



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 31, 2023 – 03:09 AM EDT

PDB ID : 1CES
Title : CRYSTALS OF DEMETALLIZED CONCANAVALIN A SOAKED WITH ZINC HAVE A ZINC ION BOUND IN THE S1 SITE
Authors : Bouckaert, J.; Loris, R.; Poortmans, F.; Wyns, L.
Deposited on : 1996-02-15
Resolution : 2.70 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.34
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) : 2.34

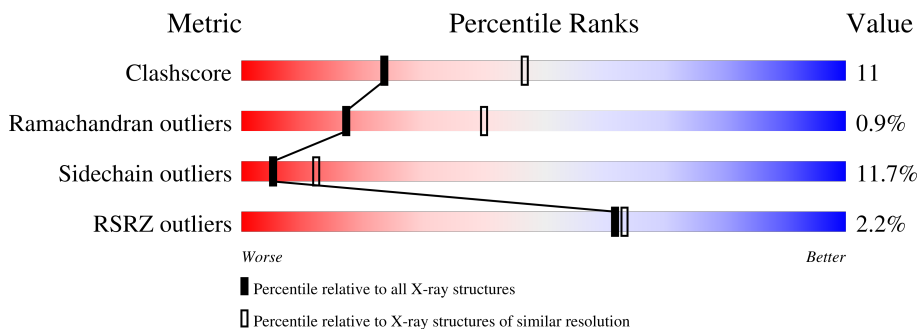
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 $\leq 5\%$. 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	237	
1	B	237	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3450 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 CONCANAVALIN A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	225	1712	1086	286	338	2	0	0	2
1	B	225	1697	1080	282	333	2	0	0	2

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	151	ASP	GLU	conflict	UNP P02866
A	155	GLU	ARG	conflict	UNP P02866
B	151	ASP	GLU	conflict	UNP P02866
B	155	GLU	ARG	conflict	UNP P02866

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

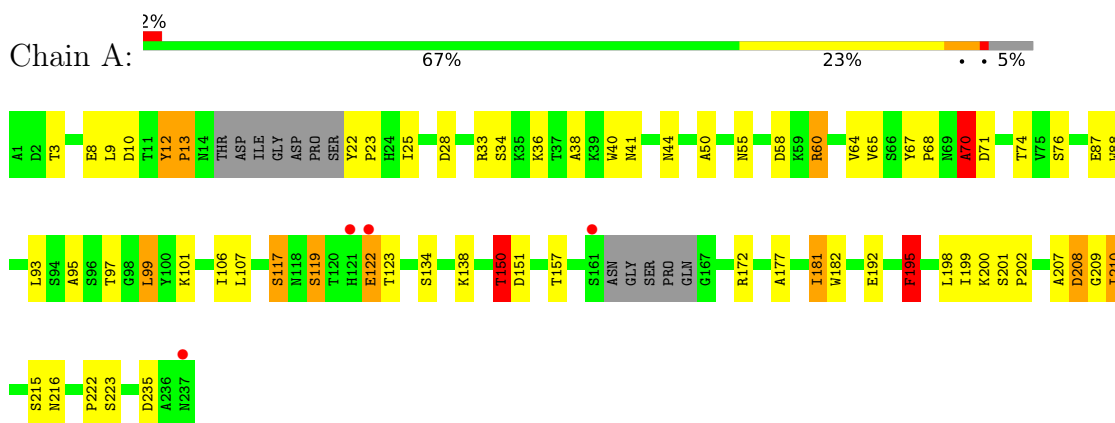
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	19	Total 19	O 19	0	0
3	B	20	Total 20	O 20	0	0

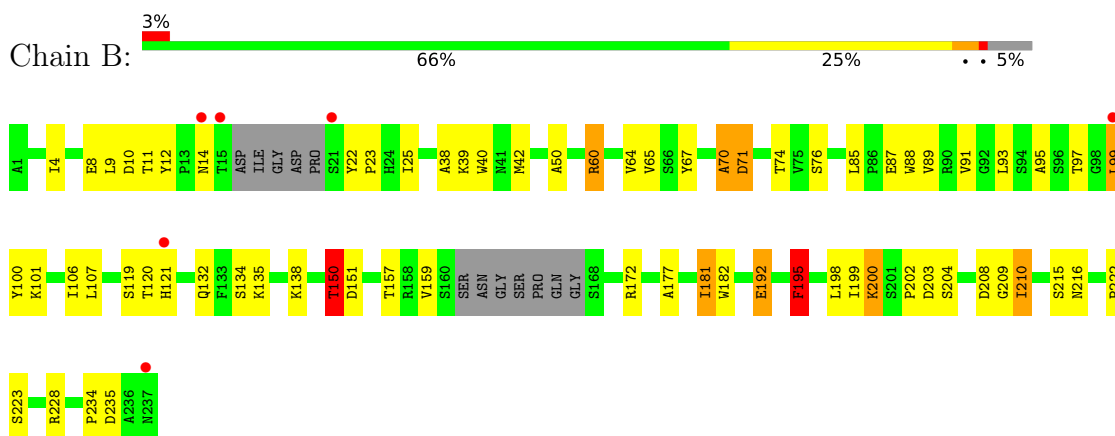
3 Residue-property plots [i](#)

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: CONCANAVALIN A



• Molecule 1: CONCANAVALIN A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	61.31Å 86.20Å 91.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.70 9.97 – 2.70	Depositor EDS
% Data completeness (in resolution range)	91.5 (10.00-2.70) 92.5 (9.97-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.93 (at 2.71Å)	Xtrriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.204 , 0.249 0.188 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	39.0	Xtrriage
Anisotropy	0.373	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 53.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3450	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.94% 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:
ZN

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	1.02	13/1750 (0.7%)	1.19	16/2381 (0.7%)
1	B	0.99	10/1735 (0.6%)	1.22	17/2363 (0.7%)
All	All	1.01	23/3485 (0.7%)	1.20	33/4744 (0.7%)

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

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	70	ALA	CA-CB	-14.60	1.21	1.52
1	A	70	ALA	CA-CB	-13.12	1.25	1.52
1	B	12	TYR	CE1-CZ	-10.65	1.24	1.38
1	B	12	TYR	CG-CD2	-9.64	1.26	1.39
1	A	12	TYR	CE1-CZ	-9.57	1.26	1.38
1	B	172	ARG	CZ-NH1	-9.51	1.20	1.33
1	A	192	GLU	CD-OE1	-9.27	1.15	1.25
1	A	181	ILE	CB-CG2	-9.24	1.24	1.52
1	A	172	ARG	CZ-NH1	-9.16	1.21	1.33
1	A	12	TYR	CG-CD2	-8.97	1.27	1.39
1	A	12	TYR	CE2-CZ	-8.82	1.27	1.38
1	B	12	TYR	CE2-CZ	-8.01	1.28	1.38
1	B	12	TYR	CG-CD1	-7.88	1.28	1.39
1	B	192	GLU	CD-OE1	-7.82	1.17	1.25
1	A	12	TYR	CG-CD1	-7.02	1.30	1.39
1	A	195	PHE	CG-CD1	-7.00	1.28	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	172	ARG	CZ-NH2	-6.88	1.24	1.33
1	B	181	ILE	CB-CG2	-6.55	1.32	1.52
1	A	195	PHE	CE1-CZ	-5.72	1.26	1.37
1	B	195	PHE	CG-CD2	-5.70	1.30	1.38
1	A	195	PHE	CE2-CZ	-5.58	1.26	1.37
1	A	195	PHE	CG-CD2	-5.46	1.30	1.38
1	B	195	PHE	CG-CD1	-5.20	1.30	1.38

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	192	GLU	OE1-CD-OE2	-18.39	101.24	123.30
1	A	192	GLU	OE1-CD-OE2	-15.61	104.57	123.30
1	B	99	LEU	CA-CB-CG	13.16	145.56	115.30
1	A	99	LEU	CA-CB-CG	11.53	141.82	115.30
1	A	70	ALA	N-CA-C	11.27	141.42	111.00
1	B	181	ILE	CG1-CB-CG2	-10.88	87.47	111.40
1	A	172	ARG	NE-CZ-NH1	10.64	125.62	120.30
1	B	172	ARG	NE-CZ-NH1	10.03	125.31	120.30
1	B	192	GLU	CG-CD-OE2	9.49	137.29	118.30
1	A	192	GLU	CG-CD-OE2	8.10	134.51	118.30
1	B	70	ALA	N-CA-C	8.00	132.61	111.00
1	B	208	ASP	CB-CG-OD1	7.99	125.49	118.30
1	A	172	ARG	NH1-CZ-NH2	-7.62	111.02	119.40
1	B	172	ARG	NH1-CZ-NH2	-7.51	111.14	119.40
1	B	200	LYS	CD-CE-NZ	7.02	127.85	111.70
1	A	200	LYS	CD-CE-NZ	7.01	127.82	111.70
1	A	208	ASP	CB-CG-OD2	6.75	124.37	118.30
1	B	71	ASP	N-CA-C	-6.49	93.48	111.00
1	B	70	ALA	CB-CA-C	-6.49	100.37	110.10
1	B	172	ARG	NE-CZ-NH2	6.42	123.51	120.30
1	A	208	ASP	CB-CG-OD1	6.32	123.98	118.30
1	A	208	ASP	OD1-CG-OD2	-6.15	111.61	123.30
1	A	123	THR	N-CA-C	5.95	127.07	111.00
1	A	12	TYR	CZ-CE2-CD2	5.81	125.03	119.80
1	B	12	TYR	CD1-CE1-CZ	5.74	124.97	119.80
1	B	12	TYR	CZ-CE2-CD2	5.68	124.92	119.80
1	B	208	ASP	OD1-CG-OD2	-5.46	112.92	123.30
1	B	99	LEU	CB-CG-CD1	-5.46	101.72	111.00
1	A	12	TYR	CD1-CE1-CZ	5.41	124.67	119.80
1	B	172	ARG	CB-CG-CD	-5.41	97.54	111.60
1	A	195	PHE	CB-CG-CD1	5.26	124.48	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	ARG	NE-CZ-NH2	5.24	122.92	120.30
1	A	70	ALA	CB-CA-C	-5.12	102.42	110.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	70	ALA	Mainchain

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	1712	0	1668	39	0
1	B	1697	0	1646	39	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	19	0	0	0	0
3	B	20	0	0	2	0
All	All	3450	0	3314	75	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 11.

All (75) 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:50:ALA:HB3	1:A:195:PHE:CE1	1.90	1.06
1:A:50:ALA:HB3	1:A:195:PHE:HE1	1.28	0.95
1:A:67:TYR:O	1:A:70:ALA:HB2	1.70	0.91
1:A:117:SER:H	1:A:122:GLU:HB2	1.48	0.79
1:B:67:TYR:O	1:B:70:ALA:HB3	1.82	0.78
1:B:150:THR:O	1:B:151:ASP:HB2	1.82	0.78
1:B:9:LEU:HD21	1:B:65:VAL:HG21	1.65	0.77
1:A:97:THR:HG23	1:A:157:THR:HG21	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:ALA:CB	1:A:195:PHE:HE1	1.97	0.76
1:B:97:THR:HG23	1:B:157:THR:HG21	1.75	0.69
1:A:9:LEU:HD21	1:A:65:VAL:HG21	1.77	0.66
1:A:119:SER:O	1:A:122:GLU:HG3	1.97	0.64
1:B:67:TYR:O	1:B:70:ALA:CB	2.45	0.64
1:B:25:ILE:HD12	1:B:65:VAL:HG23	1.80	0.63
1:A:150:THR:O	1:A:151:ASP:HB2	1.97	0.63
1:A:12:TYR:CD1	1:A:207:ALA:HB1	2.33	0.62
1:A:50:ALA:CB	1:A:195:PHE:CE1	2.73	0.62
1:A:25:ILE:HD12	1:A:65:VAL:HG23	1.81	0.62
1:A:199:ILE:HD11	1:A:210:ILE:HD11	1.82	0.62
1:A:117:SER:H	1:A:122:GLU:CB	2.13	0.61
1:A:60:ARG:HD2	1:A:76:SER:HB3	1.83	0.60
1:B:85:LEU:HD13	1:B:181:ILE:HD11	1.83	0.60
1:B:199:ILE:HD11	1:B:210:ILE:HD11	1.83	0.60
1:A:208:ASP:OD1	1:A:209:GLY:N	2.34	0.60
1:A:101:LYS:O	1:A:202:PRO:HD2	2.01	0.60
1:A:50:ALA:HB3	1:A:195:PHE:CD1	2.38	0.58
1:A:68:PRO:C	1:A:70:ALA:H	2.04	0.58
1:B:89:VAL:HG21	1:B:181:ILE:HD13	1.85	0.57
1:A:117:SER:N	1:A:122:GLU:HB2	2.20	0.55
1:A:25:ILE:HD12	1:A:65:VAL:CG2	2.39	0.53
1:B:22:TYR:HD1	1:B:23:PRO:O	1.93	0.52
1:B:93:LEU:HD21	1:B:195:PHE:CD2	2.45	0.52
1:A:25:ILE:CG2	1:A:38:ALA:HB3	2.41	0.51
1:B:40:TRP:CH2	1:B:42:MET:HG2	2.46	0.51
1:A:177:ALA:HB2	1:B:177:ALA:HB2	1.92	0.50
1:B:25:ILE:HD12	1:B:65:VAL:CG2	2.39	0.50
1:B:60:ARG:HD2	1:B:76:SER:HB3	1.93	0.50
1:A:93:LEU:HD13	1:A:106:ILE:HG13	1.93	0.49
1:B:120:THR:O	1:B:121:HIS:HB2	2.12	0.49
1:B:93:LEU:HD21	1:B:195:PHE:HD2	1.78	0.48
1:A:33:ARG:HD3	1:A:33:ARG:HA	1.77	0.48
1:A:23:PRO:HB2	1:A:40:TRP:O	2.14	0.47
1:B:87:GLU:HG3	1:B:182:TRP:O	2.14	0.47
1:A:41:ASN:HB2	1:A:71:ASP:OD2	2.15	0.47
1:A:88:TRP:CG	1:B:138:LYS:HD2	2.50	0.47
1:B:95:ALA:HA	1:B:209:GLY:O	2.14	0.47
1:A:117:SER:N	1:A:122:GLU:CB	2.78	0.46
1:A:138:LYS:HD2	1:B:88:TRP:CG	2.50	0.46
1:B:101:LYS:O	1:B:202:PRO:HD2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:ALA:HB3	1:B:195:PHE:CE1	2.51	0.46
1:A:95:ALA:HA	1:A:209:GLY:O	2.15	0.45
1:B:4:ILE:HD13	1:B:215:SER:HB3	1.97	0.45
1:B:222:PRO:HB3	1:B:234:PRO:HB3	1.99	0.45
1:B:93:LEU:CD2	1:B:195:PHE:CD2	3.00	0.45
1:B:181:ILE:HD13	1:B:181:ILE:HG21	1.15	0.44
1:B:93:LEU:HD13	1:B:106:ILE:HG13	2.00	0.44
1:B:11:THR:HG22	1:B:23:PRO:HB3	1.99	0.43
1:A:28:ASP:OD1	1:A:34:SER:HA	2.18	0.43
1:A:181:ILE:HG21	1:A:181:ILE:HD13	1.36	0.43
1:B:25:ILE:CG2	1:B:38:ALA:HB3	2.49	0.43
1:B:195:PHE:C	1:B:195:PHE:CD1	2.92	0.43
1:B:100:TYR:HB3	1:B:203:ASP:OD2	2.19	0.43
1:A:87:GLU:HG3	1:A:182:TRP:O	2.19	0.42
1:B:91:VAL:HG22	3:B:257:HOH:O	2.19	0.42
1:B:9:LEU:CD2	1:B:65:VAL:HG21	2.41	0.41
1:B:204:SER:HB3	3:B:251:HOH:O	2.18	0.41
1:A:44:ASN:HD21	1:A:201:SER:HB3	1.86	0.41
1:A:9:LEU:CD2	1:A:65:VAL:HG21	2.48	0.41
1:A:12:TYR:HA	1:A:13:PRO:HD3	1.80	0.41
1:A:3:THR:O	1:A:215:SER:HA	2.20	0.41
1:A:55:ASN:HD21	1:A:58:ASP:CG	2.24	0.40
1:B:22:TYR:CE1	1:B:39:LYS:HA	2.56	0.40
1:B:195:PHE:C	1:B:195:PHE:HD1	2.25	0.40
1:B:70:ALA:HB1	1:B:71:ASP:O	2.22	0.40
1:B:89:VAL:HG22	1:B:181:ILE:HG23	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	219/237 (92%)	206 (94%)	10 (5%)	3 (1%)	11	28
1	B	219/237 (92%)	204 (93%)	14 (6%)	1 (0%)	29	54
All	All	438/474 (92%)	410 (94%)	24 (6%)	4 (1%)	17	40

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	70	ALA
1	A	13	PRO
1	B	150	THR
1	A	150	THR

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	190/203 (94%)	169 (89%)	21 (11%)	6	14
1	B	186/203 (92%)	163 (88%)	23 (12%)	4	11
All	All	376/406 (93%)	332 (88%)	44 (12%)	5	12

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	GLU
1	A	10	ASP
1	A	22	TYR
1	A	36	LYS
1	A	60	ARG
1	A	64	VAL
1	A	74	THR
1	A	99	LEU
1	A	107	LEU
1	A	117	SER
1	A	119	SER
1	A	122	GLU

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Mol	Chain	Res	Type
1	A	134	SER
1	A	150	THR
1	A	195	PHE
1	A	198	LEU
1	A	210	ILE
1	A	216	ASN
1	A	222	PRO
1	A	223	SER
1	A	235	ASP
1	B	8	GLU
1	B	10	ASP
1	B	14	ASN
1	B	60	ARG
1	B	64	VAL
1	B	74	THR
1	B	99	LEU
1	B	107	LEU
1	B	119	SER
1	B	132	GLN
1	B	134	SER
1	B	135	LYS
1	B	150	THR
1	B	159	VAL
1	B	192	GLU
1	B	195	PHE
1	B	198	LEU
1	B	200	LYS
1	B	210	ILE
1	B	216	ASN
1	B	223	SER
1	B	228	ARG
1	B	235	ASP

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

Mol	Chain	Res	Type
1	A	43	GLN
1	A	69	ASN
1	A	205	HIS
1	B	14	ASN
1	B	43	GLN
1	B	205	HIS

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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	225/237 (94%)	-0.60	4 (1%) 68 70	3, 18, 59, 92	0
1	B	225/237 (94%)	-0.55	6 (2%) 54 55	4, 21, 65, 124	0
All	All	450/474 (94%)	-0.57	10 (2%) 62 63	3, 19, 65, 124	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	161	SER	17.7
1	B	15	THR	12.8
1	B	237	ASN	5.0
1	B	14	ASN	3.6
1	A	237	ASN	3.2
1	B	21	SER	3.0
1	A	121	HIS	2.6
1	B	99	LEU	2.3
1	B	121	HIS	2.0
1	A	122	GLU	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 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	ZN	A	238	1/1	0.88	0.09	53,53,53,53	1
2	ZN	B	238	1/1	0.96	0.05	31,31,31,31	1

6.5 Other polymers [i](#)

There are no such residues in this entry.