wwPDB X-ray Structure Validation Summary Report (i)

May 26, 2020 – 03:39 pm BST

PDB ID	:	3UJ0
Title	:	Crystal structure of the inositol 1,4,5-trisphosphate receptor with ligand bound form.
Authors	:	Ikura, M.; Seo, M.D.; Ishiyama, N.; Stathopulos, P.
Deposited on	:	2011-11-07
Resolution	:	3.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see references (i)) were used in the production of this report:

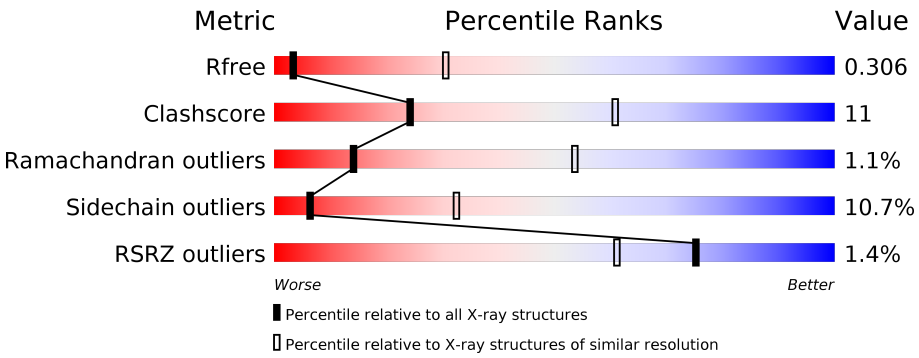
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.60 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	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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 <=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	604	% 58% 23% • 17%
1	B	604	% 57% 23% • 17%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7779 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 Inositol 1,4,5-trisphosphate receptor type 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	502	3850	2438	681	724	7	0	0	0
1	B	502	3872	2453	687	725	7	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ALA	CYS	engineered mutation	UNP P29994
A	37	ALA	CYS	engineered mutation	UNP P29994
A	56	ALA	CYS	engineered mutation	UNP P29994
A	61	ALA	CYS	engineered mutation	UNP P29994
A	206	ALA	CYS	engineered mutation	UNP P29994
A	214	ALA	CYS	engineered mutation	UNP P29994
A	253	ALA	CYS	engineered mutation	UNP P29994
A	292	ALA	CYS	engineered mutation	UNP P29994
A	326	ALA	CYS	engineered mutation	UNP P29994
A	394	ALA	CYS	engineered mutation	UNP P29994
A	530	ALA	CYS	engineered mutation	UNP P29994
A	553	ALA	CYS	engineered mutation	UNP P29994
A	556	ALA	CYS	engineered mutation	UNP P29994
B	15	ALA	CYS	engineered mutation	UNP P29994
B	37	ALA	CYS	engineered mutation	UNP P29994
B	56	ALA	CYS	engineered mutation	UNP P29994
B	61	ALA	CYS	engineered mutation	UNP P29994
B	206	ALA	CYS	engineered mutation	UNP P29994
B	214	ALA	CYS	engineered mutation	UNP P29994
B	253	ALA	CYS	engineered mutation	UNP P29994
B	292	ALA	CYS	engineered mutation	UNP P29994
B	326	ALA	CYS	engineered mutation	UNP P29994
B	394	ALA	CYS	engineered mutation	UNP P29994
B	530	ALA	CYS	engineered mutation	UNP P29994
B	553	ALA	CYS	engineered mutation	UNP P29994

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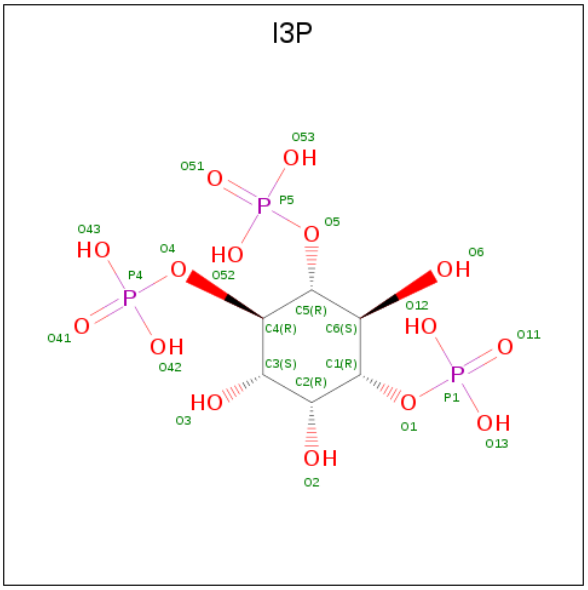
Chain	Residue	Modelled	Actual	Comment	Reference
B	556	ALA	CYS	engineered mutation	UNP P29994

- Molecule 2 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (three-letter code: I3P) (formula: $C_6H_{15}O_{15}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
2	A	1	24	6	15	3	0	0
			Total	C	O	P		
2	B	1	24	6	15	3	0	0

- Molecule 3 is water.

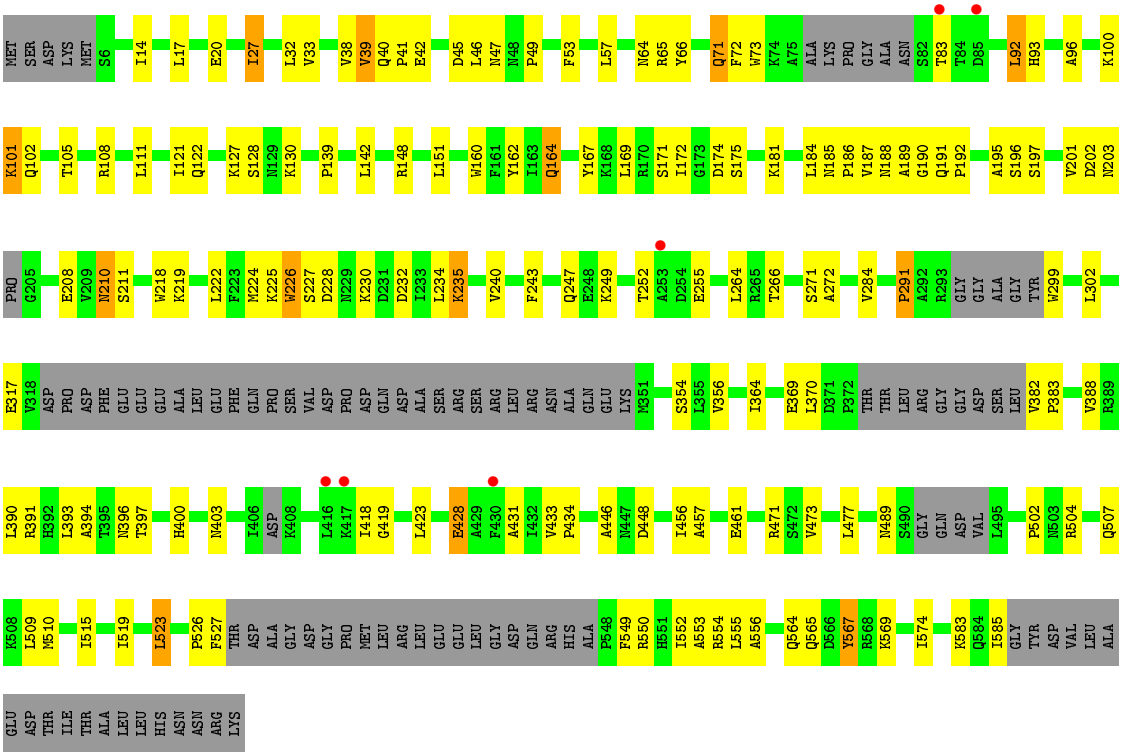
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	5	5	5	0	0
			Total	O		
3	B	4	4	4	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

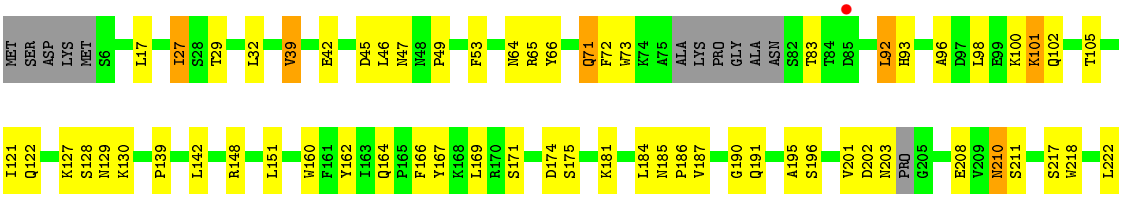
- Molecule 1: Inositol 1,4,5-trisphosphate receptor type 1

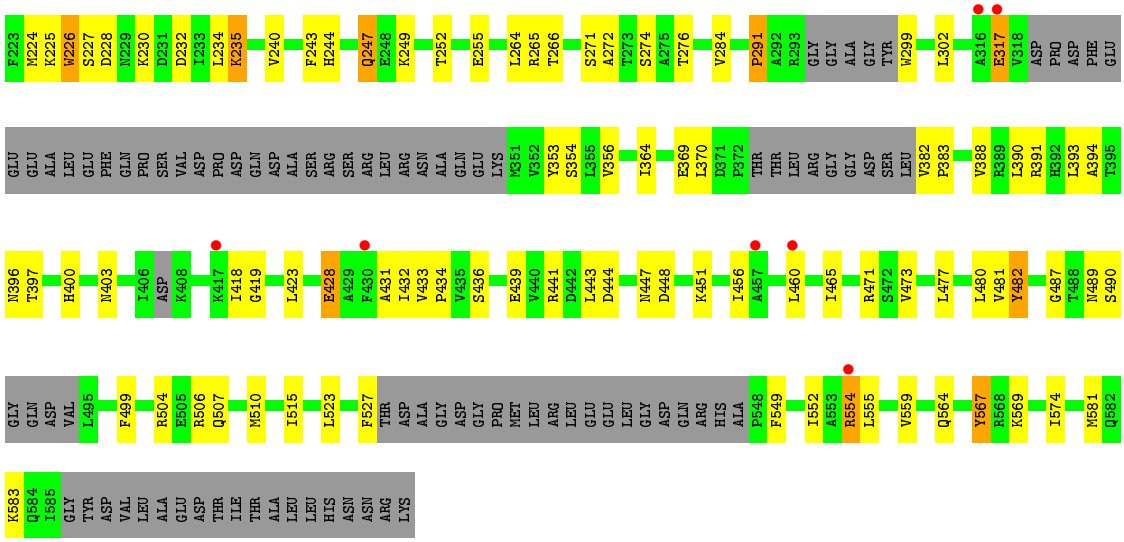
Chain A:



- Molecule 1: Inositol 1,4,5-trisphosphate receptor type 1

Chain B:




F223 M224 K225 W226 S227 D228 N229 K230 D231 D232 I233 L234 K235 V240 F243 H244 Q247 E248 K249 T252 E255 L264 R265 T266 S271 A272 T273 S274 A275 T276 V284 P291 A292 R293 GLY GLY ALA GLY TYR W299 L302 A316 E317 V318 ASP PRO ASP PHE GLU
GLU GLU ALA LEU GLU PHE GLN PRO SER VAL ASP PRO ASP GLN ASP ALA SER ARG SER ARG LEU ARG ASN ALA GLN GLU LYS M351 V352 Y353 S354 L355 V356 I364 E369 L370 D371 P372 THR THR LEU ARG GLY GLY ASP SER LEU V382 P383 V388 R389 L390 R391 H392 L393 A394 T395
N396 T397 H400 N403 I406 ASP K408 K417 I418 G419 L423 E428 A429 F430 A431 I432 V433 P434 V435 S436 E439 V440 R441 D442 L443 D444 N447 D448 K451 I456 A457 L460 I465 R471 S472 V473 L477 L480 V481 Y482 G487 T488 N489 S490
GLY GLN ASP VAL L495 F499 R504 E505 R506 Q507 M510 I515 L523 F527 THR ASP ALA GLY ASP GLY PRO MET LEU ARG LEU GLU GLU LEU GLY ASP GLN ARG HIS ALA P548 F549 I552 A553 R554 L555 V559 Q564 Y567 R568 K569 I574 M581 Q582
K583 Q584 I585 GLY TYR ASP VAL LEU ALA GLU ASP THR ILE THR ALA LEU LEU HIS ASN ASN ARG LYS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	189.17Å 78.72Å 134.11Å 90.00° 124.49° 90.00°	Depositor
Resolution (Å)	50.00 – 3.60 44.42 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.00-3.60) 99.6 (44.42-3.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.90 (at 3.57Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.258 , 0.308 0.247 , 0.306	Depositor DCC
R_{free} test set	981 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å^2)	110.6	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 91.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	7779	wwPDB-VP
Average B, all atoms (Å^2)	133.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.80% 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: I3P

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	0.48	2/3920 (0.1%)	0.57	0/5309
1	B	0.48	2/3943 (0.1%)	0.57	0/5336
All	All	0.48	4/7863 (0.1%)	0.57	0/10645

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	73	TRP	CD2-CE2	5.18	1.47	1.41
1	A	73	TRP	CD2-CE2	5.15	1.47	1.41
1	A	226	TRP	CD2-CE2	5.05	1.47	1.41
1	B	226	TRP	CD2-CE2	5.03	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3850	0	3728	89	0
1	B	3872	0	3766	81	0
2	A	24	0	9	0	0
2	B	24	0	9	2	0
3	A	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	4	0	0	0	0
All	All	7779	0	7512	168	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 11.

The worst 5 of 168 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:564:GLN:HB3	1:A:574:ILE:HD12	1.53	0.90
1:B:196:SER:HB2	1:B:208:GLU:O	1.76	0.86
1:A:196:SER:HB2	1:A:208:GLU:O	1.77	0.85
1:A:49:PRO:HG2	1:A:291:PRO:HG2	1.59	0.83
1:B:171:SER:O	1:B:174:ASP:HB2	1.80	0.82

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	484/604 (80%)	420 (87%)	57 (12%)	7 (1%)	11 48
1	B	484/604 (80%)	423 (87%)	57 (12%)	4 (1%)	19 59
All	All	968/1208 (80%)	843 (87%)	114 (12%)	11 (1%)	14 53

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	550	ARG
1	A	226	TRP
1	B	226	TRP

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Mol	Chain	Res	Type
1	A	53	PHE
1	A	189	ALA

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	399/520 (77%)	358 (90%)	41 (10%)	7 34
1	B	403/520 (78%)	358 (89%)	45 (11%)	6 30
All	All	802/1040 (77%)	716 (89%)	86 (11%)	6 32

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	567	TYR
1	B	102	GLN
1	B	515	ILE
1	A	585	ILE
1	B	42	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	122	GLN
1	B	194	HIS
1	B	524	GLN
1	B	185	ASN
1	B	207	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates 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	I3P	A	1000	-	24,24,24	0.68	0	36,39,39	0.95	0
2	I3P	B	1000	-	24,24,24	0.72	0	36,39,39	0.89	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
2	I3P	A	1000	-	-	3/15/39/39	0/1/1/1
2	I3P	B	1000	-	-	4/15/39/39	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1000	I3P	C5-O5-P5-O51
2	A	1000	I3P	C5-O5-P5-O52

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Mol	Chain	Res	Type	Atoms
2	B	1000	I3P	C3-C4-O4-P4
2	B	1000	I3P	C5-C4-O4-P4
2	A	1000	I3P	C4-O4-P4-O42

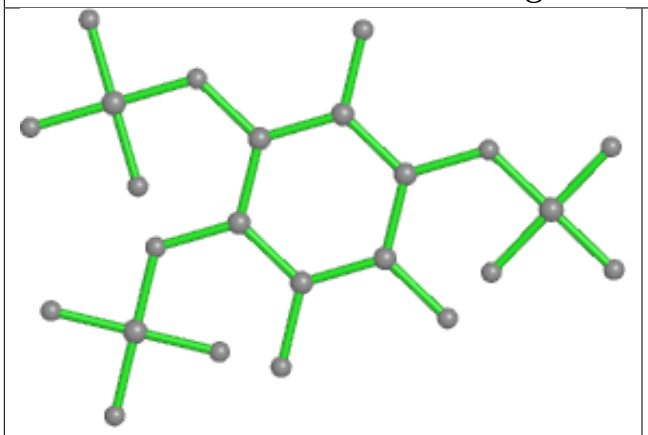
There are no ring outliers.

1 monomer is involved in 2 short contacts:

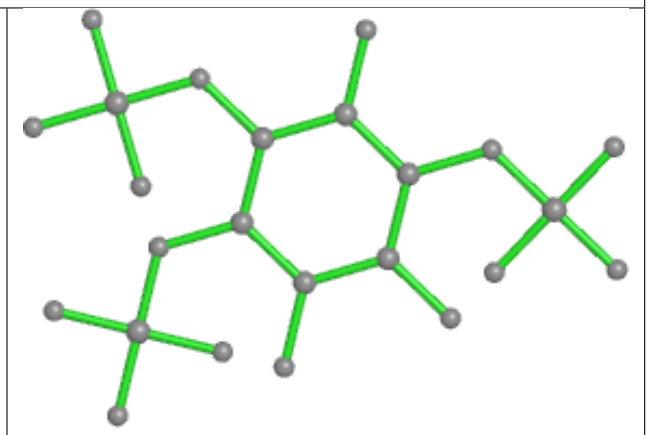
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1000	I3P	2	0

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 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.

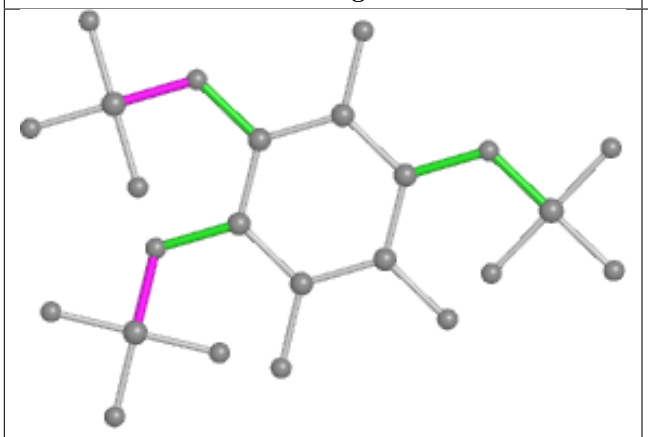
Ligand I3P A 1000



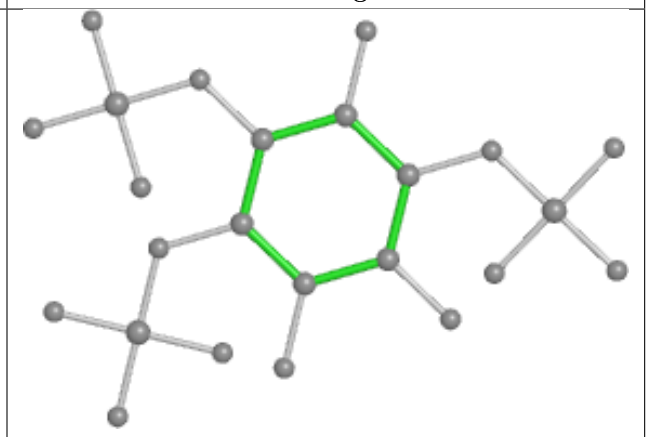
Bond lengths



Bond angles

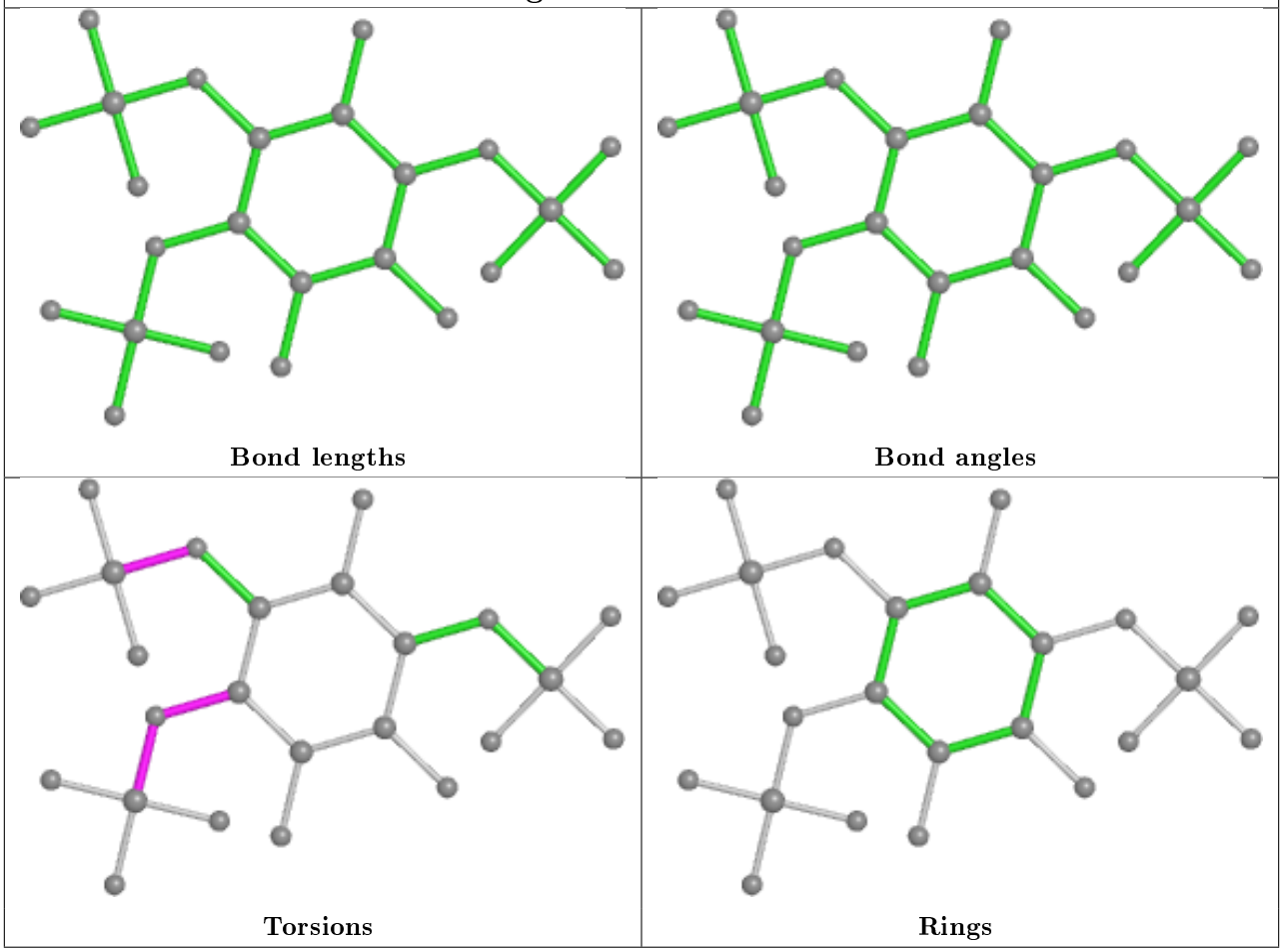


Torsions



Rings

Ligand I3P B 1000



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	502/604 (83%)	0.00	6 (1%)	79	66	80, 130, 185, 208	0
1	B	502/604 (83%)	-0.02	8 (1%)	72	57	78, 130, 182, 210	0
All	All	1004/1208 (83%)	-0.01	14 (1%)	75	61	78, 130, 184, 210	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	253	ALA	3.8
1	B	316	ALA	3.3
1	A	85	ASP	3.3
1	B	457	ALA	2.8
1	A	83	THR	2.5

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

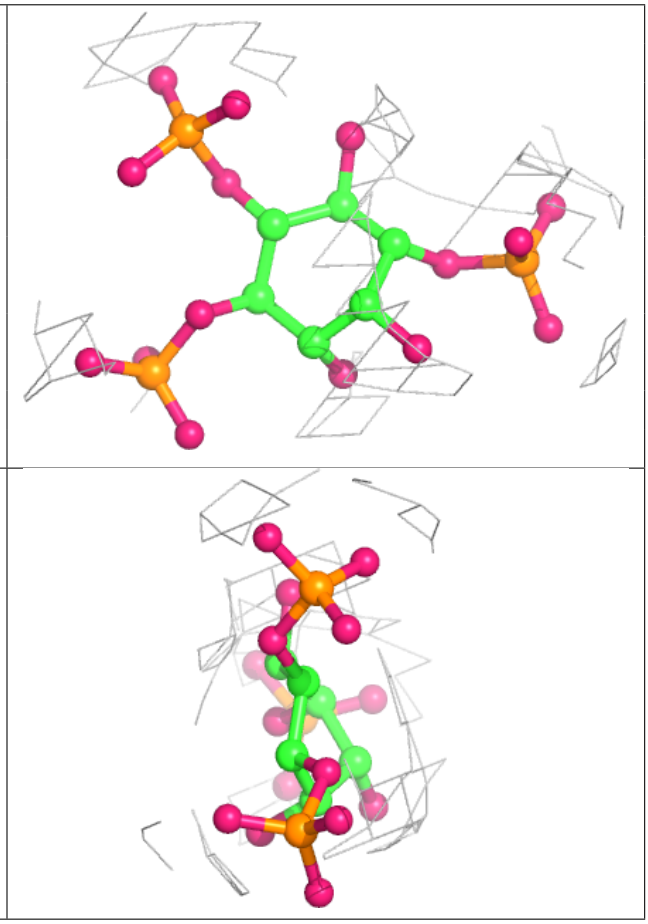
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

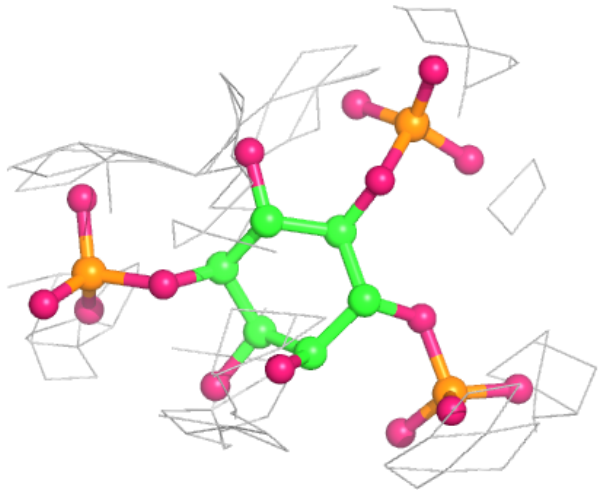
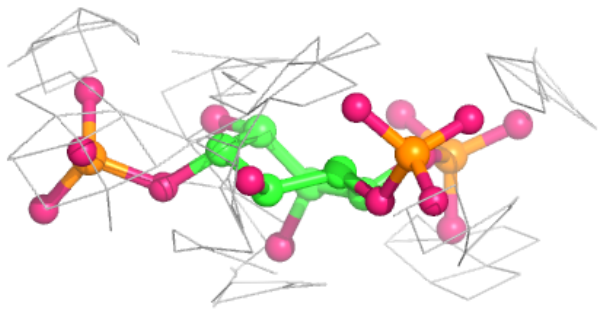
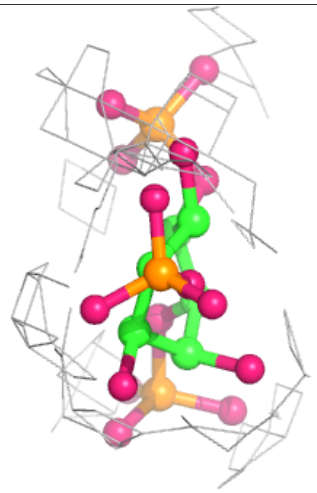
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	I3P	A	1000	24/24	0.91	0.17	136,156,165,168	0
2	I3P	B	1000	24/24	0.92	0.13	141,148,156,162	0

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 I3P A 1000:

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 I3P B 1000: 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.