



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:52 AM GMT

PDB ID : 3CGE  
Title : Pyridine Nucleotide Complexes with Bacillus anthracis Coenzyme A-Disulfide  
Reductase: A Structural Analysis of Dual NAD(P)H Specificity  
Authors : Wallen, J.R.  
Deposited on : 2008-03-05  
Resolution : 2.26 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

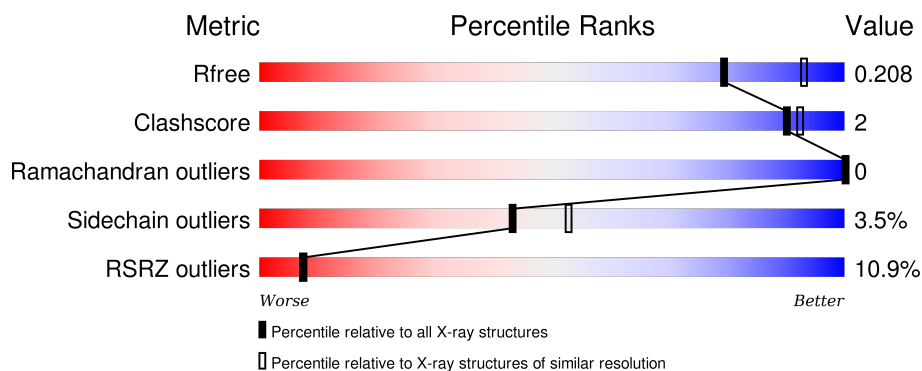
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.26 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	1640 (2.28-2.24)
Clashscore	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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	480	<div> <div>11%</div> <div> <div></div> <div>84%</div> <div>7%</div> <div>8%</div> </div> </div>
1	B	480	<div> <div>9%</div> <div> <div></div> <div>85%</div> <div>7%</div> <div>8%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7659 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 Pyridine nucleotide-disulfide oxidoreductase, class I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	0	2	0
			3491	2205	603	668	15			
1	B	444	Total	C	N	O	S	0	0	0
			3479	2197	602	665	15			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	EXPRESSION TAG	UNP Q81TK8
A	-34	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-33	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-32	SER	-	EXPRESSION TAG	UNP Q81TK8
A	-31	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-30	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-29	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-28	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-27	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-26	HIS	-	EXPRESSION TAG	UNP Q81TK8
A	-25	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-24	MET	-	EXPRESSION TAG	UNP Q81TK8
A	-23	ALA	-	EXPRESSION TAG	UNP Q81TK8
A	-22	SER	-	EXPRESSION TAG	UNP Q81TK8
A	-21	MET	-	EXPRESSION TAG	UNP Q81TK8
A	-20	THR	-	EXPRESSION TAG	UNP Q81TK8
A	-19	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-18	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-17	GLN	-	EXPRESSION TAG	UNP Q81TK8
A	-16	GLN	-	EXPRESSION TAG	UNP Q81TK8
A	-15	MET	-	EXPRESSION TAG	UNP Q81TK8
A	-14	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	-13	ARG	-	EXPRESSION TAG	UNP Q81TK8
A	-12	THR	-	EXPRESSION TAG	UNP Q81TK8
A	-11	LEU	-	EXPRESSION TAG	UNP Q81TK8

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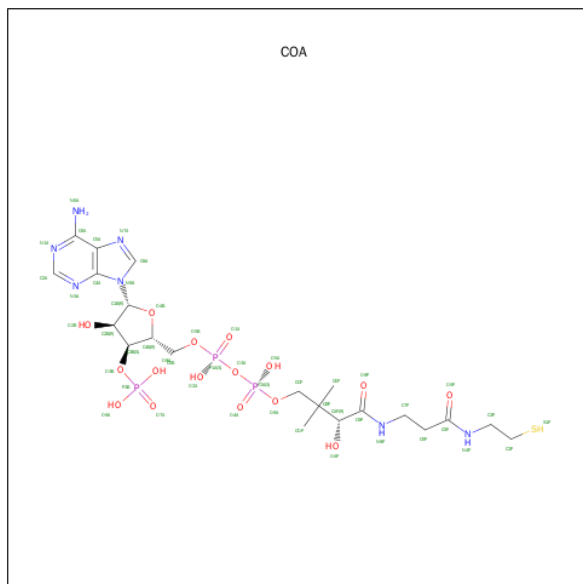
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	TYR	-	EXPRESSION TAG	UNP Q81TK8
A	-9	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-8	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-7	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-6	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-5	LYS	-	EXPRESSION TAG	UNP Q81TK8
A	-4	ASP	-	EXPRESSION TAG	UNP Q81TK8
A	-3	ARG	-	EXPRESSION TAG	UNP Q81TK8
A	-2	TRP	-	EXPRESSION TAG	UNP Q81TK8
A	-1	GLY	-	EXPRESSION TAG	UNP Q81TK8
A	0	SER	-	EXPRESSION TAG	UNP Q81TK8
B	-35	MET	-	EXPRESSION TAG	UNP Q81TK8
B	-34	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-33	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-32	SER	-	EXPRESSION TAG	UNP Q81TK8
B	-31	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-30	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-29	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-28	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-27	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-26	HIS	-	EXPRESSION TAG	UNP Q81TK8
B	-25	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-24	MET	-	EXPRESSION TAG	UNP Q81TK8
B	-23	ALA	-	EXPRESSION TAG	UNP Q81TK8
B	-22	SER	-	EXPRESSION TAG	UNP Q81TK8
B	-21	MET	-	EXPRESSION TAG	UNP Q81TK8
B	-20	THR	-	EXPRESSION TAG	UNP Q81TK8
B	-19	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-18	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-17	GLN	-	EXPRESSION TAG	UNP Q81TK8
B	-16	GLN	-	EXPRESSION TAG	UNP Q81TK8
B	-15	MET	-	EXPRESSION TAG	UNP Q81TK8
B	-14	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	-13	ARG	-	EXPRESSION TAG	UNP Q81TK8
B	-12	THR	-	EXPRESSION TAG	UNP Q81TK8
B	-11	LEU	-	EXPRESSION TAG	UNP Q81TK8
B	-10	TYR	-	EXPRESSION TAG	UNP Q81TK8
B	-9	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-8	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-7	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-6	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-5	LYS	-	EXPRESSION TAG	UNP Q81TK8

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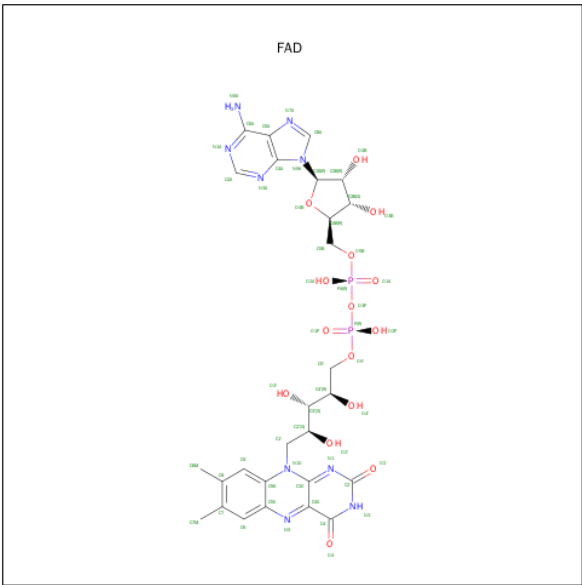
Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	ASP	-	EXPRESSION TAG	UNP Q81TK8
B	-3	ARG	-	EXPRESSION TAG	UNP Q81TK8
B	-2	TRP	-	EXPRESSION TAG	UNP Q81TK8
B	-1	GLY	-	EXPRESSION TAG	UNP Q81TK8
B	0	SER	-	EXPRESSION TAG	UNP Q81TK8

- Molecule 2 is COENZYME A (three-letter code: COA) (formula:  $C_{21}H_{36}N_7O_{16}P_3S$ ).



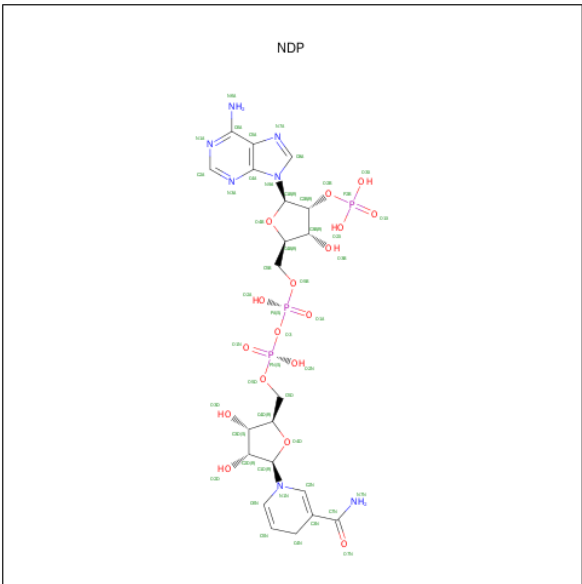
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0
2	B	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



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

- Molecule 4 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
4	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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

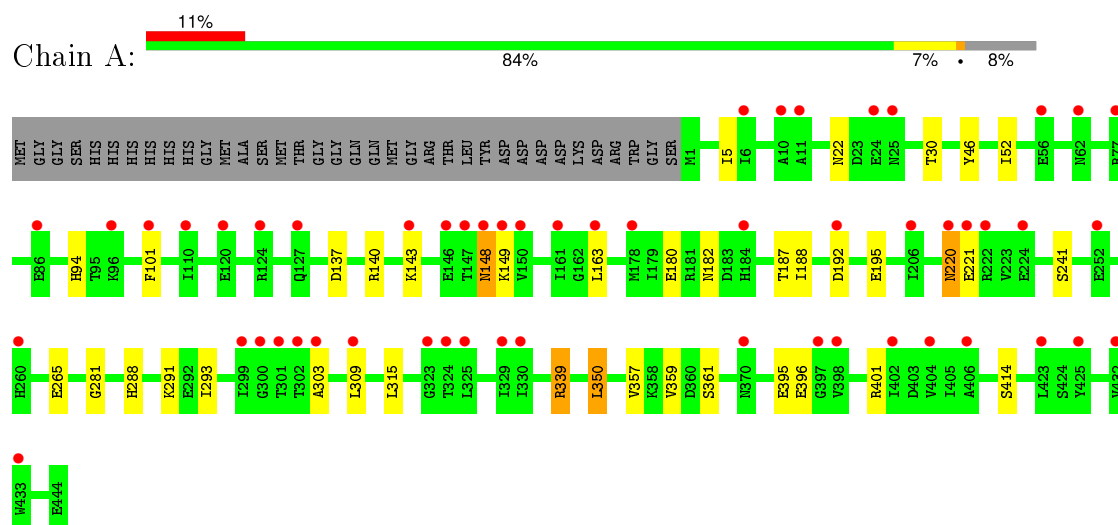
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	189	Total	O	0	0
			189	189		
5	B	202	Total	O	0	0
			202	202		

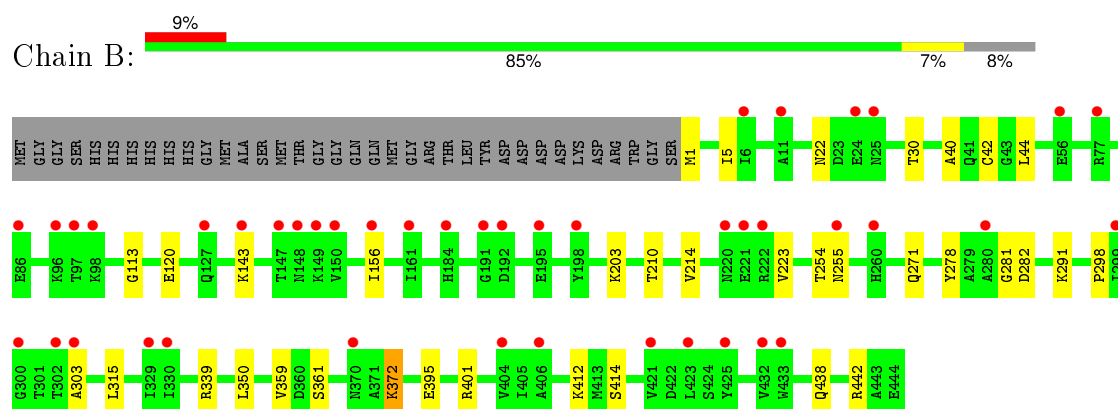
### 3 Residue-property plots [i](#)

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: Pyridine nucleotide-disulfide oxidoreductase, class I



- Molecule 1: Pyridine nucleotide-disulfide oxidoreductase, class I





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.33Å 81.60Å 98.38Å 90.00° 104.11° 90.00°	Depositor
Resolution (Å)	42.11 – 2.26 42.09 – 2.26	Depositor EDS
% Data completeness (in resolution range)	99.5 (42.11-2.26) 99.5 (42.09-2.26)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.91 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.177 , 0.214 0.173 , 0.208	Depositor DCC
$R_{free}$ test set	3078 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	38.0	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 41.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 60595 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7659	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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: COA, NDP, FAD

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	0.38	0/3555	0.53	0/4801
1	B	0.38	0/3537	0.53	0/4777
All	All	0.38	0/7092	0.53	0/9578

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3491	0	3523	18	0
1	B	3479	0	3509	15	0
2	A	48	0	32	0	0
2	B	48	0	32	0	0
3	A	53	0	31	0	0
3	B	53	0	31	0	0
4	A	48	0	26	0	0
4	B	48	0	26	1	0
5	A	189	0	0	1	0
5	B	202	0	0	0	0
All	All	7659	0	7210	33	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 2.

All (33) 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:220:ASN:HD22	1:A:220:ASN:H	1.38	0.71
1:A:220:ASN:CG	1:A:221:GLU:H	1.97	0.67
1:A:137:ASP:OD1	1:A:140:ARG:NH2	2.37	0.57
1:A:291:LYS:HG2	1:A:350:LEU:HD11	1.86	0.57
1:A:359:VAL:HG12	1:A:361:SER:HB2	1.88	0.55
1:A:220:ASN:CG	1:A:221:GLU:N	2.61	0.54
1:B:359:VAL:HG12	1:B:361:SER:HB2	1.92	0.52
1:B:291:LYS:HG2	1:B:350:LEU:HD11	1.90	0.51
1:A:288:HIS:HB3	1:A:291:LYS:HB2	1.93	0.50
1:A:46:TYR:HB2	1:A:52:ILE:HD12	1.93	0.50
1:A:188:ILE:HD12	1:A:339:ARG:HG2	1.96	0.48
1:B:271:GLN:HG2	1:B:278:TYR:CE2	2.50	0.47
1:B:254:THR:O	1:B:255:ASN:HB2	2.14	0.46
1:A:220:ASN:H	1:A:220:ASN:ND2	2.09	0.46
1:B:438:GLN:O	1:B:442:ARG:HG2	2.15	0.46
1:B:156:ILE:HD12	1:B:214:VAL:HG21	1.98	0.46
1:A:192:ASP:HA	1:A:195:GLU:OE1	2.17	0.45
1:A:94:HIS:HB2	1:A:101:PHE:HE2	1.82	0.44
1:B:113:GLY:HA2	1:B:282:ASP:HB2	1.99	0.44
1:B:5:ILE:HB	1:B:30:THR:HG22	1.98	0.44
1:A:5:ILE:HB	1:A:30:THR:HG22	1.98	0.43
1:B:143:LYS:HE2	1:B:143:LYS:HB2	1.86	0.43
1:B:298:PRO:O	4:B:802:NDP:O2D	2.30	0.43
1:A:180:GLU:OE2	1:A:182:ASN:ND2	2.52	0.43
1:B:22:ASN:HB2	1:B:315:LEU:HD13	2.02	0.42
1:A:148:ASN:HD22	1:A:149:LYS:H	1.67	0.42
1:B:372:LYS:HE3	1:B:372:LYS:HA	2.02	0.42
1:B:281:GLY:HA2	1:B:303:ALA:HA	2.02	0.41
1:B:40:ALA:HB1	1:B:42:CYS:SG	2.61	0.41
1:A:281:GLY:HA2	1:A:303:ALA:HA	2.02	0.41
1:A:22:ASN:HB2	1:A:315:LEU:HD13	2.03	0.41
1:B:372:LYS:HD3	1:B:395:GLU:OE2	2.21	0.41
1:A:395:GLU:HG3	5:A:825:HOH:O	2.21	0.41

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	444/480 (92%)	433 (98%)	11 (2%)	0	100	100
1	B	442/480 (92%)	429 (97%)	13 (3%)	0	100	100
All	All	886/960 (92%)	862 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	372/398 (94%)	356 (96%)	16 (4%)	35	41
1	B	370/398 (93%)	359 (97%)	11 (3%)	48	59
All	All	742/796 (93%)	715 (96%)	27 (4%)	43	51

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	LYS
1	A	148	ASN
1	A	163	LEU
1	A	187	THR
1	A	220	ASN
1	A	241	SER
1	A	265[A]	GLU
1	A	265[B]	GLU

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Mol	Chain	Res	Type
1	A	293	ILE
1	A	309	LEU
1	A	339	ARG
1	A	350	LEU
1	A	357	VAL
1	A	396	GLU
1	A	401	ARG
1	A	414	SER
1	B	1	MET
1	B	44	LEU
1	B	120	GLU
1	B	203	LYS
1	B	210	THR
1	B	223	VAL
1	B	339	ARG
1	B	372	LYS
1	B	401	ARG
1	B	412	LYS
1	B	414	SER

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

Mol	Chain	Res	Type
1	A	184	HIS
1	A	220	ASN
1	A	275	GLN
1	A	334	ASN
1	B	2	ASN
1	B	184	HIS
1	B	220	ASN
1	B	304	ASN
1	B	334	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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

6 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	COA	A	445	-	40,50,50	0.66	0	50,75,75	1.99	8 (16%)
3	FAD	A	446	-	48,58,58	0.90	3 (6%)	54,89,89	2.14	9 (16%)
4	NDP	A	803	-	42,52,52	1.56	5 (11%)	55,80,80	1.84	4 (7%)
2	COA	B	445	-	40,50,50	0.68	0	50,75,75	1.98	7 (14%)
3	FAD	B	446	-	48,58,58	0.90	3 (6%)	54,89,89	2.01	10 (18%)
4	NDP	B	802	-	42,52,52	1.55	5 (11%)	55,80,80	1.97	5 (9%)

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	COA	A	445	-	-	0/44/64/64	0/3/3/3
3	FAD	A	446	-	-	0/30/50/50	0/6/6/6
4	NDP	A	803	-	-	0/30/77/77	0/5/5/5
2	COA	B	445	-	-	0/44/64/64	0/3/3/3
3	FAD	B	446	-	-	0/30/50/50	0/6/6/6
4	NDP	B	802	-	-	0/30/77/77	0/5/5/5

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	446	FAD	C4X-N5	2.04	1.36	1.33
3	B	446	FAD	C10-N10	2.04	1.41	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	802	NDP	C2N-C3N	2.13	1.39	1.34
4	A	803	NDP	C2N-C3N	2.23	1.40	1.34
3	A	446	FAD	O4B-C1B	2.30	1.44	1.41
3	B	446	FAD	C4X-N5	2.38	1.37	1.33
4	B	802	NDP	C2A-N1A	2.48	1.38	1.33
4	A	803	NDP	C2A-N1A	2.60	1.38	1.33
3	A	446	FAD	C9A-N10	2.73	1.42	1.38
3	B	446	FAD	C9A-N10	2.90	1.42	1.38
4	A	803	NDP	C6N-C5N	3.25	1.39	1.33
4	B	802	NDP	C6N-C5N	3.26	1.39	1.33
4	B	802	NDP	C2A-N3A	3.63	1.38	1.32
4	A	803	NDP	C2A-N3A	3.76	1.38	1.32
4	B	802	NDP	O7N-C7N	6.61	1.41	1.24
4	A	803	NDP	O7N-C7N	6.63	1.41	1.24

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	802	NDP	N3A-C2A-N1A	-12.55	119.28	128.89
4	A	803	NDP	N3A-C2A-N1A	-11.58	120.02	128.89
3	A	446	FAD	N3A-C2A-N1A	-10.72	120.69	128.89
2	B	445	COA	N3A-C2A-N1A	-10.21	121.08	128.89
2	A	445	COA	N3A-C2A-N1A	-10.17	121.11	128.89
3	B	446	FAD	N3A-C2A-N1A	-9.39	121.71	128.89
2	B	445	COA	C2P-C3P-N4P	-4.05	104.37	112.37
2	A	445	COA	C2P-C3P-N4P	-3.83	104.81	112.37
4	B	802	NDP	PN-O3-PA	-3.54	122.78	132.73
4	A	803	NDP	PN-O3-PA	-3.42	123.12	132.73
3	A	446	FAD	C4X-C4-N3	-3.23	119.18	123.59
3	B	446	FAD	C4-C4X-C10	-3.22	117.88	119.94
2	A	445	COA	P2A-O3A-P1A	-2.95	124.44	132.73
2	A	445	COA	C6P-C7P-N8P	-2.95	105.42	111.88
3	B	446	FAD	C4X-C4-N3	-2.74	119.84	123.59
2	B	445	COA	C6P-C7P-N8P	-2.73	105.89	111.88
2	B	445	COA	P2A-O3A-P1A	-2.71	125.12	132.73
3	A	446	FAD	C4-C4X-C10	-2.52	118.33	119.94
2	A	445	COA	C4A-C5A-N7A	-2.35	107.32	109.48
4	A	803	NDP	C1B-N9A-C4A	-2.34	123.42	126.94
3	B	446	FAD	P-O3P-PA	-2.32	126.21	132.73
2	B	445	COA	C4A-C5A-N7A	-2.27	107.39	109.48
3	B	446	FAD	C4A-C5A-N7A	-2.24	107.42	109.48
3	A	446	FAD	C1B-N9A-C4A	-2.14	123.70	126.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	802	NDP	C1B-N9A-C4A	-2.13	123.72	126.94
3	A	446	FAD	P-O3P-PA	-2.05	126.98	132.73
4	B	802	NDP	O4D-C1D-N1N	2.06	112.42	108.07
2	A	445	COA	O6A-CCP-CBP	2.18	114.05	110.55
3	A	446	FAD	C5X-C9A-N10	2.20	119.29	117.62
3	A	446	FAD	C1'-N10-C9A	2.32	121.46	118.86
3	B	446	FAD	C5X-C9A-N10	2.34	119.40	117.62
2	A	445	COA	C7P-N8P-C9P	2.39	127.27	122.53
2	B	445	COA	O6A-CCP-CBP	2.40	114.41	110.55
4	B	802	NDP	O4B-C1B-N9A	2.44	113.22	108.10
3	B	446	FAD	C4-C4X-N5	2.49	121.74	118.72
4	A	803	NDP	O4D-C1D-N1N	2.50	113.34	108.07
2	A	445	COA	C3P-N4P-C5P	2.54	127.78	122.79
3	B	446	FAD	C1'-N10-C9A	2.85	122.06	118.86
2	B	445	COA	C7P-N8P-C9P	2.85	128.18	122.53
3	B	446	FAD	C4X-N5-C5X	4.20	121.59	116.76
3	A	446	FAD	C4X-N5-C5X	4.21	121.60	116.76
3	B	446	FAD	C4-N3-C2	6.30	120.70	115.25
3	A	446	FAD	C4-N3-C2	6.79	121.11	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	802	NDP	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	444/480 (92%)	0.88	54 (12%) <b>5</b> <b>5</b>	51, 58, 67, 71	0
1	B	444/480 (92%)	0.84	43 (9%) <b>10</b> <b>11</b>	50, 58, 66, 72	0
All	All	888/960 (92%)	0.86	97 (10%) <b>7</b> <b>7</b>	50, 58, 66, 72	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	147	THR	5.7
1	A	147	THR	5.3
1	B	260	HIS	5.1
1	A	24	GLU	5.0
1	A	370	ASN	4.6
1	A	220	ASN	4.2
1	A	260	HIS	4.1
1	A	96	LYS	3.9
1	A	221	GLU	3.9
1	A	25	ASN	3.9
1	B	148	ASN	3.7
1	A	150	VAL	3.7
1	B	370	ASN	3.6
1	B	24	GLU	3.6
1	B	192	ASP	3.5
1	B	255	ASN	3.5
1	B	220	ASN	3.4
1	B	191	GLY	3.4
1	A	127	GLN	3.4
1	B	423	LEU	3.3
1	B	96	LYS	3.3
1	B	432	VAL	3.2
1	B	150	VAL	3.2
1	A	329	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	330	ILE	3.2
1	A	192	ASP	3.2
1	A	432	VAL	3.1
1	A	86	GLU	3.1
1	A	163	LEU	3.0
1	A	146	GLU	2.9
1	B	221	GLU	2.9
1	A	398	VAL	2.8
1	B	421	VAL	2.7
1	A	124	ARG	2.7
1	A	148	ASN	2.7
1	B	25	ASN	2.7
1	A	77	ARG	2.7
1	B	77	ARG	2.7
1	A	425	TYR	2.7
1	A	11	ALA	2.6
1	A	397	GLY	2.6
1	A	149	LYS	2.6
1	B	195	GLU	2.6
1	B	184	HIS	2.6
1	A	404	VAL	2.6
1	A	143	LYS	2.6
1	A	423	LEU	2.6
1	B	329	ILE	2.6
1	B	425	TYR	2.5
1	A	62	ASN	2.5
1	B	303	ALA	2.5
1	A	299	ILE	2.5
1	B	198	TYR	2.5
1	B	86	GLU	2.5
1	A	300	GLY	2.5
1	B	97	THR	2.5
1	B	161	ILE	2.4
1	A	161	ILE	2.4
1	A	330	ILE	2.4
1	B	127	GLN	2.4
1	B	149	LYS	2.4
1	A	252	GLU	2.3
1	B	98	LYS	2.3
1	B	302	THR	2.3
1	B	11	ALA	2.3
1	A	303	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	6	ILE	2.3
1	A	224	GLU	2.3
1	A	433	TRP	2.3
1	A	184	HIS	2.2
1	B	56	GLU	2.2
1	B	404	VAL	2.2
1	A	178	MET	2.2
1	B	300	GLY	2.2
1	B	299	ILE	2.2
1	A	325	LEU	2.2
1	B	280	ALA	2.2
1	B	156	ILE	2.2
1	B	433	TRP	2.2
1	B	222	ARG	2.2
1	A	10	ALA	2.2
1	A	206	ILE	2.1
1	A	110	ILE	2.1
1	A	402	ILE	2.1
1	B	6	ILE	2.1
1	A	309	LEU	2.1
1	A	302	THR	2.1
1	A	301	THR	2.1
1	A	406	ALA	2.1
1	B	143	LYS	2.1
1	A	324	THR	2.1
1	A	101	PHE	2.0
1	A	222	ARG	2.0
1	B	406	ALA	2.0
1	A	56	GLU	2.0
1	A	323	GLY	2.0
1	A	120	GLU	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	COA	A	445	48/48	0.89	0.23	0.68	52,59,66,67	0
2	COA	B	445	48/48	0.90	0.21	0.13	50,57,65,65	0
4	NDP	A	803	48/48	0.94	0.18	-0.27	42,46,52,54	0
4	NDP	B	802	48/48	0.94	0.17	-0.41	42,46,49,50	0
3	FAD	A	446	53/53	0.96	0.11	-2.04	31,36,39,39	0
3	FAD	B	446	53/53	0.97	0.11	-2.07	30,34,37,37	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.