



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 7, 2017 – 02:09 AM EST

PDB ID : 4KUG
Title : Crystal structure of 3-hydroxybutylryl-CoA dehydrogenase with NAD from Clostridium butyricum
Authors : Kim, E.J.; Kim, S.; Kim, K.J.
Deposited on : unknown
Resolution : 2.30 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

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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20030345

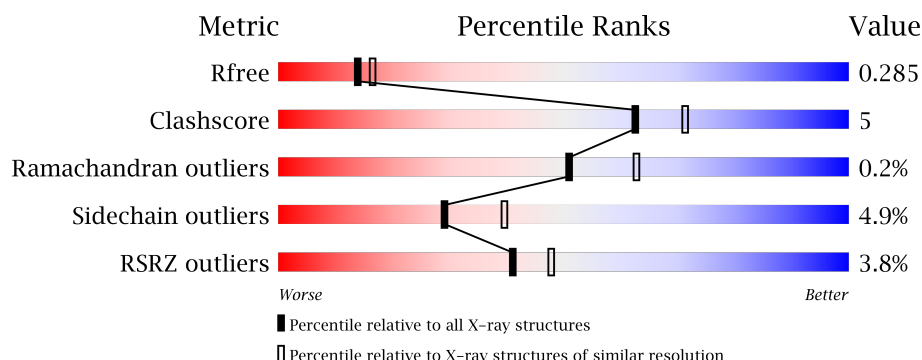
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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	290	<div> <div>2%</div> <div>83%</div> <div>13%</div> <div>..</div> </div>
1	B	290	<div> <div>4%</div> <div>85%</div> <div>11%</div> <div>..</div> </div>
1	C	290	<div> <div>4%</div> <div>83%</div> <div>13%</div> <div>..</div> </div>
1	D	290	<div> <div>4%</div> <div>80%</div> <div>16%</div> <div>..</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8910 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 3-hydroxybutyryl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	282	Total	C	N	O	S	0	0	0
			2129	1352	353	409	15			
1	B	282	Total	C	N	O	S	0	0	0
			2129	1352	353	409	15			
1	C	282	Total	C	N	O	S	0	0	0
			2129	1352	353	409	15			
1	D	282	Total	C	N	O	S	0	0	0
			2129	1352	353	409	15			

There are 32 discrepancies between the modelled and reference sequences:

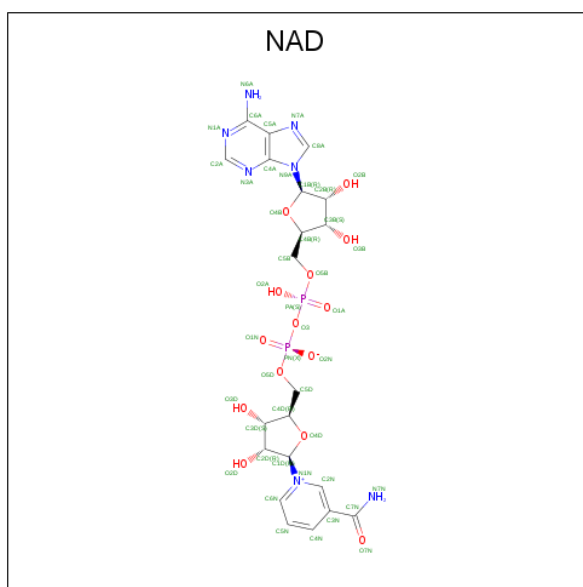
Chain	Residue	Modelled	Actual	Comment	Reference
A	283	SER	-	EXPRESSION TAG	UNP C4IEM5
A	284	LYS	-	EXPRESSION TAG	UNP C4IEM5
A	285	HIS	-	EXPRESSION TAG	UNP C4IEM5
A	286	HIS	-	EXPRESSION TAG	UNP C4IEM5
A	287	HIS	-	EXPRESSION TAG	UNP C4IEM5
A	288	HIS	-	EXPRESSION TAG	UNP C4IEM5
A	289	HIS	-	EXPRESSION TAG	UNP C4IEM5
A	290	HIS	-	EXPRESSION TAG	UNP C4IEM5
B	283	SER	-	EXPRESSION TAG	UNP C4IEM5
B	284	LYS	-	EXPRESSION TAG	UNP C4IEM5
B	285	HIS	-	EXPRESSION TAG	UNP C4IEM5
B	286	HIS	-	EXPRESSION TAG	UNP C4IEM5
B	287	HIS	-	EXPRESSION TAG	UNP C4IEM5
B	288	HIS	-	EXPRESSION TAG	UNP C4IEM5
B	289	HIS	-	EXPRESSION TAG	UNP C4IEM5
B	290	HIS	-	EXPRESSION TAG	UNP C4IEM5
C	283	SER	-	EXPRESSION TAG	UNP C4IEM5
C	284	LYS	-	EXPRESSION TAG	UNP C4IEM5
C	285	HIS	-	EXPRESSION TAG	UNP C4IEM5
C	286	HIS	-	EXPRESSION TAG	UNP C4IEM5
C	287	HIS	-	EXPRESSION TAG	UNP C4IEM5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	288	HIS	-	EXPRESSION TAG	UNP C4IEM5
C	289	HIS	-	EXPRESSION TAG	UNP C4IEM5
C	290	HIS	-	EXPRESSION TAG	UNP C4IEM5
D	283	SER	-	EXPRESSION TAG	UNP C4IEM5
D	284	LYS	-	EXPRESSION TAG	UNP C4IEM5
D	285	HIS	-	EXPRESSION TAG	UNP C4IEM5
D	286	HIS	-	EXPRESSION TAG	UNP C4IEM5
D	287	HIS	-	EXPRESSION TAG	UNP C4IEM5
D	288	HIS	-	EXPRESSION TAG	UNP C4IEM5
D	289	HIS	-	EXPRESSION TAG	UNP C4IEM5
D	290	HIS	-	EXPRESSION TAG	UNP C4IEM5

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

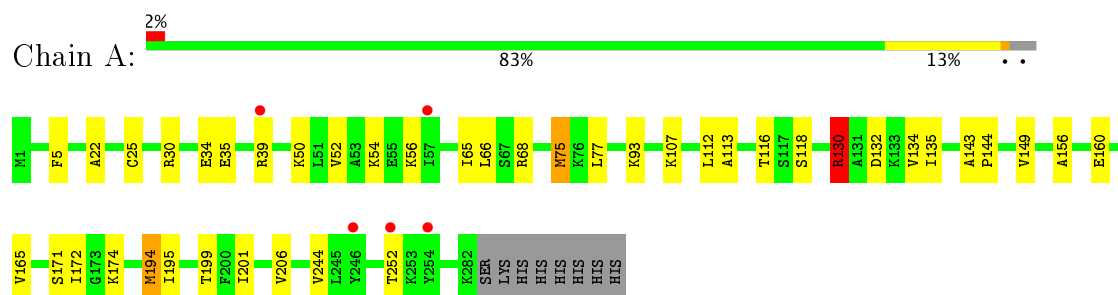


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	52	Total 52	O 52	0	0
3	B	57	Total 57	O 57	0	0
3	C	49	Total 49	O 49	0	0
3	D	60	Total 60	O 60	0	0

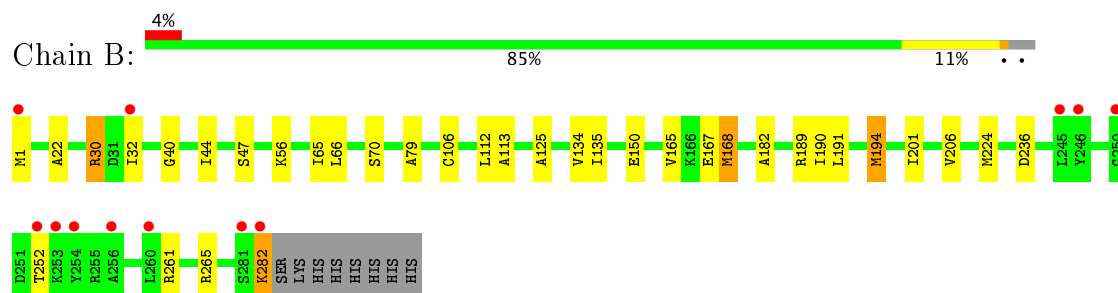
3 Residue-property plots [i](#)

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

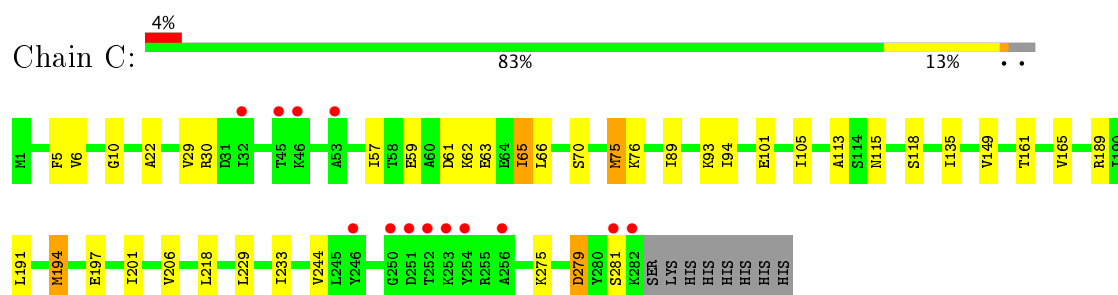
- Molecule 1: 3-hydroxybutyryl-CoA dehydrogenase



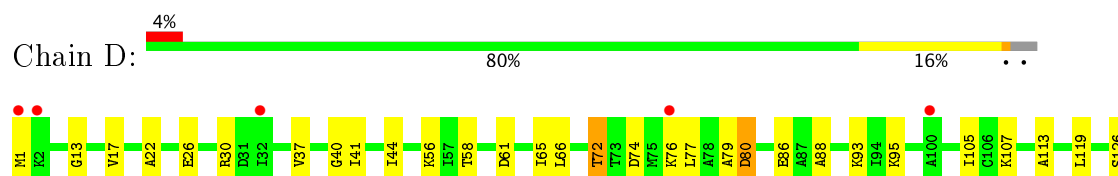
- Molecule 1: 3-hydroxybutyryl-CoA dehydrogenase

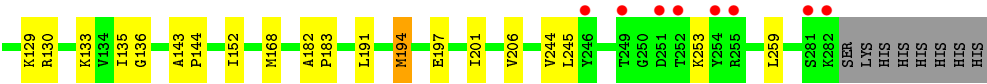


- Molecule 1: 3-hydroxybutyryl-CoA dehydrogenase



- Molecule 1: 3-hydroxybutyryl-CoA dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	148.45Å 148.45Å 201.63Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.81 – 2.30 43.77 – 2.30	Depositor EDS
% Data completeness (in resolution range)	89.4 (43.81-2.30) 89.4 (43.77-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 2.29Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.218 , 0.281 0.223 , 0.285	Depositor DCC
R_{free} test set	3331 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	43.3	Xtriage
Anisotropy	0.325	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.022 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8910	wwPDB-VP
Average B, all atoms (Å ²)	53.0	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 49.81 % 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 7.0794e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: NAD

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	0.87	0/2155	0.94	1/2901 (0.0%)
1	B	0.88	1/2155 (0.0%)	0.98	6/2901 (0.2%)
1	C	0.64	0/2155	0.79	0/2901
1	D	0.65	0/2155	0.79	1/2901 (0.0%)
All	All	0.77	1/8620 (0.0%)	0.88	8/11604 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	150	GLU	CD-OE2	5.44	1.31	1.25

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	265	ARG	NE-CZ-NH2	-8.89	115.86	120.30
1	A	130	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	B	236	ASP	CB-CG-OD1	6.06	123.75	118.30
1	D	182	ALA	C-N-CD	5.92	140.84	128.40
1	B	189	ARG	NE-CZ-NH1	-5.92	117.34	120.30
1	B	182	ALA	C-N-CD	5.78	140.53	128.40
1	B	265	ARG	NE-CZ-NH1	5.23	122.91	120.30
1	B	261	ARG	NE-CZ-NH1	5.07	122.84	120.30

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	2129	0	2211	23	0
1	B	2129	0	2211	21	0
1	C	2129	0	2211	26	0
1	D	2129	0	2211	28	0
2	A	44	0	26	1	0
2	B	44	0	26	0	0
2	C	44	0	26	2	0
2	D	44	0	26	1	0
3	A	52	0	0	1	0
3	B	57	0	0	1	0
3	C	49	0	0	0	0
3	D	60	0	0	2	0
All	All	8910	0	8948	88	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 5.

All (88) 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:B:22:ALA:HA	1:B:65:ILE:HD12	1.42	0.97
1:C:22:ALA:HA	1:C:65:ILE:HD13	1.55	0.89
1:D:22:ALA:HA	1:D:65:ILE:HD12	1.66	0.77
1:A:194:MET:HE2	1:B:194:MET:HE2	1.68	0.72
1:A:130:ARG:HG2	1:A:130:ARG:O	1.89	0.70
1:C:89:ILE:HD11	1:C:94:ILE:HD12	1.74	0.69
1:A:194:MET:HE2	1:B:194:MET:CE	2.23	0.68
1:D:80:ASP:O	1:D:107:LYS:NZ	2.27	0.68
1:C:22:ALA:HA	1:C:65:ILE:CD1	2.24	0.67
1:A:22:ALA:HA	1:A:65:ILE:HD12	1.79	0.65
1:B:113:ALA:HA	1:B:135:ILE:O	2.00	0.61
1:C:194:MET:HE2	1:D:194:MET:HE2	1.82	0.61
1:B:1:MET:SD	1:B:168:MET:HB2	2.42	0.60
1:B:22:ALA:HA	1:B:65:ILE:CD1	2.26	0.60
1:A:194:MET:HE1	1:B:194:MET:SD	2.45	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:LEU:HA	1:B:194:MET:HE3	1.88	0.56
1:A:194:MET:CE	1:B:194:MET:CE	2.83	0.55
1:D:79:ALA:CB	1:D:105:ILE:O	2.54	0.55
1:C:89:ILE:HG23	2:C:301:NAD:H8A	1.87	0.55
1:A:113:ALA:HA	1:A:135:ILE:O	2.07	0.55
1:A:195:ILE:O	1:A:199:THR:HG23	2.07	0.55
1:D:30:ARG:NH1	2:D:301:NAD:N1A	2.56	0.54
1:C:113:ALA:HA	1:C:135:ILE:O	2.09	0.53
1:D:72:THR:HG21	1:D:77:LEU:HD12	1.90	0.52
1:B:79:ALA:HA	1:B:106:CYS:HA	1.92	0.52
2:A:301:NAD:O7N	2:A:301:NAD:O1N	2.29	0.51
1:D:40:GLY:O	1:D:44:ILE:HG13	2.10	0.51
1:D:13:GLY:O	1:D:17:VAL:HG23	2.11	0.51
1:D:74:ASP:OD1	1:D:76:LYS:HG3	2.10	0.51
1:C:189:ARG:NE	1:D:197:GLU:OE2	2.37	0.50
1:C:118:SER:HB2	1:C:244:VAL:HG21	1.94	0.50
1:A:118:SER:HA	3:A:412:HOH:O	2.11	0.49
1:C:191:LEU:HA	1:C:194:MET:HE3	1.93	0.49
1:B:30:ARG:C	1:B:30:ARG:HD3	2.33	0.49
1:B:112:LEU:O	1:B:134:VAL:HA	2.13	0.48
1:A:194:MET:CE	1:B:194:MET:SD	3.01	0.48
1:C:62:LYS:HG2	1:C:66:LEU:CD2	2.43	0.48
1:D:183:PRO:HB2	1:D:245:LEU:HD23	1.96	0.48
1:C:161:THR:O	1:C:165:VAL:HG23	2.14	0.48
1:A:194:MET:HG3	1:B:190:ILE:CG2	2.43	0.48
1:B:135:ILE:HG21	1:B:165:VAL:HG21	1.96	0.48
1:C:194:MET:HE2	1:D:194:MET:CE	2.44	0.48
1:C:61:ASP:O	1:C:62:LYS:C	2.53	0.47
1:D:191:LEU:HA	1:D:194:MET:HE3	1.95	0.47
1:A:135:ILE:HG21	1:A:165:VAL:HG21	1.96	0.47
1:D:1:MET:HB2	1:D:168:MET:SD	2.54	0.47
1:D:259:LEU:C	1:D:259:LEU:HD23	2.35	0.47
1:C:201:ILE:HG23	1:C:206:VAL:HB	1.96	0.47
1:B:40:GLY:O	1:B:44:ILE:HG13	2.15	0.46
1:A:112:LEU:O	1:A:134:VAL:HA	2.16	0.46
1:A:118:SER:HB2	1:A:244:VAL:HG21	1.98	0.46
1:D:37:VAL:O	1:D:41:ILE:HG13	2.16	0.46
1:D:56:LYS:NZ	3:D:413:HOH:O	2.48	0.46
1:C:5:PHE:CZ	1:C:30:ARG:HB2	2.51	0.45
1:B:167:GLU:HB3	3:B:454:HOH:O	2.15	0.45
1:B:201:ILE:HG23	1:B:206:VAL:HB	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:LYS:HA	1:B:282:LYS:HD3	1.90	0.45
1:A:65:ILE:HD13	1:A:68:ARG:NH2	2.31	0.45
1:D:130:ARG:HG2	1:D:133:LYS:HB2	1.99	0.45
1:D:113:ALA:HA	1:D:135:ILE:O	2.17	0.44
1:C:115:ASN:O	2:C:301:NAD:H6N	2.17	0.44
1:C:275:LYS:NZ	1:C:279:ASP:OD1	2.50	0.44
1:D:201:ILE:HG23	1:D:206:VAL:HB	1.99	0.44
1:C:6:VAL:O	1:C:29:VAL:HA	2.18	0.44
1:D:58:THR:N	1:D:61:ASP:OD2	2.39	0.44
1:A:201:ILE:HG23	1:A:206:VAL:HB	1.98	0.43
1:C:76:LYS:HA	1:C:105:ILE:HD13	2.00	0.43
1:C:75:MET:HE3	1:C:101:GLU:HB3	1.99	0.43
1:C:194:MET:CE	1:D:194:MET:CE	2.96	0.43
1:A:172:ILE:HG13	1:A:174:LYS:HG2	2.00	0.43
1:A:25:CYS:O	1:A:68:ARG:HD2	2.19	0.43
1:A:65:ILE:HD13	1:A:68:ARG:HH21	1.83	0.43
1:B:135:ILE:HD13	1:B:165:VAL:HG21	1.99	0.43
1:A:5:PHE:CZ	1:A:30:ARG:HB2	2.54	0.42
1:C:197:GLU:OE1	1:D:253:LYS:HE2	2.19	0.42
1:B:125:ALA:HB2	1:B:134:VAL:HB	2.02	0.42
1:C:229:LEU:O	1:C:233:ILE:HG13	2.19	0.42
1:D:95:LYS:CE	1:D:119:LEU:HD12	2.49	0.42
1:D:143:ALA:N	1:D:144:PRO:CD	2.83	0.42
1:C:218:LEU:HA	1:C:218:LEU:HD23	1.82	0.42
1:C:59:GLU:HG3	1:C:63:GLU:OE1	2.20	0.42
1:A:143:ALA:N	1:A:144:PRO:CD	2.83	0.41
1:D:244:VAL:HG23	3:D:408:HOH:O	2.20	0.41
1:A:132:ASP:HA	1:A:156:ALA:O	2.20	0.41
1:C:57:ILE:HB	1:C:61:ASP:CB	2.51	0.41
1:D:86:GLU:OE2	1:D:88:ALA:N	2.51	0.41
1:A:116:THR:HG23	1:A:116:THR:O	2.21	0.40
1:D:136:GLY:HA3	1:D:152:ILE:HB	2.03	0.40

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	280/290 (97%)	269 (96%)	10 (4%)	1 (0%)	38	47
1	B	280/290 (97%)	270 (96%)	10 (4%)	0	100	100
1	C	280/290 (97%)	268 (96%)	11 (4%)	1 (0%)	38	47
1	D	280/290 (97%)	267 (95%)	13 (5%)	0	100	100
All	All	1120/1160 (97%)	1074 (96%)	44 (4%)	2 (0%)	51	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	75	MET
1	C	10	GLY

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	228/236 (97%)	210 (92%)	18 (8%)	14	18
1	B	228/236 (97%)	217 (95%)	11 (5%)	30	40
1	C	228/236 (97%)	220 (96%)	8 (4%)	41	56
1	D	228/236 (97%)	220 (96%)	8 (4%)	41	56
All	All	912/944 (97%)	867 (95%)	45 (5%)	29	39

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	GLU
1	A	35	GLU
1	A	39	ARG
1	A	50	LYS

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Mol	Chain	Res	Type
1	A	52	VAL
1	A	54	LYS
1	A	56	LYS
1	A	66	LEU
1	A	75	MET
1	A	77	LEU
1	A	93	LYS
1	A	107	LYS
1	A	130	ARG
1	A	149	VAL
1	A	160	GLU
1	A	171	SER
1	A	194	MET
1	A	252	THR
1	B	30	ARG
1	B	32	ILE
1	B	47	SER
1	B	56	LYS
1	B	66	LEU
1	B	70	SER
1	B	168	MET
1	B	194	MET
1	B	224	MET
1	B	252	THR
1	B	282	LYS
1	C	65	ILE
1	C	70	SER
1	C	75	MET
1	C	93	LYS
1	C	149	VAL
1	C	194	MET
1	C	279	ASP
1	C	281	SER
1	D	26	GLU
1	D	66	LEU
1	D	72	THR
1	D	80	ASP
1	D	93	LYS
1	D	126	SER
1	D	129	LYS
1	D	194	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no

such sidechains identified.

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 ⓘ

4 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	NAD	A	301	-	41,48,48	1.23	4 (9%)	43,73,73	2.27	11 (25%)
2	NAD	B	301	-	41,48,48	1.13	3 (7%)	43,73,73	2.32	12 (27%)
2	NAD	C	301	-	41,48,48	0.98	2 (4%)	43,73,73	2.10	10 (23%)
2	NAD	D	301	-	41,48,48	1.13	2 (4%)	43,73,73	1.81	9 (20%)

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	301	-	-	0/22/62/62	0/5/5/5
2	NAD	B	301	-	-	0/22/62/62	0/5/5/5
2	NAD	C	301	-	-	0/22/62/62	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	D	301	-	-	0/22/62/62	0/5/5/5

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	NAD	C2B-C1B	-2.69	1.49	1.53
2	C	301	NAD	C2A-N3A	2.16	1.35	1.32
2	A	301	NAD	C2A-N3A	2.42	1.36	1.32
2	B	301	NAD	C5A-C4A	2.67	1.46	1.40
2	A	301	NAD	C5A-C4A	2.74	1.46	1.40
2	A	301	NAD	C4A-N3A	2.91	1.39	1.35
2	C	301	NAD	C5A-C4A	3.00	1.47	1.40
2	D	301	NAD	C5A-C4A	3.25	1.47	1.40
2	D	301	NAD	O4D-C1D	3.53	1.46	1.41
2	A	301	NAD	O4D-C1D	3.72	1.46	1.41
2	B	301	NAD	O4D-C1D	4.11	1.46	1.41

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	NAD	N3A-C2A-N1A	-10.22	119.96	128.86
2	B	301	NAD	N3A-C2A-N1A	-9.76	120.36	128.86
2	C	301	NAD	N3A-C2A-N1A	-8.72	121.26	128.86
2	D	301	NAD	N3A-C2A-N1A	-7.82	122.05	128.86
2	A	301	NAD	C1B-N9A-C4A	-5.04	117.93	126.64
2	C	301	NAD	C4B-O4B-C1B	-4.84	104.62	109.77
2	B	301	NAD	C1B-N9A-C4A	-4.52	118.82	126.64
2	D	301	NAD	C1B-N9A-C4A	-3.99	119.75	126.64
2	C	301	NAD	C1B-N9A-C4A	-3.82	120.04	126.64
2	B	301	NAD	O7N-C7N-C3N	-3.72	115.27	119.62
2	D	301	NAD	C4B-O4B-C1B	-3.48	106.07	109.77
2	A	301	NAD	C4B-O4B-C1B	-3.42	106.13	109.77
2	B	301	NAD	O3D-C3D-C4D	-3.35	101.32	111.09
2	A	301	NAD	O7N-C7N-N7N	-3.17	118.07	122.58
2	B	301	NAD	C5N-C4N-C3N	-2.93	116.90	120.35
2	A	301	NAD	C5A-C6A-N6A	-2.69	114.99	120.47
2	A	301	NAD	O3D-C3D-C4D	-2.62	103.44	111.09
2	D	301	NAD	O7N-C7N-N7N	-2.60	118.88	122.58
2	C	301	NAD	O7N-C7N-N7N	-2.56	118.94	122.58
2	C	301	NAD	O3D-C3D-C4D	-2.38	104.13	111.09
2	C	301	NAD	C5A-C6A-N6A	-2.37	115.65	120.47
2	D	301	NAD	C4A-C5A-N7A	-2.34	107.15	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	NAD	O3D-C3D-C4D	-2.03	105.16	111.09
2	B	301	NAD	O2N-PN-O1N	2.01	122.70	112.28
2	D	301	NAD	C3N-C7N-N7N	2.03	120.09	117.77
2	B	301	NAD	O2A-PA-O1A	2.10	123.15	112.28
2	C	301	NAD	O2A-PA-O1A	2.11	123.22	112.28
2	B	301	NAD	C4D-O4D-C1D	2.12	112.03	109.77
2	D	301	NAD	O2A-PA-O1A	2.22	123.78	112.28
2	D	301	NAD	C2A-N1A-C6A	2.26	122.73	118.77
2	A	301	NAD	O2A-PA-O1A	2.34	124.37	112.28
2	A	301	NAD	C2A-N1A-C6A	2.35	122.88	118.77
2	A	301	NAD	C2D-C3D-C4D	2.37	107.23	102.62
2	B	301	NAD	N6A-C6A-N1A	2.48	123.69	118.77
2	C	301	NAD	C2A-N1A-C6A	2.52	123.18	118.77
2	B	301	NAD	C2D-C3D-C4D	2.76	107.99	102.62
2	A	301	NAD	O7N-C7N-C3N	2.81	122.91	119.62
2	A	301	NAD	N6A-C6A-N1A	2.81	124.33	118.77
2	C	301	NAD	C3N-C7N-N7N	3.04	121.25	117.77
2	B	301	NAD	C2N-C3N-C4N	3.43	122.18	118.26
2	C	301	NAD	N6A-C6A-N1A	3.47	125.65	118.77
2	B	301	NAD	C2A-N1A-C6A	3.74	125.31	118.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	NAD	1	0
2	C	301	NAD	2	0
2	D	301	NAD	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, 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	282/290 (97%)	-0.02	5 (1%) 69 74	26, 43, 81, 99	0
1	B	282/290 (97%)	0.09	12 (4%) 36 43	29, 43, 67, 100	0
1	C	282/290 (97%)	0.10	13 (4%) 33 40	41, 57, 81, 97	0
1	D	282/290 (97%)	0.09	13 (4%) 33 40	43, 58, 80, 100	0
All	All	1128/1160 (97%)	0.07	43 (3%) 41 48	26, 52, 80, 100	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	32	ILE	5.1
1	C	281	SER	3.9
1	C	252	THR	3.8
1	B	281	SER	3.8
1	C	246	TYR	3.7
1	C	32	ILE	3.7
1	D	281	SER	3.6
1	D	1	MET	3.5
1	B	282	LYS	3.4
1	C	46	LYS	3.2
1	B	246	TYR	3.1
1	D	282	LYS	3.1
1	A	39	ARG	3.1
1	C	53	ALA	3.0
1	C	256	ALA	2.9
1	B	32	ILE	2.8
1	C	250	GLY	2.8
1	D	254	TYR	2.8
1	A	254	TYR	2.7
1	B	254	TYR	2.7
1	B	1	MET	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	254	TYR	2.7
1	D	100	ALA	2.6
1	B	253	LYS	2.6
1	D	252	THR	2.5
1	A	252	THR	2.5
1	B	252	THR	2.5
1	D	2	LYS	2.5
1	B	250	GLY	2.5
1	D	246	TYR	2.5
1	A	246	TYR	2.4
1	C	253	LYS	2.4
1	D	76	LYS	2.3
1	B	245	LEU	2.2
1	B	256	ALA	2.2
1	A	57	ILE	2.2
1	C	282	LYS	2.1
1	C	251	ASP	2.1
1	B	260	LEU	2.1
1	D	251	ASP	2.1
1	D	249	THR	2.1
1	D	255	ARG	2.1
1	C	45	THR	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, 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
2	NAD	C	301	44/44	0.92	0.15	0.07	59,72,81,83	0
2	NAD	D	301	44/44	0.91	0.14	-0.08	61,76,82,85	0
2	NAD	B	301	44/44	0.92	0.13	-0.21	41,53,63,73	0
2	NAD	A	301	44/44	0.95	0.12	-0.33	44,54,63,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.