



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 05:55 PM UTC

PDB ID : 8QBX / pdb_00008qbx
EMDB ID : EMD-18323
Title : Chimeric Adenovirus-derived dodecamer
Authors : Buzas, D.; Borucu, U.; Bufton, J.; Kapadalakere, S.Y.; Toelzer, C.
Deposited on : 2023-08-25
Resolution : 2.20 Å(reported)

This is a Full wwPDB EM Validation 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/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

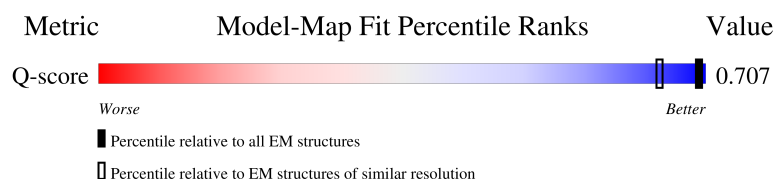
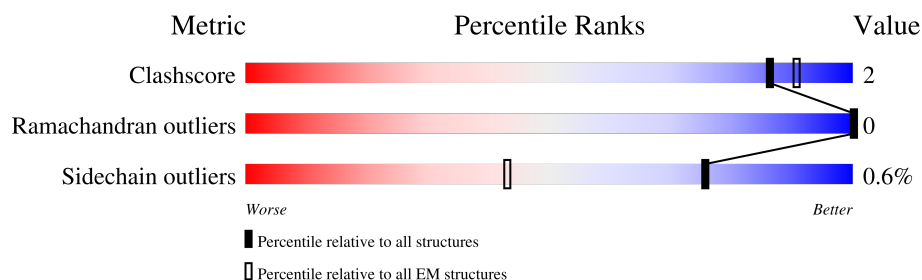
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 2.20 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.



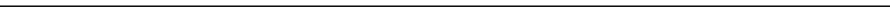
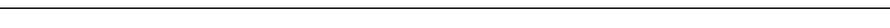
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3184 (1.71 - 2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	555	
1	AA	555	
1	AB	555	
1	B	555	

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Mol	Chain	Length	Quality of chain
1	BA	555	
1	BB	555	
1	C	555	
1	CA	555	
1	CB	555	
1	D	555	
1	DA	555	
1	DB	555	
1	E	555	
1	EA	555	
1	EB	555	
1	F	555	
1	FA	555	
1	FB	555	
1	G	555	
1	GA	555	
1	GB	555	
1	H	555	
1	HA	555	
1	HB	555	
1	I	555	
1	IA	555	
1	IB	555	
1	J	555	
1	JA	555	

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Mol	Chain	Length	Quality of chain
1	K	555	
1	KA	555	
1	L	555	
1	LA	555	
1	M	555	
1	MA	555	
1	N	555	
1	NA	555	
1	O	555	
1	OA	555	
1	P	555	
1	PA	555	
1	Q	555	
1	QA	555	
1	R	555	
1	RA	555	
1	S	555	
1	SA	555	
1	T	555	
1	TA	555	
1	UA	555	
1	V	555	
1	VA	555	
1	W	555	
1	WA	555	

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Mol	Chain	Length	Quality of chain
1	X	555	 68% • 27%
1	XA	555	 69% • 27%
1	Y	555	 68% • 27%
1	YA	555	 68% 5% 27%
1	Z	555	 68% • 27%
1	ZA	555	 68% • 27%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 183706 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 Penton protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	403	Total 3061	C 1957	N 531	O 560	S 13	0	0
1	C	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	A	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	B	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	D	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	E	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	G	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	H	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	I	403	Total 3061	C 1957	N 531	O 560	S 13	0	0
1	J	403	Total 3056	C 1954	N 528	O 561	S 13	0	0
1	K	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	L	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	M	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	N	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	O	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	P	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	Q	403	Total 3062	C 1957	N 531	O 561	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	S	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	T	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	V	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	W	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	X	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	Y	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	Z	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	AA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	BA	403	Total 3056	C 1954	N 528	O 561	S 13	0	0
1	CA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	DA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	EA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	FA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	GA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	HA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	IA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	JA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	KA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	LA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	MA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	NA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	OA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	PA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	QA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	RA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	SA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	TA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	UA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	VA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	WA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	XA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	YA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	ZA	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	AB	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	BB	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	CB	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	DB	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	EB	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	FB	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	GB	403	Total 3062	C 1957	N 531	O 561	S 13	0	0
1	HB	403	Total 3062	C 1957	N 531	O 561	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	IB	403	Total 3062	C 1957	N 531	O 561	S 13	0	0

There are 1980 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	2	MET	ARG	conflict	UNP Q2Y0H9
F	?	-	VAL	deletion	UNP Q2Y0H9
F	?	-	LEU	deletion	UNP Q2Y0H9
F	?	-	GLY	deletion	UNP Q2Y0H9
F	?	-	GLY	deletion	UNP Q2Y0H9
F	?	-	ALA	deletion	UNP Q2Y0H9
F	?	-	VAL	deletion	UNP Q2Y0H9
F	?	-	VAL	deletion	UNP Q2Y0H9
F	21	ALA	GLN	conflict	UNP Q2Y0H9
F	22	MET	-	insertion	UNP Q2Y0H9
F	23	ALA	-	insertion	UNP Q2Y0H9
F	24	ALA	-	insertion	UNP Q2Y0H9
F	27	ALA	MET	conflict	UNP Q2Y0H9
F	28	MET	ILE	conflict	UNP Q2Y0H9
F	36	TYR	PHE	conflict	UNP Q2Y0H9
F	64	ARG	LYS	conflict	UNP Q2Y0H9
F	153	GLU	-	insertion	UNP Q2Y0H9
F	154	PHE	-	insertion	UNP Q2Y0H9
F	160	GLY	-	insertion	UNP Q2Y0H9
F	161	PRO	-	insertion	UNP Q2Y0H9
F	162	VAL	-	insertion	UNP Q2Y0H9
F	163	ASN	-	insertion	UNP Q2Y0H9
F	164	ASP	-	insertion	UNP Q2Y0H9
F	314	ALA	-	insertion	UNP Q2Y0H9
F	315	ARG	-	insertion	UNP Q2Y0H9
F	330	VAL	-	insertion	UNP Q2Y0H9
F	331	ASP	-	insertion	UNP Q2Y0H9
F	344	LEU	-	insertion	UNP Q2Y0H9
F	345	GLU	-	insertion	UNP Q2Y0H9
F	357	SER	-	insertion	UNP Q2Y0H9
F	358	ARG	-	insertion	UNP Q2Y0H9
F	418	VAL	ALA	conflict	UNP Q2Y0H9
F	442	SER	ASN	conflict	UNP Q2Y0H9
C	2	MET	ARG	conflict	UNP Q2Y0H9
C	?	-	VAL	deletion	UNP Q2Y0H9
C	?	-	LEU	deletion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	GLY	deletion	UNP Q2Y0H9
C	?	-	GLY	deletion	UNP Q2Y0H9
C	?	-	ALA	deletion	UNP Q2Y0H9
C	?	-	VAL	deletion	UNP Q2Y0H9
C	?	-	VAL	deletion	UNP Q2Y0H9
C	21	ALA	GLN	conflict	UNP Q2Y0H9
C	22	MET	-	insertion	UNP Q2Y0H9
C	23	ALA	-	insertion	UNP Q2Y0H9
C	24	ALA	-	insertion	UNP Q2Y0H9
C	27	ALA	MET	conflict	UNP Q2Y0H9
C	28	MET	ILE	conflict	UNP Q2Y0H9
C	36	TYR	PHE	conflict	UNP Q2Y0H9
C	64	ARG	LYS	conflict	UNP Q2Y0H9
C	153	GLU	-	insertion	UNP Q2Y0H9
C	154	PHE	-	insertion	UNP Q2Y0H9
C	160	GLY	-	insertion	UNP Q2Y0H9
C	161	PRO	-	insertion	UNP Q2Y0H9
C	162	VAL	-	insertion	UNP Q2Y0H9
C	163	ASN	-	insertion	UNP Q2Y0H9
C	164	ASP	-	insertion	UNP Q2Y0H9
C	314	ALA	-	insertion	UNP Q2Y0H9
C	315	ARG	-	insertion	UNP Q2Y0H9
C	330	VAL	-	insertion	UNP Q2Y0H9
C	331	ASP	-	insertion	UNP Q2Y0H9
C	344	LEU	-	insertion	UNP Q2Y0H9
C	345	GLU	-	insertion	UNP Q2Y0H9
C	357	SER	-	insertion	UNP Q2Y0H9
C	358	ARG	-	insertion	UNP Q2Y0H9
C	418	VAL	ALA	conflict	UNP Q2Y0H9
C	442	SER	ASN	conflict	UNP Q2Y0H9
A	2	MET	ARG	conflict	UNP Q2Y0H9
A	?	-	VAL	deletion	UNP Q2Y0H9
A	?	-	LEU	deletion	UNP Q2Y0H9
A	?	-	GLY	deletion	UNP Q2Y0H9
A	?	-	GLY	deletion	UNP Q2Y0H9
A	?	-	ALA	deletion	UNP Q2Y0H9
A	?	-	VAL	deletion	UNP Q2Y0H9
A	?	-	VAL	deletion	UNP Q2Y0H9
A	21	ALA	GLN	conflict	UNP Q2Y0H9
A	22	MET	-	insertion	UNP Q2Y0H9
A	23	ALA	-	insertion	UNP Q2Y0H9
A	24	ALA	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	27	ALA	MET	conflict	UNP Q2Y0H9
A	28	MET	ILE	conflict	UNP Q2Y0H9
A	36	TYR	PHE	conflict	UNP Q2Y0H9
A	64	ARG	LYS	conflict	UNP Q2Y0H9
A	153	GLU	-	insertion	UNP Q2Y0H9
A	154	PHE	-	insertion	UNP Q2Y0H9
A	160	GLY	-	insertion	UNP Q2Y0H9
A	161	PRO	-	insertion	UNP Q2Y0H9
A	162	VAL	-	insertion	UNP Q2Y0H9
A	163	ASN	-	insertion	UNP Q2Y0H9
A	164	ASP	-	insertion	UNP Q2Y0H9
A	314	ALA	-	insertion	UNP Q2Y0H9
A	315	ARG	-	insertion	UNP Q2Y0H9
A	330	VAL	-	insertion	UNP Q2Y0H9
A	331	ASP	-	insertion	UNP Q2Y0H9
A	344	LEU	-	insertion	UNP Q2Y0H9
A	345	GLU	-	insertion	UNP Q2Y0H9
A	357	SER	-	insertion	UNP Q2Y0H9
A	358	ARG	-	insertion	UNP Q2Y0H9
A	418	VAL	ALA	conflict	UNP Q2Y0H9
A	442	SER	ASN	conflict	UNP Q2Y0H9
B	2	MET	ARG	conflict	UNP Q2Y0H9
B	?	-	VAL	deletion	UNP Q2Y0H9
B	?	-	LEU	deletion	UNP Q2Y0H9
B	?	-	GLY	deletion	UNP Q2Y0H9
B	?	-	GLY	deletion	UNP Q2Y0H9
B	?	-	ALA	deletion	UNP Q2Y0H9
B	?	-	VAL	deletion	UNP Q2Y0H9
B	?	-	VAL	deletion	UNP Q2Y0H9
B	21	ALA	GLN	conflict	UNP Q2Y0H9
B	22	MET	-	insertion	UNP Q2Y0H9
B	23	ALA	-	insertion	UNP Q2Y0H9
B	24	ALA	-	insertion	UNP Q2Y0H9
B	27	ALA	MET	conflict	UNP Q2Y0H9
B	28	MET	ILE	conflict	UNP Q2Y0H9
B	36	TYR	PHE	conflict	UNP Q2Y0H9
B	64	ARG	LYS	conflict	UNP Q2Y0H9
B	153	GLU	-	insertion	UNP Q2Y0H9
B	154	PHE	-	insertion	UNP Q2Y0H9
B	160	GLY	-	insertion	UNP Q2Y0H9
B	161	PRO	-	insertion	UNP Q2Y0H9
B	162	VAL	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	163	ASN	-	insertion	UNP Q2Y0H9
B	164	ASP	-	insertion	UNP Q2Y0H9
B	314	ALA	-	insertion	UNP Q2Y0H9
B	315	ARG	-	insertion	UNP Q2Y0H9
B	330	VAL	-	insertion	UNP Q2Y0H9
B	331	ASP	-	insertion	UNP Q2Y0H9
B	344	LEU	-	insertion	UNP Q2Y0H9
B	345	GLU	-	insertion	UNP Q2Y0H9
B	357	SER	-	insertion	UNP Q2Y0H9
B	358	ARG	-	insertion	UNP Q2Y0H9
B	418	VAL	ALA	conflict	UNP Q2Y0H9
B	442	SER	ASN	conflict	UNP Q2Y0H9
D	2	MET	ARG	conflict	UNP Q2Y0H9
D	?	-	VAL	deletion	UNP Q2Y0H9
D	?	-	LEU	deletion	UNP Q2Y0H9
D	?	-	GLY	deletion	UNP Q2Y0H9
D	?	-	GLY	deletion	UNP Q2Y0H9
D	?	-	ALA	deletion	UNP Q2Y0H9
D	?	-	VAL	deletion	UNP Q2Y0H9
D	?	-	VAL	deletion	UNP Q2Y0H9
D	21	ALA	GLN	conflict	UNP Q2Y0H9
D	22	MET	-	insertion	UNP Q2Y0H9
D	23	ALA	-	insertion	UNP Q2Y0H9
D	24	ALA	-	insertion	UNP Q2Y0H9
D	27	ALA	MET	conflict	UNP Q2Y0H9
D	28	MET	ILE	conflict	UNP Q2Y0H9
D	36	TYR	PHE	conflict	UNP Q2Y0H9
D	64	ARG	LYS	conflict	UNP Q2Y0H9
D	153	GLU	-	insertion	UNP Q2Y0H9
D	154	PHE	-	insertion	UNP Q2Y0H9
D	160	GLY	-	insertion	UNP Q2Y0H9
D	161	PRO	-	insertion	UNP Q2Y0H9
D	162	VAL	-	insertion	UNP Q2Y0H9
D	163	ASN	-	insertion	UNP Q2Y0H9
D	164	ASP	-	insertion	UNP Q2Y0H9
D	314	ALA	-	insertion	UNP Q2Y0H9
D	315	ARG	-	insertion	UNP Q2Y0H9
D	330	VAL	-	insertion	UNP Q2Y0H9
D	331	ASP	-	insertion	UNP Q2Y0H9
D	344	LEU	-	insertion	UNP Q2Y0H9
D	345	GLU	-	insertion	UNP Q2Y0H9
D	357	SER	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	358	ARG	-	insertion	UNP Q2Y0H9
D	418	VAL	ALA	conflict	UNP Q2Y0H9
D	442	SER	ASN	conflict	UNP Q2Y0H9
E	2	MET	ARG	conflict	UNP Q2Y0H9
E	?	-	VAL	deletion	UNP Q2Y0H9
E	?	-	LEU	deletion	UNP Q2Y0H9
E	?	-	GLY	deletion	UNP Q2Y0H9
E	?	-	GLY	deletion	UNP Q2Y0H9
E	?	-	ALA	deletion	UNP Q2Y0H9
E	?	-	VAL	deletion	UNP Q2Y0H9
E	?	-	VAL	deletion	UNP Q2Y0H9
E	21	ALA	GLN	conflict	UNP Q2Y0H9
E	22	MET	-	insertion	UNP Q2Y0H9
E	23	ALA	-	insertion	UNP Q2Y0H9
E	24	ALA	-	insertion	UNP Q2Y0H9
E	27	ALA	MET	conflict	UNP Q2Y0H9
E	28	MET	ILE	conflict	UNP Q2Y0H9
E	36	TYR	PHE	conflict	UNP Q2Y0H9
E	64	ARG	LYS	conflict	UNP Q2Y0H9
E	153	GLU	-	insertion	UNP Q2Y0H9
E	154	PHE	-	insertion	UNP Q2Y0H9
E	160	GLY	-	insertion	UNP Q2Y0H9
E	161	PRO	-	insertion	UNP Q2Y0H9
E	162	VAL	-	insertion	UNP Q2Y0H9
E	163	ASN	-	insertion	UNP Q2Y0H9
E	164	ASP	-	insertion	UNP Q2Y0H9
E	314	ALA	-	insertion	UNP Q2Y0H9
E	315	ARG	-	insertion	UNP Q2Y0H9
E	330	VAL	-	insertion	UNP Q2Y0H9
E	331	ASP	-	insertion	UNP Q2Y0H9
E	344	LEU	-	insertion	UNP Q2Y0H9
E	345	GLU	-	insertion	UNP Q2Y0H9
E	357	SER	-	insertion	UNP Q2Y0H9
E	358	ARG	-	insertion	UNP Q2Y0H9
E	418	VAL	ALA	conflict	UNP Q2Y0H9
E	442	SER	ASN	conflict	UNP Q2Y0H9
G	2	MET	ARG	conflict	UNP Q2Y0H9
G	?	-	VAL	deletion	UNP Q2Y0H9
G	?	-	LEU	deletion	UNP Q2Y0H9
G	?	-	GLY	deletion	UNP Q2Y0H9
G	?	-	GLY	deletion	UNP Q2Y0H9
G	?	-	ALA	deletion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	VAL	deletion	UNP Q2Y0H9
G	?	-	VAL	deletion	UNP Q2Y0H9
G	21	ALA	GLN	conflict	UNP Q2Y0H9
G	22	MET	-	insertion	UNP Q2Y0H9
G	23	ALA	-	insertion	UNP Q2Y0H9
G	24	ALA	-	insertion	UNP Q2Y0H9
G	27	ALA	MET	conflict	UNP Q2Y0H9
G	28	MET	ILE	conflict	UNP Q2Y0H9
G	36	TYR	PHE	conflict	UNP Q2Y0H9
G	64	ARG	LYS	conflict	UNP Q2Y0H9
G	153	GLU	-	insertion	UNP Q2Y0H9
G	154	PHE	-	insertion	UNP Q2Y0H9
G	160	GLY	-	insertion	UNP Q2Y0H9
G	161	PRO	-	insertion	UNP Q2Y0H9
G	162	VAL	-	insertion	UNP Q2Y0H9
G	163	ASN	-	insertion	UNP Q2Y0H9
G	164	ASP	-	insertion	UNP Q2Y0H9
G	314	ALA	-	insertion	UNP Q2Y0H9
G	315	ARG	-	insertion	UNP Q2Y0H9
G	330	VAL	-	insertion	UNP Q2Y0H9
G	331	ASP	-	insertion	UNP Q2Y0H9
G	344	LEU	-	insertion	UNP Q2Y0H9
G	345	GLU	-	insertion	UNP Q2Y0H9
G	357	SER	-	insertion	UNP Q2Y0H9
G	358	ARG	-	insertion	UNP Q2Y0H9
G	418	VAL	ALA	conflict	UNP Q2Y0H9
G	442	SER	ASN	conflict	UNP Q2Y0H9
H	2	MET	ARG	conflict	UNP Q2Y0H9
H	?	-	VAL	deletion	UNP Q2Y0H9
H	?	-	LEU	deletion	UNP Q2Y0H9
H	?	-	GLY	deletion	UNP Q2Y0H9
H	?	-	GLY	deletion	UNP Q2Y0H9
H	?	-	ALA	deletion	UNP Q2Y0H9
H	?	-	VAL	deletion	UNP Q2Y0H9
H	?	-	VAL	deletion	UNP Q2Y0H9
H	21	ALA	GLN	conflict	UNP Q2Y0H9
H	22	MET	-	insertion	UNP Q2Y0H9
H	23	ALA	-	insertion	UNP Q2Y0H9
H	24	ALA	-	insertion	UNP Q2Y0H9
H	27	ALA	MET	conflict	UNP Q2Y0H9
H	28	MET	ILE	conflict	UNP Q2Y0H9
H	36	TYR	PHE	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
H	64	ARG	LYS	conflict	UNP Q2Y0H9
H	153	GLU	-	insertion	UNP Q2Y0H9
H	154	PHE	-	insertion	UNP Q2Y0H9
H	160	GLY	-	insertion	UNP Q2Y0H9
H	161	PRO	-	insertion	UNP Q2Y0H9
H	162	VAL	-	insertion	UNP Q2Y0H9
H	163	ASN	-	insertion	UNP Q2Y0H9
H	164	ASP	-	insertion	UNP Q2Y0H9
H	314	ALA	-	insertion	UNP Q2Y0H9
H	315	ARG	-	insertion	UNP Q2Y0H9
H	330	VAL	-	insertion	UNP Q2Y0H9
H	331	ASP	-	insertion	UNP Q2Y0H9
H	344	LEU	-	insertion	UNP Q2Y0H9
H	345	GLU	-	insertion	UNP Q2Y0H9
H	357	SER	-	insertion	UNP Q2Y0H9
H	358	ARG	-	insertion	UNP Q2Y0H9
H	418	VAL	ALA	conflict	UNP Q2Y0H9
H	442	SER	ASN	conflict	UNP Q2Y0H9
I	2	MET	ARG	conflict	UNP Q2Y0H9
I	?	-	VAL	deletion	UNP Q2Y0H9
I	?	-	LEU	deletion	UNP Q2Y0H9
I	?	-	GLY	deletion	UNP Q2Y0H9
I	?	-	GLY	deletion	UNP Q2Y0H9
I	?	-	ALA	deletion	UNP Q2Y0H9
I	?	-	VAL	deletion	UNP Q2Y0H9
I	?	-	VAL	deletion	UNP Q2Y0H9
I	21	ALA	GLN	conflict	UNP Q2Y0H9
I	22	MET	-	insertion	UNP Q2Y0H9
I	23	ALA	-	insertion	UNP Q2Y0H9
I	24	ALA	-	insertion	UNP Q2Y0H9
I	27	ALA	MET	conflict	UNP Q2Y0H9
I	28	MET	ILE	conflict	UNP Q2Y0H9
I	36	TYR	PHE	conflict	UNP Q2Y0H9
I	64	ARG	LYS	conflict	UNP Q2Y0H9
I	153	GLU	-	insertion	UNP Q2Y0H9
I	154	PHE	-	insertion	UNP Q2Y0H9
I	160	GLY	-	insertion	UNP Q2Y0H9
I	161	PRO	-	insertion	UNP Q2Y0H9
I	162	VAL	-	insertion	UNP Q2Y0H9
I	163	ASN	-	insertion	UNP Q2Y0H9
I	164	ASP	-	insertion	UNP Q2Y0H9
I	314	ALA	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
I	315	ARG	-	insertion	UNP Q2Y0H9
I	330	VAL	-	insertion	UNP Q2Y0H9
I	331	ASP	-	insertion	UNP Q2Y0H9
I	344	LEU	-	insertion	UNP Q2Y0H9
I	345	GLU	-	insertion	UNP Q2Y0H9
I	357	SER	-	insertion	UNP Q2Y0H9
I	358	ARG	-	insertion	UNP Q2Y0H9
I	418	VAL	ALA	conflict	UNP Q2Y0H9
I	442	SER	ASN	conflict	UNP Q2Y0H9
J	2	MET	ARG	conflict	UNP Q2Y0H9
J	?	-	VAL	deletion	UNP Q2Y0H9
J	?	-	LEU	deletion	UNP Q2Y0H9
J	?	-	GLY	deletion	UNP Q2Y0H9
J	?	-	GLY	deletion	UNP Q2Y0H9
J	?	-	ALA	deletion	UNP Q2Y0H9
J	?	-	VAL	deletion	UNP Q2Y0H9
J	?	-	VAL	deletion	UNP Q2Y0H9
J	21	ALA	GLN	conflict	UNP Q2Y0H9
J	22	MET	-	insertion	UNP Q2Y0H9
J	23	ALA	-	insertion	UNP Q2Y0H9
J	24	ALA	-	insertion	UNP Q2Y0H9
J	27	ALA	MET	conflict	UNP Q2Y0H9
J	28	MET	ILE	conflict	UNP Q2Y0H9
J	36	TYR	PHE	conflict	UNP Q2Y0H9
J	64	ARG	LYS	conflict	UNP Q2Y0H9
J	153	GLU	-	insertion	UNP Q2Y0H9
J	154	PHE	-	insertion	UNP Q2Y0H9
J	160	GLY	-	insertion	UNP Q2Y0H9
J	161	PRO	-	insertion	UNP Q2Y0H9
J	162	VAL	-	insertion	UNP Q2Y0H9
J	163	ASN	-	insertion	UNP Q2Y0H9
J	164	ASP	-	insertion	UNP Q2Y0H9
J	314	ALA	-	insertion	UNP Q2Y0H9
J	315	ARG	-	insertion	UNP Q2Y0H9
J	330	VAL	-	insertion	UNP Q2Y0H9
J	331	ASP	-	insertion	UNP Q2Y0H9
J	344	LEU	-	insertion	UNP Q2Y0H9
J	345	GLU	-	insertion	UNP Q2Y0H9
J	357	SER	-	insertion	UNP Q2Y0H9
J	358	ARG	-	insertion	UNP Q2Y0H9
J	418	VAL	ALA	conflict	UNP Q2Y0H9
J	442	SER	ASN	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
K	2	MET	ARG	conflict	UNP Q2Y0H9
K	?	-	VAL	deletion	UNP Q2Y0H9
K	?	-	LEU	deletion	UNP Q2Y0H9
K	?	-	GLY	deletion	UNP Q2Y0H9
K	?	-	GLY	deletion	UNP Q2Y0H9
K	?	-	ALA	deletion	UNP Q2Y0H9
K	?	-	VAL	deletion	UNP Q2Y0H9
K	?	-	VAL	deletion	UNP Q2Y0H9
K	21	ALA	GLN	conflict	UNP Q2Y0H9
K	22	MET	-	insertion	UNP Q2Y0H9
K	23	ALA	-	insertion	UNP Q2Y0H9
K	24	ALA	-	insertion	UNP Q2Y0H9
K	27	ALA	MET	conflict	UNP Q2Y0H9
K	28	MET	ILE	conflict	UNP Q2Y0H9
K	36	TYR	PHE	conflict	UNP Q2Y0H9
K	64	ARG	LYS	conflict	UNP Q2Y0H9
K	153	GLU	-	insertion	UNP Q2Y0H9
K	154	PHE	-	insertion	UNP Q2Y0H9
K	160	GLY	-	insertion	UNP Q2Y0H9
K	161	PRO	-	insertion	UNP Q2Y0H9
K	162	VAL	-	insertion	UNP Q2Y0H9
K	163	ASN	-	insertion	UNP Q2Y0H9
K	164	ASP	-	insertion	UNP Q2Y0H9
K	314	ALA	-	insertion	UNP Q2Y0H9
K	315	ARG	-	insertion	UNP Q2Y0H9
K	330	VAL	-	insertion	UNP Q2Y0H9
K	331	ASP	-	insertion	UNP Q2Y0H9
K	344	LEU	-	insertion	UNP Q2Y0H9
K	345	GLU	-	insertion	UNP Q2Y0H9
K	357	SER	-	insertion	UNP Q2Y0H9
K	358	ARG	-	insertion	UNP Q2Y0H9
K	418	VAL	ALA	conflict	UNP Q2Y0H9
K	442	SER	ASN	conflict	UNP Q2Y0H9
L	2	MET	ARG	conflict	UNP Q2Y0H9
L	?	-	VAL	deletion	UNP Q2Y0H9
L	?	-	LEU	deletion	UNP Q2Y0H9
L	?	-	GLY	deletion	UNP Q2Y0H9
L	?	-	GLY	deletion	UNP Q2Y0H9
L	?	-	ALA	deletion	UNP Q2Y0H9
L	?	-	VAL	deletion	UNP Q2Y0H9
L	?	-	VAL	deletion	UNP Q2Y0H9
L	21	ALA	GLN	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
L	22	MET	-	insertion	UNP Q2Y0H9
L	23	ALA	-	insertion	UNP Q2Y0H9
L	24	ALA	-	insertion	UNP Q2Y0H9
L	27	ALA	MET	conflict	UNP Q2Y0H9
L	28	MET	ILE	conflict	UNP Q2Y0H9
L	36	TYR	PHE	conflict	UNP Q2Y0H9
L	64	ARG	LYS	conflict	UNP Q2Y0H9
L	153	GLU	-	insertion	UNP Q2Y0H9
L	154	PHE	-	insertion	UNP Q2Y0H9
L	160	GLY	-	insertion	UNP Q2Y0H9
L	161	PRO	-	insertion	UNP Q2Y0H9
L	162	VAL	-	insertion	UNP Q2Y0H9
L	163	ASN	-	insertion	UNP Q2Y0H9
L	164	ASP	-	insertion	UNP Q2Y0H9
L	314	ALA	-	insertion	UNP Q2Y0H9
L	315	ARG	-	insertion	UNP Q2Y0H9
L	330	VAL	-	insertion	UNP Q2Y0H9
L	331	ASP	-	insertion	UNP Q2Y0H9
L	344	LEU	-	insertion	UNP Q2Y0H9
L	345	GLU	-	insertion	UNP Q2Y0H9
L	357	SER	-	insertion	UNP Q2Y0H9
L	358	ARG	-	insertion	UNP Q2Y0H9
L	418	VAL	ALA	conflict	UNP Q2Y0H9
L	442	SER	ASN	conflict	UNP Q2Y0H9
M	2	MET	ARG	conflict	UNP Q2Y0H9
M	?	-	VAL	deletion	UNP Q2Y0H9
M	?	-	LEU	deletion	UNP Q2Y0H9
M	?	-	GLY	deletion	UNP Q2Y0H9
M	?	-	GLY	deletion	UNP Q2Y0H9
M	?	-	ALA	deletion	UNP Q2Y0H9
M	?	-	VAL	deletion	UNP Q2Y0H9
M	?	-	VAL	deletion	UNP Q2Y0H9
M	21	ALA	GLN	conflict	UNP Q2Y0H9
M	22	MET	-	insertion	UNP Q2Y0H9
M	23	ALA	-	insertion	UNP Q2Y0H9
M	24	ALA	-	insertion	UNP Q2Y0H9
M	27	ALA	MET	conflict	UNP Q2Y0H9
M	28	MET	ILE	conflict	UNP Q2Y0H9
M	36	TYR	PHE	conflict	UNP Q2Y0H9
M	64	ARG	LYS	conflict	UNP Q2Y0H9
M	153	GLU	-	insertion	UNP Q2Y0H9
M	154	PHE	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
M	160	GLY	-	insertion	UNP Q2Y0H9
M	161	PRO	-	insertion	UNP Q2Y0H9
M	162	VAL	-	insertion	UNP Q2Y0H9
M	163	ASN	-	insertion	UNP Q2Y0H9
M	164	ASP	-	insertion	UNP Q2Y0H9
M	314	ALA	-	insertion	UNP Q2Y0H9
M	315	ARG	-	insertion	UNP Q2Y0H9
M	330	VAL	-	insertion	UNP Q2Y0H9
M	331	ASP	-	insertion	UNP Q2Y0H9
M	344	LEU	-	insertion	UNP Q2Y0H9
M	345	GLU	-	insertion	UNP Q2Y0H9
M	357	SER	-	insertion	UNP Q2Y0H9
M	358	ARG	-	insertion	UNP Q2Y0H9
M	418	VAL	ALA	conflict	UNP Q2Y0H9
M	442	SER	ASN	conflict	UNP Q2Y0H9
N	2	MET	ARG	conflict	UNP Q2Y0H9
N	?	-	VAL	deletion	UNP Q2Y0H9
N	?	-	LEU	deletion	UNP Q2Y0H9
N	?	-	GLY	deletion	UNP Q2Y0H9
N	?	-	GLY	deletion	UNP Q2Y0H9
N	?	-	ALA	deletion	UNP Q2Y0H9
N	?	-	VAL	deletion	UNP Q2Y0H9
N	?	-	VAL	deletion	UNP Q2Y0H9
N	21	ALA	GLN	conflict	UNP Q2Y0H9
N	22	MET	-	insertion	UNP Q2Y0H9
N	23	ALA	-	insertion	UNP Q2Y0H9
N	24	ALA	-	insertion	UNP Q2Y0H9
N	27	ALA	MET	conflict	UNP Q2Y0H9
N	28	MET	ILE	conflict	UNP Q2Y0H9
N	36	TYR	PHE	conflict	UNP Q2Y0H9
N	64	ARG	LYS	conflict	UNP Q2Y0H9
N	153	GLU	-	insertion	UNP Q2Y0H9
N	154	PHE	-	insertion	UNP Q2Y0H9
N	160	GLY	-	insertion	UNP Q2Y0H9
N	161	PRO	-	insertion	UNP Q2Y0H9
N	162	VAL	-	insertion	UNP Q2Y0H9
N	163	ASN	-	insertion	UNP Q2Y0H9
N	164	ASP	-	insertion	UNP Q2Y0H9
N	314	ALA	-	insertion	UNP Q2Y0H9
N	315	ARG	-	insertion	UNP Q2Y0H9
N	330	VAL	-	insertion	UNP Q2Y0H9
N	331	ASP	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
N	344	LEU	-	insertion	UNP Q2Y0H9
N	345	GLU	-	insertion	UNP Q2Y0H9
N	357	SER	-	insertion	UNP Q2Y0H9
N	358	ARG	-	insertion	UNP Q2Y0H9
N	418	VAL	ALA	conflict	UNP Q2Y0H9
N	442	SER	ASN	conflict	UNP Q2Y0H9
O	2	MET	ARG	conflict	UNP Q2Y0H9
O	?	-	VAL	deletion	UNP Q2Y0H9
O	?	-	LEU	deletion	UNP Q2Y0H9
O	?	-	GLY	deletion	UNP Q2Y0H9
O	?	-	GLY	deletion	UNP Q2Y0H9
O	?	-	ALA	deletion	UNP Q2Y0H9
O	?	-	VAL	deletion	UNP Q2Y0H9
O	?	-	VAL	deletion	UNP Q2Y0H9
O	21	ALA	GLN	conflict	UNP Q2Y0H9
O	22	MET	-	insertion	UNP Q2Y0H9
O	23	ALA	-	insertion	UNP Q2Y0H9
O	24	ALA	-	insertion	UNP Q2Y0H9
O	27	ALA	MET	conflict	UNP Q2Y0H9
O	28	MET	ILE	conflict	UNP Q2Y0H9
O	36	TYR	PHE	conflict	UNP Q2Y0H9
O	64	ARG	LYS	conflict	UNP Q2Y0H9
O	153	GLU	-	insertion	UNP Q2Y0H9
O	154	PHE	-	insertion	UNP Q2Y0H9
O	160	GLY	-	insertion	UNP Q2Y0H9
O	161	PRO	-	insertion	UNP Q2Y0H9
O	162	VAL	-	insertion	UNP Q2Y0H9
O	163	ASN	-	insertion	UNP Q2Y0H9
O	164	ASP	-	insertion	UNP Q2Y0H9
O	314	ALA	-	insertion	UNP Q2Y0H9
O	315	ARG	-	insertion	UNP Q2Y0H9
O	330	VAL	-	insertion	UNP Q2Y0H9
O	331	ASP	-	insertion	UNP Q2Y0H9
O	344	LEU	-	insertion	UNP Q2Y0H9
O	345	GLU	-	insertion	UNP Q2Y0H9
O	357	SER	-	insertion	UNP Q2Y0H9
O	358	ARG	-	insertion	UNP Q2Y0H9
O	418	VAL	ALA	conflict	UNP Q2Y0H9
O	442	SER	ASN	conflict	UNP Q2Y0H9
P	2	MET	ARG	conflict	UNP Q2Y0H9
P	?	-	VAL	deletion	UNP Q2Y0H9
P	?	-	LEU	deletion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
P	?	-	GLY	deletion	UNP Q2Y0H9
P	?	-	GLY	deletion	UNP Q2Y0H9
P	?	-	ALA	deletion	UNP Q2Y0H9
P	?	-	VAL	deletion	UNP Q2Y0H9
P	?	-	VAL	deletion	UNP Q2Y0H9
P	21	ALA	GLN	conflict	UNP Q2Y0H9
P	22	MET	-	insertion	UNP Q2Y0H9
P	23	ALA	-	insertion	UNP Q2Y0H9
P	24	ALA	-	insertion	UNP Q2Y0H9
P	27	ALA	MET	conflict	UNP Q2Y0H9
P	28	MET	ILE	conflict	UNP Q2Y0H9
P	36	TYR	PHE	conflict	UNP Q2Y0H9
P	64	ARG	LYS	conflict	UNP Q2Y0H9
P	153	GLU	-	insertion	UNP Q2Y0H9
P	154	PHE	-	insertion	UNP Q2Y0H9
P	160	GLY	-	insertion	UNP Q2Y0H9
P	161	PRO	-	insertion	UNP Q2Y0H9
P	162	VAL	-	insertion	UNP Q2Y0H9
P	163	ASN	-	insertion	UNP Q2Y0H9
P	164	ASP	-	insertion	UNP Q2Y0H9
P	314	ALA	-	insertion	UNP Q2Y0H9
P	315	ARG	-	insertion	UNP Q2Y0H9
P	330	VAL	-	insertion	UNP Q2Y0H9
P	331	ASP	-	insertion	UNP Q2Y0H9
P	344	LEU	-	insertion	UNP Q2Y0H9
P	345	GLU	-	insertion	UNP Q2Y0H9
P	357	SER	-	insertion	UNP Q2Y0H9
P	358	ARG	-	insertion	UNP Q2Y0H9
P	418	VAL	ALA	conflict	UNP Q2Y0H9
P	442	SER	ASN	conflict	UNP Q2Y0H9
Q	2	MET	ARG	conflict	UNP Q2Y0H9
Q	?	-	VAL	deletion	UNP Q2Y0H9
Q	?	-	LEU	deletion	UNP Q2Y0H9
Q	?	-	GLY	deletion	UNP Q2Y0H9
Q	?	-	GLY	deletion	UNP Q2Y0H9
Q	?	-	ALA	deletion	UNP Q2Y0H9
Q	?	-	VAL	deletion	UNP Q2Y0H9
Q	?	-	VAL	deletion	UNP Q2Y0H9
Q	21	ALA	GLN	conflict	UNP Q2Y0H9
Q	22	MET	-	insertion	UNP Q2Y0H9
Q	23	ALA	-	insertion	UNP Q2Y0H9
Q	24	ALA	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	27	ALA	MET	conflict	UNP Q2Y0H9
Q	28	MET	ILE	conflict	UNP Q2Y0H9
Q	36	TYR	PHE	conflict	UNP Q2Y0H9
Q	64	ARG	LYS	conflict	UNP Q2Y0H9
Q	153	GLU	-	insertion	UNP Q2Y0H9
Q	154	PHE	-	insertion	UNP Q2Y0H9
Q	160	GLY	-	insertion	UNP Q2Y0H9
Q	161	PRO	-	insertion	UNP Q2Y0H9
Q	162	VAL	-	insertion	UNP Q2Y0H9
Q	163	ASN	-	insertion	UNP Q2Y0H9
Q	164	ASP	-	insertion	UNP Q2Y0H9
Q	314	ALA	-	insertion	UNP Q2Y0H9
Q	315	ARG	-	insertion	UNP Q2Y0H9
Q	330	VAL	-	insertion	UNP Q2Y0H9
Q	331	ASP	-	insertion	UNP Q2Y0H9
Q	344	LEU	-	insertion	UNP Q2Y0H9
Q	345	GLU	-	insertion	UNP Q2Y0H9
Q	357	SER	-	insertion	UNP Q2Y0H9
Q	358	ARG	-	insertion	UNP Q2Y0H9
Q	418	VAL	ALA	conflict	UNP Q2Y0H9
Q	442	SER	ASN	conflict	UNP Q2Y0H9
R	2	MET	ARG	conflict	UNP Q2Y0H9
R	?	-	VAL	deletion	UNP Q2Y0H9
R	?	-	LEU	deletion	UNP Q2Y0H9
R	?	-	GLY	deletion	UNP Q2Y0H9
R	?	-	GLY	deletion	UNP Q2Y0H9
R	?	-	ALA	deletion	UNP Q2Y0H9
R	?	-	VAL	deletion	UNP Q2Y0H9
R	?	-	VAL	deletion	UNP Q2Y0H9
R	21	ALA	GLN	conflict	UNP Q2Y0H9
R	22	MET	-	insertion	UNP Q2Y0H9
R	23	ALA	-	insertion	UNP Q2Y0H9
R	24	ALA	-	insertion	UNP Q2Y0H9
R	27	ALA	MET	conflict	UNP Q2Y0H9
R	28	MET	ILE	conflict	UNP Q2Y0H9
R	36	TYR	PHE	conflict	UNP Q2Y0H9
R	64	ARG	LYS	conflict	UNP Q2Y0H9
R	153	GLU	-	insertion	UNP Q2Y0H9
R	154	PHE	-	insertion	UNP Q2Y0H9
R	160	GLY	-	insertion	UNP Q2Y0H9
R	161	PRO	-	insertion	UNP Q2Y0H9
R	162	VAL	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
R	163	ASN	-	insertion	UNP Q2Y0H9
R	164	ASP	-	insertion	UNP Q2Y0H9
R	314	ALA	-	insertion	UNP Q2Y0H9
R	315	ARG	-	insertion	UNP Q2Y0H9
R	330	VAL	-	insertion	UNP Q2Y0H9
R	331	ASP	-	insertion	UNP Q2Y0H9
R	344	LEU	-	insertion	UNP Q2Y0H9
R	345	GLU	-	insertion	UNP Q2Y0H9
R	357	SER	-	insertion	UNP Q2Y0H9
R	358	ARG	-	insertion	UNP Q2Y0H9
R	418	VAL	ALA	conflict	UNP Q2Y0H9
R	442	SER	ASN	conflict	UNP Q2Y0H9
S	2	MET	ARG	conflict	UNP Q2Y0H9
S	?	-	VAL	deletion	UNP Q2Y0H9
S	?	-	LEU	deletion	UNP Q2Y0H9
S	?	-	GLY	deletion	UNP Q2Y0H9
S	?	-	GLY	deletion	UNP Q2Y0H9
S	?	-	ALA	deletion	UNP Q2Y0H9
S	?	-	VAL	deletion	UNP Q2Y0H9
S	?	-	VAL	deletion	UNP Q2Y0H9
S	21	ALA	GLN	conflict	UNP Q2Y0H9
S	22	MET	-	insertion	UNP Q2Y0H9
S	23	ALA	-	insertion	UNP Q2Y0H9
S	24	ALA	-	insertion	UNP Q2Y0H9
S	27	ALA	MET	conflict	UNP Q2Y0H9
S	28	MET	ILE	conflict	UNP Q2Y0H9
S	36	TYR	PHE	conflict	UNP Q2Y0H9
S	64	ARG	LYS	conflict	UNP Q2Y0H9
S	153	GLU	-	insertion	UNP Q2Y0H9
S	154	PHE	-	insertion	UNP Q2Y0H9
S	160	GLY	-	insertion	UNP Q2Y0H9
S	161	PRO	-	insertion	UNP Q2Y0H9
S	162	VAL	-	insertion	UNP Q2Y0H9
S	163	ASN	-	insertion	UNP Q2Y0H9
S	164	ASP	-	insertion	UNP Q2Y0H9
S	314	ALA	-	insertion	UNP Q2Y0H9
S	315	ARG	-	insertion	UNP Q2Y0H9
S	330	VAL	-	insertion	UNP Q2Y0H9
S	331	ASP	-	insertion	UNP Q2Y0H9
S	344	LEU	-	insertion	UNP Q2Y0H9
S	345	GLU	-	insertion	UNP Q2Y0H9
S	357	SER	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
S	358	ARG	-	insertion	UNP Q2Y0H9
S	418	VAL	ALA	conflict	UNP Q2Y0H9
S	442	SER	ASN	conflict	UNP Q2Y0H9
T	2	MET	ARG	conflict	UNP Q2Y0H9
T	?	-	VAL	deletion	UNP Q2Y0H9
T	?	-	LEU	deletion	UNP Q2Y0H9
T	?	-	GLY	deletion	UNP Q2Y0H9
T	?	-	GLY	deletion	UNP Q2Y0H9
T	?	-	ALA	deletion	UNP Q2Y0H9
T	?	-	VAL	deletion	UNP Q2Y0H9
T	?	-	VAL	deletion	UNP Q2Y0H9
T	21	ALA	GLN	conflict	UNP Q2Y0H9
T	22	MET	-	insertion	UNP Q2Y0H9
T	23	ALA	-	insertion	UNP Q2Y0H9
T	24	ALA	-	insertion	UNP Q2Y0H9
T	27	ALA	MET	conflict	UNP Q2Y0H9
T	28	MET	ILE	conflict	UNP Q2Y0H9
T	36	TYR	PHE	conflict	UNP Q2Y0H9
T	64	ARG	LYS	conflict	UNP Q2Y0H9
T	153	GLU	-	insertion	UNP Q2Y0H9
T	154	PHE	-	insertion	UNP Q2Y0H9
T	160	GLY	-	insertion	UNP Q2Y0H9
T	161	PRO	-	insertion	UNP Q2Y0H9
T	162	VAL	-	insertion	UNP Q2Y0H9
T	163	ASN	-	insertion	UNP Q2Y0H9
T	164	ASP	-	insertion	UNP Q2Y0H9
T	314	ALA	-	insertion	UNP Q2Y0H9
T	315	ARG	-	insertion	UNP Q2Y0H9
T	330	VAL	-	insertion	UNP Q2Y0H9
T	331	ASP	-	insertion	UNP Q2Y0H9
T	344	LEU	-	insertion	UNP Q2Y0H9
T	345	GLU	-	insertion	UNP Q2Y0H9
T	357	SER	-	insertion	UNP Q2Y0H9
T	358	ARG	-	insertion	UNP Q2Y0H9
T	418	VAL	ALA	conflict	UNP Q2Y0H9
T	442	SER	ASN	conflict	UNP Q2Y0H9
V	2	MET	ARG	conflict	UNP Q2Y0H9
V	?	-	VAL	deletion	UNP Q2Y0H9
V	?	-	LEU	deletion	UNP Q2Y0H9
V	?	-	GLY	deletion	UNP Q2Y0H9
V	?	-	GLY	deletion	UNP Q2Y0H9
V	?	-	ALA	deletion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
V	?	-	VAL	deletion	UNP Q2Y0H9
V	?	-	VAL	deletion	UNP Q2Y0H9
V	21	ALA	GLN	conflict	UNP Q2Y0H9
V	22	MET	-	insertion	UNP Q2Y0H9
V	23	ALA	-	insertion	UNP Q2Y0H9
V	24	ALA	-	insertion	UNP Q2Y0H9
V	27	ALA	MET	conflict	UNP Q2Y0H9
V	28	MET	ILE	conflict	UNP Q2Y0H9
V	36	TYR	PHE	conflict	UNP Q2Y0H9
V	64	ARG	LYS	conflict	UNP Q2Y0H9
V	153	GLU	-	insertion	UNP Q2Y0H9
V	154	PHE	-	insertion	UNP Q2Y0H9
V	160	GLY	-	insertion	UNP Q2Y0H9
V	161	PRO	-	insertion	UNP Q2Y0H9
V	162	VAL	-	insertion	UNP Q2Y0H9
V	163	ASN	-	insertion	UNP Q2Y0H9
V	164	ASP	-	insertion	UNP Q2Y0H9
V	314	ALA	-	insertion	UNP Q2Y0H9
V	315	ARG	-	insertion	UNP Q2Y0H9
V	330	VAL	-	insertion	UNP Q2Y0H9
V	331	ASP	-	insertion	UNP Q2Y0H9
V	344	LEU	-	insertion	UNP Q2Y0H9
V	345	GLU	-	insertion	UNP Q2Y0H9
V	357	SER	-	insertion	UNP Q2Y0H9
V	358	ARG	-	insertion	UNP Q2Y0H9
V	418	VAL	ALA	conflict	UNP Q2Y0H9
V	442	SER	ASN	conflict	UNP Q2Y0H9
W	2	MET	ARG	conflict	UNP Q2Y0H9
W	?	-	VAL	deletion	UNP Q2Y0H9
W	?	-	LEU	deletion	UNP Q2Y0H9
W	?	-	GLY	deletion	UNP Q2Y0H9
W	?	-	GLY	deletion	UNP Q2Y0H9
W	?	-	ALA	deletion	UNP Q2Y0H9
W	?	-	VAL	deletion	UNP Q2Y0H9
W	?	-	VAL	deletion	UNP Q2Y0H9
W	21	ALA	GLN	conflict	UNP Q2Y0H9
W	22	MET	-	insertion	UNP Q2Y0H9
W	23	ALA	-	insertion	UNP Q2Y0H9
W	24	ALA	-	insertion	UNP Q2Y0H9
W	27	ALA	MET	conflict	UNP Q2Y0H9
W	28	MET	ILE	conflict	UNP Q2Y0H9
W	36	TYR	PHE	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
W	64	ARG	LYS	conflict	UNP Q2Y0H9
W	153	GLU	-	insertion	UNP Q2Y0H9
W	154	PHE	-	insertion	UNP Q2Y0H9
W	160	GLY	-	insertion	UNP Q2Y0H9
W	161	PRO	-	insertion	UNP Q2Y0H9
W	162	VAL	-	insertion	UNP Q2Y0H9
W	163	ASN	-	insertion	UNP Q2Y0H9
W	164	ASP	-	insertion	UNP Q2Y0H9
W	314	ALA	-	insertion	UNP Q2Y0H9
W	315	ARG	-	insertion	UNP Q2Y0H9
W	330	VAL	-	insertion	UNP Q2Y0H9
W	331	ASP	-	insertion	UNP Q2Y0H9
W	344	LEU	-	insertion	UNP Q2Y0H9
W	345	GLU	-	insertion	UNP Q2Y0H9
W	357	SER	-	insertion	UNP Q2Y0H9
W	358	ARG	-	insertion	UNP Q2Y0H9
W	418	VAL	ALA	conflict	UNP Q2Y0H9
W	442	SER	ASN	conflict	UNP Q2Y0H9
X	2	MET	ARG	conflict	UNP Q2Y0H9
X	?	-	VAL	deletion	UNP Q2Y0H9
X	?	-	LEU	deletion	UNP Q2Y0H9
X	?	-	GLY	deletion	UNP Q2Y0H9
X	?	-	GLY	deletion	UNP Q2Y0H9
X	?	-	ALA	deletion	UNP Q2Y0H9
X	?	-	VAL	deletion	UNP Q2Y0H9
X	?	-	VAL	deletion	UNP Q2Y0H9
X	21	ALA	GLN	conflict	UNP Q2Y0H9
X	22	MET	-	insertion	UNP Q2Y0H9
X	23	ALA	-	insertion	UNP Q2Y0H9
X	24	ALA	-	insertion	UNP Q2Y0H9
X	27	ALA	MET	conflict	UNP Q2Y0H9
X	28	MET	ILE	conflict	UNP Q2Y0H9
X	36	TYR	PHE	conflict	UNP Q2Y0H9
X	64	ARG	LYS	conflict	UNP Q2Y0H9
X	153	GLU	-	insertion	UNP Q2Y0H9
X	154	PHE	-	insertion	UNP Q2Y0H9
X	160	GLY	-	insertion	UNP Q2Y0H9
X	161	PRO	-	insertion	UNP Q2Y0H9
X	162	VAL	-	insertion	UNP Q2Y0H9
X	163	ASN	-	insertion	UNP Q2Y0H9
X	164	ASP	-	insertion	UNP Q2Y0H9
X	314	ALA	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
X	315	ARG	-	insertion	UNP Q2Y0H9
X	330	VAL	-	insertion	UNP Q2Y0H9
X	331	ASP	-	insertion	UNP Q2Y0H9
X	344	LEU	-	insertion	UNP Q2Y0H9
X	345	GLU	-	insertion	UNP Q2Y0H9
X	357	SER	-	insertion	UNP Q2Y0H9
X	358	ARG	-	insertion	UNP Q2Y0H9
X	418	VAL	ALA	conflict	UNP Q2Y0H9
X	442	SER	ASN	conflict	UNP Q2Y0H9
Y	2	MET	ARG	conflict	UNP Q2Y0H9
Y	?	-	VAL	deletion	UNP Q2Y0H9
Y	?	-	LEU	deletion	UNP Q2Y0H9
Y	?	-	GLY	deletion	UNP Q2Y0H9
Y	?	-	GLY	deletion	UNP Q2Y0H9
Y	?	-	ALA	deletion	UNP Q2Y0H9
Y	?	-	VAL	deletion	UNP Q2Y0H9
Y	?	-	VAL	deletion	UNP Q2Y0H9
Y	21	ALA	GLN	conflict	UNP Q2Y0H9
Y	22	MET	-	insertion	UNP Q2Y0H9
Y	23	ALA	-	insertion	UNP Q2Y0H9
Y	24	ALA	-	insertion	UNP Q2Y0H9
Y	27	ALA	MET	conflict	UNP Q2Y0H9
Y	28	MET	ILE	conflict	UNP Q2Y0H9
Y	36	TYR	PHE	conflict	UNP Q2Y0H9
Y	64	ARG	LYS	conflict	UNP Q2Y0H9
Y	153	GLU	-	insertion	UNP Q2Y0H9
Y	154	PHE	-	insertion	UNP Q2Y0H9
Y	160	GLY	-	insertion	UNP Q2Y0H9
Y	161	PRO	-	insertion	UNP Q2Y0H9
Y	162	VAL	-	insertion	UNP Q2Y0H9
Y	163	ASN	-	insertion	UNP Q2Y0H9
Y	164	ASP	-	insertion	UNP Q2Y0H9
Y	314	ALA	-	insertion	UNP Q2Y0H9
Y	315	ARG	-	insertion	UNP Q2Y0H9
Y	330	VAL	-	insertion	UNP Q2Y0H9
Y	331	ASP	-	insertion	UNP Q2Y0H9
Y	344	LEU	-	insertion	UNP Q2Y0H9
Y	345	GLU	-	insertion	UNP Q2Y0H9
Y	357	SER	-	insertion	UNP Q2Y0H9
Y	358	ARG	-	insertion	UNP Q2Y0H9
Y	418	VAL	ALA	conflict	UNP Q2Y0H9
Y	442	SER	ASN	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	2	MET	ARG	conflict	UNP Q2Y0H9
Z	?	-	VAL	deletion	UNP Q2Y0H9
Z	?	-	LEU	deletion	UNP Q2Y0H9
Z	?	-	GLY	deletion	UNP Q2Y0H9
Z	?	-	GLY	deletion	UNP Q2Y0H9
Z	?	-	ALA	deletion	UNP Q2Y0H9
Z	?	-	VAL	deletion	UNP Q2Y0H9
Z	?	-	VAL	deletion	UNP Q2Y0H9
Z	21	ALA	GLN	conflict	UNP Q2Y0H9
Z	22	MET	-	insertion	UNP Q2Y0H9
Z	23	ALA	-	insertion	UNP Q2Y0H9
Z	24	ALA	-	insertion	UNP Q2Y0H9
Z	27	ALA	MET	conflict	UNP Q2Y0H9
Z	28	MET	ILE	conflict	UNP Q2Y0H9
Z	36	TYR	PHE	conflict	UNP Q2Y0H9
Z	64	ARG	LYS	conflict	UNP Q2Y0H9
Z	153	GLU	-	insertion	UNP Q2Y0H9
Z	154	PHE	-	insertion	UNP Q2Y0H9
Z	160	GLY	-	insertion	UNP Q2Y0H9
Z	161	PRO	-	insertion	UNP Q2Y0H9
Z	162	VAL	-	insertion	UNP Q2Y0H9
Z	163	ASN	-	insertion	UNP Q2Y0H9
Z	164	ASP	-	insertion	UNP Q2Y0H9
Z	314	ALA	-	insertion	UNP Q2Y0H9
Z	315	ARG	-	insertion	UNP Q2Y0H9
Z	330	VAL	-	insertion	UNP Q2Y0H9
Z	331	ASP	-	insertion	UNP Q2Y0H9
Z	344	LEU	-	insertion	UNP Q2Y0H9
Z	345	GLU	-	insertion	UNP Q2Y0H9
Z	357	SER	-	insertion	UNP Q2Y0H9
Z	358	ARG	-	insertion	UNP Q2Y0H9
Z	418	VAL	ALA	conflict	UNP Q2Y0H9
Z	442	SER	ASN	conflict	UNP Q2Y0H9
AA	2	MET	ARG	conflict	UNP Q2Y0H9
AA	?	-	VAL	deletion	UNP Q2Y0H9
AA	?	-	LEU	deletion	UNP Q2Y0H9
AA	?	-	GLY	deletion	UNP Q2Y0H9
AA	?	-	GLY	deletion	UNP Q2Y0H9
AA	?	-	ALA	deletion	UNP Q2Y0H9
AA	?	-	VAL	deletion	UNP Q2Y0H9
AA	?	-	VAL	deletion	UNP Q2Y0H9
AA	21	ALA	GLN	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
AA	22	MET	-	insertion	UNP Q2Y0H9
AA	23	ALA	-	insertion	UNP Q2Y0H9
AA	24	ALA	-	insertion	UNP Q2Y0H9
AA	27	ALA	MET	conflict	UNP Q2Y0H9
AA	28	MET	ILE	conflict	UNP Q2Y0H9
AA	36	TYR	PHE	conflict	UNP Q2Y0H9
AA	64	ARG	LYS	conflict	UNP Q2Y0H9
AA	153	GLU	-	insertion	UNP Q2Y0H9
AA	154	PHE	-	insertion	UNP Q2Y0H9
AA	160	GLY	-	insertion	UNP Q2Y0H9
AA	161	PRO	-	insertion	UNP Q2Y0H9
AA	162	VAL	-	insertion	UNP Q2Y0H9
AA	163	ASN	-	insertion	UNP Q2Y0H9
AA	164	ASP	-	insertion	UNP Q2Y0H9
AA	314	ALA	-	insertion	UNP Q2Y0H9
AA	315	ARG	-	insertion	UNP Q2Y0H9
AA	330	VAL	-	insertion	UNP Q2Y0H9
AA	331	ASP	-	insertion	UNP Q2Y0H9
AA	344	LEU	-	insertion	UNP Q2Y0H9
AA	345	GLU	-	insertion	UNP Q2Y0H9
AA	357	SER	-	insertion	UNP Q2Y0H9
AA	358	ARG	-	insertion	UNP Q2Y0H9
AA	418	VAL	ALA	conflict	UNP Q2Y0H9
AA	442	SER	ASN	conflict	UNP Q2Y0H9
BA	2	MET	ARG	conflict	UNP Q2Y0H9
BA	?	-	VAL	deletion	UNP Q2Y0H9
BA	?	-	LEU	deletion	UNP Q2Y0H9
BA	?	-	GLY	deletion	UNP Q2Y0H9
BA	?	-	GLY	deletion	UNP Q2Y0H9
BA	?	-	ALA	deletion	UNP Q2Y0H9
BA	?	-	VAL	deletion	UNP Q2Y0H9
BA	?	-	VAL	deletion	UNP Q2Y0H9
BA	21	ALA	GLN	conflict	UNP Q2Y0H9
BA	22	MET	-	insertion	UNP Q2Y0H9
BA	23	ALA	-	insertion	UNP Q2Y0H9
BA	24	ALA	-	insertion	UNP Q2Y0H9
BA	27	ALA	MET	conflict	UNP Q2Y0H9
BA	28	MET	ILE	conflict	UNP Q2Y0H9
BA	36	TYR	PHE	conflict	UNP Q2Y0H9
BA	64	ARG	LYS	conflict	UNP Q2Y0H9
BA	153	GLU	-	insertion	UNP Q2Y0H9
BA	154	PHE	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
BA	160	GLY	-	insertion	UNP Q2Y0H9
BA	161	PRO	-	insertion	UNP Q2Y0H9
BA	162	VAL	-	insertion	UNP Q2Y0H9
BA	163	ASN	-	insertion	UNP Q2Y0H9
BA	164	ASP	-	insertion	UNP Q2Y0H9
BA	314	ALA	-	insertion	UNP Q2Y0H9
BA	315	ARG	-	insertion	UNP Q2Y0H9
BA	330	VAL	-	insertion	UNP Q2Y0H9
BA	331	ASP	-	insertion	UNP Q2Y0H9
BA	344	LEU	-	insertion	UNP Q2Y0H9
BA	345	GLU	-	insertion	UNP Q2Y0H9
BA	357	SER	-	insertion	UNP Q2Y0H9
BA	358	ARG	-	insertion	UNP Q2Y0H9
BA	418	VAL	ALA	conflict	UNP Q2Y0H9
BA	442	SER	ASN	conflict	UNP Q2Y0H9
CA	2	MET	ARG	conflict	UNP Q2Y0H9
CA	?	-	VAL	deletion	UNP Q2Y0H9
CA	?	-	LEU	deletion	UNP Q2Y0H9
CA	?	-	GLY	deletion	UNP Q2Y0H9
CA	?	-	GLY	deletion	UNP Q2Y0H9
CA	?	-	ALA	deletion	UNP Q2Y0H9
CA	?	-	VAL	deletion	UNP Q2Y0H9
CA	?	-	VAL	deletion	UNP Q2Y0H9
CA	21	ALA	GLN	conflict	UNP Q2Y0H9
CA	22	MET	-	insertion	UNP Q2Y0H9
CA	23	ALA	-	insertion	UNP Q2Y0H9
CA	24	ALA	-	insertion	UNP Q2Y0H9
CA	27	ALA	MET	conflict	UNP Q2Y0H9
CA	28	MET	ILE	conflict	UNP Q2Y0H9
CA	36	TYR	PHE	conflict	UNP Q2Y0H9
CA	64	ARG	LYS	conflict	UNP Q2Y0H9
CA	153	GLU	-	insertion	UNP Q2Y0H9
CA	154	PHE	-	insertion	UNP Q2Y0H9
CA	160	GLY	-	insertion	UNP Q2Y0H9
CA	161	PRO	-	insertion	UNP Q2Y0H9
CA	162	VAL	-	insertion	UNP Q2Y0H9
CA	163	ASN	-	insertion	UNP Q2Y0H9
CA	164	ASP	-	insertion	UNP Q2Y0H9
CA	314	ALA	-	insertion	UNP Q2Y0H9
CA	315	ARG	-	insertion	UNP Q2Y0H9
CA	330	VAL	-	insertion	UNP Q2Y0H9
CA	331	ASP	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
CA	344	LEU	-	insertion	UNP Q2Y0H9
CA	345	GLU	-	insertion	UNP Q2Y0H9
CA	357	SER	-	insertion	UNP Q2Y0H9
CA	358	ARG	-	insertion	UNP Q2Y0H9
CA	418	VAL	ALA	conflict	UNP Q2Y0H9
CA	442	SER	ASN	conflict	UNP Q2Y0H9
DA	2	MET	ARG	conflict	UNP Q2Y0H9
DA	?	-	VAL	deletion	UNP Q2Y0H9
DA	?	-	LEU	deletion	UNP Q2Y0H9
DA	?	-	GLY	deletion	UNP Q2Y0H9
DA	?	-	GLY	deletion	UNP Q2Y0H9
DA	?	-	ALA	deletion	UNP Q2Y0H9
DA	?	-	VAL	deletion	UNP Q2Y0H9
DA	?	-	VAL	deletion	UNP Q2Y0H9
DA	21	ALA	GLN	conflict	UNP Q2Y0H9
DA	22	MET	-	insertion	UNP Q2Y0H9
DA	23	ALA	-	insertion	UNP Q2Y0H9
DA	24	ALA	-	insertion	UNP Q2Y0H9
DA	27	ALA	MET	conflict	UNP Q2Y0H9
DA	28	MET	ILE	conflict	UNP Q2Y0H9
DA	36	TYR	PHE	conflict	UNP Q2Y0H9
DA	64	ARG	LYS	conflict	UNP Q2Y0H9
DA	153	GLU	-	insertion	UNP Q2Y0H9
DA	154	PHE	-	insertion	UNP Q2Y0H9
DA	160	GLY	-	insertion	UNP Q2Y0H9
DA	161	PRO	-	insertion	UNP Q2Y0H9
DA	162	VAL	-	insertion	UNP Q2Y0H9
DA	163	ASN	-	insertion	UNP Q2Y0H9
DA	164	ASP	-	insertion	UNP Q2Y0H9
DA	314	ALA	-	insertion	UNP Q2Y0H9
DA	315	ARG	-	insertion	UNP Q2Y0H9
DA	330	VAL	-	insertion	UNP Q2Y0H9
DA	331	ASP	-	insertion	UNP Q2Y0H9
DA	344	LEU	-	insertion	UNP Q2Y0H9
DA	345	GLU	-	insertion	UNP Q2Y0H9
DA	357	SER	-	insertion	UNP Q2Y0H9
DA	358	ARG	-	insertion	UNP Q2Y0H9
DA	418	VAL	ALA	conflict	UNP Q2Y0H9
DA	442	SER	ASN	conflict	UNP Q2Y0H9
EA	2	MET	ARG	conflict	UNP Q2Y0H9
EA	?	-	VAL	deletion	UNP Q2Y0H9
EA	?	-	LEU	deletion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
EA	?	-	GLY	deletion	UNP Q2Y0H9
EA	?	-	GLY	deletion	UNP Q2Y0H9
EA	?	-	ALA	deletion	UNP Q2Y0H9
EA	?	-	VAL	deletion	UNP Q2Y0H9
EA	?	-	VAL	deletion	UNP Q2Y0H9
EA	21	ALA	GLN	conflict	UNP Q2Y0H9
EA	22	MET	-	insertion	UNP Q2Y0H9
EA	23	ALA	-	insertion	UNP Q2Y0H9
EA	24	ALA	-	insertion	UNP Q2Y0H9
EA	27	ALA	MET	conflict	UNP Q2Y0H9
EA	28	MET	ILE	conflict	UNP Q2Y0H9
EA	36	TYR	PHE	conflict	UNP Q2Y0H9
EA	64	ARG	LYS	conflict	UNP Q2Y0H9
EA	153	GLU	-	insertion	UNP Q2Y0H9
EA	154	PHE	-	insertion	UNP Q2Y0H9
EA	160	GLY	-	insertion	UNP Q2Y0H9
EA	161	PRO	-	insertion	UNP Q2Y0H9
EA	162	VAL	-	insertion	UNP Q2Y0H9
EA	163	ASN	-	insertion	UNP Q2Y0H9
EA	164	ASP	-	insertion	UNP Q2Y0H9
EA	314	ALA	-	insertion	UNP Q2Y0H9
EA	315	ARG	-	insertion	UNP Q2Y0H9
EA	330	VAL	-	insertion	UNP Q2Y0H9
EA	331	ASP	-	insertion	UNP Q2Y0H9
EA	344	LEU	-	insertion	UNP Q2Y0H9
EA	345	GLU	-	insertion	UNP Q2Y0H9
EA	357	SER	-	insertion	UNP Q2Y0H9
EA	358	ARG	-	insertion	UNP Q2Y0H9
EA	418	VAL	ALA	conflict	UNP Q2Y0H9
EA	442	SER	ASN	conflict	UNP Q2Y0H9
FA	2	MET	ARG	conflict	UNP Q2Y0H9
FA	?	-	VAL	deletion	UNP Q2Y0H9
FA	?	-	LEU	deletion	UNP Q2Y0H9
FA	?	-	GLY	deletion	UNP Q2Y0H9
FA	?	-	GLY	deletion	UNP Q2Y0H9
FA	?	-	ALA	deletion	UNP Q2Y0H9
FA	?	-	VAL	deletion	UNP Q2Y0H9
FA	?	-	VAL	deletion	UNP Q2Y0H9
FA	21	ALA	GLN	conflict	UNP Q2Y0H9
FA	22	MET	-	insertion	UNP Q2Y0H9
FA	23	ALA	-	insertion	UNP Q2Y0H9
FA	24	ALA	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
FA	27	ALA	MET	conflict	UNP Q2Y0H9
FA	28	MET	ILE	conflict	UNP Q2Y0H9
FA	36	TYR	PHE	conflict	UNP Q2Y0H9
FA	64	ARG	LYS	conflict	UNP Q2Y0H9
FA	153	GLU	-	insertion	UNP Q2Y0H9
FA	154	PHE	-	insertion	UNP Q2Y0H9
FA	160	GLY	-	insertion	UNP Q2Y0H9
FA	161	PRO	-	insertion	UNP Q2Y0H9
FA	162	VAL	-	insertion	UNP Q2Y0H9
FA	163	ASN	-	insertion	UNP Q2Y0H9
FA	164	ASP	-	insertion	UNP Q2Y0H9
FA	314	ALA	-	insertion	UNP Q2Y0H9
FA	315	ARG	-	insertion	UNP Q2Y0H9
FA	330	VAL	-	insertion	UNP Q2Y0H9
FA	331	ASP	-	insertion	UNP Q2Y0H9
FA	344	LEU	-	insertion	UNP Q2Y0H9
FA	345	GLU	-	insertion	UNP Q2Y0H9
FA	357	SER	-	insertion	UNP Q2Y0H9
FA	358	ARG	-	insertion	UNP Q2Y0H9
FA	418	VAL	ALA	conflict	UNP Q2Y0H9
FA	442	SER	ASN	conflict	UNP Q2Y0H9
GA	2	MET	ARG	conflict	UNP Q2Y0H9
GA	?	-	VAL	deletion	UNP Q2Y0H9
GA	?	-	LEU	deletion	UNP Q2Y0H9
GA	?	-	GLY	deletion	UNP Q2Y0H9
GA	?	-	GLY	deletion	UNP Q2Y0H9
GA	?	-	ALA	deletion	UNP Q2Y0H9
GA	?	-	VAL	deletion	UNP Q2Y0H9
GA	?	-	VAL	deletion	UNP Q2Y0H9
GA	21	ALA	GLN	conflict	UNP Q2Y0H9
GA	22	MET	-	insertion	UNP Q2Y0H9
GA	23	ALA	-	insertion	UNP Q2Y0H9
GA	24	ALA	-	insertion	UNP Q2Y0H9
GA	27	ALA	MET	conflict	UNP Q2Y0H9
GA	28	MET	ILE	conflict	UNP Q2Y0H9
GA	36	TYR	PHE	conflict	UNP Q2Y0H9
GA	64	ARG	LYS	conflict	UNP Q2Y0H9
GA	153	GLU	-	insertion	UNP Q2Y0H9
GA	154	PHE	-	insertion	UNP Q2Y0H9
GA	160	GLY	-	insertion	UNP Q2Y0H9
GA	161	PRO	-	insertion	UNP Q2Y0H9
GA	162	VAL	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
GA	163	ASN	-	insertion	UNP Q2Y0H9
GA	164	ASP	-	insertion	UNP Q2Y0H9
GA	314	ALA	-	insertion	UNP Q2Y0H9
GA	315	ARG	-	insertion	UNP Q2Y0H9
GA	330	VAL	-	insertion	UNP Q2Y0H9
GA	331	ASP	-	insertion	UNP Q2Y0H9
GA	344	LEU	-	insertion	UNP Q2Y0H9
GA	345	GLU	-	insertion	UNP Q2Y0H9
GA	357	SER	-	insertion	UNP Q2Y0H9
GA	358	ARG	-	insertion	UNP Q2Y0H9
GA	418	VAL	ALA	conflict	UNP Q2Y0H9
GA	442	SER	ASN	conflict	UNP Q2Y0H9
HA	2	MET	ARG	conflict	UNP Q2Y0H9
HA	?	-	VAL	deletion	UNP Q2Y0H9
HA	?	-	LEU	deletion	UNP Q2Y0H9
HA	?	-	GLY	deletion	UNP Q2Y0H9
HA	?	-	GLY	deletion	UNP Q2Y0H9
HA	?	-	ALA	deletion	UNP Q2Y0H9
HA	?	-	VAL	deletion	UNP Q2Y0H9
HA	?	-	VAL	deletion	UNP Q2Y0H9
HA	21	ALA	GLN	conflict	UNP Q2Y0H9
HA	22	MET	-	insertion	UNP Q2Y0H9
HA	23	ALA	-	insertion	UNP Q2Y0H9
HA	24	ALA	-	insertion	UNP Q2Y0H9
HA	27	ALA	MET	conflict	UNP Q2Y0H9
HA	28	MET	ILE	conflict	UNP Q2Y0H9
HA	36	TYR	PHE	conflict	UNP Q2Y0H9
HA	64	ARG	LYS	conflict	UNP Q2Y0H9
HA	153	GLU	-	insertion	UNP Q2Y0H9
HA	154	PHE	-	insertion	UNP Q2Y0H9
HA	160	GLY	-	insertion	UNP Q2Y0H9
HA	161	PRO	-	insertion	UNP Q2Y0H9
HA	162	VAL	-	insertion	UNP Q2Y0H9
HA	163	ASN	-	insertion	UNP Q2Y0H9
HA	164	ASP	-	insertion	UNP Q2Y0H9
HA	314	ALA	-	insertion	UNP Q2Y0H9
HA	315	ARG	-	insertion	UNP Q2Y0H9
HA	330	VAL	-	insertion	UNP Q2Y0H9
HA	331	ASP	-	insertion	UNP Q2Y0H9
HA	344	LEU	-	insertion	UNP Q2Y0H9
HA	345	GLU	-	insertion	UNP Q2Y0H9
HA	357	SER	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
HA	358	ARG	-	insertion	UNP Q2Y0H9
HA	418	VAL	ALA	conflict	UNP Q2Y0H9
HA	442	SER	ASN	conflict	UNP Q2Y0H9
IA	2	MET	ARG	conflict	UNP Q2Y0H9
IA	?	-	VAL	deletion	UNP Q2Y0H9
IA	?	-	LEU	deletion	UNP Q2Y0H9
IA	?	-	GLY	deletion	UNP Q2Y0H9
IA	?	-	GLY	deletion	UNP Q2Y0H9
IA	?	-	ALA	deletion	UNP Q2Y0H9
IA	?	-	VAL	deletion	UNP Q2Y0H9
IA	?	-	VAL	deletion	UNP Q2Y0H9
IA	21	ALA	GLN	conflict	UNP Q2Y0H9
IA	22	MET	-	insertion	UNP Q2Y0H9
IA	23	ALA	-	insertion	UNP Q2Y0H9
IA	24	ALA	-	insertion	UNP Q2Y0H9
IA	27	ALA	MET	conflict	UNP Q2Y0H9
IA	28	MET	ILE	conflict	UNP Q2Y0H9
IA	36	TYR	PHE	conflict	UNP Q2Y0H9
IA	64	ARG	LYS	conflict	UNP Q2Y0H9
IA	153	GLU	-	insertion	UNP Q2Y0H9
IA	154	PHE	-	insertion	UNP Q2Y0H9
IA	160	GLY	-	insertion	UNP Q2Y0H9
IA	161	PRO	-	insertion	UNP Q2Y0H9
IA	162	VAL	-	insertion	UNP Q2Y0H9
IA	163	ASN	-	insertion	UNP Q2Y0H9
IA	164	ASP	-	insertion	UNP Q2Y0H9
IA	314	ALA	-	insertion	UNP Q2Y0H9
IA	315	ARG	-	insertion	UNP Q2Y0H9
IA	330	VAL	-	insertion	UNP Q2Y0H9
IA	331	ASP	-	insertion	UNP Q2Y0H9
IA	344	LEU	-	insertion	UNP Q2Y0H9
IA	345	GLU	-	insertion	UNP Q2Y0H9
IA	357	SER	-	insertion	UNP Q2Y0H9
IA	358	ARG	-	insertion	UNP Q2Y0H9
IA	418	VAL	ALA	conflict	UNP Q2Y0H9
IA	442	SER	ASN	conflict	UNP Q2Y0H9
JA	2	MET	ARG	conflict	UNP Q2Y0H9
JA	?	-	VAL	deletion	UNP Q2Y0H9
JA	?	-	LEU	deletion	UNP Q2Y0H9
JA	?	-	GLY	deletion	UNP Q2Y0H9
JA	?	-	GLY	deletion	UNP Q2Y0H9
JA	?	-	ALA	deletion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
JA	?	-	VAL	deletion	UNP Q2Y0H9
JA	?	-	VAL	deletion	UNP Q2Y0H9
JA	21	ALA	GLN	conflict	UNP Q2Y0H9
JA	22	MET	-	insertion	UNP Q2Y0H9
JA	23	ALA	-	insertion	UNP Q2Y0H9
JA	24	ALA	-	insertion	UNP Q2Y0H9
JA	27	ALA	MET	conflict	UNP Q2Y0H9
JA	28	MET	ILE	conflict	UNP Q2Y0H9
JA	36	TYR	PHE	conflict	UNP Q2Y0H9
JA	64	ARG	LYS	conflict	UNP Q2Y0H9
JA	153	GLU	-	insertion	UNP Q2Y0H9
JA	154	PHE	-	insertion	UNP Q2Y0H9
JA	160	GLY	-	insertion	UNP Q2Y0H9
JA	161	PRO	-	insertion	UNP Q2Y0H9
JA	162	VAL	-	insertion	UNP Q2Y0H9
JA	163	ASN	-	insertion	UNP Q2Y0H9
JA	164	ASP	-	insertion	UNP Q2Y0H9
JA	314	ALA	-	insertion	UNP Q2Y0H9
JA	315	ARG	-	insertion	UNP Q2Y0H9
JA	330	VAL	-	insertion	UNP Q2Y0H9
JA	331	ASP	-	insertion	UNP Q2Y0H9
JA	344	LEU	-	insertion	UNP Q2Y0H9
JA	345	GLU	-	insertion	UNP Q2Y0H9
JA	357	SER	-	insertion	UNP Q2Y0H9
JA	358	ARG	-	insertion	UNP Q2Y0H9
JA	418	VAL	ALA	conflict	UNP Q2Y0H9
JA	442	SER	ASN	conflict	UNP Q2Y0H9
KA	2	MET	ARG	conflict	UNP Q2Y0H9
KA	?	-	VAL	deletion	UNP Q2Y0H9
KA	?	-	LEU	deletion	UNP Q2Y0H9
KA	?	-	GLY	deletion	UNP Q2Y0H9
KA	?	-	GLY	deletion	UNP Q2Y0H9
KA	?	-	ALA	deletion	UNP Q2Y0H9
KA	?	-	VAL	deletion	UNP Q2Y0H9
KA	?	-	VAL	deletion	UNP Q2Y0H9
KA	21	ALA	GLN	conflict	UNP Q2Y0H9
KA	22	MET	-	insertion	UNP Q2Y0H9
KA	23	ALA	-	insertion	UNP Q2Y0H9
KA	24	ALA	-	insertion	UNP Q2Y0H9
KA	27	ALA	MET	conflict	UNP Q2Y0H9
KA	28	MET	ILE	conflict	UNP Q2Y0H9
KA	36	TYR	PHE	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
KA	64	ARG	LYS	conflict	UNP Q2Y0H9
KA	153	GLU	-	insertion	UNP Q2Y0H9
KA	154	PHE	-	insertion	UNP Q2Y0H9
KA	160	GLY	-	insertion	UNP Q2Y0H9
KA	161	PRO	-	insertion	UNP Q2Y0H9
KA	162	VAL	-	insertion	UNP Q2Y0H9
KA	163	ASN	-	insertion	UNP Q2Y0H9
KA	164	ASP	-	insertion	UNP Q2Y0H9
KA	314	ALA	-	insertion	UNP Q2Y0H9
KA	315	ARG	-	insertion	UNP Q2Y0H9
KA	330	VAL	-	insertion	UNP Q2Y0H9
KA	331	ASP	-	insertion	UNP Q2Y0H9
KA	344	LEU	-	insertion	UNP Q2Y0H9
KA	345	GLU	-	insertion	UNP Q2Y0H9
KA	357	SER	-	insertion	UNP Q2Y0H9
KA	358	ARG	-	insertion	UNP Q2Y0H9
KA	418	VAL	ALA	conflict	UNP Q2Y0H9
KA	442	SER	ASN	conflict	UNP Q2Y0H9
LA	2	MET	ARG	conflict	UNP Q2Y0H9
LA	?	-	VAL	deletion	UNP Q2Y0H9
LA	?	-	LEU	deletion	UNP Q2Y0H9
LA	?	-	GLY	deletion	UNP Q2Y0H9
LA	?	-	GLY	deletion	UNP Q2Y0H9
LA	?	-	ALA	deletion	UNP Q2Y0H9
LA	?	-	VAL	deletion	UNP Q2Y0H9
LA	?	-	VAL	deletion	UNP Q2Y0H9
LA	21	ALA	GLN	conflict	UNP Q2Y0H9
LA	22	MET	-	insertion	UNP Q2Y0H9
LA	23	ALA	-	insertion	UNP Q2Y0H9
LA	24	ALA	-	insertion	UNP Q2Y0H9
LA	27	ALA	MET	conflict	UNP Q2Y0H9
LA	28	MET	ILE	conflict	UNP Q2Y0H9
LA	36	TYR	PHE	conflict	UNP Q2Y0H9
LA	64	ARG	LYS	conflict	UNP Q2Y0H9
LA	153	GLU	-	insertion	UNP Q2Y0H9
LA	154	PHE	-	insertion	UNP Q2Y0H9
LA	160	GLY	-	insertion	UNP Q2Y0H9
LA	161	PRO	-	insertion	UNP Q2Y0H9
LA	162	VAL	-	insertion	UNP Q2Y0H9
LA	163	ASN	-	insertion	UNP Q2Y0H9
LA	164	ASP	-	insertion	UNP Q2Y0H9
LA	314	ALA	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
LA	315	ARG	-	insertion	UNP Q2Y0H9
LA	330	VAL	-	insertion	UNP Q2Y0H9
LA	331	ASP	-	insertion	UNP Q2Y0H9
LA	344	LEU	-	insertion	UNP Q2Y0H9
LA	345	GLU	-	insertion	UNP Q2Y0H9
LA	357	SER	-	insertion	UNP Q2Y0H9
LA	358	ARG	-	insertion	UNP Q2Y0H9
LA	418	VAL	ALA	conflict	UNP Q2Y0H9
LA	442	SER	ASN	conflict	UNP Q2Y0H9
MA	2	MET	ARG	conflict	UNP Q2Y0H9
MA	?	-	VAL	deletion	UNP Q2Y0H9
MA	?	-	LEU	deletion	UNP Q2Y0H9
MA	?	-	GLY	deletion	UNP Q2Y0H9
MA	?	-	GLY	deletion	UNP Q2Y0H9
MA	?	-	ALA	deletion	UNP Q2Y0H9
MA	?	-	VAL	deletion	UNP Q2Y0H9
MA	?	-	VAL	deletion	UNP Q2Y0H9
MA	21	ALA	GLN	conflict	UNP Q2Y0H9
MA	22	MET	-	insertion	UNP Q2Y0H9
MA	23	ALA	-	insertion	UNP Q2Y0H9
MA	24	ALA	-	insertion	UNP Q2Y0H9
MA	27	ALA	MET	conflict	UNP Q2Y0H9
MA	28	MET	ILE	conflict	UNP Q2Y0H9
MA	36	TYR	PHE	conflict	UNP Q2Y0H9
MA	64	ARG	LYS	conflict	UNP Q2Y0H9
MA	153	GLU	-	insertion	UNP Q2Y0H9
MA	154	PHE	-	insertion	UNP Q2Y0H9
MA	160	GLY	-	insertion	UNP Q2Y0H9
MA	161	PRO	-	insertion	UNP Q2Y0H9
MA	162	VAL	-	insertion	UNP Q2Y0H9
MA	163	ASN	-	insertion	UNP Q2Y0H9
MA	164	ASP	-	insertion	UNP Q2Y0H9
MA	314	ALA	-	insertion	UNP Q2Y0H9
MA	315	ARG	-	insertion	UNP Q2Y0H9
MA	330	VAL	-	insertion	UNP Q2Y0H9
MA	331	ASP	-	insertion	UNP Q2Y0H9
MA	344	LEU	-	insertion	UNP Q2Y0H9
MA	345	GLU	-	insertion	UNP Q2Y0H9
MA	357	SER	-	insertion	UNP Q2Y0H9
MA	358	ARG	-	insertion	UNP Q2Y0H9
MA	418	VAL	ALA	conflict	UNP Q2Y0H9
MA	442	SER	ASN	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
NA	2	MET	ARG	conflict	UNP Q2Y0H9
NA	?	-	VAL	deletion	UNP Q2Y0H9
NA	?	-	LEU	deletion	UNP Q2Y0H9
NA	?	-	GLY	deletion	UNP Q2Y0H9
NA	?	-	GLY	deletion	UNP Q2Y0H9
NA	?	-	ALA	deletion	UNP Q2Y0H9
NA	?	-	VAL	deletion	UNP Q2Y0H9
NA	?	-	VAL	deletion	UNP Q2Y0H9
NA	21	ALA	GLN	conflict	UNP Q2Y0H9
NA	22	MET	-	insertion	UNP Q2Y0H9
NA	23	ALA	-	insertion	UNP Q2Y0H9
NA	24	ALA	-	insertion	UNP Q2Y0H9
NA	27	ALA	MET	conflict	UNP Q2Y0H9
NA	28	MET	ILE	conflict	UNP Q2Y0H9
NA	36	TYR	PHE	conflict	UNP Q2Y0H9
NA	64	ARG	LYS	conflict	UNP Q2Y0H9
NA	153	GLU	-	insertion	UNP Q2Y0H9
NA	154	PHE	-	insertion	UNP Q2Y0H9
NA	160	GLY	-	insertion	UNP Q2Y0H9
NA	161	PRO	-	insertion	UNP Q2Y0H9
NA	162	VAL	-	insertion	UNP Q2Y0H9
NA	163	ASN	-	insertion	UNP Q2Y0H9
NA	164	ASP	-	insertion	UNP Q2Y0H9
NA	314	ALA	-	insertion	UNP Q2Y0H9
NA	315	ARG	-	insertion	UNP Q2Y0H9
NA	330	VAL	-	insertion	UNP Q2Y0H9
NA	331	ASP	-	insertion	UNP Q2Y0H9
NA	344	LEU	-	insertion	UNP Q2Y0H9
NA	345	GLU	-	insertion	UNP Q2Y0H9
NA	357	SER	-	insertion	UNP Q2Y0H9
NA	358	ARG	-	insertion	UNP Q2Y0H9
NA	418	VAL	ALA	conflict	UNP Q2Y0H9
NA	442	SER	ASN	conflict	UNP Q2Y0H9
OA	2	MET	ARG	conflict	UNP Q2Y0H9
OA	?	-	VAL	deletion	UNP Q2Y0H9
OA	?	-	LEU	deletion	UNP Q2Y0H9
OA	?	-	GLY	deletion	UNP Q2Y0H9
OA	?	-	GLY	deletion	UNP Q2Y0H9
OA	?	-	ALA	deletion	UNP Q2Y0H9
OA	?	-	VAL	deletion	UNP Q2Y0H9
OA	?	-	VAL	deletion	UNP Q2Y0H9
OA	21	ALA	GLN	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
OA	22	MET	-	insertion	UNP Q2Y0H9
OA	23	ALA	-	insertion	UNP Q2Y0H9
OA	24	ALA	-	insertion	UNP Q2Y0H9
OA	27	ALA	MET	conflict	UNP Q2Y0H9
OA	28	MET	ILE	conflict	UNP Q2Y0H9
OA	36	TYR	PHE	conflict	UNP Q2Y0H9
OA	64	ARG	LYS	conflict	UNP Q2Y0H9
OA	153	GLU	-	insertion	UNP Q2Y0H9
OA	154	PHE	-	insertion	UNP Q2Y0H9
OA	160	GLY	-	insertion	UNP Q2Y0H9
OA	161	PRO	-	insertion	UNP Q2Y0H9
OA	162	VAL	-	insertion	UNP Q2Y0H9
OA	163	ASN	-	insertion	UNP Q2Y0H9
OA	164	ASP	-	insertion	UNP Q2Y0H9
OA	314	ALA	-	insertion	UNP Q2Y0H9
OA	315	ARG	-	insertion	UNP Q2Y0H9
OA	330	VAL	-	insertion	UNP Q2Y0H9
OA	331	ASP	-	insertion	UNP Q2Y0H9
OA	344	LEU	-	insertion	UNP Q2Y0H9
OA	345	GLU	-	insertion	UNP Q2Y0H9
OA	357	SER	-	insertion	UNP Q2Y0H9
OA	358	ARG	-	insertion	UNP Q2Y0H9
OA	418	VAL	ALA	conflict	UNP Q2Y0H9
OA	442	SER	ASN	conflict	UNP Q2Y0H9
PA	2	MET	ARG	conflict	UNP Q2Y0H9
PA	?	-	VAL	deletion	UNP Q2Y0H9
PA	?	-	LEU	deletion	UNP Q2Y0H9
PA	?	-	GLY	deletion	UNP Q2Y0H9
PA	?	-	GLY	deletion	UNP Q2Y0H9
PA	?	-	ALA	deletion	UNP Q2Y0H9
PA	?	-	VAL	deletion	UNP Q2Y0H9
PA	?	-	VAL	deletion	UNP Q2Y0H9
PA	21	ALA	GLN	conflict	UNP Q2Y0H9
PA	22	MET	-	insertion	UNP Q2Y0H9
PA	23	ALA	-	insertion	UNP Q2Y0H9
PA	24	ALA	-	insertion	UNP Q2Y0H9
PA	27	ALA	MET	conflict	UNP Q2Y0H9
PA	28	MET	ILE	conflict	UNP Q2Y0H9
PA	36	TYR	PHE	conflict	UNP Q2Y0H9
PA	64	ARG	LYS	conflict	UNP Q2Y0H9
PA	153	GLU	-	insertion	UNP Q2Y0H9
PA	154	PHE	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
PA	160	GLY	-	insertion	UNP Q2Y0H9
PA	161	PRO	-	insertion	UNP Q2Y0H9
PA	162	VAL	-	insertion	UNP Q2Y0H9
PA	163	ASN	-	insertion	UNP Q2Y0H9
PA	164	ASP	-	insertion	UNP Q2Y0H9
PA	314	ALA	-	insertion	UNP Q2Y0H9
PA	315	ARG	-	insertion	UNP Q2Y0H9
PA	330	VAL	-	insertion	UNP Q2Y0H9
PA	331	ASP	-	insertion	UNP Q2Y0H9
PA	344	LEU	-	insertion	UNP Q2Y0H9
PA	345	GLU	-	insertion	UNP Q2Y0H9
PA	357	SER	-	insertion	UNP Q2Y0H9
PA	358	ARG	-	insertion	UNP Q2Y0H9
PA	418	VAL	ALA	conflict	UNP Q2Y0H9
PA	442	SER	ASN	conflict	UNP Q2Y0H9
QA	2	MET	ARG	conflict	UNP Q2Y0H9
QA	?	-	VAL	deletion	UNP Q2Y0H9
QA	?	-	LEU	deletion	UNP Q2Y0H9
QA	?	-	GLY	deletion	UNP Q2Y0H9
QA	?	-	GLY	deletion	UNP Q2Y0H9
QA	?	-	ALA	deletion	UNP Q2Y0H9
QA	?	-	VAL	deletion	UNP Q2Y0H9
QA	?	-	VAL	deletion	UNP Q2Y0H9
QA	21	ALA	GLN	conflict	UNP Q2Y0H9
QA	22	MET	-	insertion	UNP Q2Y0H9
QA	23	ALA	-	insertion	UNP Q2Y0H9
QA	24	ALA	-	insertion	UNP Q2Y0H9
QA	27	ALA	MET	conflict	UNP Q2Y0H9
QA	28	MET	ILE	conflict	UNP Q2Y0H9
QA	36	TYR	PHE	conflict	UNP Q2Y0H9
QA	64	ARG	LYS	conflict	UNP Q2Y0H9
QA	153	GLU	-	insertion	UNP Q2Y0H9
QA	154	PHE	-	insertion	UNP Q2Y0H9
QA	160	GLY	-	insertion	UNP Q2Y0H9
QA	161	PRO	-	insertion	UNP Q2Y0H9
QA	162	VAL	-	insertion	UNP Q2Y0H9
QA	163	ASN	-	insertion	UNP Q2Y0H9
QA	164	ASP	-	insertion	UNP Q2Y0H9
QA	314	ALA	-	insertion	UNP Q2Y0H9
QA	315	ARG	-	insertion	UNP Q2Y0H9
QA	330	VAL	-	insertion	UNP Q2Y0H9
QA	331	ASP	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
QA	344	LEU	-	insertion	UNP Q2Y0H9
QA	345	GLU	-	insertion	UNP Q2Y0H9
QA	357	SER	-	insertion	UNP Q2Y0H9
QA	358	ARG	-	insertion	UNP Q2Y0H9
QA	418	VAL	ALA	conflict	UNP Q2Y0H9
QA	442	SER	ASN	conflict	UNP Q2Y0H9
RA	2	MET	ARG	conflict	UNP Q2Y0H9
RA	?	-	VAL	deletion	UNP Q2Y0H9
RA	?	-	LEU	deletion	UNP Q2Y0H9
RA	?	-	GLY	deletion	UNP Q2Y0H9
RA	?	-	GLY	deletion	UNP Q2Y0H9
RA	?	-	ALA	deletion	UNP Q2Y0H9
RA	?	-	VAL	deletion	UNP Q2Y0H9
RA	?	-	VAL	deletion	UNP Q2Y0H9
RA	21	ALA	GLN	conflict	UNP Q2Y0H9
RA	22	MET	-	insertion	UNP Q2Y0H9
RA	23	ALA	-	insertion	UNP Q2Y0H9
RA	24	ALA	-	insertion	UNP Q2Y0H9
RA	27	ALA	MET	conflict	UNP Q2Y0H9
RA	28	MET	ILE	conflict	UNP Q2Y0H9
RA	36	TYR	PHE	conflict	UNP Q2Y0H9
RA	64	ARG	LYS	conflict	UNP Q2Y0H9
RA	153	GLU	-	insertion	UNP Q2Y0H9
RA	154	PHE	-	insertion	UNP Q2Y0H9
RA	160	GLY	-	insertion	UNP Q2Y0H9
RA	161	PRO	-	insertion	UNP Q2Y0H9
RA	162	VAL	-	insertion	UNP Q2Y0H9
RA	163	ASN	-	insertion	UNP Q2Y0H9
RA	164	ASP	-	insertion	UNP Q2Y0H9
RA	314	ALA	-	insertion	UNP Q2Y0H9
RA	315	ARG	-	insertion	UNP Q2Y0H9
RA	330	VAL	-	insertion	UNP Q2Y0H9
RA	331	ASP	-	insertion	UNP Q2Y0H9
RA	344	LEU	-	insertion	UNP Q2Y0H9
RA	345	GLU	-	insertion	UNP Q2Y0H9
RA	357	SER	-	insertion	UNP Q2Y0H9
RA	358	ARG	-	insertion	UNP Q2Y0H9
RA	418	VAL	ALA	conflict	UNP Q2Y0H9
RA	442	SER	ASN	conflict	UNP Q2Y0H9
SA	2	MET	ARG	conflict	UNP Q2Y0H9
SA	?	-	VAL	deletion	UNP Q2Y0H9
SA	?	-	LEU	deletion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
SA	?	-	GLY	deletion	UNP Q2Y0H9
SA	?	-	GLY	deletion	UNP Q2Y0H9
SA	?	-	ALA	deletion	UNP Q2Y0H9
SA	?	-	VAL	deletion	UNP Q2Y0H9
SA	?	-	VAL	deletion	UNP Q2Y0H9
SA	21	ALA	GLN	conflict	UNP Q2Y0H9
SA	22	MET	-	insertion	UNP Q2Y0H9
SA	23	ALA	-	insertion	UNP Q2Y0H9
SA	24	ALA	-	insertion	UNP Q2Y0H9
SA	27	ALA	MET	conflict	UNP Q2Y0H9
SA	28	MET	ILE	conflict	UNP Q2Y0H9
SA	36	TYR	PHE	conflict	UNP Q2Y0H9
SA	64	ARG	LYS	conflict	UNP Q2Y0H9
SA	153	GLU	-	insertion	UNP Q2Y0H9
SA	154	PHE	-	insertion	UNP Q2Y0H9
SA	160	GLY	-	insertion	UNP Q2Y0H9
SA	161	PRO	-	insertion	UNP Q2Y0H9
SA	162	VAL	-	insertion	UNP Q2Y0H9
SA	163	ASN	-	insertion	UNP Q2Y0H9
SA	164	ASP	-	insertion	UNP Q2Y0H9
SA	314	ALA	-	insertion	UNP Q2Y0H9
SA	315	ARG	-	insertion	UNP Q2Y0H9
SA	330	VAL	-	insertion	UNP Q2Y0H9
SA	331	ASP	-	insertion	UNP Q2Y0H9
SA	344	LEU	-	insertion	UNP Q2Y0H9
SA	345	GLU	-	insertion	UNP Q2Y0H9
SA	357	SER	-	insertion	UNP Q2Y0H9
SA	358	ARG	-	insertion	UNP Q2Y0H9
SA	418	VAL	ALA	conflict	UNP Q2Y0H9
SA	442	SER	ASN	conflict	UNP Q2Y0H9
TA	2	MET	ARG	conflict	UNP Q2Y0H9
TA	?	-	VAL	deletion	UNP Q2Y0H9
TA	?	-	LEU	deletion	UNP Q2Y0H9
TA	?	-	GLY	deletion	UNP Q2Y0H9
TA	?	-	GLY	deletion	UNP Q2Y0H9
TA	?	-	ALA	deletion	UNP Q2Y0H9
TA	?	-	VAL	deletion	UNP Q2Y0H9
TA	?	-	VAL	deletion	UNP Q2Y0H9
TA	21	ALA	GLN	conflict	UNP Q2Y0H9
TA	22	MET	-	insertion	UNP Q2Y0H9
TA	23	ALA	-	insertion	UNP Q2Y0H9
TA	24	ALA	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
TA	27	ALA	MET	conflict	UNP Q2Y0H9
TA	28	MET	ILE	conflict	UNP Q2Y0H9
TA	36	TYR	PHE	conflict	UNP Q2Y0H9
TA	64	ARG	LYS	conflict	UNP Q2Y0H9
TA	153	GLU	-	insertion	UNP Q2Y0H9
TA	154	PHE	-	insertion	UNP Q2Y0H9
TA	160	GLY	-	insertion	UNP Q2Y0H9
TA	161	PRO	-	insertion	UNP Q2Y0H9
TA	162	VAL	-	insertion	UNP Q2Y0H9
TA	163	ASN	-	insertion	UNP Q2Y0H9
TA	164	ASP	-	insertion	UNP Q2Y0H9
TA	314	ALA	-	insertion	UNP Q2Y0H9
TA	315	ARG	-	insertion	UNP Q2Y0H9
TA	330	VAL	-	insertion	UNP Q2Y0H9
TA	331	ASP	-	insertion	UNP Q2Y0H9
TA	344	LEU	-	insertion	UNP Q2Y0H9
TA	345	GLU	-	insertion	UNP Q2Y0H9
TA	357	SER	-	insertion	UNP Q2Y0H9
TA	358	ARG	-	insertion	UNP Q2Y0H9
TA	418	VAL	ALA	conflict	UNP Q2Y0H9
TA	442	SER	ASN	conflict	UNP Q2Y0H9
UA	2	MET	ARG	conflict	UNP Q2Y0H9
UA	?	-	VAL	deletion	UNP Q2Y0H9
UA	?	-	LEU	deletion	UNP Q2Y0H9
UA	?	-	GLY	deletion	UNP Q2Y0H9
UA	?	-	GLY	deletion	UNP Q2Y0H9
UA	?	-	ALA	deletion	UNP Q2Y0H9
UA	?	-	VAL	deletion	UNP Q2Y0H9
UA	?	-	VAL	deletion	UNP Q2Y0H9
UA	21	ALA	GLN	conflict	UNP Q2Y0H9
UA	22	MET	-	insertion	UNP Q2Y0H9
UA	23	ALA	-	insertion	UNP Q2Y0H9
UA	24	ALA	-	insertion	UNP Q2Y0H9
UA	27	ALA	MET	conflict	UNP Q2Y0H9
UA	28	MET	ILE	conflict	UNP Q2Y0H9
UA	36	TYR	PHE	conflict	UNP Q2Y0H9
UA	64	ARG	LYS	conflict	UNP Q2Y0H9
UA	153	GLU	-	insertion	UNP Q2Y0H9
UA	154	PHE	-	insertion	UNP Q2Y0H9
UA	160	GLY	-	insertion	UNP Q2Y0H9
UA	161	PRO	-	insertion	UNP Q2Y0H9
UA	162	VAL	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
UA	163	ASN	-	insertion	UNP Q2Y0H9
UA	164	ASP	-	insertion	UNP Q2Y0H9
UA	314	ALA	-	insertion	UNP Q2Y0H9
UA	315	ARG	-	insertion	UNP Q2Y0H9
UA	330	VAL	-	insertion	UNP Q2Y0H9
UA	331	ASP	-	insertion	UNP Q2Y0H9
UA	344	LEU	-	insertion	UNP Q2Y0H9
UA	345	GLU	-	insertion	UNP Q2Y0H9
UA	357	SER	-	insertion	UNP Q2Y0H9
UA	358	ARG	-	insertion	UNP Q2Y0H9
UA	418	VAL	ALA	conflict	UNP Q2Y0H9
UA	442	SER	ASN	conflict	UNP Q2Y0H9
VA	2	MET	ARG	conflict	UNP Q2Y0H9
VA	?	-	VAL	deletion	UNP Q2Y0H9
VA	?	-	LEU	deletion	UNP Q2Y0H9
VA	?	-	GLY	deletion	UNP Q2Y0H9
VA	?	-	GLY	deletion	UNP Q2Y0H9
VA	?	-	ALA	deletion	UNP Q2Y0H9
VA	?	-	VAL	deletion	UNP Q2Y0H9
VA	?	-	VAL	deletion	UNP Q2Y0H9
VA	21	ALA	GLN	conflict	UNP Q2Y0H9
VA	22	MET	-	insertion	UNP Q2Y0H9
VA	23	ALA	-	insertion	UNP Q2Y0H9
VA	24	ALA	-	insertion	UNP Q2Y0H9
VA	27	ALA	MET	conflict	UNP Q2Y0H9
VA	28	MET	ILE	conflict	UNP Q2Y0H9
VA	36	TYR	PHE	conflict	UNP Q2Y0H9
VA	64	ARG	LYS	conflict	UNP Q2Y0H9
VA	153	GLU	-	insertion	UNP Q2Y0H9
VA	154	PHE	-	insertion	UNP Q2Y0H9
VA	160	GLY	-	insertion	UNP Q2Y0H9
VA	161	PRO	-	insertion	UNP Q2Y0H9
VA	162	VAL	-	insertion	UNP Q2Y0H9
VA	163	ASN	-	insertion	UNP Q2Y0H9
VA	164	ASP	-	insertion	UNP Q2Y0H9
VA	314	ALA	-	insertion	UNP Q2Y0H9
VA	315	ARG	-	insertion	UNP Q2Y0H9
VA	330	VAL	-	insertion	UNP Q2Y0H9
VA	331	ASP	-	insertion	UNP Q2Y0H9
VA	344	LEU	-	insertion	UNP Q2Y0H9
VA	345	GLU	-	insertion	UNP Q2Y0H9
VA	357	SER	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
VA	358	ARG	-	insertion	UNP Q2Y0H9
VA	418	VAL	ALA	conflict	UNP Q2Y0H9
VA	442	SER	ASN	conflict	UNP Q2Y0H9
WA	2	MET	ARG	conflict	UNP Q2Y0H9
WA	?	-	VAL	deletion	UNP Q2Y0H9
WA	?	-	LEU	deletion	UNP Q2Y0H9
WA	?	-	GLY	deletion	UNP Q2Y0H9
WA	?	-	GLY	deletion	UNP Q2Y0H9
WA	?	-	ALA	deletion	UNP Q2Y0H9
WA	?	-	VAL	deletion	UNP Q2Y0H9
WA	?	-	VAL	deletion	UNP Q2Y0H9
WA	21	ALA	GLN	conflict	UNP Q2Y0H9
WA	22	MET	-	insertion	UNP Q2Y0H9
WA	23	ALA	-	insertion	UNP Q2Y0H9
WA	24	ALA	-	insertion	UNP Q2Y0H9
WA	27	ALA	MET	conflict	UNP Q2Y0H9
WA	28	MET	ILE	conflict	UNP Q2Y0H9
WA	36	TYR	PHE	conflict	UNP Q2Y0H9
WA	64	ARG	LYS	conflict	UNP Q2Y0H9
WA	153	GLU	-	insertion	UNP Q2Y0H9
WA	154	PHE	-	insertion	UNP Q2Y0H9
WA	160	GLY	-	insertion	UNP Q2Y0H9
WA	161	PRO	-	insertion	UNP Q2Y0H9
WA	162	VAL	-	insertion	UNP Q2Y0H9
WA	163	ASN	-	insertion	UNP Q2Y0H9
WA	164	ASP	-	insertion	UNP Q2Y0H9
WA	314	ALA	-	insertion	UNP Q2Y0H9
WA	315	ARG	-	insertion	UNP Q2Y0H9
WA	330	VAL	-	insertion	UNP Q2Y0H9
WA	331	ASP	-	insertion	UNP Q2Y0H9
WA	344	LEU	-	insertion	UNP Q2Y0H9
WA	345	GLU	-	insertion	UNP Q2Y0H9
WA	357	SER	-	insertion	UNP Q2Y0H9
WA	358	ARG	-	insertion	UNP Q2Y0H9
WA	418	VAL	ALA	conflict	UNP Q2Y0H9
WA	442	SER	ASN	conflict	UNP Q2Y0H9
XA	2	MET	ARG	conflict	UNP Q2Y0H9
XA	?	-	VAL	deletion	UNP Q2Y0H9
XA	?	-	LEU	deletion	UNP Q2Y0H9
XA	?	-	GLY	deletion	UNP Q2Y0H9
XA	?	-	GLY	deletion	UNP Q2Y0H9
XA	?	-	ALA	deletion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
XA	?	-	VAL	deletion	UNP Q2Y0H9
XA	?	-	VAL	deletion	UNP Q2Y0H9
XA	21	ALA	GLN	conflict	UNP Q2Y0H9
XA	22	MET	-	insertion	UNP Q2Y0H9
XA	23	ALA	-	insertion	UNP Q2Y0H9
XA	24	ALA	-	insertion	UNP Q2Y0H9
XA	27	ALA	MET	conflict	UNP Q2Y0H9
XA	28	MET	ILE	conflict	UNP Q2Y0H9
XA	36	TYR	PHE	conflict	UNP Q2Y0H9
XA	64	ARG	LYS	conflict	UNP Q2Y0H9
XA	153	GLU	-	insertion	UNP Q2Y0H9
XA	154	PHE	-	insertion	UNP Q2Y0H9
XA	160	GLY	-	insertion	UNP Q2Y0H9
XA	161	PRO	-	insertion	UNP Q2Y0H9
XA	162	VAL	-	insertion	UNP Q2Y0H9
XA	163	ASN	-	insertion	UNP Q2Y0H9
XA	164	ASP	-	insertion	UNP Q2Y0H9
XA	314	ALA	-	insertion	UNP Q2Y0H9
XA	315	ARG	-	insertion	UNP Q2Y0H9
XA	330	VAL	-	insertion	UNP Q2Y0H9
XA	331	ASP	-	insertion	UNP Q2Y0H9
XA	344	LEU	-	insertion	UNP Q2Y0H9
XA	345	GLU	-	insertion	UNP Q2Y0H9
XA	357	SER	-	insertion	UNP Q2Y0H9
XA	358	ARG	-	insertion	UNP Q2Y0H9
XA	418	VAL	ALA	conflict	UNP Q2Y0H9
XA	442	SER	ASN	conflict	UNP Q2Y0H9
YA	2	MET	ARG	conflict	UNP Q2Y0H9
YA	?	-	VAL	deletion	UNP Q2Y0H9
YA	?	-	LEU	deletion	UNP Q2Y0H9
YA	?	-	GLY	deletion	UNP Q2Y0H9
YA	?	-	GLY	deletion	UNP Q2Y0H9
YA	?	-	ALA	deletion	UNP Q2Y0H9
YA	?	-	VAL	deletion	UNP Q2Y0H9
YA	?	-	VAL	deletion	UNP Q2Y0H9
YA	21	ALA	GLN	conflict	UNP Q2Y0H9
YA	22	MET	-	insertion	UNP Q2Y0H9
YA	23	ALA	-	insertion	UNP Q2Y0H9
YA	24	ALA	-	insertion	UNP Q2Y0H9
YA	27	ALA	MET	conflict	UNP Q2Y0H9
YA	28	MET	ILE	conflict	UNP Q2Y0H9
YA	36	TYR	PHE	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
YA	64	ARG	LYS	conflict	UNP Q2Y0H9
YA	153	GLU	-	insertion	UNP Q2Y0H9
YA	154	PHE	-	insertion	UNP Q2Y0H9
YA	160	GLY	-	insertion	UNP Q2Y0H9
YA	161	PRO	-	insertion	UNP Q2Y0H9
YA	162	VAL	-	insertion	UNP Q2Y0H9
YA	163	ASN	-	insertion	UNP Q2Y0H9
YA	164	ASP	-	insertion	UNP Q2Y0H9
YA	314	ALA	-	insertion	UNP Q2Y0H9
YA	315	ARG	-	insertion	UNP Q2Y0H9
YA	330	VAL	-	insertion	UNP Q2Y0H9
YA	331	ASP	-	insertion	UNP Q2Y0H9
YA	344	LEU	-	insertion	UNP Q2Y0H9
YA	345	GLU	-	insertion	UNP Q2Y0H9
YA	357	SER	-	insertion	UNP Q2Y0H9
YA	358	ARG	-	insertion	UNP Q2Y0H9
YA	418	VAL	ALA	conflict	UNP Q2Y0H9
YA	442	SER	ASN	conflict	UNP Q2Y0H9
ZA	2	MET	ARG	conflict	UNP Q2Y0H9
ZA	?	-	VAL	deletion	UNP Q2Y0H9
ZA	?	-	LEU	deletion	UNP Q2Y0H9
ZA	?	-	GLY	deletion	UNP Q2Y0H9
ZA	?	-	GLY	deletion	UNP Q2Y0H9
ZA	?	-	ALA	deletion	UNP Q2Y0H9
ZA	?	-	VAL	deletion	UNP Q2Y0H9
ZA	?	-	VAL	deletion	UNP Q2Y0H9
ZA	21	ALA	GLN	conflict	UNP Q2Y0H9
ZA	22	MET	-	insertion	UNP Q2Y0H9
ZA	23	ALA	-	insertion	UNP Q2Y0H9
ZA	24	ALA	-	insertion	UNP Q2Y0H9
ZA	27	ALA	MET	conflict	UNP Q2Y0H9
ZA	28	MET	ILE	conflict	UNP Q2Y0H9
ZA	36	TYR	PHE	conflict	UNP Q2Y0H9
ZA	64	ARG	LYS	conflict	UNP Q2Y0H9
ZA	153	GLU	-	insertion	UNP Q2Y0H9
ZA	154	PHE	-	insertion	UNP Q2Y0H9
ZA	160	GLY	-	insertion	UNP Q2Y0H9
ZA	161	PRO	-	insertion	UNP Q2Y0H9
ZA	162	VAL	-	insertion	UNP Q2Y0H9
ZA	163	ASN	-	insertion	UNP Q2Y0H9
ZA	164	ASP	-	insertion	UNP Q2Y0H9
ZA	314	ALA	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
ZA	315	ARG	-	insertion	UNP Q2Y0H9
ZA	330	VAL	-	insertion	UNP Q2Y0H9
ZA	331	ASP	-	insertion	UNP Q2Y0H9
ZA	344	LEU	-	insertion	UNP Q2Y0H9
ZA	345	GLU	-	insertion	UNP Q2Y0H9
ZA	357	SER	-	insertion	UNP Q2Y0H9
ZA	358	ARG	-	insertion	UNP Q2Y0H9
ZA	418	VAL	ALA	conflict	UNP Q2Y0H9
ZA	442	SER	ASN	conflict	UNP Q2Y0H9
AB	2	MET	ARG	conflict	UNP Q2Y0H9
AB	?	-	VAL	deletion	UNP Q2Y0H9
AB	?	-	LEU	deletion	UNP Q2Y0H9
AB	?	-	GLY	deletion	UNP Q2Y0H9
AB	?	-	GLY	deletion	UNP Q2Y0H9
AB	?	-	ALA	deletion	UNP Q2Y0H9
AB	?	-	VAL	deletion	UNP Q2Y0H9
AB	?	-	VAL	deletion	UNP Q2Y0H9
AB	21	ALA	GLN	conflict	UNP Q2Y0H9
AB	22	MET	-	insertion	UNP Q2Y0H9
AB	23	ALA	-	insertion	UNP Q2Y0H9
AB	24	ALA	-	insertion	UNP Q2Y0H9
AB	27	ALA	MET	conflict	UNP Q2Y0H9
AB	28	MET	ILE	conflict	UNP Q2Y0H9
AB	36	TYR	PHE	conflict	UNP Q2Y0H9
AB	64	ARG	LYS	conflict	UNP Q2Y0H9
AB	153	GLU	-	insertion	UNP Q2Y0H9
AB	154	PHE	-	insertion	UNP Q2Y0H9
AB	160	GLY	-	insertion	UNP Q2Y0H9
AB	161	PRO	-	insertion	UNP Q2Y0H9
AB	162	VAL	-	insertion	UNP Q2Y0H9
AB	163	ASN	-	insertion	UNP Q2Y0H9
AB	164	ASP	-	insertion	UNP Q2Y0H9
AB	314	ALA	-	insertion	UNP Q2Y0H9
AB	315	ARG	-	insertion	UNP Q2Y0H9
AB	330	VAL	-	insertion	UNP Q2Y0H9
AB	331	ASP	-	insertion	UNP Q2Y0H9
AB	344	LEU	-	insertion	UNP Q2Y0H9
AB	345	GLU	-	insertion	UNP Q2Y0H9
AB	357	SER	-	insertion	UNP Q2Y0H9
AB	358	ARG	-	insertion	UNP Q2Y0H9
AB	418	VAL	ALA	conflict	UNP Q2Y0H9
AB	442	SER	ASN	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
BB	2	MET	ARG	conflict	UNP Q2Y0H9
BB	?	-	VAL	deletion	UNP Q2Y0H9
BB	?	-	LEU	deletion	UNP Q2Y0H9
BB	?	-	GLY	deletion	UNP Q2Y0H9
BB	?	-	GLY	deletion	UNP Q2Y0H9
BB	?	-	ALA	deletion	UNP Q2Y0H9
BB	?	-	VAL	deletion	UNP Q2Y0H9
BB	?	-	VAL	deletion	UNP Q2Y0H9
BB	21	ALA	GLN	conflict	UNP Q2Y0H9
BB	22	MET	-	insertion	UNP Q2Y0H9
BB	23	ALA	-	insertion	UNP Q2Y0H9
BB	24	ALA	-	insertion	UNP Q2Y0H9
BB	27	ALA	MET	conflict	UNP Q2Y0H9
BB	28	MET	ILE	conflict	UNP Q2Y0H9
BB	36	TYR	PHE	conflict	UNP Q2Y0H9
BB	64	ARG	LYS	conflict	UNP Q2Y0H9
BB	153	GLU	-	insertion	UNP Q2Y0H9
BB	154	PHE	-	insertion	UNP Q2Y0H9
BB	160	GLY	-	insertion	UNP Q2Y0H9
BB	161	PRO	-	insertion	UNP Q2Y0H9
BB	162	VAL	-	insertion	UNP Q2Y0H9
BB	163	ASN	-	insertion	UNP Q2Y0H9
BB	164	ASP	-	insertion	UNP Q2Y0H9
BB	314	ALA	-	insertion	UNP Q2Y0H9
BB	315	ARG	-	insertion	UNP Q2Y0H9
BB	330	VAL	-	insertion	UNP Q2Y0H9
BB	331	ASP	-	insertion	UNP Q2Y0H9
BB	344	LEU	-	insertion	UNP Q2Y0H9
BB	345	GLU	-	insertion	UNP Q2Y0H9
BB	357	SER	-	insertion	UNP Q2Y0H9
BB	358	ARG	-	insertion	UNP Q2Y0H9
BB	418	VAL	ALA	conflict	UNP Q2Y0H9
BB	442	SER	ASN	conflict	UNP Q2Y0H9
CB	2	MET	ARG	conflict	UNP Q2Y0H9
CB	?	-	VAL	deletion	UNP Q2Y0H9
CB	?	-	LEU	deletion	UNP Q2Y0H9
CB	?	-	GLY	deletion	UNP Q2Y0H9
CB	?	-	GLY	deletion	UNP Q2Y0H9
CB	?	-	ALA	deletion	UNP Q2Y0H9
CB	?	-	VAL	deletion	UNP Q2Y0H9
CB	?	-	VAL	deletion	UNP Q2Y0H9
CB	21	ALA	GLN	conflict	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
CB	22	MET	-	insertion	UNP Q2Y0H9
CB	23	ALA	-	insertion	UNP Q2Y0H9
CB	24	ALA	-	insertion	UNP Q2Y0H9
CB	27	ALA	MET	conflict	UNP Q2Y0H9
CB	28	MET	ILE	conflict	UNP Q2Y0H9
CB	36	TYR	PHE	conflict	UNP Q2Y0H9
CB	64	ARG	LYS	conflict	UNP Q2Y0H9
CB	153	GLU	-	insertion	UNP Q2Y0H9
CB	154	PHE	-	insertion	UNP Q2Y0H9
CB	160	GLY	-	insertion	UNP Q2Y0H9
CB	161	PRO	-	insertion	UNP Q2Y0H9
CB	162	VAL	-	insertion	UNP Q2Y0H9
CB	163	ASN	-	insertion	UNP Q2Y0H9
CB	164	ASP	-	insertion	UNP Q2Y0H9
CB	314	ALA	-	insertion	UNP Q2Y0H9
CB	315	ARG	-	insertion	UNP Q2Y0H9
CB	330	VAL	-	insertion	UNP Q2Y0H9
CB	331	ASP	-	insertion	UNP Q2Y0H9
CB	344	LEU	-	insertion	UNP Q2Y0H9
CB	345	GLU	-	insertion	UNP Q2Y0H9
CB	357	SER	-	insertion	UNP Q2Y0H9
CB	358	ARG	-	insertion	UNP Q2Y0H9
CB	418	VAL	ALA	conflict	UNP Q2Y0H9
CB	442	SER	ASN	conflict	UNP Q2Y0H9
DB	2	MET	ARG	conflict	UNP Q2Y0H9
DB	?	-	VAL	deletion	UNP Q2Y0H9
DB	?	-	LEU	deletion	UNP Q2Y0H9
DB	?	-	GLY	deletion	UNP Q2Y0H9
DB	?	-	GLY	deletion	UNP Q2Y0H9
DB	?	-	ALA	deletion	UNP Q2Y0H9
DB	?	-	VAL	deletion	UNP Q2Y0H9
DB	?	-	VAL	deletion	UNP Q2Y0H9
DB	21	ALA	GLN	conflict	UNP Q2Y0H9
DB	22	MET	-	insertion	UNP Q2Y0H9
DB	23	ALA	-	insertion	UNP Q2Y0H9
DB	24	ALA	-	insertion	UNP Q2Y0H9
DB	27	ALA	MET	conflict	UNP Q2Y0H9
DB	28	MET	ILE	conflict	UNP Q2Y0H9
DB	36	TYR	PHE	conflict	UNP Q2Y0H9
DB	64	ARG	LYS	conflict	UNP Q2Y0H9
DB	153	GLU	-	insertion	UNP Q2Y0H9
DB	154	PHE	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
DB	160	GLY	-	insertion	UNP Q2Y0H9
DB	161	PRO	-	insertion	UNP Q2Y0H9
DB	162	VAL	-	insertion	UNP Q2Y0H9
DB	163	ASN	-	insertion	UNP Q2Y0H9
DB	164	ASP	-	insertion	UNP Q2Y0H9
DB	314	ALA	-	insertion	UNP Q2Y0H9
DB	315	ARG	-	insertion	UNP Q2Y0H9
DB	330	VAL	-	insertion	UNP Q2Y0H9
DB	331	ASP	-	insertion	UNP Q2Y0H9
DB	344	LEU	-	insertion	UNP Q2Y0H9
DB	345	GLU	-	insertion	UNP Q2Y0H9
DB	357	SER	-	insertion	UNP Q2Y0H9
DB	358	ARG	-	insertion	UNP Q2Y0H9
DB	418	VAL	ALA	conflict	UNP Q2Y0H9
DB	442	SER	ASN	conflict	UNP Q2Y0H9
EB	2	MET	ARG	conflict	UNP Q2Y0H9
EB	?	-	VAL	deletion	UNP Q2Y0H9
EB	?	-	LEU	deletion	UNP Q2Y0H9
EB	?	-	GLY	deletion	UNP Q2Y0H9
EB	?	-	GLY	deletion	UNP Q2Y0H9
EB	?	-	ALA	deletion	UNP Q2Y0H9
EB	?	-	VAL	deletion	UNP Q2Y0H9
EB	?	-	VAL	deletion	UNP Q2Y0H9
EB	21	ALA	GLN	conflict	UNP Q2Y0H9
EB	22	MET	-	insertion	UNP Q2Y0H9
EB	23	ALA	-	insertion	UNP Q2Y0H9
EB	24	ALA	-	insertion	UNP Q2Y0H9
EB	27	ALA	MET	conflict	UNP Q2Y0H9
EB	28	MET	ILE	conflict	UNP Q2Y0H9
EB	36	TYR	PHE	conflict	UNP Q2Y0H9
EB	64	ARG	LYS	conflict	UNP Q2Y0H9
EB	153	GLU	-	insertion	UNP Q2Y0H9
EB	154	PHE	-	insertion	UNP Q2Y0H9
EB	160	GLY	-	insertion	UNP Q2Y0H9
EB	161	PRO	-	insertion	UNP Q2Y0H9
EB	162	VAL	-	insertion	UNP Q2Y0H9
EB	163	ASN	-	insertion	UNP Q2Y0H9
EB	164	ASP	-	insertion	UNP Q2Y0H9
EB	314	ALA	-	insertion	UNP Q2Y0H9
EB	315	ARG	-	insertion	UNP Q2Y0H9
EB	330	VAL	-	insertion	UNP Q2Y0H9
EB	331	ASP	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
EB	344	LEU	-	insertion	UNP Q2Y0H9
EB	345	GLU	-	insertion	UNP Q2Y0H9
EB	357	SER	-	insertion	UNP Q2Y0H9
EB	358	ARG	-	insertion	UNP Q2Y0H9
EB	418	VAL	ALA	conflict	UNP Q2Y0H9
EB	442	SER	ASN	conflict	UNP Q2Y0H9
FB	2	MET	ARG	conflict	UNP Q2Y0H9
FB	?	-	VAL	deletion	UNP Q2Y0H9
FB	?	-	LEU	deletion	UNP Q2Y0H9
FB	?	-	GLY	deletion	UNP Q2Y0H9
FB	?	-	GLY	deletion	UNP Q2Y0H9
FB	?	-	ALA	deletion	UNP Q2Y0H9
FB	?	-	VAL	deletion	UNP Q2Y0H9
FB	?	-	VAL	deletion	UNP Q2Y0H9
FB	21	ALA	GLN	conflict	UNP Q2Y0H9
FB	22	MET	-	insertion	UNP Q2Y0H9
FB	23	ALA	-	insertion	UNP Q2Y0H9
FB	24	ALA	-	insertion	UNP Q2Y0H9
FB	27	ALA	MET	conflict	UNP Q2Y0H9
FB	28	MET	ILE	conflict	UNP Q2Y0H9
FB	36	TYR	PHE	conflict	UNP Q2Y0H9
FB	64	ARG	LYS	conflict	UNP Q2Y0H9
FB	153	GLU	-	insertion	UNP Q2Y0H9
FB	154	PHE	-	insertion	UNP Q2Y0H9
FB	160	GLY	-	insertion	UNP Q2Y0H9
FB	161	PRO	-	insertion	UNP Q2Y0H9
FB	162	VAL	-	insertion	UNP Q2Y0H9
FB	163	ASN	-	insertion	UNP Q2Y0H9
FB	164	ASP	-	insertion	UNP Q2Y0H9
FB	314	ALA	-	insertion	UNP Q2Y0H9
FB	315	ARG	-	insertion	UNP Q2Y0H9
FB	330	VAL	-	insertion	UNP Q2Y0H9
FB	331	ASP	-	insertion	UNP Q2Y0H9
FB	344	LEU	-	insertion	UNP Q2Y0H9
FB	345	GLU	-	insertion	UNP Q2Y0H9
FB	357	SER	-	insertion	UNP Q2Y0H9
FB	358	ARG	-	insertion	UNP Q2Y0H9
FB	418	VAL	ALA	conflict	UNP Q2Y0H9
FB	442	SER	ASN	conflict	UNP Q2Y0H9
GB	2	MET	ARG	conflict	UNP Q2Y0H9
GB	?	-	VAL	deletion	UNP Q2Y0H9
GB	?	-	LEU	deletion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
GB	?	-	GLY	deletion	UNP Q2Y0H9
GB	?	-	GLY	deletion	UNP Q2Y0H9
GB	?	-	ALA	deletion	UNP Q2Y0H9
GB	?	-	VAL	deletion	UNP Q2Y0H9
GB	?	-	VAL	deletion	UNP Q2Y0H9
GB	21	ALA	GLN	conflict	UNP Q2Y0H9
GB	22	MET	-	insertion	UNP Q2Y0H9
GB	23	ALA	-	insertion	UNP Q2Y0H9
GB	24	ALA	-	insertion	UNP Q2Y0H9
GB	27	ALA	MET	conflict	UNP Q2Y0H9
GB	28	MET	ILE	conflict	UNP Q2Y0H9
GB	36	TYR	PHE	conflict	UNP Q2Y0H9
GB	64	ARG	LYS	conflict	UNP Q2Y0H9
GB	153	GLU	-	insertion	UNP Q2Y0H9
GB	154	PHE	-	insertion	UNP Q2Y0H9
GB	160	GLY	-	insertion	UNP Q2Y0H9
GB	161	PRO	-	insertion	UNP Q2Y0H9
GB	162	VAL	-	insertion	UNP Q2Y0H9
GB	163	ASN	-	insertion	UNP Q2Y0H9
GB	164	ASP	-	insertion	UNP Q2Y0H9
GB	314	ALA	-	insertion	UNP Q2Y0H9
GB	315	ARG	-	insertion	UNP Q2Y0H9
GB	330	VAL	-	insertion	UNP Q2Y0H9
GB	331	ASP	-	insertion	UNP Q2Y0H9
GB	344	LEU	-	insertion	UNP Q2Y0H9
GB	345	GLU	-	insertion	UNP Q2Y0H9
GB	357	SER	-	insertion	UNP Q2Y0H9
GB	358	ARG	-	insertion	UNP Q2Y0H9
GB	418	VAL	ALA	conflict	UNP Q2Y0H9
GB	442	SER	ASN	conflict	UNP Q2Y0H9
HB	2	MET	ARG	conflict	UNP Q2Y0H9
HB	?	-	VAL	deletion	UNP Q2Y0H9
HB	?	-	LEU	deletion	UNP Q2Y0H9
HB	?	-	GLY	deletion	UNP Q2Y0H9
HB	?	-	GLY	deletion	UNP Q2Y0H9
HB	?	-	ALA	deletion	UNP Q2Y0H9
HB	?	-	VAL	deletion	UNP Q2Y0H9
HB	?	-	VAL	deletion	UNP Q2Y0H9
HB	21	ALA	GLN	conflict	UNP Q2Y0H9
HB	22	MET	-	insertion	UNP Q2Y0H9
HB	23	ALA	-	insertion	UNP Q2Y0H9
HB	24	ALA	-	insertion	UNP Q2Y0H9

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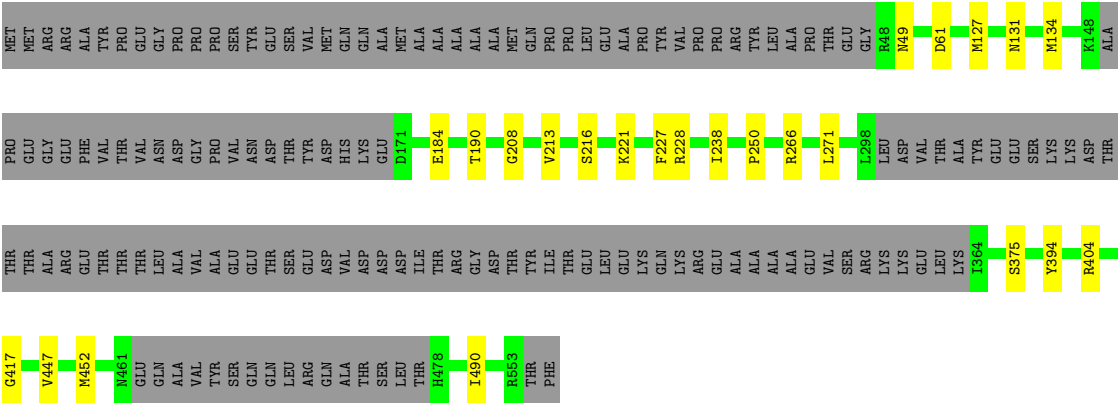
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Chain	Residue	Modelled	Actual	Comment	Reference
HB	27	ALA	MET	conflict	UNP Q2Y0H9
HB	28	MET	ILE	conflict	UNP Q2Y0H9
HB	36	TYR	PHE	conflict	UNP Q2Y0H9
HB	64	ARG	LYS	conflict	UNP Q2Y0H9
HB	153	GLU	-	insertion	UNP Q2Y0H9
HB	154	PHE	-	insertion	UNP Q2Y0H9
HB	160	GLY	-	insertion	UNP Q2Y0H9
HB	161	PRO	-	insertion	UNP Q2Y0H9
HB	162	VAL	-	insertion	UNP Q2Y0H9
HB	163	ASN	-	insertion	UNP Q2Y0H9
HB	164	ASP	-	insertion	UNP Q2Y0H9
HB	314	ALA	-	insertion	UNP Q2Y0H9
HB	315	ARG	-	insertion	UNP Q2Y0H9
HB	330	VAL	-	insertion	UNP Q2Y0H9
HB	331	ASP	-	insertion	UNP Q2Y0H9
HB	344	LEU	-	insertion	UNP Q2Y0H9
HB	345	GLU	-	insertion	UNP Q2Y0H9
HB	357	SER	-	insertion	UNP Q2Y0H9
HB	358	ARG	-	insertion	UNP Q2Y0H9
HB	418	VAL	ALA	conflict	UNP Q2Y0H9
HB	442	SER	ASN	conflict	UNP Q2Y0H9
IB	2	MET	ARG	conflict	UNP Q2Y0H9
IB	?	-	VAL	deletion	UNP Q2Y0H9
IB	?	-	LEU	deletion	UNP Q2Y0H9
IB	?	-	GLY	deletion	UNP Q2Y0H9
IB	?	-	GLY	deletion	UNP Q2Y0H9
IB	?	-	ALA	deletion	UNP Q2Y0H9
IB	?	-	VAL	deletion	UNP Q2Y0H9
IB	?	-	VAL	deletion	UNP Q2Y0H9
IB	21	ALA	GLN	conflict	UNP Q2Y0H9
IB	22	MET	-	insertion	UNP Q2Y0H9
IB	23	ALA	-	insertion	UNP Q2Y0H9
IB	24	ALA	-	insertion	UNP Q2Y0H9
IB	27	ALA	MET	conflict	UNP Q2Y0H9
IB	28	MET	ILE	conflict	UNP Q2Y0H9
IB	36	TYR	PHE	conflict	UNP Q2Y0H9
IB	64	ARG	LYS	conflict	UNP Q2Y0H9
IB	153	GLU	-	insertion	UNP Q2Y0H9
IB	154	PHE	-	insertion	UNP Q2Y0H9
IB	160	GLY	-	insertion	UNP Q2Y0H9
IB	161	PRO	-	insertion	UNP Q2Y0H9
IB	162	VAL	-	insertion	UNP Q2Y0H9

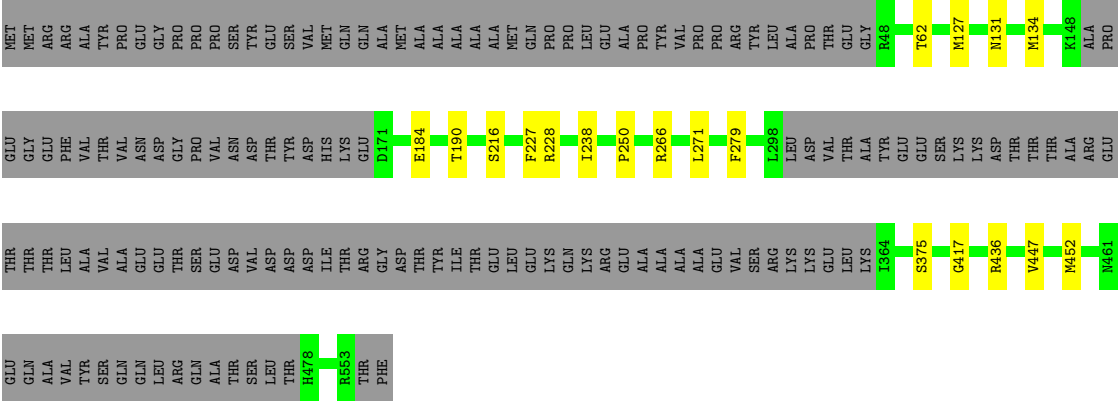
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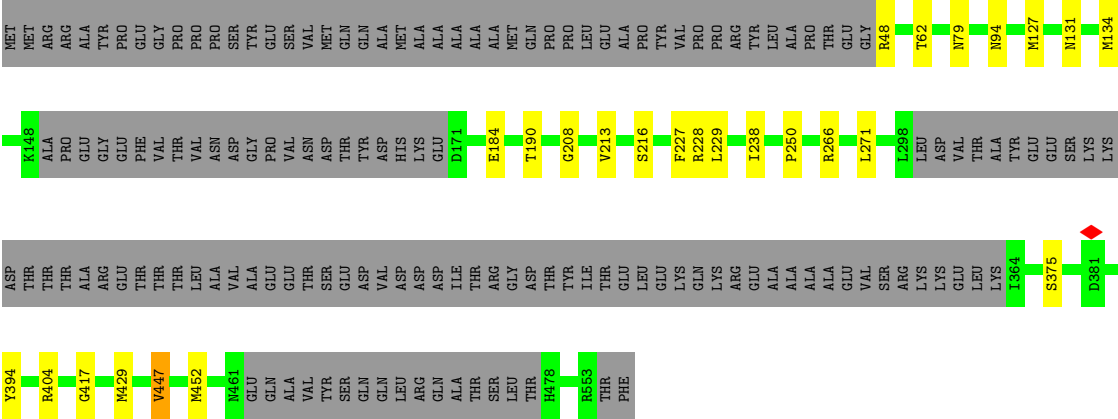
Chain	Residue	Modelled	Actual	Comment	Reference
IB	163	ASN	-	insertion	UNP Q2Y0H9
IB	164	ASP	-	insertion	UNP Q2Y0H9
IB	314	ALA	-	insertion	UNP Q2Y0H9
IB	315	ARG	-	insertion	UNP Q2Y0H9
IB	330	VAL	-	insertion	UNP Q2Y0H9
IB	331	ASP	-	insertion	UNP Q2Y0H9
IB	344	LEU	-	insertion	UNP Q2Y0H9
IB	345	GLU	-	insertion	UNP Q2Y0H9
IB	357	SER	-	insertion	UNP Q2Y0H9
IB	358	ARG	-	insertion	UNP Q2Y0H9
IB	418	VAL	ALA	conflict	UNP Q2Y0H9
IB	442	SER	ASN	conflict	UNP Q2Y0H9



• Molecule 1: Penton protein

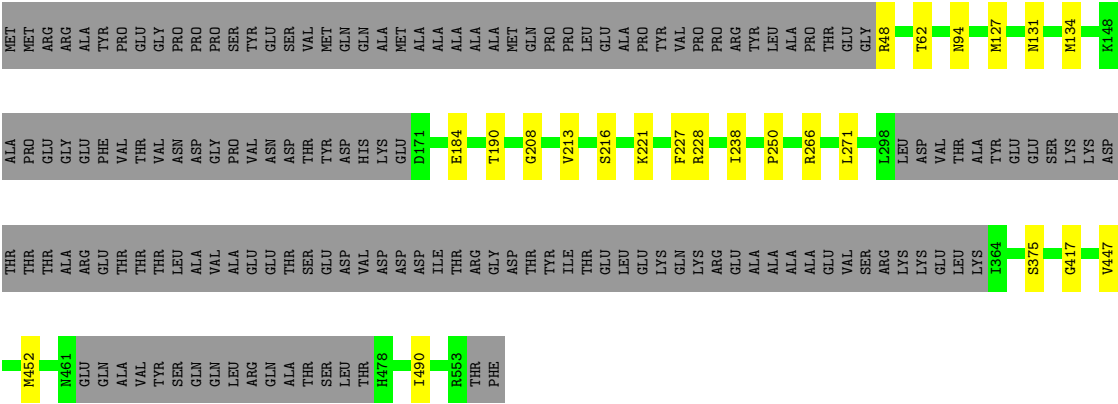


• Molecule 1: Penton protein

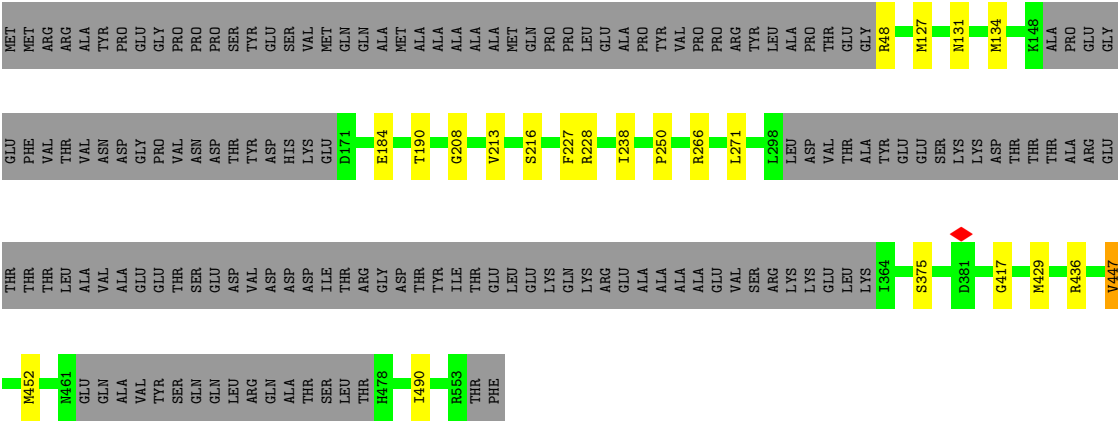


• Molecule 1: Penton protein

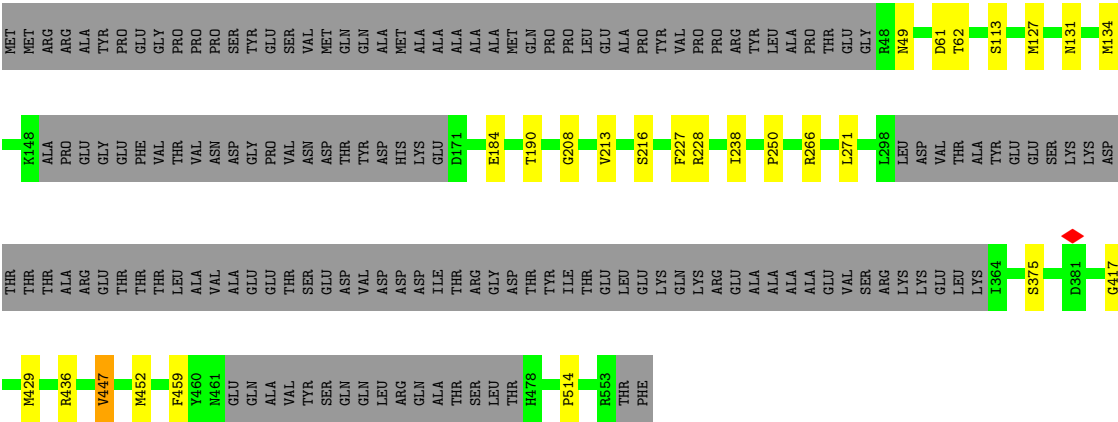




● Molecule 1: Penton protein

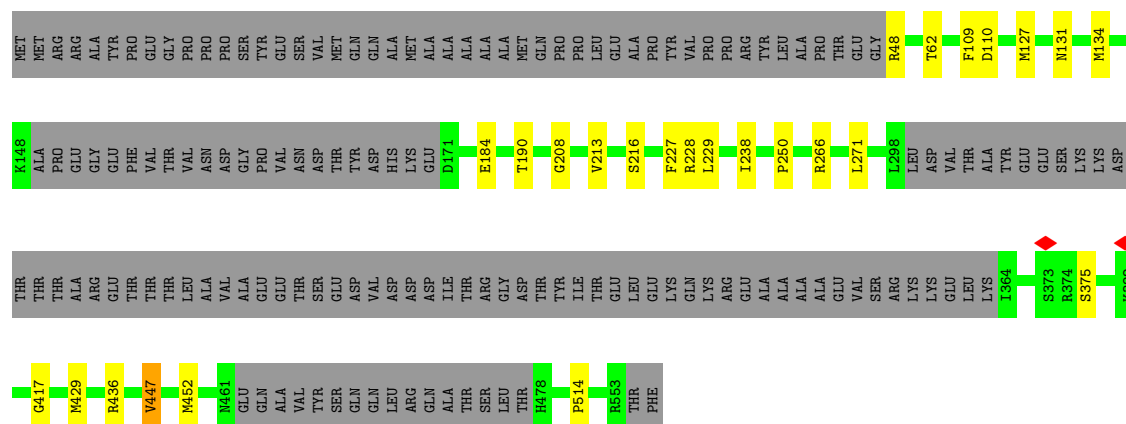


● Molecule 1: Penton protein

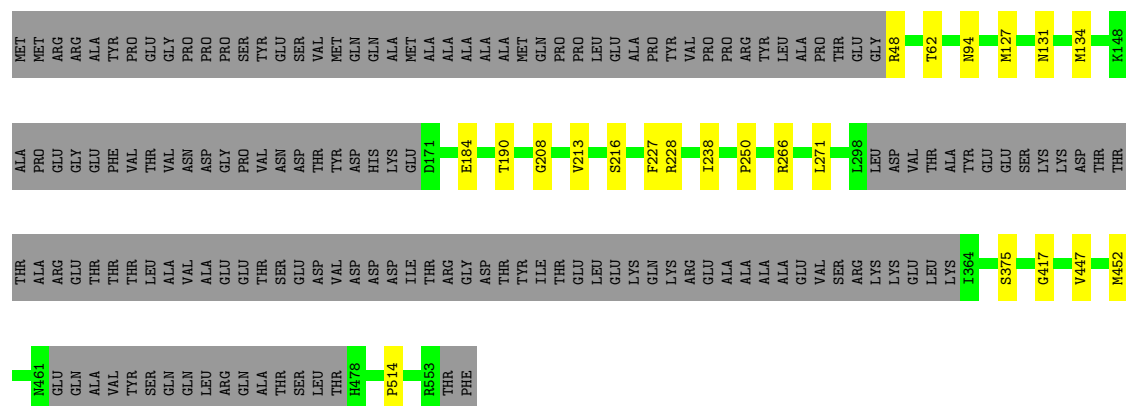


● Molecule 1: Penton protein

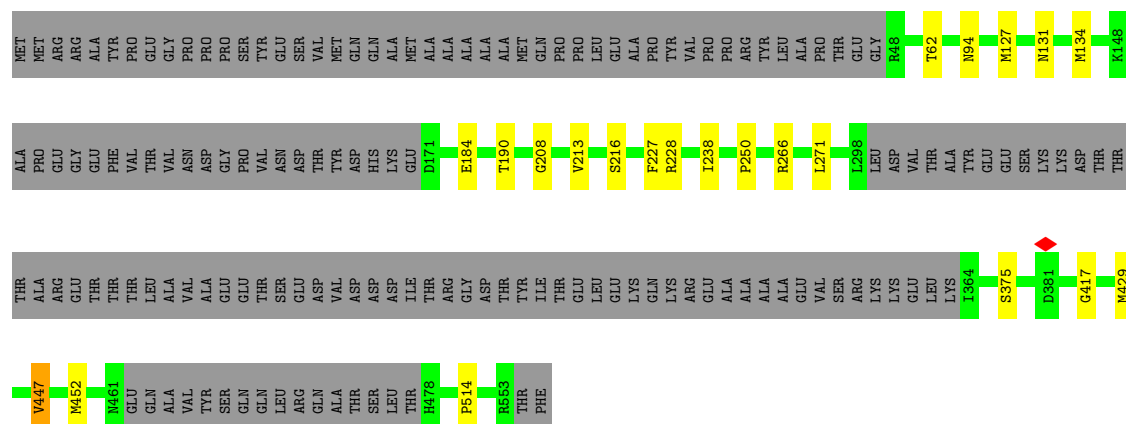




- Molecule 1: Penton protein

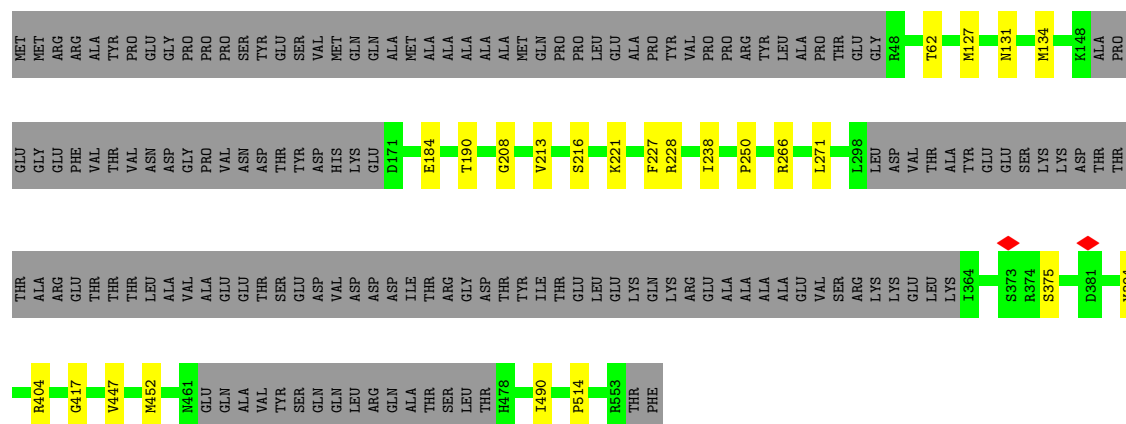


- Molecule 1: Penton protein

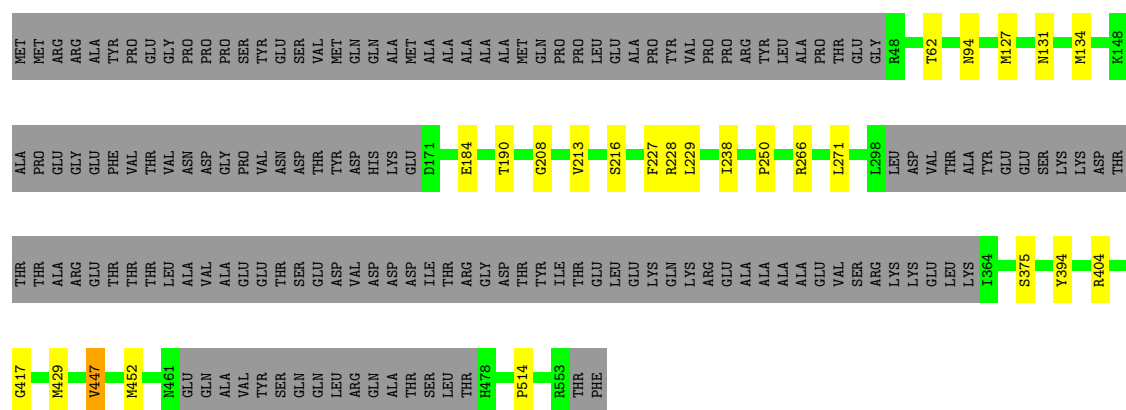


- Molecule 1: Penton protein

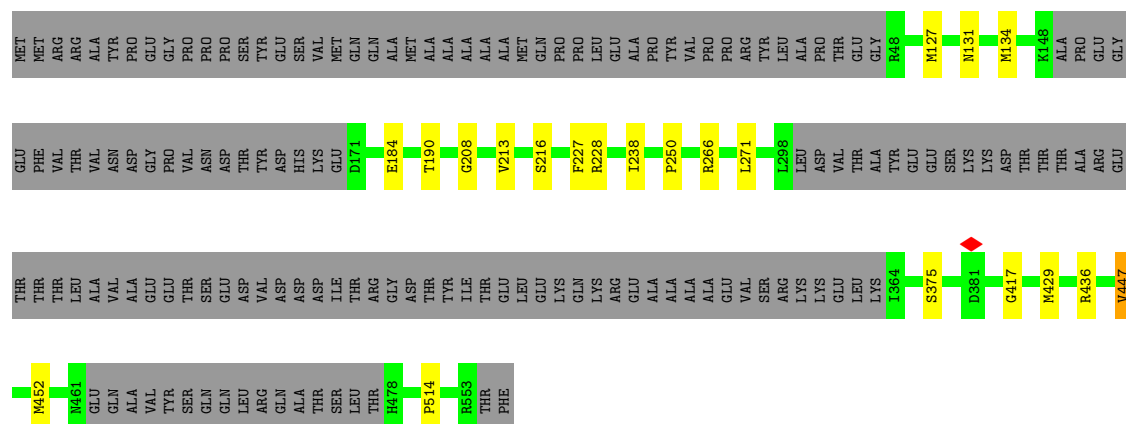




- Molecule 1: Penton protein

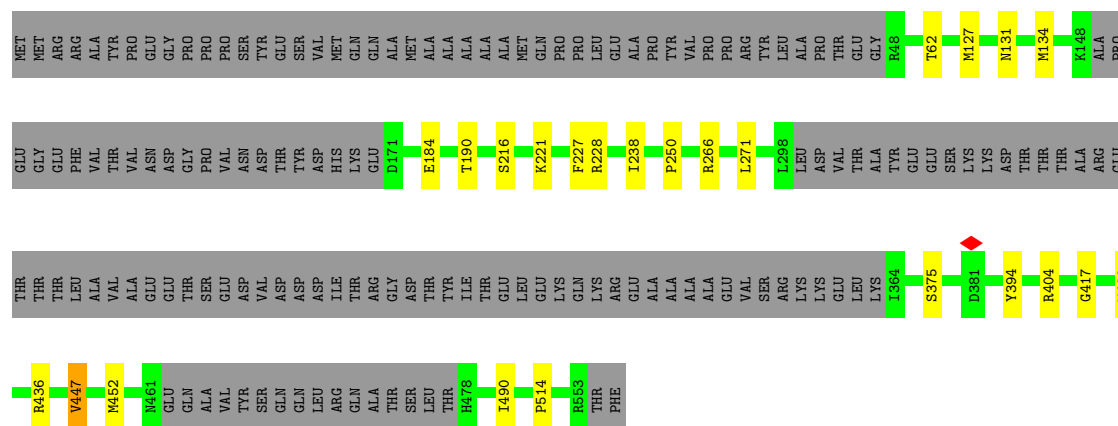


- Molecule 1: Penton protein



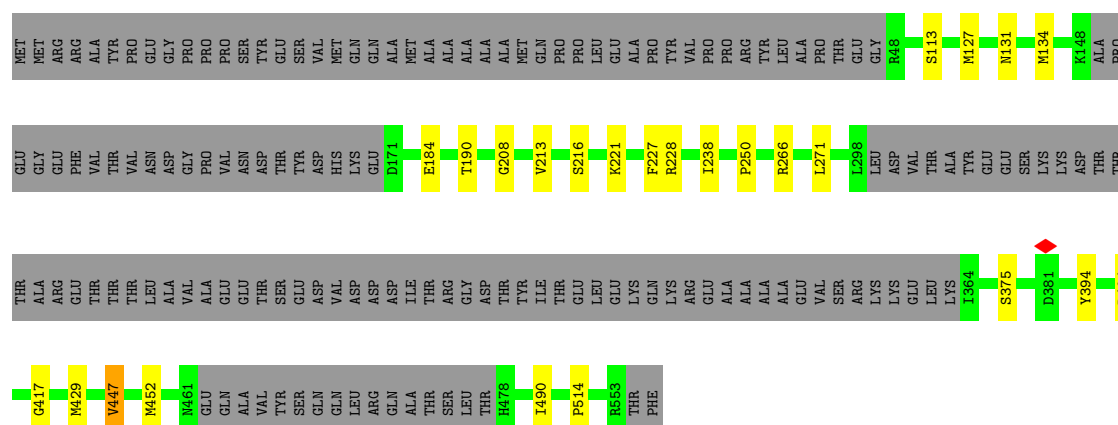
- Molecule 1: Penton protein





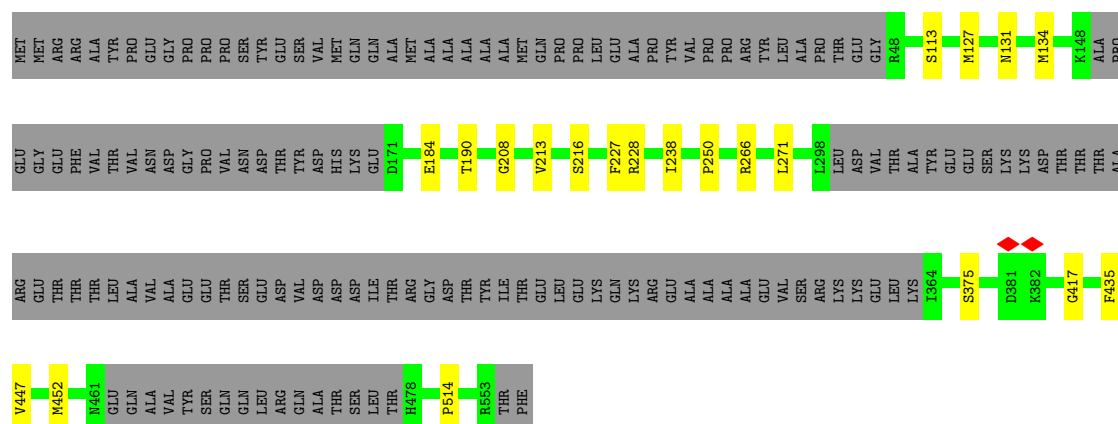
• Molecule 1: Penton protein

Chain P: 68% 27%



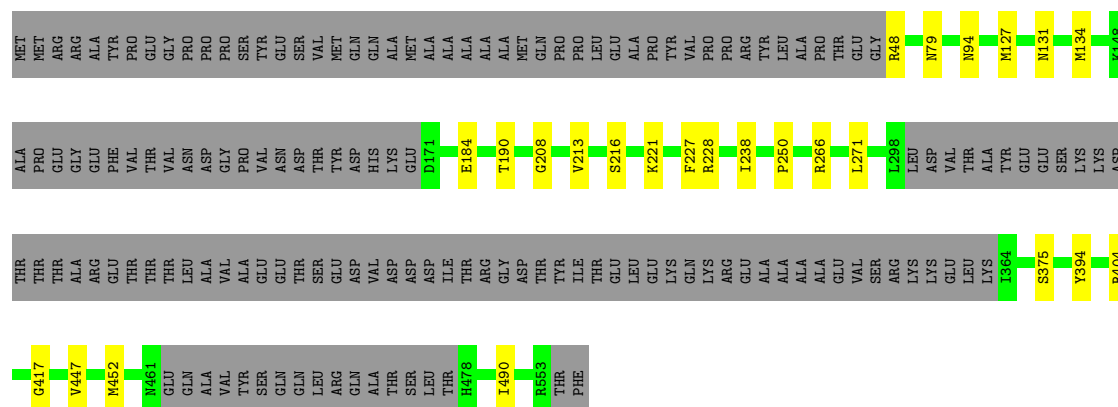
• Molecule 1: Penton protein

Chain Q: 69% 27%

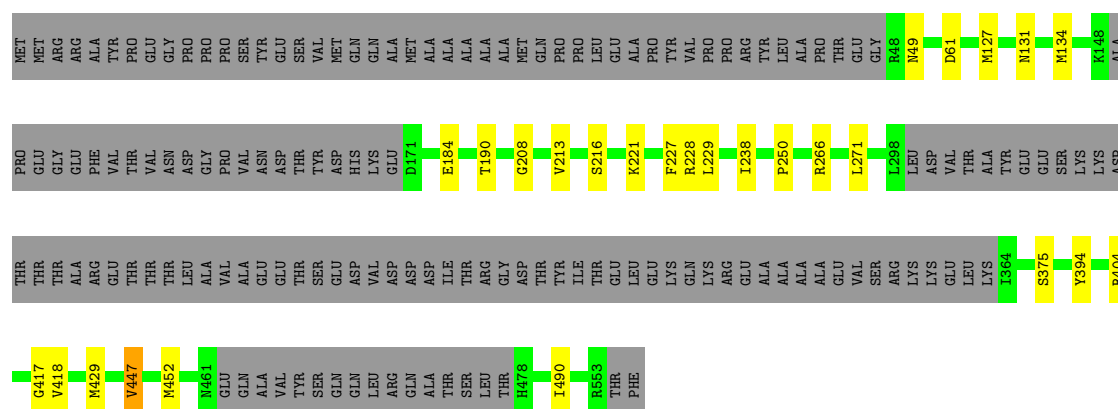


• Molecule 1: Penton protein

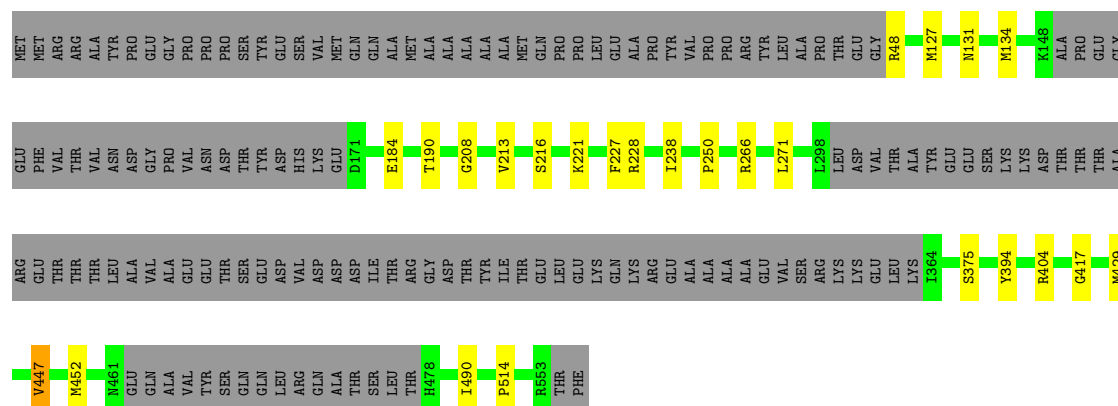
Chain R: 69% 27%



- Molecule 1: Penton protein

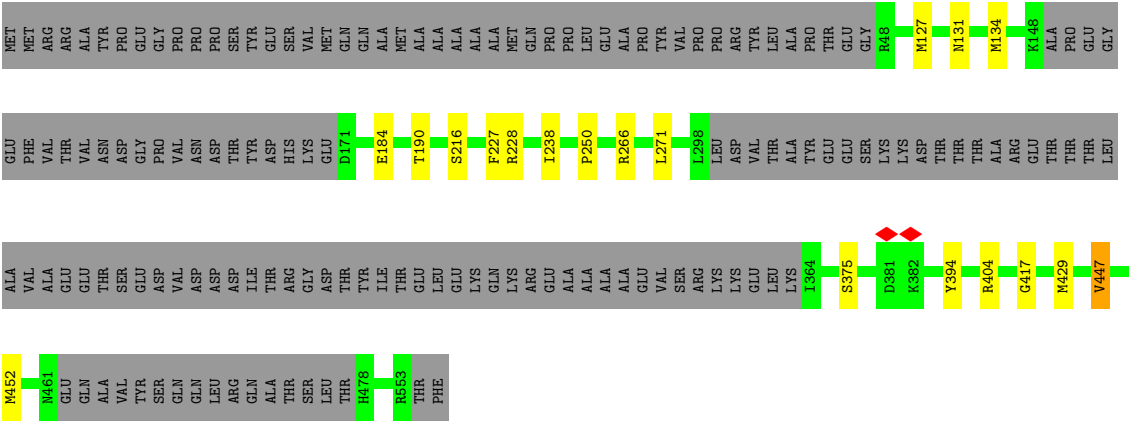


- Molecule 1: Penton protein

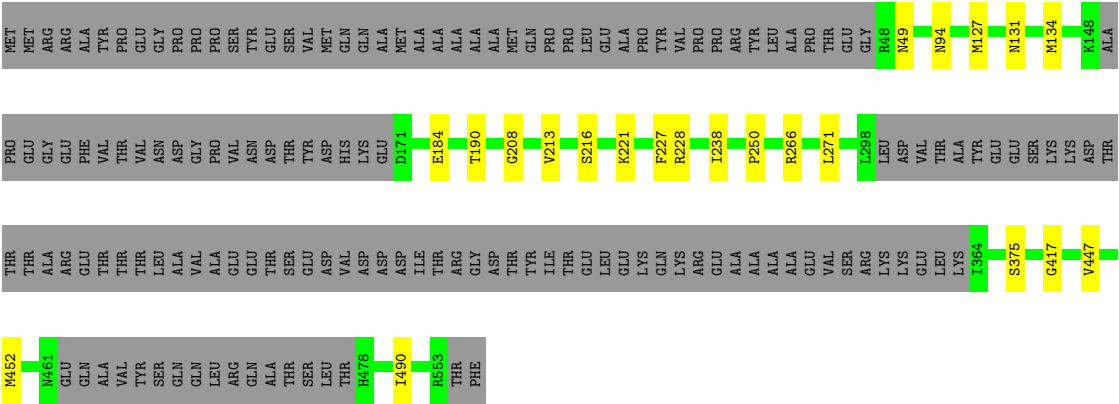


- Molecule 1: Penton protein

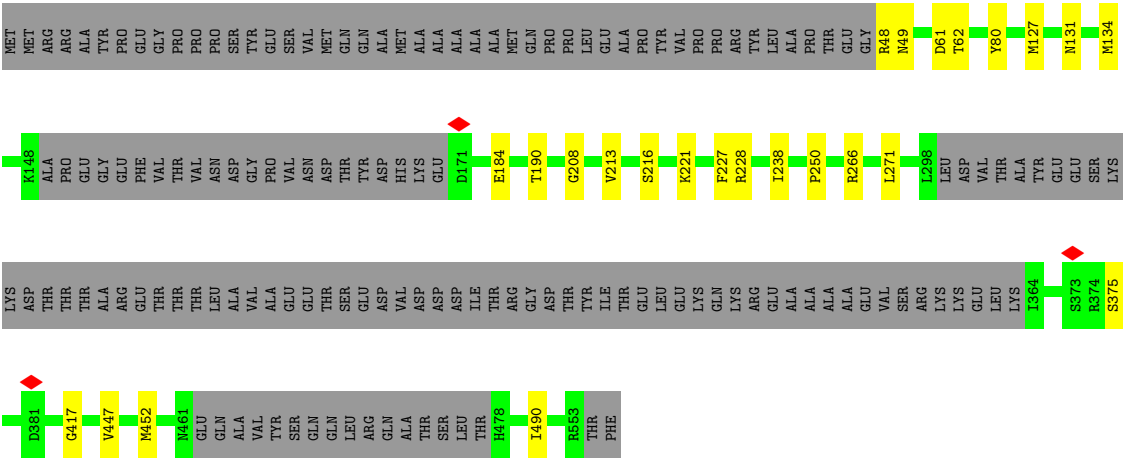




• Molecule 1: Penton protein



• Molecule 1: Penton protein



• Molecule 1: Penton protein

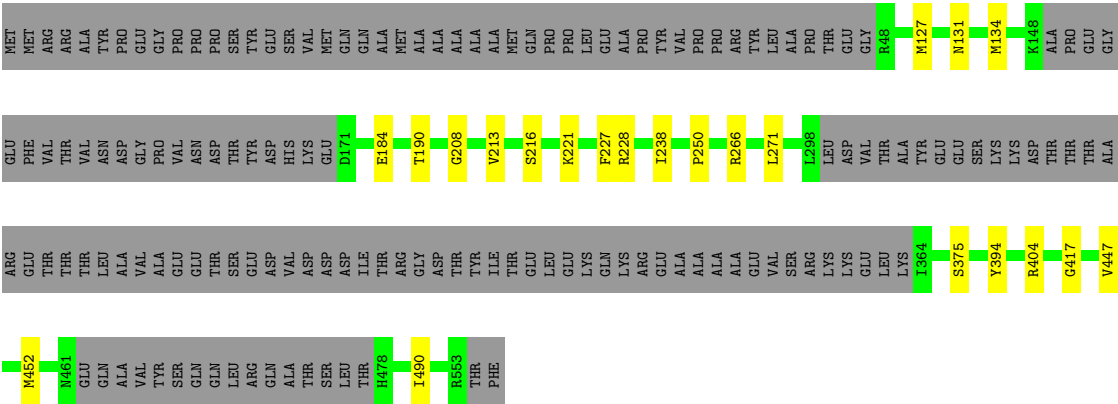
[illegible][illegible]

V447	THR	ALA
M452	THR	PRO
F459	ARG	GLY
M461	GLU	PHE
GLU	THR	VAL
GLN	THR	VAL
ALA	LEU	ASN
VAL	ALA	ASP
TYR	VAL	GLY
SER	ALA	PRO
GLN	GLU	VAL
LEU	THR	ASN
ARG	SER	ASP
GLN	GLU	THR
ALA	GLU	TYR
ALA	ASP	ASP
THR	VAL	LYS
SER	ASP	GLU
LEU	ILE	D171
THR	THR	E184
H478	ARG	T190
I490	GLY	G208
P514	ASP	V213
R553	THR	S216
THR	THR	K221
PHE	LYS	F227
	GLN	R228
	LYS	I238
	ARG	P250
	GLU	R266
	ALA	L271
	VAL	I298
	GLU	LEU
	SER	ASP
	ARG	VAL
	LYS	THR
	LEU	ALA
	LYS	TYR
	THR	GLU
	GLY	SER
	THR	LYS
	VAL	ASP
	THR	THR
	GLU	GLY
	ARG	R48
	LYS	T62
	THR	S113
	LEU	M127
	ALA	M131
	PRO	M134
	THR	R148

Chain KA:

69%

27%

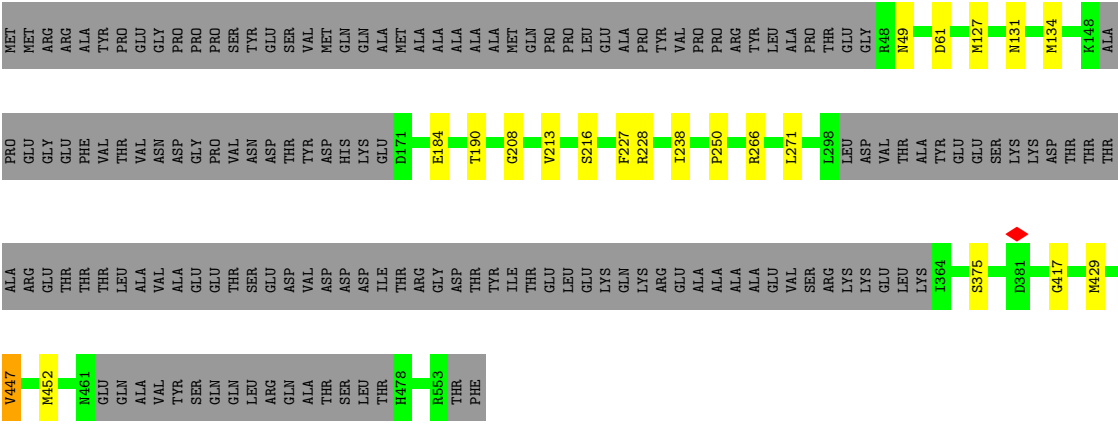


• Molecule 1: Penton protein

Chain LA:

69%

27%



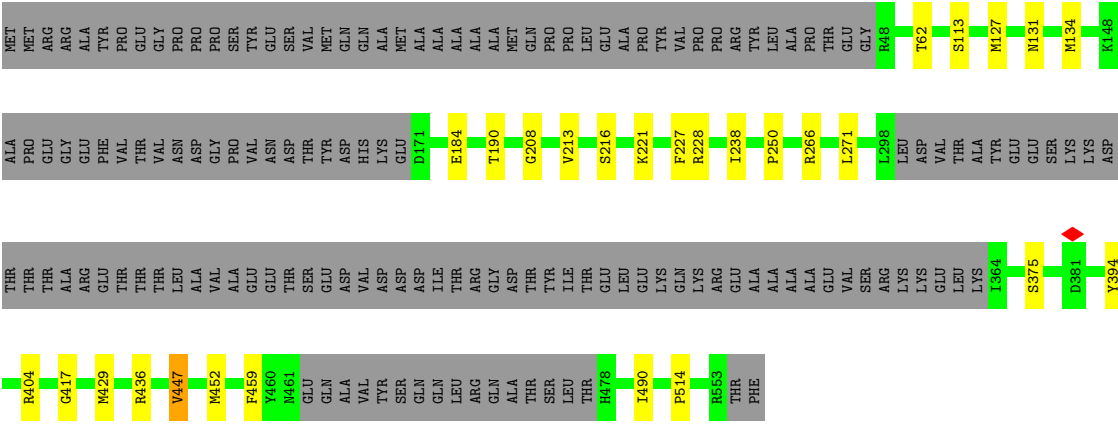
• Molecule 1: Penton protein

Chain MA:

68%

5%

27%



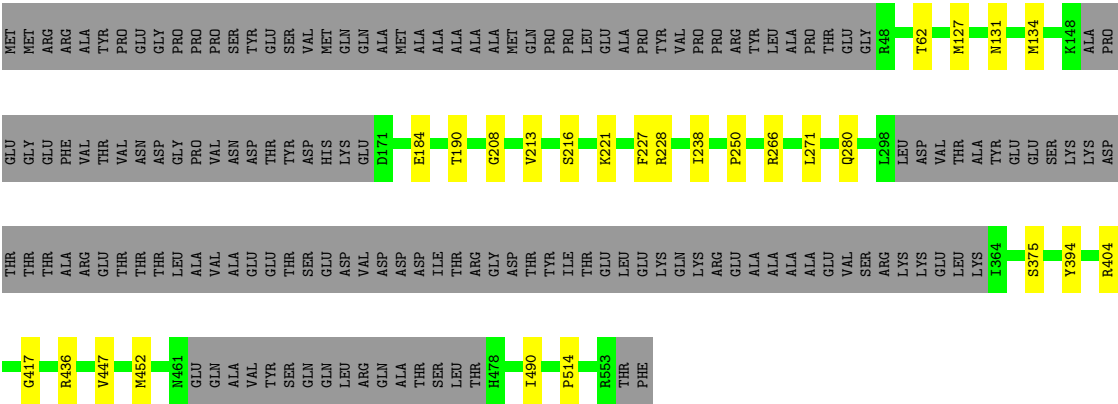
• Molecule 1: Penton protein

Chain NA:

68%

5%

27%



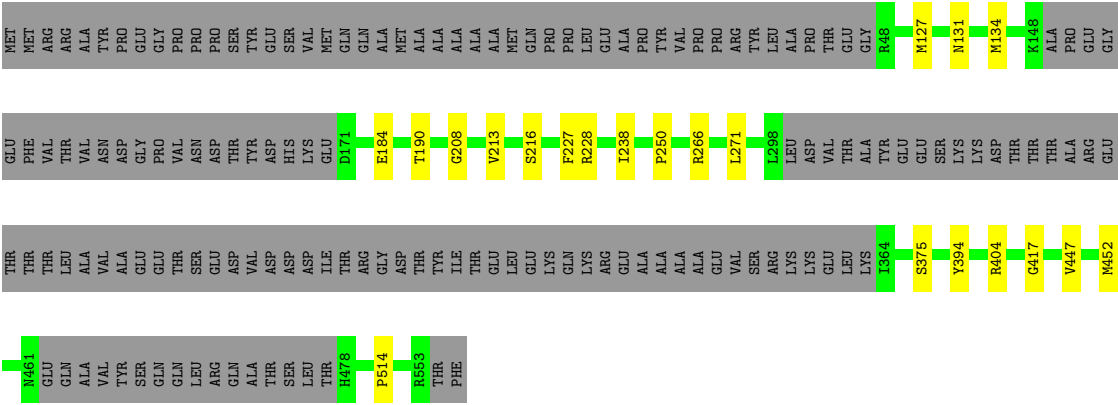
• Molecule 1: Penton protein

Chain OA:

69%

•

27%



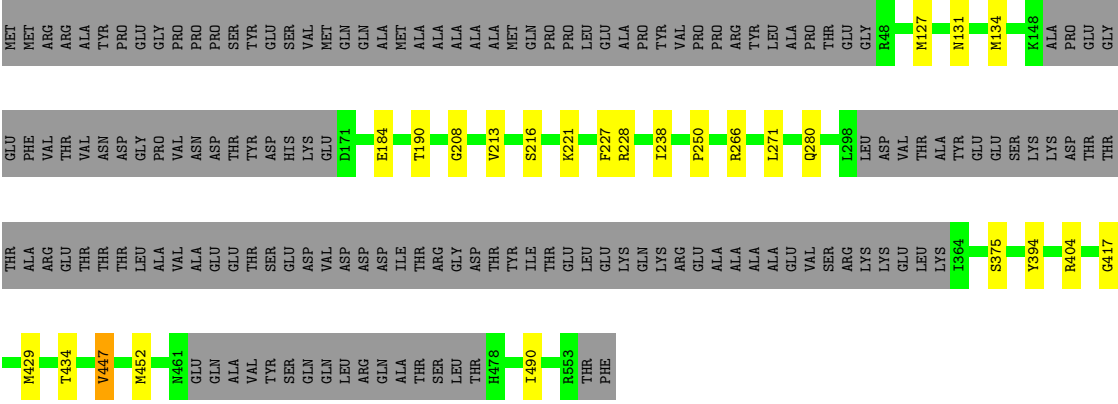
• Molecule 1: Penton protein

Chain PA:

68%

•

27%



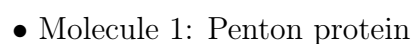
• Molecule 1: Penton protein

GLU	THR	ALA	MET
GLN	THR	PRO	ARG
ALA	THR	GLU	ARG
VAL	LEU	GLY	ALA
THR	ALA	GLU	ALA
SER	VAL	PHE	TYR
GLN	ALA	VAL	PRO
GLN	GLU	THR	GLU
LEU	GLU	VAL	GLY
ARG	THR	ASN	PRO
GLN	SER	ASP	PRO
ALA	GLU	GLY	SER
THR	ASP	PRO	TYR
SER	VAL	VAL	GLU
LEU	ASP	ASN	SER
THR	ASP	THR	VAL
R478	ASP	TYR	MET
P514	ILE	THR	GLN
R553	ARG	ASP	GLN
THR	THR	LYS	ALA
PHE	THR	GLY	MET
	THR	D171	ALA
	ILE	E184	ALA
	GLU	T190	ALA
	LEU	S216	MET
	LYS	F227	GLN
	GLN	R228	PRO
	LYS	I238	LEU
	ARG	P250	GLU
	GLU	R266	ALA
	ALA	L271	PRO
	ALA	I298	ARG
	ALA	LEU	TYR
	LYS	ASP	LEU
	GLU	VAL	ALA
	LEU	THR	PRO
	LYS	ALA	THR
	T364	TYR	GLY
	S375	GLU	R48
	G417	SER	T62
	M429	LYS	Q93
	V447	ASP	M127
	M452	THR	N131
	V463	THR	M134
		ALA	M134
		ARG	V148
		GLU	

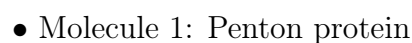
M452	ALA	THR	ALA	PRO	MET
N461	GLU	ARG	GLU	GLY	ARG
	GLN	THR	THR	GLU	ALA
	ALA	THR	THR	PHE	TYR
	VAL	THR	LEU	VAL	GLU
	TYR	ALA	ALA	VAL	GLY
	SER	VAL	VAL	ASN	PRO
	GLN	ALA	ASP	ASP	PRO
	GLN	GLU	GLY	GLY	PRO
	LEU	GLU	GLU	PRO	SER
	ARG	GLU	VAL	SER	TYR
	ALA	SER	ASN	GLU	GLY
	ALA	ASP	ASP	VAL	VAL
	THR	GLU	THR	THR	MET
	SER	VAL	TYR	TYR	GLN
	LEU	ASP	ASP	ASP	GLN
	THR	ASP	HIS	HIS	GLY
H478	ALA	ASP	LYS	LYS	MET
	THR	ILE	GLU	GLU	ALA
P514	ALA	THR	D171	ALA	ALA
	THR	ARG	ALA	ALA	ALA
R553	GLY	THR	E184	ALA	ALA
	THR	ASP	ALA	ALA	ALA
PHE	THR	THR	T190	ALA	MET
	PHE	TYR	G208	GLN	GLN
		ILE			PRO
		THR	V213	LEU	LEU
		LEU	S216	GLU	GLU
		GLU			ALA
		LYS	F227	PRO	ALA
		GLN	R228	TYR	TYR
		LYS		VAL	VAL
		ARG	I238	PRO	PRO
		GLU		PRO	PRO
		ALA	P250	ARG	ARG
		ALA		TYR	TYR
		ALA	R266	LEU	LEU
		GLU		ALA	ALA
		GLU	L271	PRO	PRO
		VAL		THR	THR
		SER		GLU	GLY
		ARG	L298	GLY	GLY
		LYS	LEU	ASP	R46
		LYS	ASP	VAL	N49
		GLU	THR	THR	
		LEU	ALA	ALA	D61
		LEU	TYR	TYR	T62
	I364		GLU	GLU	M127
S375			GLU	GLU	
			SER	SER	
			LYS	LYS	N131
D381			LYS	LYS	
			ASP	ASP	M134
G417			THR	THR	
			THR	THR	N138

[illegible]

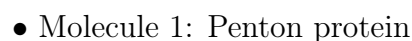
Device Type	Percentage
Smartphone	67%
Tablet	5%
Other mobile device	27%



Response	Percentage
Doing a good job	68%
Doing a bad job	27%



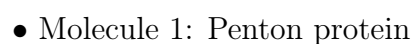
Response	Percentage
Doing a good job	68%
Doing a bad job	27%



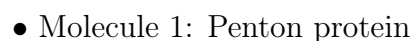
[illegible][illegible][illegible]

[illegible][illegible][illegible]

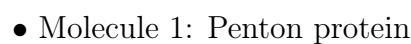
Response	Percentage
Yes	69%
No	27%



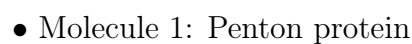
Response	Percentage
Yes, more action should be taken	68%
No, the U.S. is already doing enough	27%
Don't know	5%



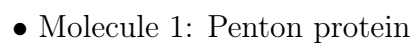
Government	Percentage
Current government	69%
Previous government	27%



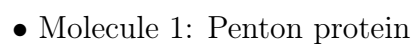
69% . 27%



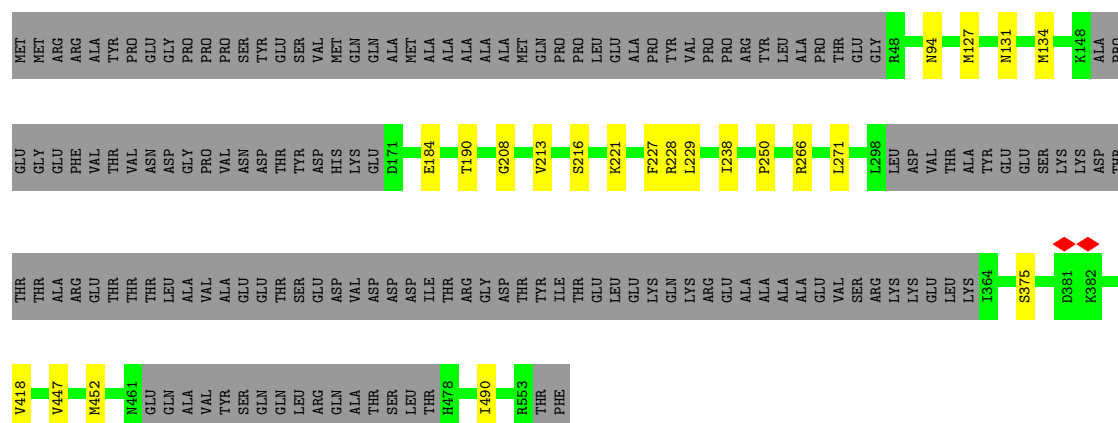
App Type	Percentage
Mobile app	68%
Mobile app	5%
Mobile app	27%



Opinion	Percentage
Doing a good job	69%
Doing a bad job	27%



Response	Percentage
Yes	68%
No	27%
Don't know	5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	566795	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.06	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.309	Depositor
Minimum map value	-0.169	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.0232	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.22	0/3138	0.44	0/4293
1	AA	0.22	0/3138	0.44	0/4293
1	AB	0.22	0/3138	0.44	0/4293
1	B	0.22	0/3138	0.44	0/4293
1	BA	0.22	0/3132	0.44	0/4286
1	BB	0.22	0/3138	0.44	0/4293
1	C	0.22	0/3138	0.44	0/4293
1	CA	0.22	0/3138	0.44	0/4293
1	CB	0.22	0/3138	0.44	0/4293
1	D	0.22	0/3138	0.44	0/4293
1	DA	0.22	0/3138	0.44	0/4293
1	DB	0.22	0/3138	0.44	0/4293
1	E	0.22	0/3138	0.44	0/4293
1	EA	0.22	0/3138	0.44	0/4293
1	EB	0.22	0/3138	0.44	0/4293
1	F	0.22	0/3137	0.44	0/4292
1	FA	0.22	0/3138	0.44	0/4293
1	FB	0.22	0/3138	0.44	0/4293
1	G	0.22	0/3138	0.44	0/4293
1	GA	0.22	0/3138	0.44	0/4293
1	GB	0.22	0/3138	0.44	0/4293
1	H	0.22	0/3138	0.44	0/4293
1	HA	0.22	0/3138	0.44	0/4293
1	HB	0.22	0/3138	0.44	0/4293
1	I	0.22	0/3137	0.44	0/4292
1	IA	0.22	0/3138	0.44	0/4293
1	IB	0.22	0/3138	0.44	0/4293
1	J	0.22	0/3132	0.44	0/4286
1	JA	0.22	0/3138	0.44	0/4293
1	K	0.22	0/3138	0.44	0/4293
1	KA	0.22	0/3138	0.44	0/4293
1	L	0.22	0/3138	0.44	0/4293
1	LA	0.22	0/3138	0.44	0/4293
1	M	0.22	0/3138	0.44	0/4293

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	MA	0.22	0/3138	0.44	0/4293
1	N	0.22	0/3138	0.44	0/4293
1	NA	0.22	0/3138	0.44	0/4293
1	O	0.22	0/3138	0.44	0/4293
1	OA	0.22	0/3138	0.44	0/4293
1	P	0.22	0/3138	0.44	0/4293
1	PA	0.22	0/3138	0.44	0/4293
1	Q	0.22	0/3138	0.44	0/4293
1	QA	0.22	0/3138	0.44	0/4293
1	R	0.22	0/3138	0.44	0/4293
1	RA	0.22	0/3138	0.44	0/4293
1	S	0.22	0/3138	0.44	0/4293
1	SA	0.22	0/3138	0.44	0/4293
1	T	0.22	0/3138	0.44	0/4293
1	TA	0.22	0/3138	0.44	0/4293
1	UA	0.22	0/3138	0.44	0/4293
1	V	0.22	0/3138	0.44	0/4293
1	VA	0.22	0/3138	0.44	0/4293
1	W	0.22	0/3138	0.44	0/4293
1	WA	0.22	0/3138	0.44	0/4293
1	X	0.22	0/3138	0.44	0/4293
1	XA	0.22	0/3138	0.44	0/4293
1	Y	0.22	0/3138	0.44	0/4293
1	YA	0.22	0/3138	0.44	0/4293
1	Z	0.22	0/3138	0.44	0/4293
1	ZA	0.22	0/3138	0.44	0/4293
All	All	0.22	0/188266	0.44	0/257564

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

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	3062	0	2857	13	0
1	AA	3062	0	2857	15	0
1	AB	3062	0	2857	13	0
1	B	3062	0	2857	12	0
1	BA	3056	0	2846	21	0
1	BB	3062	0	2857	14	0
1	C	3062	0	2857	16	0
1	CA	3062	0	2857	11	0
1	CB	3062	0	2857	11	0
1	D	3062	0	2857	17	0
1	DA	3062	0	2857	13	0
1	DB	3062	0	2857	15	0
1	E	3062	0	2857	13	0
1	EA	3062	0	2857	10	0
1	EB	3062	0	2857	13	0
1	F	3061	0	2854	14	0
1	FA	3062	0	2857	12	0
1	FB	3062	0	2857	9	0
1	G	3062	0	2857	13	0
1	GA	3062	0	2857	15	0
1	GB	3062	0	2857	18	0
1	H	3062	0	2857	18	0
1	HA	3062	0	2857	12	0
1	HB	3062	0	2857	13	0
1	I	3061	0	2854	20	0
1	IA	3062	0	2857	12	0
1	IB	3062	0	2857	13	0
1	J	3056	0	2846	13	0
1	JA	3062	0	2857	16	0
1	K	3062	0	2857	13	0
1	KA	3062	0	2857	11	0
1	L	3062	0	2857	13	0
1	LA	3062	0	2857	12	0
1	M	3062	0	2857	15	0
1	MA	3062	0	2857	17	0
1	N	3062	0	2857	12	0
1	NA	3062	0	2857	15	0
1	O	3062	0	2857	14	0
1	OA	3062	0	2857	11	0
1	P	3062	0	2857	14	0
1	PA	3062	0	2857	15	0
1	Q	3062	0	2857	12	0
1	QA	3062	0	2857	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	3062	0	2857	10	0
1	RA	3062	0	2857	13	0
1	S	3062	0	2857	16	0
1	SA	3062	0	2857	14	0
1	T	3062	0	2857	15	0
1	TA	3062	0	2857	19	0
1	UA	3062	0	2857	13	0
1	V	3062	0	2857	14	0
1	VA	3062	0	2857	14	0
1	W	3062	0	2857	16	0
1	WA	3062	0	2857	17	0
1	X	3062	0	2857	14	0
1	XA	3062	0	2857	10	0
1	Y	3062	0	2857	15	0
1	YA	3062	0	2857	17	0
1	Z	3062	0	2857	16	0
1	ZA	3062	0	2857	13	0
All	All	183706	0	171392	740	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 2.

All (740) 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:BA:62:THR:HG23	1:DB:514:PRO:HD3	1.62	0.82
1:I:514:PRO:HD3	1:TA:62:THR:HG23	1.73	0.71
1:O:266:ARG:NH2	1:O:417:GLY:O	2.29	0.66
1:J:266:ARG:NH2	1:J:417:GLY:O	2.29	0.66
1:IA:266:ARG:NH2	1:IA:417:GLY:O	2.29	0.66
1:RA:266:ARG:NH2	1:RA:417:GLY:O	2.29	0.66
1:DB:266:ARG:NH2	1:DB:417:GLY:O	2.29	0.66
1:E:266:ARG:NH2	1:E:417:GLY:O	2.29	0.66
1:I:266:ARG:NH2	1:I:417:GLY:O	2.29	0.66
1:L:266:ARG:NH2	1:L:417:GLY:O	2.29	0.66
1:PA:266:ARG:NH2	1:PA:417:GLY:O	2.29	0.66
1:HB:266:ARG:NH2	1:HB:417:GLY:O	2.29	0.66
1:K:266:ARG:NH2	1:K:417:GLY:O	2.29	0.66
1:P:266:ARG:NH2	1:P:417:GLY:O	2.29	0.66
1:R:266:ARG:NH2	1:R:417:GLY:O	2.29	0.66
1:S:266:ARG:NH2	1:S:417:GLY:O	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:266:ARG:NH2	1:BA:417:GLY:O	2.29	0.66
1:YA:266:ARG:NH2	1:YA:417:GLY:O	2.29	0.66
1:AA:266:ARG:NH2	1:AA:417:GLY:O	2.29	0.66
1:WA:266:ARG:NH2	1:WA:417:GLY:O	2.29	0.66
1:B:266:ARG:NH2	1:B:417:GLY:O	2.29	0.66
1:DA:266:ARG:NH2	1:DA:417:GLY:O	2.29	0.66
1:OA:266:ARG:NH2	1:OA:417:GLY:O	2.29	0.66
1:BB:266:ARG:NH2	1:BB:417:GLY:O	2.29	0.66
1:EB:266:ARG:NH2	1:EB:417:GLY:O	2.29	0.66
1:CB:266:ARG:NH2	1:CB:417:GLY:O	2.29	0.65
1:T:266:ARG:NH2	1:T:417:GLY:O	2.29	0.65
1:GA:266:ARG:NH2	1:GA:417:GLY:O	2.29	0.65
1:HA:266:ARG:NH2	1:HA:417:GLY:O	2.29	0.65
1:UA:266:ARG:NH2	1:UA:417:GLY:O	2.29	0.65
1:N:266:ARG:NH2	1:N:417:GLY:O	2.29	0.65
1:Y:266:ARG:NH2	1:Y:417:GLY:O	2.29	0.65
1:GB:266:ARG:NH2	1:GB:417:GLY:O	2.29	0.65
1:A:266:ARG:NH2	1:A:417:GLY:O	2.29	0.65
1:M:266:ARG:NH2	1:M:417:GLY:O	2.29	0.65
1:Q:266:ARG:NH2	1:Q:417:GLY:O	2.29	0.65
1:EA:266:ARG:NH2	1:EA:417:GLY:O	2.29	0.65
1:JA:266:ARG:NH2	1:JA:417:GLY:O	2.29	0.65
1:J:62:THR:HG23	1:O:514:PRO:HD3	1.76	0.65
1:KA:266:ARG:NH2	1:KA:417:GLY:O	2.29	0.65
1:XA:266:ARG:NH2	1:XA:417:GLY:O	2.29	0.65
1:D:266:ARG:NH2	1:D:417:GLY:O	2.29	0.65
1:H:266:ARG:NH2	1:H:417:GLY:O	2.29	0.65
1:FA:266:ARG:NH2	1:FA:417:GLY:O	2.29	0.65
1:TA:266:ARG:NH2	1:TA:417:GLY:O	2.29	0.65
1:G:266:ARG:NH2	1:G:417:GLY:O	2.29	0.65
1:W:266:ARG:NH2	1:W:417:GLY:O	2.29	0.65
1:VA:266:ARG:NH2	1:VA:417:GLY:O	2.29	0.65
1:IB:266:ARG:NH2	1:IB:417:GLY:O	2.29	0.65
1:S:460:TYR:HB2	1:JA:459:PHE:CD1	2.32	0.65
1:LA:266:ARG:NH2	1:LA:417:GLY:O	2.29	0.65
1:MA:266:ARG:NH2	1:MA:417:GLY:O	2.29	0.65
1:CA:266:ARG:NH2	1:CA:417:GLY:O	2.29	0.65
1:F:266:ARG:NH2	1:F:417:GLY:O	2.29	0.64
1:X:266:ARG:NH2	1:X:417:GLY:O	2.29	0.64
1:NA:266:ARG:NH2	1:NA:417:GLY:O	2.29	0.64
1:QA:266:ARG:NH2	1:QA:417:GLY:O	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ZA:266:ARG:NH2	1:ZA:417:GLY:O	2.29	0.64
1:S:460:TYR:HB2	1:JA:459:PHE:CG	2.31	0.64
1:AB:266:ARG:NH2	1:AB:417:GLY:O	2.29	0.64
1:FB:266:ARG:NH2	1:FB:417:GLY:O	2.29	0.64
1:SA:266:ARG:NH2	1:SA:417:GLY:O	2.29	0.64
1:V:266:ARG:NH2	1:V:417:GLY:O	2.29	0.64
1:C:266:ARG:NH2	1:C:417:GLY:O	2.29	0.64
1:Z:266:ARG:NH2	1:Z:417:GLY:O	2.29	0.64
1:M:94:ASN:OD1	1:MA:436:ARG:NH1	2.30	0.64
1:I:62:THR:HG23	1:J:514:PRO:HD3	1.81	0.63
1:I:110:ASP:OD2	1:BA:48:ARG:HA	2.02	0.60
1:BA:94:ASN:OD1	1:DB:436:ARG:NH1	2.32	0.60
1:H:514:PRO:HD3	1:GB:62:THR:HG23	1.84	0.58
1:WA:62:THR:HG23	1:HB:514:PRO:HD3	1.86	0.57
1:H:61:ASP:OD1	1:GA:49:ASN:ND2	2.35	0.57
1:C:62:THR:HG23	1:WA:514:PRO:HD3	1.86	0.56
1:H:49:ASN:ND2	1:GA:61:ASP:OD1	2.34	0.55
1:D:79:ASN:O	1:Y:279:PHE:HB2	2.07	0.55
1:BA:62:THR:CG2	1:DB:514:PRO:HD3	2.35	0.55
1:MA:62:THR:HG23	1:EB:514:PRO:HD3	1.88	0.55
1:DA:436:ARG:HD2	1:IA:436:ARG:HD2	1.89	0.54
1:E:62:THR:HG23	1:BB:514:PRO:HD3	1.89	0.53
1:J:94:ASN:OD1	1:O:436:ARG:NH1	2.40	0.53
1:FA:94:ASN:OD1	1:VA:436:ARG:NH1	2.40	0.53
1:C:436:ARG:NH1	1:ZA:94:ASN:OD1	2.37	0.53
1:D:216:SER:OG	1:D:375:SER:O	2.27	0.53
1:ZA:216:SER:OG	1:ZA:375:SER:O	2.27	0.53
1:E:216:SER:OG	1:E:375:SER:O	2.27	0.52
1:H:216:SER:OG	1:H:375:SER:O	2.27	0.52
1:I:48:ARG:CZ	1:BA:552:SER:HB2	2.40	0.52
1:R:216:SER:OG	1:R:375:SER:O	2.27	0.52
1:CA:216:SER:OG	1:CA:375:SER:O	2.27	0.52
1:FA:216:SER:OG	1:FA:375:SER:O	2.27	0.52
1:QA:514:PRO:HD3	1:AB:62:THR:HG23	1.90	0.52
1:C:94:ASN:OD1	1:WA:436:ARG:NH1	2.42	0.52
1:C:216:SER:OG	1:C:375:SER:O	2.27	0.52
1:P:216:SER:OG	1:P:375:SER:O	2.27	0.52
1:Q:216:SER:OG	1:Q:375:SER:O	2.27	0.52
1:N:216:SER:OG	1:N:375:SER:O	2.27	0.52
1:T:61:ASP:OD1	1:GB:49:ASN:ND2	2.25	0.52
1:W:216:SER:OG	1:W:375:SER:O	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:216:SER:OG	1:DA:375:SER:O	2.27	0.52
1:YA:216:SER:OG	1:YA:375:SER:O	2.27	0.52
1:BB:216:SER:OG	1:BB:375:SER:O	2.27	0.52
1:I:48:ARG:NH1	1:BA:552:SER:HA	2.24	0.52
1:EA:216:SER:OG	1:EA:375:SER:O	2.27	0.52
1:XA:216:SER:OG	1:XA:375:SER:O	2.27	0.52
1:M:216:SER:OG	1:M:375:SER:O	2.27	0.52
1:T:216:SER:OG	1:T:375:SER:O	2.27	0.52
1:Y:216:SER:OG	1:Y:375:SER:O	2.27	0.52
1:CA:94:ASN:OD1	1:HA:436:ARG:NH1	2.38	0.52
1:SA:216:SER:OG	1:SA:375:SER:O	2.27	0.52
1:TA:216:SER:OG	1:TA:375:SER:O	2.27	0.52
1:EB:216:SER:OG	1:EB:375:SER:O	2.27	0.52
1:I:216:SER:OG	1:I:375:SER:O	2.27	0.52
1:L:216:SER:OG	1:L:375:SER:O	2.27	0.52
1:IA:216:SER:OG	1:IA:375:SER:O	2.27	0.52
1:GB:216:SER:OG	1:GB:375:SER:O	2.27	0.52
1:IB:216:SER:OG	1:IB:375:SER:O	2.27	0.52
1:F:216:SER:OG	1:F:375:SER:O	2.27	0.52
1:AA:216:SER:OG	1:AA:375:SER:O	2.27	0.52
1:HA:216:SER:OG	1:HA:375:SER:O	2.27	0.52
1:VA:216:SER:OG	1:VA:375:SER:O	2.27	0.52
1:WA:216:SER:OG	1:WA:375:SER:O	2.27	0.52
1:O:216:SER:OG	1:O:375:SER:O	2.27	0.52
1:Z:216:SER:OG	1:Z:375:SER:O	2.27	0.52
1:RA:216:SER:OG	1:RA:375:SER:O	2.27	0.52
1:UA:216:SER:OG	1:UA:375:SER:O	2.27	0.52
1:X:216:SER:OG	1:X:375:SER:O	2.27	0.52
1:GA:216:SER:OG	1:GA:375:SER:O	2.27	0.52
1:KA:216:SER:OG	1:KA:375:SER:O	2.27	0.52
1:QA:216:SER:OG	1:QA:375:SER:O	2.27	0.52
1:B:216:SER:OG	1:B:375:SER:O	2.27	0.51
1:I:48:ARG:NH2	1:BA:552:SER:HB2	2.25	0.51
1:S:216:SER:OG	1:S:375:SER:O	2.27	0.51
1:JA:216:SER:OG	1:JA:375:SER:O	2.27	0.51
1:LA:216:SER:OG	1:LA:375:SER:O	2.27	0.51
1:OA:216:SER:OG	1:OA:375:SER:O	2.27	0.51
1:D:94:ASN:OD1	1:Y:436:ARG:NH1	2.40	0.51
1:K:94:ASN:OD1	1:TA:436:ARG:NH1	2.41	0.51
1:V:216:SER:OG	1:V:375:SER:O	2.27	0.51
1:G:216:SER:OG	1:G:375:SER:O	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:216:SER:OG	1:J:375:SER:O	2.27	0.51
1:MA:216:SER:OG	1:MA:375:SER:O	2.27	0.51
1:A:216:SER:OG	1:A:375:SER:O	2.27	0.51
1:K:216:SER:OG	1:K:375:SER:O	2.27	0.51
1:BA:216:SER:OG	1:BA:375:SER:O	2.27	0.51
1:CB:216:SER:OG	1:CB:375:SER:O	2.27	0.51
1:HB:216:SER:OG	1:HB:375:SER:O	2.27	0.51
1:RA:227:PHE:O	1:RA:228:ARG:HG2	2.11	0.51
1:AB:216:SER:OG	1:AB:375:SER:O	2.27	0.51
1:A:227:PHE:O	1:A:228:ARG:HG2	2.11	0.51
1:O:227:PHE:O	1:O:228:ARG:HG2	2.11	0.51
1:DA:227:PHE:O	1:DA:228:ARG:HG2	2.11	0.51
1:MA:227:PHE:O	1:MA:228:ARG:HG2	2.11	0.51
1:NA:216:SER:OG	1:NA:375:SER:O	2.27	0.51
1:FB:216:SER:OG	1:FB:375:SER:O	2.27	0.51
1:FB:227:PHE:O	1:FB:228:ARG:HG2	2.11	0.51
1:E:227:PHE:O	1:E:228:ARG:HG2	2.11	0.50
1:J:227:PHE:O	1:J:228:ARG:HG2	2.11	0.50
1:WA:227:PHE:O	1:WA:228:ARG:HG2	2.11	0.50
1:AB:227:PHE:O	1:AB:228:ARG:HG2	2.11	0.50
1:DB:216:SER:OG	1:DB:375:SER:O	2.27	0.50
1:EB:227:PHE:O	1:EB:228:ARG:HG2	2.11	0.50
1:L:227:PHE:O	1:L:228:ARG:HG2	2.11	0.50
1:W:61:ASP:OD1	1:RA:49:ASN:ND2	2.35	0.50
1:KA:227:PHE:O	1:KA:228:ARG:HG2	2.11	0.50
1:UA:227:PHE:O	1:UA:228:ARG:HG2	2.11	0.50
1:DB:227:PHE:O	1:DB:228:ARG:HG2	2.11	0.50
1:H:227:PHE:O	1:H:228:ARG:HG2	2.11	0.50
1:BA:227:PHE:O	1:BA:228:ARG:HG2	2.11	0.50
1:GA:227:PHE:O	1:GA:228:ARG:HG2	2.11	0.50
1:NA:227:PHE:O	1:NA:228:ARG:HG2	2.11	0.50
1:EA:227:PHE:O	1:EA:228:ARG:HG2	2.11	0.50
1:ZA:227:PHE:O	1:ZA:228:ARG:HG2	2.11	0.50
1:K:227:PHE:O	1:K:228:ARG:HG2	2.11	0.50
1:L:127:MET:HE3	1:L:452:MET:HE2	1.94	0.50
1:Q:227:PHE:O	1:Q:228:ARG:HG2	2.11	0.50
1:FA:227:PHE:O	1:FA:228:ARG:HG2	2.11	0.50
1:PA:216:SER:OG	1:PA:375:SER:O	2.27	0.50
1:CB:227:PHE:O	1:CB:228:ARG:HG2	2.11	0.50
1:D:227:PHE:O	1:D:228:ARG:HG2	2.11	0.50
1:P:227:PHE:O	1:P:228:ARG:HG2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:227:PHE:O	1:Y:228:ARG:HG2	2.11	0.50
1:IA:227:PHE:O	1:IA:228:ARG:HG2	2.11	0.50
1:V:127:MET:HE3	1:V:452:MET:HE2	1.94	0.50
1:X:227:PHE:O	1:X:228:ARG:HG2	2.11	0.50
1:AA:227:PHE:O	1:AA:228:ARG:HG2	2.11	0.50
1:HA:227:PHE:O	1:HA:228:ARG:HG2	2.11	0.50
1:JA:227:PHE:O	1:JA:228:ARG:HG2	2.11	0.50
1:TA:227:PHE:O	1:TA:228:ARG:HG2	2.11	0.50
1:UA:127:MET:HE3	1:UA:452:MET:HE2	1.94	0.50
1:EB:127:MET:HE3	1:EB:452:MET:HE2	1.94	0.50
1:I:227:PHE:O	1:I:228:ARG:HG2	2.11	0.50
1:T:127:MET:HE3	1:T:452:MET:HE2	1.94	0.50
1:T:227:PHE:O	1:T:228:ARG:HG2	2.11	0.50
1:IA:127:MET:HE3	1:IA:452:MET:HE2	1.94	0.50
1:OA:227:PHE:O	1:OA:228:ARG:HG2	2.11	0.50
1:QA:227:PHE:O	1:QA:228:ARG:HG2	2.11	0.50
1:SA:127:MET:HE3	1:SA:452:MET:HE2	1.94	0.50
1:GB:127:MET:HE3	1:GB:452:MET:HE2	1.94	0.50
1:HB:227:PHE:O	1:HB:228:ARG:HG2	2.12	0.50
1:IB:127:MET:HE3	1:IB:452:MET:HE2	1.94	0.50
1:IB:227:PHE:O	1:IB:228:ARG:HG2	2.11	0.50
1:B:127:MET:HE3	1:B:452:MET:HE2	1.94	0.50
1:E:127:MET:HE3	1:E:452:MET:HE2	1.94	0.50
1:I:127:MET:HE3	1:I:452:MET:HE2	1.94	0.50
1:O:127:MET:HE3	1:O:452:MET:HE2	1.94	0.50
1:Q:127:MET:HE3	1:Q:452:MET:HE2	1.94	0.50
1:NA:127:MET:HE3	1:NA:452:MET:HE2	1.94	0.50
1:D:48:ARG:NH1	1:WA:113:SER:OG	2.42	0.49
1:W:127:MET:HE3	1:W:452:MET:HE2	1.94	0.49
1:W:227:PHE:O	1:W:228:ARG:HG2	2.11	0.49
1:OA:127:MET:HE3	1:OA:452:MET:HE2	1.94	0.49
1:SA:227:PHE:O	1:SA:228:ARG:HG2	2.11	0.49
1:ZA:127:MET:HE3	1:ZA:452:MET:HE2	1.94	0.49
1:DB:127:MET:HE3	1:DB:452:MET:HE2	1.94	0.49
1:Y:48:ARG:NH1	1:MA:113:SER:OG	2.43	0.49
1:KA:127:MET:HE3	1:KA:452:MET:HE2	1.94	0.49
1:TA:127:MET:HE3	1:TA:452:MET:HE2	1.94	0.49
1:VA:227:PHE:O	1:VA:228:ARG:HG2	2.11	0.49
1:XA:227:PHE:O	1:XA:228:ARG:HG2	2.11	0.49
1:K:127:MET:HE3	1:K:452:MET:HE2	1.94	0.49
1:N:227:PHE:O	1:N:228:ARG:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JA:127:MET:HE3	1:JA:452:MET:HE2	1.94	0.49
1:PA:127:MET:HE3	1:PA:452:MET:HE2	1.94	0.49
1:BB:227:PHE:O	1:BB:228:ARG:HG2	2.11	0.49
1:FB:127:MET:HE3	1:FB:452:MET:HE2	1.94	0.49
1:HB:127:MET:HE3	1:HB:452:MET:HE2	1.94	0.49
1:D:127:MET:HE3	1:D:452:MET:HE2	1.94	0.49
1:R:227:PHE:O	1:R:228:ARG:HG2	2.11	0.49
1:S:227:PHE:O	1:S:228:ARG:HG2	2.11	0.49
1:CA:227:PHE:O	1:CA:228:ARG:HG2	2.11	0.49
1:GA:127:MET:HE3	1:GA:452:MET:HE2	1.94	0.49
1:LA:227:PHE:O	1:LA:228:ARG:HG2	2.12	0.49
1:BB:127:MET:HE3	1:BB:452:MET:HE2	1.94	0.49
1:Z:227:PHE:O	1:Z:228:ARG:HG2	2.11	0.49
1:EA:127:MET:HE3	1:EA:452:MET:HE2	1.94	0.49
1:PA:227:PHE:O	1:PA:228:ARG:HG2	2.11	0.49
1:F:227:PHE:O	1:F:228:ARG:HG2	2.12	0.49
1:B:227:PHE:O	1:B:228:ARG:HG2	2.11	0.49
1:FA:127:MET:HE3	1:FA:452:MET:HE2	1.94	0.49
1:G:227:PHE:O	1:G:228:ARG:HG2	2.11	0.49
1:S:127:MET:HE3	1:S:452:MET:HE2	1.94	0.49
1:BA:127:MET:HE3	1:BA:452:MET:HE2	1.94	0.49
1:YA:227:PHE:O	1:YA:228:ARG:HG2	2.11	0.49
1:V:227:PHE:O	1:V:228:ARG:HG2	2.11	0.49
1:GB:227:PHE:O	1:GB:228:ARG:HG2	2.12	0.49
1:F:127:MET:HE3	1:F:452:MET:HE2	1.94	0.49
1:C:127:MET:HE3	1:C:452:MET:HE2	1.94	0.49
1:Z:127:MET:HE3	1:Z:452:MET:HE2	1.94	0.49
1:CA:127:MET:HE3	1:CA:452:MET:HE2	1.94	0.49
1:L:514:PRO:HD3	1:DB:62:THR:HG23	1.95	0.49
1:R:127:MET:HE3	1:R:452:MET:HE2	1.94	0.49
1:HA:127:MET:HE3	1:HA:452:MET:HE2	1.94	0.49
1:C:227:PHE:O	1:C:228:ARG:HG2	2.11	0.48
1:M:227:PHE:O	1:M:228:ARG:HG2	2.11	0.48
1:DA:127:MET:HE3	1:DA:452:MET:HE2	1.94	0.48
1:WA:127:MET:HE3	1:WA:452:MET:HE2	1.94	0.48
1:YA:127:MET:HE3	1:YA:452:MET:HE2	1.94	0.48
1:A:127:MET:HE3	1:A:452:MET:HE2	1.94	0.48
1:H:113:SER:OG	1:GA:48:ARG:NH1	2.41	0.48
1:Y:127:MET:HE3	1:Y:452:MET:HE2	1.94	0.48
1:XA:127:MET:HE3	1:XA:452:MET:HE2	1.94	0.48
1:N:127:MET:HE3	1:N:452:MET:HE2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:127:MET:HE3	1:P:452:MET:HE2	1.94	0.48
1:X:127:MET:HE3	1:X:452:MET:HE2	1.94	0.48
1:LA:127:MET:HE3	1:LA:452:MET:HE2	1.94	0.48
1:RA:127:MET:HE3	1:RA:452:MET:HE2	1.94	0.48
1:G:436:ARG:NH1	1:UA:94:ASN:OD1	2.41	0.48
1:M:127:MET:HE3	1:M:452:MET:HE2	1.94	0.48
1:G:127:MET:HE3	1:G:452:MET:HE2	1.94	0.48
1:J:127:MET:HE3	1:J:452:MET:HE2	1.94	0.48
1:MA:127:MET:HE3	1:MA:452:MET:HE2	1.94	0.48
1:H:127:MET:HE3	1:H:452:MET:HE2	1.94	0.48
1:CB:127:MET:HE3	1:CB:452:MET:HE2	1.94	0.48
1:S:48:ARG:NH1	1:DB:113:SER:OG	2.46	0.48
1:QA:127:MET:HE3	1:QA:452:MET:HE2	1.94	0.48
1:VA:127:MET:HE3	1:VA:452:MET:HE2	1.94	0.48
1:WA:459:PHE:CG	1:HB:460:TYR:HB2	2.49	0.48
1:M:62:THR:HG23	1:MA:514:PRO:HD3	1.95	0.48
1:P:514:PRO:HD3	1:SA:62:THR:HG23	1.96	0.48
1:R:250:PRO:HG2	1:R:271:LEU:O	2.14	0.47
1:GA:127:MET:HE2	1:GA:134:MET:HE3	1.96	0.47
1:KA:250:PRO:HG2	1:KA:271:LEU:O	2.14	0.47
1:UA:250:PRO:HG2	1:UA:271:LEU:O	2.14	0.47
1:VA:250:PRO:HG2	1:VA:271:LEU:O	2.14	0.47
1:AB:127:MET:HE3	1:AB:452:MET:HE2	1.94	0.47
1:C:250:PRO:HG2	1:C:271:LEU:O	2.14	0.47
1:Q:250:PRO:HG2	1:Q:271:LEU:O	2.14	0.47
1:UA:127:MET:HE2	1:UA:134:MET:HE3	1.97	0.47
1:DB:250:PRO:HG2	1:DB:271:LEU:O	2.14	0.47
1:H:127:MET:HE2	1:H:134:MET:HE3	1.97	0.47
1:H:250:PRO:HG2	1:H:271:LEU:O	2.14	0.47
1:T:127:MET:HE2	1:T:134:MET:HE3	1.97	0.47
1:V:127:MET:HE2	1:V:134:MET:HE3	1.97	0.47
1:Z:127:MET:HE2	1:Z:134:MET:HE3	1.97	0.47
1:AA:127:MET:HE3	1:AA:452:MET:HE2	1.94	0.47
1:BB:250:PRO:HG2	1:BB:271:LEU:O	2.14	0.47
1:F:250:PRO:HG2	1:F:271:LEU:O	2.14	0.47
1:C:279:PHE:HB2	1:ZA:79:ASN:O	2.14	0.47
1:T:250:PRO:HG2	1:T:271:LEU:O	2.14	0.47
1:Z:250:PRO:HG2	1:Z:271:LEU:O	2.14	0.47
1:CA:127:MET:HE2	1:CA:134:MET:HE3	1.97	0.47
1:IA:250:PRO:HG2	1:IA:271:LEU:O	2.14	0.47
1:JA:127:MET:HE2	1:JA:134:MET:HE3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:PA:250:PRO:HG2	1:PA:271:LEU:O	2.14	0.47
1:CB:127:MET:HE2	1:CB:134:MET:HE3	1.97	0.47
1:IB:127:MET:HE2	1:IB:134:MET:HE3	1.97	0.47
1:IB:250:PRO:HG2	1:IB:271:LEU:O	2.14	0.47
1:A:250:PRO:HG2	1:A:271:LEU:O	2.14	0.47
1:O:127:MET:HE2	1:O:134:MET:HE3	1.97	0.47
1:R:127:MET:HE2	1:R:134:MET:HE3	1.97	0.47
1:X:250:PRO:HG2	1:X:271:LEU:O	2.14	0.47
1:HA:250:PRO:HG2	1:HA:271:LEU:O	2.14	0.47
1:PA:127:MET:HE2	1:PA:134:MET:HE3	1.97	0.47
1:QA:250:PRO:HG2	1:QA:271:LEU:O	2.14	0.47
1:SA:250:PRO:HG2	1:SA:271:LEU:O	2.14	0.47
1:XA:127:MET:HE2	1:XA:134:MET:HE3	1.97	0.47
1:I:250:PRO:HG2	1:I:271:LEU:O	2.14	0.47
1:DA:61:ASP:OD1	1:AB:49:ASN:ND2	2.32	0.47
1:DA:127:MET:HE2	1:DA:134:MET:HE3	1.97	0.47
1:IA:127:MET:HE2	1:IA:134:MET:HE3	1.97	0.47
1:AB:127:MET:HE2	1:AB:134:MET:HE3	1.97	0.47
1:EB:250:PRO:HG2	1:EB:271:LEU:O	2.14	0.47
1:D:62:THR:HG23	1:Y:514:PRO:HD3	1.97	0.47
1:G:127:MET:HE2	1:G:134:MET:HE3	1.97	0.47
1:K:127:MET:HE2	1:K:134:MET:HE3	1.97	0.47
1:Q:435:PHE:CE2	1:QA:93:GLN:HG3	2.49	0.47
1:AA:250:PRO:HG2	1:AA:271:LEU:O	2.14	0.47
1:CA:250:PRO:HG2	1:CA:271:LEU:O	2.14	0.47
1:GA:250:PRO:HG2	1:GA:271:LEU:O	2.14	0.47
1:LA:250:PRO:HG2	1:LA:271:LEU:O	2.14	0.47
1:MA:250:PRO:HG2	1:MA:271:LEU:O	2.14	0.47
1:OA:127:MET:HE2	1:OA:134:MET:HE3	1.97	0.47
1:AB:250:PRO:HG2	1:AB:271:LEU:O	2.14	0.47
1:HB:250:PRO:HG2	1:HB:271:LEU:O	2.14	0.47
1:A:49:ASN:ND2	1:LA:61:ASP:OD1	2.35	0.47
1:A:127:MET:HE2	1:A:134:MET:HE3	1.97	0.47
1:B:250:PRO:HG2	1:B:271:LEU:O	2.14	0.47
1:M:127:MET:HE2	1:M:134:MET:HE3	1.97	0.47
1:BA:250:PRO:HG2	1:BA:271:LEU:O	2.14	0.47
1:DA:250:PRO:HG2	1:DA:271:LEU:O	2.14	0.47
1:HA:127:MET:HE2	1:HA:134:MET:HE3	1.97	0.47
1:VA:127:MET:HE2	1:VA:134:MET:HE3	1.97	0.47
1:CB:250:PRO:HG2	1:CB:271:LEU:O	2.14	0.47
1:GB:221:LYS:NZ	1:GB:490:ILE:O	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:250:PRO:HG2	1:L:271:LEU:O	2.14	0.47
1:O:250:PRO:HG2	1:O:271:LEU:O	2.14	0.47
1:P:250:PRO:HG2	1:P:271:LEU:O	2.14	0.47
1:X:514:PRO:HD3	1:VA:62:THR:HG23	1.97	0.47
1:LA:127:MET:HE2	1:LA:134:MET:HE3	1.97	0.47
1:NA:250:PRO:HG2	1:NA:271:LEU:O	2.14	0.47
1:OA:250:PRO:HG2	1:OA:271:LEU:O	2.14	0.47
1:RA:250:PRO:HG2	1:RA:271:LEU:O	2.14	0.47
1:XA:250:PRO:HG2	1:XA:271:LEU:O	2.14	0.47
1:ZA:127:MET:HE2	1:ZA:134:MET:HE3	1.97	0.47
1:DB:127:MET:HE2	1:DB:134:MET:HE3	1.97	0.47
1:FB:127:MET:HE2	1:FB:134:MET:HE3	1.97	0.47
1:G:250:PRO:HG2	1:G:271:LEU:O	2.14	0.47
1:H:459:PHE:CG	1:AA:460:TYR:HB2	2.50	0.47
1:K:250:PRO:HG2	1:K:271:LEU:O	2.15	0.47
1:L:127:MET:HE2	1:L:134:MET:HE3	1.97	0.47
1:EA:250:PRO:HG2	1:EA:271:LEU:O	2.14	0.47
1:ZA:250:PRO:HG2	1:ZA:271:LEU:O	2.14	0.47
1:B:436:ARG:HD2	1:YA:436:ARG:HD2	1.97	0.46
1:J:250:PRO:HG2	1:J:271:LEU:O	2.14	0.46
1:W:250:PRO:HG2	1:W:271:LEU:O	2.14	0.46
1:D:250:PRO:HG2	1:D:271:LEU:O	2.14	0.46
1:E:127:MET:HE2	1:E:134:MET:HE3	1.97	0.46
1:E:250:PRO:HG2	1:E:271:LEU:O	2.14	0.46
1:L:131:ASN:HA	1:L:184:GLU:HG2	1.98	0.46
1:M:250:PRO:HG2	1:M:271:LEU:O	2.14	0.46
1:N:131:ASN:HA	1:N:184:GLU:HG2	1.98	0.46
1:Q:131:ASN:HA	1:Q:184:GLU:HG2	1.98	0.46
1:S:250:PRO:HG2	1:S:271:LEU:O	2.14	0.46
1:X:131:ASN:HA	1:X:184:GLU:HG2	1.98	0.46
1:FA:250:PRO:HG2	1:FA:271:LEU:O	2.14	0.46
1:MA:127:MET:HE2	1:MA:134:MET:HE3	1.97	0.46
1:WA:250:PRO:HG2	1:WA:271:LEU:O	2.14	0.46
1:XA:221:LYS:NZ	1:XA:490:ILE:O	2.46	0.46
1:EB:127:MET:HE2	1:EB:134:MET:HE3	1.97	0.46
1:GB:250:PRO:HG2	1:GB:271:LEU:O	2.14	0.46
1:GB:436:ARG:NH1	1:IB:94:ASN:OD1	2.46	0.46
1:A:61:ASP:OD1	1:LA:49:ASN:ND2	2.36	0.46
1:I:131:ASN:HA	1:I:184:GLU:HG2	1.98	0.46
1:P:131:ASN:HA	1:P:184:GLU:HG2	1.98	0.46
1:Q:127:MET:HE2	1:Q:134:MET:HE3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FA:131:ASN:HA	1:FA:184:GLU:HG2	1.98	0.46
1:KA:131:ASN:HA	1:KA:184:GLU:HG2	1.98	0.46
1:LA:131:ASN:HA	1:LA:184:GLU:HG2	1.98	0.46
1:QA:127:MET:HE2	1:QA:134:MET:HE3	1.97	0.46
1:SA:127:MET:HE2	1:SA:134:MET:HE3	1.97	0.46
1:TA:250:PRO:HG2	1:TA:271:LEU:O	2.14	0.46
1:BB:131:ASN:HA	1:BB:184:GLU:HG2	1.98	0.46
1:E:131:ASN:HA	1:E:184:GLU:HG2	1.98	0.46
1:O:131:ASN:HA	1:O:184:GLU:HG2	1.98	0.46
1:V:250:PRO:HG2	1:V:271:LEU:O	2.14	0.46
1:Y:131:ASN:HA	1:Y:184:GLU:HG2	1.98	0.46
1:Y:250:PRO:HG2	1:Y:271:LEU:O	2.14	0.46
1:JA:250:PRO:HG2	1:JA:271:LEU:O	2.14	0.46
1:NA:131:ASN:HA	1:NA:184:GLU:HG2	1.98	0.46
1:UA:221:LYS:NZ	1:UA:490:ILE:O	2.46	0.46
1:WA:131:ASN:HA	1:WA:184:GLU:HG2	1.98	0.46
1:WA:459:PHE:CD1	1:HB:460:TYR:HB2	2.50	0.46
1:ZA:131:ASN:HA	1:ZA:184:GLU:HG2	1.98	0.46
1:AB:131:ASN:HA	1:AB:184:GLU:HG2	1.98	0.46
1:DB:131:ASN:HA	1:DB:184:GLU:HG2	1.98	0.46
1:HB:127:MET:HE2	1:HB:134:MET:HE3	1.97	0.46
1:C:127:MET:HE2	1:C:134:MET:HE3	1.97	0.46
1:C:131:ASN:HA	1:C:184:GLU:HG2	1.98	0.46
1:E:228:ARG:HA	1:E:238:ILE:HD11	1.98	0.46
1:K:131:ASN:HA	1:K:184:GLU:HG2	1.98	0.46
1:Q:228:ARG:HA	1:Q:238:ILE:HD11	1.98	0.46
1:W:127:MET:HE2	1:W:134:MET:HE3	1.97	0.46
1:Y:127:MET:HE2	1:Y:134:MET:HE3	1.97	0.46
1:CA:131:ASN:HA	1:CA:184:GLU:HG2	1.98	0.46
1:FB:250:PRO:HG2	1:FB:271:LEU:O	2.14	0.46
1:B:131:ASN:HA	1:B:184:GLU:HG2	1.98	0.46
1:O:228:ARG:HA	1:O:238:ILE:HD11	1.98	0.46
1:T:228:ARG:HA	1:T:238:ILE:HD11	1.98	0.46
1:V:228:ARG:HA	1:V:238:ILE:HD11	1.98	0.46
1:DA:131:ASN:HA	1:DA:184:GLU:HG2	1.98	0.46
1:EA:127:MET:HE2	1:EA:134:MET:HE3	1.97	0.46
1:JA:131:ASN:HA	1:JA:184:GLU:HG2	1.98	0.46
1:NA:127:MET:HE2	1:NA:134:MET:HE3	1.97	0.46
1:VA:131:ASN:HA	1:VA:184:GLU:HG2	1.98	0.46
1:XA:131:ASN:HA	1:XA:184:GLU:HG2	1.98	0.46
1:XA:228:ARG:HA	1:XA:238:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:127:MET:HE2	1:BB:134:MET:HE3	1.97	0.46
1:GB:131:ASN:HA	1:GB:184:GLU:HG2	1.98	0.46
1:P:127:MET:HE2	1:P:134:MET:HE3	1.97	0.46
1:AA:127:MET:HE2	1:AA:134:MET:HE3	1.97	0.46
1:GA:228:ARG:HA	1:GA:238:ILE:HD11	1.98	0.46
1:KA:127:MET:HE2	1:KA:134:MET:HE3	1.97	0.46
1:OA:228:ARG:HA	1:OA:238:ILE:HD11	1.98	0.46
1:SA:131:ASN:HA	1:SA:184:GLU:HG2	1.98	0.46
1:TA:127:MET:HE2	1:TA:134:MET:HE3	1.97	0.46
1:YA:127:MET:HE2	1:YA:134:MET:HE3	1.97	0.46
1:HB:131:ASN:HA	1:HB:184:GLU:HG2	1.98	0.46
1:IB:228:ARG:HA	1:IB:238:ILE:HD11	1.98	0.46
1:D:131:ASN:HA	1:D:184:GLU:HG2	1.98	0.46
1:R:131:ASN:HA	1:R:184:GLU:HG2	1.98	0.46
1:S:127:MET:HE2	1:S:134:MET:HE3	1.97	0.46
1:BA:131:ASN:HA	1:BA:184:GLU:HG2	1.98	0.46
1:FA:127:MET:HE2	1:FA:134:MET:HE3	1.97	0.46
1:IA:228:ARG:HA	1:IA:238:ILE:HD11	1.98	0.46
1:JA:228:ARG:HA	1:JA:238:ILE:HD11	1.98	0.46
1:RA:127:MET:HE2	1:RA:134:MET:HE3	1.97	0.46
1:TA:131:ASN:HA	1:TA:184:GLU:HG2	1.98	0.46
1:ZA:228:ARG:HA	1:ZA:238:ILE:HD11	1.98	0.46
1:IB:131:ASN:HA	1:IB:184:GLU:HG2	1.98	0.46
1:D:127:MET:HE2	1:D:134:MET:HE3	1.97	0.46
1:G:228:ARG:HA	1:G:238:ILE:HD11	1.98	0.46
1:I:127:MET:HE2	1:I:134:MET:HE3	1.97	0.46
1:J:131:ASN:HA	1:J:184:GLU:HG2	1.98	0.46
1:N:127:MET:HE2	1:N:134:MET:HE3	1.97	0.46
1:S:221:LYS:NZ	1:S:490:ILE:O	2.46	0.46
1:Z:131:ASN:HA	1:Z:184:GLU:HG2	1.98	0.46
1:SA:228:ARG:HA	1:SA:238:ILE:HD11	1.98	0.46
1:YA:131:ASN:HA	1:YA:184:GLU:HG2	1.98	0.46
1:EB:228:ARG:HA	1:EB:238:ILE:HD11	1.98	0.46
1:A:131:ASN:HA	1:A:184:GLU:HG2	1.98	0.46
1:A:228:ARG:HA	1:A:238:ILE:HD11	1.98	0.46
1:M:131:ASN:HA	1:M:184:GLU:HG2	1.98	0.46
1:N:250:PRO:HG2	1:N:271:LEU:O	2.14	0.46
1:MA:131:ASN:HA	1:MA:184:GLU:HG2	1.98	0.46
1:MA:228:ARG:HA	1:MA:238:ILE:HD11	1.98	0.46
1:TA:228:ARG:HA	1:TA:238:ILE:HD11	1.98	0.46
1:UA:228:ARG:HA	1:UA:238:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:250:PRO:HG2	1:YA:271:LEU:O	2.14	0.46
1:DB:228:ARG:HA	1:DB:238:ILE:HD11	1.98	0.46
1:GB:127:MET:HE2	1:GB:134:MET:HE3	1.97	0.46
1:I:228:ARG:HA	1:I:238:ILE:HD11	1.98	0.45
1:J:127:MET:HE2	1:J:134:MET:HE3	1.97	0.45
1:L:228:ARG:HA	1:L:238:ILE:HD11	1.98	0.45
1:S:131:ASN:HA	1:S:184:GLU:HG2	1.98	0.45
1:W:131:ASN:HA	1:W:184:GLU:HG2	1.98	0.45
1:AA:131:ASN:HA	1:AA:184:GLU:HG2	1.98	0.45
1:HA:131:ASN:HA	1:HA:184:GLU:HG2	1.98	0.45
1:IA:131:ASN:HA	1:IA:184:GLU:HG2	1.98	0.45
1:KA:228:ARG:HA	1:KA:238:ILE:HD11	1.98	0.45
1:QA:131:ASN:HA	1:QA:184:GLU:HG2	1.98	0.45
1:WA:127:MET:HE2	1:WA:134:MET:HE3	1.96	0.45
1:B:127:MET:HE2	1:B:134:MET:HE3	1.97	0.45
1:BB:228:ARG:HA	1:BB:238:ILE:HD11	1.98	0.45
1:CB:228:ARG:HA	1:CB:238:ILE:HD11	1.98	0.45
1:G:131:ASN:HA	1:G:184:GLU:HG2	1.98	0.45
1:K:228:ARG:HA	1:K:238:ILE:HD11	1.98	0.45
1:L:221:LYS:NZ	1:L:490:ILE:O	2.46	0.45
1:FA:228:ARG:HA	1:FA:238:ILE:HD11	1.98	0.45
1:EB:131:ASN:HA	1:EB:184:GLU:HG2	1.98	0.45
1:T:131:ASN:HA	1:T:184:GLU:HG2	1.98	0.45
1:V:221:LYS:NZ	1:V:490:ILE:O	2.46	0.45
1:BA:127:MET:HE2	1:BA:134:MET:HE3	1.97	0.45
1:DA:228:ARG:HA	1:DA:238:ILE:HD11	1.98	0.45
1:RA:131:ASN:HA	1:RA:184:GLU:HG2	1.98	0.45
1:F:127:MET:HE2	1:F:134:MET:HE3	1.97	0.45
1:AA:228:ARG:HA	1:AA:238:ILE:HD11	1.98	0.45
1:CA:228:ARG:HA	1:CA:238:ILE:HD11	1.98	0.45
1:FB:228:ARG:HA	1:FB:238:ILE:HD11	1.98	0.45
1:F:221:LYS:NZ	1:F:490:ILE:O	2.46	0.45
1:D:228:ARG:HA	1:D:238:ILE:HD11	1.98	0.45
1:J:228:ARG:HA	1:J:238:ILE:HD11	1.98	0.45
1:S:228:ARG:HA	1:S:238:ILE:HD11	1.98	0.45
1:X:127:MET:HE2	1:X:134:MET:HE3	1.97	0.45
1:EA:228:ARG:HA	1:EA:238:ILE:HD11	1.98	0.45
1:F:131:ASN:HA	1:F:184:GLU:HG2	1.98	0.45
1:C:228:ARG:HA	1:C:238:ILE:HD11	1.98	0.45
1:P:228:ARG:HA	1:P:238:ILE:HD11	1.98	0.45
1:V:131:ASN:HA	1:V:184:GLU:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:228:ARG:HA	1:Y:238:ILE:HD11	1.98	0.45
1:Z:459:PHE:CG	1:YA:460:TYR:HB2	2.50	0.45
1:EA:131:ASN:HA	1:EA:184:GLU:HG2	1.98	0.45
1:NA:228:ARG:HA	1:NA:238:ILE:HD11	1.98	0.45
1:UA:131:ASN:HA	1:UA:184:GLU:HG2	1.98	0.45
1:ZA:221:LYS:NZ	1:ZA:490:ILE:O	2.46	0.45
1:FB:131:ASN:HA	1:FB:184:GLU:HG2	1.98	0.45
1:W:228:ARG:HA	1:W:238:ILE:HD11	1.98	0.45
1:Z:228:ARG:HA	1:Z:238:ILE:HD11	1.98	0.45
1:BA:228:ARG:HA	1:BA:238:ILE:HD11	1.98	0.45
1:LA:228:ARG:HA	1:LA:238:ILE:HD11	1.98	0.45
1:PA:131:ASN:HA	1:PA:184:GLU:HG2	1.98	0.45
1:F:228:ARG:HA	1:F:238:ILE:HD11	1.98	0.45
1:GA:131:ASN:HA	1:GA:184:GLU:HG2	1.98	0.45
1:HA:221:LYS:NZ	1:HA:490:ILE:O	2.46	0.45
1:HA:228:ARG:HA	1:HA:238:ILE:HD11	1.98	0.45
1:PA:221:LYS:NZ	1:PA:490:ILE:O	2.46	0.45
1:RA:228:ARG:HA	1:RA:238:ILE:HD11	1.98	0.45
1:B:62:THR:HG23	1:M:514:PRO:HD3	1.99	0.45
1:P:221:LYS:NZ	1:P:490:ILE:O	2.46	0.45
1:JA:514:PRO:HD3	1:RA:62:THR:HG23	1.99	0.45
1:QA:228:ARG:HA	1:QA:238:ILE:HD11	1.98	0.45
1:WA:228:ARG:HA	1:WA:238:ILE:HD11	1.98	0.45
1:GB:228:ARG:HA	1:GB:238:ILE:HD11	1.98	0.45
1:H:228:ARG:HA	1:H:238:ILE:HD11	1.98	0.44
1:YA:228:ARG:HA	1:YA:238:ILE:HD11	1.98	0.44
1:M:228:ARG:HA	1:M:238:ILE:HD11	1.98	0.44
1:S:514:PRO:HD3	1:JA:62:THR:HG23	1.99	0.44
1:IA:113:SER:OG	1:VA:48:ARG:NH1	2.46	0.44
1:PA:228:ARG:HA	1:PA:238:ILE:HD11	1.98	0.44
1:SA:221:LYS:NZ	1:SA:490:ILE:O	2.46	0.44
1:AB:221:LYS:NZ	1:AB:490:ILE:O	2.46	0.44
1:HB:228:ARG:HA	1:HB:238:ILE:HD11	1.98	0.44
1:L:62:THR:HG23	1:Z:514:PRO:HD3	1.99	0.44
1:N:228:ARG:HA	1:N:238:ILE:HD11	1.98	0.44
1:CB:131:ASN:HA	1:CB:184:GLU:HG2	1.98	0.44
1:R:228:ARG:HA	1:R:238:ILE:HD11	1.98	0.44
1:X:228:ARG:HA	1:X:238:ILE:HD11	1.98	0.44
1:GA:221:LYS:NZ	1:GA:490:ILE:O	2.46	0.44
1:B:228:ARG:HA	1:B:238:ILE:HD11	1.98	0.44
1:E:48:ARG:NH1	1:TA:113:SER:OG	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:131:ASN:HA	1:H:184:GLU:HG2	1.98	0.44
1:Z:62:THR:HG23	1:YA:514:PRO:HD3	1.99	0.44
1:AB:228:ARG:HA	1:AB:238:ILE:HD11	1.98	0.44
1:RA:514:PRO:HD3	1:BB:62:THR:HG23	2.00	0.44
1:VA:228:ARG:HA	1:VA:238:ILE:HD11	1.98	0.44
1:OA:131:ASN:HA	1:OA:184:GLU:HG2	1.98	0.44
1:PA:434:THR:HG22	1:GB:53:TYR:CD1	2.53	0.44
1:H:459:PHE:CD1	1:AA:460:TYR:HB2	2.53	0.43
1:GA:62:THR:HG23	1:NA:514:PRO:HD3	2.01	0.43
1:MA:459:PHE:CG	1:EB:460:TYR:HB2	2.53	0.43
1:TA:221:LYS:NZ	1:TA:490:ILE:O	2.46	0.43
1:H:436:ARG:NH1	1:GB:94:ASN:OD1	2.51	0.43
1:I:514:PRO:HD3	1:TA:62:THR:CG2	2.46	0.43
1:W:221:LYS:NZ	1:W:490:ILE:O	2.46	0.43
1:BA:436:ARG:NH1	1:YA:94:ASN:OD1	2.51	0.43
1:A:221:LYS:NZ	1:A:490:ILE:O	2.46	0.43
1:Q:514:PRO:HD3	1:QA:62:THR:HG23	2.00	0.43
1:C:221:LYS:NZ	1:C:490:ILE:O	2.46	0.43
1:I:436:ARG:NH1	1:TA:94:ASN:OD1	2.45	0.43
1:P:113:SER:OG	1:X:48:ARG:NH1	2.44	0.43
1:CB:221:LYS:NZ	1:CB:490:ILE:O	2.46	0.43
1:PA:434:THR:HG22	1:GB:53:TYR:CG	2.54	0.43
1:O:221:LYS:NZ	1:O:490:ILE:O	2.46	0.42
1:IB:221:LYS:NZ	1:IB:490:ILE:O	2.46	0.42
1:GA:80:TYR:CE1	1:NA:280:GLN:HG2	2.53	0.42
1:N:436:ARG:HD2	1:T:436:ARG:HD2	2.01	0.42
1:T:221:LYS:NZ	1:T:490:ILE:O	2.46	0.42
1:DA:221:LYS:NZ	1:DA:490:ILE:O	2.46	0.42
1:F:514:PRO:HD3	1:HB:62:THR:HG23	2.00	0.42
1:Y:229:LEU:HD23	1:Y:229:LEU:HA	1.92	0.42
1:H:62:THR:HG23	1:AA:514:PRO:HD3	2.02	0.42
1:T:61:ASP:CG	1:GB:49:ASN:HD22	2.18	0.42
1:KA:221:LYS:NZ	1:KA:490:ILE:O	2.46	0.42
1:T:80:TYR:CE1	1:PA:280:GLN:HG2	2.55	0.41
1:D:79:ASN:HB3	1:Y:279:PHE:CD2	2.55	0.41
1:I:229:LEU:HD23	1:I:229:LEU:HA	1.92	0.41
1:K:62:THR:HG23	1:TA:514:PRO:HD3	2.02	0.41
1:W:49:ASN:ND2	1:RA:61:ASP:OD1	2.41	0.41
1:NA:221:LYS:NZ	1:NA:490:ILE:O	2.46	0.41
1:TA:208:GLY:C	1:TA:213:VAL:HG22	2.46	0.41
1:E:208:GLY:C	1:E:213:VAL:HG22	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:VA:208:GLY:C	1:VA:213:VAL:HG22	2.46	0.41
1:C:208:GLY:C	1:C:213:VAL:HG22	2.46	0.41
1:B:279:PHE:HB2	1:V:79:ASN:O	2.20	0.41
1:H:208:GLY:C	1:H:213:VAL:HG22	2.46	0.41
1:I:109:PHE:CD2	1:BA:51:ILE:HG12	2.55	0.41
1:I:208:GLY:C	1:I:213:VAL:HG22	2.46	0.41
1:J:208:GLY:C	1:J:213:VAL:HG22	2.46	0.41
1:FA:221:LYS:NZ	1:FA:490:ILE:O	2.46	0.41
1:OA:208:GLY:C	1:OA:213:VAL:HG22	2.46	0.41
1:RA:208:GLY:C	1:RA:213:VAL:HG22	2.46	0.41
1:WA:208:GLY:C	1:WA:213:VAL:HG22	2.46	0.41
1:WA:221:LYS:NZ	1:WA:490:ILE:O	2.46	0.41
1:YA:208:GLY:C	1:YA:213:VAL:HG22	2.46	0.41
1:ZA:208:GLY:C	1:ZA:213:VAL:HG22	2.46	0.41
1:E:94:ASN:OD1	1:BB:436:ARG:NH1	2.52	0.41
1:G:490:ILE:HD12	1:G:490:ILE:HA	1.93	0.41
1:K:208:GLY:C	1:K:213:VAL:HG22	2.46	0.41
1:S:208:GLY:C	1:S:213:VAL:HG22	2.46	0.41
1:T:208:GLY:C	1:T:213:VAL:HG22	2.46	0.41
1:Z:208:GLY:C	1:Z:213:VAL:HG22	2.46	0.41
1:FA:208:GLY:C	1:FA:213:VAL:HG22	2.46	0.41
1:DB:208:GLY:C	1:DB:213:VAL:HG22	2.46	0.41
1:C:49:ASN:ND2	1:EB:61:ASP:OD1	2.32	0.41
1:D:208:GLY:C	1:D:213:VAL:HG22	2.46	0.41
1:N:208:GLY:C	1:N:213:VAL:HG22	2.46	0.41
1:P:208:GLY:C	1:P:213:VAL:HG22	2.46	0.41
1:UA:208:GLY:C	1:UA:213:VAL:HG22	2.46	0.41
1:YA:221:LYS:NZ	1:YA:490:ILE:O	2.46	0.41
1:BB:208:GLY:C	1:BB:213:VAL:HG22	2.46	0.41
1:GB:208:GLY:C	1:GB:213:VAL:HG22	2.46	0.41
1:F:208:GLY:C	1:F:213:VAL:HG22	2.46	0.41
1:C:429:MET:HG3	1:C:447:VAL:HG21	2.03	0.41
1:D:229:LEU:HD23	1:D:229:LEU:HA	1.92	0.41
1:H:429:MET:HG3	1:H:447:VAL:HG21	2.03	0.41
1:Q:208:GLY:C	1:Q:213:VAL:HG22	2.46	0.41
1:Z:459:PHE:CD1	1:YA:460:TYR:HB2	2.56	0.41
1:AA:61:ASP:OD1	1:FA:49:ASN:ND2	2.40	0.41
1:AA:208:GLY:C	1:AA:213:VAL:HG22	2.46	0.41
1:AA:429:MET:HG3	1:AA:447:VAL:HG21	2.03	0.41
1:AA:436:ARG:HD2	1:NA:436:ARG:HD2	2.02	0.41
1:BA:208:GLY:C	1:BA:213:VAL:HG22	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:429:MET:HG3	1:DA:447:VAL:HG21	2.03	0.41
1:IA:429:MET:HG3	1:IA:447:VAL:HG21	2.03	0.41
1:MA:221:LYS:NZ	1:MA:490:ILE:O	2.46	0.41
1:PA:429:MET:HG3	1:PA:447:VAL:HG21	2.03	0.41
1:QA:429:MET:HG3	1:QA:447:VAL:HG21	2.03	0.41
1:VA:221:LYS:NZ	1:VA:490:ILE:O	2.46	0.41
1:FB:208:GLY:C	1:FB:213:VAL:HG22	2.46	0.41
1:IB:208:GLY:C	1:IB:213:VAL:HG22	2.46	0.41
1:D:429:MET:HG3	1:D:447:VAL:HG21	2.03	0.41
1:G:208:GLY:C	1:G:213:VAL:HG22	2.46	0.41
1:L:208:GLY:C	1:L:213:VAL:HG22	2.46	0.41
1:M:429:MET:HG3	1:M:447:VAL:HG21	2.03	0.41
1:N:429:MET:HG3	1:N:447:VAL:HG21	2.03	0.41
1:O:429:MET:HG3	1:O:447:VAL:HG21	2.03	0.41
1:P:429:MET:HG3	1:P:447:VAL:HG21	2.03	0.41
1:R:429:MET:HG3	1:R:447:VAL:HG21	2.03	0.41
1:W:429:MET:HG3	1:W:447:VAL:HG21	2.03	0.41
1:Y:208:GLY:C	1:Y:213:VAL:HG22	2.46	0.41
1:HA:62:THR:HG23	1:OA:514:PRO:HD3	2.02	0.41
1:JA:429:MET:HG3	1:JA:447:VAL:HG21	2.03	0.41
1:LA:429:MET:HG3	1:LA:447:VAL:HG21	2.03	0.41
1:SA:208:GLY:C	1:SA:213:VAL:HG22	2.46	0.41
1:TA:229:LEU:HD23	1:TA:229:LEU:HA	1.92	0.41
1:VA:429:MET:HG3	1:VA:447:VAL:HG21	2.03	0.41
1:AB:429:MET:HG3	1:AB:447:VAL:HG21	2.03	0.41
1:EB:429:MET:HG3	1:EB:447:VAL:HG21	2.03	0.41
1:IB:229:LEU:HD23	1:IB:229:LEU:HA	1.92	0.41
1:A:394:TYR:O	1:A:404:ARG:HD2	2.22	0.40
1:L:394:TYR:O	1:L:404:ARG:HD2	2.22	0.40
1:S:394:TYR:O	1:S:404:ARG:HD2	2.22	0.40
1:W:229:LEU:HD23	1:W:229:LEU:HA	1.92	0.40
1:X:429:MET:HG3	1:X:447:VAL:HG21	2.03	0.40
1:CA:429:MET:HG3	1:CA:447:VAL:HG21	2.03	0.40
1:DA:229:LEU:HD23	1:DA:229:LEU:HA	1.92	0.40
1:EA:394:TYR:O	1:EA:404:ARG:HD2	2.22	0.40
1:KA:208:GLY:C	1:KA:213:VAL:HG22	2.46	0.40
1:XA:208:GLY:C	1:XA:213:VAL:HG22	2.46	0.40
1:YA:48:ARG:NH1	1:ZA:113:SER:OG	2.52	0.40
1:YA:394:TYR:O	1:YA:404:ARG:HD2	2.22	0.40
1:F:110:ASP:OD2	1:J:48:ARG:HA	2.22	0.40
1:G:429:MET:HG3	1:G:447:VAL:HG21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:429:MET:HG3	1:K:447:VAL:HG21	2.03	0.40
1:M:208:GLY:C	1:M:213:VAL:HG22	2.46	0.40
1:N:514:PRO:HD3	1:NA:62:THR:HG23	2.03	0.40
1:W:394:TYR:O	1:W:404:ARG:HD2	2.22	0.40
1:Z:429:MET:HG3	1:Z:447:VAL:HG21	2.03	0.40
1:EA:429:MET:HG3	1:EA:447:VAL:HG21	2.03	0.40
1:GA:208:GLY:C	1:GA:213:VAL:HG22	2.46	0.40
1:NA:394:TYR:O	1:NA:404:ARG:HD2	2.22	0.40
1:OA:394:TYR:O	1:OA:404:ARG:HD2	2.22	0.40
1:BB:429:MET:HG3	1:BB:447:VAL:HG21	2.03	0.40
1:CB:394:TYR:O	1:CB:404:ARG:HD2	2.22	0.40
1:CB:429:MET:HG3	1:CB:447:VAL:HG21	2.03	0.40
1:F:429:MET:HG3	1:F:447:VAL:HG21	2.03	0.40
1:D:394:TYR:O	1:D:404:ARG:HD2	2.22	0.40
1:G:48:ARG:NH1	1:JA:113:SER:OG	2.49	0.40
1:I:429:MET:HG3	1:I:447:VAL:HG21	2.03	0.40
1:M:229:LEU:HD23	1:M:229:LEU:HA	1.92	0.40
1:P:394:TYR:O	1:P:404:ARG:HD2	2.22	0.40
1:Q:113:SER:OG	1:R:48:ARG:NH1	2.52	0.40
1:S:429:MET:HG3	1:S:447:VAL:HG21	2.03	0.40
1:T:394:TYR:O	1:T:404:ARG:HD2	2.22	0.40
1:V:208:GLY:C	1:V:213:VAL:HG22	2.46	0.40
1:CA:208:GLY:C	1:CA:213:VAL:HG22	2.46	0.40
1:KA:394:TYR:O	1:KA:404:ARG:HD2	2.22	0.40
1:MA:394:TYR:O	1:MA:404:ARG:HD2	2.22	0.40
1:MA:429:MET:HG3	1:MA:447:VAL:HG21	2.03	0.40
1:PA:208:GLY:C	1:PA:213:VAL:HG22	2.46	0.40
1:SA:394:TYR:O	1:SA:404:ARG:HD2	2.22	0.40
1:UA:429:MET:HG3	1:UA:447:VAL:HG21	2.03	0.40
1:EB:394:TYR:O	1:EB:404:ARG:HD2	2.22	0.40
1:GB:490:ILE:HD12	1:GB:490:ILE:HA	1.93	0.40
1:F:394:TYR:O	1:F:404:ARG:HD2	2.22	0.40
1:A:208:GLY:C	1:A:213:VAL:HG22	2.46	0.40
1:B:436:ARG:NH1	1:V:94:ASN:OD1	2.51	0.40
1:E:221:LYS:NZ	1:E:490:ILE:O	2.46	0.40
1:O:394:TYR:O	1:O:404:ARG:HD2	2.22	0.40
1:V:48:ARG:NH1	1:Z:113:SER:OG	2.51	0.40
1:V:394:TYR:O	1:V:404:ARG:HD2	2.22	0.40
1:W:208:GLY:C	1:W:213:VAL:HG22	2.46	0.40
1:W:418:VAL:CG2	1:W:452:MET:HB3	2.52	0.40
1:X:208:GLY:C	1:X:213:VAL:HG22	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:221:LYS:NZ	1:X:490:ILE:O	2.46	0.40
1:X:394:TYR:O	1:X:404:ARG:HD2	2.22	0.40
1:BA:221:LYS:NZ	1:BA:490:ILE:O	2.46	0.40
1:BA:429:MET:HG3	1:BA:447:VAL:HG21	2.03	0.40
1:JA:208:GLY:C	1:JA:213:VAL:HG22	2.46	0.40
1:JA:221:LYS:NZ	1:JA:490:ILE:O	2.46	0.40
1:LA:208:GLY:C	1:LA:213:VAL:HG22	2.46	0.40
1:TA:394:TYR:O	1:TA:404:ARG:HD2	2.22	0.40
1:AB:394:TYR:O	1:AB:404:ARG:HD2	2.22	0.40
1:K:514:PRO:HD3	1:O:62:THR:HG23	2.03	0.40
1:M:394:TYR:O	1:M:404:ARG:HD2	2.22	0.40
1:Z:394:TYR:O	1:Z:404:ARG:HD2	2.22	0.40
1:BA:394:TYR:O	1:BA:404:ARG:HD2	2.22	0.40
1:HA:208:GLY:C	1:HA:213:VAL:HG22	2.46	0.40
1:IA:208:GLY:C	1:IA:213:VAL:HG22	2.46	0.40
1:MA:208:GLY:C	1:MA:213:VAL:HG22	2.46	0.40
1:NA:208:GLY:C	1:NA:213:VAL:HG22	2.46	0.40
1:PA:394:TYR:O	1:PA:404:ARG:HD2	2.22	0.40
1:SA:418:VAL:CG2	1:SA:452:MET:HB3	2.52	0.40
1:SA:429:MET:HG3	1:SA:447:VAL:HG21	2.03	0.40
1:TA:429:MET:HG3	1:TA:447:VAL:HG21	2.03	0.40
1:UA:418:VAL:CG2	1:UA:452:MET:HB3	2.52	0.40
1:WA:429:MET:HG3	1:WA:447:VAL:HG21	2.03	0.40
1:BB:418:VAL:CG2	1:BB:452:MET:HB3	2.52	0.40
1:DB:418:VAL:CG2	1:DB:452:MET:HB3	2.52	0.40
1:HB:429:MET:HG3	1:HB:447:VAL:HG21	2.03	0.40
1:IB:418:VAL:CG2	1:IB:452:MET:HB3	2.52	0.40

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 PDB entries followed by that with respect to all EM entries.

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	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	AA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	AB	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	B	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	BA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	BB	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	C	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	CA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	CB	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	D	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	DA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	DB	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	E	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	EA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	EB	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	F	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	FA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	FB	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	G	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	GA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	GB	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	H	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	HA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	HB	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	I	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	IA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	IB	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	J	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	JA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	K	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	KA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	L	395/555 (71%)	372 (94%)	23 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	M	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	MA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	N	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	NA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	O	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	OA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	P	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	PA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	Q	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	QA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	R	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	RA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	S	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	SA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	T	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	TA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	UA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	V	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	VA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	W	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	WA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	X	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	XA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	Y	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	YA	395/555 (71%)	373 (94%)	22 (6%)	0	100	100
1	Z	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
1	ZA	395/555 (71%)	372 (94%)	23 (6%)	0	100	100
All	All	23700/33300 (71%)	22349 (94%)	1351 (6%)	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 PDB entries followed by that with respect to all EM entries.

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	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	AA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	AB	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	B	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	BA	312/494 (63%)	310 (99%)	2 (1%)	78	89
1	BB	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	C	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	CA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	CB	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	D	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	DA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	DB	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	E	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	EA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	EB	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	F	312/494 (63%)	310 (99%)	2 (1%)	78	89
1	FA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	FB	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	G	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	GA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	GB	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	H	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	HA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	HB	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	I	312/494 (63%)	310 (99%)	2 (1%)	78	89
1	IA	313/494 (63%)	311 (99%)	2 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	IB	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	J	312/494 (63%)	310 (99%)	2 (1%)	78	89
1	JA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	K	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	KA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	L	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	LA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	M	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	MA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	N	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	NA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	O	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	OA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	P	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	PA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	Q	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	QA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	R	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	RA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	S	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	SA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	T	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	TA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	UA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	V	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	VA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	W	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	WA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	X	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	XA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	Y	313/494 (63%)	311 (99%)	2 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	YA	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	Z	313/494 (63%)	311 (99%)	2 (1%)	78	89
1	ZA	313/494 (63%)	311 (99%)	2 (1%)	78	89
All	All	18776/29640 (63%)	18656 (99%)	120 (1%)	76	89

All (120) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	190	THR
1	F	447	VAL
1	C	190	THR
1	C	447	VAL
1	A	190	THR
1	A	447	VAL
1	B	190	THR
1	B	447	VAL
1	D	190	THR
1	D	447	VAL
1	E	190	THR
1	E	447	VAL
1	G	190	THR
1	G	447	VAL
1	H	190	THR
1	H	447	VAL
1	I	190	THR
1	I	447	VAL
1	J	190	THR
1	J	447	VAL
1	K	190	THR
1	K	447	VAL
1	L	190	THR
1	L	447	VAL
1	M	190	THR
1	M	447	VAL
1	N	190	THR
1	N	447	VAL
1	O	190	THR
1	O	447	VAL
1	P	190	THR
1	P	447	VAL
1	Q	190	THR

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Mol	Chain	Res	Type
1	Q	447	VAL
1	R	190	THR
1	R	447	VAL
1	S	190	THR
1	S	447	VAL
1	T	190	THR
1	T	447	VAL
1	V	190	THR
1	V	447	VAL
1	W	190	THR
1	W	447	VAL
1	X	190	THR
1	X	447	VAL
1	Y	190	THR
1	Y	447	VAL
1	Z	190	THR
1	Z	447	VAL
1	AA	190	THR
1	AA	447	VAL
1	BA	190	THR
1	BA	447	VAL
1	CA	190	THR
1	CA	447	VAL
1	DA	190	THR
1	DA	447	VAL
1	EA	190	THR
1	EA	447	VAL
1	FA	190	THR
1	FA	447	VAL
1	GA	190	THR
1	GA	447	VAL
1	HA	190	THR
1	HA	447	VAL
1	IA	190	THR
1	IA	447	VAL
1	JA	190	THR
1	JA	447	VAL
1	KA	190	THR
1	KA	447	VAL
1	LA	190	THR
1	LA	447	VAL
1	MA	190	THR

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Mol	Chain	Res	Type
1	MA	447	VAL
1	NA	190	THR
1	NA	447	VAL
1	OA	190	THR
1	OA	447	VAL
1	PA	190	THR
1	PA	447	VAL
1	QA	190	THR
1	QA	447	VAL
1	RA	190	THR
1	RA	447	VAL
1	SA	190	THR
1	SA	447	VAL
1	TA	190	THR
1	TA	447	VAL
1	UA	190	THR
1	UA	447	VAL
1	VA	190	THR
1	VA	447	VAL
1	WA	190	THR
1	WA	447	VAL
1	XA	190	THR
1	XA	447	VAL
1	YA	190	THR
1	YA	447	VAL
1	ZA	190	THR
1	ZA	447	VAL
1	AB	190	THR
1	AB	447	VAL
1	BB	190	THR
1	BB	447	VAL
1	CB	190	THR
1	CB	447	VAL
1	DB	190	THR
1	DB	447	VAL
1	EB	190	THR
1	EB	447	VAL
1	FB	190	THR
1	FB	447	VAL
1	GB	190	THR
1	GB	447	VAL
1	HB	190	THR

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Mol	Chain	Res	Type
1	HB	447	VAL
1	IB	190	THR
1	IB	447	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 oligosaccharides 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.

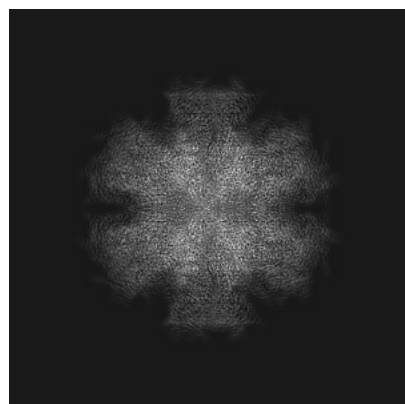
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18323. These allow visual inspection of the internal detail of the map and identification of artifacts.

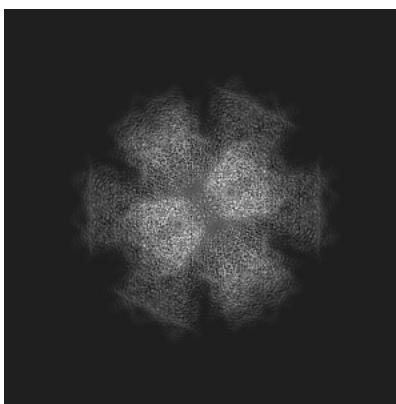
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

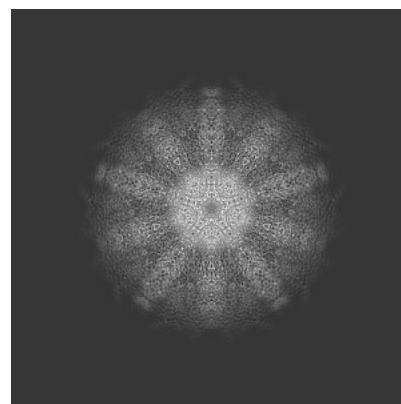
6.1.1 Primary map



X

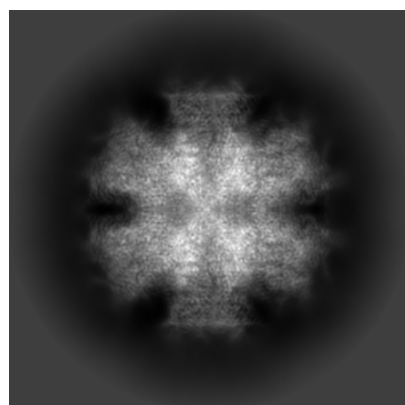


Y

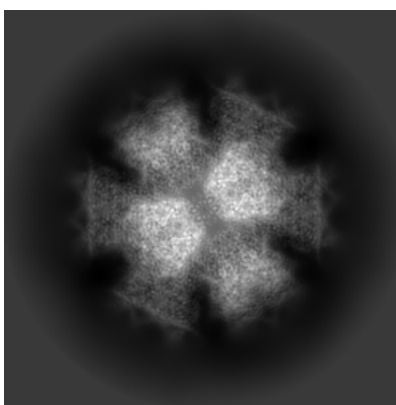


Z

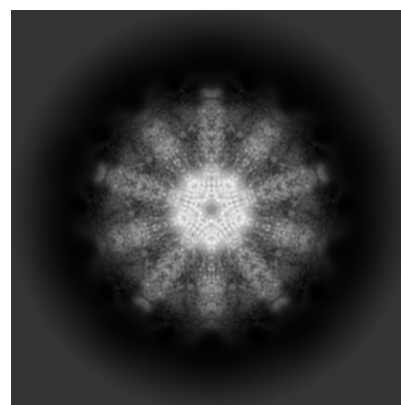
6.1.2 Raw map



X



Y

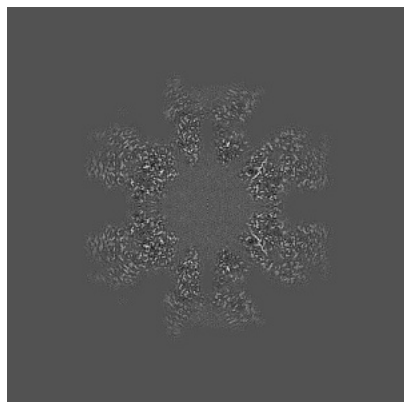


Z

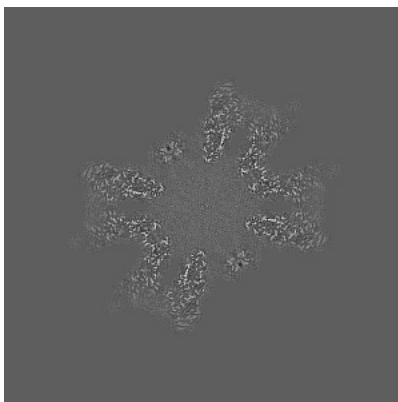
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

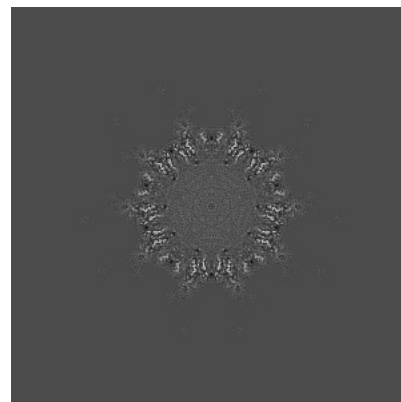
6.2.1 Primary map



X Index: 200

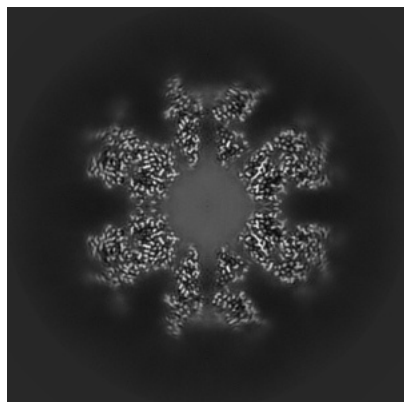


Y Index: 200

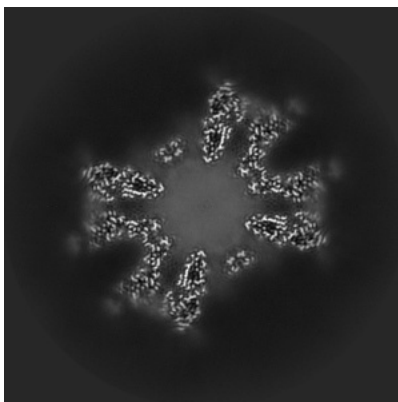


Z Index: 200

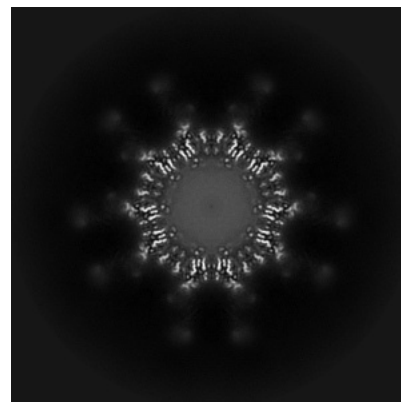
6.2.2 Raw map



X Index: 200



Y Index: 200

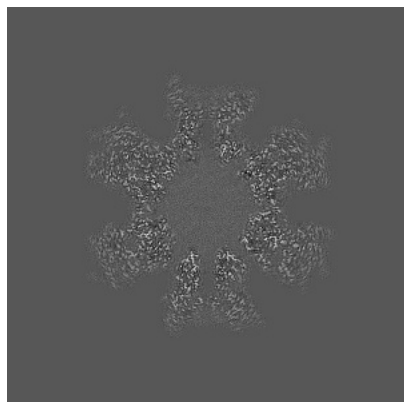


Z Index: 200

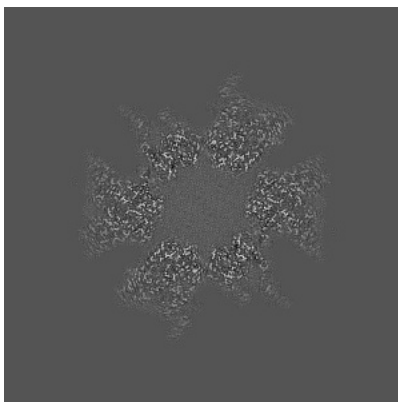
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

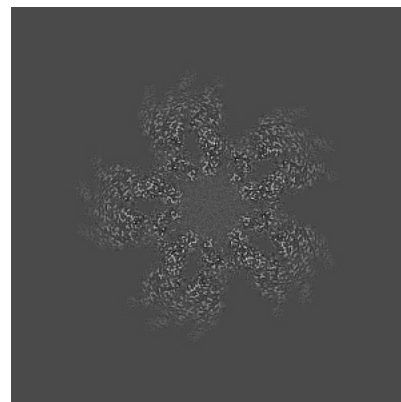
6.3.1 Primary map



X Index: 203

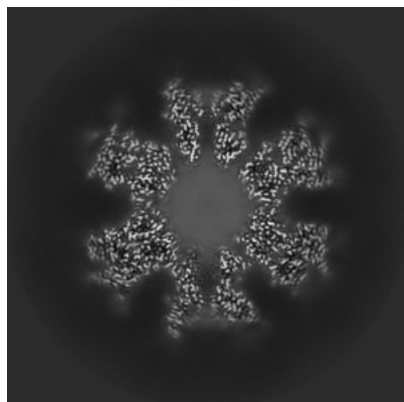


Y Index: 216

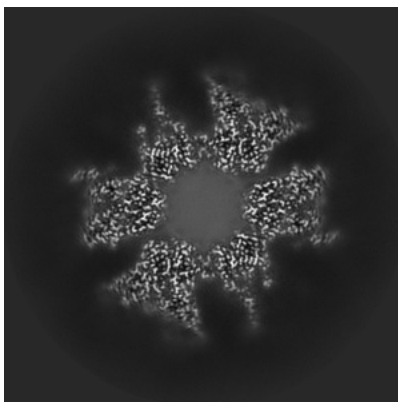


Z Index: 169

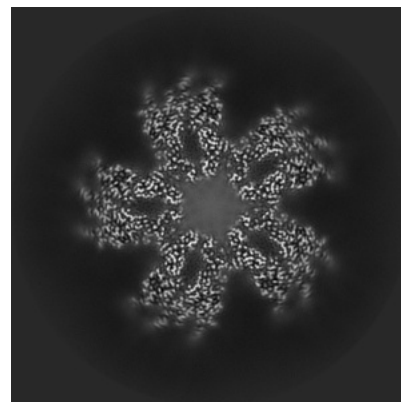
6.3.2 Raw map



X Index: 197



Y Index: 184

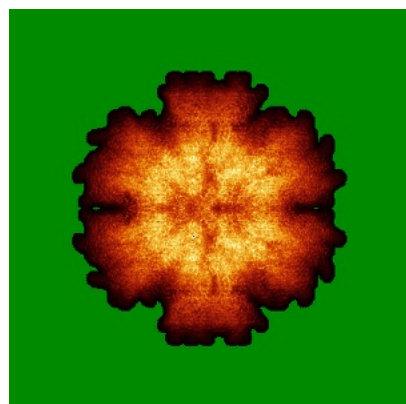


Z Index: 169

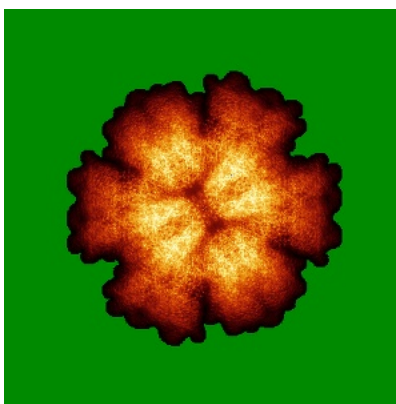
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

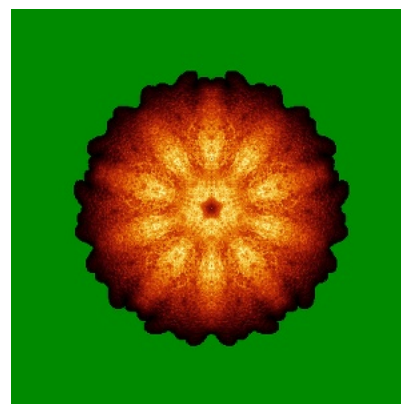
6.4.1 Primary map



X

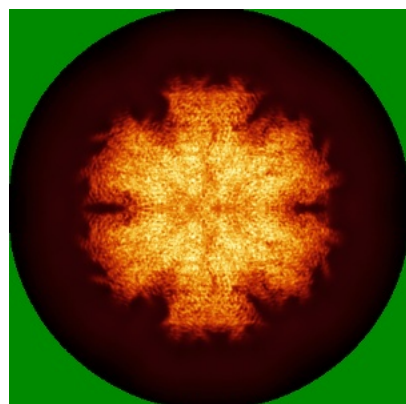


Y

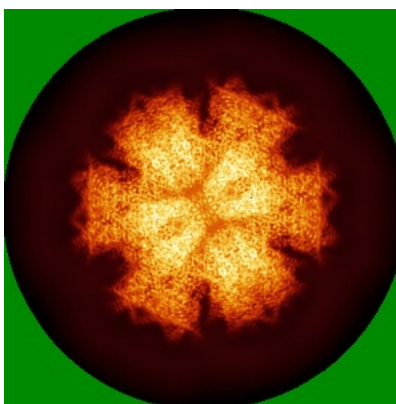


Z

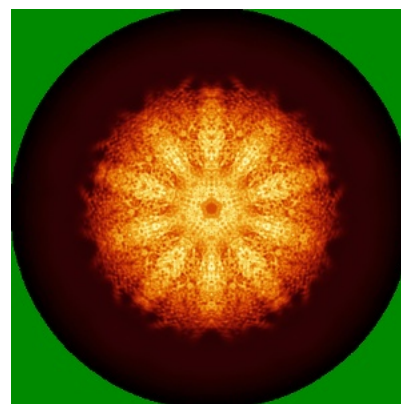
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

This section was not generated.

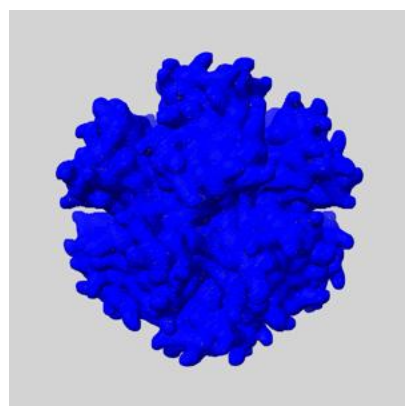
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

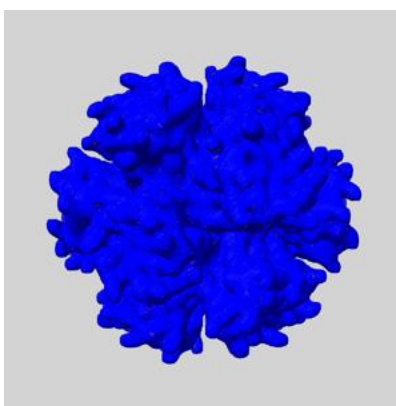
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

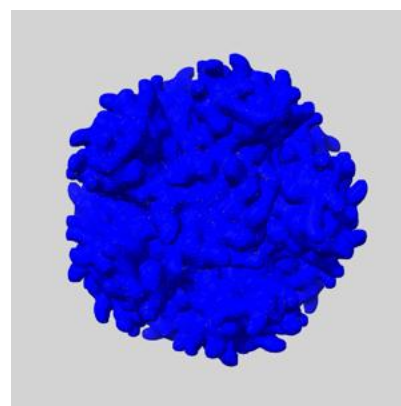
6.6.1 emd_18323_msk_1.map [i](#)



X



Y

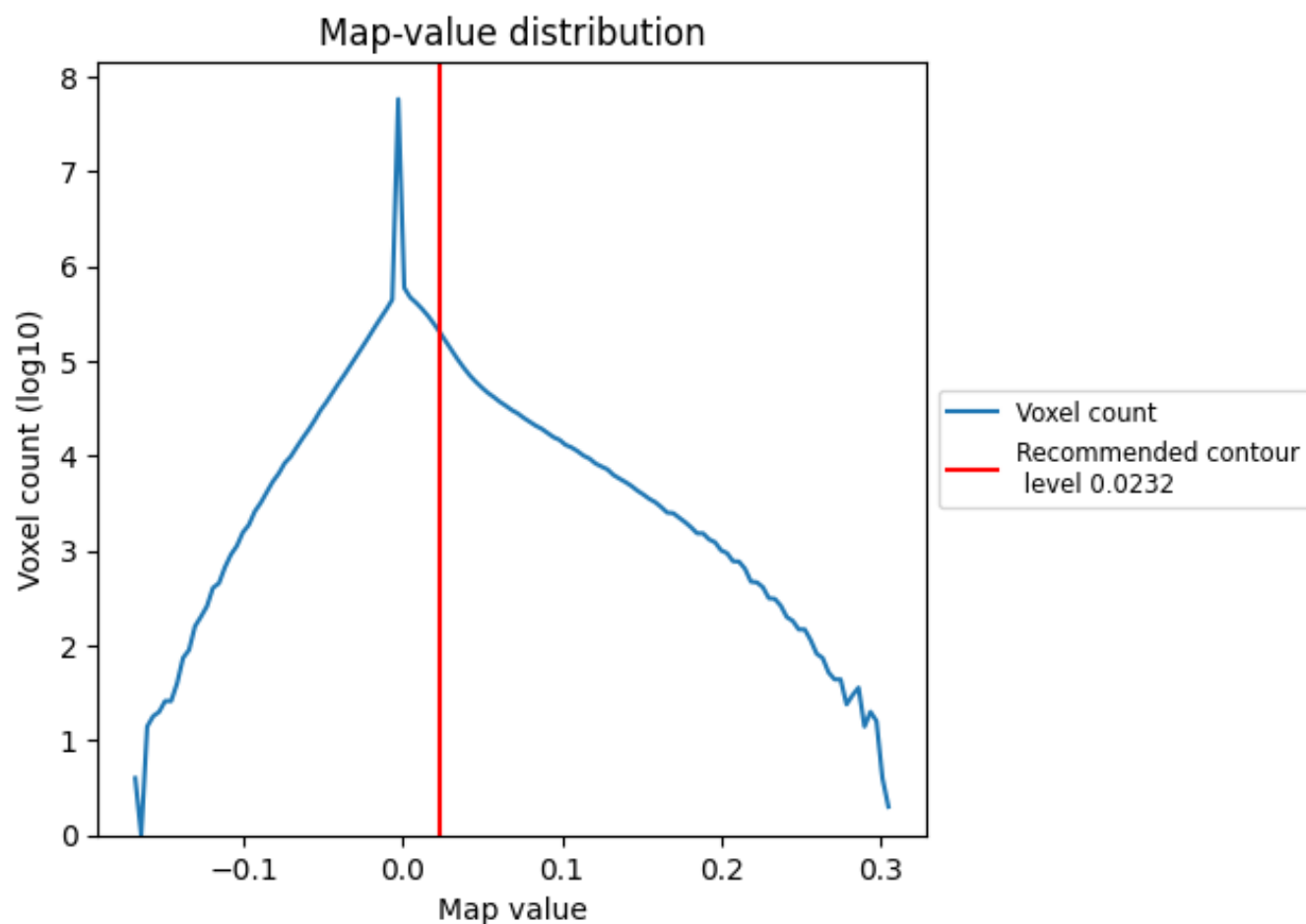


Z

7 Map analysis [i](#)

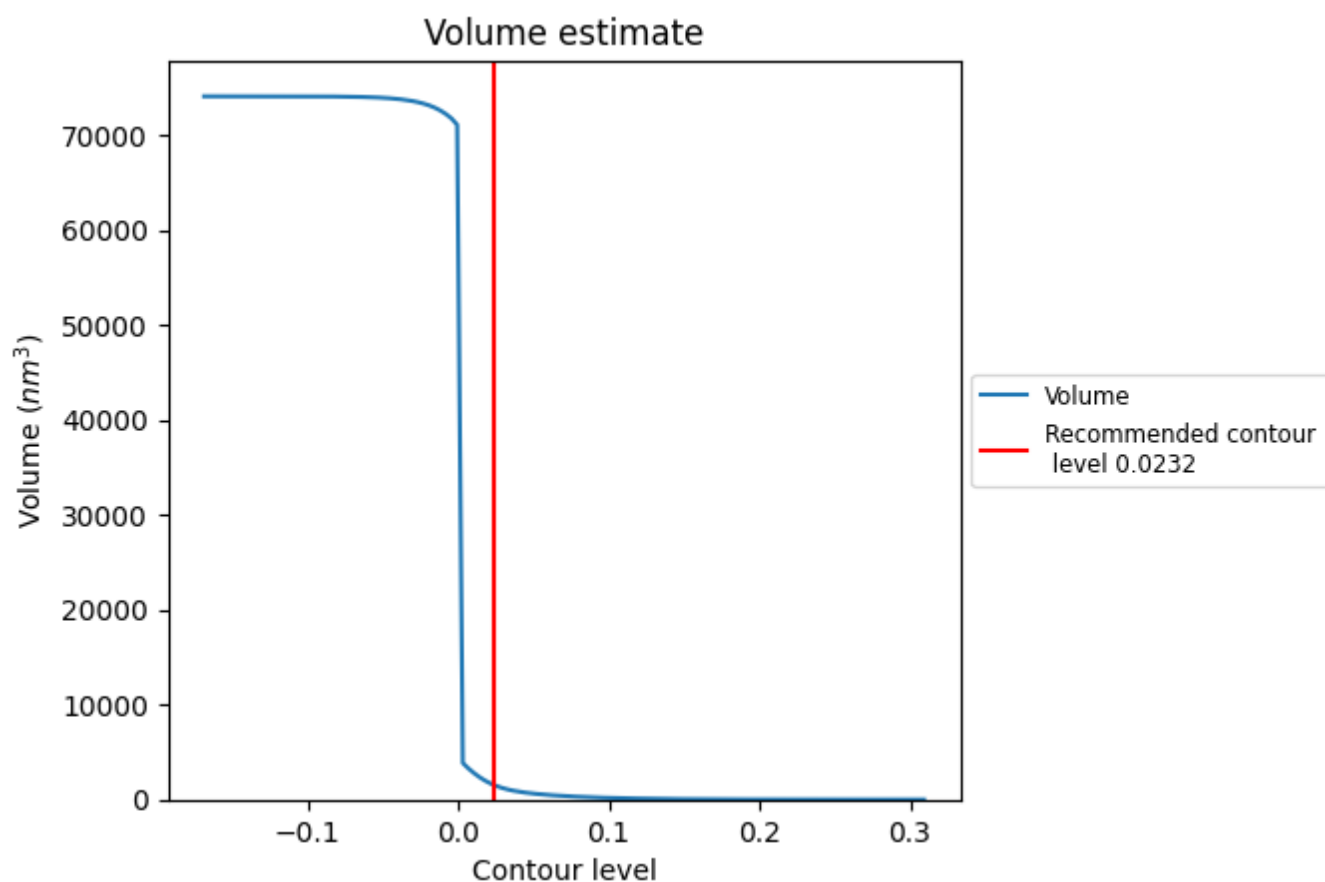
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

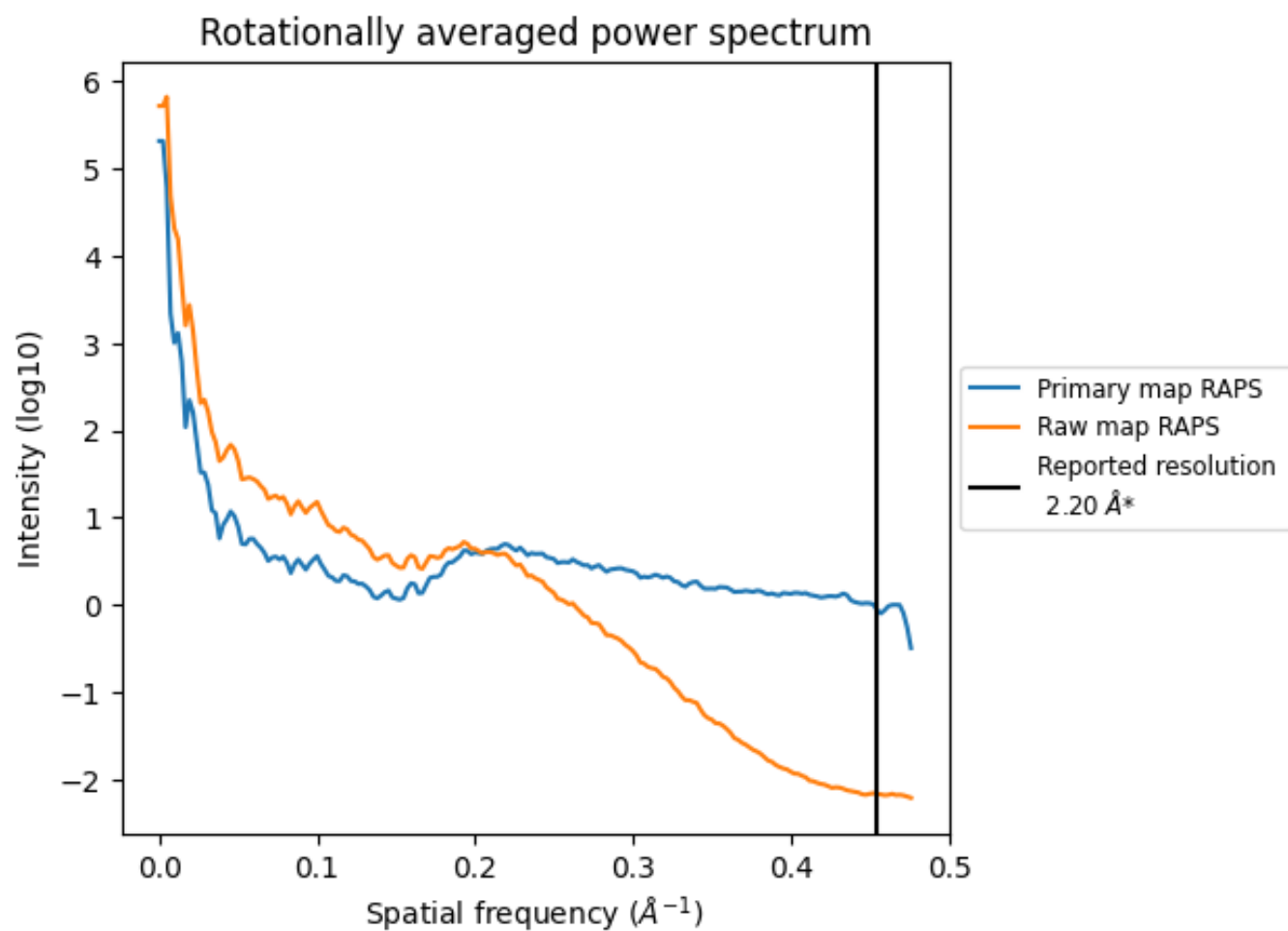
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1586 nm³; this corresponds to an approximate mass of 1433 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

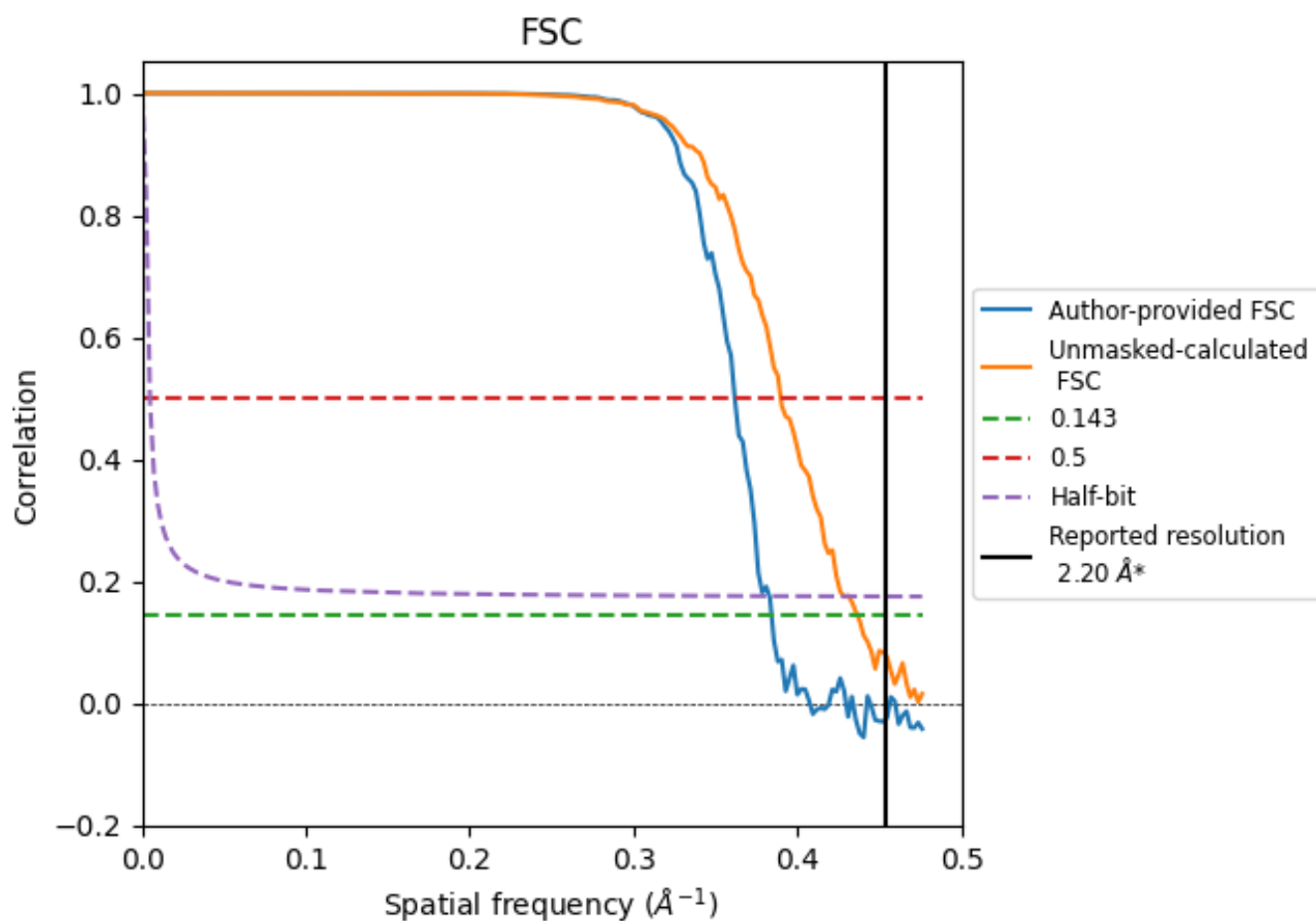


*Reported resolution corresponds to spatial frequency of 0.455 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.455 Å⁻¹

8.2 Resolution estimates [i](#)

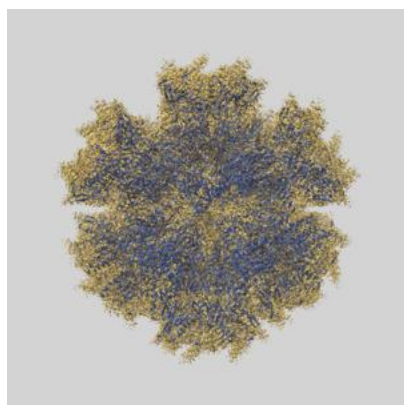
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	2.60	2.76	2.61
Unmasked-calculated*	2.29	2.56	2.33

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.60 differs from the reported value 2.2 by more than 10 %

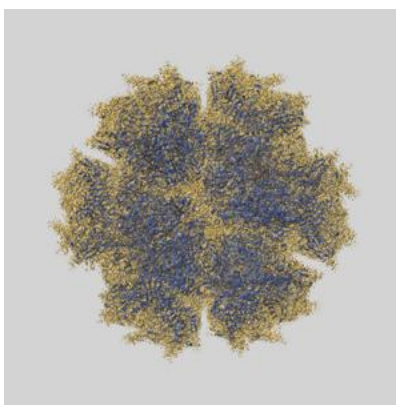
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18323 and PDB model 8QBX. Per-residue inclusion information can be found in [section 3](#) on [page 57](#).

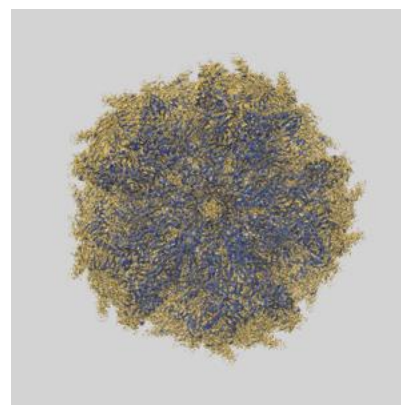
9.1 Map-model overlay [i](#)



X



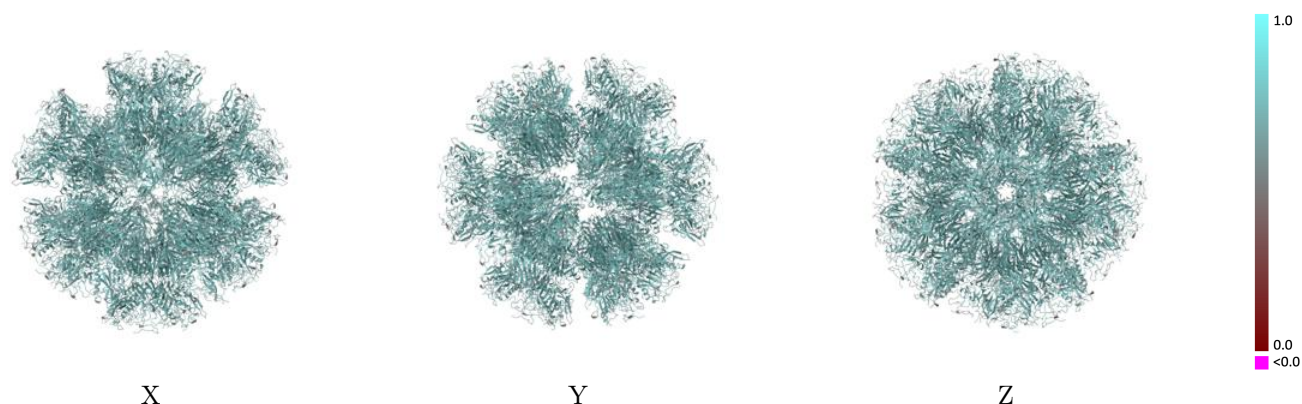
Y



Z

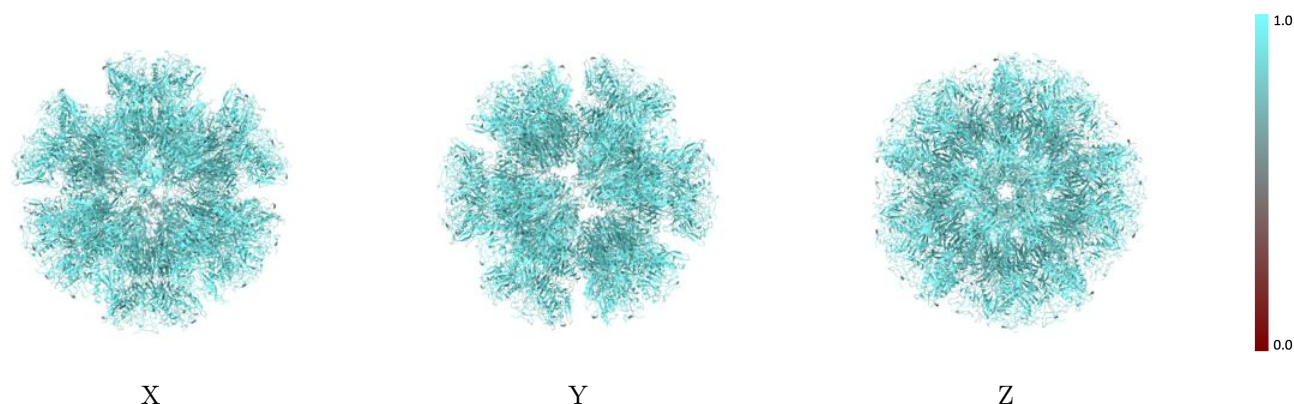
The images above show the 3D surface view of the map at the recommended contour level 0.0232 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



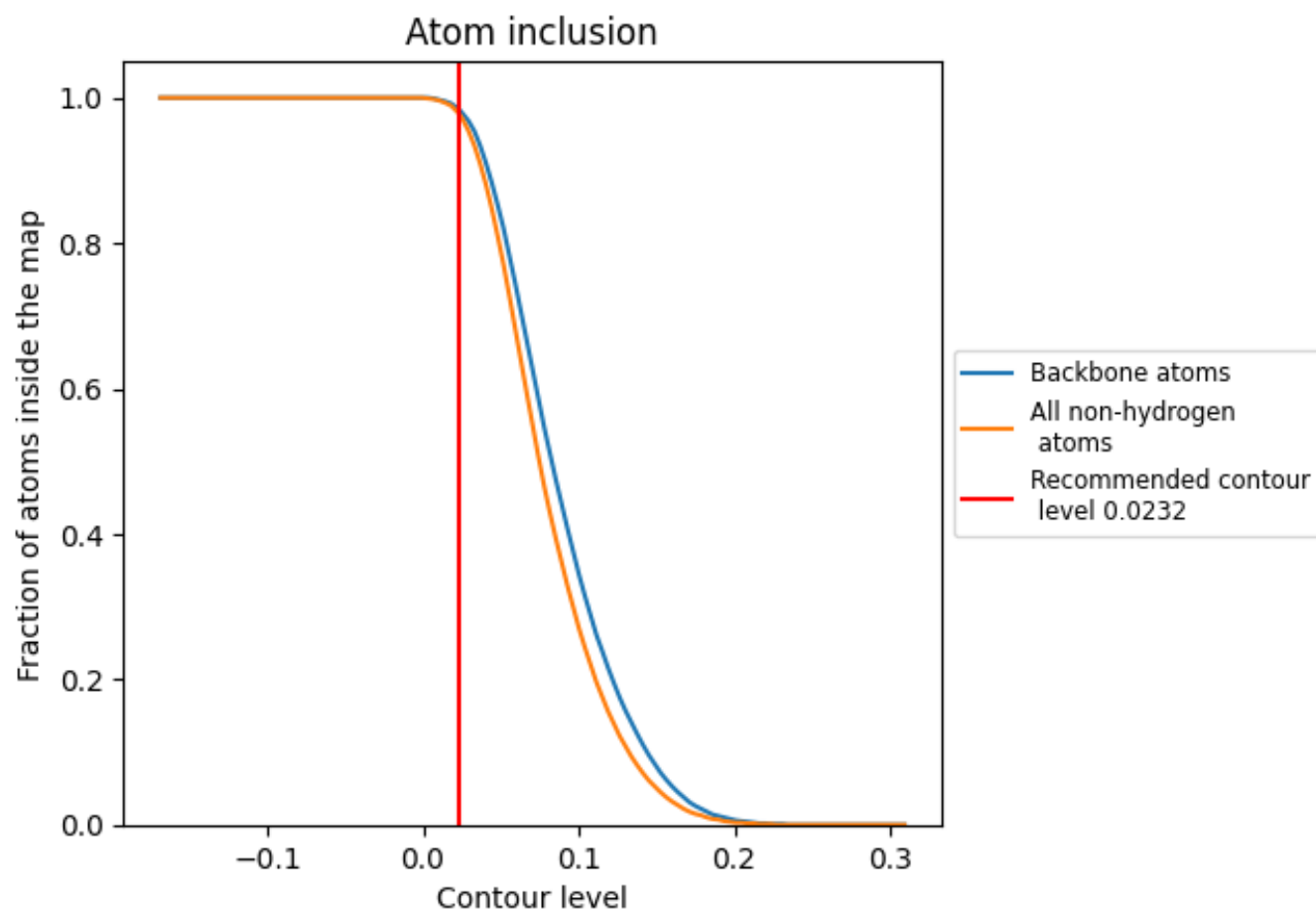
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0232).

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0232) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9780	 0.7070
A	 0.9790	 0.7090
AA	 0.9800	 0.7090
AB	 0.9810	 0.7090
B	 0.9790	 0.7110
BA	 0.9770	 0.7040
BB	 0.9780	 0.7070
C	 0.9750	 0.6930
CA	 0.9780	 0.7100
CB	 0.9770	 0.7040
D	 0.9790	 0.7030
DA	 0.9790	 0.7090
DB	 0.9760	 0.7030
E	 0.9790	 0.7120
EA	 0.9780	 0.7060
EB	 0.9820	 0.7120
F	 0.9780	 0.7110
FA	 0.9800	 0.7140
FB	 0.9790	 0.7100
G	 0.9770	 0.7030
GA	 0.9750	 0.7070
GB	 0.9750	 0.6980
H	 0.9780	 0.7000
HA	 0.9780	 0.7090
HB	 0.9770	 0.7050
I	 0.9740	 0.6980
IA	 0.9790	 0.7060
IB	 0.9770	 0.7090
J	 0.9770	 0.6990
JA	 0.9730	 0.6960
K	 0.9810	 0.7120
KA	 0.9800	 0.7070
L	 0.9790	 0.7070
LA	 0.9790	 0.7080
M	 0.9810	 0.7100



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Chain	Atom inclusion	Q-score
MA	 0.9760	 0.7050
N	 0.9810	 0.7090
NA	 0.9810	 0.7080
O	 0.9760	 0.7080
OA	 0.9770	 0.7120
P	 0.9780	 0.7070
PA	 0.9800	 0.7120
Q	 0.9780	 0.7060
QA	 0.9790	 0.7070
R	 0.9790	 0.7120
RA	 0.9790	 0.7060
S	 0.9820	 0.7100
SA	 0.9780	 0.7070
T	 0.9790	 0.7090
TA	 0.9780	 0.7080
UA	 0.9790	 0.7110
V	 0.9780	 0.7060
VA	 0.9740	 0.7010
W	 0.9810	 0.7110
WA	 0.9720	 0.6930
X	 0.9790	 0.7080
XA	 0.9790	 0.7130
Y	 0.9760	 0.7090
YA	 0.9770	 0.7100
Z	 0.9780	 0.7040
ZA	 0.9790	 0.7080