



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Feb 17, 2018 – 02:54 am GMT

PDB ID : 4A8C
EMDB ID: : EMD-1983
Title : Symmetrized cryo-EM reconstruction of E. coli DegQ 12-mer in complex with a binding peptide
Authors : Malet, H.; Canellas, F.; Sawa, J.; Yan, J.; Thalassinos, K.; Ehrmann, M.; Clausen, T.; Saibil, H.R.
Deposited on : 2011-11-20
Resolution : 7.50 Å(reported)
Based on PDB ID : 3STJ

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30686

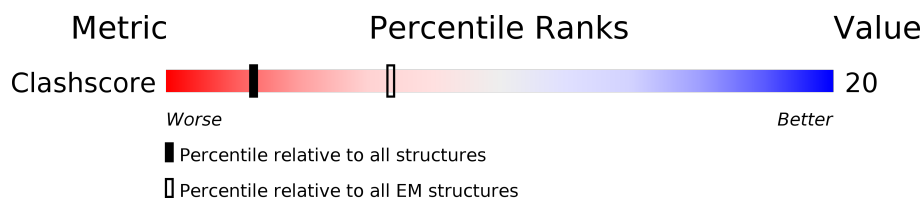
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY













The reported resolution of this entry is 7.50 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)	EM structures (#Entries)
Clashscore	136279	1886

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	436	 87% 9%
1	B	436	 87% 9%
1	C	436	 87% 9%
1	D	436	 87% 9%
1	E	436	 87% 9%
1	F	436	 87% 9%
1	G	436	 87% 9%
1	H	436	 87% 9%
1	I	436	 87% 9%
1	J	436	 87% 9%
1	K	436	 86% 9%
1	L	436	 88% 9%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4740 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEGQ.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	395	Total C 395 395	0	395
1	B	395	Total C 395 395	0	395
1	C	395	Total C 395 395	0	395
1	D	395	Total C 395 395	0	395
1	E	395	Total C 395 395	0	395
1	F	395	Total C 395 395	0	395
1	G	395	Total C 395 395	0	395
1	H	395	Total C 395 395	0	395
1	I	395	Total C 395 395	0	395
1	J	395	Total C 395 395	0	395
1	K	395	Total C 395 395	0	395
1	L	395	Total C 395 395	0	395

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	187	ALA	SER	engineered mutation	UNP P39099
A	429	LEU	-	expression tag	UNP P39099
A	430	GLU	-	expression tag	UNP P39099
A	431	HIS	-	expression tag	UNP P39099
A	432	HIS	-	expression tag	UNP P39099

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Chain	Residue	Modelled	Actual	Comment	Reference
A	433	HIS	-	expression tag	UNP P39099
A	434	HIS	-	expression tag	UNP P39099
A	435	HIS	-	expression tag	UNP P39099
A	436	HIS	-	expression tag	UNP P39099
B	187	ALA	SER	engineered mutation	UNP P39099
B	429	LEU	-	expression tag	UNP P39099
B	430	GLU	-	expression tag	UNP P39099
B	431	HIS	-	expression tag	UNP P39099
B	432	HIS	-	expression tag	UNP P39099
B	433	HIS	-	expression tag	UNP P39099
B	434	HIS	-	expression tag	UNP P39099
B	435	HIS	-	expression tag	UNP P39099
B	436	HIS	-	expression tag	UNP P39099
C	187	ALA	SER	engineered mutation	UNP P39099
C	429	LEU	-	expression tag	UNP P39099
C	430	GLU	-	expression tag	UNP P39099
C	431	HIS	-	expression tag	UNP P39099
C	432	HIS	-	expression tag	UNP P39099
C	433	HIS	-	expression tag	UNP P39099
C	434	HIS	-	expression tag	UNP P39099
C	435	HIS	-	expression tag	UNP P39099
C	436	HIS	-	expression tag	UNP P39099
D	187	ALA	SER	engineered mutation	UNP P39099
D	429	LEU	-	expression tag	UNP P39099
D	430	GLU	-	expression tag	UNP P39099
D	431	HIS	-	expression tag	UNP P39099
D	432	HIS	-	expression tag	UNP P39099
D	433	HIS	-	expression tag	UNP P39099
D	434	HIS	-	expression tag	UNP P39099
D	435	HIS	-	expression tag	UNP P39099
D	436	HIS	-	expression tag	UNP P39099
E	187	ALA	SER	engineered mutation	UNP P39099
E	429	LEU	-	expression tag	UNP P39099
E	430	GLU	-	expression tag	UNP P39099
E	431	HIS	-	expression tag	UNP P39099
E	432	HIS	-	expression tag	UNP P39099
E	433	HIS	-	expression tag	UNP P39099
E	434	HIS	-	expression tag	UNP P39099
E	435	HIS	-	expression tag	UNP P39099
E	436	HIS	-	expression tag	UNP P39099
F	187	ALA	SER	engineered mutation	UNP P39099
F	429	LEU	-	expression tag	UNP P39099

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Chain	Residue	Modelled	Actual	Comment	Reference
F	430	GLU	-	expression tag	UNP P39099
F	431	HIS	-	expression tag	UNP P39099
F	432	HIS	-	expression tag	UNP P39099
F	433	HIS	-	expression tag	UNP P39099
F	434	HIS	-	expression tag	UNP P39099
F	435	HIS	-	expression tag	UNP P39099
F	436	HIS	-	expression tag	UNP P39099
G	187	ALA	SER	engineered mutation	UNP P39099
G	429	LEU	-	expression tag	UNP P39099
G	430	GLU	-	expression tag	UNP P39099
G	431	HIS	-	expression tag	UNP P39099
G	432	HIS	-	expression tag	UNP P39099
G	433	HIS	-	expression tag	UNP P39099
G	434	HIS	-	expression tag	UNP P39099
G	435	HIS	-	expression tag	UNP P39099
G	436	HIS	-	expression tag	UNP P39099
H	187	ALA	SER	engineered mutation	UNP P39099
H	429	LEU	-	expression tag	UNP P39099
H	430	GLU	-	expression tag	UNP P39099
H	431	HIS	-	expression tag	UNP P39099
H	432	HIS	-	expression tag	UNP P39099
H	433	HIS	-	expression tag	UNP P39099
H	434	HIS	-	expression tag	UNP P39099
H	435	HIS	-	expression tag	UNP P39099
H	436	HIS	-	expression tag	UNP P39099
I	187	ALA	SER	engineered mutation	UNP P39099
I	429	LEU	-	expression tag	UNP P39099
I	430	GLU	-	expression tag	UNP P39099
I	431	HIS	-	expression tag	UNP P39099
I	432	HIS	-	expression tag	UNP P39099
I	433	HIS	-	expression tag	UNP P39099
I	434	HIS	-	expression tag	UNP P39099
I	435	HIS	-	expression tag	UNP P39099
I	436	HIS	-	expression tag	UNP P39099
J	187	ALA	SER	engineered mutation	UNP P39099
J	429	LEU	-	expression tag	UNP P39099
J	430	GLU	-	expression tag	UNP P39099
J	431	HIS	-	expression tag	UNP P39099
J	432	HIS	-	expression tag	UNP P39099
J	433	HIS	-	expression tag	UNP P39099
J	434	HIS	-	expression tag	UNP P39099
J	435	HIS	-	expression tag	UNP P39099

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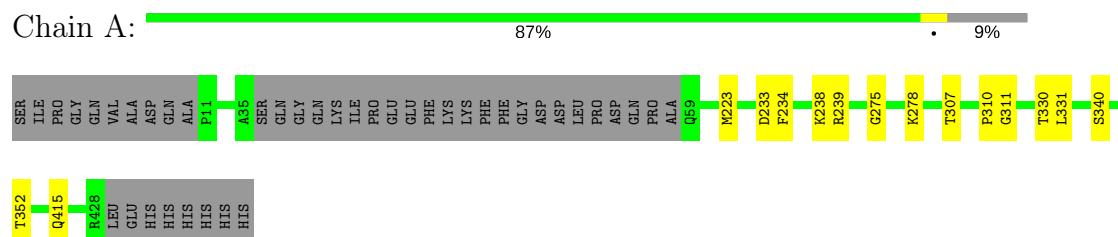
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Chain	Residue	Modelled	Actual	Comment	Reference
J	436	HIS	-	expression tag	UNP P39099
K	187	ALA	SER	engineered mutation	UNP P39099
K	429	LEU	-	expression tag	UNP P39099
K	430	GLU	-	expression tag	UNP P39099
K	431	HIS	-	expression tag	UNP P39099
K	432	HIS	-	expression tag	UNP P39099
K	433	HIS	-	expression tag	UNP P39099
K	434	HIS	-	expression tag	UNP P39099
K	435	HIS	-	expression tag	UNP P39099
K	436	HIS	-	expression tag	UNP P39099
L	187	ALA	SER	engineered mutation	UNP P39099
L	429	LEU	-	expression tag	UNP P39099
L	430	GLU	-	expression tag	UNP P39099
L	431	HIS	-	expression tag	UNP P39099
L	432	HIS	-	expression tag	UNP P39099
L	433	HIS	-	expression tag	UNP P39099
L	434	HIS	-	expression tag	UNP P39099
L	435	HIS	-	expression tag	UNP P39099
L	436	HIS	-	expression tag	UNP P39099

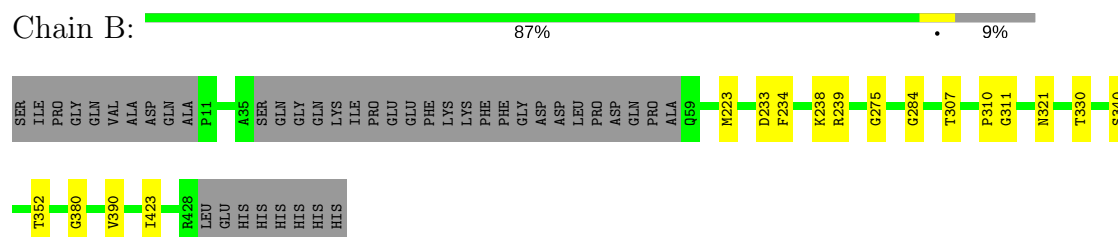
3 Residue-property plots [i](#)

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. 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.

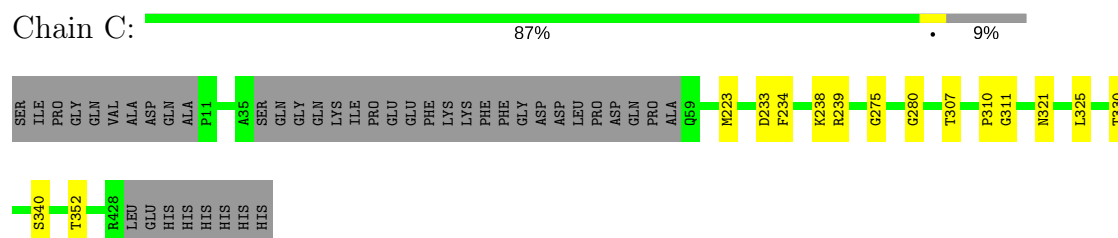
- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEQQ



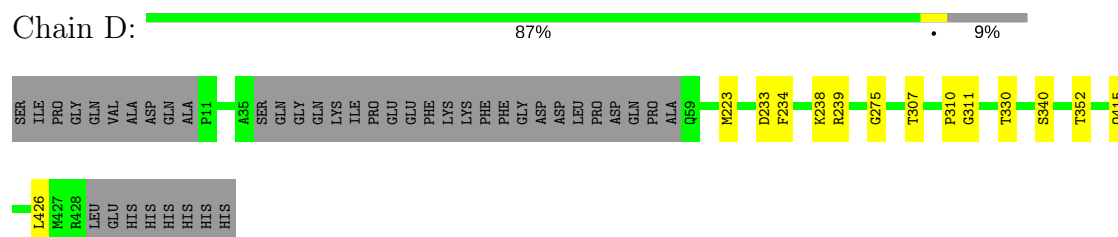
- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEQQ




- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEQQ

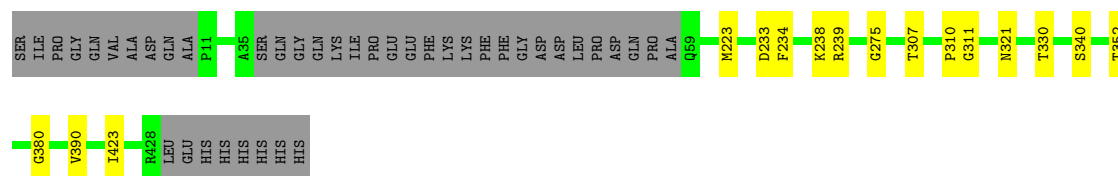


- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEQQ




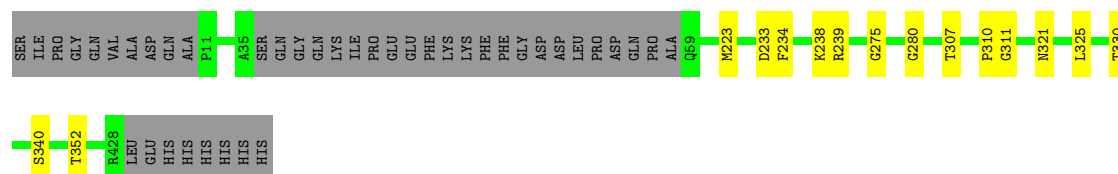
- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEQQ

Chain E:  87% 9%




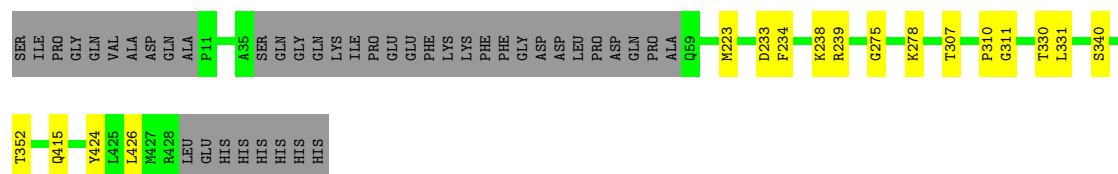
- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEGQ

Chain F:  87% 9%




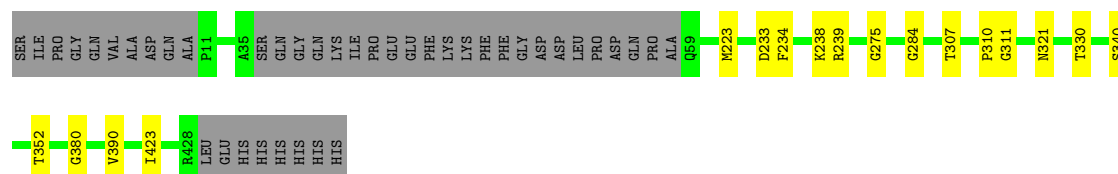
- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEGQ

Chain G:  87% 9%




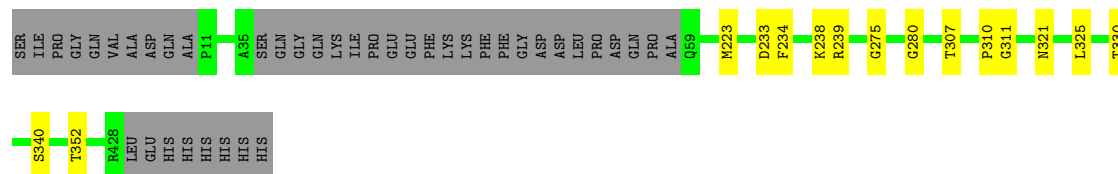
- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEGQ

Chain H:  87% 9%




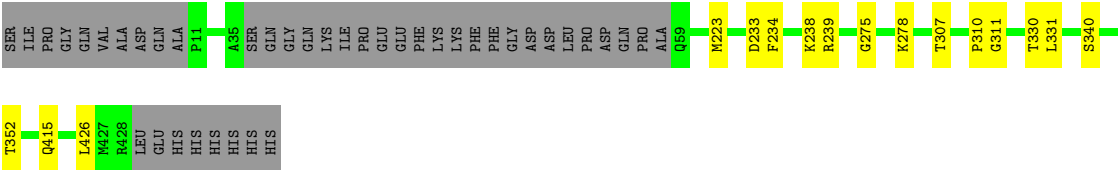
- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEGQ

Chain I:  87% 9%

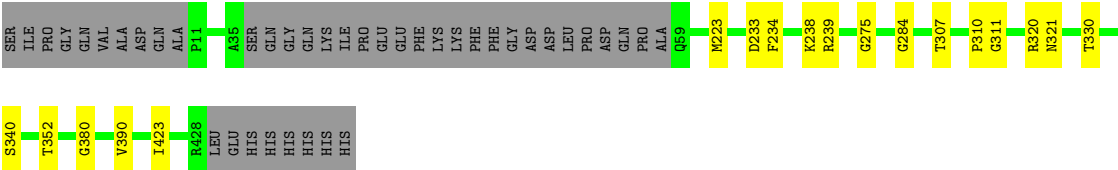
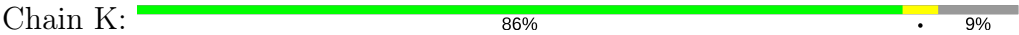


- Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEGQ

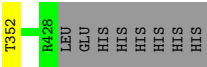
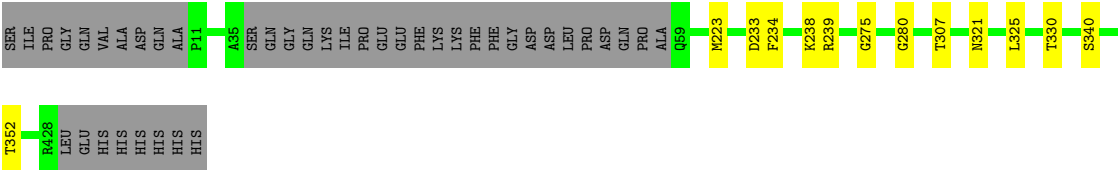
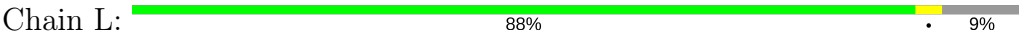
Chain J:  87% 9%



● Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEGQ



● Molecule 1: PERIPLASMIC PH-DEPENDENT SERINE ENDOPROTEASE DEGQ



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	29432	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	PHASE FLIPPING, FULL CTF CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	395	0	0	8	0
1	B	395	0	0	11	0
1	C	395	0	0	9	0
1	D	395	0	0	8	0
1	E	395	0	0	10	0
1	F	395	0	0	9	0
1	G	395	0	0	10	0
1	H	395	0	0	11	0
1	I	395	0	0	9	0
1	J	395	0	0	9	0
1	K	395	0	0	12	0
1	L	395	0	0	8	0
All	All	4740	0	0	94	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 20.

All (94) 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:G:415:GLN:CA	1:K:321:ASN:CA	2.56	0.83
1:F:280:GLY:CA	1:K:380:GLY:CA	2.61	0.79
1:H:321:ASN:CA	1:J:415:GLN:CA	2.63	0.77
1:C:280:GLY:CA	1:H:380:GLY:CA	2.63	0.77
1:F:321:ASN:CA	1:K:390:VAL:CA	2.64	0.76
1:B:380:GLY:CA	1:I:280:GLY:CA	2.63	0.76
1:B:321:ASN:CA	1:D:415:GLN:CA	2.65	0.75
1:C:321:ASN:CA	1:H:390:VAL:CA	2.65	0.74
1:E:380:GLY:CA	1:L:280:GLY:CA	2.65	0.74
1:E:390:VAL:CA	1:L:321:ASN:CA	2.67	0.73
1:C:325:LEU:CA	1:H:423:ILE:CA	2.66	0.72
1:B:390:VAL:CA	1:I:321:ASN:CA	2.69	0.70
1:G:233:ASP:CA	1:G:234:PHE:CA	2.70	0.70
1:D:233:ASP:CA	1:D:234:PHE:CA	2.70	0.69
1:L:233:ASP:CA	1:L:234:PHE:CA	2.72	0.68
1:E:233:ASP:CA	1:E:234:PHE:CA	2.72	0.67
1:G:275:GLY:CA	1:G:330:THR:CA	2.73	0.67
1:I:238:LYS:CA	1:I:239:ARG:CA	2.72	0.67
1:B:233:ASP:CA	1:B:234:PHE:CA	2.73	0.67
1:D:238:LYS:CA	1:D:239:ARG:CA	2.74	0.66
1:J:233:ASP:CA	1:J:234:PHE:CA	2.73	0.66
1:K:233:ASP:CA	1:K:234:PHE:CA	2.74	0.66
1:A:275:GLY:CA	1:A:330:THR:CA	2.75	0.65
1:I:233:ASP:CA	1:I:234:PHE:CA	2.75	0.65
1:K:275:GLY:CA	1:K:330:THR:CA	2.74	0.65
1:E:423:ILE:CA	1:L:325:LEU:CA	2.75	0.65
1:A:233:ASP:CA	1:A:234:PHE:CA	2.76	0.63
1:F:233:ASP:CA	1:F:234:PHE:CA	2.77	0.62
1:E:275:GLY:CA	1:E:330:THR:CA	2.77	0.62
1:J:275:GLY:CA	1:J:330:THR:CA	2.78	0.62
1:L:238:LYS:CA	1:L:239:ARG:CA	2.78	0.62
1:D:275:GLY:CA	1:D:330:THR:CA	2.77	0.61
1:H:233:ASP:CA	1:H:234:PHE:CA	2.78	0.61
1:I:275:GLY:CA	1:I:330:THR:CA	2.77	0.61
1:J:238:LYS:CA	1:J:239:ARG:CA	2.78	0.61
1:B:275:GLY:CA	1:B:330:THR:CA	2.79	0.61
1:B:423:ILE:CA	1:I:325:LEU:CA	2.79	0.61
1:F:325:LEU:CA	1:K:423:ILE:CA	2.79	0.60
1:L:275:GLY:CA	1:L:330:THR:CA	2.79	0.60
1:F:275:GLY:CA	1:F:330:THR:CA	2.79	0.60
1:C:233:ASP:CA	1:C:234:PHE:CA	2.80	0.60
1:H:275:GLY:CA	1:H:330:THR:CA	2.80	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:238:LYS:CA	1:K:239:ARG:CA	2.81	0.59
1:C:275:GLY:CA	1:C:330:THR:CA	2.81	0.58
1:C:223:MET:CA	1:C:307:THR:CA	2.82	0.58
1:E:223:MET:CA	1:E:307:THR:CA	2.82	0.57
1:J:223:MET:CA	1:J:307:THR:CA	2.83	0.57
1:A:223:MET:CA	1:A:307:THR:CA	2.82	0.57
1:D:223:MET:CA	1:D:307:THR:CA	2.82	0.57
1:G:223:MET:CA	1:G:307:THR:CA	2.82	0.57
1:F:223:MET:CA	1:F:307:THR:CA	2.82	0.57
1:H:223:MET:CA	1:H:307:THR:CA	2.82	0.56
1:I:223:MET:CA	1:I:307:THR:CA	2.83	0.56
1:B:223:MET:CA	1:B:307:THR:CA	2.82	0.56
1:E:238:LYS:CA	1:E:239:ARG:CA	2.83	0.56
1:K:223:MET:CA	1:K:307:THR:CA	2.82	0.56
1:L:223:MET:CA	1:L:307:THR:CA	2.83	0.56
1:A:415:GLN:CA	1:E:321:ASN:CA	2.85	0.55
1:B:238:LYS:CA	1:B:239:ARG:CA	2.87	0.52
1:C:238:LYS:CA	1:C:239:ARG:CA	2.86	0.52
1:J:340:SER:CA	1:J:352:THR:CA	2.90	0.50
1:E:340:SER:CA	1:E:352:THR:CA	2.92	0.48
1:F:238:LYS:CA	1:F:239:ARG:CA	2.92	0.47
1:A:238:LYS:CA	1:A:239:ARG:CA	2.93	0.47
1:G:424:TYR:CA	1:K:320:ARG:CA	2.92	0.47
1:J:310:PRO:CA	1:J:311:GLY:CA	2.93	0.47
1:K:310:PRO:CA	1:K:311:GLY:CA	2.93	0.46
1:C:340:SER:CA	1:C:352:THR:CA	2.94	0.46
1:D:310:PRO:CA	1:D:311:GLY:CA	2.94	0.46
1:I:310:PRO:CA	1:I:311:GLY:CA	2.94	0.46
1:E:310:PRO:CA	1:E:311:GLY:CA	2.94	0.46
1:G:426:LEU:CA	1:K:284:GLY:CA	2.94	0.46
1:B:310:PRO:CA	1:B:311:GLY:CA	2.93	0.46
1:F:310:PRO:CA	1:F:311:GLY:CA	2.94	0.46
1:G:238:LYS:CA	1:G:239:ARG:CA	2.94	0.46
1:D:340:SER:CA	1:D:352:THR:CA	2.95	0.45
1:G:340:SER:CA	1:G:352:THR:CA	2.95	0.45
1:G:310:PRO:CA	1:G:311:GLY:CA	2.94	0.45
1:H:340:SER:CA	1:H:352:THR:CA	2.94	0.45
1:F:340:SER:CA	1:F:352:THR:CA	2.94	0.45
1:H:310:PRO:CA	1:H:311:GLY:CA	2.94	0.45
1:A:340:SER:CA	1:A:352:THR:CA	2.95	0.44
1:C:310:PRO:CA	1:C:311:GLY:CA	2.95	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:340:SER:CA	1:I:352:THR:CA	2.95	0.44
1:K:340:SER:CA	1:K:352:THR:CA	2.95	0.44
1:A:310:PRO:CA	1:A:311:GLY:CA	2.95	0.44
1:A:278:LYS:CA	1:A:331:LEU:CA	2.95	0.44
1:B:340:SER:CA	1:B:352:THR:CA	2.95	0.44
1:H:284:GLY:CA	1:J:426:LEU:CA	2.97	0.43
1:L:340:SER:CA	1:L:352:THR:CA	2.97	0.43
1:H:238:LYS:CA	1:H:239:ARG:CA	2.97	0.43
1:G:278:LYS:CA	1:G:331:LEU:CA	2.97	0.42
1:J:278:LYS:CA	1:J:331:LEU:CA	2.98	0.42
1:B:284:GLY:CA	1:D:426:LEU:CA	2.99	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.