



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 28, 2016 – 03:53 PM EST

PDB ID : 5GIE  
Title : Crystal structure of VDR in complex with DLAM-4P (P21 form)  
Authors : Asano, L.; Shimizu, T.  
Deposited on : 2016-06-23  
Resolution : 2.39 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

<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028320  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20028320

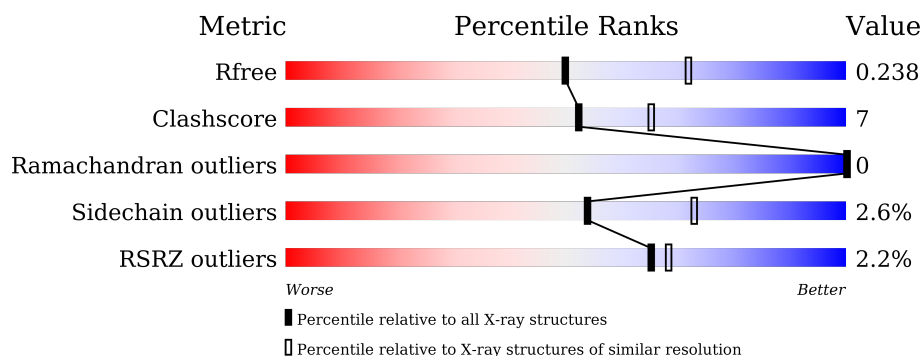
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.39 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))
$R_{free}$	91344	4019 (2.40-2.36)
Clashscore	102246	4595 (2.40-2.36)
Ramachandran outliers	100387	4520 (2.40-2.36)
Sidechain outliers	100360	4522 (2.40-2.36)
RSRZ outliers	91569	4034 (2.40-2.36)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	256	 <div>87% 10% ..</div>
1	D	256	 <div>70% 20% 10%</div>
2	C	10	 <div>80% 20%</div>
2	E	10	 <div>80% 20%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	VDP	A	501	-	-	-	X
3	VDP	D	501	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4091 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.

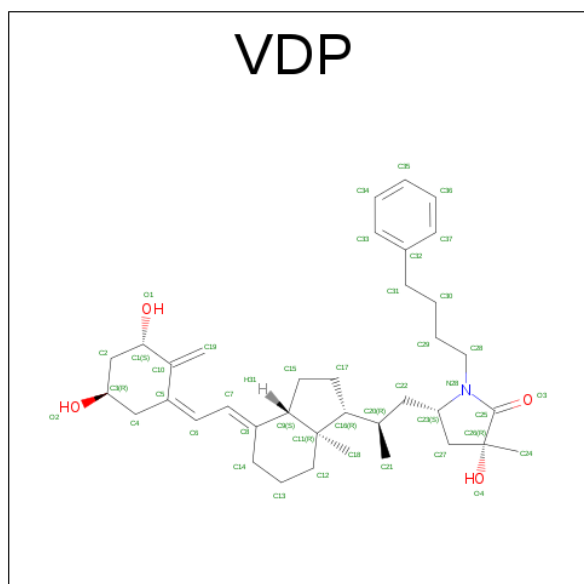
- Molecule 1 is a protein called Vitamin D3 receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	1	0
			1964	1249	330	372	13			
1	D	230	Total	C	N	O	S	0	0	0
			1764	1126	294	333	11			

- Molecule 2 is a protein called SRC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	S	0	0	0
			78	50	14	12	2			
2	E	10	Total	C	N	O	S	0	0	0
			82	53	15	12	2			

- Molecule 3 is (3R,5S)-5-[(2R)-2-[(1R,3aS,4E,7aR)-7a-methyl-4-[(2Z)-2-[(3S,5R)-2-methylidene-3,5-bis(oxidanyl)cyclohexylidene]ethylidene]-2,3,3a,5,6,7-hexahydro-1H-inden-1-yl]propyl]-3-methyl-3-oxidanyl-1-(4-phenylbutyl)pyrrolidin-2-one (three-letter code: VDP) (formula: C<sub>37</sub>H<sub>53</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			42	37	1	4		
3	D	1	Total	C	N	O	0	0
			42	37	1	4		

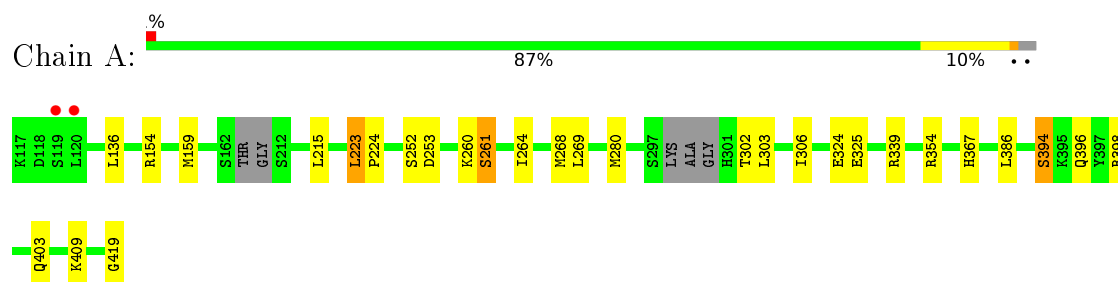
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	82	Total	O	0	0
			82	82		
4	C	2	Total	O	0	0
			2	2		
4	D	34	Total	O	0	0
			34	34		
4	E	1	Total	O	0	0
			1	1		

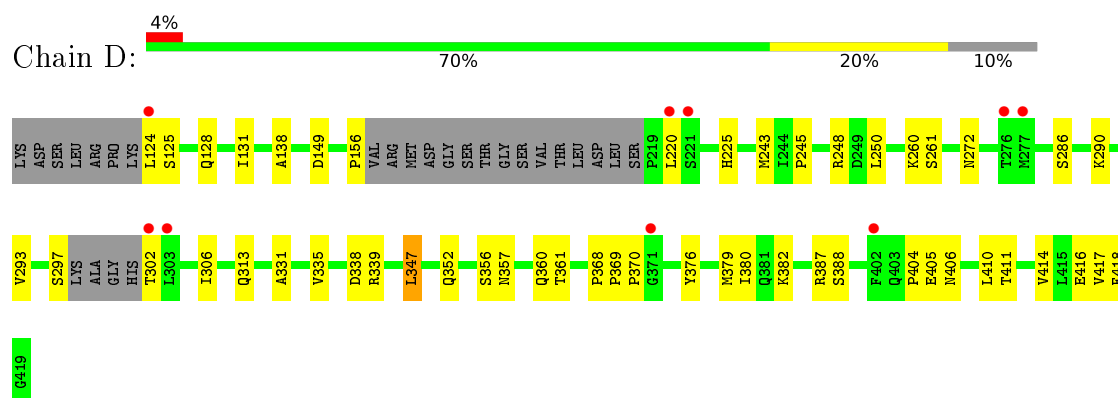
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

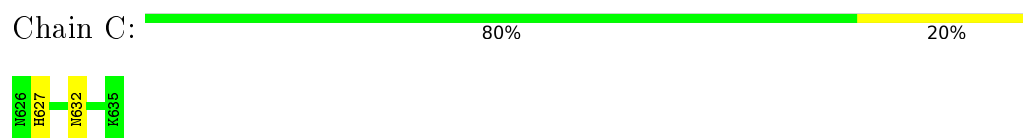
- Molecule 1: Vitamin D3 receptor



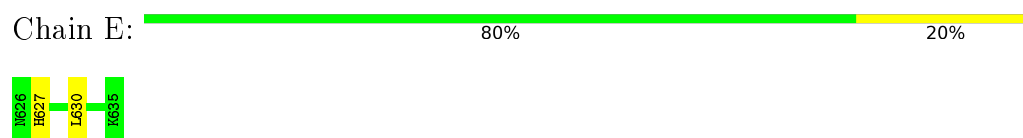
- Molecule 1: Vitamin D3 receptor



- Molecule 2: SRC1



- Molecule 2: SRC1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.36 Å 42.08 Å 96.80 Å 90.00° 94.55° 90.00°	Depositor
Resolution (Å)	38.57 – 2.39 48.25 – 2.39	Depositor EDS
% Data completeness (in resolution range)	98.4 (38.57-2.39) 86.4 (48.25-2.39)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.60 (at 2.39 Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155)	Depositor
R, $R_{free}$	0.207 , 0.234 0.209 , 0.238	Depositor DCC
$R_{free}$ test set	1845 reflections (9.45%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.5	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 43.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4091	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.39 % 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 7.0799e-03. 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: VDP

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	0.37	0/2007	0.50	0/2725
1	D	0.38	0/1801	0.51	0/2450
2	C	0.26	0/79	0.46	0/106
2	E	0.29	0/83	0.53	0/110
All	All	0.37	0/3970	0.50	0/5391

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	D	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	368	PRO	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	1964	0	1929	18	0
1	D	1764	0	1704	34	0
2	C	78	0	78	2	0
2	E	82	0	89	5	0
3	A	42	0	0	0	0
3	D	42	0	0	0	0
4	A	82	0	0	5	1
4	C	2	0	0	0	0
4	D	34	0	0	3	0
4	E	1	0	0	0	0
All	All	4091	0	3800	52	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 7.

All (52) 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:280:MET:O	4:A:601:HOH:O	1.82	0.98
1:D:149:ASP:OD2	4:D:601:HOH:O	1.89	0.89
1:A:303:LEU:HA	1:A:306:ILE:HG22	1.53	0.88
1:A:253:ASP:OD1	4:A:602:HOH:O	2.02	0.77
1:A:354:ARG:NH2	4:A:604:HOH:O	2.23	0.71
1:D:382:LYS:NZ	4:D:603:HOH:O	2.23	0.70
1:A:419:GLY:O	4:A:603:HOH:O	2.10	0.69
1:A:260:LYS:HE3	2:C:627:HIS:NE2	2.08	0.69
1:D:352:GLN:OE1	4:D:602:HOH:O	2.12	0.66
1:A:264:ILE:O	1:A:268:MET:HG3	1.99	0.63
1:D:125:SER:H	1:D:128:GLN:HE21	1.45	0.63
1:A:302:THR:HA	1:A:396:GLN:HE22	1.63	0.63
1:D:131:ILE:HD13	1:D:245:PRO:HG2	1.82	0.60
1:D:356:SER:O	1:D:360:GLN:HG3	2.02	0.59
1:D:260:LYS:HD2	2:E:627:HIS:CE1	2.38	0.58
1:D:376:TYR:O	1:D:380:ILE:HG12	2.04	0.56
1:D:220:LEU:HD21	1:D:406:ASN:OD1	2.04	0.56
1:D:293:VAL:HG23	1:D:306:ILE:HG21	1.87	0.56
1:D:125:SER:H	1:D:128:GLN:NE2	2.02	0.56
1:D:417:VAL:HG22	2:E:630:LEU:HD11	1.86	0.56
1:A:302:THR:HA	1:A:396:GLN:NE2	2.21	0.56
1:D:357:ASN:O	1:D:361:THR:HG23	2.06	0.56
1:A:269:LEU:HG	1:A:386:LEU:HD11	1.88	0.55
1:A:394:SER:OG	1:A:398:ARG:NH1	2.42	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:293:VAL:O	1:D:297:SER:OG	2.24	0.52
1:D:302:THR:O	1:D:306:ILE:HG13	2.12	0.49
1:D:272:ASN:ND2	1:D:313:GLN:OE1	2.37	0.49
1:D:411:THR:OG1	1:D:414:VAL:HG12	2.12	0.49
1:D:338:ASP:OD1	1:D:387:ARG:NH1	2.42	0.49
1:A:159:MET:SD	1:A:215:LEU:HD23	2.52	0.49
1:D:260:LYS:NZ	2:E:627:HIS:HE1	2.10	0.49
1:A:136:LEU:HD11	1:A:324:GLU:HG3	1.94	0.48
1:A:403:GLN:HG3	4:A:640:HOH:O	2.12	0.48
1:D:156:PRO:HD3	1:D:225:HIS:CE1	2.49	0.48
1:D:416:GLU:CD	2:E:627:HIS:HA	2.35	0.46
1:D:411:THR:H	1:D:414:VAL:CG1	2.29	0.46
1:D:414:VAL:HG23	1:D:418:PHE:CD2	2.50	0.46
1:D:331:ALA:O	1:D:335:VAL:HG22	2.16	0.46
1:D:379:MET:O	1:D:382:LYS:HB2	2.16	0.46
1:A:325:GLU:OE1	1:A:367:HIS:ND1	2.44	0.45
2:C:632:ASN:HB2	1:D:404:PRO:HG2	1.98	0.44
1:D:417:VAL:CG2	2:E:630:LEU:HD11	2.47	0.44
1:D:138:ALA:HA	1:D:243:MET:HE1	1.99	0.43
1:A:223:LEU:HD13	1:A:409:LYS:HB2	2.00	0.43
1:D:250:LEU:HD13	1:D:347:LEU:HD13	2.00	0.43
1:D:369:PRO:HA	1:D:370:PRO:HA	1.71	0.43
1:D:138:ALA:HA	1:D:243:MET:CE	2.49	0.43
1:A:154:ARG:HD2	1:A:224:PRO:HB3	2.01	0.42
1:D:290:LYS:HB2	1:D:290:LYS:HE3	1.79	0.42
1:D:335:VAL:O	1:D:335:VAL:HG23	2.20	0.42
1:D:261:SER:HB2	1:D:339:ARG:HD2	2.02	0.41
1:A:261:SER:HB3	1:A:339:ARG:HD2	2.02	0.41

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)
4:A:679:HOH:O	4:A:682:HOH:O[2_455]	2.02	0.18

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	246/256 (96%)	243 (99%)	3 (1%)	0	100	100
1	D	224/256 (88%)	220 (98%)	4 (2%)	0	100	100
2	C	8/10 (80%)	8 (100%)	0	0	100	100
2	E	8/10 (80%)	7 (88%)	1 (12%)	0	100	100
All	All	486/532 (91%)	478 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	221/234 (94%)	217 (98%)	4 (2%)	66	83
1	D	192/234 (82%)	185 (96%)	7 (4%)	42	61
2	C	9/10 (90%)	9 (100%)	0	100	100
2	E	10/10 (100%)	10 (100%)	0	100	100
All	All	432/488 (88%)	421 (98%)	11 (2%)	54	74

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	223	LEU
1	A	252	SER

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	261	SER
1	A	394	SER
1	D	124	LEU
1	D	248	ARG
1	D	286	SER
1	D	347	LEU
1	D	388	SER
1	D	405	GLU
1	D	410	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	272	ASN
1	A	313	GLN
1	A	357	ASN
1	A	396	GLN
1	D	128	GLN
1	D	374	GLN
2	E	627	HIS

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

2 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	$\# Z  > 2$
3	VDP	A	501	-	44,46,46	0.62	1 (2%)	50,68,68	2.18	14 (28%)
3	VDP	D	501	-	44,46,46	0.59	1 (2%)	50,68,68	2.18	12 (24%)

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	VDP	A	501	-	-	0/20/83/83	0/5/5/5
3	VDP	D	501	-	-	0/20/83/83	0/5/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	VDP	C11-C9	-2.22	1.52	1.56
3	D	501	VDP	C11-C9	-2.02	1.52	1.56

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	VDP	C29-C28-N28	-6.36	104.94	113.60
3	D	501	VDP	C6-C7-C8	-5.98	118.33	125.82
3	A	501	VDP	C6-C7-C8	-5.72	118.65	125.82
3	D	501	VDP	C11-C16-C20	-4.86	111.59	119.49
3	A	501	VDP	C14-C8-C7	-4.86	119.69	125.50
3	D	501	VDP	C20-C22-C23	-4.46	101.98	116.52
3	A	501	VDP	C11-C9-C8	-4.02	106.36	112.72
3	D	501	VDP	C14-C8-C7	-3.95	120.77	125.50
3	D	501	VDP	C11-C9-C8	-3.88	106.58	112.72
3	A	501	VDP	C4-C5-C6	-3.50	116.72	120.55
3	D	501	VDP	C29-C28-N28	-3.19	109.25	113.60
3	A	501	VDP	C3-C2-C1	-3.17	107.63	110.90
3	A	501	VDP	C20-C22-C23	-2.93	106.96	116.52
3	D	501	VDP	C21-C20-C22	-2.39	107.08	110.69
3	A	501	VDP	C30-C31-C32	-2.35	104.89	113.67

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	VDP	C11-C16-C20	-2.32	115.72	119.49
3	D	501	VDP	C4-C5-C6	-2.29	118.04	120.55
3	D	501	VDP	C18-C11-C16	-2.27	107.45	111.76
3	D	501	VDP	C1-C10-C19	-2.22	117.94	121.85
3	A	501	VDP	C18-C11-C16	-2.21	107.56	111.76
3	A	501	VDP	C21-C20-C22	-2.03	107.62	110.69
3	A	501	VDP	C22-C20-C16	3.00	113.83	109.60
3	A	501	VDP	C9-C11-C16	3.00	102.90	99.75
3	D	501	VDP	C22-C20-C16	4.98	116.63	109.60
3	A	501	VDP	C28-N28-C25	5.20	129.74	122.48
3	D	501	VDP	C28-N28-C25	7.00	132.24	122.48

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	251/256 (98%)	-0.13	2 (0%) 87 88	20, 35, 65, 84	0
1	D	230/256 (89%)	0.26	9 (3%) 43 47	24, 50, 76, 85	0
2	C	10/10 (100%)	0.07	0 100 100	37, 41, 57, 72	0
2	E	10/10 (100%)	0.41	0 100 100	47, 52, 63, 77	0
All	All	501/532 (94%)	0.07	11 (2%) 65 68	20, 43, 73, 85	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	220	LEU	4.6
1	D	371	GLY	4.3
1	D	124	LEU	3.9
1	D	276	THR	3.5
1	D	221	SER	2.8
1	A	119	SER	2.4
1	D	277	MET	2.4
1	D	303	LEU	2.3
1	D	302	THR	2.3
1	D	402	PHE	2.1
1	A	120	LEU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	VDP	A	501	42/42	0.91	0.19	2.12	27,41,79,80	0
3	VDP	D	501	42/42	0.85	0.28	2.09	37,49,103,105	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.