



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2023 – 08:55 PM EDT

PDB ID : 5T16  
Title : Crystal structure of yeast RNase III (Rnt1p) complexed with a non-hydrolyzable RNA substrate analog  
Authors : Song, H.; Ji, X.  
Deposited on : 2016-08-18  
Resolution : 2.78 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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<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>.

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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 : 2.35  
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

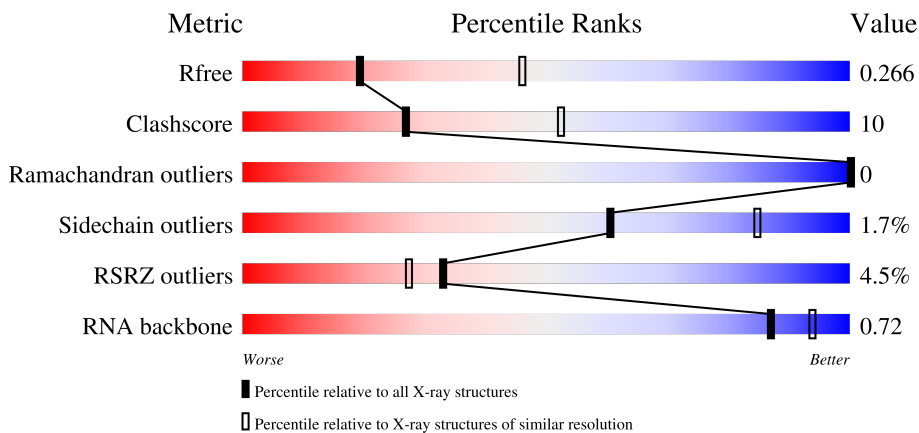
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

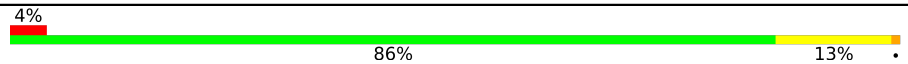
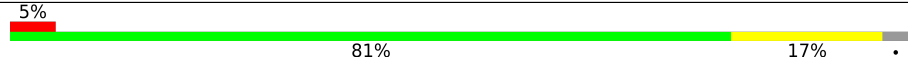


The reported resolution of this entry is 2.78 Å.

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	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)
RSRZ outliers	127900	4027 (2.80-2.76)
RNA backbone	3102	1092 (3.06-2.50)

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  $\geq 3$ , 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	276	 4% 86% 13%
1	B	276	 5% 81% 17%
1	I	276	 5% 81% 19%
1	J	276	 5% 74% 22%

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Mol	Chain	Length	Quality of chain
2	C	119	64% 29% • 5%
2	D	119	74% 21% • • •
2	E	119	67% 29% • •
2	F	119	65% 31% • •
2	K	119	77% 18% • •
2	L	119	71% 25% • •
2	M	119	66% 26% • 6%
2	N	119	69% 28% • • •
3	G	34	50% 44% 6%
3	H	34	50% 44% 6%
3	O	34	44% 47% 6% •
3	P	34	41% 50% 6% •

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
4	EDO	F	201	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 19568 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 Ribonuclease 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	276	Total 2212	C 1406	N 389	O 409	S 8	0	0	0
1	B	269	Total 2161	C 1374	N 381	O 398	S 8	0	0	0
1	I	276	Total 2212	C 1406	N 389	O 409	S 8	0	0	0
1	J	267	Total 2141	C 1361	N 379	O 393	S 8	0	0	0

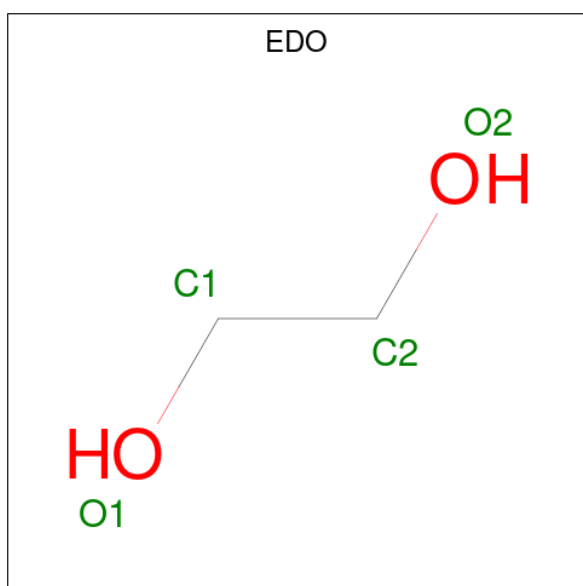
- Molecule 2 is a protein called Ribonuclease 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	113	Total 925	C 589	N 150	O 185	S 1	0	0	0
2	D	116	Total 959	C 609	N 160	O 189	S 1	0	0	0
2	E	115	Total 948	C 603	N 156	O 188	S 1	0	0	0
2	F	115	Total 948	C 603	N 156	O 188	S 1	0	0	0
2	K	114	Total 936	C 595	N 154	O 186	S 1	0	0	0
2	L	116	Total 959	C 609	N 160	O 189	S 1	0	0	0
2	M	112	Total 917	C 584	N 148	O 184	S 1	0	0	0
2	N	117	Total 968	C 614	N 161	O 192	S 1	0	0	0

- Molecule 3 is a RNA chain called RNA substrate analog.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	G	34	Total	C	N	O	P	S	0	0	0
			721	323	127	236	33	2			
3	H	34	Total	C	N	O	P	S	0	0	0
			721	323	127	236	33	2			
3	O	34	Total	C	N	O	P	S	0	0	0
			721	323	127	236	33	2			
3	P	34	Total	C	N	O	P	S	0	0	0
			721	323	127	236	33	2			

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	I	1	Total	C	O	0	0
			4	2	2		
4	J	1	Total	C	O	0	0
			4	2	2		

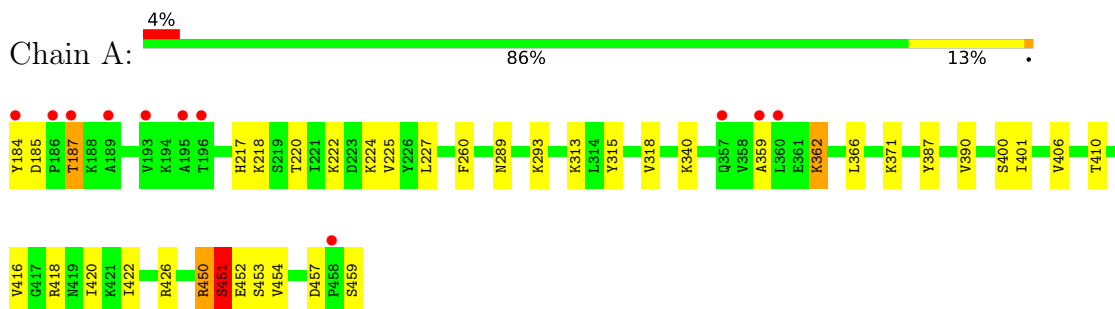
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	43	Total	O	0	0
			43	43		
5	B	44	Total	O	0	0
			44	44		
5	C	15	Total	O	0	0
			15	15		
5	D	12	Total	O	0	0
			12	12		
5	E	7	Total	O	0	0
			7	7		
5	F	9	Total	O	0	0
			9	9		
5	G	20	Total	O	0	0
			20	20		
5	H	25	Total	O	0	0
			25	25		
5	I	51	Total	O	0	0
			51	51		
5	J	46	Total	O	0	0
			46	46		
5	K	12	Total	O	0	0
			12	12		
5	L	13	Total	O	0	0
			13	13		
5	M	6	Total	O	0	0
			6	6		
5	N	14	Total	O	0	0
			14	14		
5	O	27	Total	O	0	0
			27	27		
5	P	14	Total	O	0	0
			14	14		

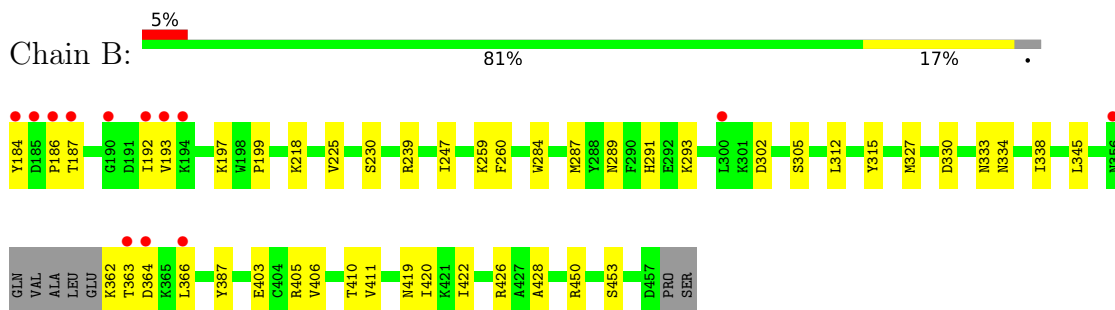
### 3 Residue-property plots [i](#)

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: Ribonuclease 3



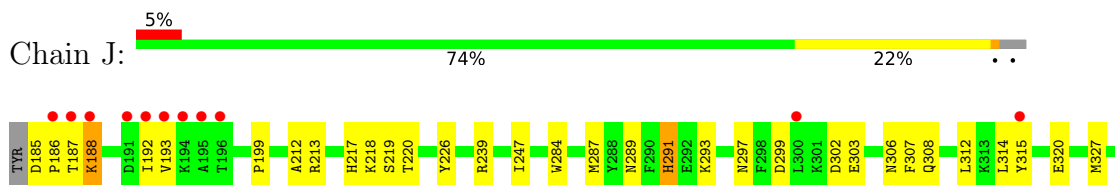
- Molecule 1: Ribonuclease 3



- Molecule 1: Ribonuclease 3

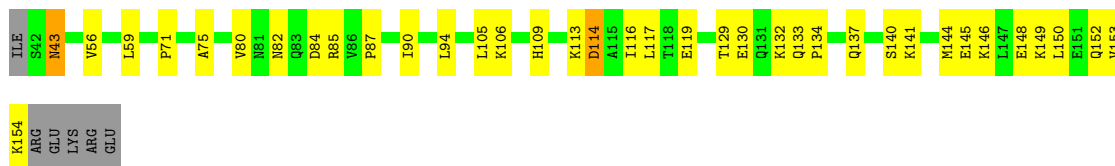


- Molecule 1: Ribonuclease 3

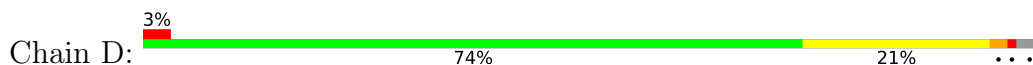




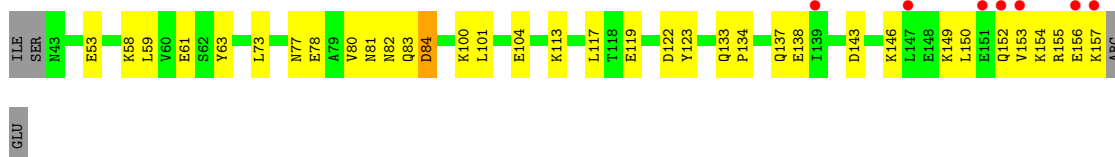
• Molecule 2: Ribonuclease 3



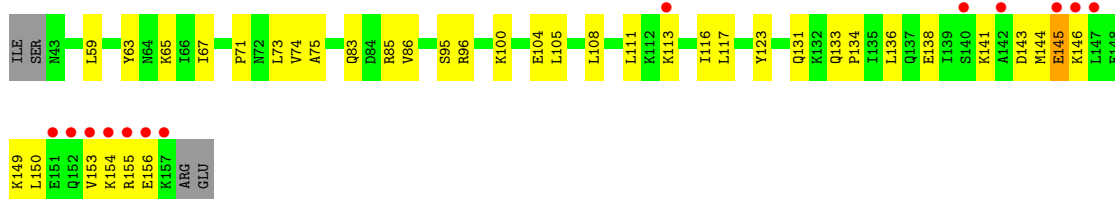
• Molecule 2: Ribonuclease 3



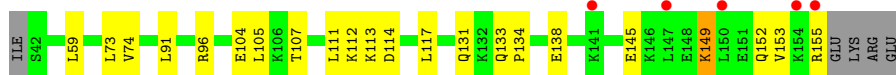
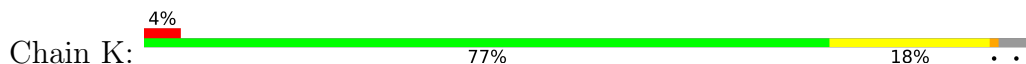
• Molecule 2: Ribonuclease 3



• Molecule 2: Ribonuclease 3



• Molecule 2: Ribonuclease 3



• Molecule 2: Ribonuclease 3





- Molecule 2: Ribonuclease 3



GLU

- Molecule 2: Ribonuclease 3



K157  
R158  
E159

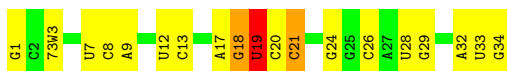
- Molecule 3: RNA substrate analog



- Molecule 3: RNA substrate analog

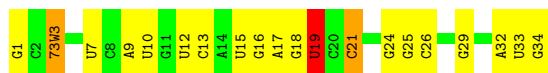


- Molecule 3: RNA substrate analog



- Molecule 3: RNA substrate analog





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.04Å 164.06Å 176.85Å 90.00° 96.78° 90.00°	Depositor
Resolution (Å)	38.98 – 2.78 39.94 – 2.78	Depositor EDS
% Data completeness (in resolution range)	98.0 (38.98-2.78) 98.2 (39.94-2.78)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.24 (at 2.77Å)	Xtrriage
Refinement program	PHENIX (dev_2376: ???)	Depositor
R, $R_{free}$	0.226 , 0.265 0.226 , 0.266	Depositor DCC
$R_{free}$ test set	998 reflections (1.16%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	61.3	Xtrriage
Anisotropy	0.382	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 30.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	19568	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.09 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2043e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: 73W, EDO

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	0.53	0/2252	0.67	0/3036
1	B	0.54	0/2199	0.68	0/2961
1	I	0.53	0/2252	0.72	1/3036 (0.0%)
1	J	0.56	1/2178 (0.0%)	0.68	0/2933
2	C	0.53	0/937	0.71	0/1267
2	D	0.57	0/971	0.76	1/1310 (0.1%)
2	E	0.63	0/960	0.77	0/1296
2	F	0.63	0/960	0.99	3/1296 (0.2%)
2	K	0.62	0/948	0.83	2/1281 (0.2%)
2	L	0.54	0/971	0.69	0/1310
2	M	0.61	0/929	0.72	0/1257
2	N	0.70	1/980 (0.1%)	0.87	1/1322 (0.1%)
3	G	0.70	0/782	1.10	1/1215 (0.1%)
3	H	0.69	0/782	1.23	3/1215 (0.2%)
3	O	0.70	0/782	1.17	2/1215 (0.2%)
3	P	0.66	0/782	1.24	6/1215 (0.5%)
All	All	0.59	2/19665 (0.0%)	0.84	20/27165 (0.1%)

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	2
2	C	0	1
2	K	0	1
2	M	0	1
2	N	0	2
All	All	0	7

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	153	VAL	CA-CB	5.17	1.65	1.54
1	J	404	CYS	CB-SG	-5.07	1.73	1.81

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	144	MET	CB-CA-C	-15.60	79.20	110.40
2	F	145	GLU	N-CA-CB	-12.78	87.60	110.60
3	P	19	U	C5-C4-O4	9.09	131.35	125.90
3	H	19	U	C5-C4-O4	8.22	130.83	125.90
3	P	19	U	N3-C4-O4	-7.64	114.05	119.40

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	450	ARG	Peptide
1	A	451	SER	Peptide
2	C	114	ASP	Peptide
2	K	114	ASP	Peptide
2	M	114	ASP	Peptide

## 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	2212	0	2270	31	0
1	B	2161	0	2218	30	0
1	I	2212	0	2270	43	0
1	J	2141	0	2202	46	0
2	C	925	0	945	34	0
2	D	959	0	985	30	0
2	E	948	0	972	32	0
2	F	948	0	972	37	0
2	K	936	0	958	19	0
2	L	959	0	985	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	M	917	0	934	26	0
2	N	968	0	991	34	0
3	G	721	0	356	12	0
3	H	721	0	356	14	0
3	O	721	0	356	13	0
3	P	721	0	356	16	0
4	A	4	0	6	0	0
4	E	4	0	6	0	0
4	F	4	0	6	1	0
4	H	4	0	6	0	0
4	I	20	0	30	2	0
4	J	4	0	6	2	0
5	A	43	0	0	4	0
5	B	44	0	0	2	0
5	C	15	0	0	6	0
5	D	12	0	0	1	0
5	E	7	0	0	1	0
5	F	9	0	0	0	0
5	G	20	0	0	3	0
5	H	25	0	0	2	0
5	I	51	0	0	4	0
5	J	46	0	0	6	0
5	K	12	0	0	1	0
5	L	13	0	0	0	0
5	M	6	0	0	1	0
5	N	14	0	0	0	0
5	O	27	0	0	2	0
5	P	14	0	0	2	0
All	All	19568	0	18186	382	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.

The worst 5 of 382 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:D:145:GLU:HA	2:D:148:GLU:HG2	1.55	0.89
2:K:107:THR:HG21	2:L:139:ILE:HD12	1.55	0.88
3:P:3:73W:SP2	5:P:111:HOH:O	2.33	0.84
2:F:145:GLU:HA	2:F:149:LYS:HE2	1.60	0.83
1:I:450:ARG:HA	1:I:453:SER:HB3	1.60	0.83

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	274/276 (99%)	267 (97%)	7 (3%)	0	100	100
1	B	265/276 (96%)	260 (98%)	5 (2%)	0	100	100
1	I	274/276 (99%)	268 (98%)	6 (2%)	0	100	100
1	J	263/276 (95%)	257 (98%)	6 (2%)	0	100	100
2	C	111/119 (93%)	108 (97%)	3 (3%)	0	100	100
2	D	114/119 (96%)	113 (99%)	1 (1%)	0	100	100
2	E	113/119 (95%)	108 (96%)	5 (4%)	0	100	100
2	F	113/119 (95%)	110 (97%)	3 (3%)	0	100	100
2	K	112/119 (94%)	108 (96%)	4 (4%)	0	100	100
2	L	114/119 (96%)	113 (99%)	1 (1%)	0	100	100
2	M	110/119 (92%)	106 (96%)	4 (4%)	0	100	100
2	N	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
All	All	1978/2056 (96%)	1930 (98%)	48 (2%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	242/242 (100%)	239 (99%)	3 (1%)	71	90
1	B	236/242 (98%)	235 (100%)	1 (0%)	91	96
1	I	242/242 (100%)	240 (99%)	2 (1%)	81	93
1	J	234/242 (97%)	231 (99%)	3 (1%)	69	89
2	C	106/112 (95%)	104 (98%)	2 (2%)	57	83
2	D	109/112 (97%)	105 (96%)	4 (4%)	34	65
2	E	108/112 (96%)	106 (98%)	2 (2%)	57	83
2	F	108/112 (96%)	106 (98%)	2 (2%)	57	83
2	K	107/112 (96%)	105 (98%)	2 (2%)	57	83
2	L	109/112 (97%)	105 (96%)	4 (4%)	34	65
2	M	105/112 (94%)	100 (95%)	5 (5%)	25	55
2	N	110/112 (98%)	110 (100%)	0	100	100
All	All	1816/1864 (97%)	1786 (98%)	30 (2%)	60	85

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	362	LYS
2	M	118	THR
1	J	188	LYS
2	M	148	GLU
2	L	158	ARG

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

Mol	Chain	Res	Type
2	E	133	GLN
1	J	291	HIS
2	L	152	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	G	32/34 (94%)	5 (15%)	0
3	H	32/34 (94%)	5 (15%)	0
3	O	32/34 (94%)	5 (15%)	0
3	P	32/34 (94%)	5 (15%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	128/136 (94%)	20 (15%)	0

5 of 20 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	G	17	A
3	G	18	G
3	G	19	U
3	G	24	G
3	G	29	G

There are no RNA pucker outliers to report.

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

4 non-standard protein/DNA/RNA residues are 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	73W	H	3	3	18,21,22	1.33	2 (11%)	26,30,33	1.24	2 (7%)
3	73W	P	3	3	18,21,22	1.63	3 (16%)	26,30,33	1.20	2 (7%)
3	73W	G	3	3	18,21,22	1.38	2 (11%)	26,30,33	1.12	2 (7%)
3	73W	O	3	3	18,21,22	1.30	2 (11%)	26,30,33	1.08	3 (11%)

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	73W	H	3	3	-	0/7/25/26	0/2/2/2
3	73W	P	3	3	-	2/7/25/26	0/2/2/2
3	73W	G	3	3	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	73W	O	3	3	-	2/7/25/26	0/2/2/2

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	3	73W	O5'-C5'	-4.35	1.34	1.44
3	H	3	73W	C2-N1	3.71	1.48	1.40
3	G	3	73W	C2-N1	3.39	1.47	1.40
3	O	3	73W	C2-N1	3.39	1.47	1.40
3	P	3	73W	C2-N1	3.21	1.46	1.40

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	3	73W	C2'-C3'-C4'	-3.60	95.64	102.64
3	P	3	73W	O4'-C1'-N1	3.09	115.42	108.36
3	G	3	73W	C2'-C3'-C4'	-3.00	96.81	102.64
3	O	3	73W	C2'-C3'-C4'	-2.88	97.04	102.64
3	G	3	73W	O4'-C1'-N1	2.47	114.02	108.36

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	P	3	73W	O4'-C4'-C5'-O5'
3	O	3	73W	O4'-C4'-C5'-O5'
3	P	3	73W	C3'-C4'-C5'-O5'
3	G	3	73W	O4'-C4'-C5'-O5'
3	O	3	73W	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	3	73W	2	0
3	P	3	73W	3	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

10 ligands are 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
4	EDO	A	501	-	3,3,3	0.45	0	2,2,2	0.39	0
4	EDO	F	201	-	3,3,3	0.59	0	2,2,2	0.21	0
4	EDO	I	504	-	3,3,3	0.49	0	2,2,2	0.46	0
4	EDO	I	501	-	3,3,3	0.58	0	2,2,2	0.28	0
4	EDO	H	101	-	3,3,3	0.46	0	2,2,2	0.47	0
4	EDO	I	502	-	3,3,3	0.54	0	2,2,2	0.24	0
4	EDO	I	505	-	3,3,3	0.66	0	2,2,2	0.11	0
4	EDO	J	501	-	3,3,3	0.62	0	2,2,2	0.07	0
4	EDO	I	503	-	3,3,3	0.52	0	2,2,2	0.31	0
4	EDO	E	201	-	3,3,3	0.51	0	2,2,2	0.20	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
4	EDO	A	501	-	-	1/1/1/1	-
4	EDO	F	201	-	-	0/1/1/1	-
4	EDO	I	504	-	-	1/1/1/1	-
4	EDO	I	501	-	-	1/1/1/1	-
4	EDO	H	101	-	-	1/1/1/1	-
4	EDO	I	502	-	-	1/1/1/1	-
4	EDO	I	505	-	-	1/1/1/1	-
4	EDO	J	501	-	-	0/1/1/1	-
4	EDO	I	503	-	-	1/1/1/1	-
4	EDO	E	201	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	EDO	O1-C1-C2-O2
4	I	503	EDO	O1-C1-C2-O2
4	I	505	EDO	O1-C1-C2-O2
4	I	501	EDO	O1-C1-C2-O2
4	I	504	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	201	EDO	1	0
4	I	501	EDO	2	0
4	J	501	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	276/276 (100%)	0.05	11 (3%) 38 33	34, 50, 77, 86	0
1	B	269/276 (97%)	0.03	13 (4%) 30 24	34, 51, 78, 89	0
1	I	276/276 (100%)	0.06	14 (5%) 28 22	34, 49, 79, 100	0
1	J	267/276 (96%)	0.05	15 (5%) 24 19	32, 49, 77, 87	0
2	C	113/119 (94%)	-0.02	0 100 100	42, 61, 83, 98	0
2	D	116/119 (97%)	0.01	4 (3%) 45 39	37, 60, 85, 93	0
2	E	115/119 (96%)	0.32	7 (6%) 21 16	41, 68, 91, 97	0
2	F	115/119 (96%)	0.35	13 (11%) 5 3	46, 68, 91, 95	0
2	K	114/119 (95%)	0.12	5 (4%) 34 28	40, 63, 87, 92	0
2	L	116/119 (97%)	0.05	5 (4%) 35 30	41, 64, 87, 92	0
2	M	112/119 (94%)	0.17	3 (2%) 54 49	41, 64, 85, 96	0
2	N	117/119 (98%)	0.23	7 (5%) 21 16	40, 65, 88, 95	0
3	G	33/34 (97%)	-0.58	0 100 100	35, 54, 79, 83	0
3	H	33/34 (97%)	-0.82	0 100 100	38, 54, 68, 73	0
3	O	33/34 (97%)	-0.66	0 100 100	35, 54, 75, 78	0
3	P	33/34 (97%)	-0.81	0 100 100	36, 54, 68, 74	0
All	All	2138/2192 (97%)	0.05	97 (4%) 33 27	32, 56, 84, 100	0

The worst 5 of 97 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	358	VAL	7.5
2	F	142	ALA	5.6
1	B	363	THR	5.1
1	A	359	ALA	4.5
2	L	157	LYS	4.3

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	73W	G	3	20/21	0.95	0.14	49,58,77,79	0
3	73W	P	3	20/21	0.95	0.14	44,56,93,95	0
3	73W	O	3	20/21	0.96	0.14	48,58,83,87	0
3	73W	H	3	20/21	0.96	0.13	42,55,81,85	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	EDO	F	201	4/4	0.61	0.76	83,84,86,87	0
4	EDO	I	501	4/4	0.76	0.40	58,58,70,80	0
4	EDO	J	501	4/4	0.81	0.60	68,75,76,82	0
4	EDO	I	505	4/4	0.82	0.48	56,60,62,62	0
4	EDO	I	503	4/4	0.84	0.43	58,64,66,70	0
4	EDO	I	504	4/4	0.86	0.26	54,54,54,55	0
4	EDO	I	502	4/4	0.88	0.29	69,72,75,75	0
4	EDO	E	201	4/4	0.92	0.11	70,77,77,80	0
4	EDO	A	501	4/4	0.94	0.17	56,57,57,60	0
4	EDO	H	101	4/4	0.94	0.47	58,58,64,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.