



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 12:24 pm GMT

PDB ID : 4YYZ
Title : 11B-HYDROXYSTEROID DEHYDROGENASE TYPE I IN COMPLEX
WITH INHIBITOR
Authors : Branden, G.; Boden, C.; Ogg, D.
Deposited on : 2015-03-24
Resolution : 3.20 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

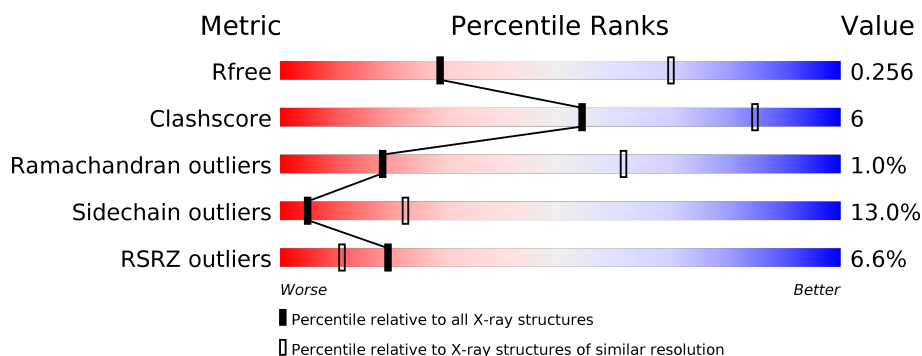
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	100719	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)

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	 5% 78% 20% •
1	B	259	 8% 73% 24% •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4210 atoms, of which 104 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 Corticosteroid 11-beta-dehydrogenase isozyme 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	0	0
			1986	1265	338	369	14			
1	B	258	Total	C	N	O	S	0	0	0
			1974	1256	337	367	14			

There are 8 discrepancies between the modelled and reference sequences:

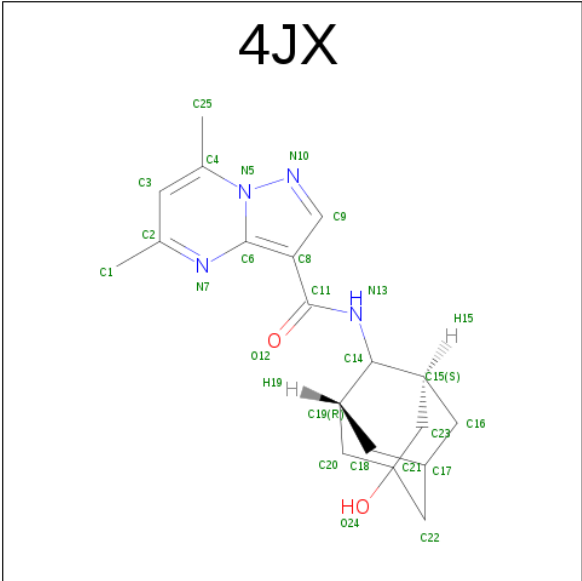
Chain	Residue	Modelled	Actual	Comment	Reference
A	179	LEU	MET	conflict	UNP P28845
A	262	ARG	LEU	conflict	UNP P28845
A	272	SER	CYS	conflict	UNP P28845
A	278	GLU	PHE	conflict	UNP P28845
B	179	LEU	MET	conflict	UNP P28845
B	262	ARG	LEU	conflict	UNP P28845
B	272	SER	CYS	conflict	UNP P28845
B	278	GLU	PHE	conflict	UNP P28845

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			76	21	28	7	17	3		
2	B	1	Total	C	H	N	O	P	0	0
			76	21	28	7	17	3		

- Molecule 3 is N-[(1R,2s,3S,5s,7s)-5-hydroxytricyclo[3.3.1.1 3,7]dec-2-yl]-5,7-dimethylpyrazolo[1,5-a]pyrimidine-3-carboxamide (three-letter code: 4JX) (formula: C₁₉H₂₄N₄O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			49	19	24	4	2		

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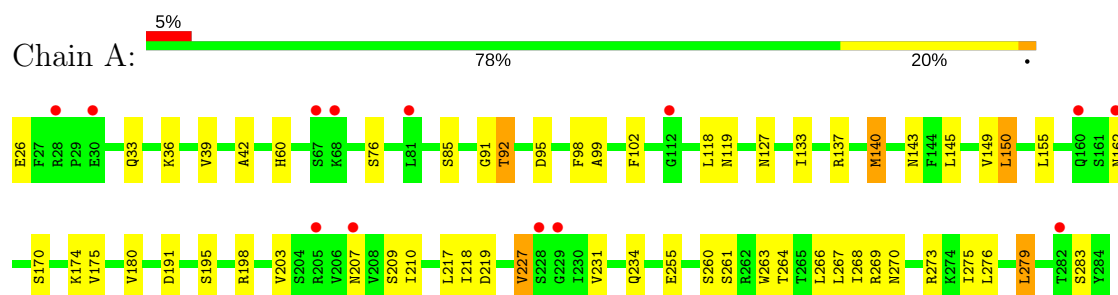
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	H	N	O	0	0
			49	19	24	4	2		

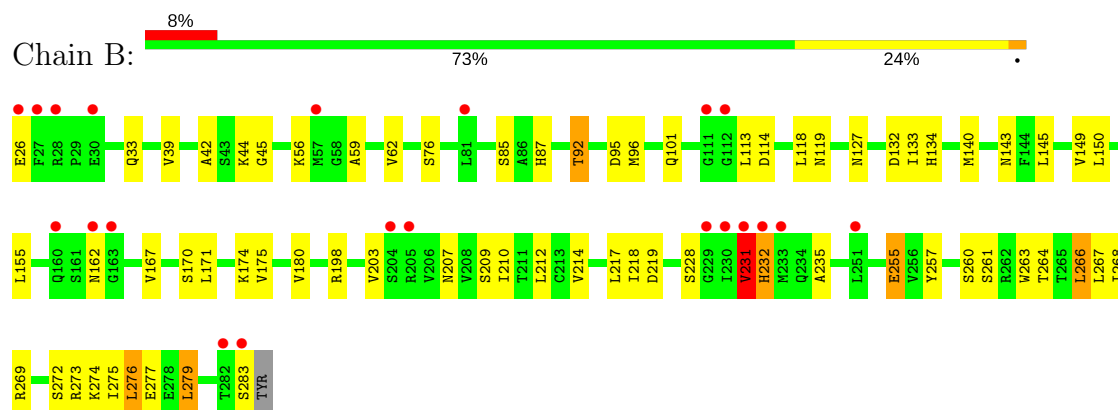
3 Residue-property plots [i](#)

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: Corticosteroid 11-beta-dehydrogenase isozyme 1



- Molecule 1: Corticosteroid 11-beta-dehydrogenase isozyme 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	107.79Å 107.79Å 136.02Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.75 – 3.20 19.51 – 3.20	Depositor EDS
% Data completeness (in resolution range)	97.1 (19.75-3.20) 97.1 (19.51-3.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 3.22Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.218 , 0.267 0.215 , 0.256	Depositor DCC
R_{free} test set	751 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	113.4	Xtriage
Anisotropy	0.338	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 122.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.015 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4210	wwPDB-VP
Average B, all atoms (Å ²)	139.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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: 4JX, NAP

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	0.55	0/2019	0.76	0/2726
1	B	0.53	0/2006	0.76	1/2708 (0.0%)
All	All	0.54	0/4025	0.76	1/5434 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	231	VAL	C-N-CA	5.71	135.97	121.70

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	1986	0	2035	28	0
1	B	1974	0	2026	33	0
2	A	48	28	25	1	0
2	B	48	28	25	3	0
3	A	25	24	24	0	0
3	B	25	24	24	0	0
All	All	4106	104	4159	50	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 6.

All (50) 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:140:MET:SD	1:A:140:MET:CE	2.02	1.47
1:B:231:VAL:HA	1:B:232:HIS:HB3	1.28	1.16
1:A:175:VAL:HG22	1:B:273:ARG:HD3	1.59	0.82
1:A:99:ALA:HB1	1:A:150:LEU:CD1	2.13	0.78
1:B:261:SER:HB3	1:B:264:THR:HG23	1.76	0.67
1:B:45:GLY:HA3	2:B:301:NAP:O2N	1.95	0.66
1:A:198:ARG:HG3	1:A:210:ILE:HB	1.78	0.66
1:A:261:SER:HB3	1:A:264:THR:HG23	1.78	0.66
1:A:91:GLY:HA3	1:A:102:PHE:HZ	1.60	0.65
1:B:198:ARG:HG3	1:B:210:ILE:HB	1.80	0.64
1:B:263:TRP:HA	1:B:266:LEU:HD12	1.84	0.60
1:B:273:ARG:HD2	1:B:277:GLU:OE2	2.02	0.60
1:B:218:ILE:HB	2:B:301:NAP:N7N	2.18	0.58
1:A:175:VAL:CG2	1:B:273:ARG:HD3	2.30	0.58
1:B:231:VAL:HA	1:B:232:HIS:CB	2.18	0.54
1:A:118:LEU:HD22	1:A:150:LEU:HD23	1.90	0.53
1:A:276:LEU:HD13	1:B:267:LEU:HB3	1.90	0.53
1:A:273:ARG:HG3	1:B:175:VAL:HG22	1.92	0.51
1:A:231:VAL:HG11	1:B:283:SER:O	2.11	0.50
1:A:275:ILE:O	1:A:279:LEU:HB2	2.12	0.50
1:B:214:VAL:HB	1:B:257:TYR:HD1	1.77	0.49
1:B:217:LEU:HD23	1:B:235:ALA:HB2	1.94	0.49
1:A:95:ASP:O	1:A:98:PHE:HB2	2.14	0.48
1:B:212:LEU:O	1:B:255:GLU:HA	2.14	0.47
1:A:174:LYS:HB2	1:A:268:ILE:HD11	1.97	0.46
1:A:267:LEU:O	1:B:272:SER:HB3	2.15	0.46
1:B:231:VAL:CA	1:B:232:HIS:HB3	2.20	0.45
1:A:217:LEU:HD21	1:A:227:VAL:HG11	1.98	0.45
1:A:133:ILE:HG21	1:B:149:VAL:HG22	1.99	0.45
1:A:99:ALA:HB1	1:A:150:LEU:HD11	1.96	0.44
1:A:264:THR:HB	1:B:276:LEU:HD21	1.99	0.44
1:A:36:LYS:HA	1:A:60:HIS:HB2	2.00	0.44
1:A:149:VAL:HG22	1:B:133:ILE:HG21	1.98	0.44
1:A:60:HIS:ND1	1:A:85:SER:HB3	2.33	0.44
1:B:118:LEU:HD12	1:B:167:VAL:HG22	2.00	0.43
1:A:276:LEU:HD13	1:B:267:LEU:HD13	1.99	0.43
1:B:174:LYS:HB2	1:B:268:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:LYS:HG3	2:B:301:NAP:H3B	2.01	0.43
1:A:218:ILE:HB	2:A:301:NAP:N7N	2.33	0.43
1:A:39:VAL:HG12	1:A:42:ALA:HB2	2.00	0.43
1:A:92:THR:HG23	1:A:95:ASP:H	1.84	0.42
1:B:39:VAL:HG12	1:B:42:ALA:HB2	2.01	0.42
1:A:191:ASP:O	1:A:195:SER:HB2	2.18	0.42
1:B:132:ASP:OD1	1:B:134:HIS:HB2	2.18	0.42
1:B:92:THR:HG23	1:B:95:ASP:H	1.83	0.42
1:B:62:VAL:HG22	1:B:87:HIS:HB2	2.02	0.41
1:B:118:LEU:CD2	1:B:150:LEU:HD13	2.51	0.41
1:A:137:ARG:HH22	1:B:96:MET:HG3	1.84	0.40
1:B:171:LEU:HD12	1:B:171:LEU:HA	1.90	0.40
1:B:275:ILE:O	1:B:279:LEU:HB2	2.21	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%)	240 (93%)	15 (6%)	2 (1%)	22	65
1	B	256/259 (99%)	236 (92%)	17 (7%)	3 (1%)	15	56
All	All	513/518 (99%)	476 (93%)	32 (6%)	5 (1%)	18	61

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	59	ALA
1	B	232	HIS
1	A	219	ASP
1	B	219	ASP
1	A	234	GLN

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	216/216 (100%)	190 (88%)	26 (12%)	6	26
1	B	215/216 (100%)	185 (86%)	30 (14%)	4	18
All	All	431/432 (100%)	375 (87%)	56 (13%)	5	22

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	GLU
1	A	33	GLN
1	A	76	SER
1	A	92	THR
1	A	119	ASN
1	A	127	ASN
1	A	140	MET
1	A	143	ASN
1	A	145	LEU
1	A	150	LEU
1	A	155	LEU
1	A	162	ASN
1	A	170	SER
1	A	180	VAL
1	A	203	VAL
1	A	207	ASN
1	A	209	SER
1	A	227	VAL
1	A	255	GLU
1	A	260	SER
1	A	263	TRP
1	A	266	LEU
1	A	269	ARG
1	A	270	ASN
1	A	279	LEU
1	A	283	SER
1	B	26	GLU

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Mol	Chain	Res	Type
1	B	33	GLN
1	B	56	LYS
1	B	76	SER
1	B	85	SER
1	B	92	THR
1	B	101	GLN
1	B	113	LEU
1	B	114	ASP
1	B	119	ASN
1	B	127	ASN
1	B	140	MET
1	B	143	ASN
1	B	145	LEU
1	B	155	LEU
1	B	162	ASN
1	B	170	SER
1	B	180	VAL
1	B	203	VAL
1	B	207	ASN
1	B	209	SER
1	B	228	SER
1	B	231	VAL
1	B	255	GLU
1	B	260	SER
1	B	266	LEU
1	B	269	ARG
1	B	274	LYS
1	B	276	LEU
1	B	279	LEU

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	72	GLN
1	A	77	HIS
1	A	134	HIS
1	A	162	ASN
1	A	270	ASN
1	B	77	HIS
1	B	119	ASN
1	B	127	ASN
1	B	162	ASN

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 ⓘ

4 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	NAP	A	301	-	44,52,52	0.57	0	51,80,80	0.91	1 (1%)
3	4JX	A	302	-	24,29,29	0.31	0	28,46,46	0.76	1 (3%)
2	NAP	B	301	-	44,52,52	0.67	0	51,80,80	0.95	2 (3%)
3	4JX	B	302	-	24,29,29	0.35	0	28,46,46	0.80	2 (7%)

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	NAP	A	301	-	-	0/27/67/67	0/5/5/5
3	4JX	A	302	-	-	0/6/39/39	0/2/5/5
2	NAP	B	301	-	-	0/27/67/67	0/5/5/5
3	4JX	B	302	-	-	0/6/39/39	0/2/5/5

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	NAP	O2X-P2B-O2B	-3.40	90.52	106.00
2	A	301	NAP	O2X-P2B-O2B	-3.16	91.62	106.00
3	B	302	4JX	C4-C3-C2	2.02	122.06	119.29
2	B	301	NAP	O3X-P2B-O2X	2.14	116.23	107.61
3	B	302	4JX	C25-C4-N5	2.56	120.89	118.12
3	A	302	4JX	C25-C4-N5	2.93	121.29	118.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	NAP	1	0
2	B	301	NAP	3	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%)	0.05	13 (5%) 30 17	87, 136, 175, 199	0
1	B	258/259 (99%)	0.27	21 (8%) 13 7	88, 138, 190, 215	0
All	All	517/518 (99%)	0.16	34 (6%) 19 11	87, 138, 187, 215	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	57	MET	9.7
1	B	233	MET	5.3
1	B	160	GLN	5.1
1	B	26	GLU	5.1
1	B	229	GLY	4.6
1	A	282	THR	4.0
1	B	232	HIS	3.9
1	B	28	ARG	3.9
1	A	112	GLY	3.8
1	B	112	GLY	3.7
1	B	27	PHE	3.5
1	B	204	SER	3.5
1	B	230	ILE	3.2
1	B	162	ASN	3.1
1	B	205	ARG	3.1
1	A	207	ASN	3.0
1	B	231	VAL	3.0
1	A	160	GLN	3.0
1	A	30	GLU	2.9
1	B	282	THR	2.9
1	A	68	LYS	2.8
1	B	81	LEU	2.8
1	A	28	ARG	2.8
1	B	251	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	30	GLU	2.7
1	A	81	LEU	2.6
1	B	163	GLY	2.5
1	A	229	GLY	2.5
1	B	283	SER	2.5
1	A	67	SER	2.4
1	A	162	ASN	2.2
1	A	205	ARG	2.1
1	A	228	SER	2.1
1	B	111	GLY	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
3	4JX	A	302	25/25	0.93	0.30	1.32	126,133,148,148	0
3	4JX	B	302	25/25	0.90	0.26	0.37	108,116,139,140	0
2	NAP	A	301	48/48	0.92	0.17	-0.66	98,122,143,147	0
2	NAP	B	301	48/48	0.95	0.15	-0.88	100,113,127,130	0

6.5 Other polymers [i](#)

There are no such residues in this entry.