wwPDB X-ray Structure Validation Summary Report (i)

May 24, 2020 – 04:29 am BST

PDB ID	:	4HEL
Title	:	Crystal structure analysis of apo-GroEL structure
Authors	:	Saxena, A.K.; Meena, S.R.
Deposited on	:	2012-10-04
Resolution	:	3.20 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
https://www.wwpdb.org/validation/2017/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:

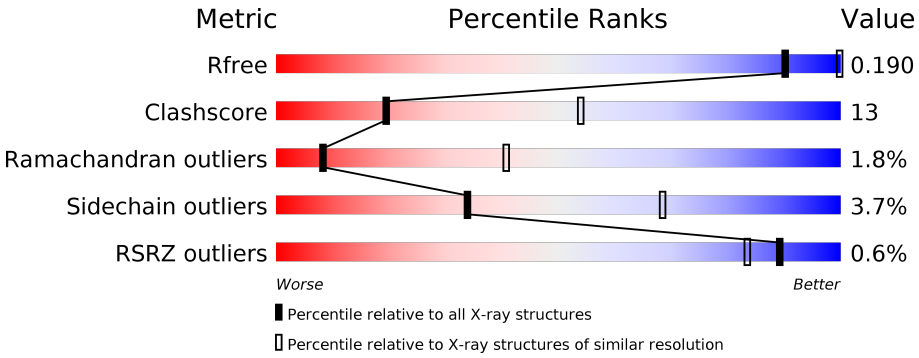
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.20 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}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 respectively. 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	525	% 74% 24% ·
1	B	525	75% 23% ·
1	C	525	76% 22% ·
1	D	525	% 70% 28% ·
1	E	525	% 76% 22% ·
1	F	525	74% 23% ·

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Mol	Chain	Length	Quality of chain
1	G	525	76% 22%
1	H	525	% 73% 26%
1	I	525	74% 24%
1	J	525	71% 27%
1	K	525	2% 70% 26%
1	L	525	% 73% 24%
1	M	525	74% 21%
1	N	525	75% 24%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 54997 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 60 kDa chaperonin 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	B	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	C	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	D	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	E	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	F	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	G	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	H	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	I	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	J	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	K	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	L	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	M	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			
1	N	525	Total	C	N	O	S	0	0	0
			3864	2403	667	774	20			

- Molecule 2 is water.

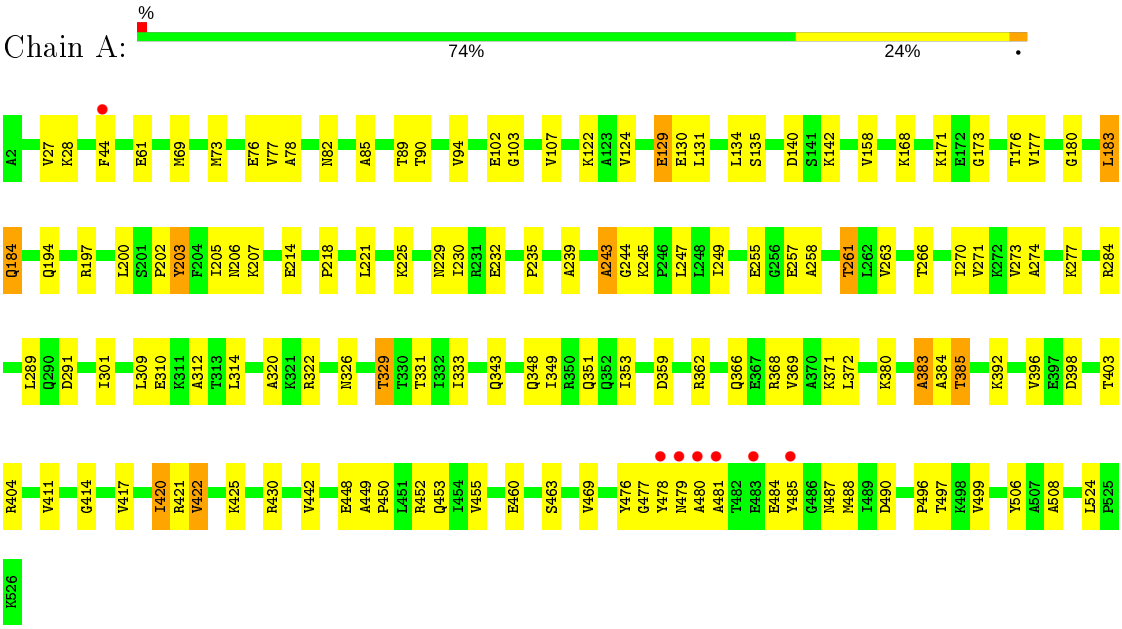
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	60	Total O 60 60	0	0
2	B	83	Total O 83 83	0	0
2	C	65	Total O 65 65	0	0
2	D	62	Total O 62 62	0	0
2	E	79	Total O 79 79	0	0
2	F	53	Total O 53 53	0	0
2	G	74	Total O 74 74	0	0
2	H	52	Total O 52 52	0	0
2	I	64	Total O 64 64	0	0
2	J	75	Total O 75 75	0	0
2	K	55	Total O 55 55	0	0
2	L	64	Total O 64 64	0	0
2	M	57	Total O 57 57	0	0
2	N	58	Total O 58 58	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 the various outlier classes 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.

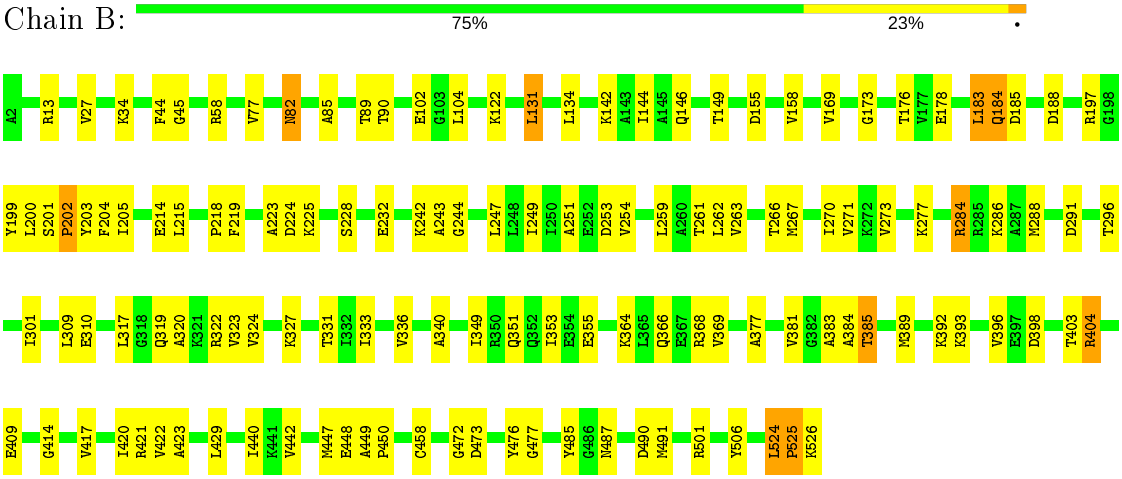
- Molecule 1: 60 kDa chaperonin 4

Chain A:



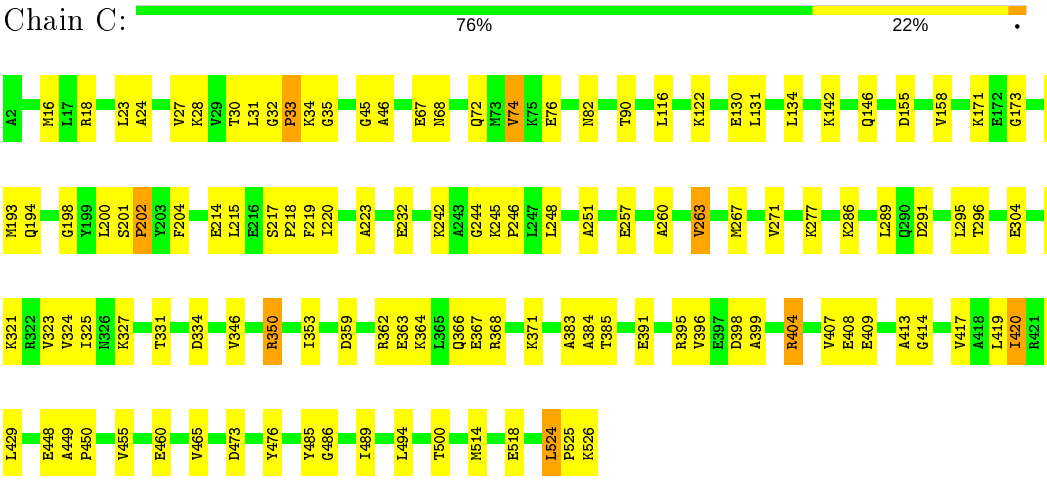
- Molecule 1: 60 kDa chaperonin 4

Chain B:



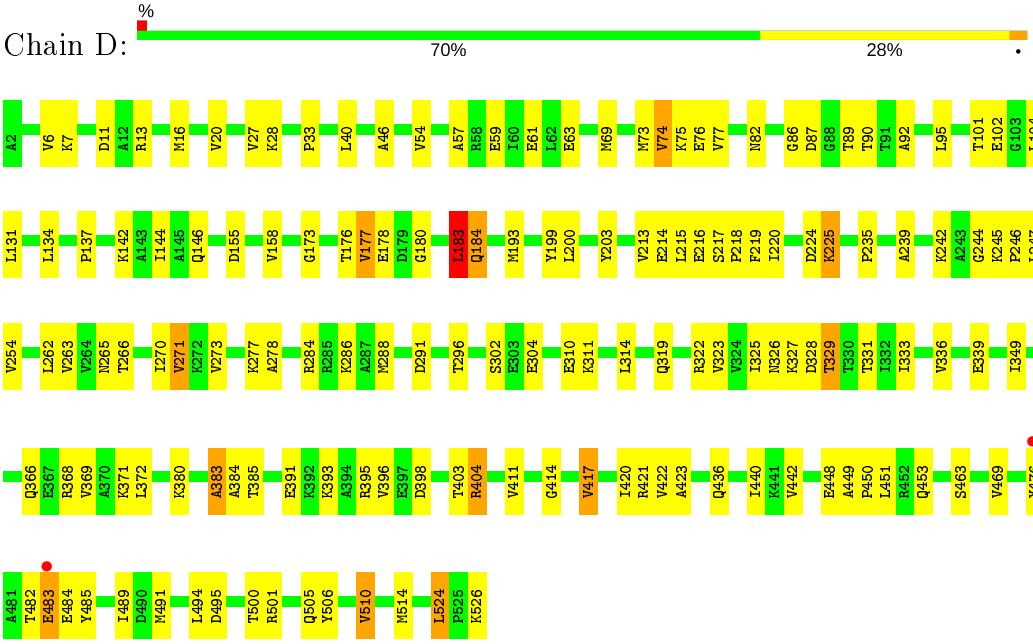
- Molecule 1: 60 kDa chaperonin 4

Chain C:



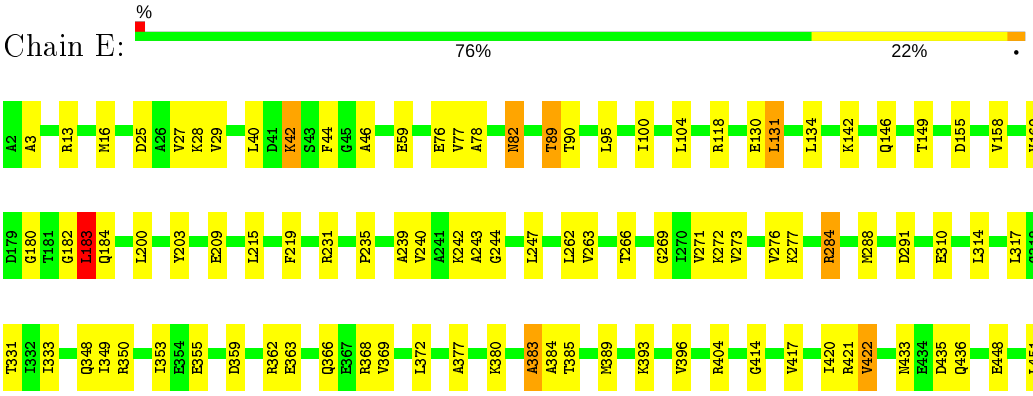
- Molecule 1: 60 kDa chaperonin 4

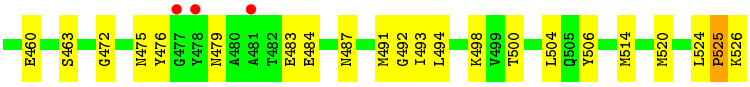
Chain D:



- Molecule 1: 60 kDa chaperonin 4

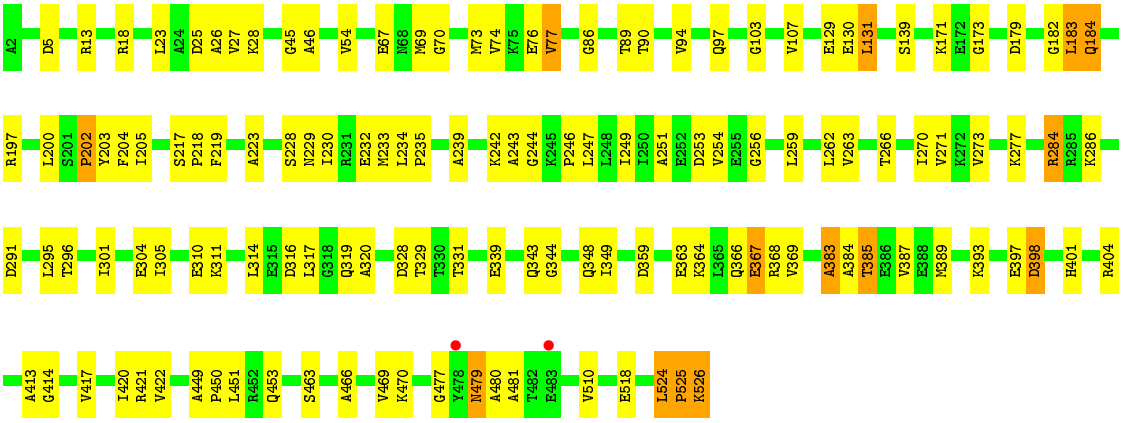
Chain E:





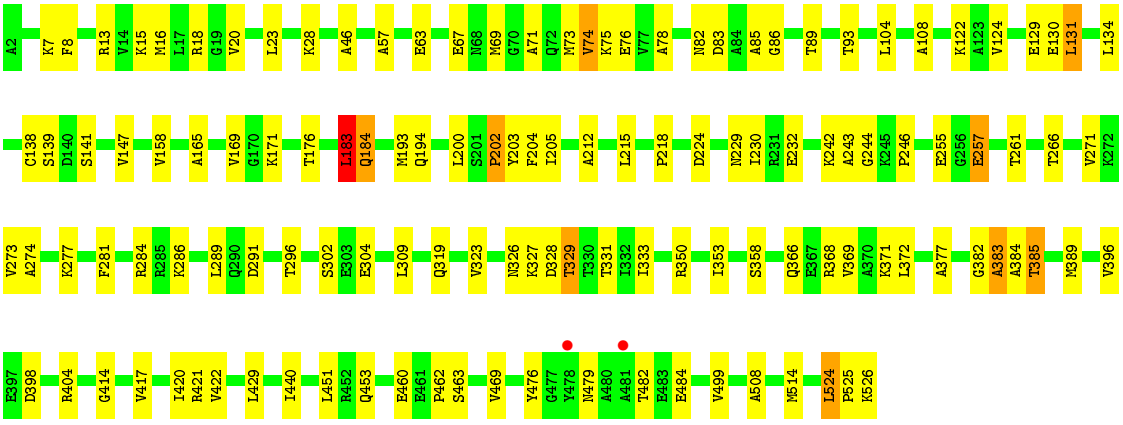
- Molecule 1: 60 kDa chaperonin 4

Chain F:



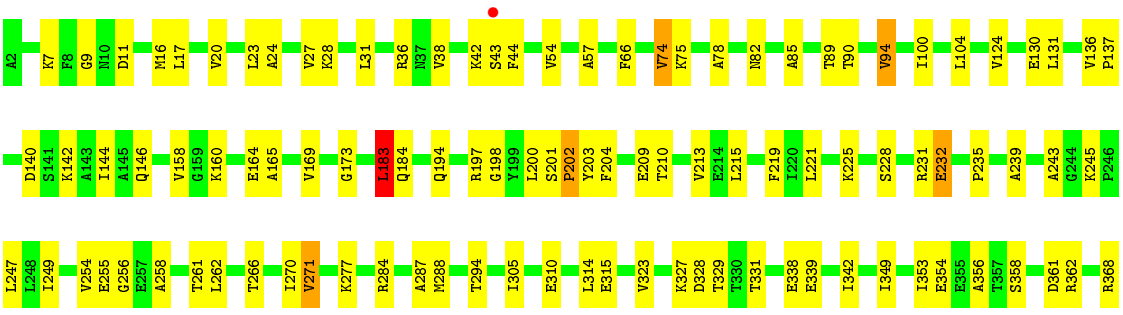
- Molecule 1: 60 kDa chaperonin 4

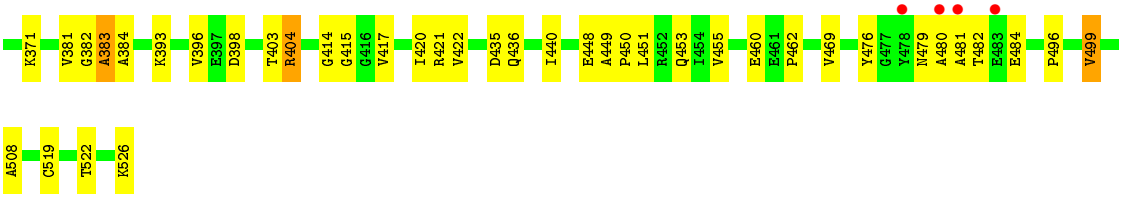
Chain G:



- Molecule 1: 60 kDa chaperonin 4

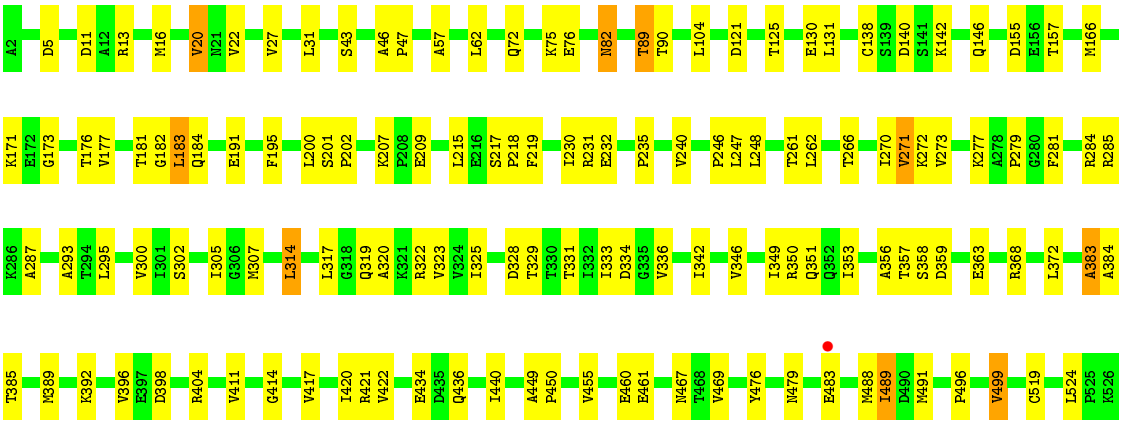
Chain H:





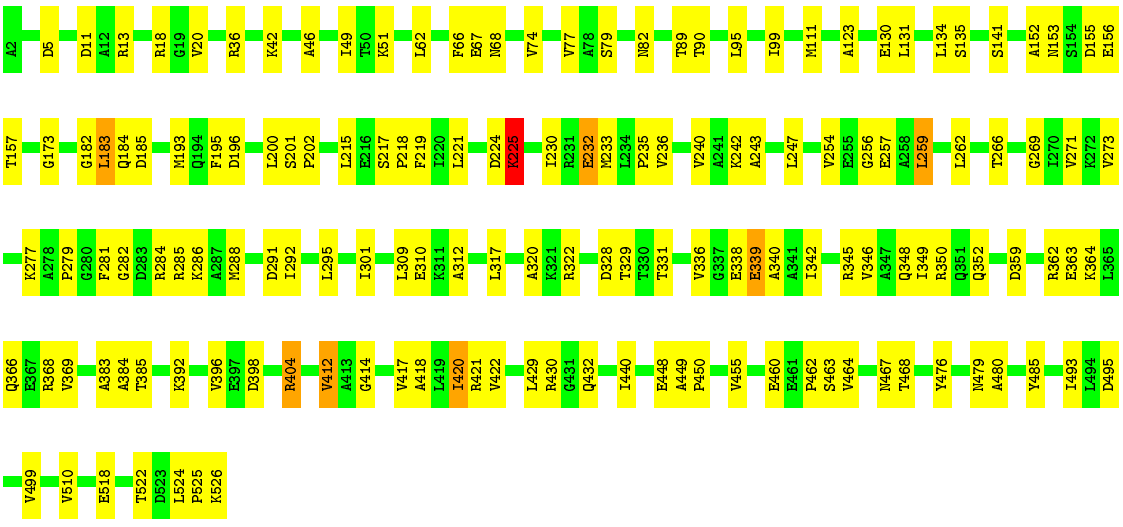
• Molecule 1: 60 kDa chaperonin 4

Chain I:



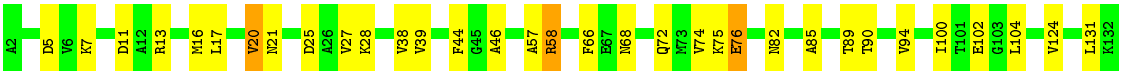
• Molecule 1: 60 kDa chaperonin 4

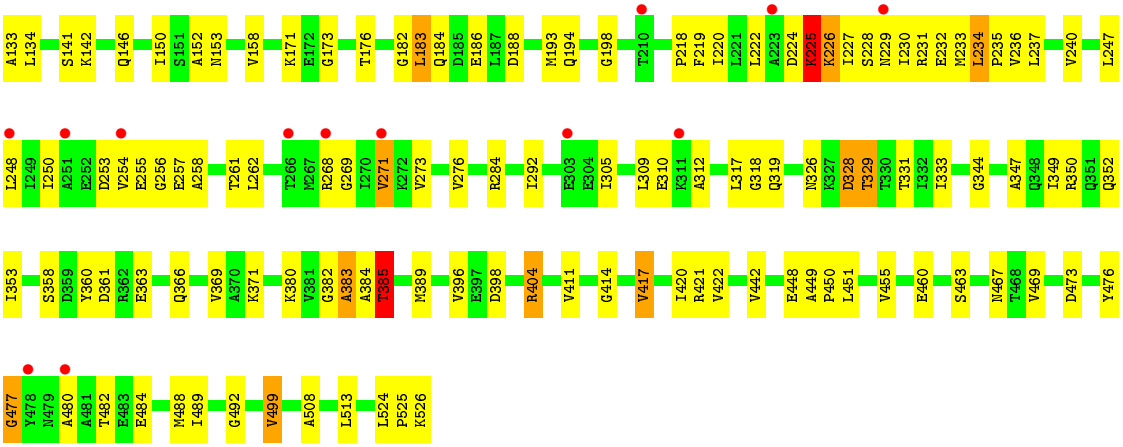
Chain J:



• Molecule 1: 60 kDa chaperonin 4

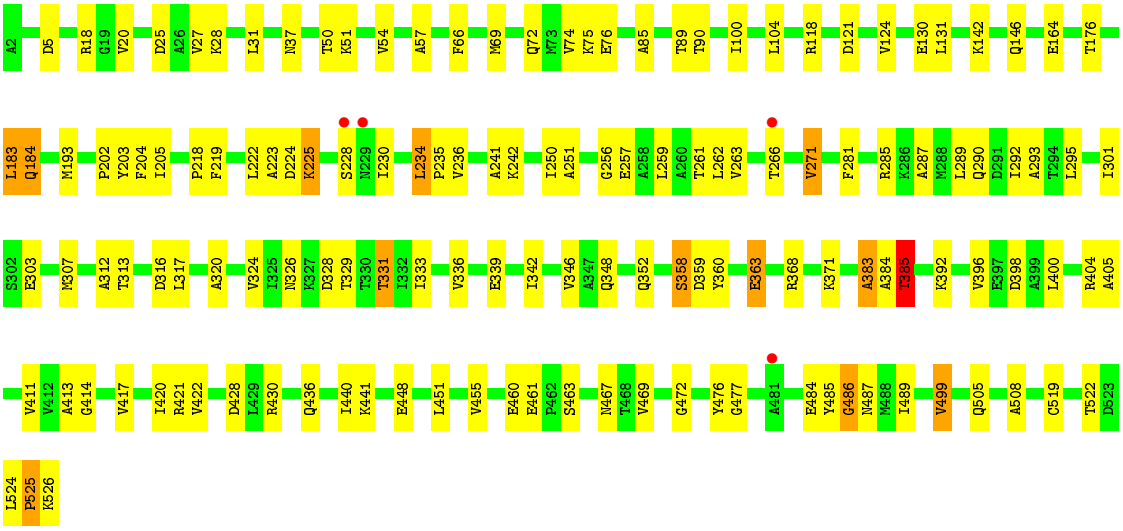
Chain K:





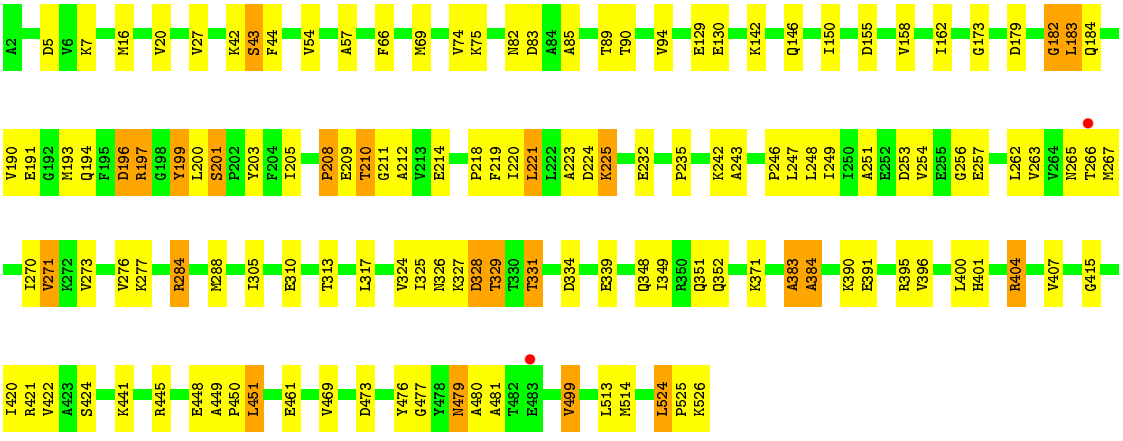
• Molecule 1: 60 kDa chaperonin 4

Chain L:



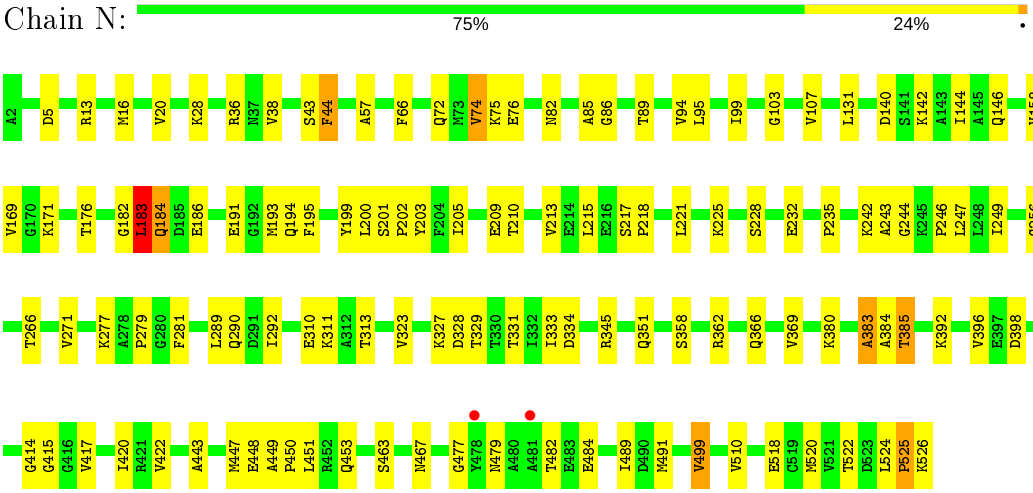
• Molecule 1: 60 kDa chaperonin 4

Chain M:



• Molecule 1: 60 kDa chaperonin 4

Chain N:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	136.24Å 261.83Å 282.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.38 – 3.20 59.09 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (59.38-3.20) 100.0 (59.09-3.20)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.36 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.198 , 0.223 0.189 , 0.190	Depositor DCC
R_{free} test set	8373 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	48.3	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 38.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	54997	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.59	0/3892	0.72	1/5254 (0.0%)
1	B	0.59	0/3892	0.69	0/5254
1	C	0.55	0/3892	0.70	2/5254 (0.0%)
1	D	0.56	0/3892	0.70	0/5254
1	E	0.61	0/3892	0.73	0/5254
1	F	0.58	0/3892	0.71	2/5254 (0.0%)
1	G	0.59	0/3892	0.70	1/5254 (0.0%)
1	H	0.58	0/3892	0.71	1/5254 (0.0%)
1	I	0.56	0/3892	0.68	2/5254 (0.0%)
1	J	0.55	0/3892	0.68	1/5254 (0.0%)
1	K	0.52	0/3892	0.67	1/5254 (0.0%)
1	L	0.55	0/3892	0.70	2/5254 (0.0%)
1	M	0.60	0/3892	0.74	1/5254 (0.0%)
1	N	0.58	0/3892	0.70	1/5254 (0.0%)
All	All	0.57	0/54488	0.70	15/73556 (0.0%)

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	K	477	GLY	N-CA-C	6.93	130.42	113.10
1	C	295	LEU	CA-CB-CG	6.61	130.49	115.30
1	N	477	GLY	N-CA-C	6.48	129.29	113.10
1	J	295	LEU	CA-CB-CG	6.38	129.97	115.30
1	A	477	GLY	N-CA-C	6.25	128.73	113.10

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	3864	0	3989	93	0
1	B	3864	0	3989	103	0
1	C	3864	0	3989	92	0
1	D	3864	0	3989	127	0
1	E	3864	0	3989	108	0
1	F	3864	0	3989	97	0
1	G	3864	0	3989	86	0
1	H	3864	0	3989	97	0
1	I	3864	0	3989	100	0
1	J	3864	0	3989	118	0
1	K	3864	0	3989	140	0
1	L	3864	0	3989	105	0
1	M	3864	0	3989	93	0
1	N	3864	0	3989	81	0
2	A	60	0	0	17	0
2	B	83	0	0	32	0
2	C	65	0	0	14	0
2	D	62	0	0	32	0
2	E	79	0	0	32	0
2	F	53	0	0	5	0
2	G	74	0	0	10	0
2	H	52	0	0	20	0
2	I	64	0	0	24	0
2	J	75	0	0	43	0
2	K	55	0	0	33	0
2	L	64	0	0	28	0
2	M	57	0	0	13	0
2	N	58	0	0	13	0
All	All	54997	0	55846	1407	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 13.

The worst 5 of 1407 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:K:234:LEU:HA	2:K:630:HOH:O	1.37	1.24
1:K:234:LEU:HD23	2:K:630:HOH:O	1.35	1.24
1:K:384:ALA:HA	2:L:635:HOH:O	1.36	1.22
1:K:219:PHE:HA	2:K:636:HOH:O	1.39	1.18
1:H:261:THR:HB	2:H:647:HOH:O	1.47	1.12

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	523/525 (100%)	499 (95%)	15 (3%)	9 (2%)	9	42
1	B	523/525 (100%)	499 (95%)	18 (3%)	6 (1%)	14	51
1	C	523/525 (100%)	496 (95%)	18 (3%)	9 (2%)	9	42
1	D	523/525 (100%)	494 (94%)	21 (4%)	8 (2%)	10	44
1	E	523/525 (100%)	493 (94%)	22 (4%)	8 (2%)	10	44
1	F	523/525 (100%)	496 (95%)	17 (3%)	10 (2%)	8	39
1	G	523/525 (100%)	498 (95%)	17 (3%)	8 (2%)	10	44
1	H	523/525 (100%)	488 (93%)	24 (5%)	11 (2%)	7	37
1	I	523/525 (100%)	492 (94%)	26 (5%)	5 (1%)	15	54
1	J	523/525 (100%)	491 (94%)	24 (5%)	8 (2%)	10	44
1	K	523/525 (100%)	486 (93%)	28 (5%)	9 (2%)	9	42
1	L	523/525 (100%)	486 (93%)	25 (5%)	12 (2%)	6	34
1	M	523/525 (100%)	487 (93%)	18 (3%)	18 (3%)	3	24
1	N	523/525 (100%)	492 (94%)	22 (4%)	9 (2%)	9	42
All	All	7322/7350 (100%)	6897 (94%)	295 (4%)	130 (2%)	8	41

5 of 130 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	480	ALA
1	B	183	LEU
1	B	184	GLN
1	C	202	PRO
1	E	44	PHE

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	405/405 (100%)	388 (96%)	17 (4%)	30	65
1	B	405/405 (100%)	395 (98%)	10 (2%)	47	77
1	C	405/405 (100%)	393 (97%)	12 (3%)	41	73
1	D	405/405 (100%)	391 (96%)	14 (4%)	36	69
1	E	405/405 (100%)	393 (97%)	12 (3%)	41	73
1	F	405/405 (100%)	390 (96%)	15 (4%)	34	68
1	G	405/405 (100%)	390 (96%)	15 (4%)	34	68
1	H	405/405 (100%)	390 (96%)	15 (4%)	34	68
1	I	405/405 (100%)	386 (95%)	19 (5%)	26	62
1	J	405/405 (100%)	390 (96%)	15 (4%)	34	68
1	K	405/405 (100%)	384 (95%)	21 (5%)	23	59
1	L	405/405 (100%)	393 (97%)	12 (3%)	41	73
1	M	405/405 (100%)	386 (95%)	19 (5%)	26	62
1	N	405/405 (100%)	392 (97%)	13 (3%)	39	71
All	All	5670/5670 (100%)	5461 (96%)	209 (4%)	34	68

5 of 209 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	524	LEU
1	I	232	GLU
1	M	479	ASN

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Mol	Chain	Res	Type
1	H	183	LEU
1	H	398	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	433	ASN
1	F	37	ASN
1	K	146	GLN
1	E	366	GLN
1	I	72	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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	525/525 (100%)	-0.47	7 (1%) 77 65	10, 32, 68, 153	0
1	B	525/525 (100%)	-0.41	0 100 100	11, 35, 69, 95	0
1	C	525/525 (100%)	-0.40	0 100 100	13, 40, 77, 102	0
1	D	525/525 (100%)	-0.31	5 (0%) 82 72	13, 39, 88, 153	0
1	E	525/525 (100%)	-0.42	3 (0%) 89 83	11, 30, 63, 180	0
1	F	525/525 (100%)	-0.42	2 (0%) 92 89	9, 38, 73, 163	0
1	G	525/525 (100%)	-0.42	2 (0%) 92 89	10, 34, 74, 122	0
1	H	525/525 (100%)	-0.39	5 (0%) 82 72	11, 38, 74, 140	0
1	I	525/525 (100%)	-0.37	1 (0%) 95 94	12, 41, 79, 170	0
1	J	525/525 (100%)	-0.35	0 100 100	13, 40, 82, 122	0
1	K	525/525 (100%)	-0.10	13 (2%) 57 43	10, 48, 121, 151	0
1	L	525/525 (100%)	-0.25	4 (0%) 86 78	13, 46, 94, 126	0
1	M	525/525 (100%)	-0.35	2 (0%) 92 89	11, 37, 80, 160	0
1	N	525/525 (100%)	-0.35	2 (0%) 92 89	9, 37, 72, 140	0
All	All	7350/7350 (100%)	-0.36	46 (0%) 89 83	9, 38, 85, 180	0

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	478	TYR	5.1
1	L	481	ALA	4.5
1	K	478	TYR	4.3
1	E	481	ALA	4.2
1	H	43	SER	4.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.