



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 7, 2020 – 01:05 PM EDT

PDB ID : 2P1P
Title : Mechanism of Auxin Perception by the TIR1 ubiquitin ligase
Authors : Tan, X.; Calderon-Villalobos, L.I.A.; Sharon, M.; Robinson, C.V.; Estelle, M.; Zheng, N.
Deposited on : 2007-03-06
Resolution : 2.21 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 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 : 2.14.6
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) : 2.14.6

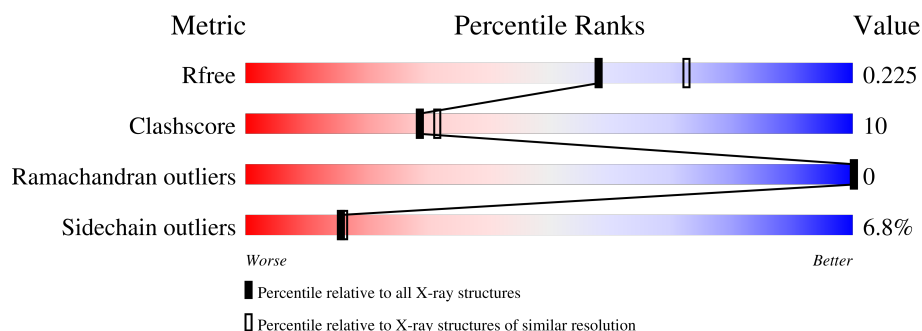
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	160	
2	B	594	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5713 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.

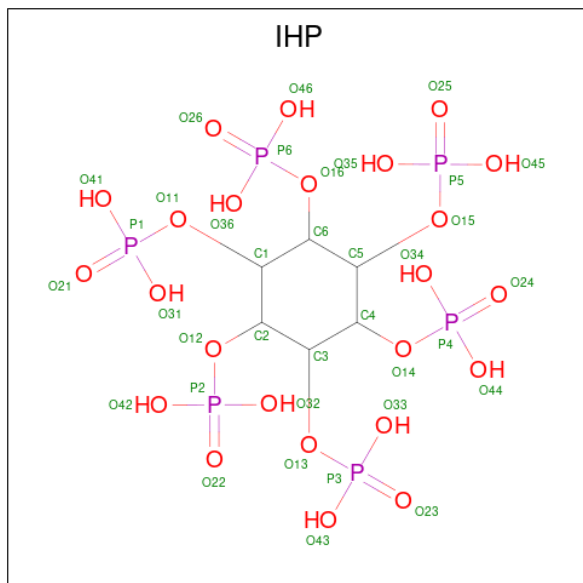
- Molecule 1 is a protein called SKP1-like protein 1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	91	Total	C	N	O	S	0	0	0
			730	460	116	152	2			

- Molecule 2 is a protein called TRANSPORT INHIBITOR RESPONSE 1 protein.

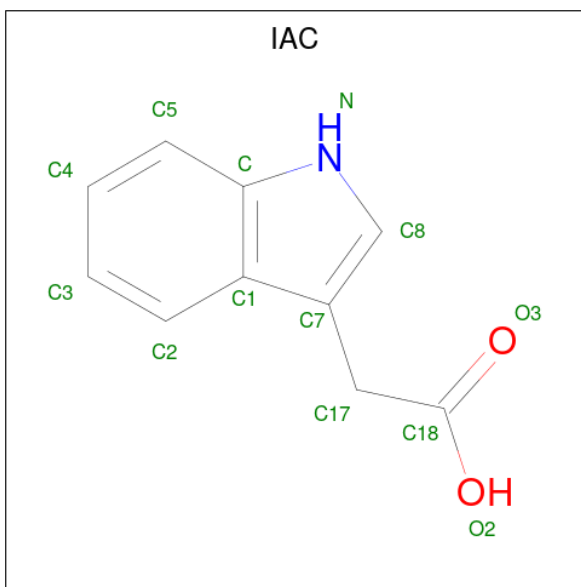
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	571	Total	C	N	O	S	0	0	0
			4495	2871	759	828	37			

- Molecule 3 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O	P	0	0
			36	6	24	6		

- Molecule 4 is 1H-INDOL-3-YLACETIC ACID (three-letter code: IAC) (formula: $C_{10}H_9NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			13	10	1	2		

- Molecule 5 is water.

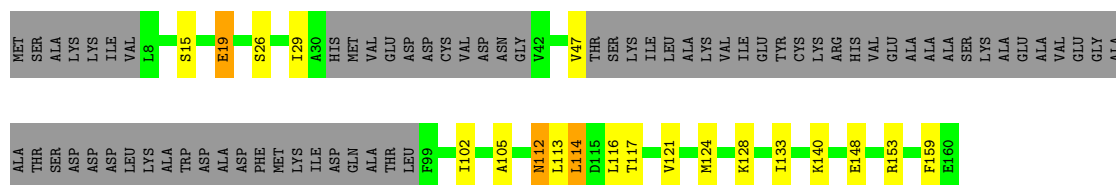
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	31	Total	O	0	0
			31	31		
5	B	408	Total	O	0	0
			408	408		

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. 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. 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.

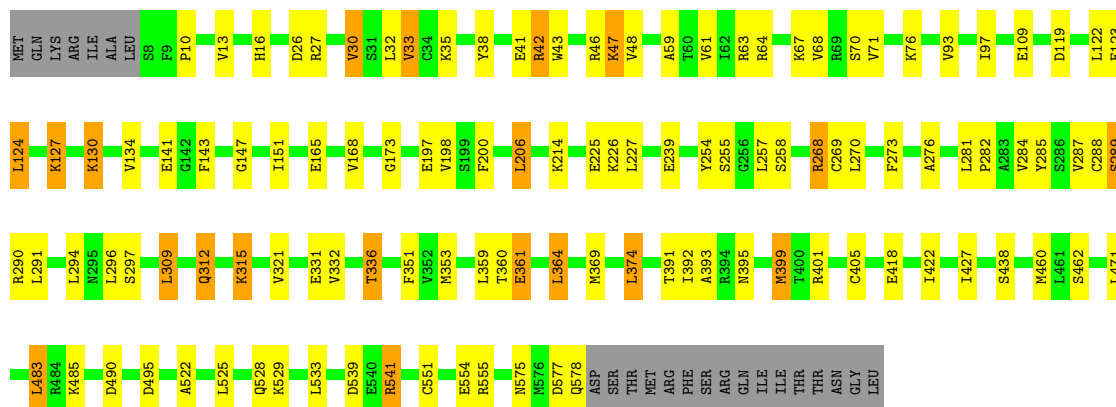
- Molecule 1: SKP1-like protein 1A

Chain A:  44% 11% . 43%



- Molecule 2: TRANSPORT INHIBITOR RESPONSE 1 protein

Chain B:  76% 16% . .



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	102.08Å 80.41Å 124.90Å 90.00° 105.16° 90.00°	Depositor
Resolution (Å)	50.00 – 2.21 49.27 – 2.21	Depositor EDS
% Data completeness (in resolution range)	89.2 (50.00-2.21) 89.3 (49.27-2.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.47 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.160 , 0.237 0.230 , 0.225	Depositor DCC
R_{free} test set	2180 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 54.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5713	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% 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: IHP, IAC

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	0.63	0/739	0.71	0/998
2	B	0.86	1/4593 (0.0%)	0.91	8/6226 (0.1%)
All	All	0.83	1/5332 (0.0%)	0.89	8/7224 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	297	SER	CB-OG	-6.35	1.33	1.42

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	399	MET	CG-SD-CE	-9.76	84.58	100.20
2	B	555	ARG	NE-CZ-NH1	6.50	123.55	120.30
2	B	490	ASP	CB-CG-OD2	6.01	123.71	118.30
2	B	483	LEU	CB-CG-CD2	5.41	120.19	111.00
2	B	541	ARG	NE-CZ-NH1	5.26	122.93	120.30
2	B	268	ARG	NE-CZ-NH1	5.15	122.87	120.30
2	B	206	LEU	CA-CB-CG	5.12	127.07	115.30
2	B	374	LEU	CA-CB-CG	5.11	127.06	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	730	0	708	17	0
2	B	4495	0	4529	87	0
3	B	36	0	6	2	0
4	B	13	0	8	0	0
5	A	31	0	0	1	0
5	B	408	0	0	18	0
All	All	5713	0	5251	102	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 10.

All (102) 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)
2:B:551:CYS:HB2	5:B:858:HOH:O	1.03	1.18
2:B:225:GLU:HG2	5:B:854:HOH:O	1.52	1.10
2:B:460:MET:SD	5:B:957:HOH:O	2.11	1.06
2:B:418:GLU:HG2	5:B:734:HOH:O	1.61	1.00
2:B:369:MET:HG2	2:B:395:ASN:ND2	1.85	0.90
1:A:124:MET:O	1:A:128:LYS:HE2	1.73	0.87
2:B:59:ALA:O	2:B:63:ARG:HG2	1.77	0.84
2:B:47:LYS:HD2	5:B:750:HOH:O	1.78	0.83
2:B:130:LYS:HD3	5:B:704:HOH:O	1.83	0.78
2:B:460:MET:CE	2:B:485:LYS:NZ	2.47	0.78
2:B:575:ASN:HD22	2:B:577:ASP:H	1.32	0.77
2:B:76:LYS:NZ	2:B:141:GLU:OE2	2.16	0.77
2:B:460:MET:CE	2:B:485:LYS:HZ2	1.98	0.76
2:B:122:LEU:HB3	2:B:151:ILE:HD11	1.68	0.75
2:B:290:ARG:HD2	5:B:651:HOH:O	1.90	0.72
2:B:460:MET:HE1	2:B:485:LYS:HZ2	1.56	0.71
2:B:369:MET:HG2	2:B:395:ASN:HD21	1.57	0.70
1:A:112:ASN:O	1:A:116:LEU:HG	1.91	0.69
1:A:116:LEU:HB3	5:A:168:HOH:O	1.92	0.68
2:B:460:MET:HE2	2:B:485:LYS:NZ	2.10	0.67
2:B:529:LYS:CD	5:B:826:HOH:O	2.41	0.67
2:B:369:MET:HE3	2:B:391:THR:CG2	2.26	0.66
2:B:438:SER:HB3	2:B:462:SER:HB2	1.76	0.66
2:B:38:TYR:O	2:B:42:ARG:HG3	1.96	0.65
2:B:405:CYS:SG	5:B:892:HOH:O	2.54	0.65
2:B:460:MET:HE1	2:B:485:LYS:NZ	2.08	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:97:ILE:HG22	2:B:124:LEU:HD13	1.79	0.65
2:B:122:LEU:HB3	2:B:151:ILE:CD1	2.28	0.63
2:B:528:GLN:HE22	2:B:578:GLN:HG3	1.62	0.63
2:B:288:CYS:HB3	2:B:312:GLN:HB2	1.82	0.62
2:B:539:ASP:OD2	2:B:541:ARG:HD3	2.00	0.62
1:A:112:ASN:HD22	1:A:112:ASN:N	1.99	0.61
2:B:47:LYS:HG3	2:B:70:SER:HB3	1.84	0.60
2:B:93:VAL:HG22	2:B:97:ILE:HD12	1.84	0.60
2:B:541:ARG:HD2	2:B:554:GLU:OE1	2.02	0.60
2:B:119:ASP:O	2:B:123:GLU:HG3	2.02	0.59
2:B:285:TYR:HA	2:B:288:CYS:SG	2.42	0.59
2:B:529:LYS:HD3	5:B:826:HOH:O	2.03	0.59
1:A:102:ILE:HG12	1:A:117:THR:HB	1.84	0.59
2:B:225:GLU:CD	2:B:225:GLU:H	2.05	0.59
2:B:575:ASN:ND2	2:B:577:ASP:H	2.00	0.58
2:B:239:GLU:HG2	2:B:269:CYS:HB2	1.87	0.57
1:A:112:ASN:HD22	1:A:112:ASN:H	1.52	0.56
1:A:26:SER:HB3	1:A:29:ILE:HD12	1.87	0.56
2:B:27:ARG:NH2	5:B:726:HOH:O	2.39	0.55
2:B:460:MET:HE3	5:B:672:HOH:O	2.06	0.54
2:B:460:MET:CE	5:B:672:HOH:O	2.55	0.54
2:B:151:ILE:HD12	2:B:151:ILE:N	2.23	0.54
2:B:42:ARG:HB3	2:B:64:ARG:O	2.08	0.54
2:B:270:LEU:HD12	2:B:291:LEU:HD11	1.89	0.53
2:B:351:PHE:HB2	5:B:846:HOH:O	2.08	0.53
2:B:364:LEU:HD13	2:B:392:ILE:HD13	1.91	0.53
2:B:294:LEU:HG	2:B:296:LEU:HG	1.92	0.52
2:B:332:VAL:O	2:B:336:THR:HG22	2.10	0.51
2:B:332:VAL:O	2:B:336:THR:CG2	2.58	0.51
1:A:105:ALA:HB2	1:A:113:LEU:HG	1.92	0.50
2:B:46:ARG:HB2	2:B:47:LYS:HE3	1.93	0.50
2:B:290:ARG:HD2	5:B:674:HOH:O	2.13	0.49
2:B:254:TYR:OH	2:B:282:PRO:HB2	2.13	0.49
1:A:19:GLU:H	1:A:19:GLU:CD	2.16	0.49
1:A:148:GLU:HG3	2:B:32:LEU:HD22	1.94	0.48
2:B:460:MET:CE	2:B:485:LYS:HZ1	2.24	0.48
2:B:214:LYS:NZ	5:B:982:HOH:O	2.31	0.48
1:A:133:ILE:HG21	2:B:33:VAL:HG11	1.95	0.48
2:B:528:GLN:HE22	2:B:578:GLN:CG	2.27	0.48
2:B:26:ASP:O	2:B:30:VAL:HG13	2.13	0.48
2:B:143:PHE:CZ	2:B:168:VAL:HG22	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:288:CYS:CB	2:B:312:GLN:HB2	2.44	0.47
3:B:595:IHP:O46	3:B:595:IHP:O25	2.32	0.47
1:A:26:SER:CB	1:A:29:ILE:HD12	2.45	0.47
2:B:399:MET:HE1	2:B:401:ARG:O	2.15	0.46
2:B:393:ALA:HB2	2:B:427:ILE:HD13	1.97	0.46
2:B:281:LEU:O	2:B:284:VAL:HB	2.15	0.46
2:B:43:TRP:HE3	2:B:67:LYS:HD2	1.81	0.46
2:B:10:PRO:HG2	2:B:13:VAL:HG23	1.98	0.46
2:B:173:GLY:HA3	2:B:197:GLU:O	2.16	0.45
2:B:268:ARG:NH1	2:B:290:ARG:HD3	2.32	0.44
2:B:68:VAL:HG11	2:B:71:VAL:HG12	1.98	0.44
2:B:273:PHE:O	2:B:276:ALA:HB2	2.18	0.44
2:B:93:VAL:HG22	2:B:97:ILE:CD1	2.46	0.44
2:B:109:GLU:HG2	2:B:134:VAL:HB	2.00	0.43
2:B:331:GLU:HG3	5:B:907:HOH:O	2.18	0.43
2:B:97:ILE:HG22	2:B:124:LEU:CD1	2.47	0.43
2:B:200:PHE:CE2	2:B:226:LYS:HD2	2.53	0.43
2:B:296:LEU:HD11	2:B:309:LEU:HD13	2.01	0.43
2:B:460:MET:HE2	2:B:485:LYS:HZ1	1.79	0.43
1:A:159:PHE:HE2	2:B:61:VAL:HG22	1.84	0.43
2:B:147:GLY:O	2:B:151:ILE:HD13	2.18	0.43
3:B:595:IHP:H3	5:B:641:HOH:O	2.19	0.43
2:B:46:ARG:HB2	2:B:47:LYS:CE	2.49	0.42
2:B:130:LYS:H	2:B:130:LYS:HD3	1.84	0.42
2:B:200:PHE:CE1	2:B:226:LYS:HB3	2.55	0.41
2:B:127:LYS:HB2	2:B:127:LYS:HE2	1.69	0.41
1:A:102:ILE:HD11	1:A:121:VAL:HG21	2.01	0.41
1:A:114:LEU:HD13	2:B:16:HIS:CD2	2.55	0.41
1:A:102:ILE:HD11	1:A:121:VAL:CG2	2.50	0.41
1:A:102:ILE:CD1	1:A:121:VAL:HG21	2.50	0.41
2:B:360:THR:HB	2:B:361:GLU:OE2	2.21	0.41
2:B:495:ASP:CG	2:B:522:ALA:HB2	2.42	0.41
2:B:43:TRP:O	2:B:67:LYS:HD3	2.21	0.41
2:B:289:SER:O	2:B:315:LYS:HG3	2.21	0.40
2:B:287:VAL:CG1	2:B:291:LEU:HD21	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	85/160 (53%)	84 (99%)	1 (1%)	0	100	100
2	B	569/594 (96%)	554 (97%)	15 (3%)	0	100	100
All	All	654/754 (87%)	638 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	82/137 (60%)	75 (92%)	7 (8%)	10	9
2	B	504/525 (96%)	471 (94%)	33 (6%)	17	18
All	All	586/662 (88%)	546 (93%)	40 (7%)	16	16

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	SER
1	A	19	GLU
1	A	47	VAL
1	A	112	ASN
1	A	114	LEU
1	A	140	LYS
1	A	153	ARG
2	B	30	VAL

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Mol	Chain	Res	Type
2	B	33	VAL
2	B	35	LYS
2	B	41	GLU
2	B	42	ARG
2	B	47	LYS
2	B	48	VAL
2	B	124	LEU
2	B	127	LYS
2	B	130	LYS
2	B	165	GLU
2	B	198	VAL
2	B	206	LEU
2	B	227	LEU
2	B	255	SER
2	B	257	LEU
2	B	258	SER
2	B	289	SER
2	B	309	LEU
2	B	312	GLN
2	B	315	LYS
2	B	321	VAL
2	B	336	THR
2	B	353	MET
2	B	359	LEU
2	B	361	GLU
2	B	364	LEU
2	B	374	LEU
2	B	422	ILE
2	B	471	LEU
2	B	483	LEU
2	B	525	LEU
2	B	533	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	ASN
2	B	317	GLN
2	B	383	GLN
2	B	395	ASN
2	B	430	HIS
2	B	501	ASN

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Mol	Chain	Res	Type
2	B	528	GLN
2	B	575	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
3	IHP	B	595	-	36,36,36	1.65	9 (25%)	54,60,60	1.16	4 (7%)
4	IAC	B	601	-	10,14,14	1.32	2 (20%)	11,19,19	1.10	2 (18%)

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
3	IHP	B	595	-	-	6/30/54/54	0/1/1/1
4	IAC	B	601	-	-	0/2/4/4	0/2/2/2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	595	IHP	P3-O43	4.32	1.71	1.54
3	B	595	IHP	P3-O33	3.69	1.69	1.54
3	B	595	IHP	P2-O32	3.18	1.67	1.54
3	B	595	IHP	P4-O14	3.02	1.65	1.59
3	B	595	IHP	P2-O12	2.62	1.64	1.59
3	B	595	IHP	P5-O15	2.56	1.64	1.59
4	B	601	IAC	C3-C2	2.41	1.42	1.36
3	B	595	IHP	P1-O31	2.28	1.63	1.54
3	B	595	IHP	P2-O42	2.09	1.62	1.54
4	B	601	IAC	C4-C5	2.07	1.41	1.36
3	B	595	IHP	P1-O41	2.01	1.62	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	595	IHP	O13-C3-C2	-3.15	101.26	108.69
3	B	595	IHP	O43-P3-O23	2.62	120.94	110.68
4	B	601	IAC	C2-C1-C	2.40	121.36	118.17
3	B	595	IHP	O31-P1-O21	2.36	119.93	110.68
3	B	595	IHP	O12-C2-C3	-2.18	103.55	108.69
4	B	601	IAC	C3-C2-C1	-2.05	118.05	120.89

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	595	IHP	C1-O11-P1-O21
3	B	595	IHP	C1-O11-P1-O41
3	B	595	IHP	C4-O14-P4-O24
3	B	595	IHP	C5-O15-P5-O35
3	B	595	IHP	C1-O11-P1-O31
3	B	595	IHP	C4-O14-P4-O34

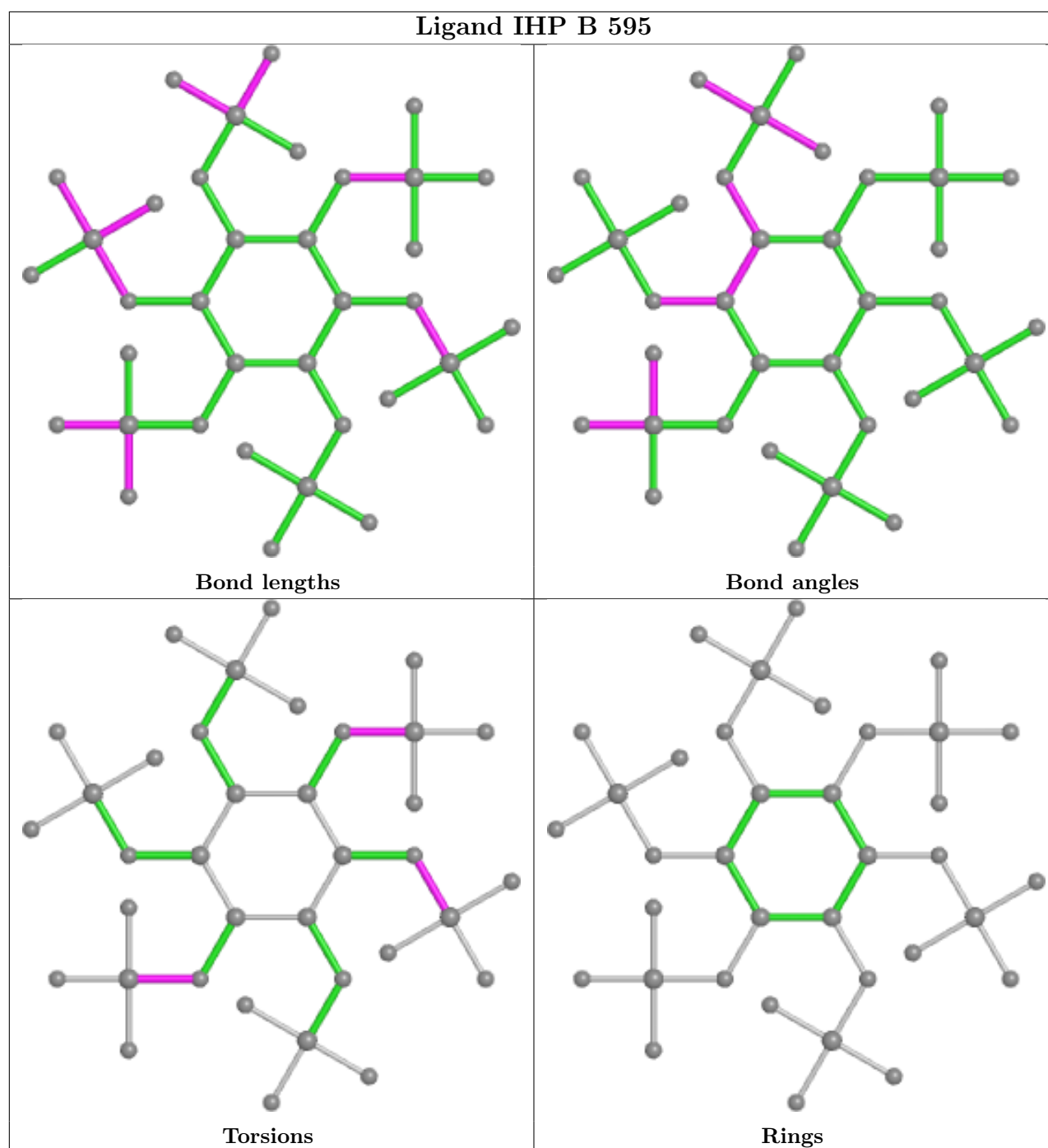
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	595	IHP	2	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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

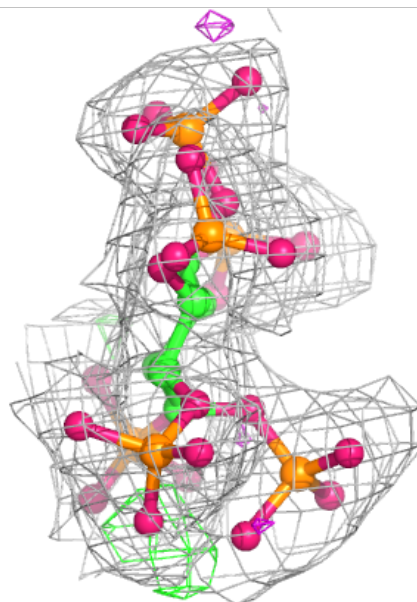
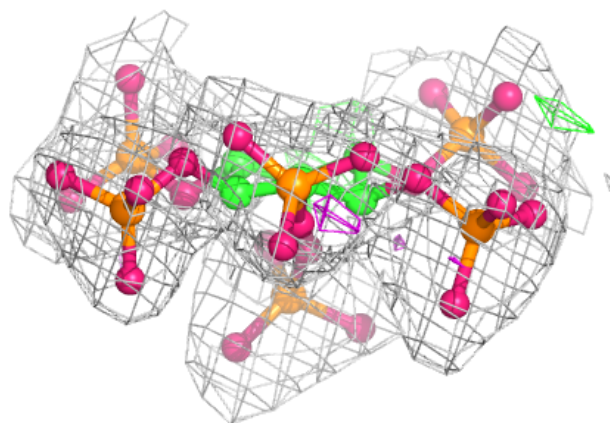
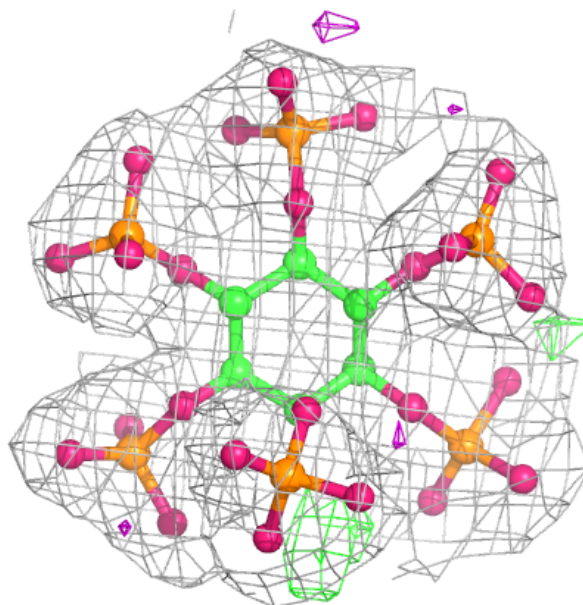
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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 IHP B 595:

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



6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.