



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:19 AM GMT

PDB ID : 2KCE
Title : BINDING OF THE ANTICANCER DRUG ZD1694 TO E. COLI THYMIDYLATE SYNTHASE: ASSESSING SPECIFICITY AND AFFINITY
Authors : Rutenber, E.E.; Stroud, R.M.
Deposited on : 1997-06-09
Resolution : 2.20 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

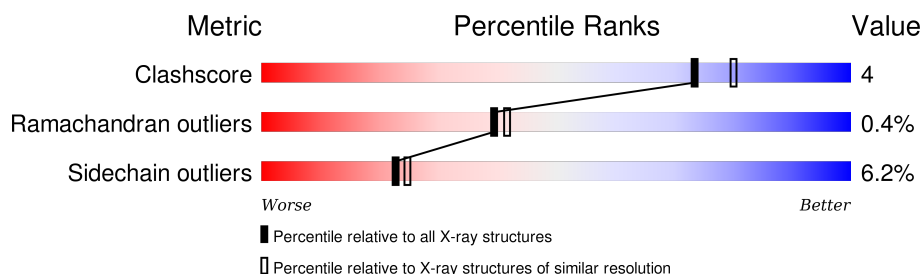
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	264	 80% 16% • •
1	B	264	 83% 14% •

2 Entry composition [i](#)

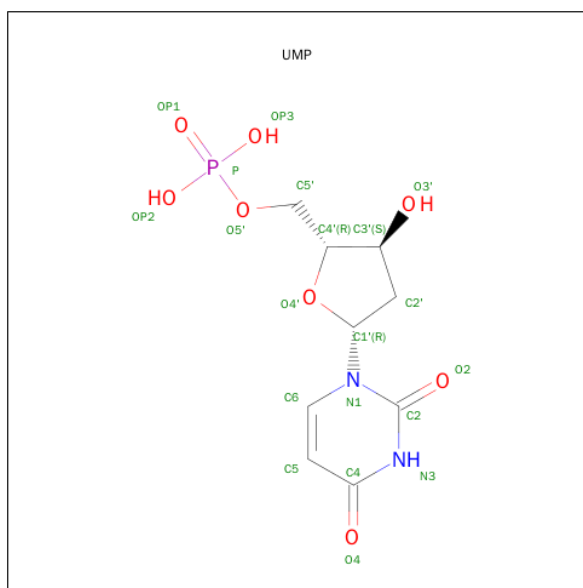
There are 4 unique types of molecules in this entry. The entry contains 6081 atoms, of which 1432 are hydrogens and 0 are deuteriums.

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 THYMIDYLATE SYNTHASE.

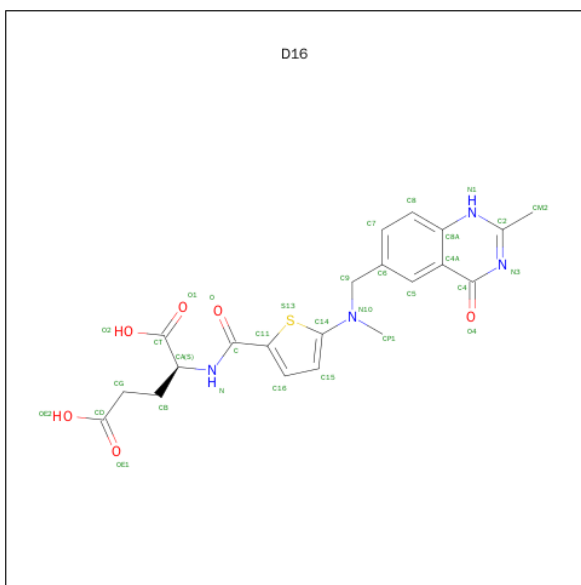
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	264	Total	C	H	N	O	S	0	0	0
			2619	1374	469	371	393	12			
1	B	264	Total	C	H	N	O	S	0	0	0
			2619	1374	469	371	393	12			

- Molecule 2 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (three-letter code: UMP) (formula: $C_9H_{13}N_2O_8P$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			21	9	1	2	8	1		
2	B	1	Total	C	H	N	O	P	0	0
			21	9	1	2	8	1		

- Molecule 3 is TOMUDEX (three-letter code: D16) (formula: $C_{21}H_{22}N_4O_6S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 33	C 21	H 1	N 4	O 6	S 1	0	0
3	B	1	Total 33	C 21	H 1	N 4	O 6	S 1	0	0

- Molecule 4 is water.

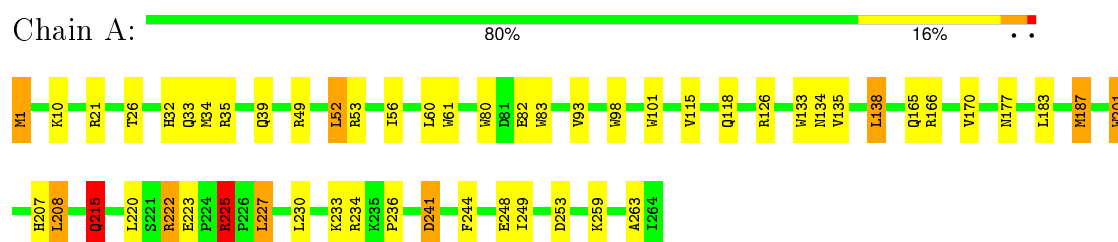
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	142	Total 426	H 284	O 142	0	0
4	B	103	Total 309	H 206	O 103	0	0

3 Residue-property plots [i](#)

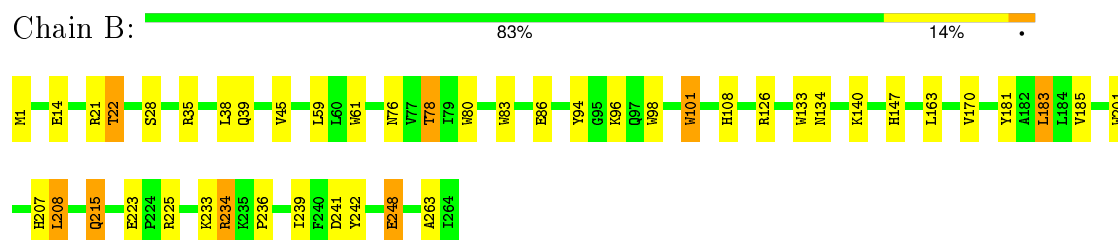
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). 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.

Note EDS was not executed.

• Molecule 1: THYMIDYLATE SYNTHASE



• Molecule 1: THYMIDYLATE SYNTHASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	126.80 Å 126.80 Å 67.56 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	7.00 – 2.20	Depositor
% Data completeness (in resolution range)	99.0 (7.00-2.20)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6081	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: D16, UMP

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	0.79	0/2210	1.48	33/3000 (1.1%)
1	B	0.78	0/2210	1.45	36/3000 (1.2%)
All	All	0.79	0/4420	1.46	69/6000 (1.1%)

There are no bond length outliers.

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	126	ARG	NE-CZ-NH2	-10.81	114.89	120.30
1	A	98	TRP	CD1-CG-CD2	9.08	113.56	106.30
1	B	35	ARG	NE-CZ-NH2	-8.99	115.81	120.30
1	A	61	TRP	CD1-CG-CD2	8.74	113.29	106.30
1	A	80	TRP	CD1-CG-CD2	8.47	113.08	106.30
1	B	133	TRP	CD1-CG-CD2	8.36	112.99	106.30
1	B	80	TRP	CD1-CG-CD2	8.36	112.98	106.30
1	B	201	TRP	CD1-CG-CD2	8.16	112.83	106.30
1	B	83	TRP	CD1-CG-CD2	8.07	112.76	106.30
1	A	21	ARG	NE-CZ-NH2	-7.86	116.37	120.30
1	B	80	TRP	CE2-CD2-CG	-7.79	101.06	107.30
1	B	133	TRP	CE2-CD2-CG	-7.75	101.10	107.30
1	A	21	ARG	NE-CZ-NH1	7.65	124.12	120.30
1	A	83	TRP	CD1-CG-CD2	7.53	112.33	106.30
1	A	222	ARG	NE-CZ-NH1	7.50	124.05	120.30
1	A	61	TRP	CE2-CD2-CG	-7.47	101.33	107.30
1	A	80	TRP	CE2-CD2-CG	-7.44	101.35	107.30
1	A	98	TRP	CE2-CD2-CG	-7.37	101.41	107.30
1	A	234	ARG	NE-CZ-NH1	7.34	123.97	120.30
1	A	133	TRP	CD1-CG-CD2	7.26	112.11	106.30
1	A	126	ARG	NE-CZ-NH1	7.25	123.92	120.30
1	B	83	TRP	CE2-CD2-CG	-7.19	101.55	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	98	TRP	CD1-CG-CD2	7.18	112.04	106.30
1	B	201	TRP	CE2-CD2-CG	-7.17	101.56	107.30
1	A	101	TRP	CE2-CD2-CG	-7.05	101.66	107.30
1	A	133	TRP	CE2-CD2-CG	-7.02	101.68	107.30
1	B	22	THR	CA-C-N	7.00	130.21	116.20
1	A	101	TRP	CD1-CG-CD2	7.00	111.90	106.30
1	A	201	TRP	CE2-CD2-CG	-6.95	101.74	107.30
1	A	83	TRP	CE2-CD2-CG	-6.94	101.75	107.30
1	A	201	TRP	CD1-CG-CD2	6.78	111.72	106.30
1	B	101	TRP	CE2-CD2-CG	-6.67	101.97	107.30
1	B	98	TRP	CE2-CD2-CG	-6.53	102.08	107.30
1	B	61	TRP	CD1-CG-CD2	6.53	111.52	106.30
1	A	187	MET	CG-SD-CE	-6.41	89.94	100.20
1	B	61	TRP	CE2-CD2-CG	-6.33	102.24	107.30
1	B	35	ARG	NE-CZ-NH1	6.30	123.45	120.30
1	B	80	TRP	CG-CD2-CE3	6.08	139.37	133.90
1	B	234	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	B	201	TRP	CB-CG-CD1	-5.90	119.33	127.00
1	B	215	GLN	CA-CB-CG	5.88	126.34	113.40
1	A	222	ARG	NE-CZ-NH2	-5.88	117.36	120.30
1	B	80	TRP	CB-CG-CD1	-5.84	119.41	127.00
1	B	201	TRP	CG-CD2-CE3	5.83	139.15	133.90
1	B	208	LEU	CA-CB-CG	5.83	128.72	115.30
1	B	126	ARG	NE-CZ-NH2	-5.83	117.38	120.30
1	A	225	ARG	NE-CZ-NH1	5.83	123.22	120.30
1	B	201	TRP	CG-CD1-NE1	-5.81	104.29	110.10
1	B	101	TRP	CD1-CG-CD2	5.79	110.93	106.30
1	B	78	THR	N-CA-CB	-5.79	99.30	110.30
1	B	45	VAL	CA-CB-CG2	-5.64	102.43	110.90
1	A	98	TRP	CG-CD1-NE1	-5.63	104.47	110.10
1	B	80	TRP	CG-CD1-NE1	-5.53	104.57	110.10
1	A	49	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	B	126	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	A	215	GLN	CA-CB-CG	5.39	125.26	113.40
1	B	101	TRP	CG-CD2-CE3	5.38	138.74	133.90
1	A	34	MET	CA-CB-CG	5.31	122.33	113.30
1	A	80	TRP	CG-CD1-NE1	-5.30	104.80	110.10
1	A	1	MET	CA-CB-CG	5.29	122.30	113.30
1	A	61	TRP	CG-CD1-NE1	-5.29	104.81	110.10
1	A	208	LEU	CA-CB-CG	5.24	127.34	115.30
1	B	234	ARG	NE-CZ-NH2	-5.21	117.70	120.30
1	B	83	TRP	CG-CD2-CE3	5.18	138.57	133.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	21	ARG	NE-CZ-NH1	5.13	122.86	120.30
1	B	83	TRP	CB-CG-CD1	-5.11	120.36	127.00
1	A	35	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	A	83	TRP	CG-CD1-NE1	-5.04	105.06	110.10
1	B	22	THR	O-C-N	-5.04	114.63	123.20

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	A	2150	469	2081	22	0
1	B	2150	469	2081	12	0
2	A	20	1	10	1	0
2	B	20	1	10	0	0
3	A	32	1	20	1	0
3	B	32	1	20	1	0
4	A	142	284	0	1	0
4	B	103	206	0	1	0
All	All	4649	1432	4222	35	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 4.

All (35) 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:233:LYS:HE3	1:A:248:GLU:HB2	1.82	0.61
1:A:10:LYS:NZ	1:A:32:HIS:HD2	1.98	0.60
1:B:22:THR:HG21	1:B:263:ALA:HB1	1.86	0.58
1:A:177:ASN:HD21	2:A:565:UMP:HN3	1.51	0.57
1:A:225:ARG:HD3	1:A:253:ASP:O	2.04	0.56
1:A:215:GLN:NE2	1:A:215:GLN:H	2.04	0.55
1:B:28:SER:HB3	1:B:207:HIS:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:VAL:HB	1:A:208:LEU:HD13	1.89	0.53
1:B:234:ARG:O	1:B:236:PRO:HD3	2.10	0.52
1:A:10:LYS:HZ3	1:A:32:HIS:HD2	1.58	0.52
1:A:82:GLU:HG2	4:A:811:HOH:O	2.10	0.52
1:A:135:VAL:HA	1:A:138:LEU:HD22	1.93	0.51
1:A:165:GLN:HE22	1:A:177:ASN:ND2	2.10	0.49
1:A:52:LEU:HD11	1:A:249:ILE:HG13	1.96	0.47
1:A:165:GLN:HE22	1:A:177:ASN:HD22	1.63	0.46
1:A:215:GLN:HE21	1:A:215:GLN:H	1.61	0.46
1:A:183:LEU:HG	1:A:187:MET:CE	2.45	0.46
1:B:170:VAL:HB	1:B:208:LEU:HD13	1.98	0.46
1:B:1:MET:N	4:B:792:HOH:O	2.44	0.46
1:A:56:ILE:HG12	1:A:183:LEU:HD21	1.99	0.45
1:A:236:PRO:HB3	1:A:241:ASP:HB3	1.99	0.45
1:B:147:HIS:HB2	1:B:163:LEU:HD11	1.98	0.44
1:A:26:THR:HB	1:A:207:HIS:HB2	2.00	0.44
1:B:181:TYR:O	1:B:185:VAL:HG23	2.18	0.44
3:B:568:D16:H15	3:B:568:D16:HP11	1.81	0.43
1:B:101:TRP:O	1:B:108:HIS:HA	2.19	0.43
1:A:115:VAL:HA	1:A:118:GLN:HE21	1.84	0.42
1:B:59:LEU:HD23	1:B:183:LEU:HD12	2.02	0.42
1:A:1:MET:HE3	1:A:227:LEU:HD11	2.02	0.42
1:B:239:ILE:HA	1:B:242:TYR:HE1	1.86	0.41
1:B:233:LYS:HD2	1:B:248:GLU:HG2	2.01	0.41
1:A:263:ALA:O	3:A:566:D16:HM22	2.20	0.41
1:A:33:GLN:HA	1:A:201:TRP:O	2.21	0.41
1:A:53:ARG:HA	1:A:244:PHE:HE1	1.86	0.41
1:B:236:PRO:HB3	1:B:241:ASP:HB2	2.02	0.40

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	262/264 (99%)	258 (98%)	3 (1%)	1 (0%)	39	42
1	B	262/264 (99%)	255 (97%)	6 (2%)	1 (0%)	39	42
All	All	524/528 (99%)	513 (98%)	9 (2%)	2 (0%)	39	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	94	TYR
1	A	93	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	233/233 (100%)	218 (94%)	15 (6%)	22	24
1	B	233/233 (100%)	219 (94%)	14 (6%)	24	26
All	All	466/466 (100%)	437 (94%)	29 (6%)	23	25

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	52	LEU
1	A	60	LEU
1	A	134	ASN
1	A	138	LEU
1	A	166	ARG
1	A	215	GLN
1	A	220	LEU
1	A	222	ARG
1	A	223	GLU
1	A	225	ARG
1	A	227	LEU
1	A	230	LEU
1	A	241	ASP

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Mol	Chain	Res	Type
1	A	259	LYS
1	B	14	GLU
1	B	38	LEU
1	B	39	GLN
1	B	76	ASN
1	B	78	THR
1	B	86	GLU
1	B	96	LYS
1	B	134	ASN
1	B	140	LYS
1	B	183	LEU
1	B	215	GLN
1	B	223	GLU
1	B	225	ARG
1	B	248	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	32	HIS
1	A	39	GLN
1	A	97	GLN
1	A	118	GLN
1	A	134	ASN
1	A	151	GLN
1	A	177	ASN
1	A	190	GLN
1	A	215	GLN
1	A	217	HIS
1	B	32	HIS
1	B	57	HIS
1	B	117	ASN
1	B	118	GLN
1	B	121	ASN
1	B	134	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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$
2	UMP	A	565	1	16,21,21	3.33	4 (25%)	20,31,31	1.32	2 (10%)
3	D16	A	566	-	25,34,34	1.32	1 (4%)	22,48,48	1.99	7 (31%)
2	UMP	B	567	1	16,21,21	2.97	3 (18%)	20,31,31	1.55	2 (10%)
3	D16	B	568	-	25,34,34	1.52	4 (16%)	22,48,48	2.00	4 (18%)

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	UMP	A	565	1	-	0/6/22/22	0/2/2/2
3	D16	A	566	-	-	0/13/25/25	0/3/3/3
2	UMP	B	567	1	-	0/6/22/22	0/2/2/2
3	D16	B	568	-	-	0/13/25/25	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	565	UMP	P-OP3	-2.28	1.46	1.54
2	A	565	UMP	P-OP2	-2.08	1.47	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	568	D16	C5-C6	2.04	1.42	1.37
3	B	568	D16	C8-C7	2.21	1.41	1.36
2	B	567	UMP	O4'-C1'	2.27	1.47	1.42
3	B	568	D16	CB-CA	2.55	1.56	1.53
3	A	566	D16	O4-C4	5.29	1.37	1.24
3	B	568	D16	O4-C4	5.44	1.37	1.24
2	B	567	UMP	C6-C5	7.44	1.54	1.38
2	A	565	UMP	C6-C5	7.79	1.55	1.38
2	B	567	UMP	C6-N1	8.15	1.47	1.35
2	A	565	UMP	C6-N1	9.94	1.49	1.35

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	567	UMP	C5-C6-N1	-5.11	108.05	120.58
2	A	565	UMP	C5-C6-N1	-3.16	112.84	120.58
3	B	568	D16	N1-C2-N3	-2.81	120.06	125.58
3	A	566	D16	N1-C2-N3	-2.61	120.46	125.58
3	A	566	D16	C4-C4A-C8A	-2.01	116.58	118.54
3	A	566	D16	C5-C4A-C8A	2.10	120.65	118.14
3	B	568	D16	CM2-C2-N1	2.31	121.13	117.21
3	A	566	D16	CM2-C2-N1	2.34	121.18	117.21
3	A	566	D16	C6-C9-N10	3.13	117.00	113.03
2	B	567	UMP	O4'-C1'-N1	3.25	113.34	107.72
2	A	565	UMP	O4'-C1'-N1	3.58	113.91	107.72
3	A	566	D16	C2-N1-C8A	4.24	120.64	115.86
3	B	568	D16	C2-N1-C8A	4.80	121.28	115.86
3	A	566	D16	CG-CB-CA	4.81	122.77	112.99
3	B	568	D16	CG-CB-CA	5.37	123.90	112.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	565	UMP	1	0
3	A	566	D16	1	0
3	B	568	D16	1	0

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](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.