



wwPDB EM Map/Model Validation Report ⓘ

Sep 27, 2016 – 02:58 PM EDT

PDB ID : 5KHU
EMDB ID: : EMD-4021
Title : Model of human Anaphase-promoting complex/Cyclosome (APC15 deletion mutant), in complex with the Mitotic checkpoint complex (APC/C-CDC20-MCC) based on cryo EM data at 4.8 Angstrom resolution
Authors : Yamaguchi, M.; VanderLinden, R.; Dube, P.; Stark, H.; Schulman, B.
Deposited on : 2016-06-15
Resolution : 4.80 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

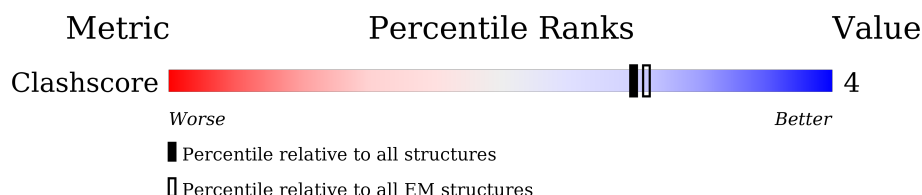
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027939

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY





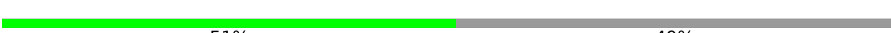






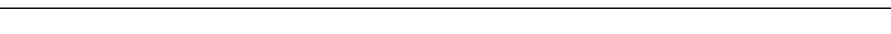
The reported resolution of this entry is 4.80 Å.

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.











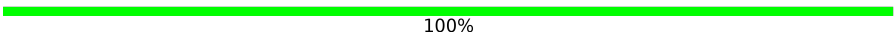


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924

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	1944	 70% 29%
2	B	84	 17% 81%
3	C	597	 77% 22%
3	P	597	 74% 26%
4	E	110	 51% 49%
5	F	824	 57% 43%
5	H	824	 58% 42%
6	G	85	 29% 71%
6	W	85	 29% 71%
7	I	808	 87% 13%
8	J	620	 81% 19%
8	K	620	 80% 20%

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Mol	Chain	Length	Quality of chain
9	L	185	 89% 9%
10	M	74	 58% 42%
11	N	822	 74% 24%
12	O	755	 81% 19%
13	Q	1050	 20% 79%
14	R	499	 74% 24%
14	S	499	 65% 33%
15	T	205	 89% 11%
16	U	9	 100%
17	X	565	 70% 30%
17	Y	565	 76% 24%

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 8453 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 Anaphase-promoting complex subunit 1.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	1374	Total C 1374 1374	0	1374

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	202	GLU	SER	engineered mutation	UNP Q9H1A4
A	286	GLU	SER	engineered mutation	UNP Q9H1A4
A	291	GLU	THR	engineered mutation	UNP Q9H1A4
A	313	GLU	SER	engineered mutation	UNP Q9H1A4
A	316	GLU	THR	engineered mutation	UNP Q9H1A4
A	317	GLU	SER	engineered mutation	UNP Q9H1A4
A	334	GLU	SER	engineered mutation	UNP Q9H1A4
A	341	GLU	SER	engineered mutation	UNP Q9H1A4
A	343	GLU	SER	engineered mutation	UNP Q9H1A4
A	355	GLU	SER	engineered mutation	UNP Q9H1A4
A	362	GLU	SER	engineered mutation	UNP Q9H1A4
A	372	GLU	SER	engineered mutation	UNP Q9H1A4
A	377	GLU	SER	engineered mutation	UNP Q9H1A4
A	?	GLU	THR	engineered mutation	UNP Q9H1A4
A	?	GLU	SER	engineered mutation	UNP Q9H1A4
A	?	GLU	SER	engineered mutation	UNP Q9H1A4
A	?	GLU	SER	engineered mutation	UNP Q9H1A4
A	671	GLN	ASN	conflict	UNP Q9H1A4
A	?	GLU	SER	engineered mutation	UNP Q9H1A4
A	?	GLU	SER	engineered mutation	UNP Q9H1A4
A	916	GLU	SER	engineered mutation	UNP Q9H1A4
A	1347	GLU	SER	engineered mutation	UNP Q9H1A4

- Molecule 2 is a protein called Anaphase-promoting complex subunit 11.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	B	16	Total C 16 16	0	16

- Molecule 3 is a protein called Cell division cycle protein 23 homolog.

Mol	Chain	Residues	Atoms	AltConf	Trace
3	C	463	Total C 463 463	0	463
3	P	442	Total C 442 442	0	442

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	542	GLU	THR	engineered mutation	UNP Q9UJX2
C	562	GLU	THR	engineered mutation	UNP Q9UJX2
C	582	GLU	THR	engineered mutation	UNP Q9UJX2
C	588	GLU	SER	engineered mutation	UNP Q9UJX2
C	596	GLU	THR	engineered mutation	UNP Q9UJX2
P	542	GLU	THR	engineered mutation	UNP Q9UJX2
P	562	GLU	THR	engineered mutation	UNP Q9UJX2
P	582	GLU	THR	engineered mutation	UNP Q9UJX2
P	588	GLU	SER	engineered mutation	UNP Q9UJX2
P	596	GLU	THR	engineered mutation	UNP Q9UJX2

- Molecule 4 is a protein called Anaphase-promoting complex subunit 16.

Mol	Chain	Residues	Atoms	AltConf	Trace
4	E	56	Total C 56 56	0	56

- Molecule 5 is a protein called Cell division cycle protein 27 homolog.

Mol	Chain	Residues	Atoms	AltConf	Trace
5	F	473	Total C 473 473	0	473
5	H	479	Total C 479 479	0	479

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	200	GLU	THR	engineered mutation	UNP P30260
F	205	GLU	THR	engineered mutation	UNP P30260
F	220	GLU	SER	engineered mutation	UNP P30260
F	241	GLU	SER	engineered mutation	UNP P30260
F	276	GLU	SER	engineered mutation	UNP P30260
F	320	GLU	SER	engineered mutation	UNP P30260
F	336	GLU	SER	engineered mutation	UNP P30260
F	339	GLU	SER	engineered mutation	UNP P30260
F	386	GLU	SER	engineered mutation	UNP P30260
F	387	GLU	SER	engineered mutation	UNP P30260
F	393	GLU	SER	engineered mutation	UNP P30260
F	426	GLU	SER	engineered mutation	UNP P30260
F	435	GLU	SER	engineered mutation	UNP P30260
F	446	GLU	THR	engineered mutation	UNP P30260
H	200	GLU	THR	engineered mutation	UNP P30260
H	205	GLU	THR	engineered mutation	UNP P30260
H	220	GLU	SER	engineered mutation	UNP P30260
H	241	GLU	SER	engineered mutation	UNP P30260
H	276	GLU	SER	engineered mutation	UNP P30260
H	320	GLU	SER	engineered mutation	UNP P30260
H	336	GLU	SER	engineered mutation	UNP P30260
H	339	GLU	SER	engineered mutation	UNP P30260
H	386	GLU	SER	engineered mutation	UNP P30260
H	387	GLU	SER	engineered mutation	UNP P30260
H	393	GLU	SER	engineered mutation	UNP P30260
H	426	GLU	SER	engineered mutation	UNP P30260
H	435	GLU	SER	engineered mutation	UNP P30260
H	446	GLU	THR	engineered mutation	UNP P30260

- Molecule 6 is a protein called Anaphase-promoting complex subunit CDC26.

Mol	Chain	Residues	Atoms	AltConf	Trace
6	G	25	Total C 25 25	0	25
6	W	25	Total C 25 25	0	25

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	51	GLU	SER	engineered mutation	UNP Q8NHZ8
G	52	GLU	SER	engineered mutation	UNP Q8NHZ8
G	82	GLU	SER	engineered mutation	UNP Q8NHZ8

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Chain	Residue	Modelled	Actual	Comment	Reference
W	51	GLU	SER	engineered mutation	UNP Q8NHZ8
W	52	GLU	SER	engineered mutation	UNP Q8NHZ8
W	82	GLU	SER	engineered mutation	UNP Q8NHZ8

- Molecule 7 is a protein called Anaphase-promoting complex subunit 4.

Mol	Chain	Residues	Atoms	AltConf	Trace
7	I	706	Total C 706 706	0	706

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	777	GLU	SER	engineered mutation	UNP Q9UJX5
I	779	GLU	SER	engineered mutation	UNP Q9UJX5

- Molecule 8 is a protein called Cell division cycle protein 16 homolog.

Mol	Chain	Residues	Atoms	AltConf	Trace
8	J	504	Total C 504 504	0	504
8	K	493	Total C 493 493	0	493

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	112	GLU	SER	engineered mutation	UNP Q13042
J	560	GLU	SER	engineered mutation	UNP Q13042
J	581	GLU	THR	engineered mutation	UNP Q13042
J	585	GLU	THR	engineered mutation	UNP Q13042
J	586	GLU	SER	engineered mutation	UNP Q13042
K	112	GLU	SER	engineered mutation	UNP Q13042
K	560	GLU	SER	engineered mutation	UNP Q13042
K	581	GLU	THR	engineered mutation	UNP Q13042
K	585	GLU	THR	engineered mutation	UNP Q13042
K	586	GLU	SER	engineered mutation	UNP Q13042

- Molecule 9 is a protein called Anaphase-promoting complex subunit 10.

Mol	Chain	Residues	Atoms	AltConf	Trace
9	L	169	Total C 169 169	0	169

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	3	GLU	THR	engineered mutation	UNP Q9UM13

- Molecule 10 is a protein called Anaphase-promoting complex subunit 13.

Mol	Chain	Residues	Atoms	AltConf	Trace
10	M	43	Total C 43 43	0	43

- Molecule 11 is a protein called Anaphase-promoting complex subunit 2.

Mol	Chain	Residues	Atoms	AltConf	Trace
11	N	627	Total C 627 627	0	627

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	218	GLU	SER	engineered mutation	UNP Q9UJX6
N	314	GLU	SER	engineered mutation	UNP Q9UJX6
N	470	GLU	SER	engineered mutation	UNP Q9UJX6
N	534	GLU	SER	engineered mutation	UNP Q9UJX6
N	811	GLU	SER	engineered mutation	UNP Q9UJX6

- Molecule 12 is a protein called Anaphase-promoting complex subunit 5.

Mol	Chain	Residues	Atoms	AltConf	Trace
12	O	608	Total C 608 608	0	608

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	178	GLU	THR	engineered mutation	UNP Q9UJX4
O	179	GLU	SER	engineered mutation	UNP Q9UJX4
O	195	GLU	SER	engineered mutation	UNP Q9UJX4
O	202	GLU	SER	engineered mutation	UNP Q9UJX4

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Chain	Residue	Modelled	Actual	Comment	Reference
O	221	GLU	SER	engineered mutation	UNP Q9UJX4
O	232	GLU	THR	engineered mutation	UNP Q9UJX4
O	364	GLU	SER	engineered mutation	UNP Q9UJX4

- Molecule 13 is a protein called Mitotic checkpoint serine/threonine-protein kinase BUB1 beta.

Mol	Chain	Residues	Atoms	AltConf	Trace
13	Q	219	Total C 219 219	0	219

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	367	GLU	SER	engineered mutation	UNP O60566
Q	435	GLU	SER	engineered mutation	UNP O60566
Q	543	GLU	SER	engineered mutation	UNP O60566
Q	600	GLU	THR	engineered mutation	UNP O60566
Q	665	GLU	SER	engineered mutation	UNP O60566
Q	670	GLU	SER	engineered mutation	UNP O60566
Q	720	GLU	SER	engineered mutation	UNP O60566
Q	1043	GLU	SER	engineered mutation	UNP O60566

- Molecule 14 is a protein called Cell division cycle protein 20 homolog.

Mol	Chain	Residues	Atoms	AltConf	Trace
14	R	378	Total C 378 378	0	378
14	S	333	Total C 333 333	0	333

- Molecule 15 is a protein called Mitotic spindle assembly checkpoint protein MAD2A.

Mol	Chain	Residues	Atoms	AltConf	Trace
15	T	183	Total C 183 183	0	183

- Molecule 16 is a protein called unknown.

Mol	Chain	Residues	Atoms	AltConf	Trace
16	U	9	Total C 9 9	0	9

- Molecule 17 is a protein called Anaphase-promoting complex subunit 7.

Mol	Chain	Residues	Atoms	AltConf	Trace
17	X	396	Total C 396 396	0	396
17	Y	432	Total C 432 432	0	432

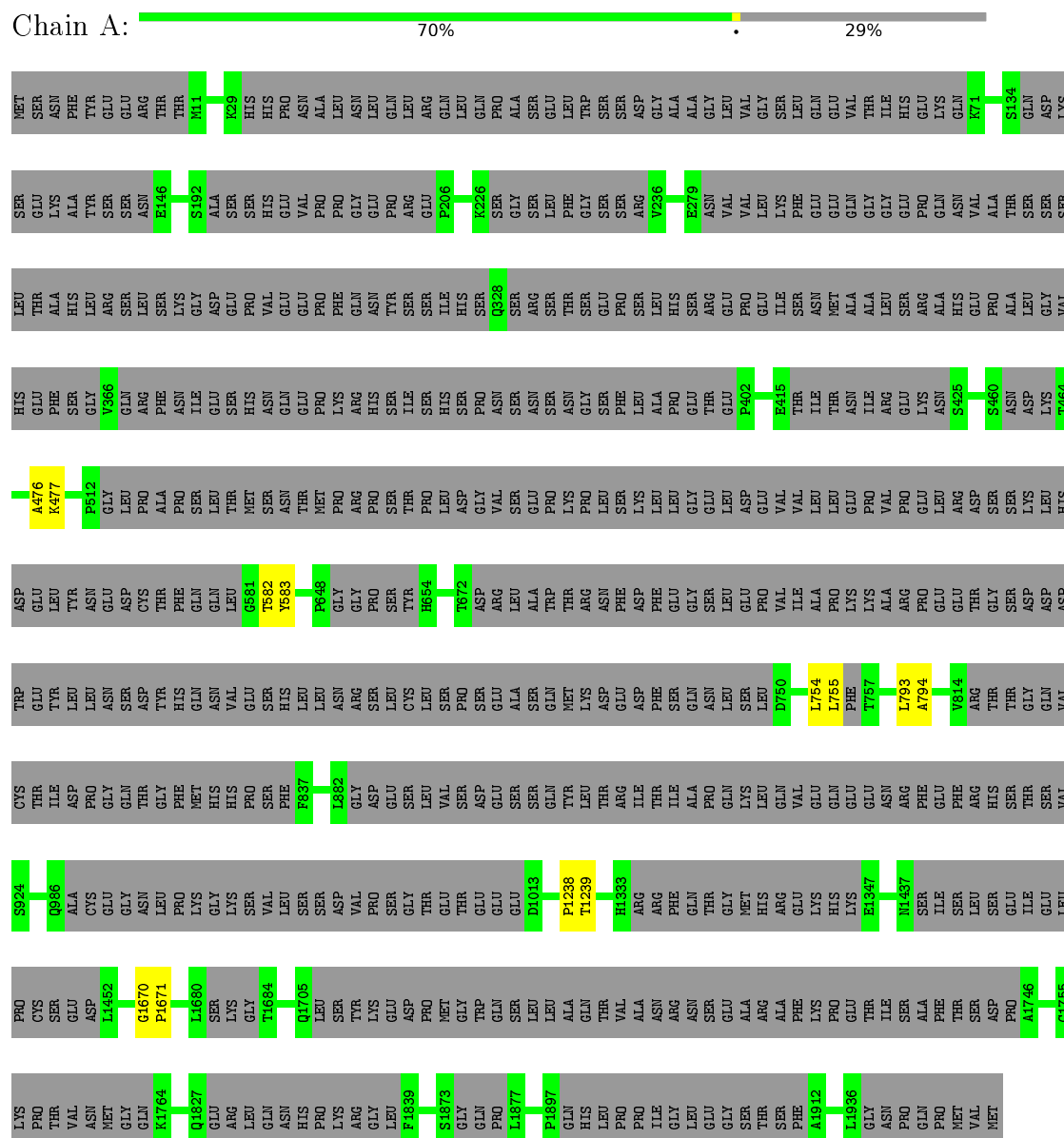
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	119	GLU	SER	engineered mutation	UNP Q9UJX3
X	120	GLU	THR	engineered mutation	UNP Q9UJX3
X	123	GLU	SER	engineered mutation	UNP Q9UJX3
X	125	GLU	SER	engineered mutation	UNP Q9UJX3
X	126	GLU	THR	engineered mutation	UNP Q9UJX3
Y	119	GLU	SER	engineered mutation	UNP Q9UJX3
Y	120	GLU	THR	engineered mutation	UNP Q9UJX3
Y	123	GLU	SER	engineered mutation	UNP Q9UJX3
Y	125	GLU	SER	engineered mutation	UNP Q9UJX3
Y	126	GLU	THR	engineered mutation	UNP Q9UJX3

3 Residue-property plots

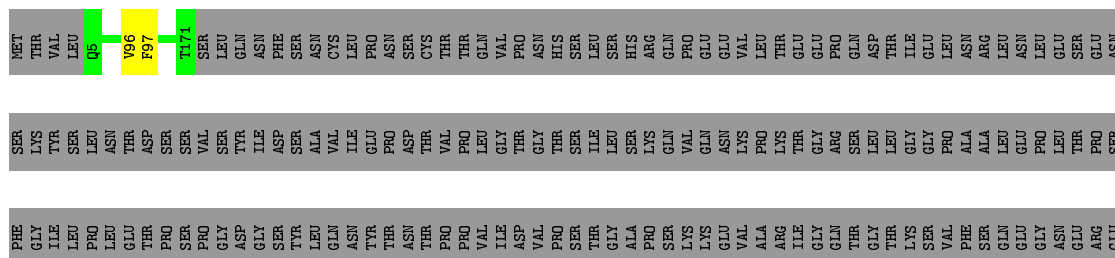
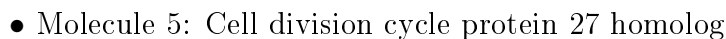
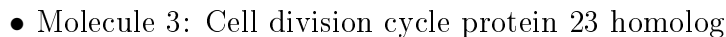
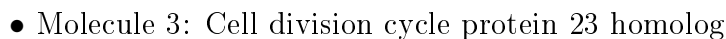
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric 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: Anaphase-promoting complex subunit 1



- Molecule 2: Anaphase-promoting complex subunit 11





VAL	THR	PRO	LEU	ALA	GLN	THR	THR	SER	SER	GLY	PRO	GLN	THR	THR	THR	THR	PRO	GLN	GLN	VAL	LEU	LEU	SER	PRO	THR	THR	ILE	THR	SER	PRO	PRO	ASN	ALA	ALA	LEU	PRO	PRO	ARG	ARG	ARG	SER	SER	ASP	GLU	GLU	THR	THR	THR	LYS	ASN	ASN	GLU	LYS	LYS	LYS	PHE	PHE	PRO
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PRO	LYS	ILE	PRO	ASN	ARG	LYS	THR	LYS	SER	LYS	THR	THR	ASN	LYS	GLY	GLY	ILE	THR	GLN	PRO	PRO	ASN	ASN	ASN	ASP	ASP	GLU	GLU	LEU	GLU	ILE	ILE	THR	THR	LYS	LYS	LEU	LEU	ASP	SER	SER	GLU	GLU	ILE	ILE	ILE	ILE	SER	SER	THR	THR	ILE	ILE	GLU	GLU	GLN	GLN	ILE	ILE	GLN	GLN	ALA	ALA	PHE	ASP	ASN	ASN	LEU	GLN	GLN	LYS	LYS	ALA	ALA	4458	4763	4767
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ASP LEU LEU ASP ASP PRO LYS GLY ALA ASN ASN GLN ILE LYS GLU ALA ILE ASP ASP LYS ARG TYR GLU GLU PRO ILE THR GLN GLU GLN GLN GLU SER SER MET THR ASP ASP ALA ASP ASP THR GLN LEU HIS ALA ALA GLU SER ASP GLU THR

- Molecule 5: Cell division cycle protein 27 homolog

Chain H:  58% 42%

MET	THR	VAL	LEU	Q5	TIT1	SER	LEU	GLN	ASN	PHE	SER	ASP	CYS	THR	THR	THR	GLN	GLY	VAL	PRO	ASN	SER	CYS	THR	THR	THR	GLN	GLY	GLU	GLU	GLU	GLU	PRO	GLN	ASP	THR	THR	ILE	GLU	GLU	LEU	ASN	ANG	LEU	LEU	ASN	ASN	ASN	LYS	THR
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SER LEU LEU THR ASP SER VAL TYR ILE ASP SER VAL VAL ILE GLU PRO THR VAL PRO LEU GLY THR GLY THR SER ILE LEU SER LYS GLN VAL GLN ASN LYS LYS PRO THR GLY ARG SER LEU LEU GLY GLY GLY PRO ALA ALA LEU GLU PRO LEU THR PRO SER PHE TYR

LEU	PRO	LEU	LEU	GLU	THR	PRO	SER	GLY	GLY	SER	TYR	LEU	GLN	ASN	TYR	THR	ASN	THR	PRO	PRO	VAL	ILE	ASP	VAL	VAL	PRO	PRO	SER	SER	THR	GLY	ALA	PRO	PRO	SER	LYS	LYS	GLU	GLU	VAL	ALA	ALA	ARG	ILE	ILE	GLY	GLY	THR	THR	THR	LYS	SER	SER	GLN	PHE	VAL	VAL	GLY	GLY	ASN	ASN	GLU	GLU	ARG	GLU	VAL	VAL	THR	THR	PRO
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ILE LEU LEU ALA GLN THR GLN SER SER GLY PRO GLN THR GLN SER THR THR THR GLN VAL LEU SER SER PRO PRO THR THR ILE THR SER SER PRO PRO ALA LEU LEU ARG ARG ARG SER SER ARG ARG LEU PHE THR THR SER SER ASP GLU GLU GLU THR THR LYS LYS ASN GLU GLU LYS LYS LYS LEU LEU MET LYS PHE PRO PRO PRO LYS THR

PRO	ASN	ARG	LYS	THR	LYS	SER	LYS	THR	ASN	LYS	GLY	ILE	THR	GLN	PRO	ASN	ASN	ASP	GLU	LEU	LEU	SER	GLU	GLY	LYS	ILE	ILE	SER	SER	THR	ILE	GLU	PRO	GLN	ILE	GLN	ALA	PHE	ASN	LEU	LEU	GLN	K456	D467	PRO	LYS	GLY	ALA	ASN	ASN
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GLN ILE LYS LYS GLU GLU ALA ILE ILE ASP LYS ARG ARG TYR LEU LEU PRO PRO ASP ASP GLU GLU GLU PRO PRO ILE ILE THR THR GLN GLN GLU GLU GLN GLN ILE ILE MET MET GLY GLY THR THR ASP ASP SER SER SER SER MET MET THR THR ASP ASP ALA ALA ASP ASP THR THR GLN GLN LEU LEU HIS HIS ALA ALA ALA ALA GLU GLU SER SER ASP ASP GLU GLU PHE PHE

- Molecule 6: Anaphase-promoting complex subunit CDC26

Chain G:  29% 71%

[illegible]

LEU
GLU
PHE

- Molecule 6: Anaphase-promoting complex subunit CDC26

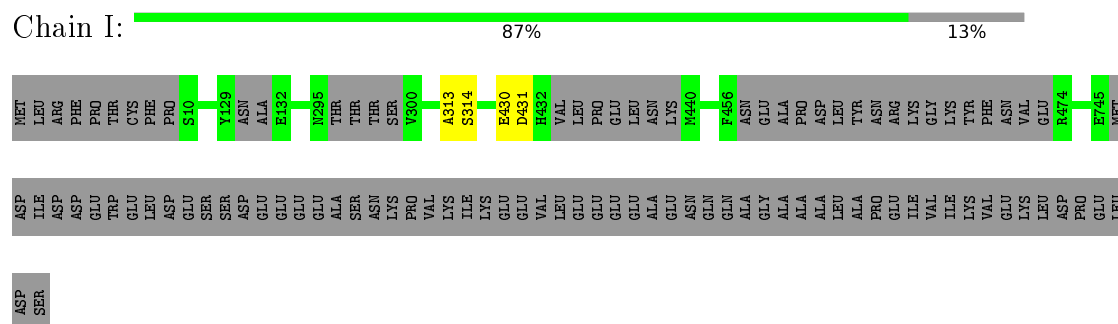
Chain W:  29% 71%

PI	D2S	LEU	GLU	LEU	THR	ARG	LYS	LYS	GLN	GLN	LYS	GLU	ASP	VAL	GLU	VAL	VAL	GLY	GLY	SER	ASP	GLY	GLY	GLY	GLY	ALA	ILE	GLY	LEU	LEU	GLU	GLU	ASP	PRO	PRO	LYS	SER	SER	ARG	GLU	GLU	GLN	MET	ILE	MET	ASN	ASP	ARG	ILE	GLY	TYR	LYS	PRO	GLN	PRO	LYS	ASN	ASN	ARG	SER	SER	GLN	PHE	GLY	GLY
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LEU
GLU
PHE

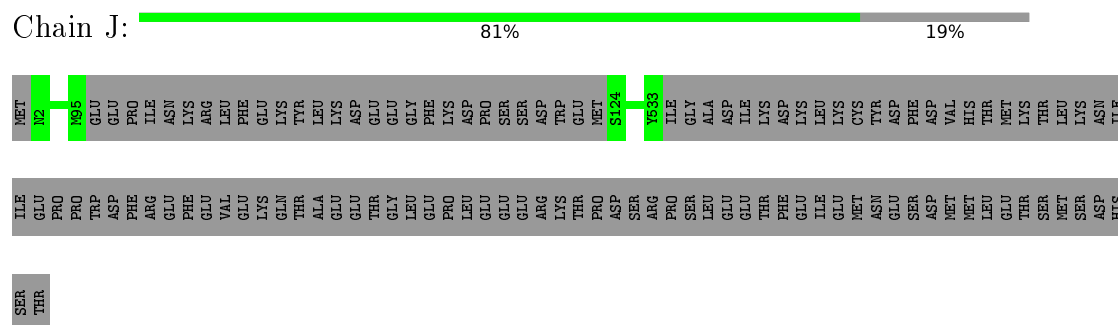
- Molecule 7: Anaphase-promoting complex subunit 4

Chain I:



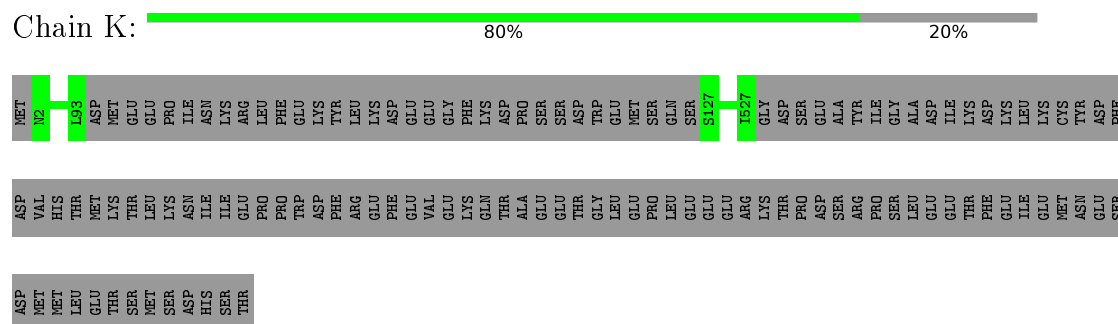
- Molecule 8: Cell division cycle protein 16 homolog

Chain J:



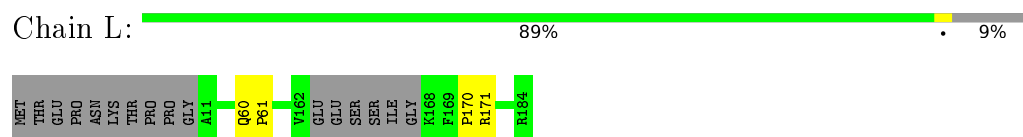
- Molecule 8: Cell division cycle protein 16 homolog

Chain K:



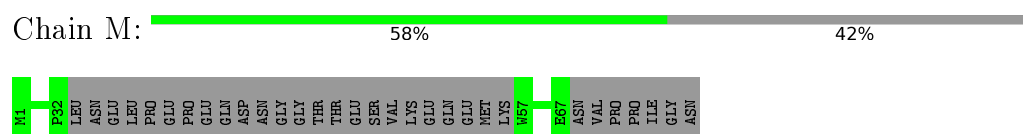
- Molecule 9: Anaphase-promoting complex subunit 10

Chain L:



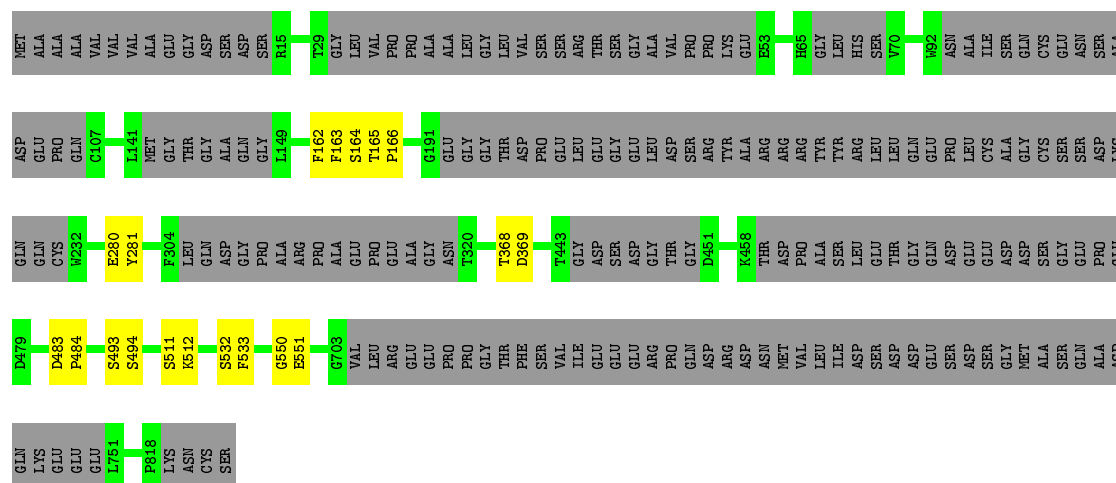
- Molecule 10: Anaphase-promoting complex subunit 13

Chain M:




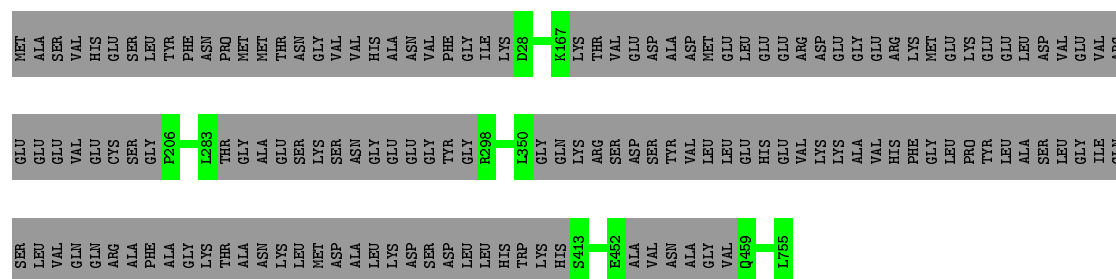
- Molecule 11: Anaphase-promoting complex subunit 2

Chain N:  74% 24%



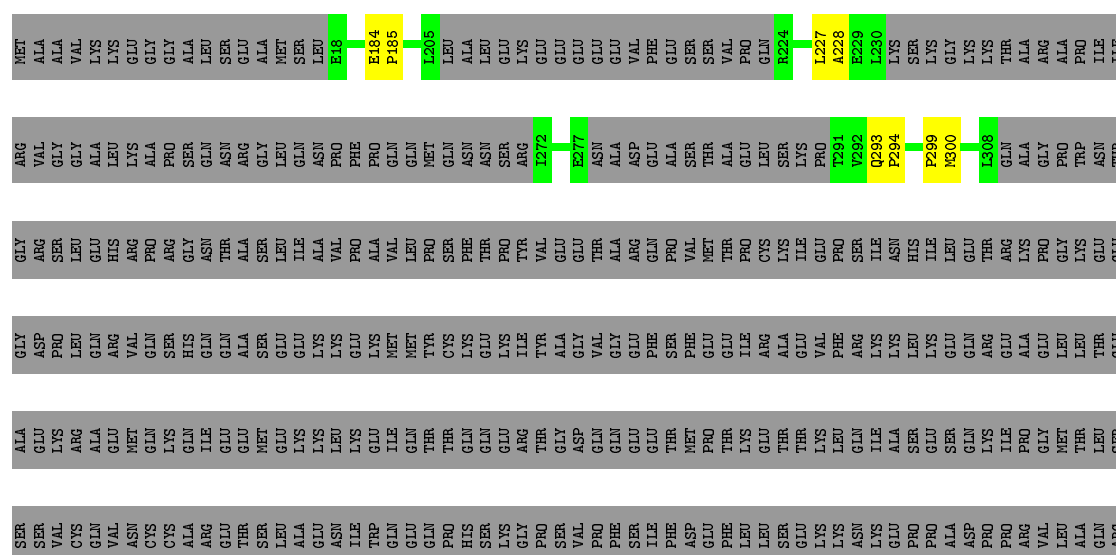
- Molecule 12: Anaphase-promoting complex subunit 5

Chain O:  81% 19%



- Molecule 13: Mitotic checkpoint serine/threonine-protein kinase BUB1 beta

Chain Q:  20% 79%



TRP	SER	VAL	HIS	VAL	GLU	SER	ARG	SER	ARG	ARG
LYS	PHE	LEU	GLU	SER	LEU	LEU	LEU	LEU	PHE	PRO
VAL	TRP	LEU	ILE	SER	ILE	SER	VAL	GLU	VAL	LEU
LYS	ARG	ARG	THR	GLN	THR	GLN	ALA	ALA	SER	VAL
LEU	SER	GLN	VAL	VAL	LEU	VAL	HIS	THR	PRO	LEU
THR	GLN	LEU	ILE	PRO	PRO	PRO	SER	PHE	THR	THR
GLU	ASN	ASP	ILE	TRP	LEU	ASP	GLU	LEU	HIS	LYS
PRO	ILE	VAL	THR	ASP	THR	ASP	CYS	GLU	GLU	SER
ALA	GLU	THR	LEU	TYR	GLU	PHE	ILE	PHE	ILE	GLU
LEU	LEU	LEU	LEU	ILE	ILE	ASP	GLY	SER	MET	SER
LEU	LEU	LEU	THR	ILE	ASN	ARG	ASP	GLY	SER	ILE
LEU	SER	SER	THR	ASN	LEU	LEU	ARG	SER	LEU	THR
PHE	ASP	GLY	ILE	LEU	LEU	PRO	ARG	LYS	LYS	THR
GLN	GLY	VAL	VAL	VAL	GLU	MET	ALA	ASP	ALA	ASN
	GLU	ARG	GLU	GLU	LEU	GLU	LYS	SER	LEU	GLU
	LEU	THR	MET	LYS	THR	VAL	VAL	PRO	VAL	ASP
	TRP	VAL	LEU	GLU	LEU	GLU	ALA	SER	SER	VAL
	ASN	GLN	HIS	ARG	LEU	ARG	SER	ASP	ASP	SER
	LYS	ILE	LYS	LEU	ILE	LEU	THR	PRO	PRO	PRO
	PHE	LEU	ALA	ASN	GLU	GLU	SER	GLU	ARG	VAL
	ARG	GLY	ILE	VAL	GLY	ASP	ILE	LEU	CYS	CYS
	ILE	LYS	HIS	ASP	GLY	PHE	LEU	LEU	PRO	ASP
	LEU	ILE	GLY	THR	GLU	HIS	GLU	PRO	GLY	GLU
	ASN	ASN	SER	SER	SER	SER	ASN	GLU	ASP	GLU
	ASP	CYS	PRO	PRO	ASP	CYS	GLU	GLU	ASP	ASP
	GLU	SER	ARG	TYR	TYR	TYR	ASN	VAL	VAL	PRO
	ALA	SER	CYS	GLN	GLN	CYS	LYS	LYS	LYS	LEU
	THR	PRO	LEU	LEU	ILE	ILE	GLU	THR	THR	SER
	VAL	GLN	ILE	GLN	GLN	ARG	LEU	THR	GLU	GLU
	VAL	VAL	ARG	GLY	GLY	THR	ASN	GLU	ALA	ALA
	LEU	ASN	ASN	CYS	TYR	CYS	GLU	ASN	GLN	ILE
	GLY	ARG	ASN	ILE	ILE	ILE	GLN	GLN	GLN	ALA
	GLU	PHE	ILE	VAL	VAL	THR	SER	THR	THR	THR
	LEU	GLY	HIS	HIS	ASN	ASN	ASN	GLY	GLY	GLY
	VAL	LEU	LYS	CYS	LYS	PHE	THR	THR	GLN	CYS
	PHE	LEU	LEU	LEU	LEU	LEU	TRP	TRP	GLN	PRO
	ASN	LEU	ASN	THR	LEU	VAL	CYS	THR	ASN	ASN
	ASP	LEU	ASN	LEU	ALA	ALA	ASN	LEU	ASN	THR
	THR	PHE	GLN	GLN	GLN	GLN	THR	LEU	THR	GLU
	THR	THR	LYS	ASP	ASP	ASP	TYR	GLU	ILE	GLU
	PHE	GLU	LEU	LEU	LEU	LEU	ARG	LYS	LYS	THR
	SER	LEU	ILE	GLN	ALA	ALA	SER	GLN	LEU	CYS
	HIS	GLN	VAL	HIS	GLU	GLU	GLU	GLU	GLU	THR
	LEU	VAL	ASP	SER	LEU	THR	LYS	LEU	PRO	ASP
	ASN	PHE	PHE	THR	THR	THR	ILE	ILE	ILE	ALA
	LYS	TRP	SER	TYR	VAL	VAL	SER	SER	ILE	ARG
	ASP	GLY	THR	ILE	ILE	ILE	LEU	GLU	GLU	ALA
	LEU	CTR	SER	THR	LYS	THR	PRO	LEU	ASP	ALA

- Molecule 14: Cell division cycle protein 20 homolog

Chain R: 74% 24%

[illegible]

- Molecule 14: Cell division cycle protein 20 homolog

Chain S:  65% . 33%

[illegible]

HIS
GLN
GLY
R498

- Molecule 15: Mitotic spindle assembly checkpoint protein MAD2A

Chain T:

89%

11%

MET	ALA	LEU	GLN	LEU	SER	ARG	GLU	GLN	GLY	ILE	T12	T167	LYS	THR	ALA	LYS	ASP	SER	ALA	PRO	ARG	GLU	K119	D205
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- Molecule 16: unknown

Chain U:

100%

There are no outlier residues recorded for this chain.

- Molecule 17: Anaphase-promoting complex subunit 7

Chain X:

70%

30%

MET	R36	I110	SER	LYS	THR	SER	VAL	GLY	ARG	PRO	GLU	GLY	ASN	GLU	ALA	GLU	PRO	GLN	SER	GLN	CYS	I132	I1452	GLU	ASP	PRO	VAL	THR	GLN	LYS	LYS	THR	LEU	ASP	LYS	ALA	THR	GLN	TYR	ILE	LYS	ALA	VAL	LYS	LYS	GLU
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LEU	LEU	SER	ARG	GLU	GLN	LYS	TYR	GLU	ASP	ILE	ALA	LEU	LEU	ASN	ALA	LEU	ALA	ASN	GLN	SER	CYS	VAL	LEU	HIS	ILE	GLY	GLY	ASP	PHE	VAL	ALA	VAL	ASN	TYR	GLU	GLU	ALA	TRP	MET	ASP	GLN	TYR	ILE	ALA	SER	LEU	ASP	ASN	LYS
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SER	LEU	GLU	GLY	MET	GLN	LYS	MET	LYS	VAL	LYS	ARG	GLU	PRO	THR	ASP	ALA	THR	GLN	GLU	ASP	VAL	ASP	MET	GLU	GLY	GLY	GLU	GLU	ASP	ASP	ILE	GLY	SER	ASP	SER	ALA	ALA	TRP	ALA	ASP	GLN	GLY	GLU	TRP	PHE	GLY	MET	GLN
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- Molecule 17: Anaphase-promoting complex subunit 7

Chain Y:

76%

24%

MET	R36	I110	SER	LYS	THR	SER	VAL	GLY	ARG	PRO	GLU	GLU	ASN	GLU	ALA	GLU	PRO	GLN	SER	GLN	CYS	I132	R488	GLU	GLN	LYS	TYR	GLU	ASP	GLY	ILE	ALA	LEU	LEU	ARG	ASN	ALA	LEU	ASN	GLN	SER	ASP	CYS	VAL	LEU	HIS	ARG	ILE	GLY	GLU	GLY	ASP	PHE	LEU	VAL
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ALA	VAL	ASN	GLU	TYR	GLN	GLU	ALA	GLN	ASP	ASP	TYR	ILE	ALA	LEU	SER	LEU	ASP	PRO	ASN	ASP	GLN	SER	LYS	LEU	GLU	GLY	MET	GLN	LYS	MET	GLU	LYS	GLU	PRO	THR	ASP	ALA	THR	GLN	GLU	GLU	ASP	VAL	ASP	MET	GLU	GLY	SER	GLY	GLU	GLY	ASP	LEU	GLU
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GLY	SER	ASP	SER	ALA	ALA	GLN	TRP	ASP	GLN	GLU	GLN	TRP	PHE	GLY	MET	GLN
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4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	268851	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	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	1374	0	0	6	0
2	B	16	0	0	1	0
3	C	463	0	0	1	0
3	P	442	0	0	1	0
4	E	56	0	0	0	0
5	F	473	0	0	1	0
5	H	479	0	0	0	0
6	G	25	0	0	0	0
6	W	25	0	0	0	0
7	I	706	0	0	2	0
8	J	504	0	0	0	0
8	K	493	0	0	0	0
9	L	169	0	0	2	0
10	M	43	0	0	0	0
11	N	627	0	0	10	0
12	O	608	0	0	0	0
13	Q	219	0	0	4	0
14	R	378	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	S	333	0	0	4	0
15	T	183	0	0	0	0
16	U	9	0	0	0	0
17	X	396	0	0	0	0
17	Y	432	0	0	0	0
All	All	8453	0	0	38	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 4.

The worst 5 of 38 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)
14:R:97:LYS:CA	14:R:98:GLU:CA	2.65	0.74
14:R:420:PHE:CA	14:R:421:ALA:CA	2.75	0.65
14:R:99:ASN:CA	14:R:100:GLN:CA	2.77	0.62
11:N:164:SER:CA	11:N:165:THR:CA	2.78	0.60
11:N:280:GLU:CA	11:N:281:TYR:CA	2.82	0.57

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 [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.