



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:28 PM GMT

PDB ID : 1XAG  
Title : CRYSTAL STRUCTURE OF STAPHYLOCOCCUS AUREUS 3-DEHYDROQUINATE SYNTHASE (DHQS) IN COMPLEX WITH ZN<sup>2+</sup>, NAD<sup>+</sup> AND CARBAPHOSPHONATE  
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Deposited on : 2004-08-25  
Resolution : 2.45 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

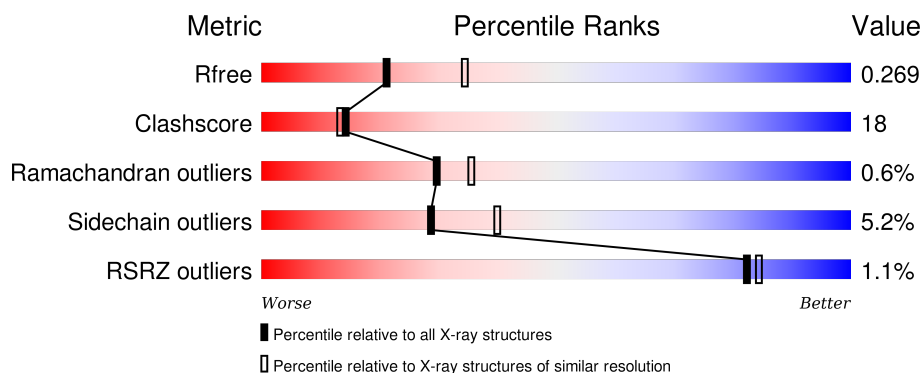
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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	354	<div> <div></div> <div>69%</div> <div>28%</div> <div>.</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3020 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 3-dehydroquinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	353	Total	C	N	O	S	0	0	0
			2842	1840	467	527	8			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	LYS	ASP	see remark 999	UNP Q6GGU4
A	23	TYR	HIS	see remark 999	UNP Q6GGU4
A	25	GLY	SER	see remark 999	UNP Q6GGU4
A	28	LEU	ILE	see remark 999	UNP Q6GGU4
A	29	ASN	ASP	see remark 999	UNP Q6GGU4
A	36	LEU	ILE	see remark 999	UNP Q6GGU4
A	41	TYR	HIS	see remark 999	UNP Q6GGU4
A	48	ASN	ASP	see remark 999	UNP Q6GGU4
A	109	VAL	ILE	see remark 999	UNP Q6GGU4
A	170	LYS	GLU	see remark 999	UNP Q6GGU4
A	226	VAL	ILE	see remark 999	UNP Q6GGU4
A	282	SER	ASN	see remark 999	UNP Q6GGU4
A	326	MET	ILE	see remark 999	UNP Q6GGU4

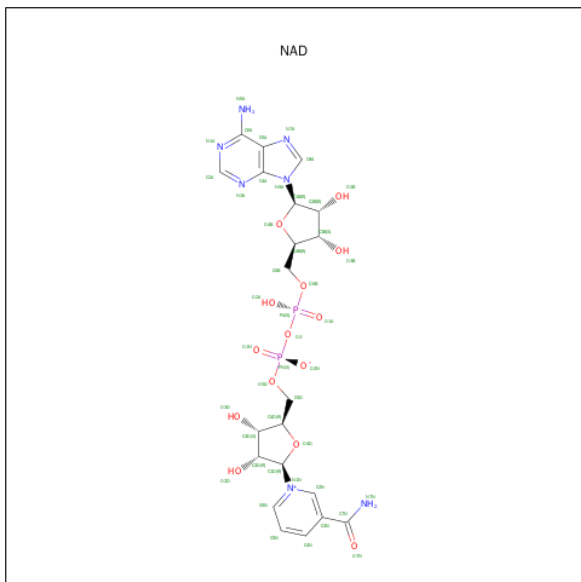
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

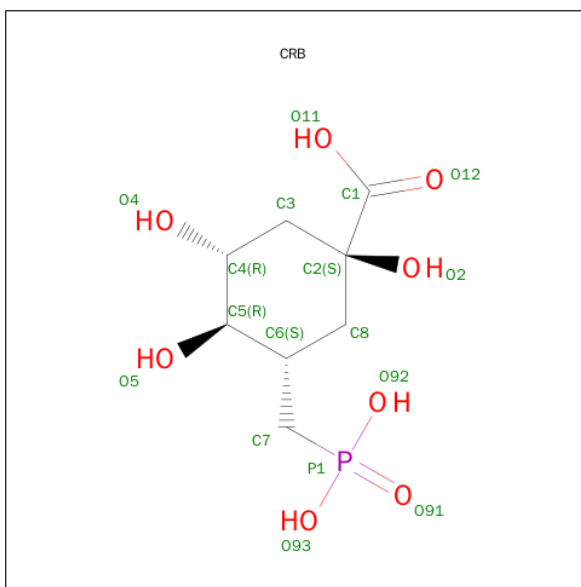
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	Cl	0	0
			5	5		

- Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula:  $C_{21}H_{27}N_7O_{14}P_2$ ).



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

- Molecule 5 is [1R-(1ALPHA,3BETA,4ALPHA,5BETA)]-5-(PHOSPHONOMETHYL)-1,3,4-TRIHYDROXYCYCLOHEXANE-1-CARBOXYLIC ACID (three-letter code: CRB) (formula:  $C_8H_{15}O_8P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	P	0	0
			17	8	8	1		

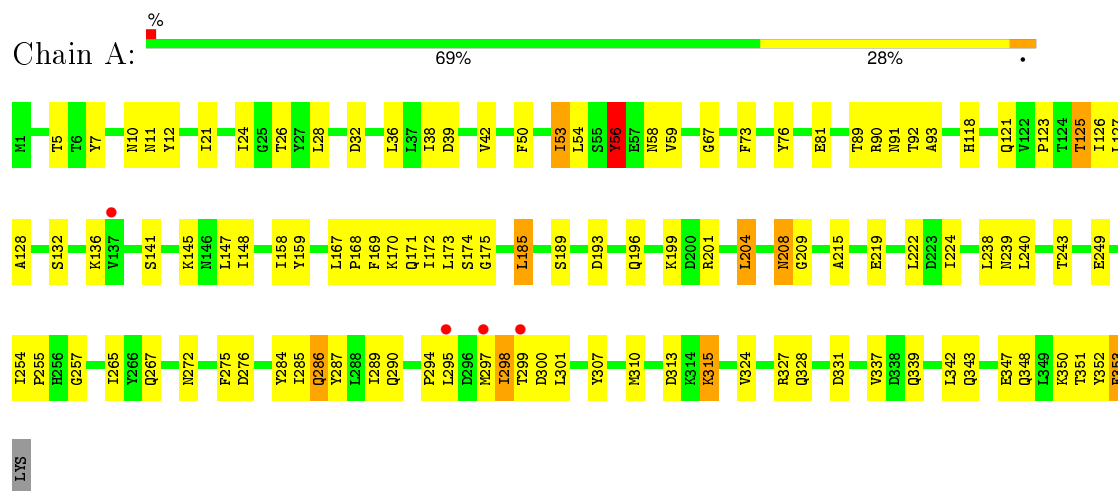
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	111	Total	O	0	0
			111	111		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 3-dehydroquinate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.29 Å 53.29 Å 240.07 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.64 – 2.45 29.64 – 2.45	Depositor EDS
% Data completeness (in resolution range)	95.2 (29.64-2.45) 95.3 (29.64-2.45)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 2.45 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.197 , 0.268 0.197 , 0.269	Depositor DCC
$R_{free}$ test set	1049 reflections (8.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	48.2	Xtriage
Anisotropy	0.513	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 51.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 12933 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3020	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.02% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CRB, ZN, NAD, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.34	0/2909	0.61	2/3939 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	58	ASN	N-CA-C	-6.52	93.39	111.00
1	A	56	TYR	N-CA-C	-5.47	96.24	111.00

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	2842	0	2806	104	0
2	A	1	0	0	0	0
3	A	5	0	0	0	0
4	A	44	0	26	2	0
5	A	17	0	12	1	0
6	A	111	0	0	2	0
All	All	3020	0	2844	104	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 18.

All (104) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:THR:HG22	1:A:128:ALA:H	1.17	1.05
1:A:7:TYR:H	1:A:11:ASN:HD21	1.33	0.77
1:A:50:PHE:O	1:A:54:LEU:HD13	1.86	0.76
1:A:313:ASP:OD2	1:A:315:LYS:HB2	1.89	0.73
1:A:125:THR:HG22	1:A:128:ALA:N	2.01	0.67
1:A:298:ILE:HD11	1:A:350:LYS:HA	1.77	0.65
1:A:327:ARG:HD2	1:A:331:ASP:OD2	1.97	0.64
1:A:53:ILE:HG12	1:A:59:VAL:HG11	1.81	0.62
1:A:39:ASP:HB3	1:A:42:VAL:HB	1.82	0.61
1:A:343:GLN:O	1:A:347:GLU:HG3	2.00	0.60
1:A:92:THR:HG22	1:A:93:ALA:N	2.16	0.60
1:A:286:GLN:HG2	1:A:287:TYR:N	2.15	0.60
1:A:32:ASP:OD2	1:A:91:ASN:HB3	2.02	0.59
1:A:89:THR:HG22	1:A:90:ARG:N	2.18	0.59
1:A:10:ASN:N	1:A:10:ASN:HD22	1.99	0.59
1:A:353:PHE:CD1	1:A:353:PHE:N	2.70	0.58
1:A:172:ILE:CG2	1:A:204:LEU:HD22	2.33	0.58
1:A:215:ALA:O	1:A:219:GLU:HG3	2.03	0.58
1:A:353:PHE:HD1	1:A:353:PHE:N	2.02	0.57
1:A:352:TYR:C	1:A:353:PHE:HD1	2.08	0.57
1:A:298:ILE:HB	1:A:301:LEU:HD22	1.86	0.56
1:A:174:SER:O	1:A:257:GLY:HA3	2.08	0.54
1:A:295:LEU:HG	1:A:353:PHE:HE2	1.73	0.53
1:A:123:PRO:HG3	1:A:132:SER:CB	2.39	0.52
1:A:348:GLN:O	1:A:351:THR:HB	2.10	0.52
1:A:123:PRO:HG3	1:A:132:SER:HB3	1.92	0.52
1:A:53:ILE:HG23	1:A:54:LEU:CD1	2.40	0.51
1:A:10:ASN:H	1:A:10:ASN:HD22	1.57	0.51
1:A:81:GLU:HA	1:A:81:GLU:OE1	2.10	0.51
1:A:126:ILE:HB	6:A:689:HOH:O	2.10	0.51
1:A:185:LEU:CD1	1:A:240:LEU:HD22	2.41	0.51
1:A:286:GLN:O	1:A:290:GLN:HG3	2.11	0.51
1:A:123:PRO:HD2	1:A:158:ILE:O	2.11	0.50
1:A:5:THR:HG21	1:A:12:TYR:CE1	2.46	0.50
1:A:172:ILE:HG22	1:A:204:LEU:HD22	1.93	0.50
1:A:285:ILE:HD13	1:A:353:PHE:HE1	1.77	0.49
1:A:127:LEU:HB2	1:A:175:GLY:HA2	1.95	0.49
1:A:185:LEU:HD13	1:A:240:LEU:HD22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:MET:SD	1:A:298:ILE:N	2.85	0.49
1:A:28:LEU:HD11	1:A:53:ILE:HD12	1.95	0.49
1:A:148:ILE:HD12	1:A:148:ILE:N	2.28	0.49
1:A:315:LYS:HB2	1:A:315:LYS:HZ3	1.78	0.48
1:A:169:PHE:CE1	1:A:173:LEU:HD21	2.49	0.48
1:A:199:LYS:HB2	1:A:199:LYS:NZ	2.29	0.48
1:A:73:PHE:CZ	1:A:148:ILE:HG12	2.49	0.48
1:A:222:LEU:O	1:A:222:LEU:HD23	2.14	0.48
1:A:199:LYS:CB	1:A:199:LYS:NZ	2.77	0.47
1:A:337:VAL:HG12	1:A:342:LEU:HG	1.97	0.47
1:A:307:TYR:OH	1:A:339:GLN:HB3	2.15	0.47
1:A:289:ILE:HG22	1:A:290:GLN:N	2.29	0.47
1:A:272:ASN:O	1:A:276:ASP:HA	2.14	0.47
1:A:21:ILE:HD11	1:A:24:ILE:HD12	1.97	0.47
1:A:24:ILE:HG22	1:A:28:LEU:CD1	2.46	0.46
1:A:67:GLY:HA2	4:A:400:NAD:O2A	2.16	0.46
1:A:7:TYR:N	1:A:11:ASN:HD21	2.08	0.46
1:A:21:ILE:CD1	1:A:24:ILE:HD12	2.45	0.46
1:A:298:ILE:CB	1:A:301:LEU:HD22	2.45	0.46
1:A:307:TYR:CZ	1:A:339:GLN:HB3	2.51	0.46
1:A:298:ILE:C	1:A:300:ASP:H	2.18	0.45
1:A:315:LYS:HE3	1:A:324:VAL:HG23	1.97	0.45
1:A:275:PHE:CD2	1:A:327:ARG:HG3	2.52	0.45
1:A:254:ILE:HD13	1:A:297:MET:HE3	1.99	0.45
1:A:224:ILE:HD12	1:A:238:LEU:HD21	1.99	0.45
1:A:7:TYR:H	1:A:11:ASN:ND2	2.07	0.45
1:A:36:LEU:HD22	1:A:54:LEU:HD11	1.99	0.45
1:A:56:TYR:N	1:A:56:TYR:CD1	2.79	0.44
1:A:243:THR:HG22	1:A:310:MET:CE	2.48	0.44
1:A:286:GLN:CG	1:A:287:TYR:N	2.80	0.44
1:A:141:SER:HB2	1:A:148:ILE:HD11	1.99	0.44
1:A:297:MET:O	1:A:300:ASP:OD2	2.35	0.44
1:A:56:TYR:HD1	1:A:56:TYR:H	1.62	0.44
1:A:328:GLN:HE21	1:A:328:GLN:HB3	1.63	0.43
1:A:254:ILE:HG21	1:A:297:MET:HE2	1.99	0.43
1:A:298:ILE:C	1:A:300:ASP:N	2.71	0.43
1:A:298:ILE:HG21	1:A:353:PHE:CE2	2.54	0.43
1:A:39:ASP:HB3	1:A:42:VAL:CG2	2.49	0.43
1:A:170:LYS:HE2	1:A:255:PRO:HG3	2.01	0.43
1:A:169:PHE:CZ	1:A:201:ARG:HG3	2.54	0.43
1:A:350:LYS:HB2	1:A:350:LYS:HE3	1.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:ILE:O	1:A:300:ASP:N	2.52	0.42
1:A:208:ASN:HD22	1:A:209:GLY:N	2.18	0.42
1:A:92:THR:CG2	1:A:93:ALA:N	2.80	0.42
1:A:89:THR:CG2	1:A:90:ARG:N	2.83	0.42
1:A:53:ILE:HG23	1:A:54:LEU:HD12	2.01	0.42
1:A:169:PHE:CZ	1:A:173:LEU:HD21	2.55	0.42
1:A:328:GLN:HG2	1:A:331:ASP:HB3	2.02	0.42
1:A:53:ILE:O	1:A:53:ILE:HG12	2.19	0.42
1:A:73:PHE:O	1:A:76:TYR:HB3	2.19	0.42
1:A:189:SER:O	1:A:193:ASP:HB2	2.19	0.42
1:A:171:GLN:NE2	4:A:400:NAD:H51A	2.35	0.41
1:A:38:ILE:HD11	1:A:42:VAL:HG12	2.02	0.41
1:A:10:ASN:ND2	1:A:10:ASN:N	2.66	0.41
1:A:39:ASP:HB3	1:A:42:VAL:CB	2.49	0.41
1:A:145:LYS:HE2	1:A:249:GLU:OE1	2.20	0.41
1:A:175:GLY:HA3	6:A:689:HOH:O	2.20	0.41
1:A:136:LYS:NZ	5:A:500:CRB:H81	2.35	0.41
1:A:89:THR:HG22	1:A:90:ARG:H	1.84	0.41
1:A:121:GLN:C	1:A:123:PRO:HD3	2.40	0.41
1:A:298:ILE:HD13	1:A:353:PHE:CD2	2.55	0.40
1:A:141:SER:HB2	1:A:148:ILE:CD1	2.51	0.40
1:A:167:LEU:HA	1:A:168:PRO:HD3	1.93	0.40
1:A:265:ILE:CD1	1:A:284:TYR:HB3	2.51	0.40
1:A:93:ALA:HA	1:A:118:HIS:O	2.21	0.40
1:A:89:THR:HG22	1:A:91:ASN:H	1.87	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	351/354 (99%)	325 (93%)	24 (7%)	2 (1%)	30	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	294	PRO
1	A	299	THR

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	305/306 (100%)	289 (95%)	16 (5%)	29	40

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	THR
1	A	53	ILE
1	A	56	TYR
1	A	125	THR
1	A	147	LEU
1	A	159	TYR
1	A	185	LEU
1	A	196	GLN
1	A	204	LEU
1	A	208	ASN
1	A	239	ASN
1	A	267	GLN
1	A	286	GLN
1	A	298	ILE
1	A	315	LYS
1	A	353	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	11	ASN

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Mol	Chain	Res	Type
1	A	33	GLN
1	A	48	ASN
1	A	60	HIS
1	A	77	GLN
1	A	143	GLN
1	A	171	GLN
1	A	192	GLN
1	A	208	ASN
1	A	290	GLN
1	A	328	GLN
1	A	344	HIS

### 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](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
4	NAD	A	400	-	38,48,48	1.83	8 (21%)	47,73,73	1.89	9 (19%)
5	CRB	A	500	2	13,17,17	1.79	3 (23%)	17,27,27	1.44	4 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAD	A	400	-	-	0/22/62/62	0/5/5/5
5	CRB	A	500	2	-	0/5/29/29	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	400	NAD	C2A-N1A	2.13	1.38	1.33
4	A	400	NAD	C5N-C4N	2.61	1.44	1.38
5	A	500	CRB	P1-C7	2.98	1.82	1.79
4	A	400	NAD	C3N-C7N	3.03	1.55	1.50
5	A	500	CRB	C4-C5	3.03	1.56	1.52
4	A	400	NAD	C6N-N1N	3.49	1.44	1.35
4	A	400	NAD	C4N-C3N	3.70	1.45	1.39
5	A	500	CRB	C8-C2	3.74	1.57	1.53
4	A	400	NAD	O4B-C1B	3.88	1.46	1.41
4	A	400	NAD	C4A-N3A	4.09	1.41	1.35
4	A	400	NAD	O4D-C1D	5.08	1.47	1.41

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	400	NAD	C5N-C4N-C3N	-5.71	113.16	120.33
4	A	400	NAD	O4B-C1B-N9A	-4.20	99.30	108.10
4	A	400	NAD	O4D-C1D-N1N	-3.77	103.99	108.13
4	A	400	NAD	C5N-C6N-N1N	-3.31	114.74	120.47
5	A	500	CRB	C3-C4-C5	-2.30	108.73	110.84
4	A	400	NAD	C4N-C3N-C7N	-2.25	115.15	121.09
5	A	500	CRB	O92-P1-C7	-2.15	101.59	106.84
4	A	400	NAD	O3-PA-O5B	2.16	108.67	102.94
5	A	500	CRB	O5-C5-C6	2.25	113.81	110.07
5	A	500	CRB	C8-C2-C3	2.26	112.84	110.33
4	A	400	NAD	C2N-C3N-C4N	3.80	122.53	118.29
4	A	400	NAD	C6N-C5N-C4N	4.55	126.32	119.44
4	A	400	NAD	C2B-C1B-N9A	4.87	121.73	114.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	400	NAD	2	0
5	A	500	CRB	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	353/354 (99%)	-0.19	4 (1%) 82 84	28, 45, 73, 108	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	299	THR	3.6
1	A	297	MET	2.8
1	A	137	VAL	2.4
1	A	295	LEU	2.1

### 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	CRB	A	500	17/17	0.97	0.22	0.85	34,43,52,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NAD	A	400	44/44	0.97	0.15	-0.34	23,38,43,49	0
3	CL	A	605	1/1	0.87	0.10	-0.73	96,96,96,96	0
3	CL	A	606	1/1	0.70	0.09	-1.83	80,80,80,80	0
2	ZN	A	601	1/1	0.91	0.10	-	114,114,114,114	0
3	CL	A	603	1/1	0.94	0.18	-	73,73,73,73	0
3	CL	A	604	1/1	0.94	0.12	-	76,76,76,76	0
3	CL	A	602	1/1	0.93	0.10	-	57,57,57,57	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.