wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 08:13 PM GMT

PDB ID	:	4QV9
Title	:	yCP beta5-C63F mutant
Authors	:	Huber, E.M.; Heinemeyer, W.; Groll, M.
Deposited on	:	2014-07-14
Resolution	:	2.60 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:

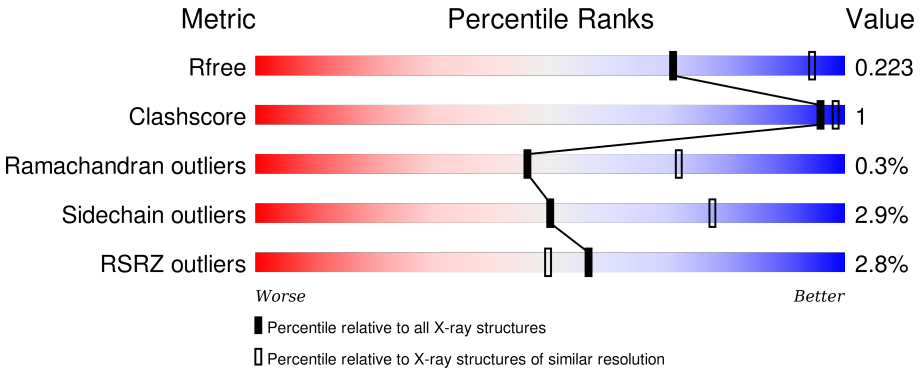
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	250	3% 98% •
1	O	250	4% 96% •
2	B	258	4% 88% 7% 5%
2	P	258	5% 87% 7% • 5%
3	C	254	6% 87% 6% • 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	9% 87% 6% 6%
4	D	260	3% 85% 5% 10%
4	R	260	4% 85% 5% 10%
5	E	234	3% 93% 6%
5	S	234	4% 93% 6%
6	F	288	3% 82% 16%
6	T	288	3% 82% 16%
7	G	252	% 90% 5%
7	U	252	3% 90% 5%
8	H	232	3% 93% 5%
8	V	232	2% 93%
9	I	205	94% 6%
9	W	205	% 95% 5%
10	J	198	% 92% 6%
10	X	198	2% 91% 7%
11	K	212	% 90% 10%
11	Y	212	% 90% 10%
12	L	222	98%
12	Z	222	% 98%
13	M	246	% 91% 5%
13	a	246	92% 5%
14	N	196	% 95% 5%
14	b	196	2% 97%

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	301	-	-	-	X
15	MG	K	302	-	-	-	X
15	MG	Z	301	-	-	-	X

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 50245 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
			1649	1051	280	312	6			
11	Y	212	Total	C	N	O	S	0	0	0
			1649	1051	280	312	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	63	PHE	CYS	ENGINEERED MUTATION	UNP P30656
Y	63	PHE	CYS	ENGINEERED MUTATION	UNP P30656

- 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 1 1	0	0
15	J	1	Total Mg 1 1	0	0
15	K	2	Total Mg 2 2	0	0
15	H	1	Total Mg 1 1	0	0
15	I	1	Total Mg 1 1	0	0
15	V	1	Total Mg 1 1	0	0
15	Z	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	Y	1	Total Mg 1 1	0	0

- Molecule 16 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0

- Molecule 17 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	30	Total O 30 30	0	0
17	B	24	Total O 24 24	0	0
17	C	20	Total O 20 20	0	0
17	D	29	Total O 29 29	0	0
17	E	18	Total O 18 18	0	0
17	F	28	Total O 28 28	0	0
17	G	46	Total O 46 46	0	0

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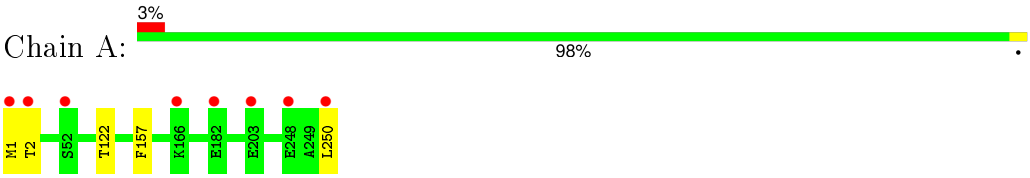
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	H	32	Total O 32 32	0	0
17	I	43	Total O 43 43	0	0
17	J	30	Total O 30 30	0	0
17	K	44	Total O 44 44	0	0
17	L	50	Total O 50 50	0	0
17	M	47	Total O 47 47	0	0
17	N	37	Total O 37 37	0	0
17	O	14	Total O 14 14	0	0
17	P	17	Total O 17 17	0	0
17	Q	23	Total O 23 23	0	0
17	R	25	Total O 25 25	0	0
17	S	9	Total O 9 9	0	0
17	T	21	Total O 21 21	0	0
17	U	32	Total O 32 32	0	0
17	V	28	Total O 28 28	0	0
17	W	34	Total O 34 34	0	0
17	X	30	Total O 30 30	0	0
17	Y	34	Total O 34 34	0	0
17	Z	31	Total O 31 31	0	0
17	a	46	Total O 46 46	0	0
17	b	35	Total O 35 35	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.

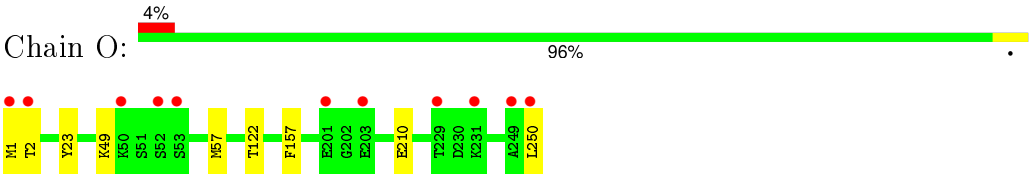
- Molecule 1: Proteasome subunit alpha type-2

Chain A:



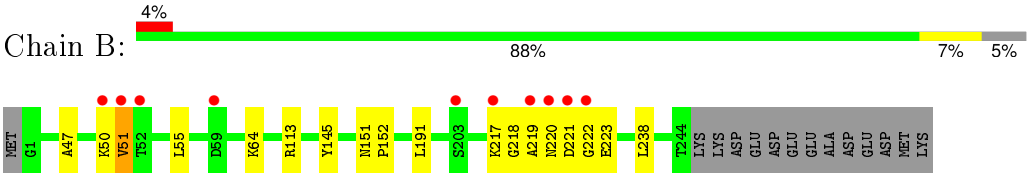
- Molecule 1: Proteasome subunit alpha type-2

Chain O:



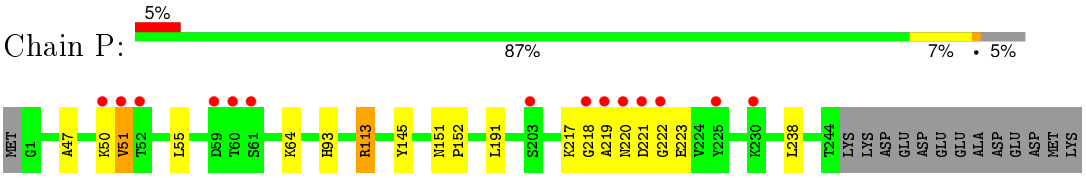
- Molecule 2: Proteasome subunit alpha type-3

Chain B:



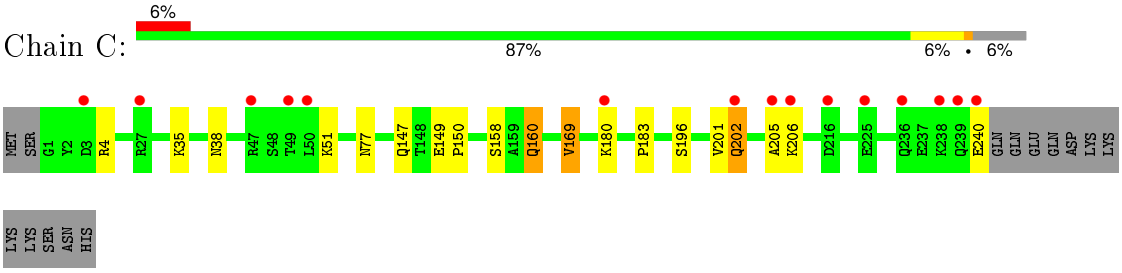
- Molecule 2: Proteasome subunit alpha type-3

Chain P:



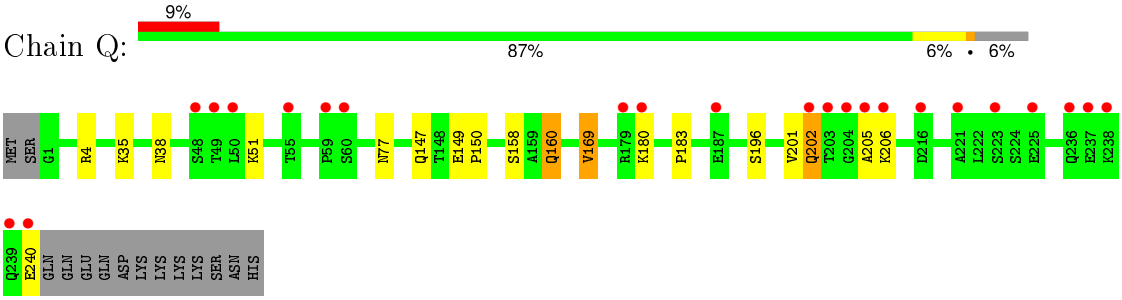
- Molecule 3: Proteasome subunit alpha type-4

Chain C:



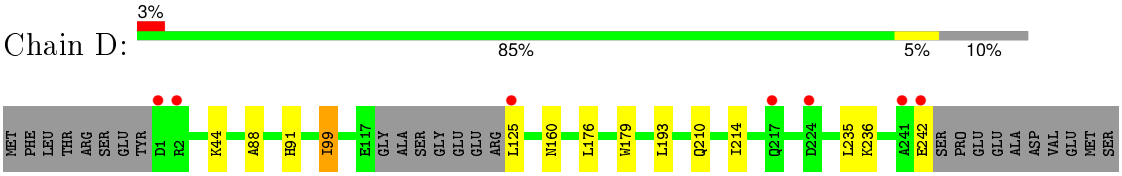
• Molecule 3: Proteasome subunit alpha type-4

Chain Q:



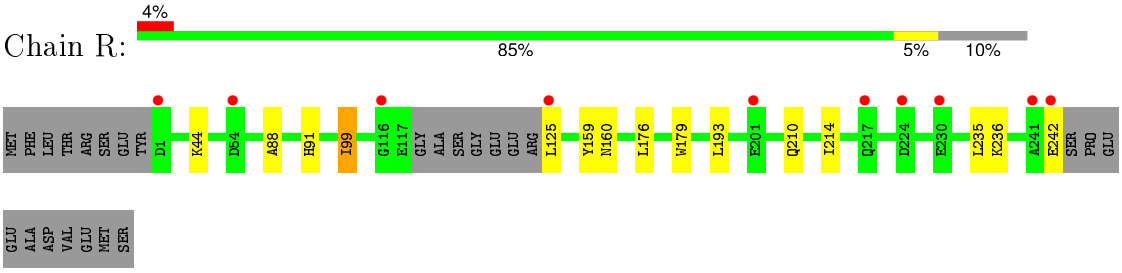
• Molecule 4: Proteasome subunit alpha type-5

Chain D:



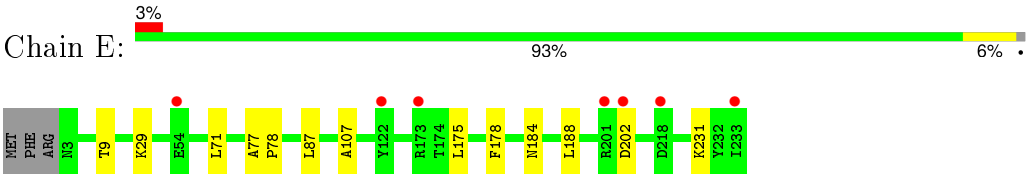
• Molecule 4: Proteasome subunit alpha type-5

Chain R:



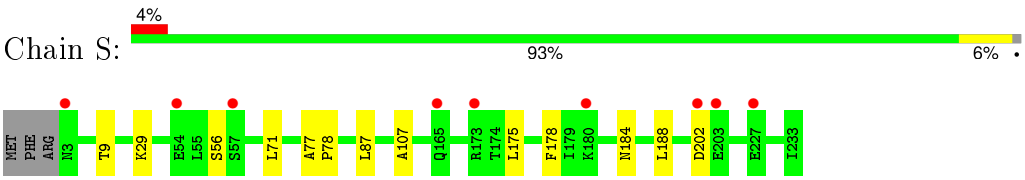
• Molecule 5: Proteasome subunit alpha type-6

Chain E:



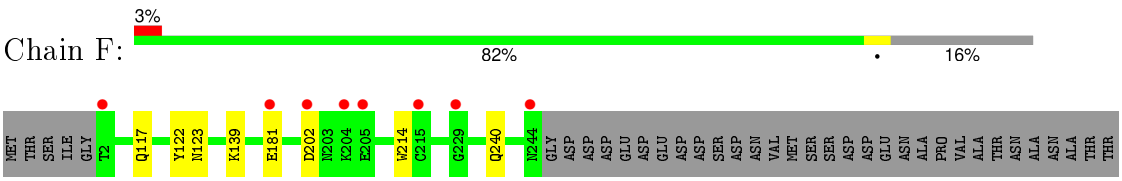
• Molecule 5: Proteasome subunit alpha type-6

Chain S:

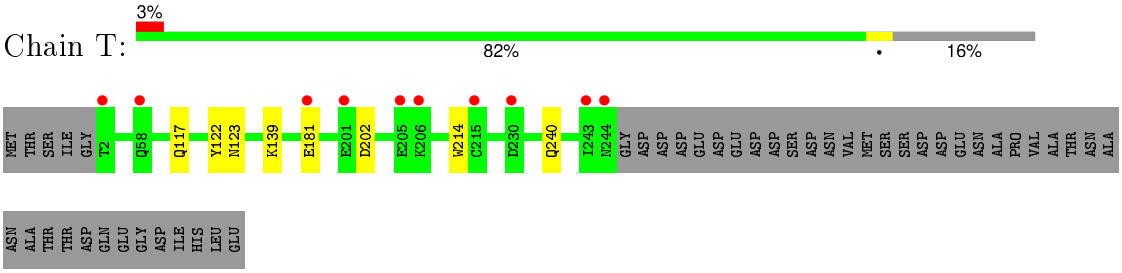


• Molecule 6: Probable proteasome subunit alpha type-7

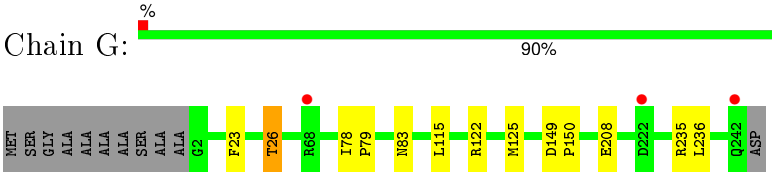
Chain F:



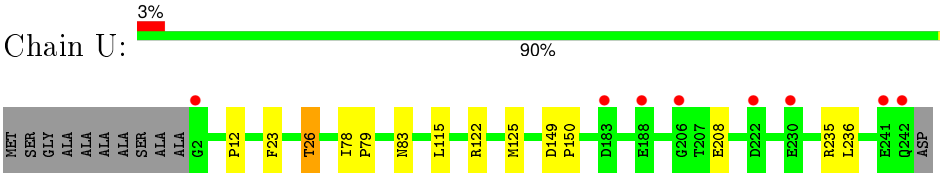
• Molecule 6: Probable proteasome subunit alpha type-7



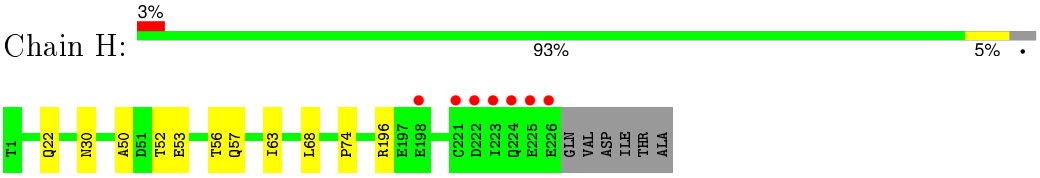
• Molecule 7: Proteasome subunit alpha type-1



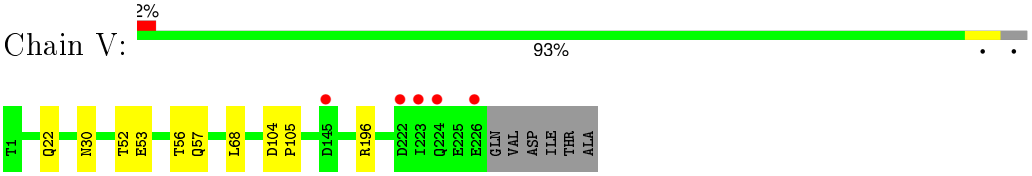
• Molecule 7: Proteasome subunit alpha type-1



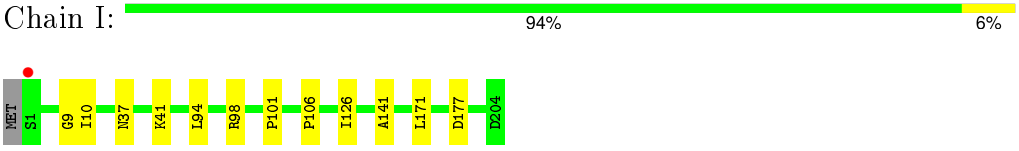
• Molecule 8: Proteasome subunit beta type-2



• Molecule 8: Proteasome subunit beta type-2

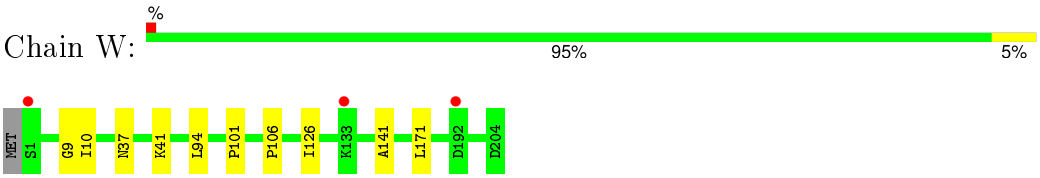


• Molecule 9: Proteasome subunit beta type-3



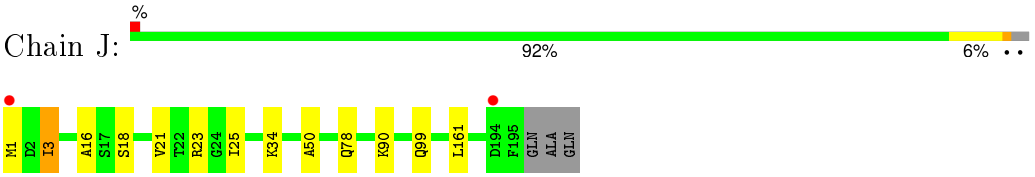
• Molecule 9: Proteasome subunit beta type-3

Chain W:



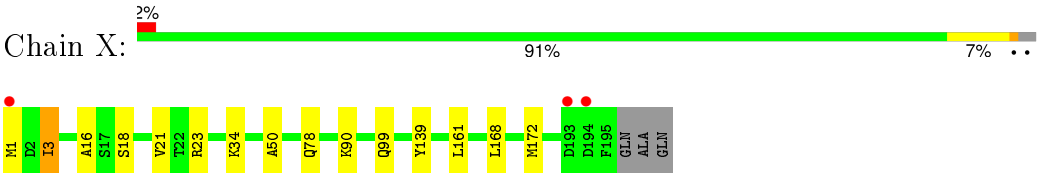
• Molecule 10: Proteasome subunit beta type-4

Chain J:



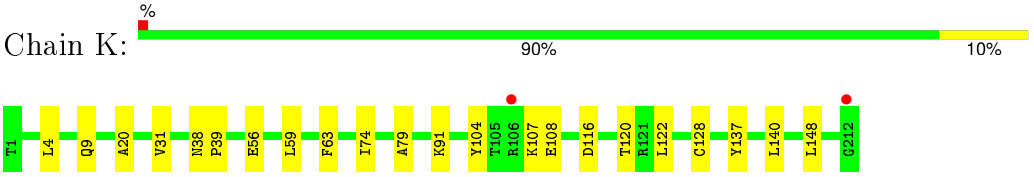
• Molecule 10: Proteasome subunit beta type-4

Chain X:



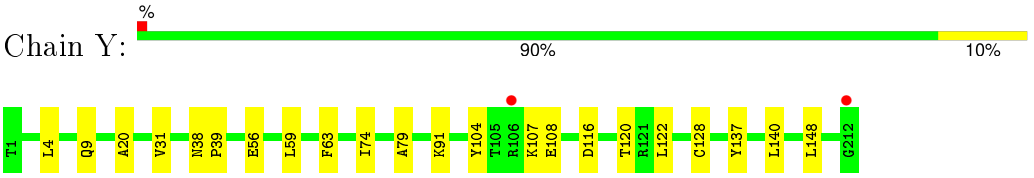
• Molecule 11: Proteasome subunit beta type-5

Chain K:



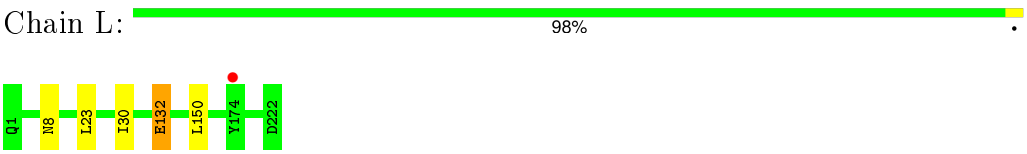
• Molecule 11: Proteasome subunit beta type-5

Chain Y:



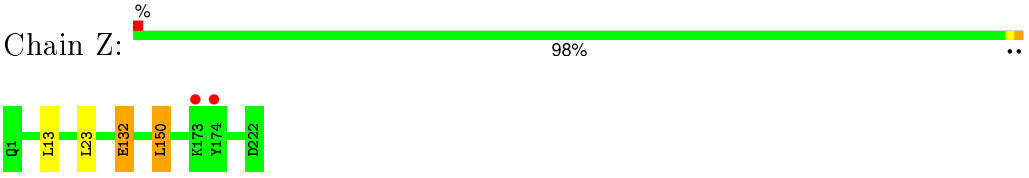
• Molecule 12: Proteasome subunit beta type-6

Chain L:



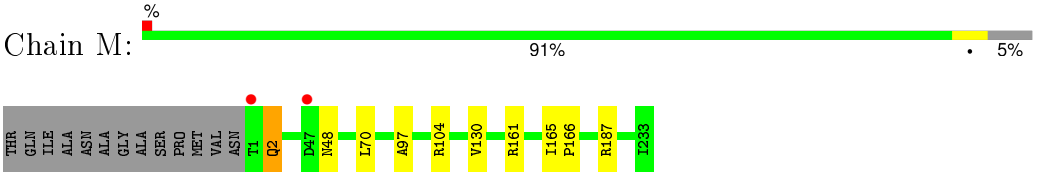
• Molecule 12: Proteasome subunit beta type-6

Chain Z:



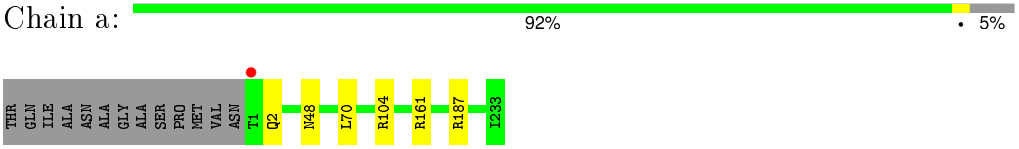
• Molecule 13: Proteasome subunit beta type-7

Chain M:



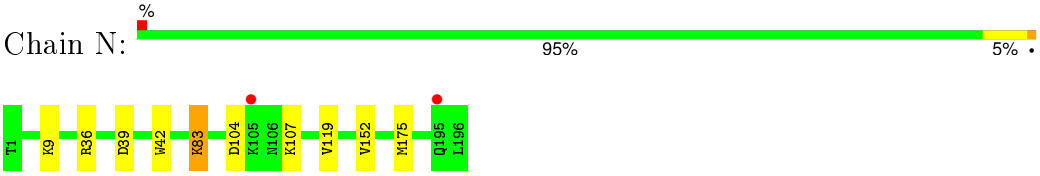
- Molecule 13: Proteasome subunit beta type-7

Chain a:



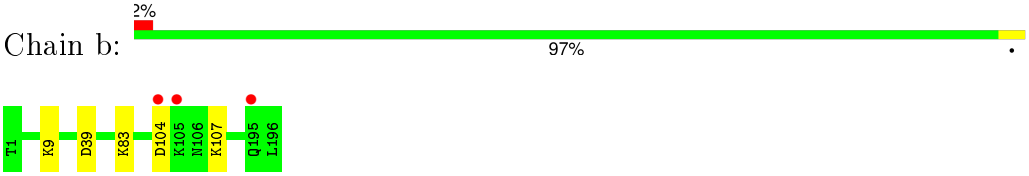
- Molecule 14: Proteasome subunit beta type-1

Chain N:



- Molecule 14: Proteasome subunit beta type-1

Chain b:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	134.20Å 300.45Å 143.41Å 90.00° 113.07° 90.00°	Depositor
Resolution (Å)	15.00 – 2.60 15.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.2 (15.00-2.60) 98.2 (15.00-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.89 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.196 , 0.218 0.202 , 0.223	Depositor DCC
R_{free} test set	15584 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	48.6	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 36.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 311693 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	50245	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

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

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	0.26	0/1952	0.46	0/2642
1	O	0.26	0/1952	0.46	0/2642
2	B	0.27	0/1934	0.49	0/2618
2	P	0.27	0/1934	0.49	0/2618
3	C	0.27	0/1910	0.50	0/2586
3	Q	0.27	0/1910	0.50	0/2586
4	D	0.26	0/1837	0.46	0/2475
4	R	0.26	0/1837	0.46	0/2475
5	E	0.26	0/1800	0.46	0/2433
5	S	0.26	0/1800	0.46	0/2433
6	F	0.27	0/1932	0.44	0/2609
6	T	0.26	0/1932	0.44	0/2609
7	G	0.27	0/1945	0.46	0/2634
7	U	0.26	0/1945	0.46	0/2634
8	H	0.24	0/1750	0.45	0/2373
8	V	0.25	0/1750	0.45	0/2373
9	I	0.27	0/1611	0.47	0/2174
9	W	0.26	0/1611	0.47	0/2174
10	J	0.26	0/1589	0.48	0/2142
10	X	0.26	0/1589	0.47	0/2142
11	K	0.32	0/1687	0.49	0/2282
11	Y	0.32	0/1687	0.49	0/2282
12	L	0.27	0/1795	0.47	0/2420
12	Z	0.26	0/1795	0.47	0/2420
13	M	0.27	0/1855	0.50	0/2514
13	a	0.27	0/1855	0.50	0/2514
14	N	0.25	0/1541	0.47	0/2087
14	b	0.25	0/1541	0.47	0/2087
All	All	0.27	0/50276	0.47	0/67978

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	1	0
1	O	1915	0	1929	4	0
2	B	1904	0	1904	6	0
2	P	1904	0	1904	9	0
3	C	1881	0	1895	6	0
3	Q	1881	0	1895	6	0
4	D	1813	0	1797	5	0
4	R	1813	0	1797	6	0
5	E	1773	0	1775	3	0
5	S	1773	0	1775	4	0
6	F	1892	0	1883	1	0
6	T	1892	0	1883	1	0
7	G	1907	0	1901	3	0
7	U	1907	0	1901	4	0
8	H	1719	0	1719	4	0
8	V	1719	0	1719	3	0
9	I	1581	0	1574	7	0
9	W	1581	0	1574	4	0
10	J	1561	0	1569	7	0
10	X	1561	0	1569	8	0
11	K	1649	0	1599	23	0
11	Y	1649	0	1599	26	0
12	L	1757	0	1711	2	0
12	Z	1757	0	1711	2	0
13	M	1824	0	1832	3	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	3	0
14	b	1512	0	1481	0	0
15	G	1	0	0	0	0
15	H	1	0	0	0	0
15	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	J	1	0	0	0	0
15	K	2	0	0	0	0
15	N	1	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	G	1	0	0	0	0
16	U	1	0	0	0	0
17	A	30	0	0	0	0
17	B	24	0	0	0	0
17	C	20	0	0	0	0
17	D	29	0	0	0	0
17	E	18	0	0	0	0
17	F	28	0	0	0	0
17	G	46	0	0	0	0
17	H	32	0	0	0	0
17	I	43	0	0	0	0
17	J	30	0	0	0	0
17	K	44	0	0	0	0
17	L	50	0	0	0	0
17	M	47	0	0	1	0
17	N	37	0	0	0	0
17	O	14	0	0	0	0
17	P	17	0	0	2	0
17	Q	23	0	0	0	0
17	R	25	0	0	0	0
17	S	9	0	0	0	0
17	T	21	0	0	0	0
17	U	32	0	0	1	0
17	V	28	0	0	0	0
17	W	34	0	0	0	0
17	X	30	0	0	0	0
17	Y	34	0	0	0	0
17	Z	31	0	0	0	0
17	a	46	0	0	0	0
17	b	35	0	0	0	0
All	All	50245	0	49138	139	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 1.

The worst 5 of 139 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)
11:K:63:PHE:HE1	11:K:79:ALA:HB1	1.33	0.91
11:Y:63:PHE:HD1	11:Y:74:ILE:HG21	1.35	0.90
11:Y:59:LEU:HG	11:Y:63:PHE:CE2	2.14	0.82
11:Y:63:PHE:HE1	11:Y:79:ALA:CB	1.92	0.82
11:K:59:LEU:O	11:K:63:PHE:HD2	1.63	0.82

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%)	240 (97%)	7 (3%)	1 (0%)	39	65
1	O	248/250 (99%)	239 (96%)	8 (3%)	1 (0%)	39	65
2	B	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	11	22
2	P	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	11	22
3	C	238/254 (94%)	233 (98%)	2 (1%)	3 (1%)	15	30
3	Q	238/254 (94%)	233 (98%)	2 (1%)	3 (1%)	15	30
4	D	231/260 (89%)	227 (98%)	4 (2%)	0	100	100
4	R	231/260 (89%)	228 (99%)	3 (1%)	0	100	100
5	E	229/234 (98%)	220 (96%)	9 (4%)	0	100	100
5	S	229/234 (98%)	220 (96%)	9 (4%)	0	100	100
6	F	241/288 (84%)	236 (98%)	5 (2%)	0	100	100
6	T	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
7	G	239/252 (95%)	236 (99%)	3 (1%)	0	100	100
7	U	239/252 (95%)	236 (99%)	3 (1%)	0	100	100
8	H	224/232 (97%)	218 (97%)	6 (3%)	0	100	100
8	V	224/232 (97%)	219 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
10	X	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
11	K	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
11	Y	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
12	L	220/222 (99%)	213 (97%)	7 (3%)	0	100	100
12	Z	220/222 (99%)	213 (97%)	7 (3%)	0	100	100
13	M	231/246 (94%)	223 (96%)	8 (4%)	0	100	100
13	a	231/246 (94%)	223 (96%)	8 (4%)	0	100	100
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%)	6118 (97%)	150 (2%)	16 (0%)	46	72

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR
2	B	51	VAL
3	C	202	GLN
2	P	51	VAL
3	Q	202	GLN

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	209/209 (100%)	206 (99%)	3 (1%)	74	90
1	O	209/209 (100%)	206 (99%)	3 (1%)	74	90
2	B	203/216 (94%)	199 (98%)	4 (2%)	63	85
2	P	203/216 (94%)	199 (98%)	4 (2%)	63	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	C	212/226 (94%)	202 (95%)	10 (5%)	32 59
3	Q	212/226 (94%)	202 (95%)	10 (5%)	32 59
4	D	194/215 (90%)	186 (96%)	8 (4%)	37 66
4	R	194/215 (90%)	186 (96%)	8 (4%)	37 66
5	E	190/193 (98%)	183 (96%)	7 (4%)	41 69
5	S	190/193 (98%)	184 (97%)	6 (3%)	46 74
6	F	201/239 (84%)	194 (96%)	7 (4%)	43 71
6	T	201/239 (84%)	194 (96%)	7 (4%)	43 71
7	G	206/210 (98%)	198 (96%)	8 (4%)	39 68
7	U	206/210 (98%)	198 (96%)	8 (4%)	39 68
8	H	185/190 (97%)	181 (98%)	4 (2%)	60 83
8	V	185/190 (97%)	181 (98%)	4 (2%)	60 83
9	I	172/173 (99%)	170 (99%)	2 (1%)	78 92
9	W	172/173 (99%)	170 (99%)	2 (1%)	78 92
10	J	173/175 (99%)	168 (97%)	5 (3%)	50 77
10	X	173/175 (99%)	168 (97%)	5 (3%)	50 77
11	K	169/169 (100%)	164 (97%)	5 (3%)	48 76
11	Y	169/169 (100%)	164 (97%)	5 (3%)	48 76
12	L	185/185 (100%)	182 (98%)	3 (2%)	70 89
12	Z	185/185 (100%)	182 (98%)	3 (2%)	70 89
13	M	199/208 (96%)	193 (97%)	6 (3%)	48 76
13	a	199/208 (96%)	193 (97%)	6 (3%)	48 76
14	N	162/162 (100%)	157 (97%)	5 (3%)	47 76
14	b	162/162 (100%)	157 (97%)	5 (3%)	47 76
All	All	5320/5540 (96%)	5167 (97%)	153 (3%)	50 77

5 of 153 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	104	ARG
3	Q	38	ASN
12	Z	150	LEU
13	M	187	ARG
1	O	122	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
12	L	70	ASN
2	P	123	GLN
12	Z	3	ASN
12	L	158	ASN
1	O	94	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	250/250 (100%)	-0.30	8 (3%) 51 44	32, 46, 83, 118	0
1	O	250/250 (100%)	-0.19	11 (4%) 38 30	37, 54, 100, 126	0
2	B	244/258 (94%)	-0.12	10 (4%) 41 33	35, 52, 97, 156	0
2	P	244/258 (94%)	-0.09	14 (5%) 27 20	38, 55, 99, 150	0
3	C	240/254 (94%)	-0.08	15 (6%) 23 17	33, 55, 118, 145	0
3	Q	240/254 (94%)	0.24	23 (9%) 10 6	42, 69, 149, 179	0
4	D	235/260 (90%)	-0.27	7 (2%) 54 47	36, 56, 89, 128	0
4	R	235/260 (90%)	-0.11	10 (4%) 39 31	39, 62, 108, 146	0
5	E	231/234 (98%)	-0.22	7 (3%) 54 47	37, 58, 94, 131	0
5	S	231/234 (98%)	-0.01	9 (3%) 43 35	41, 66, 110, 148	0
6	F	243/288 (84%)	-0.35	8 (3%) 50 43	32, 52, 99, 126	0
6	T	243/288 (84%)	-0.20	10 (4%) 41 33	36, 63, 116, 149	0
7	G	241/252 (95%)	-0.43	3 (1%) 81 77	29, 47, 80, 130	0
7	U	241/252 (95%)	-0.29	8 (3%) 50 43	37, 52, 86, 133	0
8	H	226/232 (97%)	-0.30	7 (3%) 52 45	29, 45, 76, 140	0
8	V	226/232 (97%)	-0.31	5 (2%) 65 59	32, 48, 77, 162	0
9	I	204/205 (99%)	-0.61	1 (0%) 91 90	28, 41, 67, 92	0
9	W	204/205 (99%)	-0.55	3 (1%) 76 71	29, 44, 74, 96	0
10	J	195/198 (98%)	-0.44	2 (1%) 84 81	29, 46, 72, 113	0
10	X	195/198 (98%)	-0.41	3 (1%) 76 71	31, 46, 72, 128	0
11	K	212/212 (100%)	-0.44	2 (0%) 85 83	28, 45, 67, 85	0
11	Y	212/212 (100%)	-0.49	2 (0%) 85 83	32, 46, 69, 89	0
12	L	222/222 (100%)	-0.48	1 (0%) 91 90	29, 46, 81, 120	0
12	Z	222/222 (100%)	-0.46	2 (0%) 85 83	27, 47, 84, 121	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	M	233/246 (94%)	-0.57	2 (0%) 85 83	26, 45, 68, 89	0
13	a	233/246 (94%)	-0.50	1 (0%) 93 91	27, 46, 67, 86	0
14	N	196/196 (100%)	-0.55	2 (1%) 84 81	29, 40, 68, 97	0
14	b	196/196 (100%)	-0.55	3 (1%) 76 71	30, 41, 70, 100	0
All	All	6344/6614 (95%)	-0.31	179 (2%) 56 49	26, 50, 96, 179	0

The worst 5 of 179 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	221	ASP	8.8
2	P	219	ALA	8.6
3	Q	50	LEU	7.9
3	Q	49	THR	7.2
2	P	51	VAL	6.6

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
15	MG	K	302	1/1	0.95	0.42	16.01	52,52,52,52	0
15	MG	Z	301	1/1	0.91	0.28	5.77	64,64,64,64	0
15	MG	I	301	1/1	0.95	0.28	4.96	57,57,57,57	0
15	MG	N	201	1/1	0.96	0.10	0.04	48,48,48,48	0
15	MG	J	201	1/1	0.98	0.09	-0.16	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
15	MG	V	301	1/1	0.99	0.12	-0.50	44,44,44,44	0
15	MG	G	301	1/1	0.99	0.05	-1.46	45,45,45,45	0
15	MG	Y	301	1/1	0.99	0.06	-1.77	43,43,43,43	0
15	MG	K	301	1/1	0.97	0.07	-2.11	38,38,38,38	0
15	MG	H	301	1/1	0.85	0.14	-	57,57,57,57	0
16	CL	U	301	1/1	0.99	0.16	-	43,43,43,43	0
16	CL	G	302	1/1	0.99	0.06	-	36,36,36,36	0

6.5 Other polymers (i)

There are no such residues in this entry.