



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 09:57 AM EDT

PDB ID : 6WQ1
Title : Eukaryotic LanCL2 protein
Authors : Nair, S.K.; Garg, N.
Deposited on : 2020-04-28
Resolution : 2.29 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 : 2.35.1
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) : 2.35.1

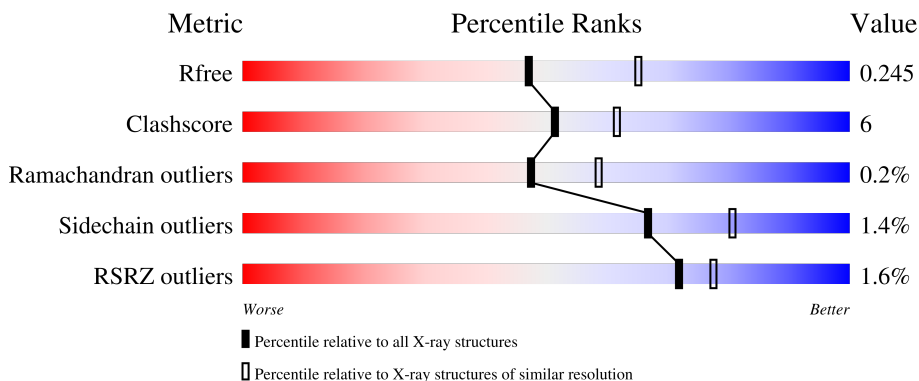
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	450	 78% 10% 12%
1	B	450	 76% 12% 12%
1	C	450	 75% 13% 12%
1	D	450	 78% 9% 12%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13475 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 LanC-like protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	396	3185	2033	554	575	23	0	0	0
1	B	396	3185	2033	554	575	23	0	0	0
1	C	395	3174	2027	550	574	23	0	0	0
1	D	396	3185	2033	554	575	23	0	0	0

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

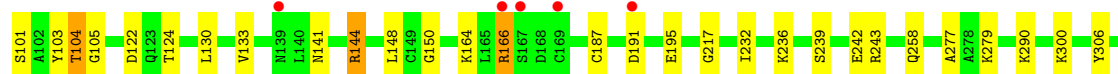
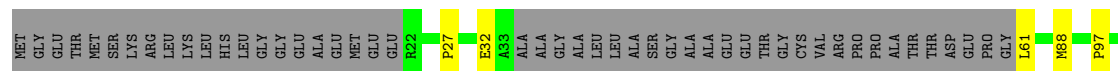
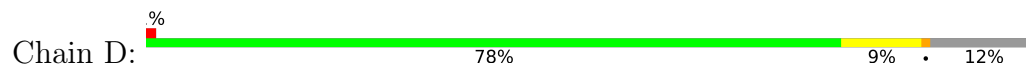
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	201	Total 201	O 201	0	0
3	B	220	Total 220	O 220	0	0
3	C	185	Total 185	O 185	0	0
3	D	136	Total 136	O 136	0	0



- Molecule 1: LanC-like protein 2



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.41Å 108.01Å 152.01Å 90.00° 91.26° 90.00°	Depositor
Resolution (Å)	37.61 – 2.29 37.99 – 2.29	Depositor EDS
% Data completeness (in resolution range)	93.8 (37.61-2.29) 93.9 (37.99-2.29)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.29Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.184 , 0.245 0.184 , 0.245	Depositor DCC
R_{free} test set	3560 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	18.6	Xtrriage
Anisotropy	0.767	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.067 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13475	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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	0.43	0/3261	0.56	0/4406
1	B	0.44	0/3261	0.59	2/4406 (0.0%)
1	C	0.39	0/3250	0.57	1/4392 (0.0%)
1	D	0.40	0/3261	0.59	1/4406 (0.0%)
All	All	0.42	0/13033	0.58	4/17610 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	166	ARG	NE-CZ-NH1	-12.21	114.20	120.30
1	C	240	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	B	96	ASP	CB-CG-OD1	6.20	123.88	118.30
1	B	96	ASP	N-CA-CB	-5.19	101.26	110.60

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	3185	0	3155	33	0
1	B	3185	0	3155	35	0
1	C	3174	0	3142	43	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3185	0	3155	33	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	201	0	0	12	1
3	B	220	0	0	11	0
3	C	185	0	0	14	0
3	D	136	0	0	13	0
All	All	13475	0	12607	142	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 6.

All (142) 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:72:ASN:ND2	3:B:603:HOH:O	1.98	0.96
1:B:211:ASN:O	3:B:601:HOH:O	1.90	0.89
1:A:33:ALA:O	3:A:601:HOH:O	1.94	0.85
1:C:247:ARG:NH1	3:C:602:HOH:O	2.09	0.83
1:B:61:LEU:N	3:B:608:HOH:O	2.11	0.83
1:C:432:LEU:O	3:C:601:HOH:O	1.98	0.82
1:D:101:SER:OG	1:D:103:TYR:O	1.98	0.81
1:D:61:LEU:N	3:D:603:HOH:O	2.16	0.79
1:B:213:GLU:OE1	3:B:605:HOH:O	2.03	0.76
1:D:290:LYS:NZ	3:D:605:HOH:O	2.18	0.76
1:A:61:LEU:N	3:A:604:HOH:O	2.18	0.75
1:B:104:THR:HG21	1:B:413:ARG:NH1	2.02	0.75
1:A:300:LYS:NZ	3:A:605:HOH:O	2.22	0.72
1:D:104:THR:HA	1:D:416:SER:HB2	1.72	0.72
1:C:314:THR:HB	1:C:316:ARG:HG3	1.71	0.71
1:D:277:ALA:O	3:D:601:HOH:O	2.13	0.67
1:C:195:GLU:OE2	1:C:197:LEU:N	2.22	0.67
1:B:141:ASN:O	3:B:607:HOH:O	2.11	0.67
1:D:402:ASP:OD2	3:D:602:HOH:O	2.14	0.66
1:C:195:GLU:OE2	1:C:196:LEU:N	2.30	0.64
1:C:69:ILE:N	1:C:69:ILE:HD12	2.13	0.64
1:C:221:GLU:HB2	3:C:656:HOH:O	1.98	0.63
1:A:61:LEU:N	3:A:611:HOH:O	2.31	0.62
1:B:95:ALA:HB3	1:B:106:TRP:CH2	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:382:ARG:NH1	1:B:437:SER:OG	2.34	0.61
1:C:208:LEU:HG	1:C:277:ALA:HB3	1.82	0.61
1:C:33:ALA:HA	3:C:723:HOH:O	1.99	0.60
1:C:183:ARG:NH2	3:C:612:HOH:O	2.34	0.60
1:B:207:LEU:HD22	1:B:219:VAL:HG11	1.83	0.60
1:B:300:LYS:HB3	1:B:306:TYR:CE2	2.38	0.59
1:C:69:ILE:HD12	1:C:69:ILE:H	1.68	0.59
1:D:148:LEU:HD23	3:D:656:HOH:O	2.03	0.59
1:C:177:LYS:NZ	3:C:606:HOH:O	2.29	0.58
1:D:130:LEU:HA	1:D:133:VAL:HG22	1.86	0.58
1:A:117:TYR:CD2	1:A:126:LEU:HG	2.39	0.58
1:C:319:HIS:HE1	1:C:362:LYS:HE2	1.70	0.57
1:C:312:ASN:OD1	1:C:314:THR:OG1	2.17	0.57
1:C:177:LYS:NZ	3:C:603:HOH:O	2.18	0.57
1:B:148:LEU:HD23	3:B:633:HOH:O	2.05	0.56
1:D:243:ARG:HG3	1:D:243:ARG:HH11	1.70	0.56
1:D:104:THR:O	3:D:606:HOH:O	2.18	0.56
1:D:191:ASP:OD2	3:D:607:HOH:O	2.18	0.56
1:D:141:ASN:N	3:D:604:HOH:O	2.16	0.55
1:B:78:GLN:O	1:B:82:LYS:HD2	2.06	0.55
1:D:232:ILE:O	1:D:236:LYS:HG3	2.07	0.55
1:A:124:THR:HG23	3:A:783:HOH:O	2.07	0.54
1:A:282:GLN:HB3	3:A:732:HOH:O	2.08	0.54
1:C:282:GLN:CD	1:D:97:PRO:HB3	2.29	0.54
1:B:31:TYR:O	1:B:33:ALA:N	2.41	0.53
1:C:411:PRO:HG2	1:C:414:PRO:HA	1.90	0.53
1:A:104:THR:HA	1:A:416:SER:HB2	1.91	0.53
1:A:133:VAL:HG11	1:A:161:ILE:HD12	1.91	0.53
1:C:155:LEU:HB2	1:C:178:LEU:HD23	1.91	0.52
1:B:382:ARG:NE	3:B:612:HOH:O	2.29	0.52
1:D:122:ASP:OD1	1:D:124:THR:HG22	2.09	0.52
1:C:23:ALA:HB2	3:C:659:HOH:O	2.08	0.52
1:A:31:TYR:HB3	1:A:388:LYS:HG3	1.90	0.51
1:A:135:ARG:NH2	3:A:617:HOH:O	2.44	0.51
1:A:395:LYS:NZ	3:A:610:HOH:O	2.31	0.51
1:D:312:ASN:N	3:D:617:HOH:O	2.43	0.51
1:D:104:THR:HA	1:D:416:SER:CB	2.41	0.51
1:A:183:ARG:HG3	3:A:686:HOH:O	2.11	0.50
1:A:413:ARG:NE	3:A:618:HOH:O	2.44	0.49
1:D:279:LYS:HD2	3:D:726:HOH:O	2.12	0.49
1:A:140:LEU:HD12	1:A:151:ASP:CG	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:LYS:HD3	3:A:619:HOH:O	2.12	0.49
1:C:436:THR:HG23	3:C:676:HOH:O	2.13	0.49
1:D:300:LYS:HB3	1:D:306:TYR:CE2	2.48	0.49
1:A:443:GLU:C	1:A:444:LEU:HD22	2.33	0.48
1:A:417:LEU:HA	1:A:422:ALA:HB3	1.95	0.48
1:D:27:PRO:O	3:D:608:HOH:O	2.19	0.48
1:A:266:MET:HB3	1:A:270:TYR:CE2	2.49	0.47
1:B:135:ARG:NH1	3:B:606:HOH:O	2.06	0.47
1:A:117:TYR:CE2	1:A:126:LEU:HG	2.49	0.47
1:C:69:ILE:CD1	3:C:631:HOH:O	2.62	0.47
1:A:412:ASP:O	1:A:414:PRO:HD3	2.15	0.46
1:B:96:ASP:HA	1:B:97:PRO:HD2	1.84	0.46
1:B:433:GLY:O	1:B:436:THR:HG22	2.15	0.46
1:C:104:THR:HA	1:C:416:SER:HB2	1.98	0.46
1:C:241:GLU:O	1:C:243:ARG:HD2	2.15	0.46
1:B:80:LYS:HE3	1:B:84:LEU:HD21	1.97	0.45
1:B:240:ARG:NE	3:B:602:HOH:O	1.94	0.45
1:C:404:GLY:HA2	3:C:725:HOH:O	2.15	0.45
1:C:319:HIS:CE1	1:C:362:LYS:HE2	2.49	0.45
1:D:144:ARG:HB3	1:D:150:GLY:HA2	1.98	0.45
1:D:166:ARG:NH2	3:D:621:HOH:O	2.49	0.45
1:B:136:THR:OG1	1:B:154:PRO:HB3	2.16	0.45
1:B:325:PRO:HG3	1:B:354:ILE:HG12	1.98	0.45
1:C:220:CYS:SG	1:C:222:SER:HB3	2.57	0.45
1:A:130:LEU:HA	1:A:133:VAL:HG22	1.99	0.45
1:B:183:ARG:HG2	3:B:794:HOH:O	2.16	0.45
1:B:240:ARG:HA	3:B:623:HOH:O	2.16	0.44
1:C:387:LYS:HD2	3:C:639:HOH:O	2.16	0.44
1:C:270:TYR:OH	1:C:292:SER:HB3	2.17	0.44
1:C:103:TYR:CD2	1:C:104:THR:HG23	2.52	0.44
1:C:236:LYS:HD2	1:C:236:LYS:HA	1.69	0.44
1:A:88:MET:HB2	1:A:421:MET:HE2	1.99	0.44
1:A:111:LEU:HD23	1:A:111:LEU:HA	1.80	0.44
1:C:69:ILE:HD13	3:C:631:HOH:O	2.17	0.44
1:C:152:ALA:HA	1:C:178:LEU:CD2	2.48	0.44
1:A:188:GLN:N	3:A:602:HOH:O	2.08	0.43
1:C:136:THR:OG1	1:C:154:PRO:HB3	2.17	0.43
1:D:395:LYS:HA	1:D:395:LYS:HD2	1.85	0.43
1:B:370:THR:O	1:B:374:GLY:N	2.44	0.43
1:A:256:ARG:HD3	1:C:127:LEU:HD22	1.99	0.43
1:D:239:SER:O	1:D:242:GLU:O	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:421:MET:HE3	1:D:421:MET:HB3	1.78	0.43
1:B:140:LEU:HB3	1:B:151:ASP:OD2	2.19	0.43
1:C:71:HIS:NE2	1:C:75:ARG:HD3	2.34	0.43
1:A:360:LEU:HD12	1:A:369:GLY:HA2	2.01	0.43
1:C:91:GLY:HA3	1:C:415:TYR:CZ	2.54	0.43
1:A:395:LYS:HA	1:A:395:LYS:HD2	1.65	0.43
1:C:143:ARG:NH2	3:C:624:HOH:O	2.52	0.43
1:A:204:LEU:O	1:A:208:LEU:HG	2.19	0.42
1:D:417:LEU:HA	1:D:422:ALA:HB3	2.01	0.42
1:D:103:TYR:O	1:D:105:GLY:N	2.52	0.42
1:B:104:THR:HA	1:B:416:SER:HB2	2.02	0.42
1:D:88:MET:HB2	1:D:421:MET:HE2	2.02	0.42
1:B:91:GLY:HA3	1:B:415:TYR:CZ	2.54	0.42
1:B:395:LYS:HA	1:B:395:LYS:HD2	1.90	0.42
1:D:361:ARG:HH11	1:D:361:ARG:HG3	1.85	0.42
1:D:103:TYR:CD2	1:D:104:THR:HG23	2.54	0.42
1:C:240:ARG:HA	1:C:240:ARG:HD2	1.58	0.42
1:A:190:SER:C	1:A:192:LEU:H	2.22	0.42
1:C:417:LEU:HA	1:C:422:ALA:HB3	2.02	0.41
1:B:430:ASP:CG	1:B:437:SER:HA	2.41	0.41
1:C:69:ILE:N	1:C:69:ILE:CD1	2.82	0.41
1:C:133:VAL:HG11	1:C:161:ILE:HD12	2.02	0.41
1:A:74:ILE:HG23	1:A:432:LEU:HD22	2.02	0.41
1:A:192:LEU:HD23	1:A:193:PRO:HD2	2.03	0.41
1:B:70:ILE:O	1:B:74:ILE:HG13	2.20	0.41
1:B:167:SER:HB3	1:B:170:GLU:OE2	2.21	0.41
1:D:164:LYS:HE3	3:D:705:HOH:O	2.20	0.41
1:B:74:ILE:HG23	1:B:432:LEU:HD22	2.03	0.41
1:C:290:LYS:NZ	1:C:343:TYR:OH	2.49	0.41
1:B:119:VAL:HG23	1:B:120:THR:HG23	2.03	0.41
1:D:258:GLN:OE1	1:D:310:LEU:HD12	2.21	0.41
1:D:104:THR:HG21	1:D:413:ARG:NH2	2.36	0.41
1:A:85:LEU:HA	1:A:85:LEU:HD23	1.82	0.40
1:B:130:LEU:HA	1:B:133:VAL:HG22	2.02	0.40
1:C:69:ILE:H	1:C:69:ILE:CD1	2.33	0.40
1:B:290:LYS:HB3	1:B:291:PRO:HD3	2.04	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)
3:A:753:HOH:O	3:A:772:HOH:O[1_655]	2.03	0.17
1:C:240:ARG:NH2	1:D:32:GLU:OE1[2_644]	2.08	0.12

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	392/450 (87%)	381 (97%)	11 (3%)	0	100	100
1	B	392/450 (87%)	380 (97%)	11 (3%)	1 (0%)	41	50
1	C	391/450 (87%)	380 (97%)	11 (3%)	0	100	100
1	D	392/450 (87%)	370 (94%)	20 (5%)	2 (0%)	29	35
All	All	1567/1800 (87%)	1511 (96%)	53 (3%)	3 (0%)	47	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	32	GLU
1	D	104	THR
1	D	217	GLY

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	339/378 (90%)	332 (98%)	7 (2%)	53	70
1	B	339/378 (90%)	338 (100%)	1 (0%)	92	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	338/378 (89%)	332 (98%)	6 (2%)	59	75
1	D	339/378 (90%)	334 (98%)	5 (2%)	65	79
All	All	1355/1512 (90%)	1336 (99%)	19 (1%)	67	81

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	126	LEU
1	A	138	ARG
1	A	166	ARG
1	A	195	GLU
1	A	300	LYS
1	A	339	LYS
1	A	413	ARG
1	B	195	GLU
1	C	170	GLU
1	C	311	SER
1	C	361	ARG
1	C	375	TYR
1	C	413	ARG
1	C	438	ARG
1	D	144	ARG
1	D	187	CYS
1	D	195	GLU
1	D	361	ARG
1	D	413	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	385	GLN
1	C	255	HIS

5.3.3 RNA

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 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 [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	396/450 (88%)	-0.37	3 (0%) 86 89	11, 19, 36, 54	0
1	B	396/450 (88%)	-0.26	9 (2%) 60 67	9, 18, 36, 56	0
1	C	395/450 (87%)	-0.18	8 (2%) 65 71	13, 23, 39, 52	0
1	D	396/450 (88%)	-0.13	6 (1%) 73 79	15, 26, 44, 58	0
All	All	1583/1800 (87%)	-0.23	26 (1%) 72 77	9, 21, 40, 58	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	166	ARG	4.5
1	D	169	CYS	4.0
1	D	139	ASN	3.6
1	B	311	SER	3.3
1	D	191	ASP	3.2
1	B	314	THR	3.1
1	C	316	ARG	3.1
1	B	310	LEU	3.0
1	C	189	GLU	2.7
1	D	311	SER	2.6
1	C	191	ASP	2.6
1	C	314	THR	2.5
1	C	166	ARG	2.5
1	B	189	GLU	2.4
1	A	139	ASN	2.3
1	A	138	ARG	2.3
1	A	191	ASP	2.2
1	C	32	GLU	2.2
1	B	166	ARG	2.1
1	B	312	ASN	2.1
1	B	302	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	233	GLU	2.1
1	C	311	SER	2.1
1	B	188	GLN	2.0
1	B	95	ALA	2.0
1	D	167	SER	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	C	501	1/1	0.99	0.08	18,18,18,18	0
2	ZN	B	501	1/1	1.00	0.10	18,18,18,18	0
2	ZN	A	501	1/1	1.00	0.05	20,20,20,20	0
2	ZN	D	501	1/1	1.00	0.10	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.