



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:08 PM GMT

PDB ID : 3SYT
Title : Crystal structure of glutamine-dependent NAD⁺ synthetase from *M. tuberculosis* bound to AMP/PPi, NAD⁺, and glutamate
Authors : Chuenchor, W.; Gerratana, B.
Deposited on : 2011-07-18
Resolution : 2.65 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 ⓘ symbol.

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

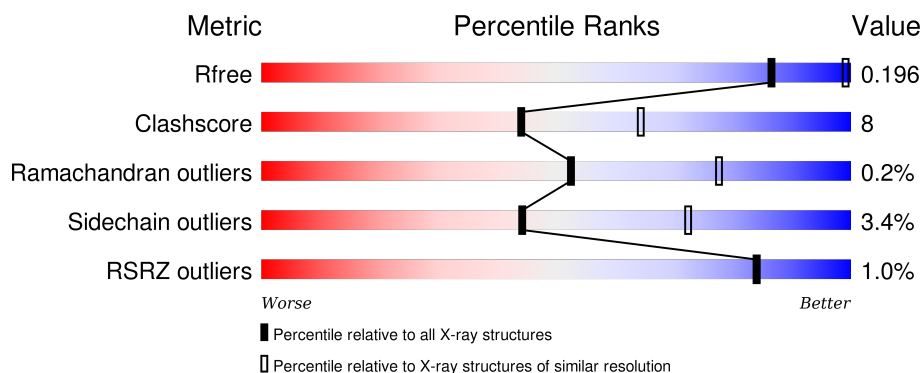
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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 $\leq 5\%$. 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	680	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 15%, green 80%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 80% 15% • • </div> </div>
1	B	680	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 14%, green 82%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 82% 14% • • </div> </div>
1	C	680	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 15%, green 80%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 80% 15% • • </div> </div>
1	D	680	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 15%, green 79%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 79% 15% 5% </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLU	A	683	-	-	-	X
2	GLU	B	683	-	-	-	X
2	GLU	C	683	-	-	-	X
2	GLU	D	683	-	-	-	X
3	GOL	A	684	-	-	-	X
4	NAD	B	680	-	-	-	X
5	AMP	A	681	-	-	-	X
6	POP	A	682	-	-	-	X
6	POP	B	682	-	-	-	X
6	POP	C	682	-	-	X	X
6	POP	D	682	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 21035 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.

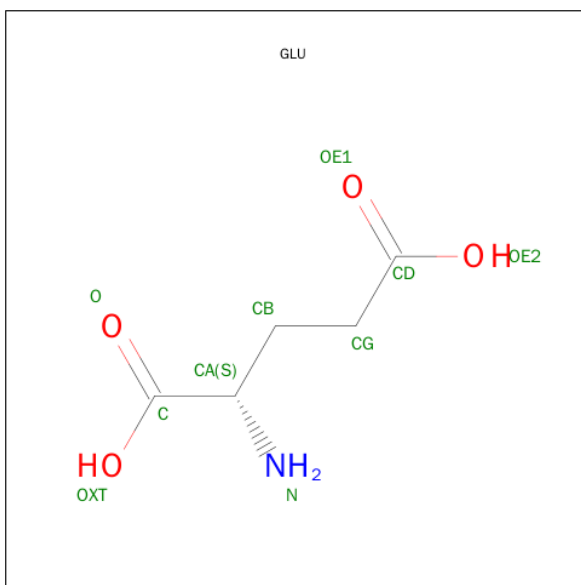
- Molecule 1 is a protein called Glutamine-dependent NAD(+) synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	660	Total	C	N	O	S	0	0	0
			5104	3235	906	947	16			
1	B	660	Total	C	N	O	S	0	0	0
			5076	3224	895	941	16			
1	C	651	Total	C	N	O	S	0	0	0
			5010	3181	888	925	16			
1	D	649	Total	C	N	O	S	0	0	0
			5003	3174	889	924	16			

There are 4 discrepancies between the modelled and reference sequences:

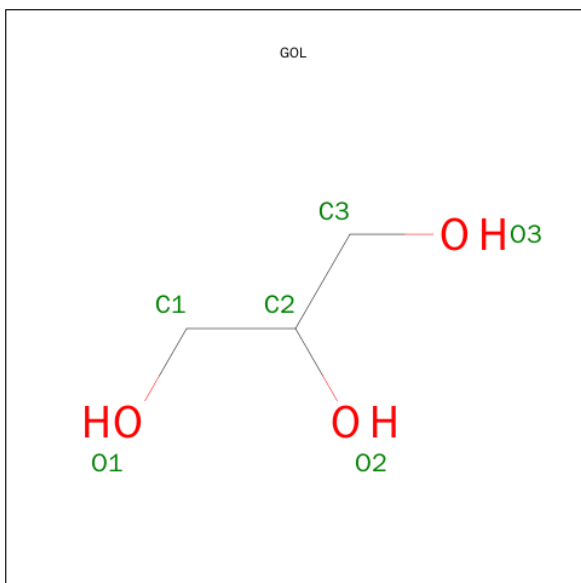
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP P0A5L6
B	0	SER	-	EXPRESSION TAG	UNP P0A5L6
C	0	SER	-	EXPRESSION TAG	UNP P0A5L6
D	0	SER	-	EXPRESSION TAG	UNP P0A5L6

- Molecule 2 is GLUTAMIC ACID (three-letter code: GLU) (formula: C₅H₉NO₄).



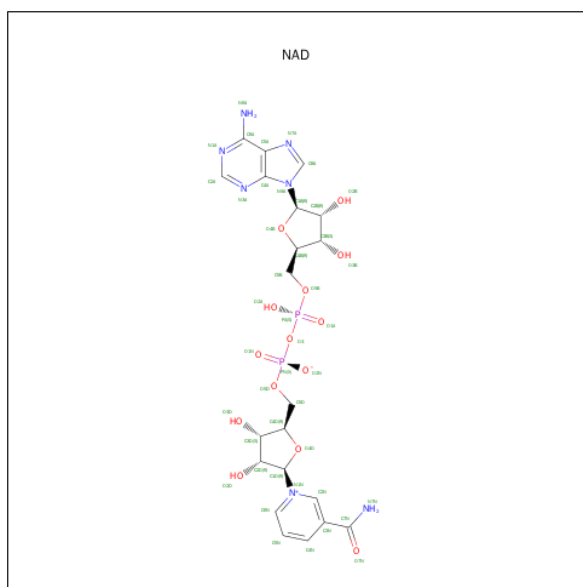
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	5	1	4		
2	B	1	Total	C	N	O	0	0
			10	5	1	4		
2	C	1	Total	C	N	O	0	0
			10	5	1	4		
2	D	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



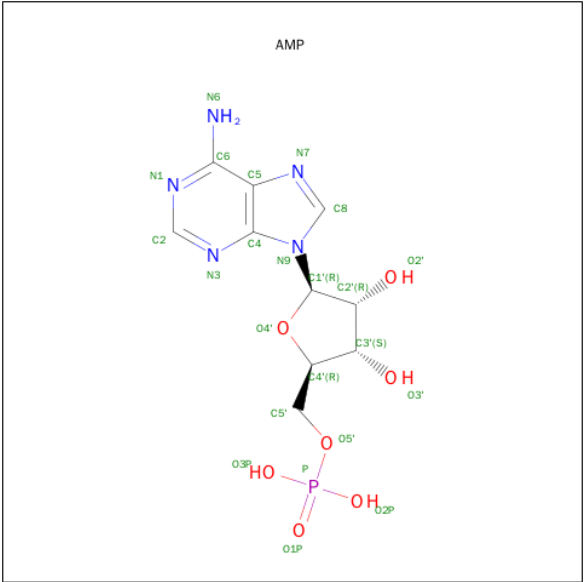
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		

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



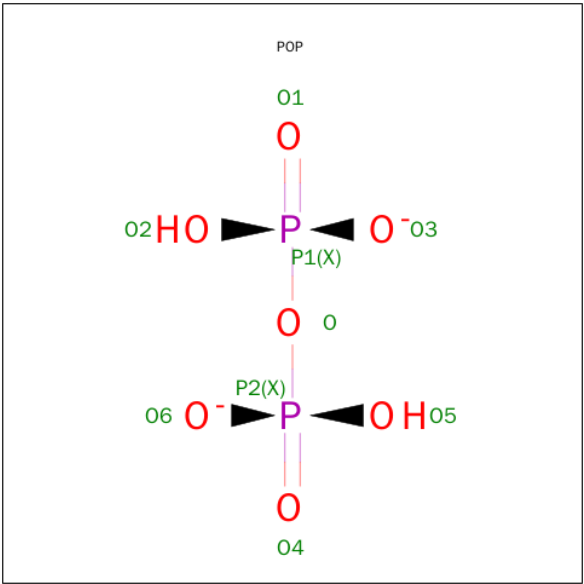
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
4	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
4	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
4	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 5 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
5	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
5	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
5	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

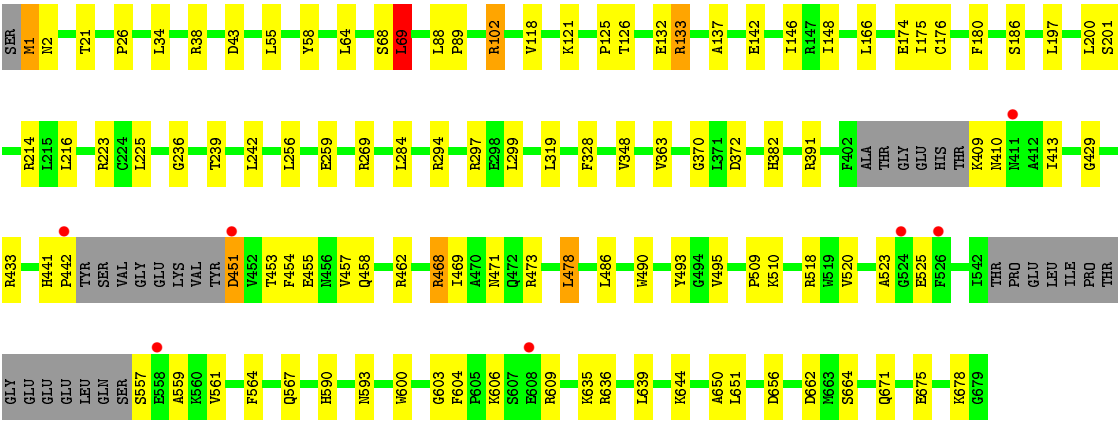
- Molecule 6 is PYROPHOSPHATE 2- (three-letter code: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).



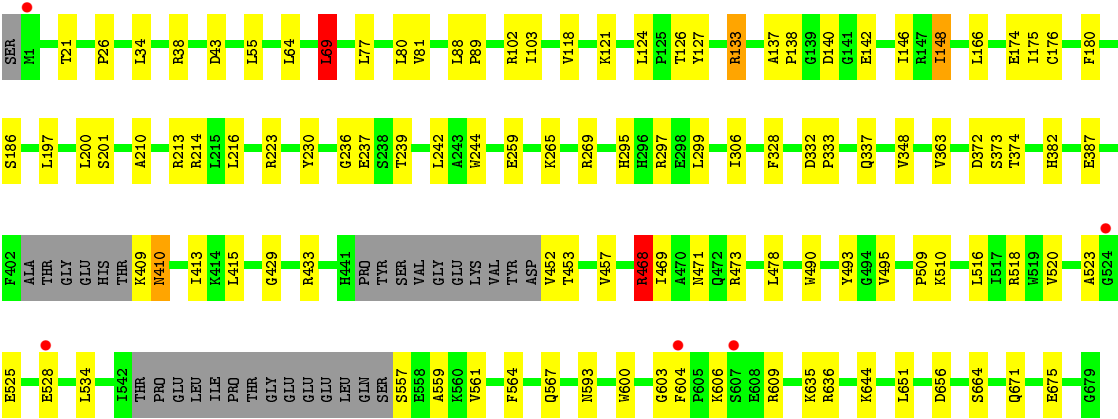
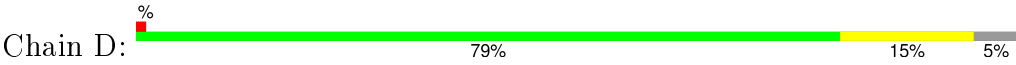
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O P 9 7 2	0	0
6	B	1	Total O P 9 7 2	0	0
6	C	1	Total O P 9 7 2	0	0
6	D	1	Total O P 9 7 2	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	133	Total O 133 133	0	0
7	B	111	Total O 111 111	0	0
7	C	108	Total O 108 108	0	0
7	D	134	Total O 134 134	0	0



● Molecule 1: Glutamine-dependent NAD(+) synthetase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	177.75Å 177.75Å 213.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.30 – 2.65 49.71 – 2.65	Depositor EDS
% Data completeness (in resolution range)	98.5 (49.30-2.65) 90.9 (49.71-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.89 (at 2.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.155 , 0.200 0.157 , 0.196	Depositor DCC
R_{free} test set	4873 reflections (5.70%)	DCC
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	1.287	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 97654 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	21035	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GOL, POP, NAD, AMP

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	0.73	4/5224 (0.1%)	0.78	4/7100 (0.1%)
1	B	0.72	0/5196	0.77	2/7065 (0.0%)
1	C	0.72	0/5127	0.77	4/6966 (0.1%)
1	D	0.73	2/5119 (0.0%)	0.77	2/6955 (0.0%)
All	All	0.72	6/20666 (0.0%)	0.77	12/28086 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	292	ASN	CG-OD1	-8.43	1.05	1.24
1	A	292	ASN	CG-ND2	-6.83	1.15	1.32
1	A	410	ASN	CG-ND2	-6.62	1.16	1.32
1	A	410	ASN	CG-OD1	-6.59	1.09	1.24
1	D	410	ASN	CG-ND2	-6.52	1.16	1.32

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	391	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	D	468	ARG	NE-CZ-NH2	-6.71	116.94	120.30
1	C	294	ARG	NE-CZ-NH2	-6.71	116.95	120.30
1	A	305	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	B	69	LEU	CA-CB-CG	-6.16	101.12	115.30

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	5104	0	4986	82	2
1	B	5076	0	4945	74	1
1	C	5010	0	4892	81	1
1	D	5003	0	4888	85	1
2	A	10	0	5	0	0
2	B	10	0	5	0	0
2	C	10	0	5	0	0
2	D	10	0	5	2	0
3	A	6	0	8	0	0
3	C	6	0	8	1	0
4	A	44	0	26	4	0
4	B	44	0	26	3	0
4	C	44	0	26	4	0
4	D	44	0	26	6	0
5	A	23	0	12	1	0
5	B	23	0	12	1	0
5	C	23	0	12	3	0
5	D	23	0	12	1	0
6	A	9	0	0	1	0
6	B	9	0	0	1	0
6	C	9	0	0	5	0
6	D	9	0	0	3	0
7	A	133	0	0	1	0
7	B	111	0	0	0	0
7	C	108	0	0	3	0
7	D	134	0	0	1	0
All	All	21035	0	19899	322	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 322 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:D:518:ARG:NH2	1:D:603:GLY:HA3	1.77	1.00

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:ARG:NH2	1:A:259:GLU:OE1	2.02	0.92
1:C:518:ARG:NH2	1:C:603:GLY:HA3	1.85	0.91
1:A:518:ARG:NH2	1:A:603:GLY:HA3	1.86	0.90
1:C:214:ARG:NH2	1:C:259:GLU:OE1	2.06	0.88

All (3) 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)
1:A:142:GLU:OE2	1:D:297:ARG:NH2[8_554]	2.02	0.18
1:B:297:ARG:NH2	1:C:142:GLU:OE2[8_554]	2.03	0.17
1:A:265:LYS:NZ	1:A:387:GLU:OE2[8_554]	2.16	0.04

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	654/680 (96%)	632 (97%)	21 (3%)	1 (0%)	52 77
1	B	654/680 (96%)	627 (96%)	26 (4%)	1 (0%)	52 77
1	C	643/680 (95%)	622 (97%)	20 (3%)	1 (0%)	52 77
1	D	641/680 (94%)	617 (96%)	23 (4%)	1 (0%)	52 77
All	All	2592/2720 (95%)	2498 (96%)	90 (4%)	4 (0%)	52 77

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	176	CYS
1	A	176	CYS
1	B	176	CYS
1	D	176	CYS

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	527/549 (96%)	505 (96%)	22 (4%)	36	64
1	B	519/549 (94%)	503 (97%)	16 (3%)	47	75
1	C	513/549 (93%)	497 (97%)	16 (3%)	47	75
1	D	513/549 (93%)	498 (97%)	15 (3%)	50	77
All	All	2072/2196 (94%)	2003 (97%)	69 (3%)	44	73

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	451	ASP
1	C	1	MET
1	D	413	ILE
1	B	468	ARG
1	B	561	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	514	GLN
1	C	590	HIS
1	D	382	HIS
1	C	111	HIS
1	D	295	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

18 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$
4	NAD	A	680	-	38,48,48	0.86	2 (5%)	47,73,73	2.04	6 (12%)
5	AMP	A	681	-	20,25,25	0.71	0	22,38,38	2.79	4 (18%)
6	POP	A	682	-	8,8,8	0.65	0	13,13,13	1.04	1 (7%)
2	GLU	A	683	-	3,9,9	0.34	0	2,11,11	0.16	0
3	GOL	A	684	-	5,5,5	0.54	0	5,5,5	0.69	0
4	NAD	B	680	-	38,48,48	0.95	1 (2%)	47,73,73	2.00	2 (4%)
5	AMP	B	681	-	20,25,25	0.65	0	22,38,38	2.50	3 (13%)
6	POP	B	682	-	8,8,8	0.81	0	13,13,13	1.03	1 (7%)
2	GLU	B	683	-	3,9,9	0.19	0	2,11,11	0.55	0
4	NAD	C	680	-	38,48,48	0.77	2 (5%)	47,73,73	2.01	3 (6%)
5	AMP	C	681	-	20,25,25	0.75	0	22,38,38	1.93	3 (13%)
6	POP	C	682	-	8,8,8	0.68	0	13,13,13	1.24	2 (15%)
2	GLU	C	683	-	3,9,9	0.11	0	2,11,11	0.38	0
3	GOL	C	684	-	5,5,5	0.58	0	5,5,5	0.53	0
4	NAD	D	680	-	38,48,48	0.92	2 (5%)	47,73,73	2.15	7 (14%)
5	AMP	D	681	-	20,25,25	0.72	0	22,38,38	2.27	4 (18%)
6	POP	D	682	-	8,8,8	0.82	0	13,13,13	1.06	1 (7%)
2	GLU	D	683	-	3,9,9	0.16	0	2,11,11	0.22	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
4	NAD	A	680	-	-	0/22/62/62	0/5/5/5
5	AMP	A	681	-	-	0/6/26/26	0/3/3/3
6	POP	A	682	-	-	0/6/6/6	0/0/0/0
2	GLU	A	683	-	-	0/3/9/9	0/0/0/0
3	GOL	A	684	-	-	0/4/4/4	0/0/0/0
4	NAD	B	680	-	-	0/22/62/62	0/5/5/5
5	AMP	B	681	-	-	0/6/26/26	0/3/3/3
6	POP	B	682	-	-	0/6/6/6	0/0/0/0
2	GLU	B	683	-	-	0/3/9/9	0/0/0/0
4	NAD	C	680	-	-	0/22/62/62	0/5/5/5
5	AMP	C	681	-	-	0/6/26/26	0/3/3/3
6	POP	C	682	-	-	0/6/6/6	0/0/0/0
2	GLU	C	683	-	-	0/3/9/9	0/0/0/0
3	GOL	C	684	-	-	0/4/4/4	0/0/0/0
4	NAD	D	680	-	-	0/22/62/62	0/5/5/5
5	AMP	D	681	-	-	0/6/26/26	0/3/3/3
6	POP	D	682	-	-	0/6/6/6	0/0/0/0
2	GLU	D	683	-	-	0/3/9/9	0/0/0/0

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	680	NAD	O4B-C1B	2.12	1.43	1.41
4	C	680	NAD	O4D-C1D	2.16	1.43	1.41
4	D	680	NAD	O4B-C1B	2.17	1.43	1.41
4	C	680	NAD	O4B-C1B	2.43	1.44	1.41
4	D	680	NAD	O4D-C1D	2.70	1.44	1.41

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	680	NAD	N3A-C2A-N1A	-12.27	119.50	128.89
4	D	680	NAD	N3A-C2A-N1A	-12.00	119.71	128.89
5	A	681	AMP	N3-C2-N1	-11.92	119.77	128.89
4	C	680	NAD	N3A-C2A-N1A	-11.44	120.14	128.89
5	B	681	AMP	N3-C2-N1	-10.48	120.87	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	680	NAD	4	0
5	A	681	AMP	1	0
6	A	682	POP	1	0
4	B	680	NAD	3	0
5	B	681	AMP	1	0
6	B	682	POP	1	0
4	C	680	NAD	4	0
5	C	681	AMP	3	0
6	C	682	POP	5	0
3	C	684	GOL	1	0
4	D	680	NAD	6	0
5	D	681	AMP	1	0
6	D	682	POP	3	0
2	D	683	GLU	2	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, 95th 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	660/680 (97%)	-0.20	6 (0%) 85 86	20, 34, 61, 95	0
1	B	660/680 (97%)	-0.18	7 (1%) 82 82	22, 35, 60, 98	0
1	C	651/680 (95%)	-0.16	7 (1%) 82 82	21, 35, 61, 99	0
1	D	649/680 (95%)	-0.22	5 (0%) 87 87	21, 34, 61, 96	0
All	All	2620/2720 (96%)	-0.19	25 (0%) 84 84	20, 35, 61, 99	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	442	PRO	3.5
1	B	558	GLU	3.3
1	C	524	GLY	3.2
1	A	524	GLY	3.0
1	B	527	GLY	2.8

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, 95th 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(\AA^2)	Q<0.9
6	POP	D	682	9/9	0.80	0.32	7.67	83,117,144,342	0
2	GLU	D	683	10/10	0.87	0.48	7.20	58,98,127,140	0
2	GLU	A	683	10/10	0.89	0.46	5.80	47,94,123,126	0
6	POP	C	682	9/9	0.69	0.46	5.35	117,148,162,288	0
6	POP	A	682	9/9	0.77	0.59	4.81	130,142,151,306	0
2	GLU	B	683	10/10	0.83	0.44	4.73	59,78,121,122	0
6	POP	B	682	9/9	0.77	0.42	3.86	101,124,141,304	0
2	GLU	C	683	10/10	0.89	0.43	3.43	54,86,116,134	0
5	AMP	A	681	23/23	0.95	0.29	2.89	31,57,110,124	0
3	GOL	A	684	6/6	0.89	0.30	2.24	40,48,62,65	0
4	NAD	B	680	44/44	0.95	0.20	2.01	26,54,134,148	0
3	GOL	C	684	6/6	0.89	0.34	2.00	50,61,66,76	0
5	AMP	B	681	23/23	0.94	0.25	1.77	41,54,101,127	0
5	AMP	D	681	23/23	0.93	0.19	1.18	30,55,97,104	0
5	AMP	C	681	23/23	0.94	0.20	1.07	39,54,101,115	0
4	NAD	A	680	44/44	0.96	0.15	0.61	29,49,122,130	0
4	NAD	C	680	44/44	0.96	0.16	0.22	31,51,134,141	0
4	NAD	D	680	44/44	0.96	0.16	0.18	28,49,135,143	0

6.5 Other polymers ⓘ

There are no such residues in this entry.