wwPDB EM Validation Summary Report ⓘ

Nov 13, 2024 – 10:11 AM JST

PDB ID	:	8JRV
EMDB ID	:	EMD-36607
Title	:	Cryo-EM structure of the glucagon receptor bound to glucagon and beta-arrestin 1
Authors	:	Chen, K.; Zhang, C.; Lin, S.; Zhao, Q.; Wu, B.
Deposited on	:	2023-06-17
Resolution	:	3.30 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp
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:

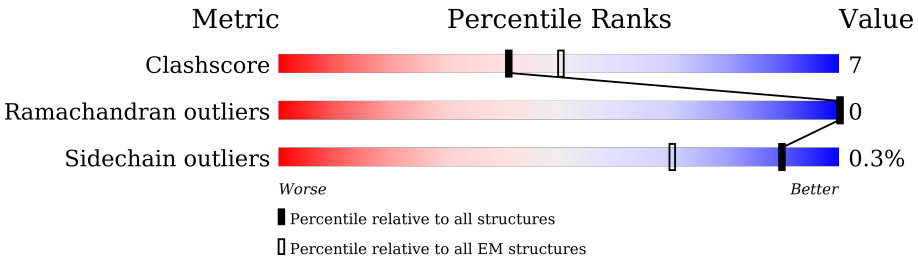
EMDB validation analysis	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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%

Mol	Chain	Length	Quality of chain
1	R	476	60% 7% 33%
2	G	29	86% 14%
3	A	627	48% 9% 43%
3	H	627	16% · 81%
3	L	627	14% · 83%
4	B	126	60% 29% · 10%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7707 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 HA signal peptide,HPC4 purification tag,Glucagon receptor,C-terminal tail of Vasopressin V2 receptor.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	319	Total	C	N	O	P	S	0	0
			2338	1525	387	412	5	9		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	2	GLY	-	linker	UNP P03435
R	3	ALA	-	linker	UNP P03435
R	4	PRO	-	linker	UNP P03435
R	17	GLY	-	linker	UNP P04070
R	18	SER	-	linker	UNP P04070
R	19	GLY	-	linker	UNP P04070
R	20	SER	-	linker	UNP P04070
R	21	ALA	-	linker	UNP P04070
R	22	GLY	-	linker	UNP P04070
R	23	SER	-	linker	UNP P04070
R	24	ALA	-	linker	UNP P04070
R	25	GLY	-	linker	UNP P04070
R	26	SER	-	linker	UNP P04070

- Molecule 2 is a protein called Glucagon.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	25	Total	C	N	O	0	0
			168	104	29	35		

- Molecule 3 is a protein called Beta-arrestin 1 and single-chain fragment variable 30 (scFv30).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	355	Total	C	N	O	S	0	0
			2632	1686	460	484	2		

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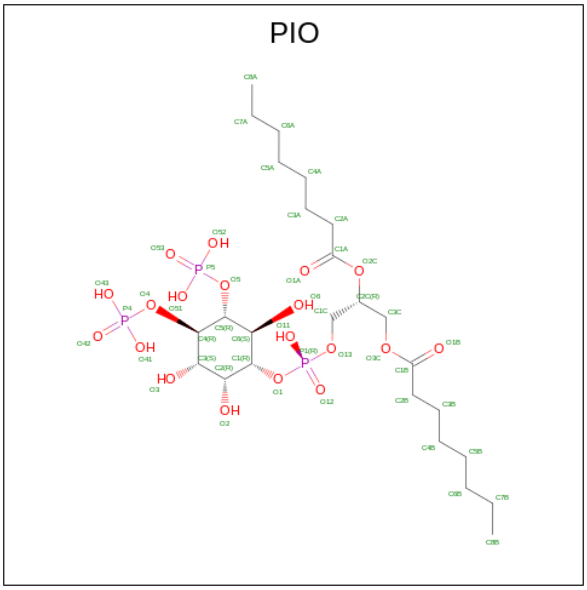
Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	117	Total	C	N	O	S	0	0
			886	569	151	163	3		
3	L	107	Total	C	N	O	S	0	0
			788	496	131	158	3		

- Molecule 4 is a protein called Nanobody 32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	113	Total	C	N	O	S	0	0
			855	535	149	167	4		

- Molecule 5 is [(2R)-2-octanoyloxy-3-[oxidanyl-[(1R,2R,3S,4R,5R,6S)-2,3,6-tris(oxidanyl)-4,5-diphosphonooxy-cyclohexyl]oxy-phosphoryl]oxy-propyl] octanoate (three-letter code: PIO) (formula: $C_{25}H_{49}O_{19}P_3$) (labeled as "Ligand of Interest" by depositor).



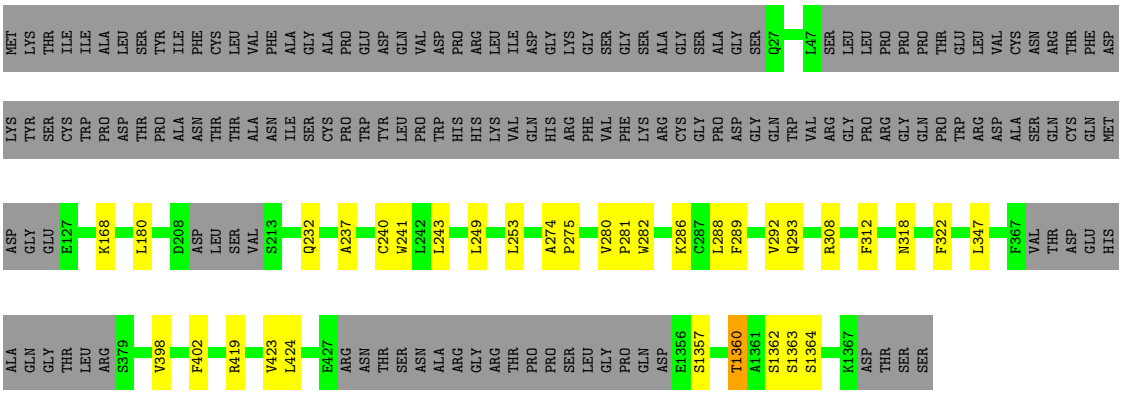
Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	O	P	0
			40	18	19	3	

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.

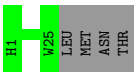
• Molecule 1: HA signal peptide,HPC4 purification tag,Glucagon receptor,C-terminal tail of Vasopressin V2 receptor

Chain R:



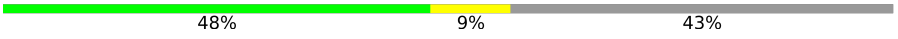
• Molecule 2: Glucagon

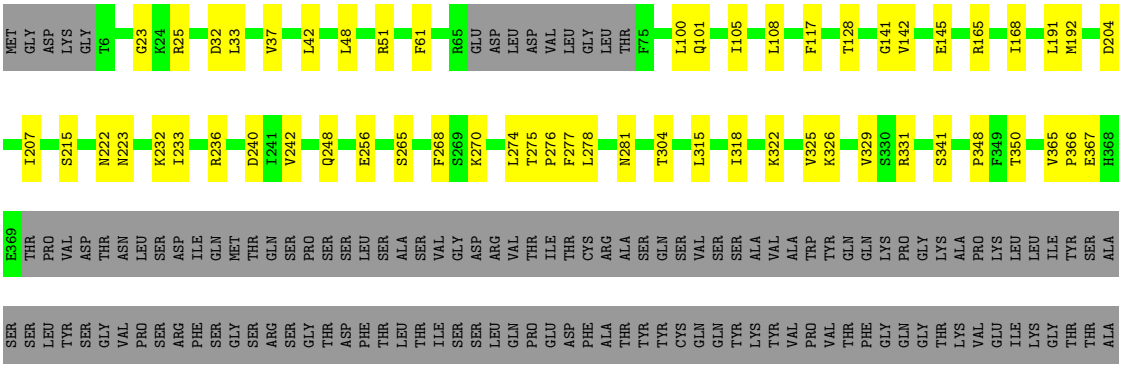
Chain G:

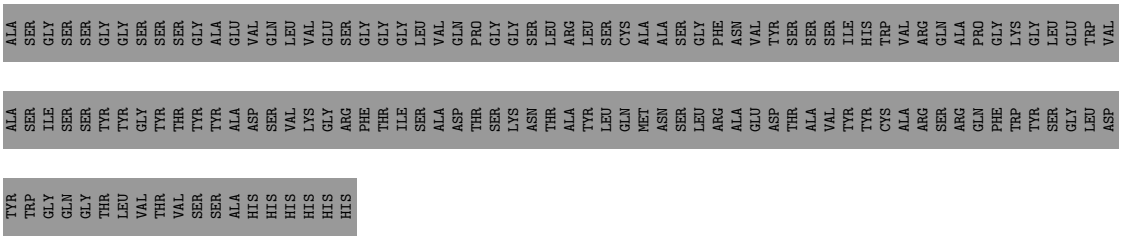


• Molecule 3: Beta-arrestin 1 and single-chain fragment variable 30 (scFv30)

Chain A:

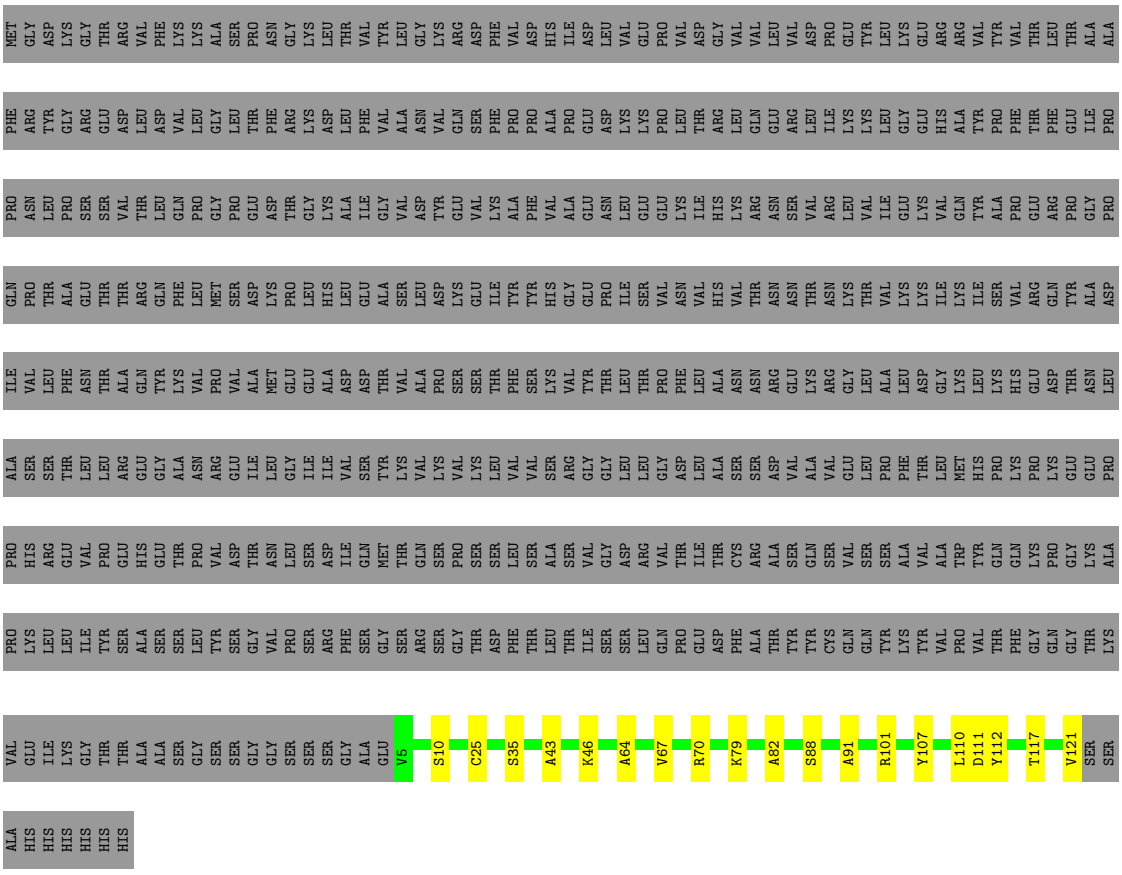






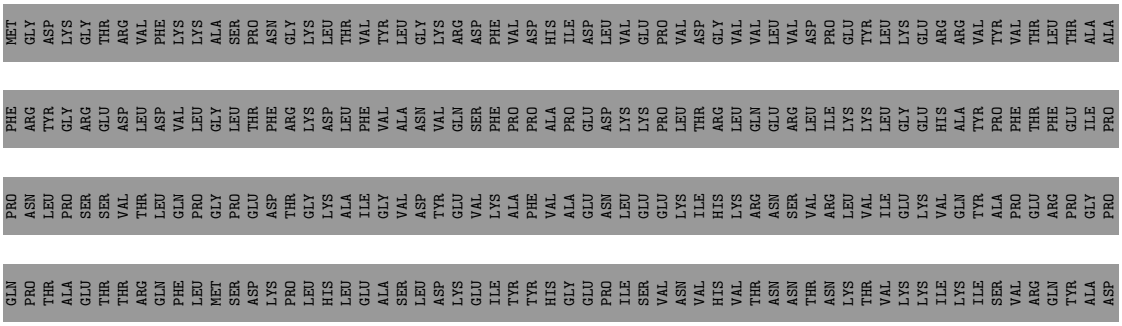
• Molecule 3: Beta-arrestin 1 and single-chain fragment variable 30 (scFv30)

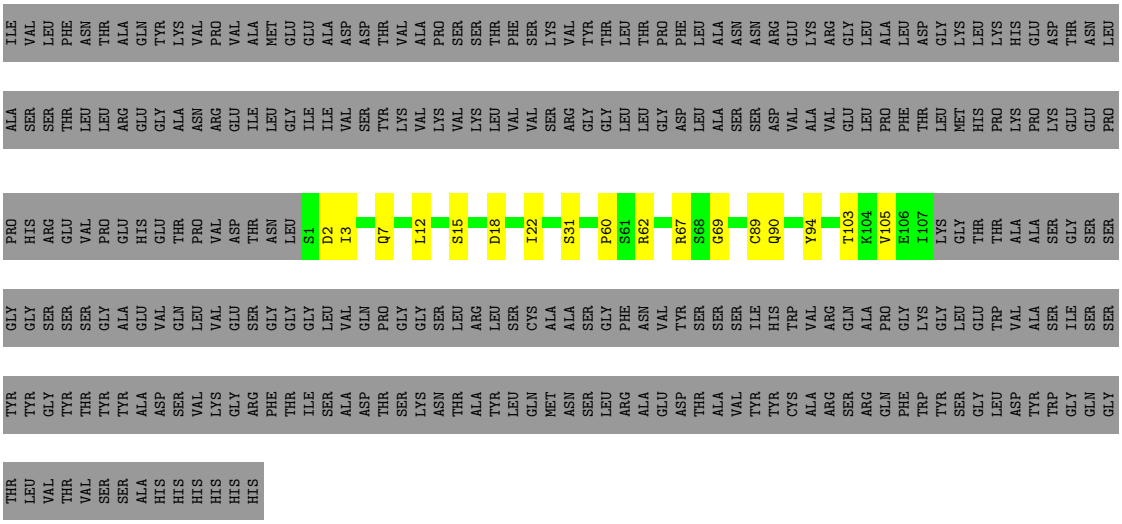
Chain H:



• Molecule 3: Beta-arrestin 1 and single-chain fragment variable 30 (scFv30)

Chain L:





• Molecule 4: Nanobody 32

Chain B:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	300738	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	70	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, PIO, TPO

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	R	0.24	0/2335	0.46	0/3189
2	G	0.23	0/171	0.33	0/233
3	A	0.25	0/2693	0.51	0/3685
3	H	0.25	0/910	0.51	0/1239
3	L	0.25	0/805	0.51	0/1098
4	B	0.26	0/871	0.55	0/1182
All	All	0.25	0/7785	0.50	0/10626

There are no bond length outliers.

There are no bond angle outliers.

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	R	2338	0	2155	19	0
2	G	168	0	125	0	0
3	A	2632	0	2529	35	0
3	H	886	0	829	12	0
3	L	788	0	749	10	0
4	B	855	0	829	28	0
5	A	40	0	24	1	0
All	All	7707	0	7240	100	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 7.

The worst 5 of 100 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)
3:A:42:LEU:HD22	3:A:108:LEU:HD12	1.70	0.74
3:H:91:ALA:HA	3:H:121:VAL:HG21	1.70	0.72
3:A:233:ILE:HB	3:A:256:GLU:HB3	1.73	0.70
4:B:82:MET:O	4:B:83:ASN:ND2	2.25	0.69
4:B:81:GLN:HE21	4:B:83:ASN:HD21	1.45	0.64

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 PDB entries followed by that with respect to all EM entries.

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	R	304/476 (64%)	285 (94%)	19 (6%)	0	100	100
2	G	23/29 (79%)	23 (100%)	0	0	100	100
3	A	351/627 (56%)	332 (95%)	19 (5%)	0	100	100
3	H	115/627 (18%)	110 (96%)	5 (4%)	0	100	100
3	L	105/627 (17%)	101 (96%)	4 (4%)	0	100	100
4	B	111/126 (88%)	105 (95%)	6 (5%)	0	100	100
All	All	1009/2512 (40%)	956 (95%)	53 (5%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM

entries.

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	R	208/403 (52%)	208 (100%)	0	100 100
2	G	13/27 (48%)	13 (100%)	0	100 100
3	A	265/538 (49%)	264 (100%)	1 (0%)	89 93
3	H	86/538 (16%)	86 (100%)	0	100 100
3	L	85/538 (16%)	85 (100%)	0	100 100
4	B	91/104 (88%)	90 (99%)	1 (1%)	70 82
All	All	748/2148 (35%)	746 (100%)	2 (0%)	90 94

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	222	ASN
4	B	109	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	219	HIS
3	A	222	ASN
4	B	83	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)

5 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	SEP	R	1362	1	8,9,10	1.54	1 (12%)	8,12,14	1.57	2 (25%)
1	SEP	R	1363	1	8,9,10	1.54	1 (12%)	8,12,14	1.66	2 (25%)
1	SEP	R	1364	1	8,9,10	1.55	1 (12%)	8,12,14	1.58	2 (25%)
1	SEP	R	1357	1	8,9,10	1.55	1 (12%)	8,12,14	1.68	2 (25%)
1	TPO	R	1360	1	8,10,11	1.67	1 (12%)	10,14,16	1.16	1 (10%)

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	SEP	R	1362	1	-	0/5/8/10	-
1	SEP	R	1363	1	-	0/5/8/10	-
1	SEP	R	1364	1	-	0/5/8/10	-
1	SEP	R	1357	1	-	0/5/8/10	-
1	TPO	R	1360	1	-	7/9/11/13	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	R	1360	TPO	P-O1P	3.43	1.61	1.50
1	R	1364	SEP	P-O1P	3.37	1.61	1.50
1	R	1357	SEP	P-O1P	3.36	1.61	1.50
1	R	1363	SEP	P-O1P	3.35	1.61	1.50
1	R	1362	SEP	P-O1P	3.35	1.61	1.50

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	R	1363	SEP	P-OG-CB	-3.17	109.56	118.30
1	R	1357	SEP	P-OG-CB	-3.08	109.80	118.30
1	R	1357	SEP	OG-CB-CA	3.08	111.14	108.14
1	R	1364	SEP	P-OG-CB	-2.94	110.21	118.30
1	R	1362	SEP	P-OG-CB	-2.92	110.26	118.30

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	R	1360	TPO	N-CA-CB-CG2
1	R	1360	TPO	N-CA-CB-OG1
1	R	1360	TPO	C-CA-CB-CG2
1	R	1360	TPO	CG2-CB-OG1-P
1	R	1360	TPO	CB-OG1-P-O3P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	R	1360	TPO	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	$\#\|Z\| > 2$
5	PIO	A	701	-	40,40,47	1.02	4 (10%)	54,58,65	1.22	5 (9%)

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
5	PIO	A	701	-	-	18/37/61/68	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	701	PIO	P5-O5	3.43	1.65	1.59
5	A	701	PIO	P4-O4	3.18	1.65	1.59
5	A	701	PIO	O3C-C1B	2.38	1.40	1.33
5	A	701	PIO	O3C-C3C	-2.08	1.40	1.45

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	701	PIO	O4-C4-C5	-5.24	96.33	108.69
5	A	701	PIO	O11-P1-O1	2.78	117.76	106.78
5	A	701	PIO	O3C-C1B-C2B	2.61	120.10	111.91
5	A	701	PIO	P1-O1-C1	-2.05	111.94	119.41
5	A	701	PIO	C5-C6-C1	-2.04	104.73	108.96

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	701	PIO	C1C-O13-P1-O12
5	A	701	PIO	C3-C4-O4-P4
5	A	701	PIO	C5-C4-O4-P4
5	A	701	PIO	C4-O4-P4-O42
5	A	701	PIO	C4-C5-O5-P5

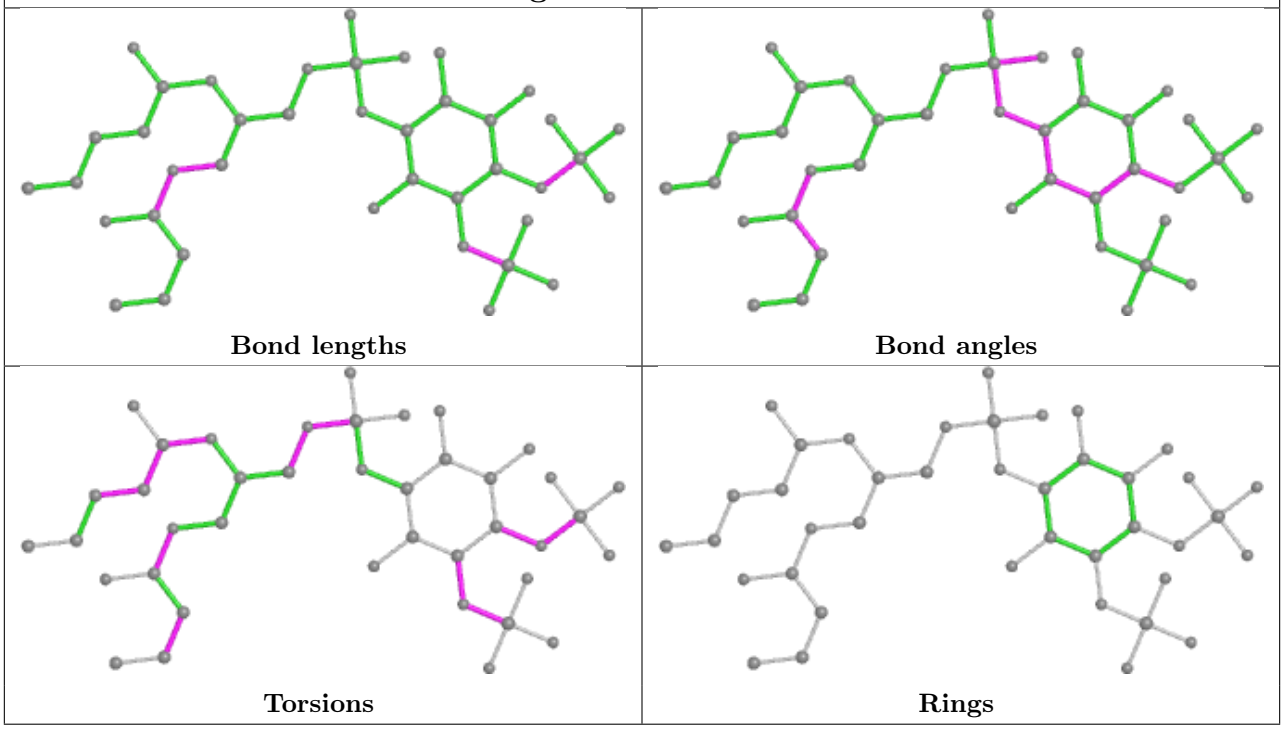
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	701	PIO	1	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 PIO A 701



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.