



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 06:06 PM UTC

PDB ID : 6G85 / pdb_00006g85
Title : Structure of Cdc14 bound to CBK1 PxL motif
Authors : Mouilleron, S.; Kataria, M.; Uhlmann, F.
Deposited on : 2018-04-07
Resolution : 1.53 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

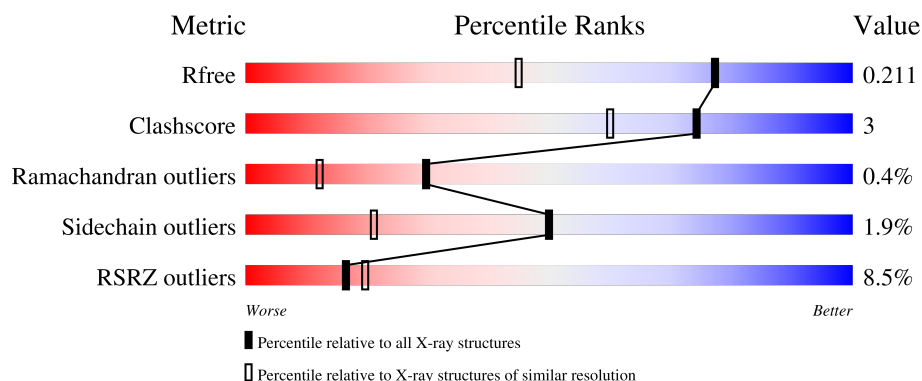
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.53 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	5890 (1.54-1.50)
Clashscore	190562	6116 (1.54-1.50)
Ramachandran outliers	187476	6002 (1.54-1.50)
Sidechain outliers	187428	5999 (1.54-1.50)
RSRZ outliers	180081	5891 (1.54-1.50)

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	374	5% 90% 6% .
1	B	374	9% 88% 7% . .
2	C	16	25% 44% 19% 38%
3	D	17	47% 82% 6% 12%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7063 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 Tyrosine-protein phosphatase CDC14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	361	Total	C	N	O	S	0	19	0
			3026	1966	511	537	12			
1	B	359	Total	C	N	O	S	0	19	0
			2990	1941	501	536	12			

- Molecule 2 is a protein called CBK1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	0	1	0
			85	57	12	16			

- Molecule 3 is a protein called CBK1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	15	Total	C	N	O	0	0	0
			106	72	15	19			

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Zn	0	0
			1	1		

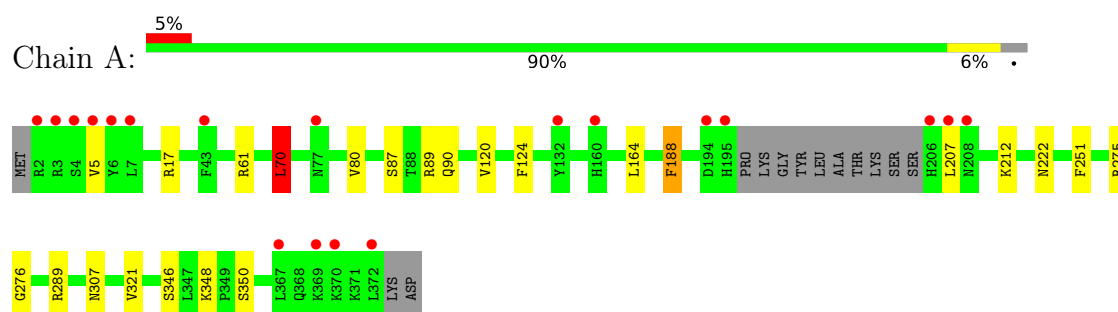
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	435	Total	O	0	7
			435	435		
9	B	352	Total	O	0	5
			352	352		
9	C	8	Total	O	0	0
			8	8		
9	D	7	Total	O	0	0
			7	7		

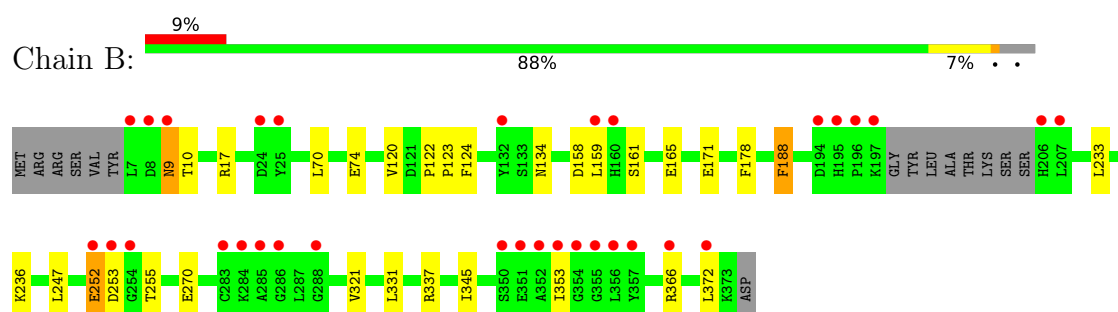
3 Residue-property plots [i](#)

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.

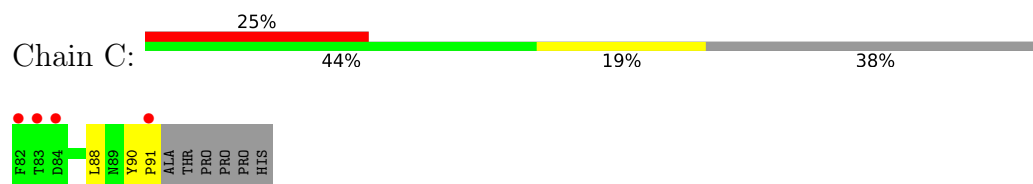
- Molecule 1: Tyrosine-protein phosphatase CDC14



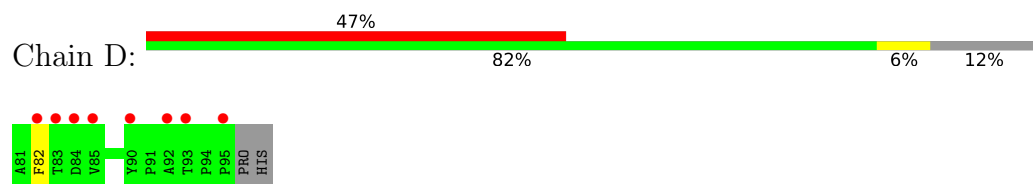
- Molecule 1: Tyrosine-protein phosphatase CDC14



- Molecule 2: CBK1



- Molecule 3: CBK1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.15Å 97.41Å 129.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.99 – 1.53 59.99 – 1.53	Depositor EDS
% Data completeness (in resolution range)	97.4 (59.99-1.53) 97.3 (59.99-1.53)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 1.53Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.182 , 0.209 0.184 , 0.211	Depositor DCC
R_{free} test set	7231 reflections (4.35%)	wwPDB-VP
Wilson B-factor (Å ²)	22.6	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7063	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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: PEG, GOL, EDO, ZN, MES

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	0.95	0/3168	0.75	2/4298 (0.0%)
1	B	0.88	0/3129	0.74	0/4246
2	C	0.51	0/91	0.55	0/126
3	D	0.53	0/111	0.69	0/156
All	All	0.91	0/6499	0.74	2/8826 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	70	LEU	CA-CB-CG	5.29	134.81	116.30
1	A	188	PHE	CA-CB-CG	5.03	118.83	113.80

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	3026	0	2952	17	0
1	B	2990	0	2917	19	0
2	C	85	0	79	2	0
3	D	106	0	98	2	0
4	A	12	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	12	0	12	1	0
5	A	6	0	8	2	0
6	A	16	0	24	5	0
7	A	7	0	10	1	0
8	A	1	0	0	0	0
9	A	435	0	0	3	0
9	B	352	0	0	4	0
9	C	8	0	0	0	0
9	D	7	0	0	0	0
All	All	7063	0	6112	38	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 3.

All (38) 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:307:ASN:ND2	9:A:504:HOH:O	2.26	0.68
1:B:236:LYS:NZ	9:B:501:HOH:O	2.29	0.65
1:A:89:ARG:HB2	5:A:402:GOL:H32	1.79	0.64
1:B:9:ASN:OD1	1:B:9:ASN:N	2.31	0.63
1:A:90:GLN:HG2	5:A:402:GOL:H31	1.81	0.60
1:A:61[B]:ARG:CZ	1:A:164:LEU:HD21	2.35	0.56
1:A:275:ARG:HH12	7:A:407:PEG:H32	1.71	0.56
1:A:70:LEU:HD21	2:C:88:LEU:HD11	1.88	0.56
6:A:405:EDO:O2	9:A:501:HOH:O	2.18	0.55
1:A:350:SER:HB2	6:A:405:EDO:H12	1.90	0.54
1:B:158:ASP:OD2	1:B:161:SER:OG	2.28	0.51
1:A:251:PHE:CE1	1:A:289:ARG:HG2	2.46	0.51
1:A:61[B]:ARG:NE	1:A:164:LEU:HD21	2.28	0.49
1:A:70:LEU:HD13	1:A:80:VAL:HG21	1.96	0.48
2:C:90:TYR:CG	2:C:91:PRO:HD2	2.49	0.48
1:B:247:LEU:HD21	1:B:353:ILE:HG22	1.95	0.48
1:B:120[B]:VAL:HG11	1:B:124:PHE:CE2	2.49	0.47
1:B:165[A]:GLU:H	1:B:165[A]:GLU:CD	2.23	0.47
1:B:252[A]:GLU:OE1	1:B:255[A]:THR:HG21	2.14	0.47
1:A:120[B]:VAL:HG11	1:A:124:PHE:CE2	2.50	0.47
1:A:17[A]:ARG:NH2	9:A:502:HOH:O	2.23	0.47
1:B:159:LEU:HD23	3:D:82:PHE:CE2	2.50	0.46
1:B:159:LEU:HB3	3:D:82:PHE:CD2	2.50	0.46
1:B:331:LEU:HD12	9:B:793:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:LEU:O	1:A:212:LYS:HE3	2.17	0.44
1:B:122:PRO:HA	1:B:123:PRO:HD3	1.88	0.43
1:A:5:VAL:HG13	6:A:406:EDO:H22	2.01	0.43
1:B:366:ARG:NH1	9:B:518:HOH:O	2.51	0.43
1:B:337[B]:ARG:HA	1:B:337[B]:ARG:HD2	1.79	0.42
1:B:134:ASN:HB3	9:B:672:HOH:O	2.20	0.42
1:A:276:GLY:HA3	6:A:403:EDO:H21	2.03	0.41
1:B:253:ASP:OD2	4:B:401:MES:H81	2.19	0.41
1:B:270:GLU:HB3	1:B:345:ILE:HD11	2.01	0.41
1:B:247:LEU:CD1	1:B:353:ILE:HA	2.51	0.40
1:A:346:SER:HG	1:A:348:LYS:H	1.68	0.40
1:B:178:PHE:HB3	1:B:188:PHE:HB3	2.03	0.40
1:A:222:ASN:HB2	6:A:404:EDO:H12	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	376/374 (100%)	365 (97%)	10 (3%)	1 (0%)	36	18
1	B	375/374 (100%)	361 (96%)	12 (3%)	2 (0%)	24	8
2	C	9/16 (56%)	8 (89%)	1 (11%)	0	100	100
3	D	13/17 (76%)	12 (92%)	1 (8%)	0	100	100
All	All	773/781 (99%)	746 (96%)	24 (3%)	3 (0%)	30	12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	321	VAL
1	B	372	LEU

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Mol	Chain	Res	Type
1	B	321	VAL

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	325/325 (100%)	322 (99%)	3 (1%)	70	49
1	B	322/325 (99%)	310 (96%)	12 (4%)	30	6
2	C	10/14 (71%)	10 (100%)	0	100	100
3	D	11/14 (79%)	11 (100%)	0	100	100
All	All	668/678 (98%)	653 (98%)	15 (2%)	50	16

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	LEU
1	A	87	SER
1	A	188	PHE
1	B	9	ASN
1	B	10	THR
1	B	17[A]	ARG
1	B	17[B]	ARG
1	B	70	LEU
1	B	74	GLU
1	B	171[A]	GLU
1	B	171[B]	GLU
1	B	188	PHE
1	B	233	LEU
1	B	252[A]	GLU
1	B	252[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	HIS
1	A	206	HIS
1	A	209	GLN
1	A	216	ASN
1	A	307	ASN
1	B	48	HIS
1	B	134	ASN
1	B	195	HIS
1	B	307	ASN
3	D	89	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 for Mogul analysis.

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	$\# Z > 2$
6	EDO	A	404	-	3,3,3	0.44	0	2,2,2	0.39	0
4	MES	A	401	-	12,12,12	1.52	2 (16%)	15,16,16	1.53	3 (20%)
7	PEG	A	407	-	6,6,6	0.50	0	5,5,5	0.38	0
5	GOL	A	402	-	5,5,5	1.19	0	5,5,5	1.03	0
6	EDO	A	403	-	3,3,3	0.39	0	2,2,2	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MES	B	401	-	12,12,12	1.45	2 (16%)	15,16,16	2.16	4 (26%)
6	EDO	A	406	-	3,3,3	0.45	0	2,2,2	0.31	0
6	EDO	A	405	-	3,3,3	0.40	0	2,2,2	0.12	0

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
6	EDO	A	404	-	-	1/1/1/1	-
4	MES	A	401	-	-	0/6/14/14	0/1/1/1
7	PEG	A	407	-	-	2/4/4/4	-
5	GOL	A	402	-	-	1/4/4/4	-
6	EDO	A	403	-	-	0/1/1/1	-
4	MES	B	401	-	-	3/6/14/14	0/1/1/1
6	EDO	A	406	-	-	0/1/1/1	-
6	EDO	A	405	-	-	0/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	401	MES	C8-S	-3.89	1.72	1.77
4	A	401	MES	C8-S	-3.09	1.73	1.77
4	A	401	MES	O1S-S	3.05	1.53	1.45
4	B	401	MES	O1S-S	2.55	1.52	1.45

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	401	MES	C7-N4-C5	4.40	122.96	111.24
4	B	401	MES	C5-N4-C3	4.14	117.77	108.84
4	B	401	MES	C2-C3-N4	-3.91	104.18	110.12
4	A	401	MES	C5-N4-C3	3.15	115.63	108.84
4	A	401	MES	C7-N4-C5	2.74	118.54	111.24
4	B	401	MES	C7-N4-C3	2.50	117.91	111.24
4	A	401	MES	O1S-S-C8	-2.07	103.59	106.73

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	401	MES	C8-C7-N4-C5
4	B	401	MES	N4-C7-C8-S
4	B	401	MES	C8-C7-N4-C3
7	A	407	PEG	O2-C3-C4-O4
5	A	402	GOL	O2-C2-C3-O3
7	A	407	PEG	C1-C2-O2-C3
6	A	404	EDO	O1-C1-C2-O2

There are no ring outliers.

7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	404	EDO	1	0
7	A	407	PEG	1	0
5	A	402	GOL	2	0
6	A	403	EDO	1	0
4	B	401	MES	1	0
6	A	406	EDO	1	0
6	A	405	EDO	2	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 [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	361/374 (96%)	0.11	19 (5%) 32 37	12, 24, 49, 88	19 (5%)
1	B	359/374 (95%)	0.47	32 (8%) 15 18	11, 27, 53, 101	19 (5%)
2	C	10/16 (62%)	2.04	4 (40%) 1 0	26, 38, 67, 70	1 (10%)
3	D	15/17 (88%)	2.67	8 (53%) 0 0	33, 43, 82, 87	0
All	All	745/781 (95%)	0.36	63 (8%) 16 20	11, 26, 53, 101	39 (5%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	353	ILE	6.8
1	B	355	GLY	6.4
1	B	356	LEU	6.1
3	D	95	PRO	6.0
1	A	195	HIS	5.5
3	D	84	ASP	5.4
1	B	7	LEU	5.2
3	D	82	PHE	5.0
1	B	372	LEU	4.8
1	A	372	LEU	4.8
1	A	206	HIS	4.8
1	A	194	ASP	4.8
2	C	82	PHE	4.6
1	B	285	ALA	4.5
1	B	206	HIS	4.2
1	B	195	HIS	4.2
1	B	352	ALA	4.1
1	A	160[A]	HIS	3.6
1	A	367	LEU	3.6
2	C	83	THR	3.5
1	B	196	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	6	TYR	3.4
1	A	132	TYR	3.3
2	C	91	PRO	3.2
1	A	43	PHE	3.2
1	B	354	GLY	3.2
1	B	8	ASP	3.2
1	B	194	ASP	3.1
3	D	83	THR	3.0
1	B	132	TYR	3.0
3	D	92	ALA	2.9
1	A	5	VAL	2.8
1	B	350	SER	2.8
1	B	357	TYR	2.8
1	B	159	LEU	2.8
1	B	254	GLY	2.8
1	A	4	SER	2.7
1	A	207	LEU	2.6
3	D	85	VAL	2.6
1	B	253	ASP	2.6
1	B	9	ASN	2.6
1	A	77	ASN	2.6
1	B	207	LEU	2.5
3	D	93	THR	2.5
3	D	90	TYR	2.5
1	B	286	GLY	2.4
1	B	288	GLY	2.4
1	A	369	LYS	2.4
1	B	25	TYR	2.3
1	B	160	HIS	2.3
1	A	2	ARG	2.3
1	B	252[A]	GLU	2.3
1	A	3	ARG	2.3
1	B	366	ARG	2.3
1	B	24	ASP	2.3
1	B	351	GLU	2.2
1	B	284[A]	LYS	2.2
1	B	283	CYS	2.1
1	A	370	LYS	2.1
1	B	197	LYS	2.1
1	A	208	ASN	2.1
1	A	7	LEU	2.0
2	C	84	ASP	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 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($\text{\AA}^2$)	Q<0.9
6	EDO	A	406	4/4	0.71	0.19	76,77,79,80	0
6	EDO	A	404	4/4	0.79	0.20	55,60,66,69	0
5	GOL	A	402	6/6	0.82	0.16	50,55,56,62	0
7	PEG	A	407	7/7	0.82	0.14	41,60,66,67	0
6	EDO	A	403	4/4	0.85	0.12	58,62,66,70	0
6	EDO	A	405	4/4	0.86	0.12	55,56,62,68	0
4	MES	B	401	12/12	0.87	0.20	27,37,48,51	12
8	ZN	A	408	1/1	0.95	0.30	58,58,58,58	0
4	MES	A	401	12/12	0.98	0.09	22,27,36,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.