



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:16 AM GMT

PDB ID : 3HFA
Title : Crystal Structure of Mycobacterium Tuberculosis Proteasome open-gate mutant
Authors : Li, D.; Li, H.
Deposited on : 2009-05-11
Resolution : 2.50 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

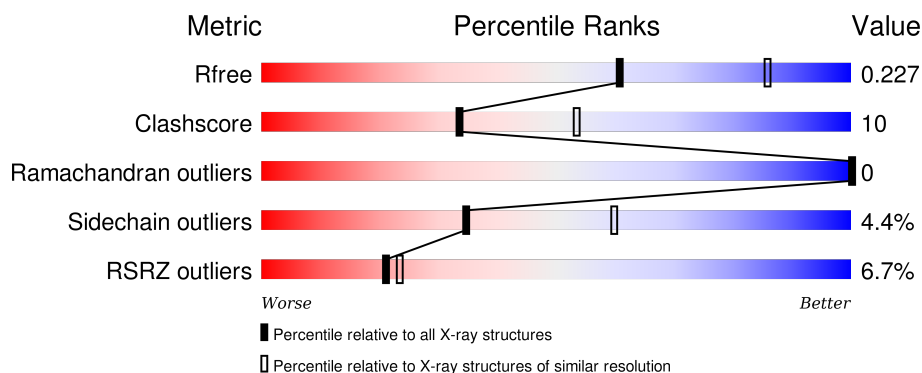
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	2	240	
1	C	240	
1	E	240	
1	G	240	
1	H	240	

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Mol	Chain	Length	Quality of chain
1	J	240	
1	L	240	
1	N	240	
1	P	240	
1	R	240	
1	T	240	
1	V	240	
1	X	240	
1	Z	240	
2	1	240	
2	A	240	
2	B	240	
2	D	240	
2	F	240	
2	I	240	
2	K	240	
2	M	240	
2	O	240	
2	Q	240	
2	S	240	
2	U	240	
2	W	240	
2	Y	240	

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
3	DMF	1	249	-	-	-	X
3	DMF	1	250	-	-	-	X
3	DMF	2	145	-	-	-	X
3	DMF	A	249	-	-	-	X
3	DMF	B	249	-	-	-	X
3	DMF	C	15	-	-	-	X
3	DMF	E	104	-	-	-	X
3	DMF	E	113	-	-	-	X
3	DMF	G	137	-	-	-	X
3	DMF	G	140	-	-	-	X
3	DMF	G	20	-	-	-	X
3	DMF	H	142	-	-	-	X
3	DMF	H	41	-	-	-	X
3	DMF	I	249	-	-	-	X
3	DMF	J	46	-	-	-	X
3	DMF	K	250	-	-	-	X
3	DMF	K	251	-	-	X	X
3	DMF	L	138	-	-	-	X
3	DMF	L	14	-	-	-	X
3	DMF	L	60	-	-	-	X
3	DMF	L	9	-	-	-	X
3	DMF	M	249	-	-	-	X
3	DMF	N	36	-	-	-	X
3	DMF	O	7	-	-	-	X
3	DMF	P	107	-	-	-	X
3	DMF	P	133	-	-	-	X
3	DMF	P	23	-	-	-	X
3	DMF	Q	249	-	-	-	X
3	DMF	Q	251	-	-	X	X
3	DMF	S	249	-	-	-	X
3	DMF	T	62	-	-	-	X
3	DMF	U	249	-	-	-	X
3	DMF	U	250	-	-	-	X
3	DMF	V	117	-	-	-	X
3	DMF	V	121	-	-	-	X
3	DMF	V	135	-	-	-	X
3	DMF	V	136	-	-	-	X
3	DMF	W	249	-	-	-	X
3	DMF	Y	249	-	-	-	X
3	DMF	Y	251	-	-	-	X
3	DMF	Z	105	-	-	-	X
3	DMF	Z	122	-	-	-	X
3	DMF	Z	27	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DMF	Z	50	-	-	-	X
3	DMF	Z	69	-	-	X	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 48523 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 (Beta subunit) PrcB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	223	Total	C	N	O	S	0	0	0
			1642	1029	283	325	5			
1	C	222	Total	C	N	O	S	0	0	0
			1638	1027	282	324	5			
1	E	223	Total	C	N	O	S	0	0	0
			1642	1029	283	325	5			
1	G	222	Total	C	N	O	S	0	0	0
			1638	1027	282	324	5			
1	J	222	Total	C	N	O	S	0	0	0
			1638	1027	282	324	5			
1	L	222	Total	C	N	O	S	0	0	0
			1638	1027	282	324	5			
1	N	223	Total	C	N	O	S	0	0	0
			1642	1029	283	325	5			
1	P	222	Total	C	N	O	S	0	0	0
			1638	1027	282	324	5			
1	R	222	Total	C	N	O	S	0	0	0
			1638	1027	282	324	5			
1	T	223	Total	C	N	O	S	0	0	0
			1642	1029	283	325	5			
1	V	226	Total	C	N	O	S	0	0	0
			1662	1040	286	331	5			
1	X	224	Total	C	N	O	S	0	0	0
			1647	1032	284	326	5			
1	Z	224	Total	C	N	O	S	0	0	0
			1647	1032	284	326	5			
1	2	222	Total	C	N	O	S	0	0	0
			1638	1027	282	324	5			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	535	HIS	-	EXPRESSION TAG	UNP O33245

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Chain	Residue	Modelled	Actual	Comment	Reference
H	536	HIS	-	EXPRESSION TAG	UNP O33245
H	537	HIS	-	EXPRESSION TAG	UNP O33245
H	538	HIS	-	EXPRESSION TAG	UNP O33245
H	539	HIS	-	EXPRESSION TAG	UNP O33245
H	540	HIS	-	EXPRESSION TAG	UNP O33245
C	535	HIS	-	EXPRESSION TAG	UNP O33245
C	536	HIS	-	EXPRESSION TAG	UNP O33245
C	537	HIS	-	EXPRESSION TAG	UNP O33245
C	538	HIS	-	EXPRESSION TAG	UNP O33245
C	539	HIS	-	EXPRESSION TAG	UNP O33245
C	540	HIS	-	EXPRESSION TAG	UNP O33245
E	535	HIS	-	EXPRESSION TAG	UNP O33245
E	536	HIS	-	EXPRESSION TAG	UNP O33245
E	537	HIS	-	EXPRESSION TAG	UNP O33245
E	538	HIS	-	EXPRESSION TAG	UNP O33245
E	539	HIS	-	EXPRESSION TAG	UNP O33245
E	540	HIS	-	EXPRESSION TAG	UNP O33245
G	535	HIS	-	EXPRESSION TAG	UNP O33245
G	536	HIS	-	EXPRESSION TAG	UNP O33245
G	537	HIS	-	EXPRESSION TAG	UNP O33245
G	538	HIS	-	EXPRESSION TAG	UNP O33245
G	539	HIS	-	EXPRESSION TAG	UNP O33245
G	540	HIS	-	EXPRESSION TAG	UNP O33245
J	535	HIS	-	EXPRESSION TAG	UNP O33245
J	536	HIS	-	EXPRESSION TAG	UNP O33245
J	537	HIS	-	EXPRESSION TAG	UNP O33245
J	538	HIS	-	EXPRESSION TAG	UNP O33245
J	539	HIS	-	EXPRESSION TAG	UNP O33245
J	540	HIS	-	EXPRESSION TAG	UNP O33245
L	535	HIS	-	EXPRESSION TAG	UNP O33245
L	536	HIS	-	EXPRESSION TAG	UNP O33245
L	537	HIS	-	EXPRESSION TAG	UNP O33245
L	538	HIS	-	EXPRESSION TAG	UNP O33245
L	539	HIS	-	EXPRESSION TAG	UNP O33245
L	540	HIS	-	EXPRESSION TAG	UNP O33245
N	535	HIS	-	EXPRESSION TAG	UNP O33245
N	536	HIS	-	EXPRESSION TAG	UNP O33245
N	537	HIS	-	EXPRESSION TAG	UNP O33245
N	538	HIS	-	EXPRESSION TAG	UNP O33245
N	539	HIS	-	EXPRESSION TAG	UNP O33245
N	540	HIS	-	EXPRESSION TAG	UNP O33245
P	535	HIS	-	EXPRESSION TAG	UNP O33245

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Chain	Residue	Modelled	Actual	Comment	Reference
P	536	HIS	-	EXPRESSION TAG	UNP O33245
P	537	HIS	-	EXPRESSION TAG	UNP O33245
P	538	HIS	-	EXPRESSION TAG	UNP O33245
P	539	HIS	-	EXPRESSION TAG	UNP O33245
P	540	HIS	-	EXPRESSION TAG	UNP O33245
R	535	HIS	-	EXPRESSION TAG	UNP O33245
R	536	HIS	-	EXPRESSION TAG	UNP O33245
R	537	HIS	-	EXPRESSION TAG	UNP O33245
R	538	HIS	-	EXPRESSION TAG	UNP O33245
R	539	HIS	-	EXPRESSION TAG	UNP O33245
R	540	HIS	-	EXPRESSION TAG	UNP O33245
T	535	HIS	-	EXPRESSION TAG	UNP O33245
T	536	HIS	-	EXPRESSION TAG	UNP O33245
T	537	HIS	-	EXPRESSION TAG	UNP O33245
T	538	HIS	-	EXPRESSION TAG	UNP O33245
T	539	HIS	-	EXPRESSION TAG	UNP O33245
T	540	HIS	-	EXPRESSION TAG	UNP O33245
V	535	HIS	-	EXPRESSION TAG	UNP O33245
V	536	HIS	-	EXPRESSION TAG	UNP O33245
V	537	HIS	-	EXPRESSION TAG	UNP O33245
V	538	HIS	-	EXPRESSION TAG	UNP O33245
V	539	HIS	-	EXPRESSION TAG	UNP O33245
V	540	HIS	-	EXPRESSION TAG	UNP O33245
X	535	HIS	-	EXPRESSION TAG	UNP O33245
X	536	HIS	-	EXPRESSION TAG	UNP O33245
X	537	HIS	-	EXPRESSION TAG	UNP O33245
X	538	HIS	-	EXPRESSION TAG	UNP O33245
X	539	HIS	-	EXPRESSION TAG	UNP O33245
X	540	HIS	-	EXPRESSION TAG	UNP O33245
Z	535	HIS	-	EXPRESSION TAG	UNP O33245
Z	536	HIS	-	EXPRESSION TAG	UNP O33245
Z	537	HIS	-	EXPRESSION TAG	UNP O33245
Z	538	HIS	-	EXPRESSION TAG	UNP O33245
Z	539	HIS	-	EXPRESSION TAG	UNP O33245
Z	540	HIS	-	EXPRESSION TAG	UNP O33245
2	535	HIS	-	EXPRESSION TAG	UNP O33245
2	536	HIS	-	EXPRESSION TAG	UNP O33245
2	537	HIS	-	EXPRESSION TAG	UNP O33245
2	538	HIS	-	EXPRESSION TAG	UNP O33245
2	539	HIS	-	EXPRESSION TAG	UNP O33245
2	540	HIS	-	EXPRESSION TAG	UNP O33245

- Molecule 2 is a protein called Proteasome (Alpha subunit) PrcA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	213	Total 1645	C 1030	N 301	O 310	S 4	0	0	0
2	A	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	B	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	F	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	I	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	K	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	M	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	O	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	Q	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	S	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	U	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	W	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	Y	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0
2	1	214	Total 1653	C 1036	N 302	O 311	S 4	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

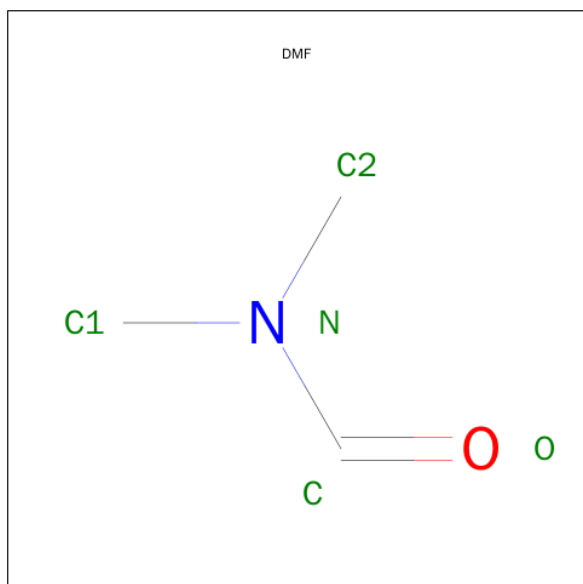
Chain	Residue	Modelled	Actual	Comment	Reference
D	9	MET	-	INITIATING METHIONINE	UNP O33244
A	9	MET	-	INITIATING METHIONINE	UNP O33244
B	9	MET	-	INITIATING METHIONINE	UNP O33244
F	9	MET	-	INITIATING METHIONINE	UNP O33244
I	9	MET	-	INITIATING METHIONINE	UNP O33244
K	9	MET	-	INITIATING METHIONINE	UNP O33244
M	9	MET	-	INITIATING METHIONINE	UNP O33244
O	9	MET	-	INITIATING METHIONINE	UNP O33244
Q	9	MET	-	INSERTION	UNP O33244
S	9	MET	-	INITIATING METHIONINE	UNP O33244
U	9	MET	-	INITIATING METHIONINE	UNP O33244
W	9	MET	-	INITIATING METHIONINE	UNP O33244

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	9	MET	-	INITIATING METHIONINE	UNP O33244
1	9	MET	-	INITIATING METHIONINE	UNP O33244

- Molecule 3 is DIMETHYLFORMAMIDE (three-letter code: DMF) (formula: C_3H_7NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	H	1	Total	C	N	O	0	0
			5	3	1	1		
3	H	1	Total	C	N	O	0	0
			5	3	1	1		
3	C	1	Total	C	N	O	0	0
			5	3	1	1		
3	E	1	Total	C	N	O	0	0
			5	3	1	1		
3	E	1	Total	C	N	O	0	0
			5	3	1	1		
3	E	1	Total	C	N	O	0	0
			5	3	1	1		
3	G	1	Total	C	N	O	0	0
			5	3	1	1		
3	G	1	Total	C	N	O	0	0
			5	3	1	1		
3	G	1	Total	C	N	O	0	0
			5	3	1	1		
3	J	1	Total	C	N	O	0	0
			5	3	1	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	L	1	Total 5	C 3	N 1	O 1	0	0
3	L	1	Total 5	C 3	N 1	O 1	0	0
3	L	1	Total 5	C 3	N 1	O 1	0	0
3	L	1	Total 5	C 3	N 1	O 1	0	0
3	N	1	Total 5	C 3	N 1	O 1	0	0
3	N	1	Total 5	C 3	N 1	O 1	0	0
3	P	1	Total 5	C 3	N 1	O 1	0	0
3	P	1	Total 5	C 3	N 1	O 1	0	0
3	P	1	Total 5	C 3	N 1	O 1	0	0
3	T	1	Total 5	C 3	N 1	O 1	0	0
3	T	1	Total 5	C 3	N 1	O 1	0	0
3	V	1	Total 5	C 3	N 1	O 1	0	0
3	V	1	Total 5	C 3	N 1	O 1	0	0
3	V	1	Total 5	C 3	N 1	O 1	0	0
3	V	1	Total 5	C 3	N 1	O 1	0	0
3	V	1	Total 5	C 3	N 1	O 1	0	0
3	V	1	Total 5	C 3	N 1	O 1	0	0
3	X	1	Total 5	C 3	N 1	O 1	0	0
3	Z	1	Total 5	C 3	N 1	O 1	0	0
3	Z	1	Total 5	C 3	N 1	O 1	0	0
3	Z	1	Total 5	C 3	N 1	O 1	0	0
3	Z	1	Total 5	C 3	N 1	O 1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	Z	1	Total 5	C 3	N 1	O 1	0	0
3	2	1	Total 5	C 3	N 1	O 1	0	0
3	2	1	Total 5	C 3	N 1	O 1	0	0
3	D	1	Total 5	C 3	N 1	O 1	0	0
3	A	1	Total 5	C 3	N 1	O 1	0	0
3	A	1	Total 5	C 3	N 1	O 1	0	0
3	B	1	Total 5	C 3	N 1	O 1	0	0
3	F	1	Total 5	C 3	N 1	O 1	0	0
3	I	1	Total 5	C 3	N 1	O 1	0	0
3	K	1	Total 5	C 3	N 1	O 1	0	0
3	K	1	Total 5	C 3	N 1	O 1	0	0
3	K	1	Total 5	C 3	N 1	O 1	0	0
3	M	1	Total 5	C 3	N 1	O 1	0	0
3	O	1	Total 5	C 3	N 1	O 1	0	0
3	Q	1	Total 5	C 3	N 1	O 1	0	0
3	Q	1	Total 5	C 3	N 1	O 1	0	0
3	Q	1	Total 5	C 3	N 1	O 1	0	0
3	S	1	Total 5	C 3	N 1	O 1	0	0
3	S	1	Total 5	C 3	N 1	O 1	0	0
3	U	1	Total 5	C 3	N 1	O 1	0	0
3	U	1	Total 5	C 3	N 1	O 1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	W	1	Total	C	N	O	0	0
			5	3	1	1		
3	Y	1	Total	C	N	O	0	0
			5	3	1	1		
3	Y	1	Total	C	N	O	0	0
			5	3	1	1		
3	Y	1	Total	C	N	O	0	0
			5	3	1	1		
3	1	1	Total	C	N	O	0	0
			5	3	1	1		
3	1	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	92	Total	O	0	0
			92	92		
4	C	43	Total	O	0	0
			43	43		
4	E	121	Total	O	0	0
			121	121		
4	G	113	Total	O	0	0
			113	113		
4	J	73	Total	O	0	0
			73	73		
4	L	109	Total	O	0	0
			109	109		
4	N	124	Total	O	0	0
			124	124		
4	P	93	Total	O	0	0
			93	93		
4	R	89	Total	O	0	0
			89	89		
4	T	96	Total	O	0	0
			96	96		
4	V	133	Total	O	0	0
			133	133		
4	X	101	Total	O	0	0
			101	101		
4	Z	91	Total	O	0	0
			91	91		

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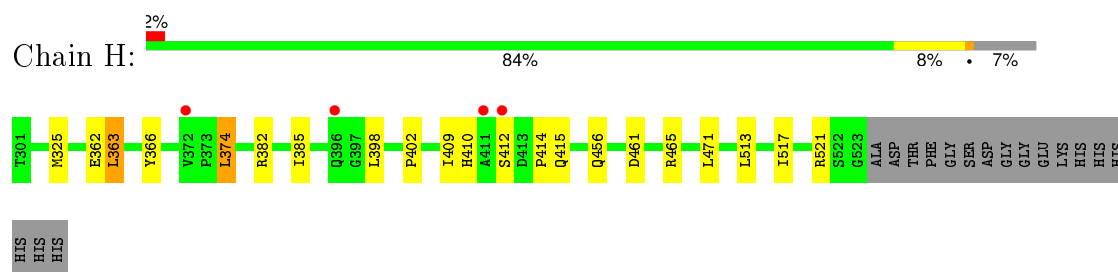
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	2	107	Total 107	O 107	0	0
4	D	49	Total 49	O 49	0	0
4	A	31	Total 31	O 31	0	0
4	B	37	Total 37	O 37	0	0
4	F	60	Total 60	O 60	0	0
4	I	35	Total 35	O 35	0	0
4	K	52	Total 52	O 52	0	0
4	M	74	Total 74	O 74	0	0
4	O	34	Total 34	O 34	0	0
4	Q	71	Total 71	O 71	0	0
4	S	35	Total 35	O 35	0	0
4	U	48	Total 48	O 48	0	0
4	W	62	Total 62	O 62	0	0
4	Y	68	Total 68	O 68	0	0
4	1	68	Total 68	O 68	0	0

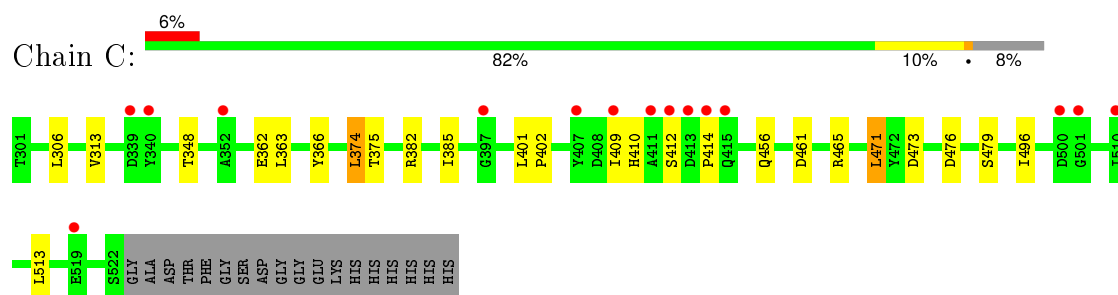
3 Residue-property plots [i](#)

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.

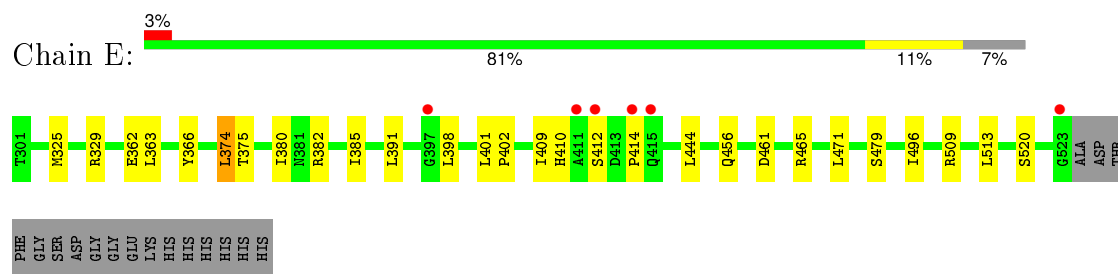
- Molecule 1: Proteasome (Beta subunit) PrcB



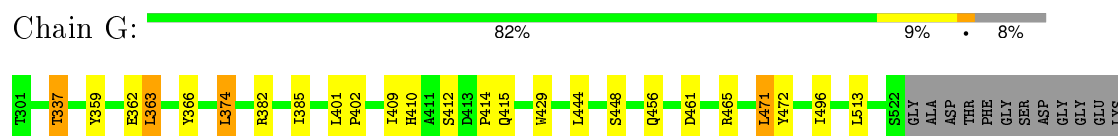
- Molecule 1: Proteasome (Beta subunit) PrcB



- Molecule 1: Proteasome (Beta subunit) PrcB




- Molecule 1: Proteasome (Beta subunit) PrcB



HIS
HIS
HIS
HIS
HIS
HIS


• Molecule 1: Proteasome (Beta subunit) PrcB

Chain J: 



GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS


• Molecule 1: Proteasome (Beta subunit) PrcB

Chain L: 



GLY
GLU
LYS
HIS
HIS
HIS
HIS
HIS


• Molecule 1: Proteasome (Beta subunit) PrcB

Chain N: 



HIS
HIS
HIS


• Molecule 1: Proteasome (Beta subunit) PrcB

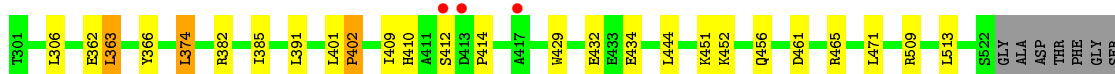
Chain P: 



HIS

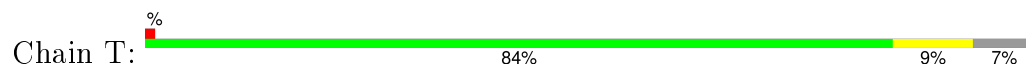
• Molecule 1: Proteasome (Beta subunit) PrcB

Chain R: 



ASP
GLY
GLY
GLY
LYS
HIS
HIS
HIS
HIS
HIS

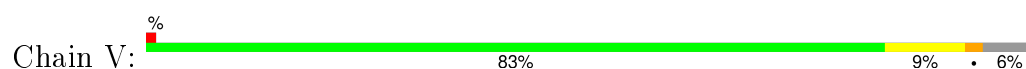
• Molecule 1: Proteasome (Beta subunit) PrcB



T301 L306 E362 L363 Y366 L374 A377 R382 I385 L391 N395 L398 I409 H410 A411 S412 D413 P414 Q415 L444 Q456 D461 R465 L471 Y472 L513 G523
ALA ASP THR PHE GLY SER ASP GLY GLY LYS HIS HIS HIS

HIS
HIS

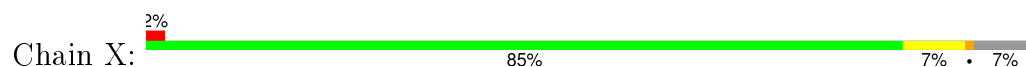
• Molecule 1: Proteasome (Beta subunit) PrcB



T301 R319 I345 R357 E362 L363 Y366 L374 T375 R382 I385 R388 I409 H410 A411 S412 D413 P414 W429 K451 Q456 D461 R465 L471 I496 L513 A514 R515 G523 T526
PHE GLY SER ASP GLY GLY LYS HIS HIS HIS HIS HIS

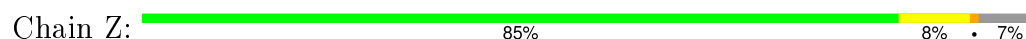
HIS
HIS
HIS
HIS

• Molecule 1: Proteasome (Beta subunit) PrcB



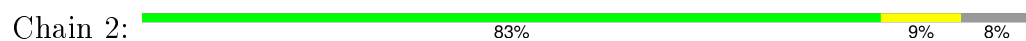
T301 N325 E362 L363 Y366 L374 R382 I385 L391 Q396 I409 H410 A411 S412 D413 P414 Q415 K451 Q456 D461 R465 L471 D509 L513 G523 A524
ASP THR PHE GLY SER ASP GLY GLY LYS HIS HIS HIS HIS HIS

• Molecule 1: Proteasome (Beta subunit) PrcB



T301 R357 E362 L363 Y366 L374 R382 I385 L398 I409 H410 A411 S412 D413 P414 W429 L444 Q456 D461 R465 L471 I496 R509 L513 A524
ASP THR PHE GLY SER ASP GLY GLY LYS HIS HIS HIS HIS HIS

• Molecule 1: Proteasome (Beta subunit) PrcB

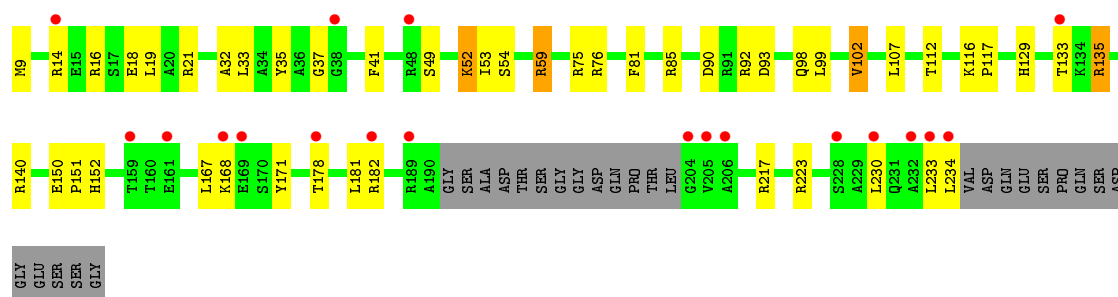


T301 L306 N335 E362 L363 Y366 L374 R382 I385 Q396 I397 L398 L401 P402 I409 H410 A411 S412 D413 P414 Q415 W429 S448 D461 L471 Y472 L513 S522
GLY ALA ASP THR PHE GLY GLY SER ASP GLY GLY LYS HIS HIS HIS HIS HIS

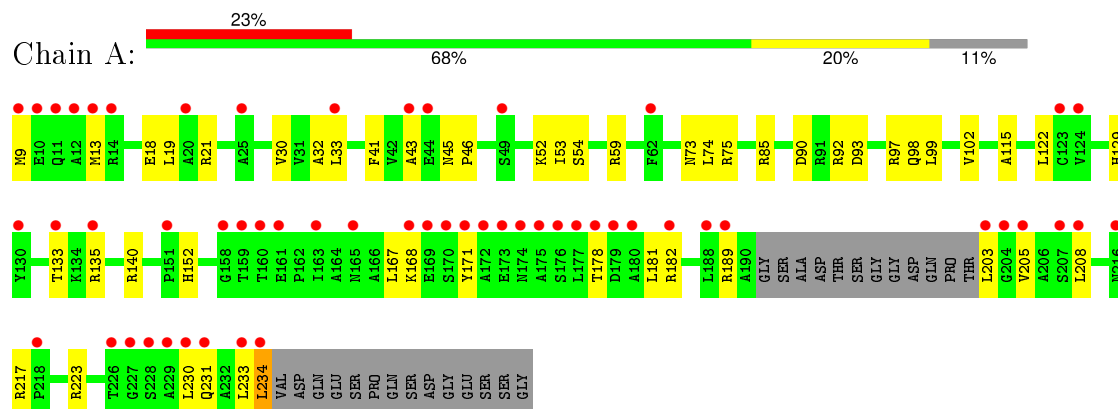
HIS
HIS

• Molecule 2: Proteasome (Alpha subunit) PrcA

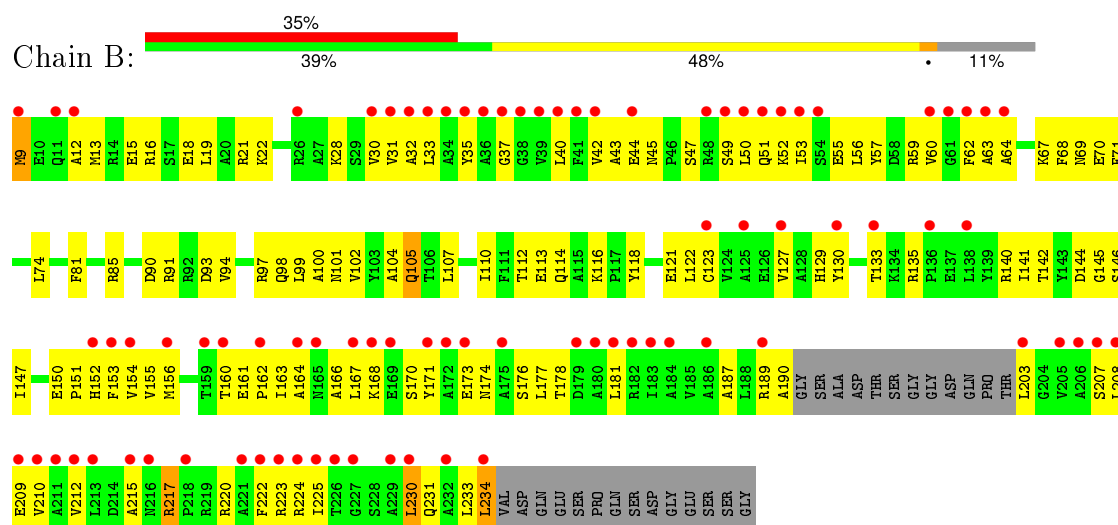




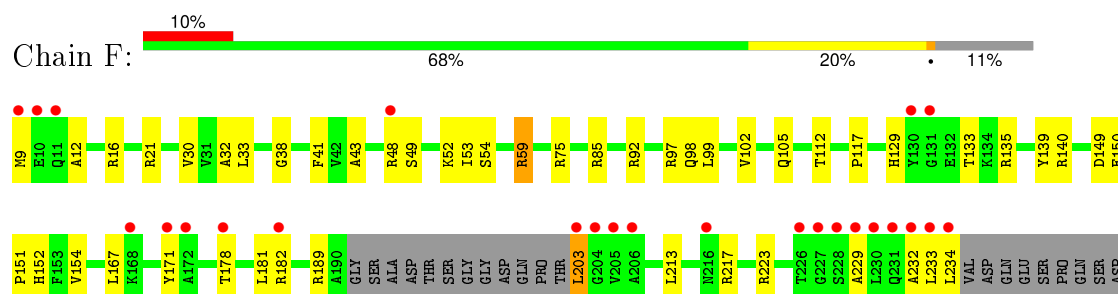
• Molecule 2: Proteasome (Alpha subunit) PrcA



• Molecule 2: Proteasome (Alpha subunit) PrcA

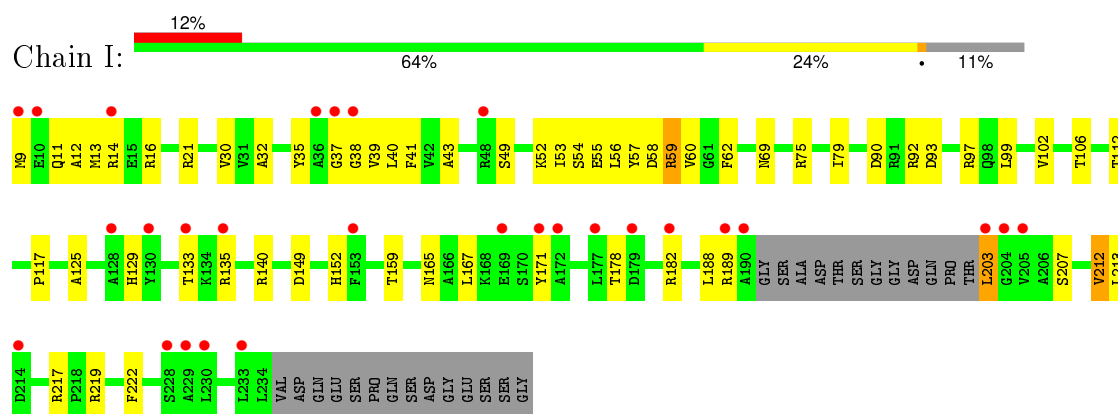


• Molecule 2: Proteasome (Alpha subunit) PrcA

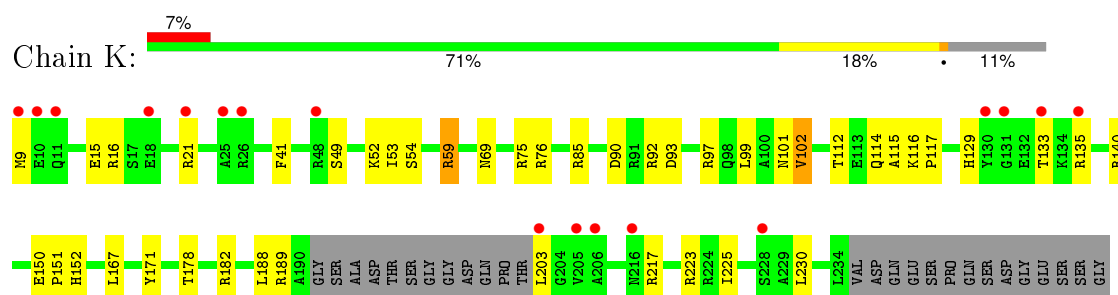


GLY
GLU
SER
SER
GLY

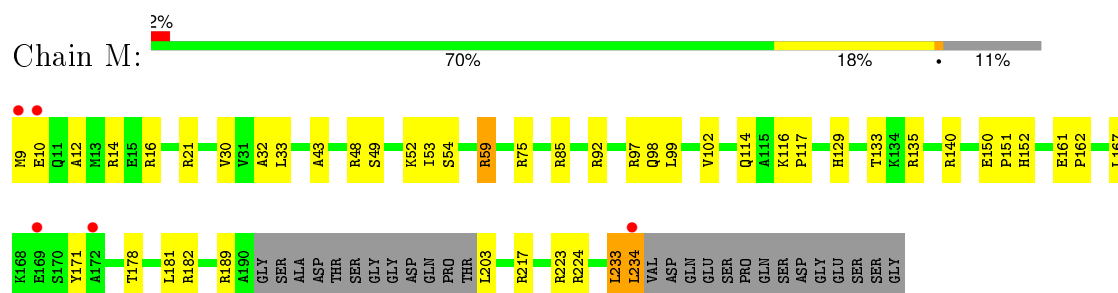
• Molecule 2: Proteasome (Alpha subunit) PrcA



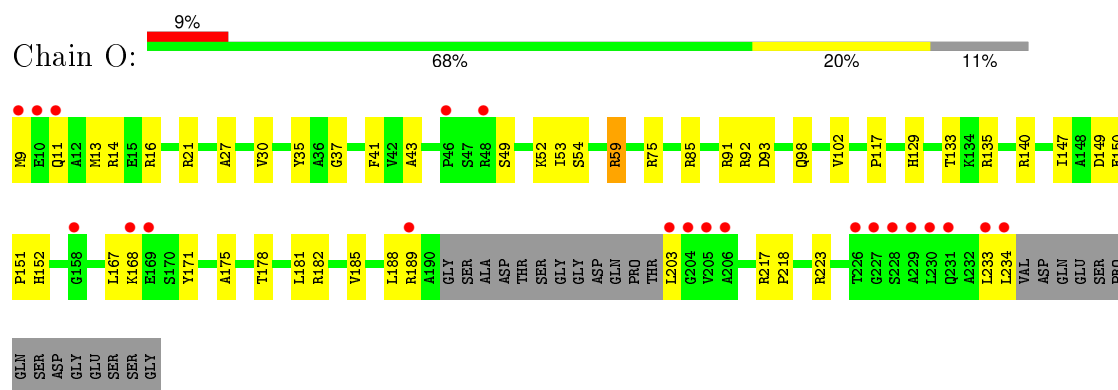
• Molecule 2: Proteasome (Alpha subunit) PrcA



• Molecule 2: Proteasome (Alpha subunit) PrcA



• Molecule 2: Proteasome (Alpha subunit) PrcA



GLN
SER
ASP
GLY
GLU
SER
SER
GLY

Chain Q: 

Chain S:

15% 71% 17% 11%

M9 E10 Q11 A12 Y13 R14 E15 S17 E18 L19 I20 R21 V30 V31 A32 L33 A36 G37 F41 F42 A43 E44 N45 P46 S47 A48 S49 K52 I53 S54 R59 R75 R85 R92 R97 Q98 V102 K116 P117 H129 Y130 G131 E132 T133 K134 R135 R140 E150 P151 H152 T159 E161 P162 I163 L167 K168 E169 S170 Y171 A172 T178 D179 R182 R189 A190 GLY SER ALA ASP THR SER GLY GLY ASP GLN PRO THR L203 G204 V205 L208 R217 G227 S228 A229 L230 L233 L234 VAL ASP GLN GLU SER PRO

Chain U:

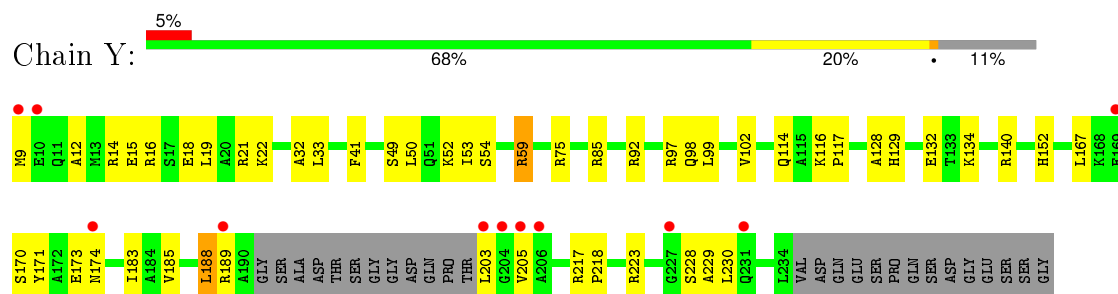
Amino Acid	Category
T226	Green
L230	Green
Q231	Red
A232	Red
L233	Red
L234	Red
VAL	Grey
ASP	Grey
GLN	Grey
GLU	Grey
GUU	Grey
SER	Grey
PRO	Grey
GLN	Grey
SER	Grey
ASP	Grey
GLY	Grey
GLU	Grey
SER	Grey
SER	Grey
GLY	Grey
G131	Green
E132	Green
K133	Green
K134	Red
K135	Red
Y139	Green
R140	Green
Y143	Green
I147	Green
A148	Green
D149	Green
E150	Green
P151	Green
H152	Green
F153	Green
V154	Green
G157	Green
G158	Red
I163	Green
K168	Green
E169	Red
S170	Green
Y171	Green
L181	Green
R182	Green
I183	Green
R189	Green
A190	Green
GLY	Grey
SER	Grey
ALA	Grey
ASP	Grey
THR	Grey
SER	Grey
GLY	Grey
ASP	Grey
GLN	Grey
PRO	Grey
THR	Grey
L203	Red
G204	Green
V205	Red
A206	Red
S207	Red
R216	Red
R217	Green
R223	Green
R224	Green
I225	Green
M9	Red
E10	Green
Q11	Green
A12	Green
M13	Green
R14	Green
E15	Green
S17	Green
L19	Green
A20	Green
R21	Green
K22	Green
G23	Green
I24	Green
A25	Green
V30	Green
F41	Green
V42	Green
A43	Green
R48	Green
S49	Green
L50	Green
Q51	Green
K52	Green
I53	Green
S54	Green
R59	Green
M69	Green
R75	Green
R76	Green
G77	Green
R85	Green
R92	Green
Q98	Green
L99	Green
V102	Green
T106	Green
I110	Green
Q114	Green
K115	Green
P117	Green
H129	Red
K136	Green

Chain W:

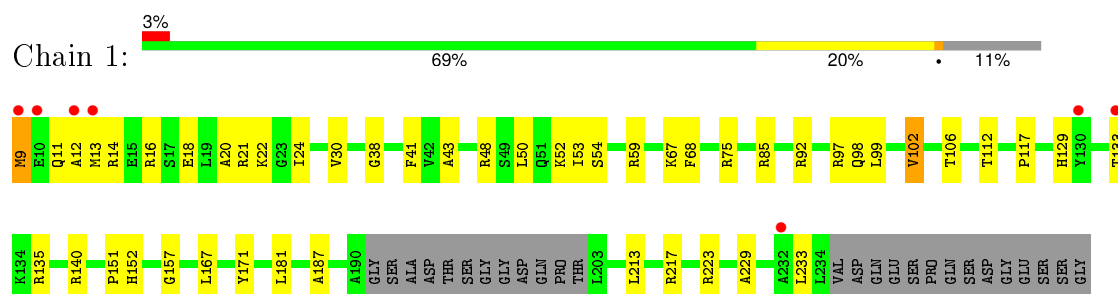
7% 65% 22% 11%

M9 E10 Q11 A12 M13 R14 E15 R16 S17 L19 K20 R21 K22 V30 I31 A32 L33 F41 V42 A43 E44 M45 P46 S47 R48 S49 K52 I53 S54 R59 M69 R75 R85 R92 R97 Q98 V102 T106 P117 H129 T133 K134 R135 E140 S150 P151 H152 V155 E161 P162 L167 K168 E169 Y170 E172 E173 T178 L181 R182 V185 A186 L187 L188 R189 A190 GLY SER ALA ASP THR SER GLY ASP GLN PRO THR L203 G204 V205 A206 S207 L213 R217 R223 Q231 A232 L233 L234 VAL ASP GLN

- Molecule 2: Proteasome (Alpha subunit) PrcA



- Molecule 2: Proteasome (Alpha subunit) PrcA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	119.16Å 221.44Å 137.12Å 90.00° 104.89° 90.00°	Depositor
Resolution (Å)	29.86 – 2.50 29.86 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.8 (29.86-2.50) 97.8 (29.86-2.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.173 , 0.214 0.198 , 0.227	Depositor DCC
R_{free} test set	11466 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	33.3	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 55.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 229841 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	48523	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	2	0.33	0/1662	0.49	0/2254
1	C	0.32	0/1662	0.50	0/2254
1	E	0.34	0/1666	0.49	0/2259
1	G	0.36	0/1662	0.50	0/2254
1	H	0.33	0/1666	0.48	0/2259
1	J	0.31	0/1662	0.48	0/2254
1	L	0.33	0/1662	0.49	0/2254
1	N	0.35	0/1666	0.49	0/2259
1	P	0.32	0/1662	0.49	0/2254
1	R	0.33	0/1662	0.49	0/2254
1	T	0.33	0/1666	0.49	0/2259
1	V	0.36	0/1686	0.50	0/2287
1	X	0.32	0/1671	0.49	0/2266
1	Z	0.32	0/1671	0.50	0/2266
2	1	0.32	0/1677	0.54	0/2264
2	A	0.32	0/1677	0.53	0/2264
2	B	0.32	0/1677	0.56	0/2264
2	D	0.36	0/1669	0.54	0/2253
2	F	0.32	0/1677	0.54	0/2264
2	I	0.32	0/1677	0.55	1/2264 (0.0%)
2	K	0.32	0/1677	0.53	0/2264
2	M	0.32	0/1677	0.54	0/2264
2	O	0.31	0/1677	0.51	0/2264
2	Q	0.33	0/1677	0.57	0/2264
2	S	0.29	0/1677	0.51	0/2264
2	U	0.32	0/1677	0.54	0/2264
2	W	0.33	0/1677	0.55	1/2264 (0.0%)
2	Y	0.33	0/1677	0.55	0/2264
All	All	0.33	0/46796	0.52	2/63318 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	I	213	LEU	N-CA-C	-5.19	96.99	111.00
2	W	213	LEU	N-CA-C	-5.11	97.20	111.00

There are no chirality outliers.

There are no planarity outliers.

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	2	1638	0	1630	16	0
1	C	1638	0	1630	23	0
1	E	1642	0	1633	28	0
1	G	1638	0	1630	21	0
1	H	1642	0	1633	15	0
1	J	1638	0	1630	15	0
1	L	1638	0	1630	21	0
1	N	1642	0	1633	19	0
1	P	1638	0	1630	18	0
1	R	1638	0	1630	23	0
1	T	1642	0	1633	19	0
1	V	1662	0	1649	22	0
1	X	1647	0	1638	16	0
1	Z	1647	0	1638	22	0
2	1	1653	0	1656	49	0
2	A	1653	0	1656	42	0
2	B	1653	0	1656	161	0
2	D	1645	0	1645	49	0
2	F	1653	0	1656	40	0
2	I	1653	0	1656	62	0
2	K	1653	0	1656	35	0
2	M	1653	0	1656	38	0
2	O	1653	0	1656	48	0
2	Q	1653	0	1656	39	0
2	S	1653	0	1656	51	0
2	U	1653	0	1656	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	W	1653	0	1656	52	0
2	Y	1653	0	1656	46	0
3	1	10	0	14	2	0
3	2	10	0	14	2	0
3	A	10	0	14	1	0
3	B	5	0	7	0	0
3	C	5	0	7	0	0
3	D	5	0	7	0	0
3	E	15	0	21	4	0
3	F	5	0	7	0	0
3	G	15	0	21	4	0
3	H	10	0	14	1	0
3	I	5	0	7	1	0
3	J	5	0	7	0	0
3	K	15	0	21	5	0
3	L	20	0	28	4	0
3	M	5	0	7	0	0
3	N	10	0	14	1	0
3	O	5	0	7	0	0
3	P	15	0	21	3	0
3	Q	15	0	21	5	0
3	S	10	0	14	1	0
3	T	10	0	14	5	0
3	U	10	0	14	1	0
3	V	25	0	35	7	0
3	W	5	0	7	1	0
3	X	5	0	7	0	0
3	Y	15	0	21	1	0
3	Z	25	0	35	7	0
4	1	68	0	0	1	0
4	2	107	0	0	3	0
4	A	31	0	0	0	0
4	B	37	0	0	4	0
4	C	43	0	0	1	0
4	D	49	0	0	5	0
4	E	121	0	0	8	0
4	F	60	0	0	4	0
4	G	113	0	0	2	0
4	H	92	0	0	0	0
4	I	35	0	0	6	0
4	J	73	0	0	2	0
4	K	52	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	109	0	0	4	0
4	M	74	0	0	5	0
4	N	124	0	0	6	0
4	O	34	0	0	4	0
4	P	93	0	0	2	0
4	Q	71	0	0	2	0
4	R	89	0	0	2	0
4	S	35	0	0	3	0
4	T	96	0	0	1	0
4	U	48	0	0	2	0
4	V	133	0	0	2	0
4	W	62	0	0	4	0
4	X	101	0	0	1	0
4	Y	68	0	0	3	0
4	Z	91	0	0	3	0
All	All	48523	0	46446	945	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 10.

The worst 5 of 945 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)
2:A:115:ALA:HB3	2:B:112:THR:CG2	1.66	1.25
2:S:116:LYS:HB2	2:1:13:MET:CE	1.68	1.23
2:B:9:MET:CE	2:B:13:MET:HE3	1.68	1.22
2:S:230:LEU:O	2:S:234:LEU:HD13	1.34	1.22
2:O:9:MET:HE2	2:O:13:MET:CE	1.77	1.15

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	2	220/240 (92%)	218 (99%)	2 (1%)	0	100	100
1	C	220/240 (92%)	220 (100%)	0	0	100	100
1	E	221/240 (92%)	219 (99%)	2 (1%)	0	100	100
1	G	220/240 (92%)	218 (99%)	2 (1%)	0	100	100
1	H	221/240 (92%)	219 (99%)	2 (1%)	0	100	100
1	J	220/240 (92%)	219 (100%)	1 (0%)	0	100	100
1	L	220/240 (92%)	218 (99%)	2 (1%)	0	100	100
1	N	221/240 (92%)	218 (99%)	3 (1%)	0	100	100
1	P	220/240 (92%)	218 (99%)	2 (1%)	0	100	100
1	R	220/240 (92%)	218 (99%)	2 (1%)	0	100	100
1	T	221/240 (92%)	219 (99%)	2 (1%)	0	100	100
1	V	224/240 (93%)	222 (99%)	2 (1%)	0	100	100
1	X	222/240 (92%)	220 (99%)	2 (1%)	0	100	100
1	Z	222/240 (92%)	221 (100%)	1 (0%)	0	100	100
2	1	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	A	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	B	210/240 (88%)	201 (96%)	9 (4%)	0	100	100
2	D	209/240 (87%)	205 (98%)	4 (2%)	0	100	100
2	F	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	I	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	K	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	M	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	O	210/240 (88%)	205 (98%)	5 (2%)	0	100	100
2	Q	210/240 (88%)	206 (98%)	4 (2%)	0	100	100
2	S	210/240 (88%)	204 (97%)	6 (3%)	0	100	100
2	U	210/240 (88%)	205 (98%)	5 (2%)	0	100	100
2	W	210/240 (88%)	207 (99%)	3 (1%)	0	100	100
2	Y	210/240 (88%)	205 (98%)	5 (2%)	0	100	100
All	All	6031/6720 (90%)	5941 (98%)	90 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	2	165/178 (93%)	160 (97%)	5 (3%)	48	76
1	C	165/178 (93%)	159 (96%)	6 (4%)	42	69
1	E	165/178 (93%)	160 (97%)	5 (3%)	48	76
1	G	165/178 (93%)	158 (96%)	7 (4%)	36	62
1	H	165/178 (93%)	159 (96%)	6 (4%)	42	69
1	J	165/178 (93%)	159 (96%)	6 (4%)	42	69
1	L	165/178 (93%)	160 (97%)	5 (3%)	48	76
1	N	165/178 (93%)	161 (98%)	4 (2%)	57	82
1	P	165/178 (93%)	160 (97%)	5 (3%)	48	76
1	R	165/178 (93%)	160 (97%)	5 (3%)	48	76
1	T	165/178 (93%)	160 (97%)	5 (3%)	48	76
1	V	167/178 (94%)	160 (96%)	7 (4%)	36	62
1	X	165/178 (93%)	160 (97%)	5 (3%)	48	76
1	Z	165/178 (93%)	160 (97%)	5 (3%)	48	76
2	1	164/184 (89%)	156 (95%)	8 (5%)	31	55
2	A	164/184 (89%)	156 (95%)	8 (5%)	31	55
2	B	164/184 (89%)	154 (94%)	10 (6%)	23	42
2	D	163/184 (89%)	156 (96%)	7 (4%)	35	61
2	F	164/184 (89%)	154 (94%)	10 (6%)	23	42
2	I	164/184 (89%)	153 (93%)	11 (7%)	20	37
2	K	164/184 (89%)	154 (94%)	10 (6%)	23	42
2	M	164/184 (89%)	153 (93%)	11 (7%)	20	37
2	O	164/184 (89%)	155 (94%)	9 (6%)	27	48
2	Q	164/184 (89%)	156 (95%)	8 (5%)	31	55
2	S	164/184 (89%)	156 (95%)	8 (5%)	31	55
2	U	164/184 (89%)	153 (93%)	11 (7%)	20	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	W	164/184 (89%)	154 (94%)	10 (6%)	23	42
2	Y	164/184 (89%)	157 (96%)	7 (4%)	35	61
All	All	4607/5068 (91%)	4403 (96%)	204 (4%)	35	60

5 of 204 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	51	GLN
2	I	69	ASN
2	W	234	LEU
2	B	105	GLN
2	F	99	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 74 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	69	ASN
2	F	129	HIS
2	Y	69	ASN
2	A	73	ASN
2	B	105	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 [i](#)

58 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	DMF	1	249	-	4,4,4	0.36	0	4,4,4	0.24	0
3	DMF	1	250	-	4,4,4	0.35	0	4,4,4	0.44	0
3	DMF	2	145	-	4,4,4	0.30	0	4,4,4	0.39	0
3	DMF	2	99	-	4,4,4	0.33	0	4,4,4	0.42	0
3	DMF	A	249	-	4,4,4	0.37	0	4,4,4	0.46	0
3	DMF	A	8	-	4,4,4	0.24	0	4,4,4	0.25	0
3	DMF	B	249	-	4,4,4	0.29	0	4,4,4	0.41	0
3	DMF	C	15	-	4,4,4	0.31	0	4,4,4	0.37	0
3	DMF	D	249	-	4,4,4	0.30	0	4,4,4	0.44	0
3	DMF	E	104	-	4,4,4	0.27	0	4,4,4	0.41	0
3	DMF	E	113	-	4,4,4	0.35	0	4,4,4	0.45	0
3	DMF	E	28	-	4,4,4	0.34	0	4,4,4	0.36	0
3	DMF	F	249	-	4,4,4	0.31	0	4,4,4	0.39	0
3	DMF	G	137	-	4,4,4	0.34	0	4,4,4	0.42	0
3	DMF	G	140	-	4,4,4	0.34	0	4,4,4	0.46	0
3	DMF	G	20	-	4,4,4	0.34	0	4,4,4	0.22	0
3	DMF	H	142	-	4,4,4	0.36	0	4,4,4	0.46	0
3	DMF	H	41	-	4,4,4	0.30	0	4,4,4	0.43	0
3	DMF	I	249	-	4,4,4	0.30	0	4,4,4	0.40	0
3	DMF	J	46	-	4,4,4	0.35	0	4,4,4	0.47	0
3	DMF	K	249	-	4,4,4	0.29	0	4,4,4	0.28	0
3	DMF	K	250	-	4,4,4	0.36	0	4,4,4	0.41	0
3	DMF	K	251	-	4,4,4	0.33	0	4,4,4	0.24	0
3	DMF	L	138	-	4,4,4	0.34	0	4,4,4	0.27	0
3	DMF	L	14	-	4,4,4	0.34	0	4,4,4	0.31	0
3	DMF	L	60	-	4,4,4	0.32	0	4,4,4	0.41	0
3	DMF	L	9	-	4,4,4	0.35	0	4,4,4	0.43	0
3	DMF	M	249	-	4,4,4	0.36	0	4,4,4	0.34	0
3	DMF	N	21	-	4,4,4	0.30	0	4,4,4	0.40	0
3	DMF	N	36	-	4,4,4	0.34	0	4,4,4	0.38	0
3	DMF	O	7	-	4,4,4	0.35	0	4,4,4	0.36	0
3	DMF	P	107	-	4,4,4	0.27	0	4,4,4	0.38	0
3	DMF	P	133	-	4,4,4	0.33	0	4,4,4	0.44	0
3	DMF	P	23	-	4,4,4	0.31	0	4,4,4	0.38	0
3	DMF	Q	249	-	4,4,4	0.31	0	4,4,4	0.33	0
3	DMF	Q	250	-	4,4,4	0.33	0	4,4,4	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DMF	Q	251	-	4,4,4	0.30	0	4,4,4	0.40	0
3	DMF	S	249	-	4,4,4	0.30	0	4,4,4	0.28	0
3	DMF	S	250	-	4,4,4	0.34	0	4,4,4	0.33	0
3	DMF	T	134	-	4,4,4	0.33	0	4,4,4	0.44	0
3	DMF	T	62	-	4,4,4	0.32	0	4,4,4	0.34	0
3	DMF	U	249	-	4,4,4	0.32	0	4,4,4	0.31	0
3	DMF	U	250	-	4,4,4	0.30	0	4,4,4	0.29	0
3	DMF	V	117	-	4,4,4	0.37	0	4,4,4	0.40	0
3	DMF	V	121	-	4,4,4	0.34	0	4,4,4	0.52	0
3	DMF	V	135	-	4,4,4	0.38	0	4,4,4	0.42	0
3	DMF	V	136	-	4,4,4	0.38	0	4,4,4	0.44	0
3	DMF	V	16	-	4,4,4	0.34	0	4,4,4	0.37	0
3	DMF	W	249	-	4,4,4	0.28	0	4,4,4	0.19	0
3	DMF	X	141	-	4,4,4	0.29	0	4,4,4	0.33	0
3	DMF	Y	249	-	4,4,4	0.45	0	4,4,4	0.53	0
3	DMF	Y	250	-	4,4,4	0.28	0	4,4,4	0.38	0
3	DMF	Y	251	-	4,4,4	0.38	0	4,4,4	0.43	0
3	DMF	Z	105	-	4,4,4	0.36	0	4,4,4	0.36	0
3	DMF	Z	122	-	4,4,4	0.33	0	4,4,4	0.35	0
3	DMF	Z	27	-	4,4,4	0.32	0	4,4,4	0.41	0
3	DMF	Z	50	-	4,4,4	0.33	0	4,4,4	0.37	0
3	DMF	Z	69	-	4,4,4	0.34	0	4,4,4	0.32	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DMF	1	249	-	-	0/2/2/2	0/0/0/0
3	DMF	1	250	-	-	0/2/2/2	0/0/0/0
3	DMF	2	145	-	-	0/2/2/2	0/0/0/0
3	DMF	2	99	-	-	0/2/2/2	0/0/0/0
3	DMF	A	249	-	-	0/2/2/2	0/0/0/0
3	DMF	A	8	-	-	0/2/2/2	0/0/0/0
3	DMF	B	249	-	-	0/2/2/2	0/0/0/0
3	DMF	C	15	-	-	0/2/2/2	0/0/0/0
3	DMF	D	249	-	-	0/2/2/2	0/0/0/0
3	DMF	E	104	-	-	0/2/2/2	0/0/0/0
3	DMF	E	113	-	-	0/2/2/2	0/0/0/0
3	DMF	E	28	-	-	0/2/2/2	0/0/0/0
3	DMF	F	249	-	-	0/2/2/2	0/0/0/0
3	DMF	G	137	-	-	0/2/2/2	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DMF	G	140	-	-	0/2/2/2	0/0/0/0
3	DMF	G	20	-	-	0/2/2/2	0/0/0/0
3	DMF	H	142	-	-	0/2/2/2	0/0/0/0
3	DMF	H	41	-	-	0/2/2/2	0/0/0/0
3	DMF	I	249	-	-	0/2/2/2	0/0/0/0
3	DMF	J	46	-	-	0/2/2/2	0/0/0/0
3	DMF	K	249	-	-	0/2/2/2	0/0/0/0
3	DMF	K	250	-	-	0/2/2/2	0/0/0/0
3	DMF	K	251	-	-	0/2/2/2	0/0/0/0
3	DMF	L	138	-	-	0/2/2/2	0/0/0/0
3	DMF	L	14	-	-	0/2/2/2	0/0/0/0
3	DMF	L	60	-	-	0/2/2/2	0/0/0/0
3	DMF	L	9	-	-	0/2/2/2	0/0/0/0
3	DMF	M	249	-	-	0/2/2/2	0/0/0/0
3	DMF	N	21	-	-	0/2/2/2	0/0/0/0
3	DMF	N	36	-	-	0/2/2/2	0/0/0/0
3	DMF	O	7	-	-	0/2/2/2	0/0/0/0
3	DMF	P	107	-	-	0/2/2/2	0/0/0/0
3	DMF	P	133	-	-	0/2/2/2	0/0/0/0
3	DMF	P	23	-	-	0/2/2/2	0/0/0/0
3	DMF	Q	249	-	-	0/2/2/2	0/0/0/0
3	DMF	Q	250	-	-	0/2/2/2	0/0/0/0
3	DMF	Q	251	-	-	0/2/2/2	0/0/0/0
3	DMF	S	249	-	-	0/2/2/2	0/0/0/0
3	DMF	S	250	-	-	0/2/2/2	0/0/0/0
3	DMF	T	134	-	-	0/2/2/2	0/0/0/0
3	DMF	T	62	-	-	0/2/2/2	0/0/0/0
3	DMF	U	249	-	-	0/2/2/2	0/0/0/0
3	DMF	U	250	-	-	0/2/2/2	0/0/0/0
3	DMF	V	117	-	-	0/2/2/2	0/0/0/0
3	DMF	V	121	-	-	0/2/2/2	0/0/0/0
3	DMF	V	135	-	-	0/2/2/2	0/0/0/0
3	DMF	V	136	-	-	0/2/2/2	0/0/0/0
3	DMF	V	16	-	-	0/2/2/2	0/0/0/0
3	DMF	W	249	-	-	0/2/2/2	0/0/0/0
3	DMF	X	141	-	-	0/2/2/2	0/0/0/0
3	DMF	Y	249	-	-	0/2/2/2	0/0/0/0
3	DMF	Y	250	-	-	0/2/2/2	0/0/0/0
3	DMF	Y	251	-	-	0/2/2/2	0/0/0/0
3	DMF	Z	105	-	-	0/2/2/2	0/0/0/0
3	DMF	Z	122	-	-	0/2/2/2	0/0/0/0
3	DMF	Z	27	-	-	0/2/2/2	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DMF	Z	50	-	-	0/2/2/2	0/0/0/0
3	DMF	Z	69	-	-	0/2/2/2	0/0/0/0

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.

32 monomers are involved in 55 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	1	249	DMF	2	0
3	2	145	DMF	1	0
3	2	99	DMF	1	0
3	A	249	DMF	1	0
3	E	104	DMF	3	0
3	E	113	DMF	1	0
3	G	137	DMF	1	0
3	G	140	DMF	2	0
3	G	20	DMF	1	0
3	H	142	DMF	1	0
3	I	249	DMF	1	0
3	K	249	DMF	1	0
3	K	251	DMF	4	0
3	L	138	DMF	3	0
3	L	9	DMF	1	0
3	N	21	DMF	1	0
3	P	107	DMF	2	0
3	P	133	DMF	1	0
3	Q	251	DMF	5	0
3	S	249	DMF	1	0
3	T	134	DMF	2	0
3	T	62	DMF	3	0
3	U	249	DMF	1	0
3	V	117	DMF	1	0
3	V	121	DMF	3	0
3	V	135	DMF	1	0
3	V	136	DMF	1	0
3	V	16	DMF	1	0
3	W	249	DMF	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	Y	249	DMF	1	0
3	Z	105	DMF	2	0
3	Z	69	DMF	5	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	2	222/240 (92%)	-0.30	1 (0%) 91 92	17, 32, 63, 84	0
1	C	222/240 (92%)	0.59	15 (6%) 20 23	26, 43, 72, 89	0
1	E	223/240 (92%)	-0.14	6 (2%) 58 62	19, 32, 67, 134	0
1	G	222/240 (92%)	-0.24	0 100 100	18, 28, 62, 83	0
1	H	223/240 (92%)	0.11	4 (1%) 71 75	22, 36, 65, 86	0
1	J	222/240 (92%)	0.16	10 (4%) 37 42	24, 38, 71, 89	0
1	L	222/240 (92%)	-0.33	5 (2%) 64 67	18, 30, 64, 83	0
1	N	223/240 (92%)	-0.35	1 (0%) 93 93	15, 30, 64, 118	0
1	P	222/240 (92%)	-0.15	4 (1%) 71 75	19, 33, 67, 85	0
1	R	222/240 (92%)	-0.09	3 (1%) 78 80	22, 34, 66, 84	0
1	T	223/240 (92%)	-0.22	2 (0%) 85 88	21, 33, 67, 98	0
1	V	226/240 (94%)	-0.34	2 (0%) 85 88	16, 29, 65, 81	0
1	X	224/240 (93%)	-0.24	5 (2%) 65 69	19, 30, 66, 124	0
1	Z	224/240 (93%)	-0.18	0 100 100	21, 34, 68, 107	0
2	1	214/240 (89%)	0.17	7 (3%) 50 55	25, 48, 89, 127	0
2	A	214/240 (89%)	1.39	56 (26%) 1 1	37, 64, 111, 131	0
2	B	214/240 (89%)	1.88	85 (39%) 0 0	40, 87, 134, 168	0
2	D	213/240 (88%)	0.34	19 (8%) 12 13	24, 49, 98, 124	0
2	F	214/240 (89%)	0.39	25 (11%) 6 6	24, 48, 96, 127	0
2	I	214/240 (89%)	0.86	28 (13%) 5 4	34, 53, 98, 125	0
2	K	214/240 (89%)	0.44	17 (7%) 15 17	25, 49, 92, 126	0
2	M	214/240 (89%)	0.04	5 (2%) 64 67	22, 45, 90, 124	0
2	O	214/240 (89%)	0.49	21 (9%) 10 10	26, 54, 95, 129	0
2	Q	214/240 (89%)	0.09	9 (4%) 40 45	20, 42, 90, 126	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	S	214/240 (89%)	0.73	36 (16%) 2 2	28, 53, 98, 126	0
2	U	214/240 (89%)	0.40	14 (6%) 22 25	22, 51, 99, 126	0
2	W	214/240 (89%)	0.30	16 (7%) 17 19	22, 46, 94, 125	0
2	Y	214/240 (89%)	0.25	11 (5%) 32 36	23, 46, 90, 127	0
All	All	6115/6720 (90%)	0.21	407 (6%) 21 23	15, 40, 90, 168	0

The worst 5 of 407 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	U	234	LEU	8.2
2	A	9	MET	8.0
2	A	203	LEU	7.1
2	Y	9	MET	7.0
2	1	9	MET	6.7

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
3	DMF	L	9	5/5	0.86	0.33	19.71	53,54,82,89	0
3	DMF	V	135	5/5	0.78	0.34	18.82	35,51,75,87	0
3	DMF	Z	105	5/5	0.93	0.34	18.82	22,57,81,82	0
3	DMF	G	20	5/5	0.88	0.30	17.04	27,40,70,93	0
3	DMF	Z	50	5/5	0.86	0.40	14.11	86,90,126,146	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	DMF	L	14	5/5	0.86	0.40	12.23	30,38,70,90	0
3	DMF	T	62	5/5	0.89	0.33	11.60	45,61,83,95	0
3	DMF	P	23	5/5	0.96	0.20	10.41	49,62,83,93	0
3	DMF	C	15	5/5	0.92	0.27	8.23	54,69,74,107	0
3	DMF	G	137	5/5	0.97	0.20	8.23	27,35,51,57	0
3	DMF	Z	27	5/5	0.91	0.25	7.34	56,66,86,97	0
3	DMF	P	133	5/5	0.93	0.23	6.95	62,69,81,113	0
3	DMF	Z	122	5/5	0.94	0.25	6.70	26,28,76,84	0
3	DMF	E	104	5/5	0.95	0.26	6.50	33,42,51,57	0
3	DMF	Y	249	5/5	0.91	0.21	6.07	19,24,64,70	0
3	DMF	S	249	5/5	0.93	0.29	5.68	37,57,66,75	0
3	DMF	1	249	5/5	0.94	0.26	5.39	19,49,53,60	0
3	DMF	L	60	5/5	0.93	0.20	5.21	35,39,50,58	0
3	DMF	N	36	5/5	0.93	0.22	5.11	35,43,74,83	0
3	DMF	Y	251	5/5	0.86	0.27	4.89	42,45,61,63	0
3	DMF	L	138	5/5	0.94	0.37	4.88	40,47,72,82	0
3	DMF	P	107	5/5	0.92	0.31	4.86	39,58,69,70	0
3	DMF	V	136	5/5	0.91	0.24	4.61	36,44,59,63	0
3	DMF	V	117	5/5	0.86	0.24	4.61	46,50,66,72	0
3	DMF	H	142	5/5	0.90	0.27	4.54	40,62,68,72	0
3	DMF	Q	249	5/5	0.97	0.20	4.38	31,39,42,58	0
3	DMF	W	249	5/5	0.96	0.16	4.30	25,31,39,60	0
3	DMF	U	249	5/5	0.95	0.20	4.14	11,23,39,54	0
3	DMF	K	251	5/5	0.88	0.23	4.11	39,50,64,80	0
3	DMF	2	145	5/5	0.93	0.22	4.11	29,42,52,58	0
3	DMF	G	140	5/5	0.96	0.19	4.10	24,33,57,59	0
3	DMF	1	250	5/5	0.88	0.22	3.87	43,63,73,87	0
3	DMF	K	250	5/5	0.91	0.25	3.84	42,58,73,78	0
3	DMF	E	113	5/5	0.94	0.31	3.69	48,56,75,77	0
3	DMF	B	249	5/5	0.93	0.27	3.28	30,46,52,59	0
3	DMF	M	249	5/5	0.97	0.18	3.12	12,15,43,51	0
3	DMF	J	46	5/5	0.93	0.21	2.90	29,54,61,63	0
3	DMF	U	250	5/5	0.89	0.20	2.84	50,54,62,63	0
3	DMF	Q	251	5/5	0.90	0.24	2.83	26,56,59,84	0
3	DMF	O	7	5/5	0.92	0.21	2.79	38,48,59,62	0
3	DMF	Z	69	5/5	0.83	0.34	2.61	53,80,102,104	0
3	DMF	H	41	5/5	0.93	0.21	2.54	53,56,63,80	0
3	DMF	V	121	5/5	0.96	0.16	2.41	26,27,49,50	0
3	DMF	I	249	5/5	0.98	0.21	2.36	41,43,50,58	0
3	DMF	A	249	5/5	0.94	0.24	2.35	23,35,53,58	0
3	DMF	2	99	5/5	0.94	0.17	1.67	33,35,64,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	DMF	D	249	5/5	0.96	0.15	1.52	21,22,39,53	0
3	DMF	T	134	5/5	0.96	0.17	1.29	33,56,59,79	0
3	DMF	N	21	5/5	0.95	0.15	0.87	17,53,56,76	0
3	DMF	Y	250	5/5	0.97	0.15	0.85	14,36,48,55	0
3	DMF	S	250	5/5	0.92	0.18	0.68	26,42,81,85	0
3	DMF	A	8	5/5	0.93	0.20	0.56	16,61,76,85	0
3	DMF	Q	250	5/5	0.95	0.14	0.50	23,37,45,58	0
3	DMF	F	249	5/5	0.97	0.13	0.45	26,28,37,42	0
3	DMF	K	249	5/5	0.98	0.12	-0.29	23,32,46,48	0
3	DMF	E	28	5/5	0.89	0.32	-	36,68,72,88	0
3	DMF	V	16	5/5	0.91	0.29	-	36,61,65,73	0
3	DMF	X	141	5/5	0.89	0.36	-	40,55,82,85	0

6.5 Other polymers ⓘ

There are no such residues in this entry.