



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 07:11 PM BST

PDB ID : 6BCY
Title : Complex of 14-3-3 theta with an IRSp53 peptide phosphorylated at T360
Authors : Kast, D.J.; Dominguez, R.
Deposited on : 2017-10-20
Resolution : 2.30 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 : 2.13.1
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) : 2.13.1

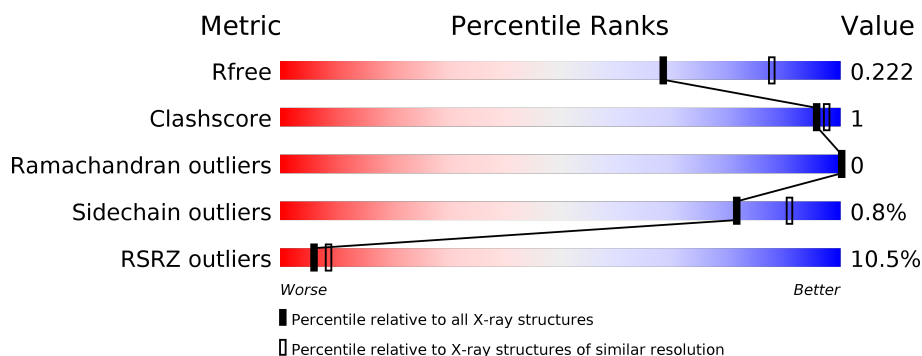
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 $\leq 5\%$. 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	245	<div> <div>11%</div> <div> <div></div> <div>92%</div> <div>6%</div> </div> </div>
1	B	245	<div> <div>6%</div> <div> <div></div> <div>89%</div> <div>6%</div> </div> </div>
1	E	245	<div> <div>10%</div> <div> <div></div> <div>92%</div> <div>6%</div> </div> </div>
1	F	245	<div> <div>10%</div> <div> <div></div> <div>89%</div> <div>6%</div> </div> </div>
2	C	13	<div> <div>15%</div> <div> <div>54%</div> <div>23%</div> <div>23%</div> </div> </div>
2	D	13	<div> <div>31%</div> <div> <div>69%</div> <div>8%</div> <div>23%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	G	13	
2	H	13	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 15870 atoms, of which 7886 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 14-3-3 protein theta.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	230	Total	C	H	N	O	S	0	5	0
			3741	1173	1870	312	375	11			
1	B	230	Total	C	H	N	O	S	0	3	0
			3722	1168	1862	310	372	10			
1	E	230	Total	C	H	N	O	S	0	3	0
			3721	1168	1859	310	374	10			
1	F	230	Total	C	H	N	O	S	0	1	0
			3698	1161	1849	308	370	10			

- Molecule 2 is a protein called Insulin receptor substrate protein of 53 kDa, peptide (IRSp53).

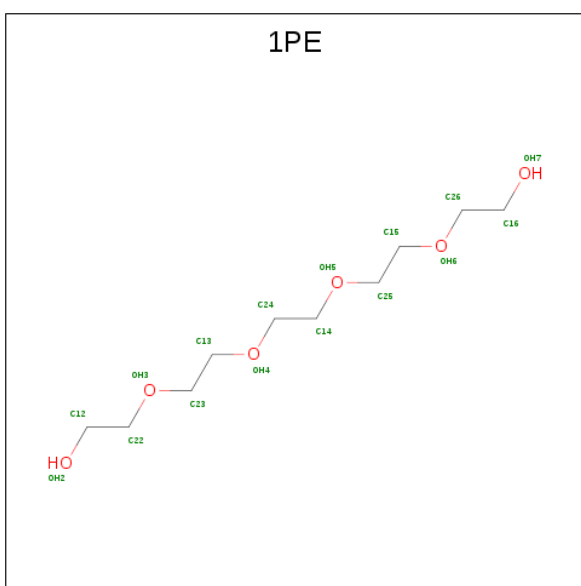
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	10	Total	C	H	N	O	P	0	0	0
			159	46	77	15	20	1			
2	D	10	Total	C	H	N	O	P	0	0	0
			159	46	77	15	20	1			
2	G	10	Total	C	H	N	O	P	0	0	0
			159	46	77	15	20	1			
2	H	9	Total	C	H	N	O	P	0	0	0
			146	42	71	14	18	1			

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



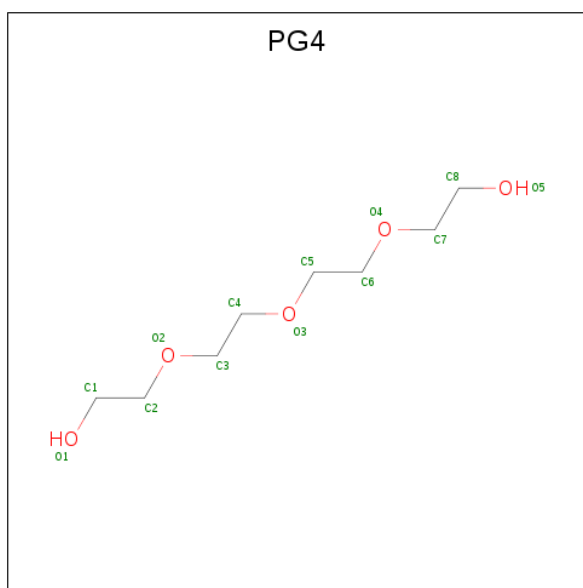
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			16	4	9	3		
3	E	1	Total	C	H	O	0	0
			16	4	9	3		

- Molecule 4 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			37	10	21	6		
4	B	1	Total	C	H	O	0	0
			37	10	21	6		

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).

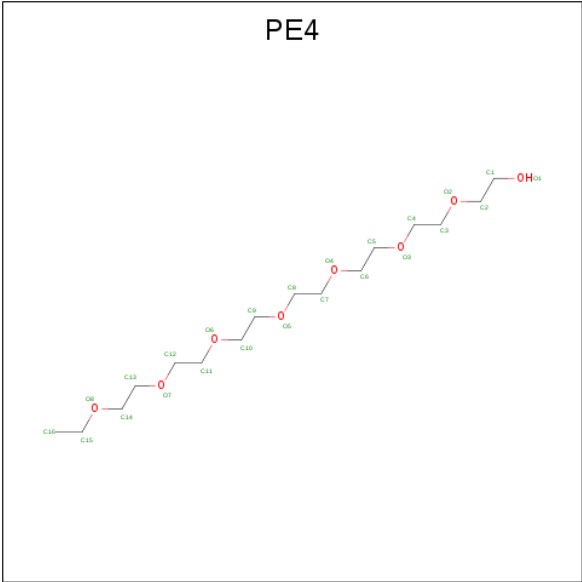


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	H	O	0	0
			30	8	17	5		
5	F	1	Total	C	H	O	0	0
			29	8	16	5		
5	F	1	Total	C	H	O	0	0
			30	8	17	5		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	1	Total	Mg	0	0
			1	1		
6	D	1	Total	Mg	0	0
			1	1		

- Molecule 7 is 2-{2-[2-(2-{2-[2-(2-ETHOXY-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHOXY]-ETHOXY}-ETHANOL (three-letter code: PE4) (formula: $C_{16}H_{34}O_8$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	E	1	Total	C	H	O	0	0
			58	16	34	8		

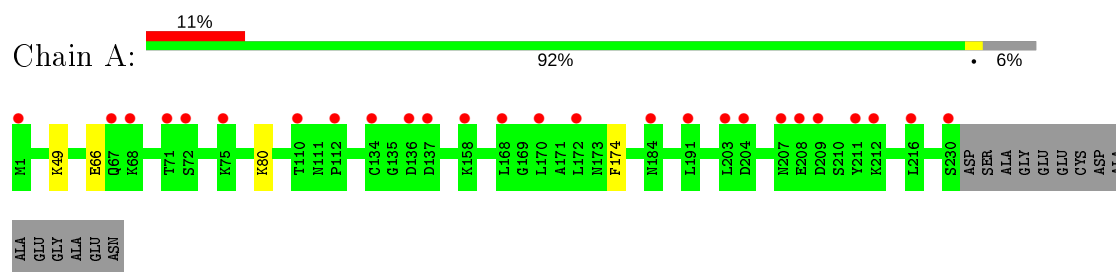
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	29	Total	O	0	0
			29	29		
8	B	38	Total	O	0	0
			38	38		
8	C	4	Total	O	0	0
			4	4		
8	D	2	Total	O	0	0
			2	2		
8	E	20	Total	O	0	0
			20	20		
8	F	14	Total	O	0	0
			14	14		
8	G	3	Total	O	0	0
			3	3		

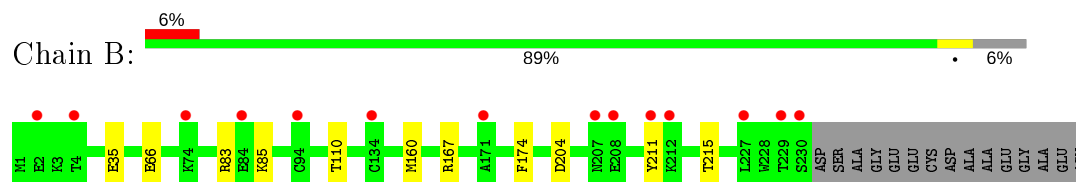
3 Residue-property plots

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 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.

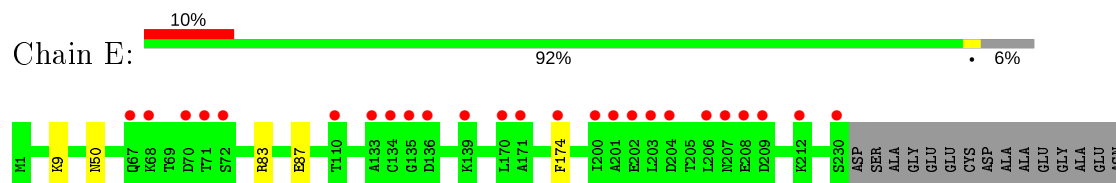
- Molecule 1: 14-3-3 protein theta



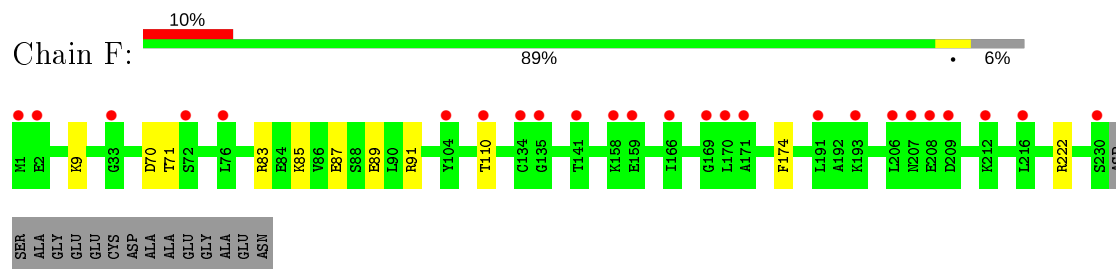
- Molecule 1: 14-3-3 protein theta



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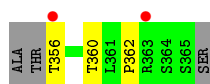


- Molecule 1: 14-3-3 protein theta

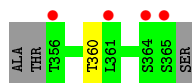


- Molecule 2: Insulin receptor substrate protein of 53 kDa, peptide (IRSp53)





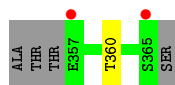
- Molecule 2: Insulin receptor substrate protein of 53 kDa, peptide (IRSp53)



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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	59.37Å 68.63Å 84.79Å 72.91° 85.59° 64.65°	Depositor
Resolution (Å)	21.85 – 2.30 29.59 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.5 (21.85-2.30) 96.6 (29.59-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.64 (at 2.31Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.192 , 0.222 0.193 , 0.222	Depositor DCC
R_{free} test set	2000 reflections (4.04%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtriage
Anisotropy	0.656	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 48.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15870	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.18% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, TPO, 1PE, PE4, PG4, PEG

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	0.24	0/1905	0.38	0/2570
1	B	0.25	0/1894	0.41	0/2555
1	E	0.24	0/1893	0.37	0/2553
1	F	0.24	0/1877	0.38	0/2531
2	C	0.22	0/70	0.42	0/91
2	D	0.23	0/70	0.41	0/91
2	G	0.23	0/70	0.51	0/91
2	H	0.26	0/63	0.35	0/81
All	All	0.24	0/7842	0.38	0/10563

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 [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	1871	1870	1870	2	0
1	B	1860	1862	1863	6	0
1	E	1862	1859	1858	4	0
1	F	1849	1849	1849	5	0
2	C	82	77	77	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	82	77	77	0	0
2	G	82	77	77	1	0
2	H	75	71	70	0	0
3	A	7	9	10	0	0
3	E	7	9	10	0	0
4	A	16	21	22	1	0
4	B	16	21	22	0	0
5	B	13	17	18	0	0
5	F	26	33	36	1	0
6	D	1	0	0	0	0
6	H	1	0	0	0	0
7	E	24	34	34	2	0
8	A	29	0	0	0	0
8	B	38	0	0	0	0
8	C	4	0	0	0	0
8	D	2	0	0	0	0
8	E	20	0	0	0	0
8	F	14	0	0	0	0
8	G	3	0	0	0	0
All	All	7984	7886	7893	17	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 1.

All (17) 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:F:83:ARG:NH1	1:F:87:GLU:OE1	2.27	0.66
1:F:87:GLU:OE2	1:F:91:ARG:NH2	2.31	0.63
1:F:70:ASP:OD1	1:F:71:THR:N	2.41	0.54
1:F:9:LYS:NZ	5:F:301:PG4:O4	2.31	0.54
1:F:85:LYS:NZ	1:F:89:GLU:OE2	2.35	0.52
1:B:35:GLU:OE2	1:B:110:THR:N	2.45	0.50
1:B:211:TYR:O	1:B:215:THR:OG1	2.23	0.48
1:E:9:LYS:NZ	7:E:301:PE4:H31	2.27	0.48
1:A:49:LYS:NZ	2:C:362:PRO:O	2.37	0.48
1:E:83:ARG:NH2	1:E:87:GLU:OE1	2.48	0.45
1:B:66:GLU:OE2	1:B:83:ARG:HD3	2.16	0.44
1:E:50:ASN:OD1	2:G:365:SER:N	2.43	0.44
4:A:301:1PE:H252	1:B:85:LYS:HG2	2.01	0.43
1:B:160:MET:O	1:B:167:ARG:NH1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:9:LYS:NZ	7:E:301:PE4:C3	2.83	0.42
1:A:66:GLU:OE2	1:A:80:LYS:HG3	2.19	0.41
1:B:204:ASP:N	1:B:204:ASP:OD1	2.53	0.41

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	233/245 (95%)	229 (98%)	4 (2%)	0	100	100
1	B	231/245 (94%)	229 (99%)	2 (1%)	0	100	100
1	E	231/245 (94%)	228 (99%)	3 (1%)	0	100	100
1	F	229/245 (94%)	225 (98%)	4 (2%)	0	100	100
2	C	7/13 (54%)	7 (100%)	0	0	100	100
2	D	7/13 (54%)	7 (100%)	0	0	100	100
2	G	7/13 (54%)	7 (100%)	0	0	100	100
2	H	6/13 (46%)	6 (100%)	0	0	100	100
All	All	951/1032 (92%)	938 (99%)	13 (1%)	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 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	208/212 (98%)	207 (100%)	1 (0%)	88	95
1	B	206/212 (97%)	205 (100%)	1 (0%)	88	95
1	E	206/212 (97%)	205 (100%)	1 (0%)	88	95
1	F	204/212 (96%)	201 (98%)	3 (2%)	65	79
2	C	9/11 (82%)	8 (89%)	1 (11%)	6	7
2	D	9/11 (82%)	9 (100%)	0	100	100
2	G	9/11 (82%)	9 (100%)	0	100	100
2	H	8/11 (73%)	8 (100%)	0	100	100
All	All	859/892 (96%)	852 (99%)	7 (1%)	81	91

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	174	PHE
1	B	174	PHE
2	C	356	THR
1	E	174	PHE
1	F	110	THR
1	F	174	PHE
1	F	222	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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
2	TPO	C	360	2	8,10,11	1.60	1 (12%)	10,14,16	1.57	1 (10%)
2	TPO	H	360	2	8,10,11	1.14	0	10,14,16	1.56	1 (10%)
2	TPO	G	360	2	8,10,11	1.11	0	10,14,16	1.49	1 (10%)
2	TPO	D	360	2,6	8,10,11	1.66	1 (12%)	10,14,16	1.51	2 (20%)

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	TPO	C	360	2	-	3/9/11/13	-
2	TPO	H	360	2	-	3/9/11/13	-
2	TPO	G	360	2	-	3/9/11/13	-
2	TPO	D	360	2,6	-	3/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	360	TPO	P-O1P	3.46	1.61	1.50
2	C	360	TPO	P-O1P	3.33	1.61	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	360	TPO	P-OG1-CB	-4.08	110.88	123.21
2	H	360	TPO	P-OG1-CB	-4.01	111.11	123.21
2	G	360	TPO	P-OG1-CB	-3.68	112.08	123.21
2	D	360	TPO	P-OG1-CB	-3.61	112.31	123.21
2	D	360	TPO	CG2-CB-CA	-2.16	108.91	113.16

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	360	TPO	O-C-CA-CB
2	C	360	TPO	CB-OG1-P-O2P
2	C	360	TPO	CB-OG1-P-O3P
2	D	360	TPO	CB-OG1-P-O3P

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Mol	Chain	Res	Type	Atoms
2	H	360	TPO	CB-OG1-P-O1P
2	G	360	TPO	CB-OG1-P-O1P
2	H	360	TPO	CB-OG1-P-O2P
2	G	360	TPO	CB-OG1-P-O2P
2	D	360	TPO	CB-OG1-P-O2P
2	H	360	TPO	O-C-CA-CB
2	G	360	TPO	O-C-CA-CB
2	D	360	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

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	PG4	F	302	-	12,12,12	0.68	0	11,11,11	0.33	0
3	PEG	A	300	-	6,6,6	0.51	0	5,5,5	0.29	0
5	PG4	B	302	-	12,12,12	0.66	0	11,11,11	0.26	0
4	1PE	A	301	-	15,15,15	0.68	0	14,14,14	0.26	0
5	PG4	F	301	-	12,12,12	0.68	0	11,11,11	0.19	0
4	1PE	B	301	-	15,15,15	0.65	0	14,14,14	0.23	0
7	PE4	E	301	-	23,23,23	0.79	0	22,22,22	0.34	0
3	PEG	E	300	-	6,6,6	0.51	0	5,5,5	0.25	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
5	PG4	F	302	-	-	6/10/10/10	-
3	PEG	A	300	-	-	1/4/4/4	-
5	PG4	B	302	-	-	6/10/10/10	-
4	1PE	A	301	-	-	5/13/13/13	-
5	PG4	F	301	-	-	2/10/10/10	-
4	1PE	B	301	-	-	5/13/13/13	-
7	PE4	E	301	-	-	10/21/21/21	-
3	PEG	E	300	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	302	PG4	O1-C1-C2-O2
7	E	301	PE4	O7-C13-C14-O8
7	E	301	PE4	O4-C7-C8-O5
7	E	301	PE4	O6-C10-C9-O5
5	B	302	PG4	O3-C5-C6-O4
5	B	302	PG4	O1-C1-C2-O2
3	E	300	PEG	O1-C1-C2-O2
4	A	301	1PE	OH2-C12-C22-OH3
4	B	301	1PE	OH5-C14-C24-OH4
5	B	302	PG4	O4-C7-C8-O5
5	F	302	PG4	O2-C3-C4-O3
4	B	301	1PE	OH7-C16-C26-OH6
3	E	300	PEG	O2-C3-C4-O4
5	F	302	PG4	C8-C7-O4-C6
5	F	302	PG4	C5-C6-O4-C7
4	A	301	1PE	C25-C15-OH6-C26
5	B	302	PG4	O2-C3-C4-O3
7	E	301	PE4	O6-C11-C12-O7
3	A	300	PEG	C1-C2-O2-C3
7	E	301	PE4	C3-C4-O3-C5
5	B	302	PG4	C1-C2-O2-C3
7	E	301	PE4	C10-C9-O5-C8
4	B	301	1PE	C15-C25-OH5-C14

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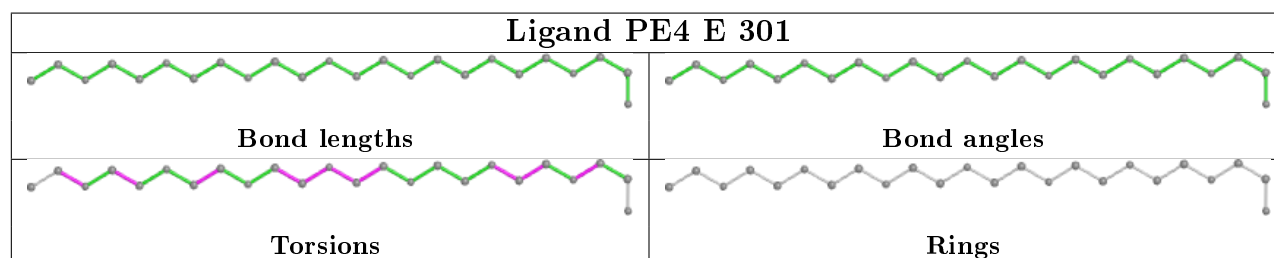
Mol	Chain	Res	Type	Atoms
7	E	301	PE4	C7-C8-O5-C9
5	F	302	PG4	O4-C7-C8-O5
4	B	301	1PE	C16-C26-OH6-C15
4	A	301	1PE	C15-C25-OH5-C14
5	F	301	PG4	C8-C7-O4-C6
4	B	301	1PE	C23-C13-OH4-C24
4	A	301	1PE	C14-C24-OH4-C13
7	E	301	PE4	C16-C15-O8-C14
5	F	301	PG4	O1-C1-C2-O2
5	B	302	PG4	C5-C6-O4-C7
4	A	301	1PE	OH4-C13-C23-OH3
5	F	302	PG4	C1-C2-O2-C3
7	E	301	PE4	C1-C2-O2-C3
7	E	301	PE4	O2-C3-C4-O3

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	301	1PE	1	0
5	F	301	PG4	1	0
7	E	301	PE4	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 ⓘ

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	230/245 (93%)	0.64	26 (11%) 5 7	27, 47, 83, 122	0
1	B	230/245 (93%)	0.41	14 (6%) 21 27	23, 42, 75, 123	0
1	E	230/245 (93%)	0.72	25 (10%) 5 8	28, 54, 100, 130	0
1	F	230/245 (93%)	0.66	25 (10%) 5 8	31, 56, 93, 141	0
2	C	9/13 (69%)	1.33	2 (22%) 0 1	47, 52, 83, 92	0
2	D	9/13 (69%)	2.17	4 (44%) 0 0	48, 57, 85, 86	0
2	G	9/13 (69%)	1.66	2 (22%) 0 1	49, 59, 82, 105	0
2	H	8/13 (61%)	1.10	2 (25%) 0 0	58, 68, 89, 93	0
All	All	955/1032 (92%)	0.64	100 (10%) 6 8	23, 50, 91, 141	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	203	LEU	6.7
1	E	201	ALA	5.5
2	G	356	THR	5.3
2	D	356	THR	5.3
1	A	230	SER	5.1
1	E	71	THR	5.0
1	A	209	ASP	4.7
1	E	206	LEU	4.7
1	E	134	CYS	4.6
1	E	136	ASP	4.6
2	C	356	THR	4.3
1	E	208	GLU	4.3
1	B	230	SER	4.3
1	B	207	ASN	4.2
1	E	204	ASP	4.1
1	E	200	ILE	4.1

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Mol	Chain	Res	Type	RSRZ
1	F	110	THR	4.1
2	D	365	SER	4.0
1	A	1	MET	3.8
1	E	70	ASP	3.7
1	A	204	ASP	3.7
1	A	134[A]	CYS	3.7
1	E	209	ASP	3.6
1	A	208	GLU	3.5
1	A	72	SER	3.5
1	A	216	LEU	3.4
1	A	67	GLN	3.4
1	A	207	ASN	3.4
1	F	207	ASN	3.4
1	E	72	SER	3.4
1	A	112	PRO	3.4
1	E	230	SER	3.3
1	F	72	SER	3.3
1	E	212	LYS	3.3
1	A	212	LYS	3.2
1	B	212	LYS	3.1
1	B	208	GLU	3.0
1	B	229	THR	3.0
1	B	74	LYS	2.9
1	E	207	ASN	2.9
1	F	230	SER	2.9
1	F	158	LYS	2.8
1	F	209	ASP	2.7
1	F	33	GLY	2.7
1	E	170	LEU	2.7
1	F	169	GLY	2.7
1	A	191	LEU	2.7
1	B	211	TYR	2.7
1	A	184[A]	ASN	2.7
2	D	361	LEU	2.7
1	F	159	GLU	2.6
1	F	166	ILE	2.6
1	F	208	GLU	2.6
1	B	134	CYS	2.5
1	E	110	THR	2.5
1	F	134	CYS	2.5
1	F	135	GLY	2.5
1	E	67	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	172	LEU	2.5
2	H	365	SER	2.4
1	A	68	LYS	2.4
1	A	71	THR	2.4
1	B	2	GLU	2.4
2	C	363	ARG	2.4
1	A	75	LYS	2.4
1	F	212	LYS	2.4
1	F	191	LEU	2.4
1	F	216	LEU	2.4
1	F	2	GLU	2.3
1	A	168	LEU	2.3
1	E	133	ALA	2.3
1	A	136	ASP	2.3
2	G	364	SER	2.3
1	B	94	CYS	2.3
1	A	203	LEU	2.3
1	F	206	LEU	2.3
1	E	174	PHE	2.3
1	F	76	LEU	2.2
1	F	104	TYR	2.2
1	F	171	ALA	2.2
1	A	137	ASP	2.2
1	E	68	LYS	2.2
2	D	364	SER	2.2
1	E	171	ALA	2.1
1	F	141	THR	2.1
1	E	135	GLY	2.1
1	A	110	THR	2.1
1	B	84	GLU	2.1
1	B	4	THR	2.1
1	A	170	LEU	2.1
1	A	158	LYS	2.1
1	F	1	MET	2.1
1	E	139	LYS	2.1
1	E	202	GLU	2.0
1	F	193	LYS	2.0
1	A	211	TYR	2.0
2	H	357	GLU	2.0
1	B	227	LEU	2.0
1	F	170	LEU	2.0
1	B	171	ALA	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(Å ²)	Q<0.9
2	TPO	H	360	11/12	0.97	0.16	43,45,53,54	0
2	TPO	G	360	11/12	0.97	0.16	41,44,51,53	0
2	TPO	D	360	11/12	0.97	0.19	31,37,41,41	0
2	TPO	C	360	11/12	0.98	0.18	36,39,45,48	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

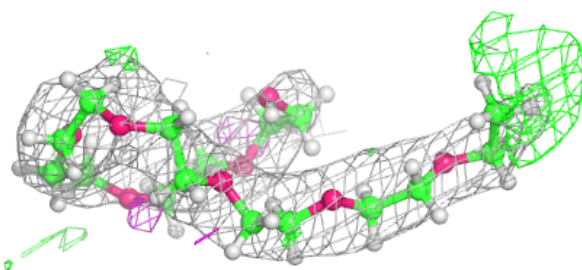
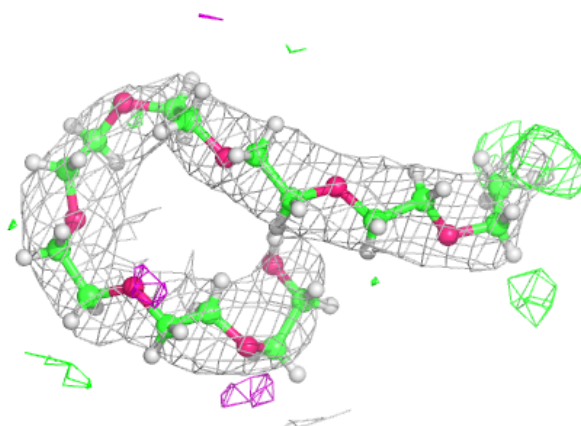
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	1PE	A	301	16/16	0.77	0.31	49,71,87,88	0
7	PE4	E	301	24/24	0.83	0.24	51,75,91,93	0
5	PG4	F	301	13/13	0.86	0.23	54,65,74,74	0
5	PG4	F	302	13/13	0.86	0.21	43,58,70,72	0
4	1PE	B	301	16/16	0.87	0.21	53,65,78,79	0
3	PEG	A	300	7/7	0.89	0.16	49,59,71,71	0
5	PG4	B	302	13/13	0.89	0.14	43,58,70,72	0
3	PEG	E	300	7/7	0.91	0.14	49,60,74,76	0
6	MG	D	401	1/1	0.92	0.18	57,57,57,57	0
6	MG	H	401	1/1	0.92	0.16	58,58,58,58	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 PE4 E 301:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.