



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:21 AM GMT

PDB ID : 2GSK  
Title : Structure of the BtuB:TonB Complex  
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Deposited on : 2006-04-26  
Resolution : 2.10 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](mailto: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.

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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

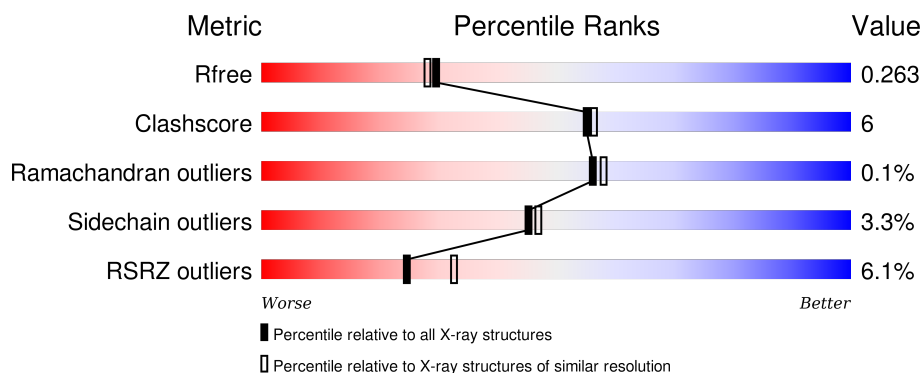
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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  $\geq 3$ , 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	590	<div> <div>4%</div> <div>84%</div> <div>16%</div> </div>
2	B	81	<div> <div>22%</div> <div>79%</div> <div>19%</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
5	LDA	A	800	-	-	-	X
5	LDA	A	801	-	-	-	X
5	LDA	A	802	-	-	-	X
5	LDA	A	803	-	-	-	X
6	OCT	A	804	-	-	-	X
6	OCT	A	805	-	-	-	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5658 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 Vitamin B12 transporter btuB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	590	Total	C	N	O	S	0	0	0
			4591	2904	779	906	2			

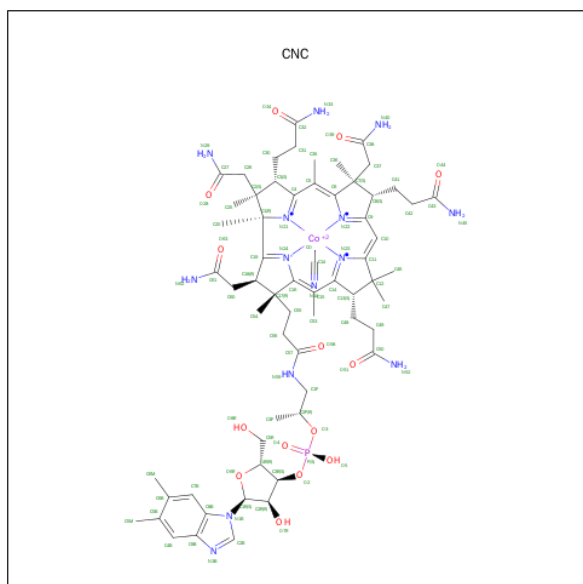
- Molecule 2 is a protein called protein TONB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	81	Total	C	N	O	S	0	0	0
			603	383	113	105	2			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

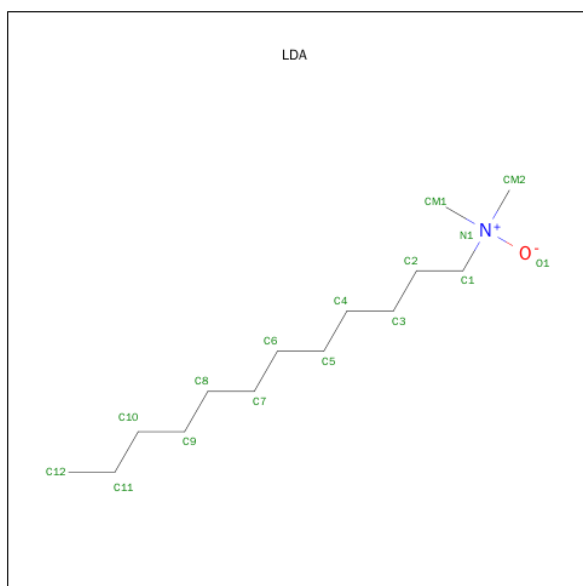
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Ca	0	0
			2	2		

- Molecule 4 is CO-CYANOCOBALAMIN (three-letter code: CNC) (formula:  $C_{63}H_{88}CoN_{14}O_{14}P$ ).



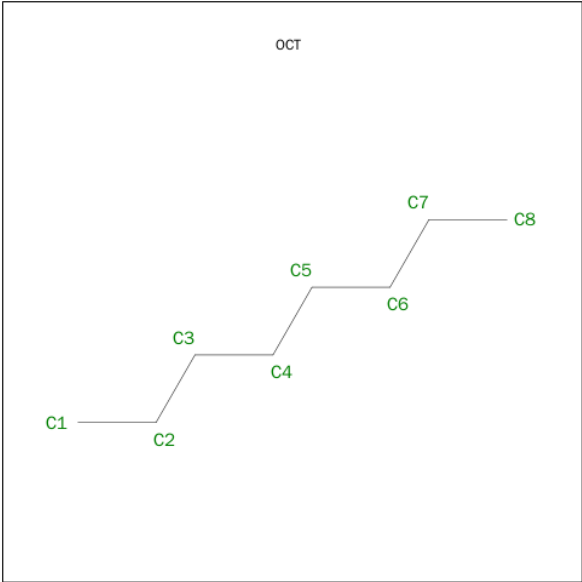
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Co	N	O	P	
			93	63	1	14	14	1	
								0	0

- Molecule 5 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula:  $C_{14}H_{31}NO$ ).



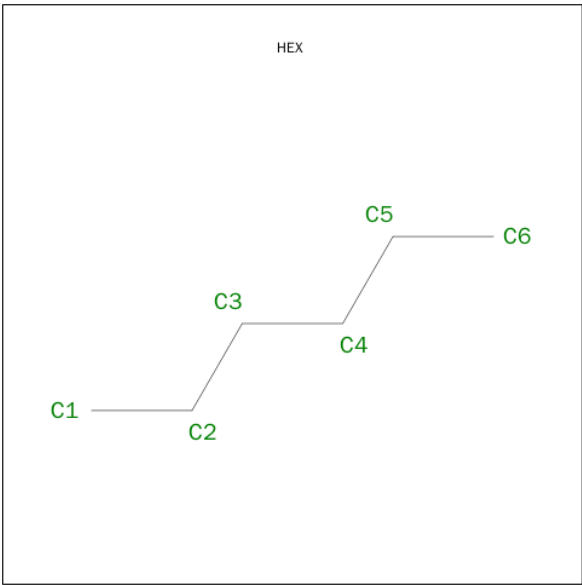
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O		
			15	13	1	1	0	0
5	A	1	Total	C	N	O		
			16	14	1	1	0	0
5	A	1	Total	C	N			
			14	13	1		0	0
5	A	1	Total	C	N	O		
			14	12	1	1	0	0

- Molecule 6 is N-OCTANE (three-letter code: OCT) (formula:  $C_8H_{18}$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	C	0	0
			8	8		
6	A	1	Total	C	0	0
			8	8		
6	A	1	Total	C	0	0
			8	8		

- Molecule 7 is HEXANE (three-letter code: HEX) (formula: C<sub>6</sub>H<sub>14</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	C	0	0
			6	6		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C 6 6	0	0

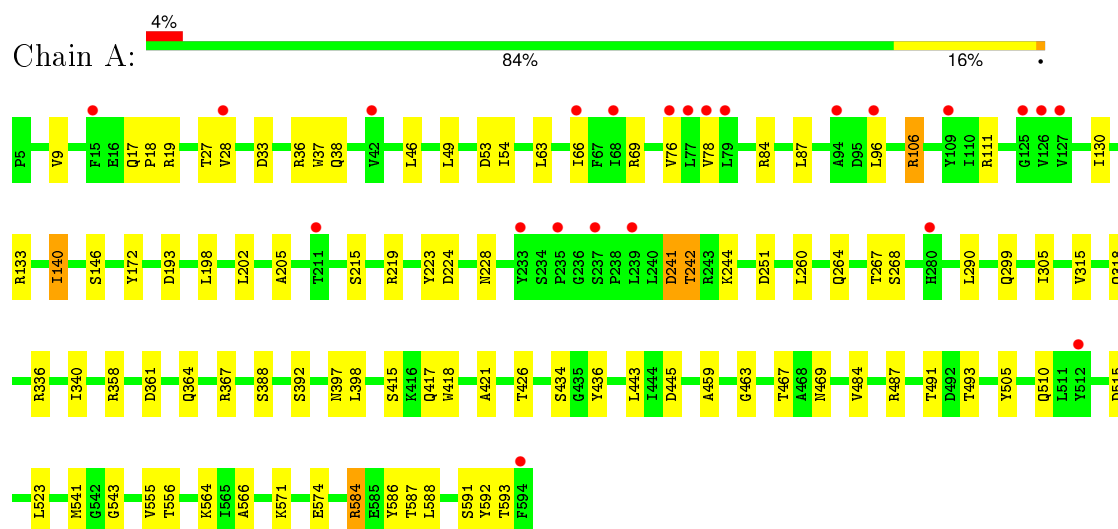
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	256	Total O 256 256	0	0
8	B	18	Total O 18 18	0	0

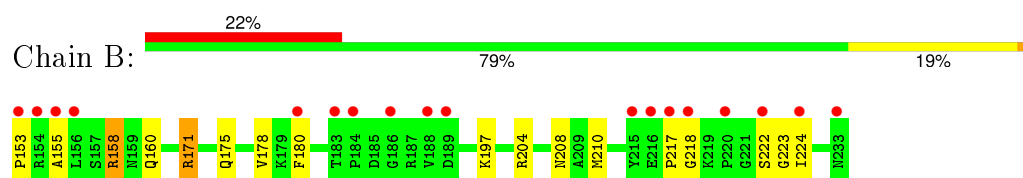
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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: Vitamin B12 transporter btuB



- Molecule 2: protein TONB





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.34Å 82.44Å 122.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.10 36.62 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.1 (40.00-2.10) 98.0 (36.62-2.10)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.43 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.196 , 0.251 0.209 , 0.263	Depositor DCC
$R_{free}$ test set	1190 reflections (2.79%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.6	Xtriage
Anisotropy	0.501	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 52.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 43954 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5658	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OCT, LDA, HEX, CA, CNC

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	1.20	9/4708 (0.2%)	1.11	16/6420 (0.2%)
2	B	0.95	0/615	0.88	0/829
All	All	1.17	9/5323 (0.2%)	1.08	16/7249 (0.2%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	241	ASP	CB-CG	-7.90	1.35	1.51
1	A	574	GLU	CD-OE1	-6.64	1.18	1.25
1	A	566	ALA	CA-CB	5.84	1.64	1.52
1	A	76	VAL	CB-CG2	5.31	1.64	1.52
1	A	223	TYR	CE1-CZ	5.19	1.45	1.38
1	A	37	TRP	CE3-CZ3	5.12	1.47	1.38
1	A	388	SER	CB-OG	-5.07	1.35	1.42
1	A	28	VAL	CB-CG1	5.07	1.63	1.52
1	A	268	SER	CB-OG	5.01	1.48	1.42

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	241	ASP	CB-CG-OD1	-16.95	103.04	118.30
1	A	251	ASP	CB-CG-OD1	12.26	129.34	118.30
1	A	251	ASP	CB-CG-OD2	-12.11	107.40	118.30
1	A	193	ASP	CB-CG-OD2	-9.35	109.89	118.30
1	A	193	ASP	CB-CG-OD1	8.59	126.03	118.30
1	A	241	ASP	CB-CG-OD2	6.88	124.49	118.30
1	A	584	ARG	NE-CZ-NH2	6.88	123.74	120.30
1	A	53	ASP	CB-CG-OD1	6.61	124.25	118.30
1	A	445	ASP	CB-CG-OD1	5.97	123.67	118.30
1	A	133	ARG	NE-CZ-NH1	5.70	123.15	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	241	ASP	CB-CA-C	-5.69	99.01	110.40
1	A	541	MET	CG-SD-CE	-5.63	91.19	100.20
1	A	140	ILE	CG1-CB-CG2	-5.61	99.05	111.40
1	A	106	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	A	69	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	A	487	ARG	NE-CZ-NH1	5.18	122.89	120.30

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	4591	0	4264	50	0
2	B	603	0	577	13	0
3	A	2	0	0	0	0
4	A	93	0	87	7	0
5	A	59	0	109	6	0
6	A	24	0	54	1	0
7	A	12	0	28	1	0
8	A	256	0	0	10	0
8	B	18	0	0	0	0
All	All	5658	0	5119	66	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 6.

All (66) 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)
2:B:155:ALA:HB1	2:B:158:ARG:HD2	1.53	0.88
1:A:467:THR:HG23	8:A:835:HOH:O	1.80	0.81
1:A:228:ASN:OD1	1:A:242:THR:HG23	1.86	0.75
4:A:701:CNC:H533	4:A:701:CNC:H492	1.71	0.72
1:A:361:ASP:OD1	1:A:367:ARG:HG3	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:588:LEU:HD13	5:A:803:LDA:H72	1.76	0.67
4:A:701:CNC:H531	4:A:701:CNC:H552	1.76	0.67
1:A:202:LEU:HD13	5:A:800:LDA:H32	1.79	0.65
2:B:178:VAL:HG11	2:B:210:MET:CE	2.27	0.64
4:A:701:CNC:H531	4:A:701:CNC:C55	2.27	0.63
1:A:305:ILE:HG21	2:B:171:ARG:HD2	1.81	0.62
1:A:392:SER:OG	1:A:415:SER:HB3	2.00	0.61
4:A:701:CNC:H362	4:A:701:CNC:H351	1.82	0.61
1:A:426:THR:HG23	6:A:804:OCT:H83	1.83	0.60
1:A:224:ASP:OD1	1:A:244:LYS:NZ	2.26	0.59
1:A:84:ARG:HD2	1:A:318:GLN:OE1	2.03	0.58
1:A:467:THR:CG2	8:A:835:HOH:O	2.46	0.57
2:B:204:ARG:HH11	2:B:208:ASN:ND2	2.02	0.57
1:A:78:VAL:HG11	1:A:96:LEU:HD21	1.88	0.55
1:A:260:LEU:HA	1:A:305:ILE:HD12	1.89	0.54
2:B:155:ALA:CB	2:B:158:ARG:HD2	2.32	0.54
1:A:146:SER:HA	5:A:803:LDA:H12	1.90	0.54
1:A:364:GLN:HG2	1:A:398:LEU:HD21	1.90	0.54
1:A:17:GLN:NE2	1:A:18:PRO:O	2.41	0.53
2:B:180:PHE:O	2:B:222:SER:O	2.27	0.53
1:A:36:ARG:NH1	1:A:515:ASP:OD1	2.42	0.53
1:A:555:VAL:HG12	1:A:556:THR:HG23	1.91	0.52
1:A:418:TRP:CE2	8:A:990:HOH:O	2.63	0.52
1:A:202:LEU:HD13	5:A:800:LDA:C3	2.40	0.50
2:B:153:PRO:CG	2:B:224:ILE:HD11	2.42	0.50
1:A:172:TYR:CE1	1:A:198:LEU:HD11	2.47	0.49
1:A:417:GLN:NE2	8:A:847:HOH:O	2.45	0.49
1:A:106:ARG:HB3	1:A:130:ILE:HB	1.95	0.49
1:A:27:THR:HG21	1:A:49:LEU:HD22	1.94	0.49
1:A:443:LEU:HD22	1:A:459:ALA:HB2	1.95	0.49
2:B:153:PRO:HG3	2:B:224:ILE:HD11	1.95	0.49
1:A:260:LEU:HA	1:A:305:ILE:CD1	2.43	0.48
1:A:63:LEU:H	4:A:701:CNC:H332	1.62	0.48
1:A:510:GLN:CG	8:A:1040:HOH:O	2.60	0.48
1:A:215:SER:OG	8:A:913:HOH:O	2.19	0.48
1:A:299:GLN:CD	8:A:1015:HOH:O	2.51	0.47
2:B:175:GLN:HG2	2:B:197:LYS:HE2	1.97	0.47
1:A:491:THR:O	1:A:493:THR:HG23	2.15	0.47
2:B:217:PRO:HA	2:B:218:GLY:HA2	1.79	0.46
1:A:205:ALA:CB	1:A:219:ARG:HG2	2.46	0.46
1:A:9:VAL:O	2:B:160:GLN:NE2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:178:VAL:HG11	2:B:210:MET:HE3	1.98	0.45
1:A:336:ARG:NH1	8:A:1043:HOH:O	2.50	0.45
1:A:267:THR:HG23	7:A:807:HEX:H52	1.99	0.45
1:A:140:ILE:HG22	1:A:592:TYR:HB3	1.99	0.45
1:A:571:LYS:NZ	8:A:889:HOH:O	2.45	0.45
1:A:436:TYR:CZ	1:A:463:GLY:HA3	2.53	0.44
1:A:305:ILE:CG2	2:B:171:ARG:HD2	2.47	0.44
4:A:701:CNC:C61	4:A:701:CNC:H551	2.48	0.44
1:A:63:LEU:HD13	4:A:701:CNC:HM63	1.99	0.43
1:A:260:LEU:HD12	1:A:305:ILE:HB	1.99	0.43
1:A:315:VAL:HG12	1:A:340:ILE:HG13	2.00	0.43
1:A:66:ILE:HD11	1:A:96:LEU:HD12	2.01	0.43
1:A:421:ALA:HB2	1:A:434:SER:HB3	2.01	0.42
1:A:38:GLN:HB2	1:A:564:LYS:HD3	2.01	0.42
1:A:523:LEU:O	1:A:543:GLY:HA2	2.19	0.42
1:A:584:ARG:HD3	1:A:586:TYR:CZ	2.55	0.41
1:A:588:LEU:CD1	5:A:803:LDA:H72	2.48	0.41
1:A:46:LEU:HB2	1:A:54:ILE:HD11	2.02	0.41
5:A:801:LDA:H22	5:A:801:LDA:HM13	1.80	0.41
1:A:33:ASP:OD2	8:A:987:HOH:O	2.21	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	588/590 (100%)	577 (98%)	11 (2%)	0	100	100
2	B	79/81 (98%)	72 (91%)	6 (8%)	1 (1%)	15	9
All	All	667/671 (99%)	649 (97%)	17 (2%)	1 (0%)	56	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	223	GLY

### 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	467/491 (95%)	452 (97%)	15 (3%)	46	48
2	B	56/69 (81%)	54 (96%)	2 (4%)	42	43
All	All	523/560 (93%)	506 (97%)	17 (3%)	45	47

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ARG
1	A	87	LEU
1	A	111	ARG
1	A	241	ASP
1	A	242	THR
1	A	264	GLN
1	A	290	LEU
1	A	358	ARG
1	A	397	ASN
1	A	469	ASN
1	A	484	VAL
1	A	505	TYR
1	A	587	THR
1	A	591	SER
1	A	593	THR
2	B	158	ARG
2	B	171	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	364	GLN

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Mol	Chain	Res	Type
1	A	417	GLN
2	B	160	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 ⓘ

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	CNC	A	701	-	75,103,103	1.34	9 (12%)	107,171,171	1.90	20 (18%)
5	LDA	A	800	-	12,14,15	0.39	0	11,14,17	0.64	0
5	LDA	A	801	-	15,15,15	3.06	2 (13%)	16,17,17	1.89	3 (18%)
5	LDA	A	802	-	13,13,15	0.55	0	12,12,17	0.65	0
5	LDA	A	803	-	11,13,15	0.86	0	11,12,17	0.71	0
6	OCT	A	804	-	7,7,7	0.39	0	6,6,6	0.25	0
6	OCT	A	805	-	7,7,7	0.60	0	6,6,6	0.82	0
6	OCT	A	806	-	7,7,7	0.54	0	6,6,6	0.46	0
7	HEX	A	807	-	5,5,5	0.24	0	4,4,4	0.16	0
7	HEX	A	808	-	5,5,5	0.39	0	4,4,4	0.30	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
4	CNC	A	701	-	-	0/51/235/235	0/3/11/11
5	LDA	A	800	-	-	0/11/12/13	0/0/0/0
5	LDA	A	801	-	-	0/13/13/13	0/0/0/0
5	LDA	A	802	-	-	0/11/11/13	0/0/0/0
5	LDA	A	803	-	-	0/10/11/13	0/0/0/0
6	OCT	A	804	-	-	0/5/5/5	0/0/0/0
6	OCT	A	805	-	-	0/5/5/5	0/0/0/0
6	OCT	A	806	-	-	0/5/5/5	0/0/0/0
7	HEX	A	807	-	-	0/3/3/3	0/0/0/0
7	HEX	A	808	-	-	0/3/3/3	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	801	LDA	O1-N1	-11.56	1.28	1.39
4	A	701	CNC	C4B-C9B	-4.06	1.35	1.41
4	A	701	CNC	C11-C10	-3.69	1.34	1.41
4	A	701	CNC	C2R-C3R	-2.78	1.46	1.53
4	A	701	CNC	O6R-C1R	-2.64	1.37	1.41
5	A	801	LDA	C1-N1	-2.23	1.47	1.51
4	A	701	CNC	C2-C3	-2.10	1.54	1.58
4	A	701	CNC	P-O2	2.12	1.65	1.59
4	A	701	CNC	C30-C3	2.32	1.57	1.54
4	A	701	CNC	C6M-C6B	3.05	1.57	1.51
4	A	701	CNC	C41-C8	3.35	1.59	1.54

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	701	CNC	C2R-C1R-N1B	-8.69	101.01	114.29
5	A	801	LDA	CM2-N1-CM1	-6.52	101.48	108.83
4	A	701	CNC	C20-C1-C19	-5.58	104.51	109.56
4	A	701	CNC	C18-C19-N24	-4.28	99.72	109.30
4	A	701	CNC	C48-C13-C12	-3.83	106.02	116.53
4	A	701	CNC	O58-C57-N59	-3.43	116.13	122.94
4	A	701	CNC	O5-P-O2	-3.22	99.64	109.36
4	A	701	CNC	C35-C5-C4	-2.98	112.91	118.25
4	A	701	CNC	O8R-C5R-C4R	-2.87	101.85	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	701	CNC	C9-C10-C11	-2.75	125.38	132.28
4	A	701	CNC	C13-C14-C15	-2.43	123.67	131.88
4	A	701	CNC	O6R-C4R-C5R	-2.37	104.03	109.17
4	A	701	CNC	C2P-C1P-N59	-2.06	109.88	112.92
4	A	701	CNC	C3-C4-C5	-2.05	124.96	131.88
4	A	701	CNC	C30-C3-C2	-2.03	115.09	119.11
5	A	801	LDA	O1-N1-CM2	2.03	111.77	109.05
5	A	801	LDA	CM1-N1-C1	2.16	116.72	109.77
4	A	701	CNC	C56-C55-C17	2.18	120.13	115.57
4	A	701	CNC	O2-C3R-C4R	2.21	118.68	109.99
4	A	701	CNC	C35-C5-C6	3.97	125.35	118.25
4	A	701	CNC	P-O3-C2P	4.30	126.56	120.92
4	A	701	CNC	O6R-C1R-N1B	4.68	117.89	108.10
4	A	701	CNC	O2-P-O3	6.13	105.90	100.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	701	CNC	7	0
5	A	800	LDA	2	0
5	A	801	LDA	1	0
5	A	803	LDA	3	0
6	A	804	OCT	1	0
7	A	807	HEX	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 ⓘ

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	590/590 (100%)	0.24	23 (3%)	43 52	23, 32, 43, 66	0
2	B	81/81 (100%)	1.19	18 (22%)	1 1	33, 42, 50, 52	0
All	All	671/671 (100%)	0.35	41 (6%)	25 33	23, 33, 46, 66	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	217	PRO	6.6
2	B	218	GLY	6.5
2	B	155	ALA	4.5
2	B	186	GLY	4.3
2	B	153	PRO	4.2
2	B	220	PRO	4.1
2	B	216	GLU	4.1
2	B	156	LEU	3.8
2	B	184	PRO	3.7
2	B	222	SER	3.7
2	B	215	TYR	3.5
1	A	127	VAL	3.2
2	B	154	ARG	3.2
1	A	78	VAL	3.1
1	A	77	LEU	3.1
2	B	188	VAL	3.1
2	B	233	ASN	3.0
1	A	109	TYR	3.0
2	B	189	ASP	2.9
1	A	96	LEU	2.8
1	A	66	ILE	2.7
1	A	15	PHE	2.7
1	A	594	PHE	2.7
1	A	233	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	235	PRO	2.6
1	A	126	VAL	2.6
2	B	224	ILE	2.6
1	A	76	VAL	2.5
1	A	94	ALA	2.5
2	B	180	PHE	2.5
1	A	79	LEU	2.5
1	A	211	THR	2.5
1	A	42	VAL	2.4
1	A	237	SER	2.4
1	A	125	GLY	2.4
1	A	28	VAL	2.3
1	A	68	ILE	2.3
1	A	280	HIS	2.2
1	A	512	TYR	2.1
1	A	239	LEU	2.1
2	B	183	THR	2.0

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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	LDA	A	801	16/16	0.79	0.23	5.86	49,55,68,69	0
5	LDA	A	803	14/16	0.69	0.26	4.07	39,52,58,61	0
6	OCT	A	804	8/8	0.76	0.25	3.67	50,52,57,57	0
5	LDA	A	800	15/16	0.79	0.25	2.88	40,46,53,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	LDA	A	802	14/16	0.83	0.17	2.47	43,47,52,52	0
6	OCT	A	805	8/8	0.83	0.21	2.22	29,36,40,42	0
6	OCT	A	806	8/8	0.78	0.19	1.66	40,48,51,51	0
7	HEX	A	807	6/6	0.93	0.14	1.20	40,42,44,47	0
4	CNC	A	701	93/93	0.97	0.13	-0.30	19,27,35,42	0
3	CA	A	1	1/1	0.99	0.07	-1.61	28,28,28,28	0
3	CA	A	2	1/1	0.99	0.07	-1.66	30,30,30,30	0
7	HEX	A	808	6/6	0.84	0.16	-	51,53,53,54	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.