Full wwPDB X-ray Structure Validation Report (i)

Jun 15, 2024 – 06:57 PM EDT

PDB ID	:	4Q16
Title	:	Structure of NAD+ Synthetase from Deinococcus radiodurans
Authors	:	Lee, J.Y.; Park, Y.W.
Deposited on	:	2014-04-03
Resolution	:	2.60 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

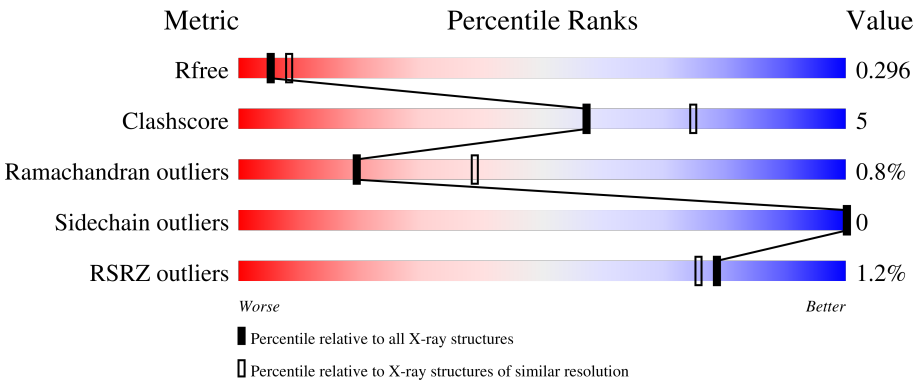
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.60 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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	287	85% 9% 6%
1	B	287	% 83% 10% 7%
1	C	287	2% 71% 18% 11%
1	D	287	% 84% 10% • 6%

2 Entry composition (i)

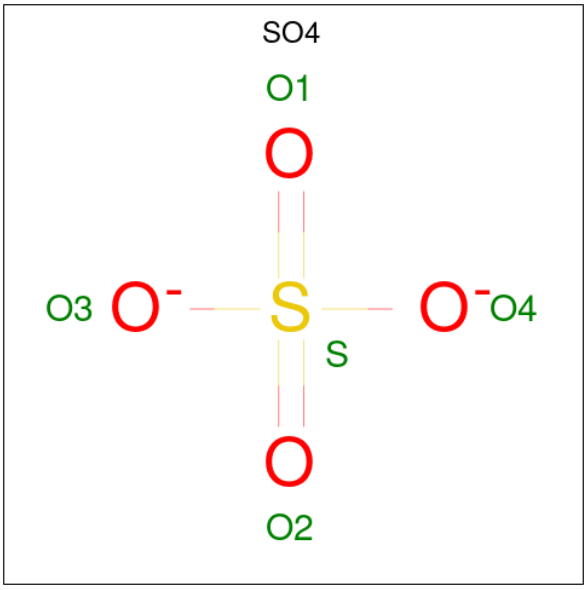
There are 3 unique types of molecules in this entry. The entry contains 8269 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NH(3)-dependent NAD(+) synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	270	2024	1266	365	390	3	10	0	0
1	B	268	1981	1244	356	378	3	10	0	0
1	C	255	1856	1165	335	353	3	10	0	0
1	D	271	2006	1259	366	378	3	11	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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

- Molecule 3 is water.

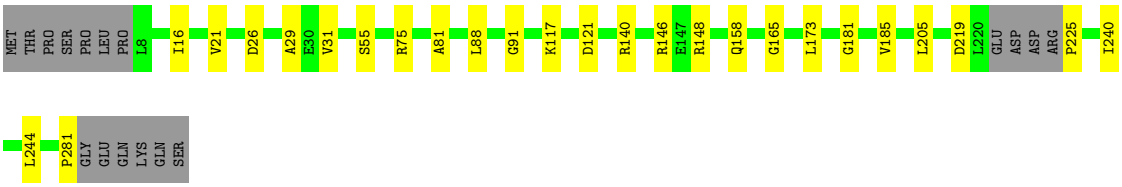
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	127	127	127	0	0
			Total	O		
3	B	85	85	85	0	0
			Total	O		
3	C	64	64	64	0	0
			Total	O		
3	D	86	86	86	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

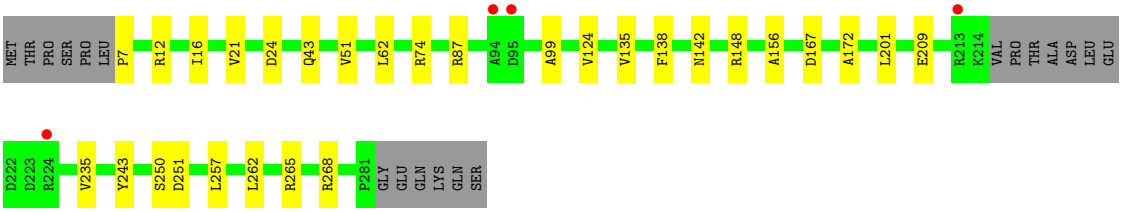
• Molecule 1: NH(3)-dependent NAD(+) synthetase

Chain A:



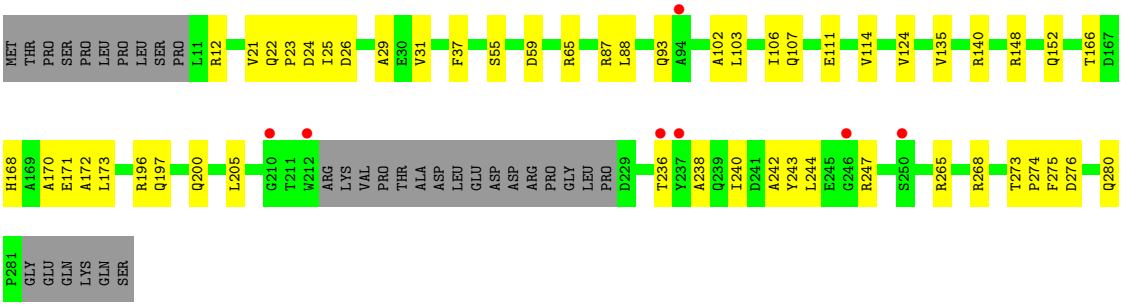
• Molecule 1: NH(3)-dependent NAD(+) synthetase

Chain B:



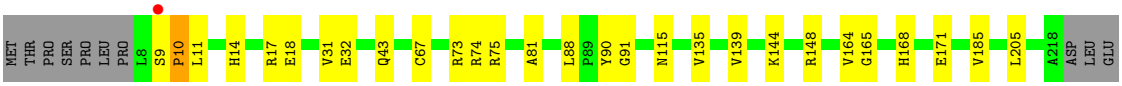
• Molecule 1: NH(3)-dependent NAD(+) synthetase

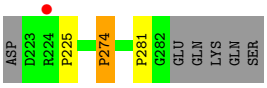
Chain C:



• Molecule 1: NH(3)-dependent NAD(+) synthetase

Chain D:


MET
THR
PRO
SER
PRO
LEU
PRO
L8
S9
P10
L11
H14
R17
E18
V31
E32
Q43
C67
R73
R74
R75
A81
L88
P89
Y90
G91
N115
V135
V139
K144
R148
V164
G165
H168
E171
V185
L205
A218
ASP
LEU
GLU


ASP
D223
R224
P225
P274
P281
G282
GLU
GLN
LYS
GLN
SER

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	113.23Å 114.15Å 121.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.38 – 2.60 50.72 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.7 (29.38-2.60) 96.0 (50.72-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.18 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.239 , 0.293 0.243 , 0.296	Depositor DCC
R_{free} test set	2487 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	35.8	Xtriage
Anisotropy	0.551	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 22.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.248 for k,h,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	8269	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% of the height of the origin peak. No significant pseudotranslation is detected.*

[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.24	0/2060	0.40	2/2800 (0.1%)
1	B	0.24	1/2018 (0.0%)	0.38	1/2747 (0.0%)
1	C	0.30	1/1889 (0.1%)	0.36	0/2570
1	D	0.24	0/2043	0.39	1/2780 (0.0%)
All	All	0.26	2/8010 (0.0%)	0.39	4/10897 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	111	GLU	CB-CG	-5.31	1.42	1.52
1	B	209	GLU	CB-CG	-5.26	1.42	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	225	PRO	N-CA-CB	5.96	110.45	103.30
1	B	7	PRO	N-CA-CB	5.89	110.37	103.30
1	A	281	PRO	N-CA-CB	5.86	110.33	103.30
1	D	281	PRO	N-CA-CB	5.69	110.13	103.30

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	2024	0	1960	15	0
1	B	1981	0	1905	17	0
1	C	1856	0	1750	31	0
1	D	2006	0	1933	15	0
2	A	10	0	0	1	0
2	B	10	0	0	0	0
2	C	10	0	0	1	0
2	D	10	0	0	0	0
3	A	127	0	0	1	0
3	B	85	0	0	5	0
3	C	64	0	0	4	0
3	D	86	0	0	0	0
All	All	8269	0	7548	76	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 (76) 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:C:59:ASP:OD2	1:C:168:HIS:NE2	2.09	0.84
1:C:280:GLN:CG	3:C:401:HOH:O	2.32	0.76
1:B:167:ASP:OD2	3:B:433:HOH:O	2.11	0.69
1:A:21:VAL:HG11	1:A:244:LEU:HB3	1.75	0.67
1:A:117:LYS:NZ	1:A:121:ASP:OD2	2.16	0.65
1:C:31:VAL:HG11	1:C:205:LEU:HD21	1.78	0.65
1:B:172:ALA:O	3:B:438:HOH:O	2.15	0.64
1:A:140:ARG:CG	3:A:423:HOH:O	2.46	0.64
1:A:75:ARG:NH1	1:A:81:ALA:O	2.34	0.61
1:B:262:LEU:O	1:B:265:ARG:NH1	2.36	0.59
1:B:268:ARG:NH1	3:B:438:HOH:O	2.20	0.59
1:C:172:ALA:O	1:C:268:ARG:NH1	2.36	0.59
1:C:12:ARG:NH1	1:C:243:TYR:O	2.33	0.58
1:D:91:GLY:O	1:D:115:ASN:ND2	2.37	0.57
1:D:32:GLU:OE2	1:D:73:ARG:NH2	2.34	0.57
1:A:55:SER:OG	2:A:301:SO4:O3	2.22	0.56
1:B:250:SER:OG	1:B:251:ASP:N	2.38	0.56
1:D:31:VAL:HG11	1:D:205:LEU:HD21	1.87	0.55
1:B:24:ASP:OD1	3:B:439:HOH:O	2.18	0.55
1:B:235:VAL:HG11	1:B:257:LEU:HD21	1.89	0.55
1:C:87:ARG:HD2	1:C:103:LEU:HD11	1.90	0.53
1:A:16:ILE:HG23	1:A:21:VAL:HB	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:165:GLY:HA3	1:D:185:VAL:HG21	1.91	0.53
1:C:242:ALA:HA	1:C:247:ARG:HE	1.74	0.52
1:A:31:VAL:HG11	1:A:205:LEU:HD21	1.91	0.52
1:D:88:LEU:HD13	1:D:148:ARG:HB3	1.91	0.52
1:A:173:LEU:HD23	1:A:240:ILE:HG23	1.92	0.52
1:B:124:VAL:HG13	1:B:135:VAL:HG21	1.94	0.50
1:C:124:VAL:HG21	1:C:140:ARG:HG3	1.93	0.50
1:C:65:ARG:NH1	1:C:106:ILE:O	2.45	0.50
1:A:165:GLY:HA3	1:A:185:VAL:HG21	1.93	0.49
1:A:158:GLN:HG3	1:B:135:VAL:HG12	1.94	0.49
1:D:14:HIS:O	1:D:17:ARG:CG	2.60	0.49
1:D:67:CYS:SG	1:D:164:VAL:HG21	2.53	0.49
1:D:17:ARG:CG	1:D:18:GLU:N	2.77	0.48
1:D:75:ARG:NH1	1:D:81:ALA:O	2.46	0.48
1:B:16:ILE:HG23	1:B:21:VAL:HB	1.94	0.48
1:C:26:ASP:HB3	1:C:29:ALA:HB3	1.95	0.48
1:C:102:ALA:O	1:C:106:ILE:HG12	2.13	0.48
1:B:12:ARG:HG3	1:B:243:TYR:CZ	2.49	0.48
1:C:273:THR:HG23	1:C:275:PHE:H	1.79	0.48
1:C:107:GLN:NE2	3:C:411:HOH:O	2.46	0.48
1:B:43:GLN:OE1	1:B:74:ARG:NH2	2.43	0.47
1:C:273:THR:HG22	1:C:276:ASP:OD2	2.14	0.47
1:C:21:VAL:HG11	1:C:244:LEU:HB3	1.96	0.47
1:C:59:ASP:HB3	1:C:166:THR:HB	1.96	0.47
1:C:25:ILE:HD13	1:C:197:GLN:HB3	1.97	0.47
1:B:148:ARG:NH1	3:B:423:HOH:O	2.34	0.47
1:A:146:ARG:HA	1:A:181:GLY:HA2	1.97	0.46
1:B:62:LEU:HD21	1:B:201:LEU:HD12	1.96	0.46
1:B:138:PHE:O	1:B:142:ASN:ND2	2.35	0.46
1:D:135:VAL:HG13	1:D:139:VAL:HB	1.95	0.46
1:A:26:ASP:HB3	1:A:29:ALA:HB3	1.97	0.46
1:C:168:HIS:CE1	1:C:170:ALA:HB3	2.51	0.45
1:C:265:ARG:NH2	3:C:409:HOH:O	2.48	0.45
1:D:43:GLN:OE1	1:D:74:ARG:NH1	2.44	0.45
1:C:88:LEU:HD23	1:C:114:VAL:HB	1.97	0.45
1:B:51:VAL:HG11	1:B:156:ALA:HB2	1.98	0.44
1:A:88:LEU:HD13	1:A:148:ARG:HB3	1.99	0.44
1:C:173:LEU:HD22	1:C:244:LEU:HD21	1.98	0.44
1:C:173:LEU:HD23	1:C:240:ILE:HG23	1.98	0.44
1:A:21:VAL:HG21	1:A:244:LEU:HD22	1.99	0.44
1:C:55:SER:OG	2:C:301:SO4:O3	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:152:GLN:NE2	3:C:405:HOH:O	2.37	0.43
1:C:22:GLN:NE2	1:C:24:ASP:O	2.52	0.42
1:C:124:VAL:HG13	1:C:135:VAL:HG21	2.02	0.42
1:B:87:ARG:HH21	1:B:99:ALA:HB3	1.85	0.42
1:C:168:HIS:CE1	1:C:171:GLU:HG3	2.55	0.42
1:D:168:HIS:CE1	1:D:171:GLU:HG3	2.54	0.42
1:A:91:GLY:H	1:A:117:LYS:HB2	1.85	0.41
1:C:196:ARG:NE	1:C:200:GLN:OE1	2.47	0.41
1:C:88:LEU:HD13	1:C:148:ARG:HB3	2.02	0.41
1:D:10:PRO:HB2	1:D:11:LEU:H	1.62	0.41
1:C:37:PHE:CD2	1:D:274:PRO:HG3	2.55	0.41
1:C:236:THR:HG22	1:C:238:ALA:H	1.85	0.41
1:D:90:TYR:CE1	1:D:144:LYS:HE2	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	266/287 (93%)	255 (96%)	10 (4%)	1 (0%)	34	57
1	B	264/287 (92%)	255 (97%)	9 (3%)	0	100	100
1	C	251/287 (88%)	237 (94%)	11 (4%)	3 (1%)	13	27
1	D	267/287 (93%)	252 (94%)	11 (4%)	4 (2%)	10	21
All	All	1048/1148 (91%)	999 (95%)	41 (4%)	8 (1%)	19	39

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	10	PRO
1	A	219	ASP

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Mol	Chain	Res	Type
1	D	9	SER
1	C	93	GLN
1	C	23	PRO
1	C	274	PRO
1	D	274	PRO
1	D	225	PRO

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	199/224 (89%)	199 (100%)	0	100	100
1	B	191/224 (85%)	191 (100%)	0	100	100
1	C	169/224 (75%)	169 (100%)	0	100	100
1	D	191/224 (85%)	191 (100%)	0	100	100
All	All	750/896 (84%)	750 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

8 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	SO4	B	302	-	4,4,4	0.15	0	6,6,6	0.07	0
2	SO4	B	301	-	4,4,4	0.15	0	6,6,6	0.09	0
2	SO4	D	302	-	4,4,4	0.14	0	6,6,6	0.07	0
2	SO4	D	301	-	4,4,4	0.15	0	6,6,6	0.09	0
2	SO4	C	301	-	4,4,4	0.13	0	6,6,6	0.09	0
2	SO4	A	302	-	4,4,4	0.14	0	6,6,6	0.07	0
2	SO4	A	301	-	4,4,4	0.14	0	6,6,6	0.08	0
2	SO4	C	302	-	4,4,4	0.14	0	6,6,6	0.04	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	SO4	1	0
2	A	301	SO4	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 (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	270/287 (94%)	-0.42	0	100	100	20, 34, 54, 77	6 (2%)
1	B	268/287 (93%)	-0.24	4 (1%)	73	70	22, 39, 64, 84	6 (2%)
1	C	255/287 (88%)	-0.02	7 (2%)	54	48	30, 47, 73, 87	6 (2%)
1	D	271/287 (94%)	-0.21	2 (0%)	87	86	27, 39, 61, 86	7 (2%)
All	All	1064/1148 (92%)	-0.23	13 (1%)	79	76	20, 39, 66, 87	25 (2%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	95	ASP	4.4
1	C	212	TRP	4.1
1	B	213	ARG	3.9
1	C	250	SER	3.2
1	B	94	ALA	3.1
1	D	224	ARG	3.0
1	C	210	GLY	2.8
1	D	9	SER	2.7
1	B	224	ARG	2.5
1	C	237	TYR	2.5
1	C	94	ALA	2.4
1	C	236	THR	2.2
1	C	246	GLY	2.2

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 monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
2	SO4	B	301	5/5	0.84	0.21	38,47,81,83	0
2	SO4	D	302	5/5	0.92	0.16	50,58,66,68	0
2	SO4	C	301	5/5	0.93	0.17	64,67,74,79	0
2	SO4	C	302	5/5	0.95	0.08	58,62,64,76	0
2	SO4	B	302	5/5	0.95	0.11	49,49,59,64	0
2	SO4	D	301	5/5	0.96	0.10	41,43,52,54	0
2	SO4	A	302	5/5	0.96	0.10	43,47,62,66	0
2	SO4	A	301	5/5	0.97	0.10	39,50,52,59	0

6.5 Other polymers (i)

There are no such residues in this entry.