



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:20 AM GMT

PDB ID : 3HZN  
Title : Structure of the Salmonella typhimurium nfnB dihydropteridine reductase  
Authors : Anderson, S.M.; Wawrzak, Z.; Onopriyenko, O.; Skarina, T.; Anderson, W.F.; Savchenko, A.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2009-06-23  
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

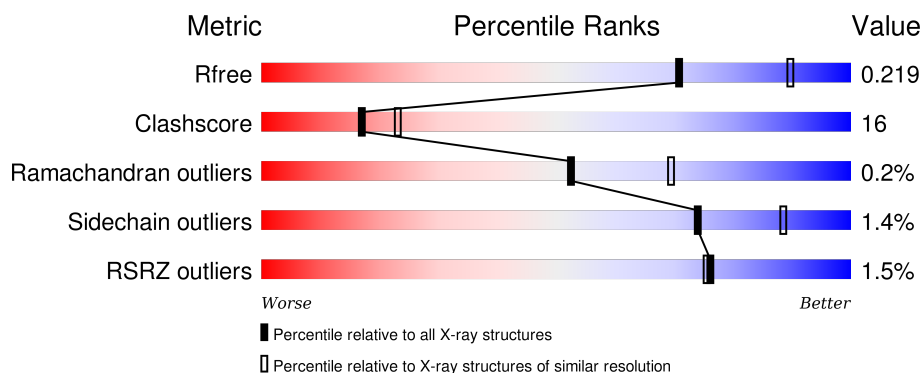
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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.



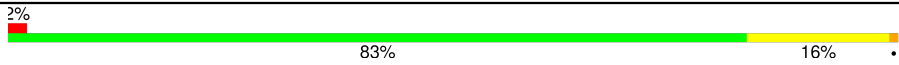


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	220	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>13%</div> <div>.</div> </div> </div>
1	B	220	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>20%</div> </div> </div>
1	C	220	<div> <div>%</div> <div> <div></div> <div>79%</div> <div>19%</div> <div>..</div> </div> </div>
1	D	220	<div> <div>%</div> <div> <div></div> <div>80%</div> <div>19%</div> <div>.</div> </div> </div>
1	E	220	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>15%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	220	
1	G	220	
1	H	220	

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
2	TLA	C	219	-	-	-	X
2	TLA	H	218	-	-	X	-
3	SIN	A	219	-	-	X	X
3	SIN	A	220	-	-	-	X
3	SIN	A	221	-	-	X	X
3	SIN	A	222	-	-	-	X
3	SIN	A	223	-	-	X	X
3	SIN	A	224	-	-	-	X
3	SIN	B	221	-	-	-	X
3	SIN	B	222	-	-	X	X
3	SIN	C	220	-	-	-	X
3	SIN	C	221	-	-	-	X
3	SIN	C	222	-	-	X	X
3	SIN	C	223	-	-	-	X
3	SIN	C	224	-	-	-	X
3	SIN	C	225	-	-	-	X
3	SIN	C	226	-	-	X	X
3	SIN	C	227	-	-	-	X
3	SIN	D	220	-	-	-	X
3	SIN	D	221	-	-	-	X
3	SIN	D	222	-	-	-	X
3	SIN	D	223	-	-	X	X
3	SIN	D	224	-	-	X	X
3	SIN	D	225	-	-	X	X
3	SIN	E	218	-	-	X	X
3	SIN	E	219	-	-	-	X
3	SIN	E	221	-	-	-	X
3	SIN	E	222	-	-	X	X
3	SIN	F	221	-	-	-	X
3	SIN	G	218	-	-	X	X
3	SIN	G	220	-	-	-	X
3	SIN	G	221	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SIN	H	219	-	-	X	X
3	SIN	H	220	-	-	-	X
3	SIN	H	221	-	-	-	X
3	SIN	H	223	-	-	-	X
4	MLI	A	225	-	-	-	X
4	MLI	A	226	-	-	-	X
4	MLI	A	227	-	-	-	X
4	MLI	B	225	-	-	X	X
4	MLI	C	231	-	-	X	X
4	MLI	C	232	-	-	-	X
4	MLI	D	226	-	-	X	X
4	MLI	D	227	-	-	X	-
4	MLI	D	228	-	-	X	X
4	MLI	E	223	-	-	X	X
4	MLI	F	224	-	-	X	-
4	MLI	G	223	-	-	-	X
4	MLI	H	224	-	-	-	X
5	CL	C	235	-	-	X	X
5	CL	C	236	-	-	X	-
5	CL	D	230	-	-	X	X
5	CL	E	225	-	-	-	X
5	CL	F	225	-	-	-	X
5	CL	G	226	-	-	-	X
6	FLC	B	218	-	-	X	X
6	FLC	F	218	-	-	X	X
8	ACT	C	233	-	-	-	X
8	ACT	D	229	-	-	-	X

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 15104 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 Oxygen-insensitive NAD(P)H nitroreductase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	Se	0	3	0
			1715	1083	291	334	1	6			
1	B	219	Total	C	N	O	S	Se	0	3	0
			1713	1082	293	331	1	6			
1	C	218	Total	C	N	O	S	Se	0	1	0
			1698	1073	289	329	1	6			
1	D	219	Total	C	N	O	S	Se	0	3	0
			1720	1089	292	332	1	6			
1	E	219	Total	C	N	O	S	Se	0	0	0
			1700	1073	291	329	1	6			
1	F	219	Total	C	N	O	S	Se	0	1	0
			1705	1076	291	331	1	6			
1	G	218	Total	C	N	O	S	Se	0	1	0
			1698	1073	289	329	1	6			
1	H	220	Total	C	N	O	S	Se	0	3	0
			1725	1088	295	335	1	6			

There are 24 discrepancies between the modelled and reference sequences:

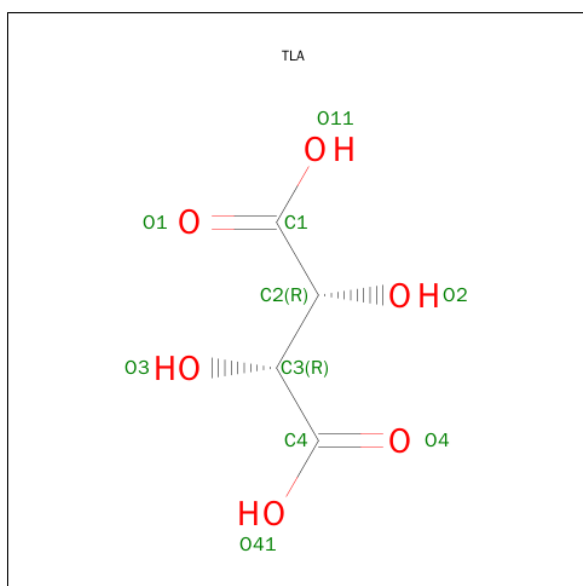
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP P15888
A	-1	ASN	-	EXPRESSION TAG	UNP P15888
A	0	ALA	-	EXPRESSION TAG	UNP P15888
B	-2	SER	-	EXPRESSION TAG	UNP P15888
B	-1	ASN	-	EXPRESSION TAG	UNP P15888
B	0	ALA	-	EXPRESSION TAG	UNP P15888
C	-2	SER	-	EXPRESSION TAG	UNP P15888
C	-1	ASN	-	EXPRESSION TAG	UNP P15888
C	0	ALA	-	EXPRESSION TAG	UNP P15888
D	-2	SER	-	EXPRESSION TAG	UNP P15888
D	-1	ASN	-	EXPRESSION TAG	UNP P15888
D	0	ALA	-	EXPRESSION TAG	UNP P15888
E	-2	SER	-	EXPRESSION TAG	UNP P15888

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	ASN	-	EXPRESSION TAG	UNP P15888
E	0	ALA	-	EXPRESSION TAG	UNP P15888
F	-2	SER	-	EXPRESSION TAG	UNP P15888
F	-1	ASN	-	EXPRESSION TAG	UNP P15888
F	0	ALA	-	EXPRESSION TAG	UNP P15888
G	-2	SER	-	EXPRESSION TAG	UNP P15888
G	-1	ASN	-	EXPRESSION TAG	UNP P15888
G	0	ALA	-	EXPRESSION TAG	UNP P15888
H	-2	SER	-	EXPRESSION TAG	UNP P15888
H	-1	ASN	-	EXPRESSION TAG	UNP P15888
H	0	ALA	-	EXPRESSION TAG	UNP P15888

- Molecule 2 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula:  $C_4H_6O_6$ ).



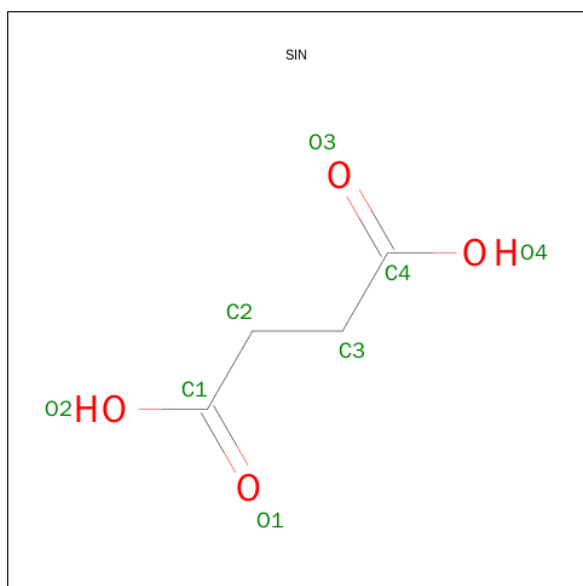
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 10 4 6	0	0
2	B	1	Total C O 10 4 6	0	0
2	C	1	Total C O 10 4 6	0	0
2	C	1	Total C O 10 4 6	0	0
2	D	1	Total C O 10 4 6	0	0
2	F	1	Total C O 10 4 6	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	H	1	Total	C	O	0	0
			10	4	6		

- Molecule 3 is SUCCINIC ACID (three-letter code: SIN) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	4	4		
3	A	1	Total	C	O	0	0
			8	4	4		
3	A	1	Total	C	O	0	0
			8	4	4		
3	A	1	Total	C	O	0	0
			8	4	4		
3	A	1	Total	C	O	0	0
			8	4	4		
3	B	1	Total	C	O	0	0
			8	4	4		
3	B	1	Total	C	O	0	0
			8	4	4		
3	B	1	Total	C	O	0	0
			8	4	4		
3	C	1	Total	C	O	0	0
			8	4	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			8	4	4		
3	C	1	Total	C	O	0	0
			8	4	4		
3	C	1	Total	C	O	0	0
			8	4	4		
3	C	1	Total	C	O	0	0
			8	4	4		
3	C	1	Total	C	O	0	0
			8	4	4		
3	C	1	Total	C	O	0	0
			8	4	4		
3	D	1	Total	C	O	0	0
			8	4	4		
3	D	1	Total	C	O	0	0
			8	4	4		
3	D	1	Total	C	O	0	0
			8	4	4		
3	D	1	Total	C	O	0	0
			8	4	4		
3	D	1	Total	C	O	0	0
			8	4	4		
3	D	1	Total	C	O	0	0
			8	4	4		
3	E	1	Total	C	O	0	0
			8	4	4		
3	E	1	Total	C	O	0	0
			8	4	4		
3	E	1	Total	C	O	0	0
			8	4	4		
3	E	1	Total	C	O	0	0
			8	4	4		
3	F	1	Total	C	O	0	0
			8	4	4		

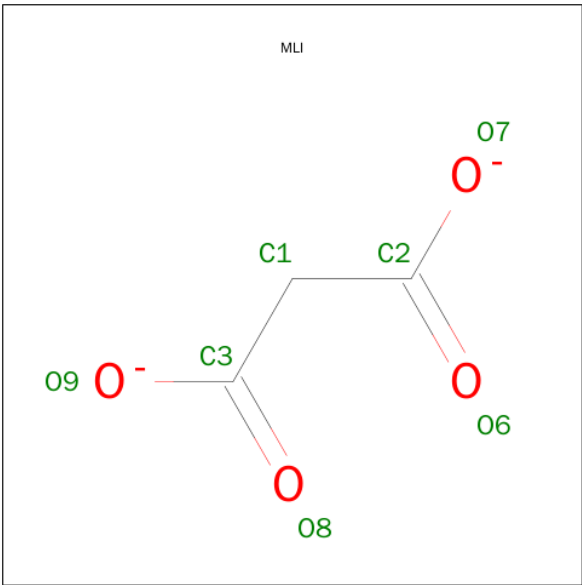
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	F	1	Total	C	O	0	0
			8	4	4		
3	F	1	Total	C	O	0	0
			8	4	4		
3	F	1	Total	C	O	0	0
			8	4	4		
3	G	1	Total	C	O	0	0
			8	4	4		
3	G	1	Total	C	O	0	0
			8	4	4		
3	G	1	Total	C	O	0	0
			8	4	4		
3	G	1	Total	C	O	0	0
			8	4	4		
3	H	1	Total	C	O	0	0
			8	4	4		
3	H	1	Total	C	O	0	0
			8	4	4		
3	H	1	Total	C	O	0	0
			8	4	4		
3	H	1	Total	C	O	0	0
			8	4	4		

- Molecule 4 is MALONATE ION (three-letter code: MLI) (formula: C<sub>3</sub>H<sub>2</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	3	4		
4	A	1	Total	C	O	0	0
			7	3	4		
4	A	1	Total	C	O	0	0
			7	3	4		
4	A	1	Total	C	O	0	0
			7	3	4		
4	B	1	Total	C	O	0	0
			7	3	4		
4	B	1	Total	C	O	0	0
			7	3	4		
4	B	1	Total	C	O	0	0
			7	3	4		
4	C	1	Total	C	O	0	0
			7	3	4		
4	C	1	Total	C	O	0	0
			7	3	4		
4	C	1	Total	C	O	0	0
			7	3	4		
4	C	1	Total	C	O	0	0
			7	3	4		
4	D	1	Total	C	O	0	0
			7	3	4		
4	D	1	Total	C	O	0	0
			7	3	4		
4	D	1	Total	C	O	0	0
			7	3	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	O	0	0
			7	3	4		
4	F	1	Total	C	O	0	0
			7	3	4		
4	G	1	Total	C	O	0	0
			7	3	4		
4	G	1	Total	C	O	0	0
			7	3	4		
4	H	1	Total	C	O	0	0
			7	3	4		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	1	Total	Cl	0	0
			1	1		
5	D	2	Total	Cl	0	0
			2	2		
5	E	2	Total	Cl	0	0
			2	2		
5	B	1	Total	Cl	0	0
			1	1		
5	C	4	Total	Cl	0	0
			4	4		
5	A	1	Total	Cl	0	0
			1	1		
5	F	1	Total	Cl	0	0
			1	1		

- Molecule 6 is CITRATE ANION (three-letter code: FLC) (formula: C<sub>6</sub>H<sub>5</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			13	6	7		
6	F	1	Total	C	O	0	0
			13	6	7		

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	H	1	Total	Na	0	0
			1	1		
7	B	1	Total	Na	0	0
			1	1		
7	C	1	Total	Na	0	0
			1	1		
7	E	1	Total	Na	0	0
			1	1		

- Molecule 8 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total	C	O	0	0
			4	2	2		
8	G	1	Total	C	O	0	0
			4	2	2		

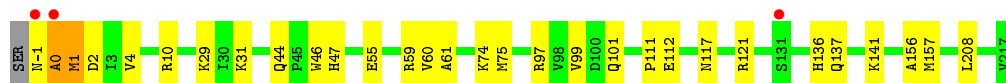
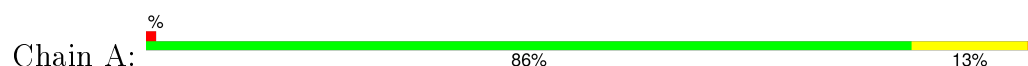
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	111	Total	O	0	3
			114	114		
9	B	66	Total	O	0	1
			67	67		
9	C	128	Total	O	0	2
			130	130		
9	D	130	Total	O	0	1
			131	131		
9	E	108	Total	O	0	1
			109	109		
9	F	113	Total	O	0	1
			114	114		
9	G	78	Total	O	0	2
			80	80		
9	H	75	Total	O	0	1
			76	76		

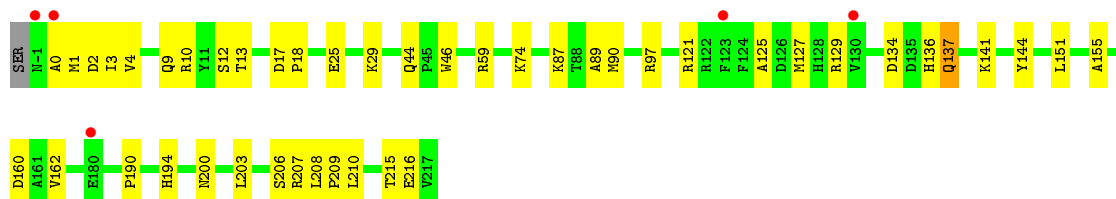
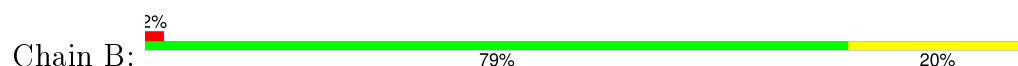
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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.

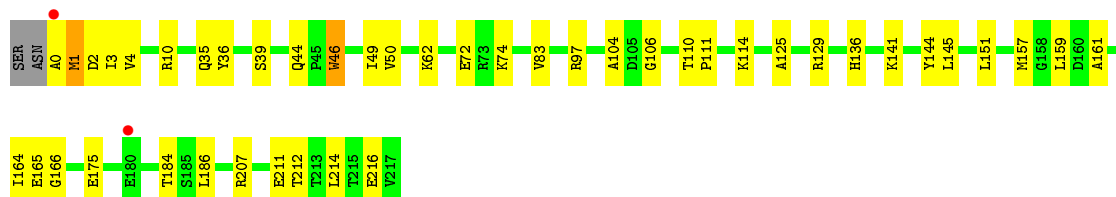
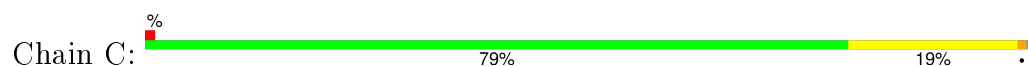
- Molecule 1: Oxygen-insensitive NAD(P)H nitroreductase



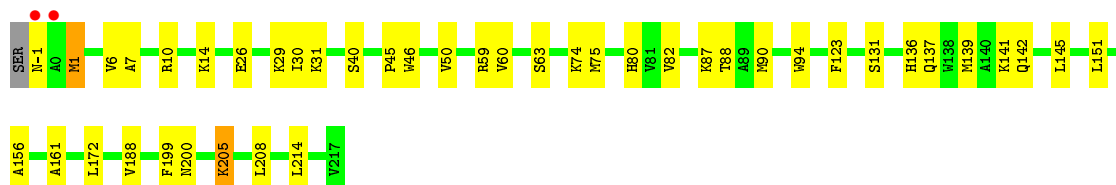
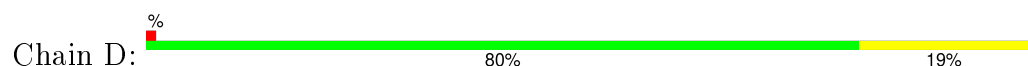
- Molecule 1: Oxygen-insensitive NAD(P)H nitroreductase



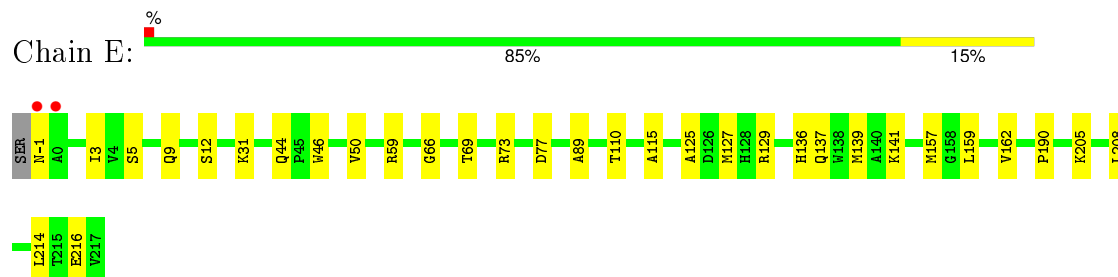
- Molecule 1: Oxygen-insensitive NAD(P)H nitroreductase



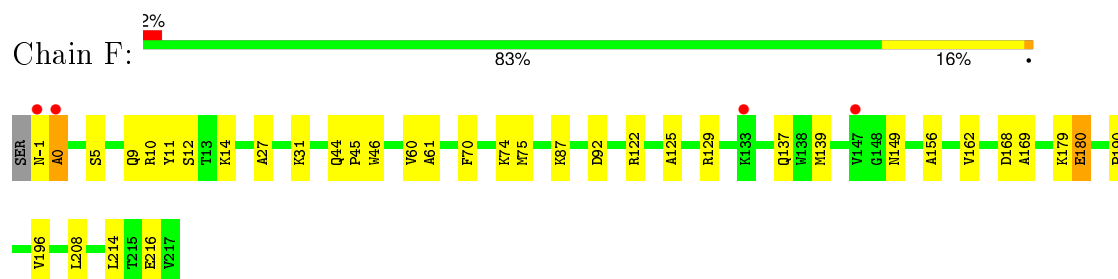
- Molecule 1: Oxygen-insensitive NAD(P)H nitroreductase



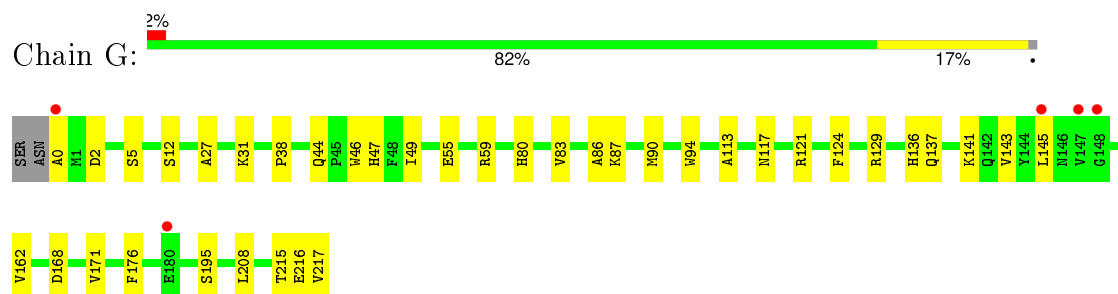
- Molecule 1: Oxygen-insensitive NAD(P)H nitroreductase



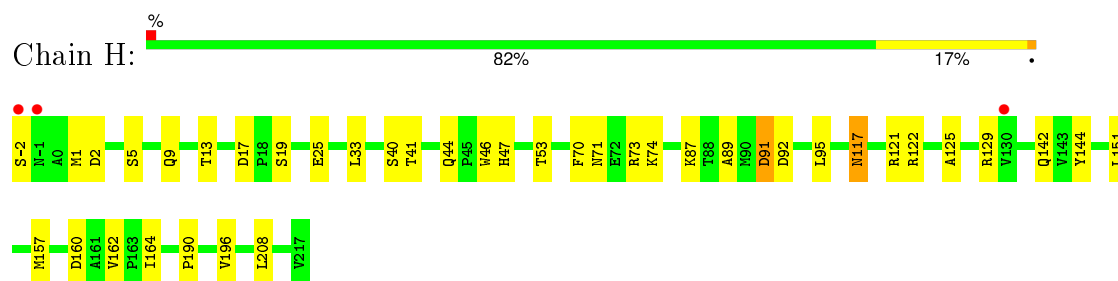
- Molecule 1: Oxygen-insensitive NAD(P)H nitroreductase



- Molecule 1: Oxygen-insensitive NAD(P)H nitroreductase



- Molecule 1: Oxygen-insensitive NAD(P)H nitroreductase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	280.34Å 96.76Å 131.84Å 90.00° 90.36° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40 30.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (30.00-2.40) 99.0 (30.00-2.40)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	7.37 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, $R_{free}$	0.177 , 0.222 0.177 , 0.219	Depositor DCC
$R_{free}$ test set	6862 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.1	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 49.9	EDS
Estimated twinning fraction	0.010 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 136446 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	15104	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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: CL, NA, MLI, TLA, ACT, FLC, SIN

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	0.48	0/1753	0.54	0/2362
1	B	0.44	0/1752	0.52	0/2361
1	C	0.53	0/1730	0.58	0/2331
1	D	0.50	0/1756	0.55	0/2366
1	E	0.48	0/1729	0.55	0/2330
1	F	0.47	0/1737	0.54	0/2341
1	G	0.45	0/1730	0.50	0/2331
1	H	0.42	0/1763	0.51	0/2375
All	All	0.47	0/13950	0.54	0/18797

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 [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	1715	0	1685	70	0
1	B	1713	0	1685	61	0
1	C	1698	0	1668	75	0
1	D	1720	0	1686	63	0
1	E	1700	0	1668	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1705	0	1672	71	0
1	G	1698	0	1668	43	0
1	H	1725	0	1696	54	0
2	A	10	0	4	1	0
2	B	10	0	4	0	0
2	C	20	0	8	0	0
2	D	10	0	4	0	0
2	F	10	0	4	1	0
2	H	10	0	4	4	0
3	A	48	0	24	33	0
3	B	24	0	12	9	0
3	C	72	0	36	28	0
3	D	56	0	28	24	0
3	E	40	0	20	14	0
3	F	32	0	16	3	0
3	G	40	0	20	10	0
3	H	40	0	20	13	0
4	A	28	0	8	0	0
4	B	21	0	6	7	0
4	C	28	0	8	10	0
4	D	21	0	6	7	0
4	E	7	0	2	7	0
4	F	7	0	2	5	0
4	G	14	0	4	2	0
4	H	7	0	2	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	4	0	0	4	0
5	D	2	0	0	3	0
5	E	2	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
6	B	13	0	5	5	0
6	F	13	0	5	19	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	E	1	0	0	0	0
7	H	1	0	0	0	0
8	C	4	0	3	0	0
8	D	4	0	3	0	0
8	G	4	0	3	0	0
9	A	114	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	B	67	0	0	2	0
9	C	130	0	0	4	0
9	D	131	0	0	5	0
9	E	109	0	0	0	0
9	F	114	0	0	10	0
9	G	80	0	0	4	0
9	H	76	0	0	6	0
All	All	15104	0	13689	455	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 16.

The worst 5 of 455 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)
3:A:219:SIN:H21	1:B:137:GLN:CB	1.52	1.39
1:D:-1:ASN:N	1:D:156:ALA:HB1	1.38	1.32
1:D:10:ARG:HE	3:D:223:SIN:C2	1.46	1.29
1:F:61:ALA:HA	1:F:75:MSE:CE	1.64	1.25
1:D:60:VAL:HG12	1:D:75:MSE:CE	1.70	1.20

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	220/220 (100%)	211 (96%)	7 (3%)	2 (1%)	21	30
1	B	220/220 (100%)	216 (98%)	4 (2%)	0	100	100
1	C	217/220 (99%)	215 (99%)	2 (1%)	0	100	100
1	D	220/220 (100%)	215 (98%)	4 (2%)	1 (0%)	34	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	217/220 (99%)	212 (98%)	5 (2%)	0	100	100
1	F	218/220 (99%)	215 (99%)	2 (1%)	1 (0%)	34	48
1	G	217/220 (99%)	211 (97%)	6 (3%)	0	100	100
1	H	221/220 (100%)	215 (97%)	6 (3%)	0	100	100
All	All	1750/1760 (99%)	1710 (98%)	36 (2%)	4 (0%)	52	69

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	0	ALA
1	A	0	ALA
1	A	1	MSE
1	D	1	MSE

### 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	183/175 (105%)	181 (99%)	2 (1%)	80	92
1	B	183/175 (105%)	181 (99%)	2 (1%)	80	92
1	C	180/175 (103%)	177 (98%)	3 (2%)	68	85
1	D	182/175 (104%)	179 (98%)	3 (2%)	70	86
1	E	180/175 (103%)	178 (99%)	2 (1%)	80	92
1	F	181/175 (103%)	178 (98%)	3 (2%)	68	85
1	G	180/175 (103%)	178 (99%)	2 (1%)	80	92
1	H	184/175 (105%)	181 (98%)	3 (2%)	70	86
All	All	1453/1400 (104%)	1433 (99%)	20 (1%)	74	88

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	205	LYS
1	E	-1	ASN
1	G	216	GLU
1	D	46	TRP
1	D	131	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	200	ASN
1	E	136	HIS
1	H	117	ASN
1	E	-1	ASN
1	E	35	GLN

### 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 91 ligands modelled in this entry, 16 are monoatomic - leaving 75 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
2	TLA	A	218	-	3,9,9	0.36	0	6,12,12	0.90	0
3	SIN	A	219	-	1,7,7	0.08	0	2,8,8	0.85	0
3	SIN	A	220	-	1,7,7	0.01	0	2,8,8	0.68	0
3	SIN	A	221	-	1,7,7	0.30	0	2,8,8	2.27	1 (50%)
3	SIN	A	222	-	1,7,7	0.02	0	2,8,8	0.81	0
3	SIN	A	223	-	1,7,7	0.13	0	2,8,8	1.75	1 (50%)
3	SIN	A	224	-	1,7,7	0.14	0	2,8,8	2.30	1 (50%)
4	MLI	A	225	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	A	226	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	A	227	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	A	228	-	0,6,6	0.00	-	0,7,7	0.00	-
6	FLC	B	218	-	3,12,12	1.04	0	3,17,17	1.63	1 (33%)
2	TLA	B	219	-	3,9,9	0.48	0	6,12,12	1.70	2 (33%)
3	SIN	B	220	-	1,7,7	0.10	0	2,8,8	1.31	0
3	SIN	B	221	-	1,7,7	0.16	0	2,8,8	0.98	0
3	SIN	B	222	-	1,7,7	0.05	0	2,8,8	0.71	0
4	MLI	B	223	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	B	224	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	B	225	-	0,6,6	0.00	-	0,7,7	0.00	-
2	TLA	C	218	-	3,9,9	0.43	0	6,12,12	0.88	0
2	TLA	C	219	-	3,9,9	0.41	0	6,12,12	0.79	0
3	SIN	C	220	-	1,7,7	0.16	0	2,8,8	1.16	0
3	SIN	C	221	-	1,7,7	0.06	0	2,8,8	1.06	0
3	SIN	C	222	-	1,7,7	0.21	0	2,8,8	0.69	0
3	SIN	C	223	-	1,7,7	0.01	0	2,8,8	0.76	0
3	SIN	C	224	-	1,7,7	0.08	0	2,8,8	1.12	0
3	SIN	C	225	-	1,7,7	0.15	0	2,8,8	2.05	1 (50%)
3	SIN	C	226	-	1,7,7	0.26	0	2,8,8	0.68	0
3	SIN	C	227	-	1,7,7	0.03	0	2,8,8	0.61	0
3	SIN	C	228	-	1,7,7	0.05	0	2,8,8	0.79	0
4	MLI	C	229	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	C	230	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	C	231	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	C	232	-	0,6,6	0.00	-	0,7,7	0.00	-
8	ACT	C	233	-	1,3,3	1.15	0	0,3,3	0.00	-
2	TLA	D	218	-	3,9,9	0.72	0	6,12,12	1.54	2 (33%)
3	SIN	D	219	-	1,7,7	0.08	0	2,8,8	1.72	0
3	SIN	D	220	-	1,7,7	0.01	0	2,8,8	1.17	0
3	SIN	D	221	-	1,7,7	0.01	0	2,8,8	2.40	1 (50%)
3	SIN	D	222	-	1,7,7	0.05	0	2,8,8	0.80	0
3	SIN	D	223	-	1,7,7	0.17	0	2,8,8	1.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SIN	D	224	-	1,7,7	0.08	0	2,8,8	1.79	1 (50%)
3	SIN	D	225	-	1,7,7	0.07	0	2,8,8	1.18	0
4	MLI	D	226	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	D	227	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	D	228	-	0,6,6	0.00	-	0,7,7	0.00	-
8	ACT	D	229	-	1,3,3	2.16	1 (100%)	0,3,3	0.00	-
3	SIN	E	218	-	1,7,7	0.21	0	2,8,8	2.35	2 (100%)
3	SIN	E	219	-	1,7,7	0.13	0	2,8,8	0.80	0
3	SIN	E	220	-	1,7,7	0.10	0	2,8,8	0.86	0
3	SIN	E	221	-	1,7,7	0.11	0	2,8,8	1.51	0
3	SIN	E	222	-	1,7,7	0.05	0	2,8,8	0.51	0
4	MLI	E	223	-	0,6,6	0.00	-	0,7,7	0.00	-
6	FLC	F	218	-	3,12,12	1.06	0	3,17,17	0.64	0
2	TLA	F	219	-	3,9,9	0.55	0	6,12,12	1.03	0
3	SIN	F	220	-	1,7,7	0.14	0	2,8,8	0.61	0
3	SIN	F	221	-	1,7,7	0.05	0	2,8,8	1.28	0
3	SIN	F	222	-	1,7,7	0.01	0	2,8,8	1.02	0
3	SIN	F	223	-	1,7,7	0.10	0	2,8,8	1.43	0
4	MLI	F	224	-	0,6,6	0.00	-	0,7,7	0.00	-
3	SIN	G	218	-	1,7,7	0.08	0	2,8,8	1.58	0
3	SIN	G	219	-	1,7,7	0.09	0	2,8,8	0.80	0
3	SIN	G	220	-	1,7,7	0.29	0	2,8,8	3.76	2 (100%)
3	SIN	G	221	-	1,7,7	0.12	0	2,8,8	2.18	1 (50%)
3	SIN	G	222	-	1,7,7	0.10	0	2,8,8	2.32	1 (50%)
4	MLI	G	223	-	0,6,6	0.00	-	0,7,7	0.00	-
4	MLI	G	224	-	0,6,6	0.00	-	0,7,7	0.00	-
8	ACT	G	225	-	1,3,3	1.67	0	0,3,3	0.00	-
2	TLA	H	218	-	3,9,9	0.37	0	6,12,12	1.74	1 (16%)
3	SIN	H	219	-	1,7,7	0.16	0	2,8,8	1.26	0
3	SIN	H	220	-	1,7,7	0.05	0	2,8,8	1.05	0
3	SIN	H	221	-	1,7,7	0.04	0	2,8,8	0.89	0
3	SIN	H	222	-	1,7,7	0.07	0	2,8,8	1.38	0
3	SIN	H	223	-	1,7,7	0.07	0	2,8,8	1.55	0
4	MLI	H	224	-	0,6,6	0.00	-	0,7,7	0.00	-

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	TLA	A	218	-	-	0/4/12/12	0/0/0/0
3	SIN	A	219	-	-	0/1/5/5	0/0/0/0
3	SIN	A	220	-	-	0/1/5/5	0/0/0/0
3	SIN	A	221	-	-	0/1/5/5	0/0/0/0
3	SIN	A	222	-	-	0/1/5/5	0/0/0/0
3	SIN	A	223	-	-	0/1/5/5	0/0/0/0
3	SIN	A	224	-	-	0/1/5/5	0/0/0/0
4	MLI	A	225	-	-	0/0/4/4	0/0/0/0
4	MLI	A	226	-	-	0/0/4/4	0/0/0/0
4	MLI	A	227	-	-	0/0/4/4	0/0/0/0
4	MLI	A	228	-	-	0/0/4/4	0/0/0/0
6	FLC	B	218	-	-	0/6/16/16	0/0/0/0
2	TLA	B	219	-	-	0/4/12/12	0/0/0/0
3	SIN	B	220	-	-	0/1/5/5	0/0/0/0
3	SIN	B	221	-	-	0/1/5/5	0/0/0/0
3	SIN	B	222	-	-	0/1/5/5	0/0/0/0
4	MLI	B	223	-	-	0/0/4/4	0/0/0/0
4	MLI	B	224	-	-	0/0/4/4	0/0/0/0
4	MLI	B	225	-	-	0/0/4/4	0/0/0/0
2	TLA	C	218	-	-	0/4/12/12	0/0/0/0
2	TLA	C	219	-	-	0/4/12/12	0/0/0/0
3	SIN	C	220	-	-	0/1/5/5	0/0/0/0
3	SIN	C	221	-	-	0/1/5/5	0/0/0/0
3	SIN	C	222	-	-	0/1/5/5	0/0/0/0
3	SIN	C	223	-	-	0/1/5/5	0/0/0/0
3	SIN	C	224	-	-	0/1/5/5	0/0/0/0
3	SIN	C	225	-	-	0/1/5/5	0/0/0/0
3	SIN	C	226	-	-	0/1/5/5	0/0/0/0
3	SIN	C	227	-	-	0/1/5/5	0/0/0/0
3	SIN	C	228	-	-	0/1/5/5	0/0/0/0
4	MLI	C	229	-	-	0/0/4/4	0/0/0/0
4	MLI	C	230	-	-	0/0/4/4	0/0/0/0
4	MLI	C	231	-	-	0/0/4/4	0/0/0/0
4	MLI	C	232	-	-	0/0/4/4	0/0/0/0
8	ACT	C	233	-	-	0/0/0/0	0/0/0/0
2	TLA	D	218	-	-	0/4/12/12	0/0/0/0
3	SIN	D	219	-	-	0/1/5/5	0/0/0/0
3	SIN	D	220	-	-	0/1/5/5	0/0/0/0
3	SIN	D	221	-	-	0/1/5/5	0/0/0/0
3	SIN	D	222	-	-	0/1/5/5	0/0/0/0
3	SIN	D	223	-	-	0/1/5/5	0/0/0/0
3	SIN	D	224	-	-	0/1/5/5	0/0/0/0
3	SIN	D	225	-	-	0/1/5/5	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MLI	D	226	-	-	0/0/4/4	0/0/0/0
4	MLI	D	227	-	-	0/0/4/4	0/0/0/0
4	MLI	D	228	-	-	0/0/4/4	0/0/0/0
8	ACT	D	229	-	-	0/0/0/0	0/0/0/0
3	SIN	E	218	-	-	0/1/5/5	0/0/0/0
3	SIN	E	219	-	-	0/1/5/5	0/0/0/0
3	SIN	E	220	-	-	0/1/5/5	0/0/0/0
3	SIN	E	221	-	-	0/1/5/5	0/0/0/0
3	SIN	E	222	-	-	0/1/5/5	0/0/0/0
4	MLI	E	223	-	-	0/0/4/4	0/0/0/0
6	FLC	F	218	-	-	0/6/16/16	0/0/0/0
2	TLA	F	219	-	-	0/4/12/12	0/0/0/0
3	SIN	F	220	-	-	0/1/5/5	0/0/0/0
3	SIN	F	221	-	-	0/1/5/5	0/0/0/0
3	SIN	F	222	-	-	0/1/5/5	0/0/0/0
3	SIN	F	223	-	-	0/1/5/5	0/0/0/0
4	MLI	F	224	-	-	0/0/4/4	0/0/0/0
3	SIN	G	218	-	-	0/1/5/5	0/0/0/0
3	SIN	G	219	-	-	0/1/5/5	0/0/0/0
3	SIN	G	220	-	-	0/1/5/5	0/0/0/0
3	SIN	G	221	-	-	0/1/5/5	0/0/0/0
3	SIN	G	222	-	-	0/1/5/5	0/0/0/0
4	MLI	G	223	-	-	0/0/4/4	0/0/0/0
4	MLI	G	224	-	-	0/0/4/4	0/0/0/0
8	ACT	G	225	-	-	0/0/0/0	0/0/0/0
2	TLA	H	218	-	-	0/4/12/12	0/0/0/0
3	SIN	H	219	-	-	0/1/5/5	0/0/0/0
3	SIN	H	220	-	-	0/1/5/5	0/0/0/0
3	SIN	H	221	-	-	0/1/5/5	0/0/0/0
3	SIN	H	222	-	-	0/1/5/5	0/0/0/0
3	SIN	H	223	-	-	0/1/5/5	0/0/0/0
4	MLI	H	224	-	-	0/0/4/4	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	229	ACT	CH3-C	2.16	1.51	1.48

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	220	SIN	C2-C3-C4	-4.63	104.27	112.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	218	TLA	O2-C2-C1	-3.68	101.93	111.21
3	G	222	SIN	C3-C2-C1	-3.28	106.73	112.75
2	B	219	TLA	C1-C2-C3	-3.22	106.74	113.35
3	D	221	SIN	C3-C2-C1	-3.13	107.00	112.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

45 monomers are involved in 195 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	218	TLA	1	0
3	A	219	SIN	15	0
3	A	220	SIN	2	0
3	A	221	SIN	10	0
3	A	223	SIN	4	0
3	A	224	SIN	2	0
6	B	218	FLC	5	0
3	B	220	SIN	1	0
3	B	222	SIN	8	0
4	B	225	MLI	7	0
3	C	221	SIN	1	0
3	C	222	SIN	12	0
3	C	223	SIN	3	0
3	C	224	SIN	1	0
3	C	225	SIN	2	0
3	C	226	SIN	5	0
3	C	227	SIN	1	0
3	C	228	SIN	3	0
4	C	231	MLI	9	0
4	C	232	MLI	1	0
3	D	219	SIN	1	0
3	D	221	SIN	1	0
3	D	222	SIN	2	0
3	D	223	SIN	12	0
3	D	224	SIN	4	0
3	D	225	SIN	4	0
4	D	226	MLI	3	0
4	D	227	MLI	2	0
4	D	228	MLI	2	0
3	E	218	SIN	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	221	SIN	3	0
3	E	222	SIN	7	0
4	E	223	MLI	7	0
6	F	218	FLC	19	0
2	F	219	TLA	1	0
3	F	223	SIN	3	0
4	F	224	MLI	5	0
3	G	218	SIN	5	0
3	G	220	SIN	2	0
3	G	221	SIN	3	0
4	G	223	MLI	1	0
4	G	224	MLI	1	0
2	H	218	TLA	4	0
3	H	219	SIN	12	0
3	H	222	SIN	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	213/220 (96%)	-0.47	3 (1%) 78 77	20, 32, 52, 66	0
1	B	213/220 (96%)	-0.19	5 (2%) 64 63	23, 40, 61, 96	0
1	C	212/220 (96%)	-0.66	2 (0%) 85 85	17, 27, 46, 75	0
1	D	213/220 (96%)	-0.44	2 (0%) 85 85	18, 29, 46, 59	0
1	E	213/220 (96%)	-0.44	2 (0%) 85 85	21, 34, 55, 76	0
1	F	213/220 (96%)	-0.26	4 (1%) 70 69	21, 34, 58, 86	0
1	G	212/220 (96%)	-0.28	5 (2%) 62 61	25, 39, 59, 88	0
1	H	214/220 (97%)	-0.21	3 (1%) 78 77	27, 42, 65, 74	0
All	All	1703/1760 (96%)	-0.37	26 (1%) 76 75	17, 34, 57, 96	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	0	ALA	7.8
1	B	0	ALA	5.4
1	F	-1	ASN	5.4
1	B	-1	ASN	4.8
1	E	0	ALA	4.4

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

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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
3	SIN	A	221	8/8	0.85	0.53	25.49	16,23,36,47	8
3	SIN	C	225	8/8	0.86	0.35	16.61	16,25,36,39	8
4	MLI	G	223	7/7	0.95	0.52	15.84	14,17,25,25	7
4	MLI	A	227	7/7	0.96	0.58	14.72	10,16,18,18	7
3	SIN	D	221	8/8	0.80	0.33	14.46	20,27,39,47	8
6	FLC	F	218	13/13	0.83	0.38	13.14	9,26,30,36	13
3	SIN	C	220	8/8	0.88	0.20	12.64	40,61,76,76	0
4	MLI	C	231	7/7	0.88	0.55	11.53	22,29,41,43	7
4	MLI	A	225	7/7	0.77	0.43	11.06	21,26,33,33	7
3	SIN	A	222	8/8	0.90	0.41	10.64	23,61,73,82	0
3	SIN	A	223	8/8	0.78	0.38	10.17	42,47,55,59	8
3	SIN	C	223	8/8	0.65	0.39	9.96	78,92,98,98	0
4	MLI	C	232	7/7	0.74	0.41	9.94	13,26,34,38	7
4	MLI	E	223	7/7	0.89	0.31	9.24	14,17,31,37	7
8	ACT	D	229	4/4	0.93	0.23	8.94	51,52,53,54	0
3	SIN	C	221	8/8	0.80	0.40	8.71	41,44,46,48	8
3	SIN	G	220	8/8	0.87	0.30	8.36	19,26,27,33	8
4	MLI	D	226	7/7	0.79	0.39	7.83	26,31,38,42	7
3	SIN	C	226	8/8	0.87	0.27	7.83	2,12,24,29	8
3	SIN	B	222	8/8	0.75	0.39	7.75	18,24,30,31	8
3	SIN	C	224	8/8	0.75	0.37	7.60	14,27,37,38	8
3	SIN	A	224	8/8	0.76	0.30	7.59	45,49,54,55	8
5	CL	F	225	1/1	0.98	0.24	7.54	80,80,80,80	0
4	MLI	D	228	7/7	0.81	0.31	7.52	29,37,43,47	7
3	SIN	A	220	8/8	0.82	0.30	7.05	76,83,91,92	0
4	MLI	H	224	7/7	0.95	0.32	6.93	32,37,47,50	7
3	SIN	A	219	8/8	0.75	0.38	6.83	29,36,41,43	8
3	SIN	D	224	8/8	0.89	0.32	6.46	10,22,30,42	8
6	FLC	B	218	13/13	0.77	0.41	6.25	39,49,53,55	13
2	TLA	C	219	10/10	0.69	0.23	6.17	44,50,52,52	10
3	SIN	H	219	8/8	0.89	0.33	6.11	15,26,33,34	8
4	MLI	B	225	7/7	0.76	0.44	5.87	20,27,36,39	7
3	SIN	D	225	8/8	0.90	0.25	5.80	61,62,79,83	0
3	SIN	G	218	8/8	0.87	0.36	5.41	86,89,92,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	CL	C	235	1/1	0.98	0.17	5.10	28,28,28,28	1
3	SIN	C	227	8/8	0.77	0.36	4.97	35,41,44,44	8
3	SIN	H	221	8/8	0.67	0.26	4.90	92,94,95,96	0
3	SIN	E	219	8/8	0.79	0.20	4.88	75,78,83,83	0
3	SIN	E	221	8/8	0.81	0.23	4.44	82,88,91,93	0
3	SIN	F	221	8/8	0.74	0.28	4.24	93,95,99,100	0
5	CL	G	226	1/1	0.96	0.35	3.95	59,59,59,59	0
3	SIN	E	222	8/8	0.77	0.31	3.94	31,32,41,42	8
3	SIN	C	222	8/8	0.87	0.30	3.87	3,10,22,43	8
8	ACT	C	233	4/4	0.89	0.21	3.67	61,64,64,65	0
3	SIN	D	220	8/8	0.81	0.18	3.56	58,71,74,75	0
3	SIN	B	221	8/8	0.76	0.21	3.42	63,72,80,80	0
5	CL	E	225	1/1	0.98	0.30	3.42	66,66,66,66	0
3	SIN	G	221	8/8	0.82	0.27	3.42	75,79,88,89	0
5	CL	D	230	1/1	0.95	0.24	3.42	70,70,70,70	0
3	SIN	H	220	8/8	0.84	0.21	3.30	63,70,73,74	8
3	SIN	D	222	8/8	0.88	0.17	3.01	43,53,61,62	8
3	SIN	H	223	8/8	0.82	0.21	2.68	52,55,56,57	8
3	SIN	D	223	8/8	0.88	0.27	2.54	6,11,25,26	8
4	MLI	A	226	7/7	0.89	0.23	2.18	41,48,63,65	0
3	SIN	E	218	8/8	0.93	0.20	2.07	33,48,62,63	0
4	MLI	A	228	7/7	0.89	0.19	1.99	74,82,87,89	0
3	SIN	F	220	8/8	0.89	0.19	1.87	48,65,76,78	0
3	SIN	E	220	8/8	0.68	0.24	1.67	69,80,88,89	0
4	MLI	C	229	7/7	0.96	0.17	1.66	35,37,47,50	0
3	SIN	G	219	8/8	0.67	0.24	1.61	76,82,87,89	0
3	SIN	B	220	8/8	0.87	0.18	1.43	47,52,55,56	8
3	SIN	D	219	8/8	0.94	0.16	1.13	44,55,64,72	0
2	TLA	H	218	10/10	0.92	0.21	0.96	40,57,64,74	0
2	TLA	B	219	10/10	0.95	0.16	0.44	41,52,65,70	0
2	TLA	F	219	10/10	0.98	0.13	-0.35	29,37,52,54	0
4	MLI	B	223	7/7	0.96	0.11	-0.64	33,36,47,50	0
2	TLA	D	218	10/10	0.96	0.12	-0.74	24,31,37,46	0
5	CL	A	229	1/1	0.99	0.10	-1.94	57,57,57,57	0
5	CL	B	226	1/1	0.96	0.05	-2.92	68,68,68,68	0
7	NA	C	238	1/1	0.90	0.14	-	59,59,59,59	0
8	ACT	G	225	4/4	0.96	0.14	-	69,69,69,69	0
4	MLI	C	230	7/7	0.84	0.21	-	49,51,53,55	7
5	CL	D	231	1/1	0.96	0.17	-	30,30,30,30	1
2	TLA	A	218	10/10	0.79	0.31	-	47,56,58,63	10
4	MLI	D	227	7/7	0.81	0.36	-	31,32,41,43	7

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SIN	C	228	8/8	0.69	0.76	-	28,32,36,38	8
5	CL	C	234	1/1	0.98	0.04	-	53,53,53,53	0
4	MLI	B	224	7/7	0.81	0.21	-	60,61,64,65	7
7	NA	E	226	1/1	0.84	0.20	-	55,55,55,55	0
5	CL	C	237	1/1	0.99	0.27	-	68,68,68,68	0
5	CL	E	224	1/1	0.95	0.31	-	80,80,80,80	0
7	NA	B	227	1/1	0.95	0.10	-	56,56,56,56	0
3	SIN	F	223	8/8	0.76	0.32	-	81,90,93,93	0
3	SIN	H	222	8/8	0.63	0.66	-	41,51,54,56	8
4	MLI	F	224	7/7	0.84	0.19	-	47,50,51,53	7
2	TLA	C	218	10/10	0.87	0.45	-	112,115,116,116	0
3	SIN	G	222	8/8	0.73	0.26	-	32,49,57,58	8
3	SIN	F	222	8/8	0.71	0.30	-	49,56,58,58	8
7	NA	H	225	1/1	0.97	0.12	-	49,49,49,49	0
4	MLI	G	224	7/7	0.80	0.19	-	56,59,61,62	7
5	CL	C	236	1/1	0.98	0.26	-	67,67,67,67	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.