



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:48 PM UTC

PDB ID : 3TJD / pdb_00003tjd
Title : co-crystal structure of Jak2 with thienopyridine 19
Authors : Huang, X.
Deposited on : 2011-08-24
Resolution : 2.90 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

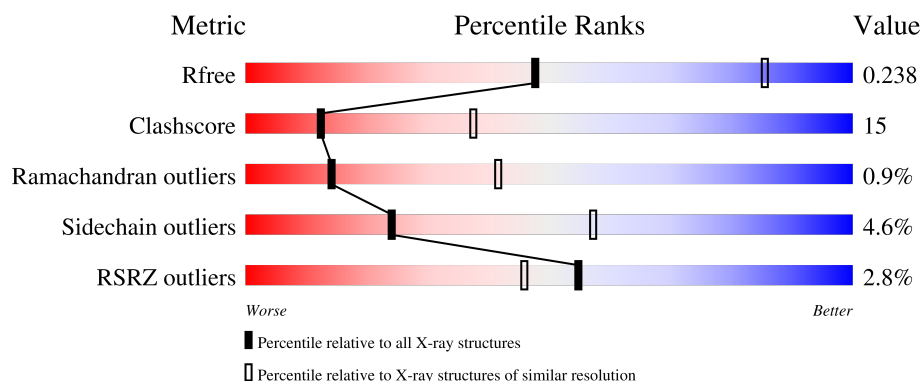
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

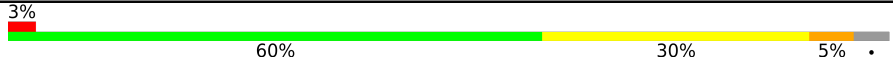
The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	298	
1	B	298	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4886 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.

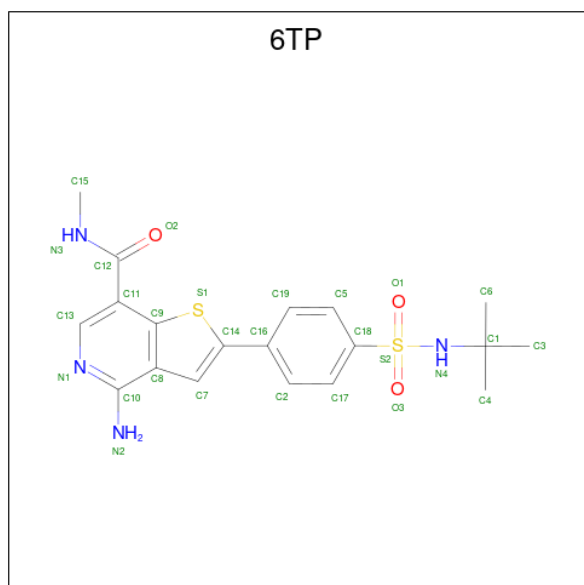
- Molecule 1 is a protein called Tyrosine-protein kinase JAK2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	P	S	0	0	0
			2373	1506	408	443	2	14			
1	B	289	Total	C	N	O	P	S	0	0	0
			2395	1519	411	449	2	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	835	GLY	-	expression tag	UNP O60674
A	836	SER	-	expression tag	UNP O60674
B	835	GLY	-	expression tag	UNP O60674
B	836	SER	-	expression tag	UNP O60674

- Molecule 2 is 4-amino-2-[4-(tert-butylsulfamoyl)phenyl]-N-methylthieno[3,2-c]pyridine-7-carboxamide (CCD ID: 6TP) (formula: C₁₉H₂₂N₄O₃S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			28	19	4	3	2		
2	B	1	Total	C	N	O	S	0	0
			28	19	4	3	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	26	Total	O	0	0
			26	26		
3	B	36	Total	O	0	0
			36	36		

4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	111.82Å 111.82Å 71.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.90 30.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.90) 94.8 (30.00-2.90)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.86Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.286 , 0.312 0.223 , 0.238	Depositor DCC
R_{free} test set	1014 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	52.6	Xtriage
Anisotropy	0.388	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 21.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4886	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6TP, PTR

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	0.80	4/2389 (0.2%)	1.07	11/3211 (0.3%)
1	B	0.78	0/2412	1.04	14/3244 (0.4%)
All	All	0.79	4/4801 (0.1%)	1.05	25/6455 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	847	ARG	C-O	-5.75	1.16	1.24
1	A	847	ARG	CZ-NH1	5.62	1.40	1.32
1	A	993	GLY	C-O	-5.49	1.20	1.24
1	A	847	ARG	CD-NE	5.28	1.53	1.46

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1049	THR	N-CA-C	-7.97	103.58	113.38
1	B	1049	THR	N-CA-C	-7.08	103.81	113.30
1	A	982	ILE	N-CA-C	-6.94	98.45	108.17
1	A	1018	ILE	N-CA-C	6.94	118.53	110.62
1	A	1068	ASP	N-CA-C	-6.75	103.54	112.72
1	B	840	ASP	CA-C-N	6.44	126.37	119.28
1	B	840	ASP	C-N-CA	6.44	126.37	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	863	VAL	N-CA-C	-6.23	99.14	108.12
1	B	965	GLU	N-CA-C	-6.06	104.68	111.28
1	B	912	LYS	N-CA-C	6.03	119.35	109.76
1	B	1010	VAL	N-CA-C	6.02	117.15	108.48
1	B	932	LEU	CA-C-N	5.87	127.18	119.84
1	B	932	LEU	C-N-CA	5.87	127.18	119.84
1	A	1087	ARG	N-CA-C	5.77	117.84	109.07
1	A	992	ILE	N-CA-C	-5.66	100.17	108.54
1	B	978	ALA	N-CA-C	-5.62	99.77	108.42
1	B	950	HIS	N-CA-C	-5.52	105.28	112.23
1	A	1020	TRP	N-CA-C	-5.50	106.42	114.39
1	A	847	ARG	NE-CZ-NH1	-5.36	116.14	121.50
1	A	869	ASP	CA-C-N	5.33	125.15	119.28
1	A	869	ASP	C-N-CA	5.33	125.15	119.28
1	B	1035	SER	N-CA-C	-5.30	105.56	112.23
1	B	1018	ILE	N-CA-C	5.21	118.37	111.17
1	B	1005	LYS	N-CA-C	5.20	118.21	109.95
1	B	976	ASP	N-CA-C	5.17	118.64	111.71

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	847	ARG	Sidechain

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	2373	0	2344	83	0
1	B	2395	0	2362	65	0
2	A	28	0	22	4	0
2	B	28	0	22	2	0
3	A	26	0	0	2	0
3	B	36	0	0	7	0
All	All	4886	0	4750	147	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 15.

All (147) 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:1069:LYS:HE3	1:A:1069:LYS:HA	1.20	1.17
1:A:1069:LYS:HA	1:A:1069:LYS:CE	1.85	1.04
1:A:977:LEU:HD21	1:A:982:ILE:HD11	1.49	0.95
1:B:890:GLU:HG2	1:B:893:ARG:HH22	1.41	0.86
1:B:854:GLN:HG3	3:B:27:HOH:O	1.76	0.84
1:A:1008:PTR:HE1	1:A:1010:VAL:HB	1.59	0.83
1:A:873:ASP:O	1:A:875:THR:HG23	1.78	0.82
1:A:966:TYR:O	1:A:969:THR:HG22	1.83	0.79
1:B:890:GLU:HG2	1:B:893:ARG:NH2	1.98	0.79
1:A:977:LEU:CD2	1:A:982:ILE:HD11	2.17	0.75
1:B:976:ASP:O	1:B:981:ASN:ND2	2.21	0.74
1:A:1087:ARG:HH11	1:A:1087:ARG:HG3	1.58	0.69
1:A:1069:LYS:HE2	1:A:1070:GLN:HG3	1.74	0.69
1:A:952:LYS:HD2	1:A:955:GLN:HE21	1.58	0.68
1:A:1027:THR:HG22	1:A:1079:ILE:HD13	1.76	0.67
1:A:946:GLU:H	1:A:946:GLU:CD	2.00	0.66
1:B:976:ASP:HB2	1:B:997:LEU:HD12	1.77	0.65
1:B:985:GLU:OE1	1:B:989:ARG:HD2	1.96	0.65
1:A:848:HIS:CG	1:A:870:PRO:HA	2.32	0.64
1:B:840:ASP:OD1	1:B:842:THR:HG22	1.97	0.64
1:A:1057:PRO:HB2	1:A:1058:PRO:HD3	1.80	0.64
1:A:1007:PTR:OH	3:A:13:HOH:O	2.15	0.63
1:B:975:ARG:HG2	1:B:1031:PHE:CD2	2.33	0.63
1:A:976:ASP:HB2	1:A:997:LEU:HD12	1.81	0.62
1:A:1069:LYS:HE2	1:A:1070:GLN:H	1.63	0.62
1:A:1069:LYS:CE	1:A:1069:LYS:CA	2.69	0.61
1:B:1057:PRO:HB2	1:B:1058:PRO:HD3	1.81	0.61
1:B:942:GLN:HG2	1:B:1051:ILE:HB	1.82	0.61
1:B:919:SER:HG	1:B:924:ASN:N	1.99	0.60
1:B:917:CYS:SG	1:B:926:LYS:HE3	2.41	0.60
1:B:846:GLU:CD	1:B:926:LYS:NZ	2.60	0.59
1:A:1044:LEU:HD23	1:A:1102:MET:HG3	1.84	0.59
1:A:1069:LYS:HD3	1:A:1077:HIS:CD2	2.38	0.59
1:B:1045:TYR:O	1:B:1049:THR:HG23	2.04	0.58
1:A:1086:GLY:O	1:A:1087:ARG:HG3	2.03	0.58
1:A:952:LYS:HD2	1:A:955:GLN:NE2	2.18	0.58
1:A:857:LYS:HZ1	1:A:885:GLN:HG2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:977:LEU:HD21	1:A:982:ILE:CD1	2.28	0.57
1:B:873:ASP:OD1	1:B:875:THR:HG23	2.05	0.56
1:B:917:CYS:HB3	1:B:926:LYS:HE3	1.86	0.56
1:A:1087:ARG:HG3	1:A:1087:ARG:NH1	2.19	0.56
1:A:917:CYS:HB3	1:A:926:LYS:HB2	1.86	0.56
1:B:1038:TRP:CE3	1:B:1106:TRP:HA	2.40	0.56
1:A:994:ASP:HB2	2:A:1:6TP:H5	1.87	0.55
1:A:1045:TYR:O	1:A:1049:THR:HG23	2.07	0.55
1:B:865:MET:HE3	1:B:878:VAL:HG11	1.88	0.55
1:B:917:CYS:HB3	1:B:926:LYS:HB2	1.89	0.54
1:B:981:ASN:OD1	2:B:1:6TP:O3	2.27	0.53
1:B:858:GLY:HA3	2:B:1:6TP:H3B	1.89	0.53
1:A:919:SER:HB3	1:A:924:ASN:ND2	2.24	0.53
1:A:1093:GLY:HA3	1:B:1112:GLN:O	2.10	0.52
1:A:932:LEU:HD12	1:A:983:LEU:CB	2.40	0.52
1:B:919:SER:HA	3:B:119:HOH:O	2.10	0.52
1:B:960:ILE:HD13	1:B:982:ILE:HD13	1.90	0.52
1:B:1095:PRO:HB2	1:B:1098:ILE:HG12	1.92	0.52
1:A:952:LYS:HE3	1:A:955:GLN:HE22	1.75	0.52
1:B:846:GLU:CD	1:B:926:LYS:HZ3	2.17	0.52
1:B:943:LYS:HD3	1:B:944:HIS:CD2	2.45	0.52
1:A:919:SER:HB3	1:A:924:ASN:HD21	1.75	0.52
1:A:870:PRO:HG2	1:A:871:LEU:HD13	1.90	0.52
1:A:932:LEU:HD12	1:A:983:LEU:HB2	1.92	0.52
1:A:873:ASP:O	1:A:874:ASN:C	2.53	0.51
1:A:1070:GLN:OE1	1:A:1073:MET:HG3	2.10	0.51
1:B:1034:ALA:CB	1:B:1110:VAL:HG13	2.41	0.51
1:B:938:ARG:HD2	3:B:48:HOH:O	2.10	0.50
1:B:976:ASP:OD1	1:B:980:ARG:NH2	2.45	0.50
1:A:974:HIS:HE1	1:A:994:ASP:O	1.95	0.50
1:B:975:ARG:NH2	3:B:18:HOH:O	2.45	0.50
1:A:849:LEU:HG	1:A:868:TYR:HD1	1.77	0.49
1:B:840:ASP:CG	1:B:842:THR:HG22	2.35	0.49
1:A:855:LEU:HD22	2:A:1:6TP:O2	2.12	0.49
1:B:1060:GLU:OE1	1:B:1063:ARG:NH2	2.46	0.48
1:B:1102:MET:HE3	1:B:1106:TRP:HH2	1.78	0.48
1:A:862:SER:O	1:A:882:LYS:HA	2.13	0.48
1:B:907:HIS:HE1	1:B:909:ASN:HD22	1.61	0.48
1:A:863:VAL:HG23	2:A:1:6TP:C6	2.44	0.48
1:A:1063:ARG:HG2	1:A:1067:ASN:HD21	1.79	0.48
1:A:1069:LYS:HE2	1:A:1070:GLN:N	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:973:ILE:CG1	1:B:1001:LEU:HD13	2.44	0.48
1:B:912:LYS:HB2	1:B:930:GLU:HG2	1.96	0.47
1:B:1021:TYR:HB3	1:B:1026:LEU:HD13	1.97	0.47
1:A:937:LEU:HD21	1:A:1047:LEU:HD21	1.97	0.47
1:A:974:HIS:HD2	1:A:977:LEU:N	2.13	0.47
1:A:1042:VAL:O	1:A:1046:GLU:HG3	2.16	0.46
1:B:1102:MET:HE3	1:B:1106:TRP:CH2	2.50	0.46
1:B:960:ILE:CD1	1:B:982:ILE:HD13	2.45	0.46
1:A:977:LEU:HA	1:A:977:LEU:HD23	1.47	0.46
1:A:907:HIS:HE1	1:A:909:ASN:HD22	1.63	0.46
1:B:930:GLU:OE1	1:B:991:LYS:NZ	2.40	0.46
1:B:955:GLN:NE2	3:B:265:HOH:O	2.49	0.46
1:B:977:LEU:HD22	1:B:978:ALA:H	1.80	0.45
1:B:980:ARG:HG2	1:B:981:ASN:OD1	2.16	0.45
1:B:917:CYS:CB	1:B:926:LYS:HE3	2.46	0.45
1:A:965:GLU:HA	1:A:965:GLU:OE1	2.16	0.45
1:B:847:ARG:HG3	1:B:848:HIS:CD2	2.51	0.45
1:A:974:HIS:CE1	1:A:994:ASP:O	2.69	0.45
1:A:1066:GLY:O	1:A:1069:LYS:HB2	2.17	0.45
1:A:869:ASP:OD2	1:A:872:GLN:HA	2.16	0.45
1:A:958:SER:O	1:A:962:LYS:HG3	2.17	0.44
1:B:850:LYS:HE2	1:B:869:ASP:HB3	1.99	0.44
1:B:1058:PRO:O	1:B:1062:MET:HG2	2.18	0.44
1:A:950:HIS:HE1	1:A:1093:GLY:O	2.00	0.44
1:A:986:ASN:OD1	1:A:986:ASN:C	2.61	0.44
1:A:1122:ARG:O	1:A:1126:ILE:HG13	2.17	0.44
1:B:1009:LYS:NZ	3:B:192:HOH:O	2.50	0.44
1:A:857:LYS:HG3	1:A:858:GLY:N	2.33	0.44
1:A:941:LEU:HD12	1:A:948:ILE:CD1	2.48	0.44
1:B:902:LEU:HG	1:B:913:TYR:HB2	1.99	0.44
1:B:977:LEU:HA	1:B:977:LEU:HD23	1.46	0.44
1:B:976:ASP:CB	1:B:997:LEU:HD12	2.47	0.43
1:A:896:GLU:CG	3:A:28:HOH:O	2.65	0.43
1:A:1007:PTR:O2P	1:A:1007:PTR:HE1	2.18	0.43
1:B:917:CYS:SG	1:B:926:LYS:CE	3.06	0.43
1:B:1045:TYR:HB2	1:B:1102:MET:HE3	2.01	0.43
1:A:888:THR:HG22	1:A:890:GLU:H	1.84	0.43
1:A:871:LEU:N	1:A:871:LEU:CD1	2.81	0.43
1:A:1124:ASP:HA	1:A:1127:ARG:HD3	2.01	0.43
1:B:1010:VAL:O	1:B:1010:VAL:HG23	2.19	0.42
1:A:1067:ASN:C	1:A:1069:LYS:H	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:917:CYS:SG	1:B:926:LYS:NZ	2.92	0.42
1:A:882:LYS:NZ	1:A:898:GLU:OE2	2.40	0.42
1:A:934:TYR:HB2	1:A:984:VAL:HB	2.02	0.42
1:B:932:LEU:HA	1:B:933:PRO:HD2	1.77	0.42
1:B:1064:MET:HE2	1:B:1081:LEU:HD11	2.01	0.42
1:A:1045:TYR:HB2	1:A:1102:MET:HE3	2.00	0.42
1:B:989:ARG:NH2	3:B:71:HOH:O	2.50	0.42
1:A:932:LEU:HA	1:A:933:PRO:HD2	1.90	0.42
1:A:941:LEU:HD12	1:A:948:ILE:HD12	2.02	0.42
1:A:914:LYS:HB2	1:A:928:ILE:O	2.20	0.42
1:A:1002:PRO:HG2	1:A:1005:LYS:HB2	2.02	0.42
1:B:898:GLU:OE1	1:B:996:GLY:HA2	2.19	0.42
1:A:943:LYS:C	1:A:944:HIS:ND1	2.78	0.42
1:B:978:ALA:HA	1:B:1043:VAL:HG22	2.01	0.42
1:A:974:HIS:HD2	1:A:976:ASP:H	1.68	0.41
1:A:895:PHE:O	1:A:899:ILE:HG13	2.21	0.41
1:A:881:VAL:HG22	1:A:928:ILE:HD12	2.03	0.41
1:A:847:ARG:H	1:A:847:ARG:HG2	1.61	0.41
1:A:873:ASP:OD1	1:A:875:THR:OG1	2.26	0.41
1:A:872:GLN:HE21	1:A:872:GLN:HB3	1.60	0.41
1:A:852:LEU:O	1:A:853:GLN:HB3	2.20	0.41
1:B:954:LEU:HD23	1:B:954:LEU:HA	1.85	0.40
1:B:973:ILE:HG13	1:B:1001:LEU:HD13	2.02	0.40
1:B:976:ASP:O	1:B:976:ASP:CG	2.64	0.40
1:A:849:LEU:HG	1:A:868:TYR:CD1	2.57	0.40
1:A:865:MET:HE3	1:A:878:VAL:HG11	2.03	0.40
1:B:1094:CYS:HA	1:B:1095:PRO:HD3	1.95	0.40
1:A:994:ASP:CB	2:A:1:6TP:H5	2.51	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	280/298 (94%)	263 (94%)	14 (5%)	3 (1%)	11	36
1	B	283/298 (95%)	270 (95%)	11 (4%)	2 (1%)	18	48
All	All	563/596 (94%)	533 (95%)	25 (4%)	5 (1%)	14	41

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1070	GLN
1	B	987	GLU
1	B	1070	GLN
1	A	987	GLU
1	A	1071	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	260/269 (97%)	245 (94%)	15 (6%)	18	49
1	B	263/269 (98%)	254 (97%)	9 (3%)	32	66
All	All	523/538 (97%)	499 (95%)	24 (5%)	24	57

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	847	ARG
1	A	871	LEU
1	A	872	GLN
1	A	897	ARG
1	A	924	ASN
1	A	925	LEU
1	A	946	GLU
1	A	969	THR
1	A	977	LEU
1	A	987	GLU
1	A	989	ARG

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Mol	Chain	Res	Type
1	A	1011	LYS
1	A	1069	LYS
1	A	1117	ARG
1	A	1121	LEU
1	B	854	GLN
1	B	925	LEU
1	B	943	LYS
1	B	949	ASP
1	B	977	LEU
1	B	1001	LEU
1	B	1026	LEU
1	B	1069	LYS
1	B	1100	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	848	HIS
1	A	872	GLN
1	A	874	ASN
1	A	909	ASN
1	A	924	ASN
1	A	950	HIS
1	A	955	GLN
1	A	974	HIS
1	A	1067	ASN
1	A	1077	HIS
1	B	843	GLN
1	B	891	HIS
1	B	909	ASN
1	B	924	ASN
1	B	955	GLN
1	B	1111	ASN
1	B	1129	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	PTR	B	1008	1	15,16,17	1.04	1 (6%)	17,22,24	0.79	0
1	PTR	A	1007	1	15,16,17	0.83	1 (6%)	17,22,24	0.78	0
1	PTR	B	1007	1	15,16,17	0.75	1 (6%)	17,22,24	0.68	0
1	PTR	A	1008	1	15,16,17	0.85	0	17,22,24	0.81	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	PTR	B	1008	1	-	1/10/11/13	0/1/1/1
1	PTR	A	1007	1	-	0/10/11/13	0/1/1/1
1	PTR	B	1007	1	-	0/10/11/13	0/1/1/1
1	PTR	A	1008	1	-	0/10/11/13	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1008	PTR	P-OH	2.39	1.64	1.59
1	A	1007	PTR	P-OH	2.18	1.63	1.59
1	B	1007	PTR	P-OH	2.18	1.63	1.59

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	1008	PTR	O-C-CA-CB

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1007	PTR	2	0
1	A	1008	PTR	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	6TP	B	1	-	30,30,30	3.17	15 (50%)	43,46,46	2.56	17 (39%)
2	6TP	A	1	-	30,30,30	3.12	10 (33%)	43,46,46	3.01	23 (53%)

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	6TP	B	1	-	-	4/22/22/22	0/3/3/3
2	6TP	A	1	-	-	5/22/22/22	0/3/3/3

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	6TP	S2-N4	10.59	1.77	1.61
2	A	1	6TP	S2-N4	9.81	1.76	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	6TP	C2-C16	6.49	1.49	1.39
2	B	1	6TP	C2-C16	6.34	1.49	1.39
2	A	1	6TP	C9-S1	-6.29	1.61	1.74
2	A	1	6TP	C19-C16	5.02	1.47	1.39
2	B	1	6TP	C19-C16	4.44	1.46	1.39
2	A	1	6TP	C8-C10	4.11	1.47	1.42
2	A	1	6TP	C18-S2	-4.00	1.70	1.76
2	B	1	6TP	C17-C18	3.94	1.45	1.38
2	B	1	6TP	C8-C10	3.93	1.47	1.42
2	B	1	6TP	C5-C18	3.83	1.44	1.38
2	B	1	6TP	C12-N3	3.21	1.37	1.33
2	B	1	6TP	C17-C2	3.03	1.43	1.38
2	B	1	6TP	O3-S2	-3.03	1.40	1.43
2	A	1	6TP	C16-C14	2.97	1.53	1.47
2	A	1	6TP	C5-C18	2.85	1.43	1.38
2	B	1	6TP	C9-S1	-2.82	1.68	1.74
2	A	1	6TP	C17-C2	2.75	1.43	1.38
2	A	1	6TP	C17-C18	2.72	1.43	1.38
2	B	1	6TP	C16-C14	2.64	1.52	1.47
2	B	1	6TP	C4-C1	-2.52	1.46	1.52
2	B	1	6TP	C13-C11	2.50	1.44	1.40
2	B	1	6TP	C18-S2	-2.15	1.73	1.76
2	B	1	6TP	C14-S1	-2.07	1.70	1.75

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	6TP	C9-S1-C14	7.15	98.91	91.52
2	A	1	6TP	C5-C18-S2	-6.43	112.68	119.76
2	A	1	6TP	C11-C9-C8	6.38	128.37	122.33
2	B	1	6TP	C5-C18-S2	-6.32	112.81	119.76
2	A	1	6TP	C17-C18-C5	5.91	128.17	120.47
2	B	1	6TP	C2-C17-C18	-5.77	113.83	119.44
2	B	1	6TP	C17-C18-C5	5.41	127.53	120.47
2	A	1	6TP	C10-C8-C7	-4.93	127.79	135.26
2	B	1	6TP	C10-C8-C7	-4.77	128.03	135.26
2	A	1	6TP	C8-C10-N2	-4.57	117.55	122.42
2	A	1	6TP	C2-C17-C18	-4.56	115.01	119.44
2	B	1	6TP	C11-C13-N1	-4.32	118.23	124.32
2	B	1	6TP	C8-C10-N2	-3.97	118.19	122.42
2	B	1	6TP	O1-S2-N4	-3.91	98.43	107.36
2	A	1	6TP	O3-S2-O1	-3.88	114.81	119.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	6TP	C11-C13-N1	-3.85	118.89	124.32
2	A	1	6TP	C16-C14-S1	3.65	125.30	119.70
2	B	1	6TP	C9-S1-C14	3.47	95.11	91.52
2	B	1	6TP	C13-N1-C10	3.38	121.91	118.64
2	B	1	6TP	C11-C9-S1	3.30	129.08	125.20
2	B	1	6TP	O3-S2-O1	3.25	123.47	119.52
2	A	1	6TP	C19-C5-C18	-3.24	116.28	119.44
2	A	1	6TP	C8-C9-S1	-3.15	103.38	112.90
2	A	1	6TP	C13-N1-C10	3.04	121.58	118.64
2	B	1	6TP	C19-C5-C18	-2.95	116.57	119.44
2	A	1	6TP	C8-C7-C14	-2.90	103.63	113.17
2	A	1	6TP	O1-S2-C18	2.79	111.50	107.98
2	A	1	6TP	C9-C8-C7	2.79	122.85	111.22
2	B	1	6TP	C11-C12-N3	-2.73	112.99	116.98
2	A	1	6TP	O2-C12-C11	2.73	126.04	121.03
2	A	1	6TP	C11-C9-S1	2.59	128.25	125.20
2	A	1	6TP	C15-N3-C12	-2.48	117.08	121.80
2	B	1	6TP	C11-C9-C8	2.42	124.62	122.33
2	B	1	6TP	C16-C14-S1	2.41	123.40	119.70
2	A	1	6TP	O2-C12-N3	-2.35	119.19	122.67
2	B	1	6TP	C8-C9-S1	-2.18	106.30	112.90
2	A	1	6TP	C3-C1-N4	2.09	115.54	108.94
2	B	1	6TP	C8-C7-C14	-2.05	106.42	113.17
2	A	1	6TP	C18-S2-N4	-2.04	104.47	108.11
2	A	1	6TP	C4-C1-C3	-2.01	105.51	109.95

There are no chirality outliers.

All (9) torsion outliers are listed below:

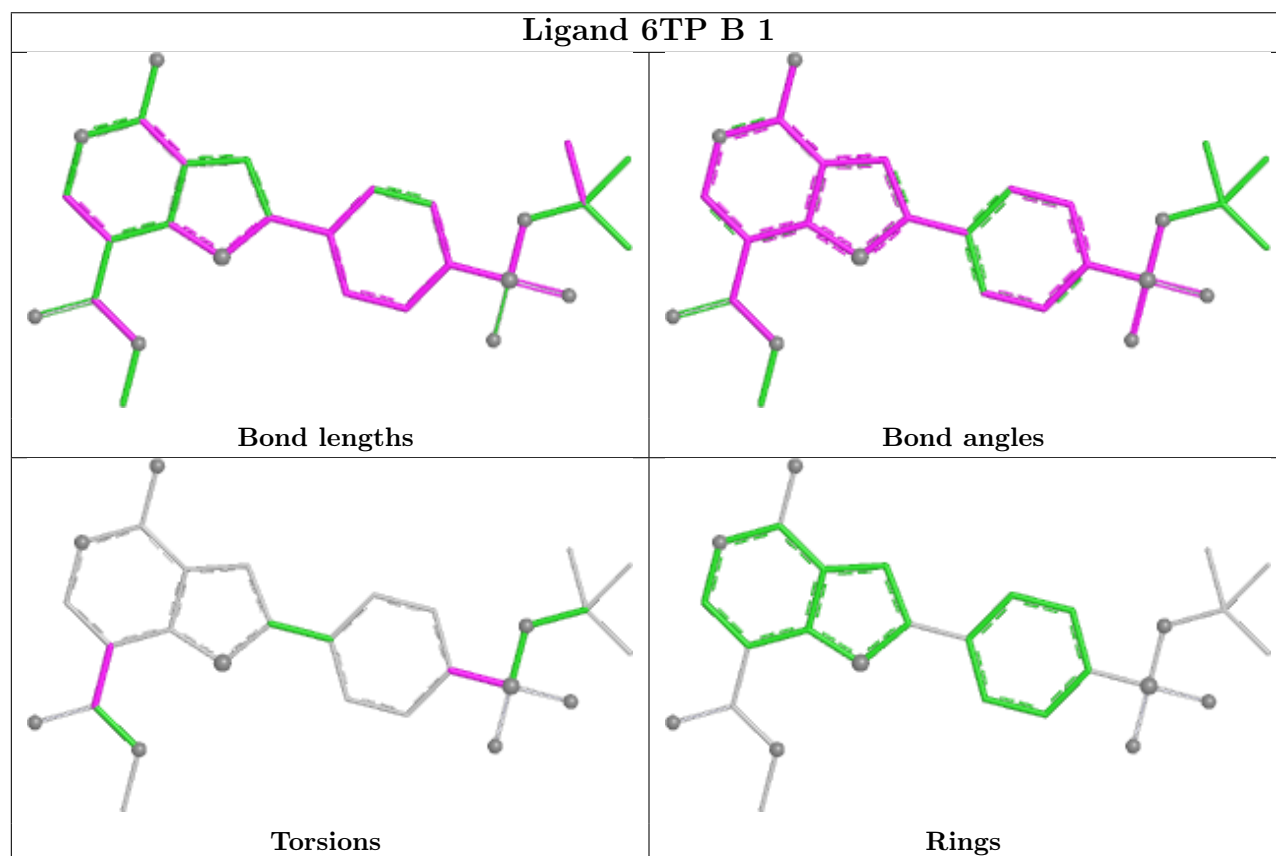
Mol	Chain	Res	Type	Atoms
2	A	1	6TP	C13-C11-C12-O2
2	B	1	6TP	C13-C11-C12-O2
2	B	1	6TP	C13-C11-C12-N3
2	A	1	6TP	C13-C11-C12-N3
2	A	1	6TP	C3-C1-N4-S2
2	A	1	6TP	C4-C1-N4-S2
2	A	1	6TP	C6-C1-N4-S2
2	B	1	6TP	C5-C18-S2-O3
2	B	1	6TP	C17-C18-S2-O3

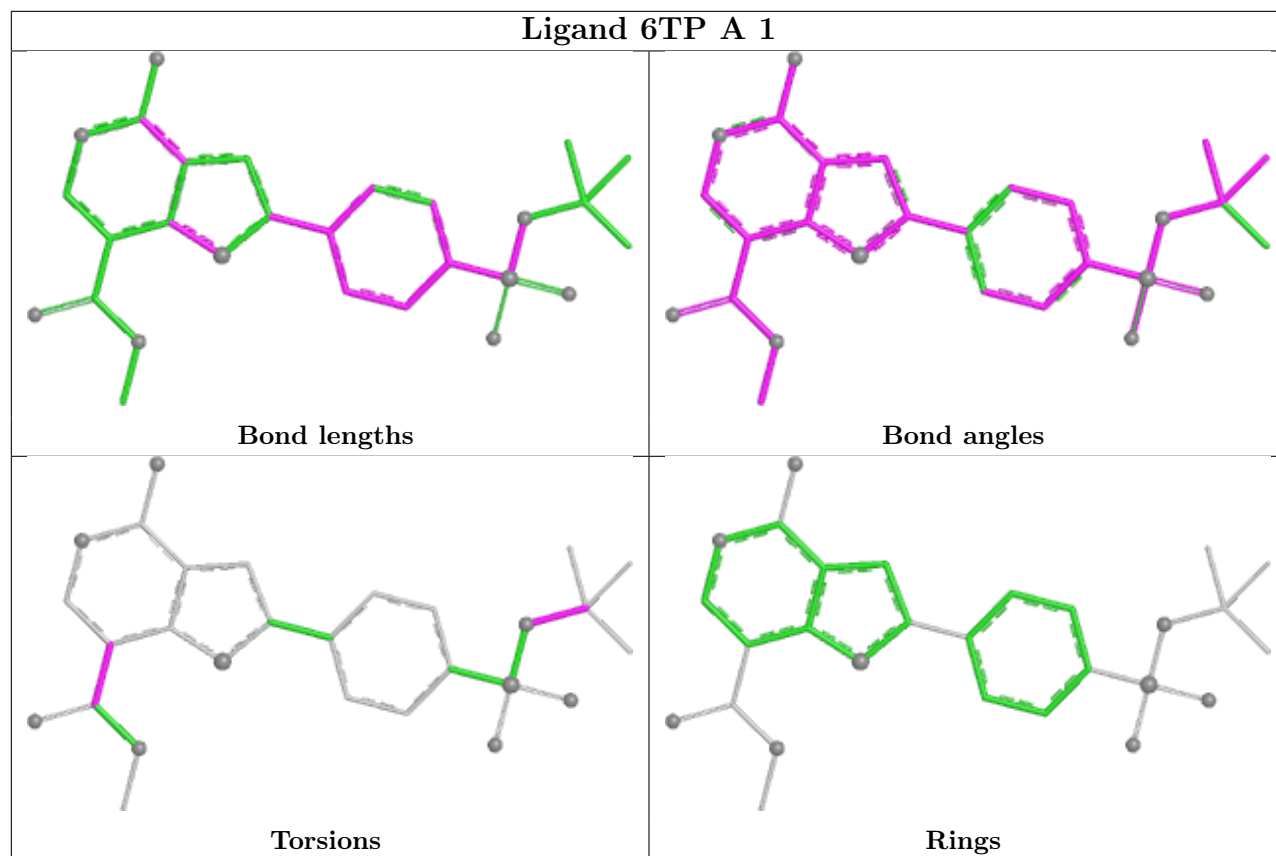
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	6TP	2	0
2	A	1	6TP	4	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	284/298 (95%)	-0.04	8 (2%) 55 46	13, 31, 64, 83	0
1	B	287/298 (96%)	-0.07	8 (2%) 55 46	12, 30, 62, 84	0
All	All	571/596 (95%)	-0.05	16 (2%) 55 46	12, 30, 64, 84	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1013	PRO	3.9
1	A	924	ASN	3.6
1	B	1011	LYS	3.2
1	A	919	SER	2.9
1	A	1014	GLY	2.8
1	B	1012	GLU	2.3
1	A	1131	ALA	2.2
1	A	885	GLN	2.1
1	A	1013	PRO	2.1
1	B	842	THR	2.1
1	B	1068	ASP	2.1
1	A	1072	GLN	2.1
1	B	981	ASN	2.0
1	B	1118	ASP	2.0
1	B	1015	GLU	2.0
1	A	1071	GLY	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($\text{\AA}^2$)	Q<0.9
1	PTR	B	1008	16/17	0.81	0.14	41,54,71,72	0
1	PTR	B	1007	16/17	0.88	0.11	42,47,52,52	0
1	PTR	A	1007	16/17	0.89	0.10	37,48,67,69	0
1	PTR	A	1008	16/17	0.89	0.11	34,38,51,52	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

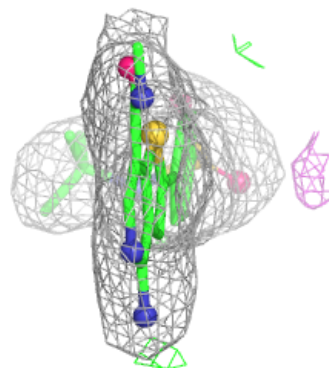
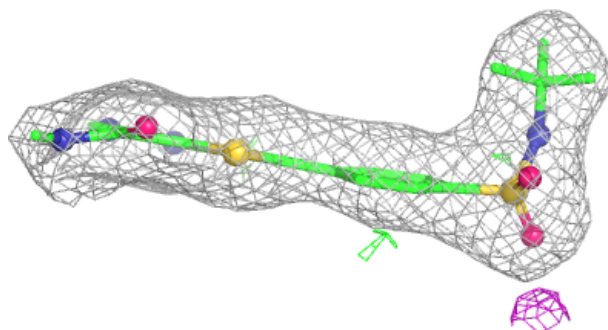
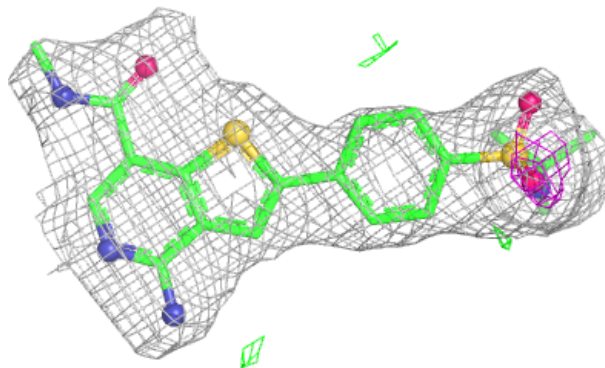
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	6TP	B	1	28/28	0.94	0.09	13,20,25,29	0
2	6TP	A	1	28/28	0.96	0.08	7,16,26,28	0

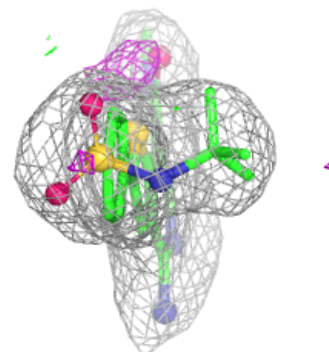
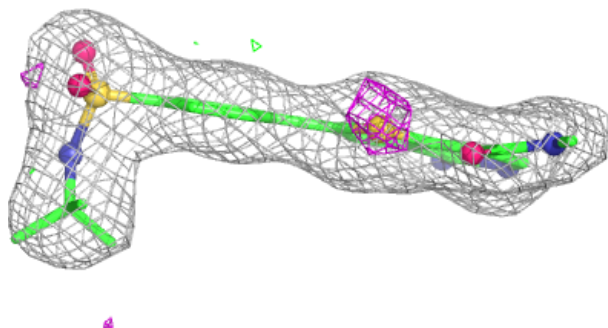
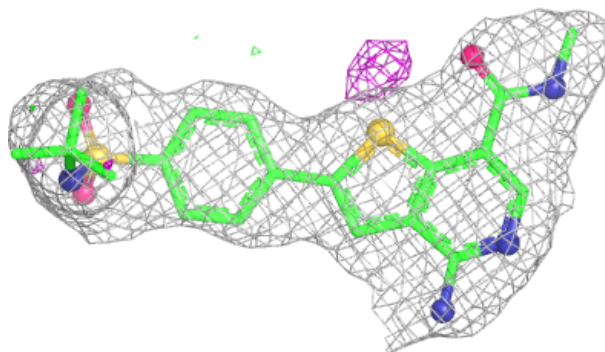
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 6TP B 1:

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

**Electron density around 6TP A 1:**

$2mF_o-DF_c$ (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.