



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:02 PM GMT

PDB ID : 4E73
Title : Crystal structure of JNK1beta-JIP in complex with an azaquinolone inhibitor
Authors : Lukacs, C.M.; Janson, C.A.
Deposited on : 2012-03-16
Resolution : 2.27 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

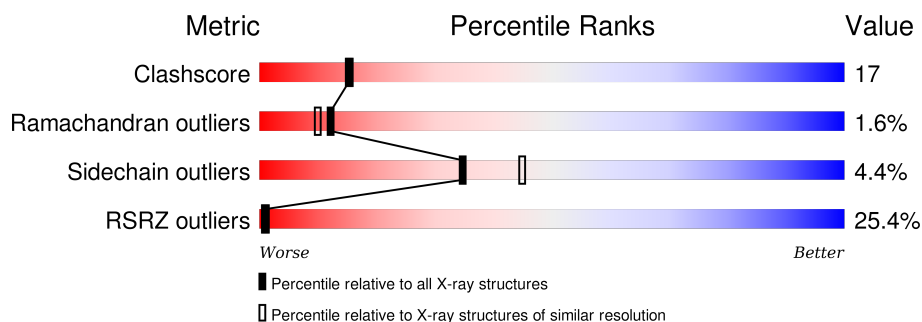
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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))
Clashscore	102246	5929 (2.30-2.26)
Ramachandran outliers	100387	5851 (2.30-2.26)
Sidechain outliers	100360	5850 (2.30-2.26)
RSRZ outliers	91569	5204 (2.30-2.26)

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	369	
2	B	11	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2784 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 Mitogen-activated protein kinase 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	1	0
			2581	1659	435	467	20			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	364	HIS	-	EXPRESSION TAG	UNP P45983
A	365	HIS	-	EXPRESSION TAG	UNP P45983
A	366	HIS	-	EXPRESSION TAG	UNP P45983
A	367	HIS	-	EXPRESSION TAG	UNP P45983
A	368	HIS	-	EXPRESSION TAG	UNP P45983
A	369	HIS	-	EXPRESSION TAG	UNP P45983

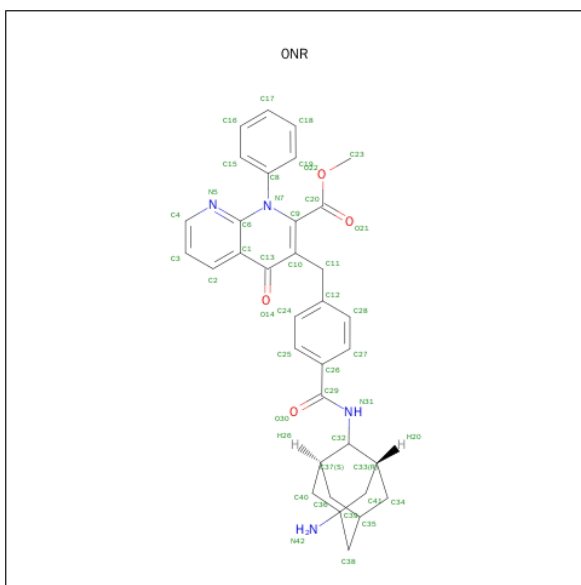
- Molecule 2 is a protein called C-Jun-amino-terminal kinase-interacting protein 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	9	Total	C	N	O	0	0	0
			72	46	14	12			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	153	LYS	ARG	CONFLICT	UNP Q9UQF2

- Molecule 3 is METHYL 3-(4-([(1R,2S,3S,5S,7S)-5-AMINOTRICYCLO[3.3.1.1^{3,7}]DEC-2-YL]CARBAMOYL)BENZYL)-4-OXO-1-PHENYL-1,4-DIHYDRO-1,8-NAPHTHYRIDINE-2-CARBOXYLATE (three-letter code: 0NR) (formula: C₃₄H₃₄N₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			42	34	4	4		

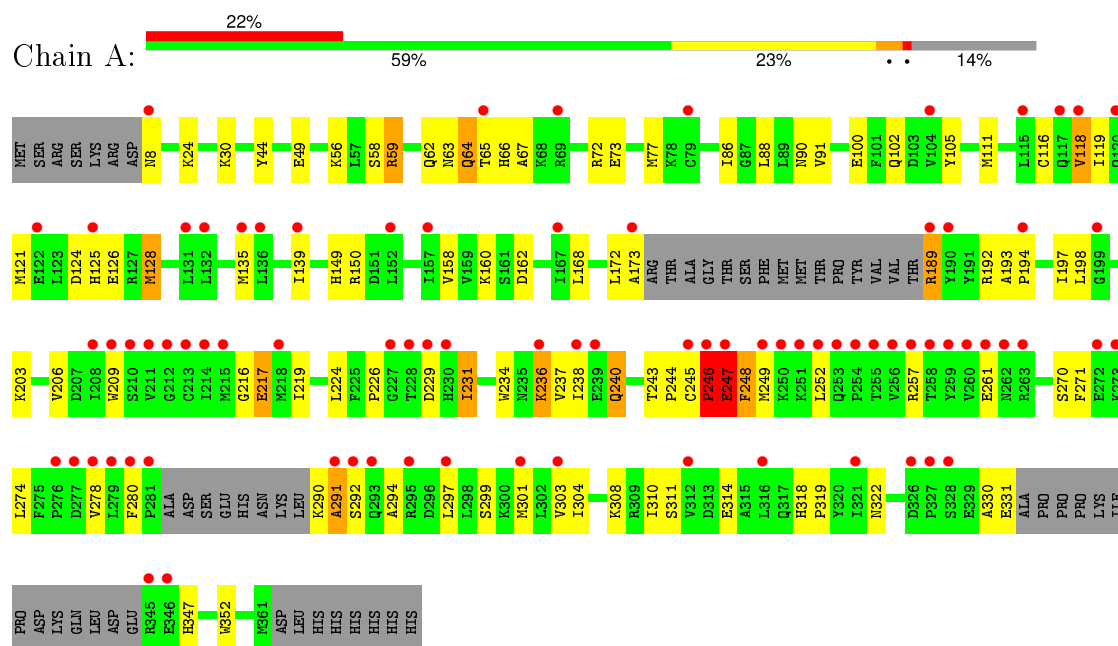
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	88	Total O 88 88	0	0
4	B	1	Total O 1 1	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 ($\text{RSRZ} > 2$). 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: Mitogen-activated protein kinase 8



• Molecule 2: C-Jun-amino-terminal kinase-interacting protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	62.90Å 79.84Å 85.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.70 – 2.27 27.69 – 2.27	Depositor EDS
% Data completeness (in resolution range)	98.9 (27.70-2.27) 99.0 (27.69-2.27)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 2.26Å)	Xtriage
Refinement program	CNX 2005	Depositor
R, R_{free}	0.247 , 0.282 0.248 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	48.8	Xtriage
Anisotropy	0.122	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 61.2	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 20301 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2784	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 4.73% 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: 0NR

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	0.32	0/2635	0.48	0/3555
2	B	0.33	0/73	0.63	0/98
All	All	0.32	0/2708	0.49	0/3653

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	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	246	PRO	Peptide

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	2581	0	2601	94	0
2	B	72	0	82	3	0
3	A	42	0	34	0	0
4	A	88	0	0	4	0
4	B	1	0	0	0	0
All	All	2784	0	2717	94	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 17.

All (94) 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:59:ARG:NH1	1:A:59:ARG:HB3	1.83	0.94
1:A:245:CYS:HB2	1:A:246:PRO:HD2	1.53	0.90
1:A:245:CYS:SG	1:A:247:GLU:HB3	2.14	0.88
1:A:231:ILE:H	1:A:231:ILE:HD13	1.42	0.84
1:A:63:ASN:HD22	1:A:65:THR:H	1.24	0.83
1:A:119:ILE:HD11	1:A:217:GLU:HB3	1.61	0.81
1:A:189:ARG:HD3	1:A:197:ILE:HG22	1.64	0.80
1:A:59:ARG:HB3	1:A:59:ARG:HH11	1.50	0.77
1:A:240:GLN:NE2	1:A:274:LEU:HD22	2.08	0.69
1:A:59:ARG:HB2	1:A:62:GLN:HB2	1.73	0.68
1:A:226:PRO:HD2	1:A:236:LYS:HD3	1.77	0.67
1:A:249:MET:O	1:A:257:ARG:HD2	1.95	0.67
1:A:216:GLY:HA3	1:A:224:LEU:HD11	1.77	0.66
1:A:63:ASN:ND2	1:A:65:THR:H	1.94	0.65
1:A:290:LYS:O	1:A:292:SER:N	2.31	0.64
1:A:271:PHE:CZ	1:A:299:SER:HA	2.31	0.64
1:A:249:MET:HA	1:A:252:LEU:HD12	1.81	0.62
1:A:197:ILE:HG13	1:A:198:LEU:CD1	2.28	0.62
1:A:118:VAL:O	1:A:121:MET:HG2	1.99	0.62
1:A:189:ARG:HG2	1:A:192:ARG:HD2	1.80	0.62
1:A:247:GLU:O	1:A:248:PHE:HB2	2.00	0.61
1:A:197:ILE:HG13	1:A:198:LEU:HD12	1.82	0.61
1:A:160:LYS:HB3	1:A:162:ASP:OD1	2.01	0.60
1:A:322:ASN:HB2	4:A:581:HOH:O	2.03	0.59
1:A:56:LYS:HE3	1:A:105:TYR:OH	2.03	0.58
1:A:58:SER:C	1:A:59:ARG:HG2	2.22	0.58
1:A:135[A]:MET:O	1:A:139:ILE:HG13	2.03	0.58
1:A:319:PRO:HA	1:A:322:ASN:HD21	1.69	0.57
1:A:245:CYS:HG	1:A:247:GLU:HB3	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:PRO:O	1:A:198:LEU:HD13	2.04	0.57
1:A:73:GLU:O	1:A:77:MET:HG3	2.04	0.57
1:A:67:ALA:HB1	1:A:352:TRP:HB3	1.87	0.57
1:A:118:VAL:HG21	2:B:160:LEU:HD21	1.85	0.56
1:A:319:PRO:HA	1:A:322:ASN:ND2	2.21	0.56
1:A:59:ARG:CZ	1:A:59:ARG:HB3	2.36	0.56
1:A:172:LEU:O	1:A:173:ALA:CB	2.54	0.55
1:A:63:ASN:HD22	1:A:65:THR:N	2.01	0.55
1:A:249:MET:HA	1:A:252:LEU:CD1	2.37	0.55
1:A:257:ARG:O	1:A:261:GLU:HB2	2.08	0.53
1:A:135[B]:MET:O	1:A:139:ILE:HG13	2.09	0.53
1:A:63:ASN:HD21	1:A:65:THR:HB	1.73	0.53
1:A:116:CYS:O	1:A:119:ILE:HG22	2.08	0.53
1:A:198:LEU:HD11	1:A:234:TRP:CE3	2.45	0.52
1:A:126:GLU:HG2	2:B:157:PRO:HG3	1.90	0.52
1:A:297:LEU:HD11	1:A:301:MET:HE2	1.92	0.51
1:A:111:MET:HG3	1:A:158:VAL:HG23	1.93	0.51
1:A:100:GLU:O	1:A:102:GLN:HG2	2.10	0.50
1:A:244:PRO:O	1:A:249:MET:HE2	2.11	0.50
1:A:59:ARG:HG3	1:A:66:HIS:CE1	2.46	0.49
1:A:270:SER:O	1:A:274:LEU:HG	2.12	0.49
1:A:203:LYS:O	1:A:206:VAL:HG12	2.12	0.49
1:A:172:LEU:O	1:A:173:ALA:HB3	2.13	0.48
1:A:234:TRP:O	1:A:238:ILE:HG12	2.12	0.48
1:A:310:ILE:HG12	1:A:311:SER:N	2.28	0.48
1:A:247:GLU:O	1:A:248:PHE:CB	2.62	0.48
1:A:229:ASP:HB3	1:A:231:ILE:HD11	1.96	0.47
1:A:231:ILE:H	1:A:231:ILE:CD1	2.11	0.47
1:A:330:ALA:O	1:A:331:GLU:HG3	2.14	0.47
1:A:318:HIS:CG	1:A:319:PRO:HD2	2.50	0.47
1:A:246:PRO:O	1:A:248:PHE:N	2.49	0.46
1:A:72:ARG:HD3	4:A:583:HOH:O	2.16	0.46
1:A:124:ASP:O	1:A:128:MET:HB2	2.15	0.46
1:A:72:ARG:NE	4:A:588:HOH:O	2.26	0.46
1:A:119:ILE:CD1	1:A:217:GLU:HB3	2.38	0.45
1:A:189:ARG:CG	1:A:192:ARG:HD2	2.45	0.45
1:A:245:CYS:HB2	1:A:246:PRO:CD	2.33	0.45
1:A:149:HIS:O	1:A:150:ARG:HB2	2.16	0.45
1:A:72:ARG:CZ	1:A:173:ALA:HB3	2.46	0.45
1:A:237:VAL:HG12	1:A:304:ILE:HD11	1.98	0.44
1:A:231:ILE:HD13	1:A:231:ILE:N	2.23	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:ASP:HB3	1:A:231:ILE:CD1	2.48	0.44
1:A:125:HIS:CD2	1:A:290:LYS:HB2	2.53	0.44
1:A:63:ASN:ND2	1:A:65:THR:N	2.64	0.43
1:A:189:ARG:NH1	1:A:192:ARG:HH11	2.15	0.43
1:A:193:ALA:HA	1:A:209:TRP:CD1	2.54	0.43
1:A:56:LYS:HE3	1:A:105:TYR:HH	1.83	0.43
1:A:310:ILE:HD11	1:A:314:GLU:HB3	2.01	0.43
1:A:240:GLN:HB3	1:A:240:GLN:HE21	1.52	0.43
1:A:126:GLU:HG2	2:B:157:PRO:CG	2.49	0.42
1:A:44:TYR:OH	1:A:49:GLU:HA	2.19	0.42
1:A:8:ASN:O	1:A:24:LYS:HE3	2.19	0.42
1:A:280:PHE:CD1	1:A:291:ALA:HA	2.54	0.42
1:A:219:ILE:HD13	1:A:280:PHE:CZ	2.55	0.42
1:A:88:LEU:HD11	1:A:91:VAL:CG2	2.50	0.41
1:A:86:ILE:HG13	1:A:168:LEU:HD12	2.03	0.41
1:A:280:PHE:HE1	1:A:294:ALA:HB3	1.86	0.41
1:A:189:ARG:CD	1:A:197:ILE:HG22	2.43	0.41
1:A:280:PHE:CE1	1:A:294:ALA:HB3	2.56	0.41
1:A:64:GLN:NE2	1:A:347:HIS:O	2.53	0.41
1:A:303:VAL:HG11	1:A:308:LYS:HB2	2.03	0.41
1:A:245:CYS:CB	1:A:246:PRO:HD2	2.33	0.40
1:A:203:LYS:NZ	4:A:586:HOH:O	2.53	0.40
1:A:243:THR:HG22	1:A:244:PRO:O	2.22	0.40
1:A:88:LEU:HD11	1:A:91:VAL:HG22	2.03	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	311/369 (84%)	293 (94%)	14 (4%)	4 (1%)	15 14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	7/11 (64%)	6 (86%)	0	1 (14%)	0	0
All	All	318/380 (84%)	299 (94%)	14 (4%)	5 (2%)	12	10

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	248	PHE
1	A	291	ALA
2	B	155	LYS
1	A	246	PRO
1	A	247	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	285/331 (86%)	272 (95%)	13 (5%)	33	43
2	B	9/11 (82%)	9 (100%)	0	100	100
All	All	294/342 (86%)	281 (96%)	13 (4%)	35	45

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	LYS
1	A	59	ARG
1	A	64	GLN
1	A	90	ASN
1	A	118	VAL
1	A	128	MET
1	A	189	ARG
1	A	217	GLU
1	A	231	ILE
1	A	236	LYS
1	A	240	GLN

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Mol	Chain	Res	Type
1	A	247	GLU
1	A	278	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	27	GLN
1	A	62	GLN
1	A	63	ASN
1	A	90	ASN
1	A	240	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	$\# Z > 2$
3	0NR	A	401	-	46,48,48	2.49	22 (47%)	50,72,72	1.20	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
3	0NR	A	401	-	-	0/22/53/53	0/4/7/7

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	0NR	C39-N42	-2.03	1.42	1.49
3	A	401	0NR	C41-C33	2.07	1.57	1.53
3	A	401	0NR	C24-C12	2.10	1.43	1.38
3	A	401	0NR	C25-C26	2.13	1.42	1.39
3	A	401	0NR	C29-N31	2.26	1.39	1.34
3	A	401	0NR	C28-C12	2.28	1.43	1.38
3	A	401	0NR	C28-C27	2.50	1.43	1.38
3	A	401	0NR	C6-N7	2.58	1.45	1.39
3	A	401	0NR	C27-C26	2.65	1.43	1.39
3	A	401	0NR	C11-C10	2.70	1.56	1.52
3	A	401	0NR	C6-N5	2.77	1.39	1.35
3	A	401	0NR	C3-C2	2.86	1.43	1.36
3	A	401	0NR	C4-N5	3.16	1.38	1.32
3	A	401	0NR	C40-C39	3.43	1.57	1.53
3	A	401	0NR	C38-C39	3.60	1.57	1.53
3	A	401	0NR	C15-C8	3.60	1.44	1.38
3	A	401	0NR	C19-C8	3.66	1.44	1.38
3	A	401	0NR	C13-C10	3.82	1.52	1.41
3	A	401	0NR	C41-C39	3.90	1.58	1.53
3	A	401	0NR	C37-C32	4.13	1.58	1.53
3	A	401	0NR	C33-C32	4.47	1.58	1.53
3	A	401	0NR	C13-C1	6.84	1.50	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	0NR	C1-C6-N5	-3.26	119.65	123.53
3	A	401	0NR	C10-C11-C12	-2.13	108.75	113.64
3	A	401	0NR	C2-C1-C6	2.04	118.90	117.00
3	A	401	0NR	C13-C1-C6	2.08	120.17	117.89
3	A	401	0NR	C8-N7-C9	2.10	121.85	119.33
3	A	401	0NR	O22-C20-O21	2.14	127.87	123.44
3	A	401	0NR	C4-N5-C6	2.92	120.55	116.93

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	318/369 (86%)	1.23	81 (25%)  	29, 56, 99, 113	0
2	B	9/11 (81%)	1.09	2 (22%)  	66, 67, 80, 82	0
All	All	327/380 (86%)	1.22	83 (25%)  	29, 56, 99, 113	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	291	ALA	7.9
1	A	253	GLN	7.9
1	A	258	THR	6.8
1	A	278	VAL	6.7
1	A	256	VAL	6.7
1	A	229	ASP	6.3
1	A	211	VAL	6.2
1	A	247	GLU	6.1
1	A	254	PRO	5.6
1	A	292	SER	5.3
1	A	250	LYS	5.2
1	A	345	ARG	5.1
1	A	135[A]	MET	4.8
1	A	228	THR	4.8
1	A	280	PHE	4.8
1	A	279	LEU	4.7
1	A	328	SER	4.6
1	A	246	PRO	4.5
1	A	273	LYS	4.5
1	A	152	LEU	4.4
1	A	326	ASP	4.3
1	A	281	PRO	4.3
1	A	214	ILE	4.3
1	A	189	ARG	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	8	ASN	4.0
1	A	276	PRO	4.0
1	A	131	LEU	3.9
1	A	136	LEU	3.7
1	A	249	MET	3.6
1	A	262	ASN	3.6
1	A	227	GLY	3.6
1	A	139	ILE	3.5
1	A	132	LEU	3.4
1	A	115	LEU	3.4
1	A	65	THR	3.3
1	A	157	ILE	3.3
1	A	190	TYR	3.2
1	A	245	CYS	3.2
1	A	210	SER	3.2
1	A	120	GLN	3.1
1	A	208	ILE	3.1
1	A	79	CYS	2.9
1	A	239	GLU	2.8
1	A	301	MET	2.8
1	A	117	GLN	2.8
1	A	303	VAL	2.8
1	A	213	CYS	2.7
1	A	260	VAL	2.7
1	A	230	HIS	2.7
1	A	118	VAL	2.7
1	A	125	HIS	2.7
1	A	327	PRO	2.7
1	A	295	ARG	2.6
2	B	158	THR	2.6
1	A	257	ARG	2.6
1	A	173	ALA	2.6
1	A	122	GLU	2.6
1	A	261	GLU	2.6
1	A	199	GLY	2.6
1	A	215	MET	2.6
1	A	194	PRO	2.5
1	A	255	THR	2.5
1	A	236	LYS	2.4
1	A	212	GLY	2.4
1	A	252	LEU	2.4
1	A	293	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	167	ILE	2.4
1	A	104	VAL	2.4
2	B	155	LYS	2.4
1	A	218	MET	2.3
1	A	272	GLU	2.3
1	A	259	TYR	2.3
1	A	321	ILE	2.3
1	A	312	VAL	2.2
1	A	263	ARG	2.2
1	A	316	LEU	2.2
1	A	297	LEU	2.2
1	A	346	GLU	2.2
1	A	238	ILE	2.2
1	A	277	ASP	2.2
1	A	69	ARG	2.1
1	A	209	TRP	2.1
1	A	251	LYS	2.1

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	0NR	A	401	42/42	0.93	0.15	-0.01	24,39,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.