53	108.05	113.15
6	H	403	PY3	C19-C11-C12	-2.52	115.41	120.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	H	403	PY3	C1-N6-C5	2.37	122.29	116.86
6	H	403	PY3	C2-C1-N6	-2.23	119.80	123.60
6	H	403	PY3	C38-C41-N42	2.17	121.06	117.04
6	H	403	PY3	C36-C35-C30	-2.15	119.69	121.11
6	H	403	PY3	N31-C26-N27	2.04	120.90	118.00

There are no chirality outliers.

All (7) torsion outliers are listed below:

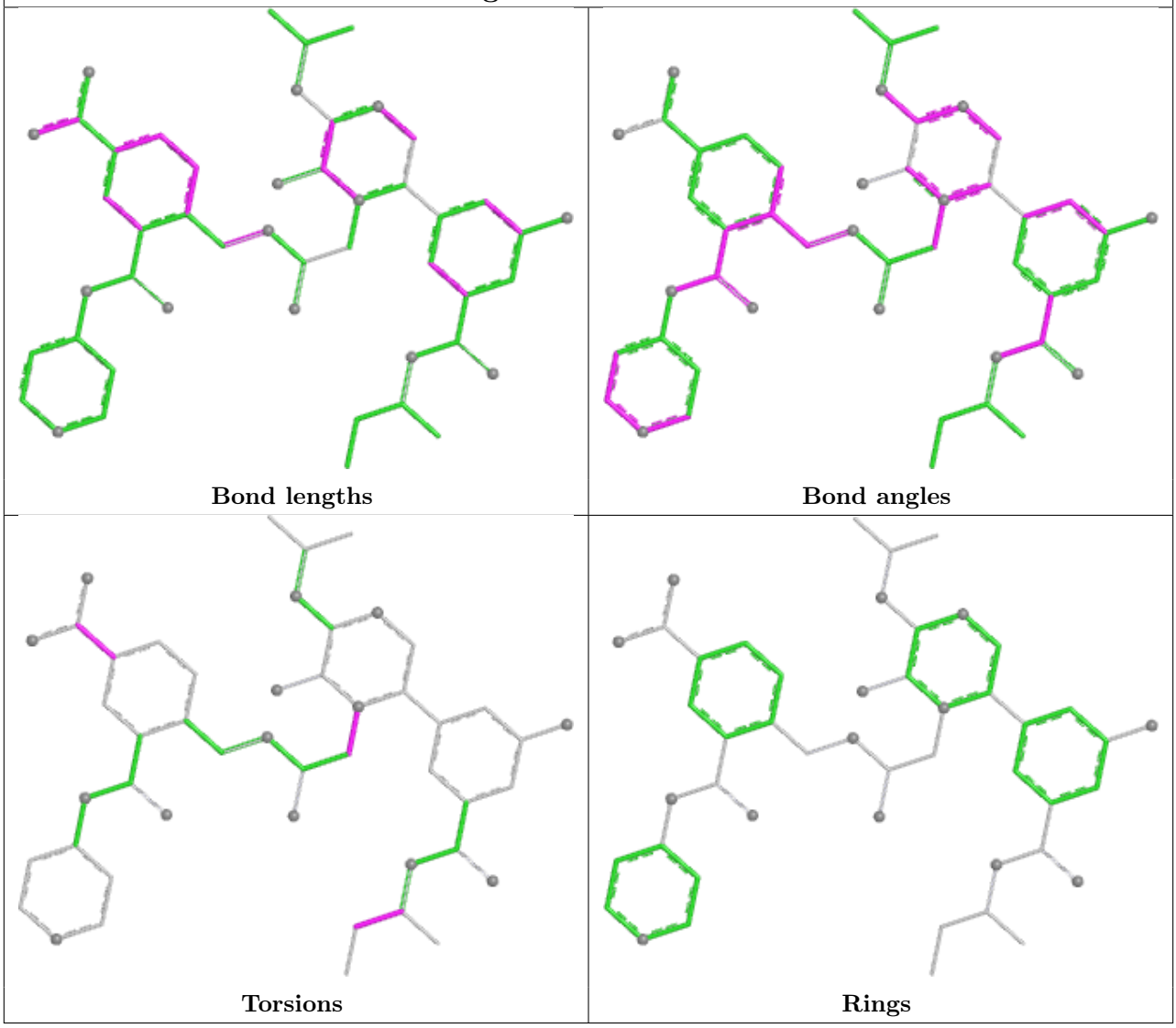
Mol	Chain	Res	Type	Atoms
6	H	403	PY3	C21-C22-N23-C29
6	H	403	PY3	N42-C43-C44-C45
6	H	403	PY3	C47-C43-C44-C45
6	H	403	PY3	C13-C14-C16-N18
6	H	403	PY3	C15-C14-C16-N18
6	H	403	PY3	C13-C14-C16-N17
6	H	403	PY3	C15-C14-C16-N17

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand PY3 H 403



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	L	132/142 (92%)	0.72	26 (19%)	1	0	13, 26, 61, 67	0
2	H	254/254 (100%)	-0.22	6 (2%)	59	57	6, 14, 34, 51	0
3	T	207/211 (98%)	0.77	28 (13%)	3	2	11, 25, 65, 82	0
All	All	593/607 (97%)	0.34	60 (10%)	7	6	6, 20, 58, 82	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	T	2	GLY	13.9
3	T	86	THR	12.9
3	T	85	SER	11.9
1	L	1	ALA	10.8
3	T	1	SER	10.4
3	T	83	VAL	10.0
3	T	3	THR	8.8
3	T	4	THR	7.4
3	T	82	ASN	7.0
1	L	2	ASN	6.5
3	T	5	ASN	6.5
3	T	84	GLU	6.1
3	T	81	GLY	5.9
1	L	3	ALA	5.1
2	H	248	PRO	5.1
3	T	162	SER	5.0
3	T	211	GLY	4.8
1	L	34	ALA	4.7
1	L	11	GLY	4.5
3	T	181	LYS	4.3
1	L	122	ALA	4.1
3	T	138	ASN	4.1
1	L	46	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
3	T	161	SER	3.6
3	T	137	ASN	3.5
3	T	160	SER	3.4
3	T	182	GLY	3.4
1	L	45	SER	3.3
1	L	18	LYS	3.3
3	T	163	SER	3.2
1	L	9	ARG	3.2
3	T	159	LYS	3.2
1	L	66	GLN	3.0
1	L	51	ALA	3.0
1	L	42	ILE	2.9
1	L	33	ASP	2.9
1	L	12	SER	2.9
1	L	4	PHE	2.8
1	L	32	LYS	2.8
3	T	136	ARG	2.8
1	L	65	LEU	2.7
1	L	8	LEU	2.7
2	H	170(F)	GLY	2.7
1	L	5	LEU	2.6
3	T	120	GLY	2.5
3	T	164	GLY	2.5
2	H	170(G)	ASP	2.5
1	L	10	PRO	2.4
2	H	62	ARG	2.4
3	T	121	THR	2.4
1	L	15	ARG	2.2
3	T	183	GLU	2.2
3	T	80	ALA	2.2
1	L	38	LYS	2.1
1	L	106	THR	2.1
1	L	24	PHE	2.1
2	H	247	ARG	2.0
2	H	76	HIS	2.0
1	L	21	GLN	2.0
3	T	156	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CGU	L	35	12/13	0.58	0.40	57,61,63,63	0
1	CGU	L	6	12/13	0.66	0.27	57,59,60,60	0
1	CGU	L	20	12/13	0.69	0.44	61,63,64,64	0
1	CGU	L	14	12/13	0.72	0.27	57,58,59,59	0
1	CGU	L	19	12/13	0.73	0.42	65,66,68,69	0
1	CGU	L	7	12/13	0.74	0.30	58,58,59,60	0
1	CGU	L	25	12/13	0.80	0.28	49,51,52,53	0
1	CGU	L	26	12/13	0.81	0.19	48,50,51,51	0
1	CGU	L	29	12/13	0.83	0.18	39,42,45,45	0
1	CGU	L	16	12/13	0.83	0.19	52,53,56,57	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

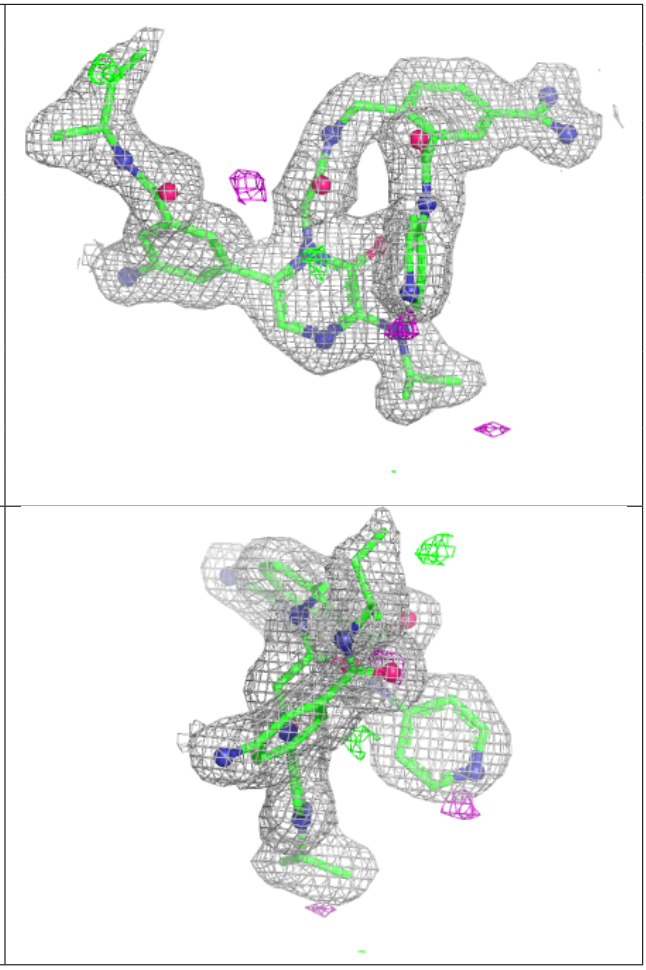
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	MG	L	402	1/1	0.74	0.19	59,59,59,59	0
4	CA	L	401	1/1	0.78	0.14	92,92,92,92	0
4	CA	H	400	1/1	0.93	0.09	46,46,46,46	0
6	PY3	H	403	48/48	0.94	0.11	11,17,23,28	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 PY3 H 403:

$2mF_o$-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.