



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:58 AM GMT

PDB ID : 3KEQ
Title : Crystal structure of a Rex-family transcriptional regulatory protein from *Streptococcus agalactiae* complexed with NAD⁺
Authors : Thiagarajan, S.; Logan, D.; von Wachenfeldt, C.
Deposited on : 2009-10-26
Resolution : 2.40 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

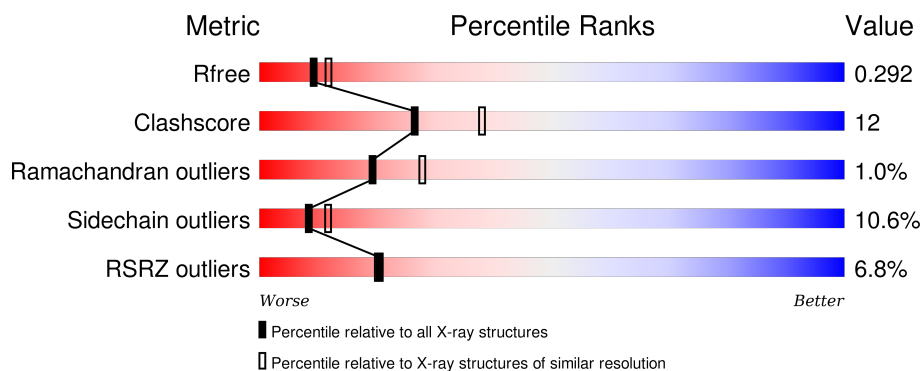
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	212	<div> <div>8%</div> <div> <div></div> <div>71%</div> <div>18%</div> <div>•</div> <div>8%</div> </div> </div>
1	B	212	<div> <div>5%</div> <div> <div></div> <div>72%</div> <div>21%</div> <div>•</div> <div>•</div> </div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3250 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 Redox-sensing transcriptional repressor rex.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	196	Total	C	N	O	S	80	0	0
			1541	984	255	296	6			
1	B	204	Total	C	N	O	S	50	0	0
			1606	1023	272	305	6			

- 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		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	31	Total	O	0	0
			31	31		

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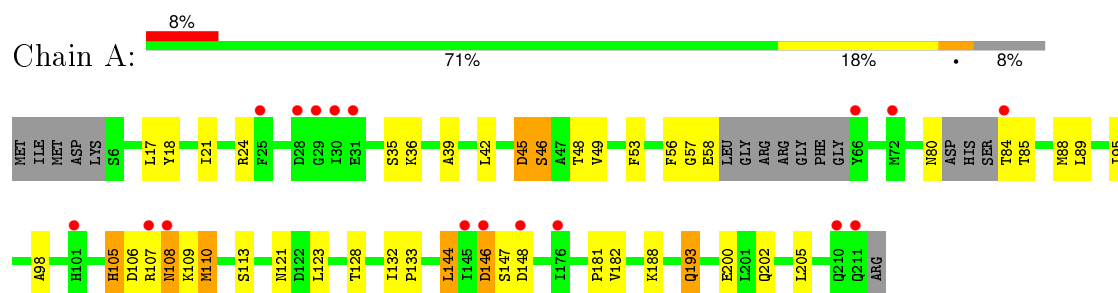
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	28	Total	O	0	0
			28	28		

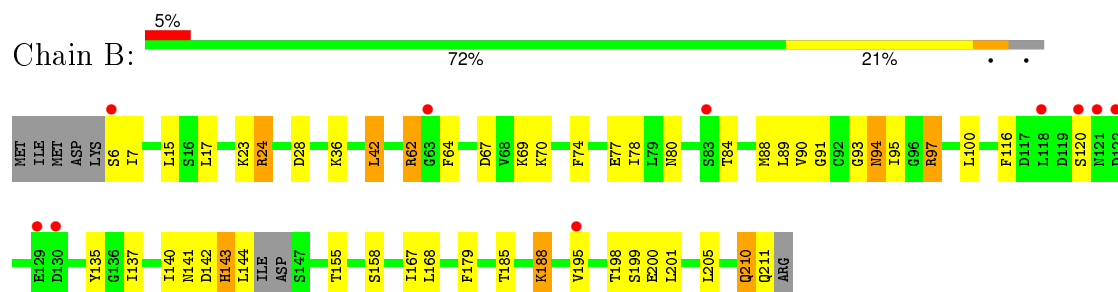
3 Residue-property plots [i](#)

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: Redox-sensing transcriptional repressor rex



- Molecule 1: Redox-sensing transcriptional repressor rex



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.67Å 71.47Å 113.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.47 – 2.40 28.47 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (28.47-2.40) 99.4 (28.47-2.40)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.223 , 0.292 0.229 , 0.292	Depositor DCC
R_{free} test set	977 reflections (5.45%)	DCC
Wilson B-factor (Å ²)	54.8	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 18935 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3250	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% 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: 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	0.81	1/1565 (0.1%)	0.83	0/2115
1	B	0.82	1/1633 (0.1%)	0.90	6/2204 (0.3%)
All	All	0.81	2/3198 (0.1%)	0.87	6/4319 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	142	ASP	CA-CB	5.92	1.67	1.53
1	A	200	GLU	CB-CG	-5.90	1.41	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	24	ARG	NE-CZ-NH1	-10.13	115.23	120.30
1	B	24	ARG	NE-CZ-NH2	5.74	123.17	120.30
1	B	77	GLU	CG-CD-OE1	5.65	129.59	118.30
1	B	62	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	B	77	GLU	CB-CA-C	5.42	121.23	110.40
1	B	188	LYS	CA-CB-CG	5.08	124.58	113.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1541	0	1546	45	0
1	B	1606	0	1614	38	0
2	A	44	0	26	8	0
3	A	31	0	0	0	0
3	B	28	0	0	0	0
All	All	3250	0	3186	74	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 12.

All (74) 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:17:LEU:HD22	1:B:42:LEU:HD11	1.38	1.02
1:A:21:ILE:HD11	1:A:42:LEU:HD21	1.55	0.88
1:A:21:ILE:CD1	1:A:42:LEU:HD21	2.05	0.85
1:A:18:TYR:HA	1:A:21:ILE:HD12	1.60	0.82
1:A:45:ASP:O	1:A:48:THR:HG22	1.80	0.82
1:A:88:MET:HE1	1:A:144:LEU:CD2	2.10	0.80
1:A:110:MET:CE	1:B:205:LEU:HD22	2.10	0.80
1:A:95:ILE:CD1	2:A:213:NAD:H2N	2.11	0.79
1:A:88:MET:CE	1:A:144:LEU:HD21	2.13	0.79
1:A:88:MET:HE1	1:A:144:LEU:HD21	1.64	0.78
1:A:95:ILE:HD11	2:A:213:NAD:H2N	1.65	0.77
1:A:95:ILE:HD11	2:A:213:NAD:C7N	2.15	0.77
1:B:17:LEU:HD22	1:B:42:LEU:CD1	2.16	0.74
1:A:45:ASP:O	1:A:48:THR:CG2	2.36	0.73
1:A:95:ILE:HD11	2:A:213:NAD:N7N	2.04	0.73
1:A:181:PRO:O	1:B:23:LYS:NZ	2.21	0.72
1:A:95:ILE:HD11	2:A:213:NAD:C2N	2.19	0.72
1:B:90:VAL:HG21	1:B:168:LEU:HD21	1.73	0.71
1:A:110:MET:HE3	1:B:205:LEU:HD22	1.73	0.70
1:A:84:THR:HG22	1:A:84:THR:O	1.91	0.70
1:B:24:ARG:HD2	1:B:28:ASP:OD2	1.91	0.69
1:A:105:HIS:HB3	1:A:108:ASN:HA	1.76	0.68
1:A:110:MET:HE1	1:B:205:LEU:HD22	1.76	0.67
1:A:39:ALA:HB2	1:A:46:SER:HA	1.78	0.64
1:B:135:TYR:CE2	1:B:143:HIS:CE1	2.87	0.62
1:A:110:MET:HE2	1:B:201:LEU:HB3	1.80	0.62
1:B:140:ILE:HG21	1:B:167:ILE:HG21	1.82	0.60
1:B:140:ILE:HG21	1:B:167:ILE:CG2	2.33	0.59
1:A:110:MET:CE	1:B:201:LEU:HB3	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:17:LEU:CD2	1:B:42:LEU:HD11	2.22	0.58
1:A:95:ILE:HD13	2:A:213:NAD:H2N	1.85	0.57
1:A:21:ILE:HD11	1:A:42:LEU:CD2	2.33	0.57
1:B:89:LEU:HD23	1:B:100:LEU:HD13	1.87	0.57
1:A:95:ILE:HD11	2:A:213:NAD:C3N	2.36	0.55
1:A:42:LEU:HD23	1:A:42:LEU:N	2.20	0.55
1:A:193:GLN:NE2	1:B:200:GLU:O	2.39	0.55
1:B:93:GLY:O	1:B:97:ARG:HB2	2.07	0.55
1:A:88:MET:HE3	1:A:144:LEU:HD21	1.88	0.54
1:B:195:VAL:CG2	1:B:195:VAL:O	2.56	0.53
1:A:105:HIS:CB	1:A:108:ASN:HA	2.40	0.52
1:A:121:ASN:ND2	1:A:123:LEU:H	2.08	0.52
1:A:128:THR:HG23	1:A:132:ILE:O	2.10	0.52
1:A:95:ILE:CD1	2:A:213:NAD:N7N	2.74	0.51
1:A:113:SER:O	1:A:133:PRO:HD2	2.11	0.51
1:A:202:GLN:HE21	1:B:80:ASN:HD21	1.59	0.51
1:B:195:VAL:HG22	1:B:195:VAL:O	2.11	0.50
1:B:88:MET:CE	1:B:144:LEU:HD11	2.42	0.49
1:A:105:HIS:O	1:A:108:ASN:ND2	2.45	0.48
1:A:39:ALA:CB	1:A:46:SER:HA	2.43	0.47
1:A:85:THR:HG23	1:A:110:MET:HA	1.95	0.47
1:B:91:GLY:O	1:B:155:THR:OG1	2.32	0.46
1:B:135:TYR:CZ	1:B:143:HIS:CE1	3.04	0.46
1:A:84:THR:CG2	1:A:84:THR:O	2.59	0.45
1:B:116:PHE:CE1	1:B:135:TYR:HB2	2.53	0.44
1:A:45:ASP:O	1:A:48:THR:HG23	2.17	0.44
1:A:110:MET:HE3	1:B:205:LEU:CD2	2.43	0.44
1:A:45:ASP:C	1:A:48:THR:HG22	2.35	0.43
1:A:57:GLY:O	1:A:58:GLU:C	2.56	0.43
1:B:88:MET:HE1	1:B:144:LEU:HD11	2.00	0.43
1:B:116:PHE:HA	1:B:135:TYR:O	2.19	0.43
1:B:94:ASN:O	1:B:97:ARG:N	2.52	0.43
1:B:140:ILE:HG23	1:B:141:ASN:N	2.33	0.42
1:B:210:GLN:HE21	1:B:210:GLN:N	2.18	0.42
1:B:210:GLN:NE2	1:B:210:GLN:N	2.67	0.42
1:B:62:ARG:C	1:B:64:PHE:H	2.23	0.42
1:B:74:PHE:CE2	1:B:78:ILE:HD11	2.54	0.42
1:A:95:ILE:O	1:A:98:ALA:HB3	2.20	0.41
1:B:137:ILE:HG22	1:B:137:ILE:O	2.20	0.41
1:B:179:PHE:CD2	1:B:195:VAL:HG22	2.55	0.41
1:B:95:ILE:HD12	1:B:95:ILE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:GLN:NE2	1:B:210:GLN:CA	2.83	0.41
1:B:67:ASP:OD2	1:B:70:LYS:HD2	2.20	0.41
1:A:53:PHE:HA	1:A:56:PHE:CD2	2.55	0.41
1:A:49:VAL:HG13	1:A:53:PHE:CE1	2.56	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	190/212 (90%)	177 (93%)	10 (5%)	3 (2%)	12	16
1	B	200/212 (94%)	189 (94%)	10 (5%)	1 (0%)	34	48
All	All	390/424 (92%)	366 (94%)	20 (5%)	4 (1%)	19	28

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	146	ASP
1	A	108	ASN
1	A	106	ASP
1	B	158	SER

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	171/185 (92%)	151 (88%)	20 (12%)	7	8
1	B	177/185 (96%)	160 (90%)	17 (10%)	10	15
All	All	348/370 (94%)	311 (89%)	37 (11%)	8	12

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LEU
1	A	24	ARG
1	A	35	SER
1	A	36	LYS
1	A	45	ASP
1	A	46	SER
1	A	80	ASN
1	A	89	LEU
1	A	105	HIS
1	A	107	ARG
1	A	109	LYS
1	A	110	MET
1	A	144	LEU
1	A	146	ASP
1	A	147	SER
1	A	148	ASP
1	A	182	VAL
1	A	188	LYS
1	A	193	GLN
1	A	205	LEU
1	B	6	SER
1	B	7	ILE
1	B	15	LEU
1	B	36	LYS
1	B	42	LEU
1	B	69	LYS
1	B	84	THR
1	B	94	ASN
1	B	97	ARG
1	B	120	SER
1	B	143	HIS
1	B	185	THR
1	B	188	LYS
1	B	198	THR
1	B	199	SER

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Mol	Chain	Res	Type
1	B	210	GLN
1	B	211	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	ASN
1	A	86	ASN
1	A	108	ASN
1	A	121	ASN
1	B	80	ASN
1	B	141	ASN
1	B	143	HIS
1	B	202	GLN
1	B	210	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	213	-	38,48,48	1.78	4 (10%)	47,73,73	2.31	7 (14%)

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	213	-	-	0/22/62/62	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	213	NAD	O4D-C4D	-2.11	1.40	1.45
2	A	213	NAD	C2A-N1A	2.25	1.38	1.33
2	A	213	NAD	C2A-N3A	3.53	1.38	1.32
2	A	213	NAD	O7N-C7N	8.19	1.41	1.24

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	213	NAD	N3A-C2A-N1A	-11.20	120.31	128.89
2	A	213	NAD	PN-O3-PA	-3.94	121.66	132.73
2	A	213	NAD	C4A-C5A-N7A	-2.61	107.08	109.48
2	A	213	NAD	O2N-PN-O1N	2.07	123.73	112.53
2	A	213	NAD	C3N-C7N-N7N	2.40	120.44	117.82
2	A	213	NAD	O2A-PA-O3	2.59	116.86	105.09
2	A	213	NAD	O4D-C1D-N1N	7.29	116.14	108.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	213	NAD	8	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	196/212 (92%)	0.33	17 (8%) 13 12	27, 63, 104, 113	17 (8%)
1	B	204/212 (96%)	0.09	10 (4%) 33 34	32, 56, 97, 109	20 (9%)
All	All	400/424 (94%)	0.21	27 (6%) 20 20	27, 58, 102, 113	37 (9%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	29	GLY	4.4
1	A	108	ASN	3.9
1	A	145	ILE	3.7
1	A	28	ASP	3.7
1	B	6	SER	3.6
1	A	211	GLN	3.4
1	B	121	ASN	3.4
1	A	30	ILE	3.3
1	B	120	SER	3.0
1	A	72	MET	2.9
1	A	66	TYR	2.9
1	A	101	HIS	2.8
1	B	129	GLU	2.8
1	A	210	GLN	2.7
1	A	146	ASP	2.6
1	A	25	PHE	2.6
1	A	176	ILE	2.4
1	B	118	LEU	2.3
1	A	107	ARG	2.2
1	B	130	ASP	2.2
1	B	63	GLY	2.1
1	B	83	SER	2.1
1	A	84	THR	2.1
1	A	148	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	122	ASP	2.1
1	A	31	GLU	2.0
1	B	195	VAL	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	A	213	44/44	0.97	0.11	-0.93	20,36,50,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.