



wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 09:16 pm BST

PDB ID : 2NWC
Title : A 3.02 angstrom crystal structure of wild-type apo GroEL in a monoclinic space group
Authors : Kiser, P.D.; Lodowski, D.T.; Palczewski, K.
Deposited on : 2006-11-14
Resolution : 3.02 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

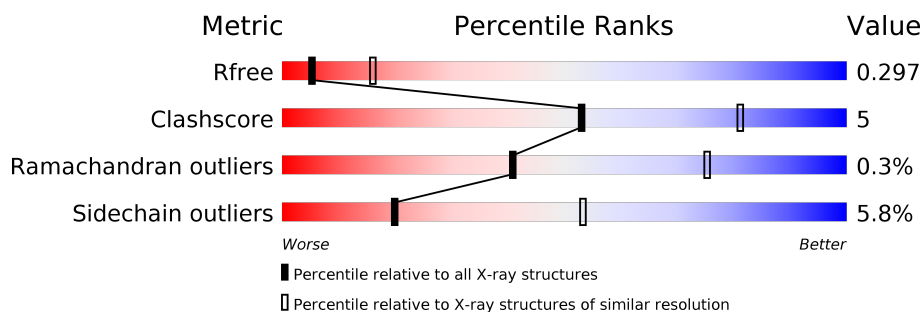
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.02 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	2399 (3.04-3.00)
Clashscore	141614	2734 (3.04-3.00)
Ramachandran outliers	138981	2640 (3.04-3.00)
Sidechain outliers	138945	2643 (3.04-3.00)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	547	80% 15% . .
1	B	547	82% 13% . .
1	C	547	80% 14% . .
1	D	547	79% 14% . .
1	E	547	80% 14% . . .
1	F	547	81% 13% . .
1	G	547	81% 13% . .

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Mol	Chain	Length	Quality of chain
1	H	547	<div><div></div><div>83%11%<div><div></div><div></div><div></div></div></div></div>
1	I	547	<div><div></div><div>80%15%<div><div></div><div></div><div></div></div></div></div>
1	J	547	<div><div></div><div>80%14%<div><div></div><div></div><div></div></div></div></div>
1	K	547	<div><div></div><div>81%12%<div><div></div><div></div><div></div></div></div></div>
1	L	547	<div><div></div><div>79%16%<div><div></div><div></div><div></div></div></div></div>
1	M	547	<div><div></div><div>82%12%<div><div></div><div></div><div></div></div></div></div>
1	N	547	<div><div></div><div>79%14%<div><div></div><div></div><div></div></div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 53970 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.

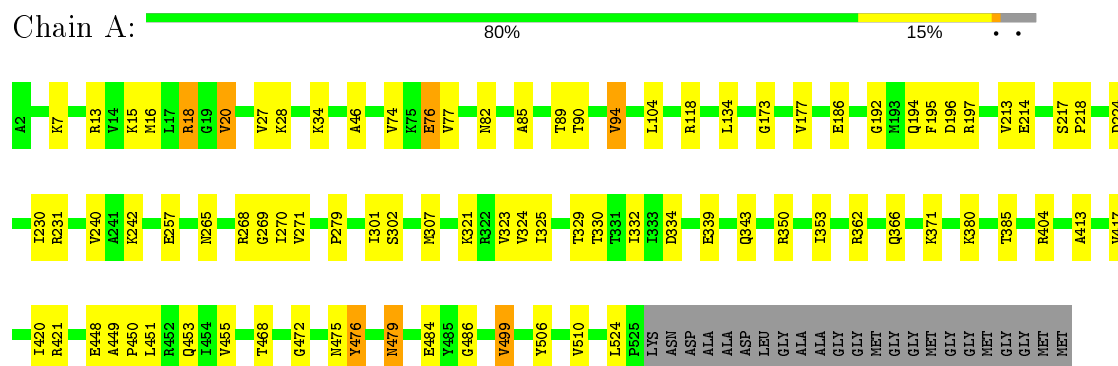
- Molecule 1 is a protein called 60 kDa chaperonin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	B	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	C	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	D	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	E	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	F	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	G	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	H	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	I	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	J	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	K	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	L	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	M	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	N	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			

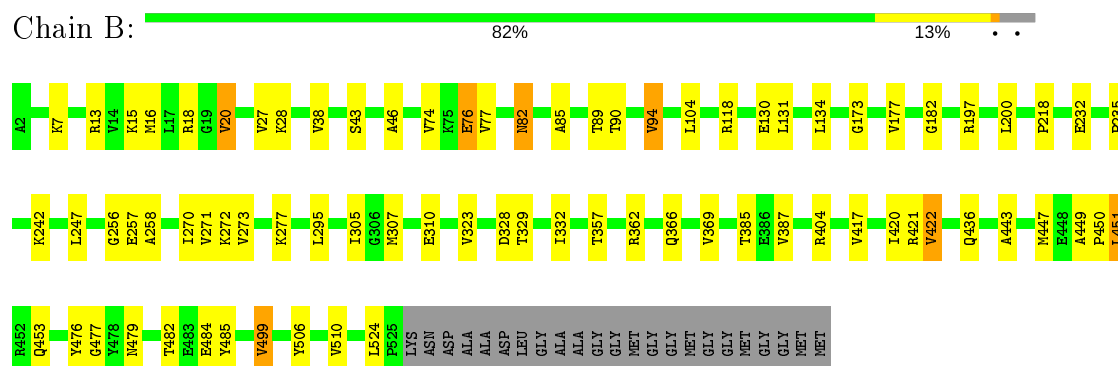
3 Residue-property plots

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. 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. 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.

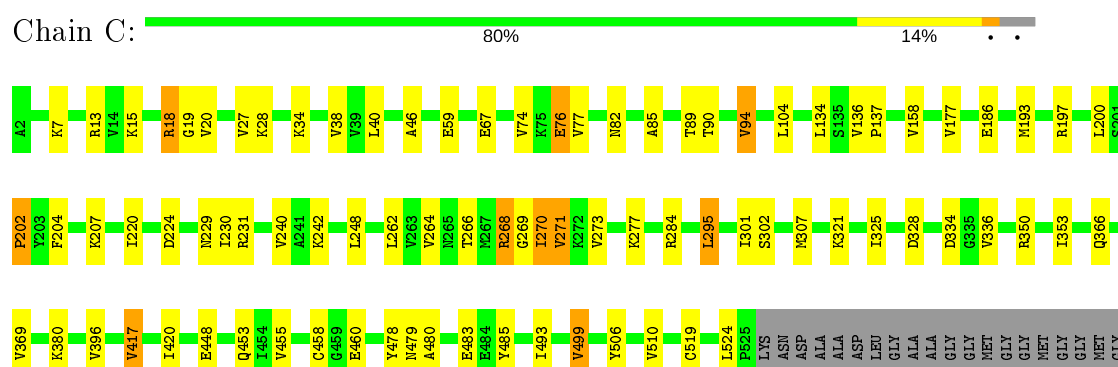
- Molecule 1: 60 kDa chaperonin



- Molecule 1: 60 kDa chaperonin




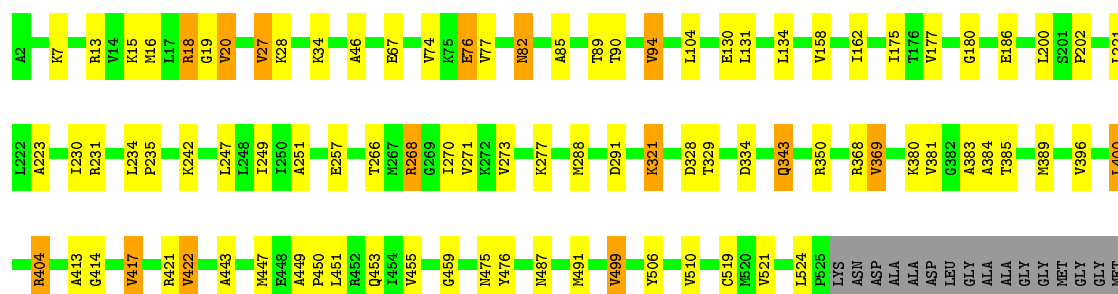
- Molecule 1: 60 kDa chaperonin



GLY
MET
MET


- Molecule 1: 60 kDa chaperonin

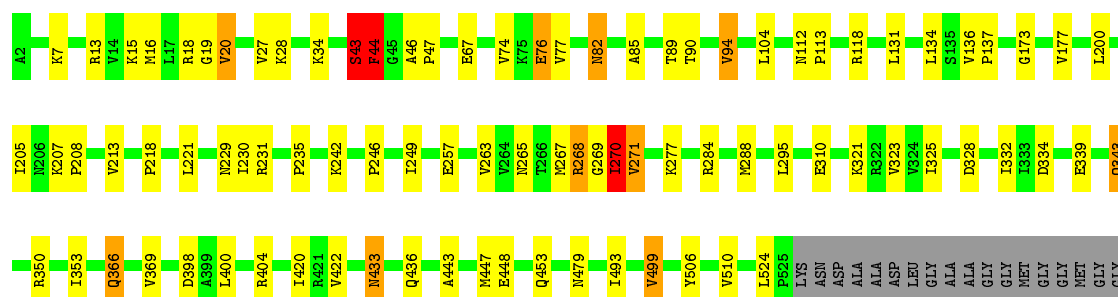
Chain D:  79% 14%



GLY
GLY
GLY
GLY
MET
MET


- Molecule 1: 60 kDa chaperonin

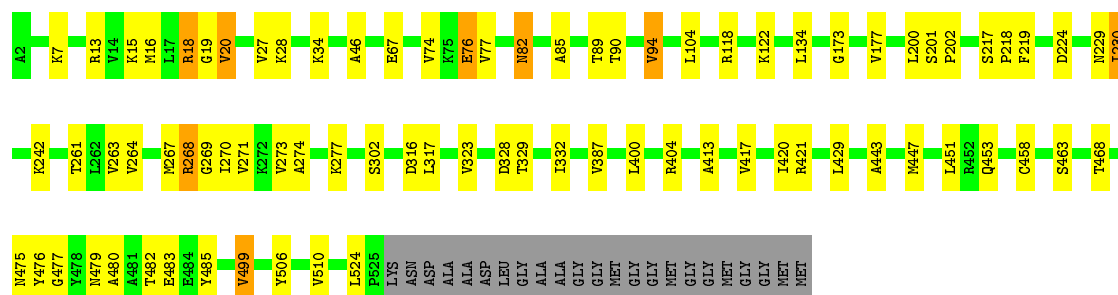
Chain E:  80% 14%




MET
GLY
GLY
MET
MET

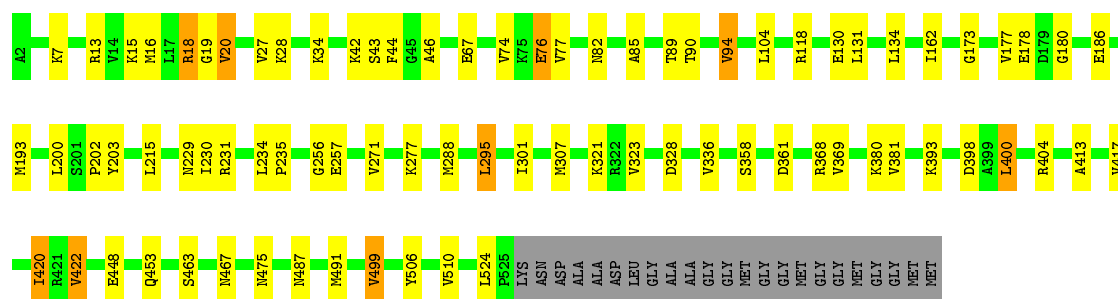
- Molecule 1: 60 kDa chaperonin

Chain F:  81% 13%



- Molecule 1: 60 kDa chaperonin

Chain G:  81% 13%



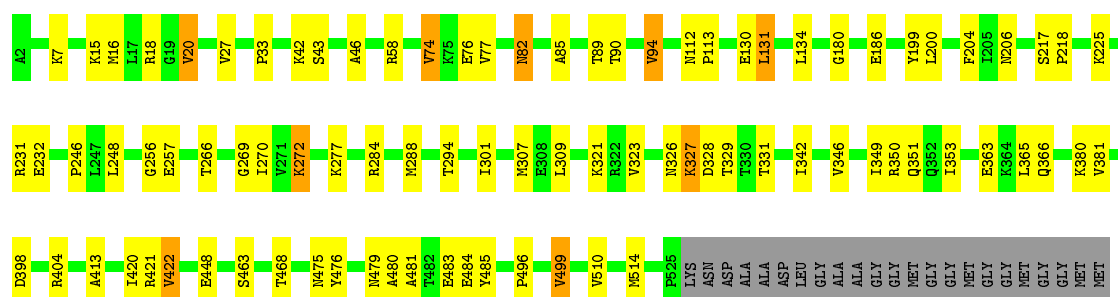
- Molecule 1: 60 kDa chaperonin

Chain H: 83% 11%



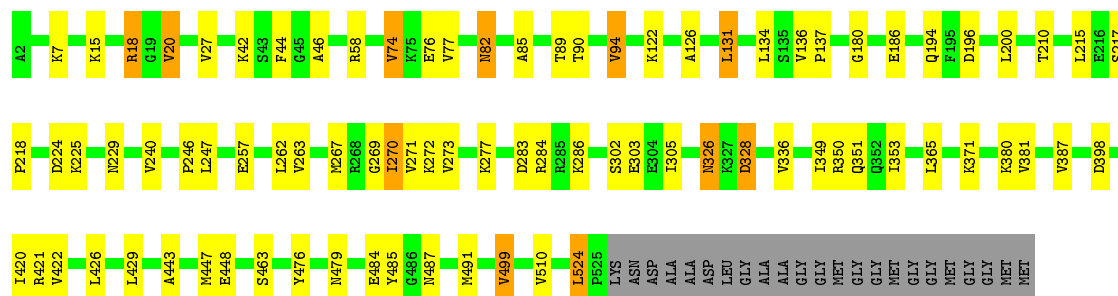
- Molecule 1: 60 kDa chaperonin

Chain I: 80% 15%



- Molecule 1: 60 kDa chaperonin

Chain J: 80% 14%



- Molecule 1: 60 kDa chaperonin

V396	E397	D398	R404	A413	R421	V422	A449	P450	T468	V469	N475	Y476	N479	T482	E483	E484	Y485	G486	N487	M491	V499	V510	L524	P525	LYS	ASN	ASP	ALA	ALA	ALA	ASP	LEU	GLY	ALA	ALA	GLY	GLY	MET	GLY	GLY	MET	GLY	GLY	MET	GLY	MET	MET
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	136.42Å 262.25Å 147.07Å 90.00° 99.83° 90.00°	Depositor
Resolution (Å)	30.00 – 3.02 49.32 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (30.00-3.02) 99.0 (49.32-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.227 , 0.263 0.271 , 0.297	Depositor DCC
R_{free} test set	10227 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	67.1	Xtriage
Anisotropy	0.415	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 12.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	53970	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.17% 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, 0.333 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	0.32	0/3883	0.50	0/5243
1	B	0.45	2/3883 (0.1%)	0.49	1/5243 (0.0%)
1	C	0.33	0/3883	0.49	0/5243
1	D	0.34	0/3883	0.50	0/5243
1	E	0.34	0/3883	0.55	2/5243 (0.0%)
1	F	0.32	0/3883	0.50	0/5243
1	G	0.33	0/3883	0.62	3/5243 (0.1%)
1	H	0.32	0/3883	0.49	0/5243
1	I	0.36	1/3883 (0.0%)	0.50	0/5243
1	J	0.32	0/3883	0.49	0/5243
1	K	0.32	0/3883	0.48	0/5243
1	L	0.33	0/3883	0.50	0/5243
1	M	0.33	0/3883	0.49	0/5243
1	N	0.34	0/3883	0.49	0/5243
All	All	0.34	3/54362 (0.0%)	0.51	6/73402 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	I	0	1
1	K	0	1
1	M	0	2
1	N	0	1
All	All	0	10

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	232	GLU	CD-OE2	16.33	1.43	1.25
1	B	232	GLU	CD-OE1	9.88	1.36	1.25
1	I	327	LYS	CE-NZ	8.56	1.70	1.49

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	18	ARG	NE-CZ-NH1	-18.59	111.01	120.30
1	G	18	ARG	NE-CZ-NH2	17.59	129.09	120.30
1	E	43	SER	N-CA-CB	-13.09	90.87	110.50
1	E	43	SER	N-CA-C	8.90	135.04	111.00
1	G	18	ARG	CD-NE-CZ	7.90	134.66	123.60

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	269	GLY	Peptide
1	C	269	GLY	Peptide
1	D	268	ARG	Peptide
1	E	43	SER	Peptide
1	F	269	GLY	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3855	0	3976	48	0
1	B	3855	0	3976	43	0
1	C	3855	0	3976	52	0
1	D	3855	0	3976	58	0
1	E	3855	0	3976	56	0
1	F	3855	0	3976	42	0
1	G	3855	0	3976	40	0
1	H	3855	0	3976	34	0
1	I	3855	0	3976	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	3855	0	3976	43	0
1	K	3855	0	3976	43	0
1	L	3855	0	3976	47	0
1	M	3855	0	3976	35	0
1	N	3855	0	3976	46	0
All	All	53970	0	55664	587	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 5.

The worst 5 of 587 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:I:327:LYS:CE	1:I:327:LYS:NZ	1.70	1.49
1:E:46:ALA:HB2	1:F:76:GLU:HG3	1.24	1.09
1:A:46:ALA:HB2	1:B:76:GLU:HG3	1.35	1.07
1:F:46:ALA:HB2	1:G:76:GLU:HG3	1.41	0.99
1:A:76:GLU:HG3	1:G:46:ALA:HB2	1.50	0.93

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	522/547 (95%)	505 (97%)	15 (3%)	2 (0%)	34	71
1	B	522/547 (95%)	507 (97%)	13 (2%)	2 (0%)	34	71
1	C	522/547 (95%)	507 (97%)	13 (2%)	2 (0%)	34	71
1	D	522/547 (95%)	512 (98%)	9 (2%)	1 (0%)	47	81
1	E	522/547 (95%)	501 (96%)	19 (4%)	2 (0%)	34	71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	522/547 (95%)	507 (97%)	15 (3%)	0	100	100
1	G	522/547 (95%)	509 (98%)	11 (2%)	2 (0%)	34	71
1	H	522/547 (95%)	508 (97%)	11 (2%)	3 (1%)	25	62
1	I	522/547 (95%)	496 (95%)	22 (4%)	4 (1%)	19	55
1	J	522/547 (95%)	505 (97%)	16 (3%)	1 (0%)	47	81
1	K	522/547 (95%)	507 (97%)	14 (3%)	1 (0%)	47	81
1	L	522/547 (95%)	504 (97%)	17 (3%)	1 (0%)	47	81
1	M	522/547 (95%)	505 (97%)	16 (3%)	1 (0%)	47	81
1	N	522/547 (95%)	508 (97%)	12 (2%)	2 (0%)	34	71
All	All	7308/7658 (95%)	7081 (97%)	203 (3%)	24 (0%)	41	75

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	44	PHE
1	E	270	ILE
1	H	44	PHE
1	I	483	GLU
1	G	43	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	404/414 (98%)	381 (94%)	23 (6%)	20	54
1	B	404/414 (98%)	384 (95%)	20 (5%)	24	59
1	C	404/414 (98%)	384 (95%)	20 (5%)	24	59
1	D	404/414 (98%)	380 (94%)	24 (6%)	19	52
1	E	404/414 (98%)	378 (94%)	26 (6%)	17	49
1	F	404/414 (98%)	382 (95%)	22 (5%)	22	56
1	G	404/414 (98%)	381 (94%)	23 (6%)	20	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	404/414 (98%)	380 (94%)	24 (6%)	19	52
1	I	404/414 (98%)	381 (94%)	23 (6%)	20	54
1	J	404/414 (98%)	381 (94%)	23 (6%)	20	54
1	K	404/414 (98%)	382 (95%)	22 (5%)	22	56
1	L	404/414 (98%)	379 (94%)	25 (6%)	18	50
1	M	404/414 (98%)	381 (94%)	23 (6%)	20	54
1	N	404/414 (98%)	373 (92%)	31 (8%)	13	41
All	All	5656/5796 (98%)	5327 (94%)	329 (6%)	20	53

5 of 329 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	328	ASP
1	I	58	ARG
1	N	94	VAL
1	G	417	VAL
1	H	224	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	475	ASN
1	H	351	GLN
1	N	265	ASN
1	G	265	ASN
1	I	146	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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.