



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:39 AM GMT

PDB ID : 3MKN
Title : Crystal structure of the E. coli pyrimidine nucleosidase YeiK bound to a competitive inhibitor
Authors : Garau, G.; Fornili, A.; Giabbai, B.; Degano, M.
Deposited on : 2010-04-15
Resolution : 2.00 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

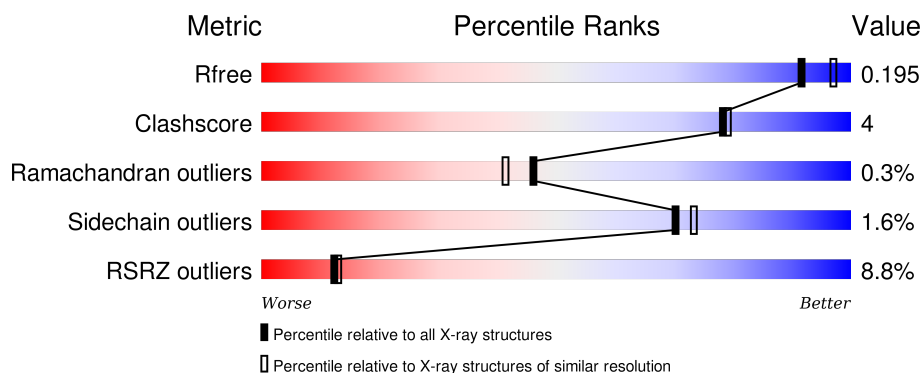
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	316	<div> <div>13%</div> <div>86%</div> <div>9% . .</div> </div>
1	B	316	<div> <div>3%</div> <div>88%</div> <div>7% 5%</div> </div>
1	C	316	<div> <div>10%</div> <div>88%</div> <div>5% 8%</div> </div>
1	D	316	<div> <div>7%</div> <div>91%</div> <div>5% .</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DNB	C	502	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9711 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 Putative uncharacterized protein YeiK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	3	0
			2276	1444	379	433	20			
1	B	301	Total	C	N	O	S	0	5	0
			2287	1455	379	433	20			
1	C	292	Total	C	N	O	S	0	1	0
			2190	1391	364	415	20			
1	D	303	Total	C	N	O	S	0	4	0
			2298	1456	384	438	20			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP C3T3U2
A	-1	SER	-	EXPRESSION TAG	UNP C3T3U2
A	0	HIS	-	EXPRESSION TAG	UNP C3T3U2
B	-2	GLY	-	EXPRESSION TAG	UNP C3T3U2
B	-1	SER	-	EXPRESSION TAG	UNP C3T3U2
B	0	HIS	-	EXPRESSION TAG	UNP C3T3U2
C	-2	GLY	-	EXPRESSION TAG	UNP C3T3U2
C	-1	SER	-	EXPRESSION TAG	UNP C3T3U2
C	0	HIS	-	EXPRESSION TAG	UNP C3T3U2
D	-2	GLY	-	EXPRESSION TAG	UNP C3T3U2
D	-1	SER	-	EXPRESSION TAG	UNP C3T3U2
D	0	HIS	-	EXPRESSION TAG	UNP C3T3U2

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

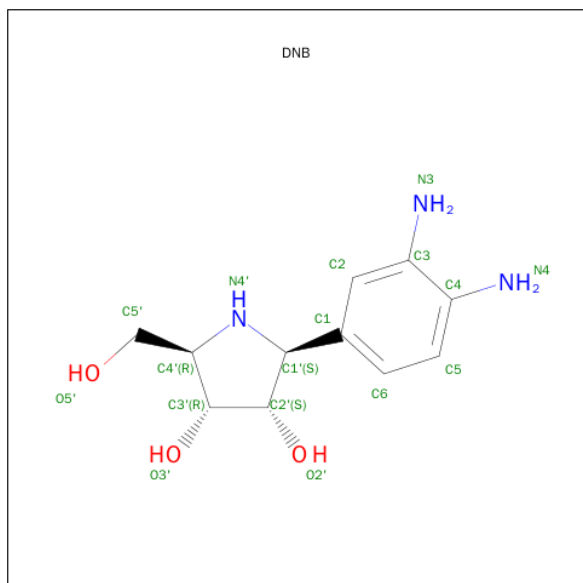
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	A	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Ca	0	0
			1	1		
2	C	1	Total	Ca	0	0
			1	1		

- Molecule 3 is (2S,3S,4R,5R)-2-(3,4-DIAMINOPHENYL)-5-(HYDROXYMETHYL)PYRROLIDINE-3,4-DIOL (three-letter code: DNB) (formula: C₁₁H₁₇N₃O₃).



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 water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	101	Total	O	0	0
			101	101		
4	B	221	Total	O	0	0
			221	221		
4	C	97	Total	O	0	0
			97	97		

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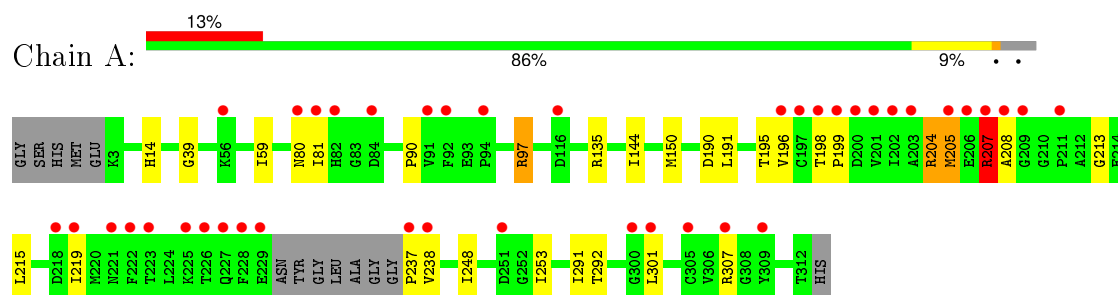
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	169	Total 169	O 169	0	0

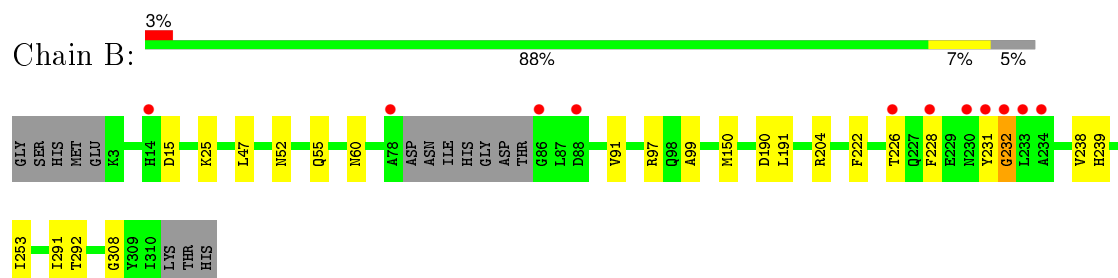
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

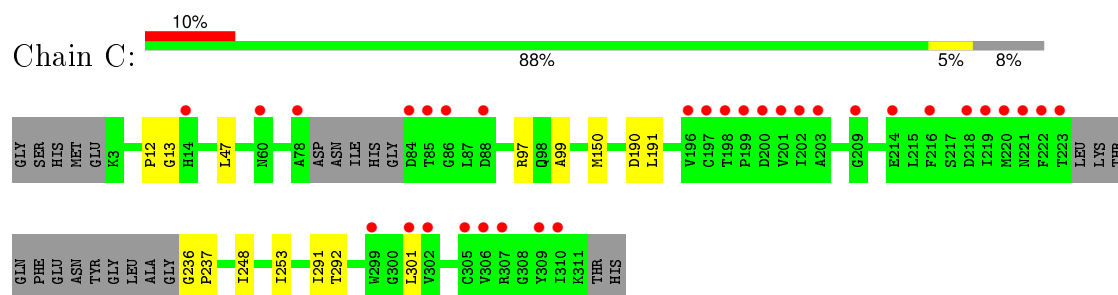
- Molecule 1: Putative uncharacterized protein YeiK



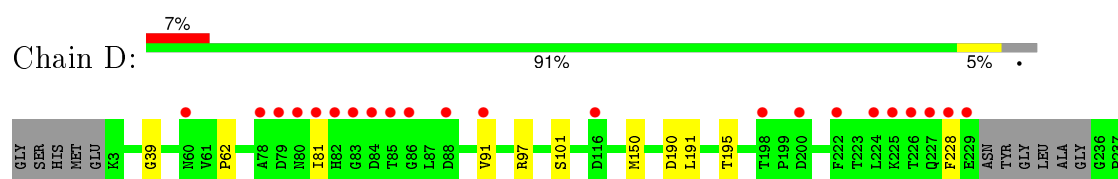
- Molecule 1: Putative uncharacterized protein YeiK



- Molecule 1: Putative uncharacterized protein YeiK



- Molecule 1: Putative uncharacterized protein YeiK





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.85Å 86.45Å 97.82Å 90.00° 98.86° 90.00°	Depositor
Resolution (Å)	44.97 – 2.00 44.97 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.3 (44.97-2.00) 97.3 (44.97-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.174 , 0.196 0.175 , 0.195	Depositor DCC
R_{free} test set	4602 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	23.7	Xtriage
Anisotropy	0.576	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.1	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 91905 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9711	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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: CA, DNB

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	1.15	12/2330 (0.5%)	0.92	9/3176 (0.3%)
1	B	0.74	0/2357	0.72	1/3209 (0.0%)
1	C	0.54	0/2234	0.58	0/3043
1	D	0.66	0/2359	0.65	0/3213
All	All	0.81	12/9280 (0.1%)	0.73	10/12641 (0.1%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	204	ARG	CZ-NH1	26.16	1.67	1.33
1	A	204	ARG	CD-NE	18.58	1.78	1.46
1	A	204	ARG	CZ-NH2	16.91	1.55	1.33
1	A	205	MET	CG-SD	13.31	2.15	1.81
1	A	208	ALA	C-N	11.19	1.53	1.33
1	A	307	ARG	CZ-NH1	10.05	1.46	1.33
1	A	204	ARG	CG-CD	9.48	1.75	1.51
1	A	213	GLY	C-O	9.16	1.38	1.23
1	A	208	ALA	C-O	8.00	1.38	1.23
1	A	207	ARG	CZ-NH1	7.85	1.43	1.33
1	A	204	ARG	NE-CZ	6.60	1.41	1.33
1	A	205	MET	SD-CE	5.10	2.06	1.77

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	ARG	NE-CZ-NH2	-27.43	106.58	120.30
1	A	204	ARG	CD-NE-CZ	-10.87	108.38	123.60
1	A	307	ARG	NE-CZ-NH2	-9.93	115.33	120.30
1	A	204	ARG	NE-CZ-NH1	9.66	125.13	120.30
1	A	207	ARG	NE-CZ-NH2	-9.49	115.55	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	205	MET	CG-SD-CE	-8.86	86.02	100.20
1	A	204	ARG	NH1-CZ-NH2	7.88	128.06	119.40
1	A	204	ARG	CG-CD-NE	-7.68	95.68	111.80
1	B	204	ARG	NE-CZ-NH2	-7.21	116.70	120.30
1	A	207	ARG	NE-CZ-NH1	5.87	123.24	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	2276	0	2272	27	1
1	B	2287	0	2307	19	1
1	C	2190	0	2201	6	0
1	D	2298	0	2302	9	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	17	0	16	2	0
3	B	17	0	16	2	0
3	C	17	0	17	0	0
3	D	17	0	16	2	0
4	A	101	0	0	2	0
4	B	221	0	0	8	0
4	C	97	0	0	0	0
4	D	169	0	0	3	0
All	All	9711	0	9147	65	2

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 4.

All (65) 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:ARG:CG	1:A:204:ARG:CD	1.75	1.58
1:A:204:ARG:CD	1:A:204:ARG:NE	1.78	1.45
1:A:205:MET:CE	1:A:205:MET:SD	2.06	1.44
1:A:205:MET:CG	1:A:205:MET:SD	2.15	1.34
1:B:15[C]:ASP:OD2	1:B:238:VAL:HA	1.73	0.88
4:B:434:HOH:O	1:D:280:VAL:HG11	1.76	0.83
1:B:15[A]:ASP:HB2	4:B:394:HOH:O	1.78	0.81
1:A:204:ARG:CZ	1:A:204:ARG:CD	2.59	0.80
1:A:204:ARG:CB	1:A:204:ARG:CD	2.59	0.80
1:B:15[B]:ASP:HB2	4:B:394:HOH:O	1.93	0.67
1:B:228:PHE:HA	1:B:232:GLY:CA	2.27	0.65
1:A:204:ARG:CG	1:A:204:ARG:NE	2.62	0.63
1:A:195:THR:OG1	1:A:238:VAL:O	2.20	0.60
1:B:228:PHE:HA	1:B:232:GLY:HA2	1.82	0.60
1:D:195:THR:OG1	1:D:238:VAL:O	2.18	0.60
1:D:62:PRO:CG	4:D:374:HOH:O	2.50	0.59
1:A:215:LEU:HG	1:A:219:ILE:HD12	1.84	0.58
1:A:81:ILE:HG13	3:A:502:DNB:N4	2.19	0.58
1:D:62:PRO:HG2	4:D:374:HOH:O	2.05	0.56
1:C:291:ILE:HG22	1:C:292:THR:HG23	1.87	0.56
1:A:248:ILE:HG21	1:A:301[A]:LEU:HD11	1.87	0.55
1:A:196:VAL:HA	1:A:237:PRO:HA	1.87	0.55
1:A:90:PRO:HG3	1:A:219:ILE:HG13	1.89	0.54
4:B:434:HOH:O	1:D:280:VAL:CG1	2.47	0.53
1:B:15[C]:ASP:HB3	4:B:394:HOH:O	2.09	0.53
1:A:196:VAL:HA	1:A:237:PRO:N	2.23	0.53
1:B:291:ILE:HG22	1:B:292:THR:HG23	1.89	0.52
1:B:55:GLN:HA	1:B:97[A]:ARG:HE	1.74	0.52
1:B:222:PHE:O	1:B:226:THR:HG22	2.09	0.52
1:A:205:MET:CE	1:A:205:MET:CG	2.87	0.52
1:D:291:ILE:HG22	1:D:292:THR:HG23	1.91	0.51
1:A:205:MET:SD	1:A:205:MET:CB	2.98	0.50
1:D:191:LEU:HD11	1:D:253:ILE:HG23	1.93	0.50
1:A:195:THR:O	1:A:237:PRO:HA	2.12	0.49
1:A:97:ARG:NH1	4:A:391:HOH:O	2.41	0.49
1:C:248:ILE:HG21	1:C:301:LEU:HD11	1.95	0.49
1:A:198:THR:HB	1:A:199:PRO:HD2	1.94	0.48
1:A:196:VAL:HA	1:A:237:PRO:CA	2.42	0.48
1:B:15[A]:ASP:OD2	1:B:239:HIS:HB2	2.13	0.48
1:D:62:PRO:HG3	4:D:374:HOH:O	2.11	0.47
1:B:191[A]:LEU:HD11	1:B:253:ILE:HG23	1.95	0.47
1:A:291:ILE:HG22	1:A:292:THR:HG23	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:ILE:O	1:A:97:ARG:NH1	2.46	0.46
1:A:191:LEU:HD11	1:A:253:ILE:HG23	1.98	0.46
3:B:502:DNB:H2	3:B:502:DNB:H2'	1.58	0.46
3:D:502:DNB:H2	3:D:502:DNB:H2'	1.76	0.45
1:B:15[C]:ASP:CG	4:B:447:HOH:O	2.55	0.45
1:A:14:HIS:CD2	1:A:219:ILE:HG23	2.52	0.45
1:A:14:HIS:HD2	1:A:219:ILE:HG23	1.83	0.44
1:D:81:ILE:HG13	3:D:502:DNB:HN4A	1.83	0.44
1:B:55:GLN:HB2	1:B:97[A]:ARG:HG2	1.98	0.44
3:A:502:DNB:H2	3:A:502:DNB:H2'	1.85	0.43
1:C:191:LEU:HD11	1:C:253:ILE:HG23	2.00	0.43
1:C:47:LEU:HD11	1:C:99:ALA:HB2	2.01	0.43
1:C:12:PRO:HA	1:C:13:GLY:HA3	1.78	0.43
3:B:502:DNB:C2	3:B:502:DNB:H5'	2.50	0.42
1:A:135:ARG:HD3	1:A:135:ARG:HA	1.87	0.42
1:C:236:GLY:HA2	1:C:237:PRO:HD3	1.87	0.42
1:B:52:ASN:ND2	4:B:314:HOH:O	2.52	0.41
1:B:91:VAL:HG22	4:B:471:HOH:O	2.20	0.41
1:B:47:LEU:HD11	1:B:99:ALA:HB2	2.04	0.40
1:B:191[A]:LEU:CD1	1:B:253:ILE:HG23	2.52	0.40
1:A:97:ARG:HD3	4:A:391:HOH:O	2.21	0.40
1:B:25:LYS:CG	1:B:308:GLY:HA3	2.51	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:ILE:O	1:A:207:ARG:NH2[2_646]	1.95	0.25
1:B:60:ASN:O	1:D:101:SER:OG[1_655]	2.09	0.11

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	302/316 (96%)	294 (97%)	7 (2%)	1 (0%)	46	41
1	B	303/316 (96%)	293 (97%)	9 (3%)	1 (0%)	46	41
1	C	287/316 (91%)	280 (98%)	7 (2%)	0	100	100
1	D	303/316 (96%)	293 (97%)	9 (3%)	1 (0%)	46	41
All	All	1195/1264 (94%)	1160 (97%)	32 (3%)	3 (0%)	46	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	232	GLY
1	A	39	GLY
1	D	39	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	248/259 (96%)	243 (98%)	5 (2%)	63	65
1	B	252/259 (97%)	249 (99%)	3 (1%)	78	81
1	C	239/259 (92%)	236 (99%)	3 (1%)	76	79
1	D	253/259 (98%)	248 (98%)	5 (2%)	63	65
All	All	992/1036 (96%)	976 (98%)	16 (2%)	70	73

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	ASN
1	A	97	ARG
1	A	150	MET
1	A	190	ASP
1	A	207	ARG
1	B	150	MET
1	B	190	ASP
1	B	231	TYR

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Mol	Chain	Res	Type
1	C	97	ARG
1	C	150	MET
1	C	190	ASP
1	D	91	VAL
1	D	97	ARG
1	D	150	MET
1	D	190	ASP
1	D	228	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	265	ASN
1	B	52	ASN
1	B	265	ASN
1	C	52	ASN
1	C	265	ASN
1	D	52	ASN
1	D	265	ASN

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](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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
3	DNB	A	502	2	18,18,18	1.17	2 (11%)	17,26,26	2.22	3 (17%)
3	DNB	B	502	2	18,18,18	1.12	1 (5%)	17,26,26	2.08	3 (17%)
3	DNB	C	502	2	18,18,18	1.11	1 (5%)	17,26,26	1.75	1 (5%)
3	DNB	D	502	2	18,18,18	1.18	2 (11%)	17,26,26	2.04	6 (35%)

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
3	DNB	A	502	2	-	0/6/22/22	0/2/2/2
3	DNB	B	502	2	-	0/6/22/22	0/2/2/2
3	DNB	C	502	2	-	0/6/22/22	0/2/2/2
3	DNB	D	502	2	-	0/6/22/22	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	502	DNB	C1-C1'	-3.20	1.47	1.51
3	A	502	DNB	C1-C1'	-3.03	1.47	1.51
3	C	502	DNB	C1-C1'	-2.89	1.48	1.51
3	B	502	DNB	C1-C1'	-2.82	1.48	1.51
3	A	502	DNB	C4'-N4'	-2.28	1.44	1.48
3	D	502	DNB	C4'-N4'	-2.23	1.44	1.48

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	DNB	C1-C1'-N4'	-7.49	102.44	113.47
3	B	502	DNB	C1-C1'-N4'	-6.61	103.74	113.47
3	C	502	DNB	C1-C1'-N4'	-6.03	104.61	113.47
3	D	502	DNB	C1-C1'-N4'	-5.31	105.66	113.47
3	D	502	DNB	C6-C1-C1'	-2.94	116.10	120.78
3	A	502	DNB	C6-C1-C1'	-2.51	116.79	120.78

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	502	DNB	C5-C6-C1	-2.44	118.69	121.20
3	D	502	DNB	C6-C5-C4	-2.26	118.63	121.37
3	A	502	DNB	C2'-C3'-C4'	2.38	107.15	103.17
3	D	502	DNB	C6-C1-C2	2.42	121.70	118.79
3	B	502	DNB	C6-C1-C2	2.51	121.81	118.79
3	D	502	DNB	C5-C4-C3	2.62	121.26	118.43
3	D	502	DNB	C2'-C3'-C4'	3.09	108.33	103.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	DNB	2	0
3	B	502	DNB	2	0
3	D	502	DNB	2	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	303/316 (95%)	0.37	41 (13%) 4 4	11, 39, 87, 110	2 (0%)
1	B	301/316 (95%)	-0.25	11 (3%) 45 47	9, 15, 38, 71	0
1	C	292/316 (92%)	0.10	32 (10%) 7 8	13, 35, 82, 96	1 (0%)
1	D	303/316 (95%)	-0.08	22 (7%) 18 19	11, 22, 51, 83	1 (0%)
All	All	1199/1264 (94%)	0.03	106 (8%) 12 13	9, 25, 77, 110	4 (0%)

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	81	ILE	9.5
1	B	231	TYR	6.6
1	D	228	PHE	6.4
1	A	198	THR	6.3
1	A	226	THR	6.2
1	D	80	ASN	6.2
1	D	83	GLY	6.0
1	C	203	ALA	5.7
1	C	201	VAL	5.7
1	D	82	HIS	5.5
1	D	84	ASP	5.2
1	C	202	ILE	5.1
1	C	223	THR	5.1
1	C	310	ILE	5.0
1	C	222	PHE	4.8
1	A	238	VAL	4.7
1	A	84	ASP	4.7
1	A	228	PHE	4.7
1	B	78	ALA	4.6
1	C	78	ALA	4.5
1	D	226	THR	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	86	GLY	4.3
1	B	226	THR	4.3
1	C	197	CYS	4.2
1	B	230	ASN	4.2
1	D	79	ASP	4.2
1	A	309	TYR	4.2
1	C	84	ASP	4.1
1	A	222	PHE	4.0
1	A	219	ILE	4.0
1	D	224	LEU	4.0
1	C	200	ASP	4.0
1	D	85	THR	4.0
1	C	199	PRO	3.9
1	C	198	THR	3.8
1	D	86	GLY	3.8
1	A	202	ILE	3.8
1	D	225	LYS	3.8
1	A	221	ASN	3.7
1	C	85	THR	3.6
1	A	197	CYS	3.6
1	A	237	PRO	3.6
1	C	221	ASN	3.6
1	A	227	GLN	3.5
1	D	227	GLN	3.4
1	A	211	PRO	3.4
1	B	86	GLY	3.4
1	A	91	VAL	3.3
1	D	229	GLU	3.2
1	A	199	PRO	3.2
1	C	301	LEU	3.2
1	A	218	ASP	3.2
1	A	305	CYS	3.2
1	C	307	ARG	3.2
1	B	232	GLY	3.1
1	C	305	CYS	3.1
1	C	309	TYR	3.1
1	A	203	ALA	3.0
1	C	302	VAL	3.0
1	A	81	ILE	3.0
1	D	91	VAL	3.0
1	C	60	ASN	2.9
1	B	233	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	222	PHE	2.9
1	C	218	ASP	2.8
1	B	228	PHE	2.7
1	A	223	THR	2.7
1	C	216	PHE	2.7
1	D	78	ALA	2.7
1	B	88	ASP	2.6
1	A	205	MET	2.6
1	A	196	VAL	2.6
1	A	82	HIS	2.6
1	D	200	ASP	2.5
1	A	208	ALA	2.5
1	C	306	VAL	2.5
1	C	88	ASP	2.4
1	A	307	ARG	2.4
1	B	234	ALA	2.4
1	A	80	ASN	2.4
1	B	14	HIS	2.4
1	A	94	PRO	2.3
1	A	207	ARG	2.3
1	A	201	VAL	2.3
1	A	209	GLY	2.3
1	A	300	GLY	2.3
1	A	229	GLU	2.3
1	C	14	HIS	2.3
1	A	116	ASP	2.3
1	D	198	THR	2.2
1	C	196	VAL	2.2
1	D	60[A]	ASN	2.2
1	A	225	LYS	2.2
1	A	92	PHE	2.2
1	C	219	ILE	2.2
1	A	301[A]	LEU	2.1
1	C	214	GLU	2.1
1	D	116	ASP	2.1
1	A	56	LYS	2.1
1	A	206	GLU	2.1
1	C	299	TRP	2.1
1	A	200	ASP	2.1
1	A	251	ASP	2.0
1	C	220	MET	2.0
1	C	209	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	88	ASP	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
3	DNB	C	502	17/17	0.61	0.30	2.79	48,60,64,64	0
3	DNB	B	502	17/17	0.69	0.24	1.10	18,42,49,49	0
3	DNB	A	502	17/17	0.88	0.16	0.57	35,41,49,49	0
3	DNB	D	502	17/17	0.84	0.22	0.32	19,35,43,44	0
2	CA	C	501	1/1	0.98	0.08	-0.55	27,27,27,27	0
2	CA	B	501	1/1	1.00	0.07	-0.74	13,13,13,13	0
2	CA	A	501	1/1	0.96	0.07	-1.19	24,24,24,24	0
2	CA	D	501	1/1	0.99	0.06	-1.56	16,16,16,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.