



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2021 – 08:44 PM EDT

PDB ID : 3KYD  
Title : Human SUMO E1 SUMO1-AMP tetrahedral intermediate mimic  
Authors : Lima, C.D.  
Deposited on : 2009-12-05  
Resolution : 2.61 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](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.

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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 : 2.23.2  
buster-report : 1.1.7 (2018)  
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

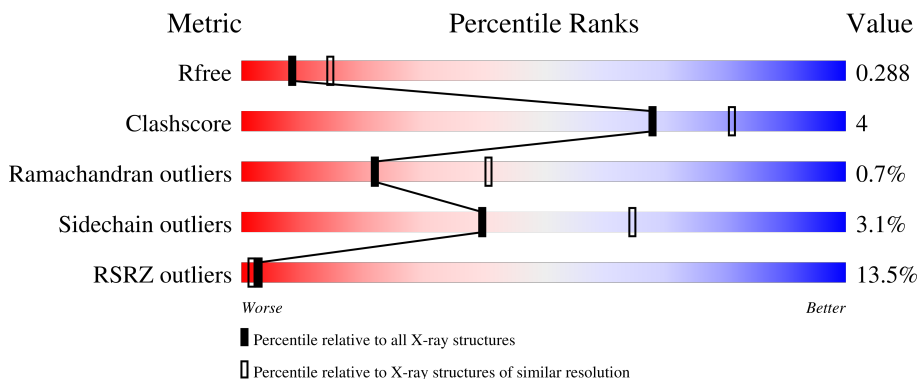
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.61 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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	346	
2	B	551	
3	D	115	

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6978 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 SUMO-activating enzyme subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	301	Total	C	N	O	S	0	0	0
			2353	1497	398	445	13			

- Molecule 2 is a protein called SUMO-activating enzyme subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	477	Total	C	N	O	S	0	0	0
			3740	2382	648	690	20			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	SER	-	expression tag	UNP Q9UBT2
B	0	LEU	-	expression tag	UNP Q9UBT2
B	229	CYS	SER	variant	UNP Q9UBT2

- Molecule 3 is a protein called Small ubiquitin-related modifier 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	77	Total	C	N	O	S	0	0	0
			631	397	108	121	5			

There are 20 discrepancies between the modelled and reference sequences:

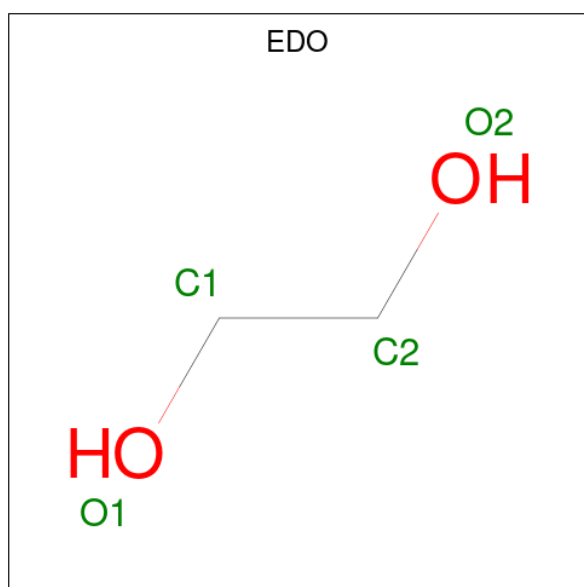
Chain	Residue	Modelled	Actual	Comment	Reference
D	-18	MET	-	expression tag	UNP P63165
D	-17	GLY	-	expression tag	UNP P63165
D	-16	SER	-	expression tag	UNP P63165
D	-15	SER	-	expression tag	UNP P63165
D	-14	HIS	-	expression tag	UNP P63165
D	-13	HIS	-	expression tag	UNP P63165
D	-12	HIS	-	expression tag	UNP P63165

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-11	HIS	-	expression tag	UNP P63165
D	-10	HIS	-	expression tag	UNP P63165
D	-9	HIS	-	expression tag	UNP P63165
D	-8	SER	-	expression tag	UNP P63165
D	-7	SER	-	expression tag	UNP P63165
D	-6	GLY	-	expression tag	UNP P63165
D	-5	LEU	-	expression tag	UNP P63165
D	-4	VAL	-	expression tag	UNP P63165
D	-3	PRO	-	expression tag	UNP P63165
D	-2	ARG	-	expression tag	UNP P63165
D	-1	SER	-	expression tag	UNP P63165
D	0	HIS	-	expression tag	UNP P63165
D	95	CYS	THR	engineered mutation	UNP P63165

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).

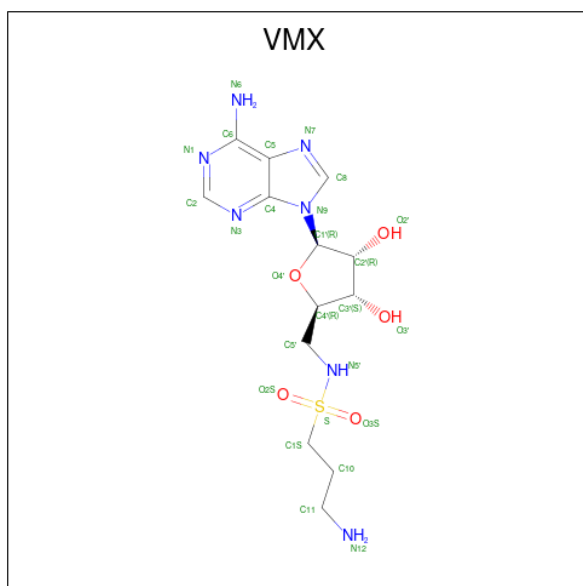


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula:  $Zn$ ).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Zn	0	0
			1	1		

- Molecule 6 is 5'-{[(3-aminopropyl)sulfonyl]amino}-5'-deoxyadenosine (three-letter code: VMX) (formula: C<sub>13</sub>H<sub>21</sub>N<sub>7</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	D	1	Total	C	N	O	S	0	0
			26	13	7	5	1		

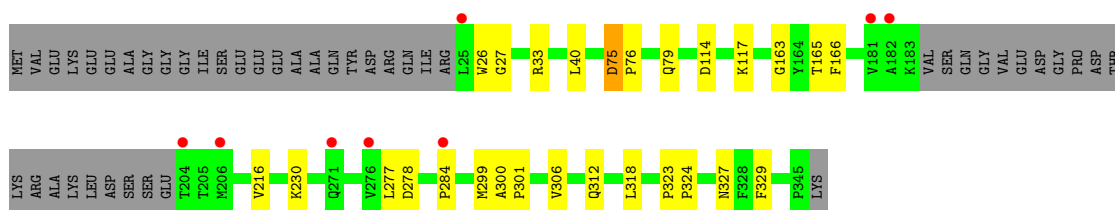
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	94	Total	O	0	0
			94	94		
7	B	101	Total	O	0	0
			101	101		
7	D	20	Total	O	0	0
			20	20		

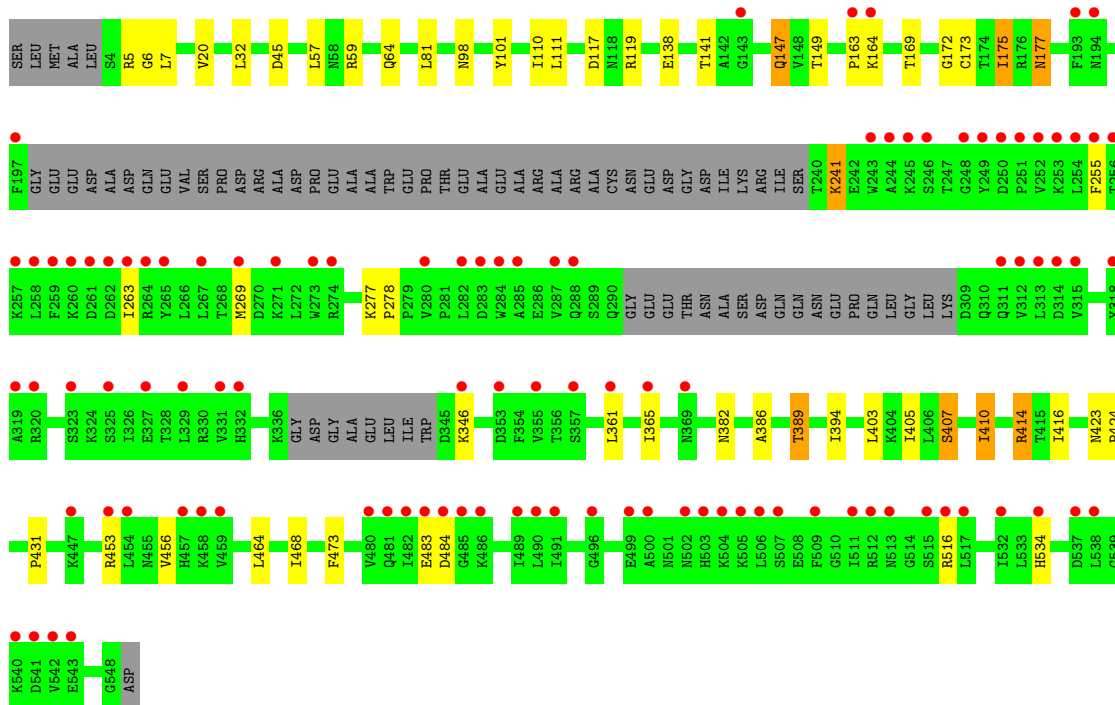
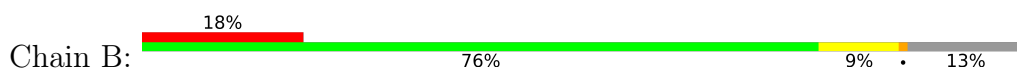
### 3 Residue-property plots [i](#)

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.

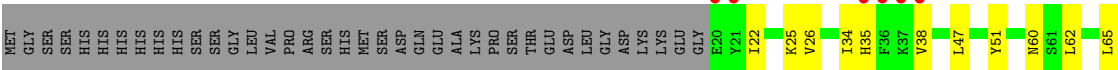
#### • Molecule 1: SUMO-activating enzyme subunit 1



#### • Molecule 2: SUMO-activating enzyme subunit 2



#### • Molecule 3: Small ubiquitin-related modifier 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.72Å 115.61Å 90.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.61 46.55 – 2.61	Depositor EDS
% Data completeness (in resolution range)	98.9 (25.00-2.61) 98.9 (46.55-2.61)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.79 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0093	Depositor
R, $R_{free}$	0.227 , 0.284 0.226 , 0.288	Depositor DCC
$R_{free}$ test set	1675 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	53.7	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 79.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6978	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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, EDO, VMX

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	0.34	0/2395	0.47	0/3232
2	B	0.33	0/3809	0.48	0/5152
3	D	0.33	0/641	0.46	0/856
All	All	0.33	0/6845	0.47	0/9240

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

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	2353	0	2360	11	0
2	B	3740	0	3796	35	0
3	D	631	0	627	10	0
4	A	8	0	12	0	0
4	D	4	0	6	0	0
5	B	1	0	0	0	0
6	D	26	0	19	1	0
7	A	94	0	0	0	0
7	B	101	0	0	2	0
7	D	20	0	0	0	0
All	All	6978	0	6820	51	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 4.

All (51) 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:166:PHE:CE2	1:A:216:VAL:HG12	2.03	0.93
2:B:423:ASN:HB2	2:B:424:PRO:HD2	1.52	0.92
2:B:147:GLN:HE22	3:D:94:GLN:H	1.28	0.79
2:B:414:ARG:HG2	2:B:431:PRO:HB2	1.73	0.70
1:A:312:GLN:HB2	2:B:389:THR:HG21	1.73	0.69
2:B:147:GLN:NE2	3:D:94:GLN:H	1.91	0.67
2:B:263:ILE:HD13	2:B:365:ILE:HG21	1.78	0.65
2:B:241:LYS:HD3	2:B:241:LYS:H	1.63	0.61
2:B:263:ILE:HB	7:B:637:HOH:O	2.07	0.54
2:B:138:GLU:HB3	2:B:149:THR:HG22	1.91	0.52
2:B:141:THR:CG2	2:B:394:ILE:HG13	2.38	0.52
1:A:277:LEU:HD13	1:A:284:PRO:HA	1.92	0.52
2:B:403:LEU:O	2:B:407:SER:HB2	2.09	0.52
2:B:117:ASP:HB3	6:D:97:VMX:H1SA	1.95	0.49
2:B:141:THR:HG22	2:B:394:ILE:HG13	1.94	0.49
2:B:423:ASN:CB	2:B:424:PRO:HD2	2.34	0.48
1:A:26:TRP:CG	1:A:27:GLY:N	2.81	0.48
1:A:33:ARG:HG2	1:A:318:LEU:O	2.14	0.48
1:A:165:THR:OG1	1:A:329:PHE:HB3	2.13	0.48
3:D:38:VAL:HG21	3:D:47:LEU:HD12	1.96	0.48
2:B:473:PHE:N	7:B:636:HOH:O	2.39	0.47
2:B:255:PHE:CE1	2:B:361:LEU:HD21	2.49	0.47
3:D:25:LYS:HG2	3:D:35:HIS:CD2	2.50	0.47
2:B:163:PRO:HD2	3:D:60:ASN:HB2	1.97	0.47
2:B:20:VAL:HG12	2:B:111:LEU:HB3	1.96	0.46
3:D:22:ILE:HG23	3:D:84:GLU:HA	1.97	0.46
3:D:65:LEU:HD12	3:D:91:TYR:CE1	2.51	0.45
2:B:172:GLY:O	2:B:386:ALA:HB2	2.18	0.45
2:B:464:LEU:HA	2:B:468:ILE:HD12	1.99	0.45
2:B:169:THR:HA	2:B:382:ASN:HB3	1.97	0.44
2:B:277:LYS:HA	2:B:278:PRO:HD3	1.84	0.44
1:A:300:ALA:HB3	1:A:301:PRO:HD3	1.98	0.44
2:B:423:ASN:HB2	2:B:424:PRO:CD	2.36	0.44
2:B:59:ARG:HH12	2:B:64:GLN:HA	1.83	0.43
2:B:98:ASN:HB3	2:B:101:TYR:CE1	2.53	0.43
3:D:34:ILE:HD12	3:D:51:TYR:CE1	2.53	0.43
2:B:147:GLN:HE22	3:D:94:GLN:N	2.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:26:VAL:HG22	3:D:88:ILE:HB	2.00	0.42
2:B:483:GLU:HB2	2:B:516:ARG:HB2	2.01	0.42
1:A:75:ASP:H	1:A:76:PRO:CD	2.31	0.42
1:A:114:ASP:HB3	1:A:117:LYS:HG2	2.02	0.42
2:B:110:ILE:H	2:B:110:ILE:HG13	1.68	0.42
2:B:414:ARG:HG2	2:B:431:PRO:CB	2.47	0.41
2:B:177:ASN:HD22	2:B:177:ASN:HA	1.58	0.41
2:B:175:ILE:H	2:B:175:ILE:HG13	1.63	0.41
1:A:323:PRO:HA	1:A:324:PRO:HD3	1.92	0.41
2:B:164:LYS:HA	2:B:164:LYS:HD3	1.97	0.41
1:A:163:GLY:HA3	1:A:306:VAL:HG21	2.03	0.40
2:B:147:GLN:HA	2:B:416:ILE:O	2.21	0.40
2:B:456:VAL:HG12	2:B:534:HIS:CE1	2.56	0.40
2:B:405:ILE:HG12	2:B:410:ILE:HG23	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	297/346 (86%)	278 (94%)	17 (6%)	2 (1%)	22	41
2	B	469/551 (85%)	443 (94%)	22 (5%)	4 (1%)	17	33
3	D	75/115 (65%)	73 (97%)	2 (3%)	0	100	100
All	All	841/1012 (83%)	794 (94%)	41 (5%)	6 (1%)	22	41

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	327	ASN
2	B	175	ILE
2	B	484	ASP

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Mol	Chain	Res	Type
2	B	346	LYS
2	B	6	GLY
1	A	75	ASP

### 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	259/296 (88%)	254 (98%)	5 (2%)	57	78
2	B	414/475 (87%)	397 (96%)	17 (4%)	30	55
3	D	71/104 (68%)	70 (99%)	1 (1%)	67	84
All	All	744/875 (85%)	721 (97%)	23 (3%)	40	65

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	LEU
1	A	79	GLN
1	A	230	LYS
1	A	278	ASP
1	A	299	MET
2	B	5	ARG
2	B	7	LEU
2	B	32	LEU
2	B	45	ASP
2	B	57	LEU
2	B	81	LEU
2	B	119	ARG
2	B	147	GLN
2	B	173	CYS
2	B	177	ASN
2	B	241	LYS
2	B	269	MET
2	B	389	THR
2	B	407	SER

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Mol	Chain	Res	Type
2	B	410	ILE
2	B	414	ARG
2	B	453	ARG
3	D	62	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	ASN
2	B	74	GLN
2	B	82	GLN
2	B	93	HIS
2	B	147	GLN
2	B	177	ASN
2	B	382	ASN
2	B	412	GLN
2	B	419	ASN
2	B	455	ASN
3	D	35	HIS
3	D	94	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](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\# Z  > 2$
4	EDO	A	348	-	3,3,3	0.46	0	2,2,2	0.29	0
4	EDO	A	347	-	3,3,3	0.41	0	2,2,2	0.43	0
4	EDO	D	98	-	3,3,3	0.46	0	2,2,2	0.34	0
6	VMX	D	97	2,3	25,28,28	1.28	2 (8%)	25,41,41	2.03	4 (16%)

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	348	-	-	1/1/1/1	-
4	EDO	A	347	-	-	1/1/1/1	-
4	EDO	D	98	-	-	0/1/1/1	-
6	VMX	D	97	2,3	-	3/11/31/31	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	97	VMX	O4'-C1'	3.71	1.46	1.41
6	D	97	VMX	C1S-S	-3.44	1.66	1.78

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	97	VMX	O3S-S-O2S	-6.58	109.82	119.35
6	D	97	VMX	C3'-C2'-C1'	4.08	107.12	100.98
6	D	97	VMX	N3-C2-N1	-4.02	122.39	128.68
6	D	97	VMX	C1'-N9-C4	-2.36	122.50	126.64

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	97	VMX	C11-C10-C1S-S

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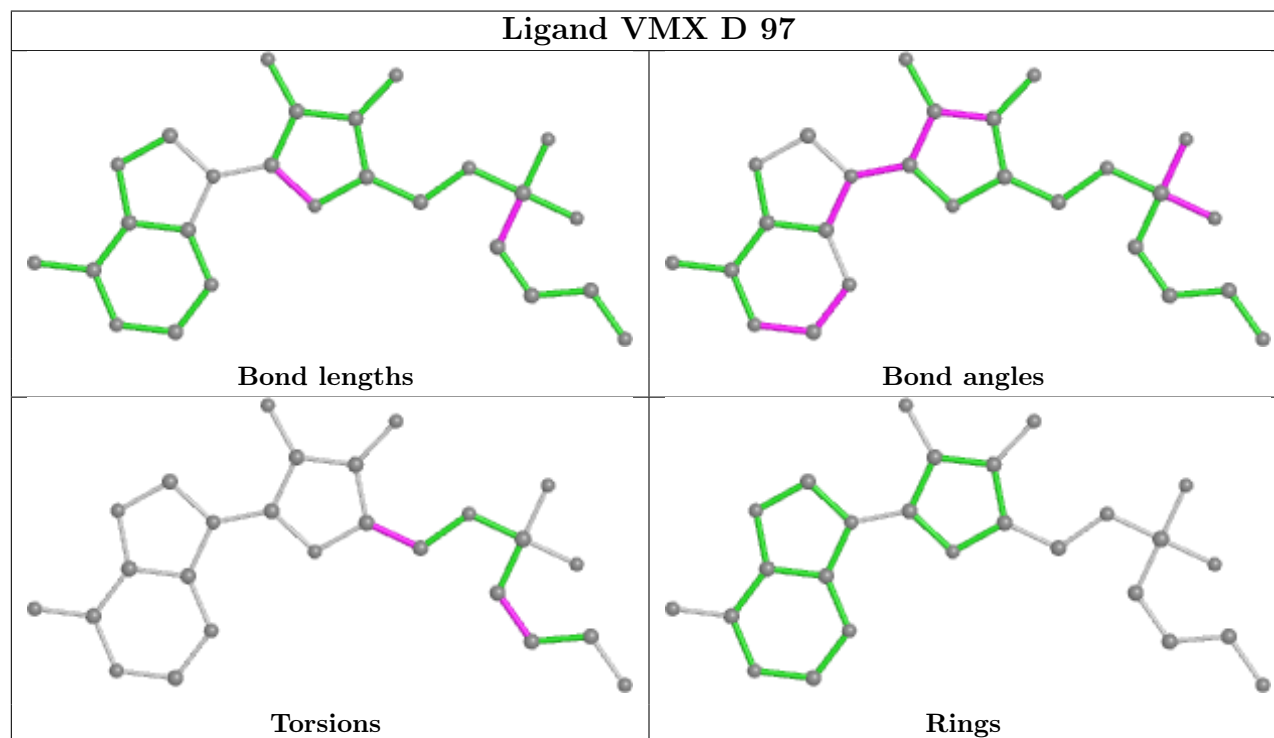
Mol	Chain	Res	Type	Atoms
6	D	97	VMX	C3'-C4'-C5'-N5'
4	A	348	EDO	O1-C1-C2-O2
6	D	97	VMX	O4'-C4'-C5'-N5'
4	A	347	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	97	VMX	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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

### 6.1 Protein, DNA and RNA chains

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	301/346 (86%)	0.03	8 (2%) 54 49	14, 21, 28, 30	0
2	B	477/551 (86%)	0.97	101 (21%) 0 0	16, 23, 31, 55	0
3	D	77/115 (66%)	0.35	6 (7%) 13 9	20, 23, 27, 28	0
All	All	855/1012 (84%)	0.59	115 (13%) 3 2	14, 22, 29, 55	0

All (115) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	490	LEU	7.0
2	B	263	ILE	6.6
2	B	511	ILE	6.6
2	B	249	TYR	6.1
2	B	243	TRP	6.0
2	B	313	LEU	5.9
2	B	541	ASP	5.9
2	B	284	TRP	5.7
2	B	245	LYS	5.6
2	B	454	LEU	5.4
2	B	319	ALA	5.2
2	B	459	VAL	5.2
2	B	486	LYS	4.9
2	B	320	ARG	4.7
2	B	507	SER	4.7
2	B	453	ARG	4.6
2	B	258	LEU	4.6
2	B	457	HIS	4.6
2	B	532	ILE	4.6
2	B	482	ILE	4.3
2	B	315	VAL	4.3
2	B	480	VAL	4.2
2	B	246	SER	4.2

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Mol	Chain	Res	Type	RSRZ
2	B	491	ILE	4.2
2	B	254	LEU	4.2
2	B	512	ARG	3.9
2	B	193	PHE	3.9
2	B	244	ALA	3.8
2	B	265	TYR	3.8
2	B	542	VAL	3.7
2	B	357	SER	3.6
2	B	516	ARG	3.6
2	B	503	HIS	3.6
2	B	500	ALA	3.5
2	B	312	VAL	3.4
2	B	273	TRP	3.4
2	B	264	ARG	3.4
2	B	513	ASN	3.4
2	B	269	MET	3.3
2	B	318	TYR	3.3
2	B	502	ASN	3.3
2	B	271	LYS	3.2
2	B	250	ASP	3.2
2	B	499	GLU	3.2
2	B	538	LEU	3.2
2	B	483	GLU	3.2
2	B	285	ALA	3.2
3	D	36	PHE	3.2
2	B	361	LEU	3.1
2	B	504	LYS	3.1
2	B	283	ASP	3.0
2	B	331	VAL	3.0
1	A	182	ALA	3.0
3	D	21	TYR	2.9
2	B	506	LEU	2.9
2	B	447	LYS	2.9
2	B	262	ASP	2.9
2	B	458	LYS	2.9
2	B	329	LEU	2.9
2	B	259	PHE	2.9
2	B	253	LYS	2.9
2	B	274	ARG	2.8
2	B	369	ASN	2.8
2	B	252	VAL	2.8
2	B	256	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	276	VAL	2.7
2	B	267	LEU	2.7
2	B	534	HIS	2.6
2	B	280	VAL	2.6
2	B	194	ASN	2.6
2	B	517	LEU	2.6
2	B	515	SER	2.6
3	D	37	LYS	2.6
1	A	204	THR	2.6
2	B	505	LYS	2.6
2	B	282	LEU	2.6
2	B	537	ASP	2.6
2	B	496	GLY	2.5
2	B	257	LYS	2.5
2	B	485	GLY	2.5
3	D	38	VAL	2.4
1	A	181	VAL	2.4
2	B	540	LYS	2.4
2	B	311	GLN	2.4
1	A	284	PRO	2.4
2	B	489	ILE	2.3
2	B	287	VAL	2.3
2	B	355	VAL	2.3
2	B	163	PRO	2.3
2	B	251	PRO	2.3
2	B	346	LYS	2.3
2	B	255	PHE	2.3
2	B	365	ILE	2.3
2	B	484	ASP	2.3
2	B	260	LYS	2.3
1	A	25	LEU	2.3
2	B	332	HIS	2.3
2	B	327	GLU	2.3
2	B	314	ASP	2.2
2	B	509	PHE	2.2
2	B	481	GLN	2.2
3	D	20	GLU	2.2
1	A	206	MET	2.2
2	B	353	ASP	2.2
2	B	325	SER	2.1
2	B	248	GLY	2.1
2	B	197	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	323	SER	2.1
2	B	261	ASP	2.1
2	B	288	GLN	2.1
2	B	164	LYS	2.1
2	B	543	GLU	2.1
3	D	35	HIS	2.0
1	A	271	GLN	2.0
2	B	143	GLY	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

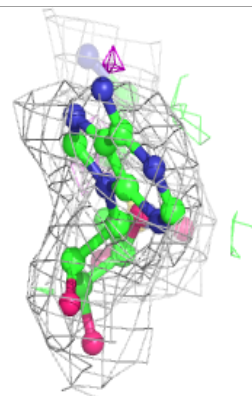
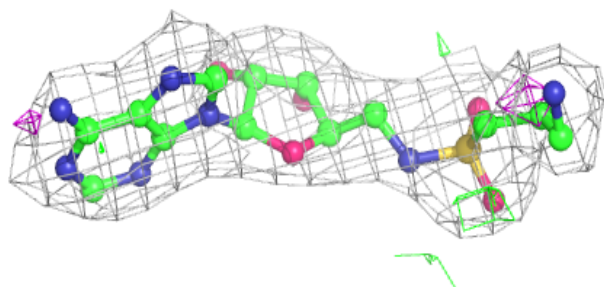
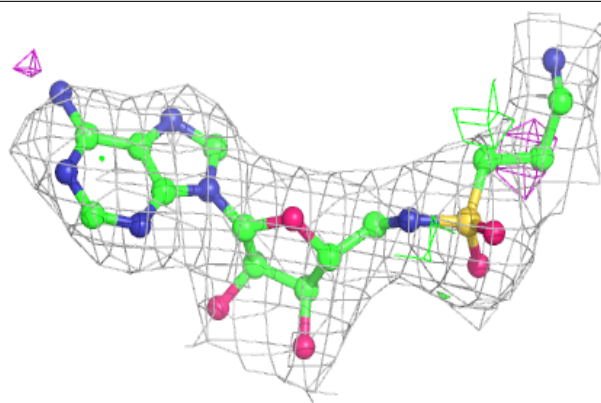
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
4	EDO	D	98	4/4	0.54	0.32	99,99,99,99	0
4	EDO	A	348	4/4	0.94	0.17	74,74,74,74	0
4	EDO	A	347	4/4	0.94	0.29	58,58,59,59	0
6	VMX	D	97	26/26	0.95	0.21	17,18,23,24	0
5	ZN	B	550	1/1	0.98	0.15	50,50,50,50	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around VMX D 97:**

$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.