



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:15 PM GMT

PDB ID : 4R02  
Title : yCP in complex with BSc4999 (alpha-Keto Phenylamide)  
Authors : Voss, C.; Scholz, C.; Knorr, S.; Beck, P.; Stein, M.; Zall, A.; Kuckelkorn, U.;  
Kloetzel, P.-M.; Groll, M.; Hamacher, K.; Schmidt, B.  
Deposited on : 2014-07-29  
Resolution : 2.50 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.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

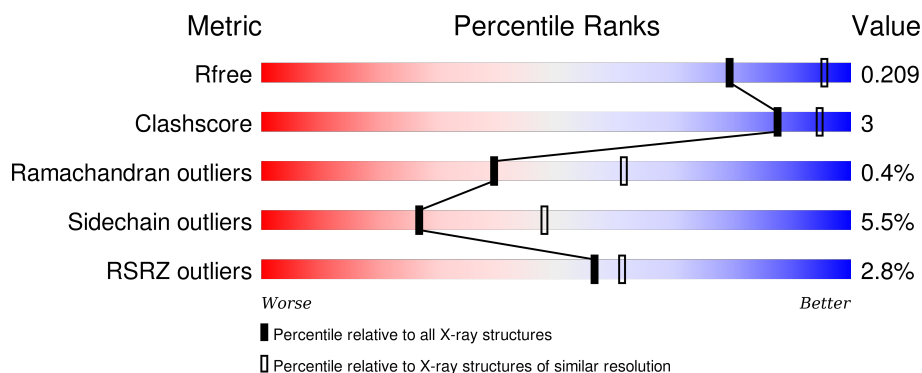
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	250	<div> <div>3%</div> <div>94%</div> <div>5%</div> </div>
1	O	250	<div> <div>3%</div> <div>93%</div> <div>6%</div> </div>
2	B	258	<div> <div>3%</div> <div>83%</div> <div>11%</div> <div>5%</div> </div>
2	P	258	<div> <div>5%</div> <div>83%</div> <div>10%</div> <div>5%</div> </div>
3	C	254	<div> <div>6%</div> <div>81%</div> <div>12%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
15	MG	I	302	-	-	-	X
15	MG	J	201	-	-	-	X
15	MG	K	303	-	-	-	X
16	3E5	K	301	-	-	-	X
16	3E5	Y	301	-	-	-	X

## 2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 52173 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	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	7			
8	V	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	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	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			
11	Y	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	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	0	0
			1757	1115	303	335	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	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	b	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

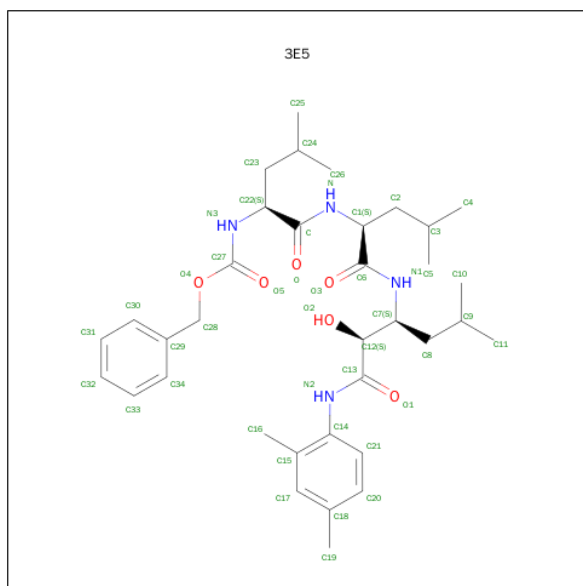
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Mg	0	0
			1	1		
15	J	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	K	2	Total	Mg	0	0
			2	2		
15	I	2	Total	Mg	0	0
			2	2		
15	V	1	Total	Mg	0	0
			1	1		
15	Z	1	Total	Mg	0	0
			1	1		
15	N	2	Total	Mg	0	0
			2	2		
15	Y	1	Total	Mg	0	0
			1	1		

- Molecule 16 is N-[(BENZYLOXY)CARBONYL]-L-LEUCYL-N-{(2S,3S)-1-[(2,4-DIMETHYLPHENYL)AMINO]-2-HYDROXY-5-METHYL-1-OXOHEXAN-3-YL}-L-LEUCINAMIDE (three-letter code: 3E5) (formula: C<sub>35</sub>H<sub>52</sub>N<sub>4</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
16	K	1	Total	C	N	O	0	0
			45	35	4	6		
16	Y	1	Total	C	N	O	0	0
			45	35	4	6		

- Molecule 17 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	121	Total O 121 121	0	0
17	B	84	Total O 84 84	0	0
17	C	88	Total O 88 88	0	0
17	D	82	Total O 82 82	0	0
17	E	44	Total O 44 44	0	0
17	F	93	Total O 93 93	0	0
17	G	117	Total O 117 117	0	0
17	H	110	Total O 110 110	0	0
17	I	106	Total O 106 106	0	0
17	J	101	Total O 101 101	0	0
17	K	119	Total O 119 119	0	0
17	L	118	Total O 118 118	0	0
17	M	141	Total O 141 141	0	0
17	N	108	Total O 108 108	0	0
17	O	79	Total O 79 79	0	0
17	P	73	Total O 73 73	0	0
17	Q	61	Total O 61 61	0	0
17	R	74	Total O 74 74	0	0
17	S	38	Total O 38 38	0	0
17	T	82	Total O 82 82	0	0
17	U	109	Total O 109 109	0	0
17	V	89	Total O 89 89	0	0

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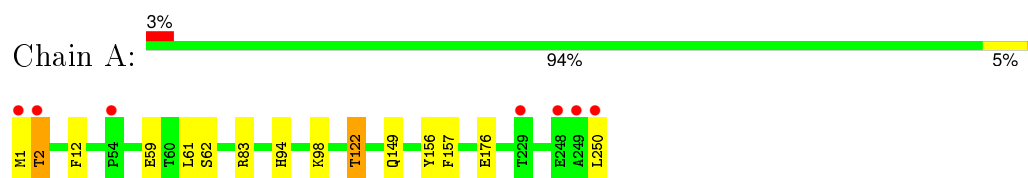
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	W	104	Total 104	O 104	0	0
17	X	92	Total 92	O 92	0	0
17	Y	114	Total 114	O 114	0	0
17	Z	126	Total 126	O 126	0	0
17	a	137	Total 137	O 137	0	0
17	b	96	Total 96	O 96	0	0

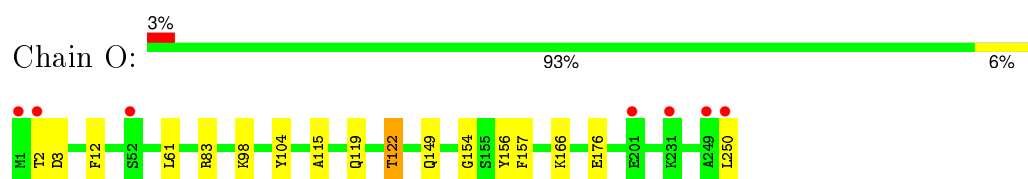
### 3 Residue-property plots [i](#)

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.

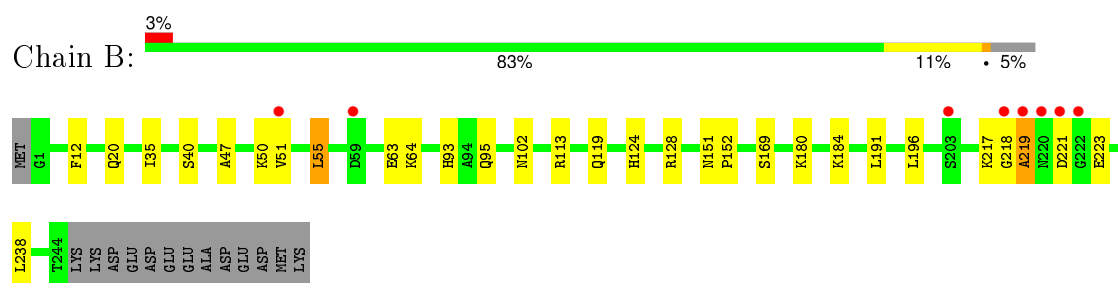
- Molecule 1: Proteasome subunit alpha type-2



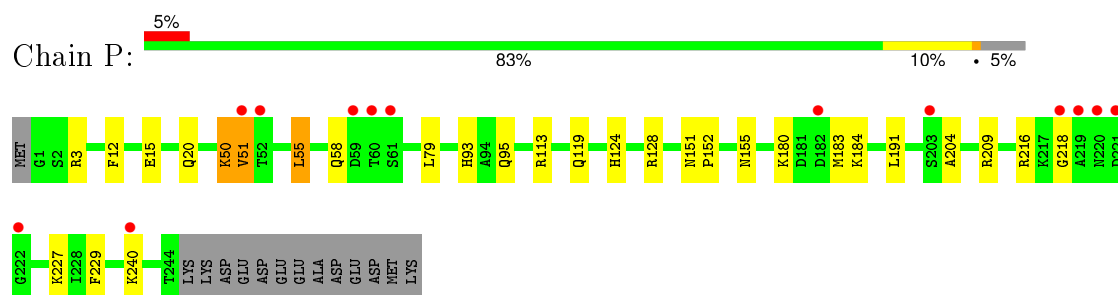
- Molecule 1: Proteasome subunit alpha type-2



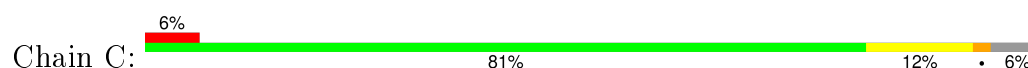
- Molecule 2: Proteasome subunit alpha type-3

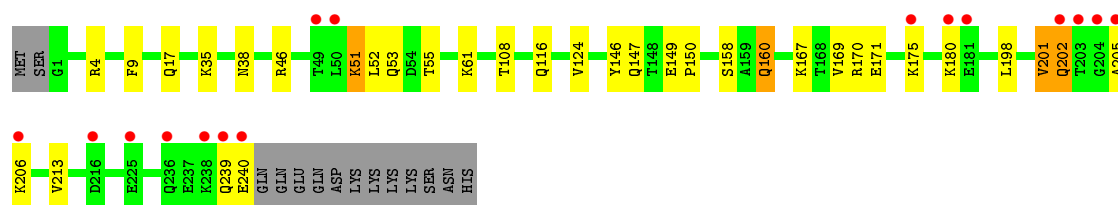


- Molecule 2: Proteasome subunit alpha type-3

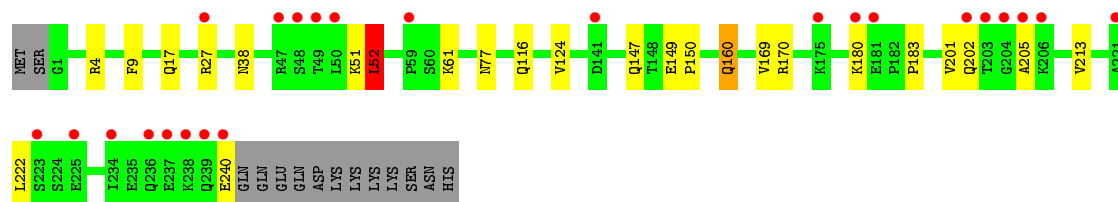
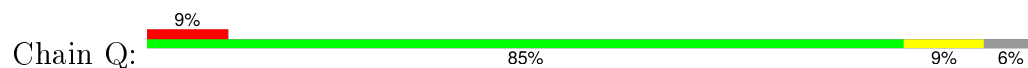


- Molecule 3: Proteasome subunit alpha type-4

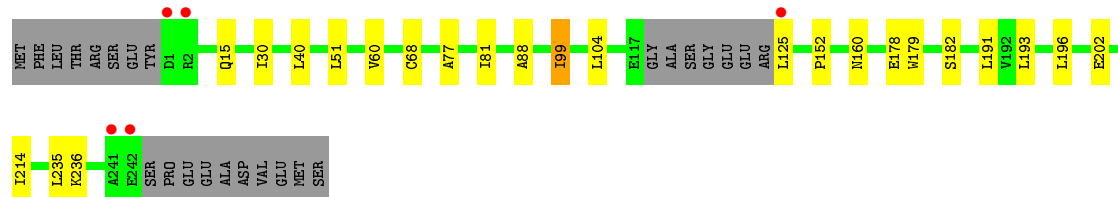
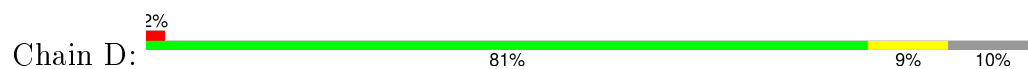




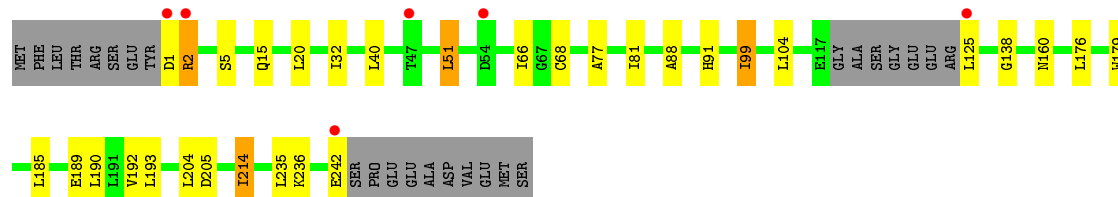
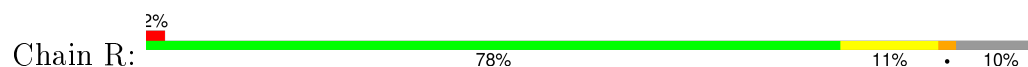
- Molecule 3: Proteasome subunit alpha type-4



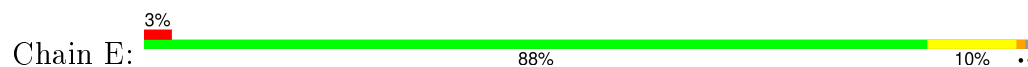
- Molecule 4: Proteasome subunit alpha type-5



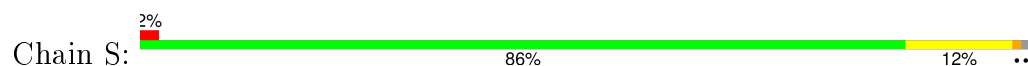
- Molecule 4: Proteasome subunit alpha type-5

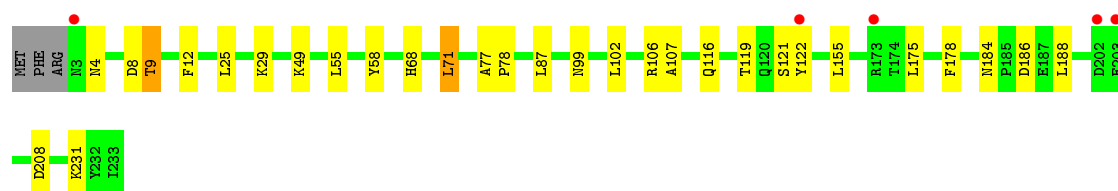


- Molecule 5: Proteasome subunit alpha type-6

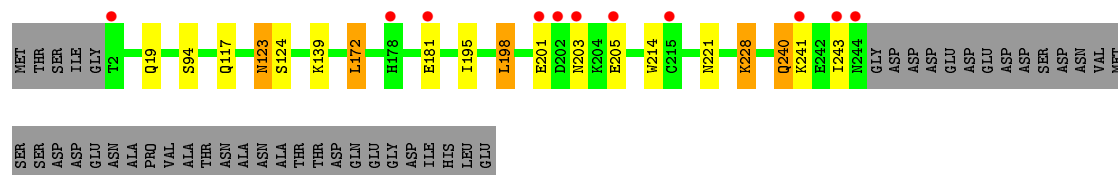
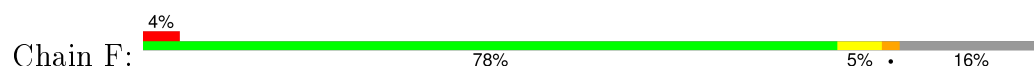


- Molecule 5: Proteasome subunit alpha type-6

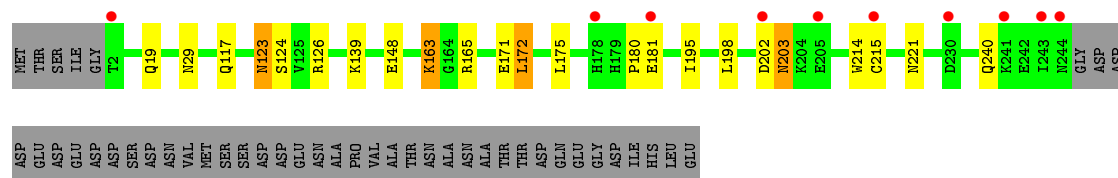




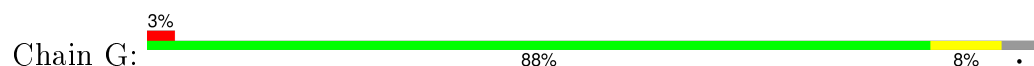
- Molecule 6: Probable proteasome subunit alpha type-7



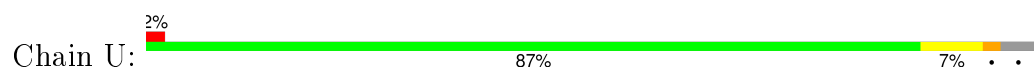
- Molecule 6: Probable proteasome subunit alpha type-7



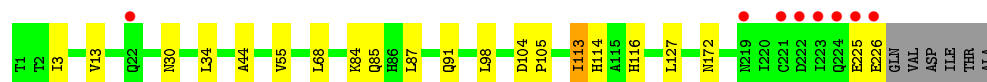
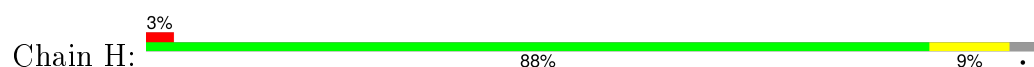
- Molecule 7: Proteasome subunit alpha type-1



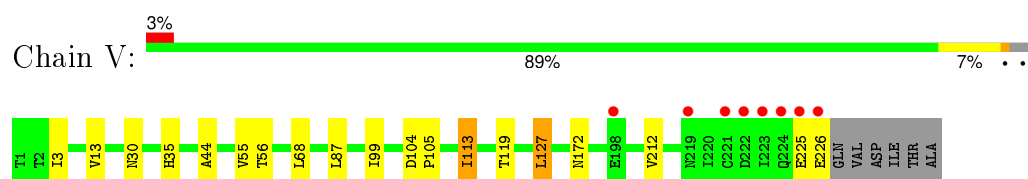
- Molecule 7: Proteasome subunit alpha type-1



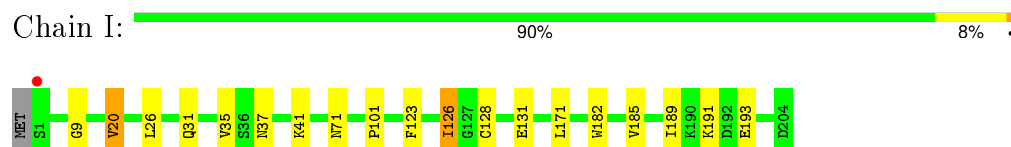
- Molecule 8: Proteasome subunit beta type-2



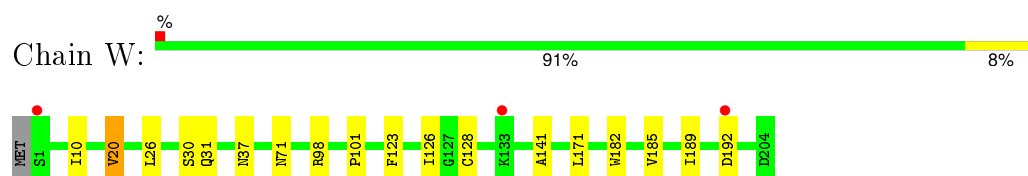
- Molecule 8: Proteasome subunit beta type-2



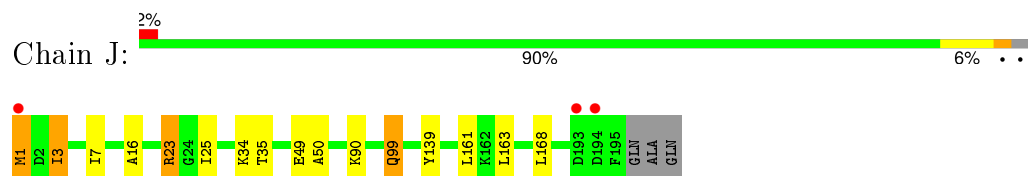
- Molecule 9: Proteasome subunit beta type-3



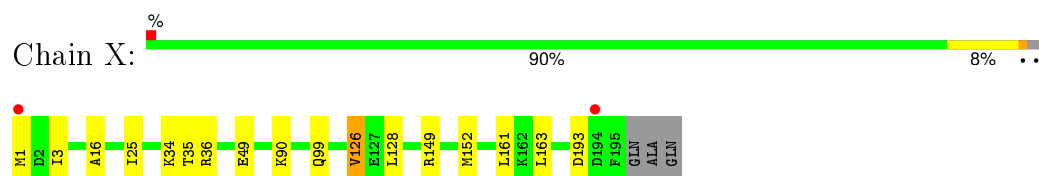
- Molecule 9: Proteasome subunit beta type-3



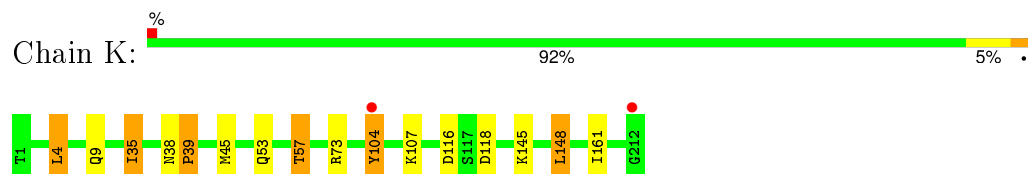
- Molecule 10: Proteasome subunit beta type-4



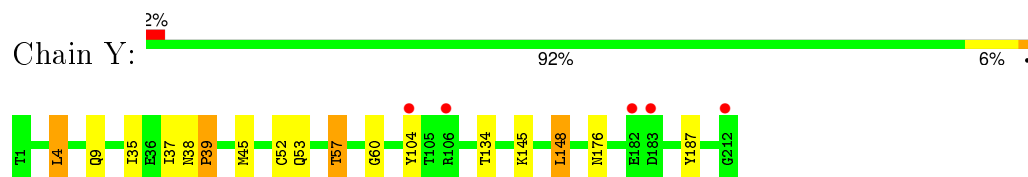
- Molecule 10: Proteasome subunit beta type-4



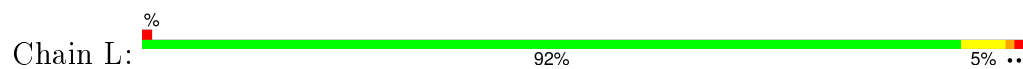
- Molecule 11: Proteasome subunit beta type-5



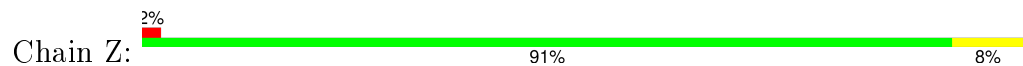
- Molecule 11: Proteasome subunit beta type-5



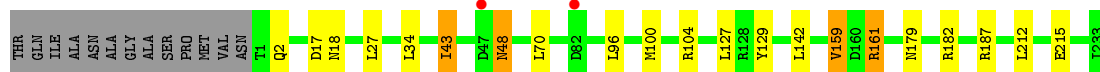
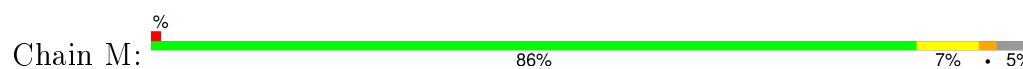
- Molecule 12: Proteasome subunit beta type-6



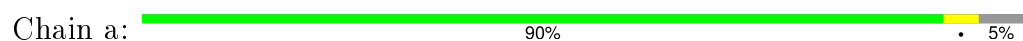
- Molecule 12: Proteasome subunit beta type-6



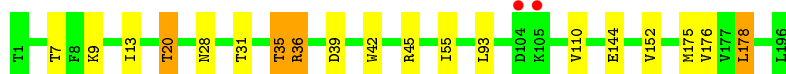
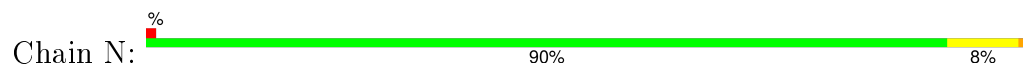
- Molecule 13: Proteasome subunit beta type-7



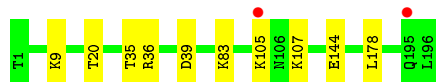
- Molecule 13: Proteasome subunit beta type-7



- Molecule 14: Proteasome subunit beta type-1



- Molecule 14: Proteasome subunit beta type-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	137.24Å 300.87Å 146.29Å 90.00° 113.20° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 15.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.0 (15.00-2.50) 97.0 (15.00-2.50)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.30 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.170 , 0.207 0.172 , 0.209	Depositor DCC
$R_{free}$ test set	18074 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.2	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 46.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 361476 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	52173	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, 3E5

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	0.27	0/1952	0.48	0/2642
1	O	0.27	0/1952	0.48	0/2642
2	B	0.27	0/1934	0.52	0/2618
2	P	0.27	0/1934	0.53	0/2618
3	C	0.28	0/1910	0.53	0/2586
3	Q	0.28	0/1910	0.54	0/2586
4	D	0.27	0/1837	0.52	0/2475
4	R	0.27	0/1837	0.53	0/2475
5	E	0.27	0/1800	0.51	1/2433 (0.0%)
5	S	0.27	0/1800	0.51	1/2433 (0.0%)
6	F	0.28	0/1932	0.51	0/2609
6	T	0.29	0/1932	0.50	0/2609
7	G	0.28	0/1945	0.50	0/2634
7	U	0.27	0/1945	0.50	0/2634
8	H	0.26	0/1750	0.51	0/2373
8	V	0.26	0/1750	0.50	0/2373
9	I	0.28	0/1611	0.51	0/2174
9	W	0.27	0/1611	0.50	0/2174
10	J	0.27	0/1589	0.50	0/2142
10	X	0.27	0/1589	0.51	0/2142
11	K	0.27	0/1681	0.52	0/2274
11	Y	0.29	0/1681	0.52	1/2274 (0.0%)
12	L	0.27	0/1795	0.51	0/2420
12	Z	0.28	0/1795	0.52	0/2420
13	M	0.28	0/1855	0.57	0/2514
13	a	0.28	0/1855	0.57	0/2514
14	N	0.26	0/1541	0.49	0/2087
14	b	0.27	0/1541	0.48	0/2087
All	All	0.27	0/50264	0.51	3/67962 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying

if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
12	L	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Y	4	LEU	CA-CB-CG	5.49	127.93	115.30
5	S	71	LEU	CA-CB-CG	5.21	127.29	115.30
5	E	71	LEU	CA-CB-CG	5.12	127.08	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	L	135	GLN	Peptide

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	8	0
1	O	1915	0	1929	9	0
2	B	1904	0	1904	14	0
2	P	1904	0	1904	19	0
3	C	1881	0	1895	15	0
3	Q	1881	0	1895	11	0
4	D	1813	0	1797	8	0
4	R	1813	0	1797	16	0
5	E	1773	0	1775	7	0
5	S	1773	0	1775	8	0
6	F	1892	0	1883	7	0
6	T	1892	0	1883	6	0
7	G	1907	0	1901	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	U	1907	0	1901	10	0
8	H	1719	0	1719	8	0
8	V	1719	0	1719	11	0
9	I	1581	0	1574	8	0
9	W	1581	0	1574	8	0
10	J	1561	0	1569	9	0
10	X	1561	0	1569	8	0
11	K	1644	0	1594	8	0
11	Y	1644	0	1594	7	0
12	L	1757	0	1711	11	0
12	Z	1757	0	1711	8	0
13	M	1824	0	1832	10	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	11	0
14	b	1512	0	1481	0	0
15	G	1	0	0	0	0
15	I	2	0	0	0	0
15	J	1	0	0	0	0
15	K	2	0	0	0	0
15	N	2	0	0	0	0
15	V	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	1	0	0	0	0
16	K	45	0	51	1	0
16	Y	45	0	51	0	0
17	A	121	0	0	0	0
17	B	84	0	0	0	0
17	C	88	0	0	0	0
17	D	82	0	0	0	0
17	E	44	0	0	0	0
17	F	93	0	0	0	0
17	G	117	0	0	0	0
17	H	110	0	0	1	0
17	I	106	0	0	0	0
17	J	101	0	0	1	0
17	K	119	0	0	0	0
17	L	118	0	0	1	0
17	M	141	0	0	1	0
17	N	108	0	0	0	0
17	O	79	0	0	0	0
17	P	73	0	0	0	0
17	Q	61	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	R	74	0	0	0	0
17	S	38	0	0	0	0
17	T	82	0	0	0	0
17	U	109	0	0	0	0
17	V	89	0	0	1	0
17	W	104	0	0	0	0
17	X	92	0	0	0	0
17	Y	114	0	0	0	0
17	Z	126	0	0	0	0
17	a	137	0	0	0	0
17	b	96	0	0	0	0
All	All	52173	0	49230	230	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 (230) 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)
4:D:99:ILE:HD11	4:D:104:LEU:HB2	1.54	0.89
11:Y:53:GLN:O	11:Y:57:THR:HG23	1.81	0.80
4:R:91:HIS:HB3	4:R:99:ILE:HG22	1.71	0.73
5:E:12:PHE:H	6:F:19:GLN:HE22	1.34	0.73
3:Q:51:LYS:O	3:Q:52:LEU:HB2	1.87	0.72
11:K:53:GLN:O	11:K:57:THR:HG23	1.89	0.72
3:C:201:VAL:HG13	3:C:202:GLN:H	1.54	0.71
5:S:12:PHE:H	6:T:19:GLN:HE22	1.40	0.70
4:R:91:HIS:CB	4:R:99:ILE:HG22	2.23	0.68
4:R:91:HIS:CG	4:R:99:ILE:HG22	2.29	0.68
10:J:23:ARG:NH1	11:K:116:ASP:OD1	2.27	0.67
10:J:3:ILE:HD12	10:J:168:LEU:HD13	1.77	0.67
14:N:35:THR:HG21	14:N:45:ARG:HE	1.59	0.67
2:P:12:PHE:H	3:Q:17:GLN:HE22	1.41	0.67
10:X:1:MET:HB2	10:X:34:LYS:HE3	1.79	0.65
2:B:12:PHE:H	3:C:17:GLN:HE22	1.44	0.64
9:I:26:LEU:HD21	9:I:185:VAL:HG23	1.79	0.63
3:Q:160:GLN:HA	3:Q:160:GLN:HE21	1.63	0.63
2:B:93:HIS:HB3	2:B:113:ARG:HH21	1.64	0.62
11:K:73:ARG:NH2	11:K:104:TYR:O	2.33	0.61
2:P:93:HIS:HB3	2:P:113:ARG:HH21	1.65	0.60
11:K:38:ASN:HB2	11:K:39:PRO:HD2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Z:172:LEU:H	12:Z:172:LEU:HD23	1.66	0.59
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.68	0.58
9:W:98:ARG:HA	9:W:126:ILE:HD11	1.84	0.58
8:H:3:ILE:HG21	8:H:44:ALA:HB3	1.86	0.58
3:C:9:PHE:H	4:D:15:GLN:HE22	1.52	0.58
11:K:35:ILE:HG22	11:K:45:MET:HE3	1.85	0.58
11:K:35:ILE:HG22	11:K:45:MET:CE	2.34	0.58
9:I:26:LEU:HD21	9:I:185:VAL:CG2	2.34	0.57
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.85	0.57
4:R:66:ILE:HD12	4:R:99:ILE:HD11	1.87	0.56
2:B:93:HIS:HB3	2:B:113:ARG:NH2	2.20	0.56
12:L:31:THR:HG22	12:L:36:ASN:HD21	1.70	0.56
6:F:123:ASN:C	6:F:123:ASN:HD22	2.09	0.56
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.88	0.56
5:E:9:THR:HG21	5:E:119:THR:HA	1.86	0.56
3:C:201:VAL:HG13	3:C:202:GLN:N	2.20	0.56
10:J:23:ARG:HH21	10:J:50:ALA:CB	2.19	0.55
12:L:31:THR:CG2	12:L:36:ASN:HD21	2.19	0.55
12:Z:195:HIS:HD2	12:Z:197:GLN:H	1.54	0.55
2:B:47:ALA:HB1	2:B:64:LYS:HD2	1.87	0.55
14:N:35:THR:CG2	14:N:45:ARG:HE	2.19	0.55
3:C:51:LYS:O	3:C:52:LEU:HB2	2.06	0.55
3:C:201:VAL:O	3:C:202:GLN:HB2	2.07	0.55
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.35	0.54
4:R:185:LEU:O	4:R:189:GLU:HG3	2.08	0.53
7:U:23:PHE:O	7:U:26:THR:HB	2.08	0.53
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.74	0.53
10:X:25:ILE:HG12	10:X:25:ILE:O	2.07	0.53
2:B:95:GLN:HE22	9:I:71:ASN:HD22	1.56	0.53
12:Z:13:LEU:HD11	12:Z:150:LEU:HD21	1.90	0.53
8:V:225:GLU:O	8:V:226:GLU:HB2	2.08	0.53
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.90	0.53
7:U:26:THR:HG21	7:U:131:ILE:HD12	1.92	0.52
13:M:161:ARG:HH11	13:M:161:ARG:HG3	1.74	0.52
3:Q:160:GLN:HE22	3:Q:170:ARG:HE	1.57	0.52
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.91	0.52
1:O:122:THR:CG2	2:P:128:ARG:HH21	2.23	0.52
11:Y:45:MET:HG2	11:Y:52:CYS:HB3	1.92	0.51
9:W:101:PRO:HB3	9:W:126:ILE:CD1	2.41	0.51
13:M:2:GLN:NE2	17:M:422:HOH:O	2.44	0.51
14:N:35:THR:HG21	14:N:45:ARG:NE	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:227:LYS:HD3	2:P:229:PHE:CE1	2.46	0.51
1:O:12:PHE:H	2:P:20:GLN:HE22	1.58	0.51
5:S:68:HIS:HE1	5:S:102:LEU:O	1.94	0.51
7:U:34:LEU:C	7:U:34:LEU:HD23	2.31	0.51
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.40	0.51
7:U:63:ILE:HD12	7:U:215:GLU:HB3	1.93	0.51
13:M:48:ASN:H	13:M:48:ASN:HD22	1.59	0.50
13:M:27:LEU:HD21	13:M:34:LEU:HD22	1.93	0.50
11:Y:38:ASN:HB2	11:Y:39:PRO:HD2	1.93	0.50
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.60	0.50
9:I:101:PRO:HB3	9:I:126:ILE:HD12	1.93	0.50
14:N:176:VAL:HG12	14:N:178:LEU:HD13	1.94	0.49
3:C:35:LYS:HG2	3:C:158:SER:O	2.12	0.49
2:P:95:GLN:HE22	9:W:71:ASN:HD22	1.60	0.49
2:P:216:ARG:HB3	2:P:218:GLY:H	1.76	0.49
14:N:20:THR:CG2	14:N:31:THR:OG1	2.60	0.49
6:T:172:LEU:HD13	6:T:195:ILE:HD13	1.94	0.49
7:G:83:ASN:C	7:G:83:ASN:HD22	2.16	0.49
10:J:23:ARG:NH2	10:J:50:ALA:CB	2.75	0.49
4:R:1:ASP:O	4:R:2:ARG:HB2	2.12	0.48
10:J:1:MET:HB2	10:J:34:LYS:HE3	1.94	0.48
7:G:30:ASN:HD22	7:G:164:PRO:HG2	1.77	0.48
11:Y:176:ASN:ND2	11:Y:187:TYR:OH	2.46	0.48
2:B:35:ILE:HD12	2:B:196:LEU:HG	1.95	0.48
8:H:87:LEU:HD12	8:H:113:ILE:HD11	1.95	0.48
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.44	0.48
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.94	0.48
10:X:149:ARG:O	10:X:152:MET:HG3	2.13	0.48
8:V:3:ILE:HG21	8:V:44:ALA:HB3	1.95	0.48
5:E:71:LEU:HD23	5:E:71:LEU:C	2.34	0.48
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.96	0.48
3:C:149:GLU:HB2	3:C:150:PRO:HD2	1.96	0.48
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.48	0.48
12:L:23:LEU:HD13	12:L:43:VAL:HG13	1.94	0.48
2:P:93:HIS:HB3	2:P:113:ARG:NH2	2.28	0.48
2:P:204:ALA:O	2:P:209:ARG:NH2	2.43	0.48
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	1.96	0.48
7:G:68:ARG:O	7:G:223:LYS:HA	2.14	0.48
12:L:195:HIS:HD2	12:L:197:GLN:H	1.62	0.47
7:U:167:GLN:HE21	7:U:171:THR:HG23	1.79	0.47
3:Q:27:ARG:HB2	3:Q:27:ARG:HH11	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:127:LEU:HG	13:M:142:LEU:HD12	1.97	0.47
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.49	0.47
8:V:113:ILE:HB	8:V:119:THR:HG22	1.96	0.47
12:L:165:ASN:HD21	8:V:212:VAL:H	1.62	0.47
14:N:13:ILE:HG21	14:N:175:MET:CE	2.45	0.47
8:V:104:ASP:HB2	8:V:105:PRO:CD	2.45	0.46
5:E:10:VAL:O	5:E:10:VAL:HG13	2.15	0.46
2:B:124:HIS:HB3	3:C:124:VAL:HG12	1.98	0.46
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.51	0.46
6:T:163:LYS:HE2	6:T:203:ASN:ND2	2.29	0.46
9:W:98:ARG:HD2	9:W:126:ILE:HG12	1.97	0.46
2:P:15:GLU:O	3:Q:27:ARG:NH1	2.48	0.46
5:E:206:THR:OG1	5:E:209:ASN:HB2	2.15	0.46
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.45	0.46
10:J:25:ILE:O	10:J:25:ILE:HG12	2.15	0.46
6:F:172:LEU:HD13	6:F:195:ILE:HD13	1.97	0.46
4:D:77:ALA:O	4:D:81:ILE:HG12	2.15	0.46
16:K:301:3E5:H44	16:K:301:3E5:O1	2.14	0.46
5:S:9:THR:HG21	5:S:119:THR:HA	1.98	0.46
8:H:104:ASP:HB2	8:H:105:PRO:CD	2.45	0.46
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.97	0.45
6:T:123:ASN:HD22	6:T:123:ASN:C	2.20	0.45
1:A:149:GLN:O	1:A:156:TYR:HA	2.17	0.45
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.52	0.45
1:A:83:ARG:HE	7:G:114:ASN:HD21	1.64	0.45
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	1.97	0.45
1:A:83:ARG:HE	7:G:114:ASN:ND2	2.14	0.45
7:G:34:LEU:HD23	7:G:34:LEU:C	2.37	0.45
4:D:60:VAL:HG11	4:D:81:ILE:HG21	1.99	0.45
12:L:8:ASN:HA	12:L:30:ILE:O	2.17	0.45
4:R:32:ILE:HD12	4:R:192:VAL:HG23	1.98	0.45
1:A:176:GLU:HG3	2:B:55:LEU:HD22	1.99	0.45
6:T:240:GLN:HA	6:T:240:GLN:HE21	1.81	0.45
3:C:46:ARG:HH12	3:C:206:LYS:HB3	1.82	0.45
2:P:151:ASN:HB2	2:P:152:PRO:HD2	1.98	0.45
6:F:123:ASN:HD22	6:F:124:SER:N	2.15	0.44
14:N:20:THR:HG23	14:N:28:ASN:HB3	1.99	0.44
2:B:151:ASN:HB2	2:B:152:PRO:HD2	1.98	0.44
7:G:73:VAL:HG12	7:G:133:THR:HB	1.98	0.44
14:N:55:ILE:HD11	14:N:93:LEU:HD13	1.99	0.44
4:R:51:LEU:C	4:R:51:LEU:HD12	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:3:ARG:NH1	5:S:122:TYR:OH	2.51	0.44
1:O:115:ALA:HB1	1:O:154:GLY:O	2.18	0.44
9:I:35:VAL:HG13	17:J:308:HOH:O	2.17	0.43
3:C:108:THR:HG21	3:C:146:TYR:HB3	1.99	0.43
4:R:99:ILE:HG13	4:R:104:LEU:HB2	1.99	0.43
6:F:228:LYS:H	6:F:228:LYS:HD3	1.81	0.43
1:O:176:GLU:HG3	2:P:55:LEU:HD22	1.99	0.43
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.53	0.43
3:C:198:LEU:HA	3:C:201:VAL:HG12	2.00	0.43
9:W:123:PHE:HA	9:W:128:CYS:O	2.18	0.43
10:X:1:MET:N	10:X:1:MET:SD	2.86	0.43
6:F:198:LEU:HD13	6:F:243:ILE:HG22	2.00	0.43
8:H:225:GLU:O	8:H:226:GLU:HB2	2.18	0.43
1:A:12:PHE:H	2:B:20:GLN:HE22	1.67	0.43
5:S:49:LYS:HB3	5:S:58:TYR:HB3	2.01	0.43
7:U:187:GLU:HG2	7:U:192:LYS:HB2	2.01	0.42
10:J:49:GLU:HB2	10:J:99:GLN:HB3	2.00	0.42
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.48	0.42
5:E:118:ASN:N	5:E:118:ASN:HD22	2.17	0.42
11:K:4:LEU:HD13	11:K:161:ILE:HD11	2.01	0.42
7:U:83:ASN:C	7:U:83:ASN:HD22	2.22	0.42
8:V:3:ILE:HG22	8:V:99:ILE:HD12	2.01	0.42
3:Q:201:VAL:HG22	3:Q:201:VAL:O	2.19	0.42
6:F:240:GLN:HA	6:F:240:GLN:HE21	1.85	0.42
2:B:219:ALA:HB3	2:B:223:GLU:HG3	2.02	0.42
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.01	0.42
8:V:87:LEU:HD12	8:V:113:ILE:HD11	2.00	0.42
4:D:30:ILE:HD12	4:D:196:LEU:HG	2.01	0.42
2:P:50:LYS:HA	2:P:50:LYS:HE3	2.02	0.42
10:X:1:MET:CB	10:X:34:LYS:HE3	2.47	0.41
3:C:160:GLN:HE22	3:C:170:ARG:HE	1.68	0.41
13:M:43:ILE:HG12	13:M:43:ILE:O	2.20	0.41
12:Z:23:LEU:HD13	12:Z:43:VAL:HG13	2.01	0.41
7:G:78:ILE:N	7:G:79:PRO:CD	2.83	0.41
2:P:50:LYS:O	2:P:51:VAL:C	2.58	0.41
11:K:145:LYS:HB2	11:K:148:LEU:HD13	2.03	0.41
2:B:47:ALA:HB1	2:B:64:LYS:CD	2.51	0.41
12:Z:43:VAL:HG12	12:Z:205:LEU:HD22	2.02	0.41
11:Y:37:ILE:HG23	11:Y:60:GLY:HA2	2.02	0.41
9:W:20:VAL:HG23	9:W:189:ILE:HB	2.01	0.41
8:H:84:LYS:HG3	8:H:85:GLN:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:17:ASP:OD1	13:M:18:ASN:N	2.54	0.41
10:X:1:MET:HB2	10:X:34:LYS:CE	2.48	0.41
8:V:99:ILE:HG13	8:V:127:LEU:HD22	2.02	0.41
12:L:13:LEU:HD11	12:L:150:LEU:HD21	2.01	0.41
6:T:123:ASN:HD22	6:T:124:SER:N	2.18	0.41
10:J:139:TYR:CZ	11:Y:134:THR:HG22	2.56	0.41
8:H:172:ASN:ND2	17:H:401:HOH:O	2.54	0.41
9:W:26:LEU:HD21	9:W:185:VAL:HG23	2.03	0.41
8:H:98:LEU:HB2	8:H:113:ILE:HG23	2.02	0.41
12:L:146:ILE:HG22	12:L:150:LEU:HD22	2.01	0.41
12:L:135:GLN:NE2	17:L:392:HOH:O	2.52	0.41
1:O:149:GLN:O	1:O:156:TYR:HA	2.21	0.41
3:C:201:VAL:CG1	3:C:202:GLN:H	2.29	0.41
7:G:83:ASN:ND2	7:G:83:ASN:C	2.74	0.41
5:S:77:ALA:N	5:S:78:PRO:CD	2.84	0.41
1:O:83:ARG:HE	7:U:114:ASN:ND2	2.19	0.41
7:U:68:ARG:O	7:U:223:LYS:HA	2.21	0.41
8:V:35:HIS:HB3	8:V:56:THR:HG21	2.03	0.41
9:I:123:PHE:HA	9:I:128:CYS:O	2.20	0.41
4:R:204:LEU:HD23	4:R:205:ASP:N	2.36	0.41
1:A:1:MET:CG	1:A:2:THR:N	2.84	0.41
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.20	0.41
4:D:178:GLU:HB3	4:D:191:LEU:HD21	2.03	0.41
2:P:155:ASN:ND2	3:Q:77:ASN:HB2	2.35	0.41
13:M:96:LEU:O	13:M:100:MET:HG2	2.21	0.41
1:O:119:GLN:O	1:O:122:THR:HB	2.21	0.40
8:H:114:HIS:CD2	8:H:116:HIS:H	2.39	0.40
13:M:179:ASN:HD22	13:M:182:ARG:HH11	1.69	0.40
4:R:77:ALA:O	4:R:81:ILE:HG12	2.21	0.40
10:X:126:VAL:HG13	10:X:128:LEU:HG	2.03	0.40
9:I:20:VAL:HG23	9:I:189:ILE:HB	2.03	0.40
1:A:122:THR:CG2	2:B:128:ARG:HH21	2.35	0.40
8:V:3:ILE:CG2	8:V:44:ALA:HB3	2.51	0.40
12:L:136:CYS:SG	12:L:150:LEU:HB3	2.61	0.40
4:R:138:GLY:HA2	4:R:214:ILE:HG12	2.04	0.40
3:Q:149:GLU:HB2	3:Q:150:PRO:HD2	2.02	0.40
1:O:98:LYS:HE3	1:O:104:TYR:CZ	2.56	0.40
8:V:172:ASN:ND2	17:V:421:HOH:O	2.53	0.40
14:N:7:THR:HG23	14:N:110:VAL:HG23	2.02	0.40
13:M:159:VAL:O	13:M:159:VAL:CG2	2.68	0.40
1:A:94:HIS:HA	1:A:98:LYS:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:152:VAL:HA	14:N:175:MET:HE1	2.02	0.40
7:U:187:GLU:HG2	7:U:192:LYS:CB	2.51	0.40
7:G:37:ARG:NH2	7:G:183:ASP:HB3	2.36	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	248/250 (99%)	241 (97%)	6 (2%)	1 (0%)	39	61
1	O	248/250 (99%)	239 (96%)	7 (3%)	2 (1%)	24	41
2	B	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	11	19
2	P	242/258 (94%)	231 (96%)	9 (4%)	2 (1%)	24	41
3	C	238/254 (94%)	231 (97%)	4 (2%)	3 (1%)	15	26
3	Q	238/254 (94%)	232 (98%)	2 (1%)	4 (2%)	11	19
4	D	231/260 (89%)	230 (100%)	1 (0%)	0	100	100
4	R	231/260 (89%)	226 (98%)	4 (2%)	1 (0%)	39	61
5	E	229/234 (98%)	221 (96%)	7 (3%)	1 (0%)	39	61
5	S	229/234 (98%)	219 (96%)	10 (4%)	0	100	100
6	F	241/288 (84%)	235 (98%)	5 (2%)	1 (0%)	39	61
6	T	241/288 (84%)	235 (98%)	5 (2%)	1 (0%)	39	61
7	G	239/252 (95%)	236 (99%)	3 (1%)	0	100	100
7	U	239/252 (95%)	238 (100%)	1 (0%)	0	100	100
8	H	224/232 (97%)	217 (97%)	7 (3%)	0	100	100
8	V	224/232 (97%)	217 (97%)	7 (3%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	W	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
10	J	193/198 (98%)	188 (97%)	5 (3%)	0	100	100
10	X	193/198 (98%)	186 (96%)	7 (4%)	0	100	100
11	K	210/212 (99%)	204 (97%)	5 (2%)	1 (0%)	34	55
11	Y	210/212 (99%)	203 (97%)	6 (3%)	1 (0%)	34	55
12	L	220/222 (99%)	214 (97%)	5 (2%)	1 (0%)	34	55
12	Z	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
13	M	231/246 (94%)	222 (96%)	9 (4%)	0	100	100
13	a	231/246 (94%)	223 (96%)	7 (3%)	1 (0%)	39	61
14	N	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
14	b	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
All	All	6284/6614 (95%)	6108 (97%)	152 (2%)	24 (0%)	39	61

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR
2	B	51	VAL
3	C	202	GLN
12	L	165	ASN
1	O	2	THR
2	P	51	VAL
2	B	218	GLY
2	B	219	ALA
2	B	221	ASP
3	C	201	VAL
2	P	183	MET
4	R	2	ARG
5	E	231	LYS
6	F	205	GLU
3	Q	52	LEU
3	Q	205	ALA
11	Y	39	PRO
3	C	205	ALA
1	O	3	ASP
3	Q	183	PRO
6	T	180	PRO
11	K	39	PRO

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Mol	Chain	Res	Type
3	Q	202	GLN
13	a	229	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	A	209/209 (100%)	203 (97%)	6 (3%)	50	77
1	O	209/209 (100%)	204 (98%)	5 (2%)	57	82
2	B	203/216 (94%)	191 (94%)	12 (6%)	24	44
2	P	203/216 (94%)	194 (96%)	9 (4%)	35	60
3	C	212/226 (94%)	195 (92%)	17 (8%)	15	28
3	Q	212/226 (94%)	200 (94%)	12 (6%)	25	46
4	D	194/215 (90%)	182 (94%)	12 (6%)	23	41
4	R	194/215 (90%)	180 (93%)	14 (7%)	18	33
5	E	190/193 (98%)	172 (90%)	18 (10%)	11	20
5	S	190/193 (98%)	173 (91%)	17 (9%)	12	23
6	F	201/239 (84%)	187 (93%)	14 (7%)	19	34
6	T	201/239 (84%)	183 (91%)	18 (9%)	12	22
7	G	206/210 (98%)	198 (96%)	8 (4%)	39	66
7	U	206/210 (98%)	194 (94%)	12 (6%)	25	45
8	H	185/190 (97%)	177 (96%)	8 (4%)	35	61
8	V	185/190 (97%)	179 (97%)	6 (3%)	46	74
9	I	172/173 (99%)	163 (95%)	9 (5%)	29	51
9	W	172/173 (99%)	165 (96%)	7 (4%)	37	63
10	J	173/175 (99%)	165 (95%)	8 (5%)	33	57
10	X	173/175 (99%)	164 (95%)	9 (5%)	29	51
11	K	169/169 (100%)	161 (95%)	8 (5%)	32	56
11	Y	169/169 (100%)	163 (96%)	6 (4%)	42	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	L	185/185 (100%)	177 (96%)	8 (4%)	35	61
12	Z	185/185 (100%)	174 (94%)	11 (6%)	24	44
13	M	199/208 (96%)	189 (95%)	10 (5%)	30	53
13	a	199/208 (96%)	189 (95%)	10 (5%)	30	53
14	N	162/162 (100%)	155 (96%)	7 (4%)	35	61
14	b	162/162 (100%)	152 (94%)	10 (6%)	23	41
All	All	5320/5540 (96%)	5029 (94%)	291 (6%)	27	48

All (291) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	GLU
1	A	61	LEU
1	A	62	SER
1	A	122	THR
1	A	157	PHE
1	A	250	LEU
2	B	40	SER
2	B	50	LYS
2	B	55	LEU
2	B	63	GLU
2	B	102	ASN
2	B	119	GLN
2	B	169	SER
2	B	180	LYS
2	B	184	LYS
2	B	191	LEU
2	B	217	LYS
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	51	LYS
3	C	53	GLN
3	C	55	THR
3	C	61	LYS
3	C	116	GLN
3	C	147	GLN
3	C	160	GLN
3	C	167	LYS
3	C	169	VAL

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Mol	Chain	Res	Type
3	C	171	GLU
3	C	175	LYS
3	C	180	LYS
3	C	213	VAL
3	C	239	GLN
3	C	240	GLU
4	D	40	LEU
4	D	51	LEU
4	D	68	CYS
4	D	99	ILE
4	D	125	LEU
4	D	152	PRO
4	D	182	SER
4	D	193	LEU
4	D	202	GLU
4	D	214	ILE
4	D	235	LEU
4	D	236	LYS
5	E	4	ASN
5	E	8	ASP
5	E	9	THR
5	E	10	VAL
5	E	29	LYS
5	E	54	GLU
5	E	55	LEU
5	E	71	LEU
5	E	99	ASN
5	E	106	ARG
5	E	116	GLN
5	E	144	LEU
5	E	180	LYS
5	E	184	ASN
5	E	186	ASP
5	E	188	LEU
5	E	207	VAL
5	E	208	ASP
6	F	94	SER
6	F	117	GLN
6	F	123	ASN
6	F	139	LYS
6	F	172	LEU
6	F	181	GLU

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Mol	Chain	Res	Type
6	F	198	LEU
6	F	201	GLU
6	F	203	ASN
6	F	214	TRP
6	F	221	ASN
6	F	228	LYS
6	F	240	GLN
6	F	241	LYS
7	G	26	THR
7	G	83	ASN
7	G	115	LEU
7	G	117	GLN
7	G	125	MET
7	G	166	GLN
7	G	235	ARG
7	G	236	LEU
8	H	13	VAL
8	H	30	ASN
8	H	34	LEU
8	H	55	VAL
8	H	68	LEU
8	H	91	GLN
8	H	113	ILE
8	H	127	LEU
9	I	20	VAL
9	I	31	GLN
9	I	37	ASN
9	I	126	ILE
9	I	131	GLU
9	I	171	LEU
9	I	182	TRP
9	I	191	LYS
9	I	193	GLU
10	J	1	MET
10	J	3	ILE
10	J	7	ILE
10	J	23	ARG
10	J	35	THR
10	J	90	LYS
10	J	99	GLN
10	J	163	LEU
11	K	4	LEU

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Mol	Chain	Res	Type
11	K	9	GLN
11	K	35	ILE
11	K	57	THR
11	K	104	TYR
11	K	107	LYS
11	K	118	ASP
11	K	148	LEU
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
12	L	108	HIS
12	L	135	GLN
12	L	150	LEU
12	L	165	ASN
12	L	172	LEU
13	M	43	ILE
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	129	TYR
13	M	159	VAL
13	M	161	ARG
13	M	187	ARG
13	M	212	LEU
13	M	215	GLU
14	N	9	LYS
14	N	20	THR
14	N	35	THR
14	N	36	ARG
14	N	39	ASP
14	N	144	GLU
14	N	178	LEU
1	O	61	LEU
1	O	122	THR
1	O	157	PHE
1	O	166	LYS
1	O	250	LEU
2	P	50	LYS
2	P	55	LEU
2	P	58	GLN
2	P	79	LEU
2	P	119	GLN

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Mol	Chain	Res	Type
2	P	180	LYS
2	P	184	LYS
2	P	191	LEU
2	P	240	LYS
3	Q	4	ARG
3	Q	38	ASN
3	Q	52	LEU
3	Q	61	LYS
3	Q	116	GLN
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	213	VAL
3	Q	222	LEU
3	Q	240	GLU
4	R	5	SER
4	R	20	LEU
4	R	40	LEU
4	R	51	LEU
4	R	68	CYS
4	R	99	ILE
4	R	125	LEU
4	R	176	LEU
4	R	190	LEU
4	R	193	LEU
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU
5	S	4	ASN
5	S	8	ASP
5	S	9	THR
5	S	25	LEU
5	S	29	LYS
5	S	55	LEU
5	S	71	LEU
5	S	99	ASN
5	S	106	ARG
5	S	116	GLN
5	S	121	SER
5	S	155	LEU

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Mol	Chain	Res	Type
5	S	184	ASN
5	S	186	ASP
5	S	188	LEU
5	S	208	ASP
5	S	231	LYS
6	T	29	ASN
6	T	117	GLN
6	T	123	ASN
6	T	126	ARG
6	T	139	LYS
6	T	148	GLU
6	T	163	LYS
6	T	165	ARG
6	T	171	GLU
6	T	172	LEU
6	T	175	LEU
6	T	181	GLU
6	T	198	LEU
6	T	202	ASP
6	T	203	ASN
6	T	214	TRP
6	T	215	CYS
6	T	221	ASN
7	U	26	THR
7	U	34	LEU
7	U	68	ARG
7	U	83	ASN
7	U	115	LEU
7	U	117	GLN
7	U	122	ARG
7	U	125	MET
7	U	154	TYR
7	U	230	GLU
7	U	235	ARG
7	U	236	LEU
8	V	13	VAL
8	V	30	ASN
8	V	55	VAL
8	V	68	LEU
8	V	113	ILE
8	V	127	LEU
9	W	20	VAL

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Mol	Chain	Res	Type
9	W	30	SER
9	W	31	GLN
9	W	37	ASN
9	W	171	LEU
9	W	182	TRP
9	W	192	ASP
10	X	3	ILE
10	X	35	THR
10	X	36	ARG
10	X	49	GLU
10	X	90	LYS
10	X	99	GLN
10	X	126	VAL
10	X	163	LEU
10	X	193	ASP
11	Y	4	LEU
11	Y	9	GLN
11	Y	35	ILE
11	Y	57	THR
11	Y	104	TYR
11	Y	148	LEU
12	Z	3	ASN
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	66	LYS
12	Z	108	HIS
12	Z	136	CYS
12	Z	150	LEU
12	Z	165	ASN
12	Z	172	LEU
12	Z	173	LYS
13	a	2	GLN
13	a	43	ILE
13	a	48	ASN
13	a	68	LYS
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
13	a	206	LEU
13	a	212	LEU

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Mol	Chain	Res	Type
14	b	9	LYS
14	b	20	THR
14	b	35	THR
14	b	36	ARG
14	b	39	ASP
14	b	83	LYS
14	b	105	LYS
14	b	107	LYS
14	b	144	GLU
14	b	178	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (140) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	20	GLN
2	B	58	GLN
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
2	B	155	ASN
2	B	176	GLN
3	C	17	GLN
3	C	38	ASN
3	C	53	GLN
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	100	ASN
4	D	225	ASN
5	E	68	HIS
5	E	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN

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Mol	Chain	Res	Type
6	F	123	ASN
6	F	191	GLN
6	F	240	GLN
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	167	GLN
7	G	175	ASN
7	G	186	ASN
8	H	30	ASN
8	H	66	HIS
8	H	114	HIS
8	H	116	HIS
8	H	165	ASN
8	H	172	ASN
8	H	189	ASN
10	J	55	GLN
10	J	118	GLN
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
12	L	3	ASN
12	L	49	ASN
12	L	70	ASN
12	L	135	GLN
12	L	159	GLN
12	L	165	ASN
12	L	195	HIS
13	M	2	GLN
13	M	18	ASN
13	M	48	ASN
13	M	108	ASN
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
14	N	161	GLN
1	O	94	HIS
2	P	20	GLN
2	P	58	GLN
2	P	95	GLN

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Mol	Chain	Res	Type
2	P	119	GLN
2	P	123	GLN
2	P	155	ASN
2	P	176	GLN
3	Q	17	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	146	GLN
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN
5	S	151	ASN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	191	GLN
6	T	203	ASN
6	T	240	GLN
7	U	6	HIS
7	U	30	ASN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	167	GLN
7	U	175	ASN
7	U	186	ASN
8	V	30	ASN

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Mol	Chain	Res	Type
8	V	66	HIS
8	V	114	HIS
8	V	116	HIS
8	V	165	ASN
8	V	172	ASN
8	V	189	ASN
10	X	37	GLN
10	X	55	GLN
10	X	86	GLN
10	X	118	GLN
10	X	191	GLN
11	Y	85	ASN
11	Y	176	ASN
11	Y	190	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	79	HIS
12	Z	80	ASN
12	Z	158	ASN
12	Z	165	ASN
12	Z	195	HIS
13	a	48	ASN
13	a	102	GLN
13	a	108	ASN
13	a	179	ASN
14	b	38	HIS
14	b	161	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 13 ligands modelled in this entry, 11 are monoatomic - leaving 2 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$
16	3E5	K	301	11	46,46,46	1.28	3 (6%)	61,62,62	1.11	5 (8%)
16	3E5	Y	301	11	46,46,46	1.28	3 (6%)	61,62,62	1.23	6 (9%)

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
16	3E5	K	301	11	-	0/49/49/49	0/2/2/2
16	3E5	Y	301	11	-	0/49/49/49	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	Y	301	3E5	C14-N2	-2.72	1.36	1.41
16	K	301	3E5	C14-N2	-2.30	1.37	1.41
16	Y	301	3E5	C14-C15	5.24	1.50	1.40
16	Y	301	3E5	O4-C27	5.35	1.46	1.35
16	K	301	3E5	O4-C27	5.40	1.46	1.35
16	K	301	3E5	C14-C15	5.48	1.50	1.40

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Y	301	3E5	C12-C13-N2	-3.88	111.94	115.43
16	Y	301	3E5	O4-C27-O5	-3.36	117.32	124.22
16	K	301	3E5	C21-C14-C15	-3.22	116.99	120.67
16	K	301	3E5	O4-C27-O5	-2.79	118.49	124.22
16	Y	301	3E5	C21-C14-C15	-2.59	117.71	120.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	K	301	3E5	O2-C12-C13	-2.06	105.67	110.47
16	K	301	3E5	C23-C22-N3	2.18	115.92	110.49
16	Y	301	3E5	C28-O4-C27	2.80	122.57	115.91
16	Y	301	3E5	C8-C7-C12	2.81	117.40	111.71
16	K	301	3E5	O4-C27-N3	3.36	117.99	110.54
16	Y	301	3E5	O4-C27-N3	3.68	118.71	110.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	K	301	3E5	1	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 ⓘ

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	250/250 (100%)	-0.41	7 (2%) 56 61	33, 45, 74, 117	0
1	O	250/250 (100%)	-0.30	7 (2%) 56 61	36, 51, 88, 125	0
2	B	244/258 (94%)	-0.28	8 (3%) 50 55	33, 50, 90, 144	0
2	P	244/258 (94%)	-0.23	13 (5%) 30 34	37, 53, 102, 153	0
3	C	240/254 (94%)	-0.08	16 (6%) 21 23	34, 55, 115, 143	0
3	Q	240/254 (94%)	0.16	24 (10%) 9 10	38, 64, 132, 161	0
4	D	235/260 (90%)	-0.42	5 (2%) 67 71	36, 54, 82, 120	0
4	R	235/260 (90%)	-0.32	6 (2%) 59 63	36, 56, 85, 136	0
5	E	231/234 (98%)	-0.26	8 (3%) 48 53	39, 57, 86, 120	0
5	S	231/234 (98%)	-0.24	5 (2%) 65 69	40, 57, 87, 120	0
6	F	243/288 (84%)	-0.38	11 (4%) 37 42	33, 49, 90, 131	0
6	T	243/288 (84%)	-0.31	10 (4%) 41 46	33, 51, 93, 124	0
7	G	241/252 (95%)	-0.46	7 (2%) 55 60	32, 46, 79, 122	0
7	U	241/252 (95%)	-0.43	5 (2%) 67 71	33, 47, 78, 106	0
8	H	226/232 (97%)	-0.34	8 (3%) 48 53	34, 44, 73, 133	0
8	V	226/232 (97%)	-0.32	8 (3%) 48 53	34, 47, 78, 159	0
9	I	204/205 (99%)	-0.55	1 (0%) 91 92	30, 45, 72, 100	0
9	W	204/205 (99%)	-0.51	3 (1%) 76 79	33, 47, 78, 106	0
10	J	195/198 (98%)	-0.46	3 (1%) 76 79	30, 45, 69, 137	0
10	X	195/198 (98%)	-0.48	2 (1%) 84 86	33, 46, 71, 125	0
11	K	212/212 (100%)	-0.42	2 (0%) 85 88	33, 46, 81, 97	0
11	Y	212/212 (100%)	-0.41	5 (2%) 62 66	33, 46, 83, 107	0
12	L	222/222 (100%)	-0.49	2 (0%) 85 88	32, 46, 75, 100	0
12	Z	222/222 (100%)	-0.48	4 (1%) 71 75	31, 45, 75, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
13	M	233/246 (94%)	-0.58	2 (0%) 85 88	29, 44, 63, 77	0
13	a	233/246 (94%)	-0.57	1 (0%) 93 93	29, 42, 61, 74	0
14	N	196/196 (100%)	-0.61	2 (1%) 84 86	31, 40, 66, 85	0
14	b	196/196 (100%)	-0.55	2 (1%) 84 86	30, 41, 65, 95	0
All	All	6344/6614 (95%)	-0.38	177 (2%) 56 61	29, 48, 86, 161	0

All (177) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	V	224	GLN	9.8
3	Q	49	THR	9.6
10	X	1	MET	9.3
3	Q	50	LEU	7.9
8	H	224	GLN	7.4
2	P	51	VAL	6.9
10	J	1	MET	6.3
3	C	240	GLU	5.5
9	W	1	SER	5.5
2	B	221	ASP	5.3
8	V	226	GLU	5.2
3	C	238	LYS	5.2
3	Q	239	GLN	5.1
10	J	194	ASP	5.1
8	V	222	ASP	5.1
10	X	194	ASP	5.1
2	P	219	ALA	5.0
3	C	206	LYS	4.9
8	H	226	GLU	4.8
3	Q	240	GLU	4.8
2	B	219	ALA	4.7
1	O	1	MET	4.7
5	S	202	ASP	4.6
3	Q	236	GLN	4.6
3	Q	202	GLN	4.4
2	P	221	ASP	4.4
9	I	1	SER	4.4
8	V	223	ILE	4.4
3	Q	48	SER	4.4
3	C	49	THR	4.3
3	Q	238	LYS	4.3
8	H	221	CYS	4.2

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Mol	Chain	Res	Type	RSRZ
8	V	221	CYS	4.1
1	O	249	ALA	4.1
3	C	239	GLN	4.1
1	A	249	ALA	4.0
8	V	225	GLU	4.0
1	A	250	LEU	4.0
7	G	242	GLN	3.9
2	B	51	VAL	3.8
8	H	222	ASP	3.8
2	P	222	GLY	3.8
6	T	244	ASN	3.7
4	D	242	GLU	3.7
6	F	205	GLU	3.7
4	R	242	GLU	3.6
6	F	178	HIS	3.6
3	Q	206	LYS	3.6
3	C	175	LYS	3.6
1	A	1	MET	3.6
2	B	222	GLY	3.6
3	C	50	LEU	3.6
5	E	202	ASP	3.5
6	T	243	ILE	3.5
2	P	240	LYS	3.5
3	Q	234	ILE	3.4
3	Q	204	GLY	3.4
2	B	218	GLY	3.4
2	P	220	ASN	3.4
3	Q	205	ALA	3.4
3	C	202	GLN	3.4
6	F	244	ASN	3.4
6	T	178	HIS	3.4
3	Q	203	THR	3.3
3	C	203	THR	3.3
6	F	243	ILE	3.2
2	P	218	GLY	3.2
7	U	242	GLN	3.2
3	C	236	GLN	3.2
2	P	52	THR	3.1
9	W	133	LYS	3.0
3	C	205	ALA	3.0
3	Q	225	GLU	3.0
3	Q	237	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	2	THR	3.0
3	Q	175	LYS	3.0
6	T	2	THR	3.0
9	W	192	ASP	3.0
2	P	59	ASP	2.9
11	K	212	GLY	2.9
6	T	215	CYS	2.9
3	Q	59	PRO	2.9
7	G	2	GLY	2.9
3	Q	47	ARG	2.9
6	F	202	ASP	2.9
1	O	2	THR	2.9
2	B	203	SER	2.9
3	C	180	LYS	2.9
1	O	201	GLU	2.8
5	E	203	GLU	2.8
2	B	220	ASN	2.8
7	U	51	PRO	2.8
3	C	204	GLY	2.8
11	Y	212	GLY	2.7
3	C	181	GLU	2.7
8	H	223	ILE	2.7
7	G	3	TYR	2.7
5	E	233	ILE	2.7
5	S	3	ASN	2.7
5	S	203	GLU	2.7
4	R	125	LEU	2.7
6	T	181	GLU	2.7
1	O	52	SER	2.6
6	F	215	CYS	2.6
6	F	203	ASN	2.6
7	G	51	PRO	2.6
11	Y	183	ASP	2.6
5	E	217	LYS	2.6
6	F	201	GLU	2.6
4	R	54	ASP	2.6
6	F	2	THR	2.6
13	a	1	THR	2.6
6	T	205	GLU	2.5
11	Y	104	TYR	2.5
14	b	195	GLN	2.5
4	D	241	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
7	G	240	ALA	2.5
3	C	216	ASP	2.5
6	T	202	ASP	2.5
11	Y	106	ARG	2.5
14	N	105	LYS	2.5
7	U	2	GLY	2.5
1	A	248	GLU	2.5
7	U	3	TYR	2.4
2	P	182	ASP	2.4
2	B	59	ASP	2.4
10	J	193	ASP	2.4
4	R	1	ASP	2.4
1	O	250	LEU	2.4
7	U	222	ASP	2.4
4	D	1	ASP	2.4
4	D	2	ARG	2.3
11	Y	182	GLU	2.3
12	Z	165	ASN	2.3
12	Z	1	GLN	2.3
6	T	241	LYS	2.3
12	Z	167	LYS	2.3
1	A	229	THR	2.3
2	P	60	THR	2.3
12	L	1	GLN	2.3
2	P	61	SER	2.3
8	H	22	GLN	2.3
4	R	2	ARG	2.3
3	Q	180	LYS	2.2
3	Q	221	ALA	2.2
4	R	47	THR	2.2
3	Q	181	GLU	2.2
13	M	82	ASP	2.2
6	F	181	GLU	2.2
1	A	54	PRO	2.2
3	Q	27	ARG	2.2
11	K	104	TYR	2.2
12	Z	210	ASP	2.2
3	C	225	GLU	2.1
7	G	241	GLU	2.1
8	H	219	ASN	2.1
8	V	219	ASN	2.1
14	b	105	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
2	P	203	SER	2.1
5	E	204	SER	2.1
5	S	173	ARG	2.1
5	E	54	GLU	2.1
12	L	172	LEU	2.1
3	Q	141	ASP	2.1
6	T	230	ASP	2.1
5	E	3	ASN	2.1
8	H	225	GLU	2.1
14	N	104	ASP	2.1
5	S	122	TYR	2.1
7	G	181	LYS	2.1
13	M	47	ASP	2.1
1	O	231	LYS	2.0
3	Q	223	SER	2.0
8	V	198	GLU	2.0
6	F	241	LYS	2.0
4	D	125	LEU	2.0
5	E	122	TYR	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(Å <sup>2</sup> )	Q<0.9
15	MG	I	302	1/1	0.90	0.33	10.27	82,82,82,82	0
15	MG	K	303	1/1	0.95	0.29	5.81	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
15	MG	J	201	1/1	0.96	0.20	4.52	61,61,61,61	0
16	3E5	Y	301	45/45	0.86	0.23	3.64	58,72,101,106	0
16	3E5	K	301	45/45	0.86	0.23	3.08	52,69,89,95	0
15	MG	V	301	1/1	0.98	0.09	-1.03	42,42,42,42	0
15	MG	K	302	1/1	0.99	0.09	-1.15	47,47,47,47	0
15	MG	G	301	1/1	0.99	0.04	-1.41	40,40,40,40	0
15	MG	N	201	1/1	0.99	0.07	-1.90	48,48,48,48	0
15	MG	Y	302	1/1	0.99	0.05	-2.46	42,42,42,42	0
15	MG	I	301	1/1	0.98	0.05	-2.99	54,54,54,54	0
15	MG	Z	301	1/1	0.97	0.05	-3.55	54,54,54,54	0
15	MG	N	202	1/1	0.89	0.36	-	82,82,82,82	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.