



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 1, 2025 – 10:33 am BST

PDB ID : 9QDF / pdb_00009qdf
Title : Yeast 20S proteasome mutant: beta1_G128V (b1-propeptide deleted) in complex with Bortezomib
Authors : Huber, E.M.; Heinemeyer, W.; Groll, M.
Deposited on : 2025-03-06
Resolution : 2.70 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.46

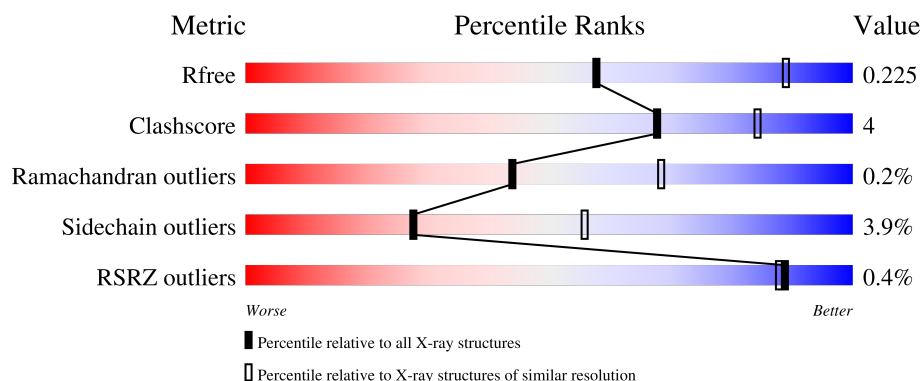
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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 ≥ 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	250	 96%
1	O	250	 95%
2	B	258	 88% 5% 5%
2	P	258	 88% 5% 5%
3	C	254	 88% 6% 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	 2% 89% 6%
4	D	260	 84% 6% 10%
4	R	260	 85% 5% 10%
5	E	234	 91% 7%
5	S	234	 92% 6%
6	F	288	 80% 16%
6	T	288	 80% 16%
7	G	252	 87% 8%
7	U	252	 87% 8%
8	H	231	 87% 8%
8	V	231	 89% 6%
9	I	205	 94% 5%
9	W	205	 92% 7%
10	J	198	 1% 87% 10%
10	X	198	 1% 85% 12%
11	K	211	 82% 14%
11	Y	211	 1% 80% 16%
12	L	222	 90% 9%
12	Z	222	 91% 9%
13	M	246	 82% 11% 5%
13	a	246	 81% 12% 5%
14	N	195	 1% 84% 12%
14	b	195	 1% 84% 14%
15	d	3	 67% 33%
15	e	3	 33% 67%

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Mol	Chain	Length	Quality of chain
15	f	3	<div><div></div><div>67%</div><div>33%</div></div>
15	g	3	<div><div></div><div>67%</div><div>33%</div></div>
15	h	3	<div><div></div><div>33%</div><div>67%</div></div>
15	i	3	<div><div></div><div>33%</div><div>67%</div></div>

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 49860 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 Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			
3	Q	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			
4	R	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			
5	S	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			

- Molecule 6 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			
6	T	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			
7	U	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			

- Molecule 8 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	221	Total	C	N	O	S	0	0	0
			1677	1057	292	321	7			
8	V	221	Total	C	N	O	S	0	0	0
			1677	1057	292	321	7			

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			
9	W	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 10 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	211	Total	C	N	O	S	0	0	0
			1637	1041	279	310	7			
11	Y	211	Total	C	N	O	S	0	0	0
			1637	1041	279	310	7			

- Molecule 12 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	Z	222	Total	C	N	O	S	0	1	0
			1767	1121	306	336	4			

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	a	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			

- Molecule 14 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	195	Total	C	N	O	S	0	0	0
			1508	954	249	298	7			
14	b	195	Total	C	N	O	S	0	0	0
			1508	954	249	298	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	128	VAL	GLY	engineered mutation	UNP P38624
b	128	VAL	GLY	engineered mutation	UNP P38624

- Molecule 15 is a protein called 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-C]PYRAZ

OLE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	d	3	Total	C	N	O	0	0	0
			35	24	5	6			
15	e	3	Total	C	N	O	0	0	0
			35	24	5	6			
15	f	3	Total	C	N	O	0	0	0
			35	24	5	6			
15	g	3	Total	C	N	O	0	0	0
			35	24	5	6			
15	h	3	Total	C	N	O	0	0	0
			35	24	5	6			
15	i	3	Total	C	N	O	0	0	0
			35	24	5	6			

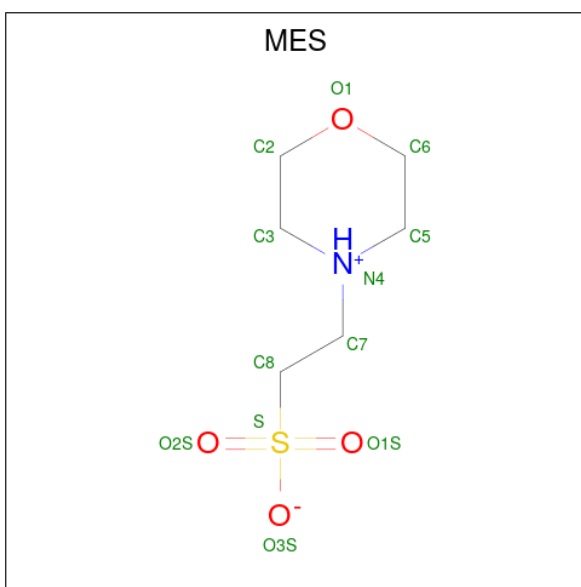
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	G	1	Total	Mg	0	0
			1	1		
16	I	1	Total	Mg	0	0
			1	1		
16	V	1	Total	Mg	0	0
			1	1		
16	Z	1	Total	Mg	0	0
			1	1		

- Molecule 17 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

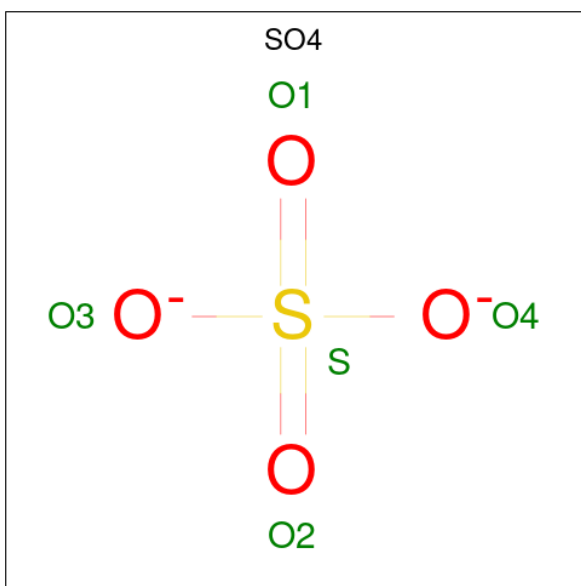
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	G	2	Total	Cl	0	0
			2	2		
17	N	1	Total	Cl	0	0
			1	1		
17	U	1	Total	Cl	0	0
			1	1		
17	b	1	Total	Cl	0	0
			1	1		

- Molecule 18 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	a	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 19 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	d	1	Total	O	S	0	0
			5	4	1		
19	g	1	Total	O	S	0	0
			5	4	1		

- Molecule 20 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
20	A	14	Total O 14 14	0	0
20	B	13	Total O 13 13	0	0
20	C	6	Total O 6 6	0	0
20	D	6	Total O 6 6	0	0
20	E	6	Total O 6 6	0	0
20	F	15	Total O 15 15	0	0
20	G	15	Total O 15 15	0	0
20	H	16	Total O 16 16	0	0
20	I	16	Total O 16 16	0	0
20	J	17	Total O 17 17	0	0
20	K	8	Total O 8 8	0	0
20	L	19	Total O 19 19	0	0
20	M	16	Total O 16 16	0	0
20	N	8	Total O 8 8	0	0
20	O	8	Total O 8 8	0	0
20	P	11	Total O 11 11	0	0
20	Q	12	Total O 12 12	0	0
20	R	11	Total O 11 11	0	0
20	S	4	Total O 4 4	0	0
20	T	14	Total O 14 14	0	0
20	U	17	Total O 17 17	0	0
20	V	20	Total O 20 20	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	W	9	Total 9	O 9	0	0
20	X	10	Total 10	O 10	0	0
20	Y	12	Total 12	O 12	0	0
20	Z	15	Total 15	O 15	0	0
20	a	18	Total 18	O 18	0	0
20	b	11	Total 11	O 11	0	0
20	d	1	Total 1	O 1	0	0
20	f	1	Total 1	O 1	0	0

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.

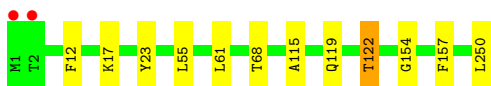
- Molecule 1: Proteasome subunit alpha type-2

Chain A:  96%




- Molecule 1: Proteasome subunit alpha type-2

Chain O:  95%




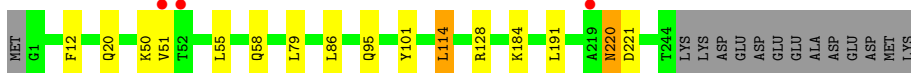
- Molecule 2: Proteasome subunit alpha type-3

Chain B:  88% 5% 5%



- Molecule 2: Proteasome subunit alpha type-3

Chain P:  88% 5% 5%

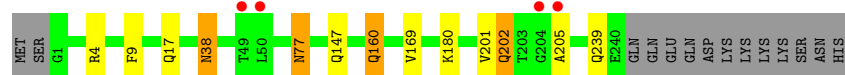


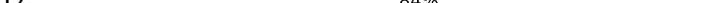
- Molecule 3: Proteasome subunit alpha type-4

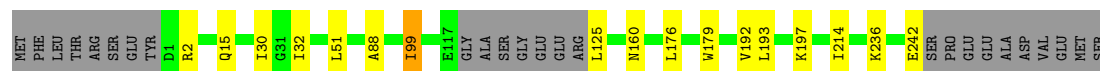
Chain C:  88% 6% 6%




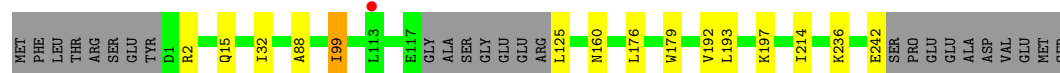
- Molecule 3: Proteasome subunit alpha type-4



- Chain D:  84% 6% 10%

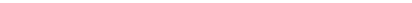


- Chain R:  85% 5% 10%



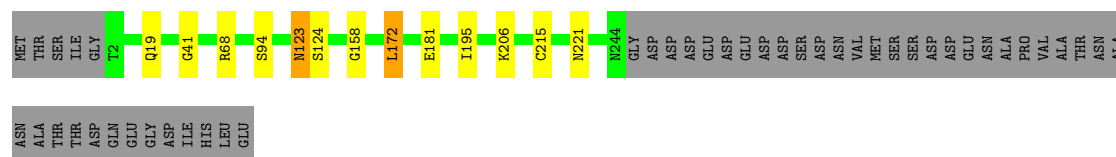
- Chain E: 91% 7% .




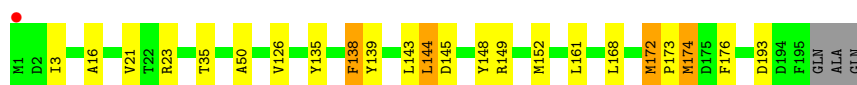
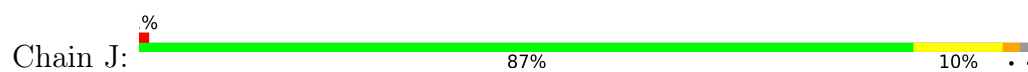
- Chain S:  92% 6% ..



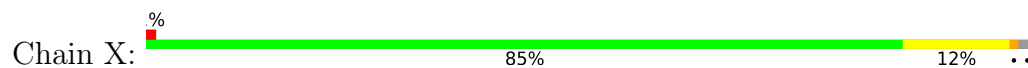
- Chain F: 80% . . 16%



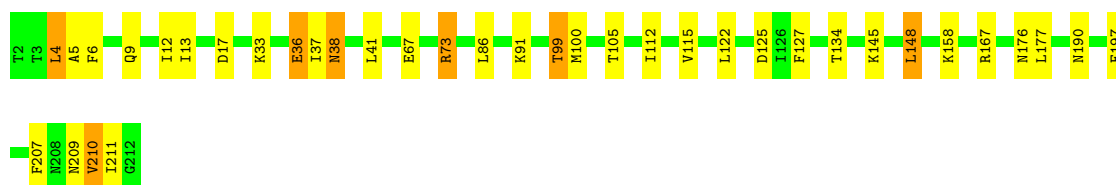
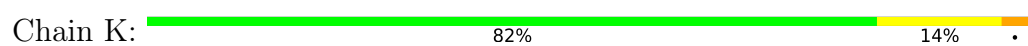
- Chain T:  80% . . 16%



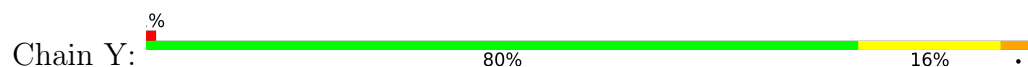
- Molecule 10: Proteasome subunit beta type-4



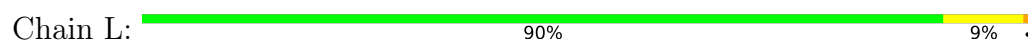
- Molecule 11: Proteasome subunit beta type-5



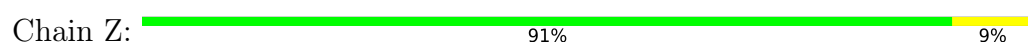
- Molecule 11: Proteasome subunit beta type-5




- Molecule 12: Proteasome subunit beta type-6

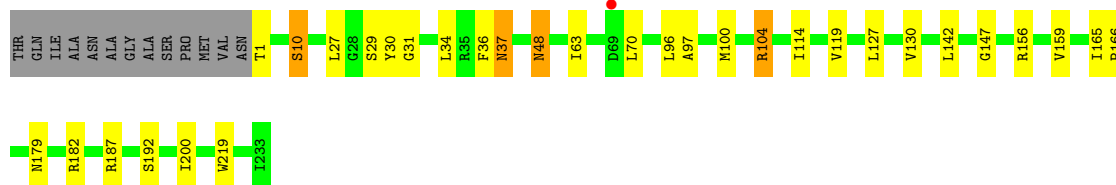


- Molecule 12: Proteasome subunit beta type-6




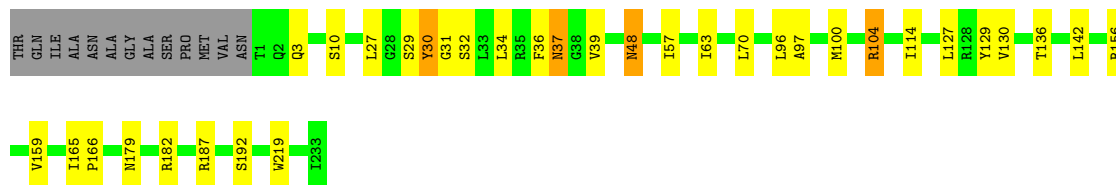
- Molecule 13: Proteasome subunit beta type-7

Chain M:  82% 11% • 5%




- Molecule 13: Proteasome subunit beta type-7

Chain a:  81% 12% • 5%




- Molecule 14: Proteasome subunit beta type-1

Chain N:  84% 12% •



- Molecule 14: Proteasome subunit beta type-1

Chain b:  84% 14% •



- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-C.]PYRAZOLE

Chain d:  67% 33%



- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-C.]PYRAZOLE

Chain e:  33% 67%



- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-C.]PYRAZOLE

Chain f:  67% 33%

VGL1
F2
A11493

- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-C.]PYRAZOLE

Chain g:  67% 33%

VGL1
F2
A11493

- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-C.]PYRAZOLE

Chain h:  33% 67%

VGL1
F2
A11493

- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-C.]PYRAZOLE

Chain i:  33% 67%

VGL1
F2
A11493

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	136.95Å 300.39Å 145.30Å 90.00° 113.18° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 15.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.4 (15.00-2.70) 96.4 (15.00-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.179 , 0.217 0.180 , 0.225	Depositor DCC
R_{free} test set	14184 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	45.5	Xtriage
Anisotropy	1.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 55.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	49860	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: SO4, MG, VGL, CL, A1I49, MES

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	1.04	0/1952	1.42	0/2642
1	O	1.04	1/1952 (0.1%)	1.43	0/2642
2	B	1.02	0/1934	1.43	0/2618
2	P	1.03	0/1934	1.43	0/2618
3	C	1.03	0/1910	1.46	0/2586
3	Q	1.04	0/1910	1.47	0/2586
4	D	1.04	0/1837	1.48	4/2475 (0.2%)
4	R	1.04	0/1837	1.48	2/2475 (0.1%)
5	E	1.04	0/1800	1.44	0/2433
5	S	1.04	0/1800	1.45	0/2433
6	F	1.02	0/1932	1.45	0/2609
6	T	1.03	0/1932	1.45	2/2609 (0.1%)
7	G	1.01	0/1945	1.42	0/2634
7	U	1.02	0/1945	1.43	0/2634
8	H	1.04	0/1708	1.41	2/2316 (0.1%)
8	V	1.03	0/1708	1.42	2/2316 (0.1%)
9	I	1.01	0/1611	1.41	1/2174 (0.0%)
9	W	1.01	0/1611	1.41	1/2174 (0.0%)
10	J	1.00	0/1589	1.40	1/2142 (0.0%)
10	X	1.01	0/1589	1.40	0/2142
11	K	1.00	0/1674	1.44	1/2264 (0.0%)
11	Y	1.01	0/1674	1.43	1/2264 (0.0%)
12	L	1.01	0/1795	1.39	0/2420
12	Z	1.00	0/1806	1.38	0/2435
13	M	1.01	0/1855	1.39	0/2514
13	a	1.01	0/1855	1.40	0/2514
14	N	1.02	0/1537	1.44	1/2082 (0.0%)
14	b	1.01	0/1537	1.43	1/2082 (0.0%)
15	d	2.02	1/11 (9.1%)	1.13	0/13
15	e	2.05	1/11 (9.1%)	1.07	0/13
15	f	2.39	1/11 (9.1%)	3.23	1/13 (7.7%)
15	g	1.83	1/11 (9.1%)	0.89	0/13

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	h	1.82	1/11 (9.1%)	0.95	0/13
15	i	2.25	1/11 (9.1%)	3.27	1/13 (7.7%)
All	All	1.02	7/50235 (0.0%)	1.43	21/67911 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	f	2	PHE	CB-CG	-7.30	1.33	1.50
15	i	2	PHE	CB-CG	-6.68	1.35	1.50
15	e	2	PHE	CB-CG	-6.16	1.36	1.50
15	d	2	PHE	CB-CG	-5.99	1.36	1.50
15	g	2	PHE	CB-CG	-5.71	1.37	1.50

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	f	2	PHE	CA-CB-CG	-10.55	103.25	113.80
15	i	2	PHE	CA-CB-CG	-9.98	103.82	113.80
14	N	94	THR	CB-CA-C	6.30	120.52	111.82
14	b	94	THR	CB-CA-C	6.28	120.48	111.82
9	I	183	GLY	CA-C-O	-6.20	118.19	122.22

There are no chirality outliers.

There are no planarity outliers.

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	1915	0	1929	4	0
1	O	1915	0	1929	6	0
2	B	1904	0	1904	9	0
2	P	1904	0	1904	8	0
3	C	1881	0	1895	12	0
3	Q	1881	0	1895	8	0
4	D	1813	0	1797	5	0
4	R	1813	0	1797	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1773	0	1775	13	0
5	S	1773	0	1775	13	0
6	F	1892	0	1883	6	0
6	T	1892	0	1883	7	0
7	G	1907	0	1901	11	0
7	U	1907	0	1901	12	0
8	H	1677	0	1678	16	0
8	V	1677	0	1678	7	0
9	I	1581	0	1574	8	0
9	W	1581	0	1574	10	0
10	J	1561	0	1569	16	0
10	X	1561	0	1569	21	0
11	K	1637	0	1585	47	0
11	Y	1637	0	1585	50	0
12	L	1757	0	1711	15	0
12	Z	1767	0	1717	13	0
13	M	1824	0	1832	27	0
13	a	1824	0	1832	23	0
14	N	1508	0	1477	29	0
14	b	1508	0	1477	28	0
15	d	35	0	11	0	0
15	e	35	0	11	2	0
15	f	35	0	11	4	0
15	g	35	0	11	4	0
15	h	35	0	11	1	0
15	i	35	0	11	2	0
16	G	1	0	0	0	0
16	I	1	0	0	0	0
16	V	1	0	0	0	0
16	Z	1	0	0	0	0
17	G	2	0	0	0	0
17	N	1	0	0	0	0
17	U	1	0	0	0	0
17	b	1	0	0	0	0
18	a	12	0	13	0	0
19	d	5	0	0	0	0
19	g	5	0	0	0	0
20	A	14	0	0	0	0
20	B	13	0	0	0	0
20	C	6	0	0	0	0
20	D	6	0	0	0	0
20	E	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	F	15	0	0	0	0
20	G	15	0	0	0	0
20	H	16	0	0	1	0
20	I	16	0	0	0	0
20	J	17	0	0	1	0
20	K	8	0	0	0	0
20	L	19	0	0	0	0
20	M	16	0	0	0	0
20	N	8	0	0	0	0
20	O	8	0	0	0	0
20	P	11	0	0	0	0
20	Q	12	0	0	0	0
20	R	11	0	0	0	0
20	S	4	0	0	0	0
20	T	14	0	0	1	0
20	U	17	0	0	0	0
20	V	20	0	0	0	0
20	W	9	0	0	0	0
20	X	10	0	0	0	0
20	Y	12	0	0	0	0
20	Z	15	0	0	0	0
20	a	18	0	0	1	0
20	b	11	0	0	0	0
20	d	1	0	0	0	0
20	f	1	0	0	0	0
All	All	49860	0	49105	349	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.

The worst 5 of 349 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)
14:N:14:LEU:HD11	14:N:100:ALA:HB3	1.30	1.10
11:K:197:PHE:CE1	11:K:207:PHE:CE1	2.43	1.06
13:a:37:ASN:HB3	14:b:135:TYR:HE2	1.20	1.06
11:K:5:ALA:HB3	11:K:100:MET:HE2	1.38	1.04
11:K:134:THR:HG22	10:X:139:TYR:CE1	1.94	1.03

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	A	248/250 (99%)	240 (97%)	8 (3%)	0	100	100
1	O	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
2	B	242/258 (94%)	233 (96%)	7 (3%)	2 (1%)	16	38
2	P	242/258 (94%)	233 (96%)	7 (3%)	2 (1%)	16	38
3	C	238/254 (94%)	230 (97%)	5 (2%)	3 (1%)	10	26
3	Q	238/254 (94%)	230 (97%)	5 (2%)	3 (1%)	10	26
4	D	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
4	R	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
5	E	229/234 (98%)	222 (97%)	7 (3%)	0	100	100
5	S	229/234 (98%)	222 (97%)	7 (3%)	0	100	100
6	F	241/288 (84%)	233 (97%)	8 (3%)	0	100	100
6	T	241/288 (84%)	234 (97%)	7 (3%)	0	100	100
7	G	239/252 (95%)	229 (96%)	10 (4%)	0	100	100
7	U	239/252 (95%)	229 (96%)	10 (4%)	0	100	100
8	H	219/231 (95%)	215 (98%)	4 (2%)	0	100	100
8	V	219/231 (95%)	215 (98%)	4 (2%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	188 (97%)	5 (3%)	0	100	100
10	X	193/198 (98%)	188 (97%)	5 (3%)	0	100	100
11	K	209/211 (99%)	205 (98%)	3 (1%)	1 (0%)	25	49
11	Y	209/211 (99%)	205 (98%)	2 (1%)	2 (1%)	13	33
12	L	220/222 (99%)	217 (99%)	3 (1%)	0	100	100
12	Z	221/222 (100%)	218 (99%)	3 (1%)	0	100	100
13	M	231/246 (94%)	222 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	a	231/246 (94%)	223 (96%)	7 (3%)	1 (0%)	30	55
14	N	193/195 (99%)	185 (96%)	8 (4%)	0	100	100
14	b	193/195 (99%)	185 (96%)	8 (4%)	0	100	100
All	All	6271/6608 (95%)	6082 (97%)	175 (3%)	14 (0%)	44	68

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
2	P	51	VAL
3	Q	202	GLN
11	Y	211	ILE

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	209/209 (100%)	204 (98%)	5 (2%)	44	73
1	O	209/209 (100%)	204 (98%)	5 (2%)	44	73
2	B	203/216 (94%)	195 (96%)	8 (4%)	27	56
2	P	203/216 (94%)	195 (96%)	8 (4%)	27	56
3	C	212/226 (94%)	205 (97%)	7 (3%)	33	62
3	Q	212/226 (94%)	205 (97%)	7 (3%)	33	62
4	D	194/215 (90%)	186 (96%)	8 (4%)	26	54
4	R	194/215 (90%)	186 (96%)	8 (4%)	26	54
5	E	190/193 (98%)	184 (97%)	6 (3%)	34	63
5	S	190/193 (98%)	185 (97%)	5 (3%)	41	70
6	F	201/239 (84%)	194 (96%)	7 (4%)	31	60
6	T	201/239 (84%)	194 (96%)	7 (4%)	31	60
7	G	206/210 (98%)	198 (96%)	8 (4%)	27	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	U	206/210 (98%)	195 (95%)	11 (5%)	19	43
8	H	180/189 (95%)	173 (96%)	7 (4%)	27	56
8	V	180/189 (95%)	173 (96%)	7 (4%)	27	56
9	I	172/173 (99%)	170 (99%)	2 (1%)	67	86
9	W	172/173 (99%)	170 (99%)	2 (1%)	67	86
10	J	173/175 (99%)	165 (95%)	8 (5%)	23	49
10	X	173/175 (99%)	165 (95%)	8 (5%)	23	49
11	K	168/168 (100%)	159 (95%)	9 (5%)	18	42
11	Y	168/168 (100%)	157 (94%)	11 (6%)	14	34
12	L	185/185 (100%)	178 (96%)	7 (4%)	28	56
12	Z	186/185 (100%)	179 (96%)	7 (4%)	28	56
13	M	199/208 (96%)	192 (96%)	7 (4%)	31	60
13	a	199/208 (96%)	189 (95%)	10 (5%)	20	46
14	N	162/162 (100%)	149 (92%)	13 (8%)	10	24
14	b	162/162 (100%)	152 (94%)	10 (6%)	15	36
15	d	1/1 (100%)	1 (100%)	0	100	100
15	e	1/1 (100%)	1 (100%)	0	100	100
15	f	1/1 (100%)	1 (100%)	0	100	100
15	g	1/1 (100%)	1 (100%)	0	100	100
15	h	1/1 (100%)	1 (100%)	0	100	100
15	i	1/1 (100%)	1 (100%)	0	100	100
All	All	5315/5542 (96%)	5107 (96%)	208 (4%)	27	56

5 of 208 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	Q	4	ARG
7	U	59	THR
14	b	13	ILE
3	Q	160	GLN
5	S	9	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 177 such sidechains are listed below:

Mol	Chain	Res	Type
5	S	120	GLN
9	W	37	ASN
6	T	19	GLN
7	U	83	ASN
10	X	133	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 9 are monoatomic - leaving 3 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	$\# Z > 2$
19	SO4	d	101	-	4,4,4	0.38	0	6,6,6	0.05	0
19	SO4	g	101	-	4,4,4	0.37	0	6,6,6	0.05	0
18	MES	a	301	-	12,12,12	0.72	0	14,16,16	0.40	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
18	MES	a	301	-	-	1/6/14/14	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	a	301	MES	N4-C7-C8-S

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 ⓘ

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, 95th 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 ²)	Q<0.9
1	A	250/250 (100%)	-0.70	1 (0%) 89 88	48, 62, 92, 148	0
1	O	250/250 (100%)	-0.67	2 (0%) 82 82	52, 69, 106, 141	0
2	B	244/258 (94%)	-0.54	3 (1%) 76 76	48, 67, 110, 155	0
2	P	244/258 (94%)	-0.49	3 (1%) 76 76	53, 71, 119, 159	0
3	C	240/254 (94%)	-0.60	1 (0%) 89 88	50, 72, 124, 147	0
3	Q	240/254 (94%)	-0.50	4 (1%) 69 68	53, 81, 141, 171	0
4	D	235/260 (90%)	-0.67	0 100 100	52, 72, 101, 125	0
4	R	235/260 (90%)	-0.62	1 (0%) 89 88	52, 73, 105, 134	0
5	E	231/234 (98%)	-0.56	0 100 100	54, 73, 104, 135	0
5	S	231/234 (98%)	-0.49	1 (0%) 89 88	54, 77, 114, 135	0
6	F	243/288 (84%)	-0.60	0 100 100	46, 67, 108, 132	0
6	T	243/288 (84%)	-0.59	0 100 100	46, 73, 117, 137	0
7	G	241/252 (95%)	-0.74	0 100 100	46, 62, 90, 120	0
7	U	241/252 (95%)	-0.72	0 100 100	50, 64, 95, 118	0
8	H	221/231 (95%)	-0.75	0 100 100	46, 57, 80, 104	0
8	V	221/231 (95%)	-0.74	0 100 100	47, 60, 81, 121	0
9	I	204/205 (99%)	-0.82	0 100 100	43, 58, 79, 111	0
9	W	204/205 (99%)	-0.85	0 100 100	44, 59, 86, 111	0
10	J	195/198 (98%)	-0.68	1 (0%) 87 86	44, 60, 84, 117	0
10	X	195/198 (98%)	-0.67	1 (0%) 87 86	47, 62, 83, 127	0
11	K	211/211 (100%)	-0.75	0 100 100	45, 59, 86, 166	0
11	Y	211/211 (100%)	-0.69	2 (0%) 81 80	46, 59, 91, 148	0
12	L	222/222 (100%)	-0.75	0 100 100	45, 60, 89, 106	0
12	Z	222/222 (100%)	-0.72	1 (0%) 87 86	38, 58, 86, 98	1 (0%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.77	1 (0%) 89 88	44, 61, 83, 104	0
13	a	233/246 (94%)	-0.78	0 100 100	43, 59, 79, 104	0
14	N	195/195 (100%)	-0.63	1 (0%) 87 86	42, 58, 109, 146	0
14	b	195/195 (100%)	-0.60	2 (1%) 79 79	46, 59, 104, 155	0
15	d	1/3 (33%)	-0.61	0 100 100	59, 59, 59, 59	0
15	e	1/3 (33%)	-1.33	0 100 100	50, 50, 50, 50	0
15	f	1/3 (33%)	0.74	0 100 100	72, 72, 72, 72	0
15	g	1/3 (33%)	-0.56	0 100 100	63, 63, 63, 63	0
15	h	1/3 (33%)	-0.81	0 100 100	57, 57, 57, 57	0
15	i	1/3 (33%)	0.89	0 100 100	77, 77, 77, 77	0
All	All	6336/6626 (95%)	-0.67	25 (0%) 89 88	38, 64, 105, 171	1 (0%)

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	219	ALA	3.6
3	Q	50	LEU	3.5
3	Q	205	ALA	3.2
2	P	219	ALA	3.1
2	P	51	VAL	2.9

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 oligosaccharides 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, 95th 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(\AA^2)	Q<0.9
16	MG	Z	301	1/1	0.75	0.35	173,173,173,173	0
17	CL	G	302	1/1	0.81	0.22	30,30,30,30	0
18	MES	a	301	12/12	0.87	0.16	133,143,149,153	0
17	CL	b	201	1/1	0.95	0.07	87,87,87,87	0
16	MG	V	301	1/1	0.95	0.10	120,120,120,120	0
16	MG	I	301	1/1	0.96	0.10	112,112,112,112	0
17	CL	N	201	1/1	0.96	0.09	76,76,76,76	0
16	MG	G	301	1/1	0.97	0.06	88,88,88,88	0
17	CL	U	301	1/1	0.97	0.04	73,73,73,73	0
19	SO4	g	101	5/5	0.97	0.16	94,101,109,111	0
19	SO4	d	101	5/5	0.98	0.13	101,102,106,107	0
17	CL	G	303	1/1	0.99	0.04	62,62,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.