



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 06:52 am GMT

PDB ID : 1PIV
Title : BINDING OF THE ANTIVIRAL DRUG WIN51711 TO THE SABIN STRAIN OF TYPE 3 POLIOVIRUS: STRUCTURAL COMPARISON WITH DRUG BINDING IN RHINOVIRUS 14
Authors : Hiremath, C.N.; Grant, R.A.; Filman, D.J.; Hogle, J.M.
Deposited on : 1995-02-02
Resolution : 2.90 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : NOT EXECUTED
EDS : NOT EXECUTED
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

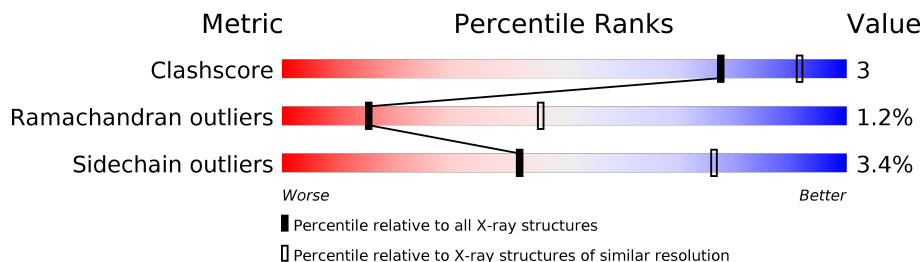
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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))
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)

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 ≥ 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	0	4	100%
2	1	301	76% 14% .. 7%
3	2	271	81% 15% ..
4	3	238	86% 12% ..
5	4	68	81% 10% 9%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6656 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 POLIOVIRUS TYPE 3 (SUBUNIT VP1).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	0	4	Total	C	N	O	0	0	0
			30	19	4	7			

- Molecule 2 is a protein called POLIOVIRUS TYPE 3 (SUBUNIT VP1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1	279	Total	C	N	O	S	0	0	0
			2214	1408	383	416	7			

- Molecule 3 is a protein called POLIOVIRUS TYPE 3 (SUBUNIT VP2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	2	266	Total	C	N	O	S	0	0	0
			2088	1330	354	392	12			

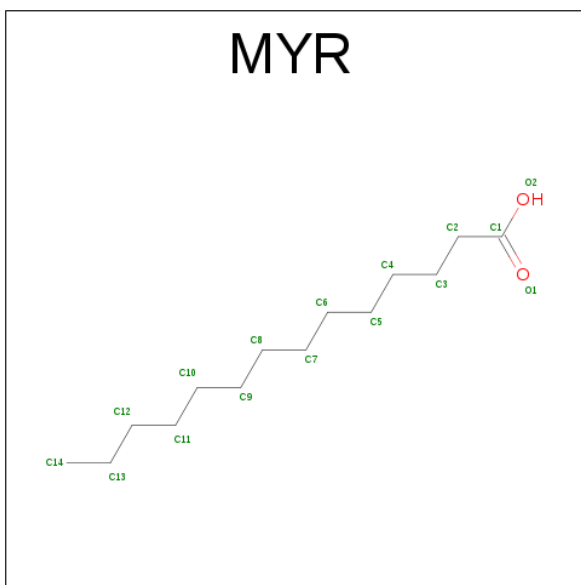
- Molecule 4 is a protein called POLIOVIRUS TYPE 3 (SUBUNIT VP3).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3	235	Total	C	N	O	S	0	0	0
			1812	1150	296	348	18			

- Molecule 5 is a protein called POLIOVIRUS TYPE 3 (SUBUNIT VP4).

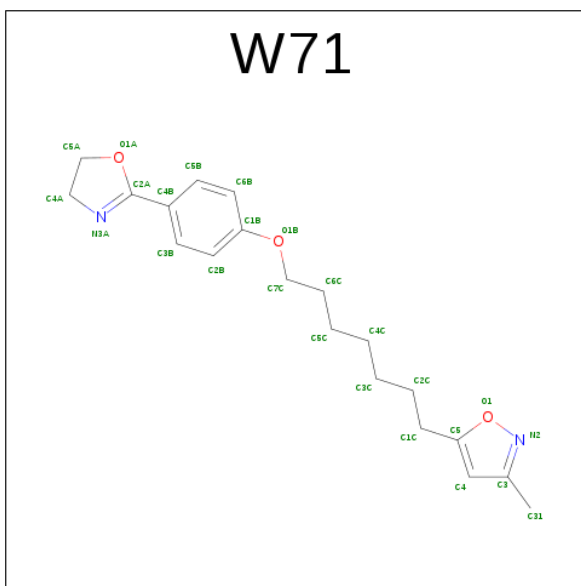
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	4	62	Total	C	N	O	0	0	0
			472	291	79	102			

- Molecule 6 is MYRISTIC ACID (three-letter code: MYR) (formula: C₁₄H₂₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	4	1	Total	C	O	0	0
			15	14	1		

- Molecule 7 is 5-(7-(4-(4,5-DIHYDRO-2-OXAZOLYL)PHENOXY)HEPTYL)-3-METHYL ISOXAZOLE (three-letter code: W71) (formula: $C_{20}H_{26}N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	1	1	Total	C	N	O	0	0
			25	20	2	3		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

Note EDS was not executed.

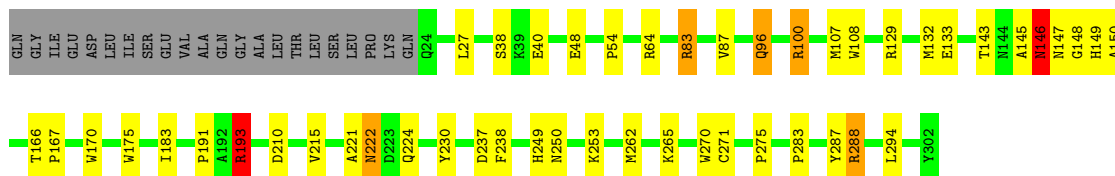
- Molecule 1: POLIOVIRUS TYPE 3 (SUBUNIT VP1)

Chain 0:  100%


There are no outlier residues recorded for this chain.

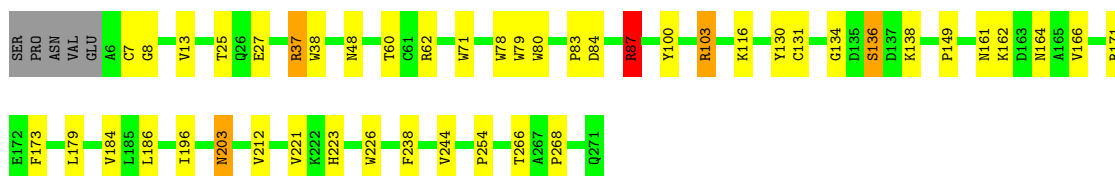
- Molecule 2: POLIOVirus TYPE 3 (SUBUNIT VP1)

Chain 1:  76% 14% 7%



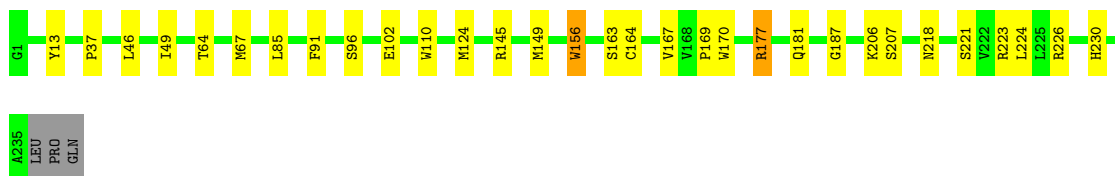
- Molecule 3: POLIOVirus TYPE 3 (SUBUNIT VP2)

Chain 2:  81% 15% 2%

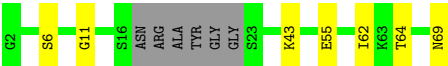
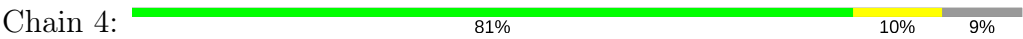


- Molecule 4: POLIOVirus TYPE 3 (SUBUNIT VP3)

Chain 3:  86% 12% 2%



- Molecule 5: POLIOVirus TYPE 3 (SUBUNIT VP4)



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	321.06Å 358.62Å 381.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.316 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6656	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MYR, W71

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	0	0.73	0/29	1.21	0/38
2	1	0.72	0/2278	1.43	22/3111 (0.7%)
3	2	0.73	0/2146	1.46	23/2926 (0.8%)
4	3	0.70	0/1857	1.36	15/2533 (0.6%)
5	4	0.68	0/479	1.33	0/647
All	All	0.71	0/6789	1.41	60/9255 (0.6%)

There are no bond length outliers.

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	175	TRP	CD1-CG-CD2	9.17	113.64	106.30
2	1	170	TRP	CD1-CG-CD2	8.82	113.36	106.30
2	1	270	TRP	CD1-CG-CD2	8.67	113.24	106.30
3	2	226	TRP	CD1-CG-CD2	8.64	113.21	106.30
2	1	175	TRP	CE2-CD2-CG	-8.51	100.49	107.30
4	3	110	TRP	CD1-CG-CD2	8.00	112.70	106.30
3	2	78	TRP	CD1-CG-CD2	7.95	112.66	106.30
3	2	62	ARG	NE-CZ-NH1	7.95	124.28	120.30
3	2	38	TRP	CD1-CG-CD2	7.93	112.64	106.30
2	1	108	TRP	CD1-CG-CD2	7.75	112.50	106.30
3	2	226	TRP	CE2-CD2-CG	-7.70	101.14	107.30
2	1	170	TRP	CE2-CD2-CG	-7.68	101.16	107.30
3	2	78	TRP	CE2-CD2-CG	-7.51	101.29	107.30
3	2	80	TRP	CD1-CG-CD2	7.47	112.28	106.30
3	2	79	TRP	CD1-CG-CD2	7.41	112.22	106.30
4	3	170	TRP	CD1-CG-CD2	7.33	112.16	106.30
4	3	110	TRP	CE2-CD2-CG	-7.32	101.44	107.30
3	2	38	TRP	CE2-CD2-CG	-7.20	101.54	107.30
3	2	71	TRP	CD1-CG-CD2	7.18	112.05	106.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	3	170	TRP	CE2-CD2-CG	-7.14	101.59	107.30
3	2	80	TRP	CE2-CD2-CG	-7.12	101.60	107.30
2	1	129	ARG	NE-CZ-NH2	-7.09	116.75	120.30
2	1	270	TRP	CE2-CD2-CG	-7.08	101.64	107.30
3	2	71	TRP	CE2-CD2-CG	-7.02	101.69	107.30
2	1	108	TRP	CE2-CD2-CG	-7.00	101.70	107.30
3	2	79	TRP	CE2-CD2-CG	-6.91	101.77	107.30
4	3	156	TRP	CD1-CG-CD2	6.78	111.73	106.30
4	3	177	ARG	NE-CZ-NH1	6.73	123.66	120.30
2	1	288	ARG	NE-CZ-NH2	-6.57	117.02	120.30
3	2	87	ARG	NE-CZ-NH1	6.45	123.53	120.30
4	3	85	LEU	CA-CB-CG	6.36	129.93	115.30
4	3	156	TRP	CE2-CD2-CG	-6.32	102.25	107.30
2	1	287	TYR	CB-CG-CD2	-6.14	117.32	121.00
3	2	37	ARG	NE-CZ-NH1	6.11	123.35	120.30
3	2	203	ASN	CB-CA-C	-5.92	98.57	110.40
3	2	100	TYR	CB-CG-CD2	-5.88	117.47	121.00
3	2	130	TYR	CB-CG-CD2	-5.84	117.49	121.00
2	1	100	ARG	NE-CZ-NH1	5.83	123.21	120.30
4	3	177	ARG	NE-CZ-NH2	-5.80	117.40	120.30
4	3	170	TRP	CG-CD2-CE3	5.79	139.11	133.90
2	1	193	ARG	NE-CZ-NH1	5.73	123.17	120.30
2	1	146	ASN	N-CA-C	5.72	126.45	111.00
2	1	64	ARG	NE-CZ-NH1	5.68	123.14	120.30
4	3	170	TRP	CB-CG-CD1	-5.65	119.66	127.00
4	3	223	ARG	NE-CZ-NH2	-5.63	117.48	120.30
2	1	270	TRP	CG-CD1-NE1	-5.50	104.60	110.10
4	3	223	ARG	NE-CZ-NH1	5.47	123.04	120.30
2	1	83	ARG	NE-CZ-NH2	-5.30	117.65	120.30
3	2	226	TRP	CG-CD1-NE1	-5.28	104.83	110.10
2	1	108	TRP	CG-CD1-NE1	-5.26	104.84	110.10
2	1	175	TRP	CG-CD2-CE3	5.26	138.63	133.90
3	2	171	ARG	NE-CZ-NH1	5.23	122.92	120.30
3	2	136	SER	N-CA-C	5.21	125.05	111.00
2	1	170	TRP	CG-CD1-NE1	-5.18	104.92	110.10
4	3	226	ARG	NE-CZ-NH1	5.17	122.89	120.30
3	2	103	ARG	NE-CZ-NH1	5.11	122.86	120.30
3	2	38	TRP	CG-CD1-NE1	-5.11	104.99	110.10
2	1	175	TRP	CG-CD1-NE1	-5.08	105.02	110.10
2	1	170	TRP	CG-CD2-CE3	5.02	138.42	133.90
4	3	145	ARG	NE-CZ-NH1	5.01	122.81	120.30

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	0	30	0	30	0	0
2	1	2214	0	2150	26	0
3	2	2088	0	2005	17	0
4	3	1812	0	1792	13	0
5	4	472	0	453	2	0
6	4	15	0	27	0	0
7	1	25	0	26	2	0
All	All	6656	0	6483	44	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 3.

All (44) 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)
2:1:294:LEU:HD13	4:3:67:MET:SD	2.37	0.65
2:1:40:GLU:HB3	5:4:64:THR:HB	1.80	0.64
3:2:116:LYS:HD2	4:3:124:MET:SD	2.38	0.63
3:2:238:PHE:HB3	3:2:244:VAL:HG21	1.82	0.61
2:1:183:ILE:HG12	7:1:303:W71:H5A1	1.82	0.61
2:1:191:PRO:HG2	4:3:13:TYR:HB2	1.86	0.58
3:2:136:SER:HB3	3:2:138:LYS:H	1.68	0.58
2:1:107:MET:HE3	2:1:167:PRO:HD2	1.86	0.57
2:1:215:VAL:HG21	3:2:221:VAL:HG12	1.87	0.56
2:1:132:MET:SD	2:1:262:MET:HG2	2.46	0.56
3:2:179:LEU:HA	3:2:184:VAL:O	2.07	0.55
2:1:143:THR:HG21	2:1:253:LYS:HD3	1.89	0.54
2:1:275:PRO:HG2	4:3:102:GLU:HG3	1.89	0.54
4:3:167:VAL:O	4:3:169:PRO:HD3	2.08	0.53
3:2:37:ARG:HG3	4:3:37:PRO:HB3	1.91	0.53
2:1:48:GLU:HA	3:2:196:ILE:HB	1.91	0.52
3:2:84:ASP:O	3:2:87:ARG:HG2	2.10	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:266:THR:HG22	3:2:268:PRO:HD3	1.94	0.50
3:2:212:VAL:HG22	4:3:37:PRO:HG2	1.95	0.48
3:2:134:GLY:HA2	3:2:173:PHE:HA	1.96	0.48
2:1:222:ASN:HB2	2:1:224:GLN:H	1.78	0.47
2:1:96:GLN:HG3	2:1:249:HIS:CE1	2.52	0.45
2:1:54:PRO:HG3	5:4:55:GLU:OE2	2.16	0.45
3:2:13:VAL:HA	3:2:25:THR:O	2.16	0.45
4:3:156:TRP:CD1	4:3:164:CYS:HB2	2.52	0.45
2:1:238:PHE:CE2	7:1:303:W71:H4	2.52	0.44
2:1:230:TYR:OH	3:2:131:CYS:HA	2.17	0.44
4:3:177:ARG:CZ	4:3:187:GLY:HA2	2.48	0.43
2:1:150:ALA:HA	2:1:250:ASN:ND2	2.33	0.43
2:1:87:VAL:HG11	2:1:262:MET:SD	2.58	0.43
4:3:46:LEU:HA	4:3:49:ILE:HD12	2.01	0.42
2:1:107:MET:HE3	2:1:166:THR:HB	2.01	0.42
2:1:288:ARG:NE	3:2:162:LYS:NZ	2.67	0.42
4:3:96:SER:O	4:3:230:HIS:HE1	2.02	0.42
3:2:60:THR:O	3:2:254:PRO:HG2	2.20	0.42
2:1:145:ALA:O	2:1:146:ASN:HB2	2.19	0.42
2:1:27:LEU:HD11	4:3:221:SER:HB3	2.02	0.41
3:2:27:GLU:HB2	3:2:203:ASN:OD1	2.19	0.41
2:1:210:ASP:O	3:2:223:HIS:HD2	2.03	0.41
2:1:146:ASN:HD22	2:1:147:ASN:N	2.18	0.41
4:3:91:PHE:CD2	4:3:181:GLN:HB2	2.55	0.41
2:1:133:GLU:HB2	2:1:265:LYS:HE2	2.02	0.40
2:1:148:GLY:O	2:1:149:HIS:ND1	2.54	0.40
2:1:133:GLU:CD	2:1:193:ARG:HD2	2.41	0.40

There are no symmetry-related clashes.

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	0	2/4 (50%)	2 (100%)	0	0	100	100
2	1	277/301 (92%)	252 (91%)	21 (8%)	4 (1%)	13	41
3	2	264/271 (97%)	243 (92%)	17 (6%)	4 (2%)	12	39
4	3	233/238 (98%)	218 (94%)	15 (6%)	0	100	100
5	4	58/68 (85%)	51 (88%)	5 (9%)	2 (3%)	4	18
All	All	834/882 (95%)	766 (92%)	58 (7%)	10 (1%)	15	46

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	237	ASP
2	1	146	ASN
2	1	221	ALA
3	2	7	CYS
3	2	8	GLY
3	2	48	ASN
5	4	43	LYS
2	1	271	CYS
3	2	166	VAL
5	4	11	GLY

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	0	4/4 (100%)	4 (100%)	0	100	100
2	1	241/259 (93%)	233 (97%)	8 (3%)	43	77
3	2	224/229 (98%)	217 (97%)	7 (3%)	45	79
4	3	210/213 (99%)	203 (97%)	7 (3%)	43	77
5	4	53/56 (95%)	50 (94%)	3 (6%)	24	56
All	All	732/761 (96%)	707 (97%)	25 (3%)	42	76

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	1	38	SER
2	1	83	ARG
2	1	96	GLN
2	1	100	ARG
2	1	146	ASN
2	1	193	ARG
2	1	222	ASN
2	1	283	PRO
3	2	83	PRO
3	2	87	ARG
3	2	103	ARG
3	2	149	PRO
3	2	161	ASN
3	2	164	ASN
3	2	186	LEU
4	3	64	THR
4	3	149	MET
4	3	163	SER
4	3	206	LYS
4	3	207	SER
4	3	218	ASN
4	3	224	LEU
5	4	6	SER
5	4	62	ILE
5	4	69	ASN

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

Mol	Chain	Res	Type
2	1	102	GLN
2	1	222	ASN
2	1	224	GLN
2	1	250	ASN
3	2	139	GLN
3	2	271	GLN
4	3	80	GLN
4	3	218	ASN
4	3	230	HIS
5	4	13	HIS
5	4	44	GLN
5	4	69	ASN

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	$\# Z > 2$
7	W71	1	303	-	24,27,27	1.80	5 (20%)	29,34,34	2.81	3 (10%)
6	MYR	4	1	5	14,14,15	0.32	0	13,13,15	0.74	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
7	W71	1	303	-	-	0/14/22/22	0/2/3/3
6	MYR	4	1	5	-	0/11/12/13	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	1	303	W71	C4B-C2A	-4.37	1.38	1.47
7	1	303	W71	C4-C5	-2.48	1.35	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	1	303	W71	C4-C3	-2.11	1.35	1.39
7	1	303	W71	O1A-C2A	3.59	1.41	1.36
7	1	303	W71	C2A-N3A	5.17	1.33	1.27

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	1	303	W71	O1A-C2A-N3A	-8.89	110.41	118.41
7	1	303	W71	C4A-N3A-C2A	6.26	112.40	106.69
7	1	303	W71	O1A-C2A-C4B	9.18	127.02	115.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	1	303	W71	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.