wwPDB X-ray Structure Validation Summary Report (i)

Jul 19, 2016 – 10:54 AM EDT

PDB ID	:	5LC1
Title	:	L-threonine dehydrogenase from Trypanosoma brucei with NAD and the inhibitor pyruvate bound.
Authors	:	Erskine, P.T.; Adjogatse, E.; Wood, S.P.; Cooper, J.B.
Deposited on	:	2016-06-18
Resolution	:	2.10 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
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

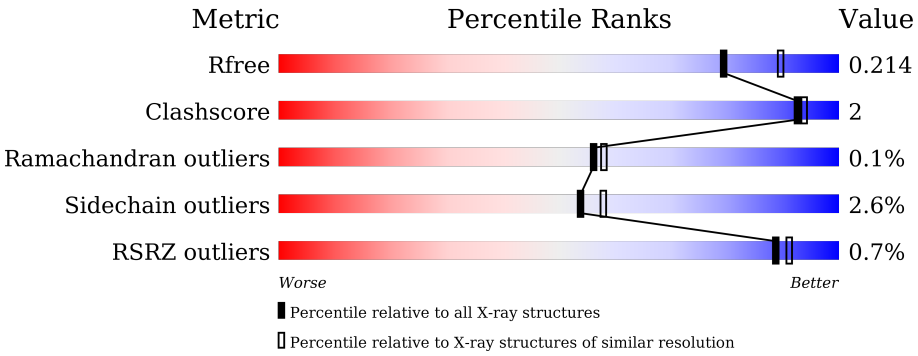
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027790
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027790

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 >=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 <=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	321	95%
1	B	321	92% 7%
1	C	321	93% 7%
1	D	321	92% 7%
1	E	321	90% 9%
1	F	321	90% 9%

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
3	PYR	A	501	-	-	-	X
3	PYR	B	501	-	-	-	X
3	PYR	C	501	-	-	-	X
3	PYR	D	501	-	-	-	X
3	PYR	E	501	-	-	-	X
3	PYR	F	501	-	-	-	X
4	BME	A	502	-	-	-	X
4	BME	B	502	-	-	-	X
5	ACT	A	503	-	-	-	X
5	ACT	B	503	-	-	-	X
6	NA	A	504	-	-	-	X
6	NA	E	503	-	-	-	X
6	NA	F	502	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 17331 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.

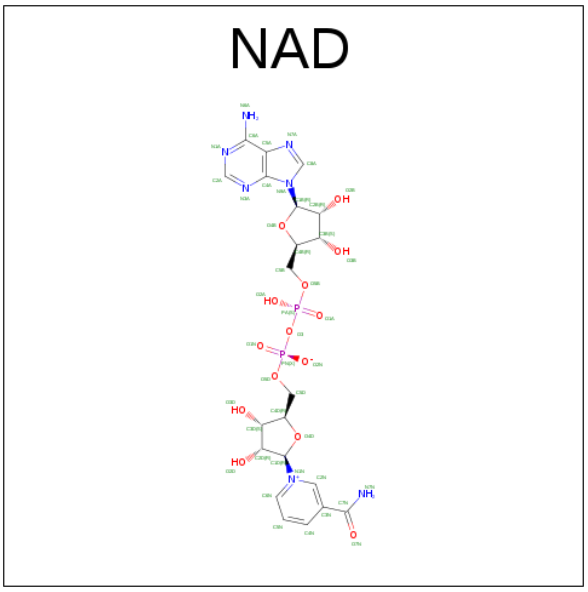
- Molecule 1 is a protein called L-threonine 3-dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	0	0
			2500	1595	416	470	19			
1	B	321	Total	C	N	O	S	0	1	0
			2520	1606	421	474	19			
1	C	320	Total	C	N	O	S	0	0	0
			2501	1595	416	471	19			
1	D	320	Total	C	N	O	S	0	1	0
			2510	1600	417	474	19			
1	E	320	Total	C	N	O	S	0	1	0
			2510	1601	418	472	19			
1	F	319	Total	C	N	O	S	0	1	0
			2502	1597	418	468	19			

There are 12 discrepancies between the modelled and reference sequences:

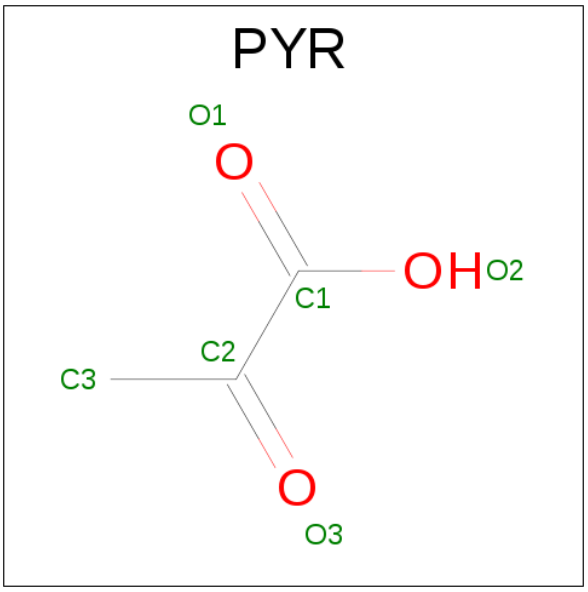
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	HIS	-	expression tag	UNP Q7YW97
A	2	MET	-	expression tag	UNP Q7YW97
B	1	HIS	-	expression tag	UNP Q7YW97
B	2	MET	-	expression tag	UNP Q7YW97
C	1	HIS	-	expression tag	UNP Q7YW97
C	2	MET	-	expression tag	UNP Q7YW97
D	1	HIS	-	expression tag	UNP Q7YW97
D	2	MET	-	expression tag	UNP Q7YW97
E	1	HIS	-	expression tag	UNP Q7YW97
E	2	MET	-	expression tag	UNP Q7YW97
F	1	HIS	-	expression tag	UNP Q7YW97
F	2	MET	-	expression tag	UNP Q7YW97

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



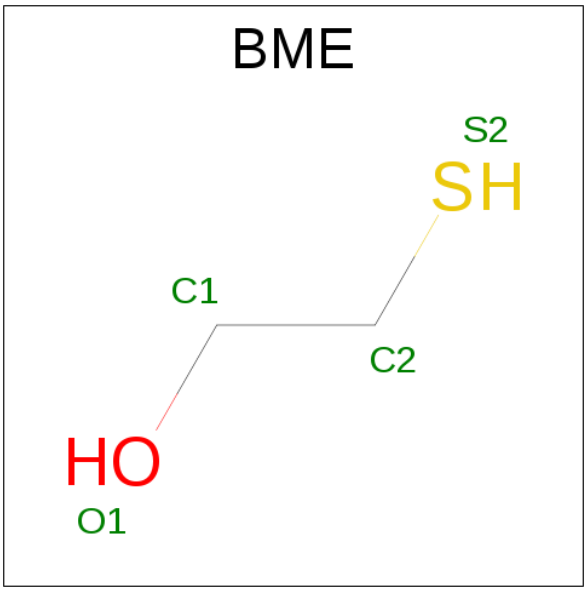
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is PYRUVIC ACID (three-letter code: PYR) (formula: $C_3H_4O_3$).



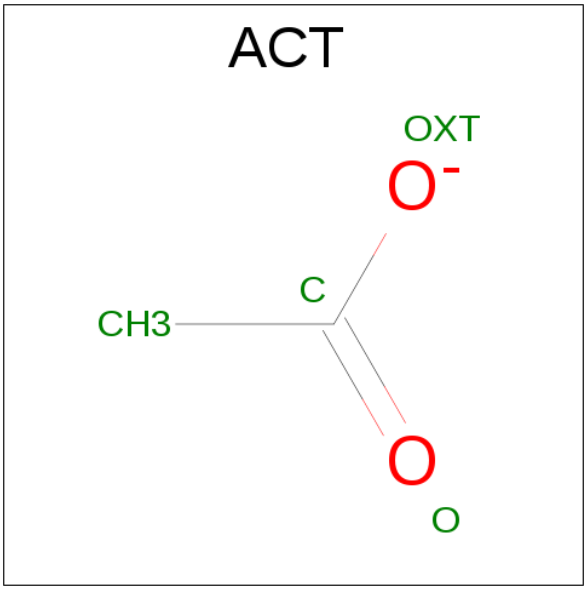
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0
3	F	1	Total C O 6 3 3	0	0

- Molecule 4 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O S 4 2 1 1	0	0
4	B	1	Total C O S 4 2 1 1	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	E	1	Total C O 4 2 2	0	0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	1	Total Na 1 1	0	0
6	E	1	Total Na 1 1	0	0
6	B	1	Total Na 1 1	0	0
6	C	1	Total Na 1 1	0	0
6	A	1	Total Na 1 1	0	0
6	F	1	Total Na 1 1	0	0

- Molecule 7 is water.

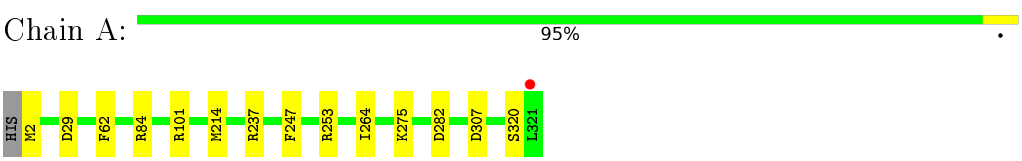
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	342	Total O 342 342	0	0
7	B	358	Total O 358 358	0	0
7	C	305	Total O 305 305	0	0
7	D	335	Total O 335 335	0	0
7	E	277	Total O 277 277	0	0
7	F	345	Total O 345 345	0	0

3 Residue-property plots (i)

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

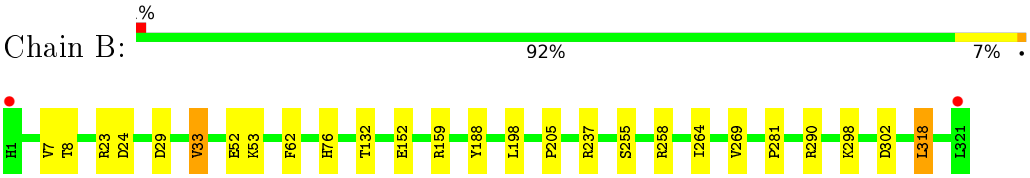
- Molecule 1: L-threonine 3-dehydrogenase

Chain A:



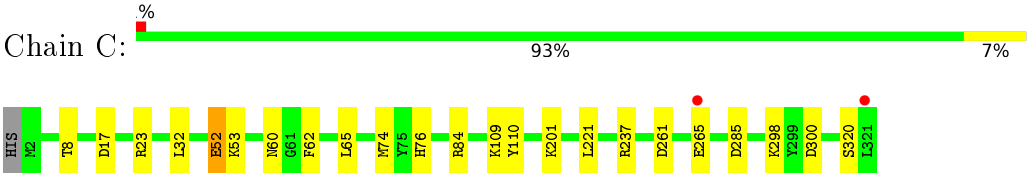
- Molecule 1: L-threonine 3-dehydrogenase

Chain B:



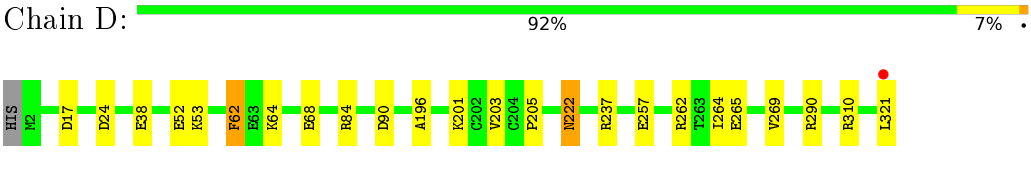
- Molecule 1: L-threonine 3-dehydrogenase

Chain C:



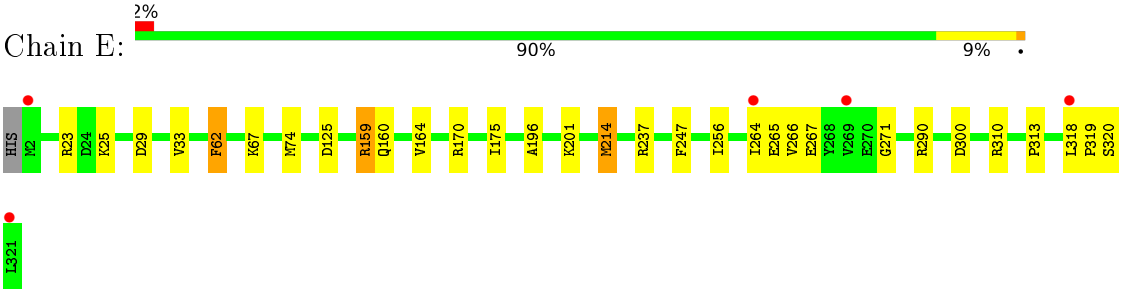
- Molecule 1: L-threonine 3-dehydrogenase

Chain D:



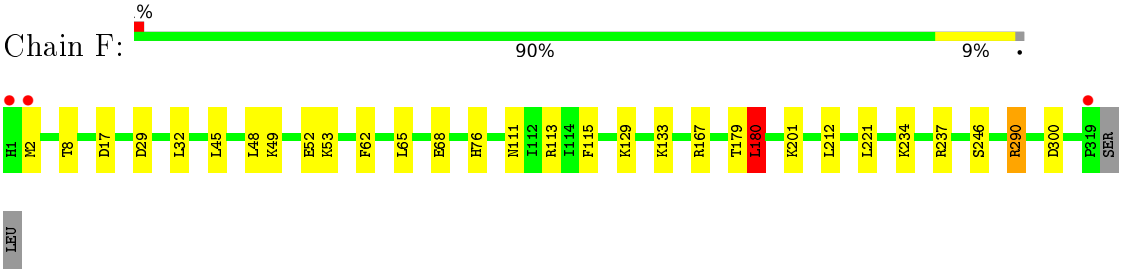
- Molecule 1: L-threonine 3-dehydrogenase

Chain E:



• Molecule 1: L-threonine 3-dehydrogenase

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	132.04Å 276.49Å 55.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	95.50 – 2.10 69.12 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.3 (95.50-2.10) 97.3 (69.12-2.10)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.66 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0151	Depositor
R, R_{free}	0.147 , 0.208 0.157 , 0.214	Depositor DCC
R_{free} test set	5563 reflections (4.99%)	DCC
Wilson B-factor (Å^2)	19.3	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 52.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	17331	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.82 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.0398e-03.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: NA, PYR, ACT, NAD, BME

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	0.83	0/2556	0.95	9/3469 (0.3%)
1	B	0.83	2/2577 (0.1%)	0.87	3/3496 (0.1%)
1	C	0.85	0/2557	0.96	8/3469 (0.2%)
1	D	0.83	0/2566	0.92	8/3481 (0.2%)
1	E	0.81	0/2566	0.92	8/3480 (0.2%)
1	F	0.83	0/2562	0.92	6/3476 (0.2%)
All	All	0.83	2/15384 (0.0%)	0.92	42/20871 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	188	TYR	CE1-CZ	6.71	1.47	1.38
1	B	152	GLU	CD-OE2	5.28	1.31	1.25

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	237	ARG	NE-CZ-NH2	-11.33	114.64	120.30
1	C	237	ARG	NE-CZ-NH1	10.49	125.54	120.30
1	A	237	ARG	NE-CZ-NH2	-9.71	115.44	120.30
1	F	237	ARG	NE-CZ-NH2	-9.49	115.56	120.30
1	D	290	ARG	NE-CZ-NH1	9.14	124.87	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	320	SER	Peptide

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	2500	0	2511	2	0
1	B	2520	0	2528	9	0
1	C	2501	0	2512	7	0
1	D	2510	0	2517	9	0
1	E	2510	0	2524	18	0
1	F	2502	0	2519	13	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	C	44	0	26	1	0
2	D	44	0	26	0	0
2	E	44	0	26	0	0
2	F	44	0	26	1	0
3	A	6	0	3	0	0
3	B	6	0	3	0	0
3	C	6	0	3	1	0
3	D	6	0	3	0	0
3	E	6	0	3	0	0
3	F	6	0	3	1	0
4	A	4	0	5	0	0
4	B	4	0	5	0	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
5	E	4	0	3	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	342	0	0	1	0
7	B	358	0	0	2	0
7	C	305	0	0	0	0
7	D	335	0	0	2	0
7	E	277	0	0	3	1
7	F	345	0	0	4	1
All	All	17331	0	15304	60	1

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.

The worst 5 of 60 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:E:196:ALA:HB2	1:E:264:ILE:HD11	1.65	0.76
1:F:179:THR:O	1:F:180:LEU:HB2	1.88	0.74
1:C:32:LEU:HD21	1:C:65:LEU:HD11	1.75	0.68
1:B:258:ARG:NH1	1:B:302:ASP:OD1	2.26	0.67
1:C:201:LYS:HE2	1:C:265:GLU:HG2	1.80	0.64

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:602:HOH:O	7:F:780:HOH:O[2_656]	1.95	0.25

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	318/321 (99%)	312 (98%)	6 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	320/321 (100%)	314 (98%)	6 (2%)	0	100	100
1	C	318/321 (99%)	312 (98%)	6 (2%)	0	100	100
1	D	319/321 (99%)	312 (98%)	7 (2%)	0	100	100
1	E	319/321 (99%)	311 (98%)	7 (2%)	1 (0%)	46	45
1	F	318/321 (99%)	311 (98%)	6 (2%)	1 (0%)	46	45
All	All	1912/1926 (99%)	1872 (98%)	38 (2%)	2 (0%)	56	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	320	SER
1	F	180	LEU

5.3.2 Protein sidechains (i)

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	277/278 (100%)	273 (99%)	4 (1%)	74	80
1	B	279/278 (100%)	270 (97%)	9 (3%)	46	48
1	C	277/278 (100%)	270 (98%)	7 (2%)	55	59
1	D	278/278 (100%)	271 (98%)	7 (2%)	55	59
1	E	278/278 (100%)	271 (98%)	7 (2%)	55	59
1	F	277/278 (100%)	268 (97%)	9 (3%)	46	48
All	All	1666/1668 (100%)	1623 (97%)	43 (3%)	54	58

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	320	SER
1	D	262	ARG
1	F	111	ASN
1	D	24	ASP

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Mol	Chain	Res	Type
1	D	52	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	291	ASN
1	F	60	ASN
1	E	60	ASN
1	A	191	HIS
1	E	311	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 23 ligands modelled in this entry, 6 are monoatomic - leaving 17 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	NAD	A	500	-	42,48,48	0.94	1 (2%)	46,73,73	1.76	6 (13%)
3	PYR	A	501	-	2,5,5	0.95	0	2,6,6	0.82	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	BME	A	502	1	3,3,3	0.52	0	1,2,2	0.05	0
5	ACT	A	503	-	0,3,3	0.00	-	0,3,3	0.00	-
2	NAD	B	500	-	42,48,48	0.94	2 (4%)	46,73,73	1.67	6 (13%)
3	PYR	B	501	-	2,5,5	0.89	0	2,6,6	0.96	0
4	BME	B	502	1	3,3,3	0.70	0	1,2,2	0.09	0
5	ACT	B	503	-	0,3,3	0.00	-	0,3,3	0.00	-
2	NAD	C	500	-	42,48,48	0.88	2 (4%)	46,73,73	1.74	8 (17%)
3	PYR	C	501	-	2,5,5	0.48	0	2,6,6	1.16	0
2	NAD	D	500	-	42,48,48	0.96	2 (4%)	46,73,73	1.58	8 (17%)
3	PYR	D	501	-	2,5,5	1.15	0	2,6,6	1.80	1 (50%)
2	NAD	E	500	-	42,48,48	1.08	3 (7%)	46,73,73	2.12	6 (13%)
3	PYR	E	501	-	2,5,5	0.32	0	2,6,6	1.01	0
5	ACT	E	502	-	0,3,3	0.00	-	0,3,3	0.00	-
2	NAD	F	500	-	42,48,48	0.99	2 (4%)	46,73,73	1.62	8 (17%)
3	PYR	F	501	-	2,5,5	0.23	0	2,6,6	0.31	0

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	500	-	-	0/22/62/62	0/5/5/5
3	PYR	A	501	-	-	0/0/4/4	0/0/0/0
4	BME	A	502	1	-	0/1/1/1	0/0/0/0
5	ACT	A	503	-	-	0/0/0/0	0/0/0/0
2	NAD	B	500	-	-	0/22/62/62	0/5/5/5
3	PYR	B	501	-	-	0/0/4/4	0/0/0/0
4	BME	B	502	1	-	0/1/1/1	0/0/0/0
5	ACT	B	503	-	-	0/0/0/0	0/0/0/0
2	NAD	C	500	-	-	0/22/62/62	0/5/5/5
3	PYR	C	501	-	-	0/0/4/4	0/0/0/0
2	NAD	D	500	-	-	0/22/62/62	0/5/5/5
3	PYR	D	501	-	-	0/0/4/4	0/0/0/0
2	NAD	E	500	-	-	0/22/62/62	0/5/5/5
3	PYR	E	501	-	-	0/0/4/4	0/0/0/0
5	ACT	E	502	-	-	0/0/0/0	0/0/0/0
2	NAD	F	500	-	-	0/22/62/62	0/5/5/5
3	PYR	F	501	-	-	0/0/4/4	0/0/0/0

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	NAD	C4A-N3A	-2.61	1.31	1.35
2	C	500	NAD	C2N-N1N	2.04	1.38	1.35
2	D	500	NAD	C5A-C4A	2.05	1.45	1.40
2	E	500	NAD	C4N-C3N	2.09	1.42	1.39
2	B	500	NAD	C2N-C3N	2.16	1.42	1.39

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	500	NAD	N3A-C2A-N1A	-7.95	122.62	128.87
2	B	500	NAD	N3A-C2A-N1A	-7.66	122.85	128.87
2	C	500	NAD	N3A-C2A-N1A	-7.55	122.94	128.87
2	A	500	NAD	N3A-C2A-N1A	-7.51	122.97	128.87
2	E	500	NAD	C1B-N9A-C4A	-5.56	120.61	126.81

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	500	NAD	1	0
3	C	501	PYR	1	0
2	F	500	NAD	1	0
3	F	501	PYR	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^{th} 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^2)	Q<0.9
1	A	320/321 (99%)	-0.51	1 (0%)	94	95	8, 18, 38, 57	0
1	B	321/321 (100%)	-0.47	2 (0%)	90	92	8, 18, 38, 92	0
1	C	320/321 (99%)	-0.47	2 (0%)	90	92	9, 18, 41, 71	0
1	D	320/321 (99%)	-0.47	1 (0%)	94	95	9, 17, 41, 86	0
1	E	320/321 (99%)	-0.31	5 (1%)	74	79	9, 21, 51, 82	0
1	F	319/321 (99%)	-0.46	3 (0%)	85	88	9, 18, 42, 80	0
All	All	1920/1926 (99%)	-0.45	14 (0%)	89	91	8, 18, 42, 92	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	HIS	4.5
1	E	321	LEU	4.3
1	C	321	LEU	4.2
1	D	321	LEU	4.0
1	F	1	HIS	3.4

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^{th} 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^2)	Q<0.9
3	PYR	E	501	6/6	0.87	0.21	11.91	26,32,35,37	0
4	BME	B	502	4/4	0.68	0.29	10.48	56,60,66,71	0
3	PYR	B	501	6/6	0.92	0.19	9.21	21,25,28,31	0
3	PYR	D	501	6/6	0.90	0.14	8.83	22,23,27,28	0
4	BME	A	502	4/4	0.85	0.21	8.29	42,44,48,52	0
3	PYR	F	501	6/6	0.92	0.15	7.73	21,25,26,27	0
3	PYR	A	501	6/6	0.94	0.13	5.22	18,20,22,27	0
3	PYR	C	501	6/6	0.90	0.16	4.78	27,29,33,33	0
6	NA	E	503	1/1	0.67	0.18	4.24	33,33,33,33	0
6	NA	A	504	1/1	0.89	0.17	3.64	29,29,29,29	0
5	ACT	B	503	4/4	0.87	0.15	3.08	29,31,37,40	0
5	ACT	A	503	4/4	0.85	0.16	2.84	28,28,29,35	0
6	NA	F	502	1/1	0.91	0.13	2.21	28,28,28,28	0
2	NAD	E	500	44/44	0.97	0.12	1.29	17,20,22,24	0
5	ACT	E	502	4/4	0.78	0.16	1.25	36,36,37,41	0
6	NA	B	504	1/1	0.92	0.11	1.24	30,30,30,30	0
2	NAD	B	500	44/44	0.97	0.11	1.21	15,18,20,23	0
2	NAD	F	500	44/44	0.98	0.09	0.07	14,17,18,20	0
2	NAD	A	500	44/44	0.98	0.09	0.02	14,15,17,19	0
2	NAD	C	500	44/44	0.98	0.08	-0.31	15,17,18,20	0
2	NAD	D	500	44/44	0.98	0.08	-0.83	12,14,16,17	0
6	NA	D	502	1/1	0.98	0.06	-1.54	20,20,20,20	0
6	NA	C	502	1/1	0.97	0.07	-2.37	21,21,21,21	0

6.5 Other polymers

There are no such residues in this entry.