



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:54 AM GMT

PDB ID : 3CM5
Title : Crystal structure of Cell-Death Related Nuclease 4 (CRN-4) bound with Mn
Authors : Hsiao, Y.-Y.; Yuan, H.S.
Deposited on : 2008-03-21
Resolution : 2.81 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

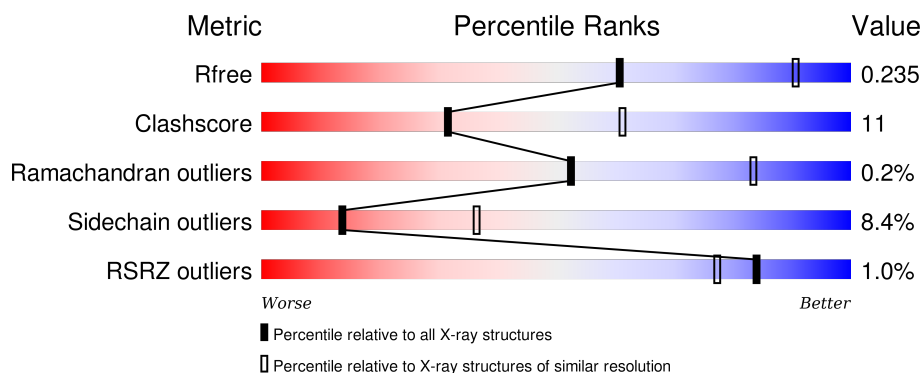
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 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	2676 (2.84-2.80)
Clashscore	102246	3124 (2.84-2.80)
Ramachandran outliers	100387	3072 (2.84-2.80)
Sidechain outliers	100360	3074 (2.84-2.80)
RSRZ outliers	91569	2690 (2.84-2.80)

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	308	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 72%, green 21%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 72% 21% • 5% </div> </div>
1	B	308	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 74%, green 19%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 74% 19% • 5% </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4877 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 Cell death-related nuclease 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	0	0
			2396	1525	404	446	21			
1	B	294	Total	C	N	O	S	0	0	0
			2396	1525	404	446	21			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	GLY	-	EXPRESSION TAG	UNP Q10905
A	-8	SER	-	EXPRESSION TAG	UNP Q10905
A	-7	PRO	-	EXPRESSION TAG	UNP Q10905
A	-6	GLY	-	EXPRESSION TAG	UNP Q10905
A	-5	ILE	-	EXPRESSION TAG	UNP Q10905
A	-4	PRO	-	EXPRESSION TAG	UNP Q10905
A	-3	GLY	-	EXPRESSION TAG	UNP Q10905
A	-2	SER	-	EXPRESSION TAG	UNP Q10905
A	-1	THR	-	EXPRESSION TAG	UNP Q10905
A	0	ARG	-	EXPRESSION TAG	UNP Q10905
B	-9	GLY	-	EXPRESSION TAG	UNP Q10905
B	-8	SER	-	EXPRESSION TAG	UNP Q10905
B	-7	PRO	-	EXPRESSION TAG	UNP Q10905
B	-6	GLY	-	EXPRESSION TAG	UNP Q10905
B	-5	ILE	-	EXPRESSION TAG	UNP Q10905
B	-4	PRO	-	EXPRESSION TAG	UNP Q10905
B	-3	GLY	-	EXPRESSION TAG	UNP Q10905
B	-2	SER	-	EXPRESSION TAG	UNP Q10905
B	-1	THR	-	EXPRESSION TAG	UNP Q10905
B	0	ARG	-	EXPRESSION TAG	UNP Q10905

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

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

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Mn 1	0	0
3	A	1	Total 1	Mn 1	0	0

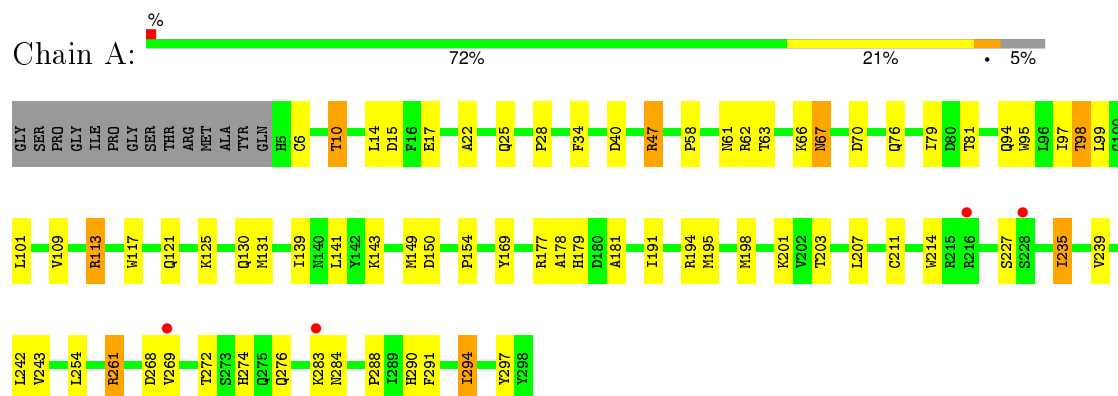
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	33	Total 33	O 33	0	0
4	B	48	Total 48	O 48	0	0

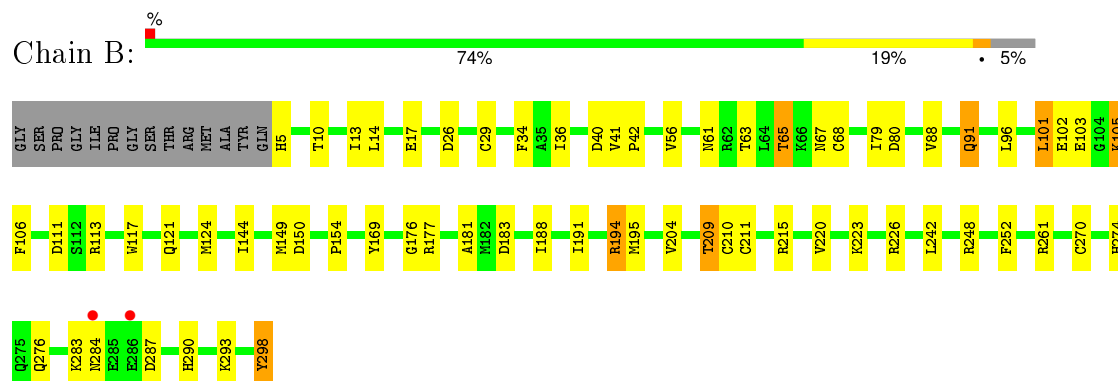
3 Residue-property plots [i](#)

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: Cell death-related nuclease 4



• Molecule 1: Cell death-related nuclease 4



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	125.13 Å 165.43 Å 64.59 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.81 29.45 – 2.81	Depositor EDS
% Data completeness (in resolution range)	91.7 (30.00-2.81) 91.7 (29.45-2.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.27 (at 2.80 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.201 , 0.239 0.202 , 0.235	Depositor DCC
R_{free} test set	1564 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	51.1	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 30641 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4877	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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: ZN, MN

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	0.63	0/2451	0.72	1/3319 (0.0%)
1	B	0.65	1/2451 (0.0%)	0.71	0/3319
All	All	0.64	1/4902 (0.0%)	0.72	1/6638 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	29	CYS	CB-SG	-5.45	1.73	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	40	ASP	CB-CG-OD1	5.58	123.32	118.30

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	2396	0	2335	53	0
1	B	2396	0	2335	53	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	33	0	0	3	0
4	B	48	0	0	4	0
All	All	4877	0	4670	101	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 (101) 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:B:191:ILE:HG22	1:B:195:MET:CE	1.79	1.12
1:A:47:ARG:HH11	1:A:47:ARG:HG2	1.22	1.03
1:A:261:ARG:HH11	1:A:261:ARG:HG2	1.22	1.00
1:B:65:THR:HG22	1:B:68:CYS:H	1.25	1.00
1:A:63:THR:H	1:B:61:ASN:HD21	1.11	0.96
1:B:274:HIS:HD2	1:B:276:GLN:H	1.13	0.96
1:B:121:GLN:HE22	1:B:242:LEU:H	1.07	0.94
1:A:121:GLN:HE22	1:A:242:LEU:H	1.16	0.93
1:B:191:ILE:HG22	1:B:195:MET:HE3	1.55	0.88
1:A:291:PHE:HA	1:A:294:ILE:HD11	1.59	0.85
1:A:274:HIS:HD2	1:A:276:GLN:H	1.23	0.84
1:B:274:HIS:CD2	1:B:276:GLN:H	1.97	0.83
1:B:88:VAL:HA	1:B:91:GLN:HG3	1.62	0.79
1:B:191:ILE:CG2	1:B:195:MET:CE	2.61	0.78
1:A:207:LEU:HD13	1:A:261:ARG:HG3	1.68	0.76
1:A:191:ILE:HG22	1:A:195:MET:HE3	1.69	0.75
1:B:209:THR:HG22	1:B:211:CYS:H	1.51	0.75
1:A:61:ASN:HD21	1:B:63:THR:H	1.34	0.73
1:B:102:GLU:HB2	1:B:105:LYS:HG3	1.69	0.73
1:B:121:GLN:NE2	1:B:242:LEU:H	1.82	0.72
1:A:47:ARG:HH11	1:A:47:ARG:CG	2.01	0.72
1:B:121:GLN:HE22	1:B:242:LEU:N	1.84	0.72
1:B:17:GLU:HG2	1:B:181:ALA:HB2	1.72	0.70
1:A:63:THR:OG1	1:B:290:HIS:HE1	1.73	0.70
1:B:65:THR:HG22	1:B:68:CYS:N	2.07	0.66
1:B:149:MET:HE3	1:B:154:PRO:HA	1.76	0.66
1:A:274:HIS:CD2	1:A:276:GLN:H	2.12	0.65
1:B:5:HIS:N	4:B:336:HOH:O	2.30	0.64
1:B:101:LEU:HD22	1:B:101:LEU:H	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:ILE:HG22	1:B:195:MET:HE1	1.77	0.62
1:A:28:PRO:HB3	1:A:294:ILE:CD1	2.29	0.62
1:A:261:ARG:CG	1:A:261:ARG:HH11	2.08	0.60
1:A:214:TRP:CZ2	1:A:243:VAL:HG21	2.36	0.60
1:A:62:ARG:HD2	4:A:327:HOH:O	2.00	0.60
1:A:62:ARG:CD	4:A:327:HOH:O	2.50	0.59
1:A:95:TRP:O	1:A:98:THR:HB	2.03	0.58
1:B:209:THR:CG2	1:B:211:CYS:H	2.15	0.58
1:A:17:GLU:HG2	1:A:181:ALA:HB2	1.86	0.58
1:A:28:PRO:HB3	1:A:294:ILE:HD13	1.84	0.58
1:A:125:LYS:HG3	1:A:297:TYR:CZ	2.39	0.57
1:B:204:VAL:HG22	1:B:252:PHE:CD1	2.39	0.57
1:A:291:PHE:HA	1:A:294:ILE:CD1	2.34	0.56
1:A:10:THR:HG21	1:A:101:LEU:HD22	1.87	0.56
1:A:194:ARG:O	1:A:198:MET:HG2	2.06	0.55
1:B:96:LEU:HD22	1:B:101:LEU:HD21	1.89	0.54
1:A:47:ARG:NH1	1:A:47:ARG:HG2	2.02	0.54
1:A:113:ARG:O	1:A:117:TRP:HB3	2.08	0.54
1:A:191:ILE:HG22	1:A:195:MET:CE	2.36	0.53
1:B:149:MET:CE	1:B:154:PRO:HA	2.38	0.53
1:A:58:PRO:HD2	1:A:79:ILE:HD13	1.91	0.53
1:A:76:GLN:HE22	1:A:79:ILE:HD11	1.72	0.53
1:B:293:LYS:HE2	1:B:298:TYR:CE2	2.44	0.52
1:A:47:ARG:HD2	4:A:333:HOH:O	2.10	0.52
1:B:284:ASN:ND2	1:B:287:ASP:HB3	2.25	0.52
1:A:261:ARG:HG2	1:A:261:ARG:NH1	2.02	0.51
1:A:66:LYS:HE3	1:A:70:ASP:OD2	2.10	0.51
1:B:191:ILE:CG2	1:B:195:MET:HE1	2.41	0.49
1:B:26:ASP:HB2	1:B:226:ARG:HG2	1.95	0.49
1:B:261:ARG:HD2	4:B:348:HOH:O	2.11	0.49
1:B:102:GLU:HB2	1:B:105:LYS:CG	2.40	0.49
1:B:149:MET:HG2	1:B:169:TYR:CE1	2.47	0.49
1:B:191:ILE:HG22	1:B:195:MET:HE2	1.88	0.48
1:A:121:GLN:HE22	1:A:242:LEU:N	1.96	0.48
1:A:149:MET:HG2	1:A:169:TYR:CE1	2.49	0.47
1:B:102:GLU:HG3	1:B:105:LYS:HE3	1.96	0.47
1:A:235:ILE:O	1:A:239:VAL:HG23	2.14	0.47
1:B:111:ASP:HB3	1:B:188:ILE:HD11	1.98	0.46
1:B:65:THR:CG2	1:B:67:ASN:ND2	2.78	0.46
1:B:41:VAL:HB	1:B:42:PRO:HD3	1.96	0.46
1:B:210:CYS:HB3	1:B:270:CYS:SG	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:GLU:HA	1:B:106:PHE:CE1	2.51	0.46
1:B:56:VAL:HG22	1:B:88:VAL:HG21	1.97	0.46
1:B:101:LEU:HD22	1:B:101:LEU:N	2.30	0.45
1:B:103:GLU:HA	1:B:106:PHE:HE1	1.82	0.45
1:A:109:VAL:HG22	1:A:139:ILE:HB	1.99	0.45
1:A:131:MET:HE3	1:A:242:LEU:HD12	1.98	0.44
1:A:125:LYS:HG3	1:A:297:TYR:OH	2.17	0.44
1:A:274:HIS:HD2	1:A:276:GLN:N	2.03	0.44
1:A:63:THR:H	1:B:61:ASN:ND2	1.95	0.43
1:B:96:LEU:CD2	1:B:101:LEU:HD21	2.48	0.43
1:B:113:ARG:O	1:B:117:TRP:HB3	2.18	0.43
1:A:130:GLN:HE22	1:A:268:ASP:HA	1.83	0.43
1:A:47:ARG:CG	1:A:47:ARG:NH1	2.70	0.43
1:A:149:MET:HE3	1:A:154:PRO:HA	2.00	0.43
1:B:13:ILE:N	1:B:13:ILE:HD12	2.34	0.43
1:A:28:PRO:HB3	1:A:294:ILE:HD11	1.98	0.43
1:A:22:ALA:H	1:A:67:ASN:ND2	2.16	0.43
1:A:269:VAL:O	1:A:269:VAL:HG12	2.19	0.42
1:B:248:ARG:NH1	4:B:302:HOH:O	2.53	0.42
1:B:88:VAL:CA	1:B:91:GLN:HG3	2.43	0.42
1:A:141:LEU:HD21	1:A:195:MET:HE3	2.02	0.42
1:A:290:HIS:ND1	1:B:80:ASP:OD1	2.43	0.42
1:B:176:GLY:HA3	1:B:183:ASP:OD2	2.20	0.42
1:A:22:ALA:H	1:A:67:ASN:HD21	1.69	0.41
1:A:191:ILE:CG2	1:A:195:MET:CE	2.99	0.41
1:A:178:ALA:O	1:A:179:HIS:HB2	2.21	0.41
1:B:194:ARG:NH1	4:B:310:HOH:O	2.54	0.41
1:A:14:LEU:HD23	1:A:15:ASP:N	2.35	0.41
1:A:149:MET:HG2	1:A:169:TYR:CZ	2.56	0.40
1:B:40:ASP:OD2	1:B:42:PRO:HD2	2.21	0.40
1:B:14:LEU:HD12	1:B:36:ILE:HG12	2.03	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	292/308 (95%)	274 (94%)	17 (6%)	1 (0%)	46	78
1	B	292/308 (95%)	282 (97%)	10 (3%)	0	100	100
All	All	584/616 (95%)	556 (95%)	27 (5%)	1 (0%)	52	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	ASP

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	263/273 (96%)	237 (90%)	26 (10%)	10	27
1	B	263/273 (96%)	245 (93%)	18 (7%)	20	48
All	All	526/546 (96%)	482 (92%)	44 (8%)	14	36

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

Mol	Chain	Res	Type
1	A	6	CYS
1	A	10	THR
1	A	25	GLN
1	A	34	PHE
1	A	47	ARG
1	A	67	ASN
1	A	81	THR
1	A	94	GLN
1	A	97	ILE
1	A	98	THR
1	A	99	LEU
1	A	113	ARG

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Mol	Chain	Res	Type
1	A	143	LYS
1	A	177	ARG
1	A	201	LYS
1	A	203	THR
1	A	211	CYS
1	A	227	SER
1	A	235	ILE
1	A	254	LEU
1	A	261	ARG
1	A	272	THR
1	A	283	LYS
1	A	284	ASN
1	A	288	PRO
1	A	294	ILE
1	B	10	THR
1	B	34	PHE
1	B	65	THR
1	B	79	ILE
1	B	91	GLN
1	B	101	LEU
1	B	105	LYS
1	B	124	MET
1	B	144	ILE
1	B	150	ASP
1	B	177	ARG
1	B	194	ARG
1	B	209	THR
1	B	215	ARG
1	B	220	VAL
1	B	223	LYS
1	B	283	LYS
1	B	298	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	A	67	ASN
1	A	121	GLN
1	A	128	ASN
1	A	130	GLN
1	A	162	ASN

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Mol	Chain	Res	Type
1	A	179	HIS
1	A	274	HIS
1	B	61	ASN
1	B	121	GLN
1	B	274	HIS
1	B	290	HIS

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 4 ligands modelled in this entry, 4 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 ⓘ

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 [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	294/308 (95%)	-0.29	4 (1%) 78 69	33, 45, 68, 76	0
1	B	294/308 (95%)	-0.45	2 (0%) 89 84	28, 41, 58, 69	0
All	All	588/616 (95%)	-0.37	6 (1%) 84 77	28, 42, 64, 76	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	286	GLU	3.6
1	A	269	VAL	2.4
1	A	228	SER	2.2
1	B	284	ASN	2.1
1	A	216	ARG	2.1
1	A	283	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(\AA^2)	Q<0.9
3	MN	B	300	1/1	0.94	0.17	0.07	43,43,43,43	0
3	MN	A	300	1/1	0.99	0.13	-0.60	38,38,38,38	0
2	ZN	B	299	1/1	0.99	0.07	-1.67	33,33,33,33	0
2	ZN	A	299	1/1	1.00	0.04	-4.35	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.