wwPDB X-ray Structure Validation Summary Report (i)

Mar 20, 2016 – 01:18 AM EDT

PDB ID	:	3H4P
Title	:	Proteasome 20S core particle from Methanocaldococcus jannaschii
Authors	:	Jeffrey, P.D.; Zhang, F.; Hu, M.; Tian, G.; Zhang, P.; Finley, D.; Shi, Y.
Deposited on	:	2009-04-20
Resolution	:	4.10 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

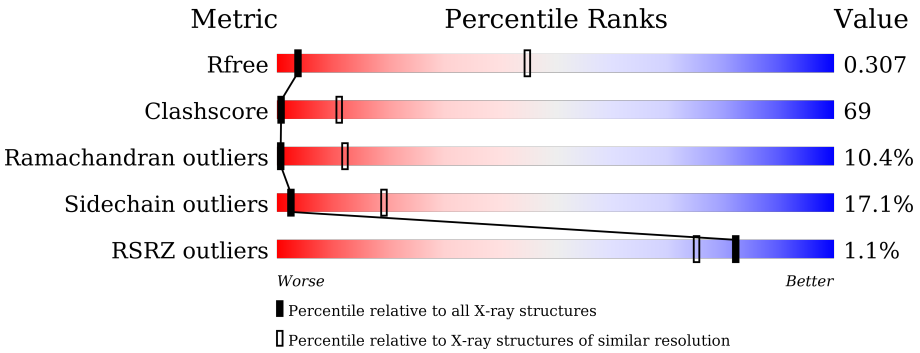
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027107
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0122
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027107

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 4.10 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	1018 (4.60-3.60)
Clashscore	102246	1117 (4.60-3.60)
Ramachandran outliers	100387	1063 (4.60-3.60)
Sidechain outliers	100360	1049 (4.60-3.60)
RSRZ outliers	91569	1022 (4.60-3.60)

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 <=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	264	2% 18% 55% 14% • 12%
1	B	264	2% 19% 53% 15% • 12%
1	C	264	% 19% 55% 13% • 12%
1	D	264	16% 56% 15% • 12%
1	E	264	3% 15% 56% 15% • 12%
1	F	264	2% 16% 58% 13% • 12%

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Mol	Chain	Length	Quality of chain
1	G	264	17% 55% 15% 12%
1	H	264	16% 56% 15% 12%
1	I	264	19% 55% 13% 12%
1	J	264	4% 19% 55% 13% 12%
1	K	264	14% 58% 14% 12%
1	L	264	17% 54% 15% 12%
1	M	264	3% 18% 55% 14% 12%
1	N	264	2% 17% 57% 13% 12%
2	a	219	73% 17% 8%
2	b	219	69% 20% 8%
2	c	219	74% 14% 8%
2	d	219	68% 22% 8%
2	e	219	68% 22% 8%
2	f	219	70% 18% 8%
2	g	219	69% 19% 8%
2	h	219	68% 22% 8%
2	i	219	68% 21% 8%
2	j	219	70% 20% 8%
2	k	219	70% 19% 8%
2	l	219	69% 19% 8%
2	m	219	68% 21% 8%
2	n	219	73% 16% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 46648 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	B	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	C	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	D	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	E	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	F	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	G	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	H	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	I	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	J	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	K	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	L	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	M	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			
1	N	232	Total	C	N	O	S	0	0	0
			1813	1150	312	346	5			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q60177

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	EXPRESSION TAG	UNP Q60177
A	0	HIS	-	EXPRESSION TAG	UNP Q60177
B	-2	GLY	-	EXPRESSION TAG	UNP Q60177
B	-1	SER	-	EXPRESSION TAG	UNP Q60177
B	0	HIS	-	EXPRESSION TAG	UNP Q60177
C	-2	GLY	-	EXPRESSION TAG	UNP Q60177
C	-1	SER	-	EXPRESSION TAG	UNP Q60177
C	0	HIS	-	EXPRESSION TAG	UNP Q60177
D	-2	GLY	-	EXPRESSION TAG	UNP Q60177
D	-1	SER	-	EXPRESSION TAG	UNP Q60177
D	0	HIS	-	EXPRESSION TAG	UNP Q60177
E	-2	GLY	-	EXPRESSION TAG	UNP Q60177
E	-1	SER	-	EXPRESSION TAG	UNP Q60177
E	0	HIS	-	EXPRESSION TAG	UNP Q60177
F	-2	GLY	-	EXPRESSION TAG	UNP Q60177
F	-1	SER	-	EXPRESSION TAG	UNP Q60177
F	0	HIS	-	EXPRESSION TAG	UNP Q60177
G	-2	GLY	-	EXPRESSION TAG	UNP Q60177
G	-1	SER	-	EXPRESSION TAG	UNP Q60177
G	0	HIS	-	EXPRESSION TAG	UNP Q60177
H	-2	GLY	-	EXPRESSION TAG	UNP Q60177
H	-1	SER	-	EXPRESSION TAG	UNP Q60177
H	0	HIS	-	EXPRESSION TAG	UNP Q60177
I	-2	GLY	-	EXPRESSION TAG	UNP Q60177
I	-1	SER	-	EXPRESSION TAG	UNP Q60177
I	0	HIS	-	EXPRESSION TAG	UNP Q60177
J	-2	GLY	-	EXPRESSION TAG	UNP Q60177
J	-1	SER	-	EXPRESSION TAG	UNP Q60177
J	0	HIS	-	EXPRESSION TAG	UNP Q60177
K	-2	GLY	-	EXPRESSION TAG	UNP Q60177
K	-1	SER	-	EXPRESSION TAG	UNP Q60177
K	0	HIS	-	EXPRESSION TAG	UNP Q60177
L	-2	GLY	-	EXPRESSION TAG	UNP Q60177
L	-1	SER	-	EXPRESSION TAG	UNP Q60177
L	0	HIS	-	EXPRESSION TAG	UNP Q60177
M	-2	GLY	-	EXPRESSION TAG	UNP Q60177
M	-1	SER	-	EXPRESSION TAG	UNP Q60177
M	0	HIS	-	EXPRESSION TAG	UNP Q60177
N	-2	GLY	-	EXPRESSION TAG	UNP Q60177
N	-1	SER	-	EXPRESSION TAG	UNP Q60177
N	0	HIS	-	EXPRESSION TAG	UNP Q60177

- Molecule 2 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	a	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	b	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	c	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	d	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	e	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	f	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	g	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	h	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	i	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	j	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	k	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	l	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	m	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			
2	n	202	Total	C	N	O	S	0	0	0
			1519	964	248	298	9			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	6	MET	-	EXPRESSION TAG	UNP Q58634
b	6	MET	-	EXPRESSION TAG	UNP Q58634
c	6	MET	-	EXPRESSION TAG	UNP Q58634
d	6	MET	-	EXPRESSION TAG	UNP Q58634
e	6	MET	-	EXPRESSION TAG	UNP Q58634
f	6	MET	-	EXPRESSION TAG	UNP Q58634
g	6	MET	-	EXPRESSION TAG	UNP Q58634
h	6	MET	-	EXPRESSION TAG	UNP Q58634
i	6	MET	-	EXPRESSION TAG	UNP Q58634
j	6	MET	-	EXPRESSION TAG	UNP Q58634
k	6	MET	-	EXPRESSION TAG	UNP Q58634
l	6	MET	-	EXPRESSION TAG	UNP Q58634

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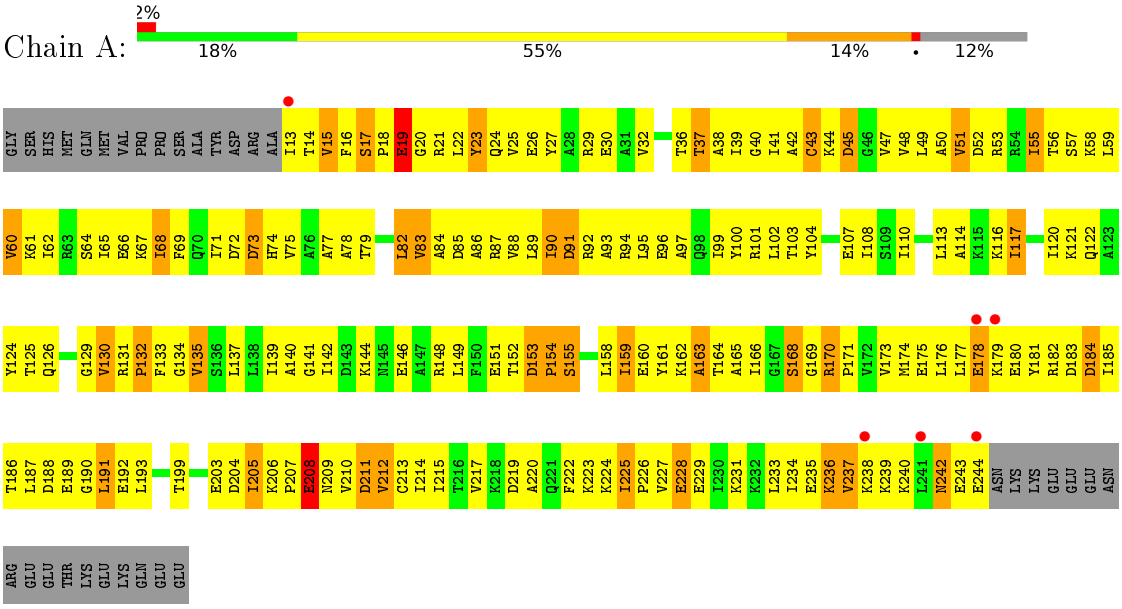
Chain	Residue	Modelled	Actual	Comment	Reference
m	6	MET	-	EXPRESSION TAG	UNP Q58634
n	6	MET	-	EXPRESSION TAG	UNP Q58634

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.

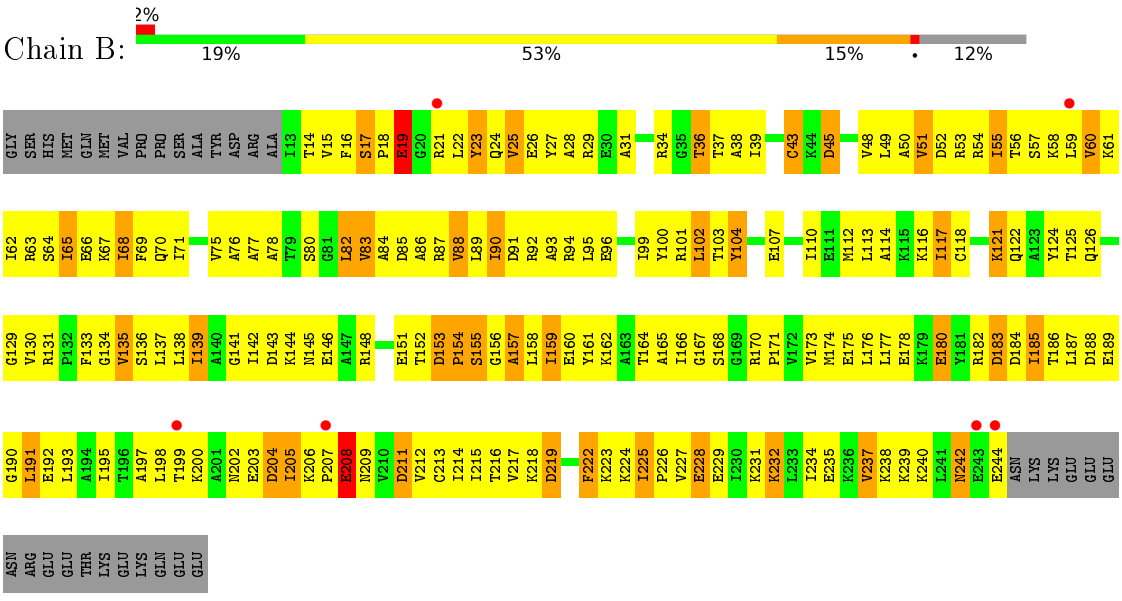
- Molecule 1: Proteasome subunit alpha

Chain A:



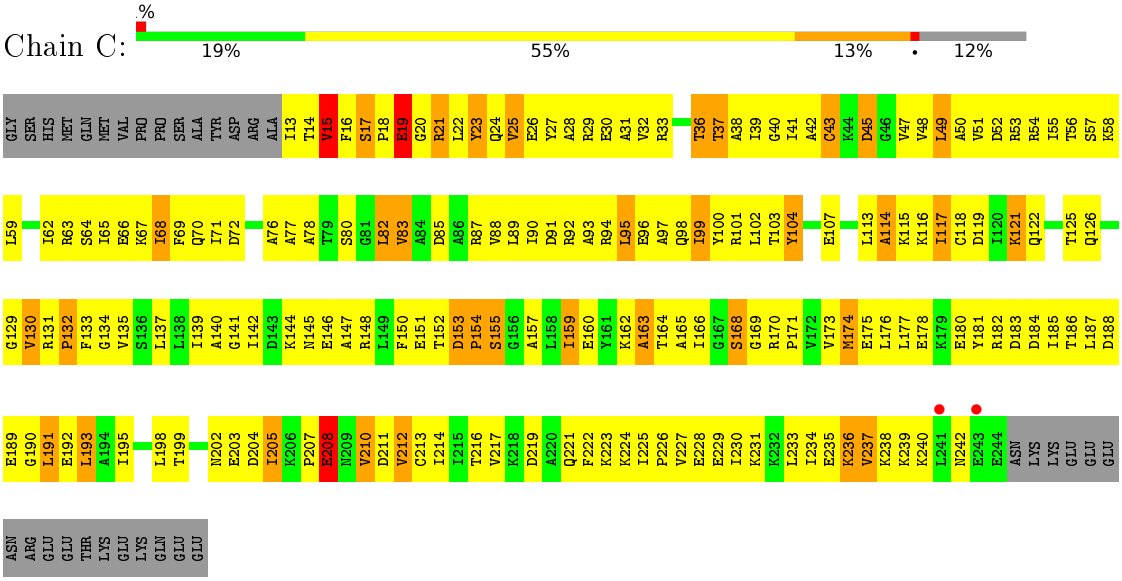
- Molecule 1: Proteasome subunit alpha

Chain B:



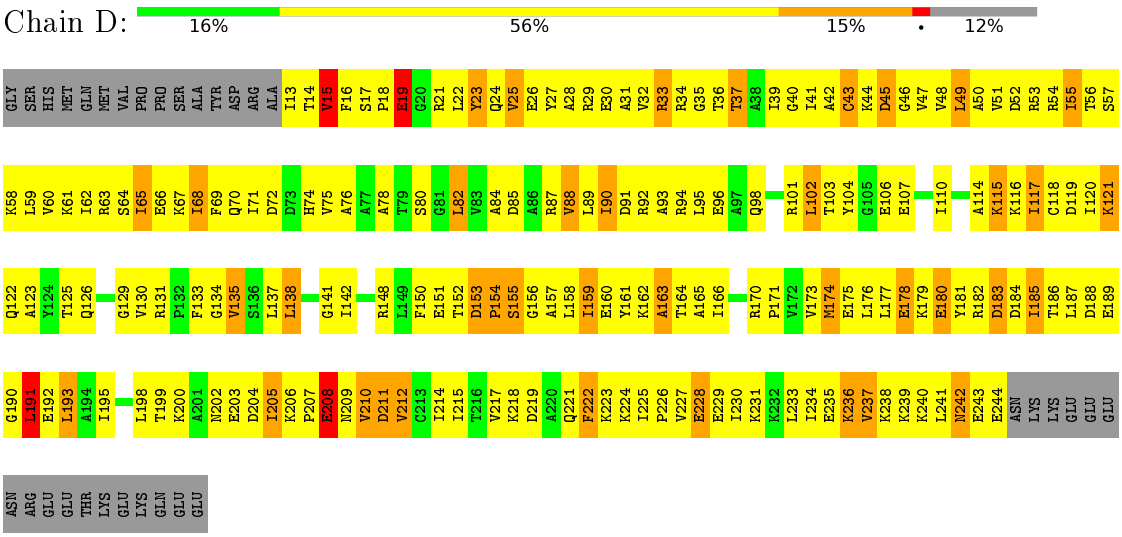
- Molecule 1: Proteasome subunit alpha

Chain C:



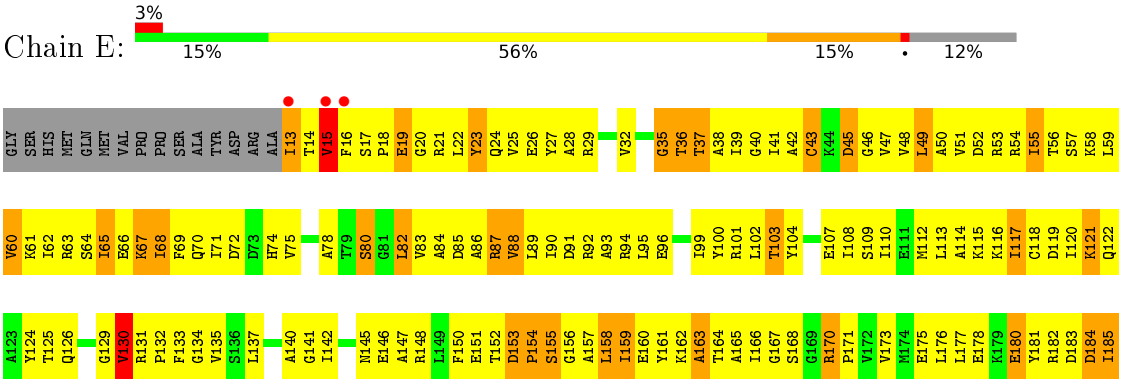
- Molecule 1: Proteasome subunit alpha

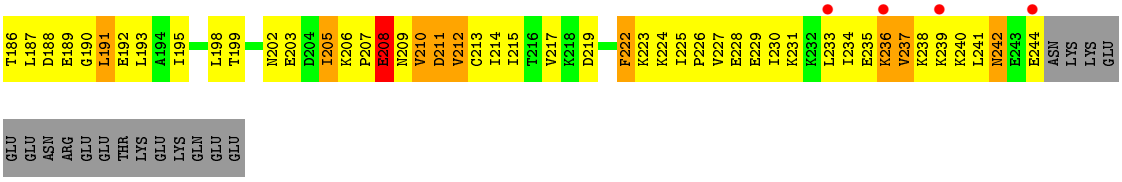
Chain D:



- Molecule 1: Proteasome subunit alpha

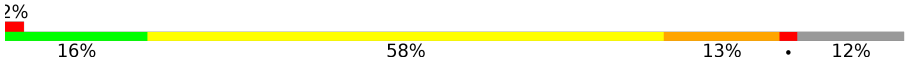
Chain E:

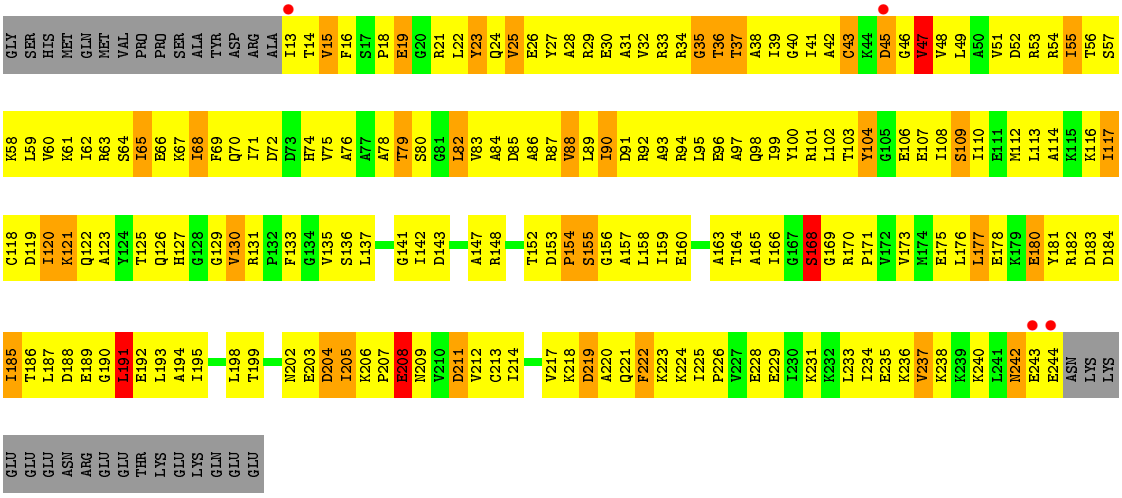




• Molecule 1: Proteasome subunit alpha

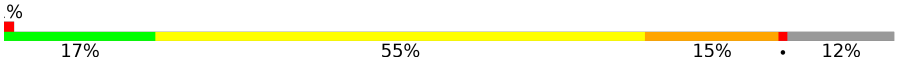
Chain F:

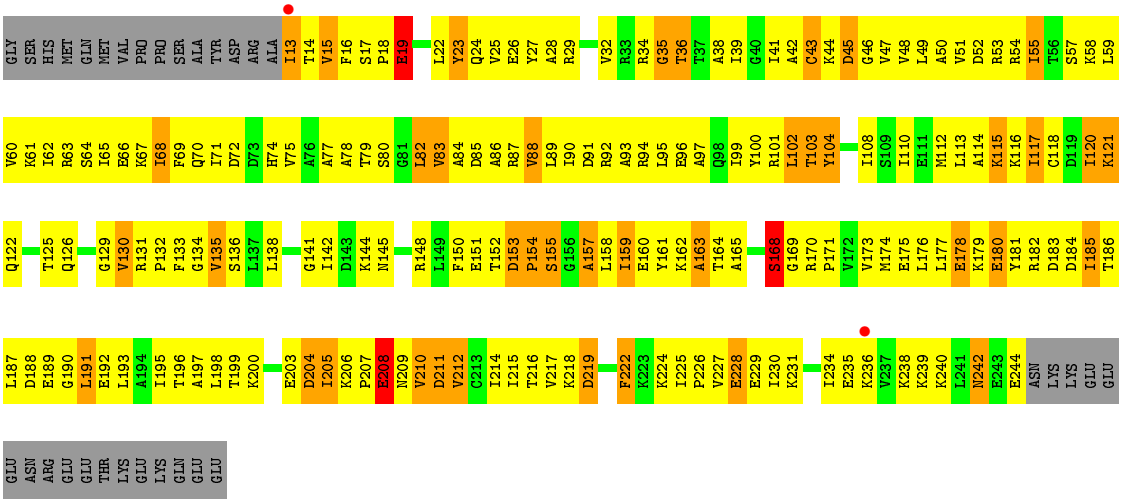




• Molecule 1: Proteasome subunit alpha

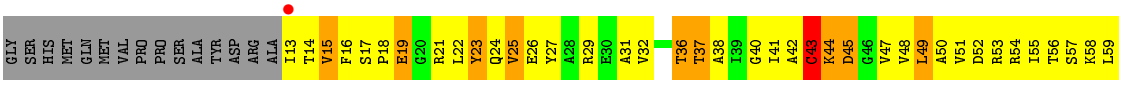
Chain G:

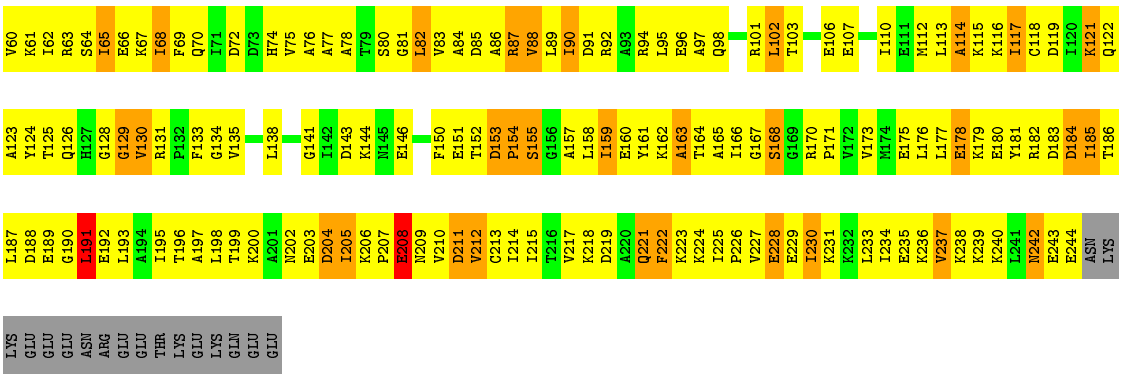




• Molecule 1: Proteasome subunit alpha

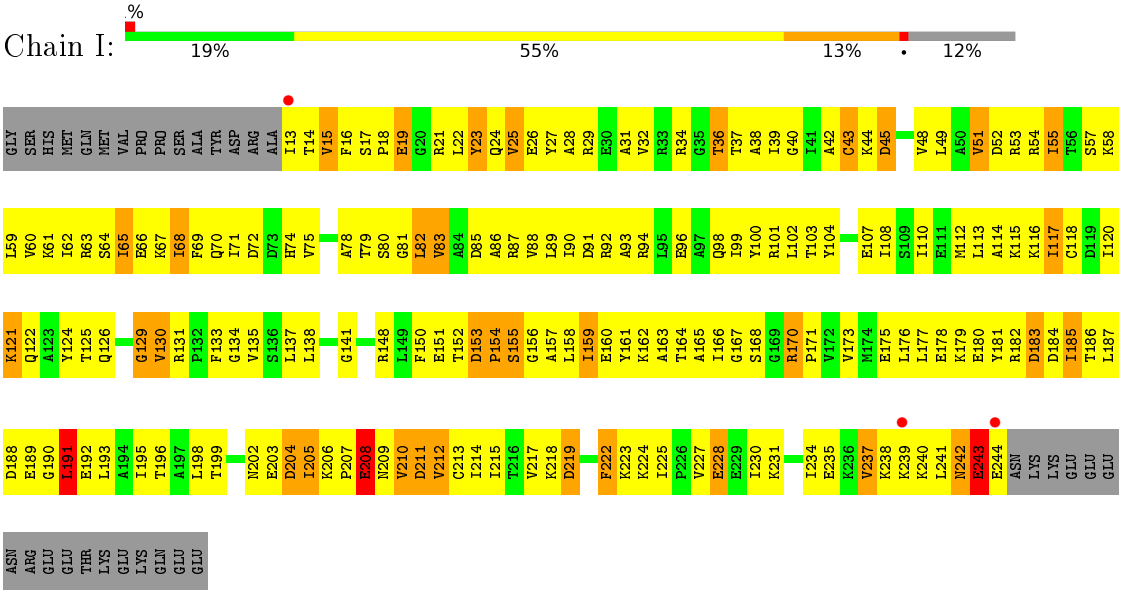
Chain H:





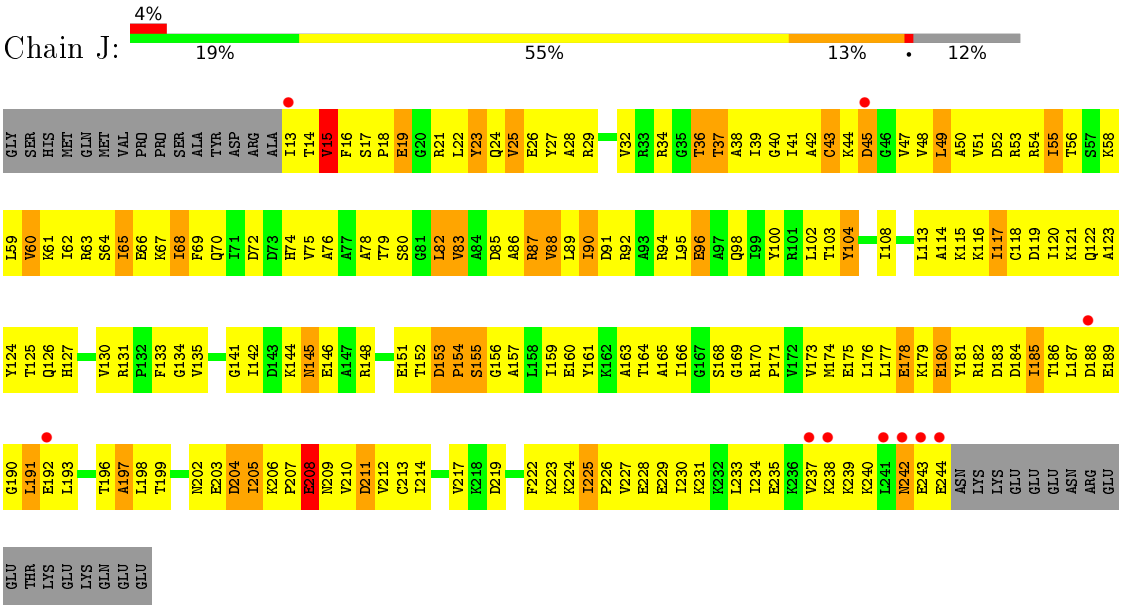
• Molecule 1: Proteasome subunit alpha

Chain I:



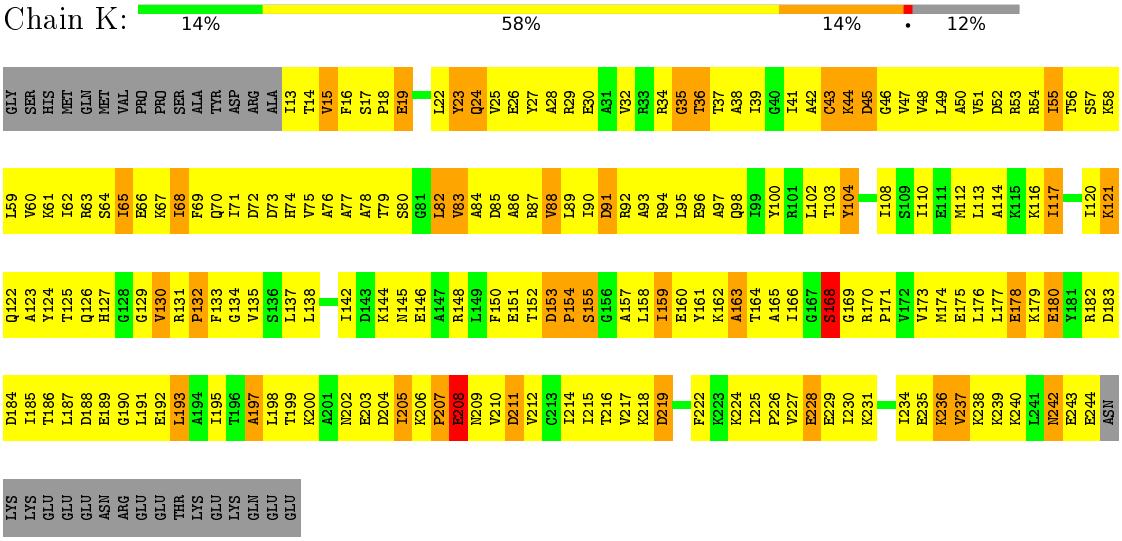
• Molecule 1: Proteasome subunit alpha

Chain J:



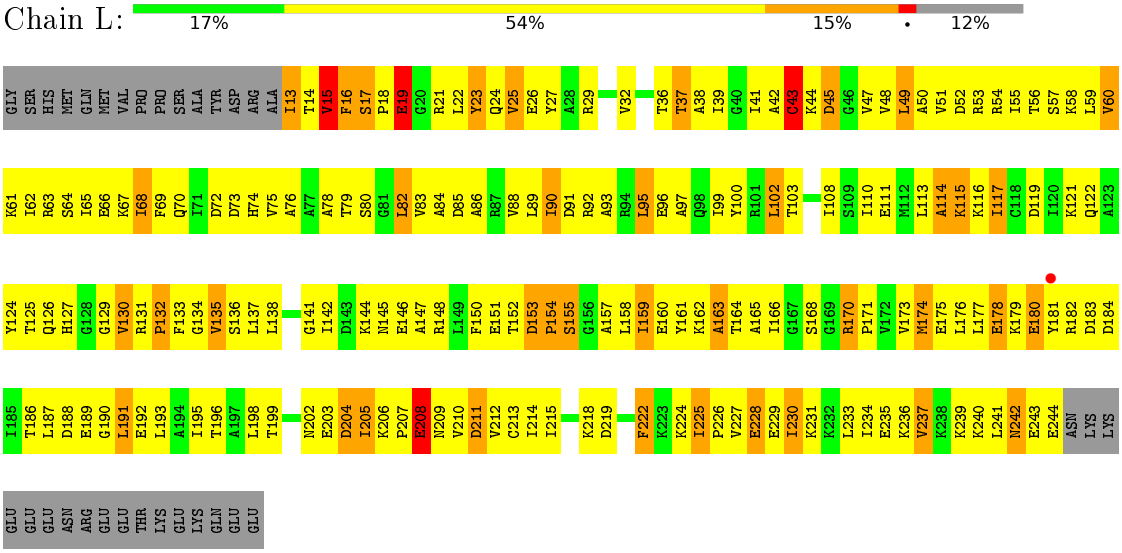
- Molecule 1: Proteasome subunit alpha

Chain K:



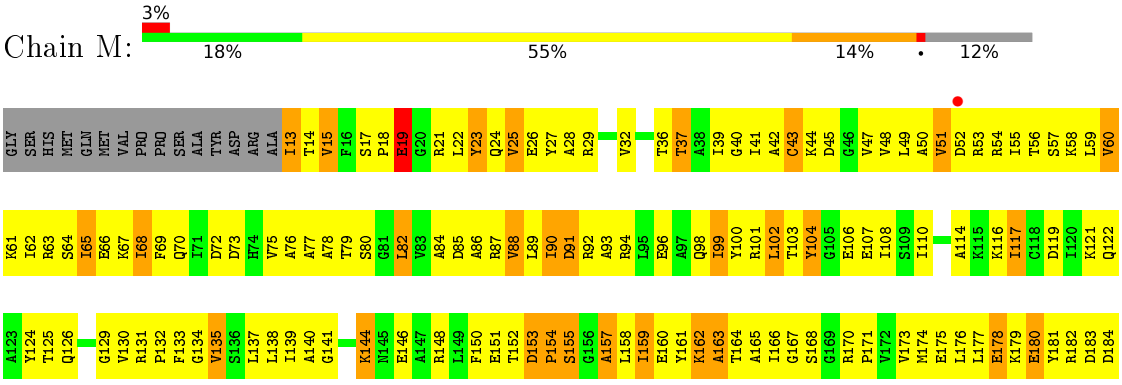
- Molecule 1: Proteasome subunit alpha

Chain L:



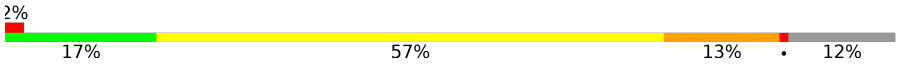
- Molecule 1: Proteasome subunit alpha

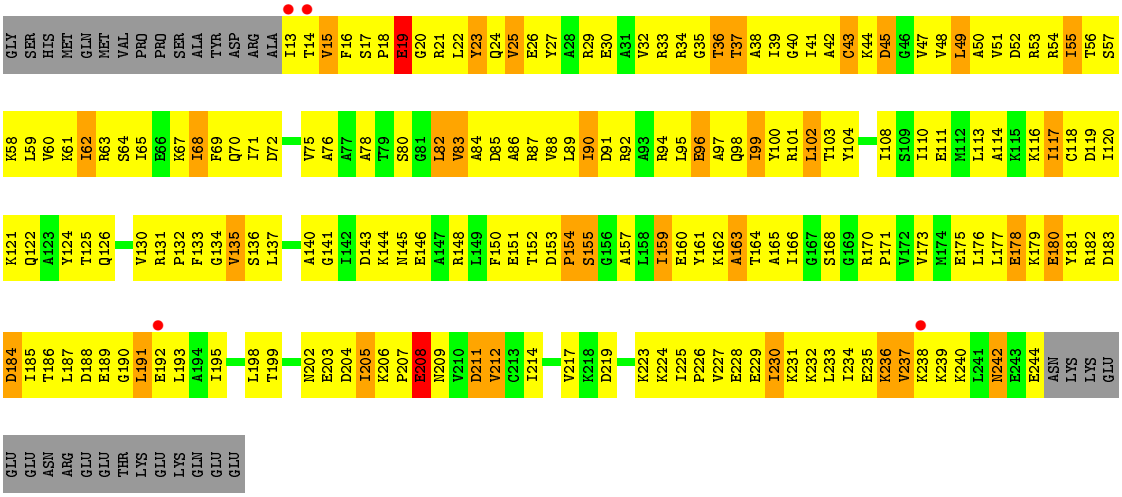
Chain M:



• Molecule 1: Proteasome subunit alpha

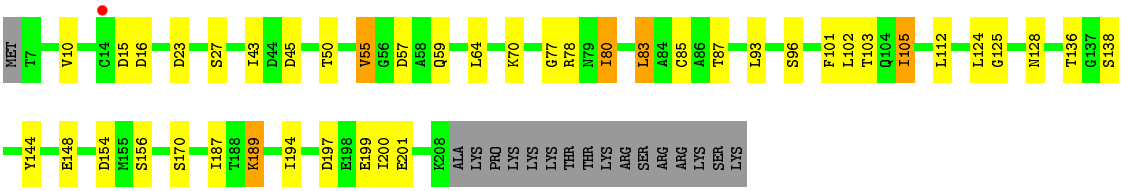
Chain N:





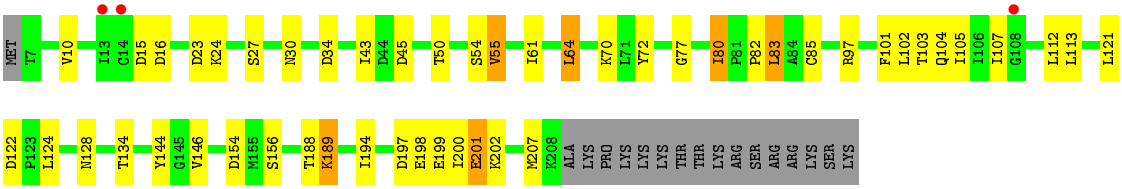
• Molecule 2: Proteasome subunit beta

Chain a:



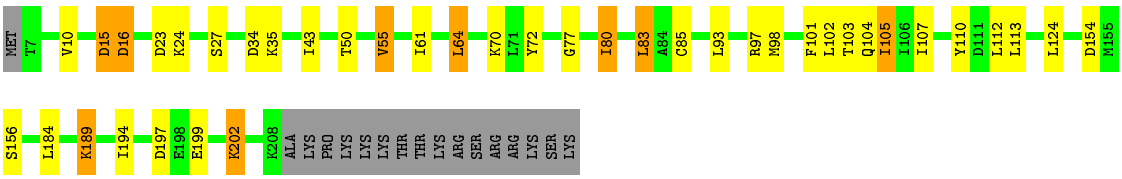
• Molecule 2: Proteasome subunit beta

Chain b:



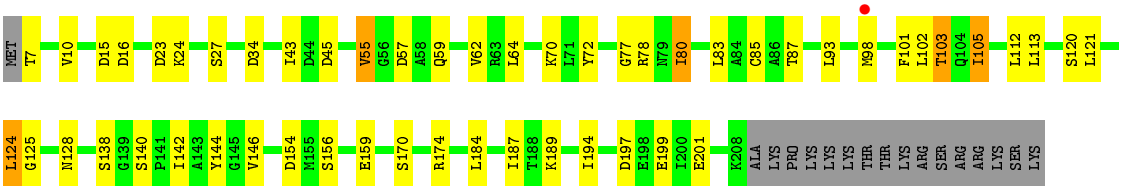
• Molecule 2: Proteasome subunit beta

Chain c:



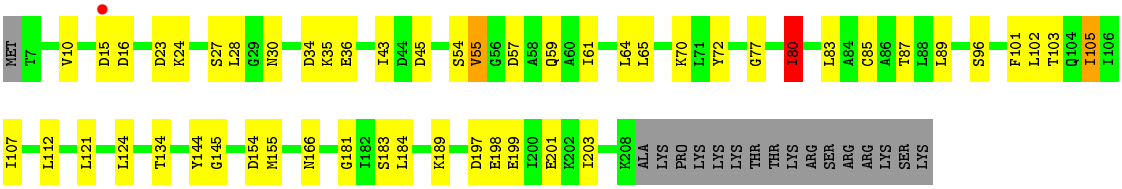
• Molecule 2: Proteasome subunit beta

Chain d:



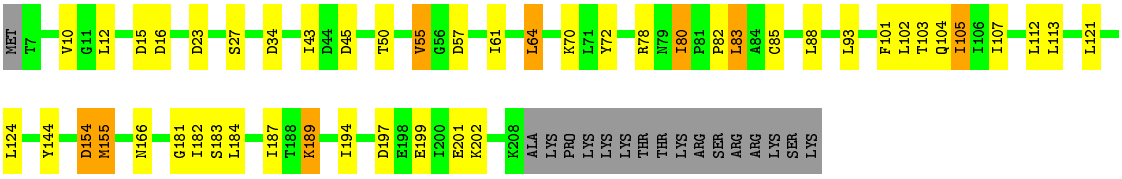
• Molecule 2: Proteasome subunit beta

Chain e:



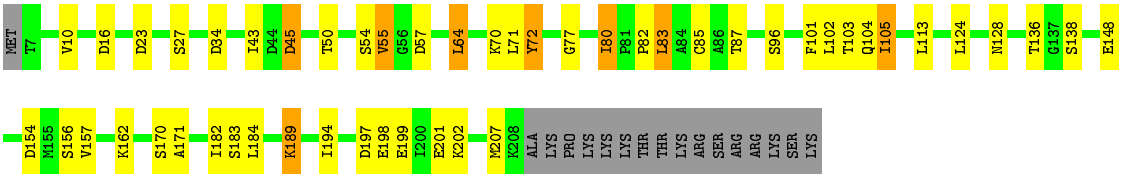
• Molecule 2: Proteasome subunit beta

Chain f:



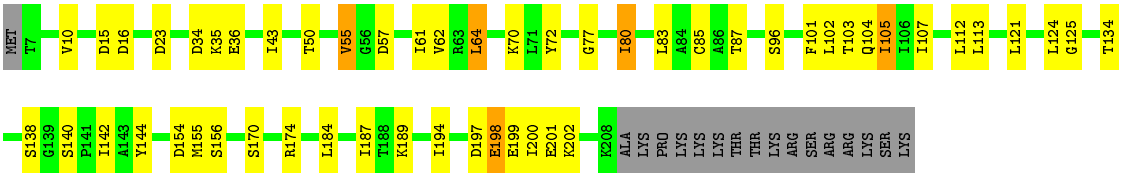
• Molecule 2: Proteasome subunit beta

Chain g:



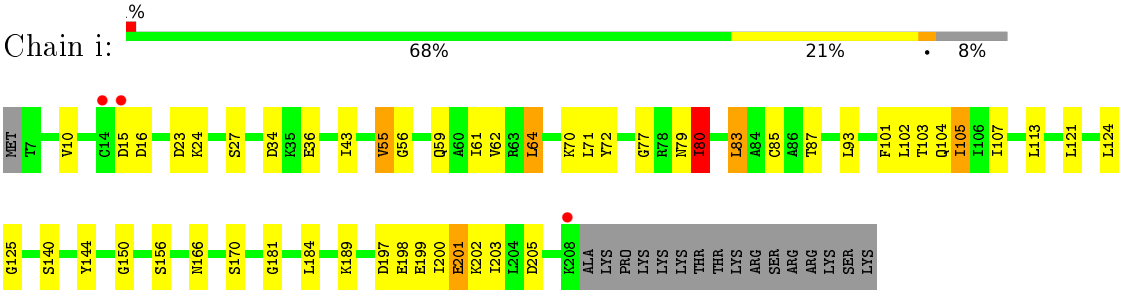
• Molecule 2: Proteasome subunit beta

Chain h:



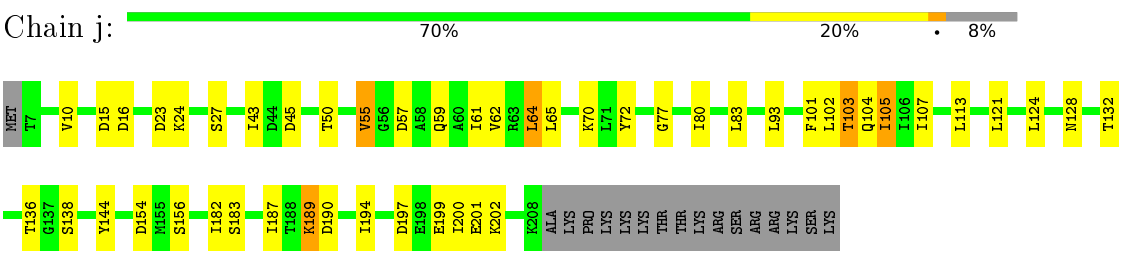
- Molecule 2: Proteasome subunit beta

Chain i:



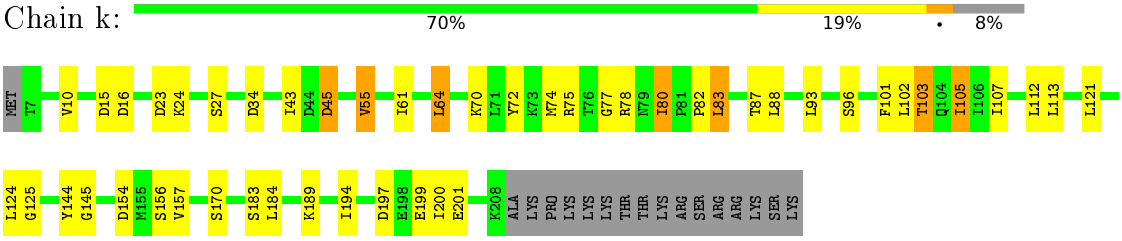
- Molecule 2: Proteasome subunit beta

Chain j:



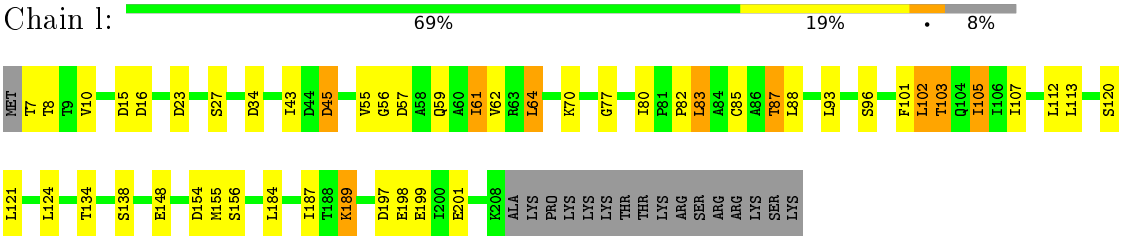
- Molecule 2: Proteasome subunit beta

Chain k:



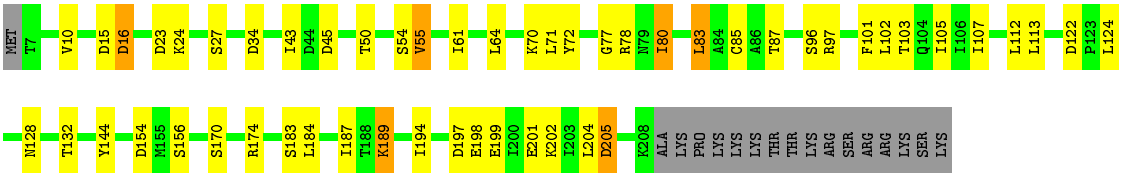
- Molecule 2: Proteasome subunit beta

Chain l:



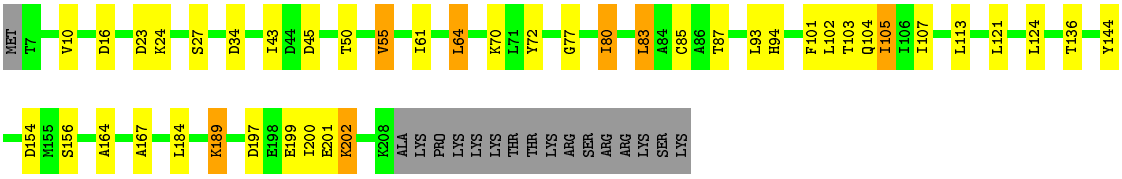
- Molecule 2: Proteasome subunit beta

Chain m:



- Molecule 2: Proteasome subunit beta

Chain n:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	206.72Å 219.54Å 149.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.98 – 4.10 49.98 – 4.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.98-4.10) 99.8 (49.98-4.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$< I/\sigma(I) >$ [1]	3.49 (at 4.14Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.254 , 0.325 0.232 , 0.307	Depositor DCC
R_{free} test set	2729 reflections (5.09%)	DCC
Wilson B-factor (Å^2)	118.1	Xtriage
Anisotropy	0.499	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 120.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Outliers	9 of 53849 reflections (0.017%)	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	46648	wwPDB-VP
Average B, all atoms (Å^2)	141.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.62 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.6646e-04.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.49	0/1832	0.66	0/2468
1	B	0.47	0/1832	0.67	0/2468
1	C	0.50	0/1832	0.69	0/2468
1	D	0.57	1/1832 (0.1%)	0.76	2/2468 (0.1%)
1	E	0.48	0/1832	0.69	1/2468 (0.0%)
1	F	0.57	0/1832	0.72	1/2468 (0.0%)
1	G	0.55	0/1832	0.73	0/2468
1	H	0.50	0/1832	0.69	1/2468 (0.0%)
1	I	0.49	0/1832	0.70	1/2468 (0.0%)
1	J	0.53	0/1832	0.69	0/2468
1	K	0.51	0/1832	0.69	0/2468
1	L	0.53	0/1832	0.70	0/2468
1	M	0.48	0/1832	0.67	0/2468
1	N	0.47	0/1832	0.65	0/2468
2	a	0.52	0/1536	0.72	0/2070
2	b	0.52	0/1536	0.74	1/2070 (0.0%)
2	c	0.51	0/1536	0.74	2/2070 (0.1%)
2	d	0.53	0/1536	0.77	1/2070 (0.0%)
2	e	0.55	0/1536	0.77	4/2070 (0.2%)
2	f	0.60	0/1536	0.80	1/2070 (0.0%)
2	g	0.58	0/1536	0.79	1/2070 (0.0%)
2	h	0.53	0/1536	0.75	1/2070 (0.0%)
2	i	0.57	0/1536	0.79	2/2070 (0.1%)
2	j	0.61	0/1536	0.84	1/2070 (0.0%)
2	k	0.59	0/1536	0.79	1/2070 (0.0%)
2	l	0.54	0/1536	0.79	3/2070 (0.1%)
2	m	0.51	0/1536	0.75	1/2070 (0.0%)
2	n	0.50	0/1536	0.74	1/2070 (0.0%)
All	All	0.53	1/47152 (0.0%)	0.73	26/63532 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	91	ASP	CB-CG	5.38	1.63	1.51

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	i	64	LEU	CA-CB-CG	7.58	132.73	115.30
2	e	64	LEU	CA-CB-CG	7.57	132.70	115.30
2	d	64	LEU	CA-CB-CG	7.28	132.04	115.30
2	l	64	LEU	CA-CB-CG	6.86	131.09	115.30
2	n	64	LEU	CA-CB-CG	6.73	130.77	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1813	0	1899	262	0
1	B	1813	0	1899	263	2
1	C	1813	0	1899	262	0
1	D	1813	0	1899	312	0
1	E	1813	0	1899	317	1
1	F	1813	0	1899	265	1
1	G	1813	0	1899	291	0
1	H	1813	0	1899	263	0
1	I	1813	0	1899	271	1
1	J	1813	0	1899	265	0
1	K	1813	0	1899	277	0
1	L	1813	0	1899	267	0
1	M	1813	0	1899	250	2
1	N	1813	0	1899	259	0
2	a	1519	0	1567	0	0
2	b	1519	0	1567	0	0
2	c	1519	0	1567	0	2
2	d	1519	0	1567	0	0
2	e	1519	0	1567	0	0
2	f	1519	0	1567	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	g	1519	0	1567	0	0
2	h	1519	0	1567	0	0
2	i	1519	0	1567	0	2
2	j	1519	0	1567	0	0
2	k	1519	0	1567	0	0
2	l	1519	0	1567	0	0
2	m	1519	0	1567	0	1
2	n	1519	0	1567	0	0
All	All	46648	0	48524	3529	7

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 69.

The worst 5 of 3529 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:178:GLU:HA	1:K:59:LEU:HD11	1.19	1.12
1:K:199:THR:HA	1:K:205:ILE:HD11	1.32	1.11
1:A:178:GLU:HA	1:B:59:LEU:HD11	1.28	1.09
1:E:38:ALA:HB2	1:E:51:VAL:HG13	1.17	1.09
1:F:190:GLY:HA2	1:F:193:LEU:HD22	1.34	1.08

The worst 5 of 7 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)
1:B:232:LYS:O	2:c:110:TYR:OH[2_565]	1.88	0.32
1:I:242:ASN:O	2:m:205:ASP:OD1[4_555]	2.00	0.20
1:M:243:GLU:N	2:i:205:ASP:OD1[4_455]	2.03	0.17
1:E:180:GLU:O	1:E:182:ARG:NH2[2_665]	2.09	0.11
1:B:231:LYS:NZ	2:c:15:ASP:OD1[2_565]	2.17	0.03

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	230/264 (87%)	163 (71%)	43 (19%)	24 (10%)	1 12
1	B	230/264 (87%)	162 (70%)	46 (20%)	22 (10%)	1 14
1	C	230/264 (87%)	155 (67%)	51 (22%)	24 (10%)	1 12
1	D	230/264 (87%)	158 (69%)	47 (20%)	25 (11%)	0 11
1	E	230/264 (87%)	158 (69%)	47 (20%)	25 (11%)	0 11
1	F	230/264 (87%)	152 (66%)	53 (23%)	25 (11%)	0 11
1	G	230/264 (87%)	156 (68%)	51 (22%)	23 (10%)	1 13
1	H	230/264 (87%)	153 (66%)	49 (21%)	28 (12%)	0 8
1	I	230/264 (87%)	159 (69%)	44 (19%)	27 (12%)	0 9
1	J	230/264 (87%)	161 (70%)	45 (20%)	24 (10%)	1 12
1	K	230/264 (87%)	151 (66%)	51 (22%)	28 (12%)	0 8
1	L	230/264 (87%)	162 (70%)	39 (17%)	29 (13%)	0 8
1	M	230/264 (87%)	159 (69%)	45 (20%)	26 (11%)	0 10
1	N	230/264 (87%)	159 (69%)	48 (21%)	23 (10%)	1 13
2	a	200/219 (91%)	135 (68%)	45 (22%)	20 (10%)	1 13
2	b	200/219 (91%)	129 (64%)	53 (26%)	18 (9%)	1 17
2	c	200/219 (91%)	140 (70%)	45 (22%)	15 (8%)	1 21
2	d	200/219 (91%)	132 (66%)	46 (23%)	22 (11%)	0 11
2	e	200/219 (91%)	136 (68%)	46 (23%)	18 (9%)	1 17
2	f	200/219 (91%)	142 (71%)	42 (21%)	16 (8%)	1 19
2	g	200/219 (91%)	132 (66%)	43 (22%)	25 (12%)	0 8
2	h	200/219 (91%)	136 (68%)	44 (22%)	20 (10%)	1 13
2	i	200/219 (91%)	130 (65%)	46 (23%)	24 (12%)	0 8
2	j	200/219 (91%)	145 (72%)	39 (20%)	16 (8%)	1 19
2	k	200/219 (91%)	126 (63%)	50 (25%)	24 (12%)	0 8
2	l	200/219 (91%)	143 (72%)	37 (18%)	20 (10%)	1 13
2	m	200/219 (91%)	139 (70%)	43 (22%)	18 (9%)	1 17
2	n	200/219 (91%)	136 (68%)	46 (23%)	18 (9%)	1 17
All	All	6020/6762 (89%)	4109 (68%)	1284 (21%)	627 (10%)	1 12

5 of 627 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	TYR
1	A	43	CYS
1	A	132	PRO
1	A	155	SER
1	A	168	SER

5.3.2 Protein sidechains (i)

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	195/224 (87%)	171 (88%)	24 (12%)	6 33
1	B	195/224 (87%)	167 (86%)	28 (14%)	4 27
1	C	195/224 (87%)	170 (87%)	25 (13%)	5 31
1	D	195/224 (87%)	170 (87%)	25 (13%)	5 31
1	E	195/224 (87%)	166 (85%)	29 (15%)	4 26
1	F	195/224 (87%)	165 (85%)	30 (15%)	3 24
1	G	195/224 (87%)	166 (85%)	29 (15%)	4 26
1	H	195/224 (87%)	162 (83%)	33 (17%)	2 20
1	I	195/224 (87%)	166 (85%)	29 (15%)	4 26
1	J	195/224 (87%)	170 (87%)	25 (13%)	5 31
1	K	195/224 (87%)	170 (87%)	25 (13%)	5 31
1	L	195/224 (87%)	166 (85%)	29 (15%)	4 26
1	M	195/224 (87%)	169 (87%)	26 (13%)	5 30
1	N	195/224 (87%)	170 (87%)	25 (13%)	5 31
2	a	163/179 (91%)	135 (83%)	28 (17%)	2 19
2	b	163/179 (91%)	126 (77%)	37 (23%)	1 9
2	c	163/179 (91%)	133 (82%)	30 (18%)	2 16
2	d	163/179 (91%)	128 (78%)	35 (22%)	1 10
2	e	163/179 (91%)	129 (79%)	34 (21%)	1 11
2	f	163/179 (91%)	125 (77%)	38 (23%)	1 8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	g	163/179 (91%)	131 (80%)	32 (20%)	1 14
2	h	163/179 (91%)	126 (77%)	37 (23%)	1 9
2	i	163/179 (91%)	132 (81%)	31 (19%)	2 14
2	j	163/179 (91%)	126 (77%)	37 (23%)	1 9
2	k	163/179 (91%)	132 (81%)	31 (19%)	2 14
2	l	163/179 (91%)	127 (78%)	36 (22%)	1 10
2	m	163/179 (91%)	124 (76%)	39 (24%)	1 7
2	n	163/179 (91%)	132 (81%)	31 (19%)	2 14
All	All	5012/5642 (89%)	4154 (83%)	858 (17%)	2 19

5 of 858 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	f	189	LYS
1	I	210	VAL
2	m	27	SER
2	g	50	THR
1	H	60	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	g	128	ASN
1	N	98	GLN

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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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	232/264 (87%)	-0.08	6 (2%) 59 48	127, 157, 221, 336	0
1	B	232/264 (87%)	0.03	6 (2%) 59 48	118, 151, 270, 519	0
1	C	232/264 (87%)	-0.25	2 (0%) 85 79	114, 132, 205, 333	0
1	D	232/264 (87%)	-0.39	0 100 100	59, 134, 205, 245	0
1	E	232/264 (87%)	-0.14	7 (3%) 54 41	82, 139, 252, 355	0
1	F	232/264 (87%)	-0.18	4 (1%) 73 63	92, 116, 204, 346	0
1	G	232/264 (87%)	-0.32	2 (0%) 85 79	106, 128, 215, 284	0
1	H	232/264 (87%)	-0.30	1 (0%) 93 90	131, 148, 187, 271	0
1	I	232/264 (87%)	-0.23	3 (1%) 79 71	90, 136, 212, 299	0
1	J	232/264 (87%)	-0.01	10 (4%) 39 29	81, 141, 259, 366	0
1	K	232/264 (87%)	-0.27	0 100 100	112, 139, 220, 291	0
1	L	232/264 (87%)	-0.24	1 (0%) 93 90	113, 135, 208, 253	0
1	M	232/264 (87%)	-0.01	9 (3%) 43 33	126, 143, 253, 507	0
1	N	232/264 (87%)	-0.16	4 (1%) 73 63	130, 147, 186, 303	0
2	a	202/219 (92%)	-0.41	1 (0%) 91 88	118, 138, 170, 185	0
2	b	202/219 (92%)	-0.13	3 (1%) 76 67	113, 131, 161, 180	0
2	c	202/219 (92%)	-0.36	0 100 100	101, 119, 195, 251	0
2	d	202/219 (92%)	-0.41	1 (0%) 91 88	107, 124, 162, 194	0
2	e	202/219 (92%)	-0.42	1 (0%) 91 88	93, 111, 159, 203	0
2	f	202/219 (92%)	-0.37	0 100 100	100, 115, 150, 175	0
2	g	202/219 (92%)	-0.32	0 100 100	110, 125, 149, 171	0
2	h	202/219 (92%)	-0.39	0 100 100	123, 139, 174, 186	0
2	i	202/219 (92%)	-0.36	3 (1%) 76 67	110, 123, 155, 170	0
2	j	202/219 (92%)	-0.48	0 100 100	72, 87, 159, 212	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
2	k	202/219 (92%)	-0.43	0	100	100	80, 102, 177, 209	0
2	l	202/219 (92%)	-0.41	0	100	100	104, 120, 160, 193	0
2	m	202/219 (92%)	-0.34	0	100	100	102, 122, 213, 254	0
2	n	202/219 (92%)	-0.26	0	100	100	122, 148, 181, 195	0
All	All	6076/6762 (89%)	-0.27	64 (1%)	82	75	59, 134, 207, 519	0

The worst 5 of 64 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	244	GLU	6.5
1	J	13	ILE	5.4
1	E	236	LYS	5.2
1	J	244	GLU	4.8
1	A	244	GLU	4.3

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.