



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 16, 2023 – 01:24 PM EST

PDB ID : 4P5O  
Title : Structure of an RBX1-UBC12 NEDD8-CUL1-DCN1 complex: a RING-E3-E2 ubiquitin-like protein-substrate intermediate trapped in action  
Authors : Scott, D.C.; Schulman, B.A.  
Deposited on : 2014-03-18  
Resolution : 3.11 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)

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>.

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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 : 2.36  
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) : 2.36

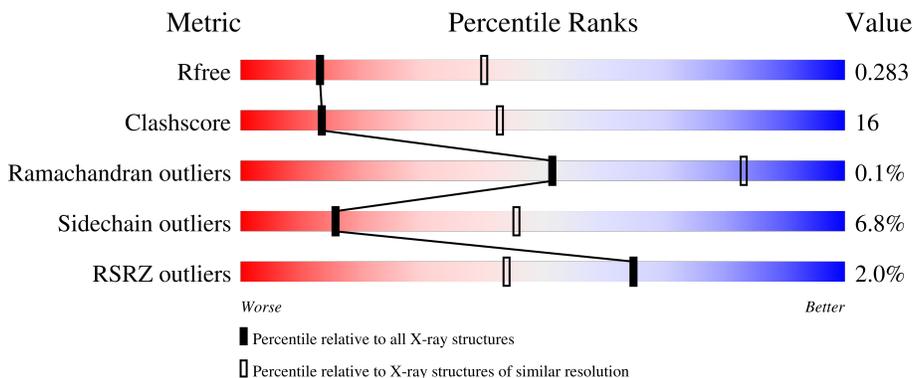
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.11 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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  $\geq 3$ , 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	368	 2% (poor fit), 55% (0 outliers), 29% (1 outlier), 11% (2+ outliers)
1	C	368	 2% (poor fit), 59% (0 outliers), 25% (1 outlier), 12% (2+ outliers)
2	B	106	 2% (poor fit), 51% (0 outliers), 17% (1 outlier), 29% (2+ outliers)
2	D	106	 52% (0 outliers), 18% (1 outlier), 28% (2+ outliers)
3	E	200	 3% (poor fit), 64% (0 outliers), 31% (1 outlier), 2% (2+ outliers)

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Mol	Chain	Length	Quality of chain
3	F	200	<p>2% 58% 37% ..</p>
4	G	189	<p>58% 28% 5% 10%</p>
4	I	189	<p>54% 31% .. 11%</p>
5	H	81	<p>% 63% 28% • 6%</p>
5	K	81	<p>7% 64% 26% • 6%</p>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13577 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 Cullin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	327	Total 2631	C 1671	N 447	O 499	S 14	0	0	0
1	C	322	Total 2556	C 1615	N 436	O 491	S 14	0	0	0

- Molecule 2 is a protein called E3 ubiquitin-protein ligase RBX1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	75	Total 619	C 393	N 112	O 105	S 9	0	0	0
2	D	76	Total 624	C 397	N 114	O 104	S 9	0	0	0

- Molecule 3 is a protein called DCN1-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	197	Total 1614	C 1039	N 264	O 302	S 9	0	0	0
3	F	195	Total 1594	C 1027	N 258	O 300	S 9	0	0	0

- Molecule 4 is a protein called NEDD8-conjugating enzyme Ubc12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	I	169	Total 1374	C 883	N 230	O 254	S 7	0	0	0
4	G	171	Total 1384	C 888	N 231	O 258	S 7	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	1	AME	-	expression tag	UNP P61081
I	103	SER	ASN	engineered mutation	UNP P61081
I	111	SER	CYS	engineered mutation	UNP P61081
I	184	HIS	-	expression tag	UNP P61081
I	185	HIS	-	expression tag	UNP P61081
I	186	HIS	-	expression tag	UNP P61081
I	187	HIS	-	expression tag	UNP P61081
I	188	HIS	-	expression tag	UNP P61081
I	189	HIS	-	expression tag	UNP P61081
G	1	AME	-	expression tag	UNP P61081
G	103	SER	ASN	engineered mutation	UNP P61081
G	111	SER	CYS	engineered mutation	UNP P61081
G	184	HIS	-	expression tag	UNP P61081
G	185	HIS	-	expression tag	UNP P61081
G	186	HIS	-	expression tag	UNP P61081
G	187	HIS	-	expression tag	UNP P61081
G	188	HIS	-	expression tag	UNP P61081
G	189	HIS	-	expression tag	UNP P61081

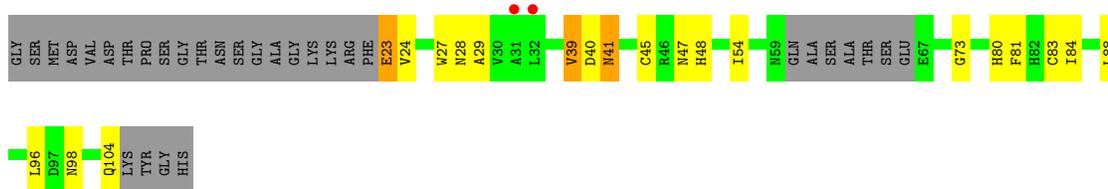
- Molecule 5 is a protein called NEDD8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	K	76	Total	C	N	O	S	0	0	0
			591	372	102	115	2			
5	H	76	Total	C	N	O	S	0	0	0
			584	367	102	113	2			

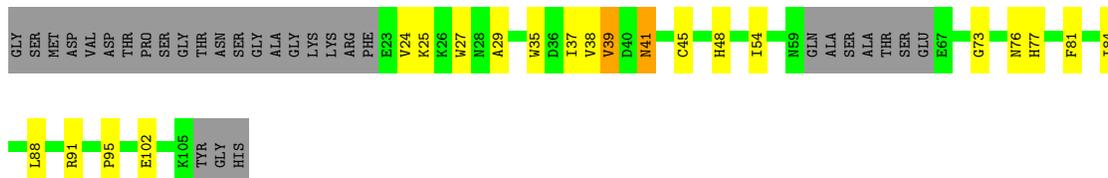
- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	3	Total	Zn	0	0
			3	3		
6	D	3	Total	Zn	0	0
			3	3		

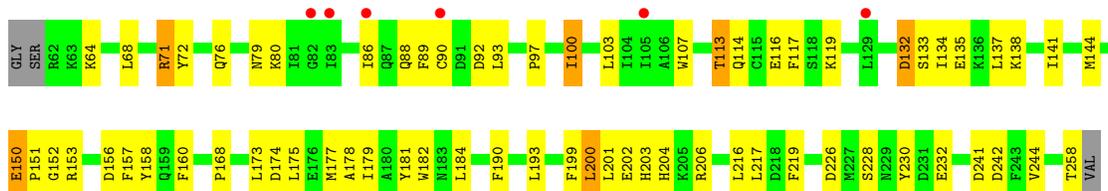




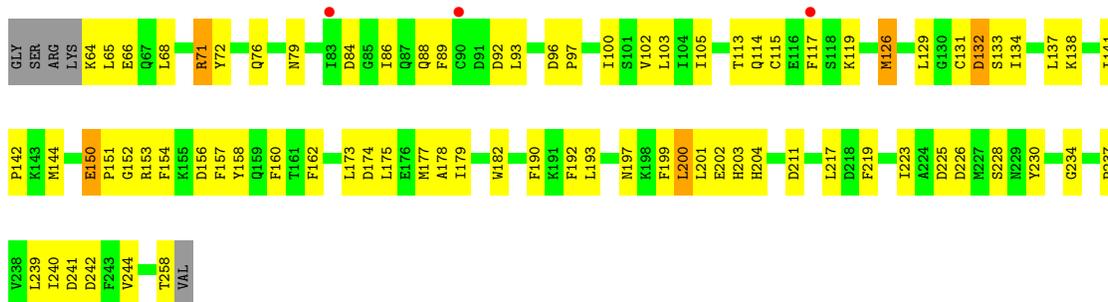
- Molecule 2: E3 ubiquitin-protein ligase RBX1



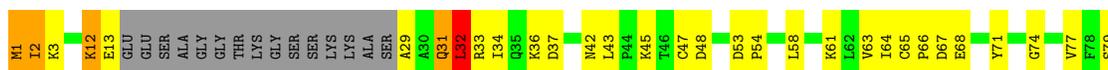
- Molecule 3: DCN1-like protein 1

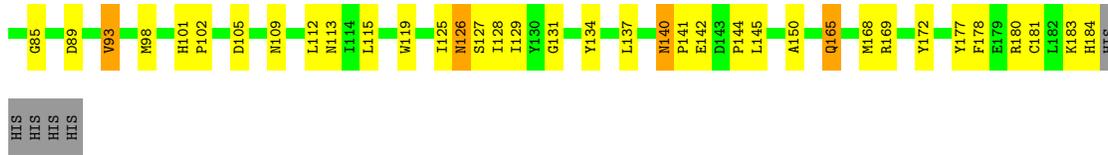


- Molecule 3: DCN1-like protein 1

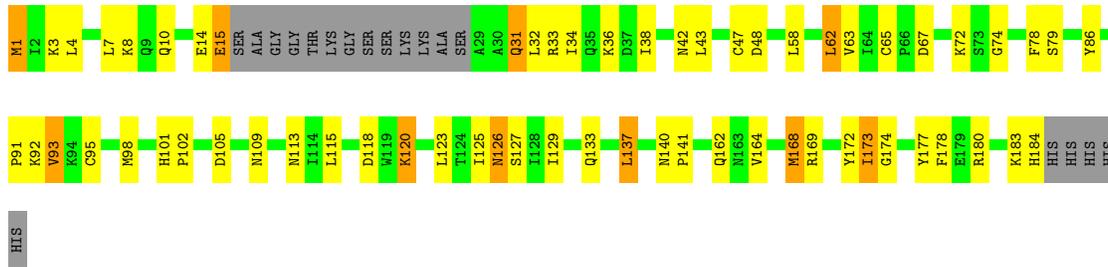


- Molecule 4: NEDD8-conjugating enzyme Ubc12

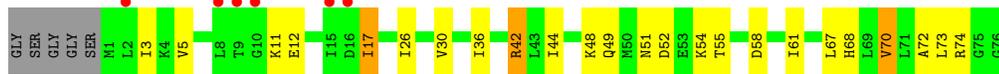




• Molecule 4: NEDD8-conjugating enzyme Ubc12



• Molecule 5: NEDD8



• Molecule 5: NEDD8



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.11Å 129.61Å 119.94Å 90.00° 111.79° 90.00°	Depositor
Resolution (Å)	42.13 – 3.11 42.13 – 3.11	Depositor EDS
% Data completeness (in resolution range)	99.5 (42.13-3.11) 99.5 (42.13-3.11)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.39 (at 3.12Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.227 , 0.284 0.226 , 0.283	Depositor DCC
$R_{free}$ test set	2314 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	68.2	Xtrriage
Anisotropy	0.907	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 38.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.439 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13577	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	97.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% of the height of the origin peak. No significant pseudotranslation is detected.*

<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

### 5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.43	0/2670	0.61	0/3587
1	C	0.43	0/2591	0.63	1/3481 (0.0%)
2	B	0.44	0/637	0.60	0/868
2	D	0.42	0/642	0.58	0/874
3	E	0.41	0/1653	0.57	1/2229 (0.0%)
3	F	0.41	0/1633	0.56	1/2204 (0.0%)
4	G	0.51	0/1404	0.65	1/1897 (0.1%)
4	I	0.55	0/1394	0.68	1/1882 (0.1%)
5	H	0.34	0/589	0.57	0/791
5	K	0.36	0/596	0.56	0/800
All	All	0.44	0/13809	0.61	5/18613 (0.0%)

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	1
1	C	0	1
3	E	0	1
3	F	0	1
All	All	0	4

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	32	LEU	CA-CB-CG	6.95	131.28	115.30
3	F	200	LEU	CA-CB-CG	6.43	130.08	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	200	LEU	CA-CB-CG	5.84	128.74	115.30
1	C	725	LEU	CA-CB-CG	5.53	128.02	115.30
4	G	62	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	418	SER	Peptide
1	C	418	SER	Peptide
3	E	150	GLU	Peptide
3	F	150	GLU	Peptide

## 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	2631	0	2660	104	0
1	C	2556	0	2547	77	0
2	B	619	0	566	17	0
2	D	624	0	575	15	0
3	E	1614	0	1570	54	1
3	F	1594	0	1544	61	0
4	G	1384	0	1361	54	1
4	I	1374	0	1364	48	0
5	H	584	0	603	15	0
5	K	591	0	616	17	0
6	B	3	0	0	0	0
6	D	3	0	0	0	0
All	All	13577	0	13406	433	1

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 16.

The worst 5 of 433 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:720:ARG:NH2	1:A:774:TYR:OH	1.89	1.03
3:E:152:GLY:HA2	3:E:153:ARG:HB2	1.53	0.91
3:E:175:LEU:HD21	3:E:200:LEU:HD13	1.56	0.85
1:C:533:LEU:HD11	2:D:24:VAL:HG22	1.60	0.84
3:F:152:GLY:HA2	3:F:153:ARG:HB2	1.63	0.79

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:258:THR:O	4:G:162:GLN:NE2[1_554]	2.14	0.06

## 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	319/368 (87%)	297 (93%)	22 (7%)	0	100	100
1	C	312/368 (85%)	289 (93%)	23 (7%)	0	100	100
2	B	71/106 (67%)	68 (96%)	2 (3%)	1 (1%)	11	40
2	D	72/106 (68%)	69 (96%)	2 (3%)	1 (1%)	11	40
3	E	195/200 (98%)	182 (93%)	13 (7%)	0	100	100
3	F	193/200 (96%)	179 (93%)	14 (7%)	0	100	100
4	G	167/189 (88%)	160 (96%)	7 (4%)	0	100	100
4	I	165/189 (87%)	158 (96%)	7 (4%)	0	100	100
5	H	74/81 (91%)	71 (96%)	3 (4%)	0	100	100
5	K	74/81 (91%)	71 (96%)	3 (4%)	0	100	100
All	All	1642/1888 (87%)	1544 (94%)	96 (6%)	2 (0%)	51	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	39	VAL
2	D	39	VAL

### 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	294/339 (87%)	268 (91%)	26 (9%)	10	36
1	C	282/339 (83%)	259 (92%)	23 (8%)	11	38
2	B	66/90 (73%)	61 (92%)	5 (8%)	13	41
2	D	66/90 (73%)	64 (97%)	2 (3%)	41	71
3	E	173/176 (98%)	166 (96%)	7 (4%)	31	65
3	F	171/176 (97%)	163 (95%)	8 (5%)	26	59
4	G	153/170 (90%)	142 (93%)	11 (7%)	14	44
4	I	153/170 (90%)	143 (94%)	10 (6%)	17	47
5	H	62/68 (91%)	57 (92%)	5 (8%)	11	39
5	K	64/68 (94%)	60 (94%)	4 (6%)	18	48
All	All	1484/1686 (88%)	1383 (93%)	101 (7%)	16	45

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	509	GLN
1	C	721	MET
5	H	71	LEU
1	C	537	ILE
1	C	682	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
5	K	41	GLN
1	C	436	ASN

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Mol	Chain	Res	Type
1	C	712	GLN
2	B	41	ASN
1	A	463	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

2 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
4	AME	I	1	4	9,10,11	1.42	2 (22%)	9,11,13	1.74	2 (22%)
4	AME	G	1	4	9,10,11	1.42	2 (22%)	9,11,13	1.56	2 (22%)

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	AME	I	1	4	-	4/9/10/12	-
4	AME	G	1	4	-	2/9/10/12	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	1	AME	CA-N	-3.02	1.42	1.46
4	I	1	AME	CA-N	-2.89	1.42	1.46
4	I	1	AME	CT1-N	2.22	1.42	1.34
4	G	1	AME	CT1-N	2.14	1.41	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	1	AME	CE-SD-CG	3.02	110.77	100.40
4	I	1	AME	CE-SD-CG	2.94	110.51	100.40
4	G	1	AME	C-CA-N	-2.50	105.21	109.73
4	I	1	AME	CT2-CT1-N	2.01	119.50	116.10

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	I	1	AME	C-CA-CB-CG
4	I	1	AME	N-CA-CB-CG
4	I	1	AME	O-C-CA-CB
4	G	1	AME	C-CA-CB-CG
4	G	1	AME	N-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	1	AME	1	0
4	G	1	AME	4	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [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	327/368 (88%)	-0.16	6 (1%) 68 47	36, 96, 170, 195	0
1	C	322/368 (87%)	-0.14	9 (2%) 53 30	37, 93, 167, 202	0
2	B	75/106 (70%)	-0.11	2 (2%) 54 31	56, 105, 156, 160	0
2	D	76/106 (71%)	-0.17	0 100 100	54, 108, 138, 157	0
3	E	197/200 (98%)	-0.16	6 (3%) 50 27	49, 98, 155, 167	0
3	F	195/200 (97%)	-0.22	3 (1%) 73 54	60, 97, 144, 164	0
4	G	170/189 (89%)	-0.17	0 100 100	35, 63, 150, 178	0
4	I	168/189 (88%)	-0.30	0 100 100	30, 63, 132, 190	0
5	H	76/81 (93%)	-0.06	1 (1%) 77 59	75, 123, 155, 168	0
5	K	76/81 (93%)	0.16	6 (7%) 12 5	68, 119, 148, 159	0
All	All	1682/1888 (89%)	-0.16	33 (1%) 65 44	30, 92, 162, 202	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	528	SER	7.1
2	B	31	ALA	4.6
1	C	669	ILE	3.6
5	K	15	ILE	3.6
1	C	579	LEU	3.4

### 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( $\text{\AA}^2$ )	Q<0.9
4	AME	I	1	11/12	0.91	0.36	76,87,100,105	0
4	AME	G	1	11/12	0.92	0.55	74,82,97,144	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( $\text{\AA}^2$ )	Q<0.9
6	ZN	D	202	1/1	0.97	0.18	78,78,78,78	0
6	ZN	B	203	1/1	0.98	0.15	109,109,109,109	0
6	ZN	B	202	1/1	0.98	0.23	82,82,82,82	0
6	ZN	D	203	1/1	0.98	0.17	103,103,103,103	0
6	ZN	B	201	1/1	0.99	0.19	93,93,93,93	0
6	ZN	D	201	1/1	0.99	0.23	103,103,103,103	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.