



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:13 PM UTC

PDB ID : 2CBL / pdb_00002cbl
Title : N-TERMINAL DOMAIN OF CBL IN COMPLEX WITH ITS BINDING SITE ON ZAP-70
Authors : Meng, W.; Sawasdikosol, S.; Burakoff, S.J.; Eck, M.J.
Deposited on : 1998-08-28
Resolution : 2.10 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

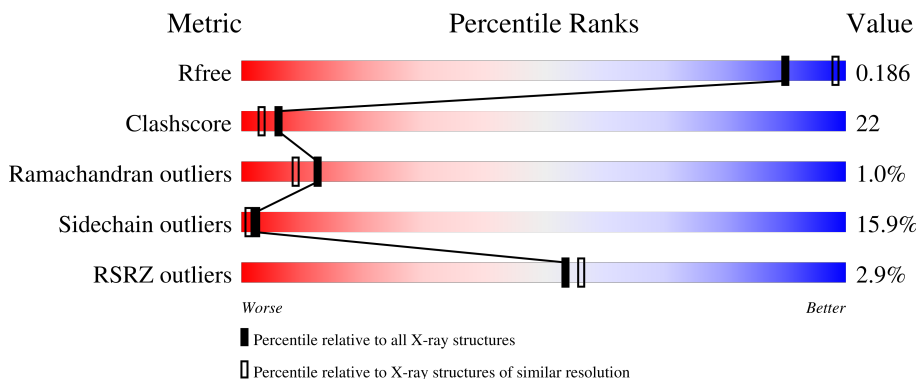
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	305	
2	B	12	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2907 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 PROTO-ONCOGENE CBL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	305	2495	1615	425	442	13	0	0	0

- Molecule 2 is a protein called ZAP-70.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	9	70	40	9	20	1	0	0	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

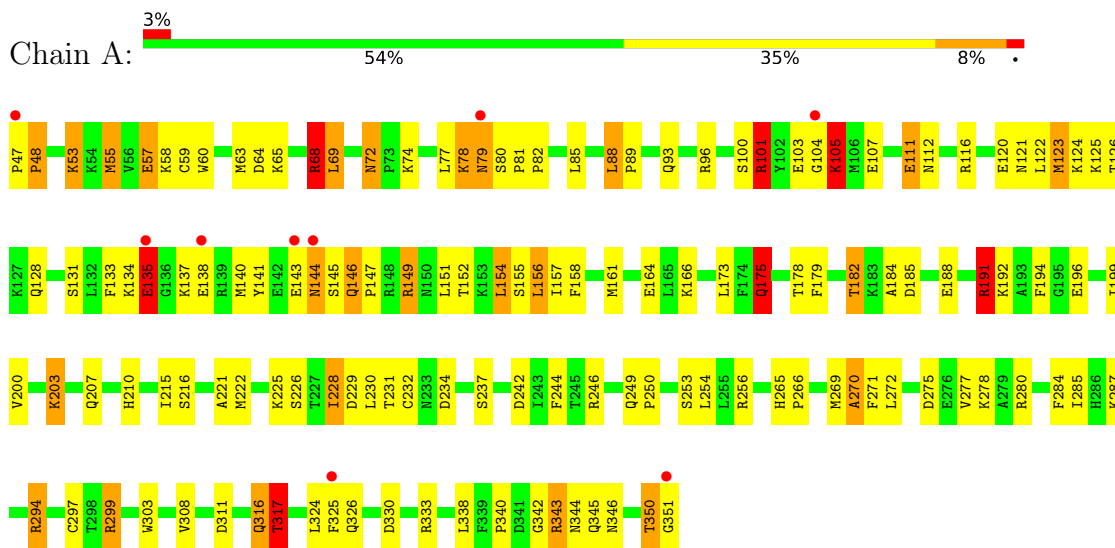
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	320	Total	O	0	0
			320	320		
4	B	21	Total	O	0	0
			21	21		

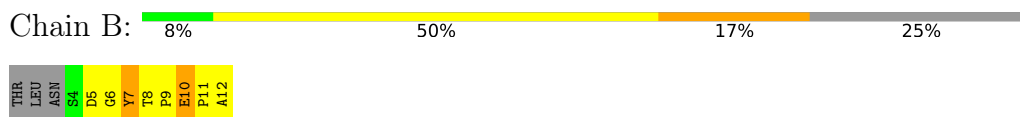
3 Residue-property plots [i](#)

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: PROTO-ONCOGENE CBL



- Molecule 2: ZAP-70



4 Data and refinement statistics

Property	Value	Source
Space group	P 6	Depositor
Cell constants a, b, c, α , β , γ	123.38Å 123.38Å 56.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.10 20.00 – 2.14	Depositor EDS
% Data completeness (in resolution range)	76.9 (20.00-2.10) 75.6 (20.00-2.14)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.14Å)	Xtrriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.173 , 0.245 0.175 , 0.186	Depositor DCC
R_{free} test set	1051 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtrriage
Anisotropy	0.607	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 86.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.045 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2907	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% 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: CA, PTR

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	0.89	5/2561 (0.2%)	1.63	30/3457 (0.9%)
2	B	0.98	0/54	2.01	2/71 (2.8%)
All	All	0.89	5/2615 (0.2%)	1.64	32/3528 (0.9%)

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	13
2	B	0	1
All	All	0	14

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	343	ARG	CD-NE	-7.74	1.35	1.46
1	A	271	PHE	N-CA	7.72	1.58	1.46
1	A	294	ARG	CD-NE	7.35	1.56	1.46
1	A	299	ARG	NE-CZ	-6.01	1.26	1.33
1	A	317	THR	CA-C	5.27	1.59	1.52

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	343	ARG	CD-NE-CZ	26.39	161.35	124.40
1	A	299	ARG	CD-NE-CZ	24.23	158.32	124.40
1	A	68	ARG	CD-NE-CZ	11.51	140.51	124.40
1	A	270	ALA	CA-C-N	-10.41	108.84	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	ALA	C-N-CA	-10.41	108.84	122.79
1	A	294	ARG	NE-CZ-NH2	9.85	128.07	119.20
1	A	294	ARG	CD-NE-CZ	-9.27	111.42	124.40
1	A	294	ARG	NE-CZ-NH1	-8.48	113.02	121.50
1	A	191	ARG	CD-NE-CZ	8.26	135.96	124.40
2	B	11	PRO	CA-C-N	8.10	136.27	121.70
2	B	11	PRO	C-N-CA	8.10	136.27	121.70
1	A	343	ARG	NE-CZ-NH1	-7.75	113.75	121.50
1	A	271	PHE	CA-CB-CG	7.23	121.03	113.80
1	A	343	ARG	NE-CZ-NH2	7.04	125.54	119.20
1	A	185	ASP	CB-CA-C	-6.96	99.67	110.81
1	A	333	ARG	CD-NE-CZ	-6.79	114.89	124.40
1	A	317	THR	CA-CB-OG1	6.75	119.73	109.60
1	A	333	ARG	NE-CZ-NH2	6.70	125.23	119.20
1	A	79	ASN	CA-CB-CG	-6.54	106.06	112.60
1	A	271	PHE	N-CA-C	-6.43	99.98	109.11
1	A	175	GLN	CA-C-O	-6.16	113.95	121.89
1	A	265	HIS	CA-C-O	5.95	123.72	119.32
1	A	308	VAL	CB-CA-C	-5.91	103.81	110.96
1	A	316	GLN	CB-CG-CD	5.73	122.34	112.60
1	A	79	ASN	N-CA-C	5.71	119.34	112.38
1	A	101	ARG	CD-NE-CZ	5.46	132.04	124.40
1	A	317	THR	CB-CA-C	-5.27	99.43	109.66
1	A	229	ASP	CA-CB-CG	-5.24	107.36	112.60
1	A	72	ASN	CA-CB-CG	-5.22	107.38	112.60
1	A	184	ALA	N-CA-C	5.22	116.66	111.07
1	A	135	GLU	CB-CA-C	5.20	119.63	110.37
1	A	68	ARG	CG-CD-NE	5.07	123.15	112.00

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104	GLY	Mainchain
1	A	105	LYS	Mainchain
1	A	135	GLU	Mainchain
1	A	138	GLU	Mainchain
1	A	144	ASN	Mainchain
1	A	175	GLN	Mainchain
1	A	194	PHE	Mainchain
1	A	199	ILE	Mainchain
1	A	226	SER	Mainchain

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Mol	Chain	Res	Type	Group
1	A	266	PRO	Mainchain
1	A	317	THR	Mainchain
1	A	338	LEU	Mainchain
1	A	88	LEU	Mainchain
2	B	10	GLU	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	2495	0	2499	111	0
2	B	70	0	50	8	0
3	A	1	0	0	0	0
4	A	320	0	0	18	0
4	B	21	0	0	3	0
All	All	2907	0	2549	115	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 22.

All (115) 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:72:ASN:HD21	1:A:74:LYS:HB2	1.12	1.09
1:A:203:LYS:H	1:A:203:LYS:HE2	1.15	1.08
1:A:326:GLN:HG2	4:A:642:HOH:O	1.63	0.98
1:A:294:ARG:HH12	1:A:316:GLN:NE2	1.69	0.90
2:B:6:GLY:HA3	4:B:37:HOH:O	1.72	0.88
1:A:203:LYS:H	1:A:203:LYS:CE	1.87	0.86
1:A:256:ARG:HH11	1:A:256:ARG:HG2	1.42	0.84
1:A:72:ASN:ND2	1:A:74:LYS:HB2	1.94	0.82
1:A:294:ARG:HH12	1:A:316:GLN:HE22	1.25	0.81
1:A:144:ASN:HA	1:A:149:ARG:HE	1.45	0.81
1:A:78:LYS:NZ	1:A:78:LYS:H	1.80	0.79
1:A:317:THR:HG21	2:B:10:GLU:HA	1.62	0.79
1:A:280:ARG:HG2	4:A:398:HOH:O	1.81	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:LYS:HA	1:A:68:ARG:HH11	1.49	0.78
1:A:60:TRP:HA	1:A:63:MET:HE3	1.69	0.74
1:A:277:VAL:HG21	1:A:294:ARG:HH11	1.52	0.73
1:A:203:LYS:HE2	1:A:203:LYS:N	2.00	0.73
1:A:122:LEU:O	1:A:126:THR:HG23	1.87	0.73
1:A:125:LYS:NZ	1:A:128:GLN:HE22	1.86	0.72
1:A:350:THR:HG22	4:A:523:HOH:O	1.89	0.72
1:A:157:ILE:HG22	1:A:161:MET:HE2	1.71	0.71
1:A:60:TRP:HD1	1:A:63:MET:HE1	1.55	0.70
1:A:225:LYS:NZ	1:A:234:ASP:OD1	2.26	0.69
1:A:278:LYS:HD3	4:A:367:HOH:O	1.92	0.68
1:A:93:GLN:HE22	1:A:96:ARG:NH1	1.92	0.67
1:A:78:LYS:H	1:A:78:LYS:HZ2	1.43	0.67
1:A:182:THR:HG21	1:A:246:ARG:HE	1.60	0.67
1:A:317:THR:HG23	2:B:8:THR:O	1.96	0.66
1:A:149:ARG:HB3	4:A:440:HOH:O	1.96	0.65
1:A:72:ASN:HD21	1:A:74:LYS:CB	1.99	0.64
1:A:93:GLN:HE22	1:A:96:ARG:HH11	1.46	0.63
1:A:72:ASN:ND2	1:A:141:TYR:CE1	2.66	0.63
1:A:125:LYS:HD3	1:A:128:GLN:NE2	2.14	0.63
1:A:256:ARG:HG2	1:A:256:ARG:NH1	2.13	0.63
1:A:82:PRO:HG3	1:A:156:LEU:HD13	1.84	0.60
1:A:182:THR:HB	1:A:242:ASP:OD1	2.01	0.60
1:A:340:PRO:HG3	1:A:346:ASN:HD22	1.65	0.60
1:A:101:ARG:HG2	1:A:101:ARG:HH11	1.66	0.60
1:A:60:TRP:HD1	1:A:63:MET:CE	2.16	0.59
1:A:287:LYS:NZ	1:A:344:ASN:ND2	2.52	0.58
1:A:123:MET:HE3	4:A:588:HOH:O	2.03	0.58
1:A:277:VAL:HG21	1:A:294:ARG:NH1	2.18	0.58
1:A:125:LYS:HZ2	1:A:128:GLN:HE22	1.49	0.58
1:A:93:GLN:NE2	1:A:96:ARG:HD3	2.19	0.58
1:A:203:LYS:H	1:A:203:LYS:CD	2.18	0.57
1:A:182:THR:HG21	1:A:246:ARG:NE	2.18	0.57
1:A:77:LEU:HA	1:A:78:LYS:HZ2	1.70	0.57
1:A:143:GLU:HB2	4:A:411:HOH:O	2.05	0.56
1:A:145:SER:O	1:A:149:ARG:HG2	2.04	0.56
1:A:294:ARG:NH1	4:A:662:HOH:O	2.38	0.56
1:A:287:LYS:HZ3	1:A:344:ASN:ND2	2.04	0.56
1:A:53:LYS:O	1:A:57:GLU:HG2	2.04	0.56
1:A:112:ASN:O	1:A:116:ARG:HG3	2.07	0.55
1:A:350:THR:CG2	4:A:523:HOH:O	2.48	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:12:ALA:HB2	4:B:48:HOH:O	2.07	0.55
1:A:317:THR:HG21	2:B:10:GLU:CA	2.36	0.55
1:A:47:PRO:CB	1:A:48:PRO:CD	2.85	0.54
1:A:55:MET:SD	1:A:123:MET:HE1	2.48	0.53
1:A:59:CYS:SG	1:A:63:MET:HE2	2.48	0.53
1:A:191:ARG:NH2	4:A:600:HOH:O	2.41	0.53
1:A:228:ILE:HG12	1:A:244:PHE:CD1	2.44	0.53
1:A:80:SER:HB2	2:B:5:ASP:OD1	2.09	0.53
1:A:203:LYS:O	1:A:207:GLN:HG3	2.11	0.51
1:A:121:ASN:HD21	1:A:231:THR:HB	1.76	0.51
1:A:284:PHE:CZ	1:A:342:GLY:HA3	2.46	0.51
1:A:47:PRO:CB	1:A:48:PRO:HD2	2.41	0.50
1:A:203:LYS:NZ	4:A:470:HOH:O	2.37	0.50
1:A:287:LYS:NZ	1:A:344:ASN:HD21	2.10	0.49
1:A:203:LYS:N	1:A:203:LYS:CD	2.75	0.49
1:A:232:CYS:HB3	4:A:468:HOH:O	2.13	0.48
2:B:9:PRO:HB3	4:B:46:HOH:O	2.14	0.48
1:A:111:GLU:O	1:A:116:ARG:NH1	2.47	0.48
1:A:88:LEU:N	1:A:89:PRO:HD2	2.29	0.48
1:A:152:THR:O	1:A:155:SER:HB2	2.14	0.47
1:A:158:PHE:HA	1:A:161:MET:HE3	1.95	0.47
1:A:287:LYS:HZ1	1:A:344:ASN:HD21	1.61	0.47
1:A:351:GLY:HA2	4:A:524:HOH:O	2.14	0.47
1:A:210:HIS:CD2	1:A:215:ILE:H	2.33	0.47
2:B:5:ASP:OD2	2:B:7:PTR:O1P	2.34	0.46
1:A:101:ARG:HH11	1:A:101:ARG:CG	2.28	0.46
1:A:78:LYS:HD3	1:A:275:ASP:OD2	2.16	0.46
1:A:149:ARG:HG2	1:A:149:ARG:H	1.57	0.45
1:A:210:HIS:HD2	1:A:215:ILE:H	1.63	0.45
1:A:294:ARG:HH11	1:A:294:ARG:HD3	1.30	0.45
1:A:93:GLN:HE22	1:A:96:ARG:HD3	1.82	0.45
1:A:146:GLN:N	1:A:147:PRO:CD	2.80	0.45
1:A:88:LEU:HB2	1:A:89:PRO:HD3	1.98	0.45
1:A:215:ILE:HG21	1:A:221:ALA:HB2	1.98	0.45
1:A:131:SER:HB3	1:A:135:GLU:OE1	2.16	0.45
1:A:60:TRP:CD1	1:A:63:MET:HE1	2.44	0.44
1:A:294:ARG:NH1	1:A:316:GLN:NE2	2.52	0.44
1:A:249:GLN:HB2	1:A:250:PRO:HA	1.99	0.44
1:A:48:PRO:HG3	1:A:120:GLU:OE2	2.18	0.43
1:A:69:LEU:HG	1:A:133:PHE:CG	2.53	0.43
1:A:351:GLY:HA3	4:A:525:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:MET:HE3	4:A:496:HOH:O	2.18	0.43
1:A:140:MET:HE1	1:A:151:LEU:HB2	2.00	0.42
1:A:164:GLU:OE2	1:A:237:SER:OG	2.25	0.42
1:A:88:LEU:N	1:A:89:PRO:CD	2.82	0.42
1:A:178:THR:O	1:A:179:PHE:C	2.62	0.42
1:A:78:LYS:HZ2	1:A:78:LYS:N	2.15	0.42
1:A:303:TRP:CD2	1:A:324:LEU:HD22	2.55	0.42
1:A:105:LYS:HA	4:A:616:HOH:O	2.19	0.42
1:A:166:LYS:NZ	4:A:361:HOH:O	2.53	0.42
1:A:154:LEU:HD12	1:A:154:LEU:HA	1.89	0.41
1:A:63:MET:HE3	1:A:63:MET:HB2	1.93	0.41
1:A:269:MET:HE3	1:A:269:MET:HB3	1.82	0.41
1:A:203:LYS:N	1:A:203:LYS:HD3	2.35	0.41
1:A:81:PRO:HA	1:A:82:PRO:HA	1.86	0.41
1:A:125:LYS:HD3	1:A:128:GLN:HE22	1.85	0.41
1:A:210:HIS:CD2	4:A:484:HOH:O	2.74	0.41
1:A:228:ILE:O	1:A:228:ILE:HG22	2.21	0.41
1:A:253:SER:O	1:A:254:LEU:C	2.63	0.41
1:A:134:LYS:HE3	1:A:134:LYS:HB2	1.86	0.40
1:A:326:GLN:HE21	1:A:330:ASP:CG	2.29	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	303/305 (99%)	288 (95%)	12 (4%)	3 (1%)	12 9
2	B	6/12 (50%)	6 (100%)	0	0	100 100
All	All	309/317 (98%)	294 (95%)	12 (4%)	3 (1%)	12 9

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	270	ALA
1	A	137	LYS
1	A	48	PRO

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	271/272 (100%)	227 (84%)	44 (16%)	2 1
2	B	6/9 (67%)	6 (100%)	0	100 100
All	All	277/281 (99%)	233 (84%)	44 (16%)	2 1

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

Mol	Chain	Res	Type
1	A	53	LYS
1	A	55	MET
1	A	57	GLU
1	A	58	LYS
1	A	64	ASP
1	A	68	ARG
1	A	69	LEU
1	A	78	LYS
1	A	79	ASN
1	A	85	LEU
1	A	100	SER
1	A	101	ARG
1	A	103	GLU
1	A	105	LYS
1	A	107	GLU
1	A	111	GLU
1	A	123	MET
1	A	124	LYS
1	A	146	GLN
1	A	149	ARG
1	A	154	LEU

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Mol	Chain	Res	Type
1	A	156	LEU
1	A	173	LEU
1	A	175	GLN
1	A	182	THR
1	A	188	GLU
1	A	191	ARG
1	A	192	LYS
1	A	196	GLU
1	A	200	VAL
1	A	203	LYS
1	A	216	SER
1	A	228	ILE
1	A	230	LEU
1	A	272	LEU
1	A	285	ILE
1	A	297	CYS
1	A	299	ARG
1	A	311	ASP
1	A	317	THR
1	A	325	PHE
1	A	343	ARG
1	A	345	GLN
1	A	350	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	93	GLN
1	A	94	HIS
1	A	121	ASN
1	A	128	GLN
1	A	146	GLN
1	A	150	ASN
1	A	210	HIS
1	A	282	GLN
1	A	286	HIS
1	A	316	GLN
1	A	326	GLN
1	A	344	ASN
1	A	345	GLN
1	A	346	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue 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
2	PTR	B	7	2	15,16,17	5.48	4 (26%)	17,22,24	3.97	3 (17%)

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	PTR	B	7	2	-	0/10/11/13	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	7	PTR	P-OH	15.22	1.88	1.59
2	B	7	PTR	P-O1P	10.19	1.82	1.50
2	B	7	PTR	P-O3P	10.15	1.92	1.54
2	B	7	PTR	P-O2P	2.46	1.64	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	7	PTR	O3P-P-OH	-10.39	74.60	105.32
2	B	7	PTR	O2P-P-OH	-8.86	79.11	105.32
2	B	7	PTR	O2P-P-O1P	8.40	143.55	110.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	7	PTR	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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	305/305 (100%)	-0.10	9 (2%) 52 55	29, 42, 71, 83	0
2	B	8/12 (66%)	0.20	0 100 100	31, 41, 55, 66	0
All	All	313/317 (98%)	-0.09	9 (2%) 53 56	29, 42, 71, 83	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	351	GLY	3.1
1	A	47	PRO	2.9
1	A	325	PHE	2.8
1	A	143	GLU	2.6
1	A	144	ASN	2.6
1	A	135	GLU	2.5
1	A	79	ASN	2.5
1	A	104	GLY	2.4
1	A	138	GLU	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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	PTR	B	7	16/17	0.96	0.09	17,36,40,47	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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
3	CA	A	352	1/1	0.99	0.23	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.