



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:56 PM GMT

PDB ID : 1D8T
Title : CRYSTAL STRUCTURE OF ELONGATION FACTOR, TU (EF-TU-MGGDP) COMPLEXED WITH GE2270A, A THIAZOLYL PEPTIDE ANTIBIOTIC
Authors : Heffron, S.E.; Journak, F.
Deposited on : 1999-10-25
Resolution : 2.35 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
<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:

MolProbitry : 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

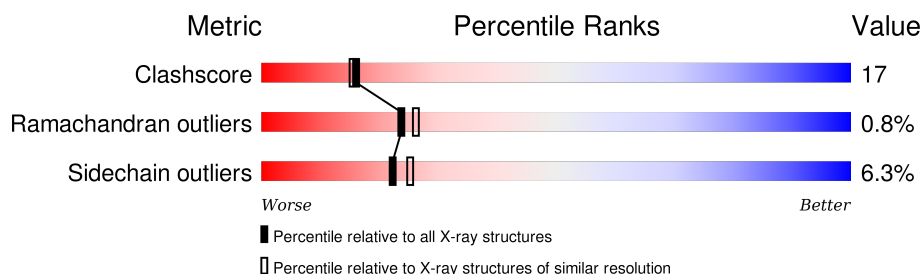
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)

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	393	 66% 30% . .
1	B	393	 68% 27% . .
2	C	15	 73% 20% 7%
2	D	15	 80% 13% 7%

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
2	MH6	C	11	-	X	-	-
2	BB8	C	8	X	-	-	-
2	MH6	D	11	-	X	-	-
2	BB8	D	8	X	-	-	-
5	ACT	A	3007	-	-	X	-
5	ACT	A	3030	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6718 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 ELONGATION FACTOR TU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	S	0	1	0
			3024	1911	520	580	13			
1	B	385	Total	C	N	O	S	0	0	0
			2963	1873	510	567	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	393	GLY	SER	CONFLICT	UNP P0A6N1
B	393	GLY	SER	CONFLICT	UNP P0A6N1

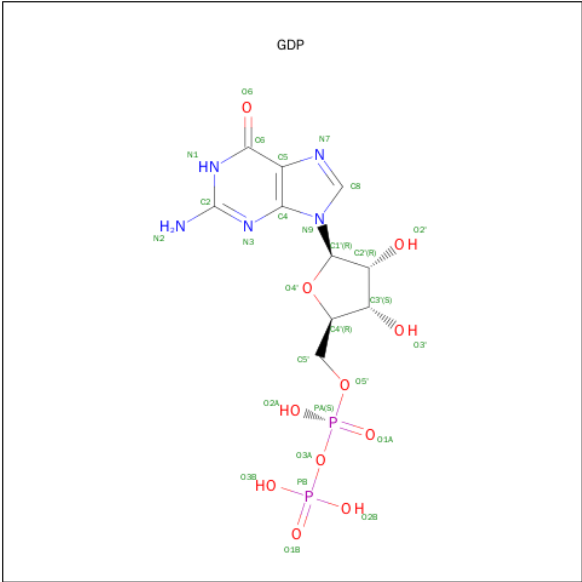
- Molecule 2 is a protein called THIOCILLIN GE2270.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	15	Total	C	N	O	S	0	0	1
			87	56	15	10	6			
2	D	15	Total	C	N	O	S	0	0	1
			87	56	15	10	6			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

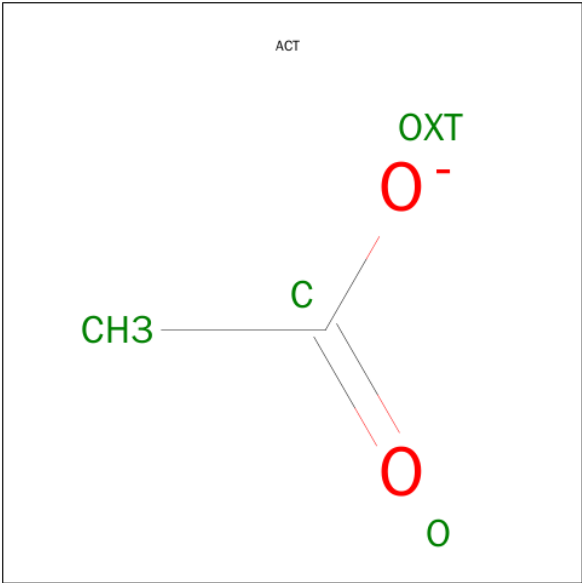
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 28	C 10	N 5	O 11	P 2	0	0
4	B	1	Total 28	C 10	N 5	O 11	P 2	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

- Molecule 6 is water.

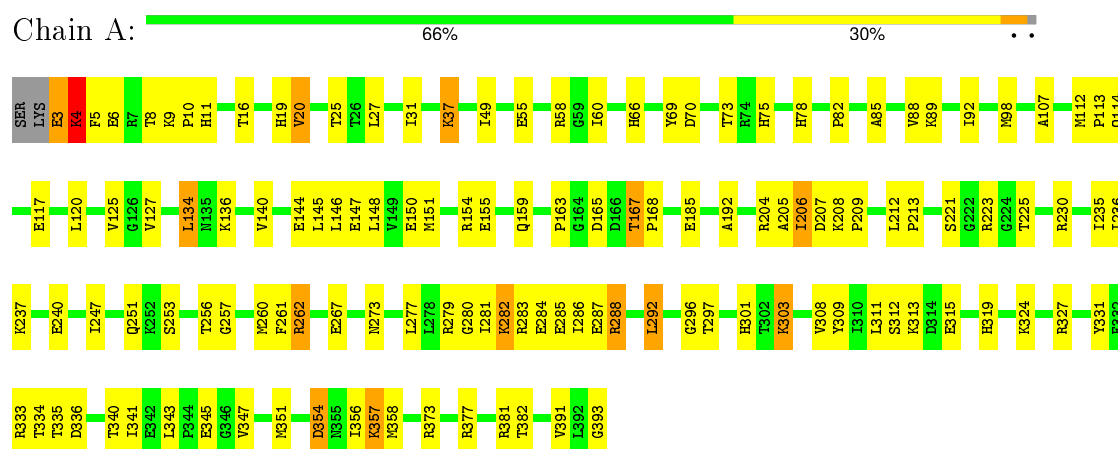
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	227	Total O 227 227	0	0
6	B	146	Total O 146 146	0	0
6	C	4	Total O 4 4	0	0
6	D	2	Total O 2 2	0	0

3 Residue-property plots

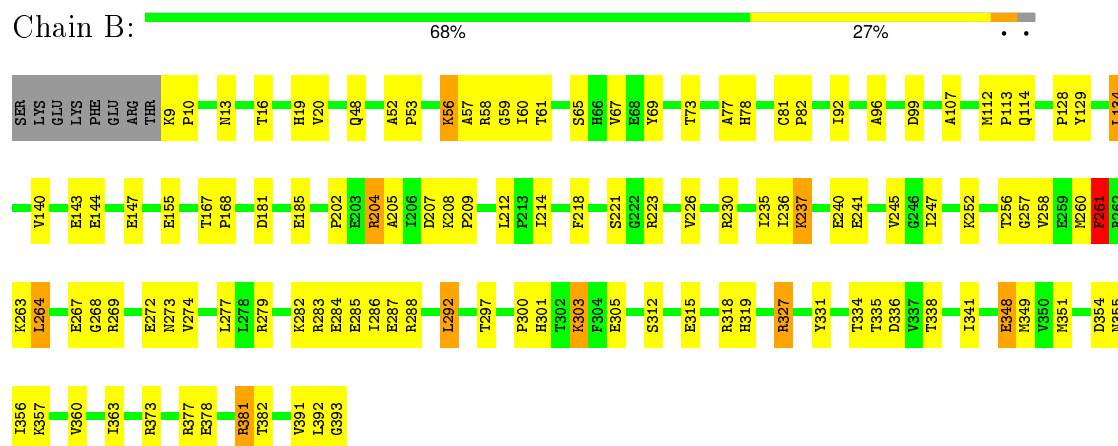
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

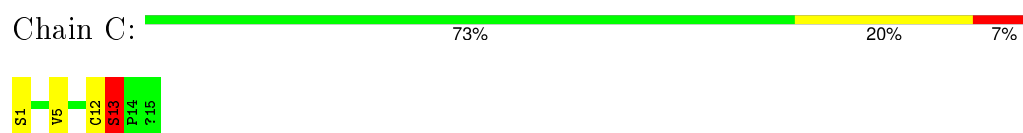
• Molecule 1: ELONGATION FACTOR TU




• Molecule 1: ELONGATION FACTOR TU



• Molecule 2: THIOCILLIN GE2270



- Molecule 2: THIOCILLIN GE2270

Chain D:  80% 13% 7%



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	133.47Å 45.17Å 144.00Å 90.00° 94.64° 90.00°	Depositor
Resolution (Å)	24.44 – 2.35	Depositor
% Data completeness (in resolution range)	86.3 (24.44-2.35)	Depositor
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.200 , 0.246	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6718	wwPDB-VP
Average B, all atoms (Å ²)	27.0	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: GDP, MG, NH2, MEN, ACT, MH6, BB9, BB8, BB7, BB6

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	0.37	0/3084	0.68	0/4173
1	B	0.34	0/3018	0.65	0/4086
2	C	2.02	1/23 (4.3%)	2.05	1/26 (3.8%)
2	D	1.95	1/23 (4.3%)	2.10	0/26
All	All	0.39	2/6148 (0.0%)	0.68	1/8311 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	2	0
2	D	2	0
All	All	4	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	SER	CA-CB	-6.38	1.43	1.52
2	D	1	SER	CA-CB	-6.33	1.43	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	13	SER	CB-CA-C	5.10	119.79	110.10

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	1	SER	CA
2	C	8	BB8	CB
2	D	1	SER	CA
2	D	8	BB8	CB

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	3024	0	3030	118	0
1	B	2963	0	2974	95	0
2	C	87	0	56	2	0
2	D	87	0	56	5	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	28	0	12	1	0
4	B	28	0	12	0	0
5	A	76	0	57	7	0
5	B	44	0	33	3	0
6	A	227	0	0	6	0
6	B	146	0	0	2	0
6	C	4	0	0	0	0
6	D	2	0	0	0	0
All	All	6718	0	6230	213	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 17.

The worst 5 of 213 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:B:327:ARG:O	1:B:327:ARG:HD2	1.46	1.13
1:B:327:ARG:HD3	1:B:338:THR:HG23	1.28	1.11
1:B:348:GLU:CD	1:B:348:GLU:H	1.72	0.93
1:A:279:ARG:HE	1:A:280:GLY:H	1.20	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:HIS:HD2	1:A:75:HIS:HD2	1.18	0.86

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	390/393 (99%)	378 (97%)	10 (3%)	2 (0%)	34	39
1	B	383/393 (98%)	371 (97%)	10 (3%)	2 (0%)	34	39
2	C	4/15 (27%)	2 (50%)	1 (25%)	1 (25%)	0	0
2	D	4/15 (27%)	2 (50%)	1 (25%)	1 (25%)	0	0
All	All	781/816 (96%)	753 (96%)	22 (3%)	6 (1%)	24	26

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
2	C	13	SER
2	D	13	SER
1	B	261	PHE
1	A	247	ILE

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	324/325 (100%)	304 (94%)	20 (6%)	23	26
1	B	317/325 (98%)	298 (94%)	19 (6%)	24	28
2	C	3/4 (75%)	1 (33%)	2 (67%)	0	0
2	D	3/4 (75%)	2 (67%)	1 (33%)	0	0
All	All	647/658 (98%)	605 (94%)	42 (6%)	22	24

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	354	ASP
1	B	65	SER
1	B	381	ARG
1	A	357	LYS
1	B	48	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	273	ASN
1	A	329	GLN
1	B	78	HIS
1	A	251	GLN
1	B	75	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

18 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	BB9	C	10	2	0,4,6	0.00	-	0,4,7	0.00	-
2	MH6	C	11	2	3,3,6	3.69	2 (66%)	1,3,7	3.03	1 (100%)
2	BB9	C	12	2	0,4,6	0.00	-	0,4,7	0.00	-
2	BB9	C	2	2	3,5,6	4.57	1 (33%)	1,5,7	3.00	1 (100%)
2	MEN	C	3	2	7,7,9	1.57	2 (28%)	6,8,11	0.51	0
2	BB6	C	4	2	4,6,7	4.49	1 (25%)	1,7,9	1.80	0
2	BB7	C	6	2	6,8,9	3.70	2 (33%)	3,9,11	1.29	0
2	BB8	C	8	2	11,11,13	2.17	5 (45%)	13,14,17	0.48	0
2	BB9	C	9	2	0,4,6	0.00	-	0,4,7	0.00	-
2	BB9	D	10	2	0,4,6	0.00	-	0,4,7	0.00	-
2	MH6	D	11	2	3,3,6	3.41	2 (66%)	1,3,7	3.21	1 (100%)
2	BB9	D	12	2	0,4,6	0.00	-	0,4,7	0.00	-
2	BB9	D	2	2	3,5,6	4.99	1 (33%)	1,5,7	2.90	1 (100%)
2	MEN	D	3	2	7,7,9	1.30	1 (14%)	6,8,11	0.63	0
2	BB6	D	4	2	4,6,7	4.09	1 (25%)	1,7,9	1.71	0
2	BB7	D	6	2	6,8,9	4.23	1 (16%)	3,9,11	1.61	1 (33%)
2	BB8	D	8	2	11,11,13	3.10	5 (45%)	13,14,17	1.53	2 (15%)
2	BB9	D	9	2	0,4,6	0.00	-	0,4,7	0.00	-

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	BB9	C	10	2	-	0/0/2/6	0/0/0/0
2	MH6	C	11	2	-	0/0/0/6	0/0/0/0
2	BB9	C	12	2	-	0/0/2/6	0/0/0/0
2	BB9	C	2	2	-	0/0/4/6	0/0/0/0
2	MEN	C	3	2	-	0/6/6/10	0/0/0/0
2	BB6	C	4	2	-	0/0/6/8	0/0/0/0
2	BB7	C	6	2	-	0/1/9/11	0/0/0/0
2	BB8	C	8	2	1/1/2/3	0/8/8/12	0/1/1/1
2	BB9	C	9	2	-	0/0/2/6	0/0/0/0
2	BB9	D	10	2	-	0/0/2/6	0/0/0/0
2	MH6	D	11	2	-	0/0/0/6	0/0/0/0
2	BB9	D	12	2	-	0/0/2/6	0/0/0/0
2	BB9	D	2	2	-	0/0/4/6	0/0/0/0
2	MEN	D	3	2	-	0/6/6/10	0/0/0/0
2	BB6	D	4	2	-	0/0/6/8	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BB7	D	6	2	-	0/1/9/11	0/0/0/0
2	BB8	D	8	2	1/1/2/3	0/8/8/12	0/1/1/1
2	BB9	D	9	2	-	0/0/2/6	0/0/0/0

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	11	MH6	CB-CA	-5.17	1.42	1.49
2	D	11	MH6	CB-CA	-4.64	1.43	1.49
2	C	6	BB7	OB2-CB1	2.01	1.46	1.41
2	C	8	BB8	CA-N	2.09	1.50	1.46
2	C	3	MEN	CB-CA	2.20	1.57	1.53

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	BB9	O-C-CA	-3.00	120.98	125.40
2	D	8	BB8	CD2-CG-CB	-2.93	116.43	120.72
2	D	2	BB9	O-C-CA	-2.90	121.13	125.40
2	D	6	BB7	O-C-CA	-2.60	120.33	125.35
2	D	8	BB8	CD1-CG-CB	2.97	125.06	120.72

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	D	8	BB8	CB
2	C	8	BB8	CB

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	12	BB9	1	0
2	D	12	BB9	2	0

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 34 ligands modelled in this entry, 2 are monoatomic - leaving 32 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	ACT	A	3002	-	1,3,3	2.34	1 (100%)	0,3,3	0.00	-
5	ACT	A	3003	-	1,3,3	2.59	1 (100%)	0,3,3	0.00	-
5	ACT	A	3004	-	1,3,3	1.77	0	0,3,3	0.00	-
5	ACT	A	3005	-	1,3,3	2.53	1 (100%)	0,3,3	0.00	-
5	ACT	A	3006	-	1,3,3	2.76	1 (100%)	0,3,3	0.00	-
5	ACT	A	3007	-	1,3,3	2.45	1 (100%)	0,3,3	0.00	-
5	ACT	A	3010	-	1,3,3	2.70	1 (100%)	0,3,3	0.00	-
5	ACT	A	3013	-	1,3,3	2.76	1 (100%)	0,3,3	0.00	-
5	ACT	A	3016	-	1,3,3	2.72	1 (100%)	0,3,3	0.00	-
5	ACT	A	3017	-	1,3,3	2.67	1 (100%)	0,3,3	0.00	-
5	ACT	A	3019	-	1,3,3	2.75	1 (100%)	0,3,3	0.00	-
5	ACT	A	3020	-	1,3,3	2.94	1 (100%)	0,3,3	0.00	-
5	ACT	A	3021	-	1,3,3	2.59	1 (100%)	0,3,3	0.00	-
5	ACT	A	3022	-	1,3,3	2.44	1 (100%)	0,3,3	0.00	-
5	ACT	A	3023	-	1,3,3	2.52	1 (100%)	0,3,3	0.00	-
5	ACT	A	3025	-	1,3,3	2.00	0	0,3,3	0.00	-
5	ACT	A	3026	-	1,3,3	2.47	1 (100%)	0,3,3	0.00	-
5	ACT	A	3028	-	1,3,3	2.64	1 (100%)	0,3,3	0.00	-
5	ACT	A	3030	-	1,3,3	2.92	1 (100%)	0,3,3	0.00	-
4	GDP	A	999	3	23,30,30	1.12	1 (4%)	30,47,47	2.45	6 (20%)
5	ACT	B	3001	-	1,3,3	2.64	1 (100%)	0,3,3	0.00	-
5	ACT	B	3008	-	1,3,3	2.38	1 (100%)	0,3,3	0.00	-
5	ACT	B	3009	-	1,3,3	2.72	1 (100%)	0,3,3	0.00	-
5	ACT	B	3011	-	1,3,3	2.49	1 (100%)	0,3,3	0.00	-
5	ACT	B	3012	-	1,3,3	2.84	1 (100%)	0,3,3	0.00	-
5	ACT	B	3014	-	1,3,3	2.26	1 (100%)	0,3,3	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ACT	B	3015	-	1,3,3	2.73	1 (100%)	0,3,3	0.00	-
5	ACT	B	3018	-	1,3,3	2.64	1 (100%)	0,3,3	0.00	-
5	ACT	B	3024	-	1,3,3	2.51	1 (100%)	0,3,3	0.00	-
5	ACT	B	3027	-	1,3,3	3.24	1 (100%)	0,3,3	0.00	-
5	ACT	B	3029	-	1,3,3	2.92	1 (100%)	0,3,3	0.00	-
4	GDP	B	999	3	23,30,30	1.19	1 (4%)	30,47,47	2.42	7 (23%)

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	ACT	A	3002	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3003	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3004	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3005	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3006	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3007	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3010	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3013	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3016	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3017	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3019	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3020	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3021	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3022	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3023	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3025	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3026	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3028	-	-	0/0/0/0	0/0/0/0
5	ACT	A	3030	-	-	0/0/0/0	0/0/0/0
4	GDP	A	999	3	-	0/12/32/32	0/3/3/3
5	ACT	B	3001	-	-	0/0/0/0	0/0/0/0
5	ACT	B	3008	-	-	0/0/0/0	0/0/0/0
5	ACT	B	3009	-	-	0/0/0/0	0/0/0/0
5	ACT	B	3011	-	-	0/0/0/0	0/0/0/0
5	ACT	B	3012	-	-	0/0/0/0	0/0/0/0
5	ACT	B	3014	-	-	0/0/0/0	0/0/0/0
5	ACT	B	3015	-	-	0/0/0/0	0/0/0/0
5	ACT	B	3018	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ACT	B	3024	-	-	0/0/0/0	0/0/0/0
5	ACT	B	3027	-	-	0/0/0/0	0/0/0/0
5	ACT	B	3029	-	-	0/0/0/0	0/0/0/0
4	GDP	B	999	3	-	0/12/32/32	0/3/3/3

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	3014	ACT	CH3-C	2.26	1.51	1.48
5	A	3002	ACT	CH3-C	2.34	1.52	1.48
5	B	3008	ACT	CH3-C	2.38	1.52	1.48
5	A	3022	ACT	CH3-C	2.44	1.52	1.48
5	A	3007	ACT	CH3-C	2.45	1.52	1.48

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	999	GDP	C5-C6-N1	-8.99	111.30	123.59
4	B	999	GDP	C5-C6-N1	-8.98	111.31	123.59
4	B	999	GDP	PA-O3A-PB	-3.19	121.99	132.67
4	A	999	GDP	O3'-C3'-C2'	-3.14	101.62	111.83
4	B	999	GDP	O3'-C3'-C4'	-3.13	101.68	111.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	3004	ACT	1	0
5	A	3007	ACT	2	0
5	A	3021	ACT	1	0
5	A	3028	ACT	1	0
5	A	3030	ACT	2	0
4	A	999	GDP	1	0
5	B	3009	ACT	1	0
5	B	3011	ACT	1	0
5	B	3012	ACT	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.