



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:19 AM GMT

PDB ID : 2WOW  
Title : TRYPANOSOMA BRUCEI TRYPANOTHIONE REDUCTASE WITH  
NADP AND TRYPANOTHIONE BOUND  
Authors : Alphey, M.S.; Fairlamb, A.H.  
Deposited on : 2009-07-30  
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](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

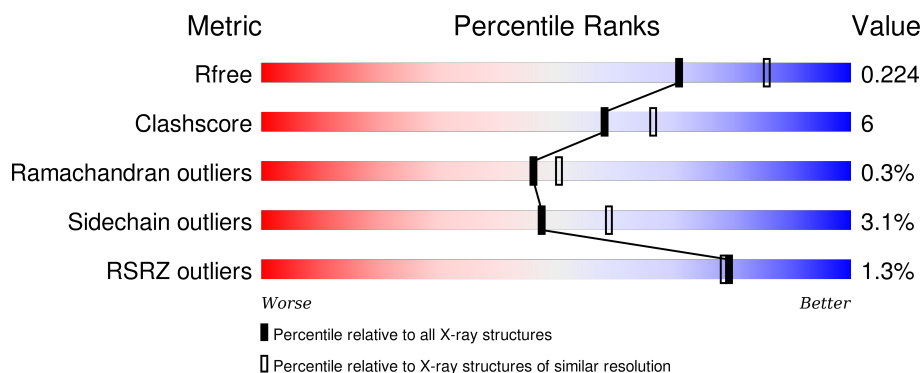
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	495	<div> <div>%</div> <div>84%14%..</div> </div>
1	B	495	<div> <div>2%</div> <div>82%16%..</div> </div>
1	C	495	<div> <div>%</div> <div>89%9%..</div> </div>
1	D	495	<div> <div>%</div> <div>87%12%. .</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
4	GCG	A	1001[A]	-	-	-	X
4	GCG	A	1001[B]	-	-	-	X
4	GCG	B	1001[A]	-	-	-	X
4	GCG	B	1001[B]	-	-	-	X
4	GCG	C	1001[A]	-	-	-	X
4	GCG	C	1001[B]	-	-	-	X
4	GCG	D	1001[A]	-	-	-	X
4	GCG	D	1001[B]	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16222 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 TRYPANOTHIONE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	490	Total	C	N	O	S	0	2	0
			3733	2374	635	704	20			
1	B	488	Total	C	N	O	S	0	1	0
			3714	2363	630	702	19			
1	C	491	Total	C	N	O	S	0	1	0
			3736	2378	634	704	20			
1	D	490	Total	C	N	O	S	0	0	0
			3717	2363	631	704	19			

There are 12 discrepancies between the modelled and reference sequences:

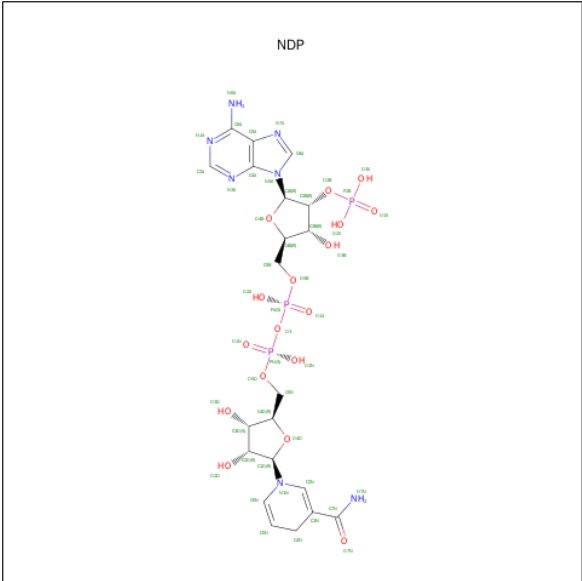
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q389T8
A	-1	SER	-	EXPRESSION TAG	UNP Q389T8
A	0	HIS	-	EXPRESSION TAG	UNP Q389T8
B	-2	GLY	-	EXPRESSION TAG	UNP Q389T8
B	-1	SER	-	EXPRESSION TAG	UNP Q389T8
B	0	HIS	-	EXPRESSION TAG	UNP Q389T8
C	-2	GLY	-	EXPRESSION TAG	UNP Q389T8
C	-1	SER	-	EXPRESSION TAG	UNP Q389T8
C	0	HIS	-	EXPRESSION TAG	UNP Q389T8
D	-2	GLY	-	EXPRESSION TAG	UNP Q389T8
D	-1	SER	-	EXPRESSION TAG	UNP Q389T8
D	0	HIS	-	EXPRESSION TAG	UNP Q389T8

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



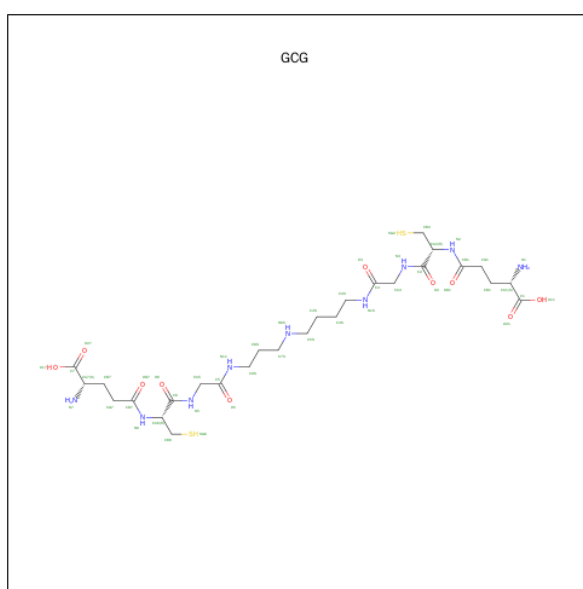
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C<sub>21</sub>H<sub>30</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is BIS(GAMMA-GLUTAMYL-CYSTEINYL-GLYCINYL)SPERMIDINE (three-letter code: GCG) (formula:  $C_{27}H_{49}N_9O_{10}S_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	1
			71	40	13	15	3		
4	B	1	Total	C	N	O	S	0	1
			71	40	13	15	3		
4	C	1	Total	C	N	O	S	0	1
			71	40	13	15	3		
4	D	1	Total	C	N	O	S	0	1
			71	40	13	15	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	174	Total	O	0	0
			174	174		

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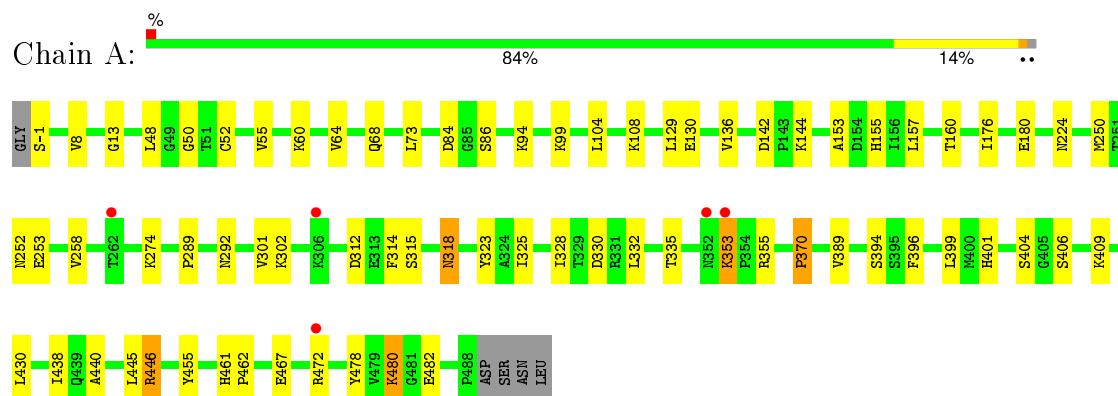
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	149	Total 149	O 149	0	0
5	C	171	Total 171	O 171	0	0
5	D	140	Total 140	O 140	0	0

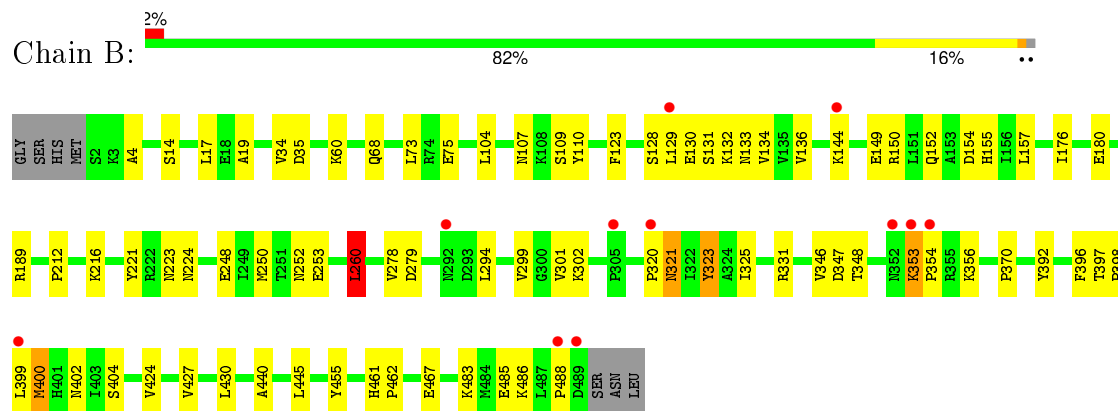
### 3 Residue-property plots [i](#)

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.

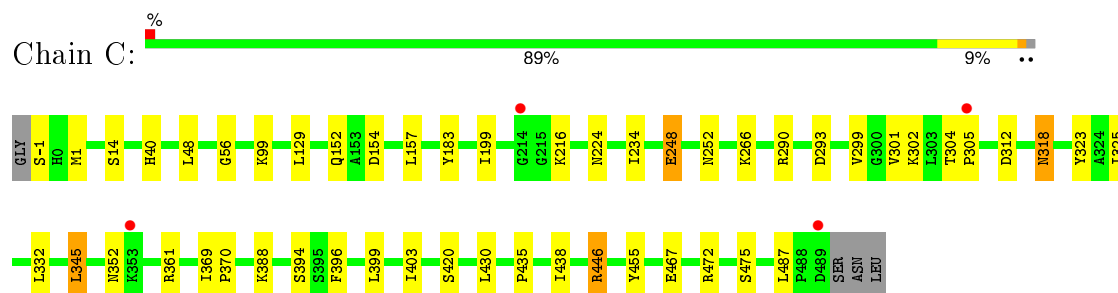
#### • Molecule 1: TRYPANOTHIONE REDUCTASE



#### • Molecule 1: TRYPANOTHIONE REDUCTASE

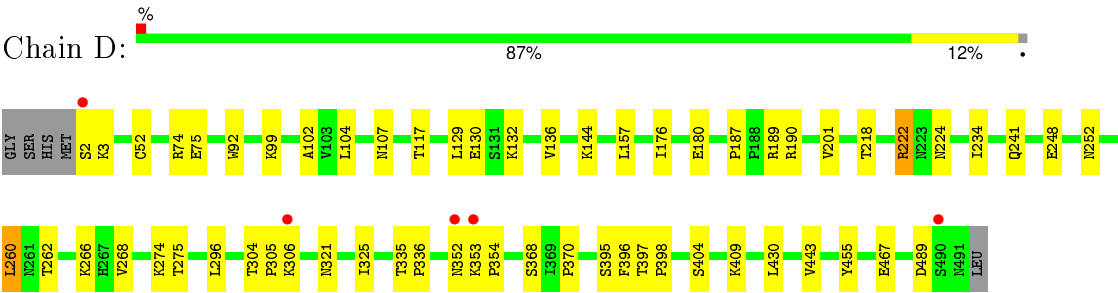


#### • Molecule 1: TRYPANOTHIONE REDUCTASE



#### • Molecule 1: TRYPANOTHIONE REDUCTASE





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.70 Å   63.70 Å   169.60 Å 90.00°   97.60°   90.00°	Depositor
Resolution (Å)	19.87 – 2.20 19.87 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.87-2.20) 99.6 (19.87-2.20)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.01 (at 2.19 Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, $R_{free}$	0.172   ,   0.226 0.172   ,   0.224	Depositor DCC
$R_{free}$ test set	5466 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.7	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 36.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 109305 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16222	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.16% 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: NDP, FAD, GCG

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	1.10	1/3818 (0.0%)	0.89	2/5179 (0.0%)
1	B	1.04	3/3792 (0.1%)	0.90	3/5145 (0.1%)
1	C	1.08	1/3819 (0.0%)	0.94	10/5181 (0.2%)
1	D	1.08	2/3795 (0.1%)	0.89	4/5149 (0.1%)
All	All	1.07	7/15224 (0.0%)	0.90	19/20654 (0.1%)

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
1	B	0	1
1	C	0	1
All	All	0	2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	455	TYR	CD1-CE1	6.35	1.48	1.39
1	B	427	VAL	CB-CG1	5.37	1.64	1.52
1	D	443	VAL	CB-CG2	5.28	1.64	1.52
1	B	455	TYR	CD1-CE1	5.24	1.47	1.39
1	C	323	TYR	CD1-CE1	5.22	1.47	1.39
1	A	258	VAL	CB-CG2	5.10	1.63	1.52
1	B	278	VAL	CA-CB	5.04	1.65	1.54

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	290	ARG	NE-CZ-NH2	-7.61	116.50	120.30
1	C	154	ASP	CB-CG-OD2	-7.40	111.64	118.30
1	B	260	LEU	CB-CG-CD2	7.12	123.10	111.00
1	C	154	ASP	CB-CG-OD1	7.01	124.61	118.30
1	C	361	ARG	NE-CZ-NH2	6.95	123.78	120.30
1	C	290	ARG	NE-CZ-NH1	6.79	123.70	120.30
1	C	312	ASP	CB-CG-OD1	6.45	124.11	118.30
1	C	361	ARG	NE-CZ-NH1	-6.22	117.19	120.30
1	B	294	LEU	CB-CG-CD1	-6.08	100.66	111.00
1	D	222	ARG	NE-CZ-NH1	6.05	123.32	120.30
1	B	260	LEU	CA-CB-CG	5.53	128.01	115.30
1	D	74	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	D	260	LEU	CB-CG-CD2	5.36	120.11	111.00
1	D	190	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	C	345	LEU	CA-CB-CG	-5.20	103.33	115.30
1	C	332	LEU	CA-CB-CG	5.19	127.23	115.30
1	C	48	LEU	CB-CG-CD2	-5.02	102.46	111.00
1	A	312	ASP	CB-CG-OD1	5.01	122.81	118.30
1	A	399	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	353	LYS	Peptide
1	C	352	ASN	Peptide

## 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	3733	0	3748	44	0
1	B	3714	0	3723	56	0
1	C	3736	0	3744	37	0
1	D	3717	0	3721	30	0
2	A	53	0	31	0	0
2	B	53	0	31	2	0
2	C	53	0	31	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	53	0	31	0	0
3	A	48	0	26	0	0
3	B	48	0	26	0	0
3	C	48	0	26	1	0
3	D	48	0	26	0	0
4	A	71	0	46	9	0
4	B	71	0	46	4	0
4	C	71	0	46	6	0
4	D	71	0	46	6	0
5	A	174	0	0	0	0
5	B	149	0	0	4	0
5	C	171	0	0	5	0
5	D	140	0	0	2	0
All	All	16222	0	15348	183	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 (183) 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)
4:C:1001[A]:GCG:HG72	4:C:1001[A]:GCG:O27	1.53	1.08
1:A:446:ARG:HG2	1:A:446:ARG:HH11	1.17	1.06
1:B:399[B]:LEU:O	1:B:400:MET:HB3	1.68	0.91
1:A:446:ARG:CG	1:A:446:ARG:HH11	1.86	0.89
1:B:347:ASP:HB3	1:B:353:LYS:HG3	1.54	0.89
1:C:318:ASN:H	1:C:318:ASN:HD22	1.22	0.88
1:C:446:ARG:HG2	1:C:446:ARG:HH21	1.39	0.87
1:B:224:ASN:HD22	1:B:252:ASN:HD21	1.22	0.84
1:A:394:SER:HA	4:B:1001[A]:GCG:HA7	1.57	0.84
1:C:455[A]:TYR:CZ	1:C:472:ARG:HD2	2.16	0.81
1:B:396:PHE:CE1	1:B:467:GLU:HG3	2.19	0.78
1:B:130:GLU:OE2	1:B:150:ARG:NH1	2.14	0.78
4:D:1001[B]:GCG:O5	4:D:1001[B]:GCG:H8S2	1.83	0.78
1:A:396:PHE:CE1	1:A:467:GLU:HG3	2.18	0.78
1:B:130:GLU:CD	1:B:150:ARG:HH12	1.87	0.77
1:C:216:LYS:HE2	5:C:2065:HOH:O	1.89	0.73
1:C:403:ILE:HD11	1:D:102:ALA:HB2	1.70	0.73
1:D:224:ASN:HD22	1:D:252:ASN:HD21	1.35	0.72
1:A:318:ASN:HD22	1:A:318:ASN:H	1.38	0.72
1:A:157:LEU:HD11	1:A:325:ILE:HG12	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:GLU:HB2	1:B:136:VAL:CG2	2.20	0.71
4:B:1001[A]:GCG:HG72	4:B:1001[A]:GCG:O17	1.83	0.71
1:D:396:PHE:CE1	1:D:467:GLU:HG3	2.27	0.69
1:C:129:LEU:HD23	1:C:299:VAL:HG21	1.73	0.69
1:D:130:GLU:HB2	1:D:136:VAL:CG2	2.23	0.69
1:B:356:LYS:HE3	5:B:2109:HOH:O	1.92	0.69
1:C:396:PHE:CE1	1:C:467:GLU:HG2	2.30	0.67
1:B:250:MET:CE	1:B:253:GLU:HG3	2.25	0.66
1:C:446:ARG:CG	1:C:446:ARG:HH21	2.08	0.66
1:B:399[A]:LEU:CD1	1:B:402:ASN:HD22	2.08	0.66
1:A:455:TYR:CZ	1:A:472:ARG:HD2	2.31	0.65
1:D:130:GLU:HB2	1:D:136:VAL:HG23	1.79	0.64
1:C:157:LEU:HD11	1:C:325:ILE:HG12	1.78	0.63
4:C:1001[A]:GCG:O27	4:C:1001[A]:GCG:CG7	2.31	0.63
1:A:353:LYS:HE3	1:A:355:ARG:HE	1.64	0.63
1:B:370:PRO:HG2	1:B:430:LEU:HD11	1.79	0.63
1:D:117:THR:O	5:D:2018:HOH:O	2.16	0.62
1:D:321:ASN:HB2	5:D:2021:HOH:O	1.99	0.62
1:C:318:ASN:N	1:C:318:ASN:HD22	1.95	0.62
1:C:157:LEU:HD13	1:C:345:LEU:HD22	1.83	0.61
1:B:399[B]:LEU:O	1:B:400:MET:CB	2.47	0.60
1:C:455[A]:TYR:OH	1:C:472:ARG:HD2	2.02	0.59
1:D:129:LEU:HD22	1:D:296:LEU:HD23	1.84	0.59
1:B:347:ASP:HB3	1:B:353:LYS:CG	2.29	0.59
1:B:131:SER:O	1:B:133:ASN:N	2.36	0.59
1:A:446:ARG:HG2	1:A:446:ARG:NH1	1.98	0.59
1:A:130:GLU:HB2	1:A:136:VAL:HG23	1.83	0.58
1:A:155:HIS:HB3	1:A:323:TYR:HE2	1.69	0.58
1:C:224:ASN:HD22	1:C:252:ASN:HD21	1.52	0.57
1:A:142:ASP:OD1	1:A:144:LYS:HE3	2.05	0.57
1:C:369:ILE:HG23	5:C:2142:HOH:O	2.05	0.57
1:A:302:LYS:H	1:A:318:ASN:ND2	2.03	0.57
1:B:250:MET:HE1	1:B:253:GLU:HG3	1.87	0.57
1:B:250:MET:HE2	1:B:253:GLU:HG3	1.87	0.56
1:A:60:LYS:C	1:A:60:LYS:HD2	2.26	0.56
1:A:289:PRO:HG3	1:A:330:ASP:HB2	1.85	0.56
4:A:1001[A]:GCG:HG72	4:A:1001[A]:GCG:O27	2.06	0.55
1:B:155:HIS:HB3	1:B:323:TYR:HE2	1.71	0.55
1:A:301:VAL:HA	1:A:318:ASN:HD21	1.72	0.55
1:A:446:ARG:CG	1:A:446:ARG:NH1	2.55	0.55
4:A:1001[A]:GCG:O6	4:A:1001[A]:GCG:OD7	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:302:LYS:H	1:C:318:ASN:ND2	2.05	0.54
4:B:1001[A]:GCG:O17	4:B:1001[A]:GCG:CG7	2.53	0.54
1:A:401:HIS:HD2	1:A:404:SER:OG	1.90	0.54
1:B:320:PRO:O	1:B:321:ASN:ND2	2.41	0.54
1:B:348:THR:HA	1:B:354:PRO:HA	1.89	0.54
1:A:84:ASP:OD1	1:A:86:SER:HB2	2.07	0.54
1:A:370:PRO:HG2	1:A:430:LEU:HD11	1.90	0.53
1:A:394:SER:OG	4:B:1001[A]:GCG:HB72	2.09	0.53
1:B:131:SER:HA	1:B:299:VAL:CG1	2.39	0.52
1:C:199:ILE:HG13	3:C:800:NDP:H5N	1.91	0.52
1:B:4:ALA:HA	1:B:152:GLN:HB3	1.91	0.52
1:C:302:LYS:H	1:C:318:ASN:HD21	1.56	0.52
1:C:293:ASP:HB2	5:C:2098:HOH:O	2.09	0.51
1:C:304:THR:HB	1:C:305:PRO:CD	2.41	0.51
1:A:250:MET:HE3	1:A:253:GLU:HG3	1.93	0.51
1:D:157:LEU:HD11	1:D:325:ILE:HG12	1.93	0.51
1:D:75:GLU:HB3	1:D:404:SER:HB2	1.92	0.51
4:D:1001[A]:GCG:C7S	4:D:1001[A]:GCG:O5	2.59	0.50
1:A:13:GLY:HA2	1:A:50:GLY:HA3	1.93	0.50
1:C:152:GLN:NE2	5:C:2048:HOH:O	2.45	0.50
1:C:396:PHE:HB2	4:D:1001[A]:GCG:HB62	1.94	0.50
1:B:19:ALA:O	1:B:346:VAL:HG21	2.11	0.49
1:B:224:ASN:ND2	1:B:252:ASN:HD21	2.00	0.49
4:C:1001[B]:GCG:OD7	4:C:1001[B]:GCG:N7	2.45	0.49
1:B:221:TYR:CE2	1:B:223:ASN:HB2	2.47	0.49
1:C:216:LYS:HE3	1:C:248:GLU:HB3	1.93	0.49
1:B:189:ARG:HA	1:B:212:PRO:HD2	1.94	0.48
1:B:68:GLN:NE2	5:B:2012:HOH:O	2.42	0.48
1:D:397:THR:HG22	1:D:398:PRO:O	2.13	0.48
1:A:130:GLU:HB2	1:A:136:VAL:CG2	2.43	0.48
1:D:266:LYS:HD2	1:D:266:LYS:N	2.28	0.48
1:B:424:VAL:HG12	1:B:445:LEU:HD11	1.95	0.48
1:D:241:GLN:OE1	1:D:370:PRO:HG3	2.13	0.48
1:B:130:GLU:HB2	1:B:136:VAL:HG23	1.95	0.48
4:D:1001[B]:GCG:O5	4:D:1001[B]:GCG:C8S	2.60	0.47
1:A:224:ASN:HD22	1:A:252:ASN:HD21	1.61	0.47
1:A:176:ILE:HB	1:A:180:GLU:HB2	1.96	0.47
1:C:40:HIS:ND1	1:C:183:TYR:OH	2.40	0.47
1:C:403:ILE:CD1	1:D:102:ALA:HB2	2.42	0.47
1:B:131:SER:HA	1:B:299:VAL:HG12	1.97	0.47
4:C:1001[A]:GCG:HN71	1:D:395:SER:H	1.59	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:92:TRP:HB3	1:D:187:PRO:HD3	1.97	0.47
1:A:302:LYS:H	1:A:318:ASN:HD21	1.62	0.47
1:B:399[A]:LEU:HD12	1:B:399[A]:LEU:HA	1.54	0.46
1:D:176:ILE:HB	1:D:180:GLU:HB2	1.97	0.46
1:A:440:ALA:HB3	1:B:440:ALA:HB3	1.98	0.46
1:B:34:VAL:HG22	1:B:123:PHE:HB2	1.97	0.46
1:C:370:PRO:HG2	1:C:430:LEU:HD11	1.98	0.46
1:B:34:VAL:HG12	2:B:700:FAD:H2A	1.96	0.46
1:C:446:ARG:NH2	1:C:446:ARG:CG	2.71	0.46
1:B:331:ARG:HG3	5:B:2031:HOH:O	2.16	0.45
1:B:176:ILE:HB	1:B:180:GLU:HB2	1.99	0.45
1:A:438:ILE:O	1:A:438:ILE:HG13	2.16	0.45
1:B:34:VAL:HA	1:B:123:PHE:O	2.17	0.45
4:D:1001[A]:GCG:HA6	4:D:1001[A]:GCG:HA51	1.61	0.45
1:B:348:THR:HG23	1:B:354:PRO:HB3	1.99	0.45
1:C:299:VAL:HG23	1:C:301:VAL:HG23	1.98	0.45
1:B:130:GLU:HB3	1:B:134:VAL:HB	1.99	0.45
1:A:406:SER:HB3	1:A:409:LYS:HG3	1.97	0.45
1:C:318:ASN:ND2	1:C:318:ASN:H	2.02	0.45
1:C:475:SER:OG	5:C:2157:HOH:O	2.05	0.45
1:D:335:THR:HB	1:D:336:PRO:HD3	1.99	0.44
1:B:399[A]:LEU:HD11	1:B:402:ASN:HD22	1.80	0.44
1:C:301:VAL:HA	1:C:318:ASN:HD21	1.82	0.44
4:A:1001[A]:GCG:CG7	4:A:1001[A]:GCG:O27	2.65	0.44
1:B:353:LYS:HB2	1:B:354:PRO:HA	1.98	0.44
1:A:314:PHE:O	1:A:315:SER:HB2	2.17	0.44
1:A:160:THR:OG1	1:A:328:ILE:HD12	2.17	0.44
2:B:700:FAD:H1'1	2:B:700:FAD:H9	1.75	0.44
1:A:445:LEU:HD12	1:A:445:LEU:N	2.32	0.43
1:C:56:GLY:HA2	2:C:700:FAD:C7	2.49	0.43
1:D:398:PRO:HD2	1:D:409:LYS:O	2.18	0.43
1:C:435:PRO:O	1:C:438:ILE:HG22	2.18	0.43
1:C:234:ILE:HG12	1:C:430:LEU:HB2	2.00	0.43
1:D:234:ILE:HG12	1:D:430:LEU:HB2	2.01	0.43
1:A:64:VAL:O	1:A:68[A]:GLN:HG3	2.19	0.43
1:C:318:ASN:ND2	1:C:318:ASN:N	2.63	0.42
1:A:73:LEU:CD2	1:B:73:LEU:HD23	2.48	0.42
1:B:60:LYS:HE2	1:B:60:LYS:HB3	1.81	0.42
1:B:157:LEU:HD11	1:B:325:ILE:HG12	2.01	0.42
1:D:218:THR:HG23	1:D:248:GLU:HG2	2.00	0.42
1:B:223:ASN:HB3	5:B:2063:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:HIS:HA	1:A:462:PRO:HA	1.82	0.42
1:B:461:HIS:HA	1:B:462:PRO:HA	1.89	0.42
1:D:304:THR:HB	1:D:305:PRO:CD	2.49	0.42
1:A:104:LEU:HG	1:A:108:LYS:HE3	2.01	0.42
1:B:299:VAL:HG23	1:B:301:VAL:HG23	2.01	0.42
1:D:201:VAL:HG12	1:D:368:SER:HB3	2.01	0.42
1:B:392:TYR:N	1:B:392:TYR:CD2	2.88	0.42
1:B:397:THR:HA	1:B:398:PRO:HD3	1.90	0.42
1:B:17:LEU:HD13	1:B:110:TYR:CE1	2.54	0.41
1:B:399[A]:LEU:CD1	1:B:402:ASN:ND2	2.81	0.41
1:D:224:ASN:ND2	1:D:252:ASN:HD21	2.11	0.41
1:A:8:VAL:HG23	1:A:153:ALA:HB2	2.01	0.41
1:C:394:SER:OG	4:D:1001[A]:GCG:HG71	2.20	0.41
1:A:389:VAL:HB	1:A:478:TYR:HB2	2.01	0.41
1:D:353:LYS:HG3	1:D:354:PRO:HD2	2.02	0.41
1:D:104:LEU:HA	1:D:107:ASN:HD22	1.85	0.41
1:A:332:LEU:HD23	1:A:332:LEU:HA	1.89	0.41
1:B:260:LEU:H	1:C:152:GLN:NE2	2.18	0.41
1:A:478:TYR:HA	1:A:482:GLU:O	2.21	0.41
1:B:189:ARG:HB3	1:B:279:ASP:OD2	2.21	0.41
1:D:268:VAL:O	1:D:275:THR:HA	2.21	0.41
1:D:304:THR:HB	1:D:305:PRO:HD2	2.03	0.40
1:A:355:ARG:HH21	1:A:355:ARG:HG2	1.86	0.40
1:B:104:LEU:HA	1:B:107:ASN:HD22	1.87	0.40
1:D:129:LEU:CD1	1:D:129:LEU:N	2.83	0.40
1:B:75:GLU:HB3	1:B:404:SER:HB2	2.02	0.40
1:A:353:LYS:HE3	1:A:355:ARG:NE	2.34	0.40
1:B:216:LYS:HE3	1:B:248:GLU:HB2	2.04	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	490/495 (99%)	475 (97%)	14 (3%)	1 (0%)	52	59
1	B	487/495 (98%)	465 (96%)	19 (4%)	3 (1%)	30	29
1	C	490/495 (99%)	473 (96%)	17 (4%)	0	100	100
1	D	488/495 (99%)	471 (96%)	15 (3%)	2 (0%)	39	42
All	All	1955/1980 (99%)	1884 (96%)	65 (3%)	6 (0%)	46	50

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	132	LYS
1	A	480	LYS
1	B	400	MET
1	D	132	LYS
1	D	352	ASN
1	B	488	PRO

### 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	405/407 (100%)	391 (96%)	14 (4%)	43	53
1	B	402/407 (99%)	388 (96%)	14 (4%)	43	53
1	C	404/407 (99%)	393 (97%)	11 (3%)	52	64
1	D	402/407 (99%)	391 (97%)	11 (3%)	52	64
All	All	1613/1628 (99%)	1563 (97%)	50 (3%)	47	59

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-1	SER
1	A	48	LEU
1	A	55	VAL
1	A	94	LYS
1	A	99	LYS

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Mol	Chain	Res	Type
1	A	129	LEU
1	A	274	LYS
1	A	292	ASN
1	A	318	ASN
1	A	335	THR
1	A	353	LYS
1	A	370	PRO
1	A	446	ARG
1	A	480	LYS
1	B	35	ASP
1	B	109	SER
1	B	128	SER
1	B	129	LEU
1	B	144	LYS
1	B	149	GLU
1	B	154	ASP
1	B	260	LEU
1	B	302	LYS
1	B	321	ASN
1	B	323	TYR
1	B	483	LYS
1	B	485	GLU
1	B	486	LYS
1	C	-1	SER
1	C	1	MET
1	C	99	LYS
1	C	248	GLU
1	C	266	LYS
1	C	318	ASN
1	C	388	LYS
1	C	399	LEU
1	C	420	SER
1	C	446	ARG
1	C	487	LEU
1	D	2	SER
1	D	3	LYS
1	D	99	LYS
1	D	144	LYS
1	D	189	ARG
1	D	222	ARG
1	D	260	LEU
1	D	262	THR

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Mol	Chain	Res	Type
1	D	274	LYS
1	D	306	LYS
1	D	489	ASP

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

Mol	Chain	Res	Type
1	A	152	GLN
1	A	224	ASN
1	A	318	ASN
1	A	401	HIS
1	B	107	ASN
1	B	133	ASN
1	B	224	ASN
1	B	321	ASN
1	B	402	ASN
1	C	0	HIS
1	C	115	ASN
1	C	152	GLN
1	C	224	ASN
1	C	318	ASN
1	C	321	ASN
1	D	107	ASN
1	D	224	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

16 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
4	GCG	A	1001[A]	-	41,47,47	0.76	1 (2%)	46,58,58	1.94	13 (28%)
4	GCG	A	1001[B]	-	41,47,47	0.91	1 (2%)	46,58,58	1.74	14 (30%)
2	FAD	A	700	-	48,58,58	1.24	5 (10%)	54,89,89	2.29	12 (22%)
3	NDP	A	800	-	42,52,52	1.69	9 (21%)	55,80,80	1.85	8 (14%)
4	GCG	B	1001[A]	-	41,47,47	0.66	0	46,58,58	1.44	4 (8%)
4	GCG	B	1001[B]	-	41,47,47	0.91	1 (2%)	46,58,58	1.60	4 (8%)
2	FAD	B	700	-	48,58,58	1.29	7 (14%)	54,89,89	2.53	10 (18%)
3	NDP	B	800	-	42,52,52	1.60	8 (19%)	55,80,80	1.98	9 (16%)
4	GCG	C	1001[A]	-	41,47,47	0.76	2 (4%)	46,58,58	1.40	9 (19%)
4	GCG	C	1001[B]	-	41,47,47	0.89	3 (7%)	46,58,58	1.29	4 (8%)
2	FAD	C	700	-	48,58,58	1.55	6 (12%)	54,89,89	1.88	10 (18%)
3	NDP	C	800	-	42,52,52	1.75	8 (19%)	55,80,80	1.83	8 (14%)
4	GCG	D	1001[A]	-	41,47,47	0.67	0	46,58,58	1.16	2 (4%)
4	GCG	D	1001[B]	-	41,47,47	0.88	2 (4%)	46,58,58	1.29	2 (4%)
2	FAD	D	700	-	48,58,58	1.56	9 (18%)	54,89,89	2.16	7 (12%)
3	NDP	D	800	-	42,52,52	1.46	4 (9%)	55,80,80	2.02	7 (12%)

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	GCG	A	1001[A]	-	-	0/53/61/61	0/0/0/0
4	GCG	A	1001[B]	-	-	0/53/61/61	0/0/0/0
2	FAD	A	700	-	-	0/30/50/50	0/6/6/6
3	NDP	A	800	-	-	0/30/77/77	0/5/5/5
4	GCG	B	1001[A]	-	-	0/53/61/61	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GCG	B	1001[B]	-	-	0/53/61/61	0/0/0/0
2	FAD	B	700	-	-	0/30/50/50	0/6/6/6
3	NDP	B	800	-	-	0/30/77/77	0/5/5/5
4	GCG	C	1001[A]	-	-	0/53/61/61	0/0/0/0
4	GCG	C	1001[B]	-	-	0/53/61/61	0/0/0/0
2	FAD	C	700	-	-	0/30/50/50	0/6/6/6
3	NDP	C	800	-	-	0/30/77/77	0/5/5/5
4	GCG	D	1001[A]	-	-	0/53/61/61	0/0/0/0
4	GCG	D	1001[B]	-	-	0/53/61/61	0/0/0/0
2	FAD	D	700	-	-	0/30/50/50	0/6/6/6
3	NDP	D	800	-	-	0/30/77/77	0/5/5/5

All (66) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	800	NDP	C4N-C5N	-4.56	1.39	1.49
3	A	800	NDP	C4N-C5N	-4.12	1.40	1.49
3	C	800	NDP	C4N-C5N	-3.83	1.40	1.49
3	B	800	NDP	C4N-C5N	-3.56	1.41	1.49
2	D	700	FAD	C4X-C10	-3.12	1.35	1.41
3	B	800	NDP	P2B-O3X	-2.82	1.44	1.54
4	D	1001[B]	GCG	CB6-CA6	-2.68	1.49	1.53
3	C	800	NDP	P2B-O3X	-2.62	1.45	1.54
3	A	800	NDP	P2B-O3X	-2.55	1.45	1.54
2	D	700	FAD	C6-C5X	-2.46	1.38	1.41
2	A	700	FAD	C9A-C5X	-2.37	1.37	1.42
2	D	700	FAD	O2'-C2'	-2.10	1.38	1.43
2	D	700	FAD	P-O2P	-2.06	1.46	1.54
2	C	700	FAD	C1'-N10	2.04	1.50	1.48
2	B	700	FAD	C1'-N10	2.05	1.50	1.48
3	B	800	NDP	P2B-O1X	2.10	1.58	1.51
4	C	1001[B]	GCG	CB2-SG2	2.11	1.86	1.81
4	C	1001[A]	GCG	CB2-SG2	2.11	1.86	1.81
2	A	700	FAD	C9A-N10	2.18	1.41	1.38
3	A	800	NDP	C2N-C3N	2.25	1.40	1.34
4	C	1001[B]	GCG	CA3-N3	2.34	1.51	1.45
4	C	1001[A]	GCG	CA3-N3	2.34	1.51	1.45
3	A	800	NDP	C1D-N1N	2.35	1.53	1.46
2	A	700	FAD	C2A-N3A	2.37	1.36	1.32
4	D	1001[B]	GCG	CG7-CD7	2.41	1.56	1.51
2	B	700	FAD	C4-N3	2.41	1.37	1.33
2	B	700	FAD	C10-N1	2.43	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	700	FAD	C9-C8	2.44	1.44	1.37
3	C	800	NDP	O4D-C1D	2.45	1.48	1.42
3	C	800	NDP	P2B-O1X	2.48	1.59	1.51
4	C	1001[B]	GCG	CG7-CD7	2.48	1.56	1.51
4	B	1001[B]	GCG	CG7-CD7	2.48	1.56	1.51
3	B	800	NDP	O4B-C4B	2.57	1.51	1.45
2	B	700	FAD	C2A-N1A	2.68	1.39	1.33
3	D	800	NDP	C2N-C3N	2.78	1.41	1.34
2	B	700	FAD	C4X-N5	2.79	1.37	1.33
3	A	800	NDP	P2B-O1X	2.80	1.60	1.51
3	C	800	NDP	C2N-C3N	2.80	1.41	1.34
3	B	800	NDP	O4B-C1B	2.82	1.44	1.41
3	A	800	NDP	O4D-C4D	2.87	1.51	1.45
2	D	700	FAD	C2A-N3A	2.93	1.37	1.32
3	C	800	NDP	C6N-C5N	3.01	1.39	1.33
4	A	1001[B]	GCG	CG7-CD7	3.04	1.57	1.51
3	B	800	NDP	PA-O1A	3.08	1.62	1.51
4	A	1001[A]	GCG	CB6-CA6	3.08	1.56	1.53
2	B	700	FAD	C5X-N5	3.13	1.40	1.35
3	D	800	NDP	PA-O1A	3.16	1.62	1.51
3	B	800	NDP	C6N-C5N	3.24	1.39	1.33
2	C	700	FAD	C2A-N3A	3.27	1.38	1.32
2	D	700	FAD	C1'-N10	3.50	1.52	1.48
3	C	800	NDP	PN-O1N	3.61	1.64	1.51
2	A	700	FAD	C4-N3	3.63	1.39	1.33
2	D	700	FAD	C4-N3	3.65	1.39	1.33
3	B	800	NDP	PN-O1N	3.69	1.64	1.51
2	A	700	FAD	C4X-N5	3.75	1.39	1.33
2	D	700	FAD	C5X-N5	3.78	1.41	1.35
3	A	800	NDP	O4D-C1D	3.98	1.51	1.42
2	D	700	FAD	C4X-N5	3.98	1.39	1.33
3	A	800	NDP	C6N-C5N	4.00	1.41	1.33
2	C	700	FAD	C5X-N5	4.07	1.41	1.35
3	D	800	NDP	C6N-C5N	4.11	1.41	1.33
2	C	700	FAD	C4-N3	4.26	1.41	1.33
2	B	700	FAD	C2A-N3A	4.37	1.39	1.32
3	A	800	NDP	PN-O1N	4.54	1.67	1.51
2	C	700	FAD	C4X-N5	4.95	1.41	1.33
3	C	800	NDP	O4B-C1B	5.77	1.48	1.41

All (123) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	700	FAD	N3A-C2A-N1A	-12.71	119.17	128.89
2	B	700	FAD	N3A-C2A-N1A	-11.67	119.96	128.89
2	A	700	FAD	N3A-C2A-N1A	-11.11	120.39	128.89
3	D	800	NDP	N3A-C2A-N1A	-10.56	120.81	128.89
3	B	800	NDP	N3A-C2A-N1A	-9.04	121.97	128.89
3	A	800	NDP	N3A-C2A-N1A	-8.37	122.48	128.89
3	C	800	NDP	N3A-C2A-N1A	-7.81	122.91	128.89
2	C	700	FAD	N3A-C2A-N1A	-7.72	122.98	128.89
4	B	1001[B]	GCG	CA6-CB6-SG6	-6.89	105.69	114.16
2	B	700	FAD	C4X-C4-N3	-4.99	116.77	123.59
4	B	1001[B]	GCG	CA2-CB2-SG2	-4.92	108.11	114.16
4	B	1001[A]	GCG	CA2-CB2-SG2	-4.92	108.11	114.16
3	D	800	NDP	C2D-C1D-N1N	-4.83	100.30	113.34
4	C	1001[B]	GCG	CA6-CB6-SG6	-4.65	108.44	114.16
3	C	800	NDP	O2B-P2B-O1X	-4.61	95.59	107.11
3	B	800	NDP	C2D-C1D-N1N	-4.51	101.15	113.34
4	D	1001[A]	GCG	CA2-CB2-SG2	-4.49	108.64	114.16
4	D	1001[B]	GCG	CA2-CB2-SG2	-4.49	108.64	114.16
4	D	1001[B]	GCG	CA6-CB6-SG6	-4.36	108.80	114.16
3	A	800	NDP	C2D-C1D-N1N	-4.24	101.88	113.34
4	A	1001[B]	GCG	CA2-CB2-SG2	-4.21	108.99	114.16
4	A	1001[A]	GCG	CA2-CB2-SG2	-4.21	108.99	114.16
4	C	1001[A]	GCG	CB6-CA6-N6	-4.08	105.67	111.40
4	B	1001[A]	GCG	C6-CA6-N6	-3.88	100.33	111.26
2	A	700	FAD	C4X-C4-N3	-3.35	119.01	123.59
2	D	700	FAD	C1B-N9A-C4A	-3.30	121.96	126.94
3	B	800	NDP	C1B-N9A-C4A	-3.30	121.96	126.94
3	D	800	NDP	O2B-P2B-O1X	-3.19	99.13	107.11
4	A	1001[B]	GCG	CA6-C6-N5	-3.12	110.59	116.72
2	A	700	FAD	C9A-C5X-N5	-3.12	117.74	122.36
4	C	1001[A]	GCG	CA6-CB6-SG6	-3.11	110.34	114.16
3	C	800	NDP	C2D-C1D-N1N	-3.08	105.03	113.34
4	A	1001[B]	GCG	C6-CA6-N6	-2.98	102.86	111.26
2	C	700	FAD	C4X-C4-N3	-2.98	119.51	123.59
2	A	700	FAD	C4A-C5A-N7A	-2.96	106.75	109.48
4	C	1001[B]	GCG	CB6-CA6-N6	-2.90	107.32	111.40
3	B	800	NDP	C3N-C2N-N1N	-2.88	119.01	123.14
3	C	800	NDP	C1B-N9A-C4A	-2.80	122.72	126.94
3	D	800	NDP	C5D-C4D-C3D	-2.68	104.58	115.21
2	C	700	FAD	C4A-C5A-N7A	-2.64	107.05	109.48
3	B	800	NDP	C5D-C4D-C3D	-2.63	104.75	115.21
4	B	1001[A]	GCG	CA6-N6-CD7	-2.63	114.88	121.58
2	B	700	FAD	O4B-C1B-N9A	-2.59	102.67	108.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	800	NDP	C1B-N9A-C4A	-2.58	123.04	126.94
4	A	1001[B]	GCG	OD1-CD1-CG1	-2.58	117.53	121.98
4	A	1001[A]	GCG	OD1-CD1-CG1	-2.58	117.53	121.98
2	A	700	FAD	C4X-C10-N10	-2.57	119.01	120.52
3	C	800	NDP	O5D-PN-O1N	-2.50	99.91	109.62
2	C	700	FAD	O2'-C2'-C1'	-2.50	103.80	109.94
4	C	1001[B]	GCG	CB1-CG1-CD1	-2.38	107.61	113.27
4	C	1001[A]	GCG	CB1-CG1-CD1	-2.38	107.61	113.27
3	B	800	NDP	O5D-PN-O1N	-2.37	100.43	109.62
4	C	1001[B]	GCG	OD1-CD1-CG1	-2.37	117.90	121.98
4	C	1001[A]	GCG	OD1-CD1-CG1	-2.37	117.90	121.98
2	B	700	FAD	C4B-O4B-C1B	-2.33	107.16	109.72
3	A	800	NDP	C3N-C2N-N1N	-2.31	119.83	123.14
4	C	1001[A]	GCG	C7S-N6S-C5S	-2.30	105.21	113.35
4	A	1001[B]	GCG	CA6-N6-CD7	-2.26	115.83	121.58
3	A	800	NDP	O3B-C3B-C4B	-2.16	104.56	111.05
4	A	1001[B]	GCG	C4S-C5S-N6S	-2.15	106.60	111.96
4	A	1001[A]	GCG	C4S-C5S-N6S	-2.15	106.60	111.96
4	D	1001[A]	GCG	C5-CA5-N5	-2.14	107.31	113.26
4	A	1001[A]	GCG	CB7-CG7-CD7	-2.13	108.19	113.27
4	A	1001[A]	GCG	CG7-CD7-N6	-2.11	112.39	115.83
4	B	1001[B]	GCG	OD7-CD7-CG7	-2.10	118.36	121.98
4	A	1001[B]	GCG	CA3-N3-C2	-2.08	116.57	121.26
4	A	1001[A]	GCG	CA3-N3-C2	-2.08	116.57	121.26
4	A	1001[B]	GCG	C2S-N1S-C3	-2.05	118.75	122.79
4	A	1001[A]	GCG	C2S-N1S-C3	-2.05	118.75	122.79
3	B	800	NDP	C1D-N1N-C2N	-2.05	117.33	120.91
4	C	1001[A]	GCG	CA6-N6-CD7	-2.05	116.36	121.58
4	C	1001[A]	GCG	C8S-C9S-N11	-2.02	106.28	112.19
3	A	800	NDP	O2X-P2B-O1X	-2.00	104.13	110.58
2	D	700	FAD	O3'-C3'-C4'	2.00	113.80	108.75
2	A	700	FAD	C6-C5X-C9A	2.03	121.66	118.98
4	A	1001[B]	GCG	CA2-C2-N3	2.04	120.72	116.72
4	A	1001[A]	GCG	CA2-C2-N3	2.04	120.72	116.72
2	B	700	FAD	O3P-PA-O5B	2.07	108.43	102.94
4	C	1001[A]	GCG	CB6-CA6-C6	2.09	114.37	109.66
4	C	1001[A]	GCG	CA5-N5-C6	2.11	126.02	121.26
2	A	700	FAD	C1'-N10-C9A	2.12	121.24	118.86
3	D	800	NDP	O3X-P2B-O2X	2.15	115.55	107.38
2	A	700	FAD	O3P-P-O5'	2.21	108.79	102.94
3	C	800	NDP	O3-PA-O5B	2.21	108.79	102.94
4	A	1001[B]	GCG	C2-CA2-N2	2.22	117.53	111.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1001[A]	GCG	C2-CA2-N2	2.22	117.53	111.26
4	B	1001[B]	GCG	C6-CA6-N6	2.23	117.55	111.26
4	A	1001[A]	GCG	OD7-CD7-N6	2.27	126.86	123.01
3	A	800	NDP	O3X-P2B-O2X	2.28	116.06	107.38
2	A	700	FAD	C2B-C1B-N9A	2.29	117.79	114.29
2	C	700	FAD	O2A-PA-O3P	2.33	115.68	105.09
4	A	1001[B]	GCG	O6-C6-N5	2.34	127.79	123.08
2	D	700	FAD	C2B-C1B-N9A	2.41	117.98	114.29
2	D	700	FAD	C4-C4X-N5	2.49	121.74	118.72
4	A	1001[A]	GCG	CA6-N6-CD7	2.51	127.98	121.58
4	A	1001[B]	GCG	C9S-N11-C5	2.53	127.77	122.79
3	D	800	NDP	O3X-P2B-O1X	2.55	118.78	110.58
3	C	800	NDP	C4N-C5N-C6N	2.59	126.85	122.58
2	D	700	FAD	C4-N3-C2	2.74	117.62	115.25
2	B	700	FAD	C5X-C9A-N10	2.79	119.74	117.62
2	C	700	FAD	C4-N3-C2	2.80	117.66	115.25
2	C	700	FAD	O3P-P-O5'	2.91	110.65	102.94
4	B	1001[A]	GCG	CB6-CA6-C6	3.08	116.62	109.66
2	B	700	FAD	O3P-P-O5'	3.14	111.27	102.94
2	B	700	FAD	C4X-N5-C5X	3.24	120.49	116.76
4	A	1001[B]	GCG	CB6-CA6-C6	3.28	117.06	109.66
4	A	1001[A]	GCG	CB6-CA6-C6	3.36	117.23	109.66
2	D	700	FAD	C4X-N5-C5X	3.49	120.78	116.76
3	B	800	NDP	O3X-P2B-O2X	3.54	120.86	107.38
2	A	700	FAD	C5X-C9A-N10	3.57	120.33	117.62
2	B	700	FAD	C2B-C1B-N9A	3.64	119.86	114.29
4	A	1001[B]	GCG	CA5-N5-C6	3.93	130.13	121.26
2	C	700	FAD	C4X-N5-C5X	4.18	121.57	116.76
2	C	700	FAD	C4X-C10-N10	4.28	123.04	120.52
2	A	700	FAD	C4-N3-C2	4.30	118.96	115.25
2	C	700	FAD	C4-C4X-N5	4.63	124.33	118.72
3	D	800	NDP	O4D-C1D-N1N	4.67	117.93	108.07
3	C	800	NDP	O4D-C1D-N1N	4.90	118.41	108.07
3	B	800	NDP	O4D-C1D-N1N	5.13	118.90	108.07
2	A	700	FAD	C4X-N5-C5X	5.91	123.56	116.76
3	A	800	NDP	O4D-C1D-N1N	6.22	121.20	108.07
4	A	1001[A]	GCG	CA6-CB6-SG6	7.70	123.62	114.16
2	B	700	FAD	C4-N3-C2	9.08	123.10	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1001[A]	GCG	9	0
4	B	1001[A]	GCG	4	0
2	B	700	FAD	2	0
4	C	1001[A]	GCG	5	0
4	C	1001[B]	GCG	1	0
2	C	700	FAD	1	0
3	C	800	NDP	1	0
4	D	1001[A]	GCG	4	0
4	D	1001[B]	GCG	2	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	490/495 (98%)	-0.47	5 (1%) 84 83	13, 22, 37, 55	0
1	B	488/495 (98%)	-0.26	11 (2%) 64 63	13, 26, 52, 74	1 (0%)
1	C	491/495 (99%)	-0.52	4 (0%) 87 87	13, 21, 35, 56	0
1	D	490/495 (98%)	-0.39	5 (1%) 84 83	13, 23, 42, 60	1 (0%)
All	All	1959/1980 (98%)	-0.41	25 (1%) 79 78	13, 23, 45, 74	2 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	2	SER	5.8
1	D	352	ASN	5.4
1	B	399[A]	LEU	4.1
1	B	352	ASN	4.0
1	A	352[A]	ASN	3.3
1	C	489	ASP	3.2
1	B	144	LYS	3.0
1	D	490	SER	3.0
1	A	353	LYS	2.8
1	B	354	PRO	2.8
1	B	353	LYS	2.7
1	C	305	PRO	2.7
1	B	489	ASP	2.6
1	A	306	LYS	2.5
1	B	488	PRO	2.5
1	D	306	LYS	2.5
1	B	305	PRO	2.4
1	D	353	LYS	2.3
1	C	214	GLY	2.2
1	A	472	ARG	2.1
1	B	292	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	262	THR	2.1
1	B	320	PRO	2.0
1	C	353	LYS	2.0
1	B	129	LEU	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
4	GCG	D	1001[A]	48/48	0.79	0.29	9.17	27,42,51,51	48
4	GCG	D	1001[B]	48/48	0.79	0.29	8.97	17,37,50,51	48
4	GCG	C	1001[A]	48/48	0.81	0.26	7.78	15,28,41,43	48
4	GCG	A	1001[A]	48/48	0.86	0.26	5.77	14,29,37,40	48
4	GCG	C	1001[B]	48/48	0.81	0.26	5.59	7,32,47,49	48
4	GCG	B	1001[B]	48/48	0.82	0.23	4.40	16,34,40,42	48
4	GCG	B	1001[A]	48/48	0.82	0.23	3.66	19,34,40,42	48
4	GCG	A	1001[B]	48/48	0.86	0.26	1.26	13,27,41,43	48
2	FAD	C	700	53/53	0.98	0.09	-0.37	12,16,18,21	0
3	NDP	C	800	48/48	0.97	0.09	-0.44	17,22,26,28	0
2	FAD	A	700	53/53	0.99	0.08	-0.47	10,14,18,21	0
3	NDP	A	800	48/48	0.98	0.09	-0.48	19,24,29,32	0
2	FAD	D	700	53/53	0.98	0.08	-0.48	12,19,24,26	0
3	NDP	B	800	48/48	0.98	0.08	-0.66	18,25,30,33	0
2	FAD	B	700	53/53	0.98	0.09	-0.88	10,20,30,33	0
3	NDP	D	800	48/48	0.97	0.08	-0.98	15,25,31,33	0

## 6.5 Other polymers

There are no such residues in this entry.