



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:03 AM GMT

PDB ID : 1Z7Q
Title : Crystal structure of the 20s proteasome from yeast in complex with the proteasome activator PA26 from Trypanosome brucei at 3.2 angstroms resolution
Authors : Forster, A.; Whitby, F.G.; Hill, C.P.
Deposited on : 2005-03-26
Resolution : 3.22 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
<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 (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

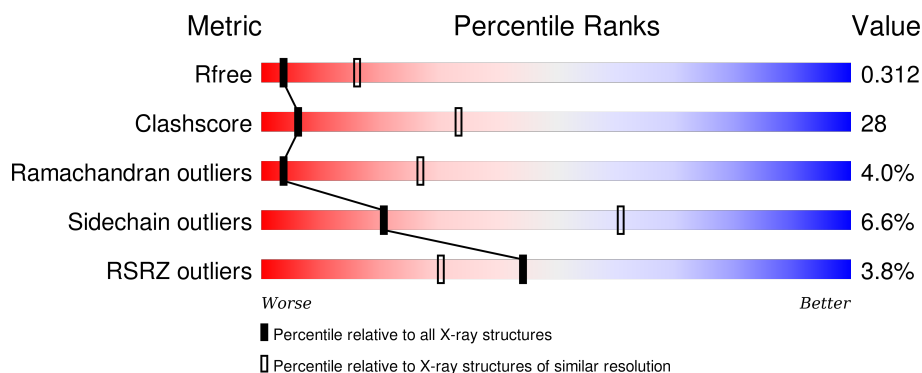
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.22 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	1095 (3.26-3.18)
Clashscore	102246	1046 (3.24-3.20)
Ramachandran outliers	100387	1026 (3.24-3.20)
Sidechain outliers	100360	1025 (3.24-3.20)
RSRZ outliers	91569	1100 (3.26-3.18)

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.

Mol	Chain	Length	Quality of chain
1	A	252	<div> <div>4%</div> <div>28% 58% 10% . .</div> </div>
1	O	252	<div> <div>5%</div> <div>29% 58% 9% . .</div> </div>
2	B	250	<div> <div>3%</div> <div>44% 46% 9% .</div> </div>
2	P	250	<div> <div>4%</div> <div>44% 46% 9% .</div> </div>
3	C	258	<div> <div>2%</div> <div>42% 41% 10% . 6%</div> </div>

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Mol	Chain	Length	Quality of chain
3	Q	258	
4	D	254	
4	R	254	
5	E	260	
5	S	260	
6	F	234	
6	T	234	
7	G	288	
7	U	288	
8	H	196	
8	V	196	
9	I	222	
9	W	222	
10	J	205	
10	X	205	
11	K	198	
11	Y	198	
12	L	212	
12	Z	212	
13	M	222	
13	a	222	
14	N	233	
14	b	233	
15	c	231	
15	d	231	

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Mol	Chain	Length	Quality of chain
15	e	231	
15	f	231	
15	g	231	
15	h	231	
15	i	231	
15	j	231	
15	k	231	
15	l	231	
15	m	231	
15	n	231	
15	o	231	
15	p	231	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 74222 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 component C7-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			
1	O	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			

- Molecule 2 is a protein called Proteasome component Y7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	249	Total	C	N	O	S	0	0	0
			1907	1214	314	376	3			
2	P	249	Total	C	N	O	S	0	0	0
			1907	1214	314	376	3			

- Molecule 3 is a protein called Proteasome component Y13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	243	Total	C	N	O	S	0	0	0
			1900	1199	320	378	3			
3	Q	243	Total	C	N	O	S	0	0	0
			1900	1199	320	378	3			

- Molecule 4 is a protein called Proteasome component PRE6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			
4	R	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			

- Molecule 5 is a protein called Proteasome component PUP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	245	Total	C	N	O	S	0	0	0
			1888	1179	317	385	7			
5	S	245	Total	C	N	O	S	0	0	0
			1888	1179	317	385	7			

- Molecule 6 is a protein called Proteasome component PRE5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	234	Total	C	N	O	S	0	0	0
			1803	1134	313	351	5			
6	T	234	Total	C	N	O	S	0	0	0
			1803	1134	313	351	5			

- Molecule 7 is a protein called Proteasome component C1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			
7	U	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			

- Molecule 8 is a protein called Proteasome component PRE3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
8	V	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 9 is a protein called Proteasome component PUP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	222	Total	C	N	O	S	0	0	0
			1685	1061	293	324	7			
9	W	222	Total	C	N	O	S	0	0	0
			1685	1061	293	324	7			

- Molecule 10 is a protein called Proteasome component PUP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 11 is a protein called Proteasome component C11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			
11	Y	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

- Molecule 12 is a protein called Proteasome component PRE2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	212	Total	C	N	O	S	0	0	0
			1646	1045	282	312	7			
12	Z	212	Total	C	N	O	S	0	0	0
			1646	1045	282	312	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	33	ARG	LYS	CONFLICT	UNP P30656
Z	33	ARG	LYS	CONFLICT	UNP P30656

- Molecule 13 is a protein called Potential proteasome component C5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
13	a	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

- Molecule 14 is a protein called Proteasome component PRE4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
14	b	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			

- Molecule 15 is a protein called proteasome activator protein PA26.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	c	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	d	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	e	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	f	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	g	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	h	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	i	230	Total 1760	C 1101	N 310	O 343	S 6	249	0	0
15	j	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	k	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	l	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	m	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	n	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	o	230	Total 1760	C 1101	N 310	O 343	S 6	219	0	0
15	p	230	Total 1760	C 1101	N 310	O 343	S 6	249	0	0

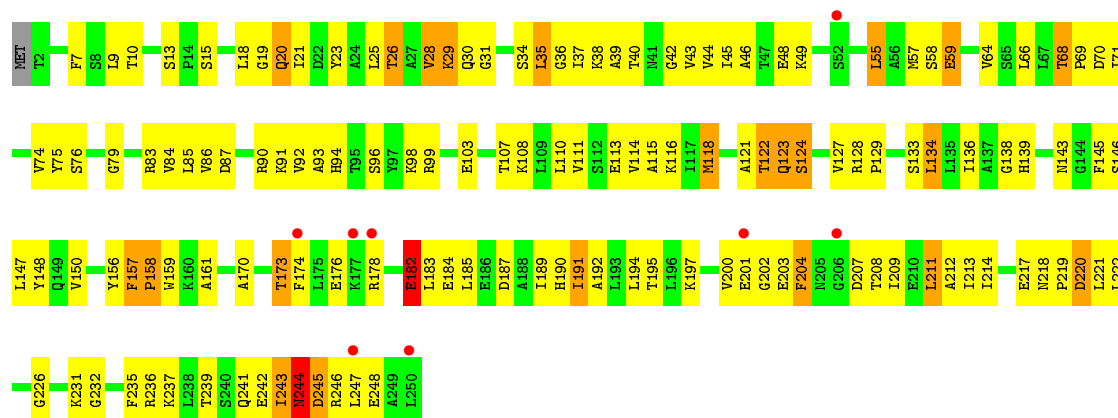
There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	1049	VAL	THR	CONFLICT	UNP Q9U8G2
c	?	-	SER	DELETION	UNP Q9U8G2
c	1171	GLY	-	INSERTION	UNP Q9U8G2
d	1049	VAL	THR	CONFLICT	UNP Q9U8G2
d	?	-	SER	DELETION	UNP Q9U8G2
d	1171	GLY	-	INSERTION	UNP Q9U8G2
e	1049	VAL	THR	CONFLICT	UNP Q9U8G2
e	?	-	SER	DELETION	UNP Q9U8G2
e	1171	GLY	-	INSERTION	UNP Q9U8G2
f	1049	VAL	THR	CONFLICT	UNP Q9U8G2
f	?	-	SER	DELETION	UNP Q9U8G2
f	1171	GLY	-	INSERTION	UNP Q9U8G2

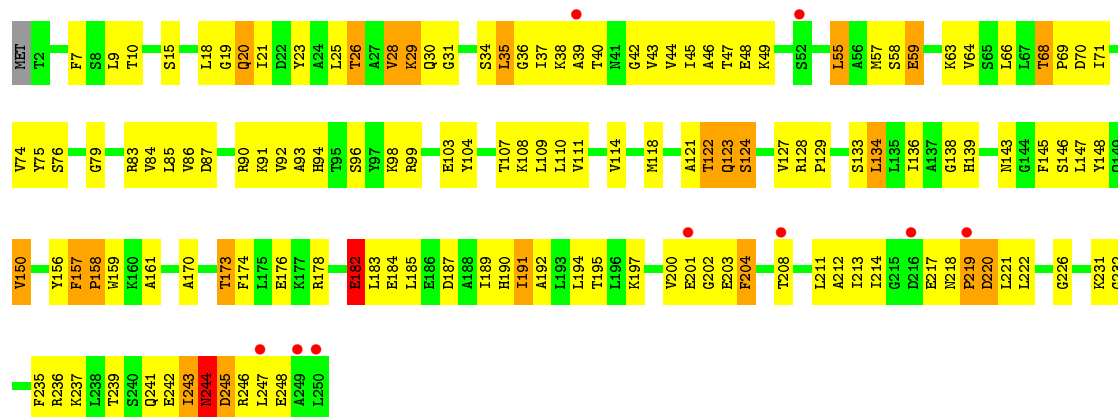
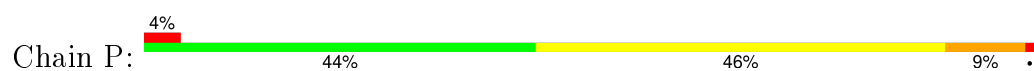
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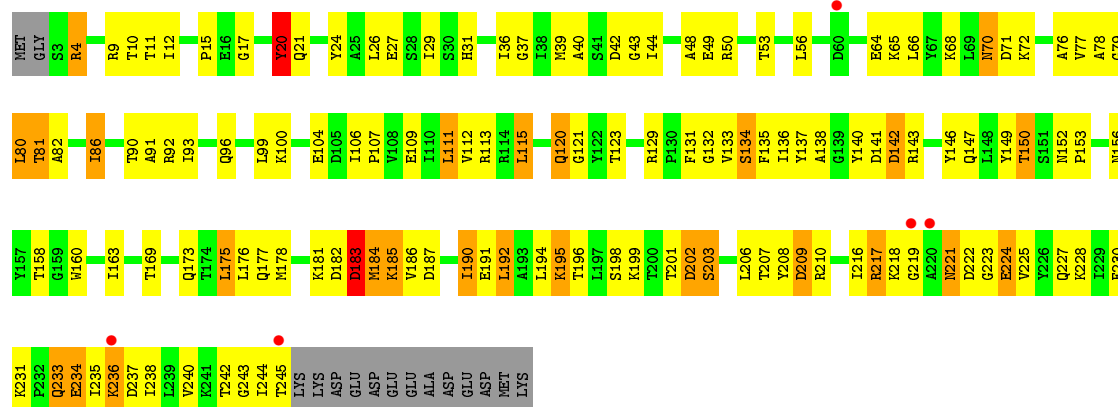
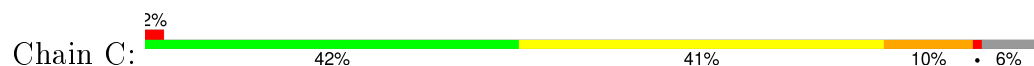
Chain	Residue	Modelled	Actual	Comment	Reference
g	1049	VAL	THR	CONFLICT	UNP Q9U8G2
g	?	-	SER	DELETION	UNP Q9U8G2
g	1171	GLY	-	INSERTION	UNP Q9U8G2
h	1049	VAL	THR	CONFLICT	UNP Q9U8G2
h	?	-	SER	DELETION	UNP Q9U8G2
h	1171	GLY	-	INSERTION	UNP Q9U8G2
i	1049	VAL	THR	CONFLICT	UNP Q9U8G2
i	?	-	SER	DELETION	UNP Q9U8G2
i	1171	GLY	-	INSERTION	UNP Q9U8G2
j	1049	VAL	THR	CONFLICT	UNP Q9U8G2
j	?	-	SER	DELETION	UNP Q9U8G2
j	1171	GLY	-	INSERTION	UNP Q9U8G2
k	1049	VAL	THR	CONFLICT	UNP Q9U8G2
k	?	-	SER	DELETION	UNP Q9U8G2
k	1171	GLY	-	INSERTION	UNP Q9U8G2
l	1049	VAL	THR	CONFLICT	UNP Q9U8G2
l	?	-	SER	DELETION	UNP Q9U8G2
l	1171	GLY	-	INSERTION	UNP Q9U8G2
m	1049	VAL	THR	CONFLICT	UNP Q9U8G2
m	?	-	SER	DELETION	UNP Q9U8G2
m	1171	GLY	-	INSERTION	UNP Q9U8G2
n	1049	VAL	THR	CONFLICT	UNP Q9U8G2
n	?	-	SER	DELETION	UNP Q9U8G2
n	1171	GLY	-	INSERTION	UNP Q9U8G2
o	1049	VAL	THR	CONFLICT	UNP Q9U8G2
o	?	-	SER	DELETION	UNP Q9U8G2
o	1171	GLY	-	INSERTION	UNP Q9U8G2
p	1049	VAL	THR	CONFLICT	UNP Q9U8G2
p	?	-	SER	DELETION	UNP Q9U8G2
p	1171	GLY	-	INSERTION	UNP Q9U8G2



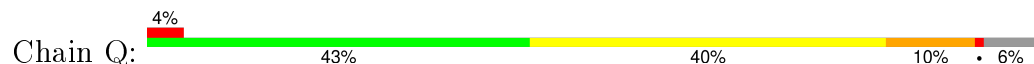
- Molecule 2: Proteasome component Y7

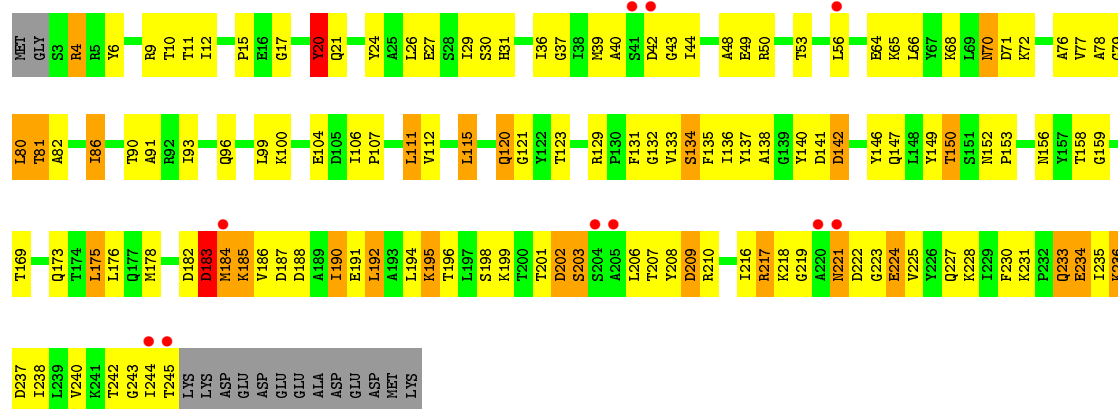


- Molecule 3: Proteasome component Y13

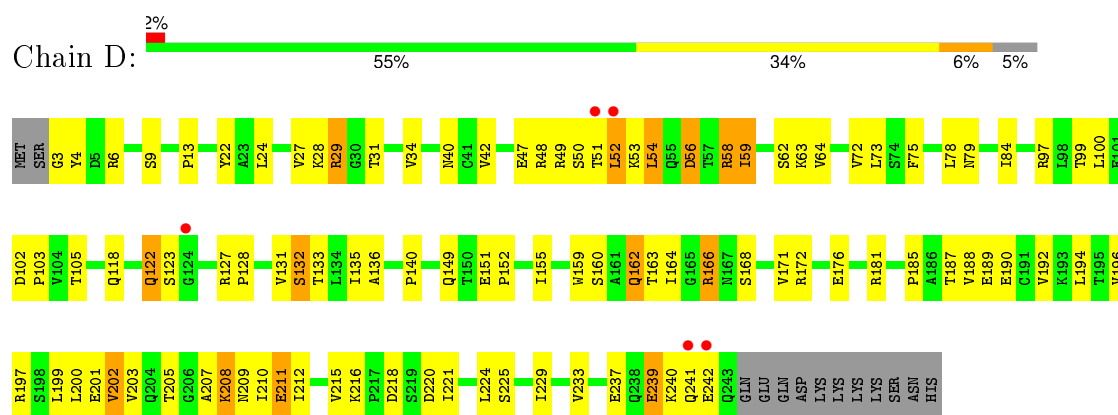


- Molecule 3: Proteasome component Y13

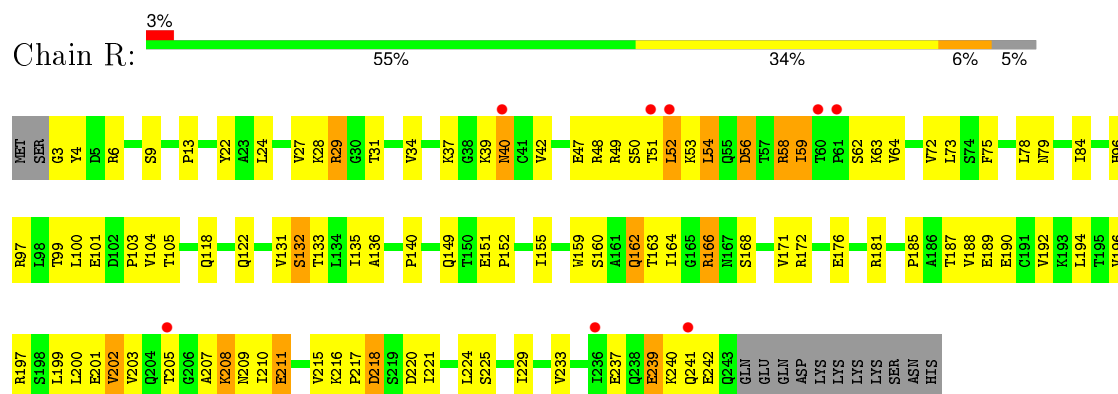




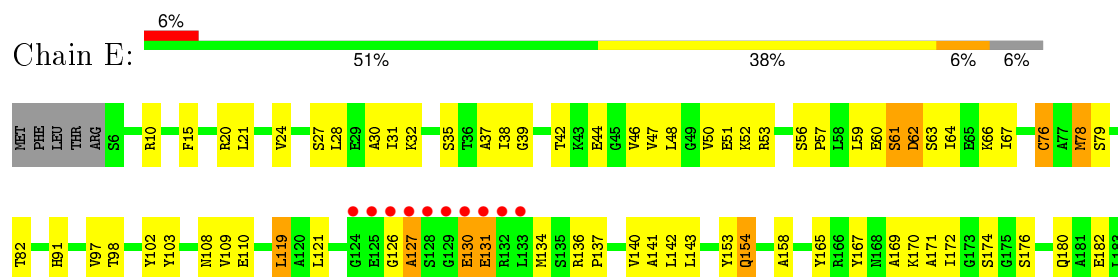
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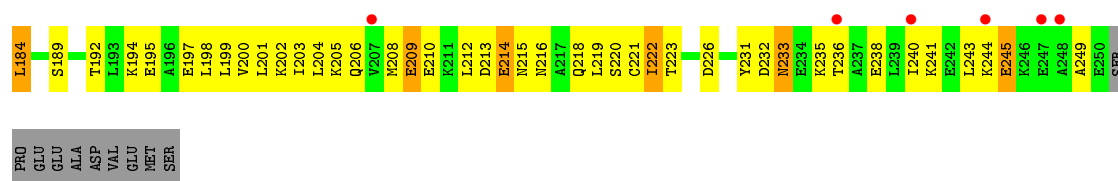


• Molecule 4: Proteasome component PRE6

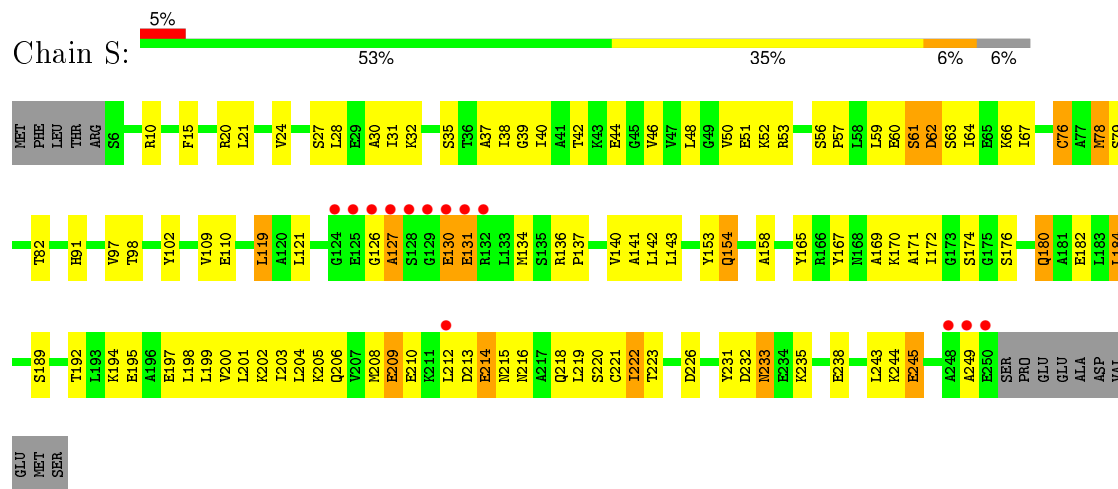


• Molecule 5: Proteasome component PUP2

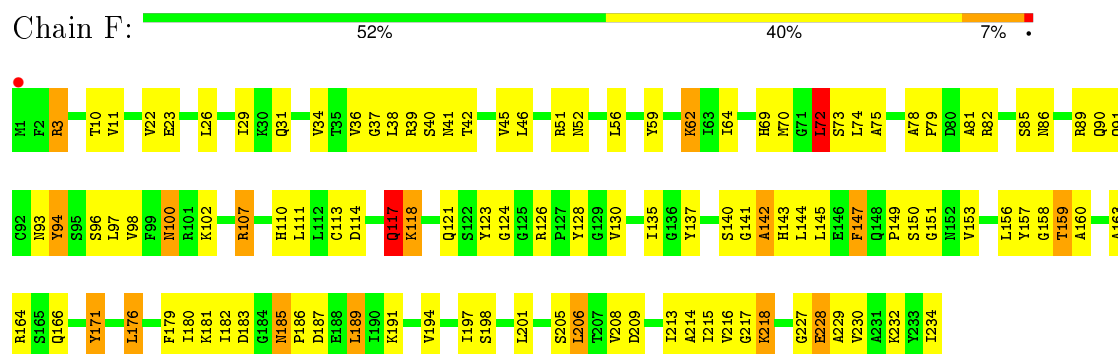




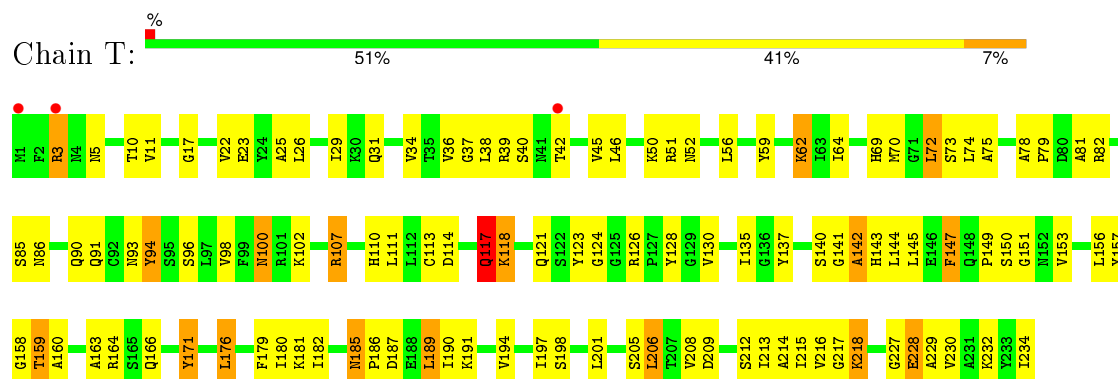
• Molecule 5: Proteasome component PUP2



• Molecule 6: Proteasome component PRE5

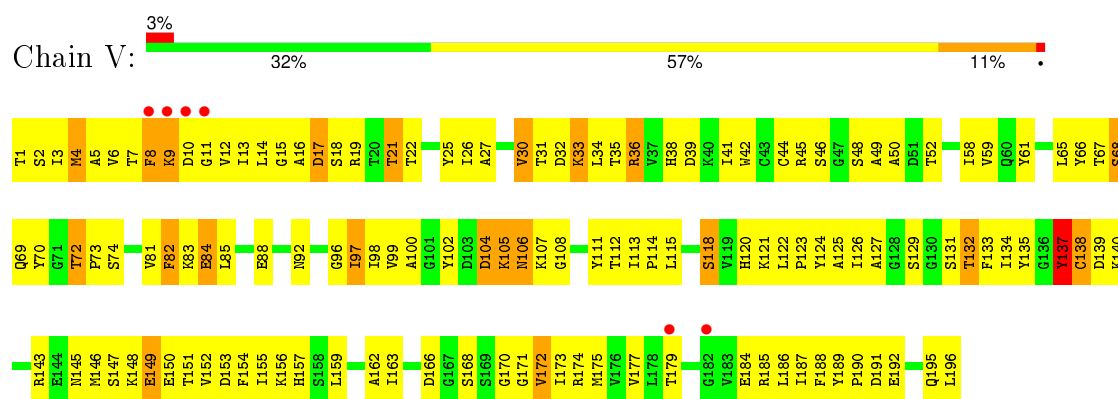


• Molecule 6: Proteasome component PRE5

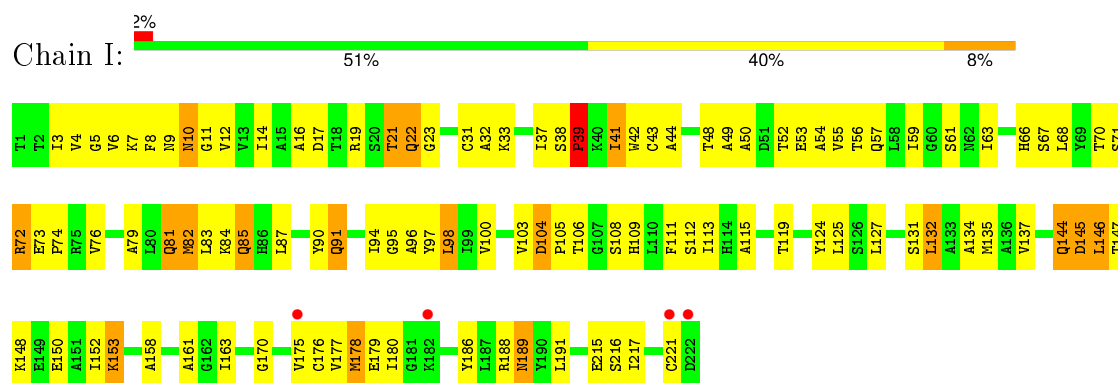


• Molecule 7: Proteasome component C1

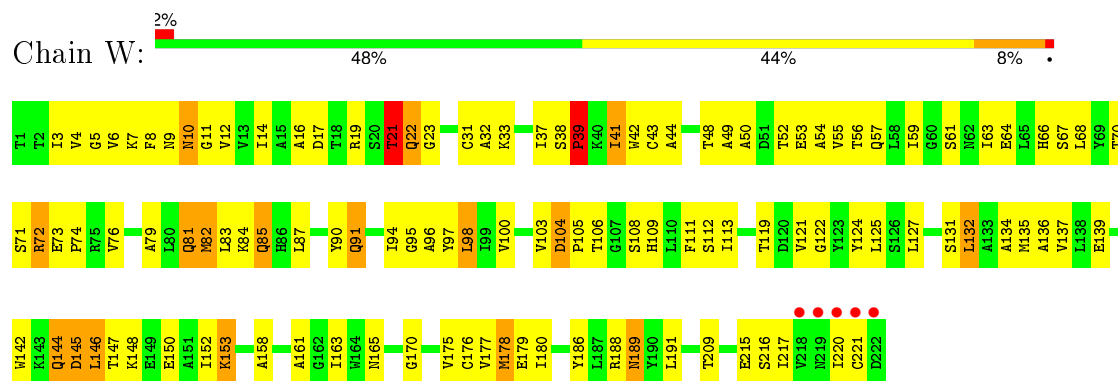




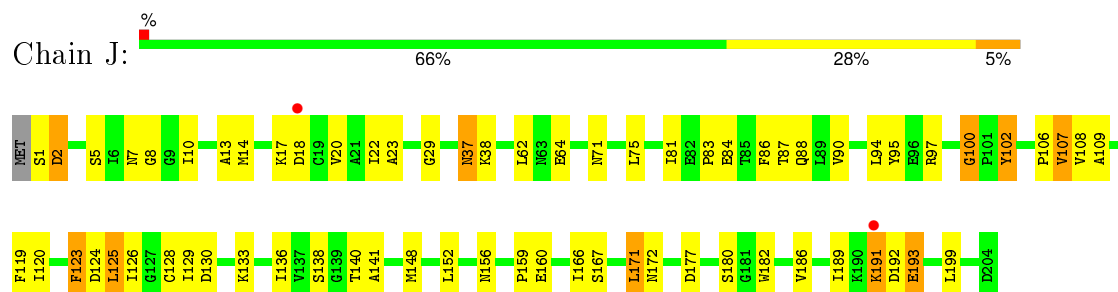
• Molecule 9: Proteasome component PUP1

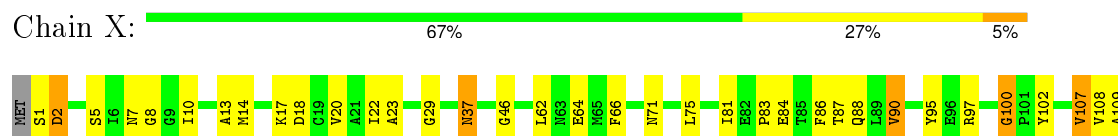


• Molecule 9: Proteasome component PUP1

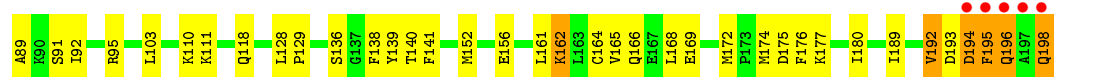
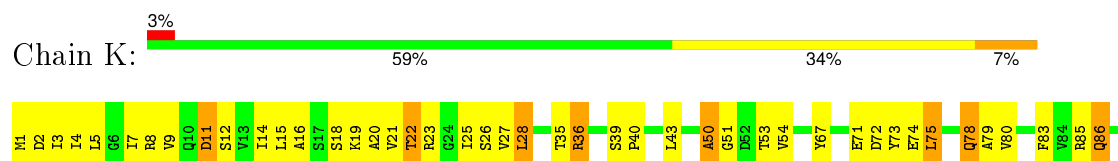


• Molecule 10: Proteasome component PUP3

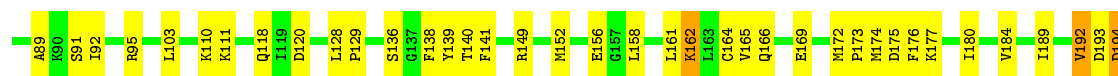
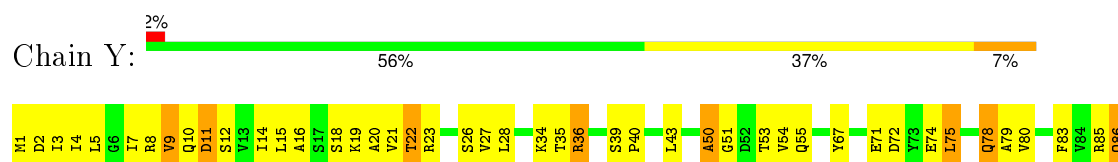




• Molecule 11: Proteasome component C11



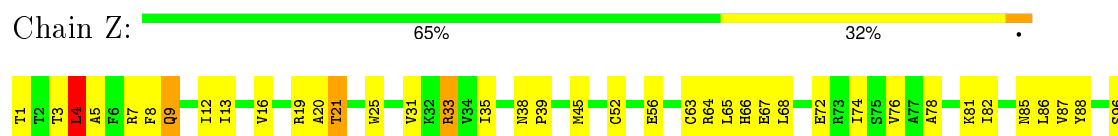
• Molecule 11: Proteasome component C11



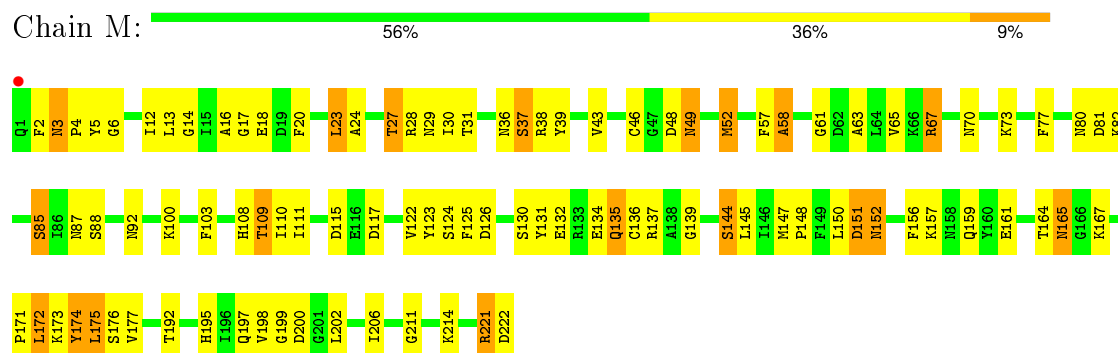
• Molecule 12: Proteasome component PRE2



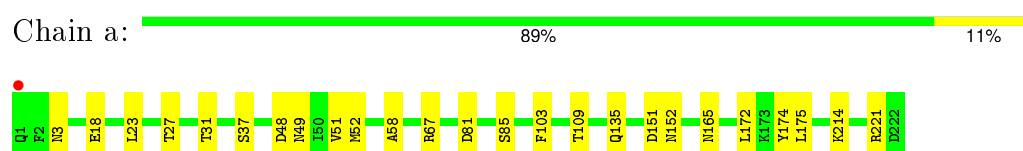
• Molecule 12: Proteasome component PRE2



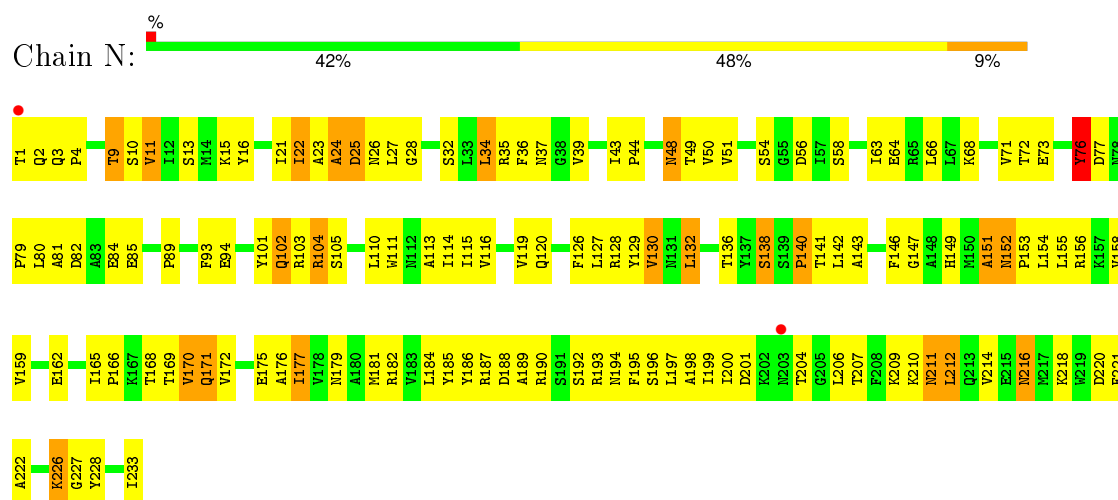
- Molecule 13: Potential proteasome component C5



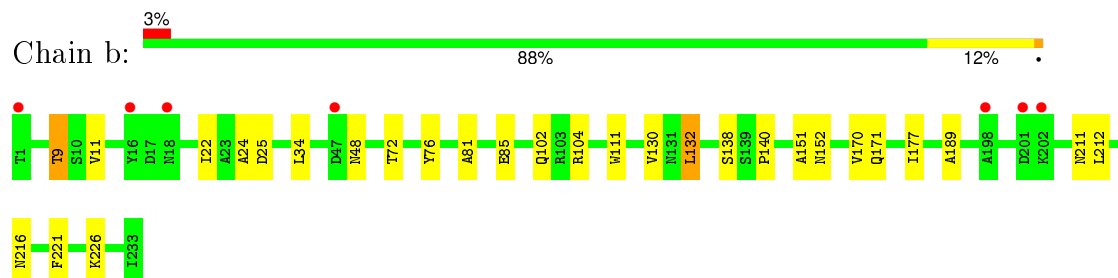
- Molecule 13: Potential proteasome component C5



- Molecule 14: Proteasome component PRE4

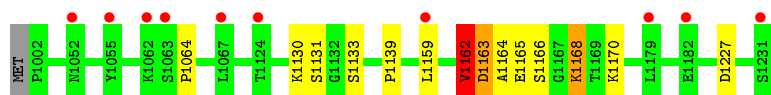


- Molecule 14: Proteasome component PRE4

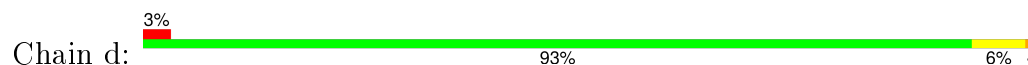


- Molecule 15: proteasome activator protein PA26

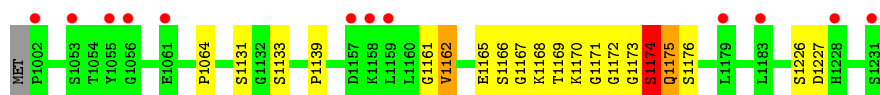




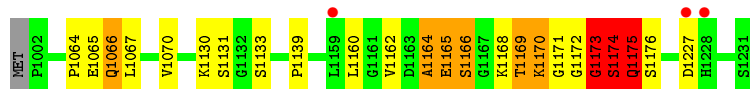
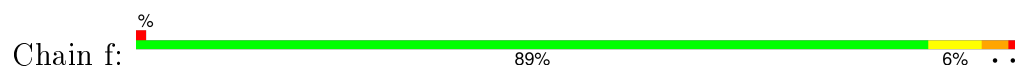
- Molecule 15: proteasome activator protein PA26



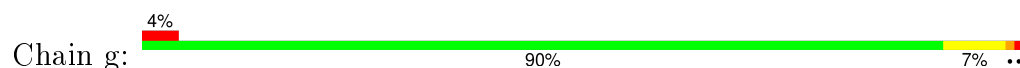
- Molecule 15: proteasome activator protein PA26



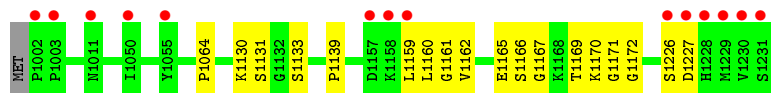
- Molecule 15: proteasome activator protein PA26



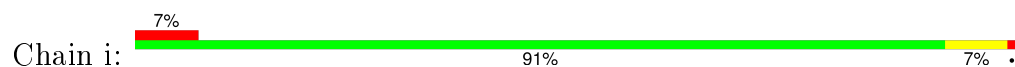
- Molecule 15: proteasome activator protein PA26



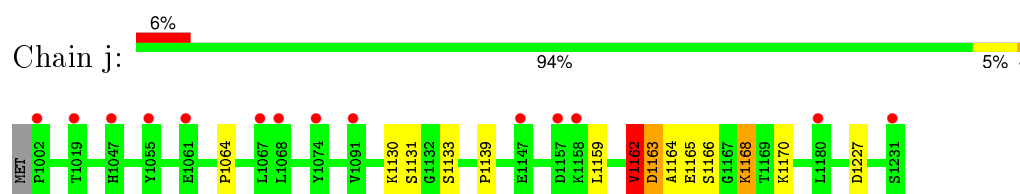
- Molecule 15: proteasome activator protein PA26



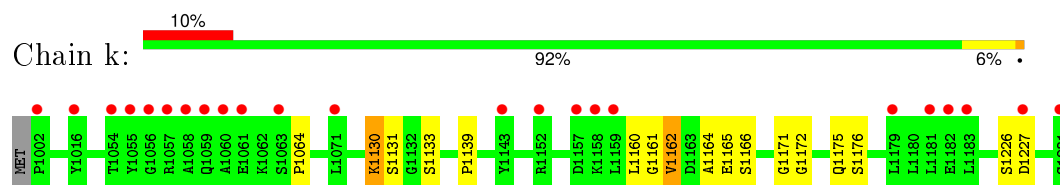
- Molecule 15: proteasome activator protein PA26



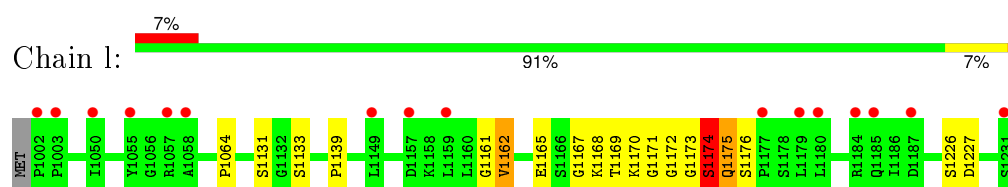
- Molecule 15: proteasome activator protein PA26



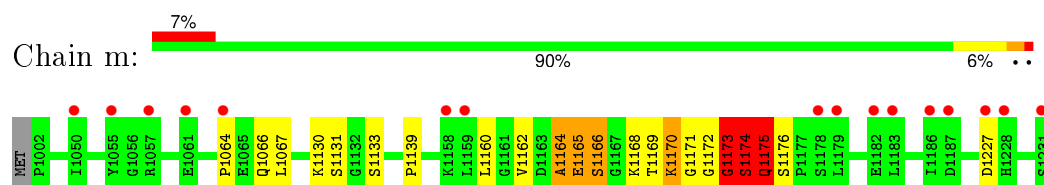
- Molecule 15: proteasome activator protein PA26



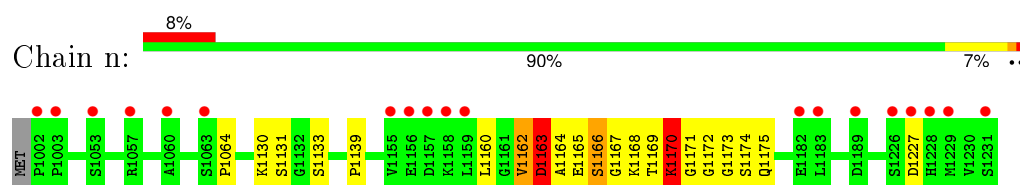
- Molecule 15: proteasome activator protein PA26



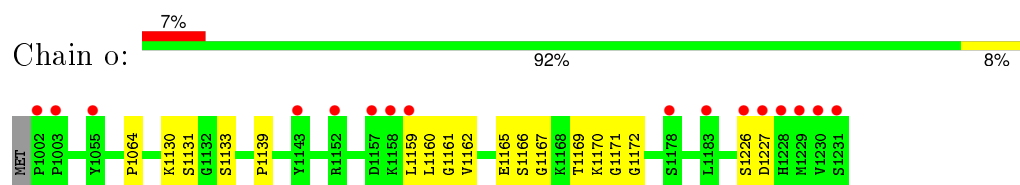
- Molecule 15: proteasome activator protein PA26



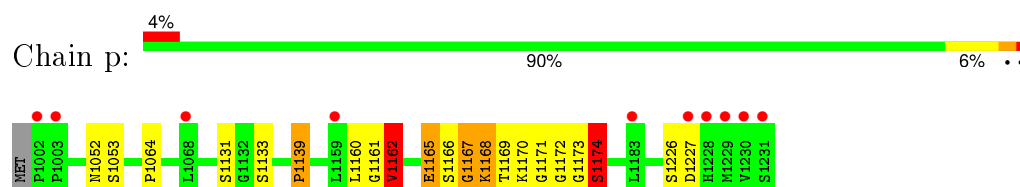
- Molecule 15: proteasome activator protein PA26



- Molecule 15: proteasome activator protein PA26



- Molecule 15: proteasome activator protein PA26



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	192.96 Å 232.13 Å 296.77 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.80 – 3.22 39.84 – 3.22	Depositor EDS
% Data completeness (in resolution range)	89.1 (39.80-3.22) 88.2 (39.84-3.22)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 3.25 Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.263 , 0.308 0.275 , 0.312	Depositor DCC
R_{free} test set	1264 reflections (0.67%)	DCC
Wilson B-factor (Å ²)	71.3	Xtriage
Anisotropy	0.529	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 53.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 189495 reflections	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	74222	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.14% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.50	0/1959	0.70	1/2652 (0.0%)
1	O	0.49	0/1959	0.70	1/2652 (0.0%)
2	B	0.47	0/1944	0.73	0/2632
2	P	0.46	0/1944	0.72	0/2632
3	C	0.47	0/1930	0.69	0/2613
3	Q	0.47	0/1930	0.69	0/2613
4	D	0.47	0/1919	0.69	0/2598
4	R	0.45	0/1919	0.69	0/2598
5	E	0.49	0/1914	0.70	0/2579
5	S	0.47	0/1914	0.70	0/2579
6	F	0.48	0/1831	0.71	1/2473 (0.0%)
6	T	0.48	0/1831	0.70	0/2473
7	G	0.47	0/1932	0.68	0/2609
7	U	0.46	0/1932	0.67	0/2609
8	H	0.51	0/1541	0.74	0/2087
8	V	0.48	0/1541	0.73	0/2087
9	I	0.49	0/1716	0.71	0/2326
9	W	0.48	0/1716	0.70	0/2326
10	J	0.49	0/1611	0.76	2/2174 (0.1%)
10	X	0.50	0/1611	0.75	1/2174 (0.0%)
11	K	0.56	0/1613	0.74	0/2173
11	Y	0.53	0/1613	0.73	0/2173
12	L	0.54	0/1683	0.74	1/2277 (0.0%)
12	Z	0.54	0/1683	0.74	1/2277 (0.0%)
13	M	0.49	0/1795	0.73	0/2420
13	a	0.50	0/1795	0.73	0/2420
14	N	0.49	0/1855	0.75	0/2514
14	b	0.49	0/1855	0.75	0/2514
15	c	0.57	2/1786 (0.1%)	0.77	6/2415 (0.2%)
15	d	0.70	9/1786 (0.5%)	0.88	15/2415 (0.6%)
15	e	0.82	11/1786 (0.6%)	1.01	22/2415 (0.9%)
15	f	0.74	5/1786 (0.3%)	1.19	18/2415 (0.7%)
15	g	0.91	9/1786 (0.5%)	1.17	20/2415 (0.8%)
15	h	0.77	7/1786 (0.4%)	0.94	20/2415 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	i	1.22	17/1786 (1.0%)	1.43	28/2415 (1.2%)
15	j	0.56	2/1786 (0.1%)	0.77	6/2415 (0.2%)
15	k	0.69	9/1786 (0.5%)	0.88	16/2415 (0.7%)
15	l	0.81	11/1786 (0.6%)	1.01	21/2415 (0.9%)
15	m	0.73	5/1786 (0.3%)	1.18	18/2415 (0.7%)
15	n	0.91	9/1786 (0.5%)	1.17	20/2415 (0.8%)
15	o	0.76	7/1786 (0.4%)	0.94	20/2415 (0.8%)
15	p	1.23	17/1786 (1.0%)	1.43	28/2415 (1.2%)
All	All	0.63	120/75490 (0.2%)	0.85	266/102064 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	O	0	1
3	C	0	1
3	Q	0	1
14	N	0	1
15	e	0	1
15	f	0	4
15	g	0	1
15	i	0	4
15	l	0	1
15	m	0	4
15	n	0	1
15	p	0	4
All	All	0	25

The worst 5 of 120 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	i	1172	GLY	C-N	32.26	1.91	1.33
15	p	1172	GLY	C-N	32.26	1.91	1.33
15	g	1163	ASP	C-O	14.32	1.50	1.23
15	n	1163	ASP	C-O	14.30	1.50	1.23
15	i	1173	GLY	N-CA	13.87	1.66	1.46

The worst 5 of 266 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	n	1174	SER	N-CA-CB	-31.23	63.65	110.50
15	g	1174	SER	N-CA-CB	-31.22	63.68	110.50
15	p	1162	VAL	O-C-N	-27.33	78.97	122.70
15	i	1162	VAL	O-C-N	-27.26	79.09	122.70
15	f	1173	GLY	O-C-N	-27.22	79.15	122.70

There are no chirality outliers.

5 of 25 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	12	TYR	Mainchain
3	C	20	TYR	Sidechain
14	N	76	TYR	Sidechain
1	O	12	TYR	Mainchain
3	Q	20	TYR	Sidechain

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	1921	0	1910	232	0
1	O	1921	0	1910	229	0
2	B	1907	0	1917	159	0
2	P	1907	0	1917	161	0
3	C	1900	0	1898	146	0
3	Q	1900	0	1898	142	0
4	D	1890	0	1900	89	0
4	R	1890	0	1900	92	0
5	E	1888	0	1856	106	0
5	S	1888	0	1856	104	0
6	F	1803	0	1809	110	0
6	T	1803	0	1809	107	0
7	G	1892	0	1883	156	0
7	U	1892	0	1883	152	0
8	H	1512	0	1481	161	0
8	V	1512	0	1481	151	0
9	I	1685	0	1688	104	0
9	W	1685	0	1688	119	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	1581	0	1574	75	0
10	X	1581	0	1574	76	0
11	K	1585	0	1590	80	0
11	Y	1585	0	1590	89	0
12	L	1646	0	1595	72	0
12	Z	1646	0	1595	71	0
13	M	1757	0	1711	93	0
13	a	1757	0	1711	0	0
14	N	1824	0	1832	158	0
14	b	1824	0	1832	0	0
15	c	1760	0	1784	0	0
15	d	1760	0	1784	0	0
15	e	1760	0	1783	0	0
15	f	1760	0	1783	0	37
15	g	1760	0	1784	0	0
15	h	1760	0	1783	0	0
15	i	1760	0	1782	0	0
15	j	1760	0	1784	0	0
15	k	1760	0	1784	0	0
15	l	1760	0	1783	0	0
15	m	1760	0	1783	0	0
15	n	1760	0	1784	0	0
15	o	1760	0	1783	0	0
15	p	1760	0	1782	0	37
All	All	74222	0	74254	3042	37

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 28.

The worst 5 of 3042 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)
8:V:8:PHE:HE2	8:V:148:LYS:HA	1.13	1.12
3:Q:175:LEU:HD11	3:Q:199:LYS:HD2	1.33	1.11
3:C:175:LEU:HD11	3:C:199:LYS:HD2	1.33	1.10
8:H:8:PHE:HE2	8:H:148:LYS:HA	1.14	1.10
2:B:222:LEU:HD11	2:B:232:GLY:HA2	1.35	1.08

The worst 5 of 37 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:f:1065:GLU:C	15:p:1167:GLY:CA[1_554]	0.47	1.73
15:f:1065:GLU:CD	15:p:1165:GLU:OE1[1_554]	0.71	1.49
15:f:1067:LEU:N	15:p:1167:GLY:O[1_554]	0.86	1.34
15:f:1066:GLN:N	15:p:1167:GLY:CA[1_554]	0.94	1.26
15:f:1066:GLN:N	15:p:1167:GLY:C[1_554]	1.01	1.19

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	241/252 (96%)	175 (73%)	53 (22%)	13 (5%)	2	19
1	O	241/252 (96%)	174 (72%)	54 (22%)	13 (5%)	2	19
2	B	247/250 (99%)	192 (78%)	39 (16%)	16 (6%)	1	13
2	P	247/250 (99%)	193 (78%)	38 (15%)	16 (6%)	1	13
3	C	241/258 (93%)	192 (80%)	35 (14%)	14 (6%)	2	17
3	Q	241/258 (93%)	192 (80%)	35 (14%)	14 (6%)	2	17
4	D	239/254 (94%)	203 (85%)	28 (12%)	8 (3%)	5	32
4	R	239/254 (94%)	203 (85%)	28 (12%)	8 (3%)	5	32
5	E	243/260 (94%)	204 (84%)	27 (11%)	12 (5%)	3	21
5	S	243/260 (94%)	201 (83%)	30 (12%)	12 (5%)	3	21
6	F	232/234 (99%)	192 (83%)	33 (14%)	7 (3%)	5	36
6	T	232/234 (99%)	191 (82%)	33 (14%)	8 (3%)	5	31
7	G	241/288 (84%)	188 (78%)	37 (15%)	16 (7%)	1	12
7	U	241/288 (84%)	188 (78%)	37 (15%)	16 (7%)	1	12
8	H	194/196 (99%)	143 (74%)	38 (20%)	13 (7%)	1	12
8	V	194/196 (99%)	142 (73%)	37 (19%)	15 (8%)	1	8
9	I	220/222 (99%)	173 (79%)	37 (17%)	10 (4%)	3	24
9	W	220/222 (99%)	174 (79%)	35 (16%)	11 (5%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	202/205 (98%)	173 (86%)	24 (12%)	5 (2%)	7	41
10	X	202/205 (98%)	174 (86%)	23 (11%)	5 (2%)	7	41
11	K	196/198 (99%)	171 (87%)	20 (10%)	5 (3%)	7	40
11	Y	196/198 (99%)	170 (87%)	21 (11%)	5 (3%)	7	40
12	L	210/212 (99%)	183 (87%)	24 (11%)	3 (1%)	14	57
12	Z	210/212 (99%)	185 (88%)	22 (10%)	3 (1%)	14	57
13	M	220/222 (99%)	193 (88%)	24 (11%)	3 (1%)	14	57
13	a	220/222 (99%)	192 (87%)	25 (11%)	3 (1%)	14	57
14	N	231/233 (99%)	176 (76%)	39 (17%)	16 (7%)	1	11
14	b	231/233 (99%)	176 (76%)	39 (17%)	16 (7%)	1	11
15	c	228/231 (99%)	207 (91%)	14 (6%)	7 (3%)	5	34
15	d	228/231 (99%)	206 (90%)	16 (7%)	6 (3%)	7	40
15	e	228/231 (99%)	206 (90%)	16 (7%)	6 (3%)	7	40
15	f	228/231 (99%)	200 (88%)	17 (8%)	11 (5%)	3	22
15	g	228/231 (99%)	202 (89%)	18 (8%)	8 (4%)	4	31
15	h	228/231 (99%)	209 (92%)	15 (7%)	4 (2%)	11	51
15	i	228/231 (99%)	207 (91%)	16 (7%)	5 (2%)	8	45
15	j	228/231 (99%)	207 (91%)	14 (6%)	7 (3%)	5	34
15	k	228/231 (99%)	206 (90%)	16 (7%)	6 (3%)	7	40
15	l	228/231 (99%)	206 (90%)	16 (7%)	6 (3%)	7	40
15	m	228/231 (99%)	199 (87%)	18 (8%)	11 (5%)	3	22
15	n	228/231 (99%)	202 (89%)	18 (8%)	8 (4%)	4	31
15	o	228/231 (99%)	209 (92%)	15 (7%)	4 (2%)	11	51
15	p	228/231 (99%)	207 (91%)	16 (7%)	5 (2%)	8	45
All	All	9506/9802 (97%)	7986 (84%)	1140 (12%)	380 (4%)	4	27

5 of 380 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	LEU
1	A	168	ALA
1	A	221	ASN
1	A	232	LYS
2	B	123	GLN

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	207/210 (99%)	185 (89%)	22 (11%)	8	34
1	O	207/210 (99%)	186 (90%)	21 (10%)	9	37
2	B	208/209 (100%)	188 (90%)	20 (10%)	10	39
2	P	208/209 (100%)	189 (91%)	19 (9%)	12	42
3	C	203/216 (94%)	181 (89%)	22 (11%)	8	34
3	Q	203/216 (94%)	181 (89%)	22 (11%)	8	34
4	D	213/226 (94%)	196 (92%)	17 (8%)	15	52
4	R	213/226 (94%)	196 (92%)	17 (8%)	15	52
5	E	201/215 (94%)	188 (94%)	13 (6%)	21	61
5	S	201/215 (94%)	187 (93%)	14 (7%)	19	58
6	F	193/193 (100%)	174 (90%)	19 (10%)	10	38
6	T	193/193 (100%)	173 (90%)	20 (10%)	9	35
7	G	201/239 (84%)	182 (90%)	19 (10%)	11	40
7	U	201/239 (84%)	183 (91%)	18 (9%)	12	43
8	H	162/162 (100%)	145 (90%)	17 (10%)	8	35
8	V	162/162 (100%)	144 (89%)	18 (11%)	8	32
9	I	181/181 (100%)	164 (91%)	17 (9%)	11	41
9	W	181/181 (100%)	164 (91%)	17 (9%)	11	41
10	J	172/173 (99%)	163 (95%)	9 (5%)	29	69
10	X	172/173 (99%)	163 (95%)	9 (5%)	29	69
11	K	175/175 (100%)	157 (90%)	18 (10%)	9	36
11	Y	175/175 (100%)	158 (90%)	17 (10%)	10	39
12	L	169/169 (100%)	159 (94%)	10 (6%)	24	65
12	Z	169/169 (100%)	158 (94%)	11 (6%)	21	61
13	M	185/185 (100%)	164 (89%)	21 (11%)	7	31
13	a	185/185 (100%)	163 (88%)	22 (12%)	6	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	199/199 (100%)	185 (93%)	14 (7%)	19	58
14	b	199/199 (100%)	184 (92%)	15 (8%)	17	55
15	c	188/189 (100%)	182 (97%)	6 (3%)	46	80
15	d	188/189 (100%)	186 (99%)	2 (1%)	80	93
15	e	188/189 (100%)	186 (99%)	2 (1%)	80	93
15	f	188/189 (100%)	182 (97%)	6 (3%)	46	80
15	g	188/189 (100%)	184 (98%)	4 (2%)	61	87
15	h	188/189 (100%)	186 (99%)	2 (1%)	80	93
15	i	188/189 (100%)	186 (99%)	2 (1%)	80	93
15	j	188/189 (100%)	182 (97%)	6 (3%)	46	80
15	k	188/189 (100%)	186 (99%)	2 (1%)	80	93
15	l	188/189 (100%)	186 (99%)	2 (1%)	80	93
15	m	188/189 (100%)	182 (97%)	6 (3%)	46	80
15	n	188/189 (100%)	184 (98%)	4 (2%)	61	87
15	o	188/189 (100%)	186 (99%)	2 (1%)	80	93
15	p	188/189 (100%)	186 (99%)	2 (1%)	80	93
All	All	7970/8150 (98%)	7444 (93%)	526 (7%)	21	61

5 of 526 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	N	226	LYS
3	Q	190	ILE
15	e	1174	SER
1	O	126	GLN
2	P	134	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 259 such sidechains are listed below:

Mol	Chain	Res	Type
3	Q	70	ASN
6	T	152	ASN
15	l	1079	HIS
3	Q	97	ASN
4	R	209	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](#)

There are no ligands in this entry.

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	243/252 (96%)	0.30	10 (4%) 41 28	47, 82, 112, 124	0
1	O	243/252 (96%)	0.27	12 (4%) 33 22	47, 82, 112, 125	0
2	B	249/250 (99%)	0.17	8 (3%) 51 38	45, 67, 102, 123	0
2	P	249/250 (99%)	0.03	9 (3%) 46 33	46, 68, 102, 123	0
3	C	243/258 (94%)	0.01	5 (2%) 67 54	32, 60, 108, 122	0
3	Q	243/258 (94%)	0.10	10 (4%) 41 28	32, 62, 108, 122	0
4	D	241/254 (94%)	0.02	5 (2%) 67 54	34, 58, 105, 135	0
4	R	241/254 (94%)	-0.02	8 (3%) 50 37	35, 61, 104, 133	0
5	E	245/260 (94%)	0.13	16 (6%) 22 13	31, 55, 108, 133	0
5	S	245/260 (94%)	0.11	13 (5%) 30 19	33, 57, 108, 134	0
6	F	234/234 (100%)	-0.14	1 (0%) 93 90	34, 58, 78, 111	0
6	T	234/234 (100%)	-0.05	3 (1%) 79 69	36, 59, 79, 111	0
7	G	243/288 (84%)	0.16	4 (1%) 74 64	48, 69, 112, 121	0
7	U	243/288 (84%)	0.27	15 (6%) 24 15	50, 70, 112, 121	0
8	H	196/196 (100%)	0.03	5 (2%) 59 47	46, 66, 91, 98	0
8	V	196/196 (100%)	0.09	6 (3%) 52 40	46, 66, 91, 98	0
9	I	222/222 (100%)	-0.07	4 (1%) 71 60	40, 60, 84, 128	0
9	W	222/222 (100%)	0.00	5 (2%) 64 52	39, 59, 84, 127	0
10	J	204/205 (99%)	-0.38	2 (0%) 84 77	28, 43, 63, 76	0
10	X	204/205 (99%)	-0.37	1 (0%) 91 87	27, 43, 62, 76	0
11	K	198/198 (100%)	-0.22	5 (2%) 61 49	23, 40, 61, 126	0
11	Y	198/198 (100%)	-0.34	3 (1%) 76 65	24, 41, 62, 126	0
12	L	212/212 (100%)	-0.39	0 100 100	17, 37, 55, 72	0
12	Z	212/212 (100%)	-0.49	0 100 100	18, 38, 54, 70	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	222/222 (100%)	-0.29	1 (0%) 91 87	24, 47, 65, 80	0
13	a	222/222 (100%)	-0.26	1 (0%) 91 87	24, 48, 66, 80	0
14	N	233/233 (100%)	-0.10	2 (0%) 85 79	34, 60, 87, 98	0
14	b	233/233 (100%)	0.05	7 (3%) 54 41	36, 61, 87, 98	0
15	c	195/231 (84%)	0.33	10 (5%) 32 20	46, 79, 110, 123	0
15	d	195/231 (84%)	0.18	6 (3%) 52 40	46, 75, 109, 125	0
15	e	195/231 (84%)	0.22	12 (6%) 24 15	40, 70, 104, 122	0
15	f	195/231 (84%)	0.00	3 (1%) 76 65	38, 69, 103, 130	0
15	g	195/231 (84%)	0.15	9 (4%) 36 24	47, 75, 110, 159	0
15	h	195/231 (84%)	0.52	14 (7%) 18 11	55, 85, 119, 168	0
15	i	192/231 (83%)	0.59	16 (8%) 14 8	56, 86, 112, 159	1 (0%)
15	j	195/231 (84%)	0.52	14 (7%) 18 11	61, 96, 124, 134	0
15	k	195/231 (84%)	0.63	23 (11%) 6 4	66, 100, 130, 138	0
15	l	195/231 (84%)	0.49	16 (8%) 14 8	64, 98, 127, 136	0
15	m	195/231 (84%)	0.36	16 (8%) 14 8	56, 96, 129, 140	0
15	n	195/231 (84%)	0.40	19 (9%) 10 7	58, 92, 130, 169	0
15	o	195/231 (84%)	0.41	16 (8%) 14 8	64, 93, 122, 167	0
15	p	192/231 (83%)	0.45	10 (5%) 31 19	57, 93, 119, 165	1 (0%)
All	All	9094/9802 (92%)	0.09	345 (3%) 44 30	17, 66, 113, 169	2 (0%)

The worst 5 of 345 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
15	p	1231	SER	9.7
15	h	1227	ASP	8.7
3	Q	245	THR	8.7
15	h	1231	SER	7.2
3	Q	244	ILE	7.1

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

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.