



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 08:01 AM GMT

PDB ID : 2P1Q  
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 : 1.91 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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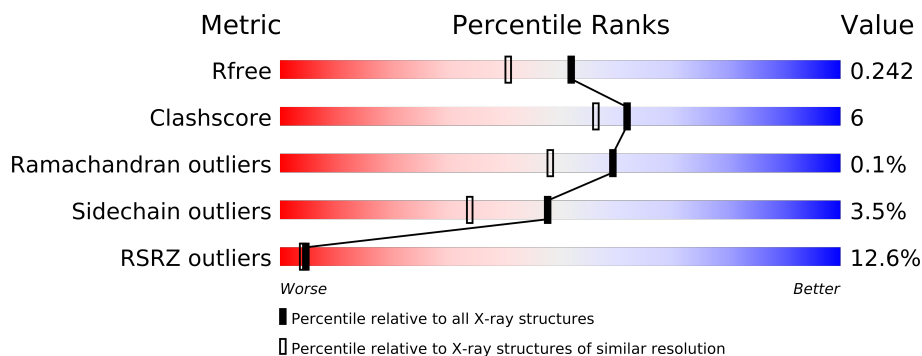
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance




The reported resolution of this entry is 1.91 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))
$R_{free}$	66092	4387 (1.94-1.90)
Clashscore	79885	5258 (1.94-1.90)
Ramachandran outliers	78287	5193 (1.94-1.90)
Sidechain outliers	78261	5194 (1.94-1.90)
RSRZ outliers	66119	4389 (1.94-1.90)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	160	
2	B	594	
3	C	13	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6401 atoms, of which 0 are hydrogen and 0 are deuterium.

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	124	Total	C	N	O	S	0	0	0
			996	631	163	197	5			

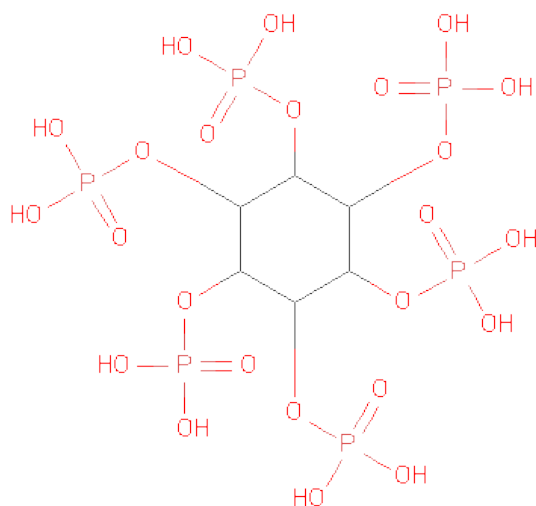
- Molecule 2 is a protein called TRANSPORT INHIBITOR RESPONSE 1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	568	Total	C	N	O	S	0	0	0
			4472	2859	755	821	37			

- Molecule 3 is a protein called Auxin-responsive protein IAA7.

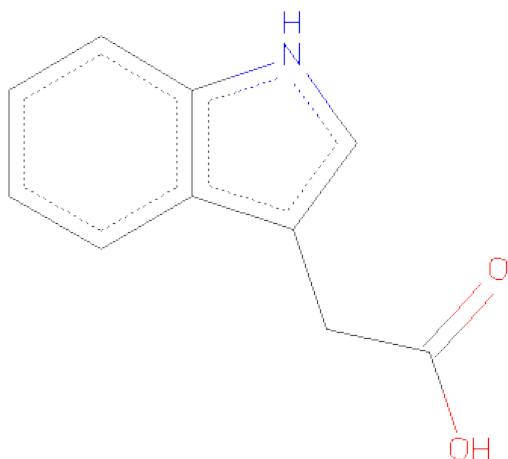
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	0	0	0
			114	74	23	17			

- Molecule 4 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula:  $C_6H_{18}O_{24}P_6$ ).



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

- Molecule 5 is 1H-INDOL-3-YLACETIC ACID (three-letter code: IAC) (formula: C<sub>10</sub>H<sub>9</sub>NO<sub>2</sub>).



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

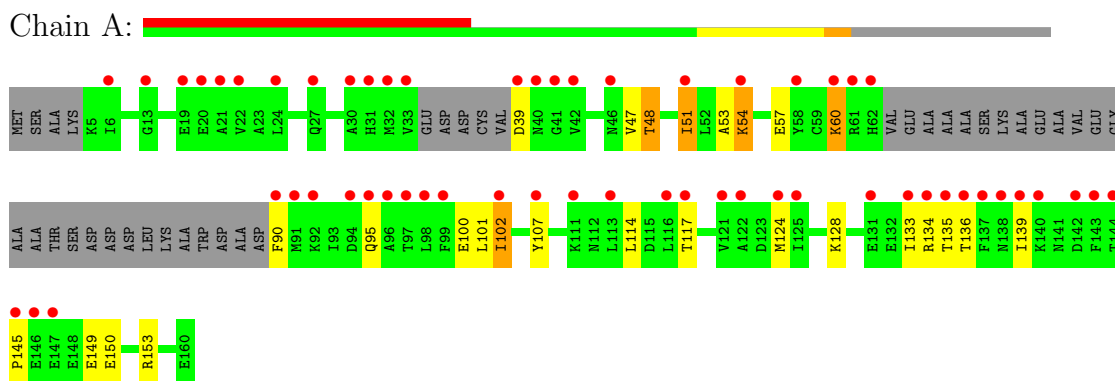
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	87	Total	O	0	0
			87	87		
6	B	666	Total	O	0	0
			666	666		
6	C	17	Total	O	0	0
			17	17		

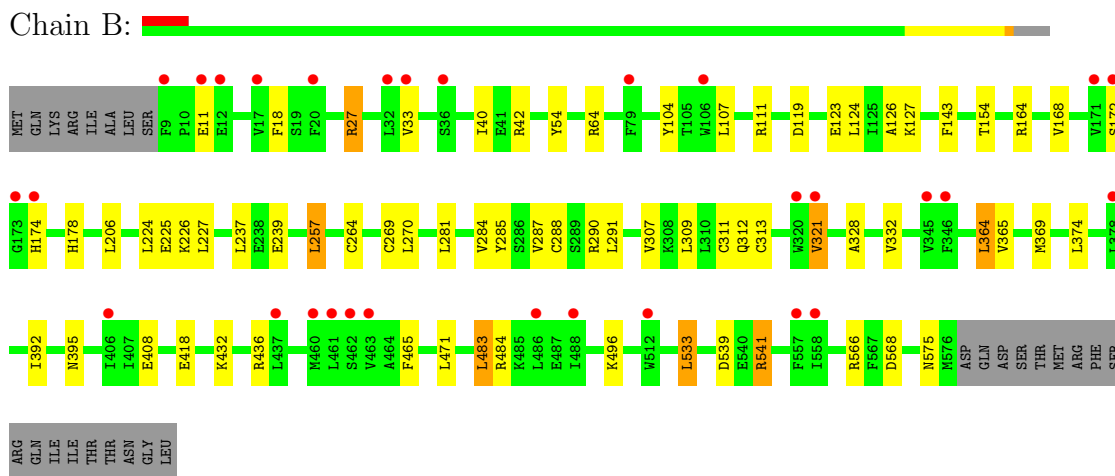
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: SKP1-like protein 1A



- Molecule 2: TRANSPORT INHIBITOR RESPONSE 1 protein



- Molecule 3: Auxin-responsive protein IAA7



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.21Å 82.47Å 125.05Å 90.00° 104.05° 90.00°	Depositor
Resolution (Å)	50.00 – 1.91 49.09 – 1.91	Depositor EDS
% Data completeness (in resolution range)	94.4 (50.00-1.91) 94.4 (49.09-1.91)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.25 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.172 , 0.213 0.245 , 0.242	Depositor DCC
$R_{free}$ test set	3723 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.5	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 55.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 73526 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6401	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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	0.98	4/1009 (0.4%)	0.74	2/1359 (0.1%)
2	B	0.77	1/4570 (0.0%)	0.84	10/6195 (0.2%)
3	C	0.98	0/118	0.84	1/159 (0.6%)
All	All	0.81	5/5697 (0.1%)	0.82	13/7713 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	60	LYS	CE-NZ	18.66	1.95	1.49
1	A	95	GLN	CD-OE1	8.08	1.41	1.24
1	A	95	GLN	CD-NE2	5.29	1.46	1.32
2	B	311	CYS	CB-SG	-5.25	1.73	1.81
1	A	135	THR	CB-OG1	5.18	1.53	1.43

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	27	ARG	NE-CZ-NH2	-10.08	115.26	120.30
1	A	60	LYS	CD-CE-NZ	-8.86	91.32	111.70
2	B	541	ARG	NE-CZ-NH2	-7.95	116.33	120.30
2	B	111	ARG	NE-CZ-NH1	-7.93	116.33	120.30
2	B	321	VAL	CB-CA-C	-6.27	99.50	111.40
2	B	533	LEU	CB-CG-CD1	6.05	121.28	111.00
2	B	321	VAL	CG1-CB-CG2	5.78	120.15	110.90
2	B	436	ARG	NE-CZ-NH1	-5.55	117.53	120.30
2	B	541	ARG	NE-CZ-NH1	5.39	123.00	120.30
1	A	51	ILE	CG1-CB-CG2	-5.36	99.60	111.40
2	B	483	LEU	CB-CG-CD2	5.35	120.09	111.00
2	B	27	ARG	NE-CZ-NH1	5.26	122.93	120.30
3	C	12	ARG	NE-CZ-NH2	-5.10	117.75	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	996	0	994	17	0
2	B	4472	0	4512	46	0
3	C	114	0	118	3	0
4	B	36	0	6	1	0
5	B	13	0	8	0	0
6	A	87	0	0	3	0
6	B	666	0	0	13	0
6	C	17	0	0	1	0
All	All	6401	0	5638	64	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (64) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:60:LYS:CE	1:A:60:LYS:NZ	1.95	1.27
2:B:11:GLU:OE1	2:B:40:ILE:HD11	1.59	1.03
2:B:369:MET:HG2	2:B:395:ASN:ND2	1.77	1.00
1:A:149:GLU:HB3	6:A:194:HOH:O	1.62	0.98
2:B:288:CYS:O	2:B:312:GLN:O	1.93	0.86
2:B:174:HIS:HD2	6:B:1107:HOH:O	1.58	0.84
2:B:418:GLU:HG2	6:B:1202:HOH:O	1.83	0.77
2:B:285:TYR:HA	2:B:288:CYS:SG	2.31	0.70
2:B:539:ASP:OD2	2:B:541:ARG:HD3	1.91	0.70
1:A:48:THR:HG22	1:A:51:ILE:H	1.56	0.70
2:B:225:GLU:HG2	6:B:1557:HOH:O	1.93	0.69
2:B:496:LYS:HE2	6:B:1158:HOH:O	1.92	0.68
2:B:288:CYS:HB2	2:B:313:CYS:SG	2.33	0.68
1:A:60:LYS:NZ	1:A:60:LYS:CD	2.57	0.68
2:B:178:HIS:NE2	6:B:1107:HOH:O	2.27	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:B:801:IHP:O44	6:B:1564:HOH:O	2.14	0.66
1:A:48:THR:HG21	6:A:181:HOH:O	1.96	0.65
1:A:102:ILE:HD13	1:A:117:THR:HB	1.80	0.63
2:B:369:MET:HG2	2:B:395:ASN:HD21	1.63	0.62
2:B:465:PHE:HZ	3:C:2:VAL:HG11	1.64	0.62
2:B:566:ARG:HG2	2:B:568:ASP:OD1	2.02	0.60
2:B:432:LYS:HG2	6:B:1414:HOH:O	2.02	0.60
2:B:364:LEU:HD13	2:B:392:ILE:HD13	1.83	0.59
2:B:539:ASP:OD2	2:B:541:ARG:CD	2.51	0.58
2:B:496:LYS:CE	6:B:1158:HOH:O	2.50	0.58
2:B:18:PHE:O	2:B:27:ARG:NH2	2.38	0.56
2:B:365:VAL:O	2:B:369:MET:HG3	2.07	0.55
2:B:281:LEU:O	2:B:284:VAL:HG22	2.08	0.54
2:B:224:LEU:HD11	2:B:257:LEU:HD11	1.88	0.54
1:A:47:VAL:HG23	1:A:107:TYR:CE2	2.44	0.53
1:A:51:ILE:HG12	1:A:100:GLU:HB3	1.89	0.53
2:B:369:MET:HG2	2:B:395:ASN:HD22	1.70	0.53
2:B:42:ARG:HB2	2:B:64:ARG:O	2.09	0.52
1:A:54:LYS:HE2	1:A:90:PHE:CE1	2.45	0.52
1:A:124:MET:O	1:A:128:LYS:HE2	2.10	0.52
2:B:11:GLU:OE1	2:B:40:ILE:CD1	2.47	0.51
1:A:48:THR:CG2	1:A:51:ILE:H	2.22	0.51
1:A:53:ALA:O	1:A:57:GLU:HG3	2.12	0.50
1:A:134:ARG:HB2	1:A:139:ILE:O	2.12	0.49
2:B:285:TYR:CD2	2:B:312:GLN:NE2	2.80	0.48
2:B:119:ASP:O	2:B:123:GLU:HG3	2.13	0.48
2:B:11:GLU:HG2	6:B:1259:HOH:O	2.13	0.48
2:B:284:VAL:O	2:B:287:VAL:HB	2.14	0.47
2:B:408:GLU:HG2	6:B:1127:HOH:O	2.14	0.47
2:B:328:ALA:HB3	6:B:1262:HOH:O	2.14	0.47
1:A:145:PRO:O	1:A:149:GLU:HG3	2.14	0.47
2:B:54:TYR:CZ	2:B:566:ARG:HD2	2.51	0.45
2:B:239:GLU:HG2	2:B:269:CYS:HB3	1.99	0.45
2:B:566:ARG:CG	2:B:568:ASP:OD1	2.65	0.44
2:B:307:VAL:HG13	2:B:332:VAL:HG11	2.00	0.44
2:B:484:ARG:HG2	6:B:1479:HOH:O	2.17	0.44
2:B:465:PHE:CZ	3:C:2:VAL:HG11	2.48	0.43
1:A:133:ILE:HG21	2:B:33:VAL:HG11	2.00	0.43
2:B:143:PHE:CZ	2:B:168:VAL:HG22	2.54	0.42
2:B:264:CYS:O	2:B:290:ARG:NH2	2.51	0.42
2:B:226:LYS:NZ	6:B:1032:HOH:O	2.52	0.42
2:B:126:ALA:HB1	2:B:154:THR:HB	2.02	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:153:ARG:NH1	6:A:194:HOH:O	2.53	0.42
2:B:104:TYR:O	2:B:107:LEU:HB2	2.19	0.41
2:B:270:LEU:HD12	2:B:291:LEU:HD11	2.02	0.41
2:B:123:GLU:O	2:B:127:LYS:HG2	2.21	0.41
1:A:47:VAL:HG23	1:A:107:TYR:CD2	2.56	0.41
2:B:127:LYS:HB2	2:B:127:LYS:HE2	1.88	0.41
3:C:12:ARG:HD3	6:C:510:HOH:O	2.21	0.41

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	118/160 (74%)	117 (99%)	1 (1%)	0	100	100
2	B	566/594 (95%)	555 (98%)	10 (2%)	1 (0%)	56	44
3	C	11/13 (85%)	11 (100%)	0	0	100	100
All	All	695/767 (91%)	683 (98%)	11 (2%)	1 (0%)	59	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	172	SER

### 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	112/137 (82%)	104 (93%)	8 (7%)	21	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	501/525 (95%)	487 (97%)	14 (3%)	56	44
3	C	12/12 (100%)	12 (100%)	0	100	100
All	All	625/674 (93%)	603 (96%)	22 (4%)	48	34

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ASP
1	A	48	THR
1	A	54	LYS
1	A	101	LEU
1	A	102	ILE
1	A	114	LEU
1	A	136	THR
1	A	150	GLU
2	B	124	LEU
2	B	164	ARG
2	B	206	LEU
2	B	227	LEU
2	B	237	LEU
2	B	257	LEU
2	B	309	LEU
2	B	321	VAL
2	B	364	LEU
2	B	374	LEU
2	B	471	LEU
2	B	483	LEU
2	B	533	LEU
2	B	575	ASN

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

Mol	Chain	Res	Type
1	A	95	GLN
2	B	174	HIS
2	B	312	GLN
2	B	317	GLN
2	B	383	GLN
2	B	395	ASN
2	B	501	ASN

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Mol	Chain	Res	Type
2	B	575	ASN
3	C	1	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates 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$
4	IHP	B	801	-	36,36,36	1.18	5 (13%)	60,60,60	1.45	10 (16%)
5	IAC	B	901	-	14,14,14	1.30	3 (21%)	19,19,19	1.04	1 (5%)

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
4	IHP	B	801	-	-	0/30/54/54	0/1/1/1
5	IAC	B	901	-	-	0/4/4/4	0/0/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	801	IHP	P2-O32	2.91	1.65	1.54
4	B	801	IHP	P2-O12	2.46	1.67	1.59
4	B	801	IHP	P3-O43	2.39	1.63	1.54
4	B	801	IHP	P3-O33	2.17	1.62	1.54
5	B	901	IAC	O2-C18	-2.16	1.22	1.30
4	B	801	IHP	P5-O15	2.15	1.66	1.59
5	B	901	IAC	C3-C2	2.13	1.41	1.36
5	B	901	IAC	C4-C5	2.09	1.41	1.36

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	801	IHP	O13-P3-O23	3.83	117.49	106.79
4	B	801	IHP	P2-O12-C2	3.28	128.87	121.96
4	B	801	IHP	O41-P1-O21	2.83	119.70	110.44
4	B	801	IHP	O45-P5-O15	-2.64	99.48	107.09
4	B	801	IHP	P1-O11-C1	2.50	127.23	121.96
4	B	801	IHP	O16-P6-O26	2.34	113.34	106.79
4	B	801	IHP	O36-P6-O16	-2.28	100.52	107.09
4	B	801	IHP	P4-O14-C4	2.28	126.75	121.96
4	B	801	IHP	O43-P3-O13	-2.24	100.65	107.09
4	B	801	IHP	O46-P6-O16	-2.09	101.07	107.09
5	B	901	IAC	C2-C1-C	2.08	122.03	119.08

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	124/160 (77%)	2.05	57 (45%) 1 0	17, 23, 28, 30	0
2	B	568/594 (95%)	0.45	30 (5%) 25 26	19, 24, 31, 36	0
3	C	13/13 (100%)	0.79	2 (15%) 3 3	22, 24, 29, 35	0
All	All	705/767 (91%)	0.74	89 (12%) 4 4	17, 24, 30, 36	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	137	PHE	6.4
1	A	39	ASP	6.0
1	A	90	PHE	6.0
1	A	40	ASN	5.5
1	A	58	TYR	5.3
1	A	125	ILE	5.1
1	A	139	ILE	5.0
1	A	124	MET	4.6
1	A	41	GLY	4.5
1	A	138	ASN	4.4
1	A	135	THR	4.3
2	B	106	TRP	4.2
1	A	94	ASP	4.2
1	A	145	PRO	4.0
1	A	131	GLU	4.0
1	A	144	THR	3.9
1	A	97	THR	3.9
1	A	99	PHE	3.9
3	C	13	LYS	3.8
1	A	92	LYS	3.8
2	B	9	PHE	3.8
1	A	140	LYS	3.6
1	A	102	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	95	GLN	3.4
1	A	111	LYS	3.3
1	A	33	VAL	3.3
1	A	136	THR	3.3
1	A	24	LEU	3.2
1	A	21	ALA	3.2
1	A	6	ILE	3.2
1	A	146	GLU	3.2
1	A	91	MET	3.2
1	A	62	HIS	3.0
1	A	61	ARG	2.9
1	A	142	ASP	2.9
1	A	96	ALA	2.9
1	A	42	VAL	2.9
3	C	1	GLN	2.9
2	B	12	GLU	2.8
1	A	20	GLU	2.8
2	B	174	HIS	2.8
1	A	143	PHE	2.8
2	B	33	VAL	2.8
1	A	22	VAL	2.7
2	B	172	SER	2.7
2	B	11	GLU	2.7
1	A	107	TYR	2.6
1	A	60	LYS	2.6
1	A	113	LEU	2.6
2	B	378	LEU	2.6
1	A	30	ALA	2.6
1	A	133	ILE	2.6
2	B	463	VAL	2.6
2	B	488	ILE	2.5
2	B	512	TRP	2.5
1	A	121	VAL	2.5
1	A	51	ILE	2.5
2	B	36	SER	2.5
1	A	46	ASN	2.5
1	A	19	GLU	2.5
1	A	147	GLU	2.4
1	A	32	MET	2.4
2	B	437	LEU	2.4
2	B	320	TRP	2.4
2	B	346	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	32	LEU	2.3
2	B	171	VAL	2.3
2	B	20	PHE	2.2
2	B	345	VAL	2.2
1	A	31	HIS	2.2
2	B	461	LEU	2.2
2	B	321	VAL	2.2
2	B	486	LEU	2.2
2	B	173	GLY	2.2
2	B	462	SER	2.2
2	B	17	VAL	2.2
1	A	13	GLY	2.2
1	A	116	LEU	2.2
1	A	27	GLN	2.1
1	A	98	LEU	2.1
2	B	406	ILE	2.1
1	A	134	ARG	2.1
2	B	79	PHE	2.1
1	A	117	THR	2.1
2	B	460	MET	2.1
2	B	558	ILE	2.1
2	B	557	PHE	2.0
1	A	122	ALA	2.0
1	A	54	LYS	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	IHP	B	801	36/36	0.14	-1.30	22,31,44,46	0
5	IAC	B	901	13/13	0.14	-1.52	17,18,19,19	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.