



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:47 AM GMT

PDB ID : 2TSR
Title : THYMIDYLATE SYNTHASE FROM RAT IN TERNARY COMPLEX
WITH DUMP AND TOMUDEX
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Deposited on : 1998-06-19
Resolution : 2.60 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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

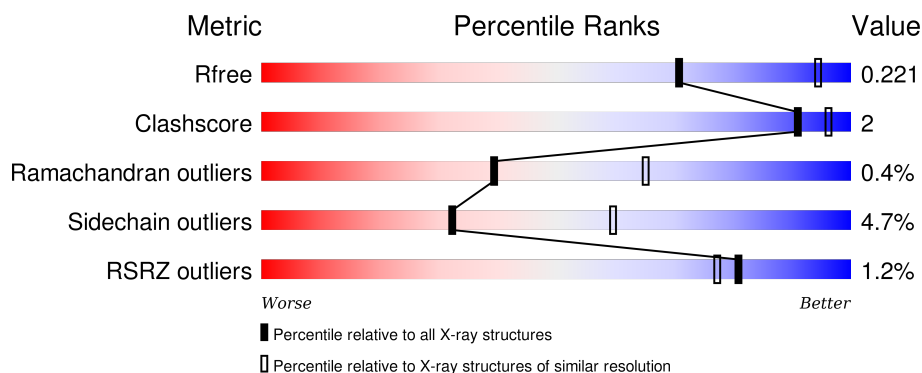
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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.

Mol	Chain	Length	Quality of chain
1	A	307	<div> <div></div> <div>84% 7% 8%</div> </div>
1	B	307	<div> <div>%</div> <div>81% 10% 8%</div> </div>
1	C	307	<div> <div>2%</div> <div>82% 9% 8%</div> </div>
1	D	307	<div> <div>%</div> <div>84% 7% 8%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	D16	A	309	-	-	-	X
3	D16	B	409	-	-	-	X
3	D16	D	609	-	-	-	X

2 Entry composition [i](#)

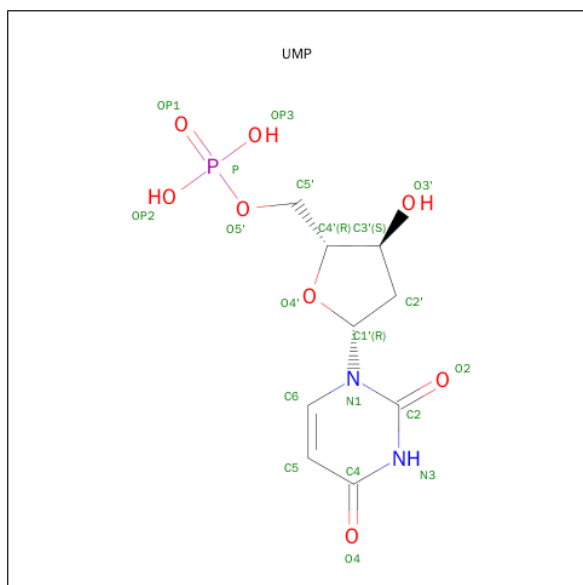
There are 4 unique types of molecules in this entry. The entry contains 9367 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 THYMIDYLATE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2271	1453	394	412	12			
1	B	281	Total	C	N	O	S	0	0	0
			2271	1453	394	412	12			
1	C	281	Total	C	N	O	S	0	0	0
			2271	1453	394	412	12			
1	D	281	Total	C	N	O	S	0	0	0
			2271	1453	394	412	12			

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



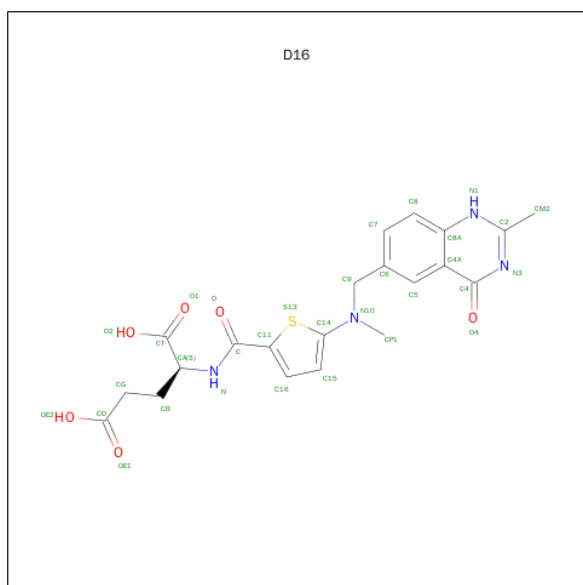
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	B	1	Total	C	N	O	P	0	0
			20	9	2	8	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	D	1	Total	C	N	O	P	0	0
			20	9	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	C	N	O	S	0	0
			32	21	4	6	1		
3	B	1	Total	C	N	O	S	0	0
			32	21	4	6	1		
3	C	1	Total	C	N	O	S	0	0
			32	21	4	6	1		
3	D	1	Total	C	N	O	S	0	0
			32	21	4	6	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	24	Total	O	0	0
			24	24		
4	B	26	Total	O	0	0
			26	26		
4	C	9	Total	O	0	0
			9	9		

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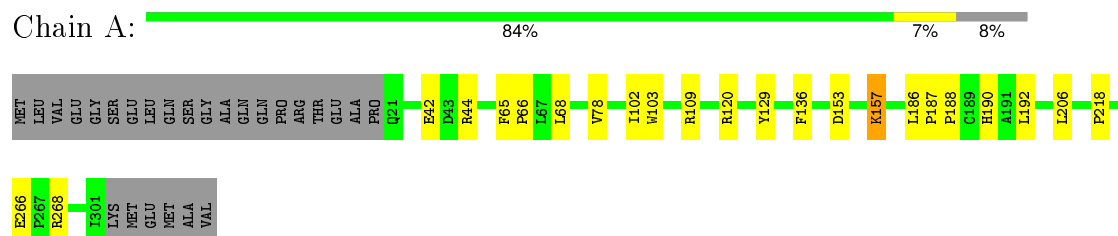
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	16	Total	O	0	0
			16	16		

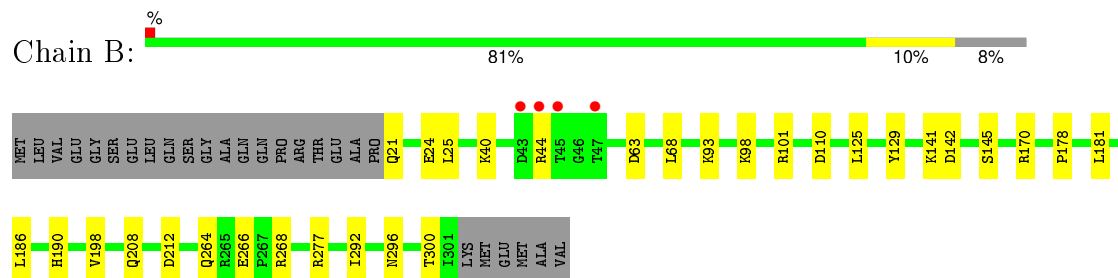
3 Residue-property plots [i](#)

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 ($RSRZ > 2$). 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.

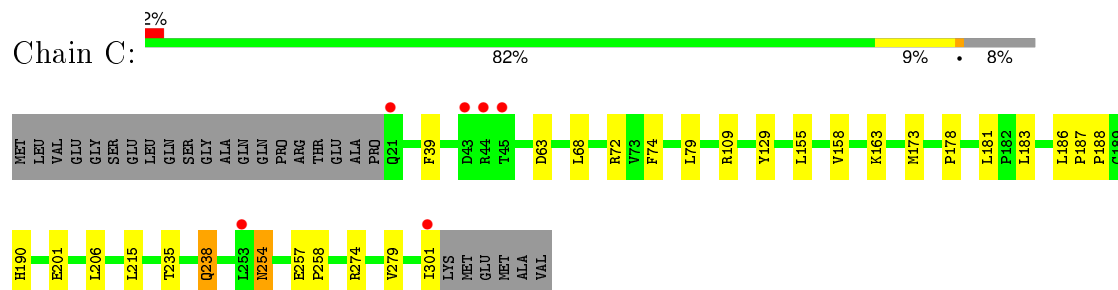
• Molecule 1: THYMIDYLATE SYNTHASE



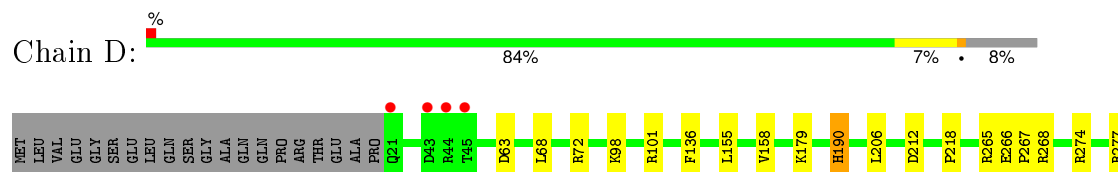
• Molecule 1: THYMIDYLATE SYNTHASE



• Molecule 1: THYMIDYLATE SYNTHASE



• Molecule 1: THYMIDYLATE SYNTHASE



N296	P299	T300	T301	LYS	MET	GLU	MET	ALA	VAL
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4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	99.70Å 101.60Å 140.80Å 90.00° 101.40° 90.00°	Depositor
Resolution (Å)	8.00 – 2.60 59.41 – 2.59	Depositor EDS
% Data completeness (in resolution range)	82.9 (8.00-2.60) 81.9 (59.41-2.59)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.54 (at 2.58Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.162 , 0.222 0.165 , 0.221	Depositor DCC
R_{free} test set	1689 reflections (4.97%)	DCC
Wilson B-factor (Å ²)	37.4	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 39.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 35237 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9367	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	0.29	0/2330	0.58	0/3152
1	B	0.30	0/2330	0.59	0/3152
1	C	0.31	0/2330	0.59	0/3152
1	D	0.30	0/2330	0.59	0/3152
All	All	0.30	0/9320	0.59	0/12608

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	2271	0	2230	11	0
1	B	2271	0	2230	9	0
1	C	2271	0	2230	10	0
1	D	2271	0	2230	9	0
2	A	20	0	11	0	0
2	B	20	0	11	2	0
2	C	20	0	11	2	0
2	D	20	0	11	3	0
3	A	32	0	20	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	32	0	20	1	0
3	C	32	0	20	1	0
3	D	32	0	20	1	0
4	A	24	0	0	0	0
4	B	26	0	0	0	0
4	C	9	0	0	1	0
4	D	16	0	0	0	0
All	All	9367	0	9044	40	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 2.

All (40) 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:44:ARG:HH11	1:B:170:ARG:NH2	1.85	0.74
1:A:68:LEU:HD12	1:A:218:PRO:HB3	1.71	0.72
1:D:190:HIS:HB3	1:D:206:LEU:HD11	1.73	0.71
1:D:212:ASP:HB2	2:D:608:UMP:H2'	1.76	0.67
1:A:186:LEU:HD12	1:A:187:PRO:HD2	1.77	0.66
1:C:190:HIS:HB2	1:C:206:LEU:HD11	1.77	0.66
2:D:608:UMP:H1'	3:D:609:D16:C4	2.26	0.66
1:A:44:ARG:HH11	1:B:170:ARG:HH21	1.44	0.63
1:B:21:GLN:HG3	1:B:25:LEU:HD12	1.82	0.62
1:A:190:HIS:HB3	1:A:206:LEU:HD11	1.83	0.61
2:B:408:UMP:H1'	3:B:409:D16:C4	2.31	0.61
2:C:508:UMP:H1'	3:C:509:D16:C4	2.34	0.57
1:D:68:LEU:HD22	1:D:218:PRO:HB3	1.90	0.53
1:C:254:ASN:ND2	1:C:254:ASN:H	2.06	0.53
1:A:102:ILE:HG13	1:A:103:TRP:CD1	2.46	0.51
2:C:508:UMP:O2	2:C:508:UMP:H2'	2.12	0.49
1:D:268:ARG:HD2	1:D:296:ASN:O	2.15	0.46
1:D:155:LEU:O	1:D:158:VAL:HG22	2.16	0.45
1:B:141:LYS:HG2	1:B:142:ASP:N	2.31	0.45
1:C:257:GLU:HB2	1:C:258:PRO:HD3	1.98	0.45
2:D:608:UMP:H2'	2:D:608:UMP:O2	2.16	0.44
1:C:163:LYS:HG3	1:C:235:THR:HG22	2.00	0.44
1:C:178:PRO:HD2	1:D:136:PHE:CE1	2.53	0.43
1:A:136:PHE:CE1	1:B:178:PRO:HD2	2.54	0.43
1:C:155:LEU:O	1:C:158:VAL:HG22	2.19	0.42
1:C:39:PHE:HD2	4:C:511:HOH:O	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:266:GLU:HA	1:D:267:PRO:HD3	1.90	0.42
1:A:153:ASP:O	1:A:157:LYS:HB2	2.19	0.42
1:B:125:LEU:HD13	1:B:186:LEU:HD21	2.01	0.42
1:B:212:ASP:HB2	2:B:408:UMP:H2"	2.02	0.42
1:B:268:ARG:HD2	1:B:296:ASN:O	2.18	0.42
1:C:254:ASN:N	1:C:254:ASN:HD22	2.18	0.41
1:C:201:GLU:HA	1:C:238:GLN:O	2.20	0.41
1:D:72:ARG:O	1:D:300:THR:HG23	2.21	0.41
1:B:24:GLU:HG3	1:B:68:LEU:HD22	2.03	0.41
1:A:109:ARG:NH2	1:A:120:ARG:O	2.54	0.41
1:C:187:PRO:HA	1:C:188:PRO:HD3	1.90	0.40
1:D:265:ARG:NH2	1:D:299:PRO:O	2.54	0.40
1:A:65:PHE:HA	1:A:66:PRO:HD3	1.84	0.40
1:A:187:PRO:HA	1:A:188:PRO:HD3	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	279/307 (91%)	264 (95%)	14 (5%)	1 (0%)	39	65
1	B	279/307 (91%)	267 (96%)	11 (4%)	1 (0%)	39	65
1	C	279/307 (91%)	264 (95%)	13 (5%)	2 (1%)	26	51
1	D	279/307 (91%)	268 (96%)	11 (4%)	0	100	100
All	All	1116/1228 (91%)	1063 (95%)	49 (4%)	4 (0%)	39	65

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	129	TYR

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Mol	Chain	Res	Type
1	C	129	TYR
1	B	129	TYR
1	C	74	PHE

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	245/266 (92%)	239 (98%)	6 (2%)	57	82
1	B	245/266 (92%)	228 (93%)	17 (7%)	19	38
1	C	245/266 (92%)	230 (94%)	15 (6%)	23	46
1	D	245/266 (92%)	237 (97%)	8 (3%)	45	73
All	All	980/1064 (92%)	934 (95%)	46 (5%)	32	59

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	GLU
1	A	78	VAL
1	A	157	LYS
1	A	192	LEU
1	A	266	GLU
1	A	268	ARG
1	B	40	LYS
1	B	44	ARG
1	B	63	ASP
1	B	93	LYS
1	B	98	LYS
1	B	101	ARG
1	B	110	ASP
1	B	145	SER
1	B	181	LEU
1	B	190	HIS
1	B	198	VAL
1	B	208	GLN

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Mol	Chain	Res	Type
1	B	264	GLN
1	B	266	GLU
1	B	277	ARG
1	B	292	ILE
1	B	300	THR
1	C	63	ASP
1	C	68	LEU
1	C	72	ARG
1	C	79	LEU
1	C	109	ARG
1	C	173	MET
1	C	181	LEU
1	C	183	LEU
1	C	186	LEU
1	C	215	LEU
1	C	238	GLN
1	C	254	ASN
1	C	274	ARG
1	C	279	VAL
1	C	301	ILE
1	D	63	ASP
1	D	98	LYS
1	D	101	ARG
1	D	179	LYS
1	D	190	HIS
1	D	274	ARG
1	D	277	ARG
1	D	300	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	GLN
1	A	205	GLN
1	B	56	GLN
1	B	205	GLN
1	B	298	HIS
1	C	56	GLN
1	C	205	GLN
1	C	254	ASN
1	D	56	GLN
1	D	165	ASN

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Mol	Chain	Res	Type
1	D	205	GLN

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 ⓘ

8 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	308	-	16,21,21	1.14	1 (6%)	23,31,31	2.89	2 (8%)
3	D16	A	309	-	25,34,34	3.29	11 (44%)	22,48,48	2.24	7 (31%)
2	UMP	B	408	-	16,21,21	1.13	1 (6%)	23,31,31	2.95	3 (13%)
3	D16	B	409	-	25,34,34	3.23	12 (48%)	22,48,48	2.18	7 (31%)
2	UMP	C	508	-	16,21,21	1.14	2 (12%)	23,31,31	2.97	3 (13%)
3	D16	C	509	-	25,34,34	3.18	11 (44%)	22,48,48	2.35	6 (27%)
2	UMP	D	608	-	16,21,21	1.15	2 (12%)	23,31,31	2.98	3 (13%)
3	D16	D	609	-	25,34,34	3.08	12 (48%)	22,48,48	2.28	6 (27%)

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	308	-	-	0/6/22/22	0/2/2/2
3	D16	A	309	-	-	0/13/25/25	0/3/3/3
2	UMP	B	408	-	-	0/6/22/22	0/2/2/2
3	D16	B	409	-	-	0/13/25/25	0/3/3/3
2	UMP	C	508	-	-	0/6/22/22	0/2/2/2
3	D16	C	509	-	-	0/13/25/25	0/3/3/3
2	UMP	D	608	-	-	0/6/22/22	0/2/2/2
3	D16	D	609	-	-	0/13/25/25	0/3/3/3

All (52) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	508	UMP	C6-C5	-2.15	1.33	1.38
2	D	608	UMP	C6-C5	-2.01	1.33	1.38
3	D	609	D16	C-N	2.08	1.38	1.34
3	B	409	D16	C-N	2.17	1.39	1.34
3	B	409	D16	C5-C6	2.64	1.43	1.37
3	C	509	D16	C14-N10	2.69	1.45	1.36
3	B	409	D16	C7-C6	2.78	1.44	1.38
3	D	609	D16	C14-N10	2.78	1.45	1.36
3	A	309	D16	C14-N10	2.79	1.45	1.36
3	D	609	D16	C7-C6	2.81	1.44	1.38
3	A	309	D16	C5-C6	2.86	1.44	1.37
3	B	409	D16	C14-N10	2.87	1.45	1.36
3	C	509	D16	C7-C6	2.88	1.44	1.38
3	A	309	D16	C7-C6	3.05	1.45	1.38
3	C	509	D16	C5-C6	3.06	1.44	1.37
3	D	609	D16	C5-C6	3.07	1.44	1.37
3	D	609	D16	C8-C7	3.12	1.43	1.36
2	B	408	UMP	C4-N3	3.13	1.38	1.33
2	C	508	UMP	C4-N3	3.13	1.38	1.33
2	A	308	UMP	C4-N3	3.21	1.39	1.33
2	D	608	UMP	C4-N3	3.23	1.39	1.33
3	C	509	D16	C8-C7	3.37	1.43	1.36
3	A	309	D16	C8-C7	3.38	1.43	1.36
3	B	409	D16	C9-C6	3.52	1.57	1.51
3	B	409	D16	C8-C7	3.56	1.44	1.36
3	C	509	D16	CB-CA	4.22	1.59	1.53
3	C	509	D16	C9-C6	4.26	1.59	1.51
3	D	609	D16	C9-C6	4.26	1.59	1.51
3	D	609	D16	CB-CA	4.32	1.59	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	609	D16	C2-N3	4.38	1.42	1.34
3	A	309	D16	C9-C6	4.38	1.59	1.51
3	C	509	D16	C2-N3	4.73	1.43	1.34
3	A	309	D16	C2-N3	4.74	1.43	1.34
3	B	409	D16	C2-N3	4.78	1.43	1.34
3	D	609	D16	C4-N3	4.92	1.42	1.33
3	B	409	D16	CB-CA	5.18	1.60	1.53
3	A	309	D16	C4-N3	5.18	1.42	1.33
3	C	509	D16	C4-N3	5.19	1.42	1.33
3	D	609	D16	C2-N1	5.21	1.43	1.34
3	A	309	D16	CB-CA	5.33	1.60	1.53
3	B	409	D16	C4-N3	5.40	1.43	1.33
3	C	509	D16	C2-N1	5.51	1.44	1.34
3	B	409	D16	C2-N1	5.68	1.44	1.34
3	A	309	D16	C2-N1	5.74	1.44	1.34
3	D	609	D16	C9-N10	5.75	1.56	1.47
3	B	409	D16	C9-N10	5.81	1.56	1.47
3	C	509	D16	C9-N10	5.98	1.56	1.47
3	A	309	D16	C9-N10	6.33	1.57	1.47
3	D	609	D16	C4-C4A	6.72	1.52	1.41
3	A	309	D16	C4-C4A	6.89	1.52	1.41
3	C	509	D16	C4-C4A	6.98	1.52	1.41
3	B	409	D16	C4-C4A	7.04	1.53	1.41

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	309	D16	N1-C2-N3	-3.40	118.89	125.58
3	D	609	D16	N1-C2-N3	-3.38	118.93	125.58
3	C	509	D16	N1-C2-N3	-3.38	118.94	125.58
3	B	409	D16	N1-C2-N3	-3.31	119.07	125.58
2	A	308	UMP	C5-C4-N3	-3.31	114.63	123.12
2	C	508	UMP	C5-C4-N3	-3.27	114.72	123.12
2	D	608	UMP	C5-C4-N3	-3.27	114.74	123.12
2	B	408	UMP	C5-C4-N3	-3.20	114.91	123.12
3	B	409	D16	C7-C8-C8A	-2.35	118.33	120.88
3	A	309	D16	C7-C8-C8A	-2.22	118.47	120.88
3	D	609	D16	C7-C8-C8A	-2.15	118.55	120.88
3	C	509	D16	C4-C4A-C8A	2.05	120.54	118.54
2	B	408	UMP	O4'-C1'-C2'	2.10	110.45	106.27
3	B	409	D16	CM2-C2-N1	2.20	120.95	117.21
3	D	609	D16	CM2-C2-N1	2.24	121.01	117.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	509	D16	CM2-C2-N1	2.28	121.08	117.21
3	A	309	D16	C4-C4A-C8A	2.33	120.81	118.54
3	A	309	D16	CM2-C2-N1	2.34	121.19	117.21
2	C	508	UMP	C2'-C1'-N1	2.49	120.21	114.16
3	B	409	D16	C4-C4A-C8A	2.53	121.01	118.54
2	D	608	UMP	C2'-C1'-N1	2.66	120.64	114.16
3	B	409	D16	C6-C9-N10	2.70	116.46	113.03
3	A	309	D16	C6-C9-N10	3.82	117.88	113.03
3	D	609	D16	C6-C9-N10	4.55	118.80	113.03
3	A	309	D16	CG-CB-CA	4.57	122.27	112.99
3	D	609	D16	CG-CB-CA	4.91	122.96	112.99
3	B	409	D16	CG-CB-CA	4.94	123.03	112.99
3	C	509	D16	C6-C9-N10	4.97	119.33	113.03
3	C	509	D16	CG-CB-CA	5.14	123.44	112.99
3	D	609	D16	C2-N1-C8A	5.66	122.24	115.86
3	B	409	D16	C2-N1-C8A	5.67	122.26	115.86
3	A	309	D16	C2-N1-C8A	5.70	122.28	115.86
3	C	509	D16	C2-N1-C8A	5.77	122.36	115.86
2	D	608	UMP	C4-N3-C2	13.16	127.17	114.14
2	B	408	UMP	C4-N3-C2	13.16	127.17	114.14
2	A	308	UMP	C4-N3-C2	13.18	127.19	114.14
2	C	508	UMP	C4-N3-C2	13.21	127.23	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	408	UMP	2	0
3	B	409	D16	1	0
2	C	508	UMP	2	0
3	C	509	D16	1	0
2	D	608	UMP	3	0
3	D	609	D16	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	281/307 (91%)	-0.66	0 100 100	10, 27, 61, 89	0
1	B	281/307 (91%)	-0.52	4 (1%) 78 74	11, 26, 63, 97	0
1	C	281/307 (91%)	-0.32	6 (2%) 67 61	15, 40, 75, 95	0
1	D	281/307 (91%)	-0.57	4 (1%) 78 74	17, 33, 62, 96	0
All	All	1124/1228 (91%)	-0.52	14 (1%) 81 77	10, 32, 67, 97	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	43	ASP	3.9
1	C	43	ASP	3.6
1	B	44	ARG	3.1
1	D	44	ARG	3.1
1	C	44	ARG	2.6
1	C	45	THR	2.6
1	D	21	GLN	2.5
1	C	253	LEU	2.4
1	D	43	ASP	2.4
1	C	301	ILE	2.3
1	B	45	THR	2.3
1	C	21	GLN	2.2
1	B	47	THR	2.1
1	D	45	THR	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	D16	B	409	32/32	0.88	0.24	4.86	60,71,85,89	0
3	D16	A	309	32/32	0.89	0.25	3.83	65,72,96,99	0
3	D16	D	609	32/32	0.92	0.21	3.33	48,59,72,72	0
3	D16	C	509	32/32	0.95	0.22	1.64	47,54,82,86	0
2	UMP	D	608	20/20	0.91	0.23	1.06	46,53,64,65	0
2	UMP	A	308	20/20	0.94	0.17	0.86	33,50,63,67	0
2	UMP	B	408	20/20	0.92	0.20	0.39	43,67,70,70	0
2	UMP	C	508	20/20	0.94	0.16	-0.04	40,52,63,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.