Full wwPDB EM Validation Report ⓘ

Nov 29, 2023 – 12:00 am GMT

PDB ID	:	8C9N
EMDB ID	:	EMD-16512
Title	:	MiniCoV-ADDomer, a SARS-CoV-2 epitope presenting viral like particle
Authors	:	Bufton, J.C.; Capin, J.; Boruku, U.; Garzoni, F.; Schaffitzel, C.; Berger, I.
Deposited on	:	2023-01-23
Resolution	:	2.36 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:

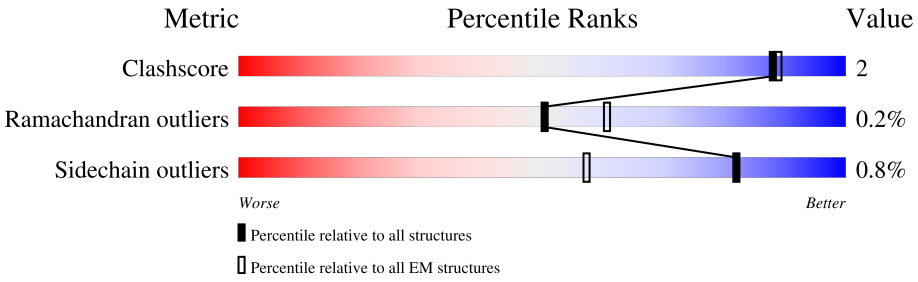
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.36 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	1	587	19% 70% 5% 26%
1	A	587	18% 70% 5% 26%
1	AA	587	20% 70% · 26%
1	AB	587	21% 70% · 26%
1	B	587	20% 70% 5% 26%
1	BA	587	20% 69% 5% 26%
1	BB	587	21% 70% · 26%
1	C	587	20% 70% 5% 26%

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Mol	Chain	Length	Quality of chain
1	CA	587	19% 70% 26%
1	CB	587	21% 70% 5% 26%
1	D	587	21% 70% 5% 26%
1	DA	587	21% 69% 5% 26%
1	DB	587	20% 69% 5% 26%
1	E	587	21% 68% 6% 26%
1	EA	587	21% 70% 5% 26%
1	EB	587	18% 70% 5% 26%
1	F	587	19% 71% 26%
1	FA	587	20% 70% 26%
1	FB	587	21% 70% 5% 26%
1	G	587	20% 68% 6% 26%
1	GA	587	20% 70% 26%
1	GB	587	21% 70% 5% 26%
1	H	587	19% 70% 5% 26%
1	HA	587	18% 70% 5% 26%
1	HB	587	21% 70% 26%
1	I	587	20% 70% 5% 26%
1	IA	587	19% 70% 5% 26%
1	J	587	19% 70% 26%
1	JA	587	19% 70% 5% 26%
1	K	587	19% 70% 26%
1	KA	587	19% 70% 26%
1	L	587	19% 69% 6% 26%
1	LA	587	19% 69% 5% 26%

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Mol	Chain	Length	Quality of chain
1	M	587	18% 69% 5% 26%
1	MA	587	19% 70% 26%
1	N	587	21% 70% 5% 26%
1	NA	587	21% 70% 5% 26%
1	O	587	19% 69% 5% 26%
1	OA	587	21% 70% 5% 26%
1	P	587	20% 69% 5% 26%
1	PA	587	21% 70% 26%
1	Q	587	20% 69% 5% 26%
1	QA	587	20% 70% 5% 26%
1	R	587	19% 70% 5% 26%
1	RA	587	18% 70% 26%
1	S	587	20% 70% 5% 26%
1	SA	587	20% 70% 5% 26%
1	T	587	20% 70% 5% 26%
1	TA	587	18% 69% 5% 26%
1	UA	587	21% 70% 26%
1	V	587	20% 70% 26%
1	VA	587	20% 68% 6% 26%
1	W	587	20% 70% 26%
1	WA	587	19% 69% 5% 26%
1	X	587	19% 69% 6% 26%
1	XA	587	21% 68% 6% 26%
1	Y	587	21% 70% 26%
1	YA	587	18% 70% 5% 26%

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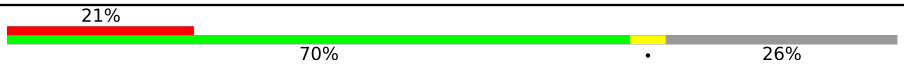
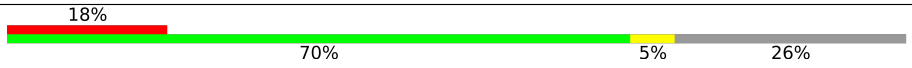
Mol	Chain	Length	Quality of chain
1	Z	587	
1	ZA	587	

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 419400 atoms, of which 207660 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	1	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	A	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	B	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	C	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	D	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	E	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	F	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	G	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	H	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	I	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	J	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	K	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	L	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	M	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	N	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	O	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	P	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	Q	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	R	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	S	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	T	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	V	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	W	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	X	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	Y	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	Z	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	AA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	BA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	CA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	DA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	EA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	FA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	GA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	HA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	IA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	JA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	KA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	LA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	MA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	NA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	OA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	PA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	QA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	RA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	SA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	TA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	UA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	VA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	WA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	XA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	YA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	ZA	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	AB	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	BB	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	CB	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	DB	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	EB	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	FB	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		
1	GB	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	HB	437	Total	C	H	N	O	S	0	0
			6990	2238	3461	602	675	14		

There are 2700 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	157	GLU	VAL	conflict	UNP Q2Y0H9
1	158	PHE	-	insertion	UNP Q2Y0H9
1	159	TYR	-	insertion	UNP Q2Y0H9
1	160	GLN	-	insertion	UNP Q2Y0H9
1	161	ALA	-	insertion	UNP Q2Y0H9
1	162	GLY	-	insertion	UNP Q2Y0H9
1	163	SER	-	insertion	UNP Q2Y0H9
1	164	THR	-	insertion	UNP Q2Y0H9
1	165	PRO	-	insertion	UNP Q2Y0H9
1	166	CYS	-	insertion	UNP Q2Y0H9
1	167	ASN	-	insertion	UNP Q2Y0H9
1	168	GLY	-	insertion	UNP Q2Y0H9
1	169	VAL	-	insertion	UNP Q2Y0H9
1	170	GLU	-	insertion	UNP Q2Y0H9
1	171	GLY	-	insertion	UNP Q2Y0H9
1	172	PHE	-	insertion	UNP Q2Y0H9
1	173	ASN	-	insertion	UNP Q2Y0H9
1	174	CYS	-	insertion	UNP Q2Y0H9
1	175	TYR	-	insertion	UNP Q2Y0H9
1	176	PHE	-	insertion	UNP Q2Y0H9
1	177	PRO	-	insertion	UNP Q2Y0H9
1	178	LEU	-	insertion	UNP Q2Y0H9
1	179	GLN	-	insertion	UNP Q2Y0H9
1	180	SER	-	insertion	UNP Q2Y0H9
1	181	TYR	-	insertion	UNP Q2Y0H9
1	182	GLY	-	insertion	UNP Q2Y0H9
1	183	PHE	-	insertion	UNP Q2Y0H9
1	184	GLN	-	insertion	UNP Q2Y0H9
1	185	PRO	-	insertion	UNP Q2Y0H9
1	186	THR	-	insertion	UNP Q2Y0H9
1	187	ASN	-	insertion	UNP Q2Y0H9
1	188	GLY	-	insertion	UNP Q2Y0H9
1	189	VAL	-	insertion	UNP Q2Y0H9
1	190	GLY	-	insertion	UNP Q2Y0H9
1	191	TYR	-	insertion	UNP Q2Y0H9
1	192	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
1	193	PRO	THR	conflict	UNP Q2Y0H9
1	341E	ALA	-	insertion	UNP Q2Y0H9
1	341F	ARG	-	insertion	UNP Q2Y0H9
1	341U	VAL	-	insertion	UNP Q2Y0H9
1	341V	ASP	-	insertion	UNP Q2Y0H9
1	342I	LEU	-	insertion	UNP Q2Y0H9
1	342J	GLU	-	insertion	UNP Q2Y0H9
1	342V	SER	-	insertion	UNP Q2Y0H9
1	342W	ARG	-	insertion	UNP Q2Y0H9
A	157	GLU	VAL	conflict	UNP Q2Y0H9
A	158	PHE	-	insertion	UNP Q2Y0H9
A	159	TYR	-	insertion	UNP Q2Y0H9
A	160	GLN	-	insertion	UNP Q2Y0H9
A	161	ALA	-	insertion	UNP Q2Y0H9
A	162	GLY	-	insertion	UNP Q2Y0H9
A	163	SER	-	insertion	UNP Q2Y0H9
A	164	THR	-	insertion	UNP Q2Y0H9
A	165	PRO	-	insertion	UNP Q2Y0H9
A	166	CYS	-	insertion	UNP Q2Y0H9
A	167	ASN	-	insertion	UNP Q2Y0H9
A	168	GLY	-	insertion	UNP Q2Y0H9
A	169	VAL	-	insertion	UNP Q2Y0H9
A	170	GLU	-	insertion	UNP Q2Y0H9
A	171	GLY	-	insertion	UNP Q2Y0H9
A	172	PHE	-	insertion	UNP Q2Y0H9
A	173	ASN	-	insertion	UNP Q2Y0H9
A	174	CYS	-	insertion	UNP Q2Y0H9
A	175	TYR	-	insertion	UNP Q2Y0H9
A	176	PHE	-	insertion	UNP Q2Y0H9
A	177	PRO	-	insertion	UNP Q2Y0H9
A	178	LEU	-	insertion	UNP Q2Y0H9
A	179	GLN	-	insertion	UNP Q2Y0H9
A	180	SER	-	insertion	UNP Q2Y0H9
A	181	TYR	-	insertion	UNP Q2Y0H9
A	182	GLY	-	insertion	UNP Q2Y0H9
A	183	PHE	-	insertion	UNP Q2Y0H9
A	184	GLN	-	insertion	UNP Q2Y0H9
A	185	PRO	-	insertion	UNP Q2Y0H9
A	186	THR	-	insertion	UNP Q2Y0H9
A	187	ASN	-	insertion	UNP Q2Y0H9
A	188	GLY	-	insertion	UNP Q2Y0H9
A	189	VAL	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	190	GLY	-	insertion	UNP Q2Y0H9
A	191	TYR	-	insertion	UNP Q2Y0H9
A	192	GLY	-	insertion	UNP Q2Y0H9
A	193	PRO	THR	conflict	UNP Q2Y0H9
A	341E	ALA	-	insertion	UNP Q2Y0H9
A	341F	ARG	-	insertion	UNP Q2Y0H9
A	341U	VAL	-	insertion	UNP Q2Y0H9
A	341V	ASP	-	insertion	UNP Q2Y0H9
A	342I	LEU	-	insertion	UNP Q2Y0H9
A	342J	GLU	-	insertion	UNP Q2Y0H9
A	342V	SER	-	insertion	UNP Q2Y0H9
A	342W	ARG	-	insertion	UNP Q2Y0H9
B	157	GLU	VAL	conflict	UNP Q2Y0H9
B	158	PHE	-	insertion	UNP Q2Y0H9
B	159	TYR	-	insertion	UNP Q2Y0H9
B	160	GLN	-	insertion	UNP Q2Y0H9
B	161	ALA	-	insertion	UNP Q2Y0H9
B	162	GLY	-	insertion	UNP Q2Y0H9
B	163	SER	-	insertion	UNP Q2Y0H9
B	164	THR	-	insertion	UNP Q2Y0H9
B	165	PRO	-	insertion	UNP Q2Y0H9
B	166	CYS	-	insertion	UNP Q2Y0H9
B	167	ASN	-	insertion	UNP Q2Y0H9
B	168	GLY	-	insertion	UNP Q2Y0H9
B	169	VAL	-	insertion	UNP Q2Y0H9
B	170	GLU	-	insertion	UNP Q2Y0H9
B	171	GLY	-	insertion	UNP Q2Y0H9
B	172	PHE	-	insertion	UNP Q2Y0H9
B	173	ASN	-	insertion	UNP Q2Y0H9
B	174	CYS	-	insertion	UNP Q2Y0H9
B	175	TYR	-	insertion	UNP Q2Y0H9
B	176	PHE	-	insertion	UNP Q2Y0H9
B	177	PRO	-	insertion	UNP Q2Y0H9
B	178	LEU	-	insertion	UNP Q2Y0H9
B	179	GLN	-	insertion	UNP Q2Y0H9
B	180	SER	-	insertion	UNP Q2Y0H9
B	181	TYR	-	insertion	UNP Q2Y0H9
B	182	GLY	-	insertion	UNP Q2Y0H9
B	183	PHE	-	insertion	UNP Q2Y0H9
B	184	GLN	-	insertion	UNP Q2Y0H9
B	185	PRO	-	insertion	UNP Q2Y0H9
B	186	THR	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	187	ASN	-	insertion	UNP Q2Y0H9
B	188	GLY	-	insertion	UNP Q2Y0H9
B	189	VAL	-	insertion	UNP Q2Y0H9
B	190	GLY	-	insertion	UNP Q2Y0H9
B	191	TYR	-	insertion	UNP Q2Y0H9
B	192	GLY	-	insertion	UNP Q2Y0H9
B	193	PRO	THR	conflict	UNP Q2Y0H9
B	341E	ALA	-	insertion	UNP Q2Y0H9
B	341F	ARG	-	insertion	UNP Q2Y0H9
B	341U	VAL	-	insertion	UNP Q2Y0H9
B	341V	ASP	-	insertion	UNP Q2Y0H9
B	342I	LEU	-	insertion	UNP Q2Y0H9
B	342J	GLU	-	insertion	UNP Q2Y0H9
B	342V	SER	-	insertion	UNP Q2Y0H9
B	342W	ARG	-	insertion	UNP Q2Y0H9
C	157	GLU	VAL	conflict	UNP Q2Y0H9
C	158	PHE	-	insertion	UNP Q2Y0H9
C	159	TYR	-	insertion	UNP Q2Y0H9
C	160	GLN	-	insertion	UNP Q2Y0H9
C	161	ALA	-	insertion	UNP Q2Y0H9
C	162	GLY	-	insertion	UNP Q2Y0H9
C	163	SER	-	insertion	UNP Q2Y0H9
C	164	THR	-	insertion	UNP Q2Y0H9
C	165	PRO	-	insertion	UNP Q2Y0H9
C	166	CYS	-	insertion	UNP Q2Y0H9
C	167	ASN	-	insertion	UNP Q2Y0H9
C	168	GLY	-	insertion	UNP Q2Y0H9
C	169	VAL	-	insertion	UNP Q2Y0H9
C	170	GLU	-	insertion	UNP Q2Y0H9
C	171	GLY	-	insertion	UNP Q2Y0H9
C	172	PHE	-	insertion	UNP Q2Y0H9
C	173	ASN	-	insertion	UNP Q2Y0H9
C	174	CYS	-	insertion	UNP Q2Y0H9
C	175	TYR	-	insertion	UNP Q2Y0H9
C	176	PHE	-	insertion	UNP Q2Y0H9
C	177	PRO	-	insertion	UNP Q2Y0H9
C	178	LEU	-	insertion	UNP Q2Y0H9
C	179	GLN	-	insertion	UNP Q2Y0H9
C	180	SER	-	insertion	UNP Q2Y0H9
C	181	TYR	-	insertion	UNP Q2Y0H9
C	182	GLY	-	insertion	UNP Q2Y0H9
C	183	PHE	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	184	GLN	-	insertion	UNP Q2Y0H9
C	185	PRO	-	insertion	UNP Q2Y0H9
C	186	THR	-	insertion	UNP Q2Y0H9
C	187	ASN	-	insertion	UNP Q2Y0H9
C	188	GLY	-	insertion	UNP Q2Y0H9
C	189	VAL	-	insertion	UNP Q2Y0H9
C	190	GLY	-	insertion	UNP Q2Y0H9
C	191	TYR	-	insertion	UNP Q2Y0H9
C	192	GLY	-	insertion	UNP Q2Y0H9
C	193	PRO	THR	conflict	UNP Q2Y0H9
C	341E	ALA	-	insertion	UNP Q2Y0H9
C	341F	ARG	-	insertion	UNP Q2Y0H9
C	341U	VAL	-	insertion	UNP Q2Y0H9
C	341V	ASP	-	insertion	UNP Q2Y0H9
C	342I	LEU	-	insertion	UNP Q2Y0H9
C	342J	GLU	-	insertion	UNP Q2Y0H9
C	342V	SER	-	insertion	UNP Q2Y0H9
C	342W	ARG	-	insertion	UNP Q2Y0H9
D	157	GLU	VAL	conflict	UNP Q2Y0H9
D	158	PHE	-	insertion	UNP Q2Y0H9
D	159	TYR	-	insertion	UNP Q2Y0H9
D	160	GLN	-	insertion	UNP Q2Y0H9
D	161	ALA	-	insertion	UNP Q2Y0H9
D	162	GLY	-	insertion	UNP Q2Y0H9
D	163	SER	-	insertion	UNP Q2Y0H9
D	164	THR	-	insertion	UNP Q2Y0H9
D	165	PRO	-	insertion	UNP Q2Y0H9
D	166	CYS	-	insertion	UNP Q2Y0H9
D	167	ASN	-	insertion	UNP Q2Y0H9
D	168	GLY	-	insertion	UNP Q2Y0H9
D	169	VAL	-	insertion	UNP Q2Y0H9
D	170	GLU	-	insertion	UNP Q2Y0H9
D	171	GLY	-	insertion	UNP Q2Y0H9
D	172	PHE	-	insertion	UNP Q2Y0H9
D	173	ASN	-	insertion	UNP Q2Y0H9
D	174	CYS	-	insertion	UNP Q2Y0H9
D	175	TYR	-	insertion	UNP Q2Y0H9
D	176	PHE	-	insertion	UNP Q2Y0H9
D	177	PRO	-	insertion	UNP Q2Y0H9
D	178	LEU	-	insertion	UNP Q2Y0H9
D	179	GLN	-	insertion	UNP Q2Y0H9
D	180	SER	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	181	TYR	-	insertion	UNP Q2Y0H9
D	182	GLY	-	insertion	UNP Q2Y0H9
D	183	PHE	-	insertion	UNP Q2Y0H9
D	184	GLN	-	insertion	UNP Q2Y0H9
D	185	PRO	-	insertion	UNP Q2Y0H9
D	186	THR	-	insertion	UNP Q2Y0H9
D	187	ASN	-	insertion	UNP Q2Y0H9
D	188	GLY	-	insertion	UNP Q2Y0H9
D	189	VAL	-	insertion	UNP Q2Y0H9
D	190	GLY	-	insertion	UNP Q2Y0H9
D	191	TYR	-	insertion	UNP Q2Y0H9
D	192	GLY	-	insertion	UNP Q2Y0H9
D	193	PRO	THR	conflict	UNP Q2Y0H9
D	341E	ALA	-	insertion	UNP Q2Y0H9
D	341F	ARG	-	insertion	UNP Q2Y0H9
D	341U	VAL	-	insertion	UNP Q2Y0H9
D	341V	ASP	-	insertion	UNP Q2Y0H9
D	342I	LEU	-	insertion	UNP Q2Y0H9
D	342J	GLU	-	insertion	UNP Q2Y0H9
D	342V	SER	-	insertion	UNP Q2Y0H9
D	342W	ARG	-	insertion	UNP Q2Y0H9
E	157	GLU	VAL	conflict	UNP Q2Y0H9
E	158	PHE	-	insertion	UNP Q2Y0H9
E	159	TYR	-	insertion	UNP Q2Y0H9
E	160	GLN	-	insertion	UNP Q2Y0H9
E	161	ALA	-	insertion	UNP Q2Y0H9
E	162	GLY	-	insertion	UNP Q2Y0H9
E	163	SER	-	insertion	UNP Q2Y0H9
E	164	THR	-	insertion	UNP Q2Y0H9
E	165	PRO	-	insertion	UNP Q2Y0H9
E	166	CYS	-	insertion	UNP Q2Y0H9
E	167	ASN	-	insertion	UNP Q2Y0H9
E	168	GLY	-	insertion	UNP Q2Y0H9
E	169	VAL	-	insertion	UNP Q2Y0H9
E	170	GLU	-	insertion	UNP Q2Y0H9
E	171	GLY	-	insertion	UNP Q2Y0H9
E	172	PHE	-	insertion	UNP Q2Y0H9
E	173	ASN	-	insertion	UNP Q2Y0H9
E	174	CYS	-	insertion	UNP Q2Y0H9
E	175	TYR	-	insertion	UNP Q2Y0H9
E	176	PHE	-	insertion	UNP Q2Y0H9
E	177	PRO	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	178	LEU	-	insertion	UNP Q2Y0H9
E	179	GLN	-	insertion	UNP Q2Y0H9
E	180	SER	-	insertion	UNP Q2Y0H9
E	181	TYR	-	insertion	UNP Q2Y0H9
E	182	GLY	-	insertion	UNP Q2Y0H9
E	183	PHE	-	insertion	UNP Q2Y0H9
E	184	GLN	-	insertion	UNP Q2Y0H9
E	185	PRO	-	insertion	UNP Q2Y0H9
E	186	THR	-	insertion	UNP Q2Y0H9
E	187	ASN	-	insertion	UNP Q2Y0H9
E	188	GLY	-	insertion	UNP Q2Y0H9
E	189	VAL	-	insertion	UNP Q2Y0H9
E	190	GLY	-	insertion	UNP Q2Y0H9
E	191	TYR	-	insertion	UNP Q2Y0H9
E	192	GLY	-	insertion	UNP Q2Y0H9
E	193	PRO	THR	conflict	UNP Q2Y0H9
E	341E	ALA	-	insertion	UNP Q2Y0H9
E	341F	ARG	-	insertion	UNP Q2Y0H9
E	341U	VAL	-	insertion	UNP Q2Y0H9
E	341V	ASP	-	insertion	UNP Q2Y0H9
E	342I	LEU	-	insertion	UNP Q2Y0H9
E	342J	GLU	-	insertion	UNP Q2Y0H9
E	342V	SER	-	insertion	UNP Q2Y0H9
E	342W	ARG	-	insertion	UNP Q2Y0H9
F	157	GLU	VAL	conflict	UNP Q2Y0H9
F	158	PHE	-	insertion	UNP Q2Y0H9
F	159	TYR	-	insertion	UNP Q2Y0H9
F	160	GLN	-	insertion	UNP Q2Y0H9
F	161	ALA	-	insertion	UNP Q2Y0H9
F	162	GLY	-	insertion	UNP Q2Y0H9
F	163	SER	-	insertion	UNP Q2Y0H9
F	164	THR	-	insertion	UNP Q2Y0H9
F	165	PRO	-	insertion	UNP Q2Y0H9
F	166	CYS	-	insertion	UNP Q2Y0H9
F	167	ASN	-	insertion	UNP Q2Y0H9
F	168	GLY	-	insertion	UNP Q2Y0H9
F	169	VAL	-	insertion	UNP Q2Y0H9
F	170	GLU	-	insertion	UNP Q2Y0H9
F	171	GLY	-	insertion	UNP Q2Y0H9
F	172	PHE	-	insertion	UNP Q2Y0H9
F	173	ASN	-	insertion	UNP Q2Y0H9
F	174	CYS	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	175	TYR	-	insertion	UNP Q2Y0H9
F	176	PHE	-	insertion	UNP Q2Y0H9
F	177	PRO	-	insertion	UNP Q2Y0H9
F	178	LEU	-	insertion	UNP Q2Y0H9
F	179	GLN	-	insertion	UNP Q2Y0H9
F	180	SER	-	insertion	UNP Q2Y0H9
F	181	TYR	-	insertion	UNP Q2Y0H9
F	182	GLY	-	insertion	UNP Q2Y0H9
F	183	PHE	-	insertion	UNP Q2Y0H9
F	184	GLN	-	insertion	UNP Q2Y0H9
F	185	PRO	-	insertion	UNP Q2Y0H9
F	186	THR	-	insertion	UNP Q2Y0H9
F	187	ASN	-	insertion	UNP Q2Y0H9
F	188	GLY	-	insertion	UNP Q2Y0H9
F	189	VAL	-	insertion	UNP Q2Y0H9
F	190	GLY	-	insertion	UNP Q2Y0H9
F	191	TYR	-	insertion	UNP Q2Y0H9
F	192	GLY	-	insertion	UNP Q2Y0H9
F	193	PRO	THR	conflict	UNP Q2Y0H9
F	341E	ALA	-	insertion	UNP Q2Y0H9
F	341F	ARG	-	insertion	UNP Q2Y0H9
F	341U	VAL	-	insertion	UNP Q2Y0H9
F	341V	ASP	-	insertion	UNP Q2Y0H9
F	342I	LEU	-	insertion	UNP Q2Y0H9
F	342J	GLU	-	insertion	UNP Q2Y0H9
F	342V	SER	-	insertion	UNP Q2Y0H9
F	342W	ARG	-	insertion	UNP Q2Y0H9
G	157	GLU	VAL	conflict	UNP Q2Y0H9
G	158	PHE	-	insertion	UNP Q2Y0H9
G	159	TYR	-	insertion	UNP Q2Y0H9
G	160	GLN	-	insertion	UNP Q2Y0H9
G	161	ALA	-	insertion	UNP Q2Y0H9
G	162	GLY	-	insertion	UNP Q2Y0H9
G	163	SER	-	insertion	UNP Q2Y0H9
G	164	THR	-	insertion	UNP Q2Y0H9
G	165	PRO	-	insertion	UNP Q2Y0H9
G	166	CYS	-	insertion	UNP Q2Y0H9
G	167	ASN	-	insertion	UNP Q2Y0H9
G	168	GLY	-	insertion	UNP Q2Y0H9
G	169	VAL	-	insertion	UNP Q2Y0H9
G	170	GLU	-	insertion	UNP Q2Y0H9
G	171	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	172	PHE	-	insertion	UNP Q2Y0H9
G	173	ASN	-	insertion	UNP Q2Y0H9
G	174	CYS	-	insertion	UNP Q2Y0H9
G	175	TYR	-	insertion	UNP Q2Y0H9
G	176	PHE	-	insertion	UNP Q2Y0H9
G	177	PRO	-	insertion	UNP Q2Y0H9
G	178	LEU	-	insertion	UNP Q2Y0H9
G	179	GLN	-	insertion	UNP Q2Y0H9
G	180	SER	-	insertion	UNP Q2Y0H9
G	181	TYR	-	insertion	UNP Q2Y0H9
G	182	GLY	-	insertion	UNP Q2Y0H9
G	183	PHE	-	insertion	UNP Q2Y0H9
G	184	GLN	-	insertion	UNP Q2Y0H9
G	185	PRO	-	insertion	UNP Q2Y0H9
G	186	THR	-	insertion	UNP Q2Y0H9
G	187	ASN	-	insertion	UNP Q2Y0H9
G	188	GLY	-	insertion	UNP Q2Y0H9
G	189	VAL	-	insertion	UNP Q2Y0H9
G	190	GLY	-	insertion	UNP Q2Y0H9
G	191	TYR	-	insertion	UNP Q2Y0H9
G	192	GLY	-	insertion	UNP Q2Y0H9
G	193	PRO	THR	conflict	UNP Q2Y0H9
G	341E	ALA	-	insertion	UNP Q2Y0H9
G	341F	ARG	-	insertion	UNP Q2Y0H9
G	341U	VAL	-	insertion	UNP Q2Y0H9
G	341V	ASP	-	insertion	UNP Q2Y0H9
G	342I	LEU	-	insertion	UNP Q2Y0H9
G	342J	GLU	-	insertion	UNP Q2Y0H9
G	342V	SER	-	insertion	UNP Q2Y0H9
G	342W	ARG	-	insertion	UNP Q2Y0H9
H	157	GLU	VAL	conflict	UNP Q2Y0H9
H	158	PHE	-	insertion	UNP Q2Y0H9
H	159	TYR	-	insertion	UNP Q2Y0H9
H	160	GLN	-	insertion	UNP Q2Y0H9
H	161	ALA	-	insertion	UNP Q2Y0H9
H	162	GLY	-	insertion	UNP Q2Y0H9
H	163	SER	-	insertion	UNP Q2Y0H9
H	164	THR	-	insertion	UNP Q2Y0H9
H	165	PRO	-	insertion	UNP Q2Y0H9
H	166	CYS	-	insertion	UNP Q2Y0H9
H	167	ASN	-	insertion	UNP Q2Y0H9
H	168	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
H	169	VAL	-	insertion	UNP Q2Y0H9
H	170	GLU	-	insertion	UNP Q2Y0H9
H	171	GLY	-	insertion	UNP Q2Y0H9
H	172	PHE	-	insertion	UNP Q2Y0H9
H	173	ASN	-	insertion	UNP Q2Y0H9
H	174	CYS	-	insertion	UNP Q2Y0H9
H	175	TYR	-	insertion	UNP Q2Y0H9
H	176	PHE	-	insertion	UNP Q2Y0H9
H	177	PRO	-	insertion	UNP Q2Y0H9
H	178	LEU	-	insertion	UNP Q2Y0H9
H	179	GLN	-	insertion	UNP Q2Y0H9
H	180	SER	-	insertion	UNP Q2Y0H9
H	181	TYR	-	insertion	UNP Q2Y0H9
H	182	GLY	-	insertion	UNP Q2Y0H9
H	183	PHE	-	insertion	UNP Q2Y0H9
H	184	GLN	-	insertion	UNP Q2Y0H9
H	185	PRO	-	insertion	UNP Q2Y0H9
H	186	THR	-	insertion	UNP Q2Y0H9
H	187	ASN	-	insertion	UNP Q2Y0H9
H	188	GLY	-	insertion	UNP Q2Y0H9
H	189	VAL	-	insertion	UNP Q2Y0H9
H	190	GLY	-	insertion	UNP Q2Y0H9
H	191	TYR	-	insertion	UNP Q2Y0H9
H	192	GLY	-	insertion	UNP Q2Y0H9
H	193	PRO	THR	conflict	UNP Q2Y0H9
H	341E	ALA	-	insertion	UNP Q2Y0H9
H	341F	ARG	-	insertion	UNP Q2Y0H9
H	341U	VAL	-	insertion	UNP Q2Y0H9
H	341V	ASP	-	insertion	UNP Q2Y0H9
H	342I	LEU	-	insertion	UNP Q2Y0H9
H	342J	GLU	-	insertion	UNP Q2Y0H9
H	342V	SER	-	insertion	UNP Q2Y0H9
H	342W	ARG	-	insertion	UNP Q2Y0H9
I	157	GLU	VAL	conflict	UNP Q2Y0H9
I	158	PHE	-	insertion	UNP Q2Y0H9
I	159	TYR	-	insertion	UNP Q2Y0H9
I	160	GLN	-	insertion	UNP Q2Y0H9
I	161	ALA	-	insertion	UNP Q2Y0H9
I	162	GLY	-	insertion	UNP Q2Y0H9
I	163	SER	-	insertion	UNP Q2Y0H9
I	164	THR	-	insertion	UNP Q2Y0H9
I	165	PRO	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
I	166	CYS	-	insertion	UNP Q2Y0H9
I	167	ASN	-	insertion	UNP Q2Y0H9
I	168	GLY	-	insertion	UNP Q2Y0H9
I	169	VAL	-	insertion	UNP Q2Y0H9
I	170	GLU	-	insertion	UNP Q2Y0H9
I	171	GLY	-	insertion	UNP Q2Y0H9
I	172	PHE	-	insertion	UNP Q2Y0H9
I	173	ASN	-	insertion	UNP Q2Y0H9
I	174	CYS	-	insertion	UNP Q2Y0H9
I	175	TYR	-	insertion	UNP Q2Y0H9
I	176	PHE	-	insertion	UNP Q2Y0H9
I	177	PRO	-	insertion	UNP Q2Y0H9
I	178	LEU	-	insertion	UNP Q2Y0H9
I	179	GLN	-	insertion	UNP Q2Y0H9
I	180	SER	-	insertion	UNP Q2Y0H9
I	181	TYR	-	insertion	UNP Q2Y0H9
I	182	GLY	-	insertion	UNP Q2Y0H9
I	183	PHE	-	insertion	UNP Q2Y0H9
I	184	GLN	-	insertion	UNP Q2Y0H9
I	185	PRO	-	insertion	UNP Q2Y0H9
I	186	THR	-	insertion	UNP Q2Y0H9
I	187	ASN	-	insertion	UNP Q2Y0H9
I	188	GLY	-	insertion	UNP Q2Y0H9
I	189	VAL	-	insertion	UNP Q2Y0H9
I	190	GLY	-	insertion	UNP Q2Y0H9
I	191	TYR	-	insertion	UNP Q2Y0H9
I	192	GLY	-	insertion	UNP Q2Y0H9
I	193	PRO	THR	conflict	UNP Q2Y0H9
I	341E	ALA	-	insertion	UNP Q2Y0H9
I	341F	ARG	-	insertion	UNP Q2Y0H9
I	341U	VAL	-	insertion	UNP Q2Y0H9
I	341V	ASP	-	insertion	UNP Q2Y0H9
I	342I	LEU	-	insertion	UNP Q2Y0H9
I	342J	GLU	-	insertion	UNP Q2Y0H9
I	342V	SER	-	insertion	UNP Q2Y0H9
I	342W	ARG	-	insertion	UNP Q2Y0H9
J	157	GLU	VAL	conflict	UNP Q2Y0H9
J	158	PHE	-	insertion	UNP Q2Y0H9
J	159	TYR	-	insertion	UNP Q2Y0H9
J	160	GLN	-	insertion	UNP Q2Y0H9
J	161	ALA	-	insertion	UNP Q2Y0H9
J	162	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
J	163	SER	-	insertion	UNP Q2Y0H9
J	164	THR	-	insertion	UNP Q2Y0H9
J	165	PRO	-	insertion	UNP Q2Y0H9
J	166	CYS	-	insertion	UNP Q2Y0H9
J	167	ASN	-	insertion	UNP Q2Y0H9
J	168	GLY	-	insertion	UNP Q2Y0H9
J	169	VAL	-	insertion	UNP Q2Y0H9
J	170	GLU	-	insertion	UNP Q2Y0H9
J	171	GLY	-	insertion	UNP Q2Y0H9
J	172	PHE	-	insertion	UNP Q2Y0H9
J	173	ASN	-	insertion	UNP Q2Y0H9
J	174	CYS	-	insertion	UNP Q2Y0H9
J	175	TYR	-	insertion	UNP Q2Y0H9
J	176	PHE	-	insertion	UNP Q2Y0H9
J	177	PRO	-	insertion	UNP Q2Y0H9
J	178	LEU	-	insertion	UNP Q2Y0H9
J	179	GLN	-	insertion	UNP Q2Y0H9
J	180	SER	-	insertion	UNP Q2Y0H9
J	181	TYR	-	insertion	UNP Q2Y0H9
J	182	GLY	-	insertion	UNP Q2Y0H9
J	183	PHE	-	insertion	UNP Q2Y0H9
J	184	GLN	-	insertion	UNP Q2Y0H9
J	185	PRO	-	insertion	UNP Q2Y0H9
J	186	THR	-	insertion	UNP Q2Y0H9
J	187	ASN	-	insertion	UNP Q2Y0H9
J	188	GLY	-	insertion	UNP Q2Y0H9
J	189	VAL	-	insertion	UNP Q2Y0H9
J	190	GLY	-	insertion	UNP Q2Y0H9
J	191	TYR	-	insertion	UNP Q2Y0H9
J	192	GLY	-	insertion	UNP Q2Y0H9
J	193	PRO	THR	conflict	UNP Q2Y0H9
J	341E	ALA	-	insertion	UNP Q2Y0H9
J	341F	ARG	-	insertion	UNP Q2Y0H9
J	341U	VAL	-	insertion	UNP Q2Y0H9
J	341V	ASP	-	insertion	UNP Q2Y0H9
J	342I	LEU	-	insertion	UNP Q2Y0H9
J	342J	GLU	-	insertion	UNP Q2Y0H9
J	342V	SER	-	insertion	UNP Q2Y0H9
J	342W	ARG	-	insertion	UNP Q2Y0H9
K	157	GLU	VAL	conflict	UNP Q2Y0H9
K	158	PHE	-	insertion	UNP Q2Y0H9
K	159	TYR	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
K	160	GLN	-	insertion	UNP Q2Y0H9
K	161	ALA	-	insertion	UNP Q2Y0H9
K	162	GLY	-	insertion	UNP Q2Y0H9
K	163	SER	-	insertion	UNP Q2Y0H9
K	164	THR	-	insertion	UNP Q2Y0H9
K	165	PRO	-	insertion	UNP Q2Y0H9
K	166	CYS	-	insertion	UNP Q2Y0H9
K	167	ASN	-	insertion	UNP Q2Y0H9
K	168	GLY	-	insertion	UNP Q2Y0H9
K	169	VAL	-	insertion	UNP Q2Y0H9
K	170	GLU	-	insertion	UNP Q2Y0H9
K	171	GLY	-	insertion	UNP Q2Y0H9
K	172	PHE	-	insertion	UNP Q2Y0H9
K	173	ASN	-	insertion	UNP Q2Y0H9
K	174	CYS	-	insertion	UNP Q2Y0H9
K	175	TYR	-	insertion	UNP Q2Y0H9
K	176	PHE	-	insertion	UNP Q2Y0H9
K	177	PRO	-	insertion	UNP Q2Y0H9
K	178	LEU	-	insertion	UNP Q2Y0H9
K	179	GLN	-	insertion	UNP Q2Y0H9
K	180	SER	-	insertion	UNP Q2Y0H9
K	181	TYR	-	insertion	UNP Q2Y0H9
K	182	GLY	-	insertion	UNP Q2Y0H9
K	183	PHE	-	insertion	UNP Q2Y0H9
K	184	GLN	-	insertion	UNP Q2Y0H9
K	185	PRO	-	insertion	UNP Q2Y0H9
K	186	THR	-	insertion	UNP Q2Y0H9
K	187	ASN	-	insertion	UNP Q2Y0H9
K	188	GLY	-	insertion	UNP Q2Y0H9
K	189	VAL	-	insertion	UNP Q2Y0H9
K	190	GLY	-	insertion	UNP Q2Y0H9
K	191	TYR	-	insertion	UNP Q2Y0H9
K	192	GLY	-	insertion	UNP Q2Y0H9
K	193	PRO	THR	conflict	UNP Q2Y0H9
K	341E	ALA	-	insertion	UNP Q2Y0H9
K	341F	ARG	-	insertion	UNP Q2Y0H9
K	341U	VAL	-	insertion	UNP Q2Y0H9
K	341V	ASP	-	insertion	UNP Q2Y0H9
K	342I	LEU	-	insertion	UNP Q2Y0H9
K	342J	GLU	-	insertion	UNP Q2Y0H9
K	342V	SER	-	insertion	UNP Q2Y0H9
K	342W	ARG	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
L	157	GLU	VAL	conflict	UNP Q2Y0H9
L	158	PHE	-	insertion	UNP Q2Y0H9
L	159	TYR	-	insertion	UNP Q2Y0H9
L	160	GLN	-	insertion	UNP Q2Y0H9
L	161	ALA	-	insertion	UNP Q2Y0H9
L	162	GLY	-	insertion	UNP Q2Y0H9
L	163	SER	-	insertion	UNP Q2Y0H9
L	164	THR	-	insertion	UNP Q2Y0H9
L	165	PRO	-	insertion	UNP Q2Y0H9
L	166	CYS	-	insertion	UNP Q2Y0H9
L	167	ASN	-	insertion	UNP Q2Y0H9
L	168	GLY	-	insertion	UNP Q2Y0H9
L	169	VAL	-	insertion	UNP Q2Y0H9
L	170	GLU	-	insertion	UNP Q2Y0H9
L	171	GLY	-	insertion	UNP Q2Y0H9
L	172	PHE	-	insertion	UNP Q2Y0H9
L	173	ASN	-	insertion	UNP Q2Y0H9
L	174	CYS	-	insertion	UNP Q2Y0H9
L	175	TYR	-	insertion	UNP Q2Y0H9
L	176	PHE	-	insertion	UNP Q2Y0H9
L	177	PRO	-	insertion	UNP Q2Y0H9
L	178	LEU	-	insertion	UNP Q2Y0H9
L	179	GLN	-	insertion	UNP Q2Y0H9
L	180	SER	-	insertion	UNP Q2Y0H9
L	181	TYR	-	insertion	UNP Q2Y0H9
L	182	GLY	-	insertion	UNP Q2Y0H9
L	183	PHE	-	insertion	UNP Q2Y0H9
L	184	GLN	-	insertion	UNP Q2Y0H9
L	185	PRO	-	insertion	UNP Q2Y0H9
L	186	THR	-	insertion	UNP Q2Y0H9
L	187	ASN	-	insertion	UNP Q2Y0H9
L	188	GLY	-	insertion	UNP Q2Y0H9
L	189	VAL	-	insertion	UNP Q2Y0H9
L	190	GLY	-	insertion	UNP Q2Y0H9
L	191	TYR	-	insertion	UNP Q2Y0H9
L	192	GLY	-	insertion	UNP Q2Y0H9
L	193	PRO	THR	conflict	UNP Q2Y0H9
L	341E	ALA	-	insertion	UNP Q2Y0H9
L	341F	ARG	-	insertion	UNP Q2Y0H9
L	341U	VAL	-	insertion	UNP Q2Y0H9
L	341V	ASP	-	insertion	UNP Q2Y0H9
L	342I	LEU	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
L	342J	GLU	-	insertion	UNP Q2Y0H9
L	342V	SER	-	insertion	UNP Q2Y0H9
L	342W	ARG	-	insertion	UNP Q2Y0H9
M	157	GLU	VAL	conflict	UNP Q2Y0H9
M	158	PHE	-	insertion	UNP Q2Y0H9
M	159	TYR	-	insertion	UNP Q2Y0H9
M	160	GLN	-	insertion	UNP Q2Y0H9
M	161	ALA	-	insertion	UNP Q2Y0H9
M	162	GLY	-	insertion	UNP Q2Y0H9
M	163	SER	-	insertion	UNP Q2Y0H9
M	164	THR	-	insertion	UNP Q2Y0H9
M	165	PRO	-	insertion	UNP Q2Y0H9
M	166	CYS	-	insertion	UNP Q2Y0H9
M	167	ASN	-	insertion	UNP Q2Y0H9
M	168	GLY	-	insertion	UNP Q2Y0H9
M	169	VAL	-	insertion	UNP Q2Y0H9
M	170	GLU	-	insertion	UNP Q2Y0H9
M	171	GLY	-	insertion	UNP Q2Y0H9
M	172	PHE	-	insertion	UNP Q2Y0H9
M	173	ASN	-	insertion	UNP Q2Y0H9
M	174	CYS	-	insertion	UNP Q2Y0H9
M	175	TYR	-	insertion	UNP Q2Y0H9
M	176	PHE	-	insertion	UNP Q2Y0H9
M	177	PRO	-	insertion	UNP Q2Y0H9
M	178	LEU	-	insertion	UNP Q2Y0H9
M	179	GLN	-	insertion	UNP Q2Y0H9
M	180	SER	-	insertion	UNP Q2Y0H9
M	181	TYR	-	insertion	UNP Q2Y0H9
M	182	GLY	-	insertion	UNP Q2Y0H9
M	183	PHE	-	insertion	UNP Q2Y0H9
M	184	GLN	-	insertion	UNP Q2Y0H9
M	185	PRO	-	insertion	UNP Q2Y0H9
M	186	THR	-	insertion	UNP Q2Y0H9
M	187	ASN	-	insertion	UNP Q2Y0H9
M	188	GLY	-	insertion	UNP Q2Y0H9
M	189	VAL	-	insertion	UNP Q2Y0H9
M	190	GLY	-	insertion	UNP Q2Y0H9
M	191	TYR	-	insertion	UNP Q2Y0H9
M	192	GLY	-	insertion	UNP Q2Y0H9
M	193	PRO	THR	conflict	UNP Q2Y0H9
M	341E	ALA	-	insertion	UNP Q2Y0H9
M	341F	ARG	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
M	341U	VAL	-	insertion	UNP Q2Y0H9
M	341V	ASP	-	insertion	UNP Q2Y0H9
M	342I	LEU	-	insertion	UNP Q2Y0H9
M	342J	GLU	-	insertion	UNP Q2Y0H9
M	342V	SER	-	insertion	UNP Q2Y0H9
M	342W	ARG	-	insertion	UNP Q2Y0H9
N	157	GLU	VAL	conflict	UNP Q2Y0H9
N	158	PHE	-	insertion	UNP Q2Y0H9
N	159	TYR	-	insertion	UNP Q2Y0H9
N	160	GLN	-	insertion	UNP Q2Y0H9
N	161	ALA	-	insertion	UNP Q2Y0H9
N	162	GLY	-	insertion	UNP Q2Y0H9
N	163	SER	-	insertion	UNP Q2Y0H9
N	164	THR	-	insertion	UNP Q2Y0H9
N	165	PRO	-	insertion	UNP Q2Y0H9
N	166	CYS	-	insertion	UNP Q2Y0H9
N	167	ASN	-	insertion	UNP Q2Y0H9
N	168	GLY	-	insertion	UNP Q2Y0H9
N	169	VAL	-	insertion	UNP Q2Y0H9
N	170	GLU	-	insertion	UNP Q2Y0H9
N	171	GLY	-	insertion	UNP Q2Y0H9
N	172	PHE	-	insertion	UNP Q2Y0H9
N	173	ASN	-	insertion	UNP Q2Y0H9
N	174	CYS	-	insertion	UNP Q2Y0H9
N	175	TYR	-	insertion	UNP Q2Y0H9
N	176	PHE	-	insertion	UNP Q2Y0H9
N	177	PRO	-	insertion	UNP Q2Y0H9
N	178	LEU	-	insertion	UNP Q2Y0H9
N	179	GLN	-	insertion	UNP Q2Y0H9
N	180	SER	-	insertion	UNP Q2Y0H9
N	181	TYR	-	insertion	UNP Q2Y0H9
N	182	GLY	-	insertion	UNP Q2Y0H9
N	183	PHE	-	insertion	UNP Q2Y0H9
N	184	GLN	-	insertion	UNP Q2Y0H9
N	185	PRO	-	insertion	UNP Q2Y0H9
N	186	THR	-	insertion	UNP Q2Y0H9
N	187	ASN	-	insertion	UNP Q2Y0H9
N	188	GLY	-	insertion	UNP Q2Y0H9
N	189	VAL	-	insertion	UNP Q2Y0H9
N	190	GLY	-	insertion	UNP Q2Y0H9
N	191	TYR	-	insertion	UNP Q2Y0H9
N	192	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
N	193	PRO	THR	conflict	UNP Q2Y0H9
N	341E	ALA	-	insertion	UNP Q2Y0H9
N	341F	ARG	-	insertion	UNP Q2Y0H9
N	341U	VAL	-	insertion	UNP Q2Y0H9
N	341V	ASP	-	insertion	UNP Q2Y0H9
N	342I	LEU	-	insertion	UNP Q2Y0H9
N	342J	GLU	-	insertion	UNP Q2Y0H9
N	342V	SER	-	insertion	UNP Q2Y0H9
N	342W	ARG	-	insertion	UNP Q2Y0H9
O	157	GLU	VAL	conflict	UNP Q2Y0H9
O	158	PHE	-	insertion	UNP Q2Y0H9
O	159	TYR	-	insertion	UNP Q2Y0H9
O	160	GLN	-	insertion	UNP Q2Y0H9
O	161	ALA	-	insertion	UNP Q2Y0H9
O	162	GLY	-	insertion	UNP Q2Y0H9
O	163	SER	-	insertion	UNP Q2Y0H9
O	164	THR	-	insertion	UNP Q2Y0H9
O	165	PRO	-	insertion	UNP Q2Y0H9
O	166	CYS	-	insertion	UNP Q2Y0H9
O	167	ASN	-	insertion	UNP Q2Y0H9
O	168	GLY	-	insertion	UNP Q2Y0H9
O	169	VAL	-	insertion	UNP Q2Y0H9
O	170	GLU	-	insertion	UNP Q2Y0H9
O	171	GLY	-	insertion	UNP Q2Y0H9
O	172	PHE	-	insertion	UNP Q2Y0H9
O	173	ASN	-	insertion	UNP Q2Y0H9
O	174	CYS	-	insertion	UNP Q2Y0H9
O	175	TYR	-	insertion	UNP Q2Y0H9
O	176	PHE	-	insertion	UNP Q2Y0H9
O	177	PRO	-	insertion	UNP Q2Y0H9
O	178	LEU	-	insertion	UNP Q2Y0H9
O	179	GLN	-	insertion	UNP Q2Y0H9
O	180	SER	-	insertion	UNP Q2Y0H9
O	181	TYR	-	insertion	UNP Q2Y0H9
O	182	GLY	-	insertion	UNP Q2Y0H9
O	183	PHE	-	insertion	UNP Q2Y0H9
O	184	GLN	-	insertion	UNP Q2Y0H9
O	185	PRO	-	insertion	UNP Q2Y0H9
O	186	THR	-	insertion	UNP Q2Y0H9
O	187	ASN	-	insertion	UNP Q2Y0H9
O	188	GLY	-	insertion	UNP Q2Y0H9
O	189	VAL	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
O	190	GLY	-	insertion	UNP Q2Y0H9
O	191	TYR	-	insertion	UNP Q2Y0H9
O	192	GLY	-	insertion	UNP Q2Y0H9
O	193	PRO	THR	conflict	UNP Q2Y0H9
O	341E	ALA	-	insertion	UNP Q2Y0H9
O	341F	ARG	-	insertion	UNP Q2Y0H9
O	341U	VAL	-	insertion	UNP Q2Y0H9
O	341V	ASP	-	insertion	UNP Q2Y0H9
O	342I	LEU	-	insertion	UNP Q2Y0H9
O	342J	GLU	-	insertion	UNP Q2Y0H9
O	342V	SER	-	insertion	UNP Q2Y0H9
O	342W	ARG	-	insertion	UNP Q2Y0H9
P	157	GLU	VAL	conflict	UNP Q2Y0H9
P	158	PHE	-	insertion	UNP Q2Y0H9
P	159	TYR	-	insertion	UNP Q2Y0H9
P	160	GLN	-	insertion	UNP Q2Y0H9
P	161	ALA	-	insertion	UNP Q2Y0H9
P	162	GLY	-	insertion	UNP Q2Y0H9
P	163	SER	-	insertion	UNP Q2Y0H9
P	164	THR	-	insertion	UNP Q2Y0H9
P	165	PRO	-	insertion	UNP Q2Y0H9
P	166	CYS	-	insertion	UNP Q2Y0H9
P	167	ASN	-	insertion	UNP Q2Y0H9
P	168	GLY	-	insertion	UNP Q2Y0H9
P	169	VAL	-	insertion	UNP Q2Y0H9
P	170	GLU	-	insertion	UNP Q2Y0H9
P	171	GLY	-	insertion	UNP Q2Y0H9
P	172	PHE	-	insertion	UNP Q2Y0H9
P	173	ASN	-	insertion	UNP Q2Y0H9
P	174	CYS	-	insertion	UNP Q2Y0H9
P	175	TYR	-	insertion	UNP Q2Y0H9
P	176	PHE	-	insertion	UNP Q2Y0H9
P	177	PRO	-	insertion	UNP Q2Y0H9
P	178	LEU	-	insertion	UNP Q2Y0H9
P	179	GLN	-	insertion	UNP Q2Y0H9
P	180	SER	-	insertion	UNP Q2Y0H9
P	181	TYR	-	insertion	UNP Q2Y0H9
P	182	GLY	-	insertion	UNP Q2Y0H9
P	183	PHE	-	insertion	UNP Q2Y0H9
P	184	GLN	-	insertion	UNP Q2Y0H9
P	185	PRO	-	insertion	UNP Q2Y0H9
P	186	THR	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
P	187	ASN	-	insertion	UNP Q2Y0H9
P	188	GLY	-	insertion	UNP Q2Y0H9
P	189	VAL	-	insertion	UNP Q2Y0H9
P	190	GLY	-	insertion	UNP Q2Y0H9
P	191	TYR	-	insertion	UNP Q2Y0H9
P	192	GLY	-	insertion	UNP Q2Y0H9
P	193	PRO	THR	conflict	UNP Q2Y0H9
P	341E	ALA	-	insertion	UNP Q2Y0H9
P	341F	ARG	-	insertion	UNP Q2Y0H9
P	341U	VAL	-	insertion	UNP Q2Y0H9
P	341V	ASP	-	insertion	UNP Q2Y0H9
P	342I	LEU	-	insertion	UNP Q2Y0H9
P	342J	GLU	-	insertion	UNP Q2Y0H9
P	342V	SER	-	insertion	UNP Q2Y0H9
P	342W	ARG	-	insertion	UNP Q2Y0H9
Q	157	GLU	VAL	conflict	UNP Q2Y0H9
Q	158	PHE	-	insertion	UNP Q2Y0H9
Q	159	TYR	-	insertion	UNP Q2Y0H9
Q	160	GLN	-	insertion	UNP Q2Y0H9
Q	161	ALA	-	insertion	UNP Q2Y0H9
Q	162	GLY	-	insertion	UNP Q2Y0H9
Q	163	SER	-	insertion	UNP Q2Y0H9
Q	164	THR	-	insertion	UNP Q2Y0H9
Q	165	PRO	-	insertion	UNP Q2Y0H9
Q	166	CYS	-	insertion	UNP Q2Y0H9
Q	167	ASN	-	insertion	UNP Q2Y0H9
Q	168	GLY	-	insertion	UNP Q2Y0H9
Q	169	VAL	-	insertion	UNP Q2Y0H9
Q	170	GLU	-	insertion	UNP Q2Y0H9
Q	171	GLY	-	insertion	UNP Q2Y0H9
Q	172	PHE	-	insertion	UNP Q2Y0H9
Q	173	ASN	-	insertion	UNP Q2Y0H9
Q	174	CYS	-	insertion	UNP Q2Y0H9
Q	175	TYR	-	insertion	UNP Q2Y0H9
Q	176	PHE	-	insertion	UNP Q2Y0H9
Q	177	PRO	-	insertion	UNP Q2Y0H9
Q	178	LEU	-	insertion	UNP Q2Y0H9
Q	179	GLN	-	insertion	UNP Q2Y0H9
Q	180	SER	-	insertion	UNP Q2Y0H9
Q	181	TYR	-	insertion	UNP Q2Y0H9
Q	182	GLY	-	insertion	UNP Q2Y0H9
Q	183	PHE	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	184	GLN	-	insertion	UNP Q2Y0H9
Q	185	PRO	-	insertion	UNP Q2Y0H9
Q	186	THR	-	insertion	UNP Q2Y0H9
Q	187	ASN	-	insertion	UNP Q2Y0H9
Q	188	GLY	-	insertion	UNP Q2Y0H9
Q	189	VAL	-	insertion	UNP Q2Y0H9
Q	190	GLY	-	insertion	UNP Q2Y0H9
Q	191	TYR	-	insertion	UNP Q2Y0H9
Q	192	GLY	-	insertion	UNP Q2Y0H9
Q	193	PRO	THR	conflict	UNP Q2Y0H9
Q	341E	ALA	-	insertion	UNP Q2Y0H9
Q	341F	ARG	-	insertion	UNP Q2Y0H9
Q	341U	VAL	-	insertion	UNP Q2Y0H9
Q	341V	ASP	-	insertion	UNP Q2Y0H9
Q	342I	LEU	-	insertion	UNP Q2Y0H9
Q	342J	GLU	-	insertion	UNP Q2Y0H9
Q	342V	SER	-	insertion	UNP Q2Y0H9
Q	342W	ARG	-	insertion	UNP Q2Y0H9
R	157	GLU	VAL	conflict	UNP Q2Y0H9
R	158	PHE	-	insertion	UNP Q2Y0H9
R	159	TYR	-	insertion	UNP Q2Y0H9
R	160	GLN	-	insertion	UNP Q2Y0H9
R	161	ALA	-	insertion	UNP Q2Y0H9
R	162	GLY	-	insertion	UNP Q2Y0H9
R	163	SER	-	insertion	UNP Q2Y0H9
R	164	THR	-	insertion	UNP Q2Y0H9
R	165	PRO	-	insertion	UNP Q2Y0H9
R	166	CYS	-	insertion	UNP Q2Y0H9
R	167	ASN	-	insertion	UNP Q2Y0H9
R	168	GLY	-	insertion	UNP Q2Y0H9
R	169	VAL	-	insertion	UNP Q2Y0H9
R	170	GLU	-	insertion	UNP Q2Y0H9
R	171	GLY	-	insertion	UNP Q2Y0H9
R	172	PHE	-	insertion	UNP Q2Y0H9
R	173	ASN	-	insertion	UNP Q2Y0H9
R	174	CYS	-	insertion	UNP Q2Y0H9
R	175	TYR	-	insertion	UNP Q2Y0H9
R	176	PHE	-	insertion	UNP Q2Y0H9
R	177	PRO	-	insertion	UNP Q2Y0H9
R	178	LEU	-	insertion	UNP Q2Y0H9
R	179	GLN	-	insertion	UNP Q2Y0H9
R	180	SER	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
R	181	TYR	-	insertion	UNP Q2Y0H9
R	182	GLY	-	insertion	UNP Q2Y0H9
R	183	PHE	-	insertion	UNP Q2Y0H9
R	184	GLN	-	insertion	UNP Q2Y0H9
R	185	PRO	-	insertion	UNP Q2Y0H9
R	186	THR	-	insertion	UNP Q2Y0H9
R	187	ASN	-	insertion	UNP Q2Y0H9
R	188	GLY	-	insertion	UNP Q2Y0H9
R	189	VAL	-	insertion	UNP Q2Y0H9
R	190	GLY	-	insertion	UNP Q2Y0H9
R	191	TYR	-	insertion	UNP Q2Y0H9
R	192	GLY	-	insertion	UNP Q2Y0H9
R	193	PRO	THR	conflict	UNP Q2Y0H9
R	341E	ALA	-	insertion	UNP Q2Y0H9
R	341F	ARG	-	insertion	UNP Q2Y0H9
R	341U	VAL	-	insertion	UNP Q2Y0H9
R	341V	ASP	-	insertion	UNP Q2Y0H9
R	342I	LEU	-	insertion	UNP Q2Y0H9
R	342J	GLU	-	insertion	UNP Q2Y0H9
R	342V	SER	-	insertion	UNP Q2Y0H9
R	342W	ARG	-	insertion	UNP Q2Y0H9
S	157	GLU	VAL	conflict	UNP Q2Y0H9
S	158	PHE	-	insertion	UNP Q2Y0H9
S	159	TYR	-	insertion	UNP Q2Y0H9
S	160	GLN	-	insertion	UNP Q2Y0H9
S	161	ALA	-	insertion	UNP Q2Y0H9
S	162	GLY	-	insertion	UNP Q2Y0H9
S	163	SER	-	insertion	UNP Q2Y0H9
S	164	THR	-	insertion	UNP Q2Y0H9
S	165	PRO	-	insertion	UNP Q2Y0H9
S	166	CYS	-	insertion	UNP Q2Y0H9
S	167	ASN	-	insertion	UNP Q2Y0H9
S	168	GLY	-	insertion	UNP Q2Y0H9
S	169	VAL	-	insertion	UNP Q2Y0H9
S	170	GLU	-	insertion	UNP Q2Y0H9
S	171	GLY	-	insertion	UNP Q2Y0H9
S	172	PHE	-	insertion	UNP Q2Y0H9
S	173	ASN	-	insertion	UNP Q2Y0H9
S	174	CYS	-	insertion	UNP Q2Y0H9
S	175	TYR	-	insertion	UNP Q2Y0H9
S	176	PHE	-	insertion	UNP Q2Y0H9
S	177	PRO	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
S	178	LEU	-	insertion	UNP Q2Y0H9
S	179	GLN	-	insertion	UNP Q2Y0H9
S	180	SER	-	insertion	UNP Q2Y0H9
S	181	TYR	-	insertion	UNP Q2Y0H9
S	182	GLY	-	insertion	UNP Q2Y0H9
S	183	PHE	-	insertion	UNP Q2Y0H9
S	184	GLN	-	insertion	UNP Q2Y0H9
S	185	PRO	-	insertion	UNP Q2Y0H9
S	186	THR	-	insertion	UNP Q2Y0H9
S	187	ASN	-	insertion	UNP Q2Y0H9
S	188	GLY	-	insertion	UNP Q2Y0H9
S	189	VAL	-	insertion	UNP Q2Y0H9
S	190	GLY	-	insertion	UNP Q2Y0H9
S	191	TYR	-	insertion	UNP Q2Y0H9
S	192	GLY	-	insertion	UNP Q2Y0H9
S	193	PRO	THR	conflict	UNP Q2Y0H9
S	341E	ALA	-	insertion	UNP Q2Y0H9
S	341F	ARG	-	insertion	UNP Q2Y0H9
S	341U	VAL	-	insertion	UNP Q2Y0H9
S	341V	ASP	-	insertion	UNP Q2Y0H9
S	342I	LEU	-	insertion	UNP Q2Y0H9
S	342J	GLU	-	insertion	UNP Q2Y0H9
S	342V	SER	-	insertion	UNP Q2Y0H9
S	342W	ARG	-	insertion	UNP Q2Y0H9
T	157	GLU	VAL	conflict	UNP Q2Y0H9
T	158	PHE	-	insertion	UNP Q2Y0H9
T	159	TYR	-	insertion	UNP Q2Y0H9
T	160	GLN	-	insertion	UNP Q2Y0H9
T	161	ALA	-	insertion	UNP Q2Y0H9
T	162	GLY	-	insertion	UNP Q2Y0H9
T	163	SER	-	insertion	UNP Q2Y0H9
T	164	THR	-	insertion	UNP Q2Y0H9
T	165	PRO	-	insertion	UNP Q2Y0H9
T	166	CYS	-	insertion	UNP Q2Y0H9
T	167	ASN	-	insertion	UNP Q2Y0H9
T	168	GLY	-	insertion	UNP Q2Y0H9
T	169	VAL	-	insertion	UNP Q2Y0H9
T	170	GLU	-	insertion	UNP Q2Y0H9
T	171	GLY	-	insertion	UNP Q2Y0H9
T	172	PHE	-	insertion	UNP Q2Y0H9
T	173	ASN	-	insertion	UNP Q2Y0H9
T	174	CYS	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
T	175	TYR	-	insertion	UNP Q2Y0H9
T	176	PHE	-	insertion	UNP Q2Y0H9
T	177	PRO	-	insertion	UNP Q2Y0H9
T	178	LEU	-	insertion	UNP Q2Y0H9
T	179	GLN	-	insertion	UNP Q2Y0H9
T	180	SER	-	insertion	UNP Q2Y0H9
T	181	TYR	-	insertion	UNP Q2Y0H9
T	182	GLY	-	insertion	UNP Q2Y0H9
T	183	PHE	-	insertion	UNP Q2Y0H9
T	184	GLN	-	insertion	UNP Q2Y0H9
T	185	PRO	-	insertion	UNP Q2Y0H9
T	186	THR	-	insertion	UNP Q2Y0H9
T	187	ASN	-	insertion	UNP Q2Y0H9
T	188	GLY	-	insertion	UNP Q2Y0H9
T	189	VAL	-	insertion	UNP Q2Y0H9
T	190	GLY	-	insertion	UNP Q2Y0H9
T	191	TYR	-	insertion	UNP Q2Y0H9
T	192	GLY	-	insertion	UNP Q2Y0H9
T	193	PRO	THR	conflict	UNP Q2Y0H9
T	341E	ALA	-	insertion	UNP Q2Y0H9
T	341F	ARG	-	insertion	UNP Q2Y0H9
T	341U	VAL	-	insertion	UNP Q2Y0H9
T	341V	ASP	-	insertion	UNP Q2Y0H9
T	342I	LEU	-	insertion	UNP Q2Y0H9
T	342J	GLU	-	insertion	UNP Q2Y0H9
T	342V	SER	-	insertion	UNP Q2Y0H9
T	342W	ARG	-	insertion	UNP Q2Y0H9
V	157	GLU	VAL	conflict	UNP Q2Y0H9
V	158	PHE	-	insertion	UNP Q2Y0H9
V	159	TYR	-	insertion	UNP Q2Y0H9
V	160	GLN	-	insertion	UNP Q2Y0H9
V	161	ALA	-	insertion	UNP Q2Y0H9
V	162	GLY	-	insertion	UNP Q2Y0H9
V	163	SER	-	insertion	UNP Q2Y0H9
V	164	THR	-	insertion	UNP Q2Y0H9
V	165	PRO	-	insertion	UNP Q2Y0H9
V	166	CYS	-	insertion	UNP Q2Y0H9
V	167	ASN	-	insertion	UNP Q2Y0H9
V	168	GLY	-	insertion	UNP Q2Y0H9
V	169	VAL	-	insertion	UNP Q2Y0H9
V	170	GLU	-	insertion	UNP Q2Y0H9
V	171	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
V	172	PHE	-	insertion	UNP Q2Y0H9
V	173	ASN	-	insertion	UNP Q2Y0H9
V	174	CYS	-	insertion	UNP Q2Y0H9
V	175	TYR	-	insertion	UNP Q2Y0H9
V	176	PHE	-	insertion	UNP Q2Y0H9
V	177	PRO	-	insertion	UNP Q2Y0H9
V	178	LEU	-	insertion	UNP Q2Y0H9
V	179	GLN	-	insertion	UNP Q2Y0H9
V	180	SER	-	insertion	UNP Q2Y0H9
V	181	TYR	-	insertion	UNP Q2Y0H9
V	182	GLY	-	insertion	UNP Q2Y0H9
V	183	PHE	-	insertion	UNP Q2Y0H9
V	184	GLN	-	insertion	UNP Q2Y0H9
V	185	PRO	-	insertion	UNP Q2Y0H9
V	186	THR	-	insertion	UNP Q2Y0H9
V	187	ASN	-	insertion	UNP Q2Y0H9
V	188	GLY	-	insertion	UNP Q2Y0H9
V	189	VAL	-	insertion	UNP Q2Y0H9
V	190	GLY	-	insertion	UNP Q2Y0H9
V	191	TYR	-	insertion	UNP Q2Y0H9
V	192	GLY	-	insertion	UNP Q2Y0H9
V	193	PRO	THR	conflict	UNP Q2Y0H9
V	341E	ALA	-	insertion	UNP Q2Y0H9
V	341F	ARG	-	insertion	UNP Q2Y0H9
V	341U	VAL	-	insertion	UNP Q2Y0H9
V	341V	ASP	-	insertion	UNP Q2Y0H9
V	342I	LEU	-	insertion	UNP Q2Y0H9
V	342J	GLU	-	insertion	UNP Q2Y0H9
V	342V	SER	-	insertion	UNP Q2Y0H9
V	342W	ARG	-	insertion	UNP Q2Y0H9
W	157	GLU	VAL	conflict	UNP Q2Y0H9
W	158	PHE	-	insertion	UNP Q2Y0H9
W	159	TYR	-	insertion	UNP Q2Y0H9
W	160	GLN	-	insertion	UNP Q2Y0H9
W	161	ALA	-	insertion	UNP Q2Y0H9
W	162	GLY	-	insertion	UNP Q2Y0H9
W	163	SER	-	insertion	UNP Q2Y0H9
W	164	THR	-	insertion	UNP Q2Y0H9
W	165	PRO	-	insertion	UNP Q2Y0H9
W	166	CYS	-	insertion	UNP Q2Y0H9
W	167	ASN	-	insertion	UNP Q2Y0H9
W	168	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
W	169	VAL	-	insertion	UNP Q2Y0H9
W	170	GLU	-	insertion	UNP Q2Y0H9
W	171	GLY	-	insertion	UNP Q2Y0H9
W	172	PHE	-	insertion	UNP Q2Y0H9
W	173	ASN	-	insertion	UNP Q2Y0H9
W	174	CYS	-	insertion	UNP Q2Y0H9
W	175	TYR	-	insertion	UNP Q2Y0H9
W	176	PHE	-	insertion	UNP Q2Y0H9
W	177	PRO	-	insertion	UNP Q2Y0H9
W	178	LEU	-	insertion	UNP Q2Y0H9
W	179	GLN	-	insertion	UNP Q2Y0H9
W	180	SER	-	insertion	UNP Q2Y0H9
W	181	TYR	-	insertion	UNP Q2Y0H9
W	182	GLY	-	insertion	UNP Q2Y0H9
W	183	PHE	-	insertion	UNP Q2Y0H9
W	184	GLN	-	insertion	UNP Q2Y0H9
W	185	PRO	-	insertion	UNP Q2Y0H9
W	186	THR	-	insertion	UNP Q2Y0H9
W	187	ASN	-	insertion	UNP Q2Y0H9
W	188	GLY	-	insertion	UNP Q2Y0H9
W	189	VAL	-	insertion	UNP Q2Y0H9
W	190	GLY	-	insertion	UNP Q2Y0H9
W	191	TYR	-	insertion	UNP Q2Y0H9
W	192	GLY	-	insertion	UNP Q2Y0H9
W	193	PRO	THR	conflict	UNP Q2Y0H9
W	341E	ALA	-	insertion	UNP Q2Y0H9
W	341F	ARG	-	insertion	UNP Q2Y0H9
W	341U	VAL	-	insertion	UNP Q2Y0H9
W	341V	ASP	-	insertion	UNP Q2Y0H9
W	342I	LEU	-	insertion	UNP Q2Y0H9
W	342J	GLU	-	insertion	UNP Q2Y0H9
W	342V	SER	-	insertion	UNP Q2Y0H9
W	342W	ARG	-	insertion	UNP Q2Y0H9
X	157	GLU	VAL	conflict	UNP Q2Y0H9
X	158	PHE	-	insertion	UNP Q2Y0H9
X	159	TYR	-	insertion	UNP Q2Y0H9
X	160	GLN	-	insertion	UNP Q2Y0H9
X	161	ALA	-	insertion	UNP Q2Y0H9
X	162	GLY	-	insertion	UNP Q2Y0H9
X	163	SER	-	insertion	UNP Q2Y0H9
X	164	THR	-	insertion	UNP Q2Y0H9
X	165	PRO	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
X	166	CYS	-	insertion	UNP Q2Y0H9
X	167	ASN	-	insertion	UNP Q2Y0H9
X	168	GLY	-	insertion	UNP Q2Y0H9
X	169	VAL	-	insertion	UNP Q2Y0H9
X	170	GLU	-	insertion	UNP Q2Y0H9
X	171	GLY	-	insertion	UNP Q2Y0H9
X	172	PHE	-	insertion	UNP Q2Y0H9
X	173	ASN	-	insertion	UNP Q2Y0H9
X	174	CYS	-	insertion	UNP Q2Y0H9
X	175	TYR	-	insertion	UNP Q2Y0H9
X	176	PHE	-	insertion	UNP Q2Y0H9
X	177	PRO	-	insertion	UNP Q2Y0H9
X	178	LEU	-	insertion	UNP Q2Y0H9
X	179	GLN	-	insertion	UNP Q2Y0H9
X	180	SER	-	insertion	UNP Q2Y0H9
X	181	TYR	-	insertion	UNP Q2Y0H9
X	182	GLY	-	insertion	UNP Q2Y0H9
X	183	PHE	-	insertion	UNP Q2Y0H9
X	184	GLN	-	insertion	UNP Q2Y0H9
X	185	PRO	-	insertion	UNP Q2Y0H9
X	186	THR	-	insertion	UNP Q2Y0H9
X	187	ASN	-	insertion	UNP Q2Y0H9
X	188	GLY	-	insertion	UNP Q2Y0H9
X	189	VAL	-	insertion	UNP Q2Y0H9
X	190	GLY	-	insertion	UNP Q2Y0H9
X	191	TYR	-	insertion	UNP Q2Y0H9
X	192	GLY	-	insertion	UNP Q2Y0H9
X	193	PRO	THR	conflict	UNP Q2Y0H9
X	341E	ALA	-	insertion	UNP Q2Y0H9
X	341F	ARG	-	insertion	UNP Q2Y0H9
X	341U	VAL	-	insertion	UNP Q2Y0H9
X	341V	ASP	-	insertion	UNP Q2Y0H9
X	342I	LEU	-	insertion	UNP Q2Y0H9
X	342J	GLU	-	insertion	UNP Q2Y0H9
X	342V	SER	-	insertion	UNP Q2Y0H9
X	342W	ARG	-	insertion	UNP Q2Y0H9
Y	157	GLU	VAL	conflict	UNP Q2Y0H9
Y	158	PHE	-	insertion	UNP Q2Y0H9
Y	159	TYR	-	insertion	UNP Q2Y0H9
Y	160	GLN	-	insertion	UNP Q2Y0H9
Y	161	ALA	-	insertion	UNP Q2Y0H9
Y	162	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	163	SER	-	insertion	UNP Q2Y0H9
Y	164	THR	-	insertion	UNP Q2Y0H9
Y	165	PRO	-	insertion	UNP Q2Y0H9
Y	166	CYS	-	insertion	UNP Q2Y0H9
Y	167	ASN	-	insertion	UNP Q2Y0H9
Y	168	GLY	-	insertion	UNP Q2Y0H9
Y	169	VAL	-	insertion	UNP Q2Y0H9
Y	170	GLU	-	insertion	UNP Q2Y0H9
Y	171	GLY	-	insertion	UNP Q2Y0H9
Y	172	PHE	-	insertion	UNP Q2Y0H9
Y	173	ASN	-	insertion	UNP Q2Y0H9
Y	174	CYS	-	insertion	UNP Q2Y0H9
Y	175	TYR	-	insertion	UNP Q2Y0H9
Y	176	PHE	-	insertion	UNP Q2Y0H9
Y	177	PRO	-	insertion	UNP Q2Y0H9
Y	178	LEU	-	insertion	UNP Q2Y0H9
Y	179	GLN	-	insertion	UNP Q2Y0H9
Y	180	SER	-	insertion	UNP Q2Y0H9
Y	181	TYR	-	insertion	UNP Q2Y0H9
Y	182	GLY	-	insertion	UNP Q2Y0H9
Y	183	PHE	-	insertion	UNP Q2Y0H9
Y	184	GLN	-	insertion	UNP Q2Y0H9
Y	185	PRO	-	insertion	UNP Q2Y0H9
Y	186	THR	-	insertion	UNP Q2Y0H9
Y	187	ASN	-	insertion	UNP Q2Y0H9
Y	188	GLY	-	insertion	UNP Q2Y0H9
Y	189	VAL	-	insertion	UNP Q2Y0H9
Y	190	GLY	-	insertion	UNP Q2Y0H9
Y	191	TYR	-	insertion	UNP Q2Y0H9
Y	192	GLY	-	insertion	UNP Q2Y0H9
Y	193	PRO	THR	conflict	UNP Q2Y0H9
Y	341E	ALA	-	insertion	UNP Q2Y0H9
Y	341F	ARG	-	insertion	UNP Q2Y0H9
Y	341U	VAL	-	insertion	UNP Q2Y0H9
Y	341V	ASP	-	insertion	UNP Q2Y0H9
Y	342I	LEU	-	insertion	UNP Q2Y0H9
Y	342J	GLU	-	insertion	UNP Q2Y0H9
Y	342V	SER	-	insertion	UNP Q2Y0H9
Y	342W	ARG	-	insertion	UNP Q2Y0H9
Z	157	GLU	VAL	conflict	UNP Q2Y0H9
Z	158	PHE	-	insertion	UNP Q2Y0H9
Z	159	TYR	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	160	GLN	-	insertion	UNP Q2Y0H9
Z	161	ALA	-	insertion	UNP Q2Y0H9
Z	162	GLY	-	insertion	UNP Q2Y0H9
Z	163	SER	-	insertion	UNP Q2Y0H9
Z	164	THR	-	insertion	UNP Q2Y0H9
Z	165	PRO	-	insertion	UNP Q2Y0H9
Z	166	CYS	-	insertion	UNP Q2Y0H9
Z	167	ASN	-	insertion	UNP Q2Y0H9
Z	168	GLY	-	insertion	UNP Q2Y0H9
Z	169	VAL	-	insertion	UNP Q2Y0H9
Z	170	GLU	-	insertion	UNP Q2Y0H9
Z	171	GLY	-	insertion	UNP Q2Y0H9
Z	172	PHE	-	insertion	UNP Q2Y0H9
Z	173	ASN	-	insertion	UNP Q2Y0H9
Z	174	CYS	-	insertion	UNP Q2Y0H9
Z	175	TYR	-	insertion	UNP Q2Y0H9
Z	176	PHE	-	insertion	UNP Q2Y0H9
Z	177	PRO	-	insertion	UNP Q2Y0H9
Z	178	LEU	-	insertion	UNP Q2Y0H9
Z	179	GLN	-	insertion	UNP Q2Y0H9
Z	180	SER	-	insertion	UNP Q2Y0H9
Z	181	TYR	-	insertion	UNP Q2Y0H9
Z	182	GLY	-	insertion	UNP Q2Y0H9
Z	183	PHE	-	insertion	UNP Q2Y0H9
Z	184	GLN	-	insertion	UNP Q2Y0H9
Z	185	PRO	-	insertion	UNP Q2Y0H9
Z	186	THR	-	insertion	UNP Q2Y0H9
Z	187	ASN	-	insertion	UNP Q2Y0H9
Z	188	GLY	-	insertion	UNP Q2Y0H9
Z	189	VAL	-	insertion	UNP Q2Y0H9
Z	190	GLY	-	insertion	UNP Q2Y0H9
Z	191	TYR	-	insertion	UNP Q2Y0H9
Z	192	GLY	-	insertion	UNP Q2Y0H9
Z	193	PRO	THR	conflict	UNP Q2Y0H9
Z	341E	ALA	-	insertion	UNP Q2Y0H9
Z	341F	ARG	-	insertion	UNP Q2Y0H9
Z	341U	VAL	-	insertion	UNP Q2Y0H9
Z	341V	ASP	-	insertion	UNP Q2Y0H9
Z	342I	LEU	-	insertion	UNP Q2Y0H9
Z	342J	GLU	-	insertion	UNP Q2Y0H9
Z	342V	SER	-	insertion	UNP Q2Y0H9
Z	342W	ARG	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
AA	157	GLU	VAL	conflict	UNP Q2Y0H9
AA	158	PHE	-	insertion	UNP Q2Y0H9
AA	159	TYR	-	insertion	UNP Q2Y0H9
AA	160	GLN	-	insertion	UNP Q2Y0H9
AA	161	ALA	-	insertion	UNP Q2Y0H9
AA	162	GLY	-	insertion	UNP Q2Y0H9
AA	163	SER	-	insertion	UNP Q2Y0H9
AA	164	THR	-	insertion	UNP Q2Y0H9
AA	165	PRO	-	insertion	UNP Q2Y0H9
AA	166	CYS	-	insertion	UNP Q2Y0H9
AA	167	ASN	-	insertion	UNP Q2Y0H9
AA	168	GLY	-	insertion	UNP Q2Y0H9
AA	169	VAL	-	insertion	UNP Q2Y0H9
AA	170	GLU	-	insertion	UNP Q2Y0H9
AA	171	GLY	-	insertion	UNP Q2Y0H9
AA	172	PHE	-	insertion	UNP Q2Y0H9
AA	173	ASN	-	insertion	UNP Q2Y0H9
AA	174	CYS	-	insertion	UNP Q2Y0H9
AA	175	TYR	-	insertion	UNP Q2Y0H9
AA	176	PHE	-	insertion	UNP Q2Y0H9
AA	177	PRO	-	insertion	UNP Q2Y0H9
AA	178	LEU	-	insertion	UNP Q2Y0H9
AA	179	GLN	-	insertion	UNP Q2Y0H9
AA	180	SER	-	insertion	UNP Q2Y0H9
AA	181	TYR	-	insertion	UNP Q2Y0H9
AA	182	GLY	-	insertion	UNP Q2Y0H9
AA	183	PHE	-	insertion	UNP Q2Y0H9
AA	184	GLN	-	insertion	UNP Q2Y0H9
AA	185	PRO	-	insertion	UNP Q2Y0H9
AA	186	THR	-	insertion	UNP Q2Y0H9
AA	187	ASN	-	insertion	UNP Q2Y0H9
AA	188	GLY	-	insertion	UNP Q2Y0H9
AA	189	VAL	-	insertion	UNP Q2Y0H9
AA	190	GLY	-	insertion	UNP Q2Y0H9
AA	191	TYR	-	insertion	UNP Q2Y0H9
AA	192	GLY	-	insertion	UNP Q2Y0H9
AA	193	PRO	THR	conflict	UNP Q2Y0H9
AA	341E	ALA	-	insertion	UNP Q2Y0H9
AA	341F	ARG	-	insertion	UNP Q2Y0H9
AA	341U	VAL	-	insertion	UNP Q2Y0H9
AA	341V	ASP	-	insertion	UNP Q2Y0H9
AA	342I	LEU	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
AA	342J	GLU	-	insertion	UNP Q2Y0H9
AA	342V	SER	-	insertion	UNP Q2Y0H9
AA	342W	ARG	-	insertion	UNP Q2Y0H9
BA	157	GLU	VAL	conflict	UNP Q2Y0H9
BA	158	PHE	-	insertion	UNP Q2Y0H9
BA	159	TYR	-	insertion	UNP Q2Y0H9
BA	160	GLN	-	insertion	UNP Q2Y0H9
BA	161	ALA	-	insertion	UNP Q2Y0H9
BA	162	GLY	-	insertion	UNP Q2Y0H9
BA	163	SER	-	insertion	UNP Q2Y0H9
BA	164	THR	-	insertion	UNP Q2Y0H9
BA	165	PRO	-	insertion	UNP Q2Y0H9
BA	166	CYS	-	insertion	UNP Q2Y0H9
BA	167	ASN	-	insertion	UNP Q2Y0H9
BA	168	GLY	-	insertion	UNP Q2Y0H9
BA	169	VAL	-	insertion	UNP Q2Y0H9
BA	170	GLU	-	insertion	UNP Q2Y0H9
BA	171	GLY	-	insertion	UNP Q2Y0H9
BA	172	PHE	-	insertion	UNP Q2Y0H9
BA	173	ASN	-	insertion	UNP Q2Y0H9
BA	174	CYS	-	insertion	UNP Q2Y0H9
BA	175	TYR	-	insertion	UNP Q2Y0H9
BA	176	PHE	-	insertion	UNP Q2Y0H9
BA	177	PRO	-	insertion	UNP Q2Y0H9
BA	178	LEU	-	insertion	UNP Q2Y0H9
BA	179	GLN	-	insertion	UNP Q2Y0H9
BA	180	SER	-	insertion	UNP Q2Y0H9
BA	181	TYR	-	insertion	UNP Q2Y0H9
BA	182	GLY	-	insertion	UNP Q2Y0H9
BA	183	PHE	-	insertion	UNP Q2Y0H9
BA	184	GLN	-	insertion	UNP Q2Y0H9
BA	185	PRO	-	insertion	UNP Q2Y0H9
BA	186	THR	-	insertion	UNP Q2Y0H9
BA	187	ASN	-	insertion	UNP Q2Y0H9
BA	188	GLY	-	insertion	UNP Q2Y0H9
BA	189	VAL	-	insertion	UNP Q2Y0H9
BA	190	GLY	-	insertion	UNP Q2Y0H9
BA	191	TYR	-	insertion	UNP Q2Y0H9
BA	192	GLY	-	insertion	UNP Q2Y0H9
BA	193	PRO	THR	conflict	UNP Q2Y0H9
BA	341E	ALA	-	insertion	UNP Q2Y0H9
BA	341F	ARG	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
BA	341U	VAL	-	insertion	UNP Q2Y0H9
BA	341V	ASP	-	insertion	UNP Q2Y0H9
BA	342I	LEU	-	insertion	UNP Q2Y0H9
BA	342J	GLU	-	insertion	UNP Q2Y0H9
BA	342V	SER	-	insertion	UNP Q2Y0H9
BA	342W	ARG	-	insertion	UNP Q2Y0H9
CA	157	GLU	VAL	conflict	UNP Q2Y0H9
CA	158	PHE	-	insertion	UNP Q2Y0H9
CA	159	TYR	-	insertion	UNP Q2Y0H9
CA	160	GLN	-	insertion	UNP Q2Y0H9
CA	161	ALA	-	insertion	UNP Q2Y0H9
CA	162	GLY	-	insertion	UNP Q2Y0H9
CA	163	SER	-	insertion	UNP Q2Y0H9
CA	164	THR	-	insertion	UNP Q2Y0H9
CA	165	PRO	-	insertion	UNP Q2Y0H9
CA	166	CYS	-	insertion	UNP Q2Y0H9
CA	167	ASN	-	insertion	UNP Q2Y0H9
CA	168	GLY	-	insertion	UNP Q2Y0H9
CA	169	VAL	-	insertion	UNP Q2Y0H9
CA	170	GLU	-	insertion	UNP Q2Y0H9
CA	171	GLY	-	insertion	UNP Q2Y0H9
CA	172	PHE	-	insertion	UNP Q2Y0H9
CA	173	ASN	-	insertion	UNP Q2Y0H9
CA	174	CYS	-	insertion	UNP Q2Y0H9
CA	175	TYR	-	insertion	UNP Q2Y0H9
CA	176	PHE	-	insertion	UNP Q2Y0H9
CA	177	PRO	-	insertion	UNP Q2Y0H9
CA	178	LEU	-	insertion	UNP Q2Y0H9
CA	179	GLN	-	insertion	UNP Q2Y0H9
CA	180	SER	-	insertion	UNP Q2Y0H9
CA	181	TYR	-	insertion	UNP Q2Y0H9
CA	182	GLY	-	insertion	UNP Q2Y0H9
CA	183	PHE	-	insertion	UNP Q2Y0H9
CA	184	GLN	-	insertion	UNP Q2Y0H9
CA	185	PRO	-	insertion	UNP Q2Y0H9
CA	186	THR	-	insertion	UNP Q2Y0H9
CA	187	ASN	-	insertion	UNP Q2Y0H9
CA	188	GLY	-	insertion	UNP Q2Y0H9
CA	189	VAL	-	insertion	UNP Q2Y0H9
CA	190	GLY	-	insertion	UNP Q2Y0H9
CA	191	TYR	-	insertion	UNP Q2Y0H9
CA	192	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
CA	193	PRO	THR	conflict	UNP Q2Y0H9
CA	341E	ALA	-	insertion	UNP Q2Y0H9
CA	341F	ARG	-	insertion	UNP Q2Y0H9
CA	341U	VAL	-	insertion	UNP Q2Y0H9
CA	341V	ASP	-	insertion	UNP Q2Y0H9
CA	342I	LEU	-	insertion	UNP Q2Y0H9
CA	342J	GLU	-	insertion	UNP Q2Y0H9
CA	342V	SER	-	insertion	UNP Q2Y0H9
CA	342W	ARG	-	insertion	UNP Q2Y0H9
DA	157	GLU	VAL	conflict	UNP Q2Y0H9
DA	158	PHE	-	insertion	UNP Q2Y0H9
DA	159	TYR	-	insertion	UNP Q2Y0H9
DA	160	GLN	-	insertion	UNP Q2Y0H9
DA	161	ALA	-	insertion	UNP Q2Y0H9
DA	162	GLY	-	insertion	UNP Q2Y0H9
DA	163	SER	-	insertion	UNP Q2Y0H9
DA	164	THR	-	insertion	UNP Q2Y0H9
DA	165	PRO	-	insertion	UNP Q2Y0H9
DA	166	CYS	-	insertion	UNP Q2Y0H9
DA	167	ASN	-	insertion	UNP Q2Y0H9
DA	168	GLY	-	insertion	UNP Q2Y0H9
DA	169	VAL	-	insertion	UNP Q2Y0H9
DA	170	GLU	-	insertion	UNP Q2Y0H9
DA	171	GLY	-	insertion	UNP Q2Y0H9
DA	172	PHE	-	insertion	UNP Q2Y0H9
DA	173	ASN	-	insertion	UNP Q2Y0H9
DA	174	CYS	-	insertion	UNP Q2Y0H9
DA	175	TYR	-	insertion	UNP Q2Y0H9
DA	176	PHE	-	insertion	UNP Q2Y0H9
DA	177	PRO	-	insertion	UNP Q2Y0H9
DA	178	LEU	-	insertion	UNP Q2Y0H9
DA	179	GLN	-	insertion	UNP Q2Y0H9
DA	180	SER	-	insertion	UNP Q2Y0H9
DA	181	TYR	-	insertion	UNP Q2Y0H9
DA	182	GLY	-	insertion	UNP Q2Y0H9
DA	183	PHE	-	insertion	UNP Q2Y0H9
DA	184	GLN	-	insertion	UNP Q2Y0H9
DA	185	PRO	-	insertion	UNP Q2Y0H9
DA	186	THR	-	insertion	UNP Q2Y0H9
DA	187	ASN	-	insertion	UNP Q2Y0H9
DA	188	GLY	-	insertion	UNP Q2Y0H9
DA	189	VAL	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
DA	190	GLY	-	insertion	UNP Q2Y0H9
DA	191	TYR	-	insertion	UNP Q2Y0H9
DA	192	GLY	-	insertion	UNP Q2Y0H9
DA	193	PRO	THR	conflict	UNP Q2Y0H9
DA	341E	ALA	-	insertion	UNP Q2Y0H9
DA	341F	ARG	-	insertion	UNP Q2Y0H9
DA	341U	VAL	-	insertion	UNP Q2Y0H9
DA	341V	ASP	-	insertion	UNP Q2Y0H9
DA	342I	LEU	-	insertion	UNP Q2Y0H9
DA	342J	GLU	-	insertion	UNP Q2Y0H9
DA	342V	SER	-	insertion	UNP Q2Y0H9
DA	342W	ARG	-	insertion	UNP Q2Y0H9
EA	157	GLU	VAL	conflict	UNP Q2Y0H9
EA	158	PHE	-	insertion	UNP Q2Y0H9
EA	159	TYR	-	insertion	UNP Q2Y0H9
EA	160	GLN	-	insertion	UNP Q2Y0H9
EA	161	ALA	-	insertion	UNP Q2Y0H9
EA	162	GLY	-	insertion	UNP Q2Y0H9
EA	163	SER	-	insertion	UNP Q2Y0H9
EA	164	THR	-	insertion	UNP Q2Y0H9
EA	165	PRO	-	insertion	UNP Q2Y0H9
EA	166	CYS	-	insertion	UNP Q2Y0H9
EA	167	ASN	-	insertion	UNP Q2Y0H9
EA	168	GLY	-	insertion	UNP Q2Y0H9
EA	169	VAL	-	insertion	UNP Q2Y0H9
EA	170	GLU	-	insertion	UNP Q2Y0H9
EA	171	GLY	-	insertion	UNP Q2Y0H9
EA	172	PHE	-	insertion	UNP Q2Y0H9
EA	173	ASN	-	insertion	UNP Q2Y0H9
EA	174	CYS	-	insertion	UNP Q2Y0H9
EA	175	TYR	-	insertion	UNP Q2Y0H9
EA	176	PHE	-	insertion	UNP Q2Y0H9
EA	177	PRO	-	insertion	UNP Q2Y0H9
EA	178	LEU	-	insertion	UNP Q2Y0H9
EA	179	GLN	-	insertion	UNP Q2Y0H9
EA	180	SER	-	insertion	UNP Q2Y0H9
EA	181	TYR	-	insertion	UNP Q2Y0H9
EA	182	GLY	-	insertion	UNP Q2Y0H9
EA	183	PHE	-	insertion	UNP Q2Y0H9
EA	184	GLN	-	insertion	UNP Q2Y0H9
EA	185	PRO	-	insertion	UNP Q2Y0H9
EA	186	THR	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
EA	187	ASN	-	insertion	UNP Q2Y0H9
EA	188	GLY	-	insertion	UNP Q2Y0H9
EA	189	VAL	-	insertion	UNP Q2Y0H9
EA	190	GLY	-	insertion	UNP Q2Y0H9
EA	191	TYR	-	insertion	UNP Q2Y0H9
EA	192	GLY	-	insertion	UNP Q2Y0H9
EA	193	PRO	THR	conflict	UNP Q2Y0H9
EA	341E	ALA	-	insertion	UNP Q2Y0H9
EA	341F	ARG	-	insertion	UNP Q2Y0H9
EA	341U	VAL	-	insertion	UNP Q2Y0H9
EA	341V	ASP	-	insertion	UNP Q2Y0H9
EA	342I	LEU	-	insertion	UNP Q2Y0H9
EA	342J	GLU	-	insertion	UNP Q2Y0H9
EA	342V	SER	-	insertion	UNP Q2Y0H9
EA	342W	ARG	-	insertion	UNP Q2Y0H9
FA	157	GLU	VAL	conflict	UNP Q2Y0H9
FA	158	PHE	-	insertion	UNP Q2Y0H9
FA	159	TYR	-	insertion	UNP Q2Y0H9
FA	160	GLN	-	insertion	UNP Q2Y0H9
FA	161	ALA	-	insertion	UNP Q2Y0H9
FA	162	GLY	-	insertion	UNP Q2Y0H9
FA	163	SER	-	insertion	UNP Q2Y0H9
FA	164	THR	-	insertion	UNP Q2Y0H9
FA	165	PRO	-	insertion	UNP Q2Y0H9
FA	166	CYS	-	insertion	UNP Q2Y0H9
FA	167	ASN	-	insertion	UNP Q2Y0H9
FA	168	GLY	-	insertion	UNP Q2Y0H9
FA	169	VAL	-	insertion	UNP Q2Y0H9
FA	170	GLU	-	insertion	UNP Q2Y0H9
FA	171	GLY	-	insertion	UNP Q2Y0H9
FA	172	PHE	-	insertion	UNP Q2Y0H9
FA	173	ASN	-	insertion	UNP Q2Y0H9
FA	174	CYS	-	insertion	UNP Q2Y0H9
FA	175	TYR	-	insertion	UNP Q2Y0H9
FA	176	PHE	-	insertion	UNP Q2Y0H9
FA	177	PRO	-	insertion	UNP Q2Y0H9
FA	178	LEU	-	insertion	UNP Q2Y0H9
FA	179	GLN	-	insertion	UNP Q2Y0H9
FA	180	SER	-	insertion	UNP Q2Y0H9
FA	181	TYR	-	insertion	UNP Q2Y0H9
FA	182	GLY	-	insertion	UNP Q2Y0H9
FA	183	PHE	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
FA	184	GLN	-	insertion	UNP Q2Y0H9
FA	185	PRO	-	insertion	UNP Q2Y0H9
FA	186	THR	-	insertion	UNP Q2Y0H9
FA	187	ASN	-	insertion	UNP Q2Y0H9
FA	188	GLY	-	insertion	UNP Q2Y0H9
FA	189	VAL	-	insertion	UNP Q2Y0H9
FA	190	GLY	-	insertion	UNP Q2Y0H9
FA	191	TYR	-	insertion	UNP Q2Y0H9
FA	192	GLY	-	insertion	UNP Q2Y0H9
FA	193	PRO	THR	conflict	UNP Q2Y0H9
FA	341E	ALA	-	insertion	UNP Q2Y0H9
FA	341F	ARG	-	insertion	UNP Q2Y0H9
FA	341U	VAL	-	insertion	UNP Q2Y0H9
FA	341V	ASP	-	insertion	UNP Q2Y0H9
FA	342I	LEU	-	insertion	UNP Q2Y0H9
FA	342J	GLU	-	insertion	UNP Q2Y0H9
FA	342V	SER	-	insertion	UNP Q2Y0H9
FA	342W	ARG	-	insertion	UNP Q2Y0H9
GA	157	GLU	VAL	conflict	UNP Q2Y0H9
GA	158	PHE	-	insertion	UNP Q2Y0H9
GA	159	TYR	-	insertion	UNP Q2Y0H9
GA	160	GLN	-	insertion	UNP Q2Y0H9
GA	161	ALA	-	insertion	UNP Q2Y0H9
GA	162	GLY	-	insertion	UNP Q2Y0H9
GA	163	SER	-	insertion	UNP Q2Y0H9
GA	164	THR	-	insertion	UNP Q2Y0H9
GA	165	PRO	-	insertion	UNP Q2Y0H9
GA	166	CYS	-	insertion	UNP Q2Y0H9
GA	167	ASN	-	insertion	UNP Q2Y0H9
GA	168	GLY	-	insertion	UNP Q2Y0H9
GA	169	VAL	-	insertion	UNP Q2Y0H9
GA	170	GLU	-	insertion	UNP Q2Y0H9
GA	171	GLY	-	insertion	UNP Q2Y0H9
GA	172	PHE	-	insertion	UNP Q2Y0H9
GA	173	ASN	-	insertion	UNP Q2Y0H9
GA	174	CYS	-	insertion	UNP Q2Y0H9
GA	175	TYR	-	insertion	UNP Q2Y0H9
GA	176	PHE	-	insertion	UNP Q2Y0H9
GA	177	PRO	-	insertion	UNP Q2Y0H9
GA	178	LEU	-	insertion	UNP Q2Y0H9
GA	179	GLN	-	insertion	UNP Q2Y0H9
GA	180	SER	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
GA	181	TYR	-	insertion	UNP Q2Y0H9
GA	182	GLY	-	insertion	UNP Q2Y0H9
GA	183	PHE	-	insertion	UNP Q2Y0H9
GA	184	GLN	-	insertion	UNP Q2Y0H9
GA	185	PRO	-	insertion	UNP Q2Y0H9
GA	186	THR	-	insertion	UNP Q2Y0H9
GA	187	ASN	-	insertion	UNP Q2Y0H9
GA	188	GLY	-	insertion	UNP Q2Y0H9
GA	189	VAL	-	insertion	UNP Q2Y0H9
GA	190	GLY	-	insertion	UNP Q2Y0H9
GA	191	TYR	-	insertion	UNP Q2Y0H9
GA	192	GLY	-	insertion	UNP Q2Y0H9
GA	193	PRO	THR	conflict	UNP Q2Y0H9
GA	341E	ALA	-	insertion	UNP Q2Y0H9
GA	341F	ARG	-	insertion	UNP Q2Y0H9
GA	341U	VAL	-	insertion	UNP Q2Y0H9
GA	341V	ASP	-	insertion	UNP Q2Y0H9
GA	342I	LEU	-	insertion	UNP Q2Y0H9
GA	342J	GLU	-	insertion	UNP Q2Y0H9
GA	342V	SER	-	insertion	UNP Q2Y0H9
GA	342W	ARG	-	insertion	UNP Q2Y0H9
HA	157	GLU	VAL	conflict	UNP Q2Y0H9
HA	158	PHE	-	insertion	UNP Q2Y0H9
HA	159	TYR	-	insertion	UNP Q2Y0H9
HA	160	GLN	-	insertion	UNP Q2Y0H9
HA	161	ALA	-	insertion	UNP Q2Y0H9
HA	162	GLY	-	insertion	UNP Q2Y0H9
HA	163	SER	-	insertion	UNP Q2Y0H9
HA	164	THR	-	insertion	UNP Q2Y0H9
HA	165	PRO	-	insertion	UNP Q2Y0H9
HA	166	CYS	-	insertion	UNP Q2Y0H9
HA	167	ASN	-	insertion	UNP Q2Y0H9
HA	168	GLY	-	insertion	UNP Q2Y0H9
HA	169	VAL	-	insertion	UNP Q2Y0H9
HA	170	GLU	-	insertion	UNP Q2Y0H9
HA	171	GLY	-	insertion	UNP Q2Y0H9
HA	172	PHE	-	insertion	UNP Q2Y0H9
HA	173	ASN	-	insertion	UNP Q2Y0H9
HA	174	CYS	-	insertion	UNP Q2Y0H9
HA	175	TYR	-	insertion	UNP Q2Y0H9
HA	176	PHE	-	insertion	UNP Q2Y0H9
HA	177	PRO	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
HA	178	LEU	-	insertion	UNP Q2Y0H9
HA	179	GLN	-	insertion	UNP Q2Y0H9
HA	180	SER	-	insertion	UNP Q2Y0H9
HA	181	TYR	-	insertion	UNP Q2Y0H9
HA	182	GLY	-	insertion	UNP Q2Y0H9
HA	183	PHE	-	insertion	UNP Q2Y0H9
HA	184	GLN	-	insertion	UNP Q2Y0H9
HA	185	PRO	-	insertion	UNP Q2Y0H9
HA	186	THR	-	insertion	UNP Q2Y0H9
HA	187	ASN	-	insertion	UNP Q2Y0H9
HA	188	GLY	-	insertion	UNP Q2Y0H9
HA	189	VAL	-	insertion	UNP Q2Y0H9
HA	190	GLY	-	insertion	UNP Q2Y0H9
HA	191	TYR	-	insertion	UNP Q2Y0H9
HA	192	GLY	-	insertion	UNP Q2Y0H9
HA	193	PRO	THR	conflict	UNP Q2Y0H9
HA	341E	ALA	-	insertion	UNP Q2Y0H9
HA	341F	ARG	-	insertion	UNP Q2Y0H9
HA	341U	VAL	-	insertion	UNP Q2Y0H9
HA	341V	ASP	-	insertion	UNP Q2Y0H9
HA	342I	LEU	-	insertion	UNP Q2Y0H9
HA	342J	GLU	-	insertion	UNP Q2Y0H9
HA	342V	SER	-	insertion	UNP Q2Y0H9
HA	342W	ARG	-	insertion	UNP Q2Y0H9
IA	157	GLU	VAL	conflict	UNP Q2Y0H9
IA	158	PHE	-	insertion	UNP Q2Y0H9
IA	159	TYR	-	insertion	UNP Q2Y0H9
IA	160	GLN	-	insertion	UNP Q2Y0H9
IA	161	ALA	-	insertion	UNP Q2Y0H9
IA	162	GLY	-	insertion	UNP Q2Y0H9
IA	163	SER	-	insertion	UNP Q2Y0H9
IA	164	THR	-	insertion	UNP Q2Y0H9
IA	165	PRO	-	insertion	UNP Q2Y0H9
IA	166	CYS	-	insertion	UNP Q2Y0H9
IA	167	ASN	-	insertion	UNP Q2Y0H9
IA	168	GLY	-	insertion	UNP Q2Y0H9
IA	169	VAL	-	insertion	UNP Q2Y0H9
IA	170	GLU	-	insertion	UNP Q2Y0H9
IA	171	GLY	-	insertion	UNP Q2Y0H9
IA	172	PHE	-	insertion	UNP Q2Y0H9
IA	173	ASN	-	insertion	UNP Q2Y0H9
IA	174	CYS	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
IA	175	TYR	-	insertion	UNP Q2Y0H9
IA	176	PHE	-	insertion	UNP Q2Y0H9
IA	177	PRO	-	insertion	UNP Q2Y0H9
IA	178	LEU	-	insertion	UNP Q2Y0H9
IA	179	GLN	-	insertion	UNP Q2Y0H9
IA	180	SER	-	insertion	UNP Q2Y0H9
IA	181	TYR	-	insertion	UNP Q2Y0H9
IA	182	GLY	-	insertion	UNP Q2Y0H9
IA	183	PHE	-	insertion	UNP Q2Y0H9
IA	184	GLN	-	insertion	UNP Q2Y0H9
IA	185	PRO	-	insertion	UNP Q2Y0H9
IA	186	THR	-	insertion	UNP Q2Y0H9
IA	187	ASN	-	insertion	UNP Q2Y0H9
IA	188	GLY	-	insertion	UNP Q2Y0H9
IA	189	VAL	-	insertion	UNP Q2Y0H9
IA	190	GLY	-	insertion	UNP Q2Y0H9
IA	191	TYR	-	insertion	UNP Q2Y0H9
IA	192	GLY	-	insertion	UNP Q2Y0H9
IA	193	PRO	THR	conflict	UNP Q2Y0H9
IA	341E	ALA	-	insertion	UNP Q2Y0H9
IA	341F	ARG	-	insertion	UNP Q2Y0H9
IA	341U	VAL	-	insertion	UNP Q2Y0H9
IA	341V	ASP	-	insertion	UNP Q2Y0H9
IA	342I	LEU	-	insertion	UNP Q2Y0H9
IA	342J	GLU	-	insertion	UNP Q2Y0H9
IA	342V	SER	-	insertion	UNP Q2Y0H9
IA	342W	ARG	-	insertion	UNP Q2Y0H9
JA	157	GLU	VAL	conflict	UNP Q2Y0H9
JA	158	PHE	-	insertion	UNP Q2Y0H9
JA	159	TYR	-	insertion	UNP Q2Y0H9
JA	160	GLN	-	insertion	UNP Q2Y0H9
JA	161	ALA	-	insertion	UNP Q2Y0H9
JA	162	GLY	-	insertion	UNP Q2Y0H9
JA	163	SER	-	insertion	UNP Q2Y0H9
JA	164	THR	-	insertion	UNP Q2Y0H9
JA	165	PRO	-	insertion	UNP Q2Y0H9
JA	166	CYS	-	insertion	UNP Q2Y0H9
JA	167	ASN	-	insertion	UNP Q2Y0H9
JA	168	GLY	-	insertion	UNP Q2Y0H9
JA	169	VAL	-	insertion	UNP Q2Y0H9
JA	170	GLU	-	insertion	UNP Q2Y0H9
JA	171	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
JA	172	PHE	-	insertion	UNP Q2Y0H9
JA	173	ASN	-	insertion	UNP Q2Y0H9
JA	174	CYS	-	insertion	UNP Q2Y0H9
JA	175	TYR	-	insertion	UNP Q2Y0H9
JA	176	PHE	-	insertion	UNP Q2Y0H9
JA	177	PRO	-	insertion	UNP Q2Y0H9
JA	178	LEU	-	insertion	UNP Q2Y0H9
JA	179	GLN	-	insertion	UNP Q2Y0H9
JA	180	SER	-	insertion	UNP Q2Y0H9
JA	181	TYR	-	insertion	UNP Q2Y0H9
JA	182	GLY	-	insertion	UNP Q2Y0H9
JA	183	PHE	-	insertion	UNP Q2Y0H9
JA	184	GLN	-	insertion	UNP Q2Y0H9
JA	185	PRO	-	insertion	UNP Q2Y0H9
JA	186	THR	-	insertion	UNP Q2Y0H9
JA	187	ASN	-	insertion	UNP Q2Y0H9
JA	188	GLY	-	insertion	UNP Q2Y0H9
JA	189	VAL	-	insertion	UNP Q2Y0H9
JA	190	GLY	-	insertion	UNP Q2Y0H9
JA	191	TYR	-	insertion	UNP Q2Y0H9
JA	192	GLY	-	insertion	UNP Q2Y0H9
JA	193	PRO	THR	conflict	UNP Q2Y0H9
JA	341E	ALA	-	insertion	UNP Q2Y0H9
JA	341F	ARG	-	insertion	UNP Q2Y0H9
JA	341U	VAL	-	insertion	UNP Q2Y0H9
JA	341V	ASP	-	insertion	UNP Q2Y0H9
JA	342I	LEU	-	insertion	UNP Q2Y0H9
JA	342J	GLU	-	insertion	UNP Q2Y0H9
JA	342V	SER	-	insertion	UNP Q2Y0H9
JA	342W	ARG	-	insertion	UNP Q2Y0H9
KA	157	GLU	VAL	conflict	UNP Q2Y0H9
KA	158	PHE	-	insertion	UNP Q2Y0H9
KA	159	TYR	-	insertion	UNP Q2Y0H9
KA	160	GLN	-	insertion	UNP Q2Y0H9
KA	161	ALA	-	insertion	UNP Q2Y0H9
KA	162	GLY	-	insertion	UNP Q2Y0H9
KA	163	SER	-	insertion	UNP Q2Y0H9
KA	164	THR	-	insertion	UNP Q2Y0H9
KA	165	PRO	-	insertion	UNP Q2Y0H9
KA	166	CYS	-	insertion	UNP Q2Y0H9
KA	167	ASN	-	insertion	UNP Q2Y0H9
KA	168	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
KA	169	VAL	-	insertion	UNP Q2Y0H9
KA	170	GLU	-	insertion	UNP Q2Y0H9
KA	171	GLY	-	insertion	UNP Q2Y0H9
KA	172	PHE	-	insertion	UNP Q2Y0H9
KA	173	ASN	-	insertion	UNP Q2Y0H9
KA	174	CYS	-	insertion	UNP Q2Y0H9
KA	175	TYR	-	insertion	UNP Q2Y0H9
KA	176	PHE	-	insertion	UNP Q2Y0H9
KA	177	PRO	-	insertion	UNP Q2Y0H9
KA	178	LEU	-	insertion	UNP Q2Y0H9
KA	179	GLN	-	insertion	UNP Q2Y0H9
KA	180	SER	-	insertion	UNP Q2Y0H9
KA	181	TYR	-	insertion	UNP Q2Y0H9
KA	182	GLY	-	insertion	UNP Q2Y0H9
KA	183	PHE	-	insertion	UNP Q2Y0H9
KA	184	GLN	-	insertion	UNP Q2Y0H9
KA	185	PRO	-	insertion	UNP Q2Y0H9
KA	186	THR	-	insertion	UNP Q2Y0H9
KA	187	ASN	-	insertion	UNP Q2Y0H9
KA	188	GLY	-	insertion	UNP Q2Y0H9
KA	189	VAL	-	insertion	UNP Q2Y0H9
KA	190	GLY	-	insertion	UNP Q2Y0H9
KA	191	TYR	-	insertion	UNP Q2Y0H9
KA	192	GLY	-	insertion	UNP Q2Y0H9
KA	193	PRO	THR	conflict	UNP Q2Y0H9
KA	341E	ALA	-	insertion	UNP Q2Y0H9
KA	341F	ARG	-	insertion	UNP Q2Y0H9
KA	341U	VAL	-	insertion	UNP Q2Y0H9
KA	341V	ASP	-	insertion	UNP Q2Y0H9
KA	342I	LEU	-	insertion	UNP Q2Y0H9
KA	342J	GLU	-	insertion	UNP Q2Y0H9
KA	342V	SER	-	insertion	UNP Q2Y0H9
KA	342W	ARG	-	insertion	UNP Q2Y0H9
LA	157	GLU	VAL	conflict	UNP Q2Y0H9
LA	158	PHE	-	insertion	UNP Q2Y0H9
LA	159	TYR	-	insertion	UNP Q2Y0H9
LA	160	GLN	-	insertion	UNP Q2Y0H9
LA	161	ALA	-	insertion	UNP Q2Y0H9
LA	162	GLY	-	insertion	UNP Q2Y0H9
LA	163	SER	-	insertion	UNP Q2Y0H9
LA	164	THR	-	insertion	UNP Q2Y0H9
LA	165	PRO	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
LA	166	CYS	-	insertion	UNP Q2Y0H9
LA	167	ASN	-	insertion	UNP Q2Y0H9
LA	168	GLY	-	insertion	UNP Q2Y0H9
LA	169	VAL	-	insertion	UNP Q2Y0H9
LA	170	GLU	-	insertion	UNP Q2Y0H9
LA	171	GLY	-	insertion	UNP Q2Y0H9
LA	172	PHE	-	insertion	UNP Q2Y0H9
LA	173	ASN	-	insertion	UNP Q2Y0H9
LA	174	CYS	-	insertion	UNP Q2Y0H9
LA	175	TYR	-	insertion	UNP Q2Y0H9
LA	176	PHE	-	insertion	UNP Q2Y0H9
LA	177	PRO	-	insertion	UNP Q2Y0H9
LA	178	LEU	-	insertion	UNP Q2Y0H9
LA	179	GLN	-	insertion	UNP Q2Y0H9
LA	180	SER	-	insertion	UNP Q2Y0H9
LA	181	TYR	-	insertion	UNP Q2Y0H9
LA	182	GLY	-	insertion	UNP Q2Y0H9
LA	183	PHE	-	insertion	UNP Q2Y0H9
LA	184	GLN	-	insertion	UNP Q2Y0H9
LA	185	PRO	-	insertion	UNP Q2Y0H9
LA	186	THR	-	insertion	UNP Q2Y0H9
LA	187	ASN	-	insertion	UNP Q2Y0H9
LA	188	GLY	-	insertion	UNP Q2Y0H9
LA	189	VAL	-	insertion	UNP Q2Y0H9
LA	190	GLY	-	insertion	UNP Q2Y0H9
LA	191	TYR	-	insertion	UNP Q2Y0H9
LA	192	GLY	-	insertion	UNP Q2Y0H9
LA	193	PRO	THR	conflict	UNP Q2Y0H9
LA	341E	ALA	-	insertion	UNP Q2Y0H9
LA	341F	ARG	-	insertion	UNP Q2Y0H9
LA	341U	VAL	-	insertion	UNP Q2Y0H9
LA	341V	ASP	-	insertion	UNP Q2Y0H9
LA	342I	LEU	-	insertion	UNP Q2Y0H9
LA	342J	GLU	-	insertion	UNP Q2Y0H9
LA	342V	SER	-	insertion	UNP Q2Y0H9
LA	342W	ARG	-	insertion	UNP Q2Y0H9
MA	157	GLU	VAL	conflict	UNP Q2Y0H9
MA	158	PHE	-	insertion	UNP Q2Y0H9
MA	159	TYR	-	insertion	UNP Q2Y0H9
MA	160	GLN	-	insertion	UNP Q2Y0H9
MA	161	ALA	-	insertion	UNP Q2Y0H9
MA	162	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
MA	163	SER	-	insertion	UNP Q2Y0H9
MA	164	THR	-	insertion	UNP Q2Y0H9
MA	165	PRO	-	insertion	UNP Q2Y0H9
MA	166	CYS	-	insertion	UNP Q2Y0H9
MA	167	ASN	-	insertion	UNP Q2Y0H9
MA	168	GLY	-	insertion	UNP Q2Y0H9
MA	169	VAL	-	insertion	UNP Q2Y0H9
MA	170	GLU	-	insertion	UNP Q2Y0H9
MA	171	GLY	-	insertion	UNP Q2Y0H9
MA	172	PHE	-	insertion	UNP Q2Y0H9
MA	173	ASN	-	insertion	UNP Q2Y0H9
MA	174	CYS	-	insertion	UNP Q2Y0H9
MA	175	TYR	-	insertion	UNP Q2Y0H9
MA	176	PHE	-	insertion	UNP Q2Y0H9
MA	177	PRO	-	insertion	UNP Q2Y0H9
MA	178	LEU	-	insertion	UNP Q2Y0H9
MA	179	GLN	-	insertion	UNP Q2Y0H9
MA	180	SER	-	insertion	UNP Q2Y0H9
MA	181	TYR	-	insertion	UNP Q2Y0H9
MA	182	GLY	-	insertion	UNP Q2Y0H9
MA	183	PHE	-	insertion	UNP Q2Y0H9
MA	184	GLN	-	insertion	UNP Q2Y0H9
MA	185	PRO	-	insertion	UNP Q2Y0H9
MA	186	THR	-	insertion	UNP Q2Y0H9
MA	187	ASN	-	insertion	UNP Q2Y0H9
MA	188	GLY	-	insertion	UNP Q2Y0H9
MA	189	VAL	-	insertion	UNP Q2Y0H9
MA	190	GLY	-	insertion	UNP Q2Y0H9
MA	191	TYR	-	insertion	UNP Q2Y0H9
MA	192	GLY	-	insertion	UNP Q2Y0H9
MA	193	PRO	THR	conflict	UNP Q2Y0H9
MA	341E	ALA	-	insertion	UNP Q2Y0H9
MA	341F	ARG	-	insertion	UNP Q2Y0H9
MA	341U	VAL	-	insertion	UNP Q2Y0H9
MA	341V	ASP	-	insertion	UNP Q2Y0H9
MA	342I	LEU	-	insertion	UNP Q2Y0H9
MA	342J	GLU	-	insertion	UNP Q2Y0H9
MA	342V	SER	-	insertion	UNP Q2Y0H9
MA	342W	ARG	-	insertion	UNP Q2Y0H9
NA	157	GLU	VAL	conflict	UNP Q2Y0H9
NA	158	PHE	-	insertion	UNP Q2Y0H9
NA	159	TYR	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
NA	160	GLN	-	insertion	UNP Q2Y0H9
NA	161	ALA	-	insertion	UNP Q2Y0H9
NA	162	GLY	-	insertion	UNP Q2Y0H9
NA	163	SER	-	insertion	UNP Q2Y0H9
NA	164	THR	-	insertion	UNP Q2Y0H9
NA	165	PRO	-	insertion	UNP Q2Y0H9
NA	166	CYS	-	insertion	UNP Q2Y0H9
NA	167	ASN	-	insertion	UNP Q2Y0H9
NA	168	GLY	-	insertion	UNP Q2Y0H9
NA	169	VAL	-	insertion	UNP Q2Y0H9
NA	170	GLU	-	insertion	UNP Q2Y0H9
NA	171	GLY	-	insertion	UNP Q2Y0H9
NA	172	PHE	-	insertion	UNP Q2Y0H9
NA	173	ASN	-	insertion	UNP Q2Y0H9
NA	174	CYS	-	insertion	UNP Q2Y0H9
NA	175	TYR	-	insertion	UNP Q2Y0H9
NA	176	PHE	-	insertion	UNP Q2Y0H9
NA	177	PRO	-	insertion	UNP Q2Y0H9
NA	178	LEU	-	insertion	UNP Q2Y0H9
NA	179	GLN	-	insertion	UNP Q2Y0H9
NA	180	SER	-	insertion	UNP Q2Y0H9
NA	181	TYR	-	insertion	UNP Q2Y0H9
NA	182	GLY	-	insertion	UNP Q2Y0H9
NA	183	PHE	-	insertion	UNP Q2Y0H9
NA	184	GLN	-	insertion	UNP Q2Y0H9
NA	185	PRO	-	insertion	UNP Q2Y0H9
NA	186	THR	-	insertion	UNP Q2Y0H9
NA	187	ASN	-	insertion	UNP Q2Y0H9
NA	188	GLY	-	insertion	UNP Q2Y0H9
NA	189	VAL	-	insertion	UNP Q2Y0H9
NA	190	GLY	-	insertion	UNP Q2Y0H9
NA	191	TYR	-	insertion	UNP Q2Y0H9
NA	192	GLY	-	insertion	UNP Q2Y0H9
NA	193	PRO	THR	conflict	UNP Q2Y0H9
NA	341E	ALA	-	insertion	UNP Q2Y0H9
NA	341F	ARG	-	insertion	UNP Q2Y0H9
NA	341U	VAL	-	insertion	UNP Q2Y0H9
NA	341V	ASP	-	insertion	UNP Q2Y0H9
NA	342I	LEU	-	insertion	UNP Q2Y0H9
NA	342J	GLU	-	insertion	UNP Q2Y0H9
NA	342V	SER	-	insertion	UNP Q2Y0H9
NA	342W	ARG	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
OA	157	GLU	VAL	conflict	UNP Q2Y0H9
OA	158	PHE	-	insertion	UNP Q2Y0H9
OA	159	TYR	-	insertion	UNP Q2Y0H9
OA	160	GLN	-	insertion	UNP Q2Y0H9
OA	161	ALA	-	insertion	UNP Q2Y0H9
OA	162	GLY	-	insertion	UNP Q2Y0H9
OA	163	SER	-	insertion	UNP Q2Y0H9
OA	164	THR	-	insertion	UNP Q2Y0H9
OA	165	PRO	-	insertion	UNP Q2Y0H9
OA	166	CYS	-	insertion	UNP Q2Y0H9
OA	167	ASN	-	insertion	UNP Q2Y0H9
OA	168	GLY	-	insertion	UNP Q2Y0H9
OA	169	VAL	-	insertion	UNP Q2Y0H9
OA	170	GLU	-	insertion	UNP Q2Y0H9
OA	171	GLY	-	insertion	UNP Q2Y0H9
OA	172	PHE	-	insertion	UNP Q2Y0H9
OA	173	ASN	-	insertion	UNP Q2Y0H9
OA	174	CYS	-	insertion	UNP Q2Y0H9
OA	175	TYR	-	insertion	UNP Q2Y0H9
OA	176	PHE	-	insertion	UNP Q2Y0H9
OA	177	PRO	-	insertion	UNP Q2Y0H9
OA	178	LEU	-	insertion	UNP Q2Y0H9
OA	179	GLN	-	insertion	UNP Q2Y0H9
OA	180	SER	-	insertion	UNP Q2Y0H9
OA	181	TYR	-	insertion	UNP Q2Y0H9
OA	182	GLY	-	insertion	UNP Q2Y0H9
OA	183	PHE	-	insertion	UNP Q2Y0H9
OA	184	GLN	-	insertion	UNP Q2Y0H9
OA	185	PRO	-	insertion	UNP Q2Y0H9
OA	186	THR	-	insertion	UNP Q2Y0H9
OA	187	ASN	-	insertion	UNP Q2Y0H9
OA	188	GLY	-	insertion	UNP Q2Y0H9
OA	189	VAL	-	insertion	UNP Q2Y0H9
OA	190	GLY	-	insertion	UNP Q2Y0H9
OA	191	TYR	-	insertion	UNP Q2Y0H9
OA	192	GLY	-	insertion	UNP Q2Y0H9
OA	193	PRO	THR	conflict	UNP Q2Y0H9
OA	341E	ALA	-	insertion	UNP Q2Y0H9
OA	341F	ARG	-	insertion	UNP Q2Y0H9
OA	341U	VAL	-	insertion	UNP Q2Y0H9
OA	341V	ASP	-	insertion	UNP Q2Y0H9
OA	342I	LEU	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
OA	342J	GLU	-	insertion	UNP Q2Y0H9
OA	342V	SER	-	insertion	UNP Q2Y0H9
OA	342W	ARG	-	insertion	UNP Q2Y0H9
PA	157	GLU	VAL	conflict	UNP Q2Y0H9
PA	158	PHE	-	insertion	UNP Q2Y0H9
PA	159	TYR	-	insertion	UNP Q2Y0H9
PA	160	GLN	-	insertion	UNP Q2Y0H9
PA	161	ALA	-	insertion	UNP Q2Y0H9
PA	162	GLY	-	insertion	UNP Q2Y0H9
PA	163	SER	-	insertion	UNP Q2Y0H9
PA	164	THR	-	insertion	UNP Q2Y0H9
PA	165	PRO	-	insertion	UNP Q2Y0H9
PA	166	CYS	-	insertion	UNP Q2Y0H9
PA	167	ASN	-	insertion	UNP Q2Y0H9
PA	168	GLY	-	insertion	UNP Q2Y0H9
PA	169	VAL	-	insertion	UNP Q2Y0H9
PA	170	GLU	-	insertion	UNP Q2Y0H9
PA	171	GLY	-	insertion	UNP Q2Y0H9
PA	172	PHE	-	insertion	UNP Q2Y0H9
PA	173	ASN	-	insertion	UNP Q2Y0H9
PA	174	CYS	-	insertion	UNP Q2Y0H9
PA	175	TYR	-	insertion	UNP Q2Y0H9
PA	176	PHE	-	insertion	UNP Q2Y0H9
PA	177	PRO	-	insertion	UNP Q2Y0H9
PA	178	LEU	-	insertion	UNP Q2Y0H9
PA	179	GLN	-	insertion	UNP Q2Y0H9
PA	180	SER	-	insertion	UNP Q2Y0H9
PA	181	TYR	-	insertion	UNP Q2Y0H9
PA	182	GLY	-	insertion	UNP Q2Y0H9
PA	183	PHE	-	insertion	UNP Q2Y0H9
PA	184	GLN	-	insertion	UNP Q2Y0H9
PA	185	PRO	-	insertion	UNP Q2Y0H9
PA	186	THR	-	insertion	UNP Q2Y0H9
PA	187	ASN	-	insertion	UNP Q2Y0H9
PA	188	GLY	-	insertion	UNP Q2Y0H9
PA	189	VAL	-	insertion	UNP Q2Y0H9
PA	190	GLY	-	insertion	UNP Q2Y0H9
PA	191	TYR	-	insertion	UNP Q2Y0H9
PA	192	GLY	-	insertion	UNP Q2Y0H9
PA	193	PRO	THR	conflict	UNP Q2Y0H9
PA	341E	ALA	-	insertion	UNP Q2Y0H9
PA	341F	ARG	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
PA	341U	VAL	-	insertion	UNP Q2Y0H9
PA	341V	ASP	-	insertion	UNP Q2Y0H9
PA	342I	LEU	-	insertion	UNP Q2Y0H9
PA	342J	GLU	-	insertion	UNP Q2Y0H9
PA	342V	SER	-	insertion	UNP Q2Y0H9
PA	342W	ARG	-	insertion	UNP Q2Y0H9
QA	157	GLU	VAL	conflict	UNP Q2Y0H9
QA	158	PHE	-	insertion	UNP Q2Y0H9
QA	159	TYR	-	insertion	UNP Q2Y0H9
QA	160	GLN	-	insertion	UNP Q2Y0H9
QA	161	ALA	-	insertion	UNP Q2Y0H9
QA	162	GLY	-	insertion	UNP Q2Y0H9
QA	163	SER	-	insertion	UNP Q2Y0H9
QA	164	THR	-	insertion	UNP Q2Y0H9
QA	165	PRO	-	insertion	UNP Q2Y0H9
QA	166	CYS	-	insertion	UNP Q2Y0H9
QA	167	ASN	-	insertion	UNP Q2Y0H9
QA	168	GLY	-	insertion	UNP Q2Y0H9
QA	169	VAL	-	insertion	UNP Q2Y0H9
QA	170	GLU	-	insertion	UNP Q2Y0H9
QA	171	GLY	-	insertion	UNP Q2Y0H9
QA	172	PHE	-	insertion	UNP Q2Y0H9
QA	173	ASN	-	insertion	UNP Q2Y0H9
QA	174	CYS	-	insertion	UNP Q2Y0H9
QA	175	TYR	-	insertion	UNP Q2Y0H9
QA	176	PHE	-	insertion	UNP Q2Y0H9
QA	177	PRO	-	insertion	UNP Q2Y0H9
QA	178	LEU	-	insertion	UNP Q2Y0H9
QA	179	GLN	-	insertion	UNP Q2Y0H9
QA	180	SER	-	insertion	UNP Q2Y0H9
QA	181	TYR	-	insertion	UNP Q2Y0H9
QA	182	GLY	-	insertion	UNP Q2Y0H9
QA	183	PHE	-	insertion	UNP Q2Y0H9
QA	184	GLN	-	insertion	UNP Q2Y0H9
QA	185	PRO	-	insertion	UNP Q2Y0H9
QA	186	THR	-	insertion	UNP Q2Y0H9
QA	187	ASN	-	insertion	UNP Q2Y0H9
QA	188	GLY	-	insertion	UNP Q2Y0H9
QA	189	VAL	-	insertion	UNP Q2Y0H9
QA	190	GLY	-	insertion	UNP Q2Y0H9
QA	191	TYR	-	insertion	UNP Q2Y0H9
QA	192	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
QA	193	PRO	THR	conflict	UNP Q2Y0H9
QA	341E	ALA	-	insertion	UNP Q2Y0H9
QA	341F	ARG	-	insertion	UNP Q2Y0H9
QA	341U	VAL	-	insertion	UNP Q2Y0H9
QA	341V	ASP	-	insertion	UNP Q2Y0H9
QA	342I	LEU	-	insertion	UNP Q2Y0H9
QA	342J	GLU	-	insertion	UNP Q2Y0H9
QA	342V	SER	-	insertion	UNP Q2Y0H9
QA	342W	ARG	-	insertion	UNP Q2Y0H9
RA	157	GLU	VAL	conflict	UNP Q2Y0H9
RA	158	PHE	-	insertion	UNP Q2Y0H9
RA	159	TYR	-	insertion	UNP Q2Y0H9
RA	160	GLN	-	insertion	UNP Q2Y0H9
RA	161	ALA	-	insertion	UNP Q2Y0H9
RA	162	GLY	-	insertion	UNP Q2Y0H9
RA	163	SER	-	insertion	UNP Q2Y0H9
RA	164	THR	-	insertion	UNP Q2Y0H9
RA	165	PRO	-	insertion	UNP Q2Y0H9
RA	166	CYS	-	insertion	UNP Q2Y0H9
RA	167	ASN	-	insertion	UNP Q2Y0H9
RA	168	GLY	-	insertion	UNP Q2Y0H9
RA	169	VAL	-	insertion	UNP Q2Y0H9
RA	170	GLU	-	insertion	UNP Q2Y0H9
RA	171	GLY	-	insertion	UNP Q2Y0H9
RA	172	PHE	-	insertion	UNP Q2Y0H9
RA	173	ASN	-	insertion	UNP Q2Y0H9
RA	174	CYS	-	insertion	UNP Q2Y0H9
RA	175	TYR	-	insertion	UNP Q2Y0H9
RA	176	PHE	-	insertion	UNP Q2Y0H9
RA	177	PRO	-	insertion	UNP Q2Y0H9
RA	178	LEU	-	insertion	UNP Q2Y0H9
RA	179	GLN	-	insertion	UNP Q2Y0H9
RA	180	SER	-	insertion	UNP Q2Y0H9
RA	181	TYR	-	insertion	UNP Q2Y0H9
RA	182	GLY	-	insertion	UNP Q2Y0H9
RA	183	PHE	-	insertion	UNP Q2Y0H9
RA	184	GLN	-	insertion	UNP Q2Y0H9
RA	185	PRO	-	insertion	UNP Q2Y0H9
RA	186	THR	-	insertion	UNP Q2Y0H9
RA	187	ASN	-	insertion	UNP Q2Y0H9
RA	188	GLY	-	insertion	UNP Q2Y0H9
RA	189	VAL	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
RA	190	GLY	-	insertion	UNP Q2Y0H9
RA	191	TYR	-	insertion	UNP Q2Y0H9
RA	192	GLY	-	insertion	UNP Q2Y0H9
RA	193	PRO	THR	conflict	UNP Q2Y0H9
RA	341E	ALA	-	insertion	UNP Q2Y0H9
RA	341F	ARG	-	insertion	UNP Q2Y0H9
RA	341U	VAL	-	insertion	UNP Q2Y0H9
RA	341V	ASP	-	insertion	UNP Q2Y0H9
RA	342I	LEU	-	insertion	UNP Q2Y0H9
RA	342J	GLU	-	insertion	UNP Q2Y0H9
RA	342V	SER	-	insertion	UNP Q2Y0H9
RA	342W	ARG	-	insertion	UNP Q2Y0H9
SA	157	GLU	VAL	conflict	UNP Q2Y0H9
SA	158	PHE	-	insertion	UNP Q2Y0H9
SA	159	TYR	-	insertion	UNP Q2Y0H9
SA	160	GLN	-	insertion	UNP Q2Y0H9
SA	161	ALA	-	insertion	UNP Q2Y0H9
SA	162	GLY	-	insertion	UNP Q2Y0H9
SA	163	SER	-	insertion	UNP Q2Y0H9
SA	164	THR	-	insertion	UNP Q2Y0H9
SA	165	PRO	-	insertion	UNP Q2Y0H9
SA	166	CYS	-	insertion	UNP Q2Y0H9
SA	167	ASN	-	insertion	UNP Q2Y0H9
SA	168	GLY	-	insertion	UNP Q2Y0H9
SA	169	VAL	-	insertion	UNP Q2Y0H9
SA	170	GLU	-	insertion	UNP Q2Y0H9
SA	171	GLY	-	insertion	UNP Q2Y0H9
SA	172	PHE	-	insertion	UNP Q2Y0H9
SA	173	ASN	-	insertion	UNP Q2Y0H9
SA	174	CYS	-	insertion	UNP Q2Y0H9
SA	175	TYR	-	insertion	UNP Q2Y0H9
SA	176	PHE	-	insertion	UNP Q2Y0H9
SA	177	PRO	-	insertion	UNP Q2Y0H9
SA	178	LEU	-	insertion	UNP Q2Y0H9
SA	179	GLN	-	insertion	UNP Q2Y0H9
SA	180	SER	-	insertion	UNP Q2Y0H9
SA	181	TYR	-	insertion	UNP Q2Y0H9
SA	182	GLY	-	insertion	UNP Q2Y0H9
SA	183	PHE	-	insertion	UNP Q2Y0H9
SA	184	GLN	-	insertion	UNP Q2Y0H9
SA	185	PRO	-	insertion	UNP Q2Y0H9
SA	186	THR	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
SA	187	ASN	-	insertion	UNP Q2Y0H9
SA	188	GLY	-	insertion	UNP Q2Y0H9
SA	189	VAL	-	insertion	UNP Q2Y0H9
SA	190	GLY	-	insertion	UNP Q2Y0H9
SA	191	TYR	-	insertion	UNP Q2Y0H9
SA	192	GLY	-	insertion	UNP Q2Y0H9
SA	193	PRO	THR	conflict	UNP Q2Y0H9
SA	341E	ALA	-	insertion	UNP Q2Y0H9
SA	341F	ARG	-	insertion	UNP Q2Y0H9
SA	341U	VAL	-	insertion	UNP Q2Y0H9
SA	341V	ASP	-	insertion	UNP Q2Y0H9
SA	342I	LEU	-	insertion	UNP Q2Y0H9
SA	342J	GLU	-	insertion	UNP Q2Y0H9
SA	342V	SER	-	insertion	UNP Q2Y0H9
SA	342W	ARG	-	insertion	UNP Q2Y0H9
TA	157	GLU	VAL	conflict	UNP Q2Y0H9
TA	158	PHE	-	insertion	UNP Q2Y0H9
TA	159	TYR	-	insertion	UNP Q2Y0H9
TA	160	GLN	-	insertion	UNP Q2Y0H9
TA	161	ALA	-	insertion	UNP Q2Y0H9
TA	162	GLY	-	insertion	UNP Q2Y0H9
TA	163	SER	-	insertion	UNP Q2Y0H9
TA	164	THR	-	insertion	UNP Q2Y0H9
TA	165	PRO	-	insertion	UNP Q2Y0H9
TA	166	CYS	-	insertion	UNP Q2Y0H9
TA	167	ASN	-	insertion	UNP Q2Y0H9
TA	168	GLY	-	insertion	UNP Q2Y0H9
TA	169	VAL	-	insertion	UNP Q2Y0H9
TA	170	GLU	-	insertion	UNP Q2Y0H9
TA	171	GLY	-	insertion	UNP Q2Y0H9
TA	172	PHE	-	insertion	UNP Q2Y0H9
TA	173	ASN	-	insertion	UNP Q2Y0H9
TA	174	CYS	-	insertion	UNP Q2Y0H9
TA	175	TYR	-	insertion	UNP Q2Y0H9
TA	176	PHE	-	insertion	UNP Q2Y0H9
TA	177	PRO	-	insertion	UNP Q2Y0H9
TA	178	LEU	-	insertion	UNP Q2Y0H9
TA	179	GLN	-	insertion	UNP Q2Y0H9
TA	180	SER	-	insertion	UNP Q2Y0H9
TA	181	TYR	-	insertion	UNP Q2Y0H9
TA	182	GLY	-	insertion	UNP Q2Y0H9
TA	183	PHE	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
TA	184	GLN	-	insertion	UNP Q2Y0H9
TA	185	PRO	-	insertion	UNP Q2Y0H9
TA	186	THR	-	insertion	UNP Q2Y0H9
TA	187	ASN	-	insertion	UNP Q2Y0H9
TA	188	GLY	-	insertion	UNP Q2Y0H9
TA	189	VAL	-	insertion	UNP Q2Y0H9
TA	190	GLY	-	insertion	UNP Q2Y0H9
TA	191	TYR	-	insertion	UNP Q2Y0H9
TA	192	GLY	-	insertion	UNP Q2Y0H9
TA	193	PRO	THR	conflict	UNP Q2Y0H9
TA	341E	ALA	-	insertion	UNP Q2Y0H9
TA	341F	ARG	-	insertion	UNP Q2Y0H9
TA	341U	VAL	-	insertion	UNP Q2Y0H9
TA	341V	ASP	-	insertion	UNP Q2Y0H9
TA	342I	LEU	-	insertion	UNP Q2Y0H9
TA	342J	GLU	-	insertion	UNP Q2Y0H9
TA	342V	SER	-	insertion	UNP Q2Y0H9
TA	342W	ARG	-	insertion	UNP Q2Y0H9
UA	157	GLU	VAL	conflict	UNP Q2Y0H9
UA	158	PHE	-	insertion	UNP Q2Y0H9
UA	159	TYR	-	insertion	UNP Q2Y0H9
UA	160	GLN	-	insertion	UNP Q2Y0H9
UA	161	ALA	-	insertion	UNP Q2Y0H9
UA	162	GLY	-	insertion	UNP Q2Y0H9
UA	163	SER	-	insertion	UNP Q2Y0H9
UA	164	THR	-	insertion	UNP Q2Y0H9
UA	165	PRO	-	insertion	UNP Q2Y0H9
UA	166	CYS	-	insertion	UNP Q2Y0H9
UA	167	ASN	-	insertion	UNP Q2Y0H9
UA	168	GLY	-	insertion	UNP Q2Y0H9
UA	169	VAL	-	insertion	UNP Q2Y0H9
UA	170	GLU	-	insertion	UNP Q2Y0H9
UA	171	GLY	-	insertion	UNP Q2Y0H9
UA	172	PHE	-	insertion	UNP Q2Y0H9
UA	173	ASN	-	insertion	UNP Q2Y0H9
UA	174	CYS	-	insertion	UNP Q2Y0H9
UA	175	TYR	-	insertion	UNP Q2Y0H9
UA	176	PHE	-	insertion	UNP Q2Y0H9
UA	177	PRO	-	insertion	UNP Q2Y0H9
UA	178	LEU	-	insertion	UNP Q2Y0H9
UA	179	GLN	-	insertion	UNP Q2Y0H9
UA	180	SER	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
UA	181	TYR	-	insertion	UNP Q2Y0H9
UA	182	GLY	-	insertion	UNP Q2Y0H9
UA	183	PHE	-	insertion	UNP Q2Y0H9
UA	184	GLN	-	insertion	UNP Q2Y0H9
UA	185	PRO	-	insertion	UNP Q2Y0H9
UA	186	THR	-	insertion	UNP Q2Y0H9
UA	187	ASN	-	insertion	UNP Q2Y0H9
UA	188	GLY	-	insertion	UNP Q2Y0H9
UA	189	VAL	-	insertion	UNP Q2Y0H9
UA	190	GLY	-	insertion	UNP Q2Y0H9
UA	191	TYR	-	insertion	UNP Q2Y0H9
UA	192	GLY	-	insertion	UNP Q2Y0H9
UA	193	PRO	THR	conflict	UNP Q2Y0H9
UA	341E	ALA	-	insertion	UNP Q2Y0H9
UA	341F	ARG	-	insertion	UNP Q2Y0H9
UA	341U	VAL	-	insertion	UNP Q2Y0H9
UA	341V	ASP	-	insertion	UNP Q2Y0H9
UA	342I	LEU	-	insertion	UNP Q2Y0H9
UA	342J	GLU	-	insertion	UNP Q2Y0H9
UA	342V	SER	-	insertion	UNP Q2Y0H9
UA	342W	ARG	-	insertion	UNP Q2Y0H9
VA	157	GLU	VAL	conflict	UNP Q2Y0H9
VA	158	PHE	-	insertion	UNP Q2Y0H9
VA	159	TYR	-	insertion	UNP Q2Y0H9
VA	160	GLN	-	insertion	UNP Q2Y0H9
VA	161	ALA	-	insertion	UNP Q2Y0H9
VA	162	GLY	-	insertion	UNP Q2Y0H9
VA	163	SER	-	insertion	UNP Q2Y0H9
VA	164	THR	-	insertion	UNP Q2Y0H9
VA	165	PRO	-	insertion	UNP Q2Y0H9
VA	166	CYS	-	insertion	UNP Q2Y0H9
VA	167	ASN	-	insertion	UNP Q2Y0H9
VA	168	GLY	-	insertion	UNP Q2Y0H9
VA	169	VAL	-	insertion	UNP Q2Y0H9
VA	170	GLU	-	insertion	UNP Q2Y0H9
VA	171	GLY	-	insertion	UNP Q2Y0H9
VA	172	PHE	-	insertion	UNP Q2Y0H9
VA	173	ASN	-	insertion	UNP Q2Y0H9
VA	174	CYS	-	insertion	UNP Q2Y0H9
VA	175	TYR	-	insertion	UNP Q2Y0H9
VA	176	PHE	-	insertion	UNP Q2Y0H9
VA	177	PRO	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
VA	178	LEU	-	insertion	UNP Q2Y0H9
VA	179	GLN	-	insertion	UNP Q2Y0H9
VA	180	SER	-	insertion	UNP Q2Y0H9
VA	181	TYR	-	insertion	UNP Q2Y0H9
VA	182	GLY	-	insertion	UNP Q2Y0H9
VA	183	PHE	-	insertion	UNP Q2Y0H9
VA	184	GLN	-	insertion	UNP Q2Y0H9
VA	185	PRO	-	insertion	UNP Q2Y0H9
VA	186	THR	-	insertion	UNP Q2Y0H9
VA	187	ASN	-	insertion	UNP Q2Y0H9
VA	188	GLY	-	insertion	UNP Q2Y0H9
VA	189	VAL	-	insertion	UNP Q2Y0H9
VA	190	GLY	-	insertion	UNP Q2Y0H9
VA	191	TYR	-	insertion	UNP Q2Y0H9
VA	192	GLY	-	insertion	UNP Q2Y0H9
VA	193	PRO	THR	conflict	UNP Q2Y0H9
VA	341E	ALA	-	insertion	UNP Q2Y0H9
VA	341F	ARG	-	insertion	UNP Q2Y0H9
VA	341U	VAL	-	insertion	UNP Q2Y0H9
VA	341V	ASP	-	insertion	UNP Q2Y0H9
VA	342I	LEU	-	insertion	UNP Q2Y0H9
VA	342J	GLU	-	insertion	UNP Q2Y0H9
VA	342V	SER	-	insertion	UNP Q2Y0H9
VA	342W	ARG	-	insertion	UNP Q2Y0H9
WA	157	GLU	VAL	conflict	UNP Q2Y0H9
WA	158	PHE	-	insertion	UNP Q2Y0H9
WA	159	TYR	-	insertion	UNP Q2Y0H9
WA	160	GLN	-	insertion	UNP Q2Y0H9
WA	161	ALA	-	insertion	UNP Q2Y0H9
WA	162	GLY	-	insertion	UNP Q2Y0H9
WA	163	SER	-	insertion	UNP Q2Y0H9
WA	164	THR	-	insertion	UNP Q2Y0H9
WA	165	PRO	-	insertion	UNP Q2Y0H9
WA	166	CYS	-	insertion	UNP Q2Y0H9
WA	167	ASN	-	insertion	UNP Q2Y0H9
WA	168	GLY	-	insertion	UNP Q2Y0H9
WA	169	VAL	-	insertion	UNP Q2Y0H9
WA	170	GLU	-	insertion	UNP Q2Y0H9
WA	171	GLY	-	insertion	UNP Q2Y0H9
WA	172	PHE	-	insertion	UNP Q2Y0H9
WA	173	ASN	-	insertion	UNP Q2Y0H9
WA	174	CYS	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
WA	175	TYR	-	insertion	UNP Q2Y0H9
WA	176	PHE	-	insertion	UNP Q2Y0H9
WA	177	PRO	-	insertion	UNP Q2Y0H9
WA	178	LEU	-	insertion	UNP Q2Y0H9
WA	179	GLN	-	insertion	UNP Q2Y0H9
WA	180	SER	-	insertion	UNP Q2Y0H9
WA	181	TYR	-	insertion	UNP Q2Y0H9
WA	182	GLY	-	insertion	UNP Q2Y0H9
WA	183	PHE	-	insertion	UNP Q2Y0H9
WA	184	GLN	-	insertion	UNP Q2Y0H9
WA	185	PRO	-	insertion	UNP Q2Y0H9
WA	186	THR	-	insertion	UNP Q2Y0H9
WA	187	ASN	-	insertion	UNP Q2Y0H9
WA	188	GLY	-	insertion	UNP Q2Y0H9
WA	189	VAL	-	insertion	UNP Q2Y0H9
WA	190	GLY	-	insertion	UNP Q2Y0H9
WA	191	TYR	-	insertion	UNP Q2Y0H9
WA	192	GLY	-	insertion	UNP Q2Y0H9
WA	193	PRO	THR	conflict	UNP Q2Y0H9
WA	341E	ALA	-	insertion	UNP Q2Y0H9
WA	341F	ARG	-	insertion	UNP Q2Y0H9
WA	341U	VAL	-	insertion	UNP Q2Y0H9
WA	341V	ASP	-	insertion	UNP Q2Y0H9
WA	342I	LEU	-	insertion	UNP Q2Y0H9
WA	342J	GLU	-	insertion	UNP Q2Y0H9
WA	342V	SER	-	insertion	UNP Q2Y0H9
WA	342W	ARG	-	insertion	UNP Q2Y0H9
XA	157	GLU	VAL	conflict	UNP Q2Y0H9
XA	158	PHE	-	insertion	UNP Q2Y0H9
XA	159	TYR	-	insertion	UNP Q2Y0H9
XA	160	GLN	-	insertion	UNP Q2Y0H9
XA	161	ALA	-	insertion	UNP Q2Y0H9
XA	162	GLY	-	insertion	UNP Q2Y0H9
XA	163	SER	-	insertion	UNP Q2Y0H9
XA	164	THR	-	insertion	UNP Q2Y0H9
XA	165	PRO	-	insertion	UNP Q2Y0H9
XA	166	CYS	-	insertion	UNP Q2Y0H9
XA	167	ASN	-	insertion	UNP Q2Y0H9
XA	168	GLY	-	insertion	UNP Q2Y0H9
XA	169	VAL	-	insertion	UNP Q2Y0H9
XA	170	GLU	-	insertion	UNP Q2Y0H9
XA	171	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
XA	172	PHE	-	insertion	UNP Q2Y0H9
XA	173	ASN	-	insertion	UNP Q2Y0H9
XA	174	CYS	-	insertion	UNP Q2Y0H9
XA	175	TYR	-	insertion	UNP Q2Y0H9
XA	176	PHE	-	insertion	UNP Q2Y0H9
XA	177	PRO	-	insertion	UNP Q2Y0H9
XA	178	LEU	-	insertion	UNP Q2Y0H9
XA	179	GLN	-	insertion	UNP Q2Y0H9
XA	180	SER	-	insertion	UNP Q2Y0H9
XA	181	TYR	-	insertion	UNP Q2Y0H9
XA	182	GLY	-	insertion	UNP Q2Y0H9
XA	183	PHE	-	insertion	UNP Q2Y0H9
XA	184	GLN	-	insertion	UNP Q2Y0H9
XA	185	PRO	-	insertion	UNP Q2Y0H9
XA	186	THR	-	insertion	UNP Q2Y0H9
XA	187	ASN	-	insertion	UNP Q2Y0H9
XA	188	GLY	-	insertion	UNP Q2Y0H9
XA	189	VAL	-	insertion	UNP Q2Y0H9
XA	190	GLY	-	insertion	UNP Q2Y0H9
XA	191	TYR	-	insertion	UNP Q2Y0H9
XA	192	GLY	-	insertion	UNP Q2Y0H9
XA	193	PRO	THR	conflict	UNP Q2Y0H9
XA	341E	ALA	-	insertion	UNP Q2Y0H9
XA	341F	ARG	-	insertion	UNP Q2Y0H9
XA	341U	VAL	-	insertion	UNP Q2Y0H9
XA	341V	ASP	-	insertion	UNP Q2Y0H9
XA	342I	LEU	-	insertion	UNP Q2Y0H9
XA	342J	GLU	-	insertion	UNP Q2Y0H9
XA	342V	SER	-	insertion	UNP Q2Y0H9
XA	342W	ARG	-	insertion	UNP Q2Y0H9
YA	157	GLU	VAL	conflict	UNP Q2Y0H9
YA	158	PHE	-	insertion	UNP Q2Y0H9
YA	159	TYR	-	insertion	UNP Q2Y0H9
YA	160	GLN	-	insertion	UNP Q2Y0H9
YA	161	ALA	-	insertion	UNP Q2Y0H9
YA	162	GLY	-	insertion	UNP Q2Y0H9
YA	163	SER	-	insertion	UNP Q2Y0H9
YA	164	THR	-	insertion	UNP Q2Y0H9
YA	165	PRO	-	insertion	UNP Q2Y0H9
YA	166	CYS	-	insertion	UNP Q2Y0H9
YA	167	ASN	-	insertion	UNP Q2Y0H9
YA	168	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
YA	169	VAL	-	insertion	UNP Q2Y0H9
YA	170	GLU	-	insertion	UNP Q2Y0H9
YA	171	GLY	-	insertion	UNP Q2Y0H9
YA	172	PHE	-	insertion	UNP Q2Y0H9
YA	173	ASN	-	insertion	UNP Q2Y0H9
YA	174	CYS	-	insertion	UNP Q2Y0H9
YA	175	TYR	-	insertion	UNP Q2Y0H9
YA	176	PHE	-	insertion	UNP Q2Y0H9
YA	177	PRO	-	insertion	UNP Q2Y0H9
YA	178	LEU	-	insertion	UNP Q2Y0H9
YA	179	GLN	-	insertion	UNP Q2Y0H9
YA	180	SER	-	insertion	UNP Q2Y0H9
YA	181	TYR	-	insertion	UNP Q2Y0H9
YA	182	GLY	-	insertion	UNP Q2Y0H9
YA	183	PHE	-	insertion	UNP Q2Y0H9
YA	184	GLN	-	insertion	UNP Q2Y0H9
YA	185	PRO	-	insertion	UNP Q2Y0H9
YA	186	THR	-	insertion	UNP Q2Y0H9
YA	187	ASN	-	insertion	UNP Q2Y0H9
YA	188	GLY	-	insertion	UNP Q2Y0H9
YA	189	VAL	-	insertion	UNP Q2Y0H9
YA	190	GLY	-	insertion	UNP Q2Y0H9
YA	191	TYR	-	insertion	UNP Q2Y0H9
YA	192	GLY	-	insertion	UNP Q2Y0H9
YA	193	PRO	THR	conflict	UNP Q2Y0H9
YA	341E	ALA	-	insertion	UNP Q2Y0H9
YA	341F	ARG	-	insertion	UNP Q2Y0H9
YA	341U	VAL	-	insertion	UNP Q2Y0H9
YA	341V	ASP	-	insertion	UNP Q2Y0H9
YA	342I	LEU	-	insertion	UNP Q2Y0H9
YA	342J	GLU	-	insertion	UNP Q2Y0H9
YA	342V	SER	-	insertion	UNP Q2Y0H9
YA	342W	ARG	-	insertion	UNP Q2Y0H9
ZA	157	GLU	VAL	conflict	UNP Q2Y0H9
ZA	158	PHE	-	insertion	UNP Q2Y0H9
ZA	159	TYR	-	insertion	UNP Q2Y0H9
ZA	160	GLN	-	insertion	UNP Q2Y0H9
ZA	161	ALA	-	insertion	UNP Q2Y0H9
ZA	162	GLY	-	insertion	UNP Q2Y0H9
ZA	163	SER	-	insertion	UNP Q2Y0H9
ZA	164	THR	-	insertion	UNP Q2Y0H9
ZA	165	PRO	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
ZA	166	CYS	-	insertion	UNP Q2Y0H9
ZA	167	ASN	-	insertion	UNP Q2Y0H9
ZA	168	GLY	-	insertion	UNP Q2Y0H9
ZA	169	VAL	-	insertion	UNP Q2Y0H9
ZA	170	GLU	-	insertion	UNP Q2Y0H9
ZA	171	GLY	-	insertion	UNP Q2Y0H9
ZA	172	PHE	-	insertion	UNP Q2Y0H9
ZA	173	ASN	-	insertion	UNP Q2Y0H9
ZA	174	CYS	-	insertion	UNP Q2Y0H9
ZA	175	TYR	-	insertion	UNP Q2Y0H9
ZA	176	PHE	-	insertion	UNP Q2Y0H9
ZA	177	PRO	-	insertion	UNP Q2Y0H9
ZA	178	LEU	-	insertion	UNP Q2Y0H9
ZA	179	GLN	-	insertion	UNP Q2Y0H9
ZA	180	SER	-	insertion	UNP Q2Y0H9
ZA	181	TYR	-	insertion	UNP Q2Y0H9
ZA	182	GLY	-	insertion	UNP Q2Y0H9
ZA	183	PHE	-	insertion	UNP Q2Y0H9
ZA	184	GLN	-	insertion	UNP Q2Y0H9
ZA	185	PRO	-	insertion	UNP Q2Y0H9
ZA	186	THR	-	insertion	UNP Q2Y0H9
ZA	187	ASN	-	insertion	UNP Q2Y0H9
ZA	188	GLY	-	insertion	UNP Q2Y0H9
ZA	189	VAL	-	insertion	UNP Q2Y0H9
ZA	190	GLY	-	insertion	UNP Q2Y0H9
ZA	191	TYR	-	insertion	UNP Q2Y0H9
ZA	192	GLY	-	insertion	UNP Q2Y0H9
ZA	193	PRO	THR	conflict	UNP Q2Y0H9
ZA	341E	ALA	-	insertion	UNP Q2Y0H9
ZA	341F	ARG	-	insertion	UNP Q2Y0H9
ZA	341U	VAL	-	insertion	UNP Q2Y0H9
ZA	341V	ASP	-	insertion	UNP Q2Y0H9
ZA	342I	LEU	-	insertion	UNP Q2Y0H9
ZA	342J	GLU	-	insertion	UNP Q2Y0H9
ZA	342V	SER	-	insertion	UNP Q2Y0H9
ZA	342W	ARG	-	insertion	UNP Q2Y0H9
AB	157	GLU	VAL	conflict	UNP Q2Y0H9
AB	158	PHE	-	insertion	UNP Q2Y0H9
AB	159	TYR	-	insertion	UNP Q2Y0H9
AB	160	GLN	-	insertion	UNP Q2Y0H9
AB	161	ALA	-	insertion	UNP Q2Y0H9
AB	162	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
AB	163	SER	-	insertion	UNP Q2Y0H9
AB	164	THR	-	insertion	UNP Q2Y0H9
AB	165	PRO	-	insertion	UNP Q2Y0H9
AB	166	CYS	-	insertion	UNP Q2Y0H9
AB	167	ASN	-	insertion	UNP Q2Y0H9
AB	168	GLY	-	insertion	UNP Q2Y0H9
AB	169	VAL	-	insertion	UNP Q2Y0H9
AB	170	GLU	-	insertion	UNP Q2Y0H9
AB	171	GLY	-	insertion	UNP Q2Y0H9
AB	172	PHE	-	insertion	UNP Q2Y0H9
AB	173	ASN	-	insertion	UNP Q2Y0H9
AB	174	CYS	-	insertion	UNP Q2Y0H9
AB	175	TYR	-	insertion	UNP Q2Y0H9
AB	176	PHE	-	insertion	UNP Q2Y0H9
AB	177	PRO	-	insertion	UNP Q2Y0H9
AB	178	LEU	-	insertion	UNP Q2Y0H9
AB	179	GLN	-	insertion	UNP Q2Y0H9
AB	180	SER	-	insertion	UNP Q2Y0H9
AB	181	TYR	-	insertion	UNP Q2Y0H9
AB	182	GLY	-	insertion	UNP Q2Y0H9
AB	183	PHE	-	insertion	UNP Q2Y0H9
AB	184	GLN	-	insertion	UNP Q2Y0H9
AB	185	PRO	-	insertion	UNP Q2Y0H9
AB	186	THR	-	insertion	UNP Q2Y0H9
AB	187	ASN	-	insertion	UNP Q2Y0H9
AB	188	GLY	-	insertion	UNP Q2Y0H9
AB	189	VAL	-	insertion	UNP Q2Y0H9
AB	190	GLY	-	insertion	UNP Q2Y0H9
AB	191	TYR	-	insertion	UNP Q2Y0H9
AB	192	GLY	-	insertion	UNP Q2Y0H9
AB	193	PRO	THR	conflict	UNP Q2Y0H9
AB	341E	ALA	-	insertion	UNP Q2Y0H9
AB	341F	ARG	-	insertion	UNP Q2Y0H9
AB	341U	VAL	-	insertion	UNP Q2Y0H9
AB	341V	ASP	-	insertion	UNP Q2Y0H9
AB	342I	LEU	-	insertion	UNP Q2Y0H9
AB	342J	GLU	-	insertion	UNP Q2Y0H9
AB	342V	SER	-	insertion	UNP Q2Y0H9
AB	342W	ARG	-	insertion	UNP Q2Y0H9
BB	157	GLU	VAL	conflict	UNP Q2Y0H9
BB	158	PHE	-	insertion	UNP Q2Y0H9
BB	159	TYR	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
BB	160	GLN	-	insertion	UNP Q2Y0H9
BB	161	ALA	-	insertion	UNP Q2Y0H9
BB	162	GLY	-	insertion	UNP Q2Y0H9
BB	163	SER	-	insertion	UNP Q2Y0H9
BB	164	THR	-	insertion	UNP Q2Y0H9
BB	165	PRO	-	insertion	UNP Q2Y0H9
BB	166	CYS	-	insertion	UNP Q2Y0H9
BB	167	ASN	-	insertion	UNP Q2Y0H9
BB	168	GLY	-	insertion	UNP Q2Y0H9
BB	169	VAL	-	insertion	UNP Q2Y0H9
BB	170	GLU	-	insertion	UNP Q2Y0H9
BB	171	GLY	-	insertion	UNP Q2Y0H9
BB	172	PHE	-	insertion	UNP Q2Y0H9
BB	173	ASN	-	insertion	UNP Q2Y0H9
BB	174	CYS	-	insertion	UNP Q2Y0H9
BB	175	TYR	-	insertion	UNP Q2Y0H9
BB	176	PHE	-	insertion	UNP Q2Y0H9
BB	177	PRO	-	insertion	UNP Q2Y0H9
BB	178	LEU	-	insertion	UNP Q2Y0H9
BB	179	GLN	-	insertion	UNP Q2Y0H9
BB	180	SER	-	insertion	UNP Q2Y0H9
BB	181	TYR	-	insertion	UNP Q2Y0H9
BB	182	GLY	-	insertion	UNP Q2Y0H9
BB	183	PHE	-	insertion	UNP Q2Y0H9
BB	184	GLN	-	insertion	UNP Q2Y0H9
BB	185	PRO	-	insertion	UNP Q2Y0H9
BB	186	THR	-	insertion	UNP Q2Y0H9
BB	187	ASN	-	insertion	UNP Q2Y0H9
BB	188	GLY	-	insertion	UNP Q2Y0H9
BB	189	VAL	-	insertion	UNP Q2Y0H9
BB	190	GLY	-	insertion	UNP Q2Y0H9
BB	191	TYR	-	insertion	UNP Q2Y0H9
BB	192	GLY	-	insertion	UNP Q2Y0H9
BB	193	PRO	THR	conflict	UNP Q2Y0H9
BB	341E	ALA	-	insertion	UNP Q2Y0H9
BB	341F	ARG	-	insertion	UNP Q2Y0H9
BB	341U	VAL	-	insertion	UNP Q2Y0H9
BB	341V	ASP	-	insertion	UNP Q2Y0H9
BB	342I	LEU	-	insertion	UNP Q2Y0H9
BB	342J	GLU	-	insertion	UNP Q2Y0H9
BB	342V	SER	-	insertion	UNP Q2Y0H9
BB	342W	ARG	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
CB	157	GLU	VAL	conflict	UNP Q2Y0H9
CB	158	PHE	-	insertion	UNP Q2Y0H9
CB	159	TYR	-	insertion	UNP Q2Y0H9
CB	160	GLN	-	insertion	UNP Q2Y0H9
CB	161	ALA	-	insertion	UNP Q2Y0H9
CB	162	GLY	-	insertion	UNP Q2Y0H9
CB	163	SER	-	insertion	UNP Q2Y0H9
CB	164	THR	-	insertion	UNP Q2Y0H9
CB	165	PRO	-	insertion	UNP Q2Y0H9
CB	166	CYS	-	insertion	UNP Q2Y0H9
CB	167	ASN	-	insertion	UNP Q2Y0H9
CB	168	GLY	-	insertion	UNP Q2Y0H9
CB	169	VAL	-	insertion	UNP Q2Y0H9
CB	170	GLU	-	insertion	UNP Q2Y0H9
CB	171	GLY	-	insertion	UNP Q2Y0H9
CB	172	PHE	-	insertion	UNP Q2Y0H9
CB	173	ASN	-	insertion	UNP Q2Y0H9
CB	174	CYS	-	insertion	UNP Q2Y0H9
CB	175	TYR	-	insertion	UNP Q2Y0H9
CB	176	PHE	-	insertion	UNP Q2Y0H9
CB	177	PRO	-	insertion	UNP Q2Y0H9
CB	178	LEU	-	insertion	UNP Q2Y0H9
CB	179	GLN	-	insertion	UNP Q2Y0H9
CB	180	SER	-	insertion	UNP Q2Y0H9
CB	181	TYR	-	insertion	UNP Q2Y0H9
CB	182	GLY	-	insertion	UNP Q2Y0H9
CB	183	PHE	-	insertion	UNP Q2Y0H9
CB	184	GLN	-	insertion	UNP Q2Y0H9
CB	185	PRO	-	insertion	UNP Q2Y0H9
CB	186	THR	-	insertion	UNP Q2Y0H9
CB	187	ASN	-	insertion	UNP Q2Y0H9
CB	188	GLY	-	insertion	UNP Q2Y0H9
CB	189	VAL	-	insertion	UNP Q2Y0H9
CB	190	GLY	-	insertion	UNP Q2Y0H9
CB	191	TYR	-	insertion	UNP Q2Y0H9
CB	192	GLY	-	insertion	UNP Q2Y0H9
CB	193	PRO	THR	conflict	UNP Q2Y0H9
CB	341E	ALA	-	insertion	UNP Q2Y0H9
CB	341F	ARG	-	insertion	UNP Q2Y0H9
CB	341U	VAL	-	insertion	UNP Q2Y0H9
CB	341V	ASP	-	insertion	UNP Q2Y0H9
CB	342I	LEU	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
CB	342J	GLU	-	insertion	UNP Q2Y0H9
CB	342V	SER	-	insertion	UNP Q2Y0H9
CB	342W	ARG	-	insertion	UNP Q2Y0H9
DB	157	GLU	VAL	conflict	UNP Q2Y0H9
DB	158	PHE	-	insertion	UNP Q2Y0H9
DB	159	TYR	-	insertion	UNP Q2Y0H9
DB	160	GLN	-	insertion	UNP Q2Y0H9
DB	161	ALA	-	insertion	UNP Q2Y0H9
DB	162	GLY	-	insertion	UNP Q2Y0H9
DB	163	SER	-	insertion	UNP Q2Y0H9
DB	164	THR	-	insertion	UNP Q2Y0H9
DB	165	PRO	-	insertion	UNP Q2Y0H9
DB	166	CYS	-	insertion	UNP Q2Y0H9
DB	167	ASN	-	insertion	UNP Q2Y0H9
DB	168	GLY	-	insertion	UNP Q2Y0H9
DB	169	VAL	-	insertion	UNP Q2Y0H9
DB	170	GLU	-	insertion	UNP Q2Y0H9
DB	171	GLY	-	insertion	UNP Q2Y0H9
DB	172	PHE	-	insertion	UNP Q2Y0H9
DB	173	ASN	-	insertion	UNP Q2Y0H9
DB	174	CYS	-	insertion	UNP Q2Y0H9
DB	175	TYR	-	insertion	UNP Q2Y0H9
DB	176	PHE	-	insertion	UNP Q2Y0H9
DB	177	PRO	-	insertion	UNP Q2Y0H9
DB	178	LEU	-	insertion	UNP Q2Y0H9
DB	179	GLN	-	insertion	UNP Q2Y0H9
DB	180	SER	-	insertion	UNP Q2Y0H9
DB	181	TYR	-	insertion	UNP Q2Y0H9
DB	182	GLY	-	insertion	UNP Q2Y0H9
DB	183	PHE	-	insertion	UNP Q2Y0H9
DB	184	GLN	-	insertion	UNP Q2Y0H9
DB	185	PRO	-	insertion	UNP Q2Y0H9
DB	186	THR	-	insertion	UNP Q2Y0H9
DB	187	ASN	-	insertion	UNP Q2Y0H9
DB	188	GLY	-	insertion	UNP Q2Y0H9
DB	189	VAL	-	insertion	UNP Q2Y0H9
DB	190	GLY	-	insertion	UNP Q2Y0H9
DB	191	TYR	-	insertion	UNP Q2Y0H9
DB	192	GLY	-	insertion	UNP Q2Y0H9
DB	193	PRO	THR	conflict	UNP Q2Y0H9
DB	341E	ALA	-	insertion	UNP Q2Y0H9
DB	341F	ARG	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
DB	341U	VAL	-	insertion	UNP Q2Y0H9
DB	341V	ASP	-	insertion	UNP Q2Y0H9
DB	342I	LEU	-	insertion	UNP Q2Y0H9
DB	342J	GLU	-	insertion	UNP Q2Y0H9
DB	342V	SER	-	insertion	UNP Q2Y0H9
DB	342W	ARG	-	insertion	UNP Q2Y0H9
EB	157	GLU	VAL	conflict	UNP Q2Y0H9
EB	158	PHE	-	insertion	UNP Q2Y0H9
EB	159	TYR	-	insertion	UNP Q2Y0H9
EB	160	GLN	-	insertion	UNP Q2Y0H9
EB	161	ALA	-	insertion	UNP Q2Y0H9
EB	162	GLY	-	insertion	UNP Q2Y0H9
EB	163	SER	-	insertion	UNP Q2Y0H9
EB	164	THR	-	insertion	UNP Q2Y0H9
EB	165	PRO	-	insertion	UNP Q2Y0H9
EB	166	CYS	-	insertion	UNP Q2Y0H9
EB	167	ASN	-	insertion	UNP Q2Y0H9
EB	168	GLY	-	insertion	UNP Q2Y0H9
EB	169	VAL	-	insertion	UNP Q2Y0H9
EB	170	GLU	-	insertion	UNP Q2Y0H9
EB	171	GLY	-	insertion	UNP Q2Y0H9
EB	172	PHE	-	insertion	UNP Q2Y0H9
EB	173	ASN	-	insertion	UNP Q2Y0H9
EB	174	CYS	-	insertion	UNP Q2Y0H9
EB	175	TYR	-	insertion	UNP Q2Y0H9
EB	176	PHE	-	insertion	UNP Q2Y0H9
EB	177	PRO	-	insertion	UNP Q2Y0H9
EB	178	LEU	-	insertion	UNP Q2Y0H9
EB	179	GLN	-	insertion	UNP Q2Y0H9
EB	180	SER	-	insertion	UNP Q2Y0H9
EB	181	TYR	-	insertion	UNP Q2Y0H9
EB	182	GLY	-	insertion	UNP Q2Y0H9
EB	183	PHE	-	insertion	UNP Q2Y0H9
EB	184	GLN	-	insertion	UNP Q2Y0H9
EB	185	PRO	-	insertion	UNP Q2Y0H9
EB	186	THR	-	insertion	UNP Q2Y0H9
EB	187	ASN	-	insertion	UNP Q2Y0H9
EB	188	GLY	-	insertion	UNP Q2Y0H9
EB	189	VAL	-	insertion	UNP Q2Y0H9
EB	190	GLY	-	insertion	UNP Q2Y0H9
EB	191	TYR	-	insertion	UNP Q2Y0H9
EB	192	GLY	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
EB	193	PRO	THR	conflict	UNP Q2Y0H9
EB	341E	ALA	-	insertion	UNP Q2Y0H9
EB	341F	ARG	-	insertion	UNP Q2Y0H9
EB	341U	VAL	-	insertion	UNP Q2Y0H9
EB	341V	ASP	-	insertion	UNP Q2Y0H9
EB	342I	LEU	-	insertion	UNP Q2Y0H9
EB	342J	GLU	-	insertion	UNP Q2Y0H9
EB	342V	SER	-	insertion	UNP Q2Y0H9
EB	342W	ARG	-	insertion	UNP Q2Y0H9
FB	157	GLU	VAL	conflict	UNP Q2Y0H9
FB	158	PHE	-	insertion	UNP Q2Y0H9
FB	159	TYR	-	insertion	UNP Q2Y0H9
FB	160	GLN	-	insertion	UNP Q2Y0H9
FB	161	ALA	-	insertion	UNP Q2Y0H9
FB	162	GLY	-	insertion	UNP Q2Y0H9
FB	163	SER	-	insertion	UNP Q2Y0H9
FB	164	THR	-	insertion	UNP Q2Y0H9
FB	165	PRO	-	insertion	UNP Q2Y0H9
FB	166	CYS	-	insertion	UNP Q2Y0H9
FB	167	ASN	-	insertion	UNP Q2Y0H9
FB	168	GLY	-	insertion	UNP Q2Y0H9
FB	169	VAL	-	insertion	UNP Q2Y0H9
FB	170	GLU	-	insertion	UNP Q2Y0H9
FB	171	GLY	-	insertion	UNP Q2Y0H9
FB	172	PHE	-	insertion	UNP Q2Y0H9
FB	173	ASN	-	insertion	UNP Q2Y0H9
FB	174	CYS	-	insertion	UNP Q2Y0H9
FB	175	TYR	-	insertion	UNP Q2Y0H9
FB	176	PHE	-	insertion	UNP Q2Y0H9
FB	177	PRO	-	insertion	UNP Q2Y0H9
FB	178	LEU	-	insertion	UNP Q2Y0H9
FB	179	GLN	-	insertion	UNP Q2Y0H9
FB	180	SER	-	insertion	UNP Q2Y0H9
FB	181	TYR	-	insertion	UNP Q2Y0H9
FB	182	GLY	-	insertion	UNP Q2Y0H9
FB	183	PHE	-	insertion	UNP Q2Y0H9
FB	184	GLN	-	insertion	UNP Q2Y0H9
FB	185	PRO	-	insertion	UNP Q2Y0H9
FB	186	THR	-	insertion	UNP Q2Y0H9
FB	187	ASN	-	insertion	UNP Q2Y0H9
FB	188	GLY	-	insertion	UNP Q2Y0H9
FB	189	VAL	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
FB	190	GLY	-	insertion	UNP Q2Y0H9
FB	191	TYR	-	insertion	UNP Q2Y0H9
FB	192	GLY	-	insertion	UNP Q2Y0H9
FB	193	PRO	THR	conflict	UNP Q2Y0H9
FB	341E	ALA	-	insertion	UNP Q2Y0H9
FB	341F	ARG	-	insertion	UNP Q2Y0H9
FB	341U	VAL	-	insertion	UNP Q2Y0H9
FB	341V	ASP	-	insertion	UNP Q2Y0H9
FB	342I	LEU	-	insertion	UNP Q2Y0H9
FB	342J	GLU	-	insertion	UNP Q2Y0H9
FB	342V	SER	-	insertion	UNP Q2Y0H9
FB	342W	ARG	-	insertion	UNP Q2Y0H9
GB	157	GLU	VAL	conflict	UNP Q2Y0H9
GB	158	PHE	-	insertion	UNP Q2Y0H9
GB	159	TYR	-	insertion	UNP Q2Y0H9
GB	160	GLN	-	insertion	UNP Q2Y0H9
GB	161	ALA	-	insertion	UNP Q2Y0H9
GB	162	GLY	-	insertion	UNP Q2Y0H9
GB	163	SER	-	insertion	UNP Q2Y0H9
GB	164	THR	-	insertion	UNP Q2Y0H9
GB	165	PRO	-	insertion	UNP Q2Y0H9
GB	166	CYS	-	insertion	UNP Q2Y0H9
GB	167	ASN	-	insertion	UNP Q2Y0H9
GB	168	GLY	-	insertion	UNP Q2Y0H9
GB	169	VAL	-	insertion	UNP Q2Y0H9
GB	170	GLU	-	insertion	UNP Q2Y0H9
GB	171	GLY	-	insertion	UNP Q2Y0H9
GB	172	PHE	-	insertion	UNP Q2Y0H9
GB	173	ASN	-	insertion	UNP Q2Y0H9
GB	174	CYS	-	insertion	UNP Q2Y0H9
GB	175	TYR	-	insertion	UNP Q2Y0H9
GB	176	PHE	-	insertion	UNP Q2Y0H9
GB	177	PRO	-	insertion	UNP Q2Y0H9
GB	178	LEU	-	insertion	UNP Q2Y0H9
GB	179	GLN	-	insertion	UNP Q2Y0H9
GB	180	SER	-	insertion	UNP Q2Y0H9
GB	181	TYR	-	insertion	UNP Q2Y0H9
GB	182	GLY	-	insertion	UNP Q2Y0H9
GB	183	PHE	-	insertion	UNP Q2Y0H9
GB	184	GLN	-	insertion	UNP Q2Y0H9
GB	185	PRO	-	insertion	UNP Q2Y0H9
GB	186	THR	-	insertion	UNP Q2Y0H9

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Chain	Residue	Modelled	Actual	Comment	Reference
GB	187	ASN	-	insertion	UNP Q2Y0H9
GB	188	GLY	-	insertion	UNP Q2Y0H9
GB	189	VAL	-	insertion	UNP Q2Y0H9
GB	190	GLY	-	insertion	UNP Q2Y0H9
GB	191	TYR	-	insertion	UNP Q2Y0H9
GB	192	GLY	-	insertion	UNP Q2Y0H9
GB	193	PRO	THR	conflict	UNP Q2Y0H9
GB	341E	ALA	-	insertion	UNP Q2Y0H9
GB	341F	ARG	-	insertion	UNP Q2Y0H9
GB	341U	VAL	-	insertion	UNP Q2Y0H9
GB	341V	ASP	-	insertion	UNP Q2Y0H9
GB	342I	LEU	-	insertion	UNP Q2Y0H9
GB	342J	GLU	-	insertion	UNP Q2Y0H9
GB	342V	SER	-	insertion	UNP Q2Y0H9
GB	342W	ARG	-	insertion	UNP Q2Y0H9
HB	157	GLU	VAL	conflict	UNP Q2Y0H9
HB	158	PHE	-	insertion	UNP Q2Y0H9
HB	159	TYR	-	insertion	UNP Q2Y0H9
HB	160	GLN	-	insertion	UNP Q2Y0H9
HB	161	ALA	-	insertion	UNP Q2Y0H9
HB	162	GLY	-	insertion	UNP Q2Y0H9
HB	163	SER	-	insertion	UNP Q2Y0H9
HB	164	THR	-	insertion	UNP Q2Y0H9
HB	165	PRO	-	insertion	UNP Q2Y0H9
HB	166	CYS	-	insertion	UNP Q2Y0H9
HB	167	ASN	-	insertion	UNP Q2Y0H9
HB	168	GLY	-	insertion	UNP Q2Y0H9
HB	169	VAL	-	insertion	UNP Q2Y0H9
HB	170	GLU	-	insertion	UNP Q2Y0H9
HB	171	GLY	-	insertion	UNP Q2Y0H9
HB	172	PHE	-	insertion	UNP Q2Y0H9
HB	173	ASN	-	insertion	UNP Q2Y0H9
HB	174	CYS	-	insertion	UNP Q2Y0H9
HB	175	TYR	-	insertion	UNP Q2Y0H9
HB	176	PHE	-	insertion	UNP Q2Y0H9
HB	177	PRO	-	insertion	UNP Q2Y0H9
HB	178	LEU	-	insertion	UNP Q2Y0H9
HB	179	GLN	-	insertion	UNP Q2Y0H9
HB	180	SER	-	insertion	UNP Q2Y0H9
HB	181	TYR	-	insertion	UNP Q2Y0H9
HB	182	GLY	-	insertion	UNP Q2Y0H9
HB	183	PHE	-	insertion	UNP Q2Y0H9

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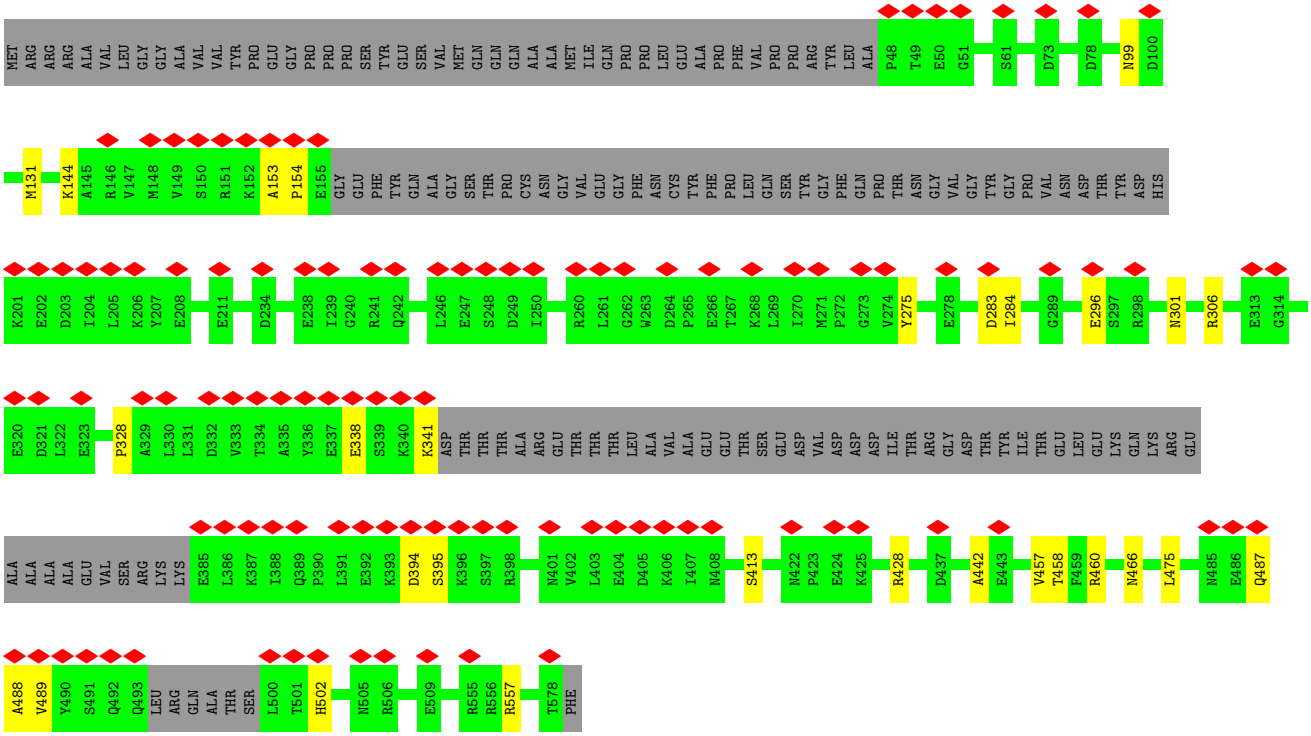
Chain	Residue	Modelled	Actual	Comment	Reference
HB	184	GLN	-	insertion	UNP Q2Y0H9
HB	185	PRO	-	insertion	UNP Q2Y0H9
HB	186	THR	-	insertion	UNP Q2Y0H9
HB	187	ASN	-	insertion	UNP Q2Y0H9
HB	188	GLY	-	insertion	UNP Q2Y0H9
HB	189	VAL	-	insertion	UNP Q2Y0H9
HB	190	GLY	-	insertion	UNP Q2Y0H9
HB	191	TYR	-	insertion	UNP Q2Y0H9
HB	192	GLY	-	insertion	UNP Q2Y0H9
HB	193	PRO	THR	conflict	UNP Q2Y0H9
HB	341E	ALA	-	insertion	UNP Q2Y0H9
HB	341F	ARG	-	insertion	UNP Q2Y0H9
HB	341U	VAL	-	insertion	UNP Q2Y0H9
HB	341V	ASP	-	insertion	UNP Q2Y0H9
HB	342I	LEU	-	insertion	UNP Q2Y0H9
HB	342J	GLU	-	insertion	UNP Q2Y0H9
HB	342V	SER	-	insertion	UNP Q2Y0H9
HB	342W	ARG	-	insertion	UNP Q2Y0H9

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

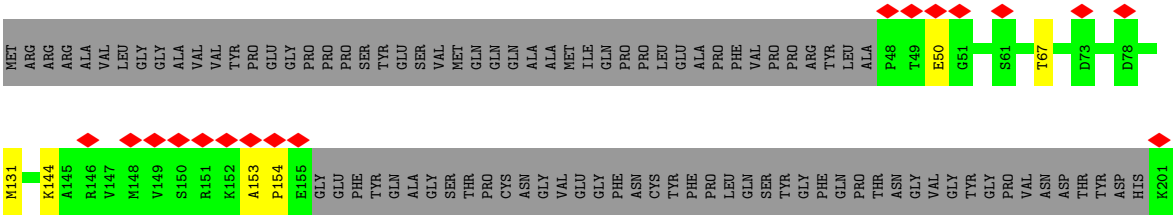
• Molecule 1: Penton protein

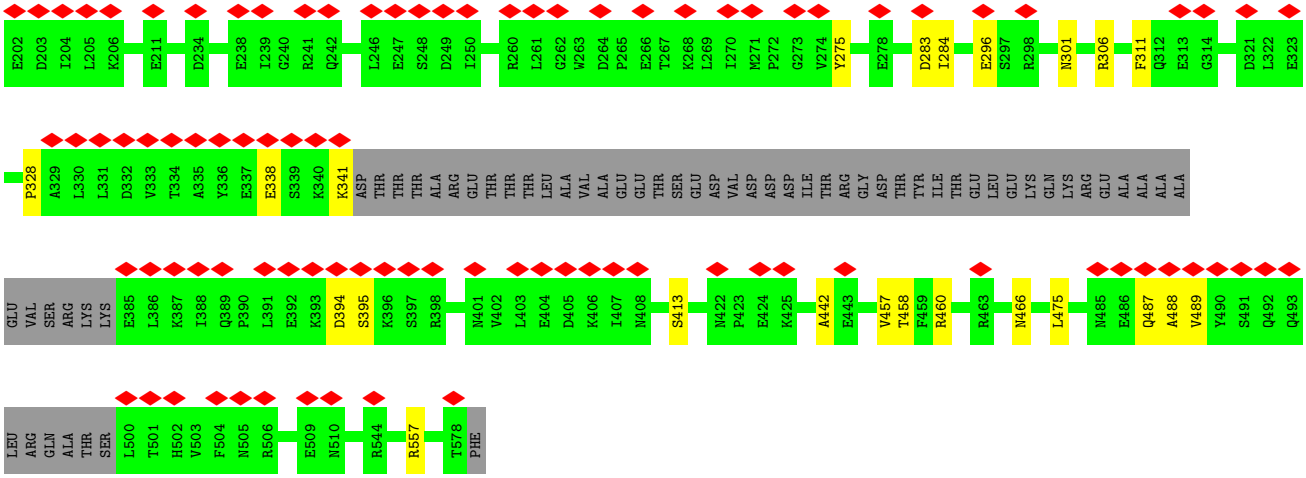
Chain 1:



• Molecule 1: Penton protein

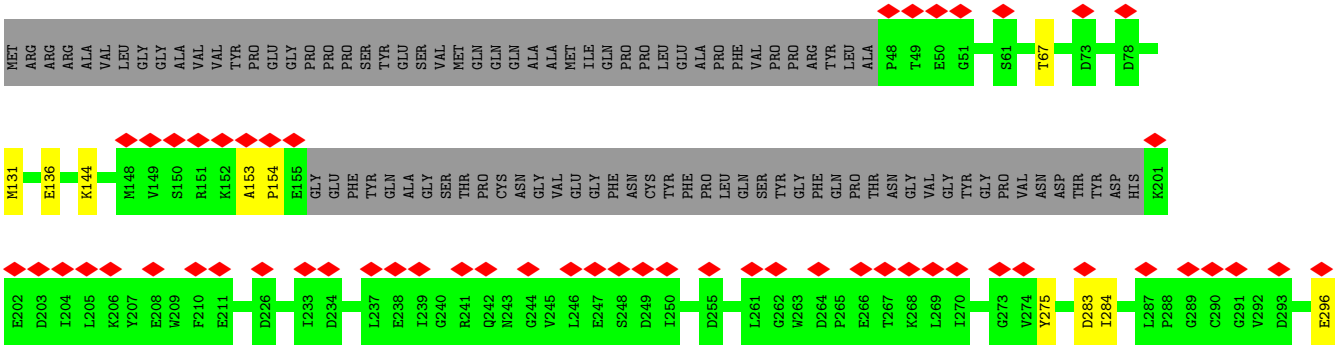
Chain A:





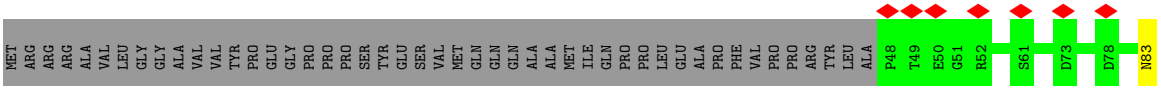
• Molecule 1: Penton protein

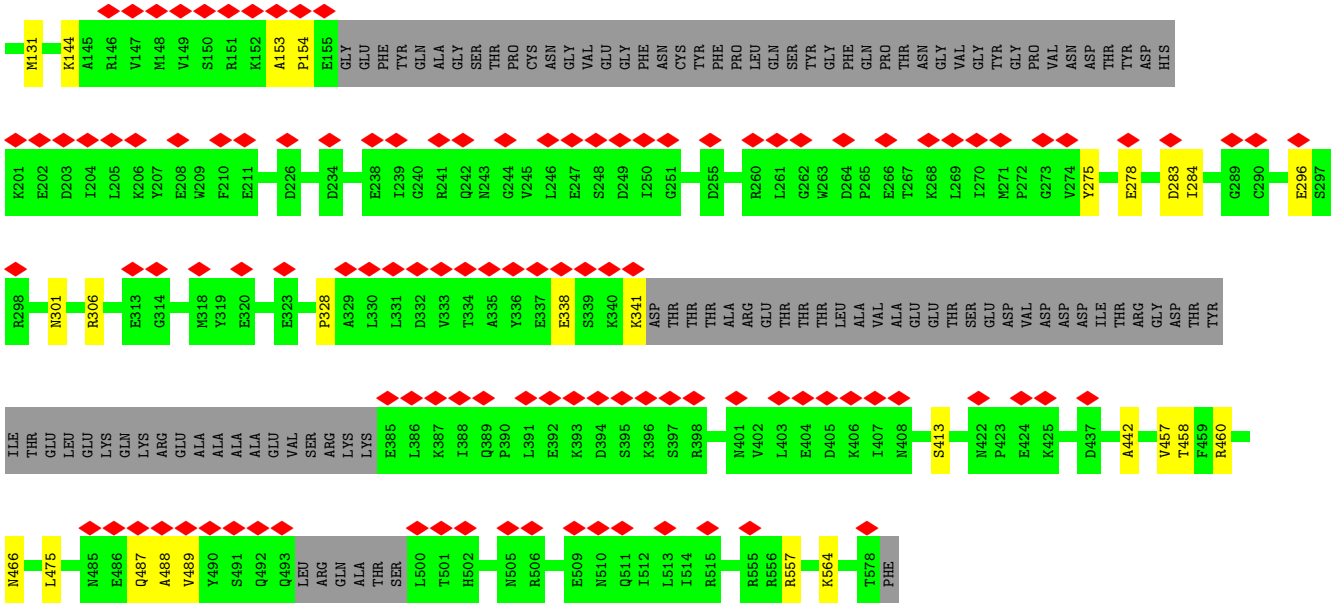
Chain B:



• Molecule 1: Penton protein

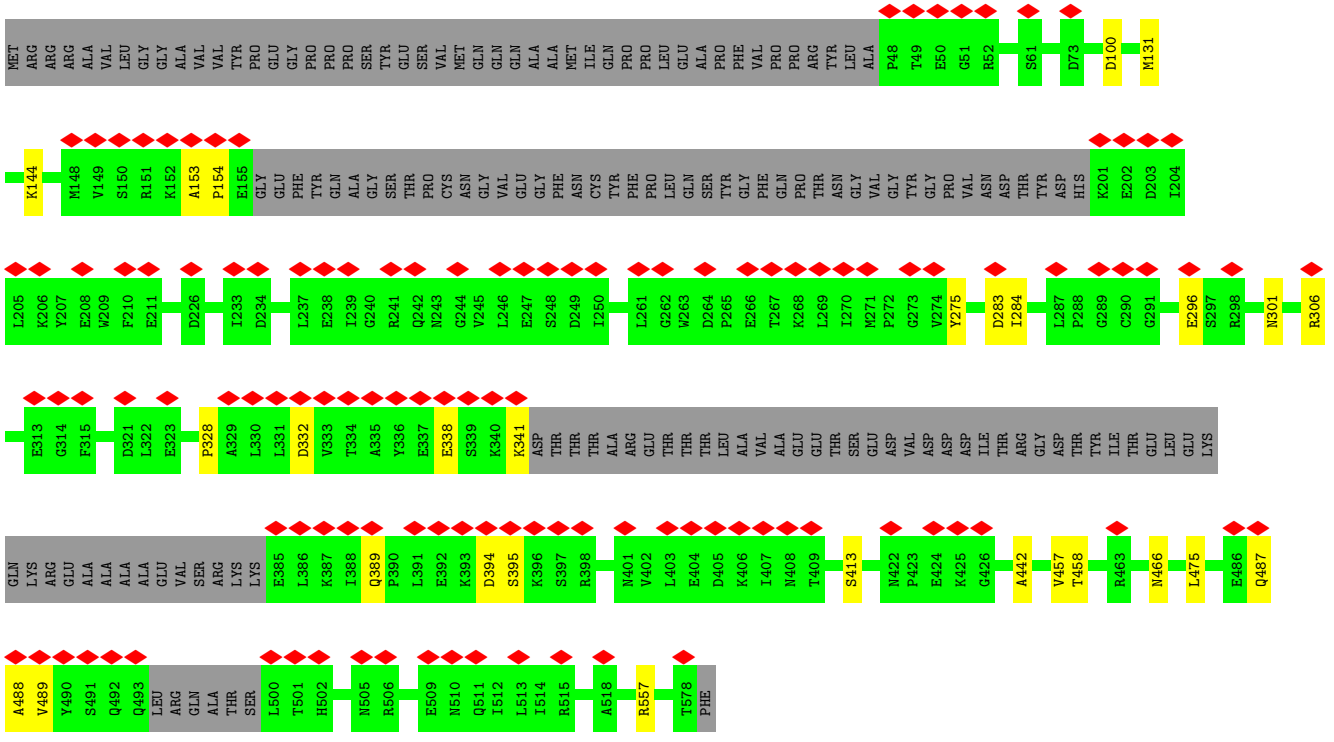
Chain C:





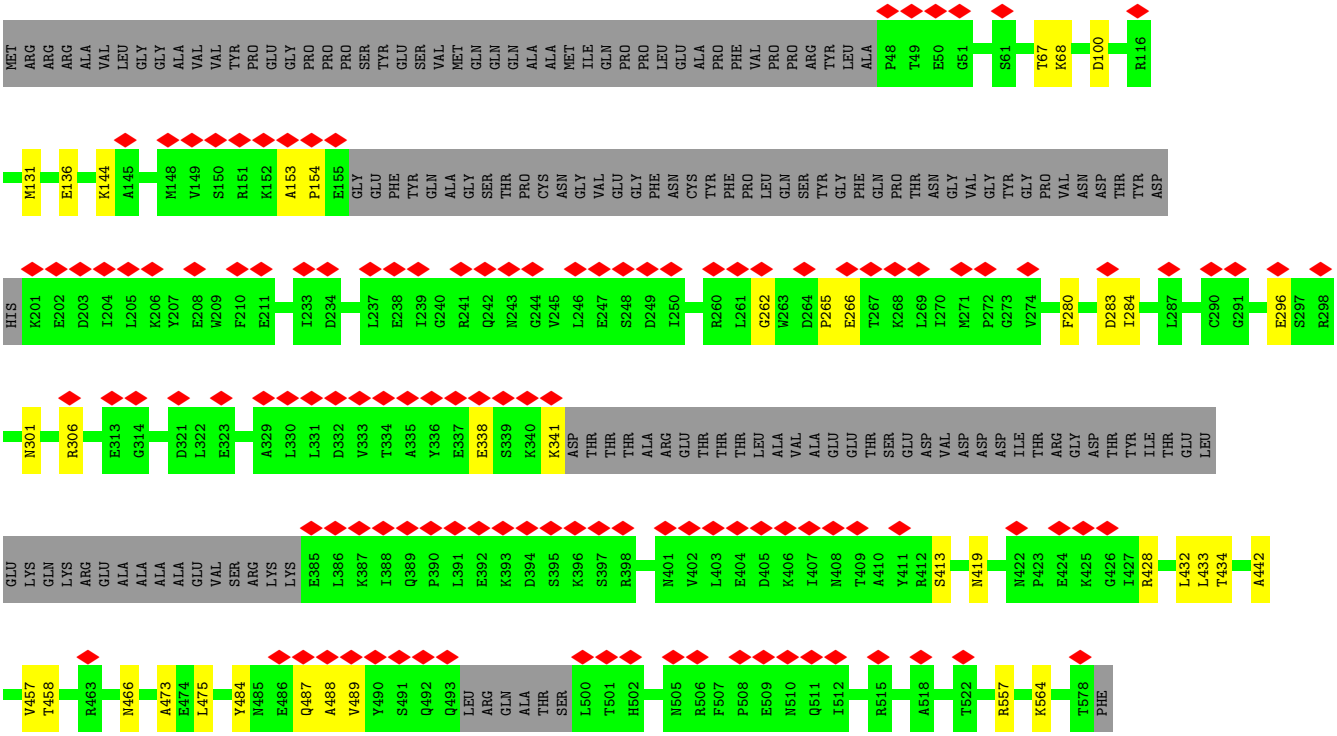
• Molecule 1: Penton protein

Chain D:



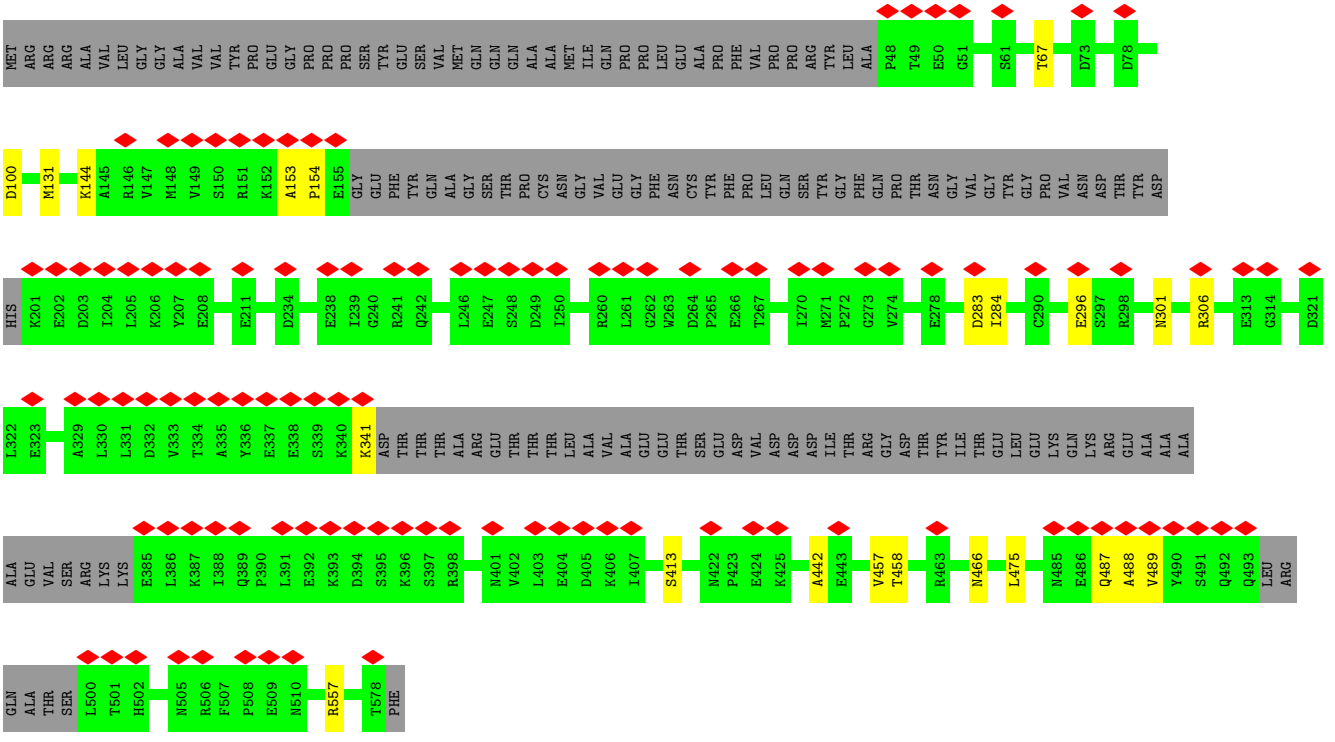
• Molecule 1: Penton protein

Chain E:



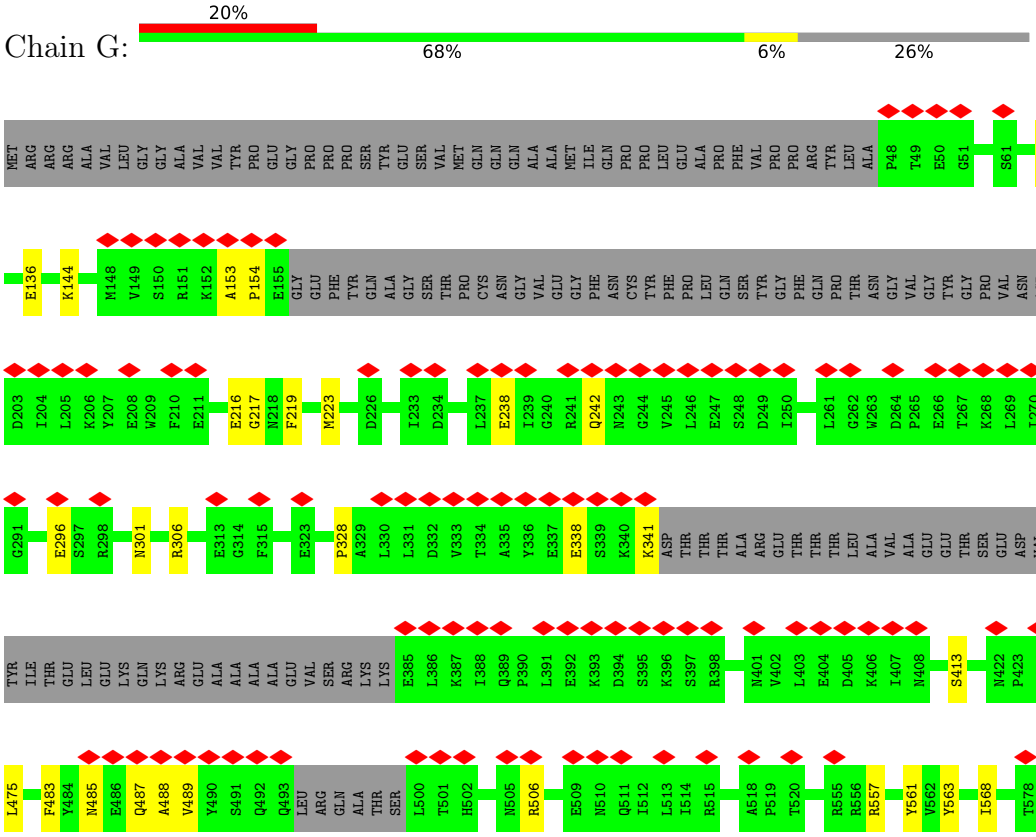
• Molecule 1: Penton protein

Chain F:



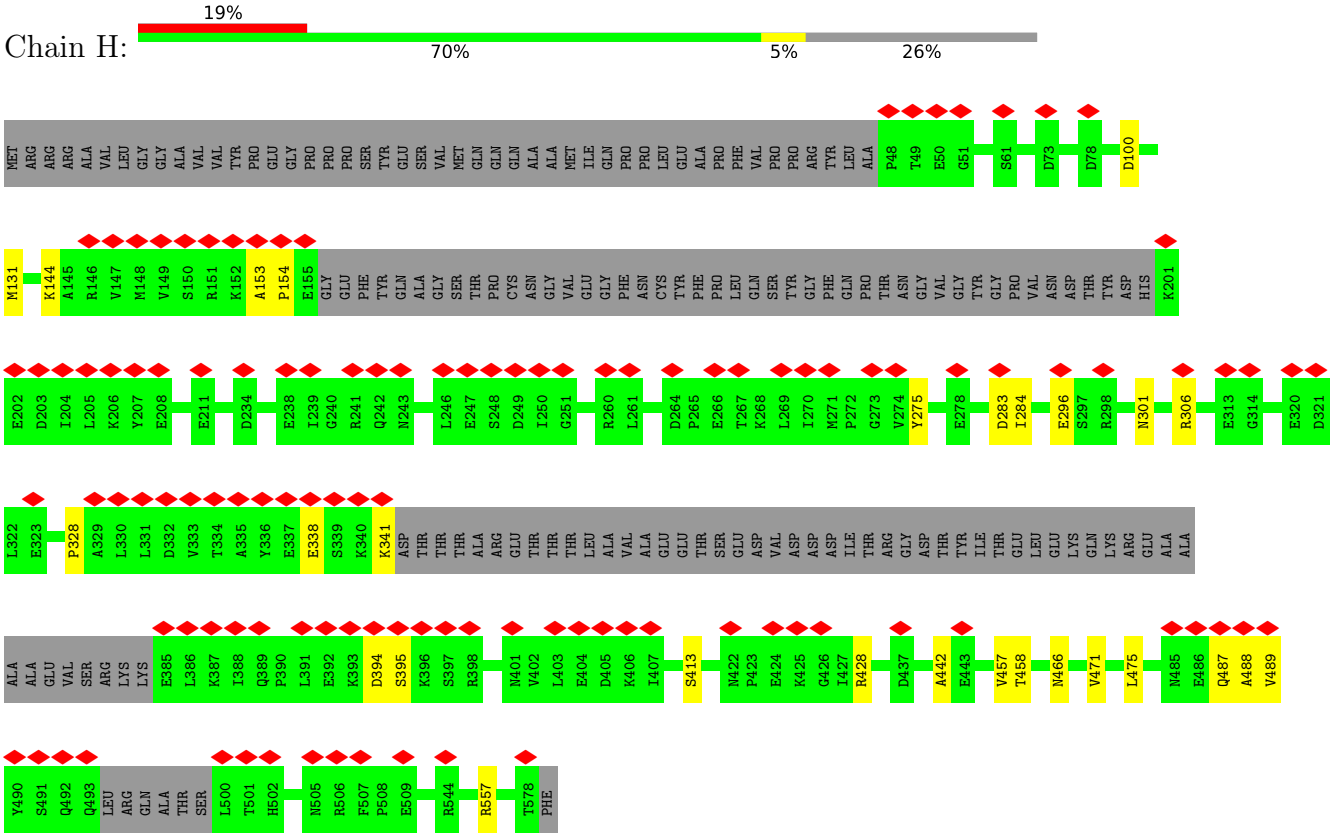
• Molecule 1: Penton protein

Chain G:



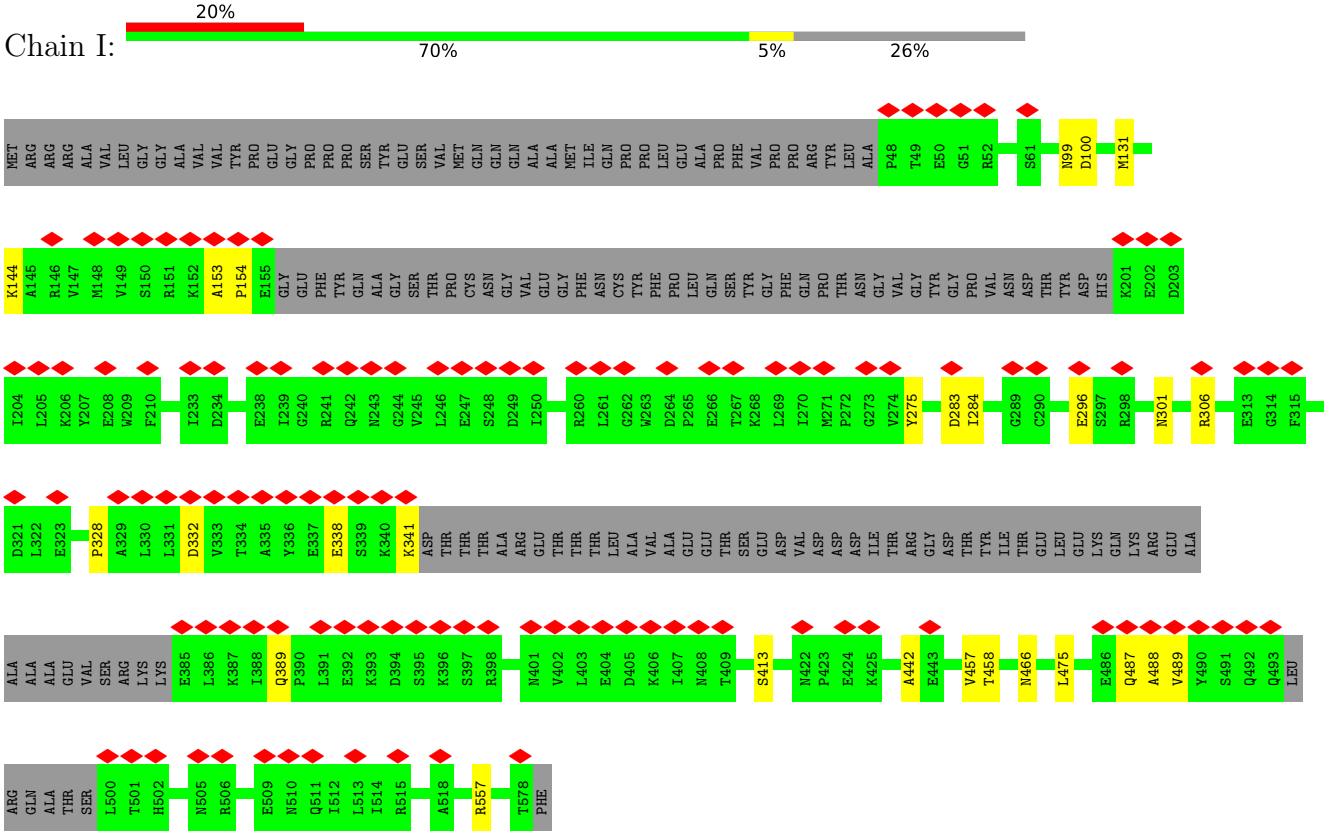
• Molecule 1: Penton protein

Chain H:



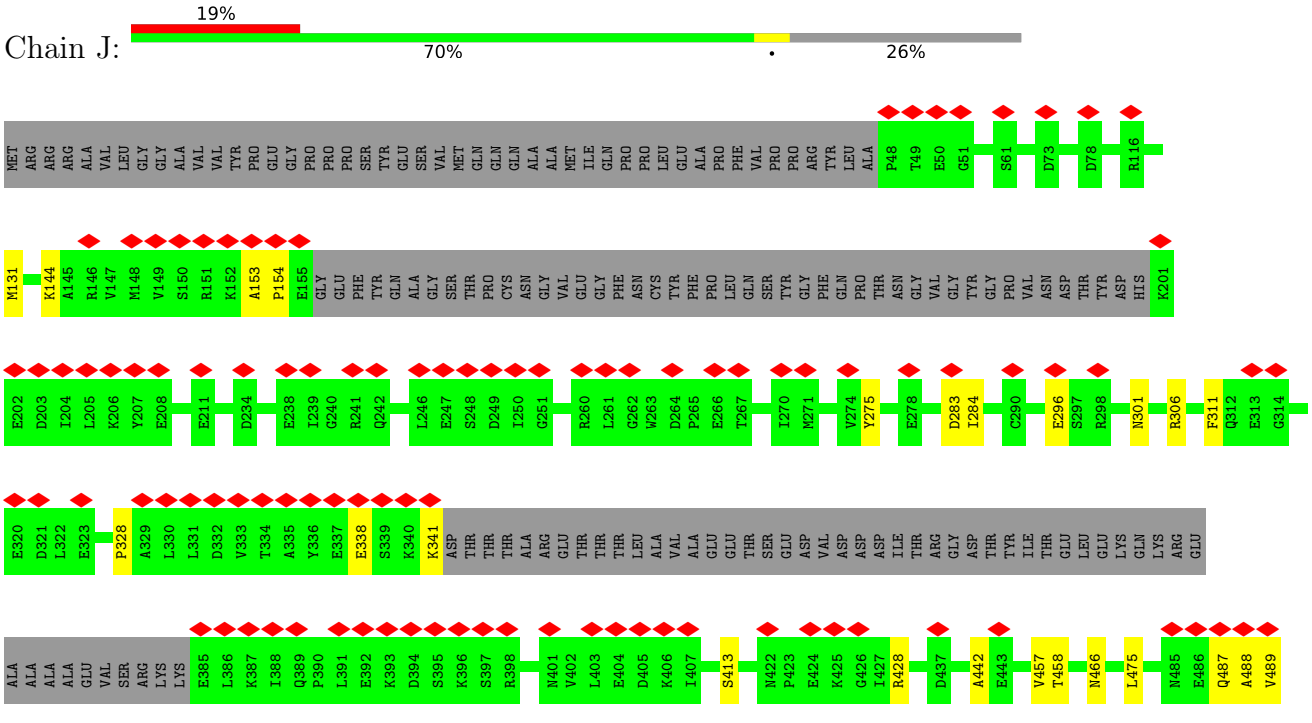
• Molecule 1: Penton protein

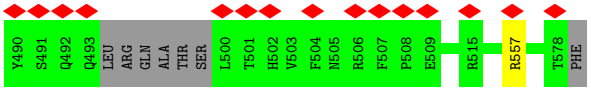
Chain I:



• Molecule 1: Penton protein

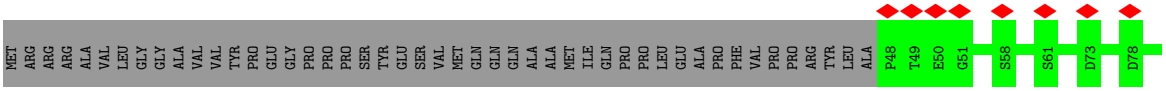
Chain J:

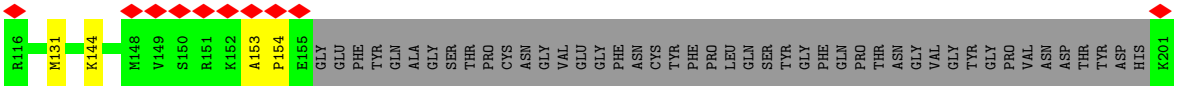


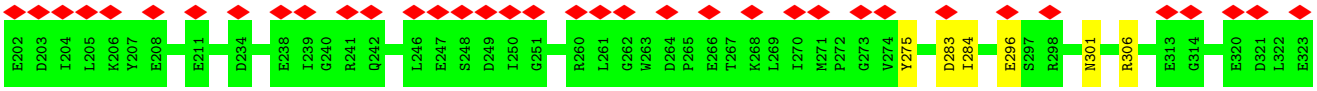


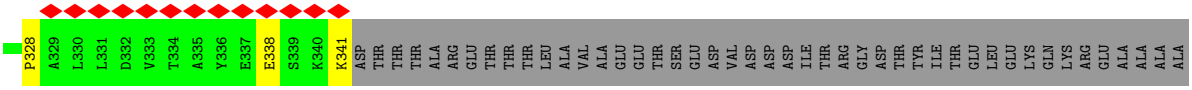
• Molecule 1: Penton protein

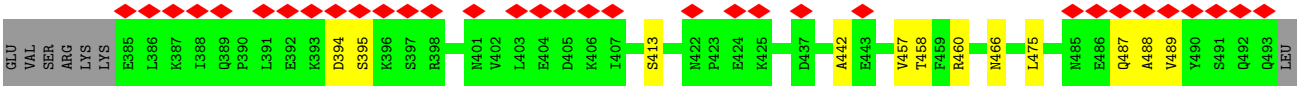
Chain K:

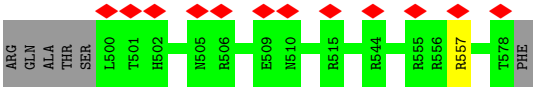






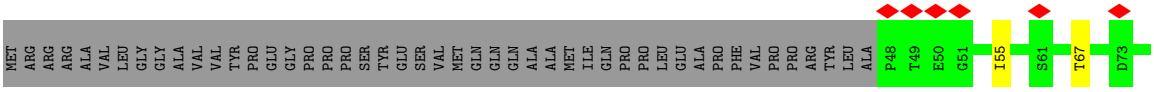


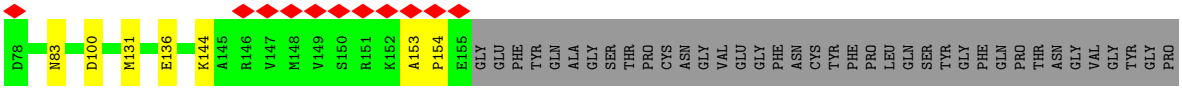


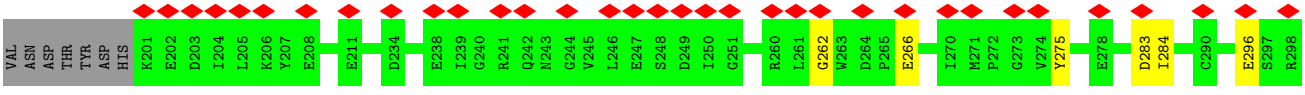


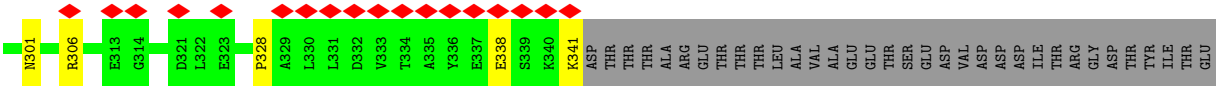
• Molecule 1: Penton protein

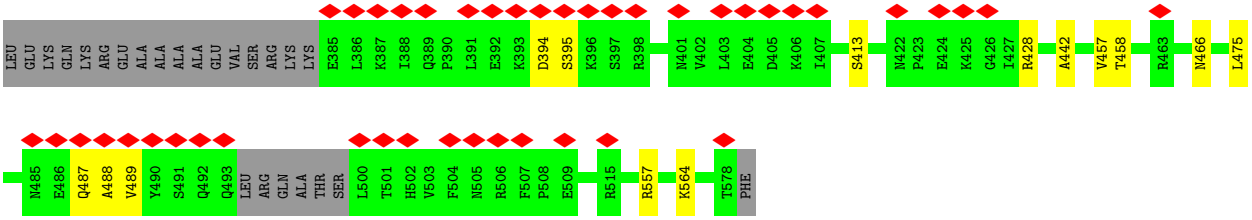
Chain L:





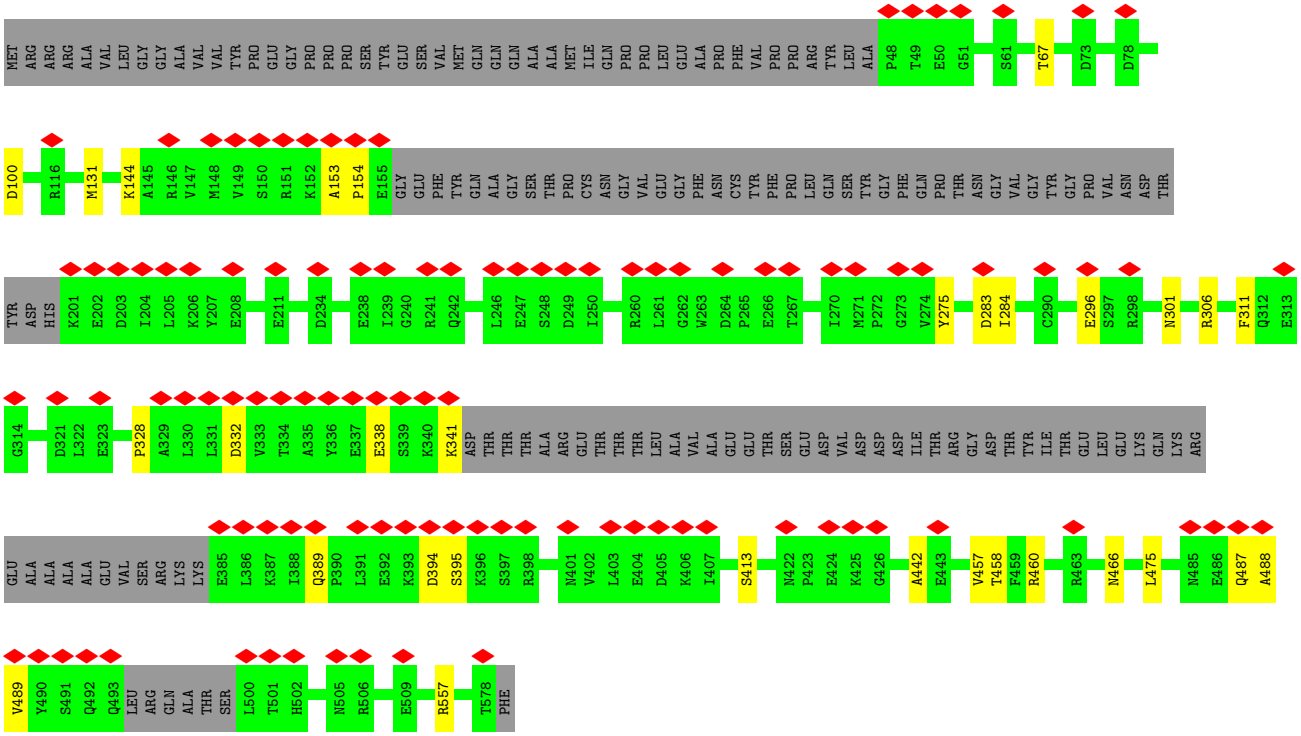






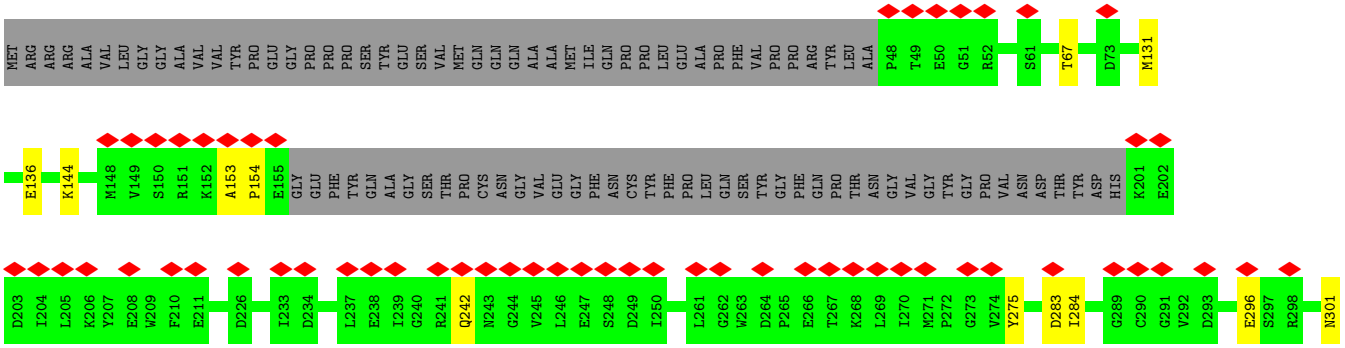
• Molecule 1: Penton protein

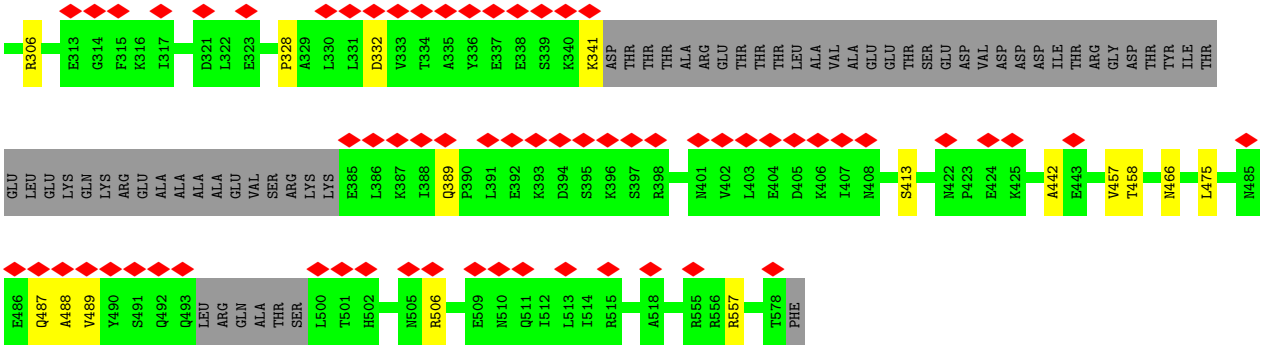
Chain M:



• Molecule 1: Penton protein

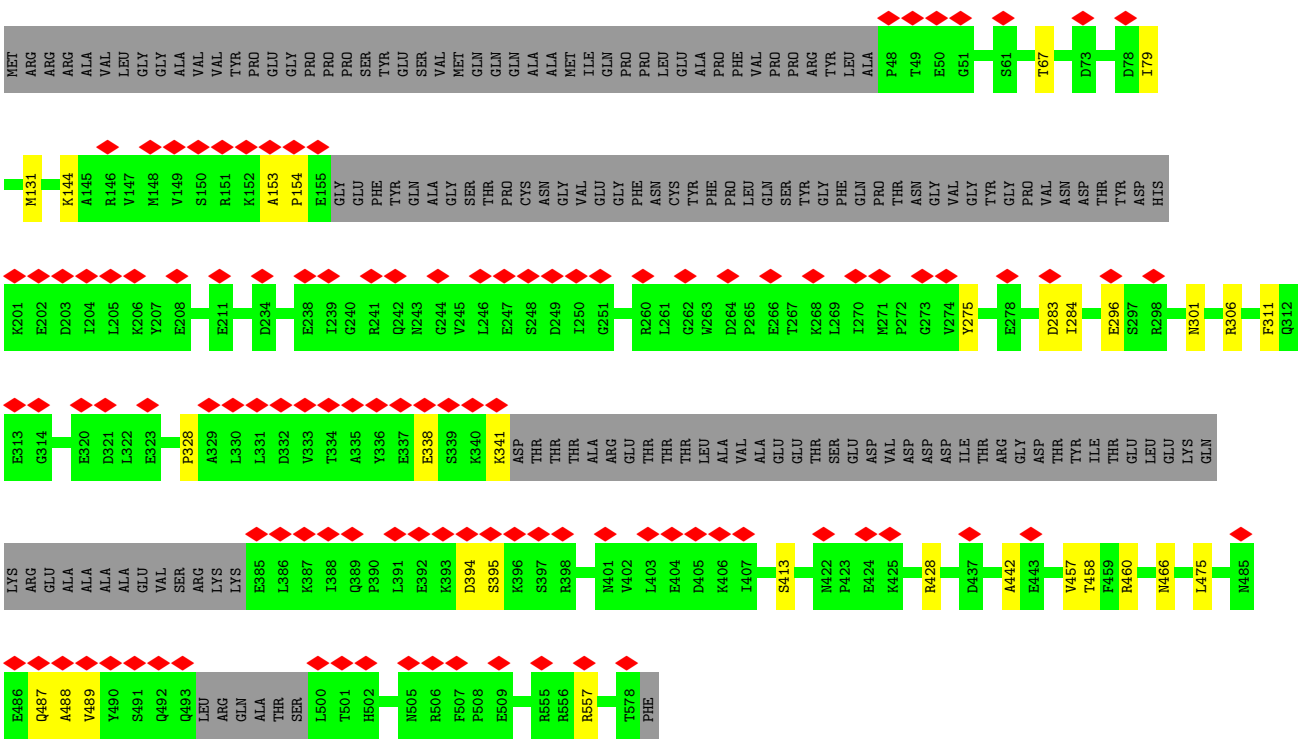
Chain N:





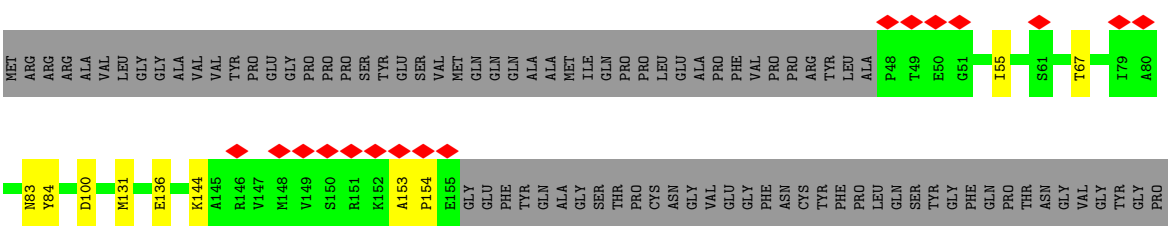
• Molecule 1: Penton protein

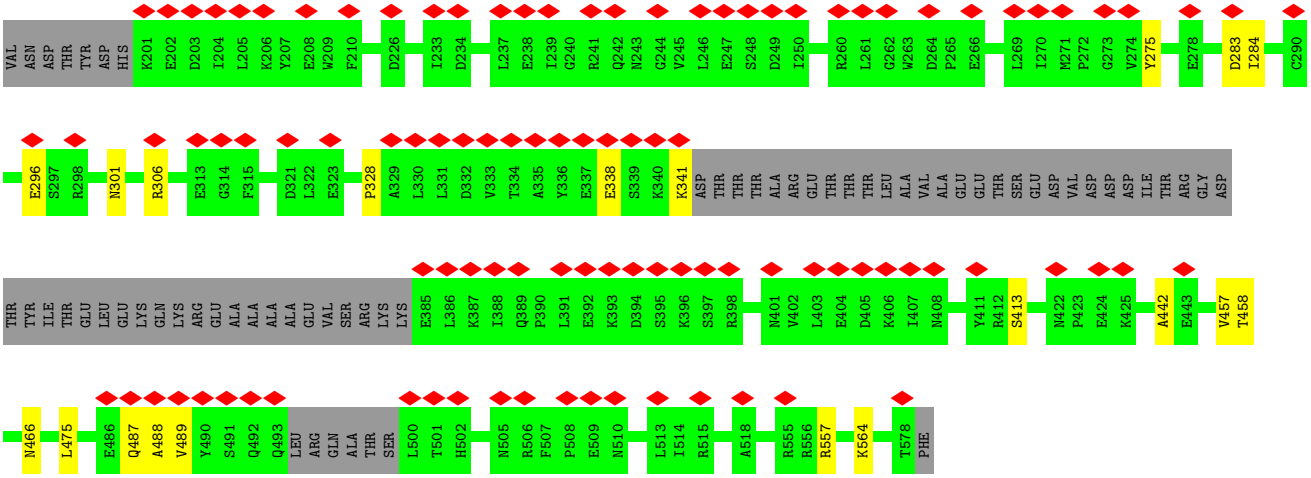
Chain O:



• Molecule 1: Penton protein

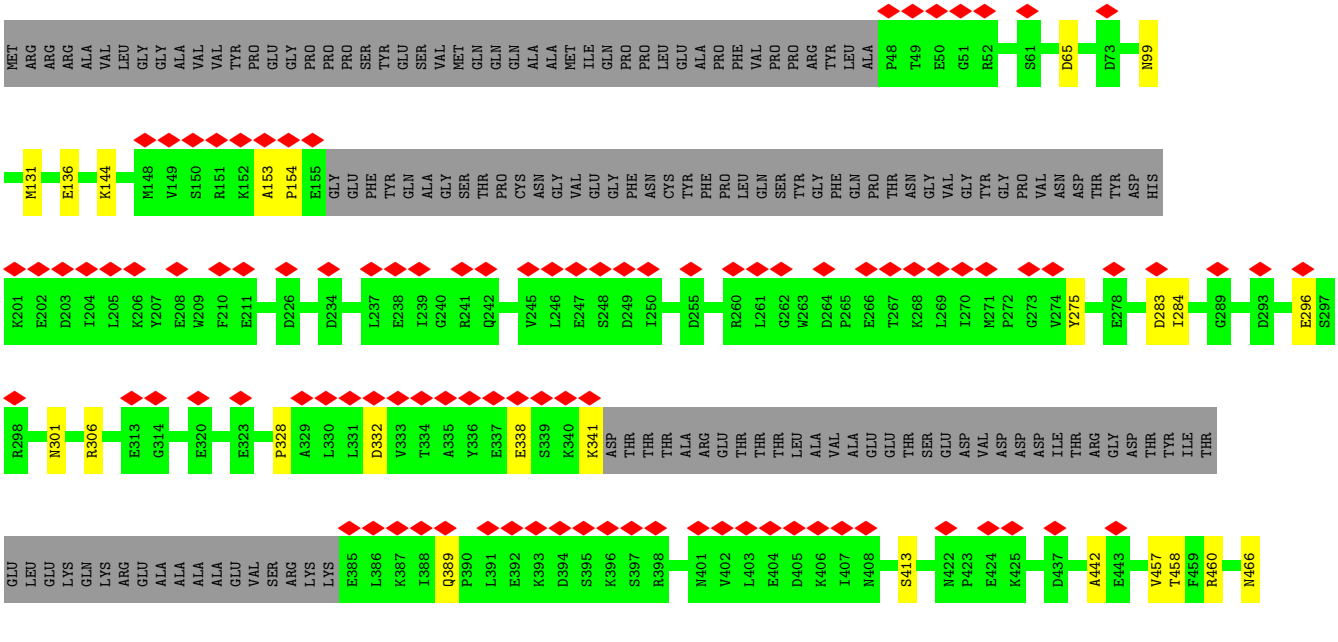
Chain P:





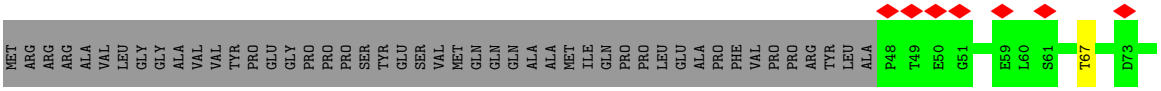
- Molecule 1: Penton protein

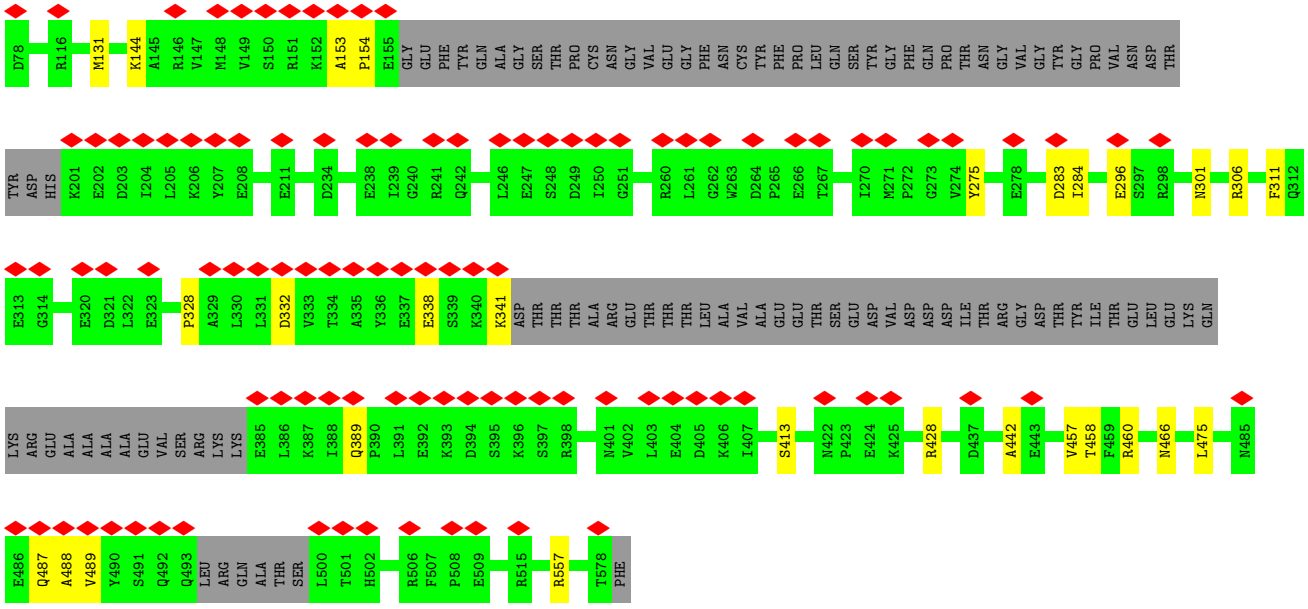
Chain Q:



- Molecule 1: Penton protein

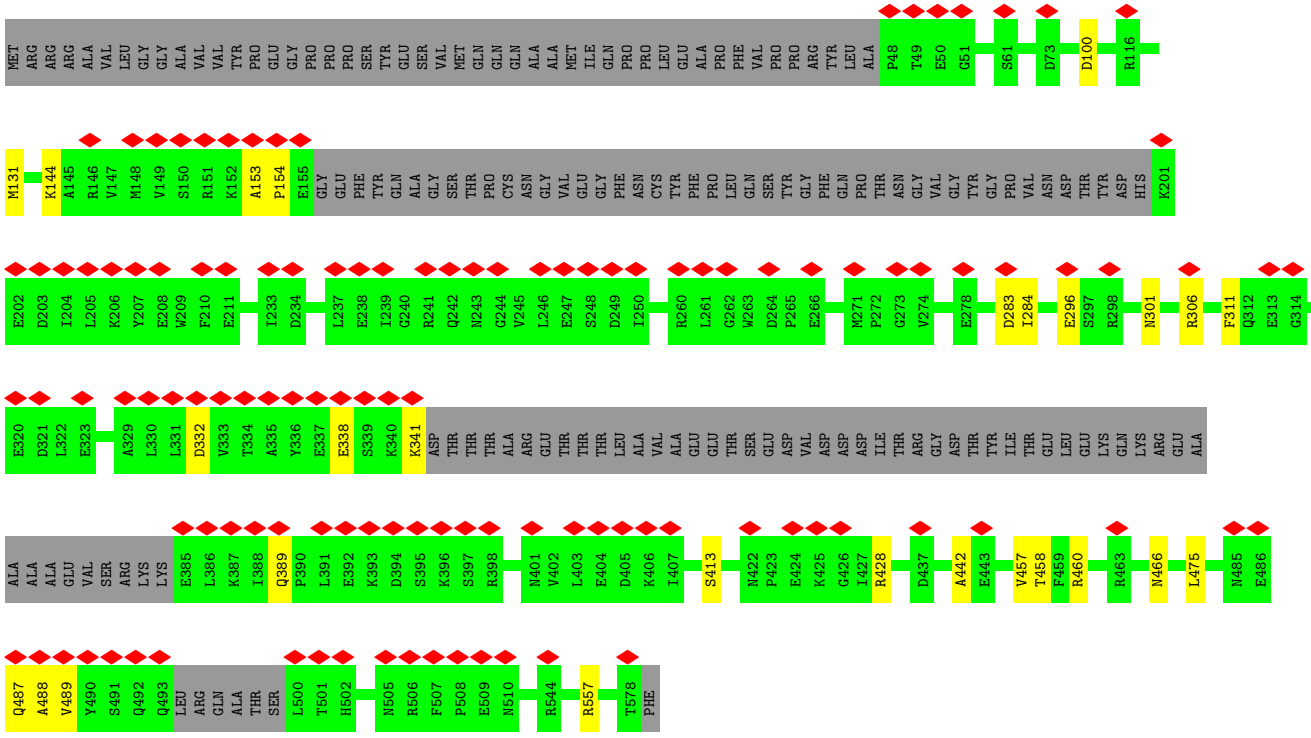
Chain R:





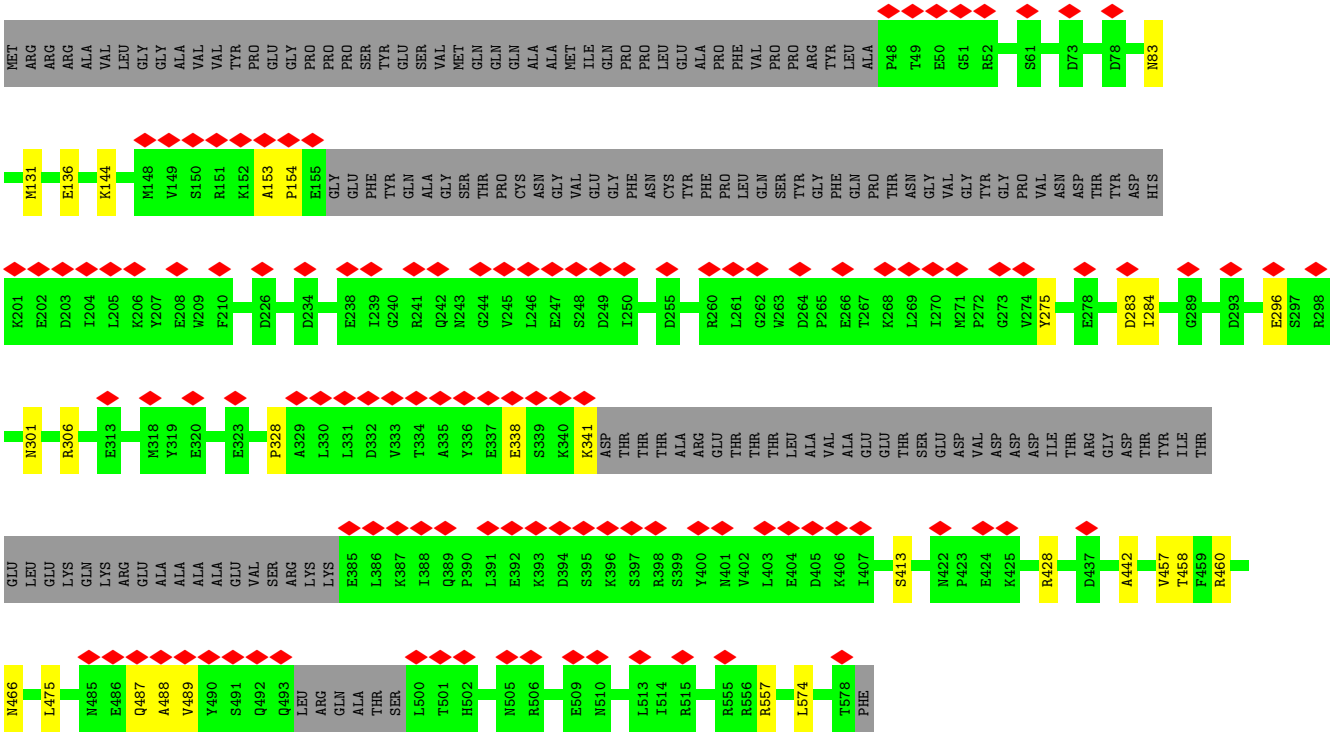
• Molecule 1: Penton protein

Chain S:

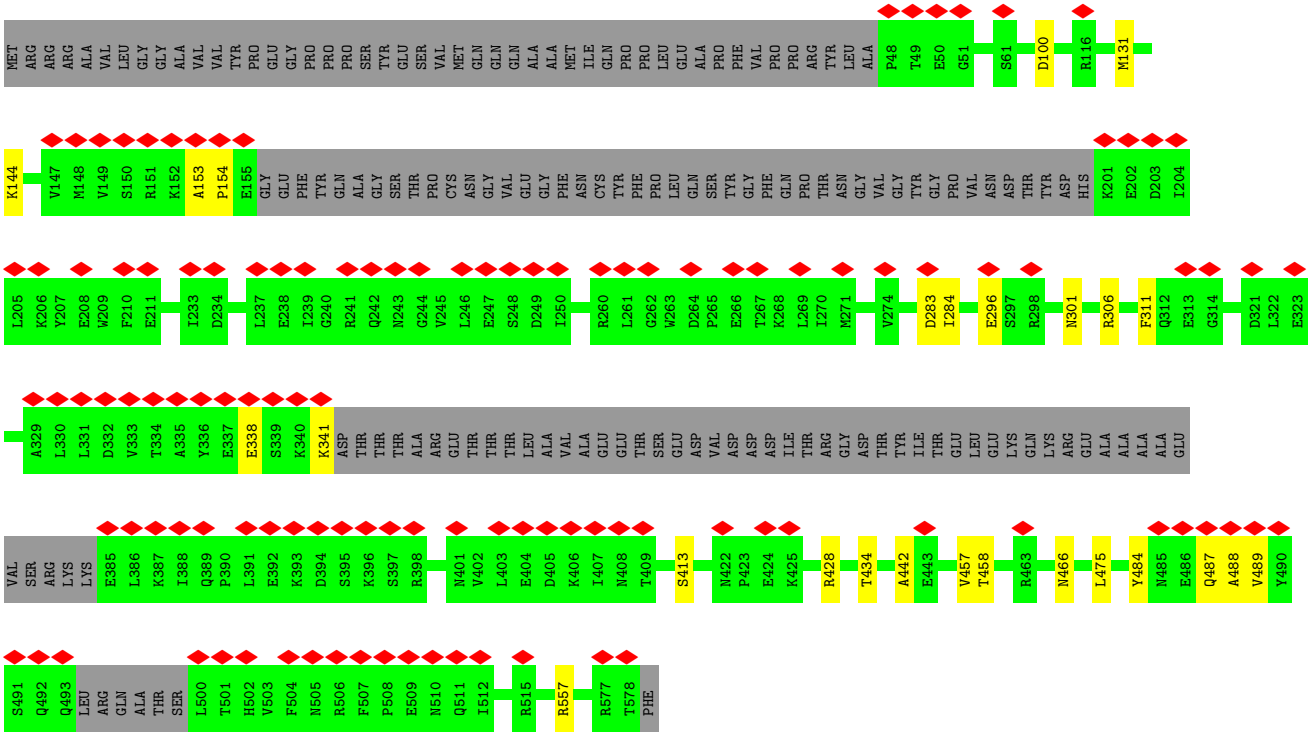


• Molecule 1: Penton protein

Chain T:

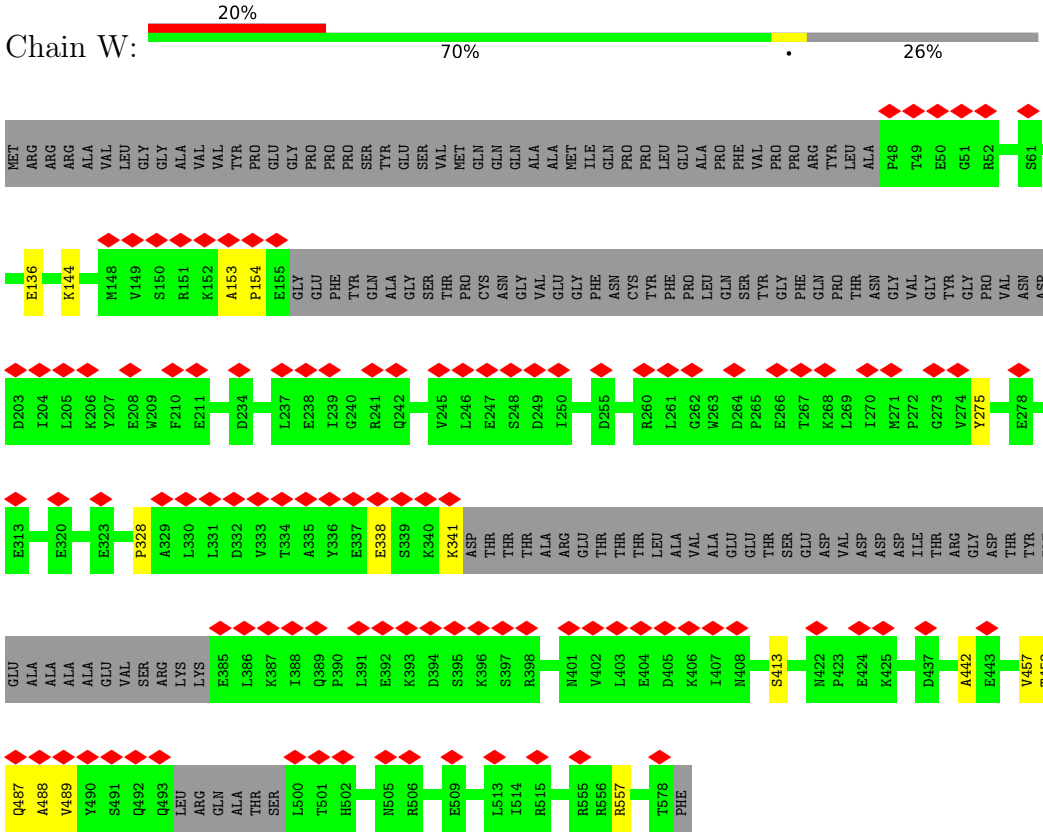


• Molecule 1: Penton protein



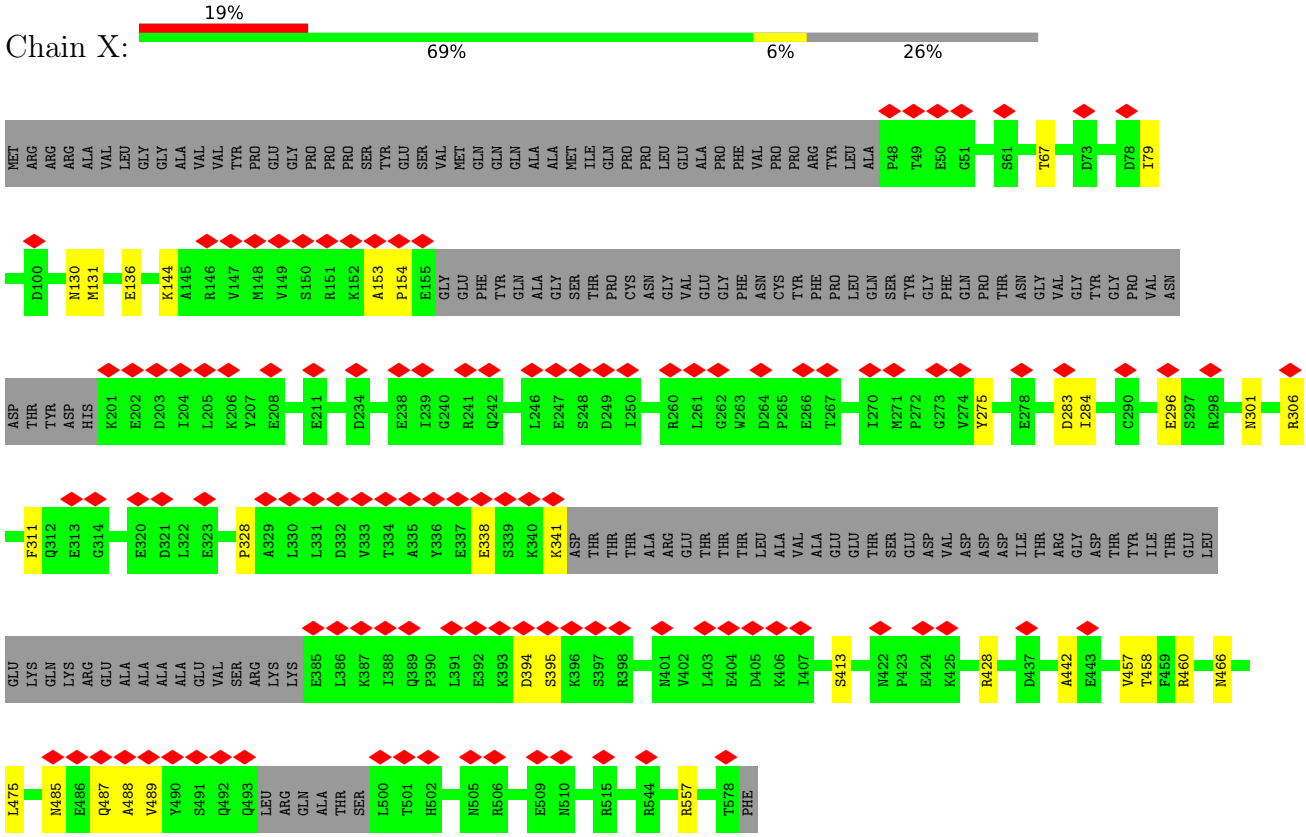
• Molecule 1: Penton protein

Chain W:



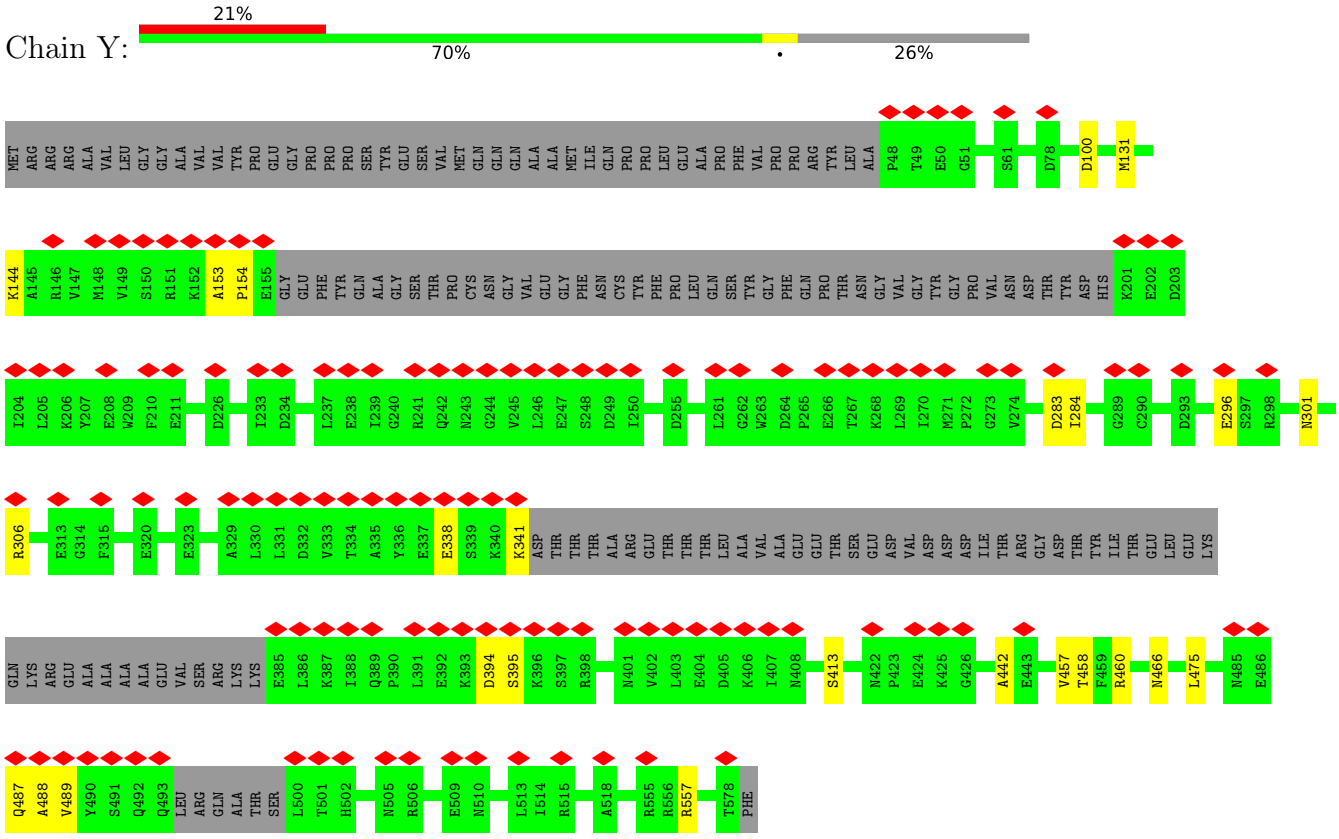
• Molecule 1: Penton protein

Chain X:



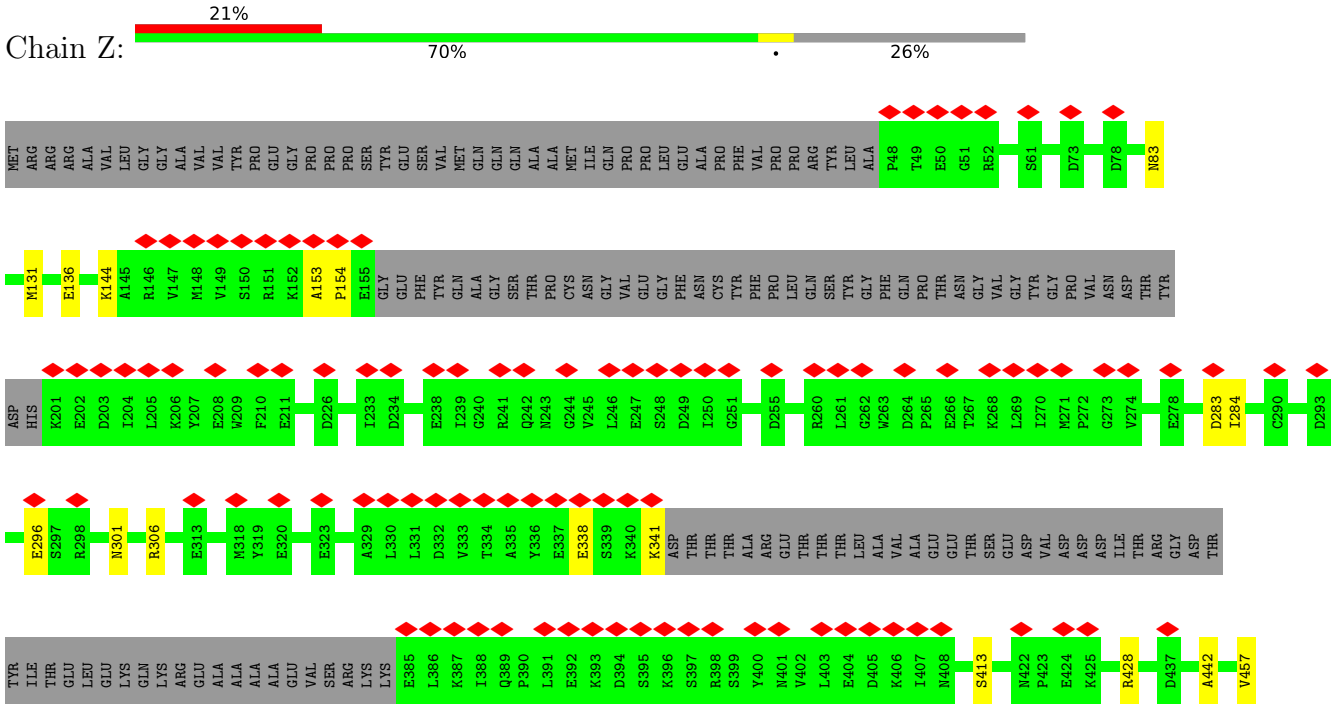
• Molecule 1: Penton protein

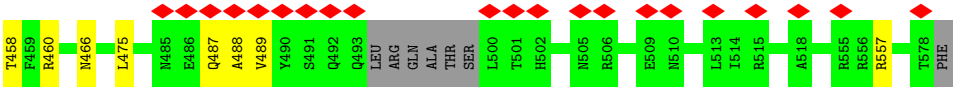
Chain Y:



• Molecule 1: Penton protein

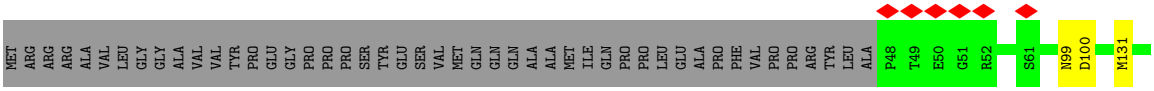
Chain Z:

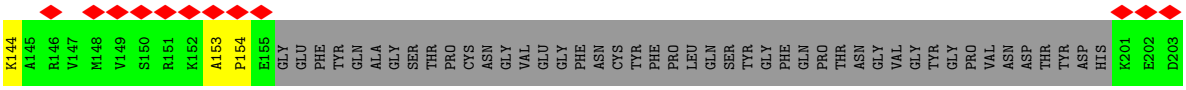


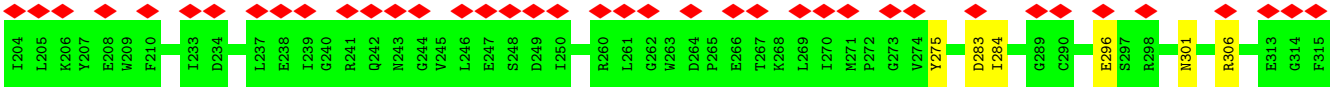


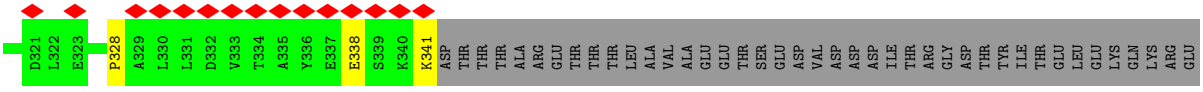
• Molecule 1: Penton protein

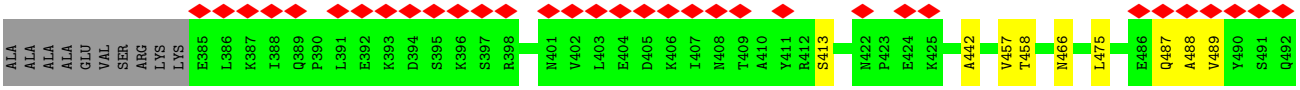
Chain AA:

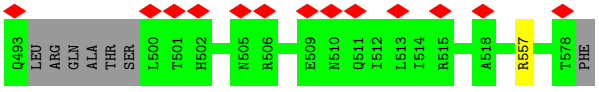






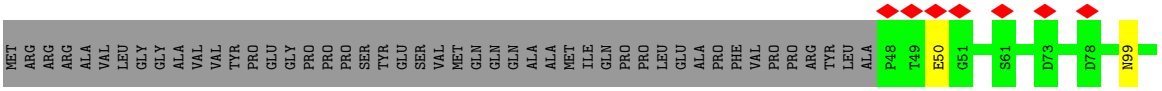


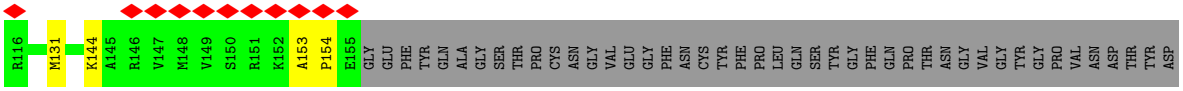


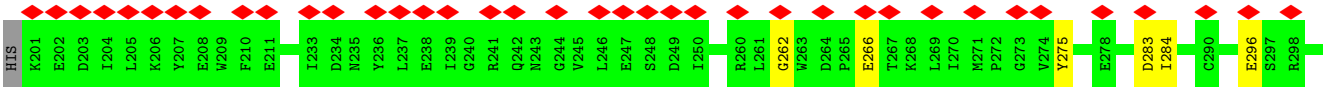


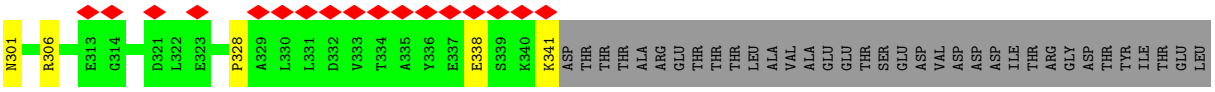
• Molecule 1: Penton protein

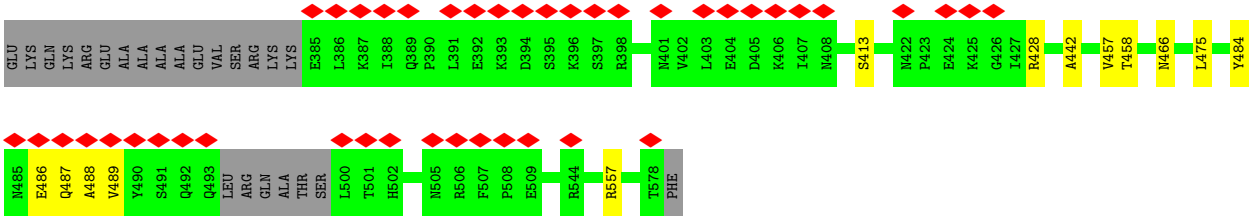
Chain BA:





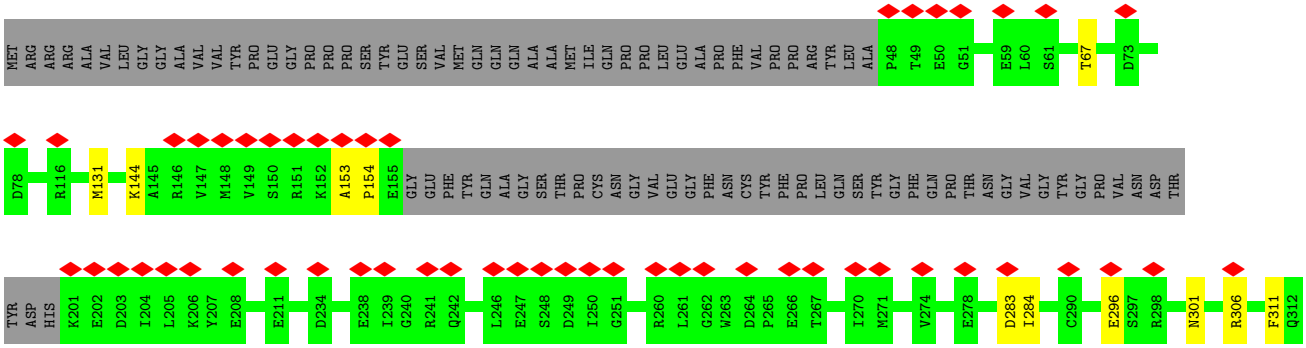


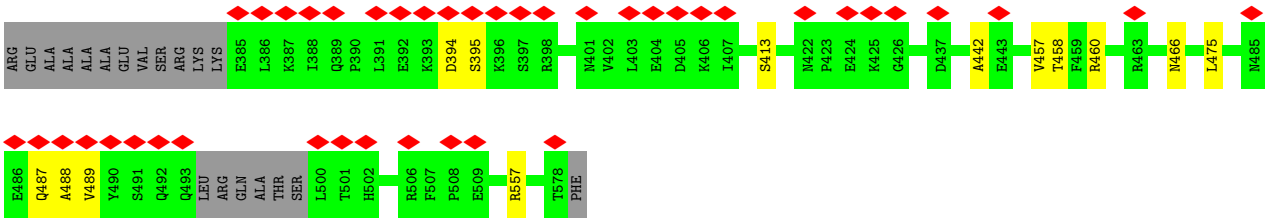




• Molecule 1: Penton protein

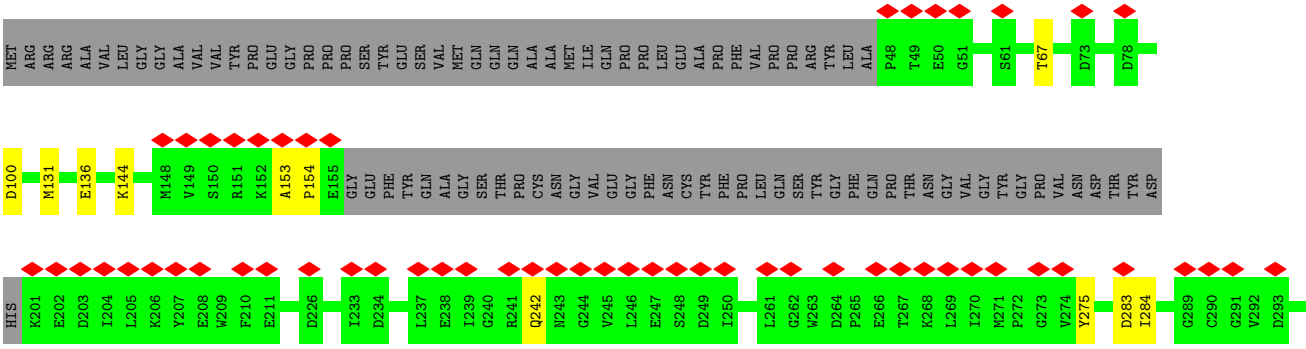
Chain CA:

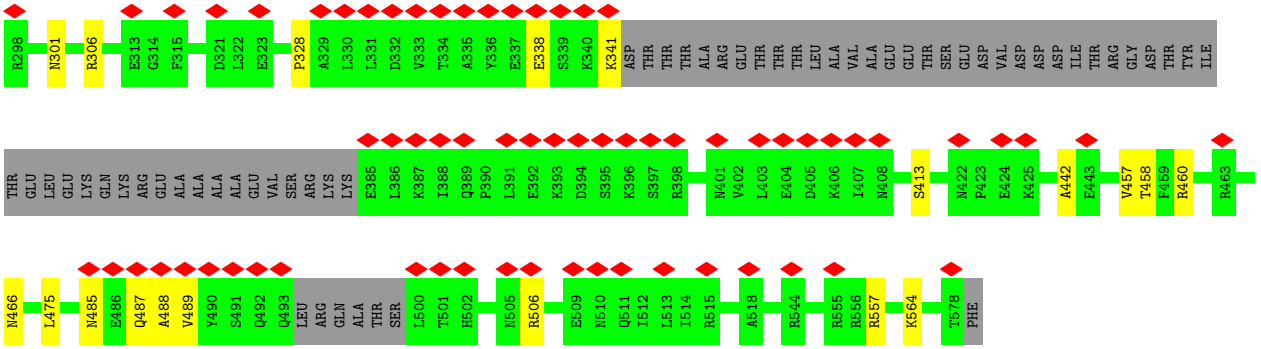




• Molecule 1: Penton protein

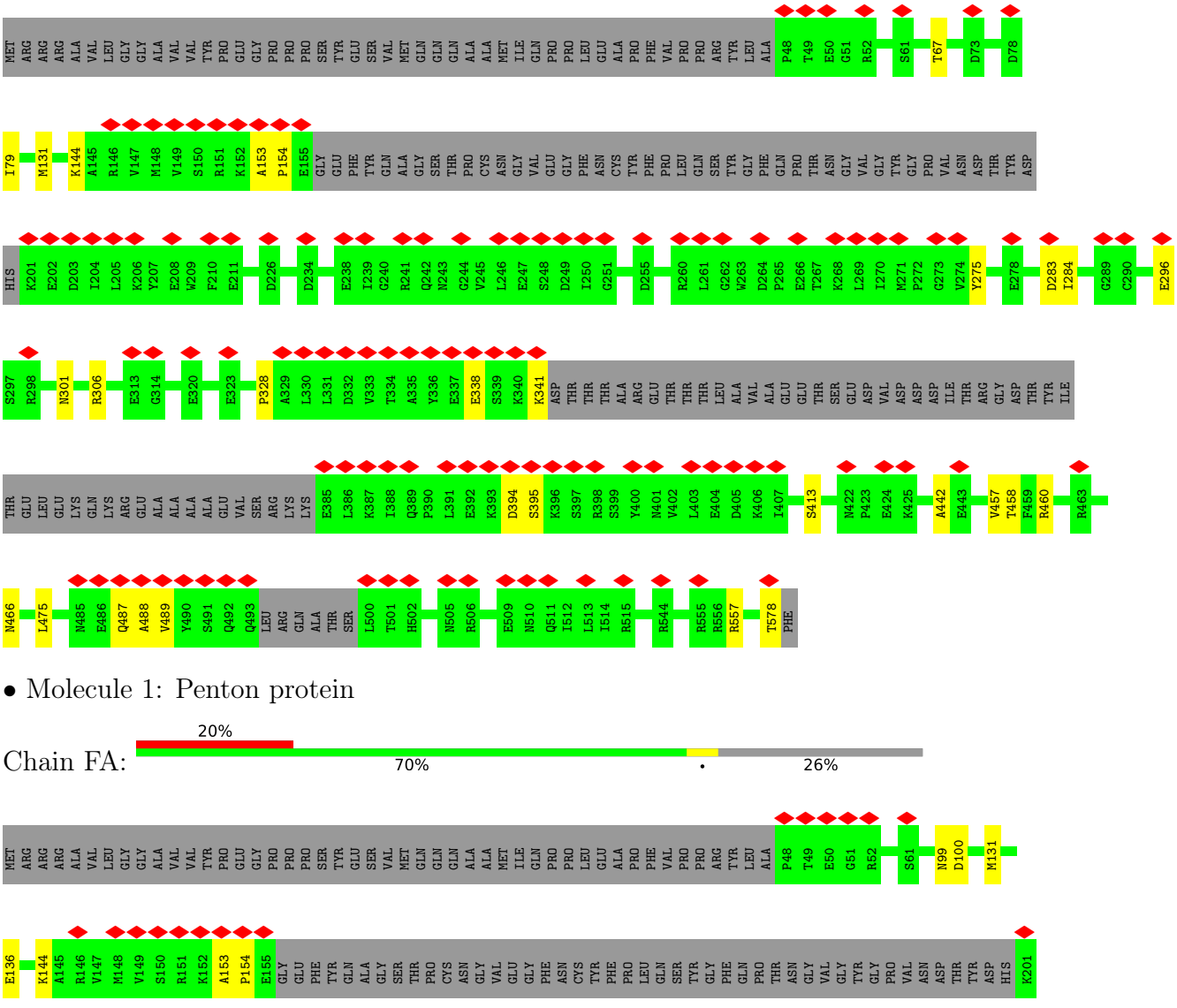
Chain DA:





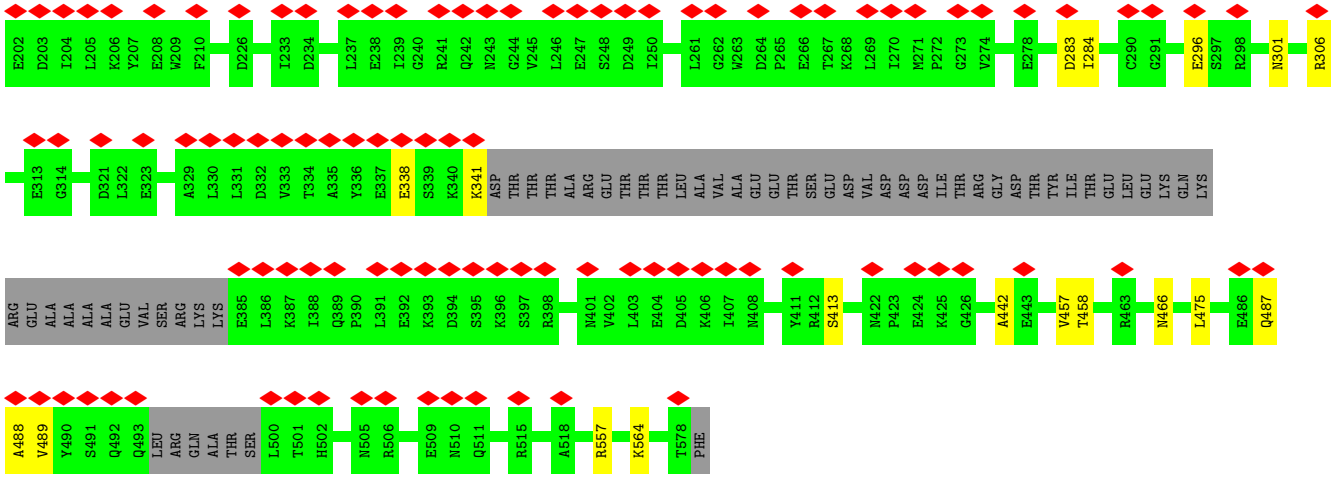
• Molecule 1: Penton protein

Chain EA:



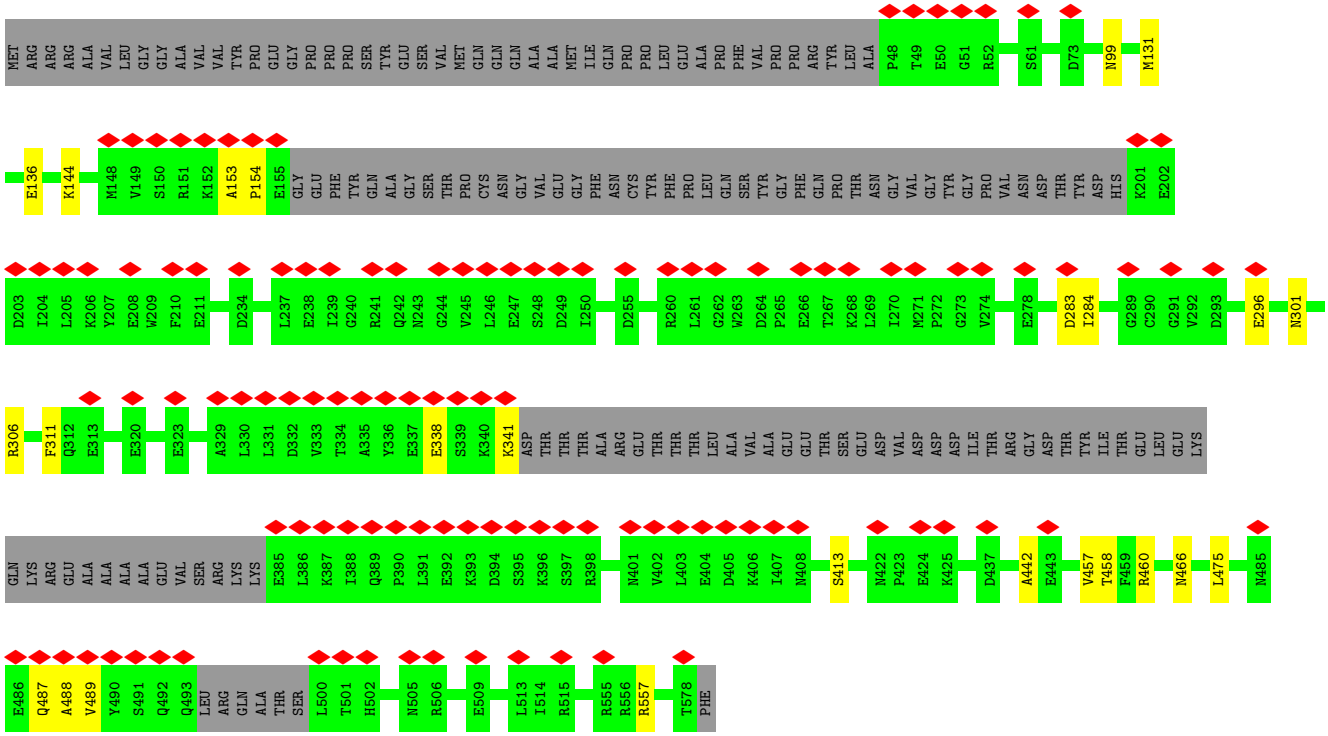
• Molecule 1: Penton protein

Chain FA:



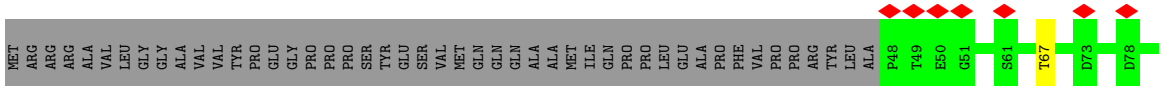
• Molecule 1: Penton protein

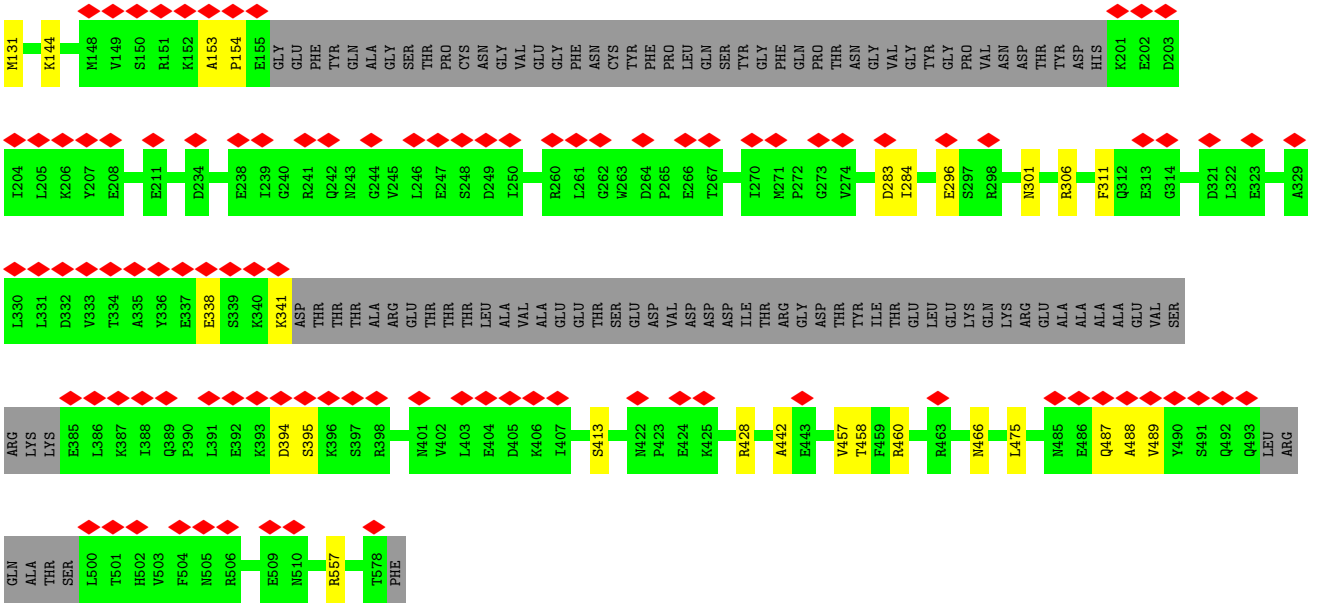
Chain GA:



• Molecule 1: Penton protein

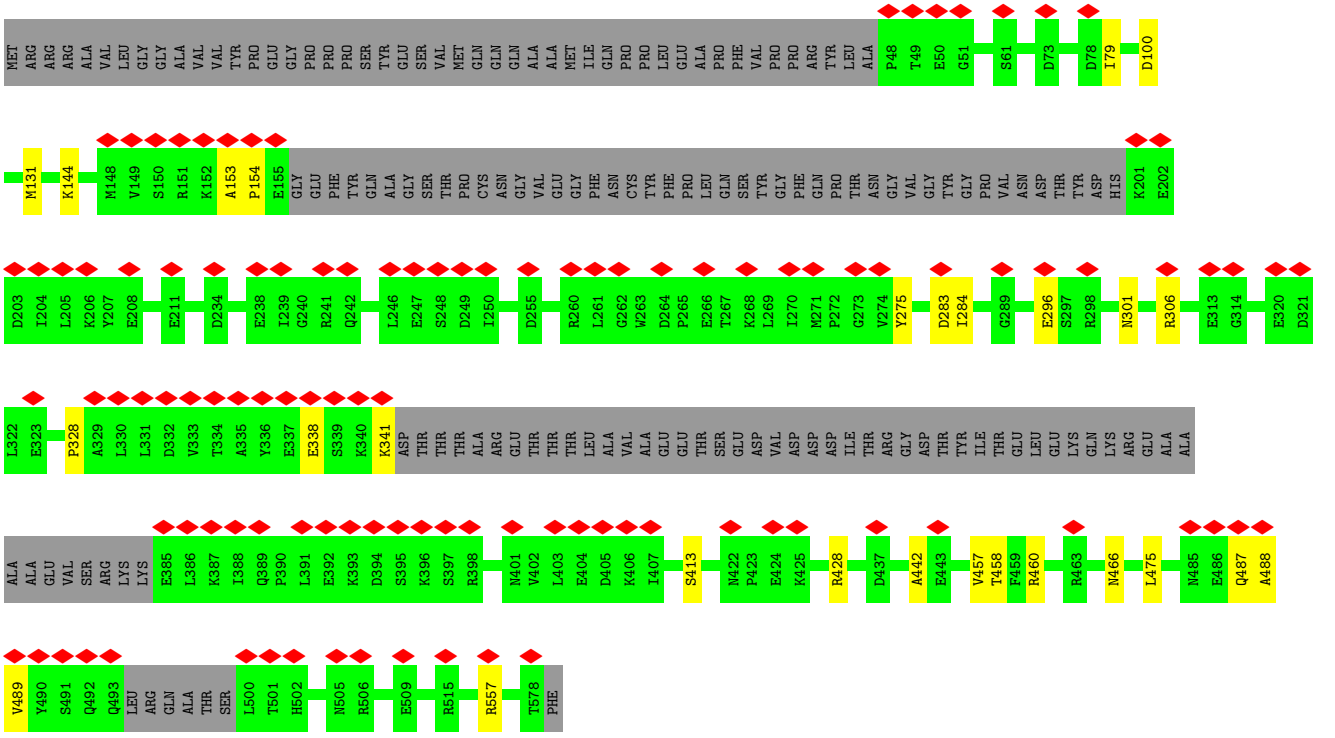
Chain HA:





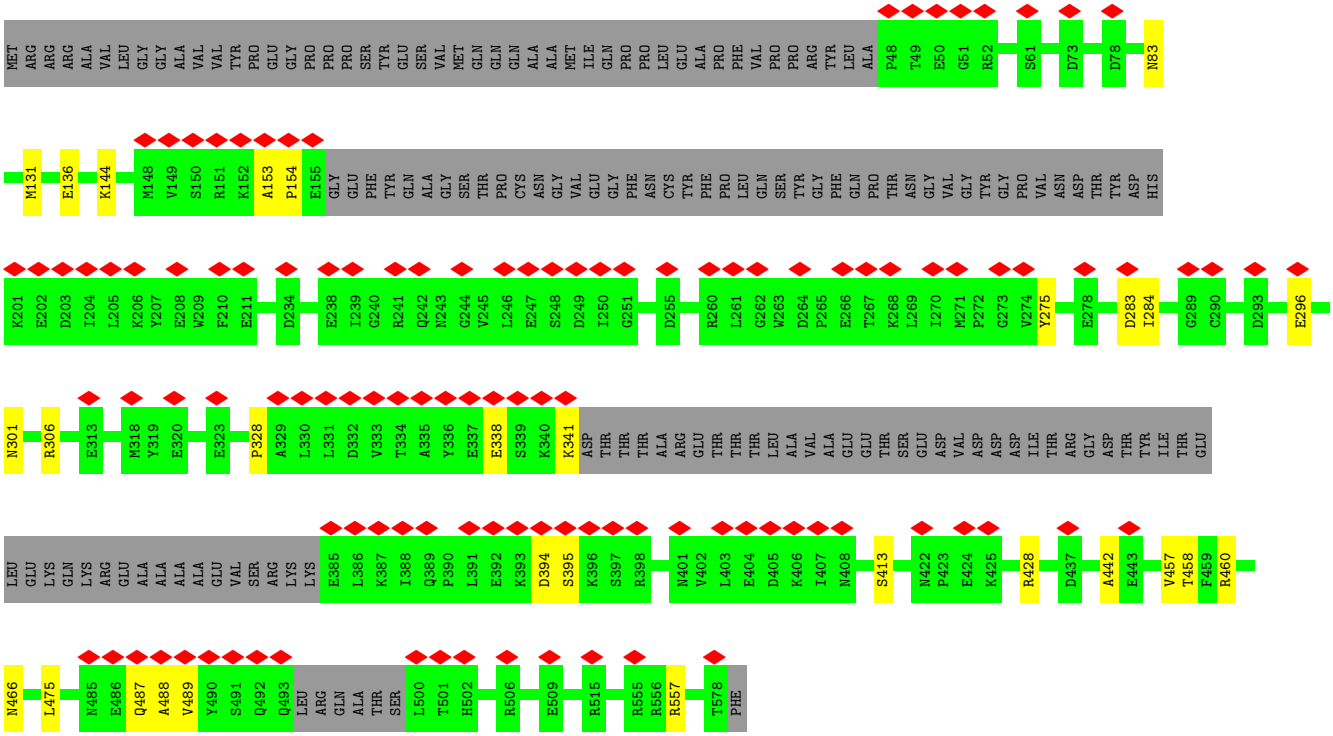
• Molecule 1: Penton protein

Chain IA:



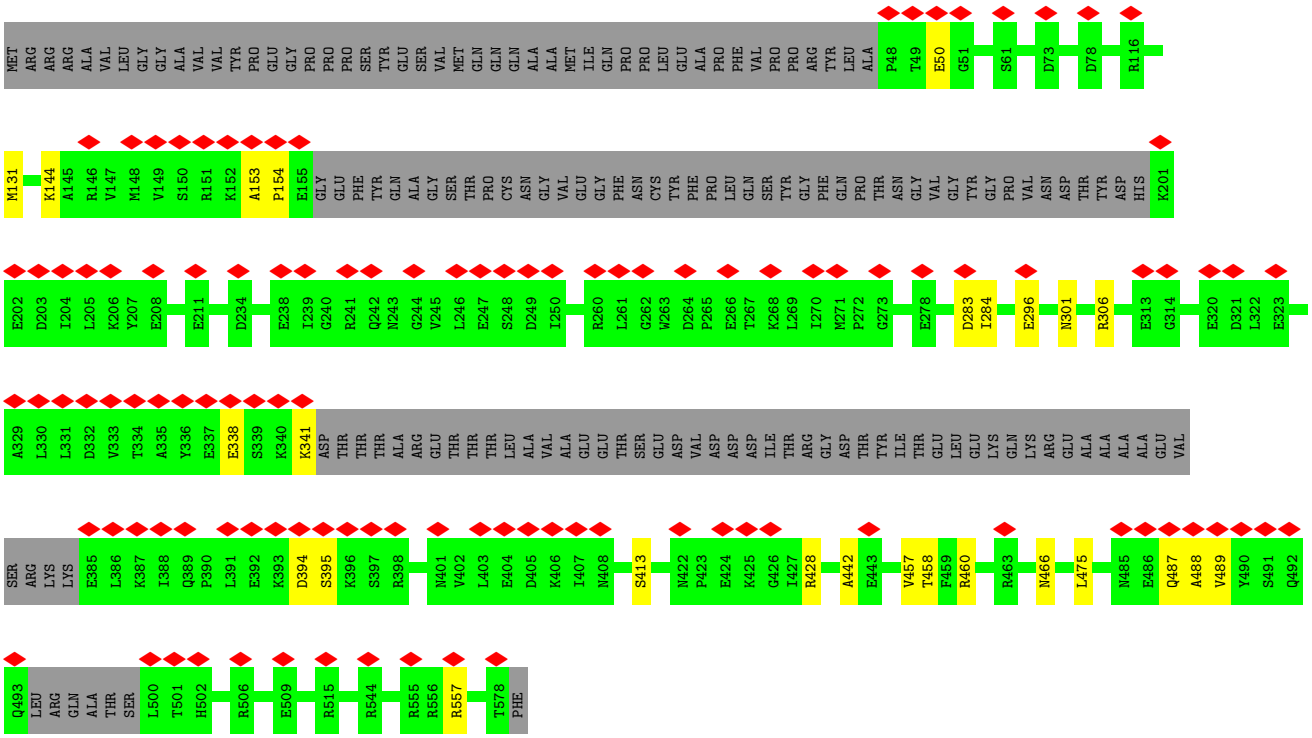
• Molecule 1: Penton protein

Chain JA:



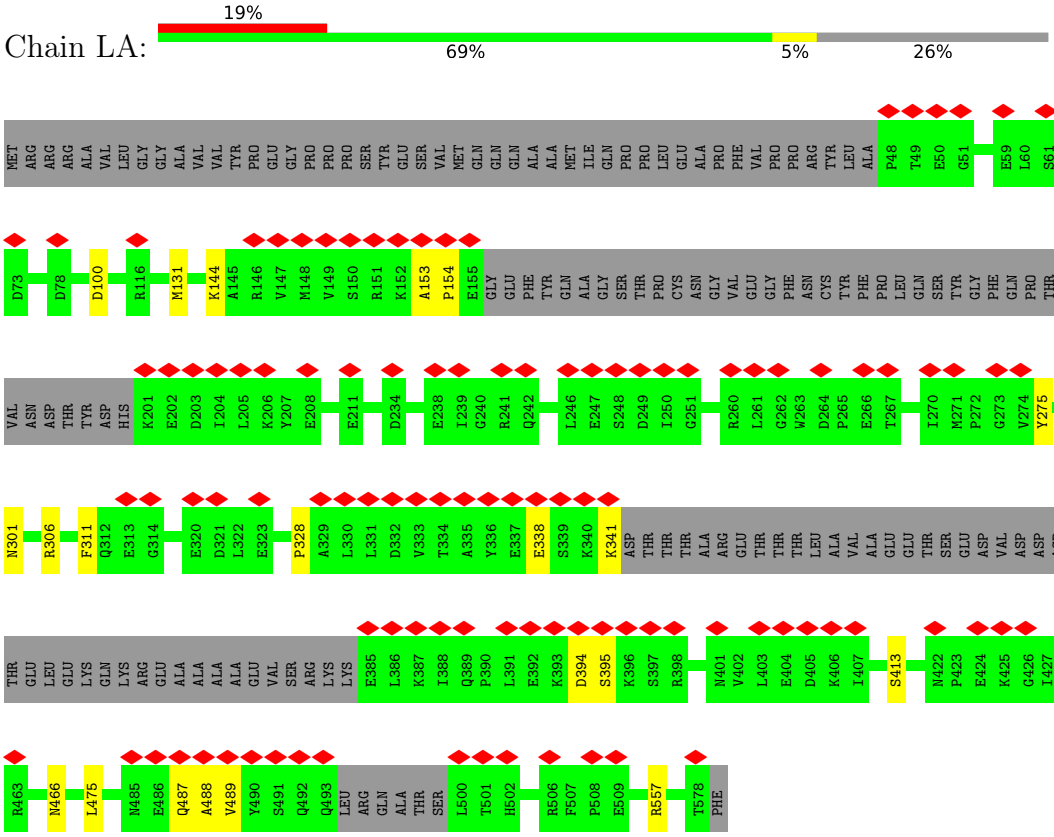
• Molecule 1: Penton protein

Chain KA:



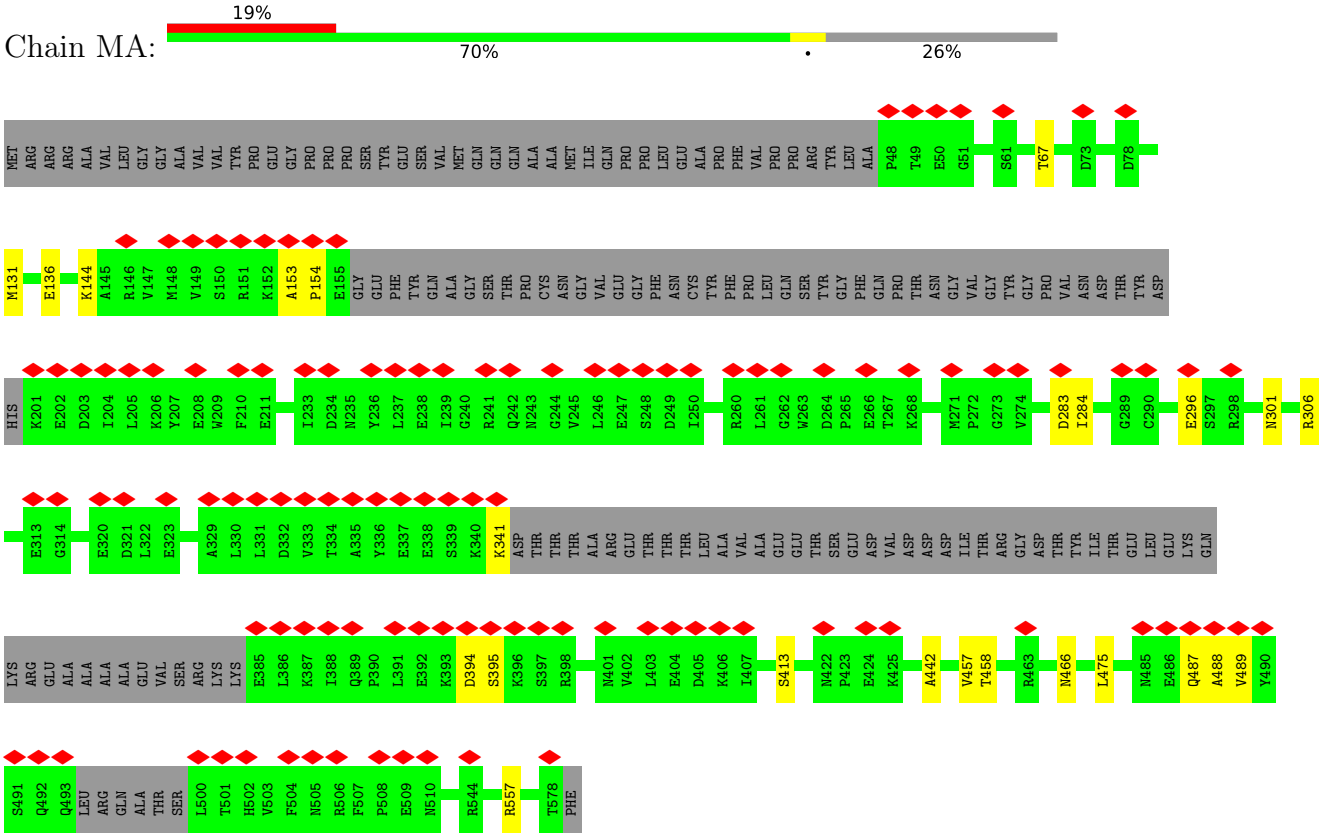
• Molecule 1: Penton protein

Chain LA:



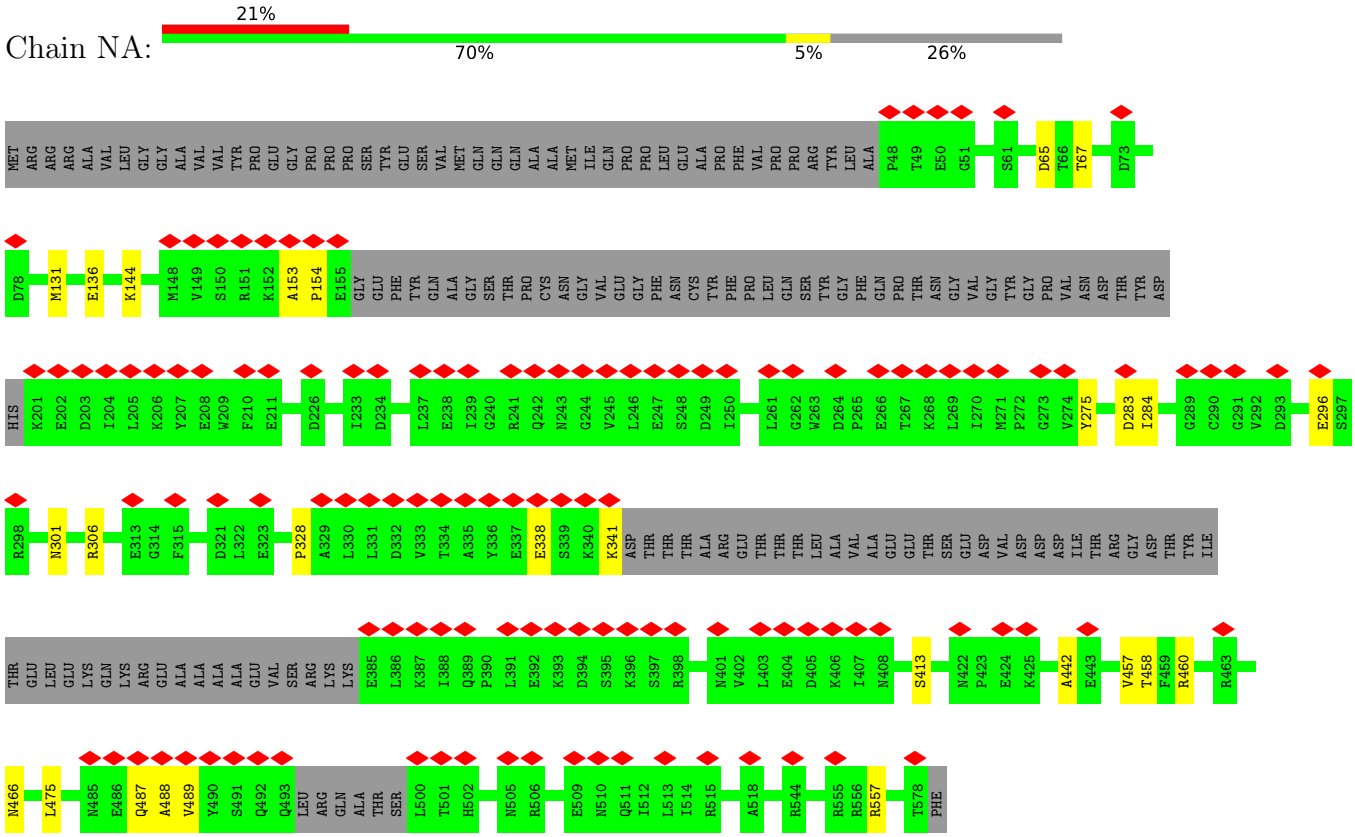
• Molecule 1: Penton protein

Chain MA:



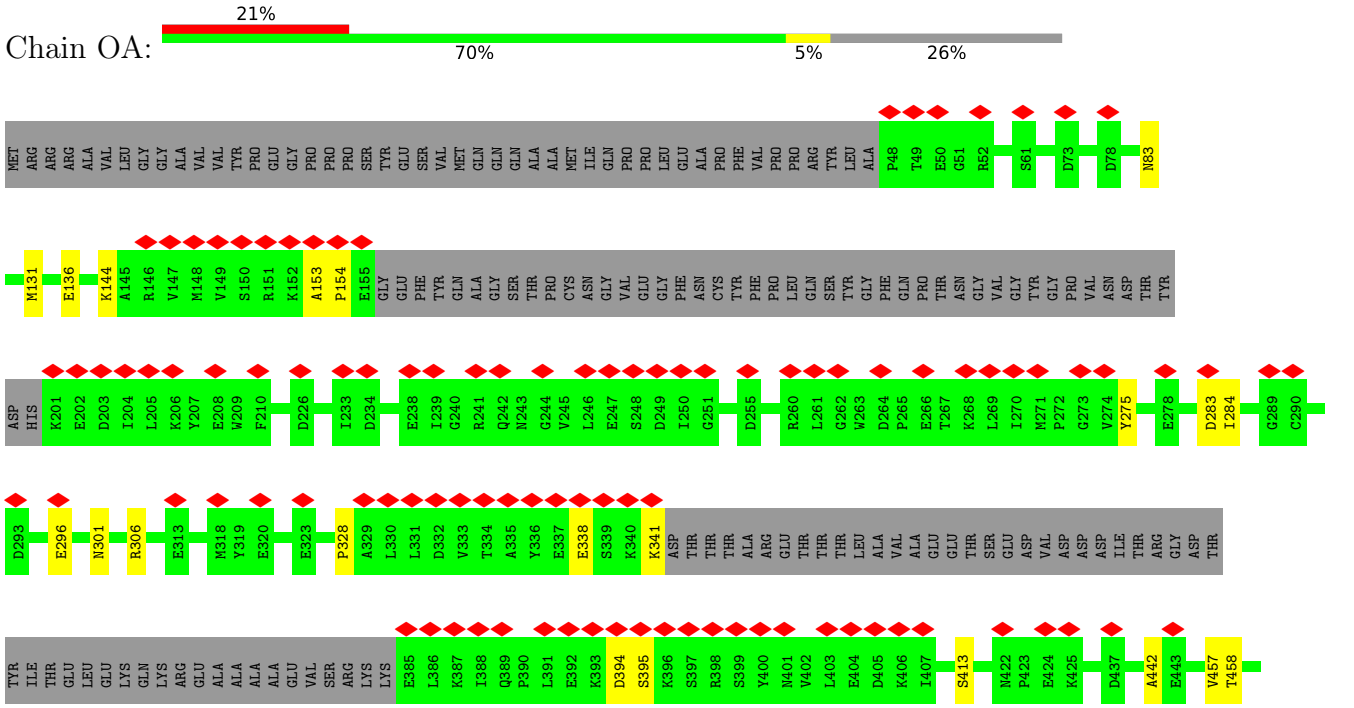
• Molecule 1: Penton protein

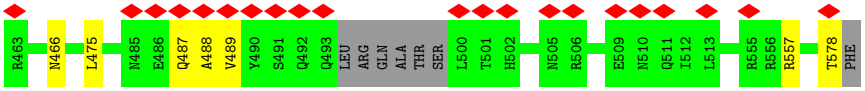
Chain NA:



• Molecule 1: Penton protein

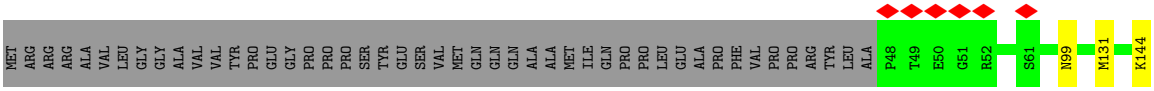
Chain OA:

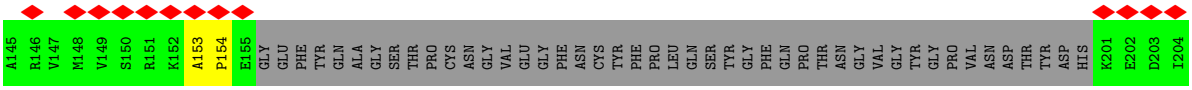


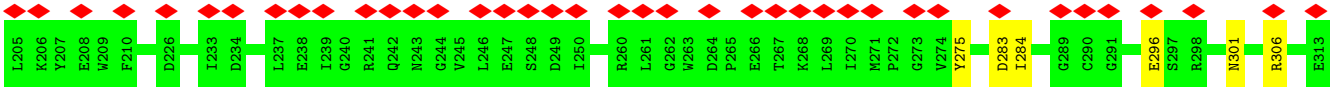


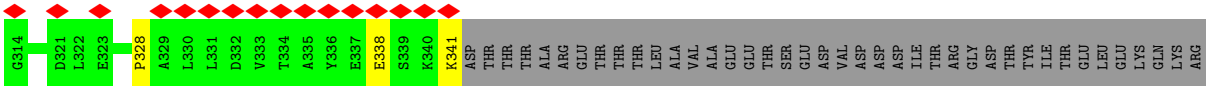
• Molecule 1: Penton protein

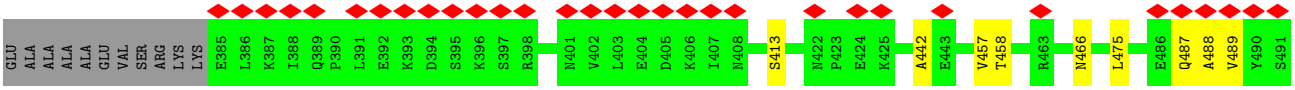
Chain PA:

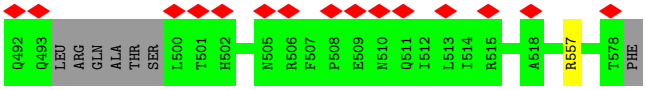






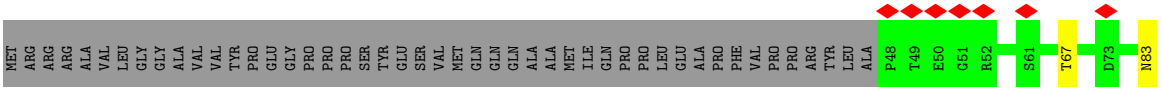


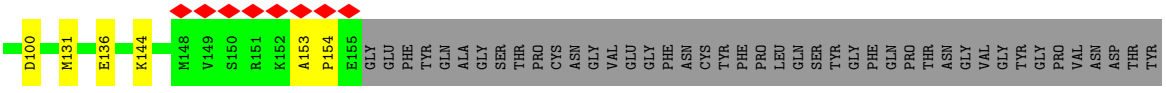


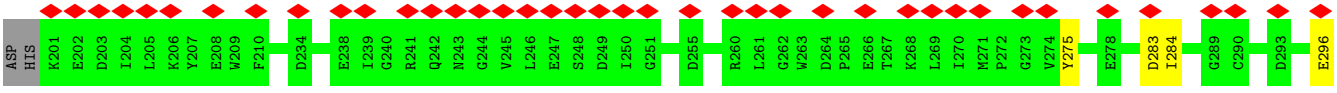


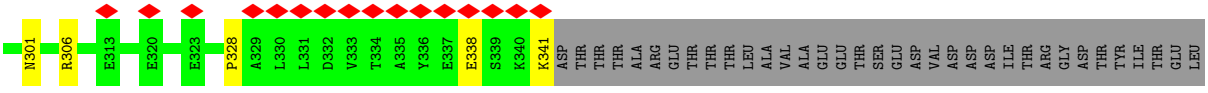
• Molecule 1: Penton protein

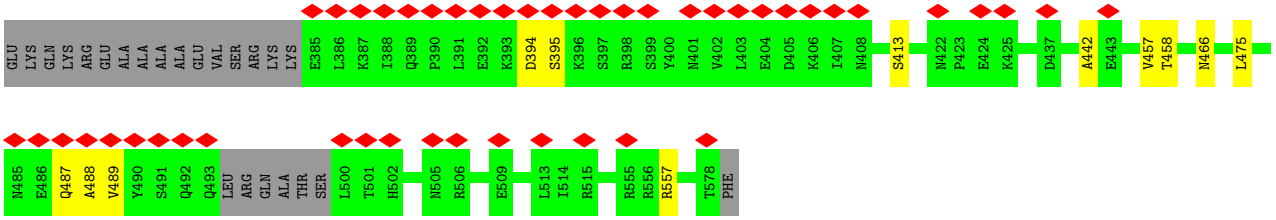
Chain QA:





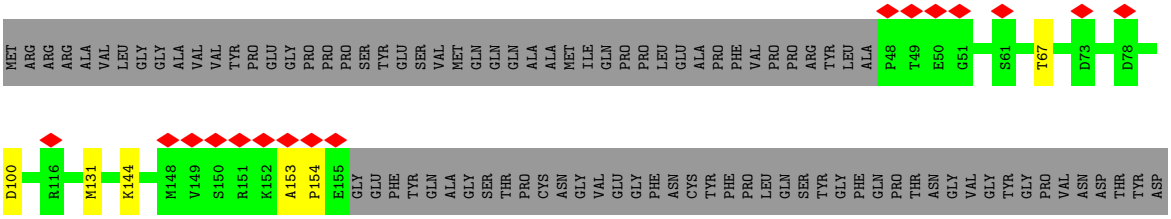


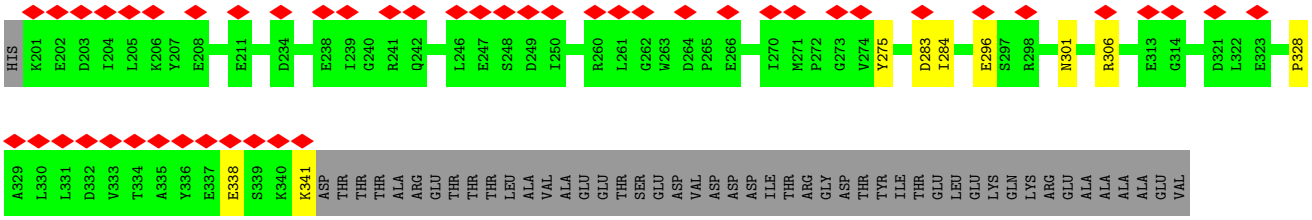


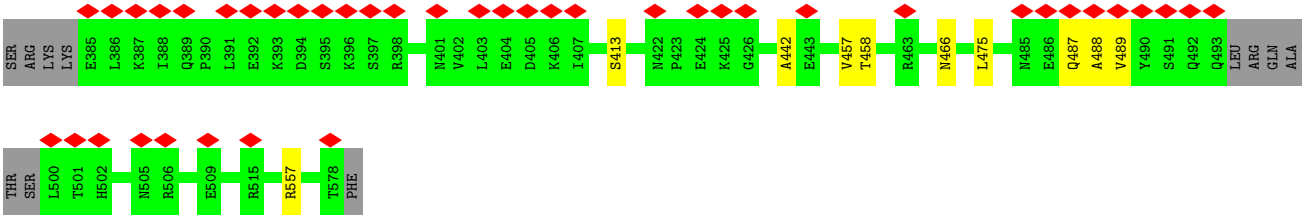


• Molecule 1: Penton protein

Chain RA:

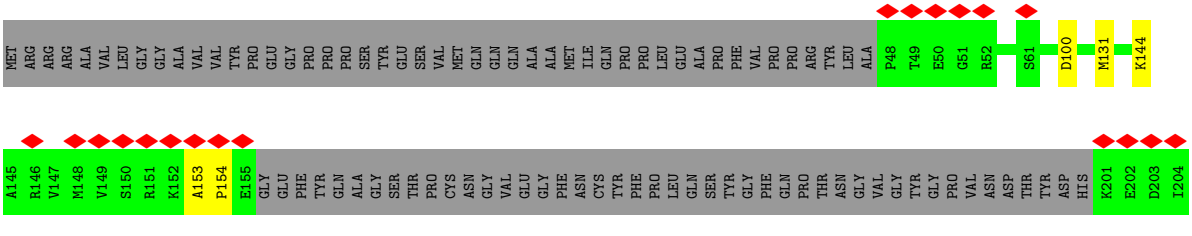


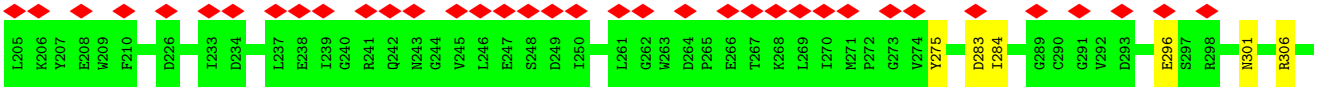


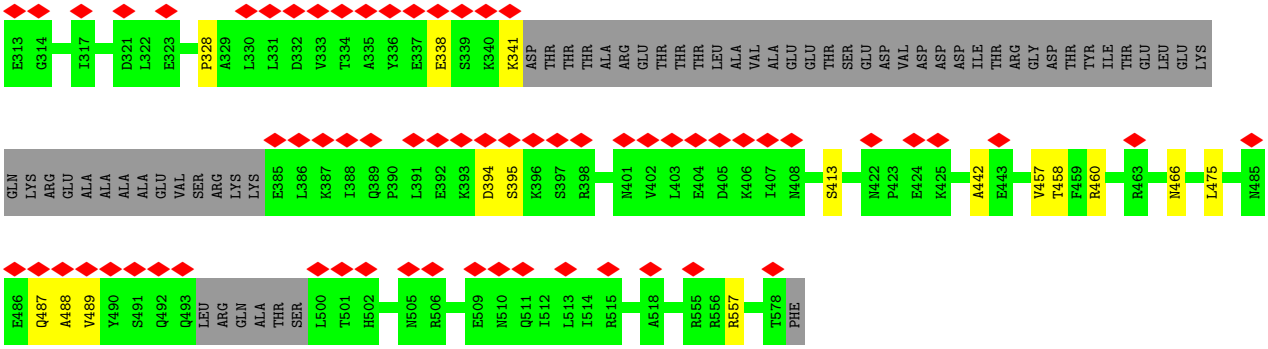


• Molecule 1: Penton protein

Chain SA:

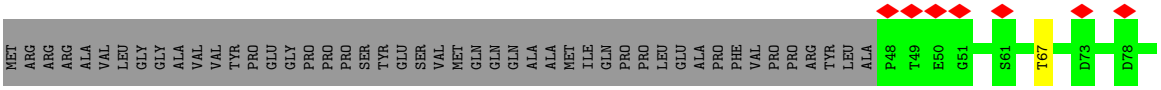


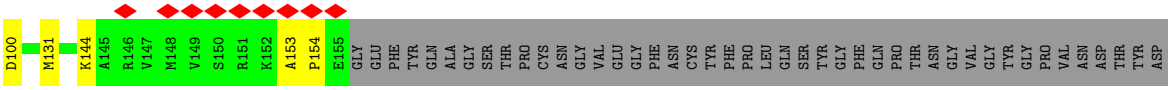


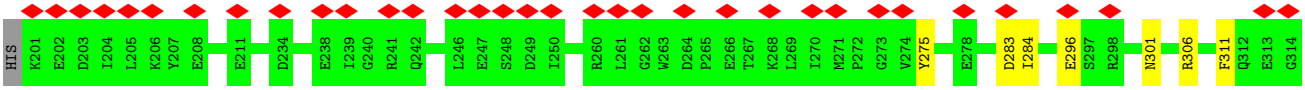


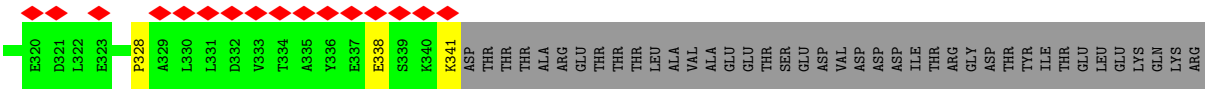
• Molecule 1: Penton protein

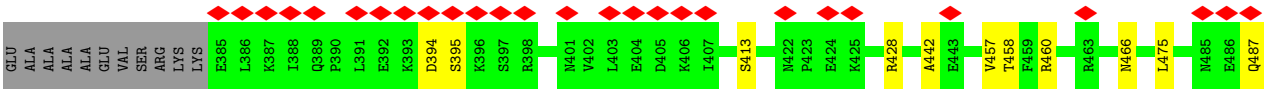
Chain TA:

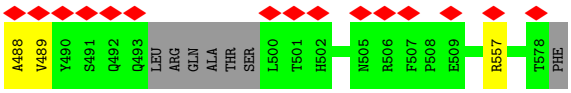






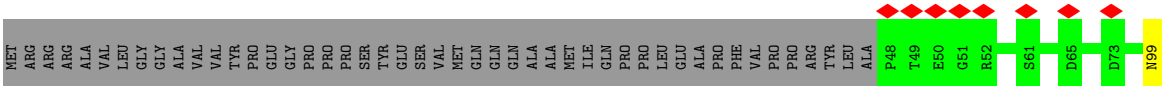


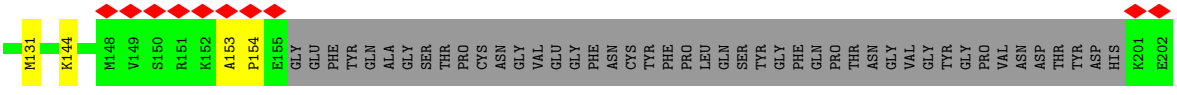


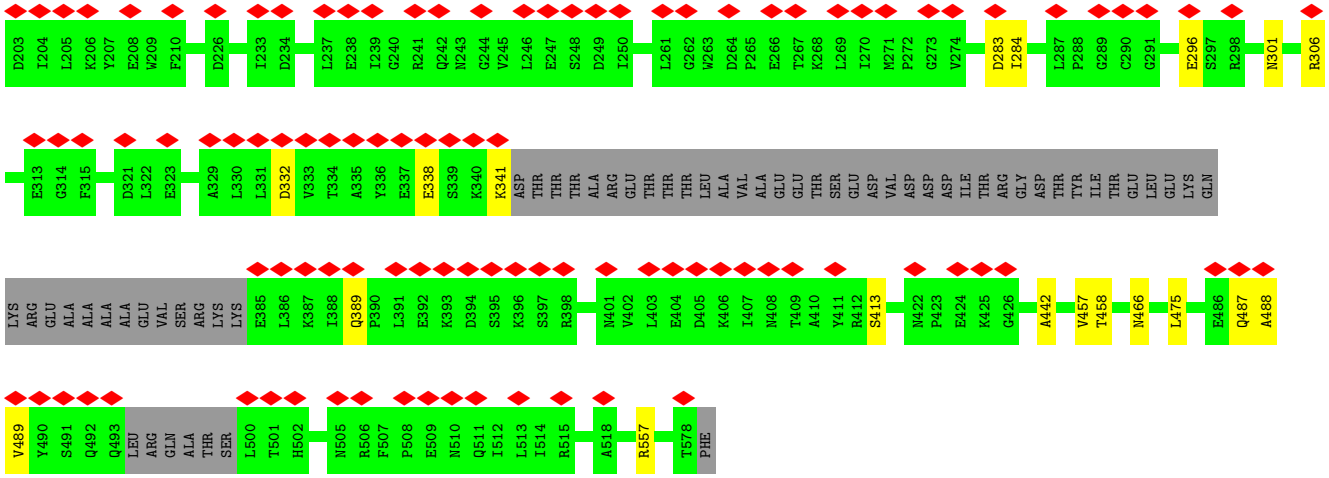


• Molecule 1: Penton protein

Chain UA:

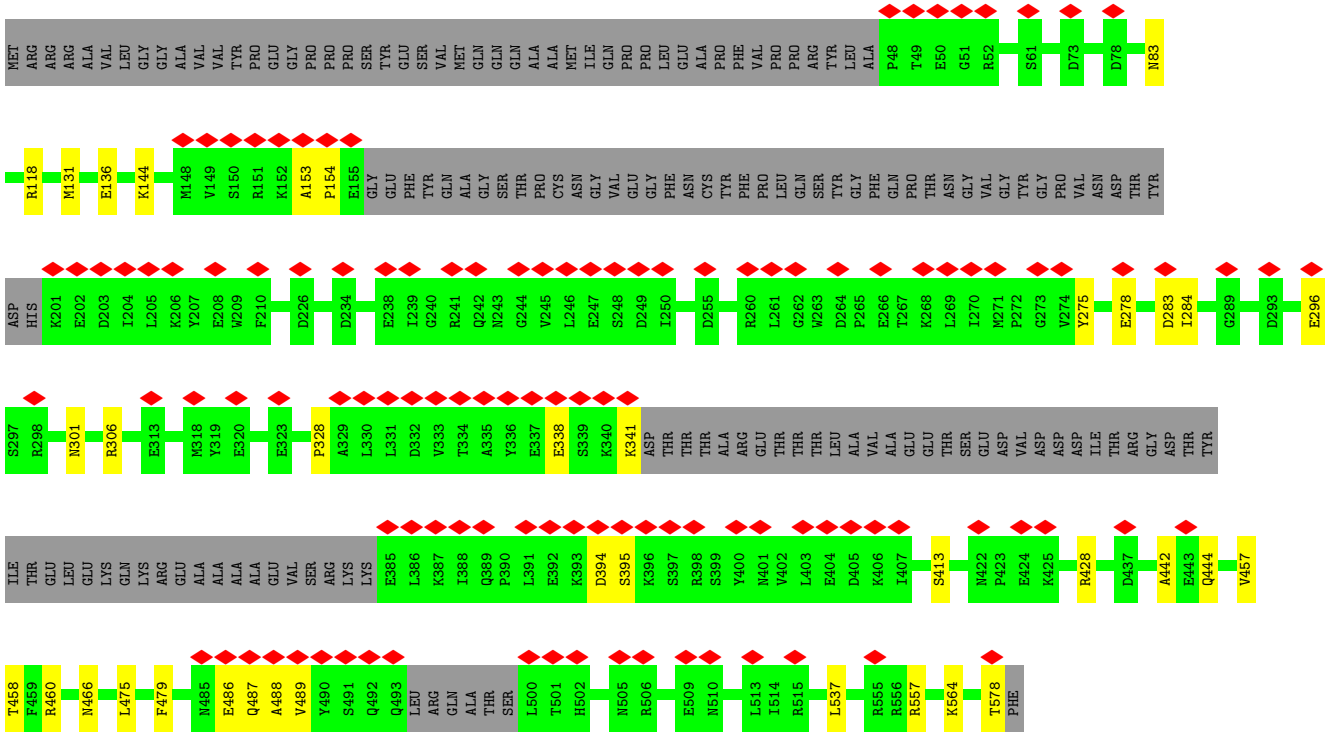






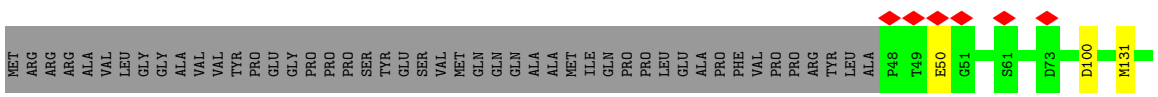
• Molecule 1: Penton protein

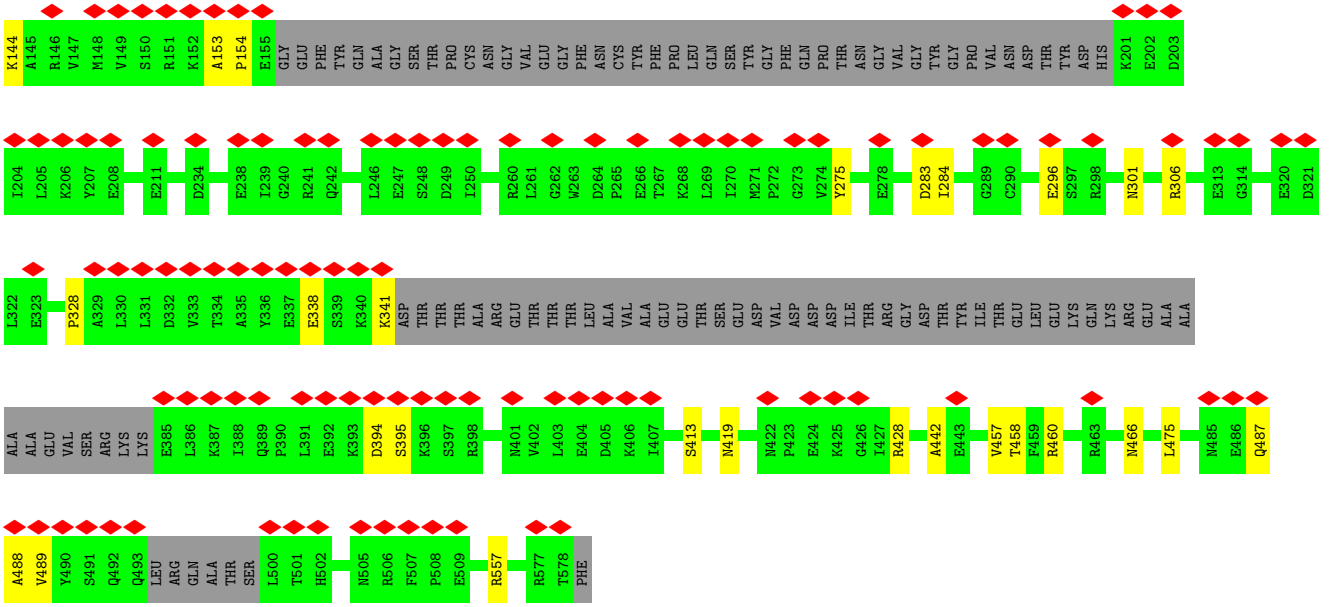
Chain VA:



• Molecule 1: Penton protein

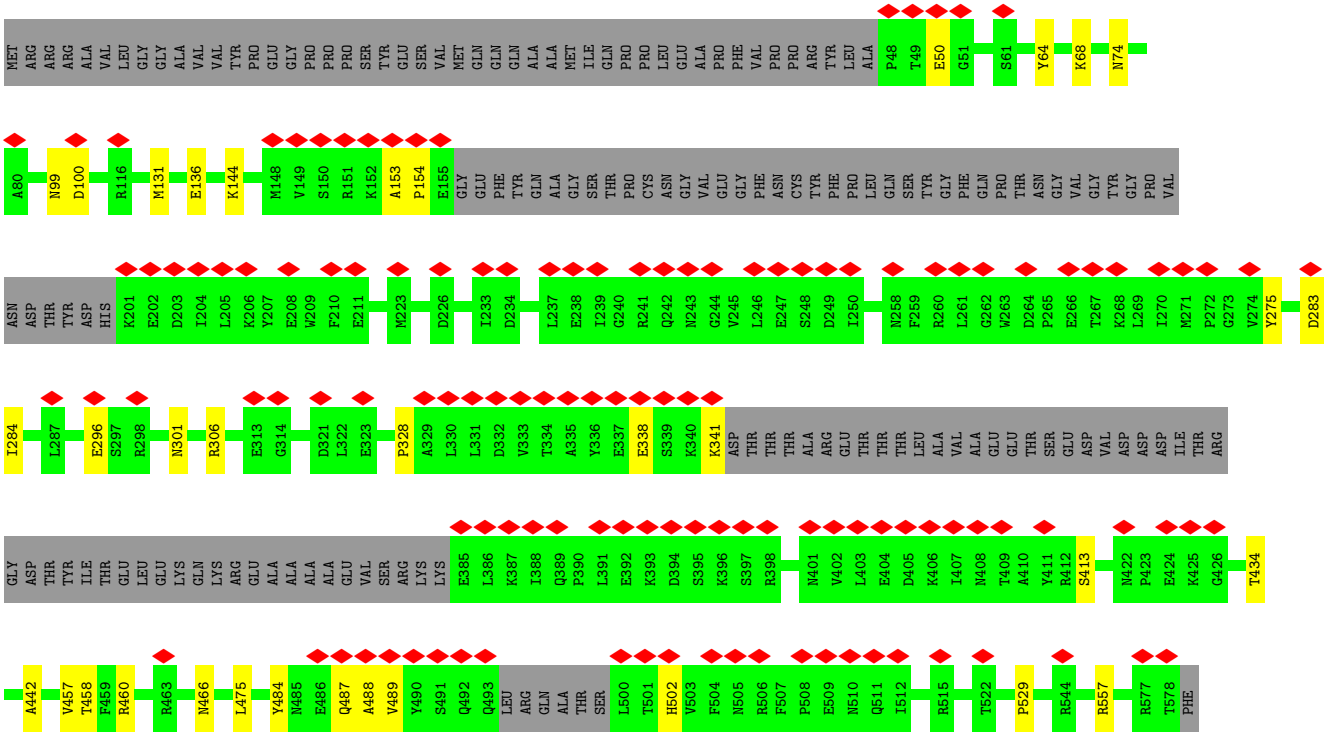
Chain WA:





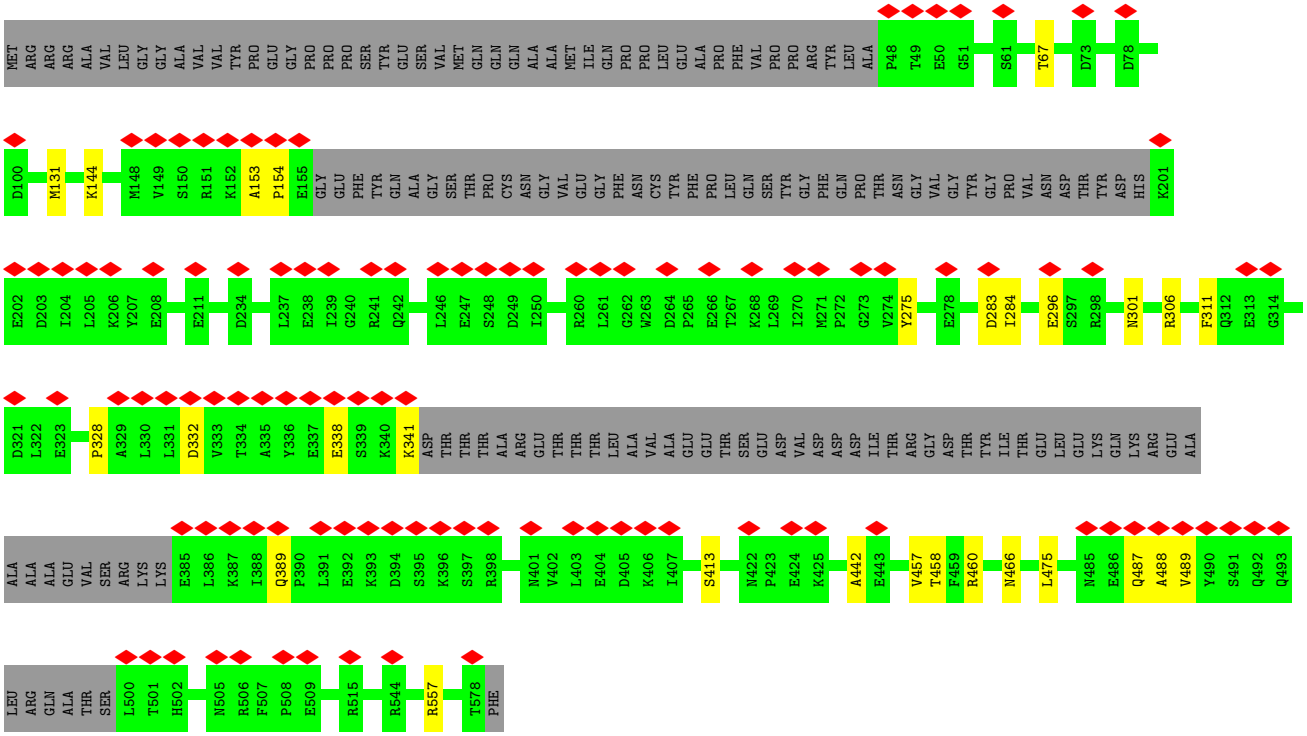
• Molecule 1: Penton protein

Chain XA:



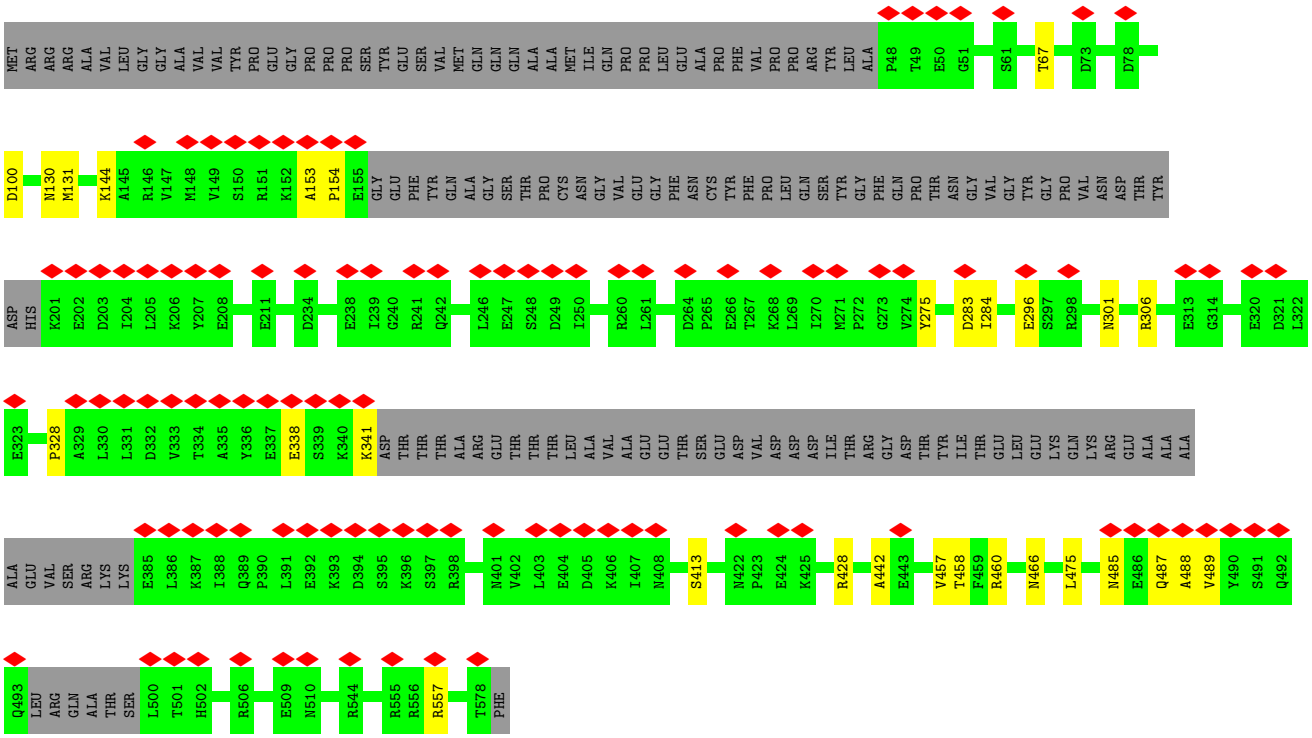
• Molecule 1: Penton protein

Chain YA:



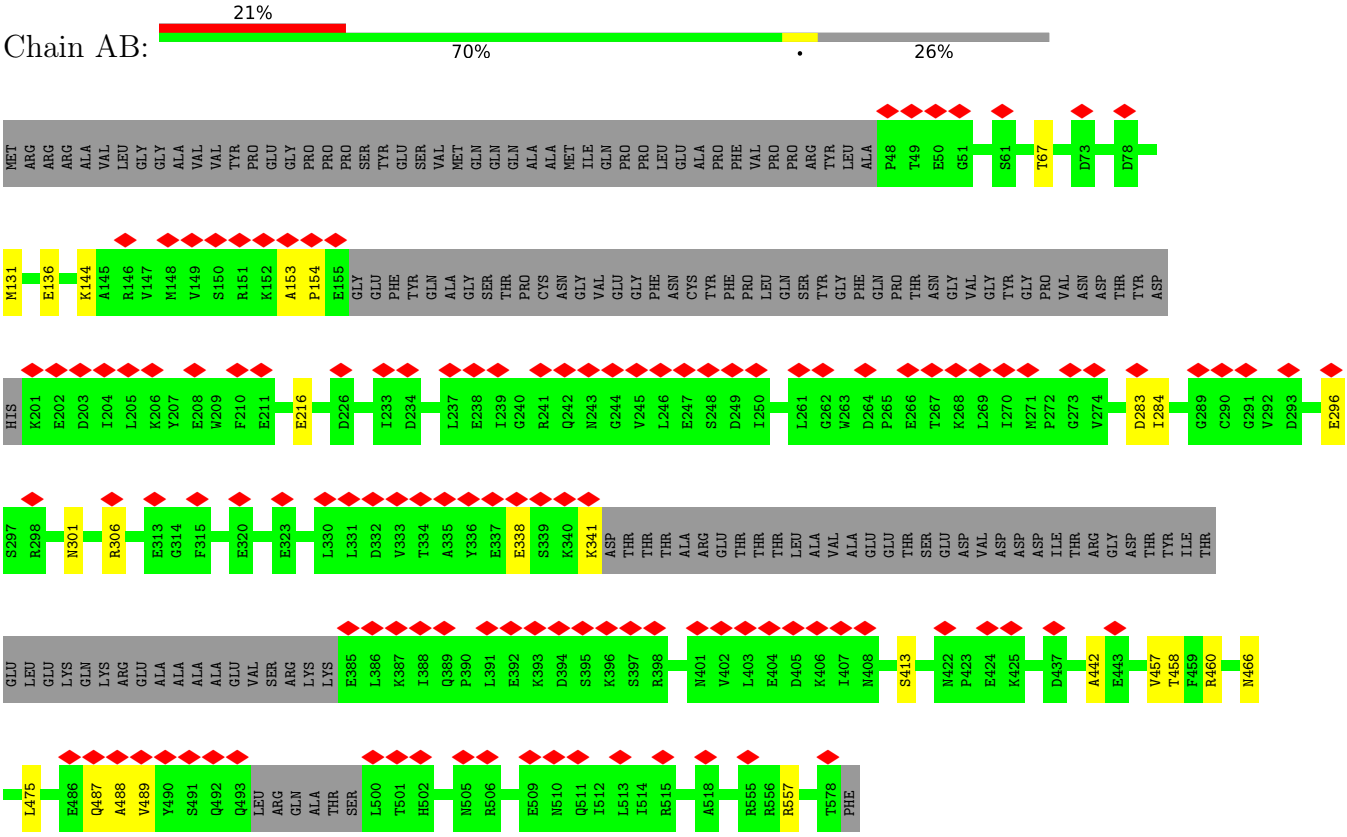
• Molecule 1: Penton protein

Chain ZA:



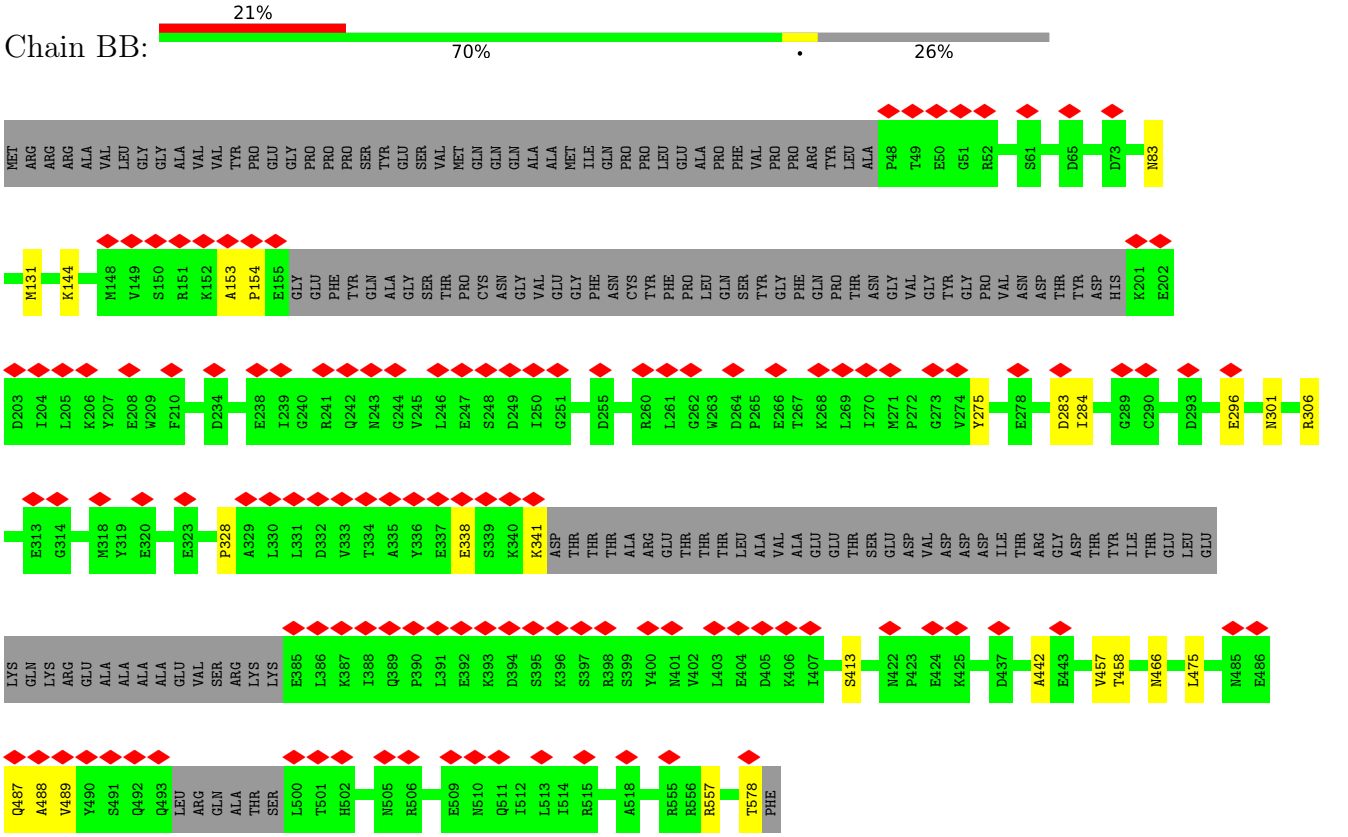
• Molecule 1: Penton protein

Chain AB:



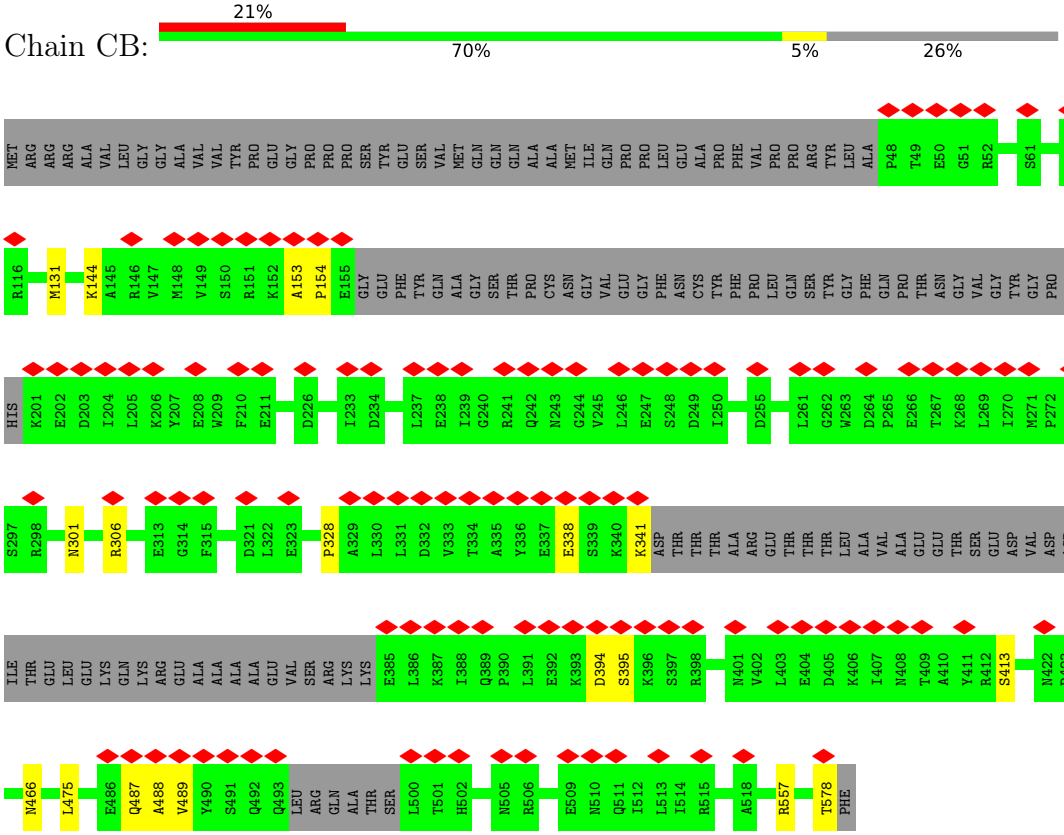
• Molecule 1: Penton protein

Chain BB:



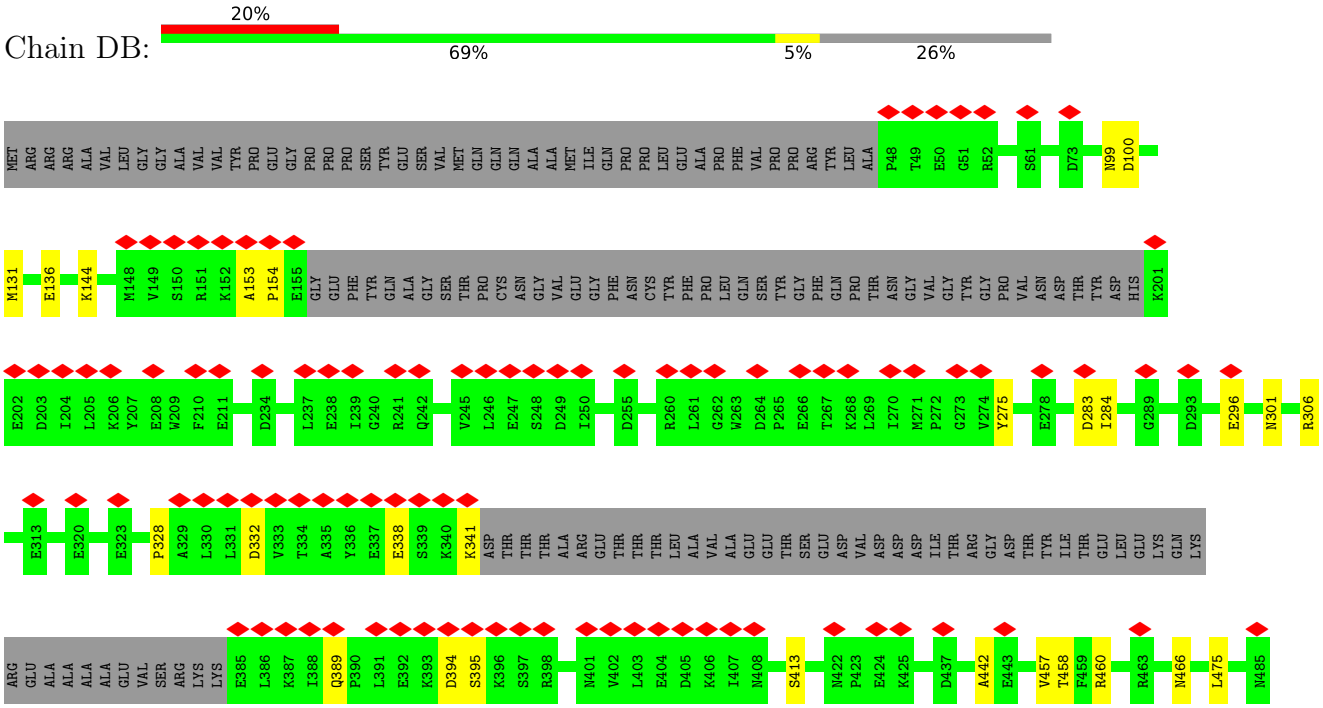
• Molecule 1: Penton protein

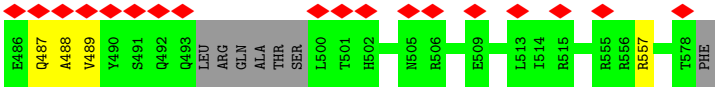
Chain CB:



• Molecule 1: Penton protein

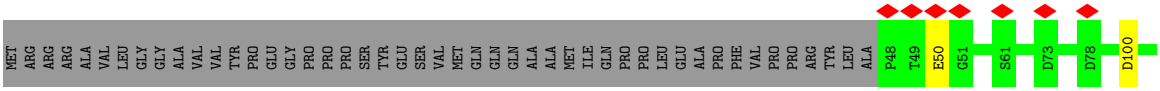
Chain DB:

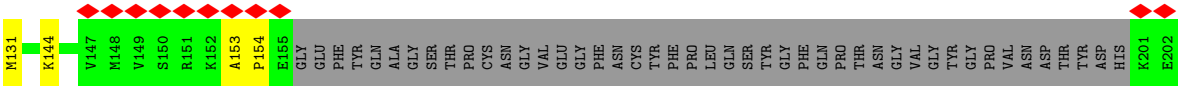


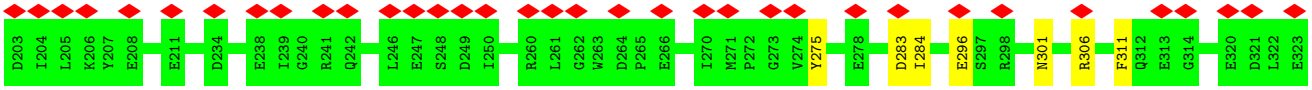


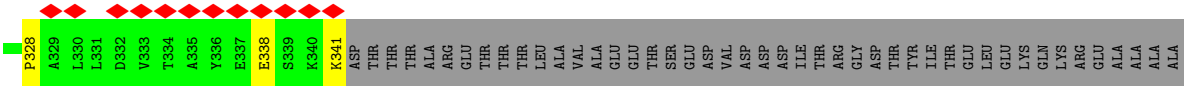
• Molecule 1: Penton protein

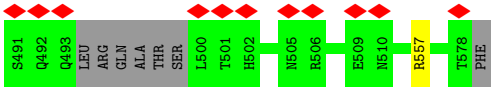
Chain EB:





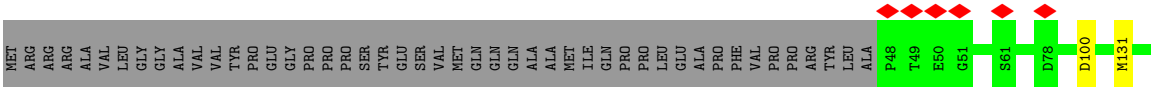


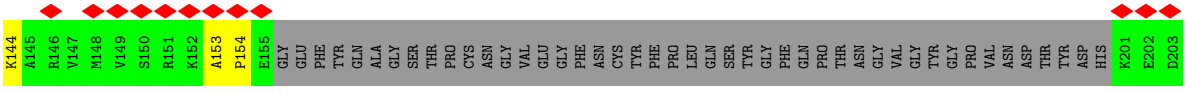


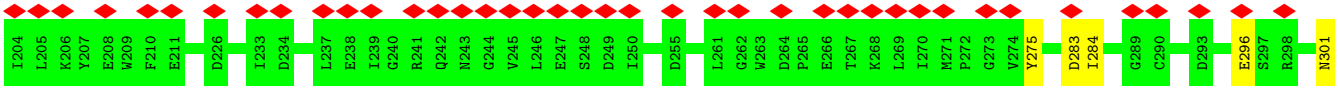


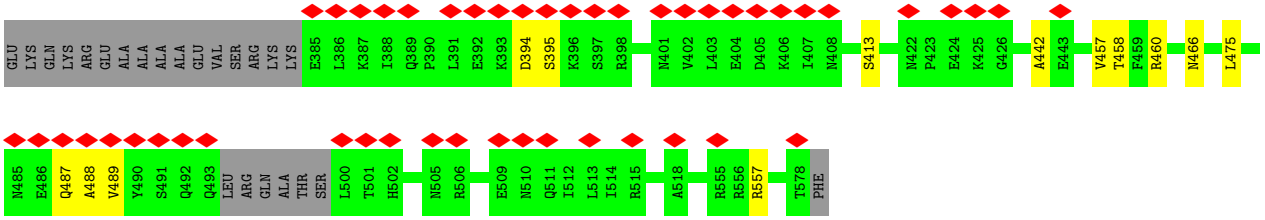
• Molecule 1: Penton protein

Chain FB:



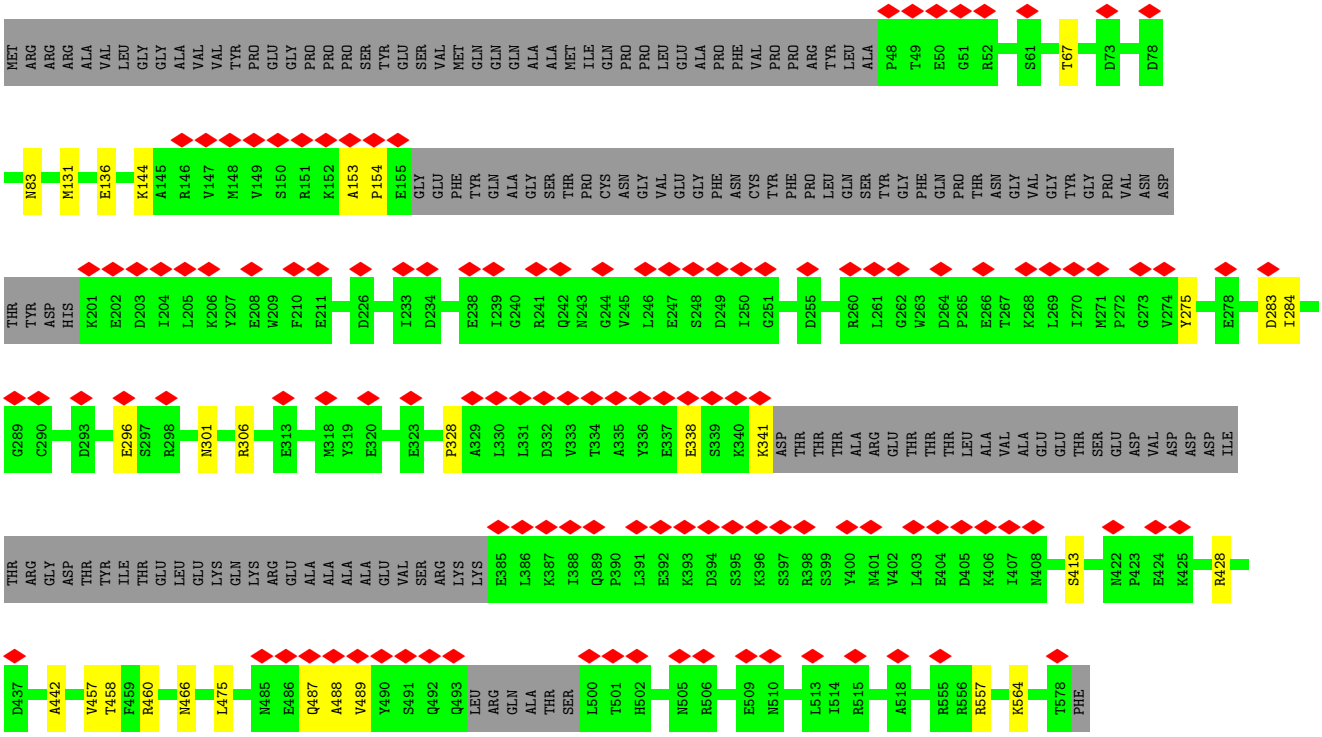






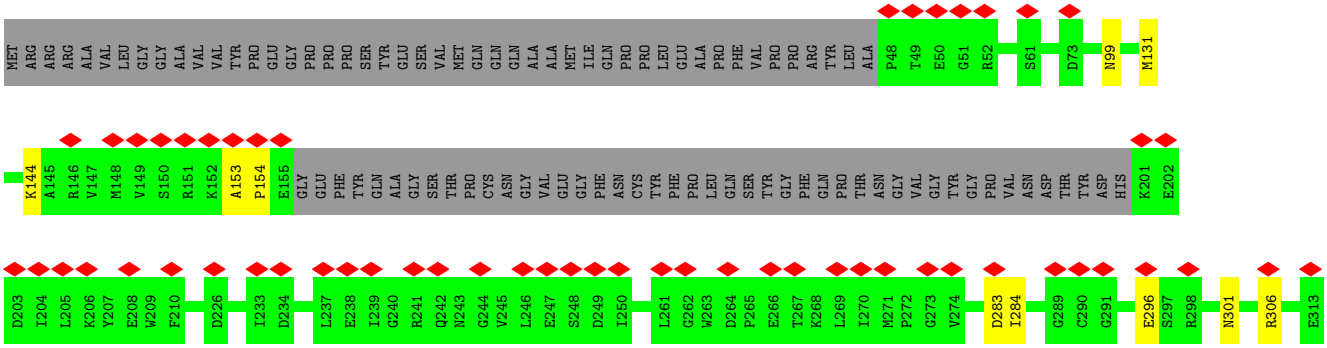
• Molecule 1: Penton protein

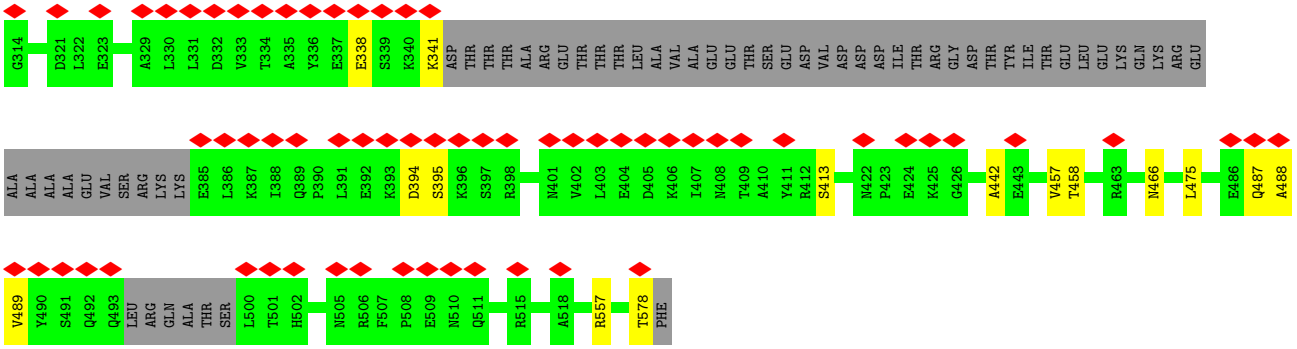
Chain GB:



• Molecule 1: Penton protein

Chain HB:




G314 D321 L322 E323 A329 L330 L331 D332 V333 T334 A335 Y336 E337 E338 S339 K340 K341 ASP THR THR THR ALA ARG GLU THR THR THR LEU ALA VAL ALA GLU GLU THR SER GLU ASP VAL ASP ASP ASP ILE THR ARG GLY ASP THR TYR ILE THR GLU LEU GLU LYS GLN LYS ARG GLU
ALA ALA ALA ALA GLU VAL SER ARG LYS LYS E385 L386 K387 T388 Q389 P390 L391 E392 K393 D394 S395 K396 S397 R398 N401 V402 L403 E404 D405 K406 I407 N408 T409 A410 Y411 R412 S413 N422 P423 E424 K425 G426 A442 E443 V457 T458 R463 N466 L475 E486 Q487 A488
V489 Y490 S491 Q492 Q493 LEU ARG GLN ALA THR SER L500 T501 H502 N505 R506 F507 P508 E509 N510 Q511 R515 A518 R557 T578 PHE

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32227	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 ($e^-/Å^2$)	1.1	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.072	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	356.99997, 356.99997, 356.99997	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	1	0.47	0/3610	0.66	2/4901 (0.0%)
1	A	0.47	0/3610	0.66	2/4901 (0.0%)
1	AA	0.47	0/3610	0.66	2/4901 (0.0%)
1	AB	0.47	0/3610	0.66	2/4901 (0.0%)
1	B	0.47	0/3610	0.66	2/4901 (0.0%)
1	BA	0.47	0/3610	0.66	2/4901 (0.0%)
1	BB	0.47	0/3610	0.66	2/4901 (0.0%)
1	C	0.47	0/3610	0.66	2/4901 (0.0%)
1	CA	0.47	0/3610	0.66	2/4901 (0.0%)
1	CB	0.47	0/3610	0.66	2/4901 (0.0%)
1	D	0.47	0/3610	0.66	2/4901 (0.0%)
1	DA	0.47	0/3610	0.66	2/4901 (0.0%)
1	DB	0.47	0/3610	0.66	2/4901 (0.0%)
1	E	0.47	0/3610	0.66	2/4901 (0.0%)
1	EA	0.47	0/3610	0.66	2/4901 (0.0%)
1	EB	0.47	0/3610	0.66	2/4901 (0.0%)
1	F	0.47	0/3610	0.66	2/4901 (0.0%)
1	FA	0.47	0/3610	0.66	2/4901 (0.0%)
1	FB	0.47	0/3610	0.66	2/4901 (0.0%)
1	G	0.47	0/3610	0.66	2/4901 (0.0%)
1	GA	0.47	0/3610	0.66	2/4901 (0.0%)
1	GB	0.47	0/3610	0.66	2/4901 (0.0%)
1	H	0.47	0/3610	0.66	2/4901 (0.0%)
1	HA	0.47	0/3610	0.66	2/4901 (0.0%)
1	HB	0.47	0/3610	0.66	2/4901 (0.0%)
1	I	0.47	0/3610	0.66	2/4901 (0.0%)
1	IA	0.47	0/3610	0.66	2/4901 (0.0%)
1	J	0.47	0/3610	0.66	2/4901 (0.0%)
1	JA	0.47	0/3610	0.66	2/4901 (0.0%)
1	K	0.47	0/3610	0.66	2/4901 (0.0%)
1	KA	0.47	0/3610	0.66	2/4901 (0.0%)
1	L	0.47	0/3610	0.66	2/4901 (0.0%)
1	LA	0.47	0/3610	0.66	2/4901 (0.0%)
1	M	0.47	0/3610	0.66	2/4901 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	MA	0.47	0/3610	0.66	2/4901 (0.0%)
1	N	0.47	0/3610	0.66	2/4901 (0.0%)
1	NA	0.47	0/3610	0.66	3/4901 (0.1%)
1	O	0.47	0/3610	0.66	2/4901 (0.0%)
1	OA	0.47	0/3610	0.66	2/4901 (0.0%)
1	P	0.47	0/3610	0.66	2/4901 (0.0%)
1	PA	0.47	0/3610	0.66	2/4901 (0.0%)
1	Q	0.47	0/3610	0.66	2/4901 (0.0%)
1	QA	0.47	0/3610	0.66	2/4901 (0.0%)
1	R	0.47	0/3610	0.66	2/4901 (0.0%)
1	RA	0.47	0/3610	0.66	2/4901 (0.0%)
1	S	0.47	0/3610	0.66	2/4901 (0.0%)
1	SA	0.47	0/3610	0.66	2/4901 (0.0%)
1	T	0.47	0/3610	0.66	2/4901 (0.0%)
1	TA	0.47	0/3610	0.66	2/4901 (0.0%)
1	UA	0.47	0/3610	0.66	2/4901 (0.0%)
1	V	0.47	0/3610	0.66	2/4901 (0.0%)
1	VA	0.47	0/3610	0.66	1/4901 (0.0%)
1	W	0.47	0/3610	0.66	2/4901 (0.0%)
1	WA	0.47	0/3610	0.66	2/4901 (0.0%)
1	X	0.47	0/3610	0.66	2/4901 (0.0%)
1	XA	0.47	0/3610	0.66	2/4901 (0.0%)
1	Y	0.47	0/3610	0.66	1/4901 (0.0%)
1	YA	0.47	0/3610	0.66	2/4901 (0.0%)
1	Z	0.47	0/3610	0.66	2/4901 (0.0%)
1	ZA	0.47	0/3610	0.66	2/4901 (0.0%)
All	All	0.47	0/216600	0.66	119/294060 (0.0%)

There are no bond length outliers.

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	MA	557	ARG	NE-CZ-NH1	5.57	123.08	120.30
1	BA	557	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	HB	557	ARG	NE-CZ-NH1	5.55	123.07	120.30
1	EA	557	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	ZA	557	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	GB	557	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	F	557	ARG	NE-CZ-NH1	5.53	123.07	120.30
1	NA	557	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	TA	557	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	E	557	ARG	NE-CZ-NH1	5.52	123.06	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	Q	557	ARG	NE-CZ-NH1	5.51	123.06	120.30
1	EB	557	ARG	NE-CZ-NH1	5.51	123.06	120.30
1	UA	557	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	T	557	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	X	557	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	Z	557	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	I	557	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	AA	557	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	OA	557	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	SA	557	ARG	NE-CZ-NH1	5.49	123.04	120.30
1	IA	557	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	WA	557	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	FB	557	ARG	NE-CZ-NH1	5.47	123.04	120.30
1	C	557	ARG	NE-CZ-NH1	5.47	123.03	120.30
1	J	557	ARG	NE-CZ-NH1	5.47	123.03	120.30
1	R	557	ARG	NE-CZ-NH1	5.47	123.03	120.30
1	DB	557	ARG	NE-CZ-NH1	5.47	123.03	120.30
1	O	557	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	W	557	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	HA	557	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	1	557	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	S	557	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	N	557	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	DA	557	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	GA	557	ARG	NE-CZ-NH1	5.45	123.02	120.30
1	A	557	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	H	557	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	CA	557	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	FA	557	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	AB	557	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	BB	557	ARG	NE-CZ-NH1	5.43	123.01	120.30
1	LA	557	ARG	NE-CZ-NH1	5.43	123.01	120.30
1	QA	557	ARG	NE-CZ-NH1	5.43	123.01	120.30
1	JA	557	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	XA	557	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	CB	557	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	VA	557	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	RA	557	ARG	NE-CZ-NH1	5.41	123.01	120.30
1	D	557	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	K	557	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	P	557	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	M	557	ARG	NE-CZ-NH1	5.39	123.00	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	KA	557	ARG	NE-CZ-NH1	5.39	122.99	120.30
1	G	557	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	B	557	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	PA	557	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	V	557	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	L	557	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	YA	557	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	Y	557	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	HB	557	ARG	NE-CZ-NH2	-5.17	117.72	120.30
1	BA	557	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	CA	557	ARG	NE-CZ-NH2	-5.15	117.72	120.30
1	FA	557	ARG	NE-CZ-NH2	-5.15	117.73	120.30
1	C	557	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	F	557	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	E	557	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	Z	557	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	GA	557	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	N	557	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	KA	557	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	RA	557	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	WA	557	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	W	557	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	BB	557	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	H	557	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	T	557	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	M	557	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	TA	557	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	OA	557	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	GB	557	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	EA	557	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	P	557	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	XA	557	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	YA	557	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	A	557	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	1	557	ARG	NE-CZ-NH2	-5.07	117.76	120.30
1	I	557	ARG	NE-CZ-NH2	-5.07	117.76	120.30
1	MA	557	ARG	NE-CZ-NH2	-5.07	117.76	120.30
1	IA	557	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	NA	557	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	R	557	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	AA	557	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	S	557	ARG	NE-CZ-NH2	-5.06	117.77	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	UA	557	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	SA	557	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	CB	557	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	DB	557	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	Q	557	ARG	NE-CZ-NH2	-5.05	117.77	120.30
1	AB	557	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	K	557	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	V	557	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	PA	557	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	HA	557	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	EB	557	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	O	557	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	DA	557	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	B	557	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	J	557	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	ZA	557	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	QA	557	ARG	NE-CZ-NH2	-5.03	117.78	120.30
1	L	557	ARG	NE-CZ-NH2	-5.03	117.78	120.30
1	D	557	ARG	NE-CZ-NH2	-5.03	117.79	120.30
1	X	557	ARG	NE-CZ-NH2	-5.03	117.78	120.30
1	FB	557	ARG	NE-CZ-NH2	-5.03	117.79	120.30
1	JA	557	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	NA	65	ASP	CB-CG-OD1	5.02	122.82	118.30
1	G	557	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	LA	65	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	3529	3461	3461	17	0
1	A	3529	3461	3461	16	0
1	AA	3529	3461	3461	14	0
1	AB	3529	3461	3461	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3529	3461	3461	15	0
1	BA	3529	3461	3461	19	0
1	BB	3529	3461	3461	12	0
1	C	3529	3461	3461	14	0
1	CA	3529	3461	3461	15	0
1	CB	3529	3461	3461	14	0
1	D	3529	3461	3461	14	0
1	DA	3529	3461	3461	22	0
1	DB	3529	3461	3461	19	0
1	E	3529	3461	3461	37	0
1	EA	3529	3461	3461	16	0
1	EB	3529	3461	3461	17	0
1	F	3529	3461	3461	10	0
1	FA	3529	3461	3461	14	0
1	FB	3529	3461	3461	16	0
1	G	3529	3461	3461	32	0
1	GA	3529	3461	3461	16	0
1	GB	3529	3461	3461	16	0
1	H	3529	3461	3461	16	0
1	HA	3529	3461	3461	14	0
1	HB	3529	3461	3461	13	0
1	I	3529	3461	3461	14	0
1	IA	3529	3461	3461	19	0
1	J	3529	3461	3461	13	0
1	JA	3529	3461	3461	15	0
1	K	3529	3461	3461	13	0
1	KA	3529	3461	3461	14	0
1	L	3529	3461	3461	21	0
1	LA	3529	3461	3461	15	0
1	M	3529	3461	3461	17	0
1	MA	3529	3461	3461	11	0
1	N	3529	3461	3461	14	0
1	NA	3529	3461	3461	15	0
1	O	3529	3461	3461	19	0
1	OA	3529	3461	3461	14	0
1	P	3529	3461	3461	18	0
1	PA	3529	3461	3461	12	0
1	Q	3529	3461	3461	19	0
1	QA	3529	3461	3461	15	0
1	R	3529	3461	3461	15	0
1	RA	3529	3461	3461	13	0
1	S	3529	3461	3461	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	SA	3529	3461	3461	13	0
1	T	3529	3461	3461	16	0
1	TA	3529	3461	3461	17	0
1	UA	3529	3461	3461	12	0
1	V	3529	3461	3461	17	0
1	VA	3529	3461	3461	29	0
1	W	3529	3461	3461	13	0
1	WA	3529	3461	3461	17	0
1	X	3529	3461	3461	19	0
1	XA	3529	3461	3461	31	0
1	Y	3529	3461	3461	12	0
1	YA	3529	3461	3461	14	0
1	Z	3529	3461	3461	13	0
1	ZA	3529	3461	3461	18	0
All	All	211740	207660	207660	806	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 (806) 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:428:ARG:NH2	1:DA:136:GLU:OE1	2.03	0.91
1:P:136:GLU:OE1	1:S:428:ARG:NH2	2.03	0.90
1:L:428:ARG:NH2	1:N:136:GLU:OE1	2.04	0.89
1:E:136:GLU:OE1	1:H:428:ARG:NH2	2.08	0.87
1:E:428:ARG:NH2	1:G:136:GLU:OE1	2.09	0.85
1:VA:460:ARG:NH2	1:XA:99:ASN:OD1	2.13	0.81
1:E:484:TYR:OH	1:G:485:ASN:OD1	2.00	0.79
1:V:100:ASP:OD2	1:GA:460:ARG:NH1	2.17	0.78
1:WA:428:ARG:NH2	1:AB:136:GLU:OE1	2.15	0.77
1:V:100:ASP:OD1	1:GA:460:ARG:NH1	2.20	0.75
1:V:100:ASP:CG	1:GA:460:ARG:NH1	2.42	0.73
1:E:266:GLU:HG3	1:G:242:GLN:OE1	1.90	0.72
1:1:428:ARG:NH2	1:B:136:GLU:OE1	2.22	0.71
1:L:457:VAL:HG13	1:N:67:THR:HG21	1.70	0.71
1:V:457:VAL:HG13	1:X:67:THR:HG21	1.72	0.71
1:XA:457:VAL:HG13	1:ZA:67:THR:HG21	1.73	0.69
1:KA:428:ARG:NH2	1:NA:136:GLU:OE1	2.24	0.69
1:E:457:VAL:HG13	1:G:67:THR:HG21	1.74	0.69
1:FA:136:GLU:OE1	1:IA:428:ARG:NH2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:WA:457:VAL:HG13	1:AB:67:THR:HG21	1.74	0.68
1:IA:460:ARG:NH1	1:XA:100:ASP:OD2	2.26	0.68
1:S:100:ASP:OD1	1:DB:460:ARG:NH1	2.27	0.67
1:K:460:ARG:NH1	1:P:100:ASP:OD2	2.27	0.66
1:CB:578:THR:N	1:EB:50:GLU:OE2	2.29	0.65
1:QA:136:GLU:OE1	1:TA:428:ARG:NH2	2.29	0.65
1:Q:460:ARG:NH1	1:FB:100:ASP:OD1	2.30	0.64
1:E:419:ASN:HD21	1:G:216:GLU:HB3	1.62	0.64
1:BA:99:ASN:OD1	1:EA:460:ARG:NH2	2.31	0.63
1:P:564:LYS:HG3	1:S:442:ALA:HB3	1.79	0.63
1:VA:486:GLU:OE2	1:XA:487:GLN:HA	1.99	0.62
1:YA:457:VAL:O	1:YA:458:THR:OG1	2.18	0.62
1:EB:457:VAL:O	1:EB:458:THR:OG1	2.18	0.62
1:D:457:VAL:O	1:D:458:THR:OG1	2.18	0.62
1:Y:457:VAL:O	1:Y:458:THR:OG1	2.18	0.62
1:XA:484:TYR:OH	1:ZA:485:ASN:OD1	2.12	0.62
1:X:457:VAL:O	1:X:458:THR:OG1	2.18	0.61
1:FB:457:VAL:O	1:FB:458:THR:OG1	2.18	0.61
1:E:100:ASP:OD2	1:ZA:460:ARG:NH1	2.34	0.61
1:WA:457:VAL:O	1:WA:458:THR:OG1	2.18	0.61
1:Q:457:VAL:O	1:Q:458:THR:OG1	2.18	0.61
1:DA:457:VAL:O	1:DA:458:THR:OG1	2.18	0.60
1:MA:457:VAL:O	1:MA:458:THR:OG1	2.18	0.60
1:1:457:VAL:O	1:1:458:THR:OG1	2.18	0.60
1:E:280:PHE:HE1	1:G:223:MET:CE	2.14	0.60
1:PA:457:VAL:O	1:PA:458:THR:OG1	2.18	0.60
1:I:457:VAL:O	1:I:458:THR:OG1	2.18	0.60
1:JA:457:VAL:O	1:JA:458:THR:OG1	2.18	0.60
1:DB:457:VAL:O	1:DB:458:THR:OG1	2.18	0.60
1:V:457:VAL:O	1:V:458:THR:OG1	2.18	0.59
1:H:457:VAL:O	1:H:458:THR:OG1	2.18	0.59
1:K:457:VAL:O	1:K:458:THR:OG1	2.18	0.59
1:M:457:VAL:O	1:M:458:THR:OG1	2.18	0.59
1:O:457:VAL:O	1:O:458:THR:OG1	2.18	0.59
1:OA:457:VAL:O	1:OA:458:THR:OG1	2.18	0.59
1:E:262:GLY:HA2	1:G:506:ARG:HH22	1.67	0.59
1:E:484:TYR:OH	1:G:485:ASN:CG	2.40	0.59
1:J:311:PHE:HB3	1:VA:83:ASN:O	2.02	0.59
1:QA:457:VAL:O	1:QA:458:THR:OG1	2.18	0.59
1:ZA:457:VAL:O	1:ZA:458:THR:OG1	2.18	0.59
1:X:460:ARG:NH1	1:WA:100:ASP:OD2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:457:VAL:O	1:BA:458:THR:OG1	2.18	0.59
1:Z:457:VAL:O	1:Z:458:THR:OG1	2.18	0.59
1:W:457:VAL:O	1:W:458:THR:OG1	2.18	0.59
1:B:457:VAL:O	1:B:458:THR:OG1	2.18	0.59
1:CB:457:VAL:O	1:CB:458:THR:OG1	2.18	0.59
1:C:457:VAL:O	1:C:458:THR:OG1	2.18	0.59
1:WA:50:GLU:OE2	1:BB:578:THR:N	2.36	0.59
1:E:457:VAL:O	1:E:458:THR:OG1	2.18	0.58
1:HB:457:VAL:O	1:HB:458:THR:OG1	2.18	0.58
1:EA:457:VAL:O	1:EA:458:THR:OG1	2.18	0.58
1:FA:457:VAL:O	1:FA:458:THR:OG1	2.18	0.58
1:E:484:TYR:HB2	1:G:483:PHE:HB3	1.86	0.58
1:TA:457:VAL:O	1:TA:458:THR:OG1	2.18	0.58
1:AB:457:VAL:O	1:AB:458:THR:OG1	2.18	0.58
1:LA:311:PHE:HB3	1:OA:83:ASN:O	2.04	0.58
1:SA:457:VAL:O	1:SA:458:THR:OG1	2.18	0.58
1:R:457:VAL:O	1:R:458:THR:OG1	2.18	0.58
1:G:457:VAL:O	1:G:458:THR:OG1	2.18	0.57
1:VA:278:GLU:OE2	1:XA:502:HIS:CE1	2.57	0.57
1:IA:457:VAL:O	1:IA:458:THR:OG1	2.18	0.57
1:BB:457:VAL:O	1:BB:458:THR:OG1	2.18	0.57
1:S:100:ASP:CG	1:DB:460:ARG:NH1	2.58	0.57
1:X:311:PHE:HB3	1:Z:83:ASN:O	2.05	0.57
1:BA:457:VAL:HG13	1:DA:67:THR:HG21	1.87	0.56
1:PA:457:VAL:HG13	1:RA:67:THR:HG21	1.87	0.56
1:A:311:PHE:HB3	1:C:83:ASN:O	2.04	0.56
1:A:457:VAL:O	1:A:458:THR:OG1	2.18	0.56
1:CA:457:VAL:O	1:CA:458:THR:OG1	2.18	0.56
1:R:311:PHE:HB3	1:T:83:ASN:O	2.06	0.56
1:RA:457:VAL:HG13	1:TA:67:THR:HG21	1.87	0.56
1:VA:479:PHE:HE1	1:XA:529:PRO:CG	2.18	0.56
1:M:301:ASN:OD1	1:M:306:ARG:NH2	2.39	0.56
1:YA:311:PHE:HB3	1:BB:83:ASN:O	2.06	0.56
1:BA:301:ASN:OD1	1:BA:306:ARG:NH2	2.39	0.56
1:CA:460:ARG:NH1	1:EB:100:ASP:OD2	2.39	0.56
1:FA:301:ASN:OD1	1:FA:306:ARG:NH2	2.39	0.56
1:MA:301:ASN:OD1	1:MA:306:ARG:NH2	2.39	0.56
1:AB:301:ASN:OD1	1:AB:306:ARG:NH2	2.39	0.56
1:FB:301:ASN:OD1	1:FB:306:ARG:NH2	2.39	0.56
1:1:301:ASN:OD1	1:1:306:ARG:NH2	2.39	0.56
1:F:457:VAL:O	1:F:458:THR:OG1	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:301:ASN:OD1	1:J:306:ARG:NH2	2.39	0.56
1:L:301:ASN:OD1	1:L:306:ARG:NH2	2.39	0.56
1:C:301:ASN:OD1	1:C:306:ARG:NH2	2.39	0.56
1:V:301:ASN:OD1	1:V:306:ARG:NH2	2.39	0.56
1:Z:301:ASN:OD1	1:Z:306:ARG:NH2	2.39	0.56
1:JA:301:ASN:OD1	1:JA:306:ARG:NH2	2.39	0.56
1:OA:301:ASN:OD1	1:OA:306:ARG:NH2	2.39	0.56
1:WA:301:ASN:OD1	1:WA:306:ARG:NH2	2.39	0.56
1:D:301:ASN:OD1	1:D:306:ARG:NH2	2.39	0.55
1:L:100:ASP:OD2	1:TA:460:ARG:NH1	2.39	0.55
1:W:301:ASN:OD1	1:W:306:ARG:NH2	2.39	0.55
1:FA:457:VAL:HG13	1:HA:67:THR:HG21	1.88	0.55
1:KA:457:VAL:O	1:KA:458:THR:OG1	2.18	0.55
1:HB:301:ASN:OD1	1:HB:306:ARG:NH2	2.39	0.55
1:N:301:ASN:OD1	1:N:306:ARG:NH2	2.39	0.55
1:TA:301:ASN:OD1	1:TA:306:ARG:NH2	2.39	0.55
1:GB:301:ASN:OD1	1:GB:306:ARG:NH2	2.39	0.55
1:E:301:ASN:OD1	1:E:306:ARG:NH2	2.39	0.55
1:P:457:VAL:HG13	1:R:67:THR:HG21	1.87	0.55
1:SA:301:ASN:OD1	1:SA:306:ARG:NH2	2.39	0.55
1:VA:278:GLU:OE2	1:XA:502:HIS:NE2	2.38	0.55
1:YA:301:ASN:OD1	1:YA:306:ARG:NH2	2.39	0.55
1:AB:144:LYS:NZ	1:AB:296:GLU:OE2	2.36	0.55
1:EB:311:PHE:HB3	1:GB:83:ASN:O	2.06	0.55
1:O:301:ASN:OD1	1:O:306:ARG:NH2	2.39	0.55
1:P:301:ASN:OD1	1:P:306:ARG:NH2	2.39	0.55
1:Q:301:ASN:OD1	1:Q:306:ARG:NH2	2.39	0.55
1:CA:301:ASN:OD1	1:CA:306:ARG:NH2	2.39	0.55
1:NA:301:ASN:OD1	1:NA:306:ARG:NH2	2.39	0.55
1:R:301:ASN:OD1	1:R:306:ARG:NH2	2.39	0.55
1:AA:457:VAL:HG13	1:CA:67:THR:HG21	1.89	0.55
1:GA:301:ASN:OD1	1:GA:306:ARG:NH2	2.39	0.55
1:RA:301:ASN:OD1	1:RA:306:ARG:NH2	2.39	0.55
1:H:301:ASN:OD1	1:H:306:ARG:NH2	2.39	0.55
1:X:301:ASN:OD1	1:X:306:ARG:NH2	2.39	0.55
1:BA:50:GLU:OE2	1:EA:578:THR:N	2.40	0.55
1:ZA:301:ASN:OD1	1:ZA:306:ARG:NH2	2.39	0.55
1:H:144:LYS:NZ	1:H:296:GLU:OE2	2.36	0.55
1:I:301:ASN:OD1	1:I:306:ARG:NH2	2.39	0.55
1:T:301:ASN:OD1	1:T:306:ARG:NH2	2.39	0.55
1:DA:301:ASN:OD1	1:DA:306:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:301:ASN:OD1	1:EA:306:ARG:NH2	2.39	0.55
1:XA:301:ASN:OD1	1:XA:306:ARG:NH2	2.39	0.55
1:EB:301:ASN:OD1	1:EB:306:ARG:NH2	2.39	0.55
1:E:67:THR:HG21	1:H:457:VAL:HG13	1.89	0.55
1:F:301:ASN:OD1	1:F:306:ARG:NH2	2.39	0.55
1:S:301:ASN:OD1	1:S:306:ARG:NH2	2.39	0.55
1:K:301:ASN:OD1	1:K:306:ARG:NH2	2.39	0.55
1:P:67:THR:HG21	1:S:457:VAL:HG13	1.88	0.55
1:NA:457:VAL:O	1:NA:458:THR:OG1	2.18	0.55
1:UA:301:ASN:OD1	1:UA:306:ARG:NH2	2.39	0.55
1:VA:301:ASN:OD1	1:VA:306:ARG:NH2	2.39	0.55
1:DB:301:ASN:OD1	1:DB:306:ARG:NH2	2.39	0.55
1:B:301:ASN:OD1	1:B:306:ARG:NH2	2.39	0.55
1:D:457:VAL:HG13	1:F:67:THR:HG21	1.89	0.55
1:M:457:VAL:HG13	1:O:67:THR:HG21	1.89	0.55
1:HA:428:ARG:NH2	1:JA:136:GLU:OE1	2.40	0.55
1:QA:301:ASN:OD1	1:QA:306:ARG:NH2	2.39	0.55
1:BB:301:ASN:OD1	1:BB:306:ARG:NH2	2.39	0.55
1:Y:301:ASN:OD1	1:Y:306:ARG:NH2	2.39	0.54
1:AA:301:ASN:OD1	1:AA:306:ARG:NH2	2.39	0.54
1:HA:301:ASN:OD1	1:HA:306:ARG:NH2	2.39	0.54
1:HA:457:VAL:O	1:HA:458:THR:OG1	2.18	0.54
1:LA:301:ASN:OD1	1:LA:306:ARG:NH2	2.39	0.54
1:T:144:LYS:NZ	1:T:296:GLU:OE2	2.36	0.54
1:AA:457:VAL:O	1:AA:458:THR:OG1	2.18	0.54
1:HA:311:PHE:HB3	1:JA:83:ASN:O	2.07	0.54
1:KA:301:ASN:OD1	1:KA:306:ARG:NH2	2.39	0.54
1:G:301:ASN:OD1	1:G:306:ARG:NH2	2.39	0.54
1:J:428:ARG:NH2	1:VA:136:GLU:OE1	2.38	0.54
1:CB:301:ASN:OD1	1:CB:306:ARG:NH2	2.39	0.54
1:GB:457:VAL:O	1:GB:458:THR:OG1	2.18	0.54
1:D:144:LYS:NZ	1:D:296:GLU:OE2	2.36	0.54
1:IA:301:ASN:OD1	1:IA:306:ARG:NH2	2.39	0.54
1:MA:144:LYS:NZ	1:MA:296:GLU:OE2	2.36	0.54
1:QA:144:LYS:NZ	1:QA:296:GLU:OE2	2.36	0.54
1:IA:460:ARG:NH1	1:XA:100:ASP:CG	2.61	0.54
1:EB:144:LYS:NZ	1:EB:296:GLU:OE2	2.36	0.54
1:A:301:ASN:OD1	1:A:306:ARG:NH2	2.39	0.54
1:J:144:LYS:NZ	1:J:296:GLU:OE2	2.36	0.54
1:HB:144:LYS:NZ	1:HB:296:GLU:OE2	2.36	0.54
1:A:460:ARG:NH1	1:CB:100:ASP:OD2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:280:PHE:CE1	1:G:223:MET:CE	2.91	0.54
1:Y:100:ASP:OD2	1:XA:460:ARG:NH1	2.41	0.54
1:UA:144:LYS:NZ	1:UA:296:GLU:OE2	2.36	0.54
1:I:457:VAL:HG13	1:LA:67:THR:HG21	1.90	0.54
1:QA:67:THR:HG21	1:TA:457:VAL:HG13	1.90	0.54
1:P:144:LYS:NZ	1:P:296:GLU:OE2	2.36	0.53
1:PA:301:ASN:OD1	1:PA:306:ARG:NH2	2.39	0.53
1:RA:144:LYS:NZ	1:RA:296:GLU:OE2	2.36	0.53
1:KA:144:LYS:NZ	1:KA:296:GLU:OE2	2.36	0.53
1:LA:100:ASP:OD2	1:WA:460:ARG:NH1	2.42	0.53
1:VA:578:THR:N	1:XA:50:GLU:OE2	2.42	0.53
1:K:144:LYS:NZ	1:K:296:GLU:OE2	2.36	0.53
1:X:428:ARG:NH2	1:Z:136:GLU:OE1	2.40	0.53
1:S:144:LYS:NZ	1:S:296:GLU:OE2	2.36	0.53
1:LA:428:ARG:NH2	1:OA:136:GLU:OE1	2.40	0.53
1:FB:144:LYS:NZ	1:FB:296:GLU:OE2	2.36	0.53
1:CA:144:LYS:NZ	1:CA:296:GLU:OE2	2.36	0.53
1:BB:144:LYS:NZ	1:BB:296:GLU:OE2	2.36	0.53
1:M:144:LYS:NZ	1:M:296:GLU:OE2	2.36	0.53
1:B:144:LYS:NZ	1:B:296:GLU:OE2	2.36	0.52
1:W:460:ARG:NH1	1:ZA:100:ASP:OD1	2.42	0.52
1:PA:144:LYS:NZ	1:PA:296:GLU:OE2	2.36	0.52
1:Q:144:LYS:NZ	1:Q:296:GLU:OE2	2.36	0.52
1:X:144:LYS:NZ	1:X:296:GLU:OE2	2.36	0.52
1:GA:311:PHE:CD1	1:IA:79:ILE:HG12	2.44	0.52
1:J:457:VAL:O	1:J:458:THR:OG1	2.18	0.52
1:P:457:VAL:O	1:P:458:THR:OG1	2.18	0.52
1:EA:394:ASP:O	1:EA:395:SER:OG	2.27	0.52
1:DB:144:LYS:NZ	1:DB:296:GLU:OE2	2.36	0.52
1:E:564:LYS:HG3	1:H:442:ALA:HB3	1.91	0.52
1:S:457:VAL:O	1:S:458:THR:OG1	2.18	0.52
1:KA:457:VAL:HG13	1:NA:67:THR:HG21	1.91	0.51
1:IA:460:ARG:NH1	1:XA:100:ASP:OD1	2.44	0.51
1:RA:457:VAL:O	1:RA:458:THR:OG1	2.18	0.51
1:WA:144:LYS:NZ	1:WA:296:GLU:OE2	2.36	0.51
1:ZA:144:LYS:NZ	1:ZA:296:GLU:OE2	2.36	0.51
1:XA:144:LYS:NZ	1:XA:296:GLU:OE2	2.36	0.51
1:DA:144:LYS:NZ	1:DA:296:GLU:OE2	2.36	0.51
1:O:144:LYS:NZ	1:O:296:GLU:OE2	2.36	0.51
1:LA:457:VAL:O	1:LA:458:THR:OG1	2.18	0.51
1:OA:144:LYS:NZ	1:OA:296:GLU:OE2	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:394:ASP:O	1:M:395:SER:OG	2.27	0.51
1:M:460:ARG:NH1	1:DB:100:ASP:OD2	2.44	0.51
1:Q:460:ARG:NH1	1:FB:100:ASP:CG	2.63	0.51
1:AA:144:LYS:NZ	1:AA:296:GLU:OE2	2.36	0.51
1:F:144:LYS:NZ	1:F:296:GLU:OE2	2.36	0.51
1:IA:144:LYS:NZ	1:IA:296:GLU:OE2	2.36	0.51
1:JA:394:ASP:O	1:JA:395:SER:OG	2.27	0.51
1:SA:144:LYS:NZ	1:SA:296:GLU:OE2	2.36	0.51
1:GA:457:VAL:O	1:GA:458:THR:OG1	2.18	0.50
1:L:564:LYS:HG3	1:O:442:ALA:HB3	1.92	0.50
1:NA:144:LYS:NZ	1:NA:296:GLU:OE2	2.36	0.50
1:TA:394:ASP:O	1:TA:395:SER:OG	2.27	0.50
1:L:144:LYS:NZ	1:L:296:GLU:OE2	2.36	0.50
1:R:144:LYS:NZ	1:R:296:GLU:OE2	2.36	0.50
1:Q:460:ARG:NH1	1:FB:100:ASP:OD2	2.43	0.50
1:AA:100:ASP:OD1	1:NA:460:ARG:NH1	2.45	0.50
1:UA:457:VAL:O	1:UA:458:THR:OG1	2.18	0.50
1:Y:144:LYS:NZ	1:Y:296:GLU:OE2	2.36	0.50
1:Z:144:LYS:NZ	1:Z:296:GLU:OE2	2.36	0.49
1:BA:262:GLY:HA2	1:DA:506:ARG:HH22	1.77	0.49
1:K:457:VAL:HG13	1:M:67:THR:HG21	1.93	0.49
1:CA:311:PHE:CD1	1:EA:79:ILE:HG12	2.48	0.49
1:VA:428:ARG:NH2	1:XA:136:GLU:OE1	2.44	0.49
1:EB:428:ARG:NH2	1:GB:136:GLU:OE1	2.42	0.49
1:VA:457:VAL:O	1:VA:458:THR:OG1	2.18	0.49
1:1:394:ASP:O	1:1:395:SER:OG	2.27	0.49
1:G:144:LYS:NZ	1:G:296:GLU:OE2	2.36	0.49
1:TA:144:LYS:NZ	1:TA:296:GLU:OE2	2.36	0.49
1:W:144:LYS:NZ	1:W:296:GLU:OE2	2.36	0.49
1:EB:457:VAL:HG13	1:GB:67:THR:HG21	1.95	0.49
1:SA:100:ASP:OD2	1:EB:460:ARG:NH1	2.45	0.49
1:CB:144:LYS:NZ	1:CB:296:GLU:OE2	2.36	0.49
1:M:100:ASP:OD2	1:S:460:ARG:NH1	2.46	0.48
1:GA:144:LYS:NZ	1:GA:296:GLU:OE2	2.36	0.48
1:LA:144:LYS:NZ	1:LA:296:GLU:OE2	2.36	0.48
1:VA:394:ASP:O	1:VA:395:SER:OG	2.27	0.48
1:JA:144:LYS:NZ	1:JA:296:GLU:OE2	2.36	0.48
1:DB:394:ASP:O	1:DB:395:SER:OG	2.27	0.48
1:T:457:VAL:O	1:T:458:THR:OG1	2.18	0.48
1:EA:144:LYS:NZ	1:EA:296:GLU:OE2	2.36	0.48
1:GB:144:LYS:NZ	1:GB:296:GLU:OE2	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FA:100:ASP:OD1	1:VA:460:ARG:NH1	2.47	0.48
1:LA:394:ASP:O	1:LA:395:SER:OG	2.27	0.48
1:VA:578:THR:C	1:XA:50:GLU:OE2	2.51	0.48
1:DB:136:GLU:OE1	1:GB:428:ARG:NH2	2.45	0.48
1:R:428:ARG:NH2	1:T:136:GLU:OE1	2.45	0.48
1:1:144:LYS:NZ	1:1:296:GLU:OE2	2.36	0.48
1:C:144:LYS:NZ	1:C:296:GLU:OE2	2.36	0.48
1:YA:144:LYS:NZ	1:YA:296:GLU:OE2	2.36	0.48
1:KA:50:GLU:OE2	1:OA:578:THR:N	2.47	0.48
1:H:100:ASP:OD2	1:R:460:ARG:NH1	2.46	0.48
1:W:136:GLU:OE1	1:Z:428:ARG:NH2	2.46	0.48
1:QA:83:ASN:O	1:TA:311:PHE:HB3	2.13	0.48
1:E:433:LEU:HD21	1:G:217:GLY:HA2	1.96	0.47
1:H:394:ASP:O	1:H:395:SER:OG	2.27	0.47
1:I:144:LYS:NZ	1:I:296:GLU:OE2	2.36	0.47
1:GA:136:GLU:OE1	1:JA:428:ARG:NH2	2.47	0.47
1:XA:457:VAL:O	1:XA:458:THR:OG1	2.18	0.47
1:E:432:LEU:HD11	1:G:561:TYR:CZ	2.49	0.47
1:S:100:ASP:CG	1:DB:460:ARG:HH11	2.18	0.47
1:DA:100:ASP:OD2	1:AB:460:ARG:NH1	2.46	0.47
1:KA:394:ASP:O	1:KA:395:SER:OG	2.27	0.47
1:HA:394:ASP:O	1:HA:395:SER:OG	2.27	0.47
1:SA:394:ASP:O	1:SA:395:SER:OG	2.27	0.47
1:D:394:ASP:O	1:D:395:SER:OG	2.27	0.47
1:P:83:ASN:O	1:S:311:PHE:HB3	2.15	0.47
1:QA:394:ASP:O	1:QA:395:SER:OG	2.27	0.47
1:Y:460:ARG:NH1	1:IA:100:ASP:OD2	2.48	0.47
1:L:67:THR:HG21	1:O:457:VAL:HG13	1.97	0.47
1:OA:283:ASP:OD2	1:OA:413:SER:OG	2.34	0.46
1:VA:144:LYS:NZ	1:VA:296:GLU:OE2	2.36	0.46
1:VA:283:ASP:OD2	1:VA:413:SER:OG	2.34	0.46
1:CB:394:ASP:O	1:CB:395:SER:OG	2.27	0.46
1:BA:283:ASP:OD2	1:BA:413:SER:OG	2.34	0.46
1:SA:283:ASP:OD2	1:SA:413:SER:OG	2.34	0.46
1:TA:283:ASP:OD2	1:TA:413:SER:OG	2.34	0.46
1:XA:283:ASP:OD2	1:XA:413:SER:OG	2.34	0.46
1:1:275:TYR:OH	1:1:328:PRO:O	2.30	0.46
1:B:283:ASP:OD2	1:B:413:SER:OG	2.34	0.46
1:D:283:ASP:OD2	1:D:413:SER:OG	2.34	0.46
1:E:144:LYS:NZ	1:E:296:GLU:OE2	2.36	0.46
1:N:144:LYS:NZ	1:N:296:GLU:OE2	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:283:ASP:OD2	1:O:413:SER:OG	2.34	0.46
1:IA:283:ASP:OD2	1:IA:413:SER:OG	2.34	0.46
1:MA:136:GLU:OE1	1:ZA:428:ARG:NH2	2.48	0.46
1:CB:283:ASP:OD2	1:CB:413:SER:OG	2.34	0.46
1:I:100:ASP:OD1	1:DA:460:ARG:NH1	2.48	0.46
1:M:283:ASP:OD2	1:M:413:SER:OG	2.34	0.46
1:BA:486:GLU:OE2	1:DA:487:GLN:HA	2.15	0.46
1:CA:283:ASP:OD2	1:CA:413:SER:OG	2.34	0.46
1:EA:283:ASP:OD2	1:EA:413:SER:OG	2.34	0.46
1:ZA:283:ASP:OD2	1:ZA:413:SER:OG	2.34	0.46
1:1:460:ARG:NH1	1:F:100:ASP:OD2	2.48	0.46
1:R:283:ASP:OD2	1:R:413:SER:OG	2.34	0.46
1:KA:283:ASP:OD2	1:KA:413:SER:OG	2.34	0.46
1:UA:283:ASP:OD2	1:UA:413:SER:OG	2.34	0.46
1:YA:283:ASP:OD2	1:YA:413:SER:OG	2.34	0.46
1:BB:283:ASP:OD2	1:BB:413:SER:OG	2.34	0.46
1:DB:99:ASN:OD1	1:GB:460:ARG:NH2	2.48	0.46
1:1:283:ASP:OD2	1:1:413:SER:OG	2.34	0.46
1:1:442:ALA:HB1	1:1:475:LEU:HD11	1.98	0.46
1:N:283:ASP:OD2	1:N:413:SER:OG	2.34	0.46
1:T:283:ASP:OD2	1:T:413:SER:OG	2.34	0.46
1:V:283:ASP:OD2	1:V:413:SER:OG	2.34	0.46
1:Y:283:ASP:OD2	1:Y:413:SER:OG	2.34	0.46
1:DA:283:ASP:OD2	1:DA:413:SER:OG	2.34	0.46
1:GA:442:ALA:HB1	1:GA:475:LEU:HD11	1.98	0.46
1:HA:460:ARG:NH1	1:TA:100:ASP:OD2	2.49	0.46
1:IA:275:TYR:OH	1:IA:328:PRO:O	2.30	0.46
1:KA:460:ARG:NH1	1:RA:100:ASP:OD2	2.49	0.46
1:Q:283:ASP:OD2	1:Q:413:SER:OG	2.34	0.46
1:CA:394:ASP:O	1:CA:395:SER:OG	2.27	0.46
1:GA:283:ASP:OD2	1:GA:413:SER:OG	2.34	0.46
1:HA:144:LYS:NZ	1:HA:296:GLU:OE2	2.36	0.46
1:MA:67:THR:HG21	1:ZA:457:VAL:HG13	1.97	0.46
1:OA:394:ASP:O	1:OA:395:SER:OG	2.27	0.46
1:SA:442:ALA:HB1	1:SA:475:LEU:HD11	1.98	0.46
1:WA:419:ASN:HD21	1:AB:216:GLU:HB3	1.80	0.46
1:HB:283:ASP:OD2	1:HB:413:SER:OG	2.34	0.46
1:F:283:ASP:OD2	1:F:413:SER:OG	2.34	0.46
1:L:283:ASP:OD2	1:L:413:SER:OG	2.34	0.46
1:Q:136:GLU:OE1	1:T:428:ARG:NH2	2.47	0.46
1:Q:442:ALA:HB1	1:Q:475:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:283:ASP:OD2	1:S:413:SER:OG	2.34	0.46
1:NA:283:ASP:OD2	1:NA:413:SER:OG	2.34	0.46
1:PA:283:ASP:OD2	1:PA:413:SER:OG	2.34	0.46
1:RA:283:ASP:OD2	1:RA:413:SER:OG	2.34	0.46
1:E:280:PHE:HE1	1:G:223:MET:HE1	1.80	0.46
1:W:275:TYR:OH	1:W:328:PRO:O	2.31	0.46
1:KA:442:ALA:HB1	1:KA:475:LEU:HD11	1.98	0.46
1:GB:442:ALA:HB1	1:GB:475:LEU:HD11	1.98	0.46
1:A:487:GLN:O	1:A:489:VAL:N	2.49	0.46
1:E:306:ARG:NH1	1:G:563:TYR:HB2	2.30	0.46
1:I:283:ASP:OD2	1:I:413:SER:OG	2.34	0.46
1:I:442:ALA:HB1	1:I:475:LEU:HD11	1.98	0.46
1:L:487:GLN:O	1:L:489:VAL:N	2.49	0.46
1:M:442:ALA:HB1	1:M:475:LEU:HD11	1.98	0.46
1:P:283:ASP:OD2	1:P:413:SER:OG	2.34	0.46
1:P:442:ALA:HB1	1:P:475:LEU:HD11	1.98	0.46
1:V:487:GLN:O	1:V:489:VAL:N	2.49	0.46
1:AA:283:ASP:OD2	1:AA:413:SER:OG	2.34	0.46
1:DA:100:ASP:OD1	1:AB:460:ARG:NH1	2.49	0.46
1:DA:442:ALA:HB1	1:DA:475:LEU:HD11	1.98	0.46
1:EA:442:ALA:HB1	1:EA:475:LEU:HD11	1.98	0.46
1:FA:487:GLN:O	1:FA:489:VAL:N	2.49	0.46
1:MA:394:ASP:O	1:MA:395:SER:OG	2.27	0.46
1:MA:487:GLN:O	1:MA:489:VAL:N	2.49	0.46
1:ZA:487:GLN:O	1:ZA:489:VAL:N	2.49	0.46
1:EB:275:TYR:OH	1:EB:328:PRO:O	2.30	0.46
1:FB:283:ASP:OD2	1:FB:413:SER:OG	2.34	0.46
1:1:487:GLN:O	1:1:489:VAL:N	2.49	0.45
1:B:442:ALA:HB1	1:B:475:LEU:HD11	1.98	0.45
1:B:487:GLN:O	1:B:489:VAL:N	2.49	0.45
1:D:100:ASP:OD2	1:YA:460:ARG:NH1	2.48	0.45
1:E:283:ASP:OD2	1:E:413:SER:OG	2.34	0.45
1:M:487:GLN:O	1:M:489:VAL:N	2.49	0.45
1:Q:487:GLN:O	1:Q:489:VAL:N	2.49	0.45
1:V:144:LYS:NZ	1:V:296:GLU:OE2	2.36	0.45
1:W:283:ASP:OD2	1:W:413:SER:OG	2.34	0.45
1:Z:487:GLN:O	1:Z:489:VAL:N	2.49	0.45
1:GA:487:GLN:O	1:GA:489:VAL:N	2.49	0.45
1:ZA:275:TYR:OH	1:ZA:328:PRO:O	2.30	0.45
1:BB:487:GLN:O	1:BB:489:VAL:N	2.49	0.45
1:DB:275:TYR:OH	1:DB:328:PRO:O	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:434:THR:HB	1:G:130:ASN:HB2	1.98	0.45
1:K:442:ALA:HB1	1:K:475:LEU:HD11	1.98	0.45
1:L:442:ALA:HB1	1:L:475:LEU:HD11	1.98	0.45
1:N:457:VAL:O	1:N:458:THR:OG1	2.18	0.45
1:V:442:ALA:HB1	1:V:475:LEU:HD11	1.98	0.45
1:X:487:GLN:O	1:X:489:VAL:N	2.49	0.45
1:CA:487:GLN:O	1:CA:489:VAL:N	2.49	0.45
1:FA:283:ASP:OD2	1:FA:413:SER:OG	2.34	0.45
1:IA:487:GLN:O	1:IA:489:VAL:N	2.50	0.45
1:JA:442:ALA:HB1	1:JA:475:LEU:HD11	1.98	0.45
1:JA:487:GLN:O	1:JA:489:VAL:N	2.49	0.45
1:LA:283:ASP:OD2	1:LA:413:SER:OG	2.34	0.45
1:FB:275:TYR:OH	1:FB:328:PRO:O	2.30	0.45
1:FB:487:GLN:O	1:FB:489:VAL:N	2.50	0.45
1:F:442:ALA:HB1	1:F:475:LEU:HD11	1.98	0.45
1:I:487:GLN:O	1:I:489:VAL:N	2.49	0.45
1:K:153:ALA:HB1	1:K:154:PRO:HD2	1.99	0.45
1:K:283:ASP:OD2	1:K:413:SER:OG	2.34	0.45
1:N:487:GLN:O	1:N:489:VAL:N	2.49	0.45
1:O:487:GLN:O	1:O:489:VAL:N	2.49	0.45
1:S:100:ASP:OD2	1:DB:460:ARG:NH1	2.39	0.45
1:X:283:ASP:OD2	1:X:413:SER:OG	2.34	0.45
1:IA:442:ALA:HB1	1:IA:475:LEU:HD11	1.98	0.45
1:LA:442:ALA:HB1	1:LA:475:LEU:HD11	1.98	0.45
1:LA:487:GLN:O	1:LA:489:VAL:N	2.49	0.45
1:QA:283:ASP:OD2	1:QA:413:SER:OG	2.34	0.45
1:ZA:442:ALA:HB1	1:ZA:475:LEU:HD11	1.98	0.45
1:CB:487:GLN:O	1:CB:489:VAL:N	2.50	0.45
1:DB:283:ASP:OD2	1:DB:413:SER:OG	2.34	0.45
1:FB:442:ALA:HB1	1:FB:475:LEU:HD11	1.98	0.45
1:GB:283:ASP:OD2	1:GB:413:SER:OG	2.34	0.45
1:A:442:ALA:HB1	1:A:475:LEU:HD11	1.98	0.45
1:D:487:GLN:O	1:D:489:VAL:N	2.49	0.45
1:J:487:GLN:O	1:J:489:VAL:N	2.49	0.45
1:M:153:ALA:HB1	1:M:154:PRO:HD2	1.99	0.45
1:S:153:ALA:HB1	1:S:154:PRO:HD2	1.99	0.45
1:DA:153:ALA:HB1	1:DA:154:PRO:HD2	1.99	0.45
1:EA:487:GLN:O	1:EA:489:VAL:N	2.50	0.45
1:GA:99:ASN:OD1	1:JA:460:ARG:NH2	2.49	0.45
1:HA:487:GLN:O	1:HA:489:VAL:N	2.49	0.45
1:JA:283:ASP:OD2	1:JA:413:SER:OG	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:TA:442:ALA:HB1	1:TA:475:LEU:HD11	1.98	0.45
1:TA:487:GLN:O	1:TA:489:VAL:N	2.49	0.45
1:XA:487:GLN:O	1:XA:489:VAL:N	2.50	0.45
1:YA:442:ALA:HB1	1:YA:475:LEU:HD11	1.98	0.45
1:GB:487:GLN:O	1:GB:489:VAL:N	2.49	0.45
1:E:265:PRO:HG2	1:G:238:GLU:HA	1.99	0.45
1:E:487:GLN:O	1:E:489:VAL:N	2.49	0.45
1:J:442:ALA:HB1	1:J:475:LEU:HD11	1.98	0.45
1:X:394:ASP:O	1:X:395:SER:OG	2.27	0.45
1:AA:153:ALA:HB1	1:AA:154:PRO:HD2	1.99	0.45
1:CA:442:ALA:HB1	1:CA:475:LEU:HD11	1.98	0.45
1:DA:487:GLN:O	1:DA:489:VAL:N	2.49	0.45
1:GA:153:ALA:HB1	1:GA:154:PRO:HD2	1.99	0.45
1:HA:283:ASP:OD2	1:HA:413:SER:OG	2.34	0.45
1:MA:153:ALA:HB1	1:MA:154:PRO:HD2	1.99	0.45
1:RA:442:ALA:HB1	1:RA:475:LEU:HD11	1.98	0.45
1:AB:442:ALA:HB1	1:AB:475:LEU:HD11	1.98	0.45
1:EB:283:ASP:OD2	1:EB:413:SER:OG	2.34	0.45
1:GB:153:ALA:HB1	1:GB:154:PRO:HD2	1.99	0.45
1:HB:394:ASP:O	1:HB:395:SER:OG	2.27	0.45
1:1:153:ALA:HB1	1:1:154:PRO:HD2	1.99	0.45
1:C:283:ASP:OD2	1:C:413:SER:OG	2.34	0.45
1:F:487:GLN:O	1:F:489:VAL:N	2.50	0.45
1:H:442:ALA:HB1	1:H:475:LEU:HD11	1.98	0.45
1:J:283:ASP:OD2	1:J:413:SER:OG	2.34	0.45
1:M:311:PHE:CD1	1:O:79:ILE:HG12	2.52	0.45
1:AA:487:GLN:O	1:AA:489:VAL:N	2.49	0.45
1:SA:153:ALA:HB1	1:SA:154:PRO:HD2	1.99	0.45
1:VA:442:ALA:HB1	1:VA:475:LEU:HD11	1.98	0.45
1:WA:283:ASP:OD2	1:WA:413:SER:OG	2.34	0.45
1:A:283:ASP:OD2	1:A:413:SER:OG	2.34	0.45
1:E:442:ALA:HB1	1:E:475:LEU:HD11	1.98	0.45
1:H:283:ASP:OD2	1:H:413:SER:OG	2.34	0.45
1:H:487:GLN:O	1:H:489:VAL:N	2.50	0.45
1:K:275:TYR:OH	1:K:328:PRO:O	2.30	0.45
1:P:487:GLN:O	1:P:489:VAL:N	2.49	0.45
1:X:442:ALA:HB1	1:X:475:LEU:HD11	1.98	0.45
1:AA:442:ALA:HB1	1:AA:475:LEU:HD11	1.98	0.45
1:BA:487:GLN:O	1:BA:489:VAL:N	2.49	0.45
1:IA:153:ALA:HB1	1:IA:154:PRO:HD2	1.99	0.45
1:MA:283:ASP:OD2	1:MA:413:SER:OG	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:UA:487:GLN:O	1:UA:489:VAL:N	2.49	0.45
1:VA:487:GLN:O	1:VA:489:VAL:N	2.49	0.45
1:AB:487:GLN:O	1:AB:489:VAL:N	2.49	0.45
1:EB:153:ALA:HB1	1:EB:154:PRO:HD2	1.99	0.45
1:G:487:GLN:O	1:G:489:VAL:N	2.49	0.45
1:H:153:ALA:HB1	1:H:154:PRO:HD2	1.99	0.45
1:BA:144:LYS:NZ	1:BA:296:GLU:OE2	2.36	0.45
1:JA:153:ALA:HB1	1:JA:154:PRO:HD2	1.99	0.45
1:NA:153:ALA:HB1	1:NA:154:PRO:HD2	1.99	0.45
1:QA:153:ALA:HB1	1:QA:154:PRO:HD2	1.99	0.45
1:RA:487:GLN:O	1:RA:489:VAL:N	2.49	0.45
1:TA:153:ALA:HB1	1:TA:154:PRO:HD2	1.99	0.45
1:TA:275:TYR:OH	1:TA:328:PRO:O	2.30	0.45
1:VA:153:ALA:HB1	1:VA:154:PRO:HD2	1.99	0.45
1:WA:153:ALA:HB1	1:WA:154:PRO:HD2	1.99	0.45
1:YA:487:GLN:O	1:YA:489:VAL:N	2.49	0.45
1:ZA:153:ALA:HB1	1:ZA:154:PRO:HD2	1.99	0.45
1:DB:487:GLN:O	1:DB:489:VAL:N	2.49	0.45
1:EB:442:ALA:HB1	1:EB:475:LEU:HD11	1.98	0.45
1:HB:487:GLN:O	1:HB:489:VAL:N	2.49	0.45
1:B:153:ALA:HB1	1:B:154:PRO:HD2	1.99	0.45
1:G:275:TYR:OH	1:G:328:PRO:O	2.30	0.45
1:FA:442:ALA:HB1	1:FA:475:LEU:HD11	1.98	0.45
1:KA:487:GLN:O	1:KA:489:VAL:N	2.50	0.45
1:VA:118:ARG:HH12	1:XA:64:TYR:CB	2.30	0.45
1:CB:275:TYR:OH	1:CB:328:PRO:O	2.30	0.45
1:EB:487:GLN:O	1:EB:489:VAL:N	2.49	0.45
1:C:487:GLN:O	1:C:489:VAL:N	2.49	0.45
1:E:153:ALA:HB1	1:E:154:PRO:HD2	1.99	0.45
1:I:153:ALA:HB1	1:I:154:PRO:HD2	1.99	0.45
1:K:487:GLN:O	1:K:489:VAL:N	2.49	0.45
1:O:442:ALA:HB1	1:O:475:LEU:HD11	1.98	0.45
1:V:428:ARG:NH2	1:X:136:GLU:OE1	2.46	0.45
1:W:487:GLN:O	1:W:489:VAL:N	2.49	0.45
1:HA:442:ALA:HB1	1:HA:475:LEU:HD11	1.98	0.45
1:MA:442:ALA:HB1	1:MA:475:LEU:HD11	1.98	0.45
1:QA:487:GLN:O	1:QA:489:VAL:N	2.49	0.45
1:WA:487:GLN:O	1:WA:489:VAL:N	2.49	0.45
1:I:275:TYR:OH	1:I:328:PRO:O	2.30	0.44
1:L:136:GLU:OE1	1:O:428:ARG:NH2	2.48	0.44
1:L:457:VAL:O	1:L:458:THR:OG1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:153:ALA:HB1	1:P:154:PRO:HD2	1.99	0.44
1:T:487:GLN:O	1:T:489:VAL:N	2.49	0.44
1:Y:153:ALA:HB1	1:Y:154:PRO:HD2	1.99	0.44
1:Y:442:ALA:HB1	1:Y:475:LEU:HD11	1.98	0.44
1:CA:153:ALA:HB1	1:CA:154:PRO:HD2	1.99	0.44
1:OA:487:GLN:O	1:OA:489:VAL:N	2.49	0.44
1:VA:118:ARG:NH1	1:XA:64:TYR:HB2	2.32	0.44
1:BB:153:ALA:HB1	1:BB:154:PRO:HD2	1.99	0.44
1:CB:442:ALA:HB1	1:CB:475:LEU:HD11	1.98	0.44
1:G:283:ASP:OD2	1:G:413:SER:OG	2.34	0.44
1:V:153:ALA:HB1	1:V:154:PRO:HD2	1.99	0.44
1:NA:442:ALA:HB1	1:NA:475:LEU:HD11	1.98	0.44
1:PA:487:GLN:O	1:PA:489:VAL:N	2.49	0.44
1:UA:153:ALA:HB1	1:UA:154:PRO:HD2	1.99	0.44
1:XA:442:ALA:HB1	1:XA:475:LEU:HD11	1.98	0.44
1:YA:153:ALA:HB1	1:YA:154:PRO:HD2	1.99	0.44
1:AB:283:ASP:OD2	1:AB:413:SER:OG	2.34	0.44
1:BB:442:ALA:HB1	1:BB:475:LEU:HD11	1.98	0.44
1:D:153:ALA:HB1	1:D:154:PRO:HD2	1.99	0.44
1:D:338:GLU:OE1	1:D:338:GLU:N	2.51	0.44
1:O:153:ALA:HB1	1:O:154:PRO:HD2	1.99	0.44
1:R:487:GLN:O	1:R:489:VAL:N	2.50	0.44
1:S:442:ALA:HB1	1:S:475:LEU:HD11	1.98	0.44
1:S:487:GLN:O	1:S:489:VAL:N	2.49	0.44
1:V:338:GLU:OE1	1:V:338:GLU:N	2.51	0.44
1:Z:153:ALA:HB1	1:Z:154:PRO:HD2	1.99	0.44
1:Z:442:ALA:HB1	1:Z:475:LEU:HD11	1.98	0.44
1:BA:275:TYR:OH	1:BA:328:PRO:O	2.30	0.44
1:BA:442:ALA:HB1	1:BA:475:LEU:HD11	1.98	0.44
1:LA:153:ALA:HB1	1:LA:154:PRO:HD2	1.99	0.44
1:NA:487:GLN:O	1:NA:489:VAL:N	2.49	0.44
1:OA:442:ALA:HB1	1:OA:475:LEU:HD11	1.98	0.44
1:PA:442:ALA:HB1	1:PA:475:LEU:HD11	1.98	0.44
1:RA:153:ALA:HB1	1:RA:154:PRO:HD2	1.99	0.44
1:SA:487:GLN:O	1:SA:489:VAL:N	2.49	0.44
1:UA:442:ALA:HB1	1:UA:475:LEU:HD11	1.98	0.44
1:VA:486:GLU:HG3	1:XA:487:GLN:OE1	2.17	0.44
1:CB:153:ALA:HB1	1:CB:154:PRO:HD2	1.99	0.44
1:DB:442:ALA:HB1	1:DB:475:LEU:HD11	1.98	0.44
1:C:442:ALA:HB1	1:C:475:LEU:HD11	1.98	0.44
1:L:275:TYR:OH	1:L:328:PRO:O	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:442:ALA:HB1	1:N:475:LEU:HD11	1.98	0.44
1:T:442:ALA:HB1	1:T:475:LEU:HD11	1.98	0.44
1:W:442:ALA:HB1	1:W:475:LEU:HD11	1.98	0.44
1:X:153:ALA:HB1	1:X:154:PRO:HD2	1.99	0.44
1:Y:338:GLU:OE1	1:Y:338:GLU:N	2.51	0.44
1:XA:338:GLU:OE1	1:XA:338:GLU:N	2.51	0.44
1:HB:442:ALA:HB1	1:HB:475:LEU:HD11	1.98	0.44
1:C:153:ALA:HB1	1:C:154:PRO:HD2	1.99	0.44
1:L:394:ASP:O	1:L:395:SER:OG	2.27	0.44
1:M:275:TYR:OH	1:M:328:PRO:O	2.30	0.44
1:R:442:ALA:HB1	1:R:475:LEU:HD11	1.98	0.44
1:Y:487:GLN:O	1:Y:489:VAL:N	2.49	0.44
1:EA:153:ALA:HB1	1:EA:154:PRO:HD2	1.99	0.44
1:UA:338:GLU:OE1	1:UA:338:GLU:N	2.51	0.44
1:WA:442:ALA:HB1	1:WA:475:LEU:HD11	1.98	0.44
1:XA:153:ALA:HB1	1:XA:154:PRO:HD2	1.99	0.44
1:XA:434:THR:HB	1:ZA:130:ASN:HB2	1.99	0.44
1:HB:153:ALA:HB1	1:HB:154:PRO:HD2	1.99	0.44
1:F:153:ALA:HB1	1:F:154:PRO:HD2	1.99	0.44
1:G:442:ALA:HB1	1:G:475:LEU:HD11	1.98	0.44
1:L:83:ASN:O	1:O:311:PHE:HB3	2.18	0.44
1:R:153:ALA:HB1	1:R:154:PRO:HD2	1.99	0.44
1:W:338:GLU:OE1	1:W:338:GLU:N	2.51	0.44
1:Z:283:ASP:OD2	1:Z:413:SER:OG	2.34	0.44
1:OA:338:GLU:OE1	1:OA:338:GLU:N	2.51	0.44
1:QA:442:ALA:HB1	1:QA:475:LEU:HD11	1.98	0.44
1:AB:153:ALA:HB1	1:AB:154:PRO:HD2	1.99	0.44
1:BB:338:GLU:OE1	1:BB:338:GLU:N	2.51	0.44
1:L:153:ALA:HB1	1:L:154:PRO:HD2	1.99	0.44
1:T:153:ALA:HB1	1:T:154:PRO:HD2	1.99	0.44
1:W:153:ALA:HB1	1:W:154:PRO:HD2	1.99	0.44
1:FA:564:LYS:HG3	1:IA:442:ALA:HB3	2.00	0.44
1:OA:153:ALA:HB1	1:OA:154:PRO:HD2	1.99	0.44
1:SA:275:TYR:OH	1:SA:328:PRO:O	2.31	0.44
1:FB:153:ALA:HB1	1:FB:154:PRO:HD2	1.99	0.44
1:HB:338:GLU:OE1	1:HB:338:GLU:N	2.51	0.44
1:G:153:ALA:HB1	1:G:154:PRO:HD2	1.99	0.44
1:J:275:TYR:OH	1:J:328:PRO:O	2.30	0.44
1:P:338:GLU:OE1	1:P:338:GLU:N	2.51	0.44
1:BA:338:GLU:OE1	1:BA:338:GLU:N	2.51	0.44
1:GB:275:TYR:OH	1:GB:328:PRO:O	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:LYS:NZ	1:A:296:GLU:OE2	2.36	0.44
1:D:442:ALA:HB1	1:D:475:LEU:HD11	1.98	0.44
1:Q:99:ASN:OD1	1:T:460:ARG:NH2	2.50	0.44
1:T:275:TYR:OH	1:T:328:PRO:O	2.30	0.44
1:BA:153:ALA:HB1	1:BA:154:PRO:HD2	1.99	0.44
1:FA:153:ALA:HB1	1:FA:154:PRO:HD2	1.99	0.44
1:HA:153:ALA:HB1	1:HA:154:PRO:HD2	1.99	0.44
1:PA:153:ALA:HB1	1:PA:154:PRO:HD2	1.99	0.44
1:E:266:GLU:CG	1:G:242:GLN:OE1	2.64	0.43
1:I:338:GLU:OE1	1:I:338:GLU:N	2.51	0.43
1:T:338:GLU:OE1	1:T:338:GLU:N	2.51	0.43
1:CA:457:VAL:HG13	1:EA:67:THR:HG21	1.98	0.43
1:RA:275:TYR:OH	1:RA:328:PRO:O	2.30	0.43
1:VA:338:GLU:OE1	1:VA:338:GLU:N	2.51	0.43
1:WA:275:TYR:OH	1:WA:328:PRO:O	2.30	0.43
1:O:460:ARG:NH1	1:QA:100:ASP:OD2	2.51	0.43
1:FA:338:GLU:OE1	1:FA:338:GLU:N	2.51	0.43
1:KA:153:ALA:HB1	1:KA:154:PRO:HD2	1.99	0.43
1:AB:338:GLU:OE1	1:AB:338:GLU:N	2.51	0.43
1:EB:338:GLU:N	1:EB:338:GLU:OE1	2.51	0.43
1:J:153:ALA:HB1	1:J:154:PRO:HD2	1.99	0.43
1:A:153:ALA:HB1	1:A:154:PRO:HD2	1.99	0.43
1:E:262:GLY:HA2	1:G:506:ARG:NH2	2.31	0.43
1:K:338:GLU:OE1	1:K:338:GLU:N	2.51	0.43
1:Q:153:ALA:HB1	1:Q:154:PRO:HD2	1.99	0.43
1:DB:153:ALA:HB1	1:DB:154:PRO:HD2	1.99	0.43
1:FB:394:ASP:O	1:FB:395:SER:OG	2.27	0.43
1:1:442:ALA:HB3	1:B:564:LYS:HG3	2.00	0.43
1:C:283:ASP:OD1	1:C:284:ILE:N	2.52	0.43
1:J:442:ALA:HB3	1:VA:564:LYS:HG3	2.01	0.43
1:N:153:ALA:HB1	1:N:154:PRO:HD2	1.99	0.43
1:Z:338:GLU:OE1	1:Z:338:GLU:N	2.51	0.43
1:JA:338:GLU:OE1	1:JA:338:GLU:N	2.51	0.43
1:WA:283:ASP:OD1	1:WA:284:ILE:N	2.52	0.43
1:WA:394:ASP:O	1:WA:395:SER:OG	2.27	0.43
1:YA:338:GLU:OE1	1:YA:338:GLU:N	2.51	0.43
1:BB:283:ASP:OD1	1:BB:284:ILE:N	2.52	0.43
1:B:283:ASP:OD1	1:B:284:ILE:N	2.52	0.43
1:W:283:ASP:OD1	1:W:284:ILE:N	2.52	0.43
1:Y:394:ASP:O	1:Y:395:SER:OG	2.27	0.43
1:RA:283:ASP:OD1	1:RA:284:ILE:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:283:ASP:OD1	1:AB:284:ILE:N	2.52	0.43
1:1:283:ASP:OD1	1:1:284:ILE:N	2.52	0.43
1:L:283:ASP:OD1	1:L:284:ILE:N	2.52	0.43
1:N:275:TYR:OH	1:N:328:PRO:O	2.30	0.43
1:P:283:ASP:OD1	1:P:284:ILE:N	2.52	0.43
1:IA:283:ASP:OD1	1:IA:284:ILE:N	2.52	0.43
1:JA:283:ASP:OD1	1:JA:284:ILE:N	2.52	0.43
1:VA:283:ASP:OD1	1:VA:284:ILE:N	2.52	0.43
1:VA:537:LEU:HD11	1:XA:68:LYS:NZ	2.34	0.43
1:FB:283:ASP:OD1	1:FB:284:ILE:N	2.52	0.43
1:E:338:GLU:OE1	1:E:338:GLU:N	2.51	0.43
1:L:55:ILE:HG21	1:O:457:VAL:HG11	2.00	0.43
1:BA:266:GLU:HG3	1:DA:242:GLN:OE1	2.18	0.43
1:EA:275:TYR:OH	1:EA:328:PRO:O	2.30	0.43
1:GA:283:ASP:OD1	1:GA:284:ILE:N	2.52	0.43
1:HA:338:GLU:OE1	1:HA:338:GLU:N	2.51	0.43
1:NA:283:ASP:OD1	1:NA:284:ILE:N	2.52	0.43
1:UA:99:ASN:OD1	1:AB:460:ARG:NH2	2.49	0.43
1:CB:283:ASP:OD1	1:CB:284:ILE:N	2.52	0.43
1:DB:283:ASP:OD1	1:DB:284:ILE:N	2.52	0.43
1:A:275:TYR:OH	1:A:328:PRO:O	2.31	0.43
1:A:338:GLU:OE1	1:A:338:GLU:N	2.51	0.43
1:B:275:TYR:OH	1:B:328:PRO:O	2.30	0.43
1:C:275:TYR:OH	1:C:328:PRO:O	2.30	0.43
1:E:280:PHE:HB3	1:G:219:PHE:CE1	2.53	0.43
1:H:283:ASP:OD1	1:H:284:ILE:N	2.52	0.43
1:H:338:GLU:OE1	1:H:338:GLU:N	2.51	0.43
1:I:283:ASP:OD1	1:I:284:ILE:N	2.52	0.43
1:O:275:TYR:OH	1:O:328:PRO:O	2.31	0.43
1:S:338:GLU:OE1	1:S:338:GLU:N	2.51	0.43
1:V:283:ASP:OD1	1:V:284:ILE:N	2.52	0.43
1:Z:283:ASP:OD1	1:Z:284:ILE:N	2.52	0.43
1:BA:484:TYR:OH	1:DA:485:ASN:OD1	2.30	0.43
1:QA:275:TYR:OH	1:QA:328:PRO:O	2.31	0.43
1:TA:283:ASP:OD1	1:TA:284:ILE:N	2.52	0.43
1:XA:275:TYR:OH	1:XA:328:PRO:O	2.31	0.43
1:ZA:283:ASP:OD1	1:ZA:284:ILE:N	2.52	0.43
1:A:394:ASP:O	1:A:395:SER:OG	2.27	0.43
1:DA:283:ASP:OD1	1:DA:284:ILE:N	2.52	0.43
1:YA:283:ASP:OD1	1:YA:284:ILE:N	2.52	0.43
1:F:283:ASP:OD1	1:F:284:ILE:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:283:ASP:OD1	1:G:284:ILE:N	2.52	0.42
1:CA:283:ASP:OD1	1:CA:284:ILE:N	2.52	0.42
1:DA:275:TYR:OH	1:DA:328:PRO:O	2.30	0.42
1:EA:338:GLU:OE1	1:EA:338:GLU:N	2.51	0.42
1:IA:338:GLU:OE1	1:IA:338:GLU:N	2.51	0.42
1:LA:275:TYR:OH	1:LA:328:PRO:O	2.31	0.42
1:LA:283:ASP:OD1	1:LA:284:ILE:N	2.52	0.42
1:PA:283:ASP:OD1	1:PA:284:ILE:N	2.52	0.42
1:RA:338:GLU:OE1	1:RA:338:GLU:N	2.51	0.42
1:SA:283:ASP:OD1	1:SA:284:ILE:N	2.52	0.42
1:T:283:ASP:OD1	1:T:284:ILE:N	2.52	0.42
1:X:283:ASP:OD1	1:X:284:ILE:N	2.52	0.42
1:EA:283:ASP:OD1	1:EA:284:ILE:N	2.52	0.42
1:HA:283:ASP:OD1	1:HA:284:ILE:N	2.52	0.42
1:MA:283:ASP:OD1	1:MA:284:ILE:N	2.52	0.42
1:D:283:ASP:OD1	1:D:284:ILE:N	2.52	0.42
1:J:283:ASP:OD1	1:J:284:ILE:N	2.52	0.42
1:K:394:ASP:O	1:K:395:SER:OG	2.27	0.42
1:Q:283:ASP:OD1	1:Q:284:ILE:N	2.52	0.42
1:QA:283:ASP:OD1	1:QA:284:ILE:N	2.52	0.42
1:K:283:ASP:OD1	1:K:284:ILE:N	2.52	0.42
1:L:262:GLY:HA2	1:N:506:ARG:HH22	1.83	0.42
1:O:283:ASP:OD1	1:O:284:ILE:N	2.52	0.42
1:R:283:ASP:OD1	1:R:284:ILE:N	2.52	0.42
1:S:283:ASP:OD1	1:S:284:ILE:N	2.52	0.42
1:Y:283:ASP:OD1	1:Y:284:ILE:N	2.52	0.42
1:FA:283:ASP:OD1	1:FA:284:ILE:N	2.52	0.42
1:NA:275:TYR:OH	1:NA:328:PRO:O	2.30	0.42
1:OA:275:TYR:OH	1:OA:328:PRO:O	2.30	0.42
1:UA:283:ASP:OD1	1:UA:284:ILE:N	2.52	0.42
1:XA:283:ASP:OD1	1:XA:284:ILE:N	2.52	0.42
1:A:50:GLU:OE2	1:HB:578:THR:N	2.53	0.42
1:P:55:ILE:HG21	1:S:457:VAL:HG11	2.00	0.42
1:P:275:TYR:OH	1:P:328:PRO:O	2.30	0.42
1:R:338:GLU:OE1	1:R:338:GLU:N	2.51	0.42
1:AA:283:ASP:OD1	1:AA:284:ILE:N	2.52	0.42
1:BA:442:ALA:HB3	1:DA:564:LYS:HG3	2.01	0.42
1:N:283:ASP:OD1	1:N:284:ILE:N	2.52	0.42
1:AA:275:TYR:OH	1:AA:328:PRO:O	2.30	0.42
1:NA:338:GLU:OE1	1:NA:338:GLU:N	2.51	0.42
1:GB:283:ASP:OD1	1:GB:284:ILE:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:ASP:OD1	1:A:284:ILE:N	2.52	0.42
1:BA:283:ASP:OD1	1:BA:284:ILE:N	2.52	0.42
1:QA:338:GLU:OE1	1:QA:338:GLU:N	2.51	0.42
1:M:283:ASP:OD1	1:M:284:ILE:N	2.52	0.42
1:KA:283:ASP:OD1	1:KA:284:ILE:N	2.52	0.42
1:LA:338:GLU:OE1	1:LA:338:GLU:N	2.51	0.42
1:PA:338:GLU:OE1	1:PA:338:GLU:N	2.51	0.42
1:ZA:338:GLU:OE1	1:ZA:338:GLU:N	2.51	0.42
1:B:338:GLU:OE1	1:B:338:GLU:N	2.51	0.42
1:E:283:ASP:OD1	1:E:284:ILE:N	2.52	0.42
1:CA:311:PHE:HD1	1:EA:79:ILE:HG12	1.83	0.42
1:TA:338:GLU:OE1	1:TA:338:GLU:N	2.51	0.42
1:EB:283:ASP:OD1	1:EB:284:ILE:N	2.52	0.42
1:C:338:GLU:OE1	1:C:338:GLU:N	2.51	0.42
1:L:266:GLU:HG3	1:N:242:GLN:OE1	2.20	0.42
1:DA:338:GLU:OE1	1:DA:338:GLU:N	2.51	0.42
1:UA:457:VAL:HG13	1:YA:67:THR:HG21	2.01	0.42
1:FB:338:GLU:OE1	1:FB:338:GLU:N	2.51	0.42
1:B:460:ARG:NH2	1:HB:99:ASN:OD1	2.51	0.41
1:E:100:ASP:CG	1:ZA:460:ARG:NH1	2.73	0.41
1:M:338:GLU:OE1	1:M:338:GLU:N	2.51	0.41
1:GA:338:GLU:OE1	1:GA:338:GLU:N	2.51	0.41
1:OA:283:ASP:OD1	1:OA:284:ILE:N	2.52	0.41
1:DB:338:GLU:OE1	1:DB:338:GLU:N	2.51	0.41
1:G:338:GLU:OE1	1:G:338:GLU:N	2.51	0.41
1:O:338:GLU:OE1	1:O:338:GLU:N	2.51	0.41
1:Q:275:TYR:OH	1:Q:328:PRO:O	2.30	0.41
1:R:275:TYR:OH	1:R:328:PRO:O	2.30	0.41
1:AA:100:ASP:CG	1:NA:460:ARG:NH1	2.73	0.41
1:AA:338:GLU:OE1	1:AA:338:GLU:N	2.51	0.41
1:GA:311:PHE:CE1	1:IA:79:ILE:HG12	2.55	0.41
1:JA:275:TYR:OH	1:JA:328:PRO:O	2.30	0.41
1:WA:338:GLU:OE1	1:WA:338:GLU:N	2.51	0.41
1:HB:283:ASP:OD1	1:HB:284:ILE:N	2.52	0.41
1:E:68:LYS:NZ	1:H:471:VAL:O	2.44	0.41
1:L:338:GLU:N	1:L:338:GLU:OE1	2.51	0.41
1:FA:144:LYS:NZ	1:FA:296:GLU:OE2	2.36	0.41
1:CB:99:ASN:OD1	1:FB:460:ARG:NH2	2.52	0.41
1:1:457:VAL:HG13	1:B:67:THR:HG21	2.01	0.41
1:J:338:GLU:OE1	1:J:338:GLU:N	2.51	0.41
1:E:306:ARG:HD3	1:G:130:ASN:ND2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:473:ALA:HB3	1:G:568:ILE:HD11	2.02	0.41
1:VA:578:THR:O	1:XA:50:GLU:OE1	2.38	0.41
1:Q:332:ASP:OD2	1:Q:389:GLN:NE2	2.53	0.41
1:CA:338:GLU:N	1:CA:338:GLU:OE1	2.51	0.41
1:UA:332:ASP:OD2	1:UA:389:GLN:NE2	2.53	0.41
1:YA:275:TYR:OH	1:YA:328:PRO:O	2.30	0.41
1:1:99:ASN:OD1	1:C:460:ARG:NH2	2.52	0.41
1:1:502:HIS:CE1	1:C:278:GLU:OE2	2.73	0.41
1:S:332:ASP:OD2	1:S:389:GLN:NE2	2.53	0.41
1:KA:338:GLU:OE1	1:KA:338:GLU:N	2.51	0.41
1:EB:442:ALA:HB3	1:GB:564:LYS:HG3	2.02	0.41
1:O:394:ASP:O	1:O:395:SER:OG	2.27	0.41
1:R:332:ASP:OD2	1:R:389:GLN:NE2	2.53	0.41
1:Q:564:LYS:HG3	1:T:442:ALA:HB3	2.02	0.41
1:V:434:THR:HB	1:X:130:ASN:HB2	2.03	0.41
1:V:484:TYR:OH	1:X:485:ASN:OD1	2.29	0.41
1:PA:99:ASN:OD1	1:SA:460:ARG:NH2	2.51	0.41
1:PA:275:TYR:OH	1:PA:328:PRO:O	2.30	0.41
1:BB:275:TYR:OH	1:BB:328:PRO:O	2.30	0.41
1:CB:338:GLU:OE1	1:CB:338:GLU:N	2.51	0.41
1:1:338:GLU:OE1	1:1:338:GLU:N	2.51	0.41
1:H:275:TYR:OH	1:H:328:PRO:O	2.30	0.41
1:I:99:ASN:OD1	1:NA:460:ARG:NH2	2.53	0.41
1:A:442:ALA:HB3	1:C:564:LYS:HG3	2.04	0.40
1:P:84:TYR:HA	1:S:311:PHE:O	2.21	0.40
1:Q:338:GLU:OE1	1:Q:338:GLU:N	2.51	0.40
1:SA:338:GLU:N	1:SA:338:GLU:OE1	2.51	0.40
1:VA:275:TYR:OH	1:VA:328:PRO:O	2.30	0.40
1:N:332:ASP:OD2	1:N:389:GLN:NE2	2.53	0.40
1:Q:460:ARG:HH11	1:FB:100:ASP:CG	2.24	0.40
1:W:99:ASN:OD1	1:Z:460:ARG:NH2	2.50	0.40
1:FA:99:ASN:OD1	1:IA:460:ARG:NH2	2.54	0.40
1:VA:444:GLN:HE22	1:XA:74:ASN:ND2	2.19	0.40
1:YA:332:ASP:OD2	1:YA:389:GLN:NE2	2.53	0.40
1:X:338:GLU:OE1	1:X:338:GLU:N	2.51	0.40
1:AA:99:ASN:OD1	1:DA:460:ARG:NH2	2.51	0.40
1:DB:332:ASP:OD2	1:DB:389:GLN:NE2	2.53	0.40
1:B:332:ASP:OD2	1:B:389:GLN:NE2	2.53	0.40
1:D:332:ASP:OD2	1:D:389:GLN:NE2	2.53	0.40
1:E:280:PHE:HB3	1:G:219:PHE:CZ	2.57	0.40
1:M:332:ASP:OD2	1:M:389:GLN:NE2	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:65:ASP:OD2	1:T:574:LEU:HB3	2.22	0.40
1:X:275:TYR:OH	1:X:328:PRO:O	2.31	0.40
1:A:67:THR:HG21	1:HB:457:VAL:HG13	2.03	0.40
1:D:275:TYR:OH	1:D:328:PRO:O	2.30	0.40
1:I:332:ASP:OD2	1:I:389:GLN:NE2	2.53	0.40
1:V:311:PHE:CD1	1:X:79:ILE:HG12	2.56	0.40
1:DA:100:ASP:CG	1:AB:460:ARG:NH1	2.75	0.40
1:GB:338:GLU:OE1	1:GB:338:GLU:N	2.51	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	1	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	A	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	AA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	AB	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	B	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	BA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	BB	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	C	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	CA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	CB	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	D	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	DA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	DB	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	E	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	EA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	EB	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	F	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	FA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	FB	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	G	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	GA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	GB	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	H	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	HA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	HB	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	I	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	IA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	J	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	JA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	K	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	KA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	L	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	LA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	M	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	MA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	N	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	NA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	O	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	OA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	P	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	PA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	Q	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	QA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56
1	R	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47 56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	RA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	S	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	SA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	T	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	TA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	UA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	V	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	VA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	W	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	WA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	X	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	XA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	Y	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	YA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	Z	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
1	ZA	429/587 (73%)	382 (89%)	46 (11%)	1 (0%)	47	56
All	All	25740/35220 (73%)	22920 (89%)	2760 (11%)	60 (0%)	50	56

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	488	ALA
1	A	488	ALA
1	B	488	ALA
1	C	488	ALA
1	D	488	ALA
1	E	488	ALA
1	F	488	ALA
1	G	488	ALA
1	H	488	ALA
1	I	488	ALA
1	J	488	ALA
1	K	488	ALA
1	L	488	ALA
1	M	488	ALA
1	N	488	ALA

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Mol	Chain	Res	Type
1	O	488	ALA
1	P	488	ALA
1	Q	488	ALA
1	R	488	ALA
1	S	488	ALA
1	T	488	ALA
1	V	488	ALA
1	W	488	ALA
1	X	488	ALA
1	Y	488	ALA
1	Z	488	ALA
1	AA	488	ALA
1	BA	488	ALA
1	CA	488	ALA
1	DA	488	ALA
1	EA	488	ALA
1	FA	488	ALA
1	GA	488	ALA
1	HA	488	ALA
1	IA	488	ALA
1	JA	488	ALA
1	KA	488	ALA
1	LA	488	ALA
1	MA	488	ALA
1	NA	488	ALA
1	OA	488	ALA
1	PA	488	ALA
1	QA	488	ALA
1	RA	488	ALA
1	SA	488	ALA
1	TA	488	ALA
1	UA	488	ALA
1	VA	488	ALA
1	WA	488	ALA
1	XA	488	ALA
1	YA	488	ALA
1	ZA	488	ALA
1	AB	488	ALA
1	BB	488	ALA
1	CB	488	ALA
1	DB	488	ALA
1	EB	488	ALA

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Mol	Chain	Res	Type
1	FB	488	ALA
1	GB	488	ALA
1	HB	488	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	1	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	A	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	AA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	AB	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	B	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	BA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	BB	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	C	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	CA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	CB	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	D	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	DA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	DB	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	E	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	EA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	EB	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	F	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	FA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	FB	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	G	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	GA	396/519 (76%)	393 (99%)	3 (1%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	GB	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	H	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	HA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	HB	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	I	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	IA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	J	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	JA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	K	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	KA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	L	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	LA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	M	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	MA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	N	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	NA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	O	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	OA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	P	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	PA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	Q	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	QA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	R	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	RA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	S	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	SA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	T	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	TA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	UA	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	V	396/519 (76%)	393 (99%)	3 (1%)	81	89
1	VA	396/519 (76%)	393 (99%)	3 (1%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	W	396/519 (76%)	393 (99%)	3 (1%)	81 89
1	WA	396/519 (76%)	393 (99%)	3 (1%)	81 89
1	X	396/519 (76%)	393 (99%)	3 (1%)	81 89
1	XA	396/519 (76%)	393 (99%)	3 (1%)	81 89
1	Y	396/519 (76%)	393 (99%)	3 (1%)	81 89
1	YA	396/519 (76%)	393 (99%)	3 (1%)	81 89
1	Z	396/519 (76%)	393 (99%)	3 (1%)	81 89
1	ZA	396/519 (76%)	393 (99%)	3 (1%)	81 89
All	All	23760/31140 (76%)	23580 (99%)	180 (1%)	82 89

All (180) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	131	MET
1	1	341	LYS
1	1	466	ASN
1	A	131	MET
1	A	341	LYS
1	A	466	ASN
1	B	131	MET
1	B	341	LYS
1	B	466	ASN
1	C	131	MET
1	C	341	LYS
1	C	466	ASN
1	D	131	MET
1	D	341	LYS
1	D	466	ASN
1	E	131	MET
1	E	341	LYS
1	E	466	ASN
1	F	131	MET
1	F	341	LYS
1	F	466	ASN
1	G	131	MET
1	G	341	LYS
1	G	466	ASN
1	H	131	MET
1	H	341	LYS

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Mol	Chain	Res	Type
1	H	466	ASN
1	I	131	MET
1	I	341	LYS
1	I	466	ASN
1	J	131	MET
1	J	341	LYS
1	J	466	ASN
1	K	131	MET
1	K	341	LYS
1	K	466	ASN
1	L	131	MET
1	L	341	LYS
1	L	466	ASN
1	M	131	MET
1	M	341	LYS
1	M	466	ASN
1	N	131	MET
1	N	341	LYS
1	N	466	ASN
1	O	131	MET
1	O	341	LYS
1	O	466	ASN
1	P	131	MET
1	P	341	LYS
1	P	466	ASN
1	Q	131	MET
1	Q	341	LYS
1	Q	466	ASN
1	R	131	MET
1	R	341	LYS
1	R	466	ASN
1	S	131	MET
1	S	341	LYS
1	S	466	ASN
1	T	131	MET
1	T	341	LYS
1	T	466	ASN
1	V	131	MET
1	V	341	LYS
1	V	466	ASN
1	W	131	MET
1	W	341	LYS

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Mol	Chain	Res	Type
1	W	466	ASN
1	X	131	MET
1	X	341	LYS
1	X	466	ASN
1	Y	131	MET
1	Y	341	LYS
1	Y	466	ASN
1	Z	131	MET
1	Z	341	LYS
1	Z	466	ASN
1	AA	131	MET
1	AA	341	LYS
1	AA	466	ASN
1	BA	131	MET
1	BA	341	LYS
1	BA	466	ASN
1	CA	131	MET
1	CA	341	LYS
1	CA	466	ASN
1	DA	131	MET
1	DA	341	LYS
1	DA	466	ASN
1	EA	131	MET
1	EA	341	LYS
1	EA	466	ASN
1	FA	131	MET
1	FA	341	LYS
1	FA	466	ASN
1	GA	131	MET
1	GA	341	LYS
1	GA	466	ASN
1	HA	131	MET
1	HA	341	LYS
1	HA	466	ASN
1	IA	131	MET
1	IA	341	LYS
1	IA	466	ASN
1	JA	131	MET
1	JA	341	LYS
1	JA	466	ASN
1	KA	131	MET
1	KA	341	LYS

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Mol	Chain	Res	Type
1	KA	466	ASN
1	LA	131	MET
1	LA	341	LYS
1	LA	466	ASN
1	MA	131	MET
1	MA	341	LYS
1	MA	466	ASN
1	NA	131	MET
1	NA	341	LYS
1	NA	466	ASN
1	OA	131	MET
1	OA	341	LYS
1	OA	466	ASN
1	PA	131	MET
1	PA	341	LYS
1	PA	466	ASN
1	QA	131	MET
1	QA	341	LYS
1	QA	466	ASN
1	RA	131	MET
1	RA	341	LYS
1	RA	466	ASN
1	SA	131	MET
1	SA	341	LYS
1	SA	466	ASN
1	TA	131	MET
1	TA	341	LYS
1	TA	466	ASN
1	UA	131	MET
1	UA	341	LYS
1	UA	466	ASN
1	VA	131	MET
1	VA	341	LYS
1	VA	466	ASN
1	WA	131	MET
1	WA	341	LYS
1	WA	466	ASN
1	XA	131	MET
1	XA	341	LYS
1	XA	466	ASN
1	YA	131	MET
1	YA	341	LYS

Continued on next page...

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Mol	Chain	Res	Type
1	YA	466	ASN
1	ZA	131	MET
1	ZA	341	LYS
1	ZA	466	ASN
1	AB	131	MET
1	AB	341	LYS
1	AB	466	ASN
1	BB	131	MET
1	BB	341	LYS
1	BB	466	ASN
1	CB	131	MET
1	CB	341	LYS
1	CB	466	ASN
1	DB	131	MET
1	DB	341	LYS
1	DB	466	ASN
1	EB	131	MET
1	EB	341	LYS
1	EB	466	ASN
1	FB	131	MET
1	FB	341	LYS
1	FB	466	ASN
1	GB	131	MET
1	GB	341	LYS
1	GB	466	ASN
1	HB	131	MET
1	HB	341	LYS
1	HB	466	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (138) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	85	GLN
1	1	419	ASN
1	1	466	ASN
1	A	85	GLN
1	A	466	ASN
1	B	85	GLN
1	B	466	ASN
1	C	85	GLN
1	C	466	ASN
1	D	85	GLN

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Mol	Chain	Res	Type
1	D	466	ASN
1	E	85	GLN
1	E	419	ASN
1	E	466	ASN
1	F	85	GLN
1	F	88	HIS
1	F	466	ASN
1	G	85	GLN
1	G	466	ASN
1	H	85	GLN
1	H	466	ASN
1	I	85	GLN
1	I	466	ASN
1	J	85	GLN
1	J	466	ASN
1	K	85	GLN
1	K	466	ASN
1	L	85	GLN
1	L	419	ASN
1	L	466	ASN
1	M	85	GLN
1	M	466	ASN
1	N	85	GLN
1	N	466	ASN
1	O	85	GLN
1	O	466	ASN
1	P	85	GLN
1	P	466	ASN
1	Q	85	GLN
1	Q	466	ASN
1	R	85	GLN
1	R	88	HIS
1	R	466	ASN
1	S	85	GLN
1	S	419	ASN
1	S	466	ASN
1	T	85	GLN
1	T	466	ASN
1	V	85	GLN
1	V	419	ASN
1	V	466	ASN
1	W	85	GLN

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Mol	Chain	Res	Type
1	W	466	ASN
1	X	85	GLN
1	X	466	ASN
1	Y	85	GLN
1	Y	466	ASN
1	Z	85	GLN
1	Z	466	ASN
1	AA	85	GLN
1	AA	466	ASN
1	BA	85	GLN
1	BA	419	ASN
1	BA	466	ASN
1	CA	85	GLN
1	CA	88	HIS
1	CA	466	ASN
1	DA	85	GLN
1	DA	466	ASN
1	EA	85	GLN
1	EA	466	ASN
1	FA	85	GLN
1	FA	466	ASN
1	GA	85	GLN
1	GA	466	ASN
1	HA	85	GLN
1	HA	88	HIS
1	HA	466	ASN
1	IA	85	GLN
1	IA	466	ASN
1	JA	85	GLN
1	JA	466	ASN
1	KA	85	GLN
1	KA	419	ASN
1	KA	466	ASN
1	LA	85	GLN
1	LA	88	HIS
1	LA	466	ASN
1	MA	85	GLN
1	MA	466	ASN
1	NA	85	GLN
1	NA	466	ASN
1	OA	85	GLN
1	OA	466	ASN

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Mol	Chain	Res	Type
1	PA	85	GLN
1	PA	466	ASN
1	QA	85	GLN
1	QA	466	ASN
1	RA	85	GLN
1	RA	88	HIS
1	RA	466	ASN
1	SA	85	GLN
1	SA	466	ASN
1	TA	85	GLN
1	TA	419	ASN
1	TA	466	ASN
1	UA	85	GLN
1	UA	466	ASN
1	VA	85	GLN
1	VA	466	ASN
1	WA	85	GLN
1	WA	419	ASN
1	WA	466	ASN
1	XA	85	GLN
1	XA	419	ASN
1	XA	466	ASN
1	YA	85	GLN
1	YA	88	HIS
1	YA	466	ASN
1	ZA	85	GLN
1	ZA	88	HIS
1	ZA	466	ASN
1	AB	85	GLN
1	AB	466	ASN
1	BB	85	GLN
1	BB	466	ASN
1	CB	85	GLN
1	CB	466	ASN
1	DB	85	GLN
1	DB	466	ASN
1	EB	85	GLN
1	EB	466	ASN
1	FB	85	GLN
1	FB	466	ASN
1	GB	85	GLN
1	GB	466	ASN

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Mol	Chain	Res	Type
1	HB	85	GLN
1	HB	466	ASN

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 monosaccharides 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.

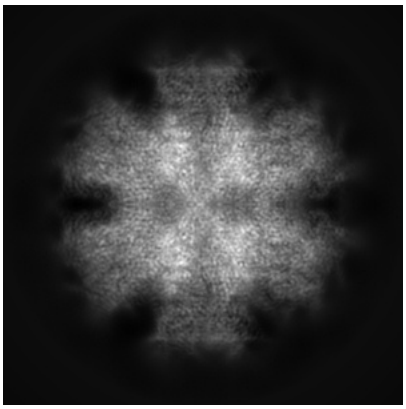
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-16512. These allow visual inspection of the internal detail of the map and identification of artifacts.

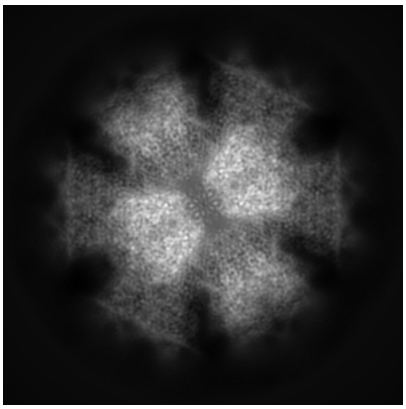
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

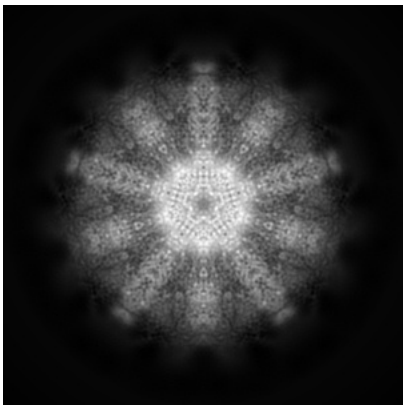
6.1.1 Primary map



X

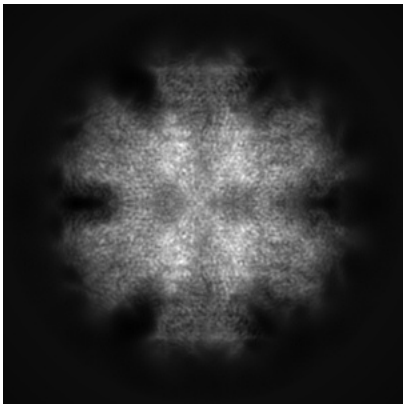


Y

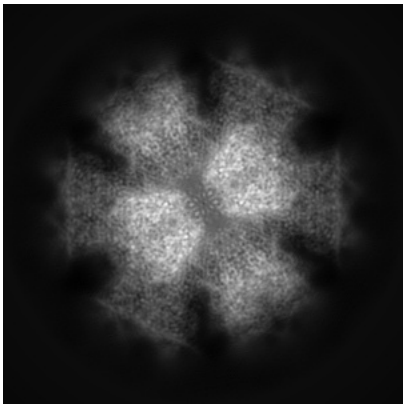


Z

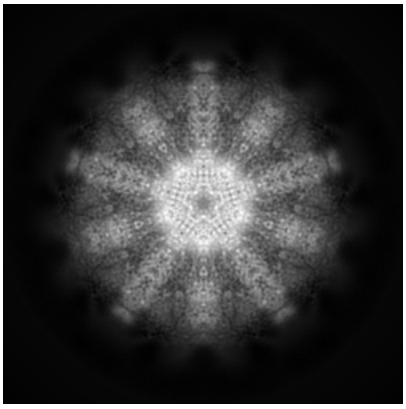
6.1.2 Raw map



X



Y

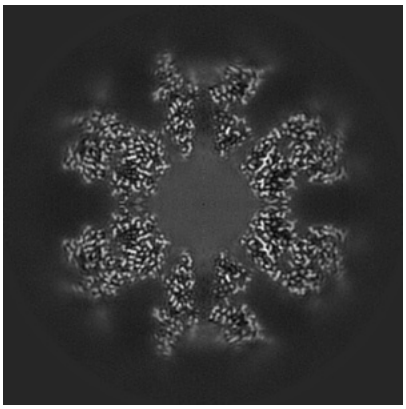


Z

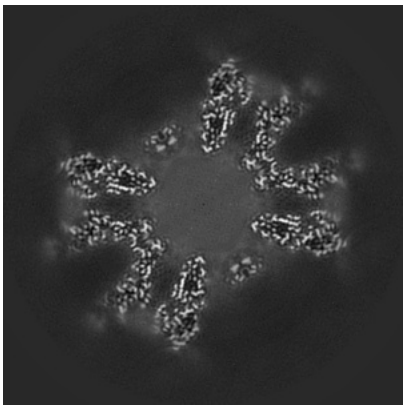
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

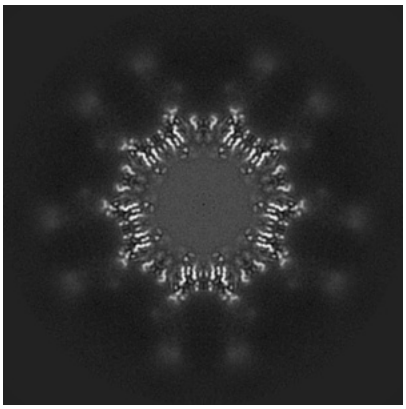
6.2.1 Primary map



X Index: 170

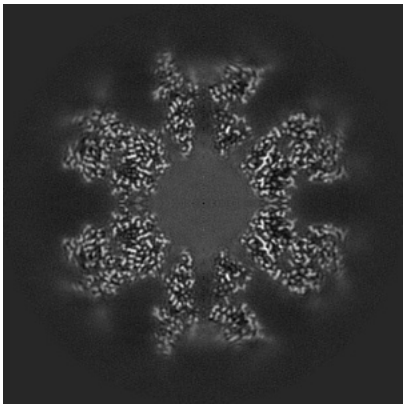


Y Index: 170

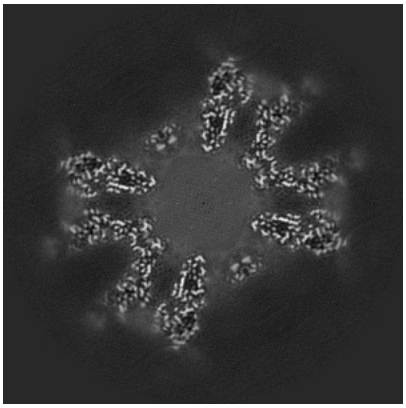


Z Index: 170

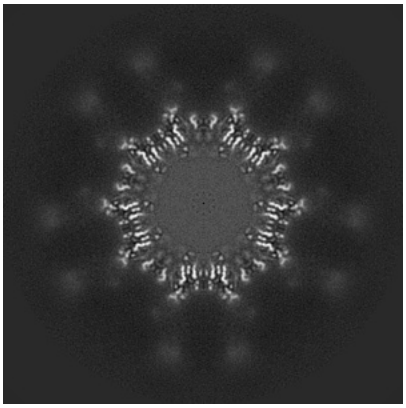
6.2.2 Raw map



X Index: 170



Y Index: 170

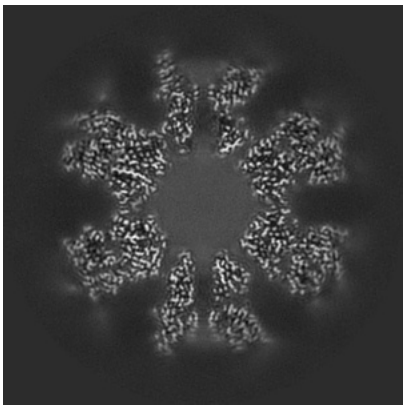


Z Index: 170

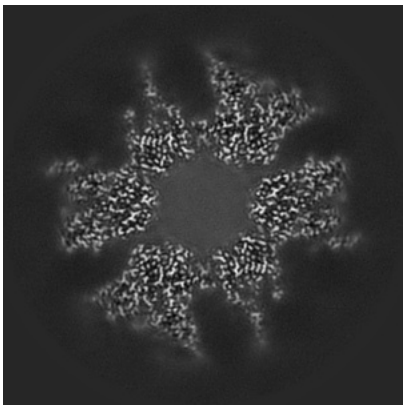
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

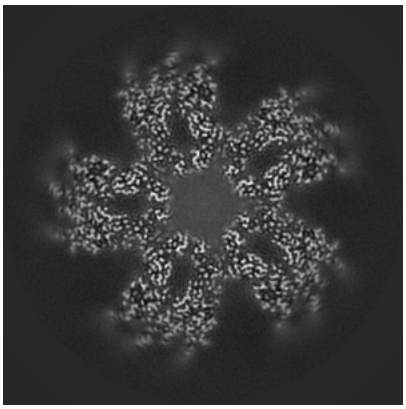
6.3.1 Primary map



X Index: 172

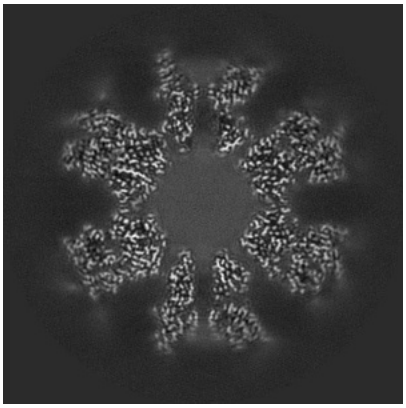


Y Index: 154

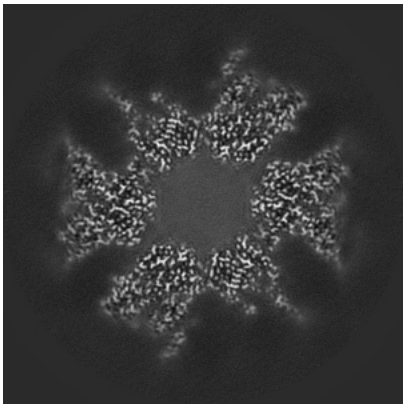


Z Index: 139

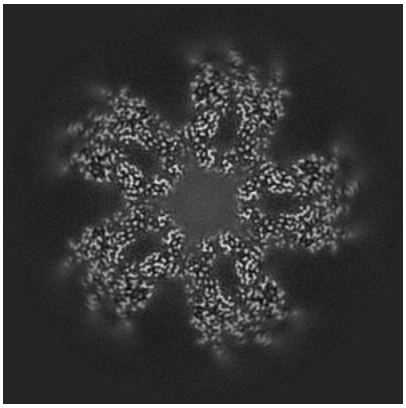
6.3.2 Raw map



X Index: 172



Y Index: 186

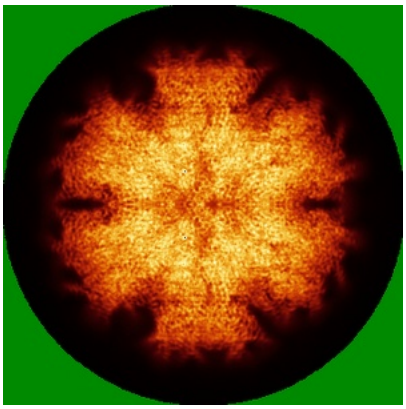


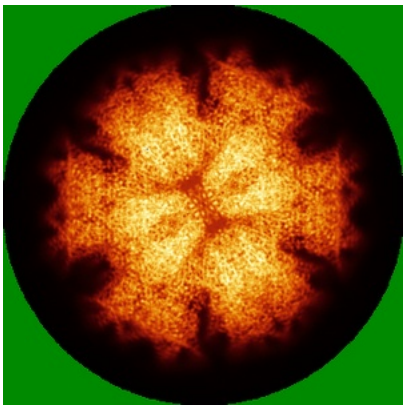
Z Index: 201

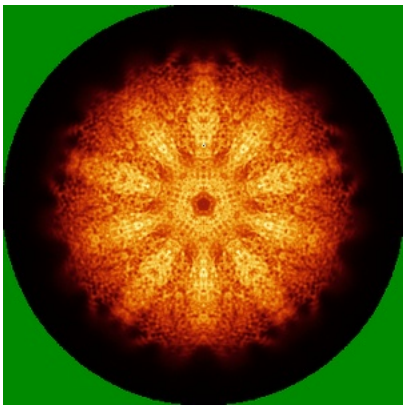
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

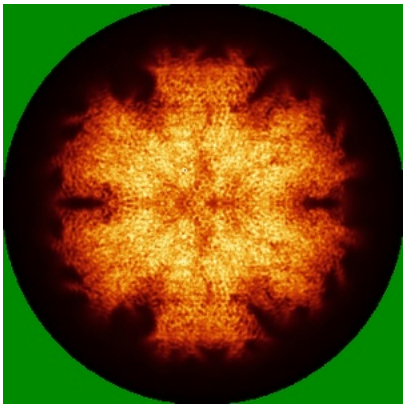
6.4.1 Primary map

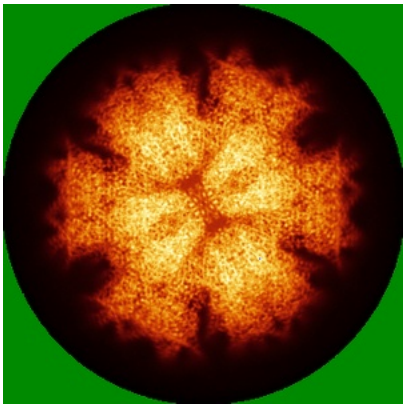

X

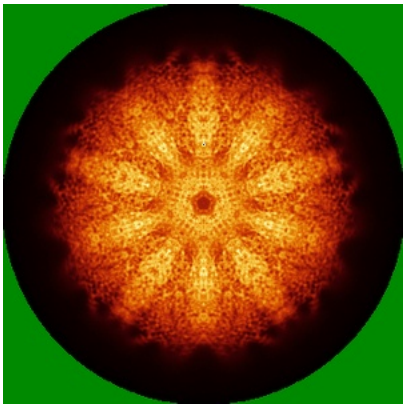

Y


Z

6.4.2 Raw map


X

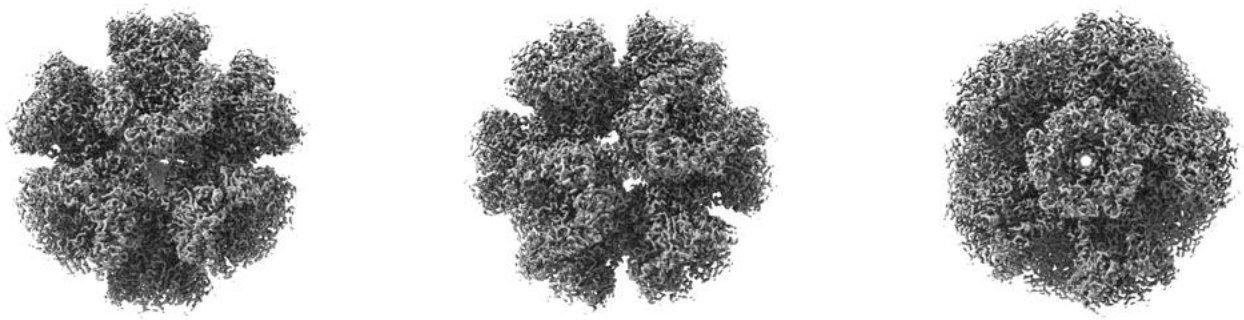

Y


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)

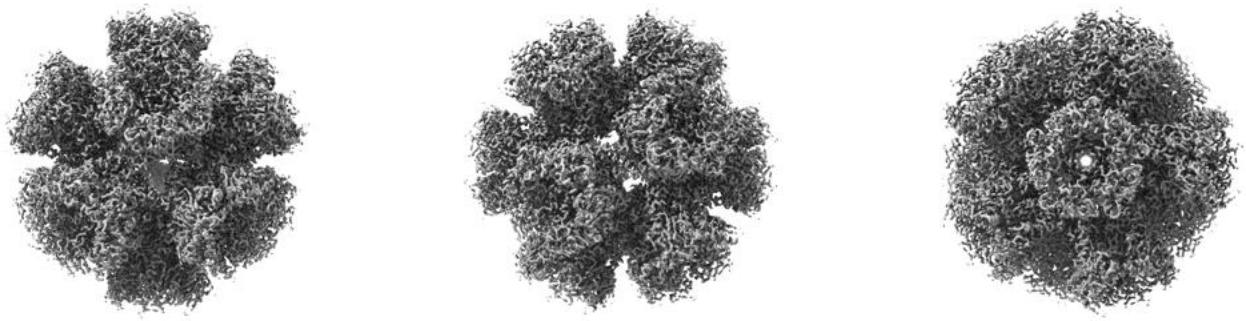
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

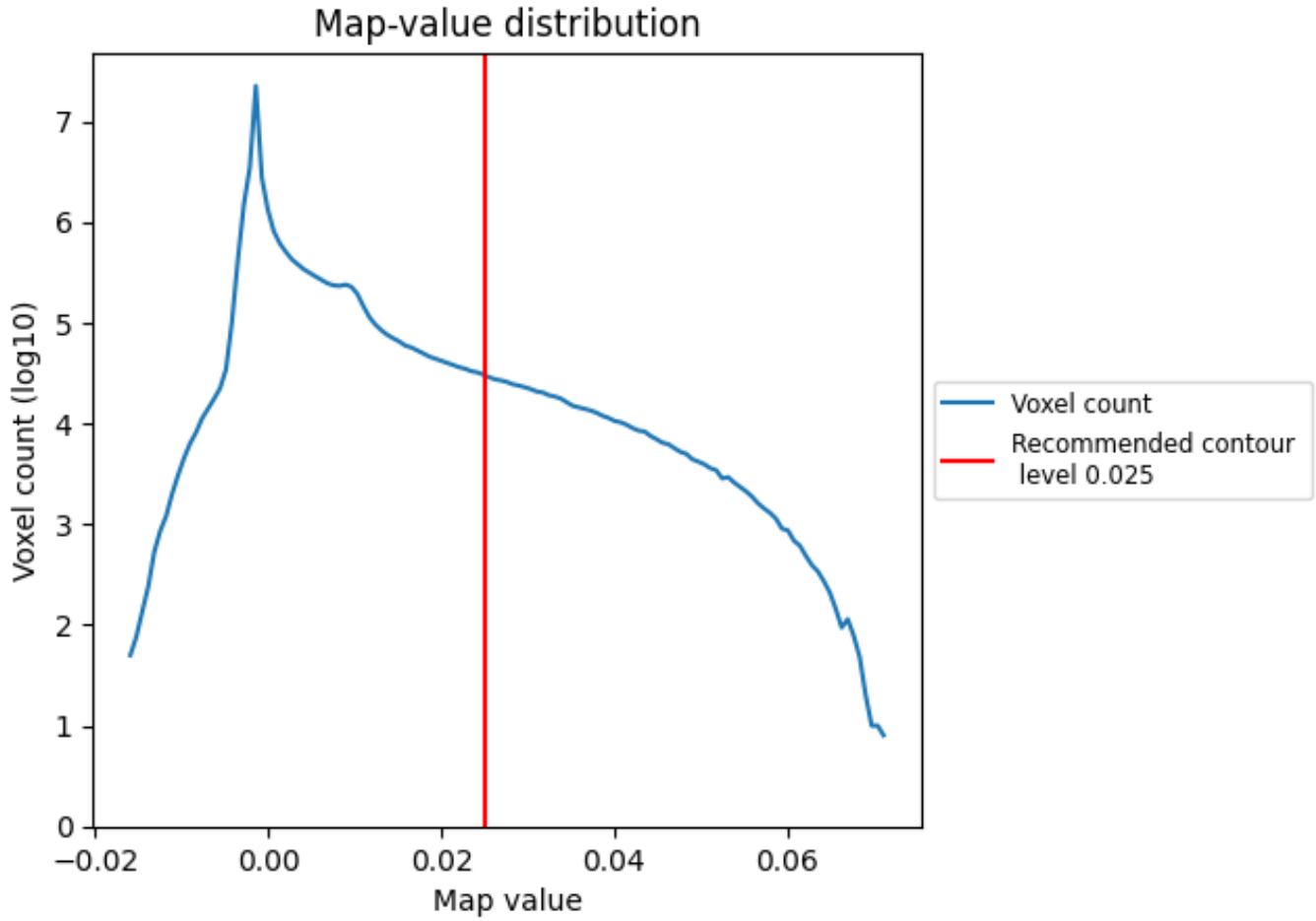
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

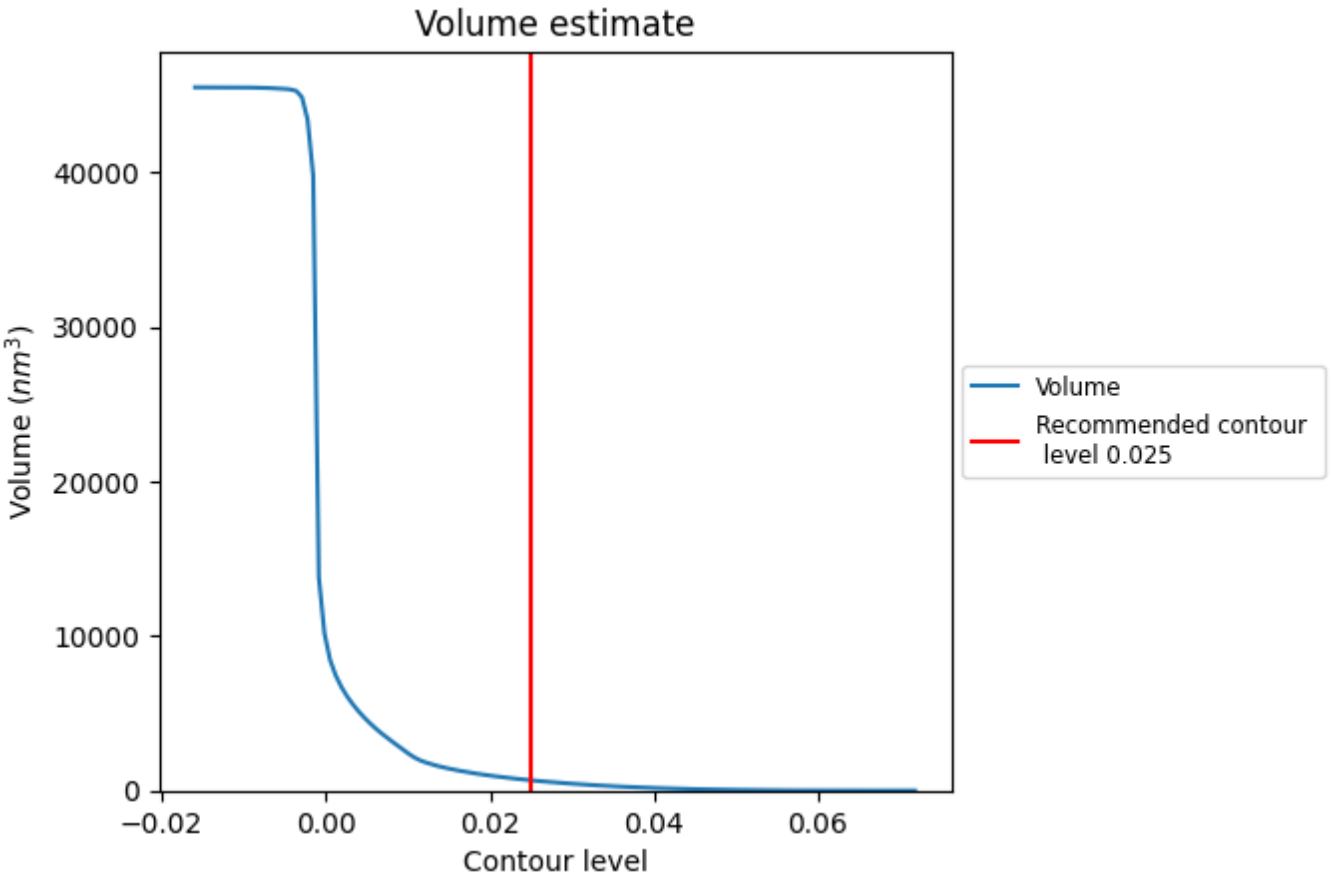
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

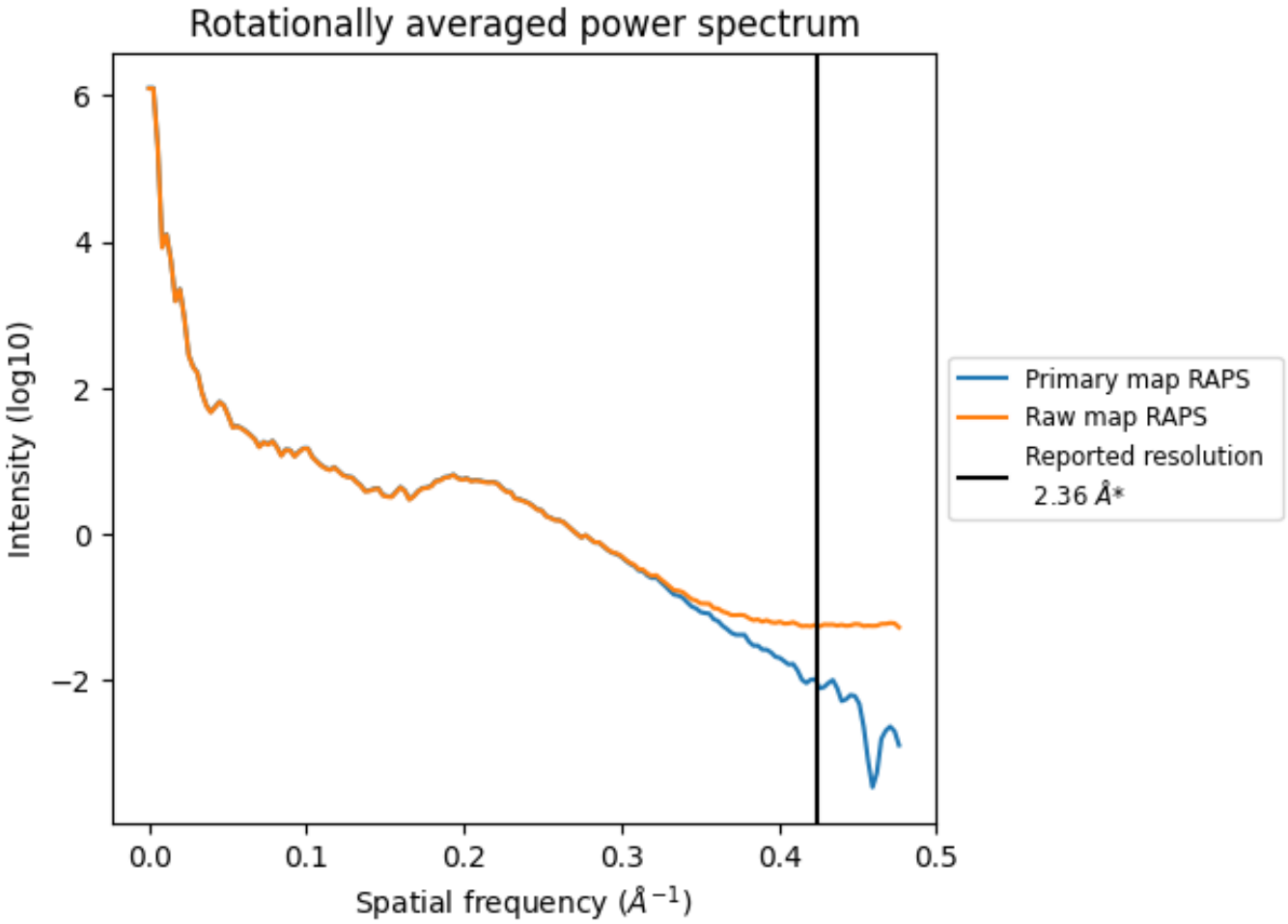
7.2 Volume estimate



The volume at the recommended contour level is 665 nm^3; this corresponds to an approximate mass of 601 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 (i)

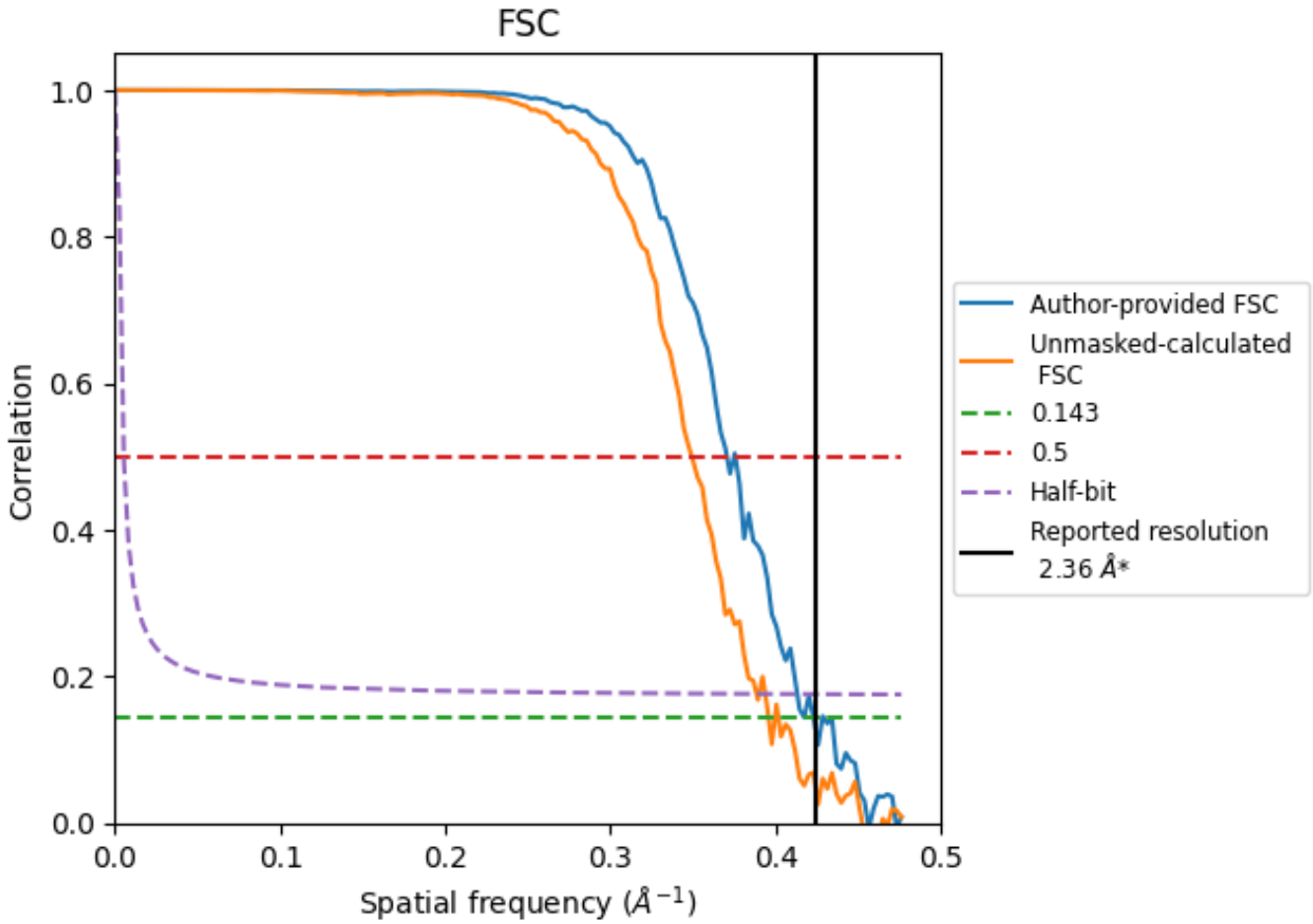


*Reported resolution corresponds to spatial frequency of 0.424 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.424 Å^{-1}

8.2 Resolution estimates (i)

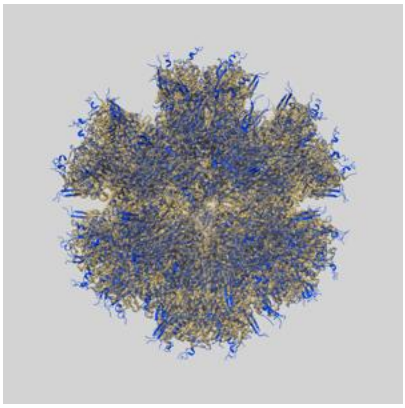
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.36	-	-
Author-provided FSC curve	2.36	2.70	2.42
Unmasked-calculated*	2.53	2.86	2.57

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

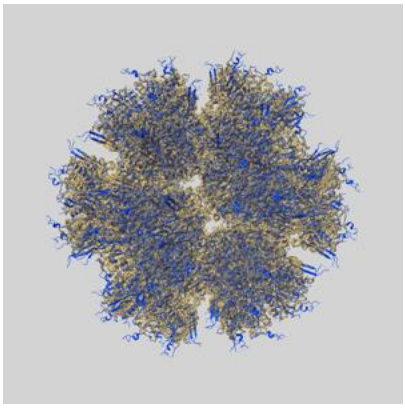
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-16512 and PDB model 8C9N. Per-residue inclusion information can be found in section 3 on page 74.

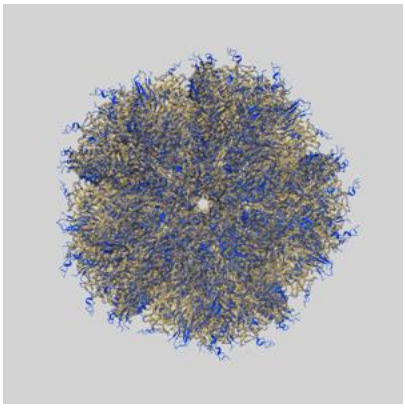
9.1 Map-model overlay



X



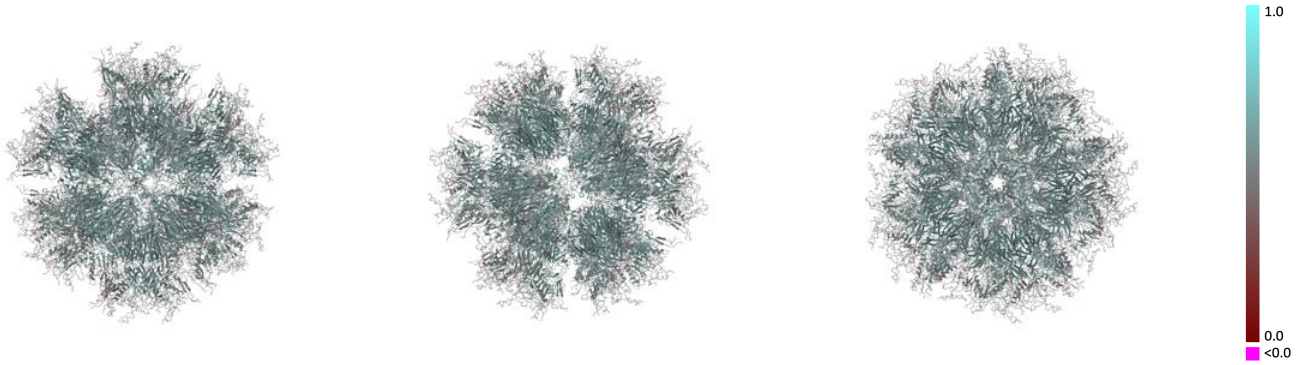
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.025 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.

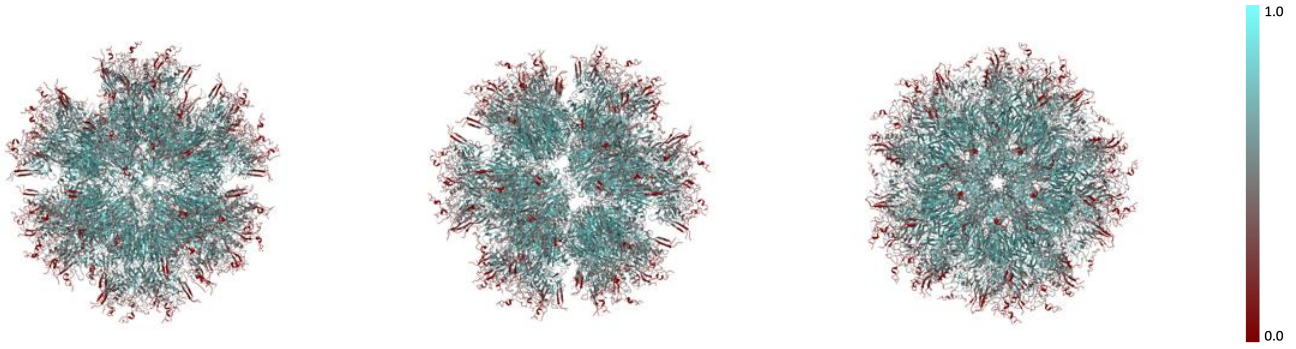
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

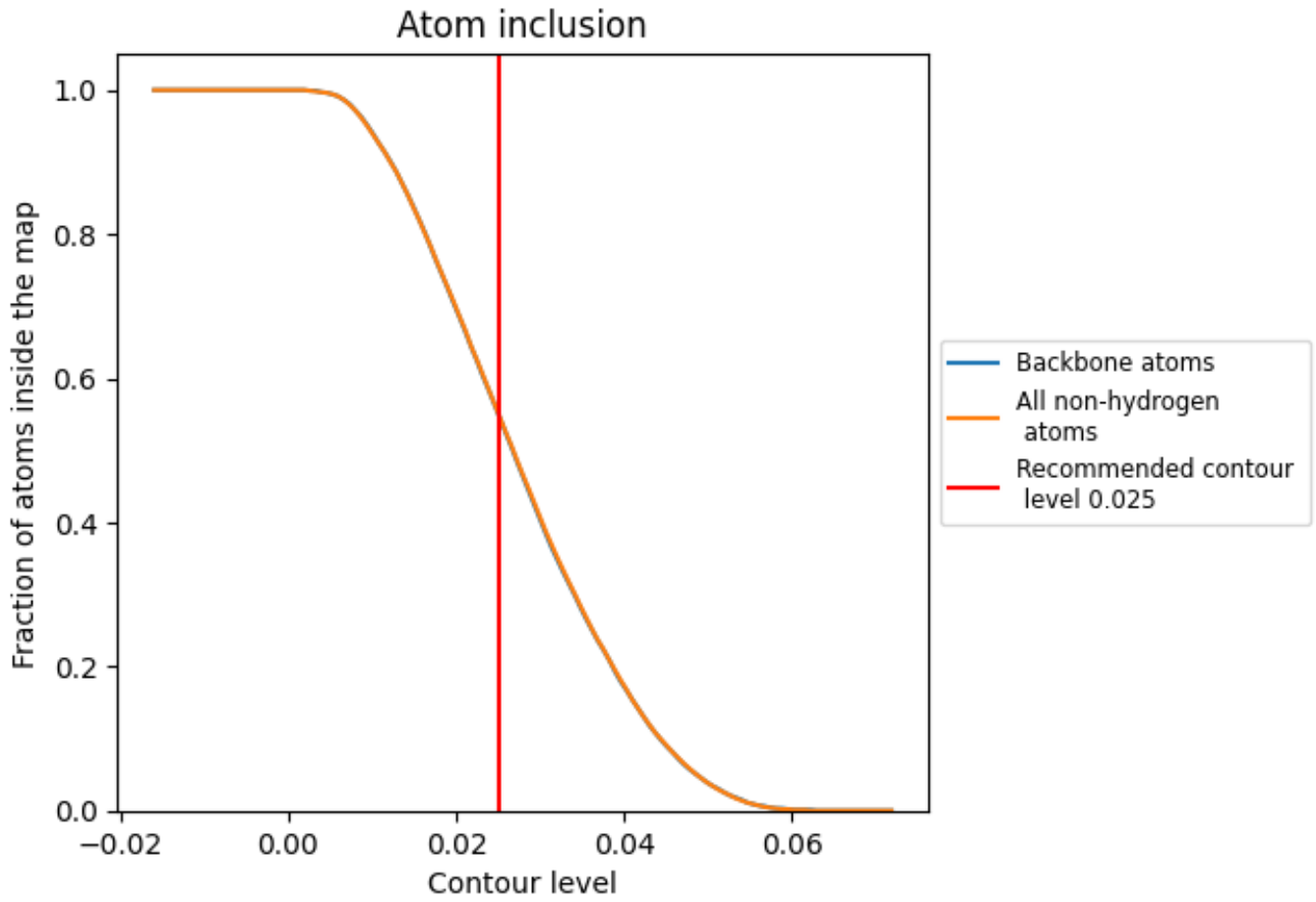
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.025).

9.4 Atom inclusion (i)



At the recommended contour level, 55% of all backbone atoms, 55% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5520	0.5440
1	0.5750	0.5560
A	0.5750	0.5590
AA	0.5580	0.5350
AB	0.5580	0.5380
B	0.5630	0.5370
BA	0.5630	0.5530
BB	0.5570	0.5320
C	0.5600	0.5320
CA	0.5740	0.5580
CB	0.5540	0.5350
D	0.5600	0.5350
DA	0.5600	0.5350
DB	0.5680	0.5410
E	0.5440	0.5220
EA	0.5640	0.5390
EB	0.5670	0.5530
F	0.5740	0.5580
FA	0.5590	0.5310
FB	0.5610	0.5370
G	0.5600	0.5350
GA	0.5670	0.5370
GB	0.5590	0.5330
H	0.5650	0.5510
HA	0.5760	0.5580
HB	0.5600	0.5350
I	0.5590	0.5400
IA	0.5790	0.5580
J	0.5740	0.5590
JA	0.5680	0.5350
K	0.5730	0.5570
KA	0.5740	0.5610
L	0.5690	0.5510
LA	0.5740	0.5580
M	0.5700	0.5560

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Chain	Atom inclusion	Q-score
MA	0.5720	0.5530
N	0.5560	0.5390
NA	0.5590	0.5390
O	0.5770	0.5560
OA	0.5640	0.5400
P	0.5580	0.5360
PA	0.5550	0.5400
Q	0.5610	0.5390
QA	0.5650	0.5420
R	0.5760	0.5580
RA	0.5750	0.5560
S	0.5600	0.5490
SA	0.5570	0.5400
T	0.5640	0.5360
TA	0.5770	0.5570
UA	0.5560	0.5340
V	0.5530	0.5310
VA	0.5620	0.5340
W	0.5680	0.5390
WA	0.5660	0.5520
X	0.5740	0.5570
XA	0.5380	0.5210
Y	0.5620	0.5380
YA	0.5770	0.5590
Z	0.5620	0.5310
ZA	0.5740	0.5570