



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:36 PM GMT

PDB ID : 3U6B
Title : Ef-tu (escherichia coli) in complex with nvp-ldi028
Authors : Palestrant, D.J.
Deposited on : 2011-10-12
Resolution : 2.12 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

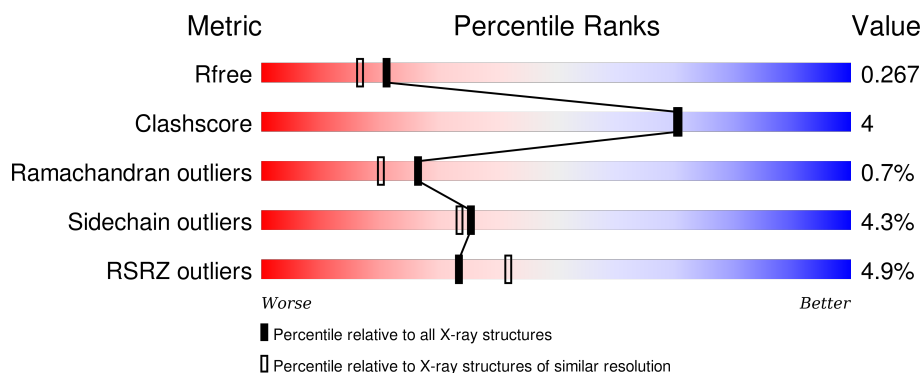
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	4587 (2.14-2.10)
Clashscore	102246	5132 (2.14-2.10)
Ramachandran outliers	100387	5080 (2.14-2.10)
Sidechain outliers	100360	5081 (2.14-2.10)
RSRZ outliers	91569	4597 (2.14-2.10)

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	394	<div> <div>3%</div> <div>81% 12% • 6%</div> </div>
1	B	394	<div> <div>7%</div> <div>82% 13% • 5%</div> </div>
2	C	12	<div> <div>8%</div> <div>75% 25%</div> </div>
2	D	12	<div> <div>58% 42%</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
2	MH6	C	11	-	X	-	-
2	MH6	D	11	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6044 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 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	369	Total	C	N	O	S	0	0	0
			2837	1802	482	540	13			
1	B	376	Total	C	N	O	S	0	0	0
			2870	1817	492	548	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	EXPRESSION TAG	UNP P0CE47
A	1	ALA	-	EXPRESSION TAG	UNP P0CE47
B	0	MET	-	EXPRESSION TAG	UNP P0CE47
B	1	ALA	-	EXPRESSION TAG	UNP P0CE47

- Molecule 2 is a protein called Thiocillin GE2270 analogue NVP-LDI028.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	12	Total	C	N	O	S	0	0	0
			84	55	13	10	6			
2	D	12	Total	C	N	O	S	0	0	0
			84	55	13	10	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	12	8BB	CYS	SEE REMARK 999	UNP Q7M0J8
D	12	8BB	CYS	SEE REMARK 999	UNP Q7M0J8

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

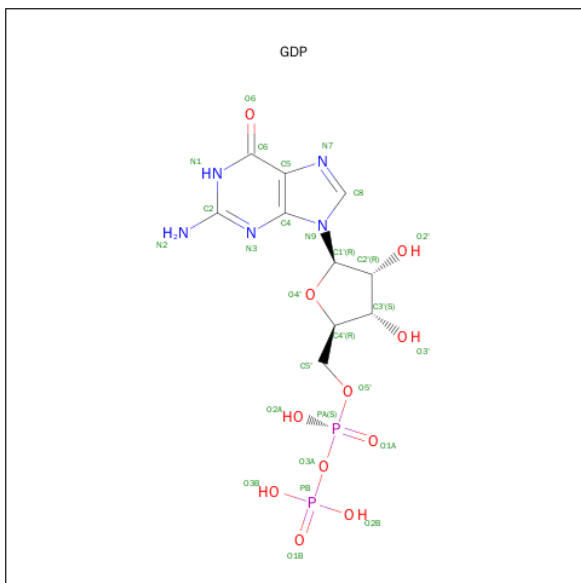
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		

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

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



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

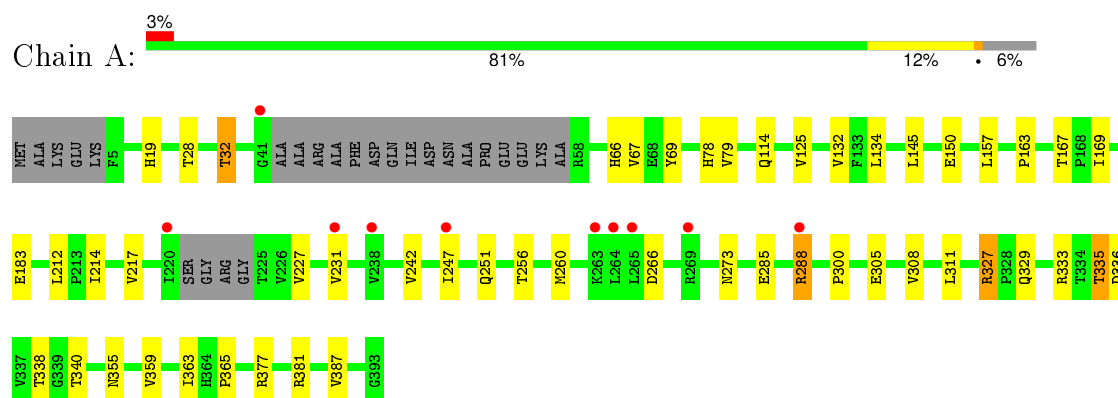
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	62	Total	O	0	0
			62	62		
5	B	47	Total	O	0	0
			47	47		
5	C	2	Total	O	0	0
			2	2		

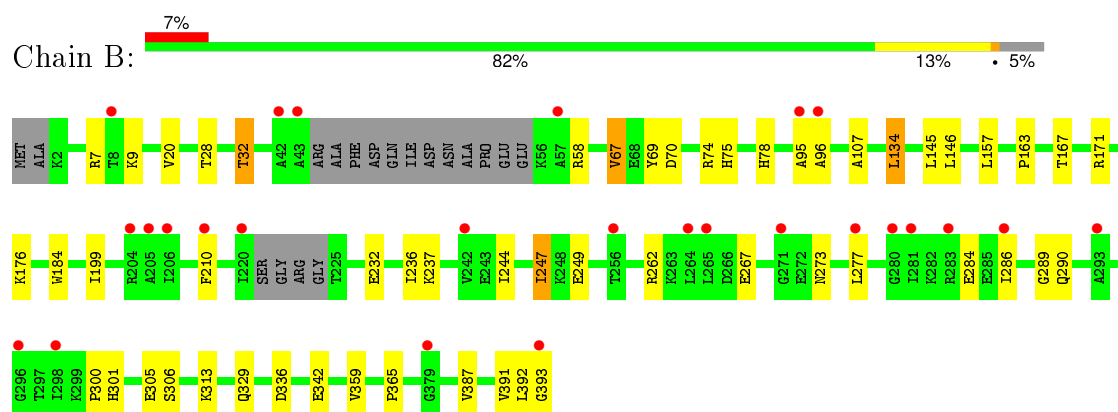
3 Residue-property plots

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.

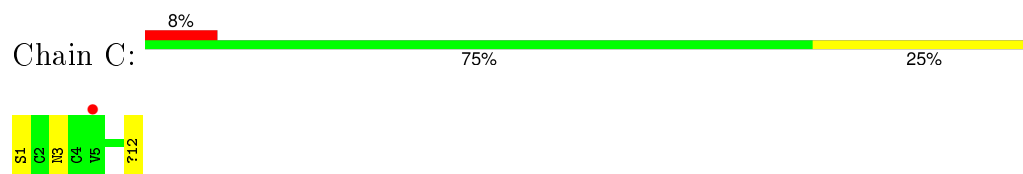
- Molecule 1: Elongation factor Tu 1



- Molecule 1: Elongation factor Tu 1

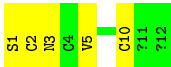


- Molecule 2: Thiocillin GE2270 analogue NVP-LDI028



- Molecule 2: Thiocillin GE2270 analogue NVP-LDI028





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	97.25Å 100.38Å 156.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.12 42.24 – 2.12	Depositor EDS
% Data completeness (in resolution range)	85.8 (8.00-2.12) 88.2 (42.24-2.12)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 2.12Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.196 , 0.257 0.203 , 0.267	Depositor DCC
R_{free} test set	1919 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.416	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.3	EDS
Estimated twinning fraction	0.118 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	1 of 39657 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6044	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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: GDP, MG, MEN, BB7, BB9, BB8, MH6, BB6, 8BB

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	0.48	0/2889	0.71	0/3913
1	B	0.49	0/2921	0.76	0/3956
2	C	2.63	1/10 (10.0%)	1.53	0/9
2	D	2.93	1/10 (10.0%)	1.45	0/9
All	All	0.51	2/5830 (0.0%)	0.74	0/7887

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	1	0
2	D	1	0
All	All	2	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	SER	CA-CB	-8.92	1.39	1.52
2	C	1	SER	CA-CB	-7.84	1.41	1.52

There are no bond angle outliers.

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	1	SER	CA
2	D	1	SER	CA

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	2837	0	2845	25	0
1	B	2870	0	2858	25	0
2	C	84	0	55	2	0
2	D	84	0	55	4	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	28	0	12	0	0
4	B	28	0	12	0	0
5	A	62	0	0	1	0
5	B	47	0	0	0	0
5	C	2	0	0	0	0
All	All	6044	0	5837	52	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 (52) 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:163:PRO:O	1:A:167:THR:HG23	1.88	0.73
1:B:74:ARG:NH2	1:B:199:ILE:O	2.20	0.68
1:B:32:THR:HG21	1:B:67:VAL:HG11	1.76	0.68
1:B:301:HIS:HD2	1:B:393:GLY:HA2	1.63	0.64
1:B:329:GLN:HE21	1:B:336:ASP:HB3	1.63	0.63
1:A:66:HIS:CE1	1:A:79:VAL:HG22	2.39	0.57
1:B:157:LEU:HD13	1:B:167:THR:HG21	1.87	0.57
1:B:176:LYS:HB3	1:B:184:TRP:CD1	2.41	0.56
1:A:167:THR:HG22	5:A:518:HOH:O	2.07	0.55
1:A:327:ARG:HG3	1:A:340:THR:HG22	1.90	0.54
1:A:329:GLN:HE21	1:A:336:ASP:HB3	1.71	0.54
1:A:28:THR:O	1:A:32:THR:HG23	2.08	0.53
1:B:69:TYR:OH	1:B:78:HIS:HD2	1.93	0.52
1:A:273:ASN:O	2:D:3:MEN:HE21	2.10	0.52
2:D:3:MEN:HE23	2:D:10:BB9:SG	2.51	0.51
1:A:150:GLU:HG2	1:A:169:ILE:HG21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:237:LYS:HG2	1:B:267:GLU:HB3	1.92	0.50
1:B:163:PRO:O	1:B:167:THR:HG23	2.12	0.50
1:A:217:VAL:HG22	1:A:227:VAL:HG12	1.95	0.49
1:B:277:LEU:HB2	2:C:12:8BB:CB	2.43	0.49
1:A:288:ARG:HG2	1:A:335:THR:HB	1.94	0.48
1:A:157:LEU:HD13	1:A:167:THR:HG21	1.95	0.48
1:A:212:LEU:HD12	1:A:231:VAL:HG22	1.94	0.48
1:B:301:HIS:CD2	1:B:393:GLY:HA2	2.48	0.48
1:B:342:GLU:HB2	1:B:359:VAL:HB	1.97	0.46
1:A:132:VAL:HB	1:A:169:ILE:HG12	1.96	0.46
1:A:69:TYR:OH	1:A:78:HIS:HD2	1.98	0.46
1:B:70:ASP:OD1	1:B:75:HIS:HD2	1.98	0.46
1:B:95:ALA:HA	1:B:96:ALA:HA	1.82	0.46
1:B:28:THR:O	1:B:32:THR:HG23	2.16	0.46
1:A:308:VAL:O	1:A:355:ASN:HA	2.17	0.45
1:B:210:PHE:CE1	1:B:236:ILE:HB	2.51	0.45
1:B:247:ILE:HD11	1:B:289:GLY:HA3	1.99	0.45
1:A:338:THR:HB	1:A:363:ILE:HG12	1.99	0.45
1:A:125:VAL:HG12	1:A:387:VAL:HG11	1.99	0.45
1:A:66:HIS:ND1	1:A:79:VAL:HG22	2.32	0.44
1:B:244:ILE:HG21	1:B:286:ILE:HG21	1.98	0.44
1:A:260:MET:HG3	2:D:3:MEN:HE22	2.00	0.44
1:B:273:ASN:O	2:C:3:MEN:HE21	2.18	0.44
1:A:19:HIS:HA	1:A:114:GLN:HB2	2.00	0.44
1:B:306:SER:HB2	1:B:387:VAL:O	2.18	0.43
1:A:305:GLU:HG2	1:A:359:VAL:HG22	2.01	0.43
1:B:305:GLU:HG3	1:B:392:LEU:HD11	2.00	0.43
1:A:32:THR:HG21	1:A:67:VAL:HG21	2.00	0.43
1:B:247:ILE:HD12	1:B:290:GLN:HG3	2.00	0.42
1:A:251:GLN:HE22	1:A:285:GLU:HB3	1.84	0.42
2:D:2:BB9:N	2:D:10:BB9:N	2.67	0.42
1:A:300:PRO:HB2	1:A:365:PRO:HB2	2.01	0.42
1:B:300:PRO:HB2	1:B:365:PRO:HB2	2.01	0.42
1:A:214:ILE:HD12	1:A:227:VAL:HB	2.02	0.42
1:B:107:ALA:HB2	1:B:134:LEU:HD22	2.02	0.41
1:B:146:LEU:HD13	1:B:171:ARG:HD3	2.01	0.41

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	363/394 (92%)	353 (97%)	8 (2%)	2 (1%)	30	24
1	B	370/394 (94%)	350 (95%)	18 (5%)	2 (0%)	34	29
2	C	2/12 (17%)	1 (50%)	1 (50%)	0	100	100
2	D	2/12 (17%)	1 (50%)	0	1 (50%)	0	0
All	All	737/812 (91%)	705 (96%)	27 (4%)	5 (1%)	26	20

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	5	VAL
1	A	333	ARG
1	B	7	ARG
1	A	247	ILE
1	B	247	ILE

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	305/325 (94%)	292 (96%)	13 (4%)	35	33
1	B	304/325 (94%)	291 (96%)	13 (4%)	35	33
2	C	1/2 (50%)	1 (100%)	0	100	100
2	D	1/2 (50%)	1 (100%)	0	100	100
All	All	611/654 (93%)	585 (96%)	26 (4%)	35	33

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	THR
1	A	134	LEU
1	A	145	LEU
1	A	183	GLU
1	A	242	VAL
1	A	256	THR
1	A	266	ASP
1	A	288	ARG
1	A	311	LEU
1	A	327	ARG
1	A	335	THR
1	A	377	ARG
1	A	381	ARG
1	B	9	LYS
1	B	20	VAL
1	B	32	THR
1	B	58	ARG
1	B	67	VAL
1	B	134	LEU
1	B	145	LEU
1	B	232	GLU
1	B	249	GLU
1	B	262	ARG
1	B	284	GLU
1	B	313	LYS
1	B	391	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	HIS
1	A	124	GLN
1	A	251	GLN
1	A	329	GLN
1	B	11	HIS
1	B	75	HIS
1	B	78	HIS
1	B	301	HIS
1	B	329	GLN

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	3.84	3 (100%)	1,3,7	1.14	0
2	8BB	C	12	2	11,16,16	2.30	2 (18%)	14,21,21	0.81	0
2	BB9	C	2	2	3,5,6	2.57	2 (66%)	1,5,7	4.95	1 (100%)
2	MEN	C	3	2	7,7,9	0.65	0	6,8,11	1.22	1 (16%)
2	BB6	C	4	2	4,6,7	2.43	2 (50%)	1,7,9	2.30	1 (100%)
2	BB7	C	6	2	6,8,9	2.19	2 (33%)	3,9,11	1.43	1 (33%)
2	BB8	C	8	2	11,11,13	2.35	4 (36%)	13,14,17	1.40	3 (23%)
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	4.32	3 (100%)	1,3,7	0.57	0
2	8BB	D	12	2	11,16,16	2.18	2 (18%)	14,21,21	0.99	1 (7%)
2	BB9	D	2	2	3,5,6	2.67	1 (33%)	1,5,7	3.71	1 (100%)
2	MEN	D	3	2	7,7,9	0.79	0	6,8,11	1.35	1 (16%)
2	BB6	D	4	2	4,6,7	2.44	2 (50%)	1,7,9	1.94	0
2	BB7	D	6	2	6,8,9	2.13	2 (33%)	3,9,11	1.47	1 (33%)
2	BB8	D	8	2	11,11,13	2.32	4 (36%)	13,14,17	0.99	1 (7%)
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	8BB	C	12	2	-	0/6/24/24	0/1/1/1
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	-	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	8BB	D	12	2	-	0/6/24/24	0/1/1/1
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
2	BB7	D	6	2	-	0/1/9/11	0/0/0/0
2	BB8	D	8	2	-	0/8/8/12	0/1/1/1
2	BB9	D	9	2	-	0/0/2/6	0/0/0/0

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	11	MH6	CB-CA	-6.36	1.40	1.49
2	C	11	MH6	CB-CA	-5.63	1.41	1.49
2	C	8	BB8	OB-CB	-5.15	1.32	1.42
2	D	8	BB8	OB-CB	-4.97	1.32	1.42
2	D	11	MH6	C-CA	-3.39	1.44	1.49
2	C	8	BB8	CG-CB	-3.23	1.47	1.51
2	C	11	MH6	C-CA	-2.80	1.45	1.49
2	C	8	BB8	CB-CA	-2.12	1.52	1.54
2	D	11	MH6	CA-N	2.01	1.34	1.27
2	C	11	MH6	CA-N	2.16	1.35	1.27
2	D	8	BB8	CE2-CZ	2.20	1.43	1.38
2	C	2	BB9	C-CA	2.38	1.48	1.45
2	D	8	BB8	CD2-CG	2.39	1.43	1.39
2	C	8	BB8	CD1-CG	2.48	1.43	1.39
2	C	4	BB6	C-CA	2.64	1.49	1.45
2	D	4	BB6	C-CA	2.80	1.49	1.45
2	D	6	BB7	C-CA	2.85	1.49	1.45
2	D	8	BB8	CD1-CG	3.27	1.44	1.39
2	C	6	BB7	C-CA	3.37	1.50	1.45
2	C	2	BB9	CA-N	3.75	1.44	1.34
2	D	12	8BB	CA-N1	3.75	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	4	BB6	CA-N	3.94	1.46	1.36
2	C	6	BB7	CA-N	4.01	1.47	1.36
2	C	4	BB6	CA-N	4.03	1.47	1.36
2	C	12	8BB	CA-N1	4.11	1.49	1.38
2	D	6	BB7	CA-N	4.16	1.47	1.36
2	D	2	BB9	CA-N	4.37	1.46	1.34
2	D	12	8BB	CA-N	6.01	1.45	1.34
2	C	12	8BB	CA-N	6.20	1.46	1.34

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	BB9	O-C-CA	-4.95	118.10	125.40
2	D	2	BB9	O-C-CA	-3.71	119.93	125.40
2	D	3	MEN	CB-CG-ND2	-2.71	112.22	116.03
2	C	8	BB8	C-CA-CB	-2.68	107.58	111.86
2	C	8	BB8	CG-CB-CA	-2.63	108.45	112.34
2	D	6	BB7	O-C-CA	-2.52	120.49	125.35
2	C	6	BB7	O-C-CA	-2.47	120.58	125.35
2	C	4	BB6	O-C-CA	-2.30	120.91	125.35
2	D	8	BB8	CG-CB-CA	-2.25	109.01	112.34
2	C	3	MEN	CB-CG-ND2	-2.12	113.04	116.03
2	D	12	8BB	O89-C88-N1	2.02	125.79	122.53
2	C	8	BB8	CD2-CG-CD1	2.15	121.04	118.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	12	8BB	1	0
2	C	3	MEN	1	0
2	D	10	BB9	2	0
2	D	2	BB9	1	0
2	D	3	MEN	3	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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$
4	GDP	A	402	3	23,30,30	1.04	1 (4%)	30,47,47	2.15	4 (13%)
4	GDP	B	401	3	23,30,30	1.00	1 (4%)	30,47,47	2.04	4 (13%)

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
4	GDP	A	402	3	-	0/12/32/32	0/3/3/3
4	GDP	B	401	3	-	0/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	401	GDP	C6-N1	3.17	1.39	1.33
4	A	402	GDP	C6-N1	3.21	1.39	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	402	GDP	C5-C6-N1	-8.34	112.19	123.59
4	B	401	GDP	C5-C6-N1	-7.78	112.95	123.59
4	B	401	GDP	N3-C2-N1	-2.81	123.16	127.44
4	A	402	GDP	N3-C2-N1	-2.68	123.36	127.44
4	A	402	GDP	C6-C5-C4	-2.37	118.06	120.90
4	B	401	GDP	C6-C5-C4	-2.04	118.46	120.90
4	B	401	GDP	C6-N1-C2	6.34	124.74	115.94
4	A	402	GDP	C6-N1-C2	6.75	125.30	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	369/394 (93%)	0.42	10 (2%) 58 65	19, 34, 58, 70	0
1	B	376/394 (95%)	0.58	26 (6%) 20 27	17, 35, 62, 86	0
2	C	3/12 (25%)	1.71	1 (33%) 0 1	50, 50, 50, 66	0
2	D	3/12 (25%)	0.94	0 100 100	45, 45, 60, 69	0
All	All	751/812 (92%)	0.51	37 (4%) 33 42	17, 35, 60, 86	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	5	VAL	4.2
1	B	42	ALA	4.2
1	B	265	LEU	3.7
1	B	393	GLY	3.6
1	B	264	LEU	3.3
1	B	204	ARG	3.2
1	B	280	GLY	3.2
1	A	264	LEU	3.2
1	A	265	LEU	3.2
1	B	96	ALA	3.1
1	A	263	LYS	3.0
1	B	281	ILE	2.9
1	B	206	ILE	2.9
1	B	286	ILE	2.9
1	B	242	VAL	2.9
1	A	220	ILE	2.9
1	B	271	GLY	2.8
1	B	277	LEU	2.7
1	A	269	ARG	2.7
1	B	43	ALA	2.5
1	B	57	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	293	ALA	2.4
1	A	288	ARG	2.4
1	B	379	GLY	2.3
1	B	283	ARG	2.3
1	B	296	GLY	2.3
1	B	95	ALA	2.3
1	B	220	ILE	2.2
1	B	298	ILE	2.2
1	B	205	ALA	2.2
1	A	238	VAL	2.2
1	A	247	ILE	2.2
1	B	256	THR	2.1
1	B	210	PHE	2.1
1	A	41	GLY	2.1
1	B	8	THR	2.1
1	A	231	VAL	2.1

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

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(Å ²)	Q<0.9
2	BB6	D	4	7/8	0.95	0.15	-	52,54,59,59	0
2	BB9	C	10	5/7	0.95	0.14	-	43,48,50,50	0
2	BB6	C	4	7/8	0.93	0.19	-	54,55,61,63	0
2	MEN	D	3	8/10	0.93	0.13	-	46,48,49,50	0
2	BB8	C	8	11/13	0.94	0.17	-	38,41,45,46	0
2	BB9	D	10	5/7	0.98	0.12	-	37,39,41,42	0
2	BB8	D	8	11/13	0.89	0.17	-	40,45,51,51	0
2	BB9	C	9	5/7	0.94	0.11	-	42,43,43,45	0
2	BB9	D	9	5/7	0.97	0.13	-	40,40,42,42	0
2	MH6	C	11	4/7	0.89	0.20	-	54,54,57,61	0
2	MH6	D	11	4/7	0.94	0.22	-	42,46,47,55	0
2	8BB	C	12	16/16	0.80	0.39	-	61,85,91,91	0
2	BB9	C	2	6/7	0.90	0.16	-	43,44,46,47	0
2	MEN	C	3	8/10	0.90	0.13	-	48,52,54,56	0
2	8BB	D	12	16/16	0.83	0.36	-	56,77,83,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	BB7	C	6	9/10	0.89	0.24	-	59,65,71,71	0
2	BB9	D	2	6/7	0.93	0.13	-	44,46,46,47	0
2	BB7	D	6	9/10	0.85	0.24	-	65,73,78,79	0

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
4	GDP	A	402	28/28	0.98	0.12	-0.30	21,24,29,31	0
4	GDP	B	401	28/28	0.98	0.12	-0.79	15,20,25,32	0
3	MG	A	401	1/1	0.96	0.08	-	25,25,25,25	0
3	MG	B	402	1/1	0.99	0.08	-	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.