



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2021 – 02:15 PM EDT

PDB ID : 3BLH
Title : Crystal Structure of Human CDK9/cyclinT1
Authors : Baumli, S.; Lolli, G.; Lowe, E.D.; Johnson, L.N.
Deposited on : 2007-12-11
Resolution : 2.48 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

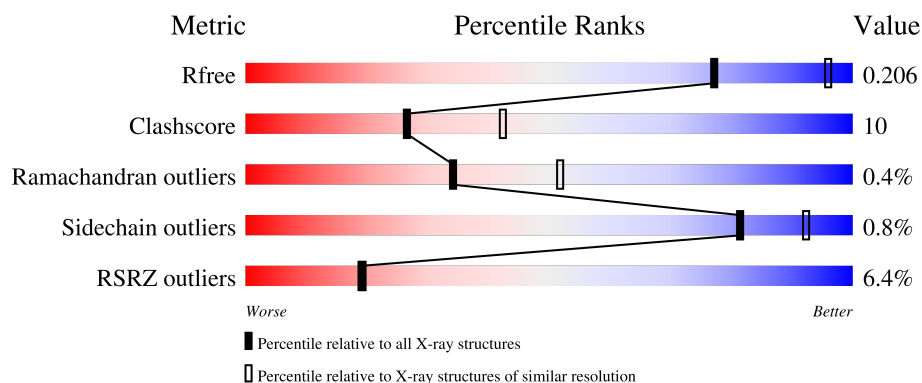
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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	331	<div> <div>6%</div> <div>68%</div> <div>19%</div> <div>12%</div> </div>
2	B	260	<div> <div>6%</div> <div>80%</div> <div>18%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	TPO	A	186	X	-	-	-
3	TRS	B	260	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4601 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 division protein kinase 9.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	P	S	0	0	0
			2365	1520	410	421	1	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P50750
A	1	PRO	-	expression tag	UNP P50750

- Molecule 2 is a protein called Cyclin-T1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	255	Total	C	N	O	S		0	0	0
			2089	1334	368	378	9				

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP O60563
B	1	PRO	-	expression tag	UNP O60563
B	77	ARG	GLN	engineered mutation	UNP O60563
B	96	GLY	GLU	engineered mutation	UNP O60563
B	241	LEU	PHE	engineered mutation	UNP O60563

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			8	4	1	3		

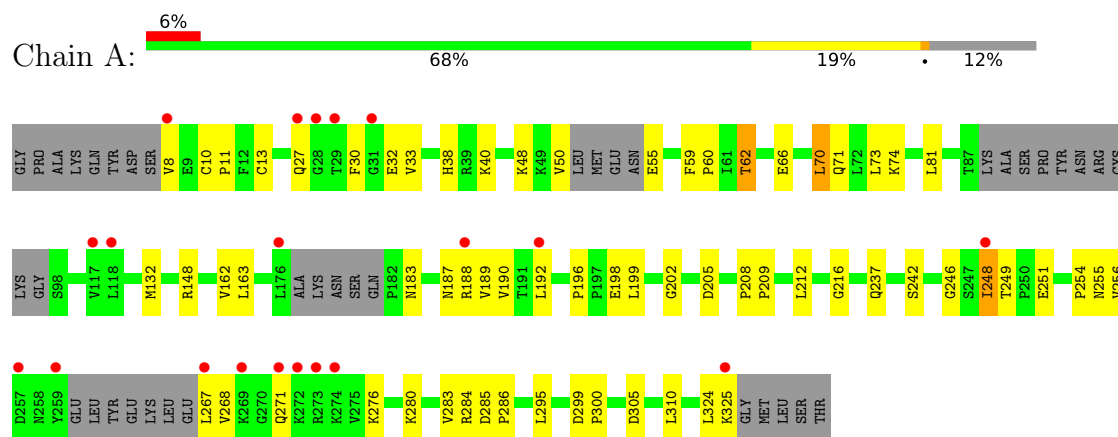
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	54	Total	O	0	0
			54	54		
4	B	85	Total	O	0	0
			85	85		

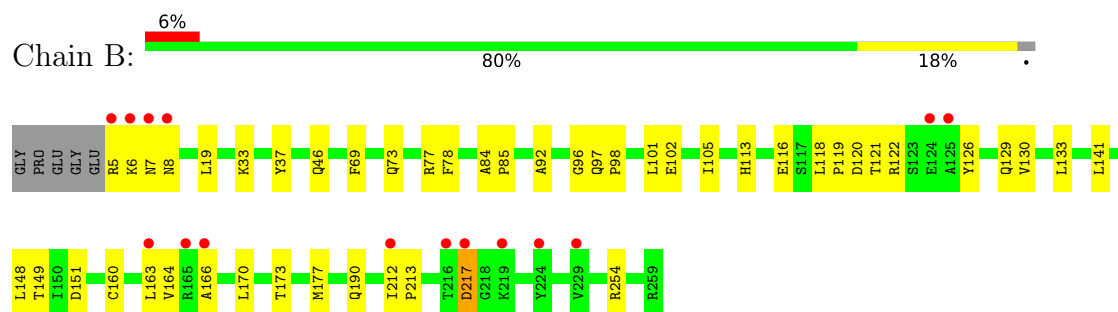
3 Residue-property plots [i](#)

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: Cell division protein kinase 9



- Molecule 2: Cyclin-T1



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	172.92Å 172.92Å 95.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.73 – 2.48 48.73 – 2.48	Depositor EDS
% Data completeness (in resolution range)	95.5 (48.73-2.48) 99.1 (48.73-2.48)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.48Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.179 , 0.221 0.167 , 0.206	Depositor DCC
R_{free} test set	1872 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	58.5	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.020 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4601	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, TRS

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	0.35	0/2400	0.50	0/3236
2	B	0.37	0/2142	0.51	0/2915
All	All	0.36	0/4542	0.51	0/6151

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	1	0

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	186	TPO	CB

There are no planarity outliers.

5.2 Too-close contacts

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	2365	0	2416	55	0
2	B	2089	0	2081	40	0
3	B	8	0	12	6	0
4	A	54	0	0	3	0
4	B	85	0	0	0	0
All	All	4601	0	4509	92	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 10.

All (92) 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)
2:B:7:ASN:HB3	2:B:8:ASN:HA	1.36	1.08
2:B:7:ASN:HB3	2:B:8:ASN:CA	1.92	1.00
2:B:254:ARG:HH12	3:B:260:TRS:H32	1.34	0.89
1:A:249:THR:HG22	1:A:251:GLU:H	1.37	0.88
1:A:71:GLN:OE1	2:B:6:LYS:HG2	1.74	0.88
1:A:189:VAL:HG23	1:A:199:LEU:HD13	1.55	0.86
1:A:248:ILE:HG22	1:A:256:VAL:HG21	1.67	0.77
2:B:7:ASN:HB3	2:B:8:ASN:C	2.08	0.74
1:A:196:PRO:HB2	1:A:198:GLU:OE1	1.88	0.72
1:A:188:ARG:O	1:A:188:ARG:HG2	1.90	0.72
2:B:254:ARG:NH1	3:B:260:TRS:H11	2.05	0.71
2:B:7:ASN:CB	2:B:8:ASN:HA	2.19	0.71
2:B:5:ARG:HG2	2:B:149:THR:HB	1.73	0.70
1:A:132:MET:HE3	4:A:378:HOH:O	1.92	0.69
2:B:84:ALA:HB3	2:B:85:PRO:HD3	1.75	0.67
1:A:254:PRO:O	1:A:255:ASN:HB2	1.94	0.67
1:A:248:ILE:CG2	1:A:256:VAL:HG21	2.26	0.65
1:A:132:MET:HE1	1:A:162:VAL:HA	1.81	0.63
1:A:276:LYS:O	1:A:280:LYS:HB2	2.00	0.61
1:A:212:LEU:HD13	1:A:305:ASP:HA	1.82	0.61
1:A:188:ARG:O	1:A:188:ARG:CG	2.50	0.60
1:A:73:LEU:O	1:A:74:LYS:HD3	2.02	0.60
2:B:254:ARG:HH12	3:B:260:TRS:C3	2.13	0.60
1:A:10:CYS:SG	1:A:13:CYS:HB3	2.43	0.59
2:B:105:ILE:HD11	2:B:130:VAL:HA	1.85	0.59
1:A:30:PHE:HZ	1:A:62:THR:HG22	1.69	0.58
1:A:66:GLU:HG2	1:A:70:LEU:HD22	1.86	0.58
2:B:105:ILE:CD1	2:B:130:VAL:HA	2.34	0.58
1:A:30:PHE:HB2	1:A:50:VAL:HA	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:118:LEU:HD12	2:B:119:PRO:HD2	1.85	0.58
1:A:187:ASN:ND2	1:A:202:GLY:HA2	2.21	0.56
1:A:38:HIS:CE1	1:A:40:LYS:HB2	2.42	0.55
1:A:248:ILE:HG13	1:A:267:LEU:HD13	1.89	0.54
1:A:268:VAL:HG21	1:A:271:GLN:HG3	1.89	0.54
2:B:166:ALA:HB1	2:B:170:LEU:HB3	1.88	0.54
1:A:242:SER:HA	1:A:246:GLY:O	2.08	0.53
1:A:30:PHE:CB	1:A:50:VAL:HA	2.39	0.52
2:B:102:GLU:HG2	2:B:126:TYR:OH	2.09	0.52
1:A:55:GLU:CD	1:A:55:GLU:N	2.64	0.52
1:A:189:VAL:HG23	1:A:199:LEU:CD1	2.34	0.51
1:A:324:LEU:O	1:A:325:LYS:HG3	2.11	0.51
1:A:8:VAL:HG23	2:B:77:ARG:HH21	1.76	0.50
1:A:38:HIS:HE1	1:A:40:LYS:HB2	1.77	0.49
2:B:77:ARG:HG2	2:B:78:PHE:CE2	2.47	0.49
1:A:71:GLN:NE2	4:A:379:HOH:O	2.45	0.49
1:A:30:PHE:HZ	1:A:62:THR:CG2	2.26	0.49
1:A:132:MET:CE	1:A:162:VAL:HA	2.43	0.49
1:A:30:PHE:CZ	1:A:62:THR:HG22	2.47	0.48
2:B:121:THR:HA	2:B:126:TYR:CD2	2.48	0.48
2:B:160:CYS:O	2:B:164:VAL:HG22	2.13	0.48
1:A:33:VAL:HG13	1:A:48:LYS:HG2	1.96	0.48
1:A:10:CYS:N	1:A:11:PRO:HD3	2.28	0.48
2:B:101:LEU:HD11	2:B:133:LEU:HD22	1.95	0.47
1:A:148:ARG:HD2	1:A:189:VAL:HG11	1.95	0.47
2:B:46:GLN:HG2	3:B:260:TRS:H21	1.97	0.47
1:A:183:ASN:HB2	1:A:205:ASP:OD1	2.15	0.46
1:A:242:SER:HB3	1:A:268:VAL:HG21	1.97	0.46
1:A:249:THR:HG22	1:A:251:GLU:HB3	1.98	0.46
1:A:249:THR:CG2	1:A:251:GLU:HB3	2.46	0.46
2:B:212:ILE:HA	2:B:213:PRO:HD3	1.83	0.46
1:A:187:ASN:O	1:A:187:ASN:OD1	2.33	0.46
2:B:254:ARG:HH12	3:B:260:TRS:H11	1.80	0.46
2:B:173:THR:O	2:B:177:MET:HG2	2.15	0.45
1:A:208:PRO:N	1:A:209:PRO:CD	2.80	0.45
2:B:217:ASP:OD1	2:B:217:ASP:N	2.49	0.45
2:B:69:PHE:CZ	2:B:73:GLN:HG3	2.52	0.45
2:B:254:ARG:CZ	3:B:260:TRS:H11	2.46	0.45
1:A:81:LEU:HG	2:B:6:LYS:HZ1	1.82	0.45
1:A:27:GLN:HA	1:A:32:GLU:HA	1.98	0.45
2:B:96:GLY:C	2:B:98:PRO:HD3	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:101:LEU:CD1	2:B:133:LEU:HD22	2.47	0.44
2:B:5:ARG:NH2	2:B:151:ASP:HB2	2.33	0.44
2:B:5:ARG:HH22	2:B:151:ASP:HB2	1.83	0.43
1:A:212:LEU:HD12	4:A:381:HOH:O	2.19	0.43
1:A:249:THR:HG22	1:A:251:GLU:N	2.19	0.43
1:A:310:LEU:HD23	1:A:310:LEU:HA	1.89	0.42
1:A:283:VAL:O	1:A:284:ARG:HB2	2.20	0.42
2:B:19:LEU:HD11	2:B:190:GLN:HG2	2.01	0.42
2:B:141:LEU:CD2	2:B:148:LEU:HD11	2.50	0.42
2:B:126:TYR:HA	2:B:129:GLN:HG2	2.01	0.41
2:B:92:ALA:HB1	2:B:97:GLN:O	2.20	0.41
2:B:166:ALA:HB1	2:B:170:LEU:HD23	2.01	0.41
1:A:192:LEU:HG	1:A:237:GLN:HE21	1.86	0.41
1:A:192:LEU:HG	1:A:237:GLN:NE2	2.36	0.41
1:A:216:GLY:HA2	1:A:295:LEU:HD13	2.03	0.41
2:B:33:LYS:HE3	2:B:37:TYR:OH	2.21	0.41
2:B:120:ASP:C	2:B:122:ARG:H	2.24	0.41
1:A:285:ASP:HA	1:A:286:PRO:HD3	1.97	0.41
1:A:299:ASP:HA	1:A:300:PRO:HD2	1.81	0.41
2:B:113:HIS:HB3	2:B:116:GLU:HB2	2.04	0.40
1:A:132:MET:HE2	1:A:163:LEU:H	1.86	0.40
1:A:59:PHE:HA	1:A:60:PRO:HD3	1.91	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	281/331 (85%)	260 (92%)	20 (7%)	1 (0%)	34	52
2	B	253/260 (97%)	242 (96%)	10 (4%)	1 (0%)	34	52
All	All	534/591 (90%)	502 (94%)	30 (6%)	2 (0%)	34	52

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	190	VAL
2	B	163	LEU

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	258/291 (89%)	255 (99%)	3 (1%)	71	87
2	B	233/236 (99%)	232 (100%)	1 (0%)	91	96
All	All	491/527 (93%)	487 (99%)	4 (1%)	81	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	THR
1	A	70	LEU
1	A	248	ILE
2	B	217	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	187	ASN
1	A	237	GLN
2	B	129	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	$\# Z > 2$
1	TPO	A	186	1	8,10,11	0.80	0	10,14,16	1.13	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
1	TPO	A	186	1	1/1/3/4	4/9/11/13	-

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	186	TPO	CB

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	186	TPO	N-CA-CB-OG1
1	A	186	TPO	C-CA-CB-CG2
1	A	186	TPO	O-C-CA-CB
1	A	186	TPO	CB-OG1-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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	$\# Z > 2$
3	TRS	B	260	-	7,7,7	0.43	0	9,9,9	0.88	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
3	TRS	B	260	-	-	9/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	260	TRS	C1-C-C2-O2
3	B	260	TRS	C3-C-C2-O2
3	B	260	TRS	C2-C-C1-O1
3	B	260	TRS	N-C-C2-O2
3	B	260	TRS	C2-C-C3-O3
3	B	260	TRS	C3-C-C1-O1
3	B	260	TRS	C1-C-C3-O3
3	B	260	TRS	N-C-C1-O1
3	B	260	TRS	N-C-C3-O3

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	260	TRS	6	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	291/331 (87%)	0.18	20 (6%)	16 16	40, 78, 132, 156	0
2	B	255/260 (98%)	0.23	15 (5%)	22 22	36, 56, 122, 182	0
All	All	546/591 (92%)	0.21	35 (6%)	19 19	36, 68, 128, 182	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	7	ASN	6.1
1	A	267	LEU	5.5
2	B	8	ASN	5.1
2	B	6	LYS	4.3
1	A	257	ASP	4.1
1	A	271	GLN	4.1
1	A	259	TYR	4.0
1	A	28	GLY	3.6
2	B	5	ARG	3.1
1	A	31	GLY	3.1
2	B	165	ARG	3.0
1	A	273	ARG	3.0
1	A	27	GLN	3.0
2	B	124	GLU	2.9
1	A	272	LYS	2.8
2	B	219	LYS	2.8
2	B	163	LEU	2.6
1	A	117	VAL	2.6
1	A	176	LEU	2.6
1	A	192	LEU	2.6
1	A	29	THR	2.3
2	B	216	THR	2.3
1	A	248	ILE	2.2
1	A	8	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	166	ALA	2.2
1	A	269	LYS	2.2
1	A	325	LYS	2.1
1	A	188	ARG	2.1
2	B	224	TYR	2.1
2	B	125	ALA	2.1
1	A	274	LYS	2.1
2	B	217	ASP	2.1
1	A	118	LEU	2.1
2	B	212	ILE	2.0
2	B	229	VAL	2.0

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
1	TPO	A	186	11/12	0.96	0.13	71,83,91,106	0

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
3	TRS	B	260	8/8	0.90	0.27	67,72,88,92	0

6.5 Other polymers [i](#)

There are no such residues in this entry.