



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 11:57 am GMT

PDB ID : 4J4H
Title : PylD in complex with pyrroline-carboxy-lysine and NADH
Authors : Quitterer, F.; Beck, P.; Bacher, A.; Groll, M.
Deposited on : 2013-02-06
Resolution : 1.80 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

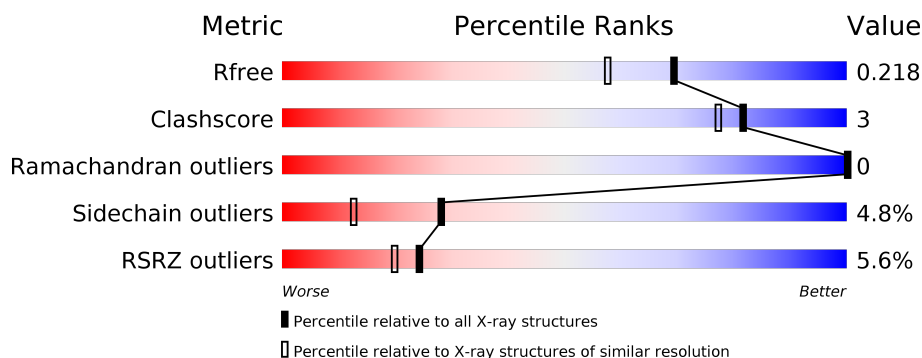
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	111664	5253 (1.80-1.80)
Clashscore	122126	6077 (1.80-1.80)
Ramachandran outliers	120053	6011 (1.80-1.80)
Sidechain outliers	120020	6010 (1.80-1.80)
RSRZ outliers	108989	5157 (1.80-1.80)

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.

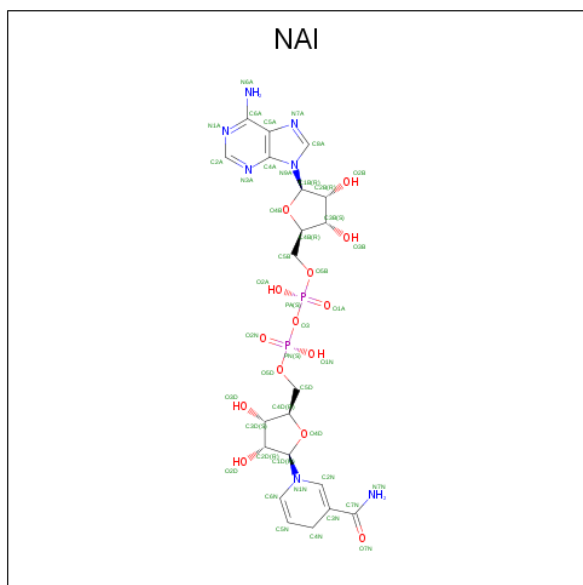
Mol	Chain	Length	Quality of chain
1	A	259	<div> <div></div> <div> <div></div> <div>93%</div> <div>6%</div> </div> </div>
1	B	259	<div> <div></div> <div> <div></div> <div>89%</div> <div>10%</div> </div> </div>
1	C	259	<div> <div></div> <div> <div></div> <div>91%</div> <div>9%</div> </div> </div>
1	D	259	<div> <div></div> <div> <div></div> <div>93%</div> <div>7%</div> </div> </div>

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 PylD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total 1952	C 1244	N 314	O 383	S 11	0	0	0
1	B	259	Total 1952	C 1244	N 314	O 383	S 11	0	0	0
1	C	259	Total 1952	C 1244	N 314	O 383	S 11	0	0	0
1	D	259	Total 1952	C 1244	N 314	O 383	S 11	0	0	0

- Molecule 2 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$).



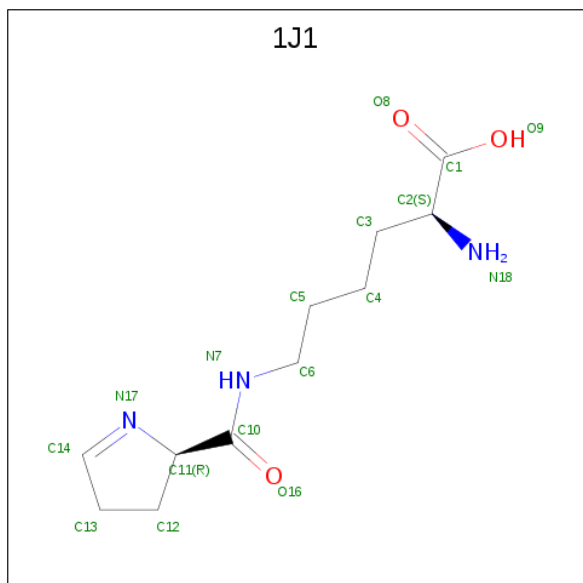
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	B	1	Total 44	C 21	N 7	O 14	P 2	0	0

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

- Molecule 3 is N 6 -[(2R)-3,4-dihydro-2H-pyrrol-2-ylcarbonyl]-L-lysine (three-letter code: 1J1) (formula: C₁₁H₁₉N₃O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	11	3	3		
3	B	1	Total	C	N	O	0	0
			17	11	3	3		
3	C	1	Total	C	N	O	0	0
			17	11	3	3		
3	D	1	Total	C	N	O	0	0
			17	11	3	3		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Na	0	0
			1	1		
4	A	1	Total	Na	0	0
			1	1		
4	D	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Na	0	0
			1	1		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mg	0	0
			1	1		
5	A	1	Total	Mg	0	0
			1	1		
5	D	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		

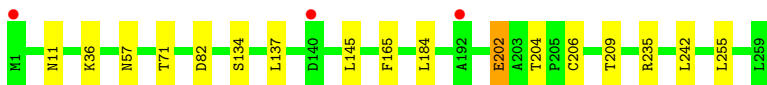
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	212	Total	O	0	0
			212	212		
6	B	204	Total	O	0	0
			204	204		
6	C	75	Total	O	0	0
			75	75		
6	D	67	Total	O	0	0
			67	67		

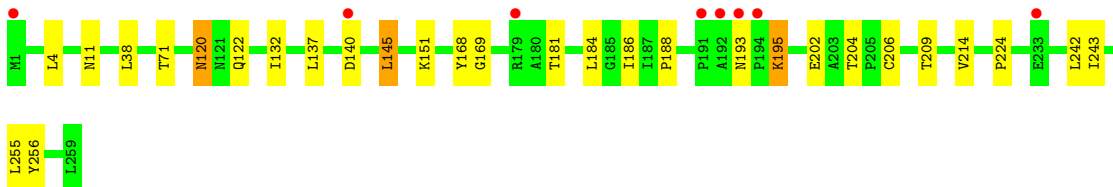
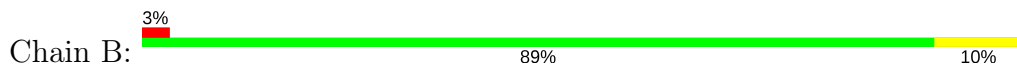
3 Residue-property plots [i](#)

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.

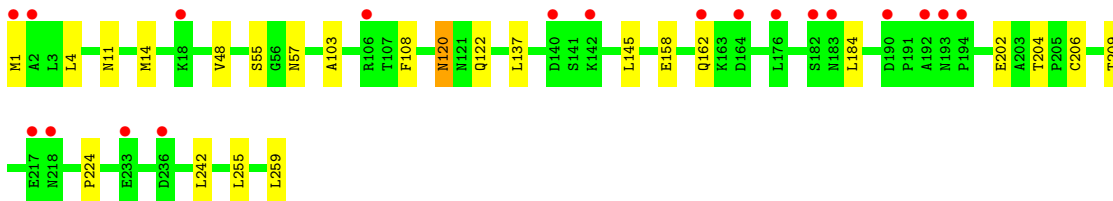
• Molecule 1: PyLD



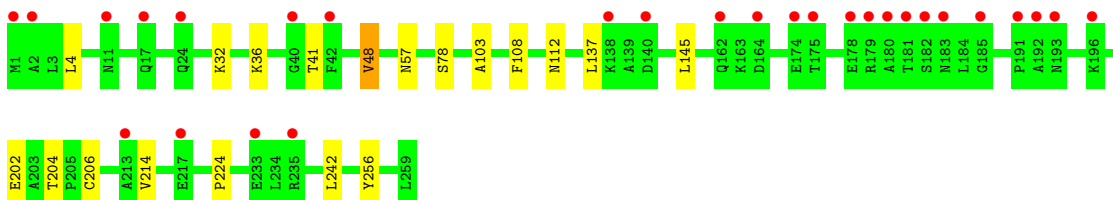
• Molecule 1: PyLD



• Molecule 1: PyLD



• Molecule 1: PyLD



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	87.25Å 260.98Å 48.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.80 10.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	92.2 (10.00-1.80) 92.8 (10.00-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.179 , 0.218 0.178 , 0.218	Depositor DCC
R_{free} test set	4797 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	23.8	Xtriage
Anisotropy	0.335	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.46 , 54.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8618	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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, 0.333 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: NA, MG, NAI, 1J1

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	0.30	0/1988	0.52	0/2700
1	B	0.31	0/1988	0.54	0/2700
1	C	0.30	0/1988	0.51	0/2700
1	D	0.29	0/1988	0.50	0/2700
All	All	0.30	0/7952	0.52	0/10800

There are no bond length outliers.

There are no bond angle outliers.

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	1952	0	1947	7	0
1	B	1952	0	1947	16	0
1	C	1952	0	1947	11	0
1	D	1952	0	1947	8	0
2	A	44	0	27	1	0
2	B	44	0	27	2	0
2	C	44	0	27	2	0
2	D	44	0	27	1	0
3	A	17	0	18	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	17	0	18	1	0
3	C	17	0	18	1	0
3	D	17	0	18	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	212	0	0	0	0
6	B	204	0	0	1	0
6	C	75	0	0	0	0
6	D	67	0	0	0	0
All	All	8618	0	7968	45	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 3.

All (45) 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:A:204:THR:HG22	1:A:206:CYS:H	1.54	0.72
1:D:204:THR:HG22	1:D:206:CYS:H	1.54	0.71
1:B:181:THR:HG21	1:B:188:PRO:HG3	1.71	0.71
1:C:204:THR:HG22	1:C:206:CYS:H	1.59	0.67
1:B:204:THR:HG22	1:B:206:CYS:H	1.60	0.67
1:C:158:GLU:O	1:C:162:GLN:HG2	1.95	0.66
1:D:41:THR:HG21	1:D:256:TYR:O	1.99	0.62
1:B:120:ASN:HD22	1:B:122:GLN:H	1.48	0.61
1:D:32:LYS:O	1:D:36:LYS:HG2	2.01	0.60
2:B:901:NAI:H42N	3:B:902:1J1:H8	1.81	0.60
1:C:202:GLU:OE1	1:C:204:THR:HB	2.01	0.59
2:A:901:NAI:H42N	3:A:902:1J1:H8	1.87	0.57
1:A:204:THR:HG21	1:A:209:THR:HG21	1.87	0.56
1:C:120:ASN:HD22	1:C:122:GLN:H	1.53	0.56
1:A:202:GLU:OE1	1:A:204:THR:HB	2.07	0.55
1:D:202:GLU:OE1	1:D:204:THR:HB	2.07	0.54
1:B:204:THR:HG21	1:B:209:THR:HG21	1.91	0.52
1:B:202:GLU:OE1	1:B:204:THR:HB	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:204:THR:HG21	1:C:209:THR:HG21	1.91	0.51
1:A:204:THR:HG22	1:A:206:CYS:N	2.26	0.49
1:D:36:LYS:HD3	1:D:41:THR:O	2.14	0.47
1:B:204:THR:HG22	1:B:206:CYS:N	2.29	0.47
1:C:224:PRO:O	2:C:901:NAI:H2N	2.14	0.47
2:C:901:NAI:H42N	3:C:902:1J1:H8	1.97	0.47
1:B:145:LEU:HD12	1:B:214:VAL:HG11	1.98	0.46
1:B:140:ASP:N	1:B:140:ASP:OD1	2.47	0.46
1:D:202:GLU:O	1:D:224:PRO:HD2	2.16	0.46
1:B:71:THR:HG22	1:B:255:LEU:HD11	1.99	0.45
1:A:206:CYS:HG	1:C:206:CYS:HG	1.64	0.45
1:A:134:SER:HB2	1:A:165:PHE:CZ	2.52	0.44
1:C:103:ALA:HB2	1:C:108:PHE:CD1	2.53	0.44
2:D:901:NAI:H42N	3:D:902:1J1:H8	2.00	0.44
1:C:202:GLU:O	1:C:224:PRO:HD2	2.18	0.44
1:B:132:ILE:HG21	1:B:243:ILE:HD13	1.98	0.44
1:B:256:TYR:OH	6:B:1177:HOH:O	2.20	0.43
1:B:202:GLU:O	1:B:224:PRO:HD2	2.18	0.43
1:D:103:ALA:HB2	1:D:108:PHE:CD1	2.54	0.43
1:C:204:THR:HG22	1:C:206:CYS:N	2.30	0.42
1:A:71:THR:HG22	1:A:255:LEU:HD11	2.00	0.42
1:C:255:LEU:O	1:C:259:LEU:HG	2.20	0.42
1:D:48:VAL:HG13	1:D:78:SER:HB3	2.01	0.42
1:B:120:ASN:ND2	1:B:122:GLN:H	2.17	0.41
1:B:168:TYR:CZ	1:B:195:LYS:HE2	2.55	0.41
1:B:169:GLY:HA3	1:B:186:ILE:HD12	2.04	0.40
1:B:224:PRO:O	2:B:901:NAI:H2N	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	257/259 (99%)	249 (97%)	8 (3%)	0	100	100
1	B	257/259 (99%)	249 (97%)	8 (3%)	0	100	100
1	C	257/259 (99%)	249 (97%)	8 (3%)	0	100	100
1	D	257/259 (99%)	250 (97%)	7 (3%)	0	100	100
All	All	1028/1036 (99%)	997 (97%)	31 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	213/214 (100%)	203 (95%)	10 (5%)	29	13
1	B	213/214 (100%)	202 (95%)	11 (5%)	25	11
1	C	213/214 (100%)	201 (94%)	12 (6%)	23	9
1	D	213/214 (100%)	205 (96%)	8 (4%)	36	20
All	All	852/856 (100%)	811 (95%)	41 (5%)	28	13

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ASN
1	A	36	LYS
1	A	57	ASN
1	A	82	ASP
1	A	137	LEU
1	A	145	LEU
1	A	184	LEU
1	A	202	GLU
1	A	235	ARG
1	A	242	LEU
1	B	4	LEU
1	B	11	ASN
1	B	38	LEU

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Mol	Chain	Res	Type
1	B	120	ASN
1	B	137	LEU
1	B	145	LEU
1	B	151	LYS
1	B	184	LEU
1	B	193	ASN
1	B	195	LYS
1	B	242	LEU
1	C	1	MET
1	C	4	LEU
1	C	11	ASN
1	C	14	MET
1	C	48	VAL
1	C	55	SER
1	C	57	ASN
1	C	120	ASN
1	C	137	LEU
1	C	145	LEU
1	C	184	LEU
1	C	242	LEU
1	D	4	LEU
1	D	48	VAL
1	D	57	ASN
1	D	112	ASN
1	D	137	LEU
1	D	145	LEU
1	D	214	VAL
1	D	242	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	ASN
1	A	13	ASN
1	A	62	ASN
1	A	72	GLN
1	A	162	GLN
1	B	11	ASN
1	B	24	GLN
1	B	62	ASN
1	B	72	GLN
1	B	94	GLN

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Mol	Chain	Res	Type
1	B	120	ASN
1	B	162	GLN
1	C	11	ASN
1	C	57	ASN
1	C	62	ASN
1	C	120	ASN
1	D	57	ASN
1	D	62	ASN
1	D	112	ASN
1	D	162	GLN

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 ⓘ

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 for Mogul analysis.

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	NAI	A	901	5	41,48,48	1.06	2 (4%)	45,73,73	1.57	6 (13%)
3	1J1	A	902	-	10,17,17	0.88	1 (10%)	10,21,21	1.75	3 (30%)
2	NAI	B	901	5	41,48,48	1.06	2 (4%)	45,73,73	1.61	6 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	1J1	B	902	-	10,17,17	0.93	1 (10%)	10,21,21	1.91	3 (30%)
2	NAI	C	901	5	41,48,48	1.07	2 (4%)	45,73,73	1.49	4 (8%)
3	1J1	C	902	-	10,17,17	0.94	1 (10%)	10,21,21	2.06	3 (30%)
2	NAI	D	901	5	41,48,48	1.09	2 (4%)	45,73,73	1.53	4 (8%)
3	1J1	D	902	-	10,17,17	0.90	1 (10%)	10,21,21	1.98	3 (30%)

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	NAI	A	901	5	-	0/25/72/72	0/5/5/5
3	1J1	A	902	-	-	0/12/23/23	0/1/1/1
2	NAI	B	901	5	-	0/25/72/72	0/5/5/5
3	1J1	B	902	-	-	0/12/23/23	0/1/1/1
2	NAI	C	901	5	-	0/25/72/72	0/5/5/5
3	1J1	C	902	-	-	0/12/23/23	0/1/1/1
2	NAI	D	901	5	-	0/25/72/72	0/5/5/5
3	1J1	D	902	-	-	0/12/23/23	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	902	1J1	C10-N7	2.39	1.38	1.33
3	A	902	1J1	C10-N7	2.39	1.38	1.33
3	B	902	1J1	C10-N7	2.48	1.38	1.33
3	C	902	1J1	C10-N7	2.58	1.38	1.33
2	A	901	NAI	C5A-C4A	3.13	1.47	1.40
2	C	901	NAI	C5A-C4A	3.16	1.47	1.40
2	D	901	NAI	C5A-C4A	3.17	1.47	1.40
2	B	901	NAI	C5A-C4A	3.17	1.47	1.40
2	C	901	NAI	C6N-C5N	3.66	1.39	1.33
2	A	901	NAI	C6N-C5N	3.69	1.40	1.33
2	B	901	NAI	C6N-C5N	3.73	1.40	1.33
2	D	901	NAI	C6N-C5N	3.77	1.40	1.33

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	NAI	N3A-C2A-N1A	-6.84	123.01	128.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	901	NAI	N3A-C2A-N1A	-6.57	123.24	128.86
2	A	901	NAI	N3A-C2A-N1A	-6.52	123.28	128.86
2	C	901	NAI	N3A-C2A-N1A	-6.35	123.43	128.86
3	C	902	1J1	C6-N7-C10	-4.78	113.81	122.59
3	B	902	1J1	C6-N7-C10	-4.65	114.05	122.59
3	D	902	1J1	C6-N7-C10	-4.49	114.35	122.59
3	A	902	1J1	C6-N7-C10	-4.02	115.21	122.59
2	B	901	NAI	C1D-N1N-C2N	-3.78	114.71	121.10
2	A	901	NAI	C1D-N1N-C2N	-3.66	114.91	121.10
2	D	901	NAI	C1D-N1N-C2N	-3.49	115.20	121.10
2	C	901	NAI	PN-O3-PA	-3.25	121.70	132.63
2	C	901	NAI	C1D-N1N-C2N	-3.20	115.70	121.10
2	D	901	NAI	PN-O3-PA	-3.18	121.95	132.63
2	B	901	NAI	C4A-C5A-N7A	-3.11	106.41	109.41
2	D	901	NAI	C4A-C5A-N7A	-3.05	106.47	109.41
2	A	901	NAI	C4A-C5A-N7A	-3.03	106.49	109.41
2	C	901	NAI	C4A-C5A-N7A	-3.02	106.50	109.41
2	B	901	NAI	PN-O3-PA	-2.81	123.17	132.63
2	A	901	NAI	PN-O3-PA	-2.51	124.21	132.63
2	B	901	NAI	C4B-O4B-C1B	-2.42	107.30	109.83
2	A	901	NAI	C4B-O4B-C1B	-2.13	107.61	109.83
2	A	901	NAI	C2D-C1D-N1N	2.14	118.75	113.32
2	B	901	NAI	C2A-N1A-C6A	2.20	122.48	118.75
3	B	902	1J1	C13-C12-C11	2.23	106.17	103.18
3	A	902	1J1	C12-C13-C14	2.26	105.67	102.78
3	A	902	1J1	C13-C12-C11	2.39	106.37	103.18
3	D	902	1J1	C13-C12-C11	2.54	106.58	103.18
3	B	902	1J1	C12-C13-C14	2.55	106.05	102.78
3	C	902	1J1	C13-C12-C11	2.68	106.76	103.18
3	D	902	1J1	C12-C13-C14	2.83	106.41	102.78
3	C	902	1J1	C12-C13-C14	2.94	106.55	102.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	NAI	1	0
3	A	902	1J1	1	0
2	B	901	NAI	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	902	1J1	1	0
2	C	901	NAI	2	0
3	C	902	1J1	1	0
2	D	901	NAI	1	0
3	D	902	1J1	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	259/259 (100%)	-0.32	3 (1%) 79 76	14, 21, 43, 58	0
1	B	259/259 (100%)	-0.21	8 (3%) 49 43	13, 21, 48, 75	0
1	C	259/259 (100%)	0.19	19 (7%) 15 12	26, 37, 65, 94	0
1	D	259/259 (100%)	0.30	28 (10%) 6 4	26, 42, 74, 86	0
All	All	1036/1036 (100%)	-0.01	58 (5%) 24 20	13, 32, 63, 94	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	192	ALA	11.4
1	C	193	ASN	10.6
1	C	192	ALA	8.2
1	D	1	MET	7.1
1	B	1	MET	6.4
1	B	193	ASN	5.2
1	D	140	ASP	5.2
1	D	175	THR	5.0
1	C	1	MET	4.9
1	C	217	GLU	4.4
1	C	164	ASP	4.2
1	D	183	ASN	4.2
1	D	179	ARG	4.2
1	D	24	GLN	4.2
1	C	140	ASP	4.1
1	C	194	PRO	4.0
1	A	192	ALA	3.9
1	D	181	THR	3.9
1	D	182	SER	3.9
1	C	190	ASP	3.7
1	D	233	GLU	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	178	GLU	3.4
1	A	140	ASP	3.3
1	C	182	SER	3.2
1	D	174	GLU	3.2
1	D	40	GLY	3.1
1	C	2	ALA	3.0
1	D	191	PRO	3.0
1	D	17	GLN	3.0
1	D	138	LYS	3.0
1	B	194	PRO	2.9
1	D	164	ASP	2.8
1	C	106	ARG	2.8
1	C	176	LEU	2.7
1	A	1	MET	2.7
1	D	192	ALA	2.7
1	C	233	GLU	2.6
1	D	185	GLY	2.6
1	D	42	PHE	2.6
1	D	2	ALA	2.6
1	D	193	ASN	2.6
1	B	140	ASP	2.6
1	C	236	ASP	2.6
1	C	183	ASN	2.5
1	D	217	GLU	2.5
1	B	233	GLU	2.5
1	B	179	ARG	2.5
1	D	180	ALA	2.5
1	D	213	ALA	2.5
1	B	191	PRO	2.4
1	C	162	GLN	2.4
1	C	18	LYS	2.4
1	D	162	GLN	2.3
1	C	218	ASN	2.2
1	C	142	LYS	2.2
1	D	196	LYS	2.1
1	D	235	ARG	2.1
1	D	11	ASN	2.1

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

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. 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
4	NA	D	903	1/1	0.86	0.18	42,42,42,42	0
4	NA	C	903	1/1	0.93	0.15	40,40,40,40	0
3	1J1	C	902	17/17	0.93	0.09	27,29,33,34	0
3	1J1	D	902	17/17	0.94	0.08	28,30,34,35	0
4	NA	B	903	1/1	0.95	0.11	32,32,32,32	0
3	1J1	A	902	17/17	0.95	0.09	17,19,22,23	0
5	MG	C	904	1/1	0.95	0.10	42,42,42,42	0
2	NAI	D	901	44/44	0.95	0.09	31,34,45,47	0
2	NAI	B	901	44/44	0.96	0.08	19,26,31,34	0
3	1J1	B	902	17/17	0.96	0.08	18,20,20,21	0
2	NAI	C	901	44/44	0.96	0.07	30,34,37,38	0
5	MG	D	904	1/1	0.97	0.14	48,48,48,48	0
2	NAI	A	901	44/44	0.97	0.08	18,23,27,27	0
5	MG	A	904	1/1	0.98	0.06	24,24,24,24	0
4	NA	A	903	1/1	0.99	0.09	31,31,31,31	0
5	MG	B	904	1/1	1.00	0.05	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.