wwPDB X-ray Structure Validation Summary Report (i)

Dec 7, 2023 – 11:27 pm GMT

PDB ID	:	2IW8
Title	:	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2-CYCLIN A F82H-L83V-H84D MUTANT WITH AN O6-CYCLOHEXYLMETHYLGUANINE INHIBITOR
Authors	:	Pratt, D.J.; Bentley, J.; Jewsbury, P.; Boyle, F.T.; Endicott, J.A.; Noble, M.E.M.
Deposited on	:	2006-06-27
Resolution	:	2.30 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

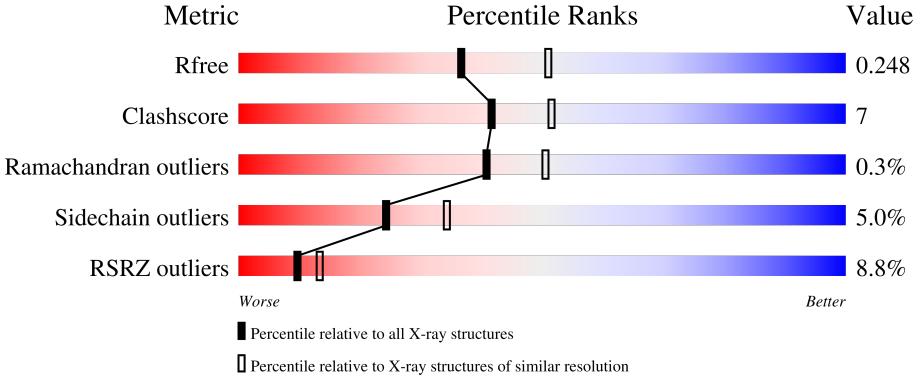
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 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 of 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	302	3% 81% 15% • •
1	C	302	11% 71% 16% • 12%
2	B	260	3% 85% 11% • •
2	D	260	17% 82% 15% • •

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9027 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 CELL DIVISION PROTEIN KINASE 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	298	2399	1552	409	429	1	8	0	1	0
1	C	266	2130	1377	364	381	1	7	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P24941
A	-2	PRO	-	expression tag	UNP P24941
A	-1	GLY	-	expression tag	UNP P24941
A	0	SER	-	expression tag	UNP P24941
A	82	HIS	PHE	engineered mutation	UNP P24941
A	83	VAL	LEU	engineered mutation	UNP P24941
A	84	ASP	HIS	engineered mutation	UNP P24941
C	-3	GLY	-	expression tag	UNP P24941
C	-2	PRO	-	expression tag	UNP P24941
C	-1	GLY	-	expression tag	UNP P24941
C	0	SER	-	expression tag	UNP P24941
C	82	HIS	PHE	engineered mutation	UNP P24941
C	83	VAL	LEU	engineered mutation	UNP P24941
C	84	ASP	HIS	engineered mutation	UNP P24941

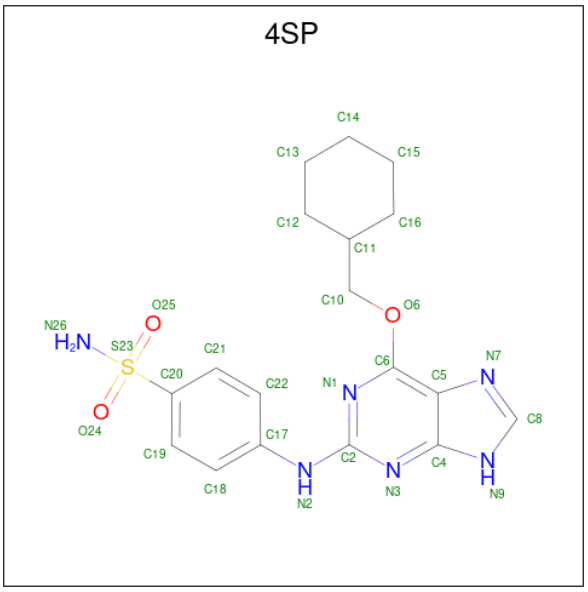
- Molecule 2 is a protein called CYCLIN-A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	255	2060	1337	336	376	11	0	0	0
2	D	255	2061	1336	336	378	11	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

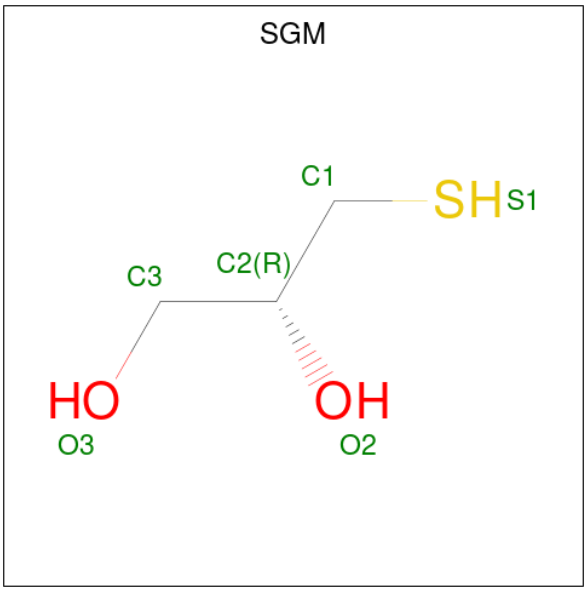
Chain	Residue	Modelled	Actual	Comment	Reference
B	173	MET	-	expression tag	UNP P20248
D	173	MET	-	expression tag	UNP P20248

- Molecule 3 is O6-CYCLOHEXYLMETHOXY-2-(4'-SULPHAMOYLANILINO) PURINE (three-letter code: 4SP) (formula: $C_{18}H_{22}N_6O_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	28	18	6	3	1	0	0
			Total	C	N	O	S		
3	C	1	28	18	6	3	1	0	0

- Molecule 4 is MONOTHIOGLYCEROL (three-letter code: SGM) (formula: $C_3H_8O_2S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
4	B	1	6	3	2	1	0	0
			Total	C	O	S		
4	D	1	6	3	2	1	0	0

- Molecule 5 is water.

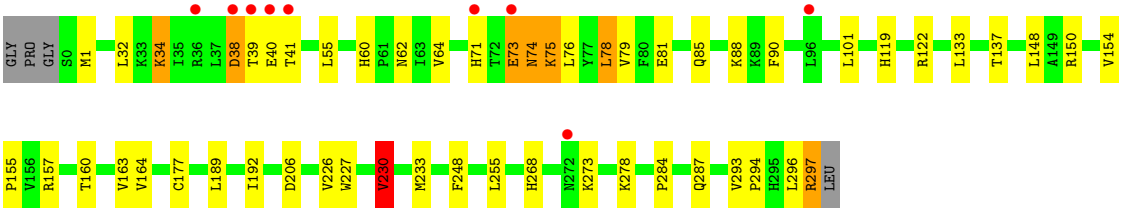
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	124	124	124	0	0
			Total	O		
5	B	96	96	96	0	0
			Total	O		
5	C	54	54	54	0	0
			Total	O		
5	D	35	35	35	0	0

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 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.

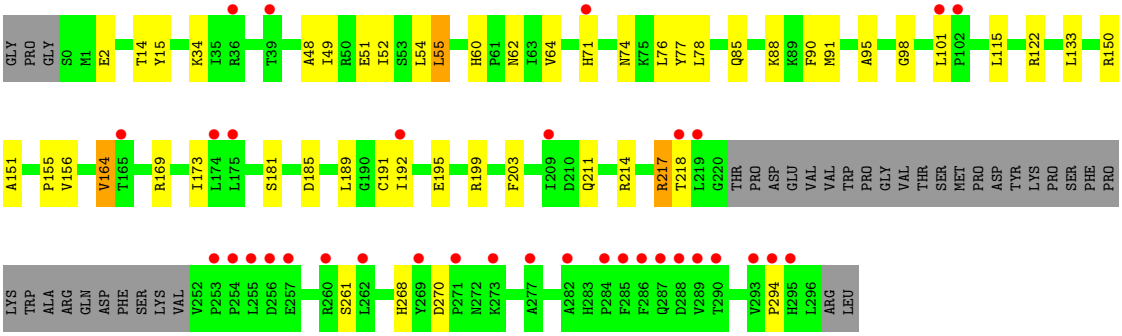
• Molecule 1: CELL DIVISION PROTEIN KINASE 2

Chain A:



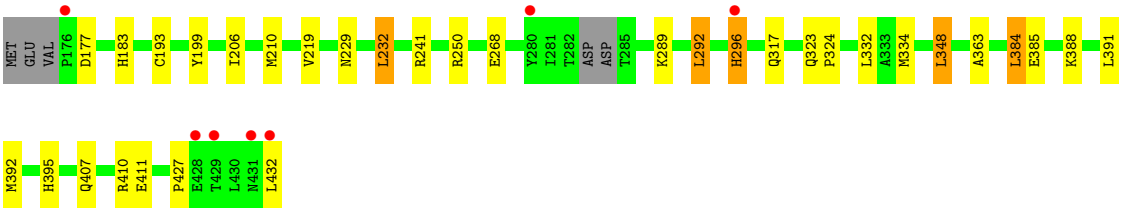
• Molecule 1: CELL DIVISION PROTEIN KINASE 2

Chain C:



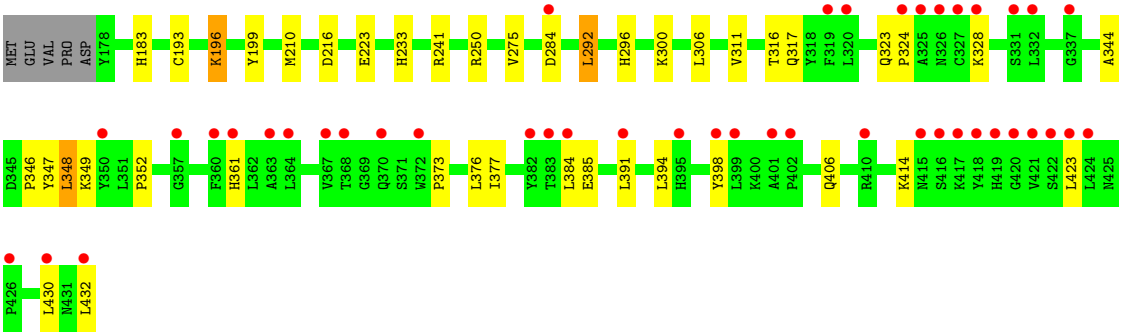
• Molecule 2: CYCLIN-A2

Chain B:



• Molecule 2: CYCLIN-A2

Chain D:


MET
GLU
VAL
PRO
ASP
Y178
H183
C193
K196
Y199
M210
D216
E223
H233
R241
R250
V275
D284
L292
H296
K300
L306
V311
T316
Q317
Y318
F319
L320
Q323
P324
A325
N326
C327
K328
S331
L332
G337
A344
D345
P346
Y347
L348
K349
Y350
L351
P352
G357
F360
H361
L362
A363
L364
V367
T368
G369
Q370
S371
W372
P373
L376
I377
Y382
T383
L384
E385
L391
L394
H395
Y398
L399
K400
A401
P402
Q406
R410
K414
M415
S416
K417
Y418
H419
G420
V421
S422
L423
L424
M425
P426
L430
M431
L432

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	73.89Å 135.32Å 148.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.30 48.82 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.5 (100.00-2.30) 96.6 (48.82-2.30)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.47 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.212 , 0.255 0.208 , 0.248	Depositor DCC
R_{free} test set	3271 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	28.6	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 44.5	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	0.93	EDS
Total number of atoms	9027	wwPDB-VP
Average B, all atoms (Å^2)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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: 4SP, SGM, 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	A	0.70	0/2452	0.74	2/3327 (0.1%)
1	C	0.55	0/2166	0.63	0/2933
2	B	0.62	0/2109	0.70	0/2861
2	D	0.50	0/2110	0.64	1/2864 (0.0%)
All	All	0.60	0/8837	0.68	3/11985 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	230	VAL	CB-CA-C	-5.61	100.74	111.40
1	A	297	ARG	NE-CZ-NH2	-5.16	117.72	120.30
2	D	241	ARG	NE-CZ-NH2	-5.04	117.78	120.30

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	2399	0	2438	42	0
1	C	2130	0	2180	36	0
2	B	2060	0	2089	28	0
2	D	2061	0	2087	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	28	0	22	1	0
3	C	28	0	22	3	0
4	B	6	0	7	0	0
4	D	6	0	8	1	0
5	A	124	0	0	3	0
5	B	96	0	0	4	0
5	C	54	0	0	3	0
5	D	35	0	0	1	0
All	All	9027	0	8853	123	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 123 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:C:155:PRO:HD2	2:D:316:THR:HG22	1.38	1.04
1:A:296:LEU:O	1:A:297:ARG:HB2	1.77	0.83
1:A:137:THR:O	1:A:293:VAL:HG13	1.77	0.83
1:A:284:PRO:O	1:A:287:GLN:HG2	1.79	0.82
1:A:268:HIS:CD2	5:A:2094:HOH:O	2.34	0.81

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	296/302 (98%)	286 (97%)	8 (3%)	2 (1%)	22 26
1	C	261/302 (86%)	245 (94%)	15 (6%)	1 (0%)	34 42
2	B	251/260 (96%)	249 (99%)	2 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	253/260 (97%)	248 (98%)	5 (2%)	0	100	100
All	All	1061/1124 (94%)	1028 (97%)	30 (3%)	3 (0%)	41	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	38	ASP
1	A	164	VAL
1	C	164	VAL

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	263/264 (100%)	242 (92%)	21 (8%)	12	15
1	C	232/264 (88%)	222 (96%)	10 (4%)	29	40
2	B	229/234 (98%)	221 (96%)	8 (4%)	36	50
2	D	229/234 (98%)	220 (96%)	9 (4%)	32	46
All	All	953/996 (96%)	905 (95%)	48 (5%)	24	34

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	391	LEU
1	C	150	ARG
1	C	2	GLU
1	C	74	ASN
1	C	217	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	62	ASN

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Mol	Chain	Res	Type
1	C	268	HIS
1	C	119	HIS
2	D	233	HIS
2	B	179	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 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	TPO	A	160	1	8,10,11	0.88	0	10,14,16	1.19	1 (10%)
1	TPO	C	160	1	8,10,11	0.98	0	10,14,16	0.86	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
1	TPO	A	160	1	-	0/9/11/13	-
1	TPO	C	160	1	-	0/9/11/13	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	160	TPO	O-C-CA	-2.01	119.50	124.78

There are no chirality outliers.

There are no torsion outliers.

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)

4 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	4SP	A	1298	-	28,31,31	2.15	5 (17%)	35,44,44	2.12	10 (28%)
4	SGM	B	1433	-	5,5,5	0.62	0	5,5,5	0.58	0
3	4SP	C	1297	-	28,31,31	1.95	4 (14%)	35,44,44	2.07	6 (17%)
4	SGM	D	1433	-	5,5,5	0.34	0	5,5,5	0.53	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
3	4SP	A	1298	-	-	4/15/23/23	0/4/4/4
4	SGM	B	1433	-	-	1/4/4/4	-
3	4SP	C	1297	-	-	4/15/23/23	0/4/4/4
4	SGM	D	1433	-	-	2/4/4/4	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1298	4SP	C20-S23	-8.88	1.63	1.77
3	C	1297	4SP	C20-S23	-7.88	1.64	1.77
3	A	1298	4SP	S23-N26	-4.08	1.52	1.60
3	C	1297	4SP	S23-N26	-3.33	1.53	1.60
3	A	1298	4SP	O24-S23	2.67	1.48	1.43

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1298	4SP	O25-S23-O24	-6.23	108.52	118.76
3	C	1297	4SP	O25-S23-O24	-6.17	108.61	118.76
3	C	1297	4SP	C2-N3-C4	5.09	121.06	115.28
3	C	1297	4SP	N3-C2-N1	-4.42	119.24	126.23
3	A	1298	4SP	C2-N1-C6	4.31	122.79	115.18

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1433	SGM	C1-C2-C3-O3
4	D	1433	SGM	O2-C2-C3-O3
3	A	1298	4SP	C19-C20-S23-O24
3	A	1298	4SP	C21-C20-S23-O24
3	C	1297	4SP	C21-C20-S23-O24

There are no ring outliers.

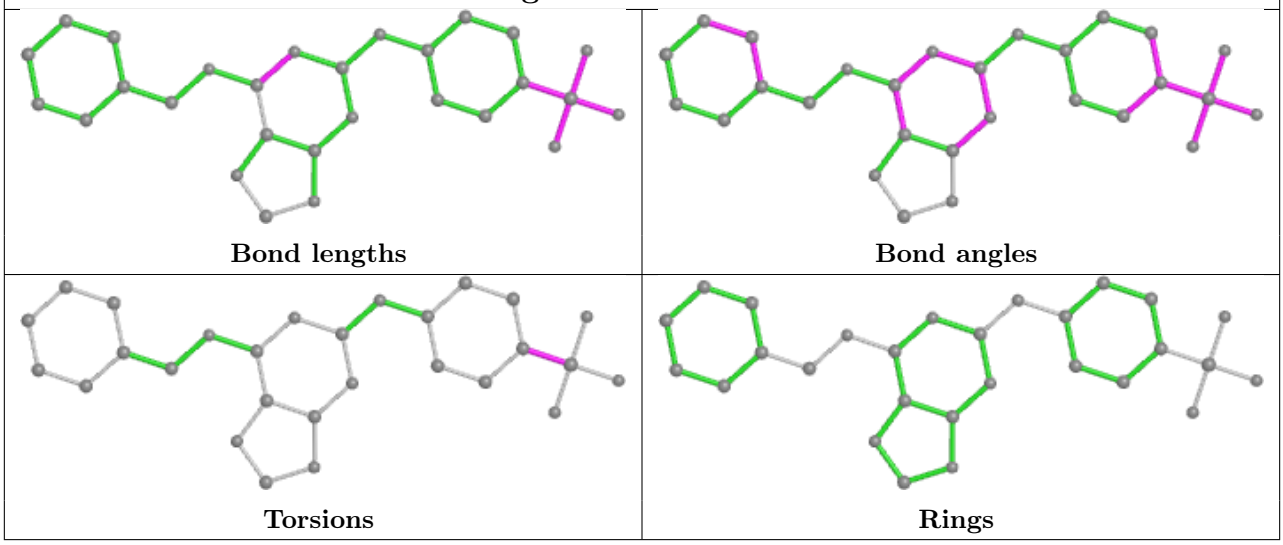
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1298	4SP	1	0
3	C	1297	4SP	3	0
4	D	1433	SGM	1	0

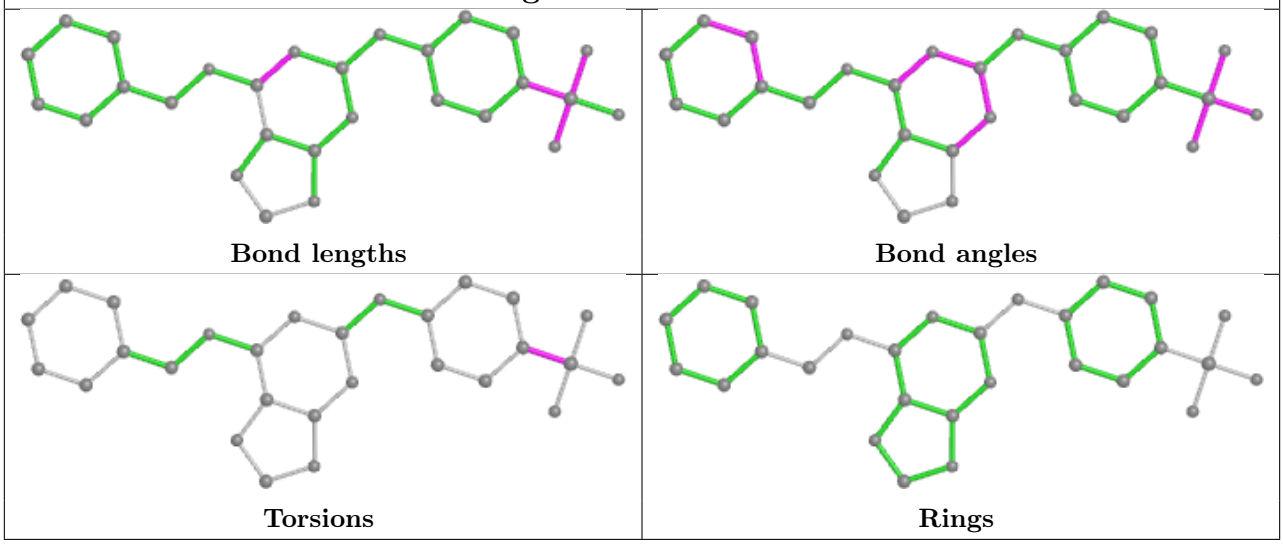
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 4SP A 1298



Ligand 4SP C 1297



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	297/302 (98%)	0.13	9 (3%) 50 57	5, 11, 28, 34	1 (0%)
1	C	265/302 (87%)	0.67	34 (12%) 3 5	4, 12, 26, 33	0
2	B	255/260 (98%)	0.09	7 (2%) 54 62	6, 13, 25, 44	0
2	D	255/260 (98%)	0.84	44 (17%) 1 1	7, 14, 25, 44	0
All	All	1072/1124 (95%)	0.42	94 (8%) 10 13	4, 13, 26, 44	1 (0%)

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	432	LEU	11.0
1	A	40	GLU	5.7
1	A	39	THR	5.7
2	D	423	LEU	5.4
2	D	419	HIS	5.0

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
1	TPO	C	160	11/12	0.96	0.12	7,10,13,13	0
1	TPO	A	160	11/12	0.99	0.14	7,10,11,12	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

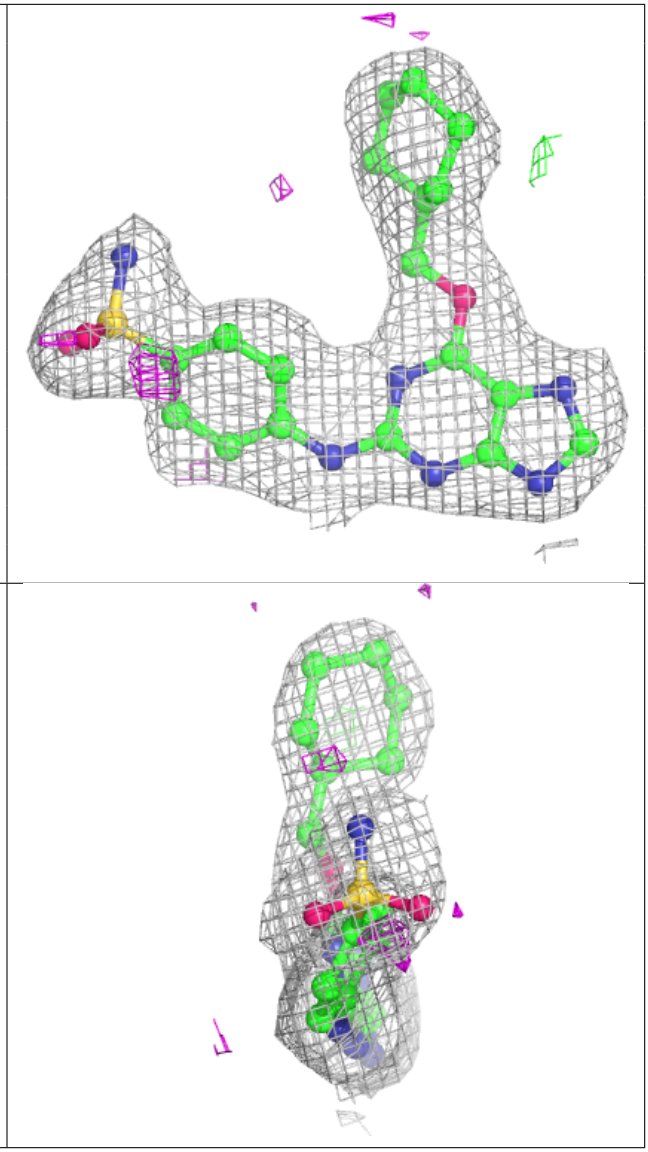
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	SGM	B	1433	6/6	0.90	0.18	28,31,32,33	0
4	SGM	D	1433	6/6	0.92	0.15	41,42,42,43	0
3	4SP	C	1297	28/28	0.94	0.14	13,15,18,19	0
3	4SP	A	1298	28/28	0.98	0.09	2,2,6,8	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.

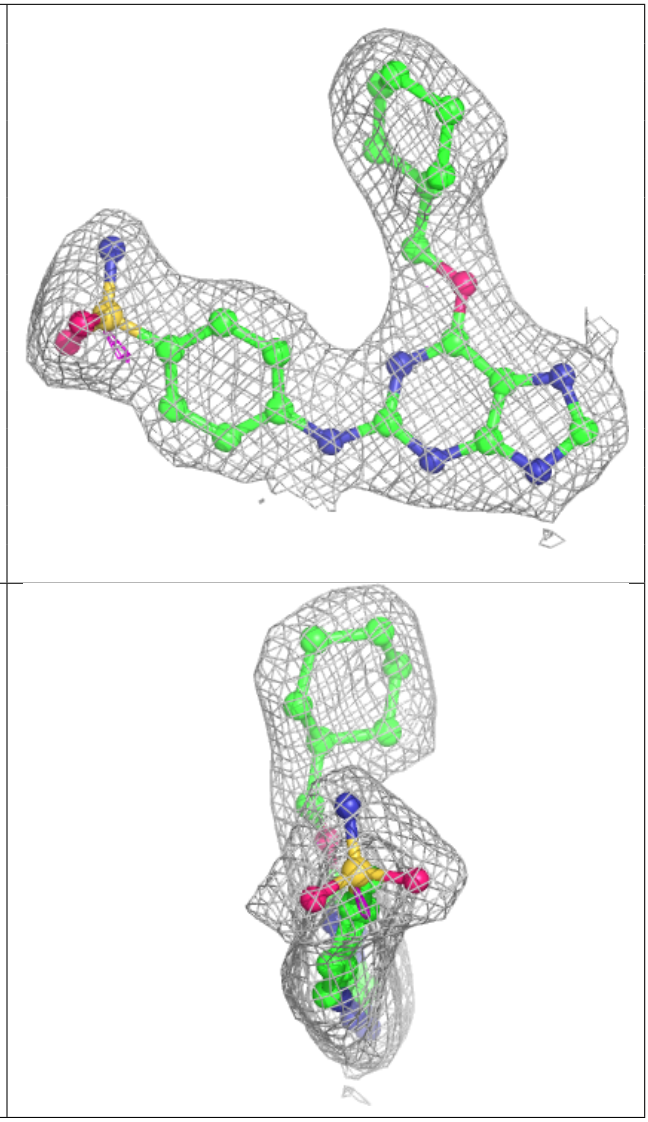
Electron density around 4SP C 1297:

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



Electron density around 4SP A 1298:

$2mF_o$-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.