



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:44 PM GMT

PDB ID : 3RUF  
Title : Alternative analogs as viable substrates of UDP-hexose 4-epimerases  
Authors : Bhatt, V.S.; Guan, W.; Wang, P.G.  
Deposited on : 2011-05-05  
Resolution : 2.00 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

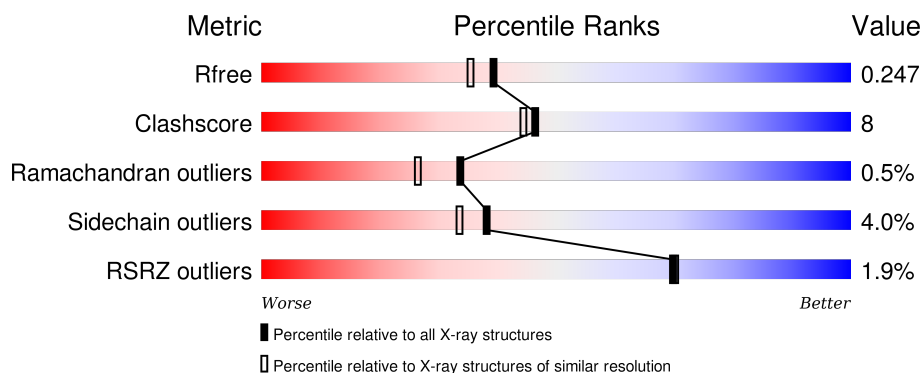
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	351	<div> <div> <div>0%</div> <div>73%</div> <div>20%</div> <div>• •</div> </div> </div>
1	B	351	<div> <div> <div>2%</div> <div>71%</div> <div>21%</div> <div>• • •</div> </div> </div>
1	S	351	<div> <div> <div>3%</div> <div>81%</div> <div>13%</div> <div>• •</div> </div> </div>
1	b	351	<div> <div> <div>2%</div> <div>90%</div> <div>5%</div> <div>•</div> </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	SO4	A	345	-	X	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11427 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 WbgU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2681	1712	459	502	8			
1	B	336	Total	C	N	O	S	0	0	0
			2681	1712	459	502	8			
1	S	336	Total	C	N	O	S	0	0	0
			2681	1712	459	502	8			
1	b	336	Total	C	N	O	S	0	0	0
			2674	1706	459	501	8			

There are 24 discrepancies between the modelled and reference sequences:

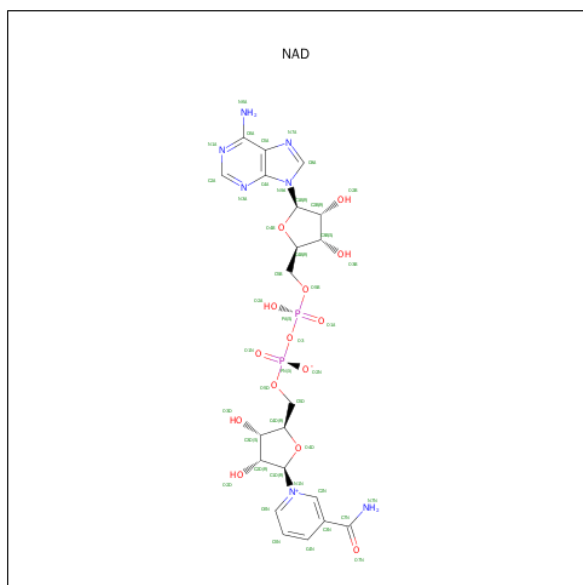
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	HIS	-	EXPRESSION TAG	UNP Q7BJX9
A	-7	HIS	-	EXPRESSION TAG	UNP Q7BJX9
A	-6	HIS	-	EXPRESSION TAG	UNP Q7BJX9
A	-5	HIS	-	EXPRESSION TAG	UNP Q7BJX9
A	-4	HIS	-	EXPRESSION TAG	UNP Q7BJX9
A	-3	HIS	-	EXPRESSION TAG	UNP Q7BJX9
B	-8	HIS	-	EXPRESSION TAG	UNP Q7BJX9
B	-7	HIS	-	EXPRESSION TAG	UNP Q7BJX9
B	-6	HIS	-	EXPRESSION TAG	UNP Q7BJX9
B	-5	HIS	-	EXPRESSION TAG	UNP Q7BJX9
B	-4	HIS	-	EXPRESSION TAG	UNP Q7BJX9
B	-3	HIS	-	EXPRESSION TAG	UNP Q7BJX9
S	-8	HIS	-	EXPRESSION TAG	UNP Q7BJX9
S	-7	HIS	-	EXPRESSION TAG	UNP Q7BJX9
S	-6	HIS	-	EXPRESSION TAG	UNP Q7BJX9
S	-5	HIS	-	EXPRESSION TAG	UNP Q7BJX9
S	-4	HIS	-	EXPRESSION TAG	UNP Q7BJX9
S	-3	HIS	-	EXPRESSION TAG	UNP Q7BJX9
b	-8	HIS	-	EXPRESSION TAG	UNP Q7BJX9
b	-7	HIS	-	EXPRESSION TAG	UNP Q7BJX9
b	-6	HIS	-	EXPRESSION TAG	UNP Q7BJX9

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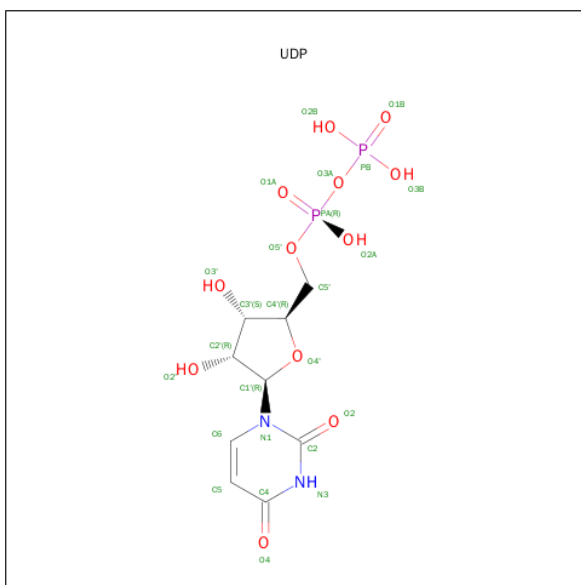
Chain	Residue	Modelled	Actual	Comment	Reference
b	-5	HIS	-	EXPRESSION TAG	UNP Q7BJX9
b	-4	HIS	-	EXPRESSION TAG	UNP Q7BJX9
b	-3	HIS	-	EXPRESSION TAG	UNP Q7BJX9

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula:  $C_{21}H_{27}N_7O_{14}P_2$ ).



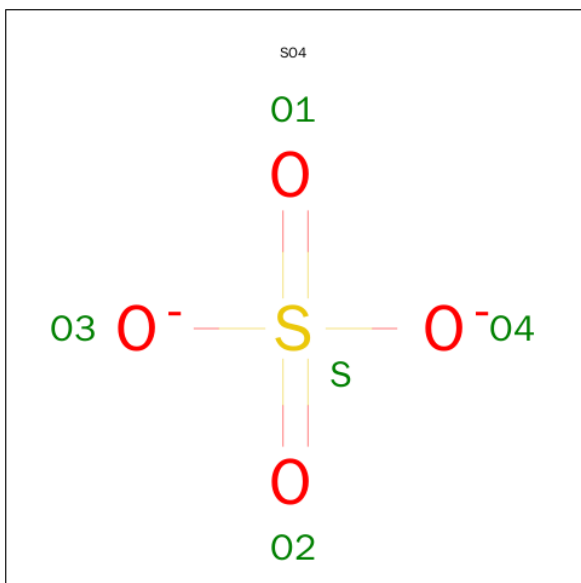
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	S	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	b	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula:  $C_9H_{14}N_2O_{12}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	B	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	S	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	b	1	Total 25	C 9	N 2	O 12	P 2	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula:  $\text{O}_4\text{S}$ ).



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

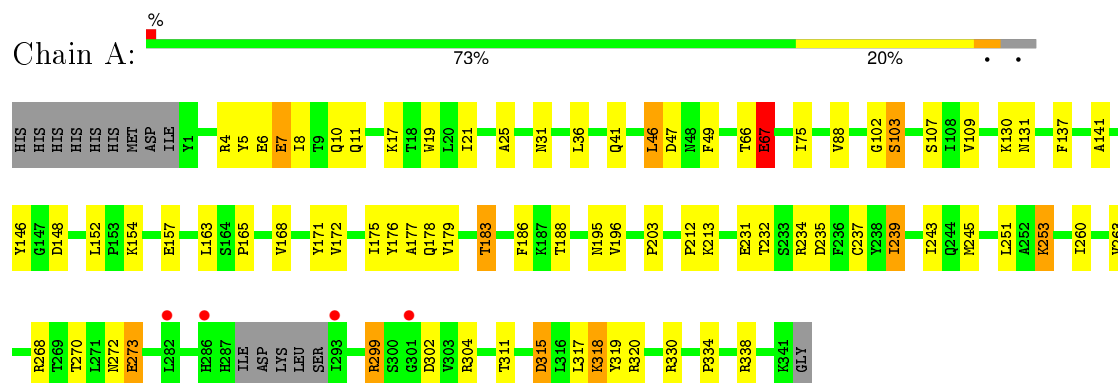
- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	111	Total	O		0	0
			111	111			
5	B	115	Total	O		0	0
			115	115			
5	S	101	Total	O		0	0
			101	101			
5	b	102	Total	O		0	0
			102	102			

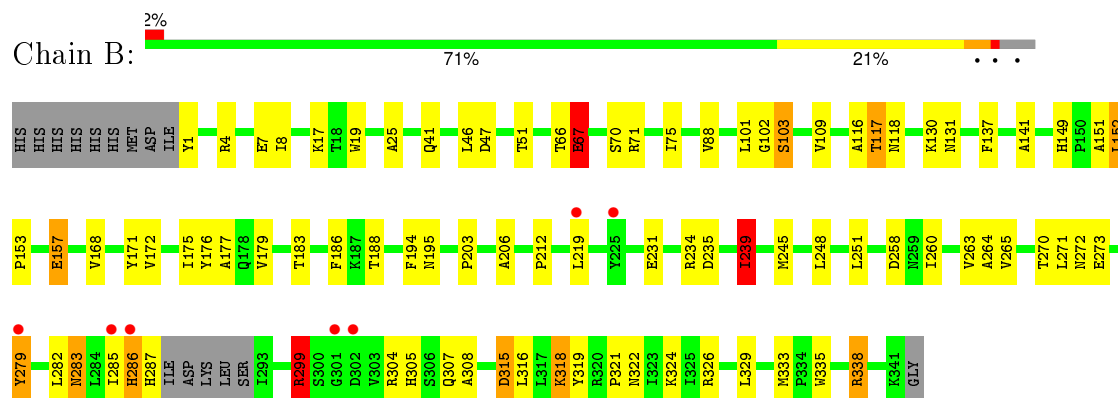
### 3 Residue-property plots [i](#)

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.

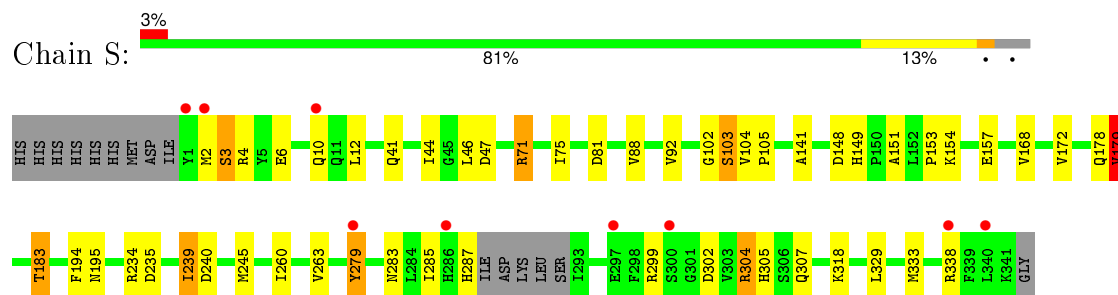
#### • Molecule 1: WbgU



#### • Molecule 1: WbgU

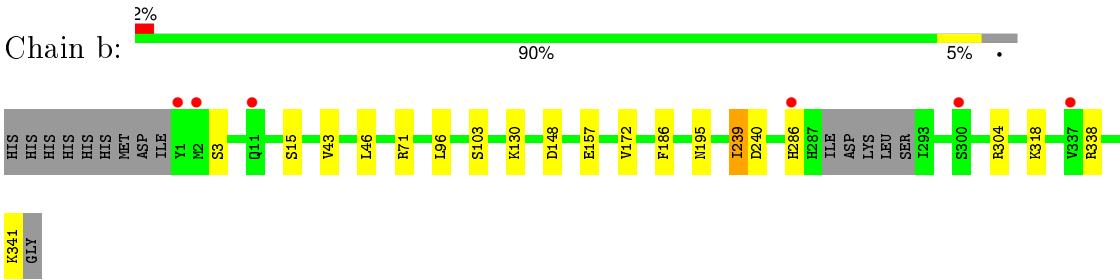


#### • Molecule 1: WbgU



#### • Molecule 1: WbgU





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.98Å 77.98Å 223.87Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.00 – 2.00 37.32 – 1.48	Depositor EDS
% Data completeness (in resolution range)	99.1 (37.00-2.00) 58.4 (37.32-1.48)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.00 (at 1.48Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.204 , 0.248 0.206 , 0.247	Depositor DCC
$R_{free}$ test set	5215 reflections (5.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.4	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 32.6	EDS
Estimated twinning fraction	0.021 for -h,-k,l 0.437 for h,-h-k,-l 0.027 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 148444 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11427	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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: UDP, SO4, NAD

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	9/2739 (0.3%)	0.92	2/3717 (0.1%)
1	B	1.17	11/2739 (0.4%)	0.96	8/3717 (0.2%)
1	S	1.03	0/2739	0.91	5/3717 (0.1%)
1	b	1.05	3/2731 (0.1%)	0.92	7/3706 (0.2%)
All	All	1.09	23/10948 (0.2%)	0.93	22/14857 (0.1%)

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	318	LYS	CD-CE	12.09	1.81	1.51
1	A	7	GLU	CB-CG	8.94	1.69	1.52
1	B	7	GLU	CB-CG	8.07	1.67	1.52
1	B	318	LYS	CB-CG	7.54	1.72	1.52
1	B	318	LYS	CE-NZ	7.39	1.67	1.49
1	A	186	PHE	CE1-CZ	6.32	1.49	1.37
1	B	1	TYR	CD1-CE1	6.19	1.48	1.39
1	A	67	GLU	CG-CD	5.92	1.60	1.51
1	A	49	PHE	CE2-CZ	5.72	1.48	1.37
1	A	5	TYR	CD2-CE2	5.70	1.47	1.39
1	b	43	VAL	CB-CG1	5.67	1.64	1.52
1	B	116	ALA	CA-CB	5.67	1.64	1.52
1	A	25	ALA	CA-CB	5.53	1.64	1.52
1	B	25	ALA	CA-CB	5.51	1.64	1.52
1	B	67	GLU	CG-CD	5.38	1.60	1.51
1	b	172	VAL	CB-CG2	5.37	1.64	1.52
1	A	176	TYR	CD2-CE2	5.31	1.47	1.39
1	A	5	TYR	CD1-CE1	5.23	1.47	1.39
1	B	318	LYS	CG-CD	5.15	1.70	1.52
1	B	137	PHE	CD1-CE1	5.14	1.49	1.39
1	A	137	PHE	CE2-CZ	5.09	1.47	1.37
1	b	186	PHE	CE2-CZ	5.04	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	186	PHE	CE1-CZ	5.00	1.46	1.37

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	258	ASP	CB-CG-OD2	7.34	124.91	118.30
1	B	299	ARG	NE-CZ-NH1	7.24	123.92	120.30
1	B	239	ILE	CB-CA-C	-6.57	98.45	111.60
1	S	240	ASP	CB-CG-OD1	6.31	123.98	118.30
1	B	260	ILE	CG1-CB-CG2	-6.29	97.57	111.40
1	b	240	ASP	CB-CG-OD1	6.19	123.87	118.30
1	S	148	ASP	CB-CG-OD1	5.93	123.63	118.30
1	A	239	ILE	CB-CA-C	-5.82	99.97	111.60
1	B	239	ILE	CG1-CB-CG2	5.67	123.87	111.40
1	S	154	LYS	CD-CE-NZ	-5.63	98.75	111.70
1	b	96	LEU	CB-CG-CD2	5.56	120.46	111.00
1	A	235	ASP	CB-CG-OD1	5.39	123.16	118.30
1	B	299	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	B	318	LYS	CG-CD-CE	5.32	127.84	111.90
1	b	195	ASN	N-CA-C	5.28	125.25	111.00
1	b	304	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	b	148	ASP	CB-CG-OD1	5.23	123.01	118.30
1	B	318	LYS	CB-CA-C	5.22	120.83	110.40
1	S	304	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	b	304	ARG	NE-CZ-NH2	-5.03	117.78	120.30
1	S	179	VAL	CG1-CB-CG2	-5.02	102.87	110.90
1	b	239	ILE	CB-CA-C	-5.01	101.57	111.60

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2681	0	2658	54	0
1	B	2681	0	2658	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S	2681	0	2658	42	0
1	b	2674	0	2651	0	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	S	44	0	26	1	0
2	b	44	0	26	0	0
3	A	25	0	11	1	0
3	B	25	0	11	0	0
3	S	25	0	11	0	0
3	b	25	0	11	0	0
4	A	5	0	0	2	0
5	A	111	0	0	1	0
5	B	115	0	0	4	0
5	S	101	0	0	5	0
5	b	102	0	0	0	0
All	All	11427	0	10773	165	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 8.

All (165) 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:318:LYS:CE	1:B:318:LYS:NZ	1.67	1.57
1:B:318:LYS:CE	1:B:318:LYS:CD	1.81	1.56
1:S:12:LEU:HD22	1:S:41:GLN:HE22	1.13	1.12
1:A:299:ARG:HH11	1:A:299:ARG:HG3	1.11	1.06
1:B:117:THR:HG22	1:B:118:ASN:OD1	1.72	0.88
1:S:12:LEU:HD22	1:S:41:GLN:NE2	1.89	0.87
1:A:299:ARG:NH1	1:A:299:ARG:HG3	1.85	0.87
1:S:179:VAL:O	1:S:183:THR:HG23	1.75	0.86
1:A:299:ARG:HH11	1:A:299:ARG:CG	1.89	0.85
1:A:19:TRP:HE1	1:A:41:GLN:HE21	1.26	0.82
1:B:179:VAL:O	1:B:183:THR:HG23	2.05	0.77
1:B:19:TRP:HE1	1:B:41:GLN:HE21	1.31	0.76
1:B:75:ILE:HD13	1:B:88:VAL:HG12	1.80	0.74
1:A:245:MET:HE2	1:A:319:TYR:CE1	2.24	0.72
1:B:270:THR:OG1	1:B:273:GLU:HG2	1.90	0.71
1:S:2:MET:HB2	1:S:6:GLU:HG3	1.71	0.71
1:A:75:ILE:HD13	1:A:88:VAL:HG12	1.73	0.70
1:S:279:TYR:HE1	1:S:283:ASN:HD21	1.38	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:329:LEU:O	1:B:333:MET:HG2	2.27	0.70
1:S:153:PRO:HG2	5:S:345:HOH:O	1.91	0.70
1:A:67:GLU:CD	1:A:67:GLU:H	1.95	0.69
1:A:46:LEU:HD23	1:A:47:ASP:N	2.07	0.68
1:S:149:HIS:HD2	1:S:151:ALA:H	1.40	0.68
1:B:17:LYS:H	1:B:41:GLN:HE22	1.42	0.67
1:S:75:ILE:HD13	1:S:88:VAL:HG12	1.75	0.67
1:B:195:ASN:ND2	1:B:234:ARG:HD2	2.10	0.66
1:S:304:ARG:HG3	1:S:305:HIS:CD2	2.31	0.66
1:B:46:LEU:HD23	1:B:47:ASP:N	2.09	0.66
1:B:245:MET:HE1	1:B:319:TYR:CD2	2.31	0.65
1:A:107:SER:HB2	1:A:165:PRO:HB2	1.78	0.65
1:B:17:LYS:H	1:B:41:GLN:NE2	1.94	0.64
1:S:329:LEU:O	1:S:333:MET:HG2	1.98	0.63
1:A:171:TYR:CE2	1:A:175:ILE:HD11	2.33	0.63
1:B:46:LEU:HD23	1:B:46:LEU:C	2.19	0.63
1:A:178:GLN:HE21	1:A:260:ILE:HD11	1.64	0.62
1:S:299:ARG:NE	5:S:463:HOH:O	2.31	0.61
1:S:10:GLN:HG2	5:S:350:HOH:O	2.00	0.61
1:A:334:PRO:O	1:A:338:ARG:HD2	2.01	0.61
1:S:149:HIS:CD2	1:S:151:ALA:H	2.17	0.61
1:A:270:THR:OG1	1:A:273:GLU:HG2	2.00	0.61
1:A:17:LYS:H	1:A:41:GLN:NE2	2.00	0.59
1:A:8:ILE:HG23	1:A:251:LEU:HD22	1.83	0.59
1:A:245:MET:HE1	1:A:319:TYR:CD2	2.38	0.58
1:S:279:TYR:CE1	1:S:283:ASN:ND2	2.71	0.58
1:B:67:GLU:CD	1:B:67:GLU:H	2.07	0.58
1:B:71:ARG:HG2	1:B:71:ARG:HH11	4.06	0.58
1:S:12:LEU:HB3	1:S:41:GLN:NE2	2.17	0.58
1:A:245:MET:HE2	1:A:319:TYR:CD1	2.38	0.58
1:A:179:VAL:O	1:A:183:THR:HG23	2.03	0.58
1:A:195:ASN:ND2	1:A:234:ARG:HD2	2.19	0.57
1:A:148:ASP:HB3	1:A:163:LEU:HD21	1.85	0.57
1:S:71:ARG:HG2	1:S:71:ARG:NH1	2.20	0.57
1:S:279:TYR:CD1	1:S:283:ASN:ND2	2.73	0.57
1:B:8:ILE:HG23	1:B:251:LEU:HD22	1.86	0.56
1:A:7:GLU:OE1	1:B:51:THR:HG22	2.05	0.56
1:S:71:ARG:HH11	1:S:71:ARG:HG2	1.70	0.56
1:B:203:PRO:HA	1:B:212:PRO:HB2	1.88	0.56
1:A:17:LYS:H	1:A:41:GLN:HE22	1.55	0.55
1:A:318:LYS:HE3	4:A:345:SO4:O2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:102:GLY:O	1:B:103:SER:HB3	2.18	0.55
1:A:318:LYS:N	1:A:318:LYS:HD3	2.20	0.54
1:B:149:HIS:HD2	1:B:151:ALA:H	1.95	0.54
1:B:149:HIS:CD2	1:B:151:ALA:H	2.67	0.53
1:B:153:PRO:HG2	5:B:348:HOH:O	26.99	0.53
1:B:71:ARG:HG2	1:B:71:ARG:NH1	4.31	0.53
1:B:315:ASP:HB3	1:B:316:LEU:HD12	1.91	0.53
1:A:66:THR:HB	1:A:67:GLU:OE2	2.08	0.53
1:A:232:THR:HG23	1:A:304:ARG:O	2.09	0.53
1:B:130:LYS:NZ	1:B:131:ASN:OD1	2.46	0.53
1:B:299:ARG:NH2	5:B:412:HOH:O	2.42	0.53
1:B:264:ALA:HB3	1:B:308:ALA:HB3	1.91	0.52
1:A:130:LYS:NZ	1:A:131:ASN:OD1	2.41	0.52
1:A:311:THR:O	1:A:315:ASP:HB2	2.09	0.52
1:B:235:ASP:HB2	1:B:307:GLN:HA	2.18	0.52
1:A:46:LEU:C	1:A:46:LEU:HD23	2.31	0.51
1:A:102:GLY:O	1:A:103:SER:HB3	2.11	0.50
1:B:171:TYR:CE2	1:B:175:ILE:HD11	2.46	0.50
1:S:285:ILE:O	1:S:287:HIS:ND1	2.42	0.50
1:A:46:LEU:C	1:A:46:LEU:CD2	2.80	0.50
1:A:317:LEU:O	1:A:318:LYS:HB2	2.12	0.50
1:B:285:ILE:HG22	1:B:285:ILE:O	2.12	0.50
1:B:265:VAL:HG12	1:B:265:VAL:O	2.12	0.50
1:B:279:TYR:CE1	1:B:283:ASN:ND2	3.82	0.49
1:A:213:LYS:HD3	3:A:344:UDP:O4	2.11	0.49
1:B:8:ILE:HD12	1:B:248:LEU:HD23	3.10	0.49
1:B:304:ARG:HG3	1:B:305:HIS:CD2	2.84	0.49
1:B:231:GLU:OE1	1:B:272:ASN:ND2	2.43	0.49
1:S:12:LEU:CD2	1:S:41:GLN:HE22	2.03	0.48
1:S:81:ASP:OD1	5:S:387:HOH:O	2.20	0.48
1:B:67:GLU:O	1:B:70:SER:OG	2.27	0.48
1:S:168:VAL:O	1:S:172:VAL:HG23	2.14	0.48
1:B:46:LEU:HD12	1:B:88:VAL:HG21	1.95	0.48
1:B:194:PHE:HB2	1:B:264:ALA:HB2	2.07	0.48
1:A:31:ASN:HB3	1:A:243:ILE:HD11	1.96	0.47
1:S:299:ARG:O	1:S:302:ASP:HB2	2.14	0.47
1:S:102:GLY:O	1:S:103:SER:HB3	2.15	0.47
1:A:231:GLU:OE1	1:A:272:ASN:ND2	2.47	0.47
1:A:67:GLU:N	1:A:67:GLU:CD	2.66	0.47
1:S:46:LEU:HD23	1:S:47:ASP:N	2.30	0.47
1:B:168:VAL:O	1:B:172:VAL:HG23	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:2:MET:O	1:S:3:SER:C	2.53	0.47
1:A:11:GLN:NE2	1:B:206:ALA:H	2.13	0.47
1:A:11:GLN:HE21	1:B:206:ALA:H	1.62	0.47
1:B:8:ILE:CD1	1:B:248:LEU:HD23	3.30	0.46
1:S:71:ARG:HH11	1:S:71:ARG:CG	2.29	0.46
1:S:245:MET:HE3	1:S:263:VAL:HG22	1.98	0.46
1:B:4:ARG:NH2	1:B:318:LYS:HD3	2.31	0.45
1:B:239:ILE:HG13	1:B:239:ILE:H	1.65	0.45
1:B:175:ILE:HG21	1:B:175:ILE:HD13	1.75	0.45
1:A:168:VAL:O	1:A:172:VAL:HG23	2.15	0.45
1:A:245:MET:HG2	1:A:263:VAL:HG22	1.97	0.45
1:B:245:MET:HG2	1:B:263:VAL:HG22	2.05	0.45
1:B:335:TRP:HA	1:B:338:ARG:HH11	3.06	0.45
1:B:130:LYS:HG2	1:B:130:LYS:HZ3	3.00	0.45
1:B:71:ARG:CG	1:B:71:ARG:HH11	3.19	0.45
1:B:141:ALA:HB1	5:B:366:HOH:O	28.70	0.45
1:A:299:ARG:O	1:A:302:ASP:HB3	2.17	0.45
1:B:101:LEU:HG	1:B:117:THR:HG21	1.99	0.45
1:S:46:LEU:CD2	2:S:343:NAD:H2A	2.46	0.45
1:A:178:GLN:NE2	1:A:260:ILE:HD11	2.29	0.44
1:S:178:GLN:NE2	1:S:260:ILE:HD11	2.33	0.44
1:B:245:MET:HE3	1:B:263:VAL:HG22	2.13	0.44
1:S:194:PHE:O	1:S:195:ASN:C	2.57	0.43
1:A:203:PRO:HA	1:A:212:PRO:HB2	2.00	0.43
1:B:4:ARG:NH1	1:B:318:LYS:HD3	2.33	0.43
1:A:146:TYR:HB3	1:A:154:LYS:HE3	2.00	0.43
1:S:44:ILE:HD12	1:S:92:VAL:HG22	1.99	0.43
1:S:260:ILE:HD12	1:S:260:ILE:N	2.34	0.43
1:B:195:ASN:HD21	1:B:234:ARG:HD2	1.84	0.43
1:B:67:GLU:CD	1:B:67:GLU:N	2.71	0.43
1:B:152:LEU:HA	1:B:153:PRO:C	2.74	0.43
1:B:265:VAL:CG1	1:B:265:VAL:O	2.65	0.43
1:B:279:TYR:O	1:B:283:ASN:HB2	2.18	0.43
1:A:253:LYS:NZ	4:A:345:SO4:O4	2.35	0.43
1:B:177:ALA:HB1	1:B:188:THR:OG1	2.19	0.43
1:A:245:MET:CE	1:A:319:TYR:CD1	3.02	0.42
1:S:4:ARG:NH2	1:S:318:LYS:HE2	2.33	0.42
1:B:286:HIS:O	1:B:287:HIS:CG	3.29	0.42
1:B:194:PHE:O	1:B:195:ASN:C	2.57	0.42
1:A:141:ALA:HB1	5:A:350:HOH:O	2.19	0.42
1:S:12:LEU:HB3	1:S:41:GLN:HE21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:LEU:CD2	1:B:46:LEU:C	2.86	0.42
1:A:4:ARG:HG2	1:A:318:LYS:HB2	2.00	0.42
1:S:245:MET:HG2	1:S:263:VAL:HG22	2.02	0.42
1:S:235:ASP:HB2	1:S:307:GLN:HA	2.01	0.42
1:S:104:VAL:N	1:S:105:PRO:HD2	2.35	0.42
1:A:177:ALA:HB1	1:A:188:THR:OG1	2.19	0.42
1:S:239:ILE:HG13	1:S:239:ILE:H	1.58	0.42
1:B:8:ILE:HD13	5:B:386:HOH:O	2.20	0.41
1:S:46:LEU:C	1:S:46:LEU:HD23	2.40	0.41
1:A:196:VAL:HA	1:A:237:CYS:O	2.19	0.41
1:B:271:LEU:HD23	1:B:271:LEU:HA	2.10	0.41
1:B:4:ARG:NH2	1:B:318:LYS:HE2	2.61	0.41
1:S:141:ALA:HB1	5:S:366:HOH:O	2.20	0.41
1:B:219:LEU:HD21	1:B:282:LEU:HD22	2.62	0.41
1:B:322:ASN:OD1	1:B:322:ASN:N	2.53	0.41
1:B:4:ARG:CZ	1:B:318:LYS:HD3	2.50	0.41
1:A:6:GLU:O	1:A:10:GLN:HG3	2.21	0.41
1:A:21:ILE:HD11	1:A:36:LEU:HD12	2.03	0.41
1:B:157:GLU:H	1:B:157:GLU:HG3	1.74	0.41
1:B:319:TYR:CZ	1:B:321:PRO:HB3	2.56	0.41
1:A:175:ILE:HD13	1:A:175:ILE:HG21	1.84	0.41
1:B:66:THR:HB	1:B:67:GLU:OE2	2.21	0.40
1:A:245:MET:CE	1:A:319:TYR:CG	3.05	0.40
1:S:195:ASN:ND2	1:S:234:ARG:HD2	2.37	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	332/351 (95%)	321 (97%)	10 (3%)	1 (0%)	46 41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	332/351 (95%)	323 (97%)	7 (2%)	2 (1%)	30	22
1	S	332/351 (95%)	321 (97%)	9 (3%)	2 (1%)	30	22
1	b	332/351 (95%)	322 (97%)	8 (2%)	2 (1%)	30	22
All	All	1328/1404 (95%)	1287 (97%)	34 (3%)	7 (0%)	34	26

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	286	HIS
1	S	3	SER
1	B	286	HIS
1	b	103	SER
1	A	103	SER
1	B	103	SER
1	S	103	SER

### 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	290/304 (95%)	275 (95%)	15 (5%)	29	23
1	B	290/304 (95%)	276 (95%)	14 (5%)	31	26
1	S	290/304 (95%)	283 (98%)	7 (2%)	57	58
1	b	289/304 (95%)	279 (96%)	10 (4%)	43	40
All	All	1159/1216 (95%)	1113 (96%)	46 (4%)	38	33

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

Mol	Chain	Res	Type
1	A	46	LEU
1	A	67	GLU
1	A	109	VAL
1	A	152	LEU

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Mol	Chain	Res	Type
1	A	157	GLU
1	A	183	THR
1	A	239	ILE
1	A	253	LYS
1	A	268	ARG
1	A	273	GLU
1	A	299	ARG
1	A	315	ASP
1	A	318	LYS
1	A	320	ARG
1	A	330	ARG
1	B	67	GLU
1	B	109	VAL
1	B	117	THR
1	B	152	LEU
1	B	157	GLU
1	B	176	TYR
1	B	239	ILE
1	B	279	TYR
1	B	283	ASN
1	B	299	ARG
1	B	315	ASP
1	B	324	LYS
1	B	326	ARG
1	B	338	ARG
1	S	71	ARG
1	S	157	GLU
1	S	179	VAL
1	S	183	THR
1	S	239	ILE
1	S	279	TYR
1	S	338	ARG
1	b	3	SER
1	b	15	SER
1	b	46	LEU
1	b	71	ARG
1	b	130	LYS
1	b	157	GLU
1	b	239	ILE
1	b	318	LYS
1	b	338	ARG
1	b	341	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	41	GLN
1	A	149	HIS
1	A	158	ASN
1	A	173	ASN
1	A	178	GLN
1	A	195	ASN
1	B	41	GLN
1	B	149	HIS
1	B	195	ASN
1	S	149	HIS
1	S	158	ASN
1	S	173	ASN
1	S	195	ASN
1	S	283	ASN
1	b	149	HIS
1	b	173	ASN
1	b	195	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length

(or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAD	A	343	-	38,48,48	1.23	3 (7%)	47,73,73	2.75	12 (25%)
3	UDP	A	344	-	18,26,26	0.99	1 (5%)	26,40,40	2.07	4 (15%)
4	SO4	A	345	-	4,4,4	2.84	4 (100%)	6,6,6	0.63	0
2	NAD	B	343	-	38,48,48	1.03	2 (5%)	47,73,73	2.55	11 (23%)
3	UDP	B	344	-	18,26,26	0.98	0	26,40,40	2.04	3 (11%)
2	NAD	S	343	-	38,48,48	1.05	1 (2%)	47,73,73	2.41	8 (17%)
3	UDP	S	344	-	18,26,26	1.10	2 (11%)	26,40,40	2.28	7 (26%)
3	UDP	b	343	-	18,26,26	0.95	0	26,40,40	2.18	4 (15%)
2	NAD	b	344	-	38,48,48	1.16	3 (7%)	47,73,73	2.23	10 (21%)

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	NAD	A	343	-	-	0/22/62/62	0/5/5/5
3	UDP	A	344	-	-	0/12/32/32	0/2/2/2
4	SO4	A	345	-	-	0/0/0/0	0/0/0/0
2	NAD	B	343	-	-	0/22/62/62	0/5/5/5
3	UDP	B	344	-	-	0/12/32/32	0/2/2/2
2	NAD	S	343	-	-	0/22/62/62	0/5/5/5
3	UDP	S	344	-	-	0/12/32/32	0/2/2/2
3	UDP	b	343	-	-	0/12/32/32	0/2/2/2
2	NAD	b	344	-	-	0/22/62/62	0/5/5/5

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	345	SO4	O1-S	-3.04	1.36	1.47
4	A	345	SO4	O4-S	-2.98	1.36	1.47
4	A	345	SO4	O3-S	-2.71	1.37	1.47
4	A	345	SO4	O2-S	-2.60	1.38	1.47
2	B	343	NAD	C2A-N3A	2.01	1.35	1.32
2	b	344	NAD	O4D-C1D	2.02	1.43	1.41
2	b	344	NAD	C2A-N3A	2.05	1.35	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	343	NAD	O3D-C3D	2.11	1.48	1.43
2	A	343	NAD	C4A-N3A	2.13	1.38	1.35
3	S	344	UDP	PB-O3B	2.24	1.62	1.54
2	S	343	NAD	C7N-N7N	2.67	1.38	1.33
3	A	344	UDP	O4'-C1'	2.76	1.44	1.41
2	B	343	NAD	O4B-C1B	2.76	1.44	1.41
3	S	344	UDP	O4'-C1'	2.89	1.44	1.41
2	b	344	NAD	C7N-N7N	2.89	1.38	1.33
2	A	343	NAD	O4B-C1B	4.62	1.47	1.41

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	343	NAD	N3A-C2A-N1A	-14.67	117.67	128.89
2	S	343	NAD	N3A-C2A-N1A	-13.50	118.55	128.89
2	B	343	NAD	N3A-C2A-N1A	-12.76	119.13	128.89
2	b	344	NAD	N3A-C2A-N1A	-10.53	120.83	128.89
2	A	343	NAD	O7N-C7N-C3N	-5.33	113.77	119.59
2	b	344	NAD	O7N-C7N-C3N	-4.75	114.40	119.59
2	B	343	NAD	O7N-C7N-C3N	-4.35	114.84	119.59
3	A	344	UDP	O3B-PB-O3A	-3.33	89.98	105.09
2	B	343	NAD	C2B-C1B-N9A	-3.29	109.27	114.29
2	A	343	NAD	PN-O3-PA	-3.18	123.81	132.73
2	S	343	NAD	O7N-C7N-C3N	-3.17	116.13	119.59
2	A	343	NAD	C2B-C1B-N9A	-3.06	109.61	114.29
2	b	344	NAD	C4A-C5A-N7A	-2.99	106.73	109.48
2	B	343	NAD	PN-O3-PA	-2.94	124.48	132.73
3	B	344	UDP	O3B-PB-O3A	-2.83	92.27	105.09
2	S	343	NAD	O3D-C3D-C4D	-2.71	102.91	111.05
2	A	343	NAD	C3N-C2N-N1N	-2.59	117.38	120.36
2	A	343	NAD	C1B-N9A-C4A	-2.52	123.14	126.94
3	b	343	UDP	O3'-C3'-C2'	-2.33	104.25	111.83
2	B	343	NAD	O2N-PN-O5D	-2.28	96.96	108.46
2	B	343	NAD	C1B-N9A-C4A	-2.18	123.66	126.94
3	A	344	UDP	C6-N1-C2	-2.17	117.76	121.28
3	S	344	UDP	O3B-PB-O3A	-2.16	95.31	105.09
2	b	344	NAD	O3D-C3D-C4D	-2.15	104.60	111.05
2	A	343	NAD	O2N-PN-O5D	-2.10	97.90	108.46
2	S	343	NAD	C1B-N9A-C4A	-2.08	123.80	126.94
2	b	344	NAD	C3N-C2N-N1N	-2.02	118.04	120.36
3	S	344	UDP	O3'-C3'-C2'	-2.00	105.31	111.83
3	S	344	UDP	O5'-PA-O1A	-2.00	101.85	109.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	343	NAD	C2A-N1A-C6A	2.11	122.54	118.77
2	A	343	NAD	C2N-C3N-C4N	2.17	120.71	118.29
3	S	344	UDP	O2A-PA-O1A	2.25	124.74	112.53
2	b	344	NAD	C2A-N1A-C6A	2.38	123.02	118.77
2	b	344	NAD	O2B-C2B-C3B	2.48	119.88	111.83
2	S	343	NAD	O2B-C2B-C3B	2.64	120.43	111.83
2	S	343	NAD	O2N-PN-O1N	2.80	127.69	112.53
2	A	343	NAD	C2A-N1A-C6A	2.81	123.78	118.77
3	B	344	UDP	O2B-PB-O1B	2.93	120.02	110.58
2	B	343	NAD	O4D-C1D-N1N	2.95	111.37	108.13
2	A	343	NAD	C3N-C7N-N7N	2.97	121.07	117.82
3	b	343	UDP	O2B-PB-O1B	2.99	120.20	110.58
2	b	344	NAD	O7N-C7N-N7N	3.06	126.90	122.59
2	B	343	NAD	C3N-C7N-N7N	3.22	121.34	117.82
2	B	343	NAD	C2N-C3N-C4N	3.23	121.88	118.29
2	b	344	NAD	C2N-C3N-C4N	3.28	121.94	118.29
3	S	344	UDP	O3A-PA-O5'	3.28	111.64	102.94
2	S	343	NAD	O4D-C1D-N1N	3.34	111.80	108.13
3	A	344	UDP	O2B-PB-O1B	3.49	121.81	110.58
2	A	343	NAD	O2N-PN-O1N	3.74	132.79	112.53
2	B	343	NAD	O2N-PN-O1N	3.80	133.10	112.53
3	S	344	UDP	O2B-PB-O1B	3.98	123.40	110.58
2	A	343	NAD	O3-PA-O5B	4.03	113.63	102.94
2	B	343	NAD	O3-PA-O5B	4.09	113.78	102.94
2	b	344	NAD	O4D-C1D-N1N	4.86	113.47	108.13
3	b	343	UDP	O3A-PA-O5'	5.39	117.25	102.94
3	b	343	UDP	C4-N3-C2	7.50	121.57	114.14
3	A	344	UDP	C4-N3-C2	7.71	121.78	114.14
3	B	344	UDP	C4-N3-C2	8.08	122.14	114.14
3	S	344	UDP	C4-N3-C2	8.51	122.57	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	344	UDP	1	0
4	A	345	SO4	2	0
2	S	343	NAD	1	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	336/351 (95%)	-0.22	4 (1%) 81 81	27, 38, 66, 82	0
1	B	336/351 (95%)	-0.21	7 (2%) 67 67	28, 39, 68, 83	0
1	S	336/351 (95%)	-0.10	9 (2%) 58 58	29, 41, 67, 92	0
1	b	336/351 (95%)	-0.07	6 (1%) 71 72	28, 41, 66, 85	0
All	All	1344/1404 (95%)	-0.15	26 (1%) 70 70	27, 40, 67, 92	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	b	2	MET	9.1
1	S	2	MET	6.1
1	B	286	HIS	5.1
1	B	301	GLY	4.9
1	b	1	TYR	4.8
1	A	301	GLY	4.6
1	S	1	TYR	4.5
1	B	225	TYR	4.1
1	b	286	HIS	3.9
1	b	300	SER	3.9
1	S	300	SER	3.8
1	A	282	LEU	3.8
1	B	279	TYR	3.8
1	S	340	LEU	3.3
1	A	293	ILE	3.1
1	B	219	LEU	2.9
1	B	285	ILE	2.7
1	A	286	HIS	2.7
1	S	10	GLN	2.6
1	S	297	GLU	2.5
1	S	338	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	S	286	HIS	2.3
1	b	337	VAL	2.2
1	S	279	TYR	2.1
1	B	302	ASP	2.1
1	b	11	GLN	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
2	NAD	S	343	44/44	0.95	0.11	0.40	29,35,40,44	0
2	NAD	b	344	44/44	0.94	0.10	0.13	30,36,41,45	0
2	NAD	B	343	44/44	0.95	0.10	0.04	27,32,39,40	0
2	NAD	A	343	44/44	0.95	0.10	-0.26	23,31,38,41	0
4	SO4	A	345	5/5	0.99	0.11	-0.27	30,30,30,30	0
3	UDP	A	344	25/25	0.91	0.12	-0.36	47,50,53,54	0
3	UDP	B	344	25/25	0.95	0.09	-0.70	45,51,53,54	0
3	UDP	S	344	25/25	0.95	0.09	-0.79	42,48,49,52	0
3	UDP	b	343	25/25	0.92	0.09	-1.31	38,49,52,52	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.