



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:29 AM GMT

PDB ID : 2HCT
Title : Acidic residues at the active sites of CD38 and ADP-ribosyl cyclase determine NAAPD synthesis and hydrolysis activities
Authors : Liu, Q.; Kriksunov, I.A.; Hao, Q.; Graeff, R.; Lee, H.C.
Deposited on : 2006-06-18
Resolution : 1.95 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 (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

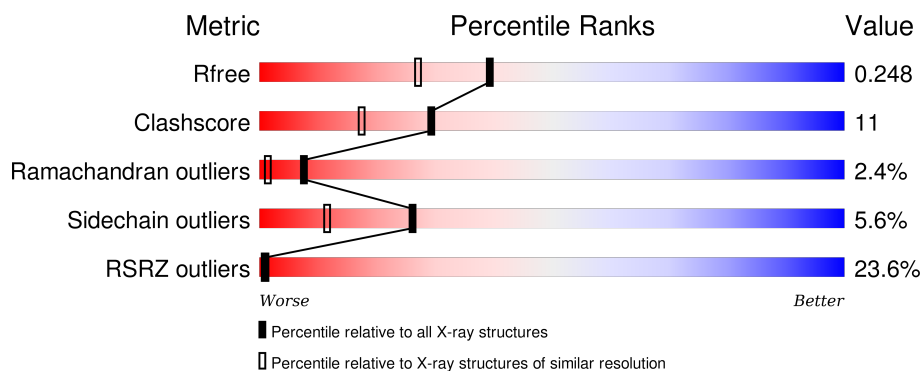
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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	262	
1	B	262	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4307 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.

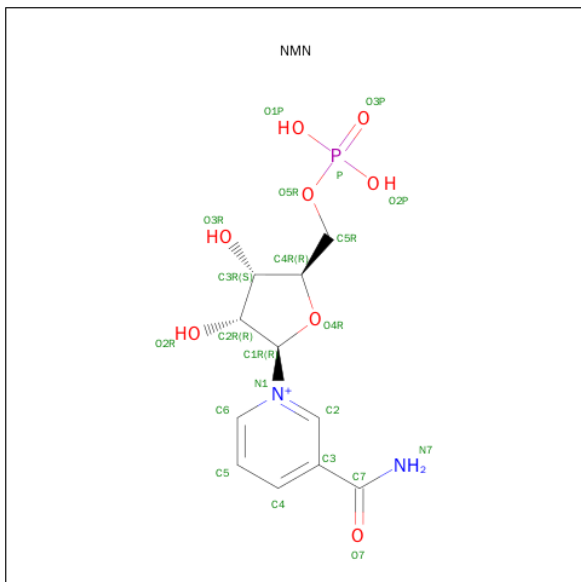
- Molecule 1 is a protein called ADP-ribosyl cyclase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2003	1263	351	373	16			
1	B	252	Total	C	N	O	S	0	0	0
			2003	1263	351	373	16			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	LYS	-	CLONING ARTIFACT	UNP P28907
A	40	ARG	-	CLONING ARTIFACT	UNP P28907
A	41	GLU	-	CLONING ARTIFACT	UNP P28907
A	42	ALA	-	CLONING ARTIFACT	UNP P28907
A	43	GLU	-	CLONING ARTIFACT	UNP P28907
A	44	ALA	-	CLONING ARTIFACT	UNP P28907
A	49	THR	-	ENGINEERED	UNP P28907
A	100	ASP	ASN	ENGINEERED	UNP P28907
A	164	ASP	ASN	ENGINEERED	UNP P28907
A	209	ASP	ASN	ENGINEERED	UNP P28907
A	219	ASP	ASN	ENGINEERED	UNP P28907
A	226	GLY	GLU	ENGINEERED	UNP P28907
B	39	LYS	-	CLONING ARTIFACT	UNP P28907
B	40	ARG	-	CLONING ARTIFACT	UNP P28907
B	41	GLU	-	CLONING ARTIFACT	UNP P28907
B	42	ALA	-	CLONING ARTIFACT	UNP P28907
B	43	GLU	-	CLONING ARTIFACT	UNP P28907
B	44	ALA	-	CLONING ARTIFACT	UNP P28907
B	49	THR	GLN	ENGINEERED	UNP P28907
B	100	ASP	ASN	ENGINEERED	UNP P28907
B	164	ASP	ASN	ENGINEERED	UNP P28907
B	209	ASP	ASN	ENGINEERED	UNP P28907
B	219	ASP	ASN	ENGINEERED	UNP P28907
B	226	GLY	GLU	ENGINEERED	UNP P28907

- Molecule 2 is BETA-NICOTINAMIDE RIBOSE MONOPHOSPHATE (three-letter code: NMN) (formula: $C_{11}H_{16}N_2O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	11	2	8	1		
2	B	1	Total	C	N	O	P	0	0
			22	11	2	8	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	142	Total	O	0	0
			142	142		
3	B	115	Total	O	0	0
			115	115		

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.

Chain A:

17% 76% 18%

LYS ARG GLU ALA GLU ALA R45 W46 R47 Q49 R58 F59 P60 V68 K69 I73 H79 V80 W86 F89 K90 T102 E103 E104 D105 Y106 Q107 M110 Q115 T116 C119 L123 L124 W125 S126 R127 D130 L131 A132 H133 Q134 Q137 V138 Q139 R140 D141 V142 F143 T144 L145 E146 L149 L150 A154 E162 F163 D164 T165 S166 K167 L168 Q171 D175 K178 D179 C180 M183 S186 V187 F188 W189 V192 S193 R194 F195 F196 V204 H205 V206 R212 S213 F222 V225 G226 V227 L230 Q236 T237 L238 G245 S246 R247 E248 D249 S250 R251 K268 R269 N270 Q286 N290 P291 E292 D293 S294 S295 C296 THR SER GLU ILE

Chain B:

29% 68% 26%

Lys ARG GLU ALA GLU ALA R46 R47 K69 I73 F89 P98 E103 E104 Q115 K121 I122 L123 W125 I126 R127 I128 K129 D130 L131 Q134 V138 Q139 R140 D141 M142 F143 T144 L145 T148 L149 G151 Y152 L153 A154 D155 M159 G161 G160 E162 F163

D164 T165 S166 K167 W176 R177 C180 S181 N182 M183 S186 M189 K190 T191 V192 S193 R194 I195 F196 A197 E198 D202 V203 V204 H205 V206 M207 D208 L209 G210 S211 R212 S213 K214 T215 F216 D217 K218 D219 F222 N229 L230 K234 V235 Q236 T237 L238 F242 V241 W242 T243

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	41.72Å 52.82Å 65.58Å 106.26° 91.85° 95.25°	Depositor
Resolution (Å)	20.00 – 1.95 30.12 – 1.95	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-1.95) 87.7 (30.12-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.195 , 0.248 0.196 , 0.248	Depositor DCC
R_{free} test set	1856 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.6	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	0 of 37215 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4307	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.98% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NMN

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	0.66	0/2053	0.69	0/2778
1	B	0.73	4/2053 (0.2%)	0.66	0/2778
All	All	0.70	4/4106 (0.1%)	0.68	0/5556

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	B	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	296	CYS	C-O	9.61	1.41	1.23
1	B	283	LYS	CE-NZ	8.13	1.69	1.49
1	B	214	LYS	CE-NZ	6.35	1.65	1.49
1	B	283	LYS	CD-CE	6.25	1.66	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	164	ASP	Peptide

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	2003	0	1914	50	0
1	B	2003	0	1914	41	0
2	A	22	0	14	2	0
2	B	22	0	14	1	0
3	A	142	0	0	9	0
3	B	115	0	0	8	0
All	All	4307	0	3856	89	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 11.

All (89) 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:283:LYS:CE	1:B:283:LYS:NZ	1.69	1.53
1:B:266:ILE:HD11	1:B:273:PHE:HB2	1.26	1.16
1:A:103:GLU:OE1	1:A:194:ARG:NH2	1.77	1.14
1:A:268:LYS:HG2	3:B:409:HOH:O	1.65	0.97
1:A:250:SER:HB2	1:A:251:ARG:NH1	1.81	0.96
1:A:103:GLU:CD	1:A:194:ARG:HH22	1.72	0.92
1:A:115:GLN:HE22	1:A:149:LEU:H	1.16	0.90
1:A:268:LYS:CG	3:B:409:HOH:O	2.22	0.86
1:B:115:GLN:HE22	1:B:149:LEU:H	1.23	0.84
1:A:140:ARG:HG2	1:A:140:ARG:O	1.76	0.83
1:A:268:LYS:HD3	3:A:343:HOH:O	1.79	0.83
1:B:230:LEU:O	1:B:269:ARG:NH1	2.11	0.82
1:A:141:ASP:HB3	3:A:432:HOH:O	1.81	0.78
1:A:250:SER:HB2	1:A:251:ARG:HH12	1.48	0.78
1:A:142:MET:N	3:A:432:HOH:O	2.20	0.74
1:A:165:THR:HG23	1:A:167:LYS:H	1.53	0.74
1:A:162:GLU:HB2	1:A:165:THR:HG22	1.71	0.71
1:A:268:LYS:HD2	1:A:268:LYS:O	1.93	0.69
1:B:176:TRP:CZ3	1:B:181:SER:HB2	2.29	0.67
1:B:279:TYR:O	1:B:281:PRO:HD3	1.97	0.65
1:A:139:GLN:C	1:A:141:ASP:H	2.00	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:ARG:HA	3:A:415:HOH:O	1.99	0.63
1:A:110:MET:HE1	1:A:150:LEU:HD13	1.81	0.62
1:B:194:ARG:HG3	1:B:229:ASN:ND2	2.14	0.62
1:B:165:THR:HG23	1:B:167:LYS:H	1.66	0.60
1:B:266:ILE:HD11	1:B:273:PHE:CB	2.16	0.60
1:A:268:LYS:CD	3:A:343:HOH:O	2.44	0.58
1:B:183:ASN:ND2	1:B:186:SER:H	2.02	0.58
1:A:140:ARG:N	3:A:428:HOH:O	2.35	0.57
1:A:268:LYS:CE	3:B:409:HOH:O	2.52	0.57
1:A:268:LYS:CD	1:A:268:LYS:O	2.52	0.57
1:B:162:GLU:HB2	1:B:165:THR:HG22	1.85	0.57
1:A:130:ASP:O	1:A:134:GLN:HG3	2.06	0.56
1:B:69:LYS:HE2	1:B:73:ILE:HD11	1.87	0.56
1:A:133:HIS:O	1:A:137:GLN:HG2	2.07	0.55
1:B:103:GLU:HG2	1:B:191:THR:OG1	2.06	0.55
1:B:180:CYS:HB2	3:B:320:HOH:O	2.06	0.55
1:A:59:PHE:HB3	1:A:60:PRO:HD3	1.88	0.54
1:B:161:GLY:C	1:B:162:GLU:HG3	2.27	0.54
1:A:165:THR:HG21	1:A:167:LYS:HB2	1.89	0.54
1:A:183:ASN:ND2	1:A:186:SER:H	2.06	0.54
1:B:255:GLN:HA	1:B:255:GLN:HE21	1.73	0.53
1:B:194:ARG:O	1:B:198:GLU:HG3	2.09	0.52
1:B:202:ASP:HB3	3:B:324:HOH:O	2.09	0.51
1:B:250:SER:HB2	1:B:251:ARG:HE	1.75	0.51
1:A:138:VAL:HA	3:A:340:HOH:O	2.11	0.51
1:A:102:THR:HG22	1:B:177:ARG:NH2	2.26	0.50
1:A:268:LYS:HE2	3:B:409:HOH:O	2.10	0.50
1:B:129:LYS:NZ	1:B:155:ASP:OD2	2.34	0.50
1:A:139:GLN:C	1:A:141:ASP:N	2.65	0.49
1:B:194:ARG:HB3	1:B:194:ARG:NH1	2.27	0.49
1:B:212:ARG:C	1:B:214:LYS:H	2.16	0.49
1:A:139:GLN:O	1:A:141:ASP:N	2.47	0.48
1:A:250:SER:CB	1:A:251:ARG:HH12	2.23	0.48
1:A:115:GLN:NE2	1:A:149:LEU:H	1.98	0.48
1:A:269:ARG:O	1:A:270:ASN:HB2	2.13	0.48
1:B:284:PHE:O	1:B:288:VAL:HG23	2.14	0.47
1:A:125:TRP:CZ2	2:A:301:NMN:H2RC	2.50	0.47
1:A:236:GLN:HG3	1:A:237:THR:OG1	2.15	0.46
1:A:106:TYR:O	1:A:110:MET:HG2	2.14	0.46
1:B:98:PRO:O	1:B:183:ASN:HA	2.14	0.46
1:B:177:ARG:HD2	3:B:375:HOH:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:CYS:HB3	3:A:384:HOH:O	2.15	0.46
1:B:250:SER:C	1:B:251:ARG:HG3	2.36	0.46
1:A:180:CYS:HB2	3:A:327:HOH:O	2.17	0.45
1:A:165:THR:CG2	1:A:167:LYS:HB2	2.46	0.45
1:B:183:ASN:HD21	1:B:186:SER:H	1.65	0.45
1:B:211:SER:O	1:B:212:ARG:HB2	2.17	0.45
1:A:110:MET:HE1	1:A:192:VAL:HG12	1.98	0.45
1:B:145:LEU:HD21	1:B:192:VAL:HG23	1.99	0.44
1:B:208:LEU:O	1:B:243:ILE:HG12	2.18	0.44
1:B:241:TRP:HB3	1:B:278:ILE:CD1	2.49	0.43
1:A:115:GLN:HE22	1:A:149:LEU:N	1.99	0.42
1:B:145:LEU:HB3	2:B:302:NMN:O2R	2.19	0.42
1:B:104:GLU:HG3	3:B:380:HOH:O	2.19	0.42
1:A:102:THR:O	1:A:105:ASP:HB2	2.19	0.42
1:A:146:GLU:OE2	2:A:301:NMN:HC2	2.20	0.42
1:B:256:ASP:HA	1:B:257:PRO:HD2	1.84	0.42
1:B:127:ARG:O	1:B:209:ASP:HB2	2.20	0.42
1:A:175:ASP:OD1	1:A:178:LYS:HG3	2.20	0.41
1:A:102:THR:CG2	1:B:177:ARG:HH21	2.34	0.41
1:A:86:TRP:CE2	1:A:90:LYS:HG3	2.56	0.41
1:B:130:ASP:O	1:B:134:GLN:HG3	2.20	0.41
1:A:286:GLN:NE2	1:A:286:GLN:HA	2.36	0.41
1:B:205:HIS:HA	1:B:239:GLU:O	2.21	0.41
1:B:266:ILE:HD12	1:B:271:ILE:O	2.21	0.40
1:B:121:LYS:HB3	1:B:141:ASP:O	2.22	0.40
1:A:48:GLN:OE1	1:A:171:GLN:HB3	2.22	0.40
1:A:69:LYS:O	1:A:73:ILE:HG12	2.22	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	250/262 (95%)	234 (94%)	12 (5%)	4 (2%)	12	3
1	B	250/262 (95%)	230 (92%)	12 (5%)	8 (3%)	5	1
All	All	500/524 (95%)	464 (93%)	24 (5%)	12 (2%)	7	1

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	248	GLU
1	B	128	ILE
1	B	212	ARG
1	B	251	ARG
1	B	293	ASP
1	B	294	SER
1	B	252	ASP
1	A	140	ARG
1	A	247	ARG
1	A	294	SER
1	B	213	SER
1	B	248	GLU

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	222/240 (92%)	213 (96%)	9 (4%)	37	22
1	B	222/240 (92%)	206 (93%)	16 (7%)	18	6
All	All	444/480 (92%)	419 (94%)	25 (6%)	26	11

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	PHE
1	A	116	THR
1	A	127	ARG
1	A	131	LEU

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Mol	Chain	Res	Type
1	A	141	ASP
1	A	164	ASP
1	A	183	ASN
1	A	236	GLN
1	A	268	LYS
1	B	47	ARG
1	B	89	PHE
1	B	131	LEU
1	B	140	ARG
1	B	177	ARG
1	B	213	SER
1	B	214	LYS
1	B	218	LYS
1	B	234	LYS
1	B	242	VAL
1	B	251	ARG
1	B	255	GLN
1	B	258	THR
1	B	264	SER
1	B	283	LYS
1	B	289	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	GLN
1	A	183	ASN
1	A	244	HIS
1	A	270	ASN
1	A	286	GLN
1	B	115	GLN
1	B	183	ASN
1	B	205	HIS
1	B	229	ASN
1	B	255	GLN
1	B	270	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	NMN	A	301	-	20,23,23	0.96	1 (5%)	26,34,34	1.23	3 (11%)
2	NMN	B	302	-	20,23,23	0.78	1 (5%)	26,34,34	1.18	2 (7%)

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	NMN	A	301	-	-	0/10/30/30	0/2/2/2
2	NMN	B	302	-	-	0/10/30/30	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	NMN	O4R-C1R	2.07	1.43	1.41
2	B	302	NMN	O4R-C1R	2.19	1.44	1.41

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	NMN	O5R-P-O3P	-2.26	101.40	107.14
2	B	302	NMN	O5R-P-O3P	-2.25	101.42	107.14
2	A	301	NMN	O7-C7-C3	2.10	121.88	119.59
2	A	301	NMN	C4R-O4R-C1R	2.11	112.04	109.72
2	B	302	NMN	O4R-C1R-N1	2.70	111.10	108.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	NMN	2	0
2	B	302	NMN	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	252/262 (96%)	1.09	44 (17%) 2 3	35, 42, 56, 62	0
1	B	252/262 (96%)	1.58	75 (29%) 1 0	31, 44, 60, 70	0
All	All	504/524 (96%)	1.34	119 (23%) 1 1	31, 43, 58, 70	0

All (119) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	249	ASP	14.4
1	B	246	GLY	13.0
1	B	213	SER	10.7
1	B	296	CYS	8.5
1	B	211	SER	7.1
1	B	292	GLU	6.7
1	B	212	ARG	6.1
1	B	124	LEU	6.1
1	B	294	SER	6.0
1	B	295	SER	5.8
1	B	288	VAL	5.6
1	A	246	GLY	5.5
1	B	293	ASP	5.1
1	A	124	LEU	5.1
1	B	216	PHE	5.0
1	A	245	GLY	4.8
1	A	47	ARG	4.8
1	B	250	SER	4.7
1	B	123	LEU	4.7
1	B	215	ILE	4.7
1	B	287	CYS	4.7
1	A	212	ARG	4.6
1	A	291	PRO	4.6
1	B	208	LEU	4.5

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Mol	Chain	Res	Type	RSRZ
1	B	282	ASP	4.5
1	B	214	LYS	4.5
1	A	213	SER	4.5
1	B	222	PHE	4.4
1	B	145	LEU	4.1
1	B	176	TRP	4.1
1	B	245	GLY	4.0
1	B	257	PRO	4.0
1	A	123	LEU	4.0
1	A	79	HIS	4.0
1	A	145	LEU	3.9
1	B	247	ARG	3.9
1	B	206	VAL	3.8
1	B	150	LEU	3.7
1	B	127	ARG	3.7
1	B	259	ILE	3.7
1	A	189	TRP	3.7
1	B	219	ASP	3.6
1	B	289	LYS	3.6
1	B	253	LEU	3.5
1	B	204	VAL	3.5
1	B	279	TYR	3.5
1	B	266	ILE	3.4
1	A	294	SER	3.4
1	A	196	PHE	3.3
1	B	144	THR	3.3
1	A	164	ASP	3.3
1	B	149	LEU	3.3
1	A	293	ASP	3.3
1	B	238	LEU	3.3
1	A	165	THR	3.2
1	A	68	VAL	3.2
1	B	138	VAL	3.2
1	B	218	LYS	3.2
1	B	256	ASP	3.1
1	A	107	GLN	3.1
1	B	89	PHE	3.1
1	B	240	ALA	3.1
1	B	189	TRP	3.1
1	A	144	THR	3.0
1	B	125	TRP	3.0
1	B	122	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	58	ARG	2.9
1	A	227	VAL	2.9
1	B	262	LEU	2.9
1	A	206	VAL	2.9
1	B	192	VAL	2.9
1	A	192	VAL	2.8
1	A	143	PHE	2.7
1	B	285	LEU	2.7
1	A	141	ASP	2.7
1	B	205	HIS	2.7
1	A	193	SER	2.7
1	B	148	THR	2.6
1	A	238	LEU	2.6
1	B	153	LEU	2.6
1	B	248	GLU	2.6
1	B	278	ILE	2.6
1	A	296	CYS	2.6
1	B	255	GLN	2.6
1	B	252	ASP	2.5
1	A	222	PHE	2.5
1	B	243	ILE	2.5
1	B	196	PHE	2.5
1	B	143	PHE	2.5
1	B	141	ASP	2.5
1	A	142	MET	2.4
1	A	80	VAL	2.4
1	A	188	PHE	2.4
1	A	226	GLY	2.3
1	B	244	HIS	2.3
1	A	168	ILE	2.3
1	B	197	ALA	2.3
1	B	177	ARG	2.3
1	B	130	ASP	2.3
1	B	151	GLY	2.3
1	B	290	ASN	2.2
1	A	125	TRP	2.2
1	B	273	PHE	2.2
1	B	249	ASP	2.2
1	B	236	GLN	2.2
1	A	45	ARG	2.2
1	A	290	ASN	2.2
1	A	204	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	292	GLU	2.2
1	A	59	PHE	2.1
1	B	271	ILE	2.1
1	A	225	VAL	2.1
1	A	154	ALA	2.1
1	B	193	SER	2.1
1	B	163	PHE	2.1
1	B	291	PRO	2.1
1	B	251	ARG	2.0
1	B	159	TRP	2.0
1	A	230	LEU	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(Å ²)	Q<0.9
2	NMN	A	301	22/22	0.86	0.15	-0.69	45,58,60,61	0
2	NMN	B	302	22/22	0.86	0.14	-1.08	44,53,66,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.