



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 10:16 AM UTC

PDB ID : 9G3O / pdb_00009g3o
EMDB ID : EMD-51005
Title : Circularly permuted lumazine synthase 24-pentamer spherical cage
Authors : Koziej, L.; Azuma, Y.
Deposited on : 2024-07-12
Resolution : 2.76 Å (reported)
Based on initial model : 1HQK

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

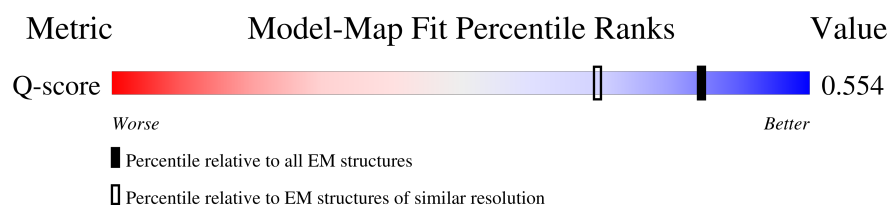
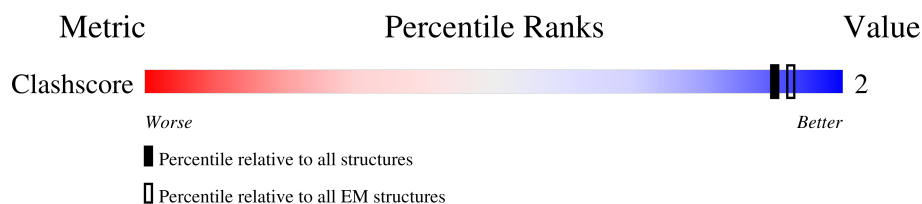
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

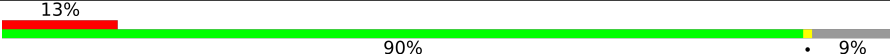
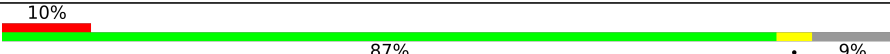
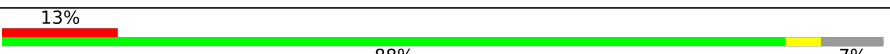
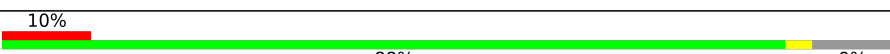
The reported resolution of this entry is 2.76 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	10642 (2.26 - 3.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	163	
1	AA	163	
1	AB	163	
1	AC	163	
1	AD	163	
1	B	163	

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Mol	Chain	Length	Quality of chain
1	BA	163	
1	BB	163	
1	BC	163	
1	BD	163	
1	C	163	
1	CA	163	
1	CB	163	
1	CC	163	
1	CD	163	
1	D	163	
1	DA	163	
1	DB	163	
1	DC	163	
1	DD	163	
1	E	163	
1	EA	163	
1	EB	163	
1	EC	163	
1	ED	163	
1	F	163	
1	FA	163	
1	FB	163	
1	FC	163	
1	FD	163	
1	G	163	

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Mol	Chain	Length	Quality of chain
1	GA	163	
1	GB	163	
1	GC	163	
1	GD	163	
1	H	163	
1	HA	163	
1	HB	163	
1	HC	163	
1	HD	163	
1	I	163	
1	IA	163	
1	IB	163	
1	IC	163	
1	ID	163	
1	J	163	
1	JA	163	
1	JB	163	
1	JC	163	
1	JD	163	
1	K	163	
1	KA	163	
1	KB	163	
1	KC	163	
1	KD	163	
1	L	163	

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Mol	Chain	Length	Quality of chain
1	LA	163	
1	LB	163	
1	LC	163	
1	LD	163	
1	M	163	
1	MA	163	
1	MB	163	
1	MC	163	
1	MD	163	
1	N	163	
1	NA	163	
1	NB	163	
1	NC	163	
1	ND	163	
1	O	163	
1	OA	163	
1	OB	163	
1	OC	163	
1	OD	163	
1	P	163	
1	PA	163	
1	PB	163	
1	PC	163	
1	PD	163	
1	Q	163	

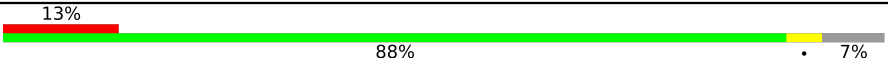
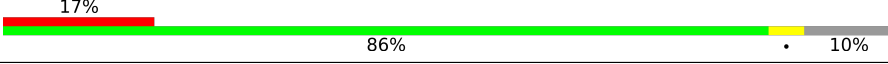
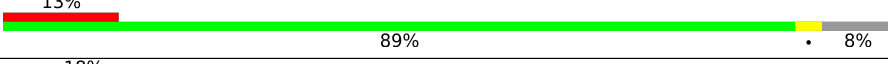
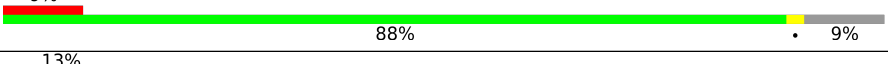
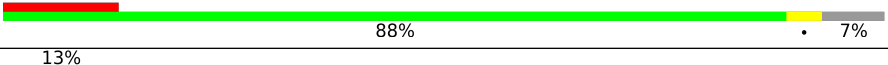
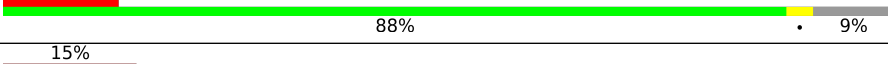
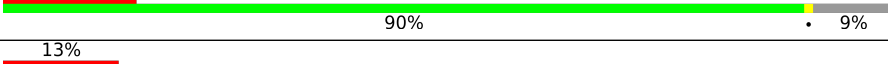
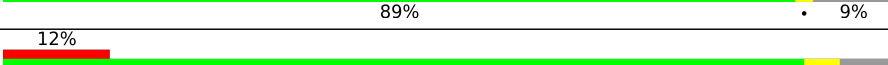
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Mol	Chain	Length	Quality of chain
1	QA	163	
1	QB	163	
1	QC	163	
1	R	163	
1	RA	163	
1	RB	163	
1	RC	163	
1	S	163	
1	SA	163	
1	SB	163	
1	SC	163	
1	T	163	
1	TA	163	
1	TB	163	
1	TC	163	
1	U	163	
1	UA	163	
1	UB	163	
1	UC	163	
1	V	163	
1	VA	163	
1	VB	163	
1	VC	163	
1	W	163	
1	WA	163	

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Mol	Chain	Length	Quality of chain
1	WB	163	
1	WC	163	
1	X	163	
1	XA	163	
1	XB	163	
1	XC	163	
1	Y	163	
1	YA	163	
1	YB	163	
1	YC	163	
1	Z	163	
1	ZA	163	
1	ZB	163	
1	ZC	163	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 133824 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 6,7-dimethyl-8-ribityllumazine synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	B	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	C	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	D	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	E	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	F	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	G	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	H	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	I	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	J	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		
1	K	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	L	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	M	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	N	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	O	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	P	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	Q	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	S	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	T	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		
1	U	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	V	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	W	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	X	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	Y	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	Z	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	AA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	BA	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	CA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	DA	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		
1	EA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	FA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	GA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	HA	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	IA	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	JA	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	KA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	LA	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	MA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	NA	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		
1	OA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	PA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	QA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	RA	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	SA	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	TA	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	UA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	VA	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	WA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	XA	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		
1	YA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	ZA	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	AB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	BB	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	CB	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	DB	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	EB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	FB	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	GB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	HB	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		
1	IB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	JB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	KB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	LB	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	MB	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	NB	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	OB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	PB	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	QB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	RB	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		
1	SB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	TB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	UB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	VB	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	WB	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	XB	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	YB	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	ZB	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	AC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	BC	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	DC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	EC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	FC	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	GC	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	HC	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	IC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	JC	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	KC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	LC	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		
1	MC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	NC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	OC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	PC	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	QC	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	RC	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	SC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	TC	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	UC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	VC	150	Total	C	N	O	S	1	0
			1127	713	201	210	3		
1	WC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	XC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	YC	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	ZC	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	AD	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	BD	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	CD	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	DD	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	ED	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	FD	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		
1	GD	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	HD	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	ID	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	JD	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	KD	151	Total	C	N	O	S	0	0
			1134	717	202	212	3		
1	LD	147	Total	C	N	O	S	0	0
			1104	699	195	207	3		
1	MD	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	ND	153	Total	C	N	O	S	0	0
			1143	722	204	214	3		
1	OD	148	Total	C	N	O	S	0	0
			1108	701	196	208	3		
1	PD	150	Total	C	N	O	S	0	0
			1127	713	201	210	3		

There are 1320 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
A	37	GLY	-	linker	UNP O66529
A	38	THR	-	linker	UNP O66529
A	39	GLY	-	linker	UNP O66529
A	40	GLY	-	linker	UNP O66529
A	41	SER	-	linker	UNP O66529
A	42	GLY	-	linker	UNP O66529
A	43	SER	-	linker	UNP O66529
A	44	SER	-	linker	UNP O66529
A	45	MET	-	linker	UNP O66529
A	46	GLU	-	linker	UNP O66529
B	1	MET	-	initiating methionine	UNP O66529
B	37	GLY	-	linker	UNP O66529
B	38	THR	-	linker	UNP O66529
B	39	GLY	-	linker	UNP O66529
B	40	GLY	-	linker	UNP O66529
B	41	SER	-	linker	UNP O66529
B	42	GLY	-	linker	UNP O66529
B	43	SER	-	linker	UNP O66529
B	44	SER	-	linker	UNP O66529
B	45	MET	-	linker	UNP O66529
B	46	GLU	-	linker	UNP O66529
C	1	MET	-	initiating methionine	UNP O66529
C	37	GLY	-	linker	UNP O66529
C	38	THR	-	linker	UNP O66529
C	39	GLY	-	linker	UNP O66529
C	40	GLY	-	linker	UNP O66529
C	41	SER	-	linker	UNP O66529
C	42	GLY	-	linker	UNP O66529
C	43	SER	-	linker	UNP O66529
C	44	SER	-	linker	UNP O66529
C	45	MET	-	linker	UNP O66529
C	46	GLU	-	linker	UNP O66529
D	1	MET	-	initiating methionine	UNP O66529
D	37	GLY	-	linker	UNP O66529
D	38	THR	-	linker	UNP O66529
D	39	GLY	-	linker	UNP O66529
D	40	GLY	-	linker	UNP O66529
D	41	SER	-	linker	UNP O66529
D	42	GLY	-	linker	UNP O66529
D	43	SER	-	linker	UNP O66529
D	44	SER	-	linker	UNP O66529
D	45	MET	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
D	46	GLU	-	linker	UNP O66529
E	1	MET	-	initiating methionine	UNP O66529
E	37	GLY	-	linker	UNP O66529
E	38	THR	-	linker	UNP O66529
E	39	GLY	-	linker	UNP O66529
E	40	GLY	-	linker	UNP O66529
E	41	SER	-	linker	UNP O66529
E	42	GLY	-	linker	UNP O66529
E	43	SER	-	linker	UNP O66529
E	44	SER	-	linker	UNP O66529
E	45	MET	-	linker	UNP O66529
E	46	GLU	-	linker	UNP O66529
F	1	MET	-	initiating methionine	UNP O66529
F	37	GLY	-	linker	UNP O66529
F	38	THR	-	linker	UNP O66529
F	39	GLY	-	linker	UNP O66529
F	40	GLY	-	linker	UNP O66529
F	41	SER	-	linker	UNP O66529
F	42	GLY	-	linker	UNP O66529
F	43	SER	-	linker	UNP O66529
F	44	SER	-	linker	UNP O66529
F	45	MET	-	linker	UNP O66529
F	46	GLU	-	linker	UNP O66529
G	1	MET	-	initiating methionine	UNP O66529
G	37	GLY	-	linker	UNP O66529
G	38	THR	-	linker	UNP O66529
G	39	GLY	-	linker	UNP O66529
G	40	GLY	-	linker	UNP O66529
G	41	SER	-	linker	UNP O66529
G	42	GLY	-	linker	UNP O66529
G	43	SER	-	linker	UNP O66529
G	44	SER	-	linker	UNP O66529
G	45	MET	-	linker	UNP O66529
G	46	GLU	-	linker	UNP O66529
H	1	MET	-	initiating methionine	UNP O66529
H	37	GLY	-	linker	UNP O66529
H	38	THR	-	linker	UNP O66529
H	39	GLY	-	linker	UNP O66529
H	40	GLY	-	linker	UNP O66529
H	41	SER	-	linker	UNP O66529
H	42	GLY	-	linker	UNP O66529
H	43	SER	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
H	44	SER	-	linker	UNP O66529
H	45	MET	-	linker	UNP O66529
H	46	GLU	-	linker	UNP O66529
I	1	MET	-	initiating methionine	UNP O66529
I	37	GLY	-	linker	UNP O66529
I	38	THR	-	linker	UNP O66529
I	39	GLY	-	linker	UNP O66529
I	40	GLY	-	linker	UNP O66529
I	41	SER	-	linker	UNP O66529
I	42	GLY	-	linker	UNP O66529
I	43	SER	-	linker	UNP O66529
I	44	SER	-	linker	UNP O66529
I	45	MET	-	linker	UNP O66529
I	46	GLU	-	linker	UNP O66529
J	1	MET	-	initiating methionine	UNP O66529
J	37	GLY	-	linker	UNP O66529
J	38	THR	-	linker	UNP O66529
J	39	GLY	-	linker	UNP O66529
J	40	GLY	-	linker	UNP O66529
J	41	SER	-	linker	UNP O66529
J	42	GLY	-	linker	UNP O66529
J	43	SER	-	linker	UNP O66529
J	44	SER	-	linker	UNP O66529
J	45	MET	-	linker	UNP O66529
J	46	GLU	-	linker	UNP O66529
K	1	MET	-	initiating methionine	UNP O66529
K	37	GLY	-	linker	UNP O66529
K	38	THR	-	linker	UNP O66529
K	39	GLY	-	linker	UNP O66529
K	40	GLY	-	linker	UNP O66529
K	41	SER	-	linker	UNP O66529
K	42	GLY	-	linker	UNP O66529
K	43	SER	-	linker	UNP O66529
K	44	SER	-	linker	UNP O66529
K	45	MET	-	linker	UNP O66529
K	46	GLU	-	linker	UNP O66529
L	1	MET	-	initiating methionine	UNP O66529
L	37	GLY	-	linker	UNP O66529
L	38	THR	-	linker	UNP O66529
L	39	GLY	-	linker	UNP O66529
L	40	GLY	-	linker	UNP O66529
L	41	SER	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
L	42	GLY	-	linker	UNP O66529
L	43	SER	-	linker	UNP O66529
L	44	SER	-	linker	UNP O66529
L	45	MET	-	linker	UNP O66529
L	46	GLU	-	linker	UNP O66529
M	1	MET	-	initiating methionine	UNP O66529
M	37	GLY	-	linker	UNP O66529
M	38	THR	-	linker	UNP O66529
M	39	GLY	-	linker	UNP O66529
M	40	GLY	-	linker	UNP O66529
M	41	SER	-	linker	UNP O66529
M	42	GLY	-	linker	UNP O66529
M	43	SER	-	linker	UNP O66529
M	44	SER	-	linker	UNP O66529
M	45	MET	-	linker	UNP O66529
M	46	GLU	-	linker	UNP O66529
N	1	MET	-	initiating methionine	UNP O66529
N	37	GLY	-	linker	UNP O66529
N	38	THR	-	linker	UNP O66529
N	39	GLY	-	linker	UNP O66529
N	40	GLY	-	linker	UNP O66529
N	41	SER	-	linker	UNP O66529
N	42	GLY	-	linker	UNP O66529
N	43	SER	-	linker	UNP O66529
N	44	SER	-	linker	UNP O66529
N	45	MET	-	linker	UNP O66529
N	46	GLU	-	linker	UNP O66529
O	1	MET	-	initiating methionine	UNP O66529
O	37	GLY	-	linker	UNP O66529
O	38	THR	-	linker	UNP O66529
O	39	GLY	-	linker	UNP O66529
O	40	GLY	-	linker	UNP O66529
O	41	SER	-	linker	UNP O66529
O	42	GLY	-	linker	UNP O66529
O	43	SER	-	linker	UNP O66529
O	44	SER	-	linker	UNP O66529
O	45	MET	-	linker	UNP O66529
O	46	GLU	-	linker	UNP O66529
P	1	MET	-	initiating methionine	UNP O66529
P	37	GLY	-	linker	UNP O66529
P	38	THR	-	linker	UNP O66529
P	39	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
P	40	GLY	-	linker	UNP O66529
P	41	SER	-	linker	UNP O66529
P	42	GLY	-	linker	UNP O66529
P	43	SER	-	linker	UNP O66529
P	44	SER	-	linker	UNP O66529
P	45	MET	-	linker	UNP O66529
P	46	GLU	-	linker	UNP O66529
Q	1	MET	-	initiating methionine	UNP O66529
Q	37	GLY	-	linker	UNP O66529
Q	38	THR	-	linker	UNP O66529
Q	39	GLY	-	linker	UNP O66529
Q	40	GLY	-	linker	UNP O66529
Q	41	SER	-	linker	UNP O66529
Q	42	GLY	-	linker	UNP O66529
Q	43	SER	-	linker	UNP O66529
Q	44	SER	-	linker	UNP O66529
Q	45	MET	-	linker	UNP O66529
Q	46	GLU	-	linker	UNP O66529
R	1	MET	-	initiating methionine	UNP O66529
R	37	GLY	-	linker	UNP O66529
R	38	THR	-	linker	UNP O66529
R	39	GLY	-	linker	UNP O66529
R	40	GLY	-	linker	UNP O66529
R	41	SER	-	linker	UNP O66529
R	42	GLY	-	linker	UNP O66529
R	43	SER	-	linker	UNP O66529
R	44	SER	-	linker	UNP O66529
R	45	MET	-	linker	UNP O66529
R	46	GLU	-	linker	UNP O66529
S	1	MET	-	initiating methionine	UNP O66529
S	37	GLY	-	linker	UNP O66529
S	38	THR	-	linker	UNP O66529
S	39	GLY	-	linker	UNP O66529
S	40	GLY	-	linker	UNP O66529
S	41	SER	-	linker	UNP O66529
S	42	GLY	-	linker	UNP O66529
S	43	SER	-	linker	UNP O66529
S	44	SER	-	linker	UNP O66529
S	45	MET	-	linker	UNP O66529
S	46	GLU	-	linker	UNP O66529
T	1	MET	-	initiating methionine	UNP O66529
T	37	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
T	38	THR	-	linker	UNP O66529
T	39	GLY	-	linker	UNP O66529
T	40	GLY	-	linker	UNP O66529
T	41	SER	-	linker	UNP O66529
T	42	GLY	-	linker	UNP O66529
T	43	SER	-	linker	UNP O66529
T	44	SER	-	linker	UNP O66529
T	45	MET	-	linker	UNP O66529
T	46	GLU	-	linker	UNP O66529
U	1	MET	-	initiating methionine	UNP O66529
U	37	GLY	-	linker	UNP O66529
U	38	THR	-	linker	UNP O66529
U	39	GLY	-	linker	UNP O66529
U	40	GLY	-	linker	UNP O66529
U	41	SER	-	linker	UNP O66529
U	42	GLY	-	linker	UNP O66529
U	43	SER	-	linker	UNP O66529
U	44	SER	-	linker	UNP O66529
U	45	MET	-	linker	UNP O66529
U	46	GLU	-	linker	UNP O66529
V	1	MET	-	initiating methionine	UNP O66529
V	37	GLY	-	linker	UNP O66529
V	38	THR	-	linker	UNP O66529
V	39	GLY	-	linker	UNP O66529
V	40	GLY	-	linker	UNP O66529
V	41	SER	-	linker	UNP O66529
V	42	GLY	-	linker	UNP O66529
V	43	SER	-	linker	UNP O66529
V	44	SER	-	linker	UNP O66529
V	45	MET	-	linker	UNP O66529
V	46	GLU	-	linker	UNP O66529
W	1	MET	-	initiating methionine	UNP O66529
W	37	GLY	-	linker	UNP O66529
W	38	THR	-	linker	UNP O66529
W	39	GLY	-	linker	UNP O66529
W	40	GLY	-	linker	UNP O66529
W	41	SER	-	linker	UNP O66529
W	42	GLY	-	linker	UNP O66529
W	43	SER	-	linker	UNP O66529
W	44	SER	-	linker	UNP O66529
W	45	MET	-	linker	UNP O66529
W	46	GLU	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
X	1	MET	-	initiating methionine	UNP O66529
X	37	GLY	-	linker	UNP O66529
X	38	THR	-	linker	UNP O66529
X	39	GLY	-	linker	UNP O66529
X	40	GLY	-	linker	UNP O66529
X	41	SER	-	linker	UNP O66529
X	42	GLY	-	linker	UNP O66529
X	43	SER	-	linker	UNP O66529
X	44	SER	-	linker	UNP O66529
X	45	MET	-	linker	UNP O66529
X	46	GLU	-	linker	UNP O66529
Y	1	MET	-	initiating methionine	UNP O66529
Y	37	GLY	-	linker	UNP O66529
Y	38	THR	-	linker	UNP O66529
Y	39	GLY	-	linker	UNP O66529
Y	40	GLY	-	linker	UNP O66529
Y	41	SER	-	linker	UNP O66529
Y	42	GLY	-	linker	UNP O66529
Y	43	SER	-	linker	UNP O66529
Y	44	SER	-	linker	UNP O66529
Y	45	MET	-	linker	UNP O66529
Y	46	GLU	-	linker	UNP O66529
Z	1	MET	-	initiating methionine	UNP O66529
Z	37	GLY	-	linker	UNP O66529
Z	38	THR	-	linker	UNP O66529
Z	39	GLY	-	linker	UNP O66529
Z	40	GLY	-	linker	UNP O66529
Z	41	SER	-	linker	UNP O66529
Z	42	GLY	-	linker	UNP O66529
Z	43	SER	-	linker	UNP O66529
Z	44	SER	-	linker	UNP O66529
Z	45	MET	-	linker	UNP O66529
Z	46	GLU	-	linker	UNP O66529
AA	1	MET	-	initiating methionine	UNP O66529
AA	37	GLY	-	linker	UNP O66529
AA	38	THR	-	linker	UNP O66529
AA	39	GLY	-	linker	UNP O66529
AA	40	GLY	-	linker	UNP O66529
AA	41	SER	-	linker	UNP O66529
AA	42	GLY	-	linker	UNP O66529
AA	43	SER	-	linker	UNP O66529
AA	44	SER	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
AA	45	MET	-	linker	UNP O66529
AA	46	GLU	-	linker	UNP O66529
BA	1	MET	-	initiating methionine	UNP O66529
BA	37	GLY	-	linker	UNP O66529
BA	38	THR	-	linker	UNP O66529
BA	39	GLY	-	linker	UNP O66529
BA	40	GLY	-	linker	UNP O66529
BA	41	SER	-	linker	UNP O66529
BA	42	GLY	-	linker	UNP O66529
BA	43	SER	-	linker	UNP O66529
BA	44	SER	-	linker	UNP O66529
BA	45	MET	-	linker	UNP O66529
BA	46	GLU	-	linker	UNP O66529
CA	1	MET	-	initiating methionine	UNP O66529
CA	37	GLY	-	linker	UNP O66529
CA	38	THR	-	linker	UNP O66529
CA	39	GLY	-	linker	UNP O66529
CA	40	GLY	-	linker	UNP O66529
CA	41	SER	-	linker	UNP O66529
CA	42	GLY	-	linker	UNP O66529
CA	43	SER	-	linker	UNP O66529
CA	44	SER	-	linker	UNP O66529
CA	45	MET	-	linker	UNP O66529
CA	46	GLU	-	linker	UNP O66529
DA	1	MET	-	initiating methionine	UNP O66529
DA	37	GLY	-	linker	UNP O66529
DA	38	THR	-	linker	UNP O66529
DA	39	GLY	-	linker	UNP O66529
DA	40	GLY	-	linker	UNP O66529
DA	41	SER	-	linker	UNP O66529
DA	42	GLY	-	linker	UNP O66529
DA	43	SER	-	linker	UNP O66529
DA	44	SER	-	linker	UNP O66529
DA	45	MET	-	linker	UNP O66529
DA	46	GLU	-	linker	UNP O66529
EA	1	MET	-	initiating methionine	UNP O66529
EA	37	GLY	-	linker	UNP O66529
EA	38	THR	-	linker	UNP O66529
EA	39	GLY	-	linker	UNP O66529
EA	40	GLY	-	linker	UNP O66529
EA	41	SER	-	linker	UNP O66529
EA	42	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
EA	43	SER	-	linker	UNP O66529
EA	44	SER	-	linker	UNP O66529
EA	45	MET	-	linker	UNP O66529
EA	46	GLU	-	linker	UNP O66529
FA	1	MET	-	initiating methionine	UNP O66529
FA	37	GLY	-	linker	UNP O66529
FA	38	THR	-	linker	UNP O66529
FA	39	GLY	-	linker	UNP O66529
FA	40	GLY	-	linker	UNP O66529
FA	41	SER	-	linker	UNP O66529
FA	42	GLY	-	linker	UNP O66529
FA	43	SER	-	linker	UNP O66529
FA	44	SER	-	linker	UNP O66529
FA	45	MET	-	linker	UNP O66529
FA	46	GLU	-	linker	UNP O66529
GA	1	MET	-	initiating methionine	UNP O66529
GA	37	GLY	-	linker	UNP O66529
GA	38	THR	-	linker	UNP O66529
GA	39	GLY	-	linker	UNP O66529
GA	40	GLY	-	linker	UNP O66529
GA	41	SER	-	linker	UNP O66529
GA	42	GLY	-	linker	UNP O66529
GA	43	SER	-	linker	UNP O66529
GA	44	SER	-	linker	UNP O66529
GA	45	MET	-	linker	UNP O66529
GA	46	GLU	-	linker	UNP O66529
HA	1	MET	-	initiating methionine	UNP O66529
HA	37	GLY	-	linker	UNP O66529
HA	38	THR	-	linker	UNP O66529
HA	39	GLY	-	linker	UNP O66529
HA	40	GLY	-	linker	UNP O66529
HA	41	SER	-	linker	UNP O66529
HA	42	GLY	-	linker	UNP O66529
HA	43	SER	-	linker	UNP O66529
HA	44	SER	-	linker	UNP O66529
HA	45	MET	-	linker	UNP O66529
HA	46	GLU	-	linker	UNP O66529
IA	1	MET	-	initiating methionine	UNP O66529
IA	37	GLY	-	linker	UNP O66529
IA	38	THR	-	linker	UNP O66529
IA	39	GLY	-	linker	UNP O66529
IA	40	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
IA	41	SER	-	linker	UNP O66529
IA	42	GLY	-	linker	UNP O66529
IA	43	SER	-	linker	UNP O66529
IA	44	SER	-	linker	UNP O66529
IA	45	MET	-	linker	UNP O66529
IA	46	GLU	-	linker	UNP O66529
JA	1	MET	-	initiating methionine	UNP O66529
JA	37	GLY	-	linker	UNP O66529
JA	38	THR	-	linker	UNP O66529
JA	39	GLY	-	linker	UNP O66529
JA	40	GLY	-	linker	UNP O66529
JA	41	SER	-	linker	UNP O66529
JA	42	GLY	-	linker	UNP O66529
JA	43	SER	-	linker	UNP O66529
JA	44	SER	-	linker	UNP O66529
JA	45	MET	-	linker	UNP O66529
JA	46	GLU	-	linker	UNP O66529
KA	1	MET	-	initiating methionine	UNP O66529
KA	37	GLY	-	linker	UNP O66529
KA	38	THR	-	linker	UNP O66529
KA	39	GLY	-	linker	UNP O66529
KA	40	GLY	-	linker	UNP O66529
KA	41	SER	-	linker	UNP O66529
KA	42	GLY	-	linker	UNP O66529
KA	43	SER	-	linker	UNP O66529
KA	44	SER	-	linker	UNP O66529
KA	45	MET	-	linker	UNP O66529
KA	46	GLU	-	linker	UNP O66529
LA	1	MET	-	initiating methionine	UNP O66529
LA	37	GLY	-	linker	UNP O66529
LA	38	THR	-	linker	UNP O66529
LA	39	GLY	-	linker	UNP O66529
LA	40	GLY	-	linker	UNP O66529
LA	41	SER	-	linker	UNP O66529
LA	42	GLY	-	linker	UNP O66529
LA	43	SER	-	linker	UNP O66529
LA	44	SER	-	linker	UNP O66529
LA	45	MET	-	linker	UNP O66529
LA	46	GLU	-	linker	UNP O66529
MA	1	MET	-	initiating methionine	UNP O66529
MA	37	GLY	-	linker	UNP O66529
MA	38	THR	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
MA	39	GLY	-	linker	UNP O66529
MA	40	GLY	-	linker	UNP O66529
MA	41	SER	-	linker	UNP O66529
MA	42	GLY	-	linker	UNP O66529
MA	43	SER	-	linker	UNP O66529
MA	44	SER	-	linker	UNP O66529
MA	45	MET	-	linker	UNP O66529
MA	46	GLU	-	linker	UNP O66529
NA	1	MET	-	initiating methionine	UNP O66529
NA	37	GLY	-	linker	UNP O66529
NA	38	THR	-	linker	UNP O66529
NA	39	GLY	-	linker	UNP O66529
NA	40	GLY	-	linker	UNP O66529
NA	41	SER	-	linker	UNP O66529
NA	42	GLY	-	linker	UNP O66529
NA	43	SER	-	linker	UNP O66529
NA	44	SER	-	linker	UNP O66529
NA	45	MET	-	linker	UNP O66529
NA	46	GLU	-	linker	UNP O66529
OA	1	MET	-	initiating methionine	UNP O66529
OA	37	GLY	-	linker	UNP O66529
OA	38	THR	-	linker	UNP O66529
OA	39	GLY	-	linker	UNP O66529
OA	40	GLY	-	linker	UNP O66529
OA	41	SER	-	linker	UNP O66529
OA	42	GLY	-	linker	UNP O66529
OA	43	SER	-	linker	UNP O66529
OA	44	SER	-	linker	UNP O66529
OA	45	MET	-	linker	UNP O66529
OA	46	GLU	-	linker	UNP O66529
PA	1	MET	-	initiating methionine	UNP O66529
PA	37	GLY	-	linker	UNP O66529
PA	38	THR	-	linker	UNP O66529
PA	39	GLY	-	linker	UNP O66529
PA	40	GLY	-	linker	UNP O66529
PA	41	SER	-	linker	UNP O66529
PA	42	GLY	-	linker	UNP O66529
PA	43	SER	-	linker	UNP O66529
PA	44	SER	-	linker	UNP O66529
PA	45	MET	-	linker	UNP O66529
PA	46	GLU	-	linker	UNP O66529
QA	1	MET	-	initiating methionine	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
QA	37	GLY	-	linker	UNP O66529
QA	38	THR	-	linker	UNP O66529
QA	39	GLY	-	linker	UNP O66529
QA	40	GLY	-	linker	UNP O66529
QA	41	SER	-	linker	UNP O66529
QA	42	GLY	-	linker	UNP O66529
QA	43	SER	-	linker	UNP O66529
QA	44	SER	-	linker	UNP O66529
QA	45	MET	-	linker	UNP O66529
QA	46	GLU	-	linker	UNP O66529
RA	1	MET	-	initiating methionine	UNP O66529
RA	37	GLY	-	linker	UNP O66529
RA	38	THR	-	linker	UNP O66529
RA	39	GLY	-	linker	UNP O66529
RA	40	GLY	-	linker	UNP O66529
RA	41	SER	-	linker	UNP O66529
RA	42	GLY	-	linker	UNP O66529
RA	43	SER	-	linker	UNP O66529
RA	44	SER	-	linker	UNP O66529
RA	45	MET	-	linker	UNP O66529
RA	46	GLU	-	linker	UNP O66529
SA	1	MET	-	initiating methionine	UNP O66529
SA	37	GLY	-	linker	UNP O66529
SA	38	THR	-	linker	UNP O66529
SA	39	GLY	-	linker	UNP O66529
SA	40	GLY	-	linker	UNP O66529
SA	41	SER	-	linker	UNP O66529
SA	42	GLY	-	linker	UNP O66529
SA	43	SER	-	linker	UNP O66529
SA	44	SER	-	linker	UNP O66529
SA	45	MET	-	linker	UNP O66529
SA	46	GLU	-	linker	UNP O66529
TA	1	MET	-	initiating methionine	UNP O66529
TA	37	GLY	-	linker	UNP O66529
TA	38	THR	-	linker	UNP O66529
TA	39	GLY	-	linker	UNP O66529
TA	40	GLY	-	linker	UNP O66529
TA	41	SER	-	linker	UNP O66529
TA	42	GLY	-	linker	UNP O66529
TA	43	SER	-	linker	UNP O66529
TA	44	SER	-	linker	UNP O66529
TA	45	MET	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
TA	46	GLU	-	linker	UNP O66529
UA	1	MET	-	initiating methionine	UNP O66529
UA	37	GLY	-	linker	UNP O66529
UA	38	THR	-	linker	UNP O66529
UA	39	GLY	-	linker	UNP O66529
UA	40	GLY	-	linker	UNP O66529
UA	41	SER	-	linker	UNP O66529
UA	42	GLY	-	linker	UNP O66529
UA	43	SER	-	linker	UNP O66529
UA	44	SER	-	linker	UNP O66529
UA	45	MET	-	linker	UNP O66529
UA	46	GLU	-	linker	UNP O66529
VA	1	MET	-	initiating methionine	UNP O66529
VA	37	GLY	-	linker	UNP O66529
VA	38	THR	-	linker	UNP O66529
VA	39	GLY	-	linker	UNP O66529
VA	40	GLY	-	linker	UNP O66529
VA	41	SER	-	linker	UNP O66529
VA	42	GLY	-	linker	UNP O66529
VA	43	SER	-	linker	UNP O66529
VA	44	SER	-	linker	UNP O66529
VA	45	MET	-	linker	UNP O66529
VA	46	GLU	-	linker	UNP O66529
WA	1	MET	-	initiating methionine	UNP O66529
WA	37	GLY	-	linker	UNP O66529
WA	38	THR	-	linker	UNP O66529
WA	39	GLY	-	linker	UNP O66529
WA	40	GLY	-	linker	UNP O66529
WA	41	SER	-	linker	UNP O66529
WA	42	GLY	-	linker	UNP O66529
WA	43	SER	-	linker	UNP O66529
WA	44	SER	-	linker	UNP O66529
WA	45	MET	-	linker	UNP O66529
WA	46	GLU	-	linker	UNP O66529
XA	1	MET	-	initiating methionine	UNP O66529
XA	37	GLY	-	linker	UNP O66529
XA	38	THR	-	linker	UNP O66529
XA	39	GLY	-	linker	UNP O66529
XA	40	GLY	-	linker	UNP O66529
XA	41	SER	-	linker	UNP O66529
XA	42	GLY	-	linker	UNP O66529
XA	43	SER	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
XA	44	SER	-	linker	UNP O66529
XA	45	MET	-	linker	UNP O66529
XA	46	GLU	-	linker	UNP O66529
YA	1	MET	-	initiating methionine	UNP O66529
YA	37	GLY	-	linker	UNP O66529
YA	38	THR	-	linker	UNP O66529
YA	39	GLY	-	linker	UNP O66529
YA	40	GLY	-	linker	UNP O66529
YA	41	SER	-	linker	UNP O66529
YA	42	GLY	-	linker	UNP O66529
YA	43	SER	-	linker	UNP O66529
YA	44	SER	-	linker	UNP O66529
YA	45	MET	-	linker	UNP O66529
YA	46	GLU	-	linker	UNP O66529
ZA	1	MET	-	initiating methionine	UNP O66529
ZA	37	GLY	-	linker	UNP O66529
ZA	38	THR	-	linker	UNP O66529
ZA	39	GLY	-	linker	UNP O66529
ZA	40	GLY	-	linker	UNP O66529
ZA	41	SER	-	linker	UNP O66529
ZA	42	GLY	-	linker	UNP O66529
ZA	43	SER	-	linker	UNP O66529
ZA	44	SER	-	linker	UNP O66529
ZA	45	MET	-	linker	UNP O66529
ZA	46	GLU	-	linker	UNP O66529
AB	1	MET	-	initiating methionine	UNP O66529
AB	37	GLY	-	linker	UNP O66529
AB	38	THR	-	linker	UNP O66529
AB	39	GLY	-	linker	UNP O66529
AB	40	GLY	-	linker	UNP O66529
AB	41	SER	-	linker	UNP O66529
AB	42	GLY	-	linker	UNP O66529
AB	43	SER	-	linker	UNP O66529
AB	44	SER	-	linker	UNP O66529
AB	45	MET	-	linker	UNP O66529
AB	46	GLU	-	linker	UNP O66529
BB	1	MET	-	initiating methionine	UNP O66529
BB	37	GLY	-	linker	UNP O66529
BB	38	THR	-	linker	UNP O66529
BB	39	GLY	-	linker	UNP O66529
BB	40	GLY	-	linker	UNP O66529
BB	41	SER	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
BB	42	GLY	-	linker	UNP O66529
BB	43	SER	-	linker	UNP O66529
BB	44	SER	-	linker	UNP O66529
BB	45	MET	-	linker	UNP O66529
BB	46	GLU	-	linker	UNP O66529
CB	1	MET	-	initiating methionine	UNP O66529
CB	37	GLY	-	linker	UNP O66529
CB	38	THR	-	linker	UNP O66529
CB	39	GLY	-	linker	UNP O66529
CB	40	GLY	-	linker	UNP O66529
CB	41	SER	-	linker	UNP O66529
CB	42	GLY	-	linker	UNP O66529
CB	43	SER	-	linker	UNP O66529
CB	44	SER	-	linker	UNP O66529
CB	45	MET	-	linker	UNP O66529
CB	46	GLU	-	linker	UNP O66529
DB	1	MET	-	initiating methionine	UNP O66529
DB	37	GLY	-	linker	UNP O66529
DB	38	THR	-	linker	UNP O66529
DB	39	GLY	-	linker	UNP O66529
DB	40	GLY	-	linker	UNP O66529
DB	41	SER	-	linker	UNP O66529
DB	42	GLY	-	linker	UNP O66529
DB	43	SER	-	linker	UNP O66529
DB	44	SER	-	linker	UNP O66529
DB	45	MET	-	linker	UNP O66529
DB	46	GLU	-	linker	UNP O66529
EB	1	MET	-	initiating methionine	UNP O66529
EB	37	GLY	-	linker	UNP O66529
EB	38	THR	-	linker	UNP O66529
EB	39	GLY	-	linker	UNP O66529
EB	40	GLY	-	linker	UNP O66529
EB	41	SER	-	linker	UNP O66529
EB	42	GLY	-	linker	UNP O66529
EB	43	SER	-	linker	UNP O66529
EB	44	SER	-	linker	UNP O66529
EB	45	MET	-	linker	UNP O66529
EB	46	GLU	-	linker	UNP O66529
FB	1	MET	-	initiating methionine	UNP O66529
FB	37	GLY	-	linker	UNP O66529
FB	38	THR	-	linker	UNP O66529
FB	39	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
FB	40	GLY	-	linker	UNP O66529
FB	41	SER	-	linker	UNP O66529
FB	42	GLY	-	linker	UNP O66529
FB	43	SER	-	linker	UNP O66529
FB	44	SER	-	linker	UNP O66529
FB	45	MET	-	linker	UNP O66529
FB	46	GLU	-	linker	UNP O66529
GB	1	MET	-	initiating methionine	UNP O66529
GB	37	GLY	-	linker	UNP O66529
GB	38	THR	-	linker	UNP O66529
GB	39	GLY	-	linker	UNP O66529
GB	40	GLY	-	linker	UNP O66529
GB	41	SER	-	linker	UNP O66529
GB	42	GLY	-	linker	UNP O66529
GB	43	SER	-	linker	UNP O66529
GB	44	SER	-	linker	UNP O66529
GB	45	MET	-	linker	UNP O66529
GB	46	GLU	-	linker	UNP O66529
HB	1	MET	-	initiating methionine	UNP O66529
HB	37	GLY	-	linker	UNP O66529
HB	38	THR	-	linker	UNP O66529
HB	39	GLY	-	linker	UNP O66529
HB	40	GLY	-	linker	UNP O66529
HB	41	SER	-	linker	UNP O66529
HB	42	GLY	-	linker	UNP O66529
HB	43	SER	-	linker	UNP O66529
HB	44	SER	-	linker	UNP O66529
HB	45	MET	-	linker	UNP O66529
HB	46	GLU	-	linker	UNP O66529
IB	1	MET	-	initiating methionine	UNP O66529
IB	37	GLY	-	linker	UNP O66529
IB	38	THR	-	linker	UNP O66529
IB	39	GLY	-	linker	UNP O66529
IB	40	GLY	-	linker	UNP O66529
IB	41	SER	-	linker	UNP O66529
IB	42	GLY	-	linker	UNP O66529
IB	43	SER	-	linker	UNP O66529
IB	44	SER	-	linker	UNP O66529
IB	45	MET	-	linker	UNP O66529
IB	46	GLU	-	linker	UNP O66529
JB	1	MET	-	initiating methionine	UNP O66529
JB	37	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
JB	38	THR	-	linker	UNP O66529
JB	39	GLY	-	linker	UNP O66529
JB	40	GLY	-	linker	UNP O66529
JB	41	SER	-	linker	UNP O66529
JB	42	GLY	-	linker	UNP O66529
JB	43	SER	-	linker	UNP O66529
JB	44	SER	-	linker	UNP O66529
JB	45	MET	-	linker	UNP O66529
JB	46	GLU	-	linker	UNP O66529
KB	1	MET	-	initiating methionine	UNP O66529
KB	37	GLY	-	linker	UNP O66529
KB	38	THR	-	linker	UNP O66529
KB	39	GLY	-	linker	UNP O66529
KB	40	GLY	-	linker	UNP O66529
KB	41	SER	-	linker	UNP O66529
KB	42	GLY	-	linker	UNP O66529
KB	43	SER	-	linker	UNP O66529
KB	44	SER	-	linker	UNP O66529
KB	45	MET	-	linker	UNP O66529
KB	46	GLU	-	linker	UNP O66529
LB	1	MET	-	initiating methionine	UNP O66529
LB	37	GLY	-	linker	UNP O66529
LB	38	THR	-	linker	UNP O66529
LB	39	GLY	-	linker	UNP O66529
LB	40	GLY	-	linker	UNP O66529
LB	41	SER	-	linker	UNP O66529
LB	42	GLY	-	linker	UNP O66529
LB	43	SER	-	linker	UNP O66529
LB	44	SER	-	linker	UNP O66529
LB	45	MET	-	linker	UNP O66529
LB	46	GLU	-	linker	UNP O66529
MB	1	MET	-	initiating methionine	UNP O66529
MB	37	GLY	-	linker	UNP O66529
MB	38	THR	-	linker	UNP O66529
MB	39	GLY	-	linker	UNP O66529
MB	40	GLY	-	linker	UNP O66529
MB	41	SER	-	linker	UNP O66529
MB	42	GLY	-	linker	UNP O66529
MB	43	SER	-	linker	UNP O66529
MB	44	SER	-	linker	UNP O66529
MB	45	MET	-	linker	UNP O66529
MB	46	GLU	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
NB	1	MET	-	initiating methionine	UNP O66529
NB	37	GLY	-	linker	UNP O66529
NB	38	THR	-	linker	UNP O66529
NB	39	GLY	-	linker	UNP O66529
NB	40	GLY	-	linker	UNP O66529
NB	41	SER	-	linker	UNP O66529
NB	42	GLY	-	linker	UNP O66529
NB	43	SER	-	linker	UNP O66529
NB	44	SER	-	linker	UNP O66529
NB	45	MET	-	linker	UNP O66529
NB	46	GLU	-	linker	UNP O66529
OB	1	MET	-	initiating methionine	UNP O66529
OB	37	GLY	-	linker	UNP O66529
OB	38	THR	-	linker	UNP O66529
OB	39	GLY	-	linker	UNP O66529
OB	40	GLY	-	linker	UNP O66529
OB	41	SER	-	linker	UNP O66529
OB	42	GLY	-	linker	UNP O66529
OB	43	SER	-	linker	UNP O66529
OB	44	SER	-	linker	UNP O66529
OB	45	MET	-	linker	UNP O66529
OB	46	GLU	-	linker	UNP O66529
PB	1	MET	-	initiating methionine	UNP O66529
PB	37	GLY	-	linker	UNP O66529
PB	38	THR	-	linker	UNP O66529
PB	39	GLY	-	linker	UNP O66529
PB	40	GLY	-	linker	UNP O66529
PB	41	SER	-	linker	UNP O66529
PB	42	GLY	-	linker	UNP O66529
PB	43	SER	-	linker	UNP O66529
PB	44	SER	-	linker	UNP O66529
PB	45	MET	-	linker	UNP O66529
PB	46	GLU	-	linker	UNP O66529
QB	1	MET	-	initiating methionine	UNP O66529
QB	37	GLY	-	linker	UNP O66529
QB	38	THR	-	linker	UNP O66529
QB	39	GLY	-	linker	UNP O66529
QB	40	GLY	-	linker	UNP O66529
QB	41	SER	-	linker	UNP O66529
QB	42	GLY	-	linker	UNP O66529
QB	43	SER	-	linker	UNP O66529
QB	44	SER	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
QB	45	MET	-	linker	UNP O66529
QB	46	GLU	-	linker	UNP O66529
RB	1	MET	-	initiating methionine	UNP O66529
RB	37	GLY	-	linker	UNP O66529
RB	38	THR	-	linker	UNP O66529
RB	39	GLY	-	linker	UNP O66529
RB	40	GLY	-	linker	UNP O66529
RB	41	SER	-	linker	UNP O66529
RB	42	GLY	-	linker	UNP O66529
RB	43	SER	-	linker	UNP O66529
RB	44	SER	-	linker	UNP O66529
RB	45	MET	-	linker	UNP O66529
RB	46	GLU	-	linker	UNP O66529
SB	1	MET	-	initiating methionine	UNP O66529
SB	37	GLY	-	linker	UNP O66529
SB	38	THR	-	linker	UNP O66529
SB	39	GLY	-	linker	UNP O66529
SB	40	GLY	-	linker	UNP O66529
SB	41	SER	-	linker	UNP O66529
SB	42	GLY	-	linker	UNP O66529
SB	43	SER	-	linker	UNP O66529
SB	44	SER	-	linker	UNP O66529
SB	45	MET	-	linker	UNP O66529
SB	46	GLU	-	linker	UNP O66529
TB	1	MET	-	initiating methionine	UNP O66529
TB	37	GLY	-	linker	UNP O66529
TB	38	THR	-	linker	UNP O66529
TB	39	GLY	-	linker	UNP O66529
TB	40	GLY	-	linker	UNP O66529
TB	41	SER	-	linker	UNP O66529
TB	42	GLY	-	linker	UNP O66529
TB	43	SER	-	linker	UNP O66529
TB	44	SER	-	linker	UNP O66529
TB	45	MET	-	linker	UNP O66529
TB	46	GLU	-	linker	UNP O66529
UB	1	MET	-	initiating methionine	UNP O66529
UB	37	GLY	-	linker	UNP O66529
UB	38	THR	-	linker	UNP O66529
UB	39	GLY	-	linker	UNP O66529
UB	40	GLY	-	linker	UNP O66529
UB	41	SER	-	linker	UNP O66529
UB	42	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
UB	43	SER	-	linker	UNP O66529
UB	44	SER	-	linker	UNP O66529
UB	45	MET	-	linker	UNP O66529
UB	46	GLU	-	linker	UNP O66529
VB	1	MET	-	initiating methionine	UNP O66529
VB	37	GLY	-	linker	UNP O66529
VB	38	THR	-	linker	UNP O66529
VB	39	GLY	-	linker	UNP O66529
VB	40	GLY	-	linker	UNP O66529
VB	41	SER	-	linker	UNP O66529
VB	42	GLY	-	linker	UNP O66529
VB	43	SER	-	linker	UNP O66529
VB	44	SER	-	linker	UNP O66529
VB	45	MET	-	linker	UNP O66529
VB	46	GLU	-	linker	UNP O66529
WB	1	MET	-	initiating methionine	UNP O66529
WB	37	GLY	-	linker	UNP O66529
WB	38	THR	-	linker	UNP O66529
WB	39	GLY	-	linker	UNP O66529
WB	40	GLY	-	linker	UNP O66529
WB	41	SER	-	linker	UNP O66529
WB	42	GLY	-	linker	UNP O66529
WB	43	SER	-	linker	UNP O66529
WB	44	SER	-	linker	UNP O66529
WB	45	MET	-	linker	UNP O66529
WB	46	GLU	-	linker	UNP O66529
XB	1	MET	-	initiating methionine	UNP O66529
XB	37	GLY	-	linker	UNP O66529
XB	38	THR	-	linker	UNP O66529
XB	39	GLY	-	linker	UNP O66529
XB	40	GLY	-	linker	UNP O66529
XB	41	SER	-	linker	UNP O66529
XB	42	GLY	-	linker	UNP O66529
XB	43	SER	-	linker	UNP O66529
XB	44	SER	-	linker	UNP O66529
XB	45	MET	-	linker	UNP O66529
XB	46	GLU	-	linker	UNP O66529
YB	1	MET	-	initiating methionine	UNP O66529
YB	37	GLY	-	linker	UNP O66529
YB	38	THR	-	linker	UNP O66529
YB	39	GLY	-	linker	UNP O66529
YB	40	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
YB	41	SER	-	linker	UNP O66529
YB	42	GLY	-	linker	UNP O66529
YB	43	SER	-	linker	UNP O66529
YB	44	SER	-	linker	UNP O66529
YB	45	MET	-	linker	UNP O66529
YB	46	GLU	-	linker	UNP O66529
ZB	1	MET	-	initiating methionine	UNP O66529
ZB	37	GLY	-	linker	UNP O66529
ZB	38	THR	-	linker	UNP O66529
ZB	39	GLY	-	linker	UNP O66529
ZB	40	GLY	-	linker	UNP O66529
ZB	41	SER	-	linker	UNP O66529
ZB	42	GLY	-	linker	UNP O66529
ZB	43	SER	-	linker	UNP O66529
ZB	44	SER	-	linker	UNP O66529
ZB	45	MET	-	linker	UNP O66529
ZB	46	GLU	-	linker	UNP O66529
AC	1	MET	-	initiating methionine	UNP O66529
AC	37	GLY	-	linker	UNP O66529
AC	38	THR	-	linker	UNP O66529
AC	39	GLY	-	linker	UNP O66529
AC	40	GLY	-	linker	UNP O66529
AC	41	SER	-	linker	UNP O66529
AC	42	GLY	-	linker	UNP O66529
AC	43	SER	-	linker	UNP O66529
AC	44	SER	-	linker	UNP O66529
AC	45	MET	-	linker	UNP O66529
AC	46	GLU	-	linker	UNP O66529
BC	1	MET	-	initiating methionine	UNP O66529
BC	37	GLY	-	linker	UNP O66529
BC	38	THR	-	linker	UNP O66529
BC	39	GLY	-	linker	UNP O66529
BC	40	GLY	-	linker	UNP O66529
BC	41	SER	-	linker	UNP O66529
BC	42	GLY	-	linker	UNP O66529
BC	43	SER	-	linker	UNP O66529
BC	44	SER	-	linker	UNP O66529
BC	45	MET	-	linker	UNP O66529
BC	46	GLU	-	linker	UNP O66529
CC	1	MET	-	initiating methionine	UNP O66529
CC	37	GLY	-	linker	UNP O66529
CC	38	THR	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
CC	39	GLY	-	linker	UNP O66529
CC	40	GLY	-	linker	UNP O66529
CC	41	SER	-	linker	UNP O66529
CC	42	GLY	-	linker	UNP O66529
CC	43	SER	-	linker	UNP O66529
CC	44	SER	-	linker	UNP O66529
CC	45	MET	-	linker	UNP O66529
CC	46	GLU	-	linker	UNP O66529
DC	1	MET	-	initiating methionine	UNP O66529
DC	37	GLY	-	linker	UNP O66529
DC	38	THR	-	linker	UNP O66529
DC	39	GLY	-	linker	UNP O66529
DC	40	GLY	-	linker	UNP O66529
DC	41	SER	-	linker	UNP O66529
DC	42	GLY	-	linker	UNP O66529
DC	43	SER	-	linker	UNP O66529
DC	44	SER	-	linker	UNP O66529
DC	45	MET	-	linker	UNP O66529
DC	46	GLU	-	linker	UNP O66529
EC	1	MET	-	initiating methionine	UNP O66529
EC	37	GLY	-	linker	UNP O66529
EC	38	THR	-	linker	UNP O66529
EC	39	GLY	-	linker	UNP O66529
EC	40	GLY	-	linker	UNP O66529
EC	41	SER	-	linker	UNP O66529
EC	42	GLY	-	linker	UNP O66529
EC	43	SER	-	linker	UNP O66529
EC	44	SER	-	linker	UNP O66529
EC	45	MET	-	linker	UNP O66529
EC	46	GLU	-	linker	UNP O66529
FC	1	MET	-	initiating methionine	UNP O66529
FC	37	GLY	-	linker	UNP O66529
FC	38	THR	-	linker	UNP O66529
FC	39	GLY	-	linker	UNP O66529
FC	40	GLY	-	linker	UNP O66529
FC	41	SER	-	linker	UNP O66529
FC	42	GLY	-	linker	UNP O66529
FC	43	SER	-	linker	UNP O66529
FC	44	SER	-	linker	UNP O66529
FC	45	MET	-	linker	UNP O66529
FC	46	GLU	-	linker	UNP O66529
GC	1	MET	-	initiating methionine	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
GC	37	GLY	-	linker	UNP O66529
GC	38	THR	-	linker	UNP O66529
GC	39	GLY	-	linker	UNP O66529
GC	40	GLY	-	linker	UNP O66529
GC	41	SER	-	linker	UNP O66529
GC	42	GLY	-	linker	UNP O66529
GC	43	SER	-	linker	UNP O66529
GC	44	SER	-	linker	UNP O66529
GC	45	MET	-	linker	UNP O66529
GC	46	GLU	-	linker	UNP O66529
HC	1	MET	-	initiating methionine	UNP O66529
HC	37	GLY	-	linker	UNP O66529
HC	38	THR	-	linker	UNP O66529
HC	39	GLY	-	linker	UNP O66529
HC	40	GLY	-	linker	UNP O66529
HC	41	SER	-	linker	UNP O66529
HC	42	GLY	-	linker	UNP O66529
HC	43	SER	-	linker	UNP O66529
HC	44	SER	-	linker	UNP O66529
HC	45	MET	-	linker	UNP O66529
HC	46	GLU	-	linker	UNP O66529
IC	1	MET	-	initiating methionine	UNP O66529
IC	37	GLY	-	linker	UNP O66529
IC	38	THR	-	linker	UNP O66529
IC	39	GLY	-	linker	UNP O66529
IC	40	GLY	-	linker	UNP O66529
IC	41	SER	-	linker	UNP O66529
IC	42	GLY	-	linker	UNP O66529
IC	43	SER	-	linker	UNP O66529
IC	44	SER	-	linker	UNP O66529
IC	45	MET	-	linker	UNP O66529
IC	46	GLU	-	linker	UNP O66529
JC	1	MET	-	initiating methionine	UNP O66529
JC	37	GLY	-	linker	UNP O66529
JC	38	THR	-	linker	UNP O66529
JC	39	GLY	-	linker	UNP O66529
JC	40	GLY	-	linker	UNP O66529
JC	41	SER	-	linker	UNP O66529
JC	42	GLY	-	linker	UNP O66529
JC	43	SER	-	linker	UNP O66529
JC	44	SER	-	linker	UNP O66529
JC	45	MET	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
JC	46	GLU	-	linker	UNP O66529
KC	1	MET	-	initiating methionine	UNP O66529
KC	37	GLY	-	linker	UNP O66529
KC	38	THR	-	linker	UNP O66529
KC	39	GLY	-	linker	UNP O66529
KC	40	GLY	-	linker	UNP O66529
KC	41	SER	-	linker	UNP O66529
KC	42	GLY	-	linker	UNP O66529
KC	43	SER	-	linker	UNP O66529
KC	44	SER	-	linker	UNP O66529
KC	45	MET	-	linker	UNP O66529
KC	46	GLU	-	linker	UNP O66529
LC	1	MET	-	initiating methionine	UNP O66529
LC	37	GLY	-	linker	UNP O66529
LC	38	THR	-	linker	UNP O66529
LC	39	GLY	-	linker	UNP O66529
LC	40	GLY	-	linker	UNP O66529
LC	41	SER	-	linker	UNP O66529
LC	42	GLY	-	linker	UNP O66529
LC	43	SER	-	linker	UNP O66529
LC	44	SER	-	linker	UNP O66529
LC	45	MET	-	linker	UNP O66529
LC	46	GLU	-	linker	UNP O66529
MC	1	MET	-	initiating methionine	UNP O66529
MC	37	GLY	-	linker	UNP O66529
MC	38	THR	-	linker	UNP O66529
MC	39	GLY	-	linker	UNP O66529
MC	40	GLY	-	linker	UNP O66529
MC	41	SER	-	linker	UNP O66529
MC	42	GLY	-	linker	UNP O66529
MC	43	SER	-	linker	UNP O66529
MC	44	SER	-	linker	UNP O66529
MC	45	MET	-	linker	UNP O66529
MC	46	GLU	-	linker	UNP O66529
NC	1	MET	-	initiating methionine	UNP O66529
NC	37	GLY	-	linker	UNP O66529
NC	38	THR	-	linker	UNP O66529
NC	39	GLY	-	linker	UNP O66529
NC	40	GLY	-	linker	UNP O66529
NC	41	SER	-	linker	UNP O66529
NC	42	GLY	-	linker	UNP O66529
NC	43	SER	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
NC	44	SER	-	linker	UNP O66529
NC	45	MET	-	linker	UNP O66529
NC	46	GLU	-	linker	UNP O66529
OC	1	MET	-	initiating methionine	UNP O66529
OC	37	GLY	-	linker	UNP O66529
OC	38	THR	-	linker	UNP O66529
OC	39	GLY	-	linker	UNP O66529
OC	40	GLY	-	linker	UNP O66529
OC	41	SER	-	linker	UNP O66529
OC	42	GLY	-	linker	UNP O66529
OC	43	SER	-	linker	UNP O66529
OC	44	SER	-	linker	UNP O66529
OC	45	MET	-	linker	UNP O66529
OC	46	GLU	-	linker	UNP O66529
PC	1	MET	-	initiating methionine	UNP O66529
PC	37	GLY	-	linker	UNP O66529
PC	38	THR	-	linker	UNP O66529
PC	39	GLY	-	linker	UNP O66529
PC	40	GLY	-	linker	UNP O66529
PC	41	SER	-	linker	UNP O66529
PC	42	GLY	-	linker	UNP O66529
PC	43	SER	-	linker	UNP O66529
PC	44	SER	-	linker	UNP O66529
PC	45	MET	-	linker	UNP O66529
PC	46	GLU	-	linker	UNP O66529
QC	1	MET	-	initiating methionine	UNP O66529
QC	37	GLY	-	linker	UNP O66529
QC	38	THR	-	linker	UNP O66529
QC	39	GLY	-	linker	UNP O66529
QC	40	GLY	-	linker	UNP O66529
QC	41	SER	-	linker	UNP O66529
QC	42	GLY	-	linker	UNP O66529
QC	43	SER	-	linker	UNP O66529
QC	44	SER	-	linker	UNP O66529
QC	45	MET	-	linker	UNP O66529
QC	46	GLU	-	linker	UNP O66529
RC	1	MET	-	initiating methionine	UNP O66529
RC	37	GLY	-	linker	UNP O66529
RC	38	THR	-	linker	UNP O66529
RC	39	GLY	-	linker	UNP O66529
RC	40	GLY	-	linker	UNP O66529
RC	41	SER	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
RC	42	GLY	-	linker	UNP O66529
RC	43	SER	-	linker	UNP O66529
RC	44	SER	-	linker	UNP O66529
RC	45	MET	-	linker	UNP O66529
RC	46	GLU	-	linker	UNP O66529
SC	1	MET	-	initiating methionine	UNP O66529
SC	37	GLY	-	linker	UNP O66529
SC	38	THR	-	linker	UNP O66529
SC	39	GLY	-	linker	UNP O66529
SC	40	GLY	-	linker	UNP O66529
SC	41	SER	-	linker	UNP O66529
SC	42	GLY	-	linker	UNP O66529
SC	43	SER	-	linker	UNP O66529
SC	44	SER	-	linker	UNP O66529
SC	45	MET	-	linker	UNP O66529
SC	46	GLU	-	linker	UNP O66529
TC	1	MET	-	initiating methionine	UNP O66529
TC	37	GLY	-	linker	UNP O66529
TC	38	THR	-	linker	UNP O66529
TC	39	GLY	-	linker	UNP O66529
TC	40	GLY	-	linker	UNP O66529
TC	41	SER	-	linker	UNP O66529
TC	42	GLY	-	linker	UNP O66529
TC	43	SER	-	linker	UNP O66529
TC	44	SER	-	linker	UNP O66529
TC	45	MET	-	linker	UNP O66529
TC	46	GLU	-	linker	UNP O66529
UC	1	MET	-	initiating methionine	UNP O66529
UC	37	GLY	-	linker	UNP O66529
UC	38	THR	-	linker	UNP O66529
UC	39	GLY	-	linker	UNP O66529
UC	40	GLY	-	linker	UNP O66529
UC	41	SER	-	linker	UNP O66529
UC	42	GLY	-	linker	UNP O66529
UC	43	SER	-	linker	UNP O66529
UC	44	SER	-	linker	UNP O66529
UC	45	MET	-	linker	UNP O66529
UC	46	GLU	-	linker	UNP O66529
VC	1	MET	-	initiating methionine	UNP O66529
VC	37	GLY	-	linker	UNP O66529
VC	38	THR	-	linker	UNP O66529
VC	39	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
VC	40	GLY	-	linker	UNP O66529
VC	41	SER	-	linker	UNP O66529
VC	42	GLY	-	linker	UNP O66529
VC	43	SER	-	linker	UNP O66529
VC	44	SER	-	linker	UNP O66529
VC	45	MET	-	linker	UNP O66529
VC	46	GLU	-	linker	UNP O66529
WC	1	MET	-	initiating methionine	UNP O66529
WC	37	GLY	-	linker	UNP O66529
WC	38	THR	-	linker	UNP O66529
WC	39	GLY	-	linker	UNP O66529
WC	40	GLY	-	linker	UNP O66529
WC	41	SER	-	linker	UNP O66529
WC	42	GLY	-	linker	UNP O66529
WC	43	SER	-	linker	UNP O66529
WC	44	SER	-	linker	UNP O66529
WC	45	MET	-	linker	UNP O66529
WC	46	GLU	-	linker	UNP O66529
XC	1	MET	-	initiating methionine	UNP O66529
XC	37	GLY	-	linker	UNP O66529
XC	38	THR	-	linker	UNP O66529
XC	39	GLY	-	linker	UNP O66529
XC	40	GLY	-	linker	UNP O66529
XC	41	SER	-	linker	UNP O66529
XC	42	GLY	-	linker	UNP O66529
XC	43	SER	-	linker	UNP O66529
XC	44	SER	-	linker	UNP O66529
XC	45	MET	-	linker	UNP O66529
XC	46	GLU	-	linker	UNP O66529
YC	1	MET	-	initiating methionine	UNP O66529
YC	37	GLY	-	linker	UNP O66529
YC	38	THR	-	linker	UNP O66529
YC	39	GLY	-	linker	UNP O66529
YC	40	GLY	-	linker	UNP O66529
YC	41	SER	-	linker	UNP O66529
YC	42	GLY	-	linker	UNP O66529
YC	43	SER	-	linker	UNP O66529
YC	44	SER	-	linker	UNP O66529
YC	45	MET	-	linker	UNP O66529
YC	46	GLU	-	linker	UNP O66529
ZC	1	MET	-	initiating methionine	UNP O66529
ZC	37	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
ZC	38	THR	-	linker	UNP O66529
ZC	39	GLY	-	linker	UNP O66529
ZC	40	GLY	-	linker	UNP O66529
ZC	41	SER	-	linker	UNP O66529
ZC	42	GLY	-	linker	UNP O66529
ZC	43	SER	-	linker	UNP O66529
ZC	44	SER	-	linker	UNP O66529
ZC	45	MET	-	linker	UNP O66529
ZC	46	GLU	-	linker	UNP O66529
AD	1	MET	-	initiating methionine	UNP O66529
AD	37	GLY	-	linker	UNP O66529
AD	38	THR	-	linker	UNP O66529
AD	39	GLY	-	linker	UNP O66529
AD	40	GLY	-	linker	UNP O66529
AD	41	SER	-	linker	UNP O66529
AD	42	GLY	-	linker	UNP O66529
AD	43	SER	-	linker	UNP O66529
AD	44	SER	-	linker	UNP O66529
AD	45	MET	-	linker	UNP O66529
AD	46	GLU	-	linker	UNP O66529
BD	1	MET	-	initiating methionine	UNP O66529
BD	37	GLY	-	linker	UNP O66529
BD	38	THR	-	linker	UNP O66529
BD	39	GLY	-	linker	UNP O66529
BD	40	GLY	-	linker	UNP O66529
BD	41	SER	-	linker	UNP O66529
BD	42	GLY	-	linker	UNP O66529
BD	43	SER	-	linker	UNP O66529
BD	44	SER	-	linker	UNP O66529
BD	45	MET	-	linker	UNP O66529
BD	46	GLU	-	linker	UNP O66529
CD	1	MET	-	initiating methionine	UNP O66529
CD	37	GLY	-	linker	UNP O66529
CD	38	THR	-	linker	UNP O66529
CD	39	GLY	-	linker	UNP O66529
CD	40	GLY	-	linker	UNP O66529
CD	41	SER	-	linker	UNP O66529
CD	42	GLY	-	linker	UNP O66529
CD	43	SER	-	linker	UNP O66529
CD	44	SER	-	linker	UNP O66529
CD	45	MET	-	linker	UNP O66529
CD	46	GLU	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
DD	1	MET	-	initiating methionine	UNP O66529
DD	37	GLY	-	linker	UNP O66529
DD	38	THR	-	linker	UNP O66529
DD	39	GLY	-	linker	UNP O66529
DD	40	GLY	-	linker	UNP O66529
DD	41	SER	-	linker	UNP O66529
DD	42	GLY	-	linker	UNP O66529
DD	43	SER	-	linker	UNP O66529
DD	44	SER	-	linker	UNP O66529
DD	45	MET	-	linker	UNP O66529
DD	46	GLU	-	linker	UNP O66529
ED	1	MET	-	initiating methionine	UNP O66529
ED	37	GLY	-	linker	UNP O66529
ED	38	THR	-	linker	UNP O66529
ED	39	GLY	-	linker	UNP O66529
ED	40	GLY	-	linker	UNP O66529
ED	41	SER	-	linker	UNP O66529
ED	42	GLY	-	linker	UNP O66529
ED	43	SER	-	linker	UNP O66529
ED	44	SER	-	linker	UNP O66529
ED	45	MET	-	linker	UNP O66529
ED	46	GLU	-	linker	UNP O66529
FD	1	MET	-	initiating methionine	UNP O66529
FD	37	GLY	-	linker	UNP O66529
FD	38	THR	-	linker	UNP O66529
FD	39	GLY	-	linker	UNP O66529
FD	40	GLY	-	linker	UNP O66529
FD	41	SER	-	linker	UNP O66529
FD	42	GLY	-	linker	UNP O66529
FD	43	SER	-	linker	UNP O66529
FD	44	SER	-	linker	UNP O66529
FD	45	MET	-	linker	UNP O66529
FD	46	GLU	-	linker	UNP O66529
GD	1	MET	-	initiating methionine	UNP O66529
GD	37	GLY	-	linker	UNP O66529
GD	38	THR	-	linker	UNP O66529
GD	39	GLY	-	linker	UNP O66529
GD	40	GLY	-	linker	UNP O66529
GD	41	SER	-	linker	UNP O66529
GD	42	GLY	-	linker	UNP O66529
GD	43	SER	-	linker	UNP O66529
GD	44	SER	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
GD	45	MET	-	linker	UNP O66529
GD	46	GLU	-	linker	UNP O66529
HD	1	MET	-	initiating methionine	UNP O66529
HD	37	GLY	-	linker	UNP O66529
HD	38	THR	-	linker	UNP O66529
HD	39	GLY	-	linker	UNP O66529
HD	40	GLY	-	linker	UNP O66529
HD	41	SER	-	linker	UNP O66529
HD	42	GLY	-	linker	UNP O66529
HD	43	SER	-	linker	UNP O66529
HD	44	SER	-	linker	UNP O66529
HD	45	MET	-	linker	UNP O66529
HD	46	GLU	-	linker	UNP O66529
ID	1	MET	-	initiating methionine	UNP O66529
ID	37	GLY	-	linker	UNP O66529
ID	38	THR	-	linker	UNP O66529
ID	39	GLY	-	linker	UNP O66529
ID	40	GLY	-	linker	UNP O66529
ID	41	SER	-	linker	UNP O66529
ID	42	GLY	-	linker	UNP O66529
ID	43	SER	-	linker	UNP O66529
ID	44	SER	-	linker	UNP O66529
ID	45	MET	-	linker	UNP O66529
ID	46	GLU	-	linker	UNP O66529
JD	1	MET	-	initiating methionine	UNP O66529
JD	37	GLY	-	linker	UNP O66529
JD	38	THR	-	linker	UNP O66529
JD	39	GLY	-	linker	UNP O66529
JD	40	GLY	-	linker	UNP O66529
JD	41	SER	-	linker	UNP O66529
JD	42	GLY	-	linker	UNP O66529
JD	43	SER	-	linker	UNP O66529
JD	44	SER	-	linker	UNP O66529
JD	45	MET	-	linker	UNP O66529
JD	46	GLU	-	linker	UNP O66529
KD	1	MET	-	initiating methionine	UNP O66529
KD	37	GLY	-	linker	UNP O66529
KD	38	THR	-	linker	UNP O66529
KD	39	GLY	-	linker	UNP O66529
KD	40	GLY	-	linker	UNP O66529
KD	41	SER	-	linker	UNP O66529
KD	42	GLY	-	linker	UNP O66529

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Chain	Residue	Modelled	Actual	Comment	Reference
KD	43	SER	-	linker	UNP O66529
KD	44	SER	-	linker	UNP O66529
KD	45	MET	-	linker	UNP O66529
KD	46	GLU	-	linker	UNP O66529
LD	1	MET	-	initiating methionine	UNP O66529
LD	37	GLY	-	linker	UNP O66529
LD	38	THR	-	linker	UNP O66529
LD	39	GLY	-	linker	UNP O66529
LD	40	GLY	-	linker	UNP O66529
LD	41	SER	-	linker	UNP O66529
LD	42	GLY	-	linker	UNP O66529
LD	43	SER	-	linker	UNP O66529
LD	44	SER	-	linker	UNP O66529
LD	45	MET	-	linker	UNP O66529
LD	46	GLU	-	linker	UNP O66529
MD	1	MET	-	initiating methionine	UNP O66529
MD	37	GLY	-	linker	UNP O66529
MD	38	THR	-	linker	UNP O66529
MD	39	GLY	-	linker	UNP O66529
MD	40	GLY	-	linker	UNP O66529
MD	41	SER	-	linker	UNP O66529
MD	42	GLY	-	linker	UNP O66529
MD	43	SER	-	linker	UNP O66529
MD	44	SER	-	linker	UNP O66529
MD	45	MET	-	linker	UNP O66529
MD	46	GLU	-	linker	UNP O66529
ND	1	MET	-	initiating methionine	UNP O66529
ND	37	GLY	-	linker	UNP O66529
ND	38	THR	-	linker	UNP O66529
ND	39	GLY	-	linker	UNP O66529
ND	40	GLY	-	linker	UNP O66529
ND	41	SER	-	linker	UNP O66529
ND	42	GLY	-	linker	UNP O66529
ND	43	SER	-	linker	UNP O66529
ND	44	SER	-	linker	UNP O66529
ND	45	MET	-	linker	UNP O66529
ND	46	GLU	-	linker	UNP O66529
OD	1	MET	-	initiating methionine	UNP O66529
OD	37	GLY	-	linker	UNP O66529
OD	38	THR	-	linker	UNP O66529
OD	39	GLY	-	linker	UNP O66529
OD	40	GLY	-	linker	UNP O66529

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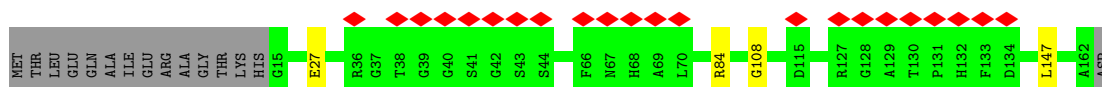
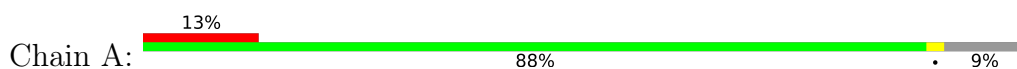
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Chain	Residue	Modelled	Actual	Comment	Reference
OD	41	SER	-	linker	UNP O66529
OD	42	GLY	-	linker	UNP O66529
OD	43	SER	-	linker	UNP O66529
OD	44	SER	-	linker	UNP O66529
OD	45	MET	-	linker	UNP O66529
OD	46	GLU	-	linker	UNP O66529
PD	1	MET	-	initiating methionine	UNP O66529
PD	37	GLY	-	linker	UNP O66529
PD	38	THR	-	linker	UNP O66529
PD	39	GLY	-	linker	UNP O66529
PD	40	GLY	-	linker	UNP O66529
PD	41	SER	-	linker	UNP O66529
PD	42	GLY	-	linker	UNP O66529
PD	43	SER	-	linker	UNP O66529
PD	44	SER	-	linker	UNP O66529
PD	45	MET	-	linker	UNP O66529
PD	46	GLU	-	linker	UNP O66529

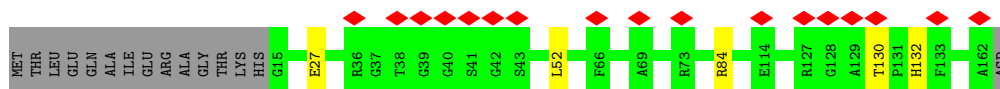
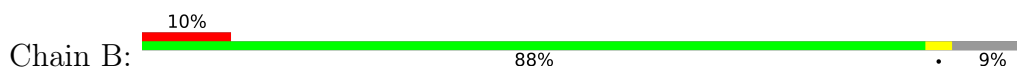
3 Residue-property plots [i](#)

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.

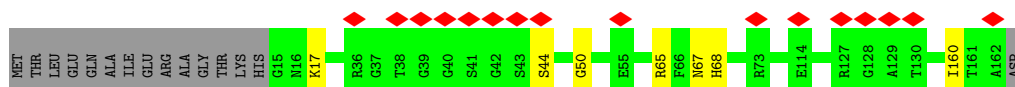
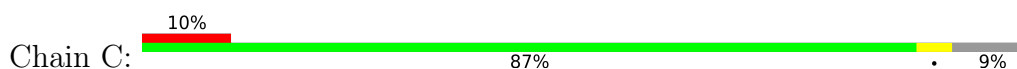
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



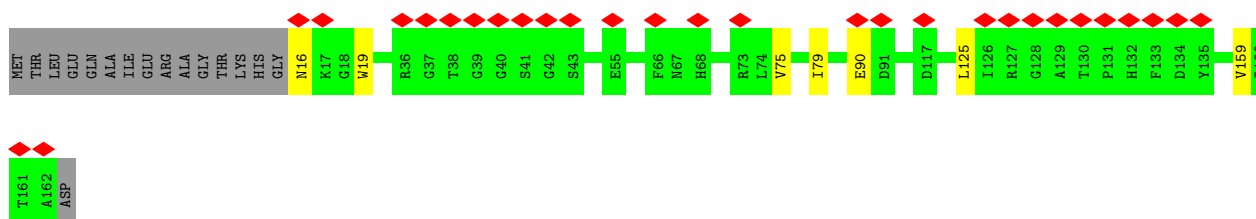
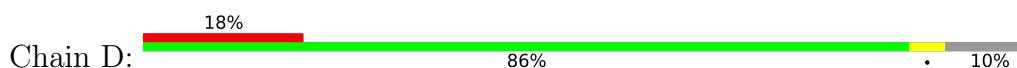
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

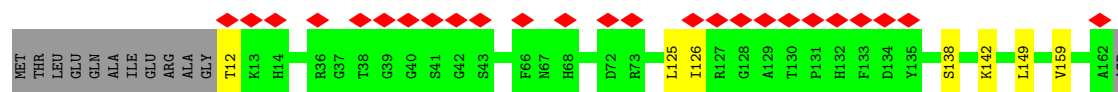


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

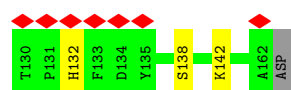
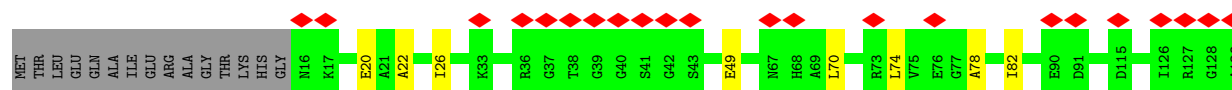
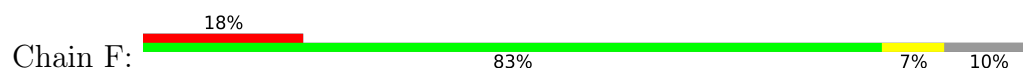


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

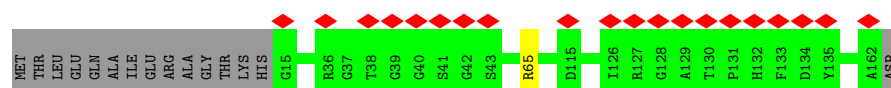
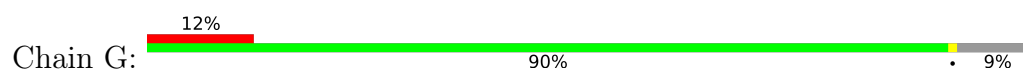




- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



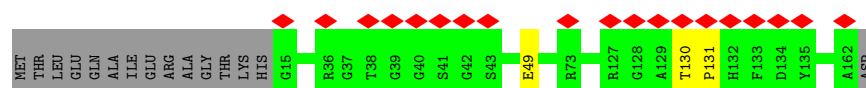
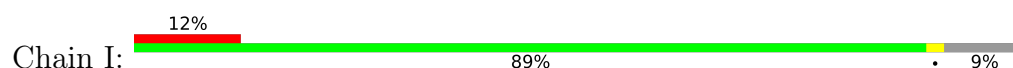
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



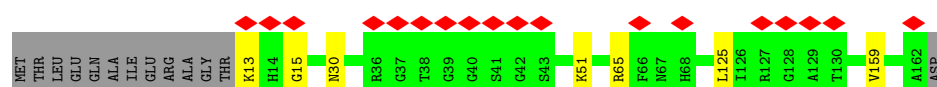
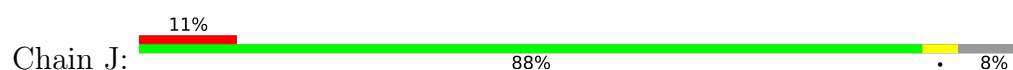
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

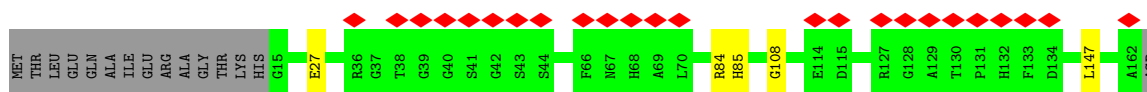


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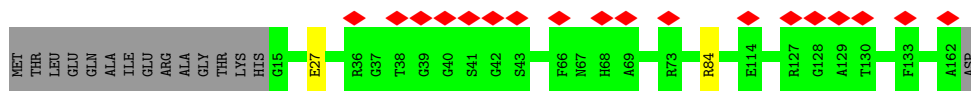
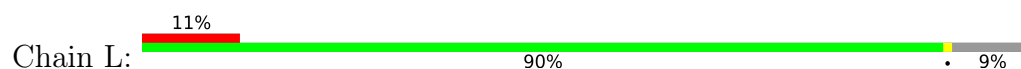


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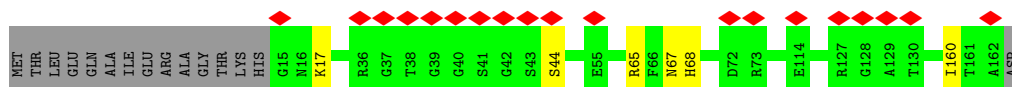
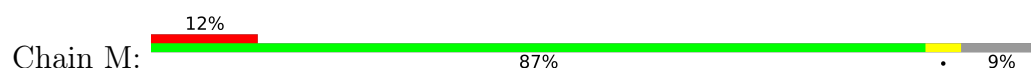




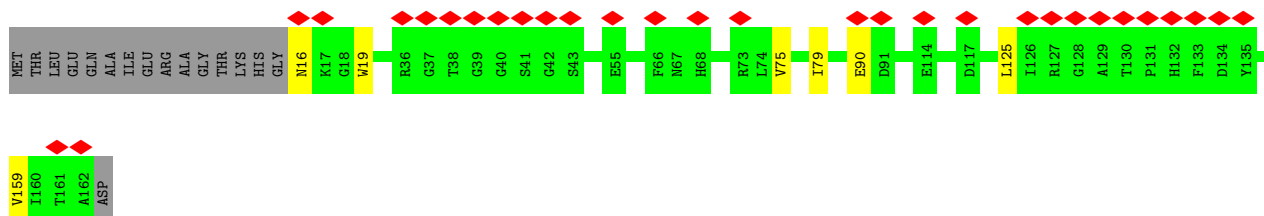
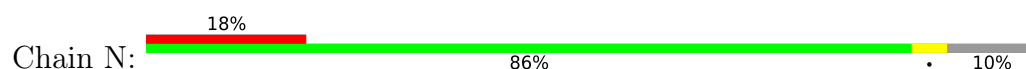
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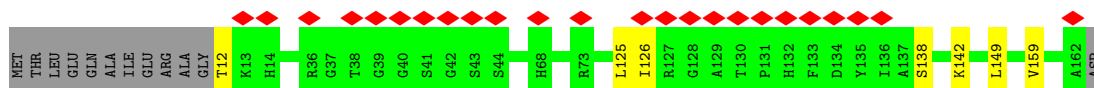
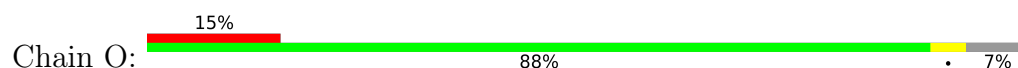
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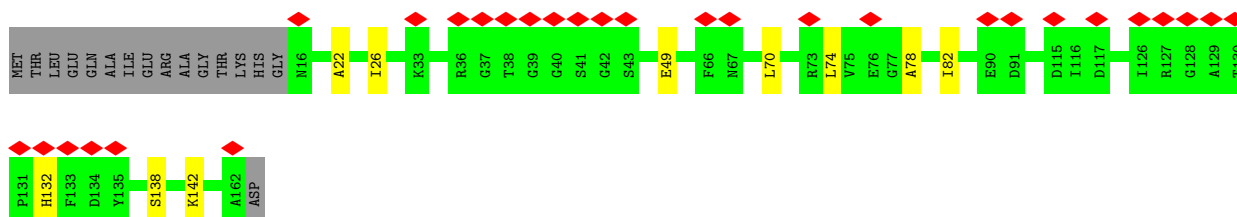
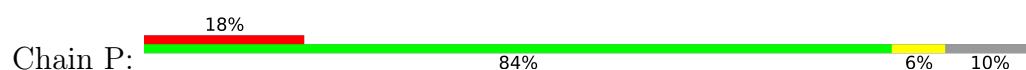
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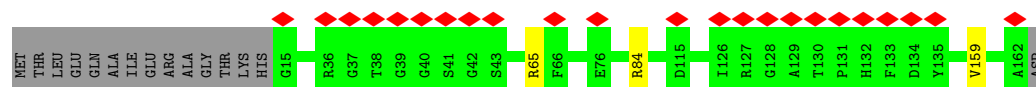
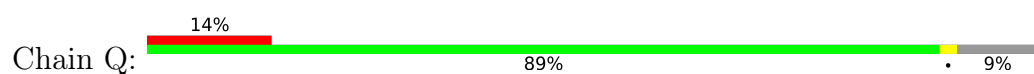
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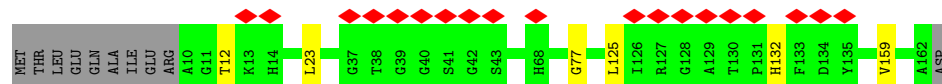
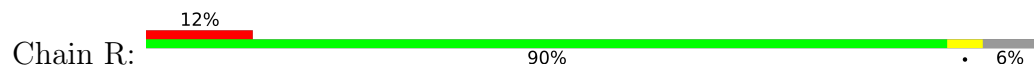
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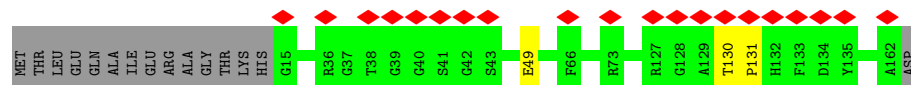
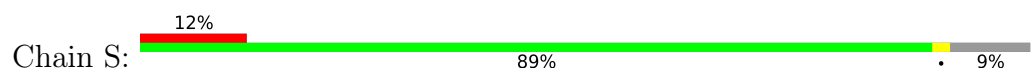
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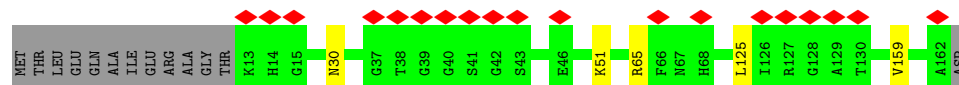
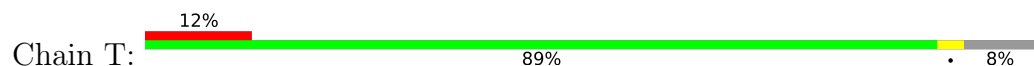
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



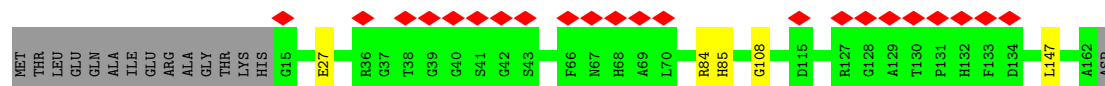
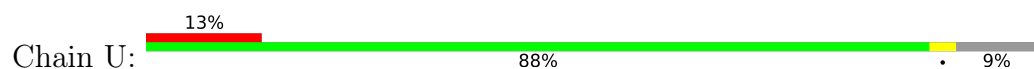
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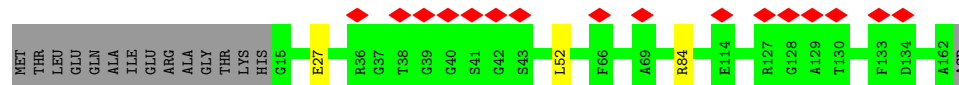
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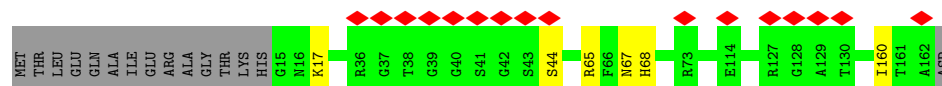
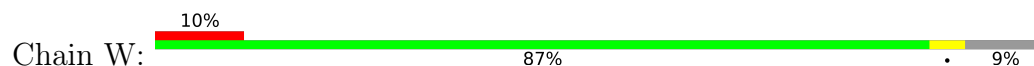
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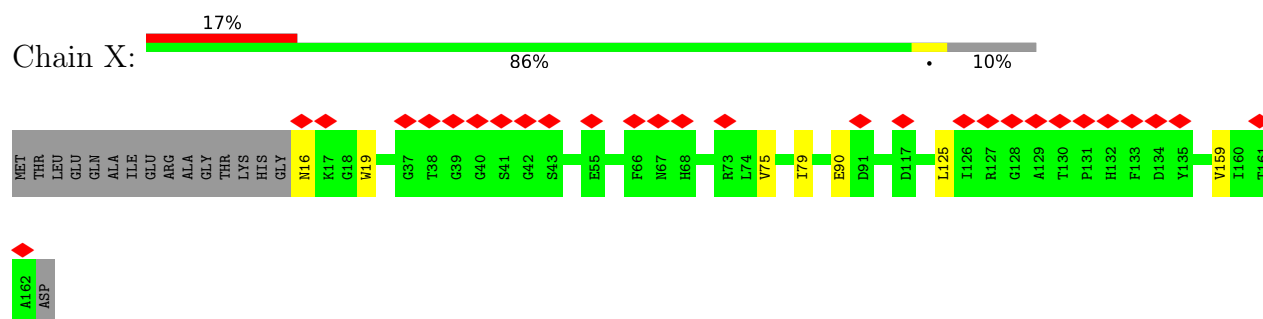
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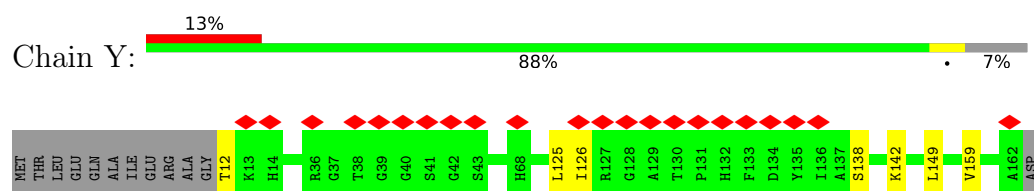
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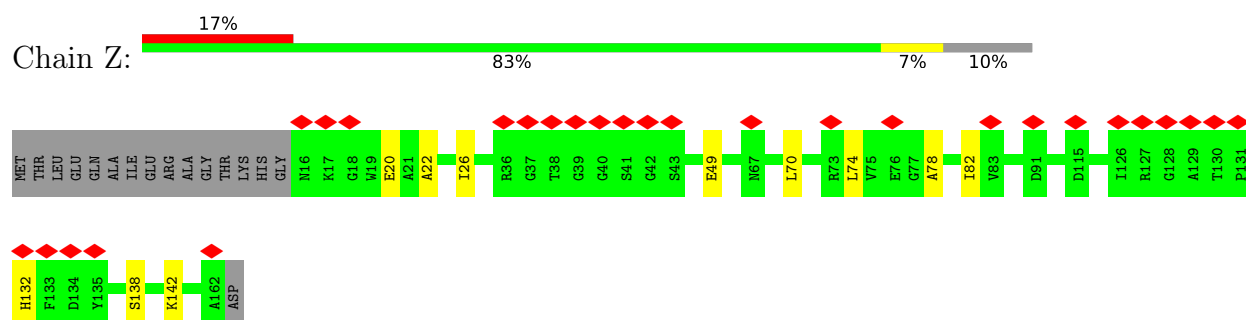
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



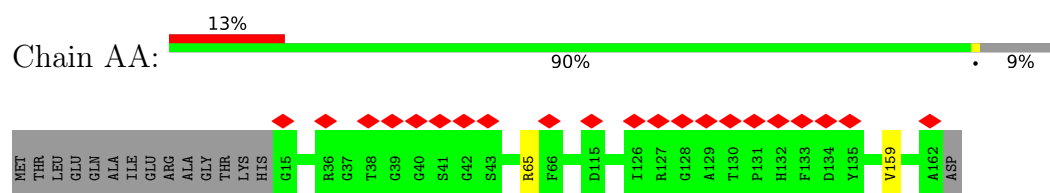
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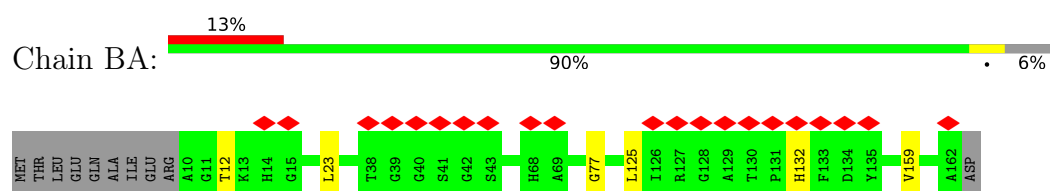
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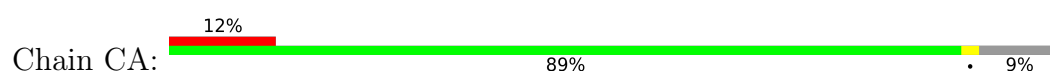
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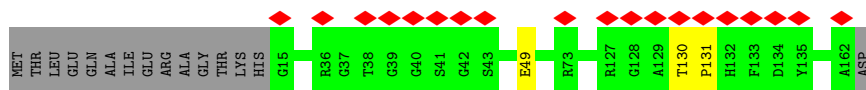


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

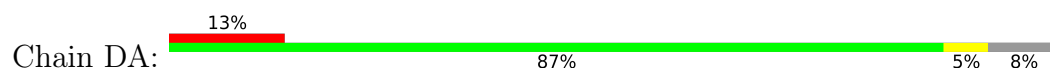


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

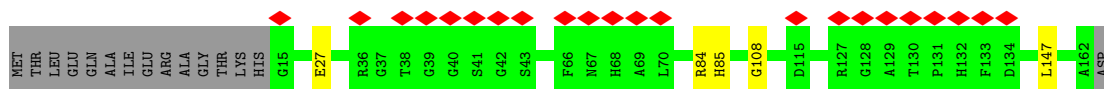
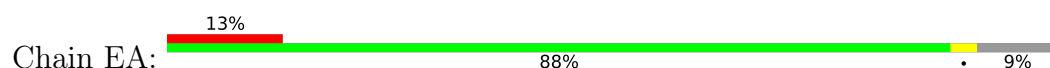




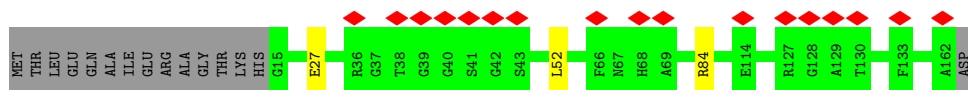
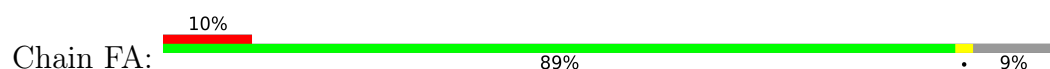
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



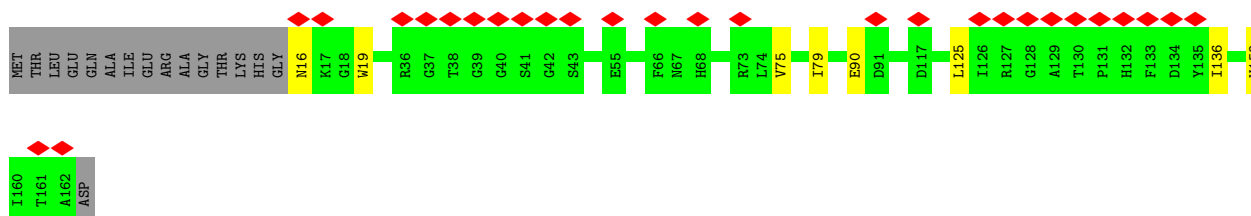
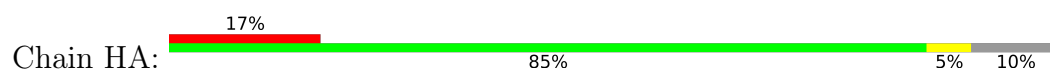
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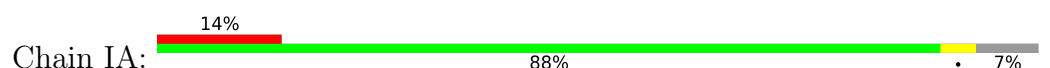
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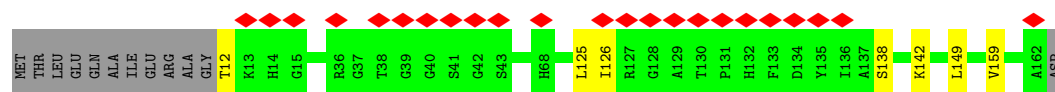


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

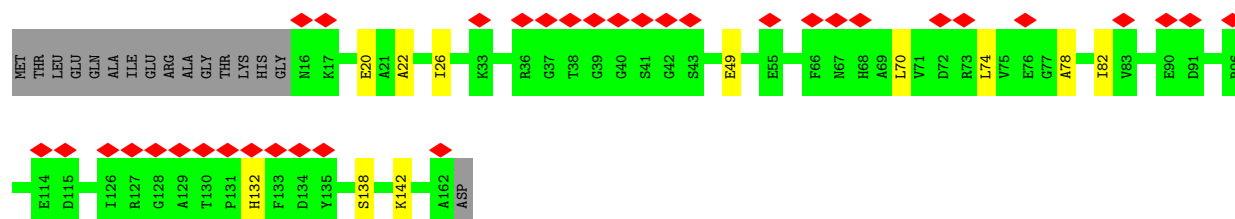
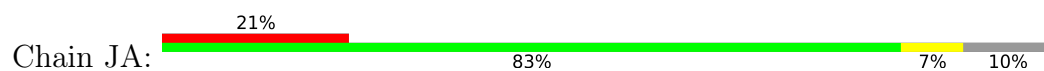


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

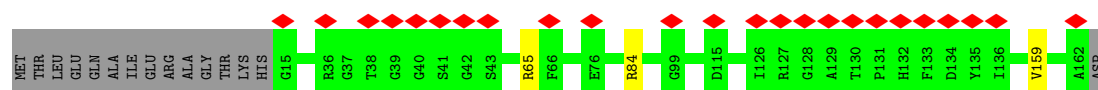
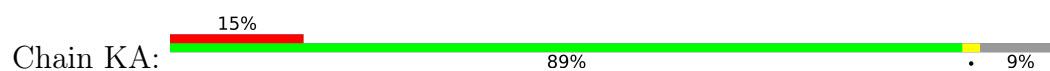




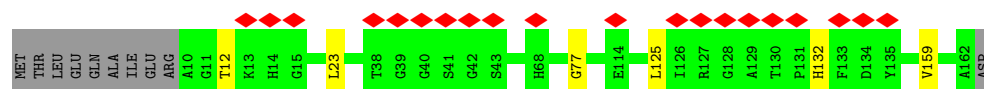
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



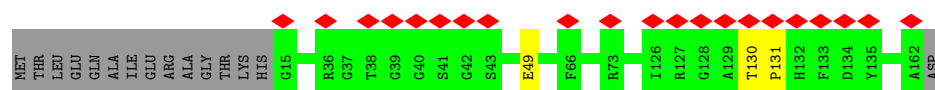
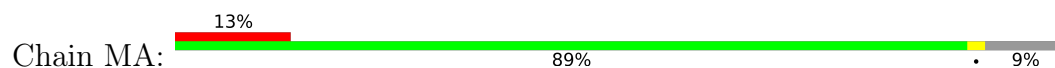
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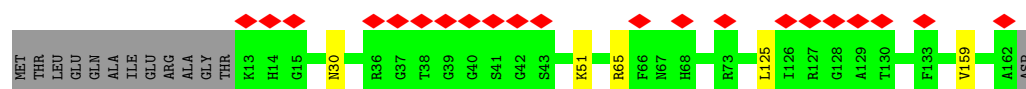
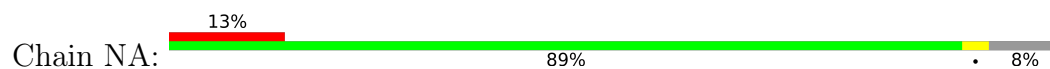
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



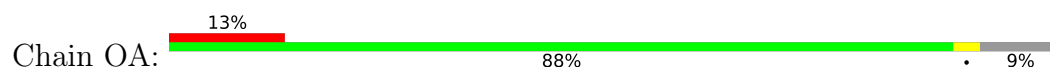
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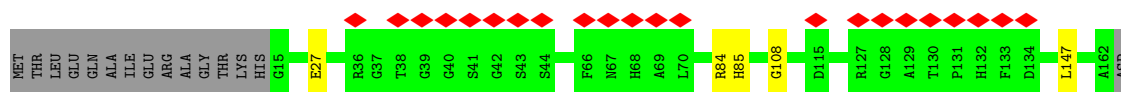


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

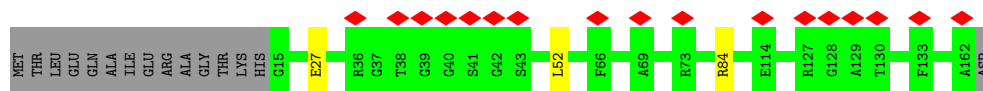
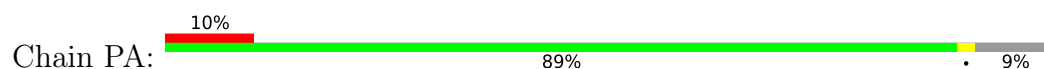


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

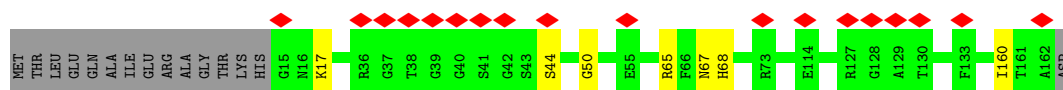
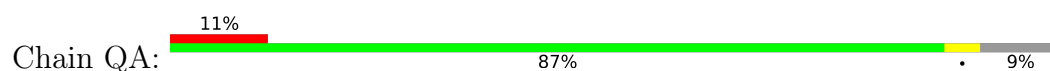




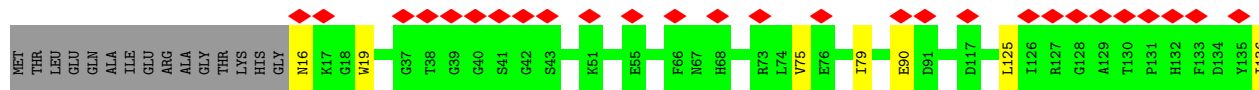
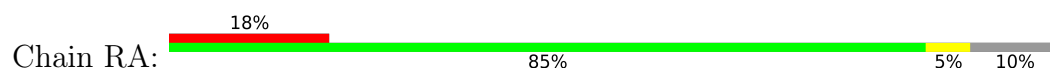
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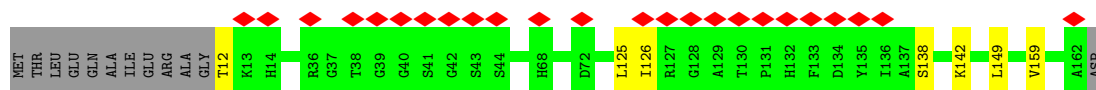
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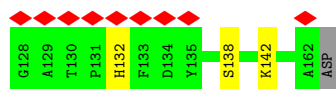
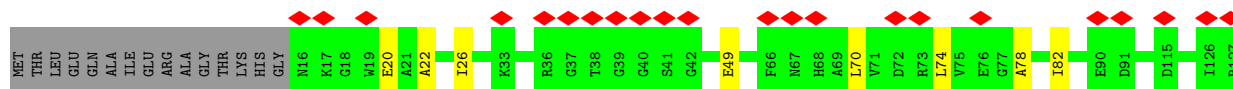
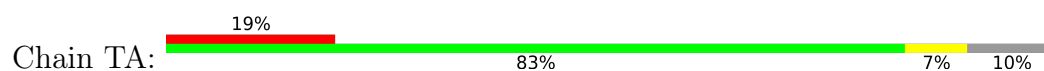
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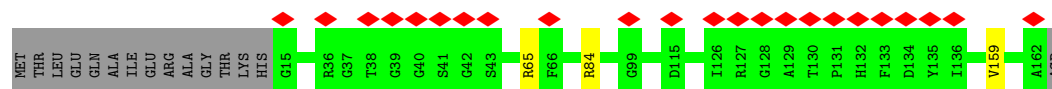
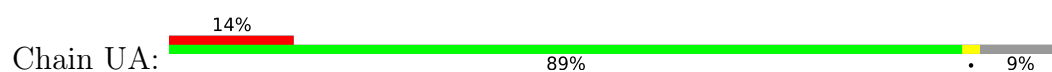
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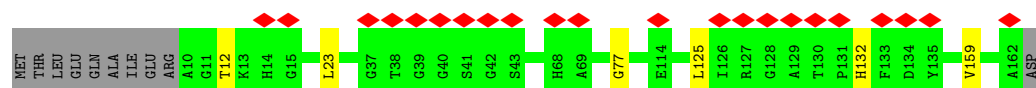
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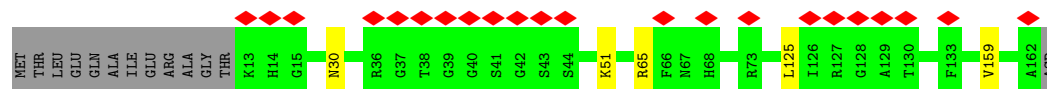
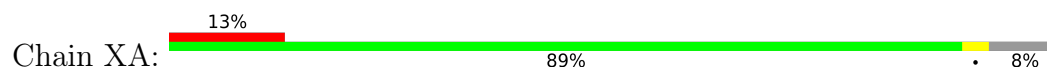
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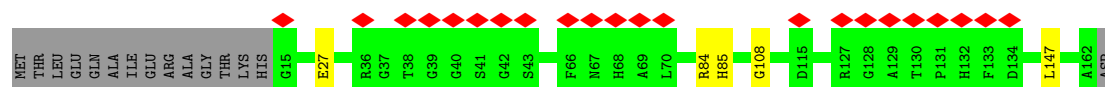
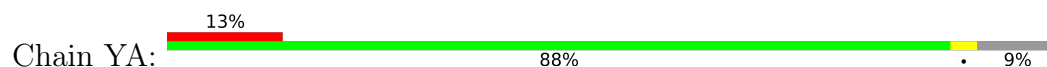
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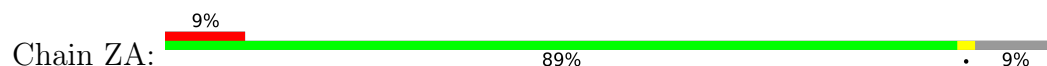
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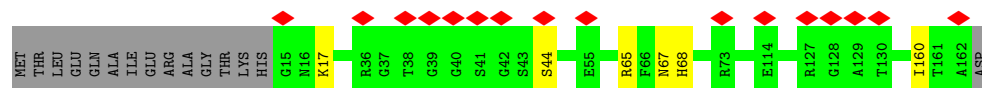
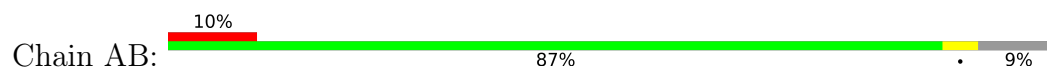
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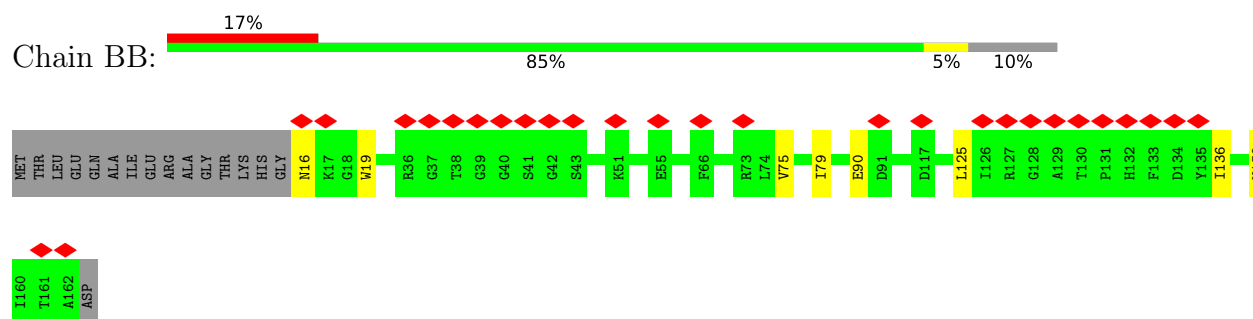
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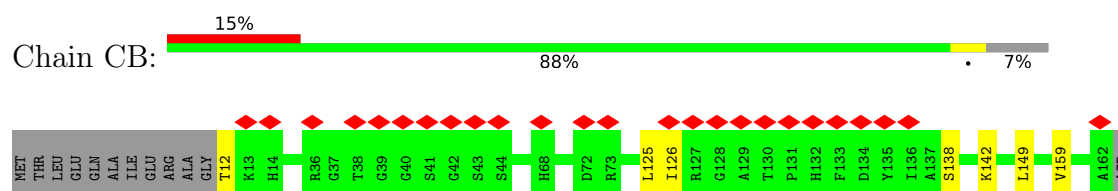
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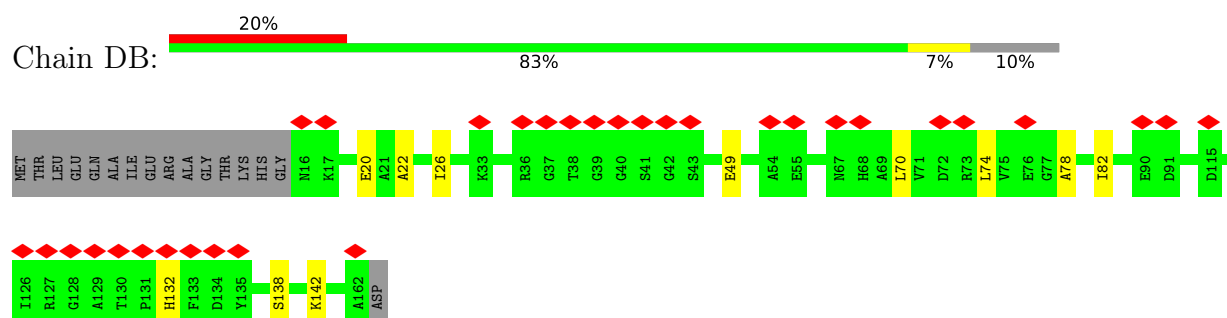
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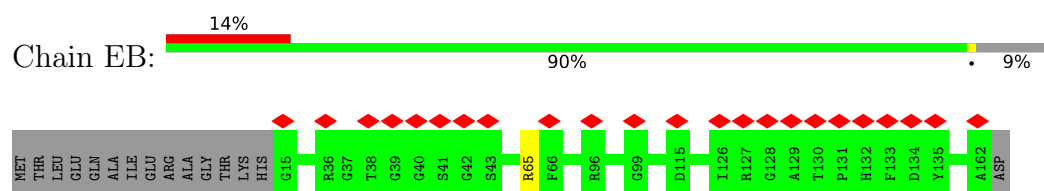
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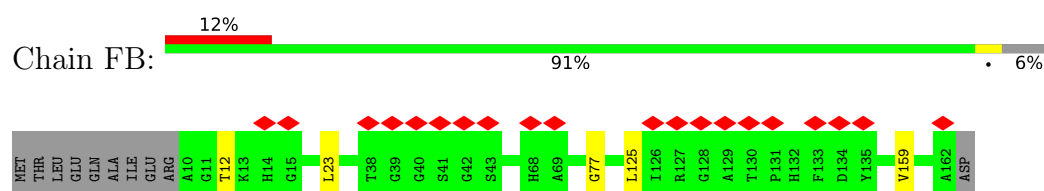
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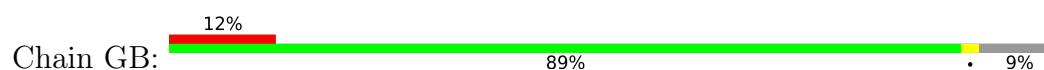
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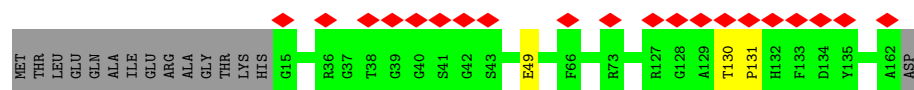


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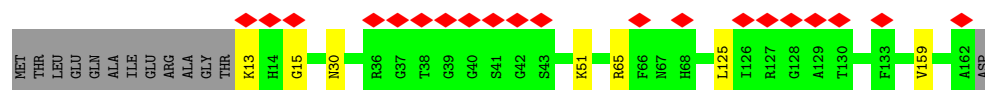
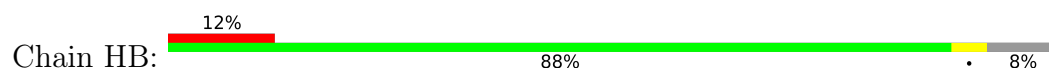


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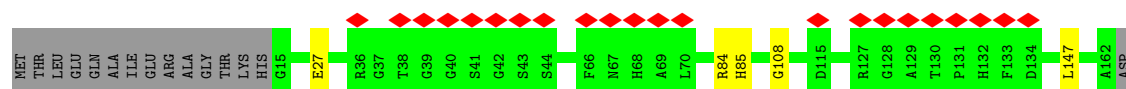




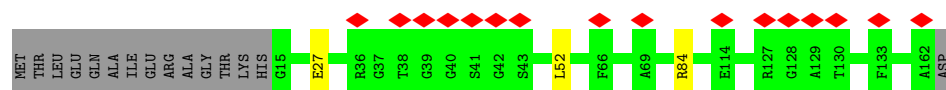
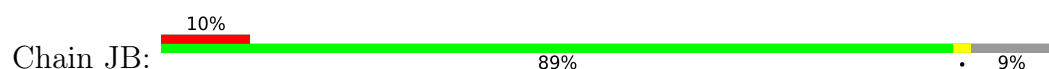
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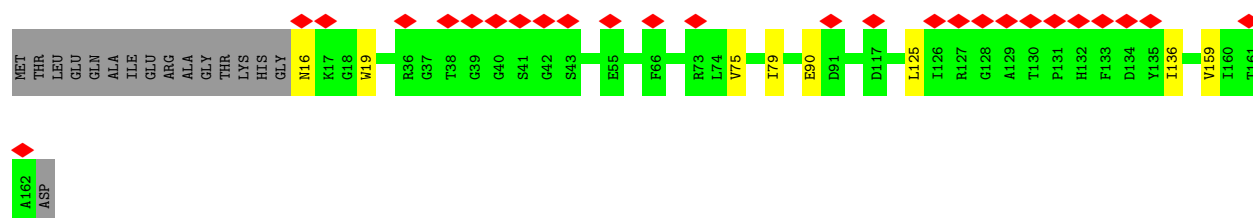
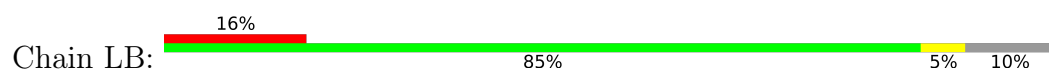
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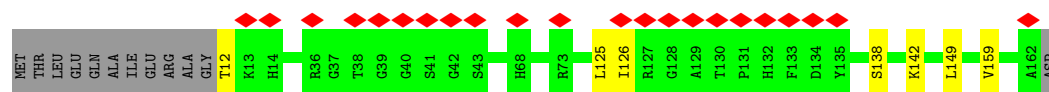


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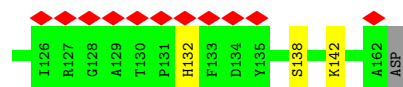
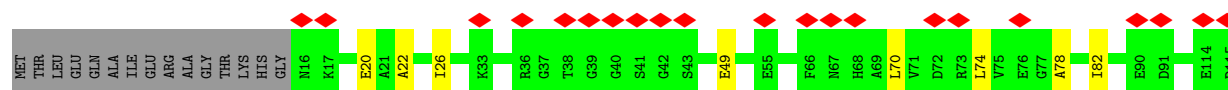
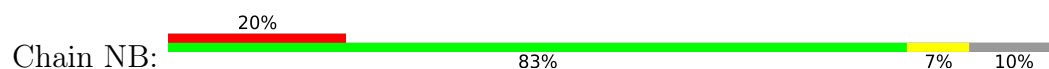


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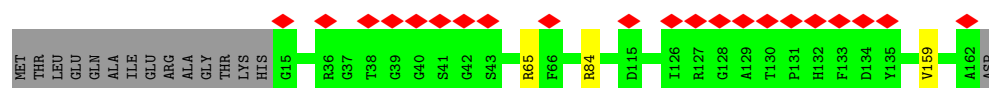
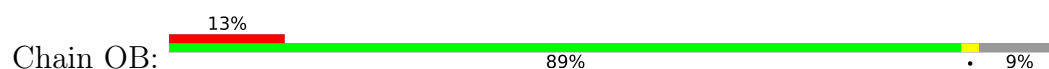




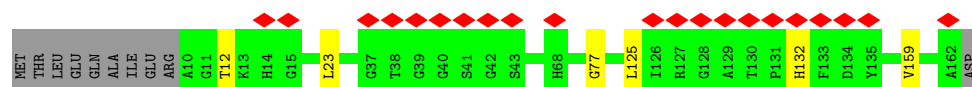
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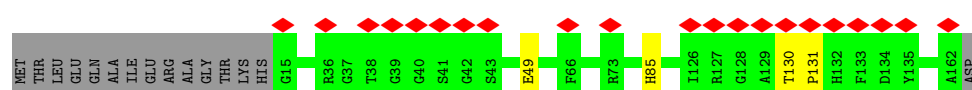
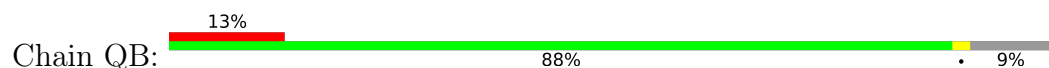
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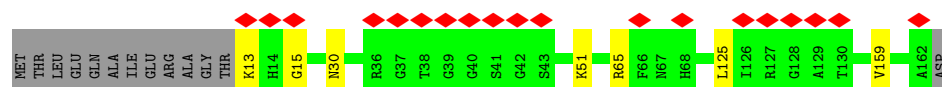
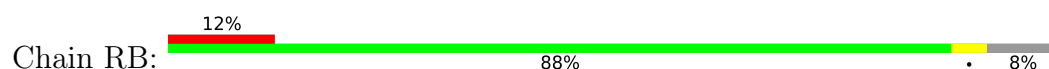
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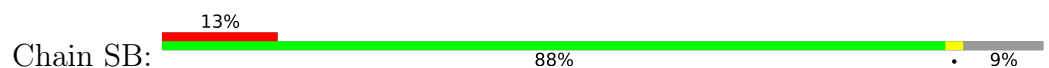
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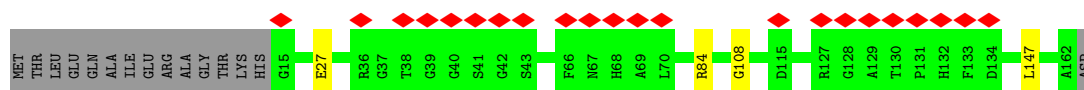


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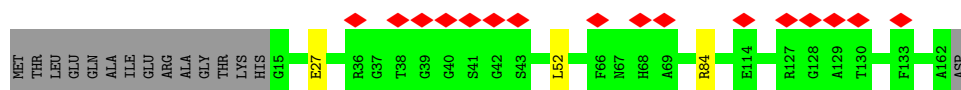
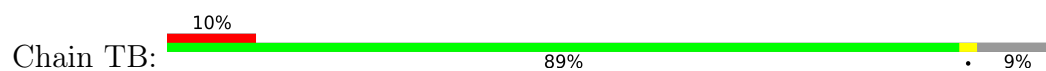


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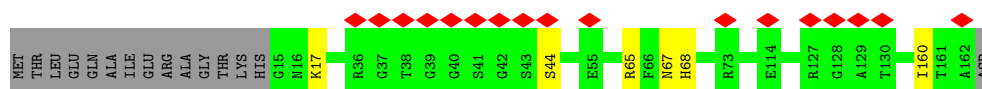




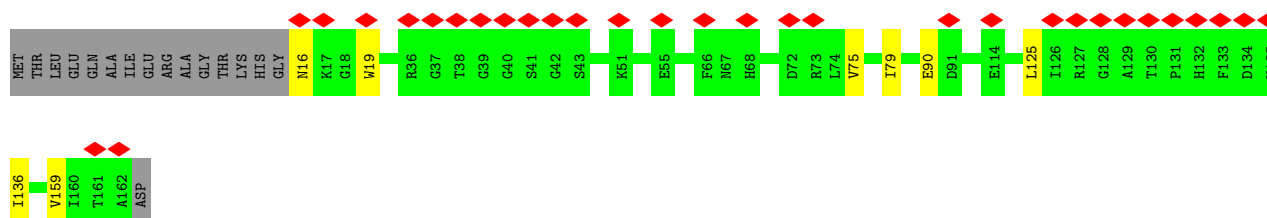
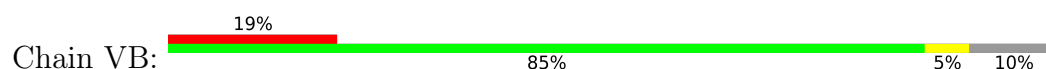
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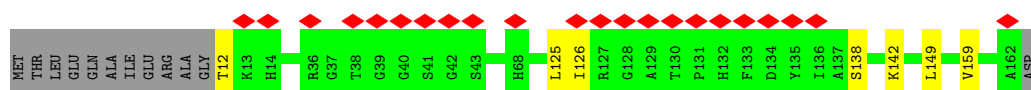
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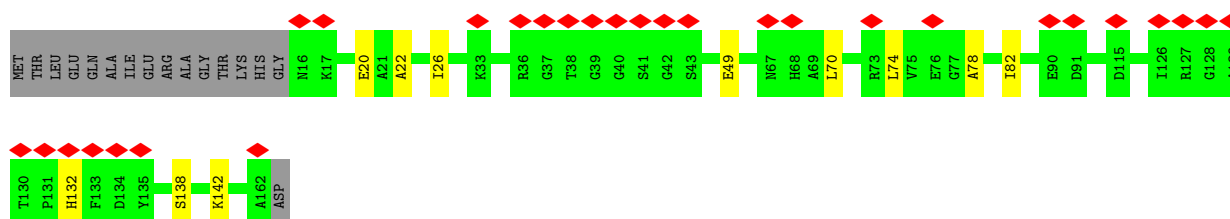
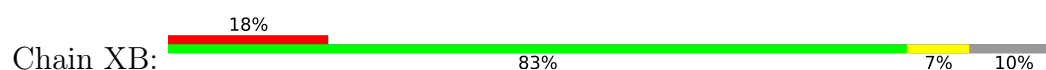
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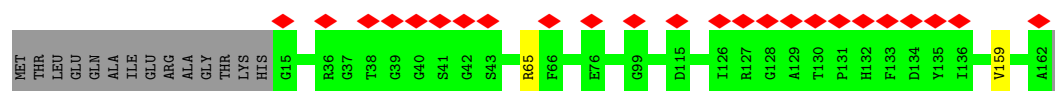
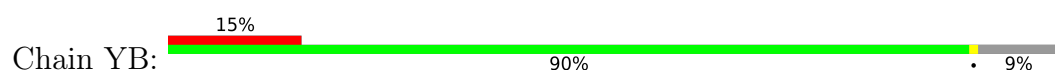
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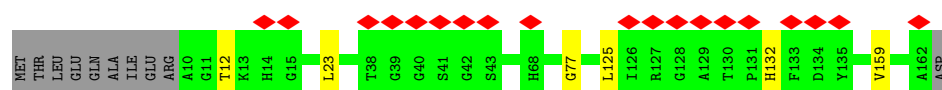
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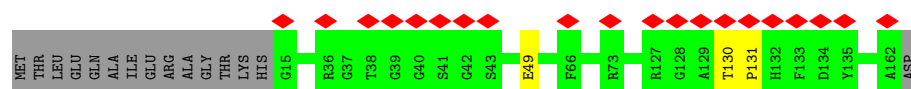
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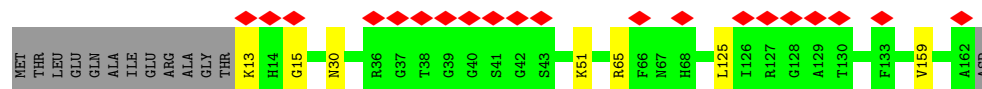
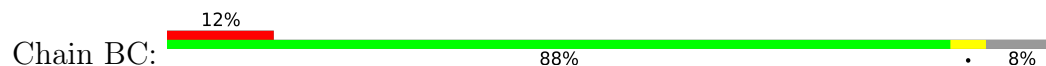
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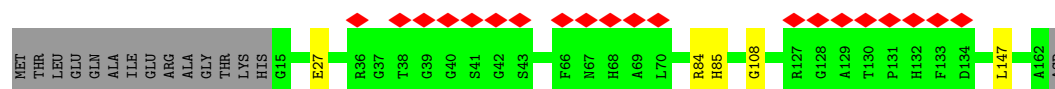
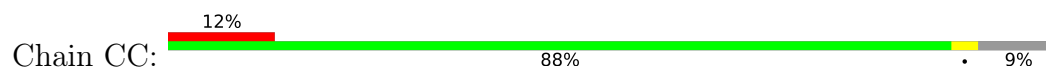
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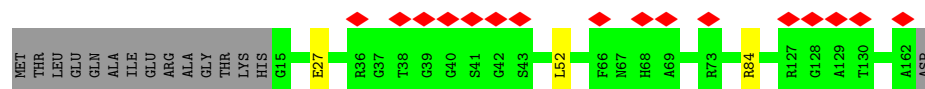
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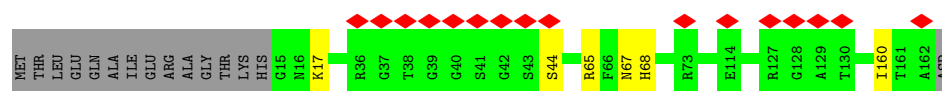
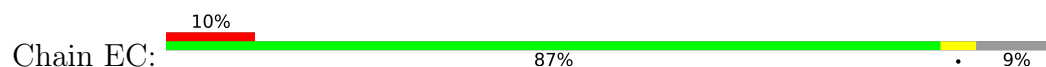
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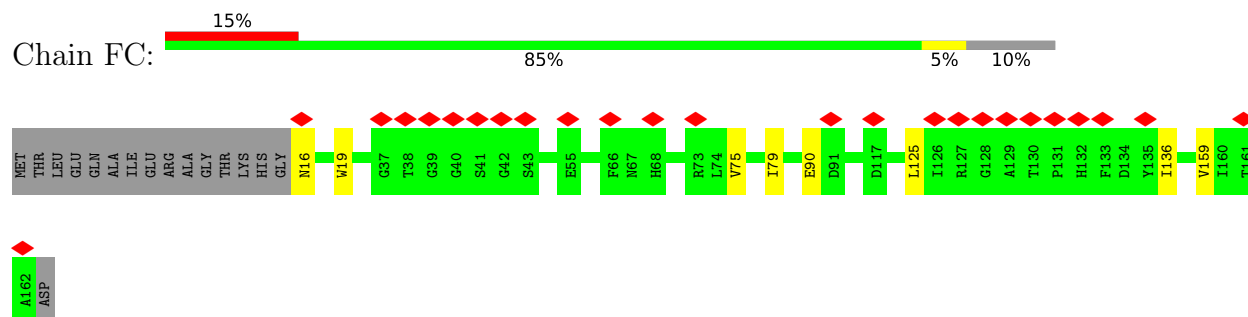
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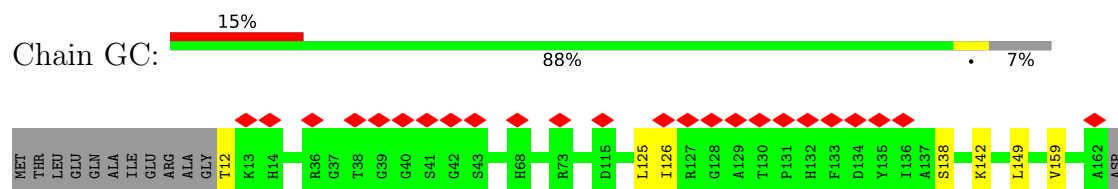
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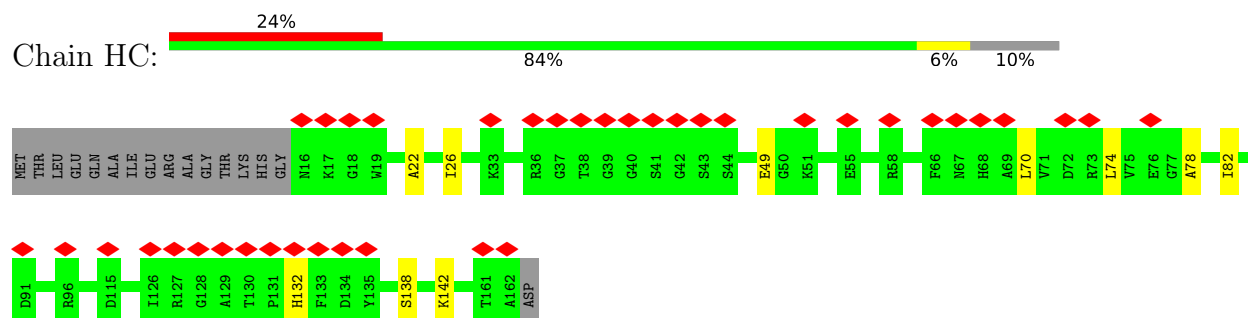
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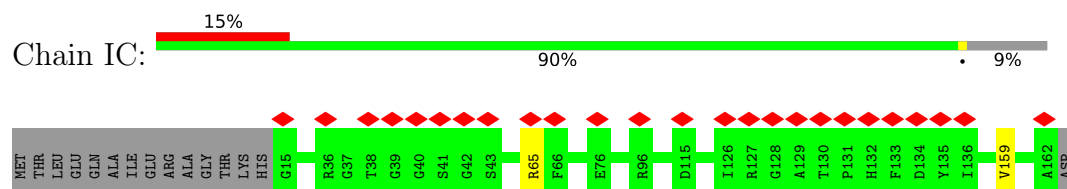
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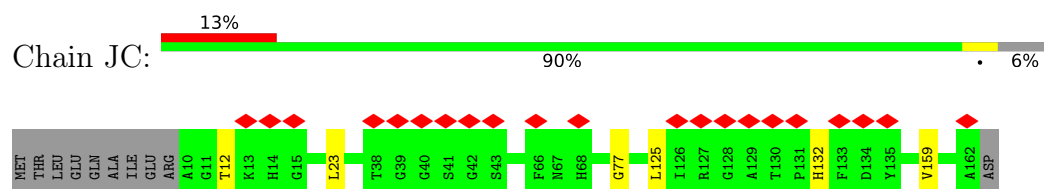
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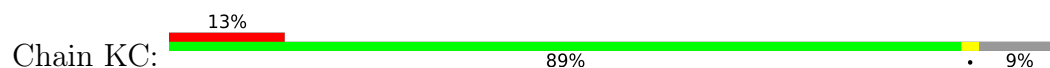
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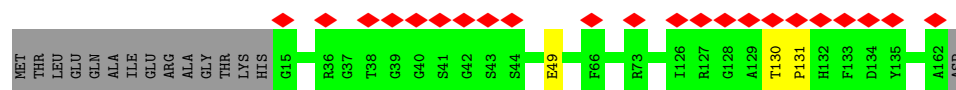


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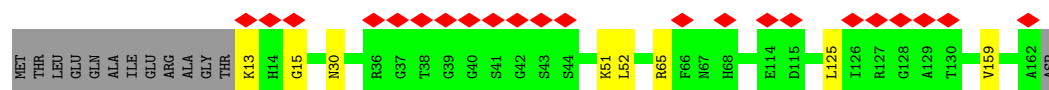


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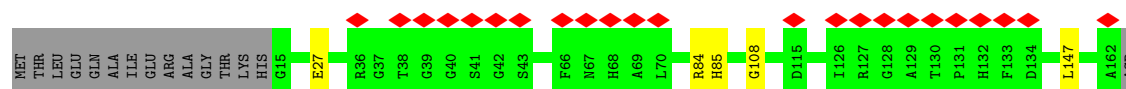




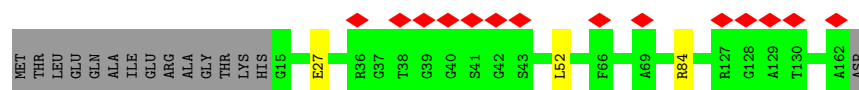
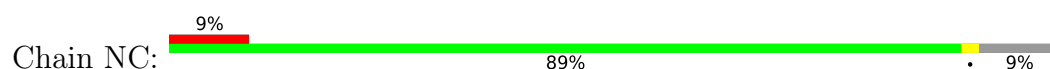
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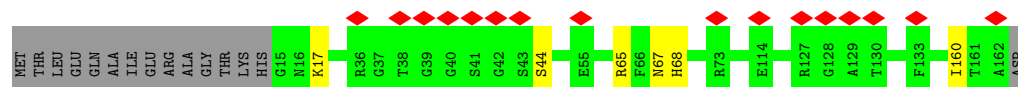
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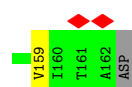
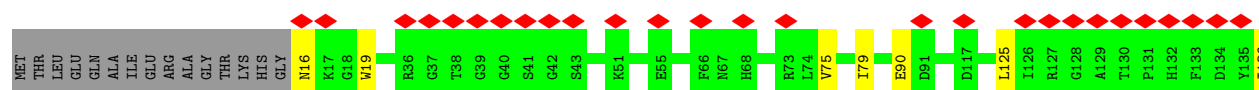
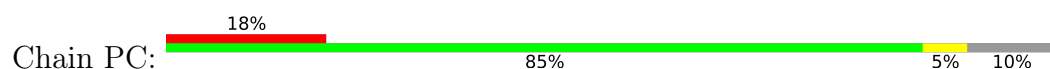
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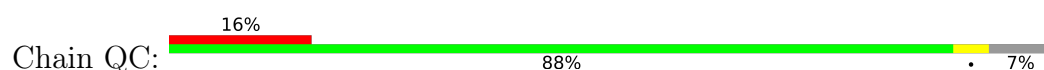
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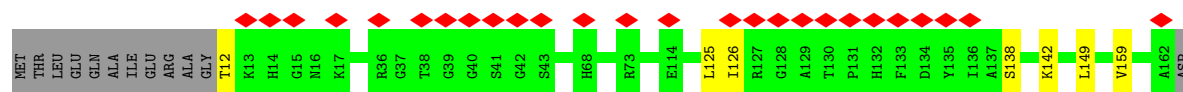


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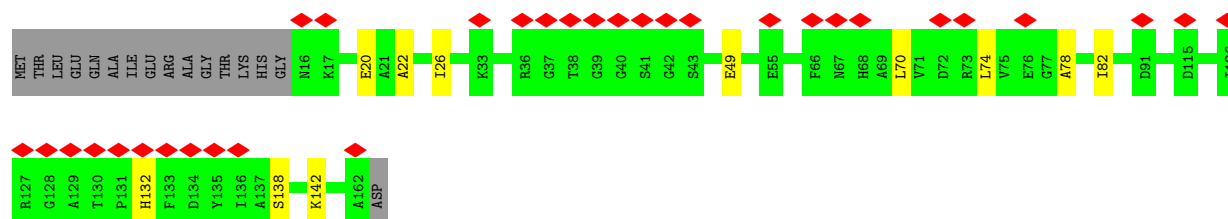
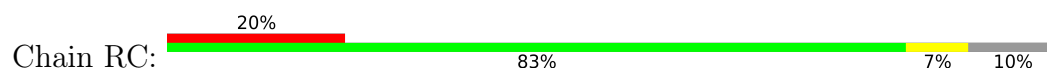


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

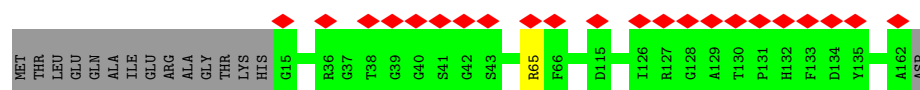
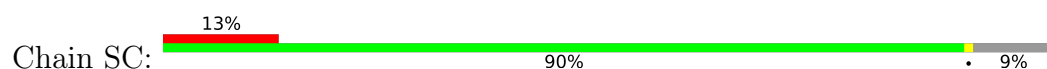




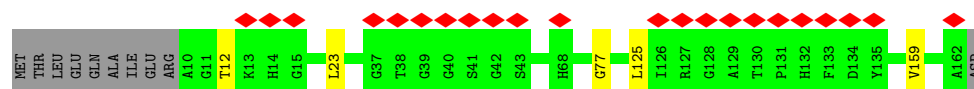
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



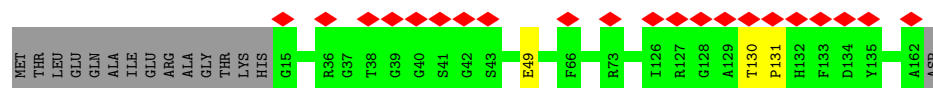
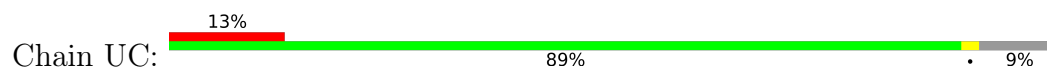
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



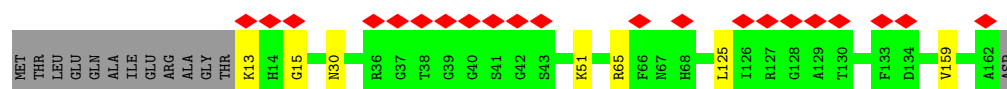
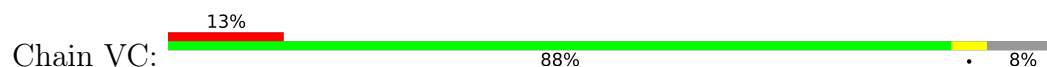
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

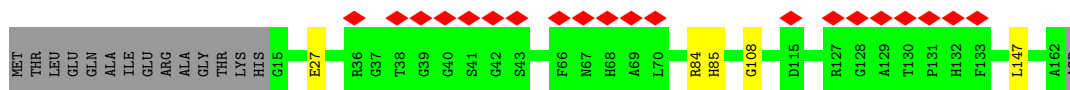


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

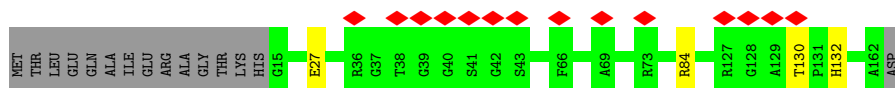
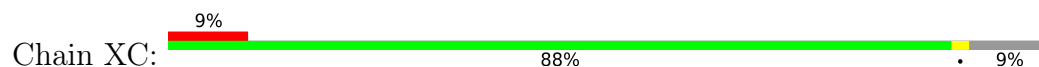


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

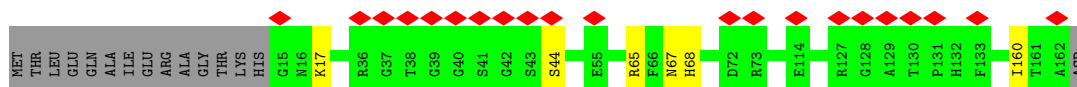




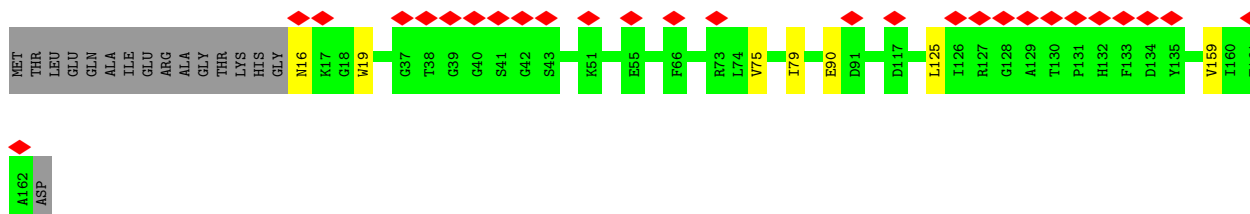
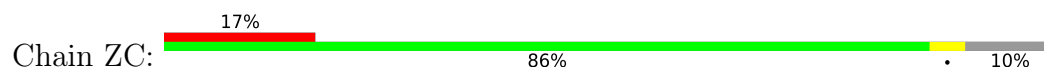
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



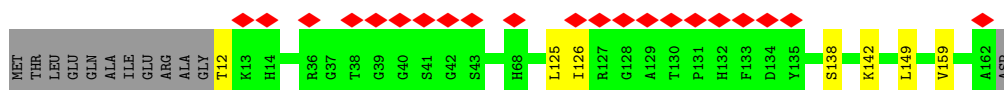
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



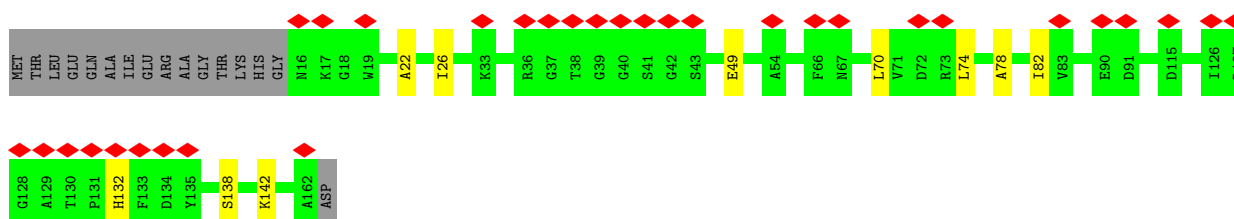
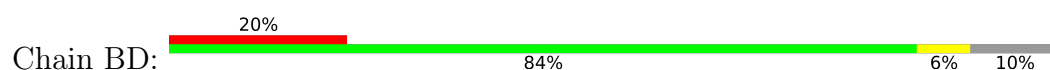
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



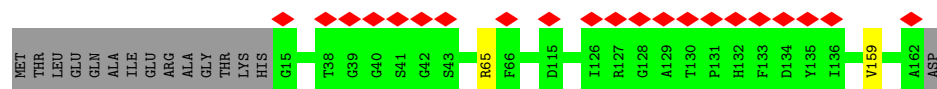
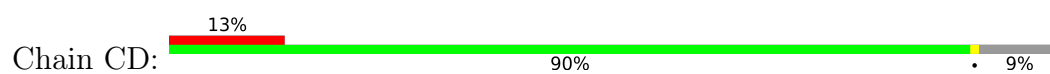
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



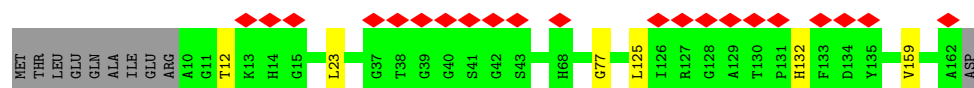
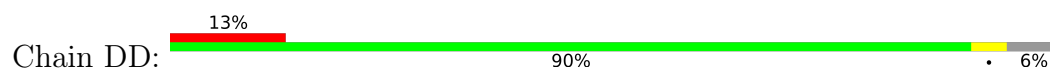
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



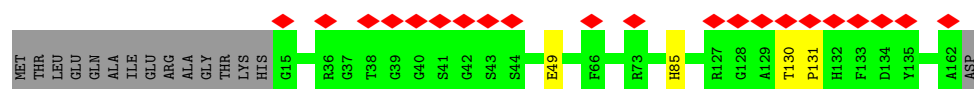
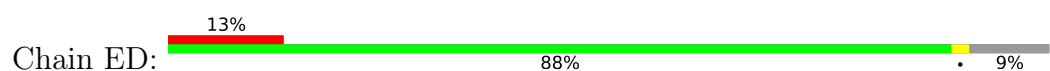
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



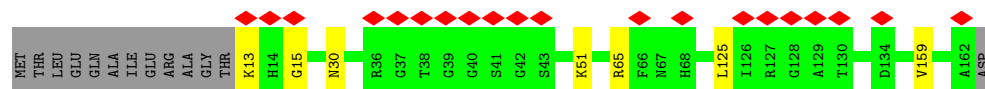
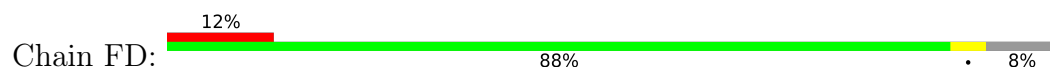
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



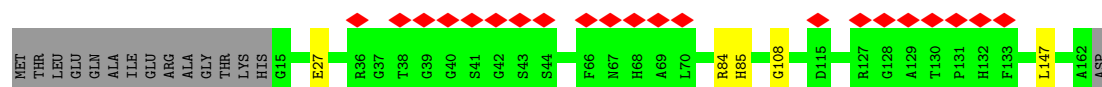
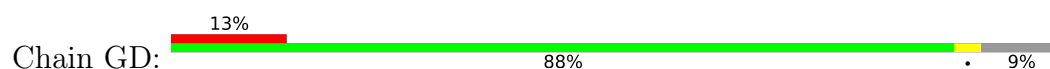
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



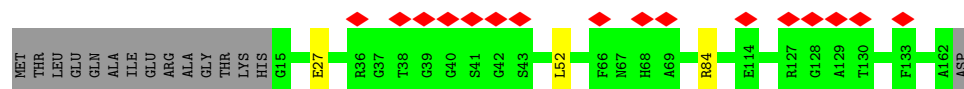
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



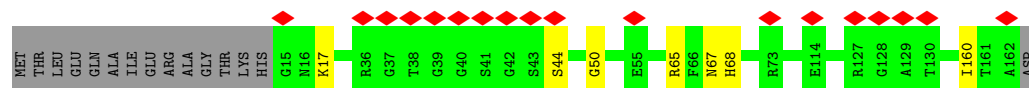
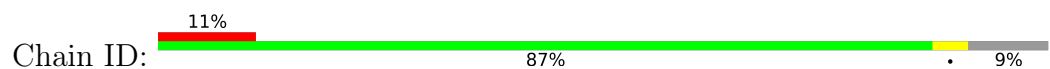
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



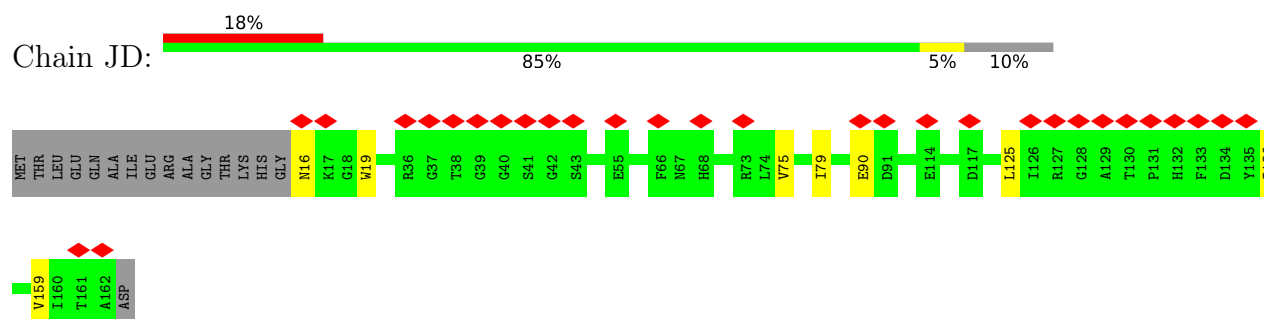
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



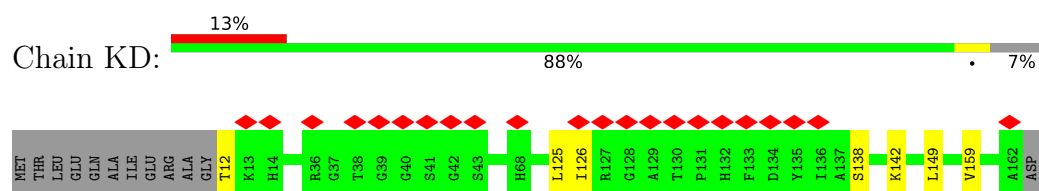
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



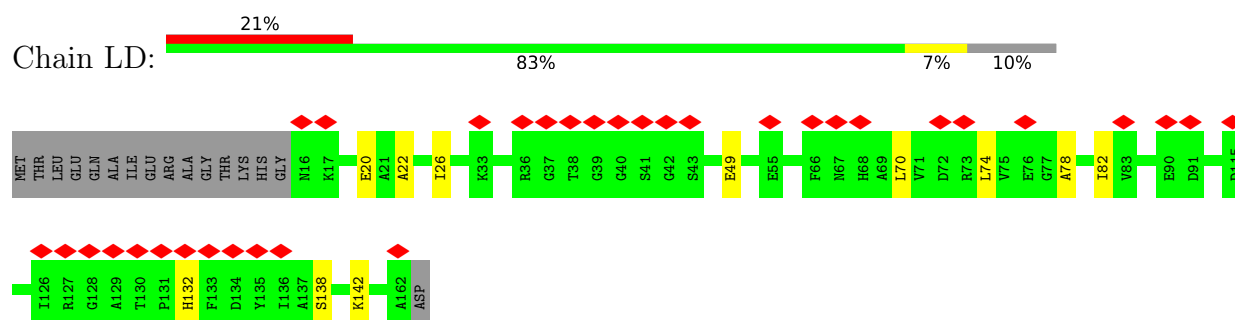
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



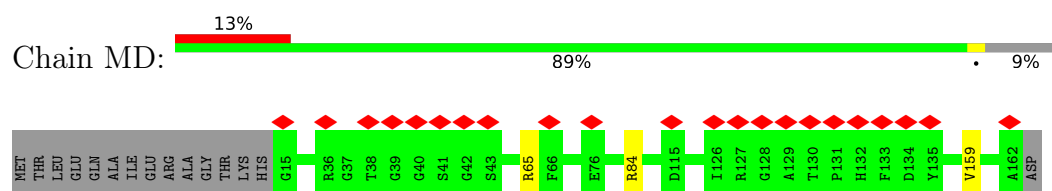
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



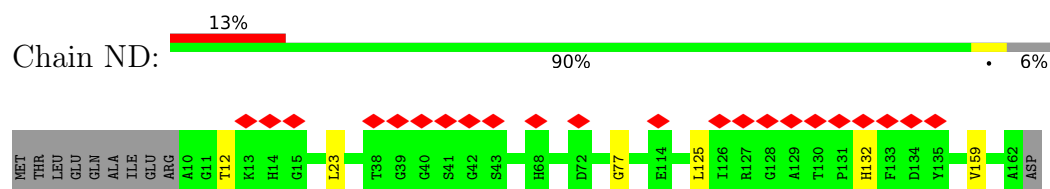
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

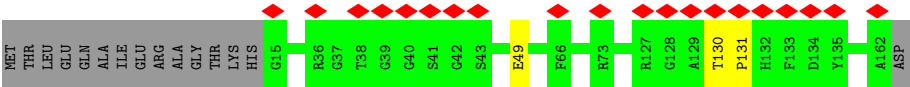


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

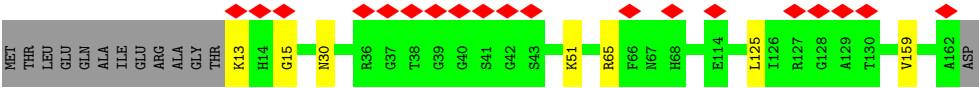
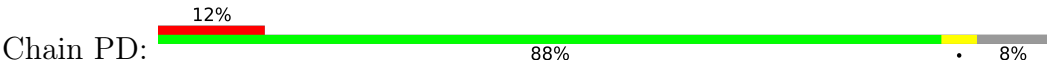


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase





• Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, T	Depositor
Number of particles used	83496	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	2.016	Depositor
Minimum map value	-0.064	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.074	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	292.4, 292.4, 292.4	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85999995, 0.85999995, 0.85999995	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	A	0.17	0/1125	0.25	0/1519
1	AA	0.17	0/1125	0.29	0/1519
1	AB	0.18	0/1125	0.31	0/1519
1	AC	0.18	0/1125	0.27	0/1519
1	AD	0.17	0/1152	0.26	0/1555
1	B	0.17	0/1125	0.26	0/1519
1	BA	0.23	0/1161	0.35	0/1567
1	BB	0.14	0/1121	0.24	0/1514
1	BC	0.18	0/1145	0.25	0/1545
1	BD	0.14	0/1121	0.25	0/1514
1	C	0.18	0/1125	0.31	0/1519
1	CA	0.19	0/1125	0.26	0/1519
1	CB	0.17	0/1152	0.26	0/1555
1	CC	0.17	0/1125	0.26	0/1519
1	CD	0.18	0/1125	0.29	0/1519
1	D	0.14	0/1121	0.24	0/1514
1	DA	0.18	0/1145	0.25	0/1545
1	DB	0.14	0/1121	0.25	0/1514
1	DC	0.18	0/1125	0.26	0/1519
1	DD	0.23	0/1161	0.35	0/1567
1	E	0.17	0/1152	0.26	0/1555
1	EA	0.17	0/1125	0.26	0/1519
1	EB	0.17	0/1125	0.29	0/1519
1	EC	0.18	0/1125	0.31	0/1519
1	ED	0.19	0/1125	0.26	0/1519
1	F	0.14	0/1121	0.25	0/1514
1	FA	0.18	0/1125	0.26	0/1519
1	FB	0.23	0/1161	0.35	0/1567
1	FC	0.14	0/1121	0.24	0/1514
1	FD	0.18	0/1145	0.25	0/1545
1	G	0.17	0/1125	0.29	0/1519
1	GA	0.18	0/1125	0.31	0/1519
1	GB	0.19	0/1125	0.26	0/1519
1	GC	0.17	0/1152	0.26	0/1555

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GD	0.17	0/1125	0.26	0/1519
1	H	0.23	0/1161	0.35	0/1567
1	HA	0.14	0/1121	0.24	0/1514
1	HB	0.18	0/1145	0.25	0/1545
1	HC	0.14	0/1121	0.25	0/1514
1	HD	0.18	0/1125	0.26	0/1519
1	I	0.18	0/1125	0.26	0/1519
1	IA	0.17	0/1152	0.26	0/1555
1	IB	0.17	0/1125	0.26	0/1519
1	IC	0.17	0/1125	0.29	0/1519
1	ID	0.18	0/1125	0.31	0/1519
1	J	0.18	0/1145	0.25	0/1545
1	JA	0.14	0/1121	0.25	0/1514
1	JB	0.18	0/1125	0.26	0/1519
1	JC	0.23	0/1161	0.35	0/1567
1	JD	0.14	0/1121	0.24	0/1514
1	K	0.17	0/1125	0.26	0/1519
1	KA	0.18	0/1125	0.29	0/1519
1	KB	0.18	0/1125	0.31	0/1519
1	KC	0.18	0/1125	0.26	0/1519
1	KD	0.17	0/1152	0.26	0/1555
1	L	0.18	0/1125	0.26	0/1519
1	LA	0.23	0/1161	0.35	0/1567
1	LB	0.14	0/1121	0.24	0/1514
1	LC	0.18	0/1145	0.25	0/1545
1	LD	0.14	0/1121	0.25	0/1514
1	M	0.18	0/1125	0.31	0/1519
1	MA	0.18	0/1125	0.26	0/1519
1	MB	0.17	0/1152	0.26	0/1555
1	MC	0.17	0/1125	0.26	0/1519
1	MD	0.18	0/1125	0.29	0/1519
1	N	0.14	0/1121	0.24	0/1514
1	NA	0.18	0/1145	0.25	0/1545
1	NB	0.14	0/1121	0.25	0/1514
1	NC	0.17	0/1125	0.26	0/1519
1	ND	0.23	0/1161	0.35	0/1567
1	O	0.17	0/1152	0.26	0/1555
1	OA	0.17	0/1125	0.26	0/1519
1	OB	0.17	0/1125	0.29	0/1519
1	OC	0.18	0/1125	0.31	0/1519
1	OD	0.19	0/1125	0.26	0/1519
1	P	0.14	0/1121	0.25	0/1514
1	PA	0.18	0/1125	0.26	0/1519

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	PB	0.23	0/1161	0.35	0/1567
1	PC	0.14	0/1121	0.24	0/1514
1	PD	0.18	0/1145	0.25	0/1545
1	Q	0.18	0/1125	0.29	0/1519
1	QA	0.18	0/1125	0.31	0/1519
1	QB	0.19	0/1125	0.26	0/1519
1	QC	0.17	0/1152	0.26	0/1555
1	R	0.23	0/1161	0.35	0/1567
1	RA	0.14	0/1121	0.24	0/1514
1	RB	0.18	0/1145	0.25	0/1545
1	RC	0.14	0/1121	0.25	0/1514
1	S	0.18	0/1125	0.26	0/1519
1	SA	0.17	0/1152	0.26	0/1555
1	SB	0.17	0/1125	0.26	0/1519
1	SC	0.17	0/1125	0.29	0/1519
1	T	0.18	0/1145	0.25	0/1545
1	TA	0.14	0/1121	0.25	0/1514
1	TB	0.18	0/1125	0.26	0/1519
1	TC	0.23	0/1161	0.35	0/1567
1	U	0.17	0/1125	0.25	0/1519
1	UA	0.18	0/1125	0.29	0/1519
1	UB	0.18	0/1125	0.31	0/1519
1	UC	0.18	0/1125	0.26	0/1519
1	V	0.18	0/1125	0.26	0/1519
1	VA	0.23	0/1161	0.35	0/1567
1	VB	0.14	0/1121	0.24	0/1514
1	VC	0.18	0/1145	0.25	0/1545
1	W	0.18	0/1125	0.31	0/1519
1	WA	0.19	0/1125	0.27	0/1519
1	WB	0.17	0/1152	0.26	0/1555
1	WC	0.17	0/1125	0.26	0/1519
1	X	0.14	0/1121	0.24	0/1514
1	XA	0.18	0/1145	0.25	0/1545
1	XB	0.14	0/1121	0.25	0/1514
1	XC	0.18	0/1125	0.26	0/1519
1	Y	0.17	0/1152	0.26	0/1555
1	YA	0.17	0/1125	0.26	0/1519
1	YB	0.17	0/1125	0.29	0/1519
1	YC	0.18	0/1125	0.31	0/1519
1	Z	0.14	0/1121	0.25	0/1514
1	ZA	0.18	0/1125	0.26	0/1519
1	ZB	0.23	0/1161	0.35	0/1567
1	ZC	0.14	0/1121	0.24	0/1514

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.18	0/135900	0.27	0/183480

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1108	0	1126	7	0
1	AA	1108	0	1126	2	0
1	AB	1108	0	1126	6	0
1	AC	1108	0	1126	2	0
1	AD	1134	0	1153	5	0
1	B	1108	0	1126	5	0
1	BA	1143	0	1161	5	0
1	BB	1104	0	1123	7	0
1	BC	1127	0	1146	5	0
1	BD	1104	0	1123	6	0
1	C	1108	0	1126	7	0
1	CA	1108	0	1126	2	0
1	CB	1134	0	1153	5	0
1	CC	1108	0	1126	8	0
1	CD	1108	0	1126	2	0
1	D	1104	0	1123	5	0
1	DA	1127	0	1146	6	0
1	DB	1104	0	1123	7	0
1	DC	1108	0	1126	4	0
1	DD	1143	0	1161	5	0
1	E	1134	0	1153	5	0
1	EA	1108	0	1126	8	0
1	EB	1108	0	1126	1	0
1	EC	1108	0	1126	6	0
1	ED	1108	0	1126	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1104	0	1123	7	0
1	FA	1108	0	1126	4	0
1	FB	1143	0	1161	4	0
1	FC	1104	0	1123	6	0
1	FD	1127	0	1146	5	0
1	G	1108	0	1126	1	0
1	GA	1108	0	1126	7	0
1	GB	1108	0	1126	2	0
1	GC	1134	0	1153	5	0
1	GD	1108	0	1126	8	0
1	H	1143	0	1161	4	0
1	HA	1104	0	1123	7	0
1	HB	1127	0	1146	5	0
1	HC	1104	0	1123	6	0
1	HD	1108	0	1126	4	0
1	I	1108	0	1126	2	0
1	IA	1134	0	1153	5	0
1	IB	1108	0	1126	8	0
1	IC	1108	0	1126	2	0
1	ID	1108	0	1126	7	0
1	J	1127	0	1146	5	0
1	JA	1104	0	1123	7	0
1	JB	1108	0	1126	4	0
1	JC	1143	0	1161	5	0
1	JD	1104	0	1123	7	0
1	K	1108	0	1126	8	0
1	KA	1108	0	1126	3	0
1	KB	1108	0	1126	7	0
1	KC	1108	0	1126	2	0
1	KD	1134	0	1153	5	0
1	L	1108	0	1126	3	0
1	LA	1143	0	1161	5	0
1	LB	1104	0	1123	7	0
1	LC	1127	0	1146	6	0
1	LD	1104	0	1123	7	0
1	M	1108	0	1126	6	0
1	MA	1108	0	1126	2	0
1	MB	1134	0	1153	5	0
1	MC	1108	0	1126	8	0
1	MD	1108	0	1126	3	0
1	N	1104	0	1123	6	0
1	NA	1127	0	1146	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	NB	1104	0	1123	7	0
1	NC	1108	0	1126	4	0
1	ND	1143	0	1161	5	0
1	O	1134	0	1153	5	0
1	OA	1108	0	1126	8	0
1	OB	1108	0	1126	3	0
1	OC	1108	0	1126	6	0
1	OD	1108	0	1126	2	0
1	P	1104	0	1123	6	0
1	PA	1108	0	1126	4	0
1	PB	1143	0	1161	5	0
1	PC	1104	0	1123	6	0
1	PD	1127	0	1146	5	0
1	Q	1108	0	1126	3	0
1	QA	1108	0	1126	7	0
1	QB	1108	0	1126	3	0
1	QC	1134	0	1153	5	0
1	R	1143	0	1161	5	0
1	RA	1104	0	1123	7	0
1	RB	1127	0	1146	5	0
1	RC	1104	0	1123	7	0
1	S	1108	0	1126	2	0
1	SA	1134	0	1153	5	0
1	SB	1108	0	1126	7	0
1	SC	1108	0	1126	1	0
1	T	1127	0	1146	4	0
1	TA	1104	0	1123	7	0
1	TB	1108	0	1126	4	0
1	TC	1143	0	1161	4	0
1	U	1108	0	1126	8	0
1	UA	1108	0	1126	3	0
1	UB	1108	0	1126	6	0
1	UC	1108	0	1126	2	0
1	V	1108	0	1126	4	0
1	VA	1143	0	1161	5	0
1	VB	1104	0	1123	7	0
1	VC	1127	0	1145	5	0
1	W	1108	0	1126	6	0
1	WA	1108	0	1126	2	0
1	WB	1134	0	1153	5	0
1	WC	1108	0	1126	8	0
1	X	1104	0	1123	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	XA	1127	0	1146	4	0
1	XB	1104	0	1123	7	0
1	XC	1108	0	1126	4	0
1	Y	1134	0	1153	5	0
1	YA	1108	0	1126	8	0
1	YB	1108	0	1126	2	0
1	YC	1108	0	1126	6	0
1	Z	1104	0	1123	7	0
1	ZA	1108	0	1126	4	0
1	ZB	1143	0	1161	5	0
1	ZC	1104	0	1123	5	0
All	All	133824	0	136031	446	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.

The worst 5 of 446 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:A:27:GLU:OE1	1:L:84:ARG:NH1	2.14	0.79
1:ZA:84:ARG:NH1	1:CC:27:GLU:OE1	2.16	0.78
1:B:84:ARG:NH1	1:GD:27:GLU:OE1	2.16	0.78
1:K:27:GLU:OE1	1:HD:84:ARG:NH1	2.17	0.78
1:TB:84:ARG:NH1	1:MC:27:GLU:OE1	2.16	0.78

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

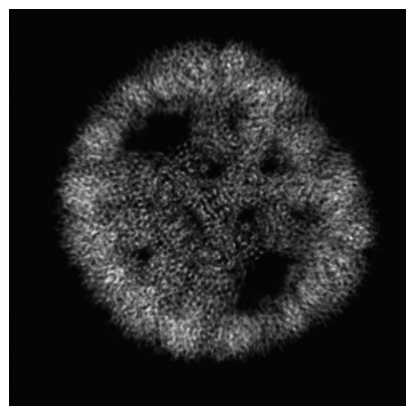
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51005. These allow visual inspection of the internal detail of the map and identification of artifacts.

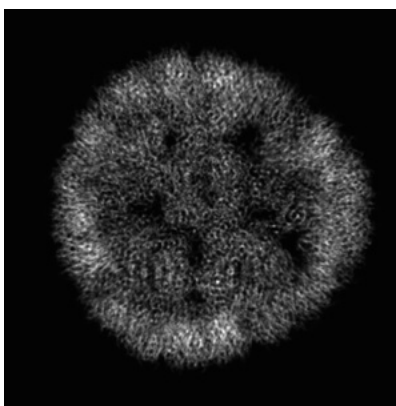
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

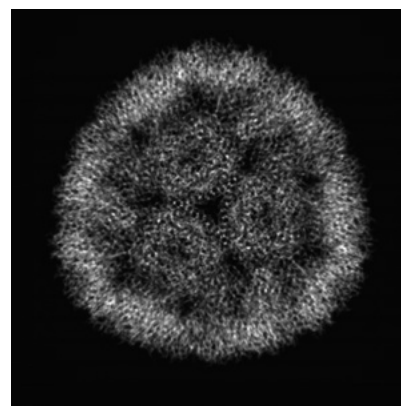
6.1.1 Primary map



X

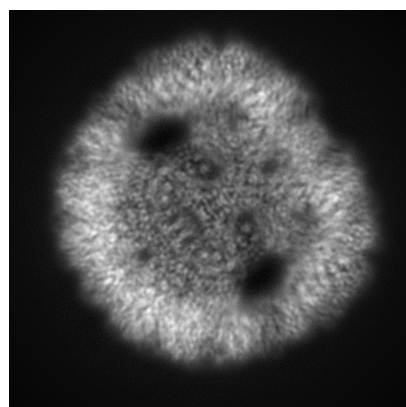


Y

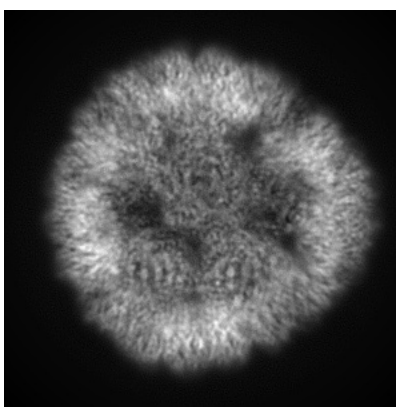


Z

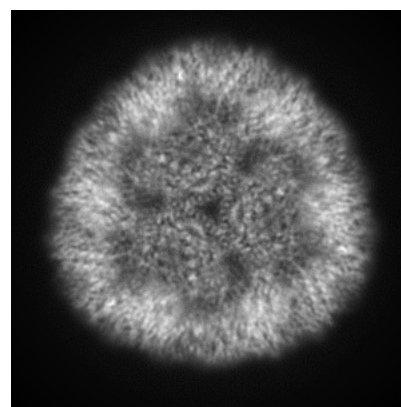
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 170

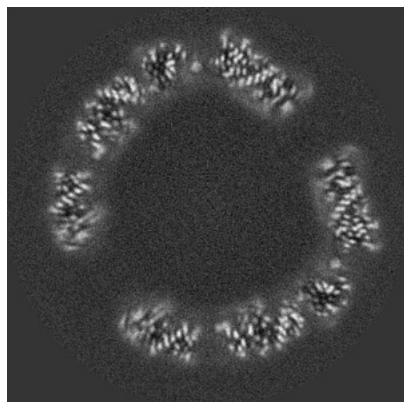


Y Index: 170

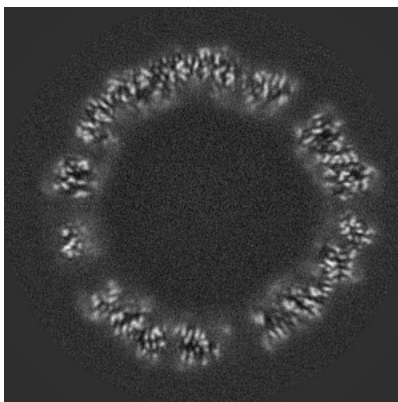


Z Index: 170

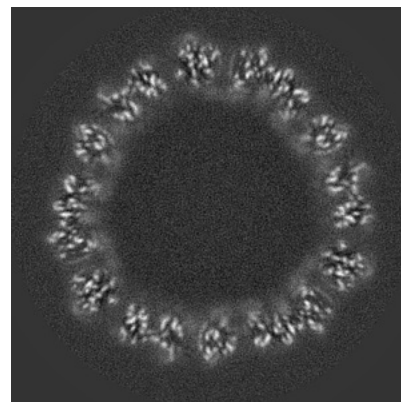
6.2.2 Raw map



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](#)

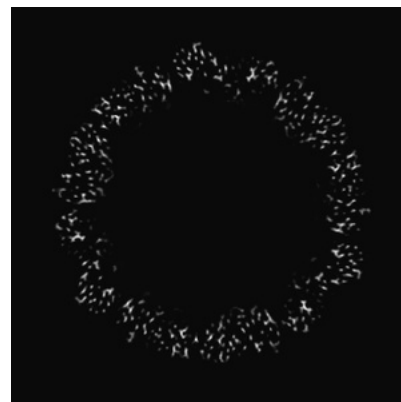
6.3.1 Primary map



X Index: 202

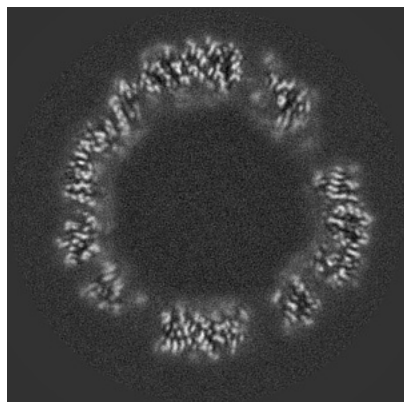


Y Index: 140

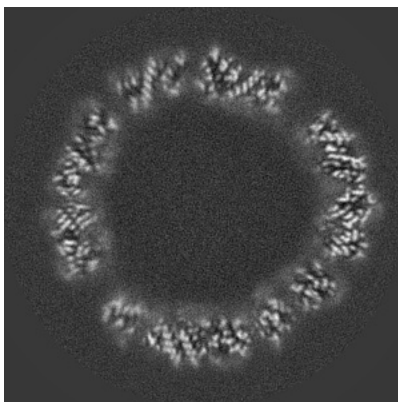


Z Index: 184

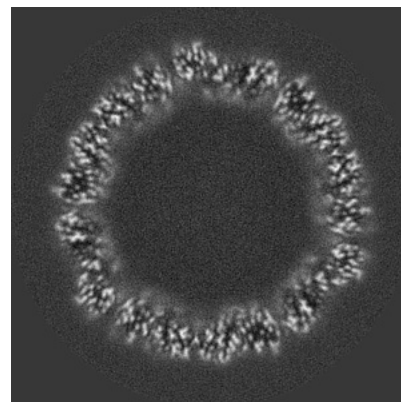
6.3.2 Raw map



X Index: 202



Y Index: 187

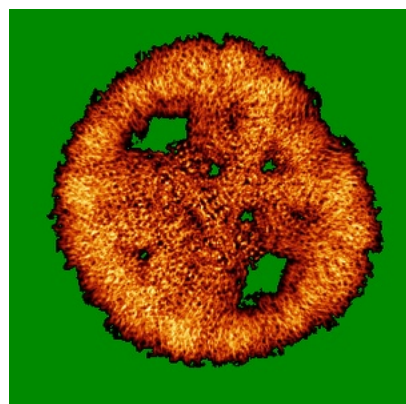


Z Index: 184

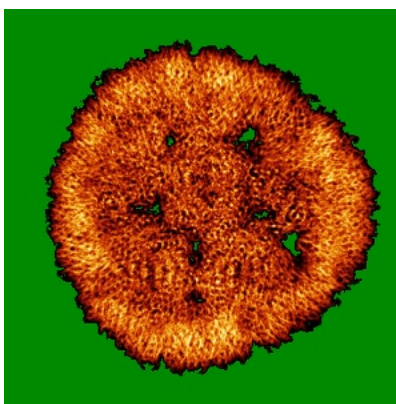
The images above show the largest variance slices of the map in three orthogonal directions.

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

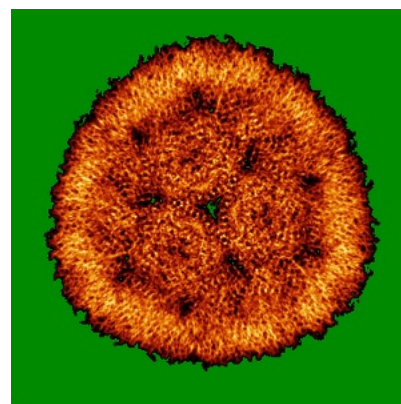
6.4.1 Primary map



X

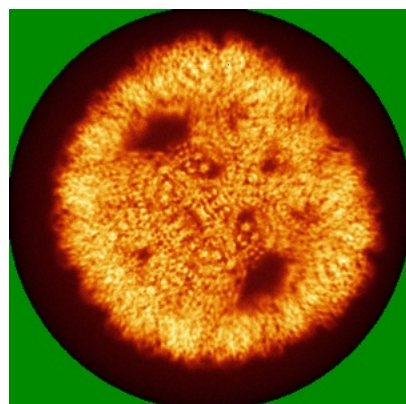


Y

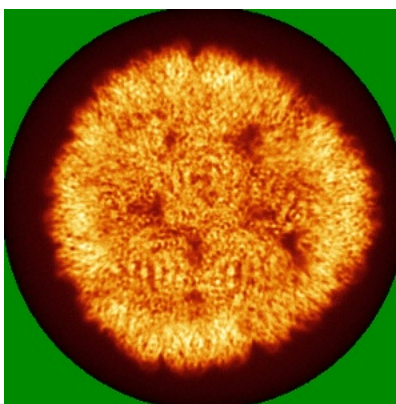


Z

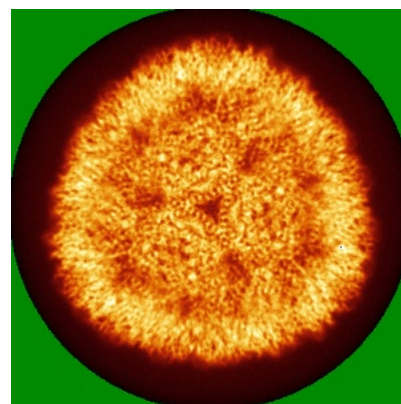
6.4.2 Raw map



X



Y



Z

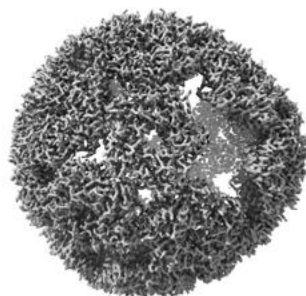
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

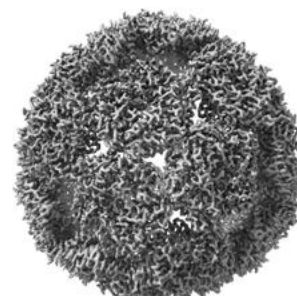
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

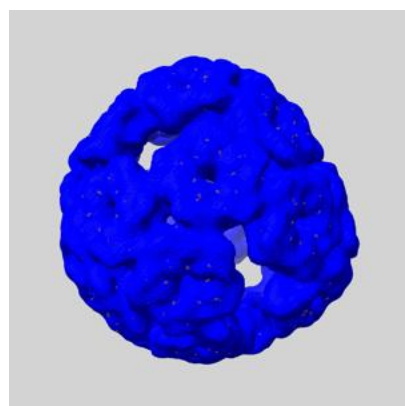
6.6 Mask visualisation [i](#)

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

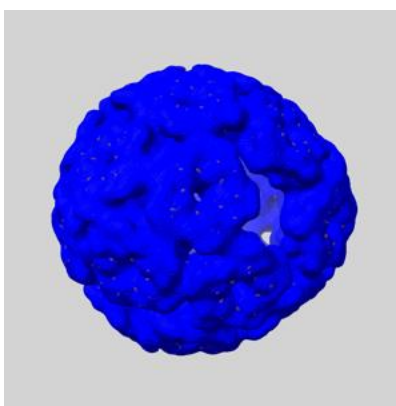
A mask typically either:

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

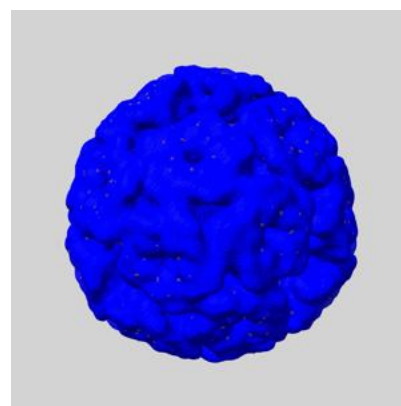
6.6.1 emd_51005_msk_1.map [i](#)



X



Y

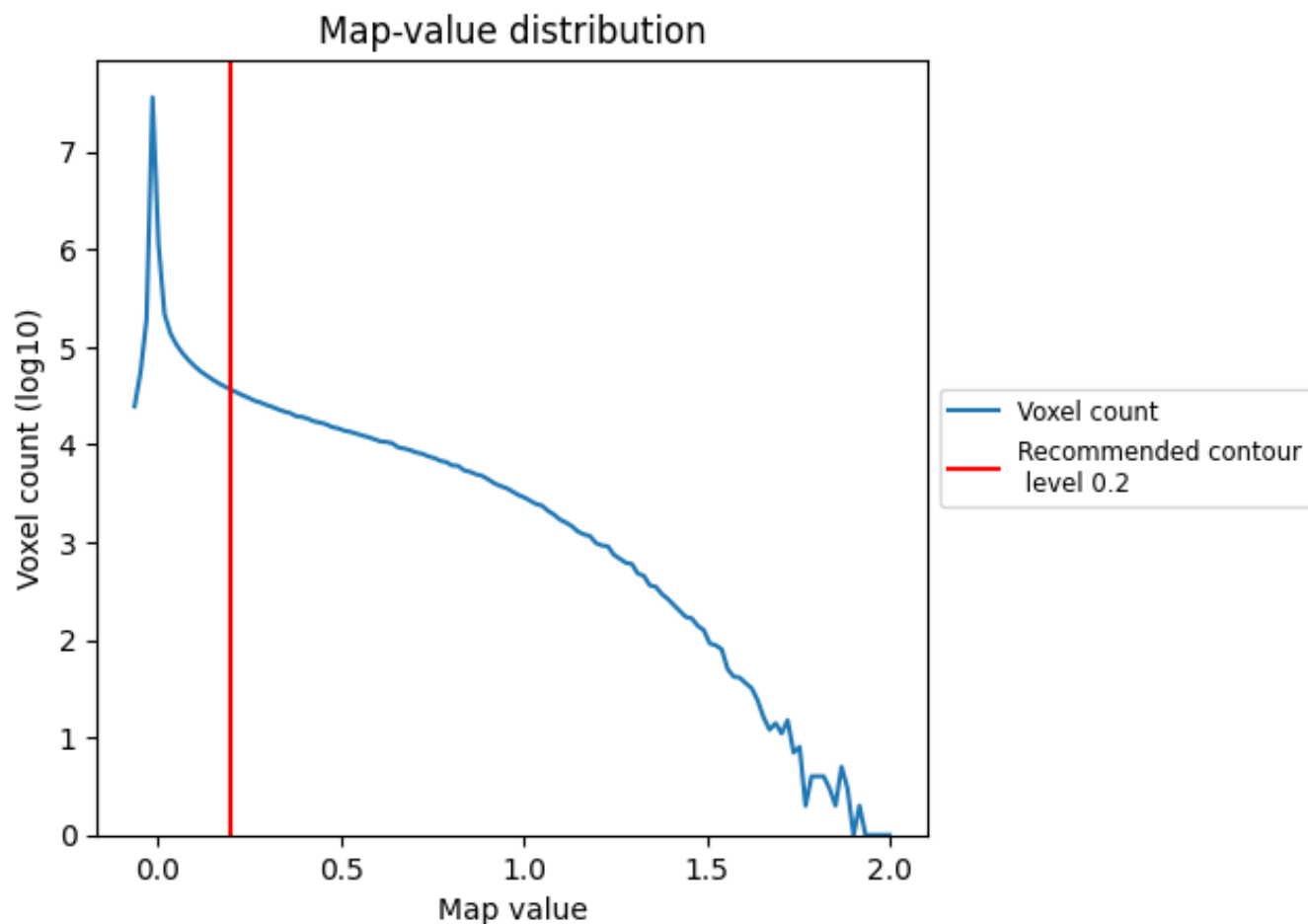


Z

7 Map analysis [i](#)

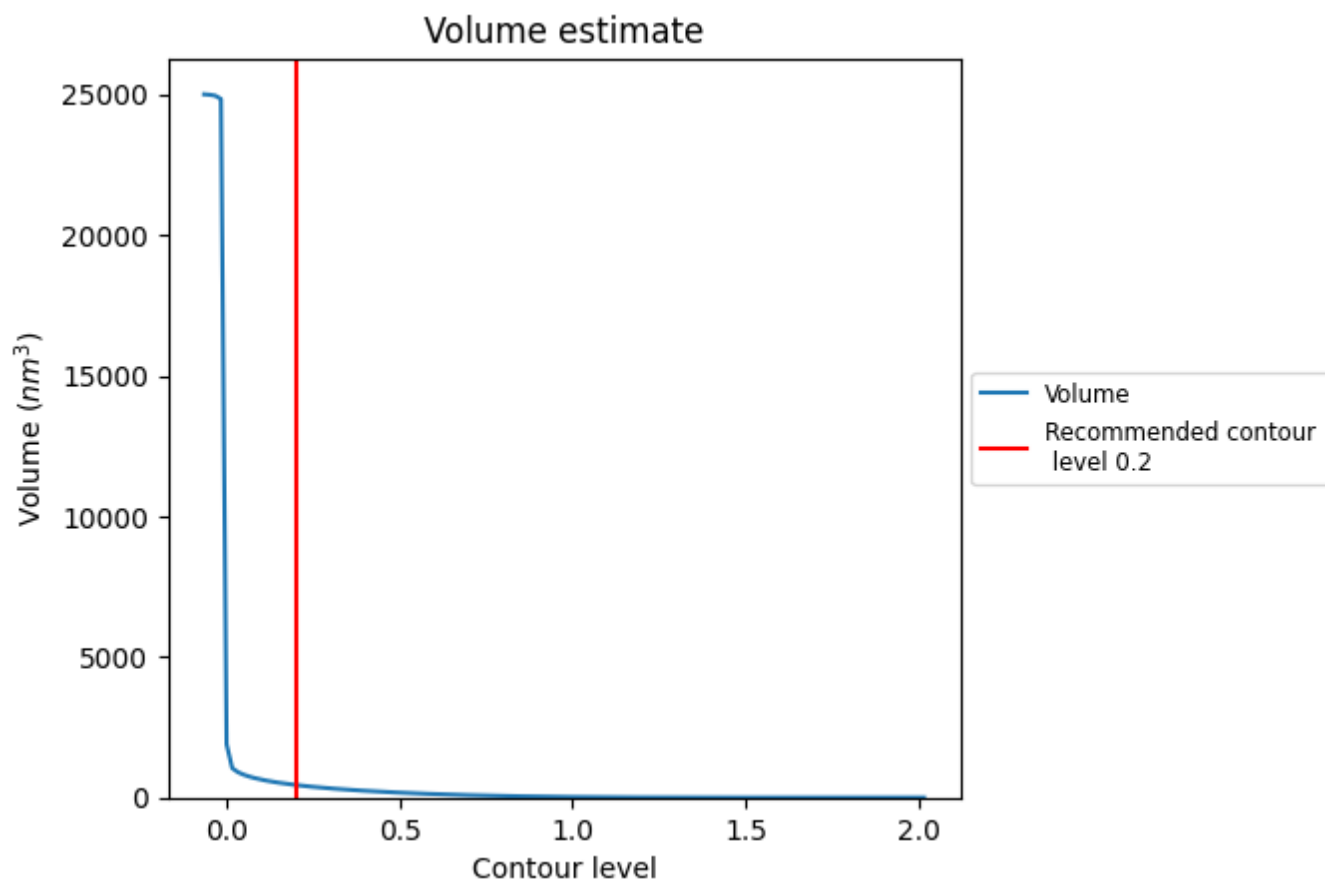
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

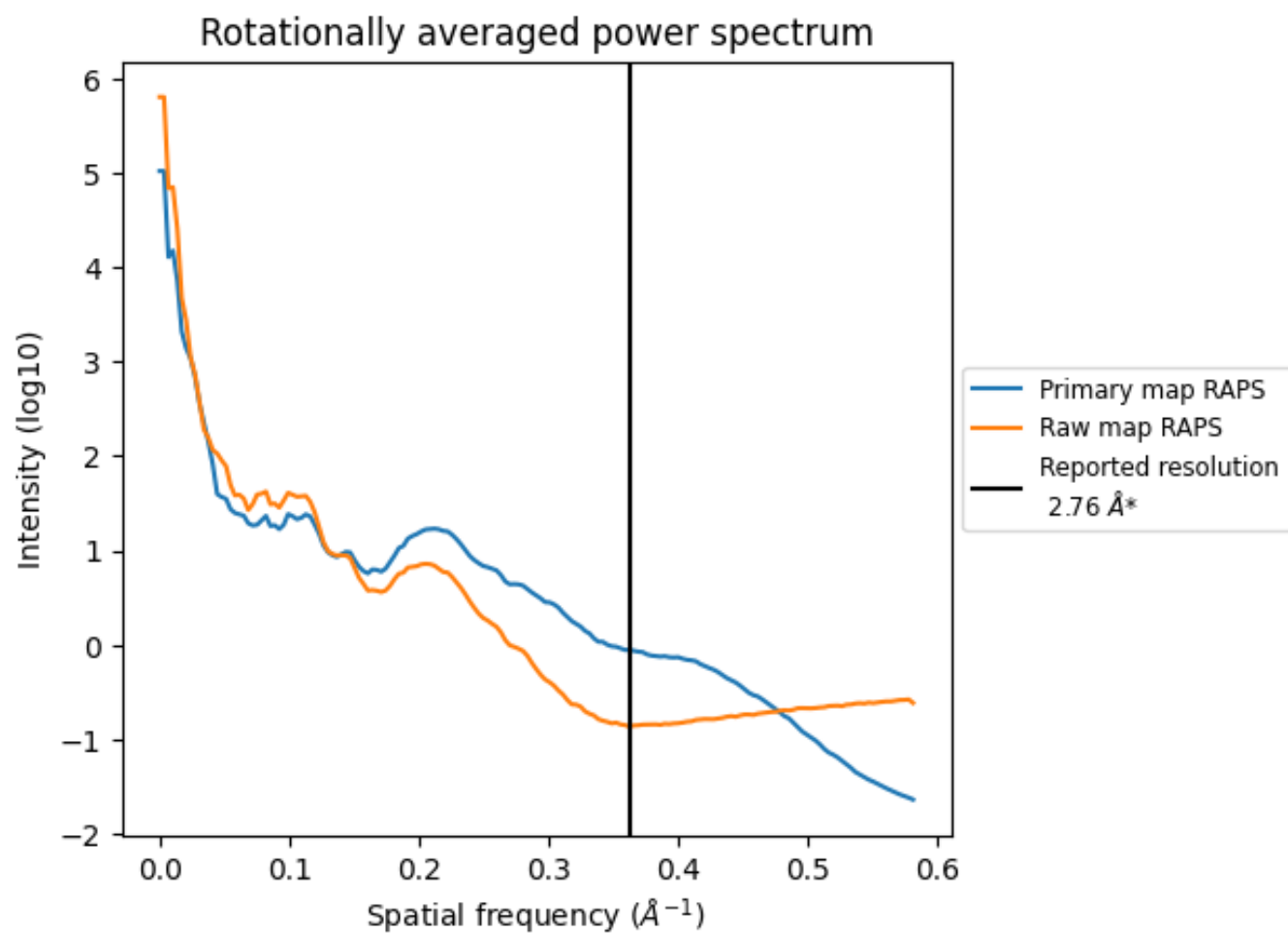
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 448 nm³; this corresponds to an approximate mass of 405 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

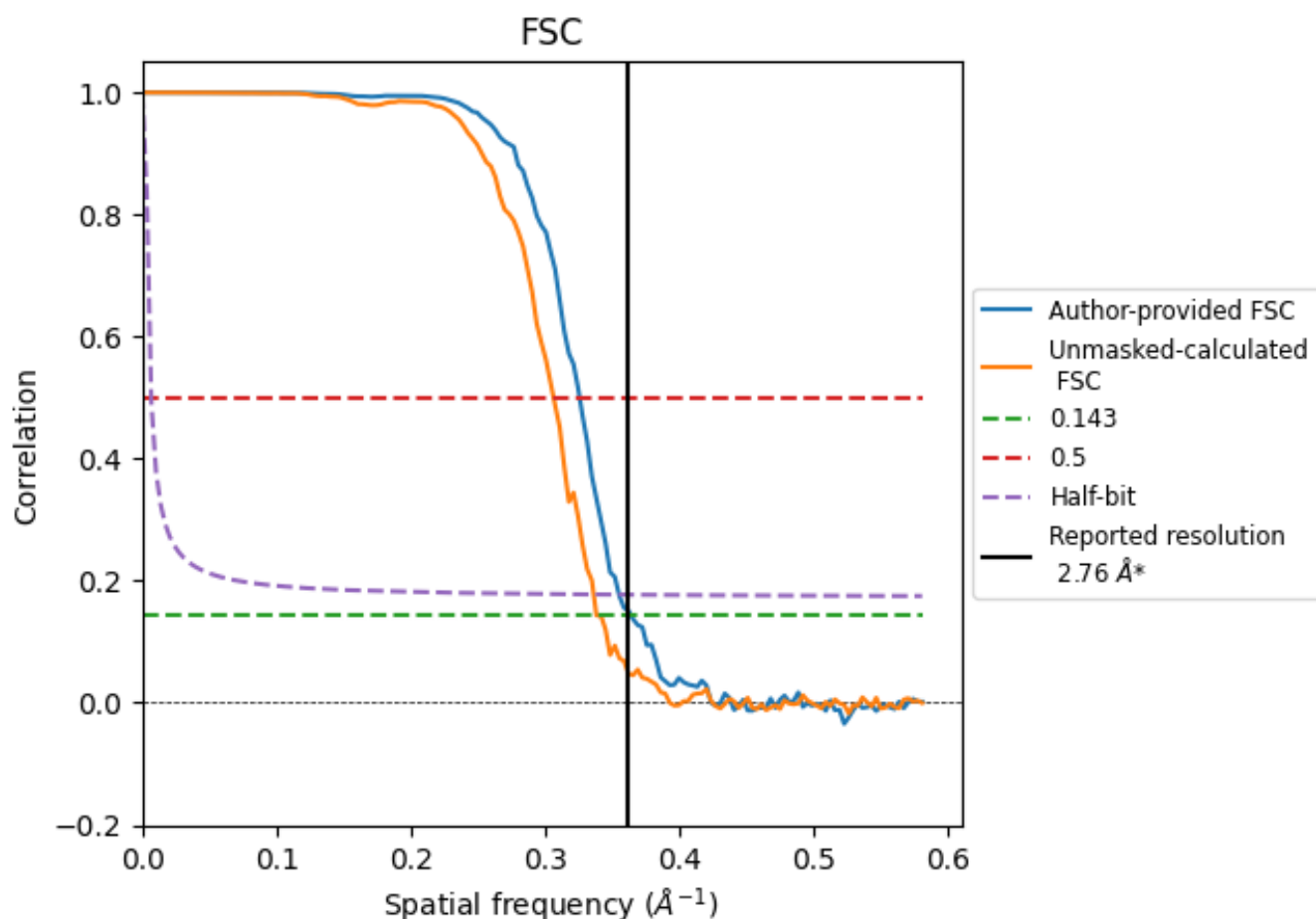


*Reported resolution corresponds to spatial frequency of 0.362 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.362 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	2.74	3.07	2.81
Unmasked-calculated*	2.95	3.26	2.97

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

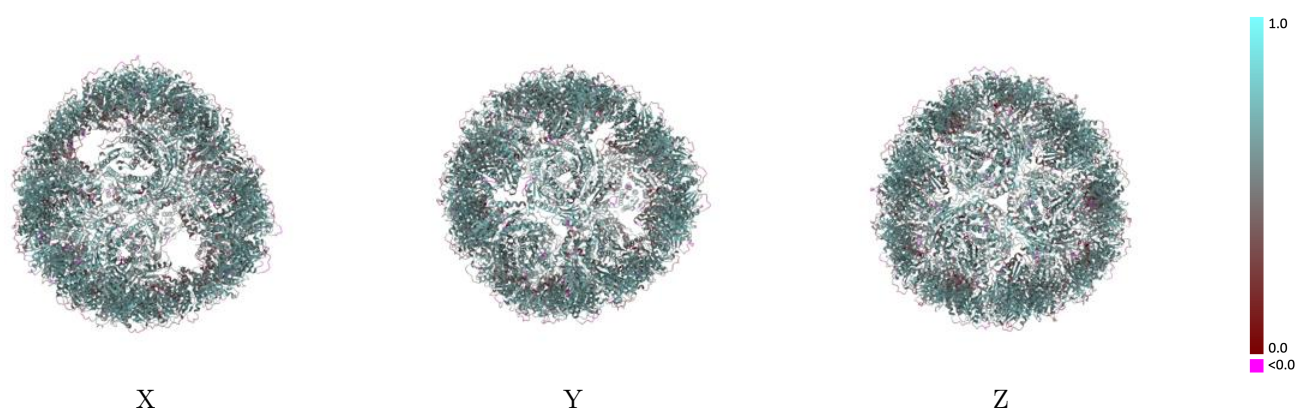
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51005 and PDB model 9G3O. Per-residue inclusion information can be found in section 3 on page 46.

9.1 Map-model overlay [i](#)

This section was not generated.

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

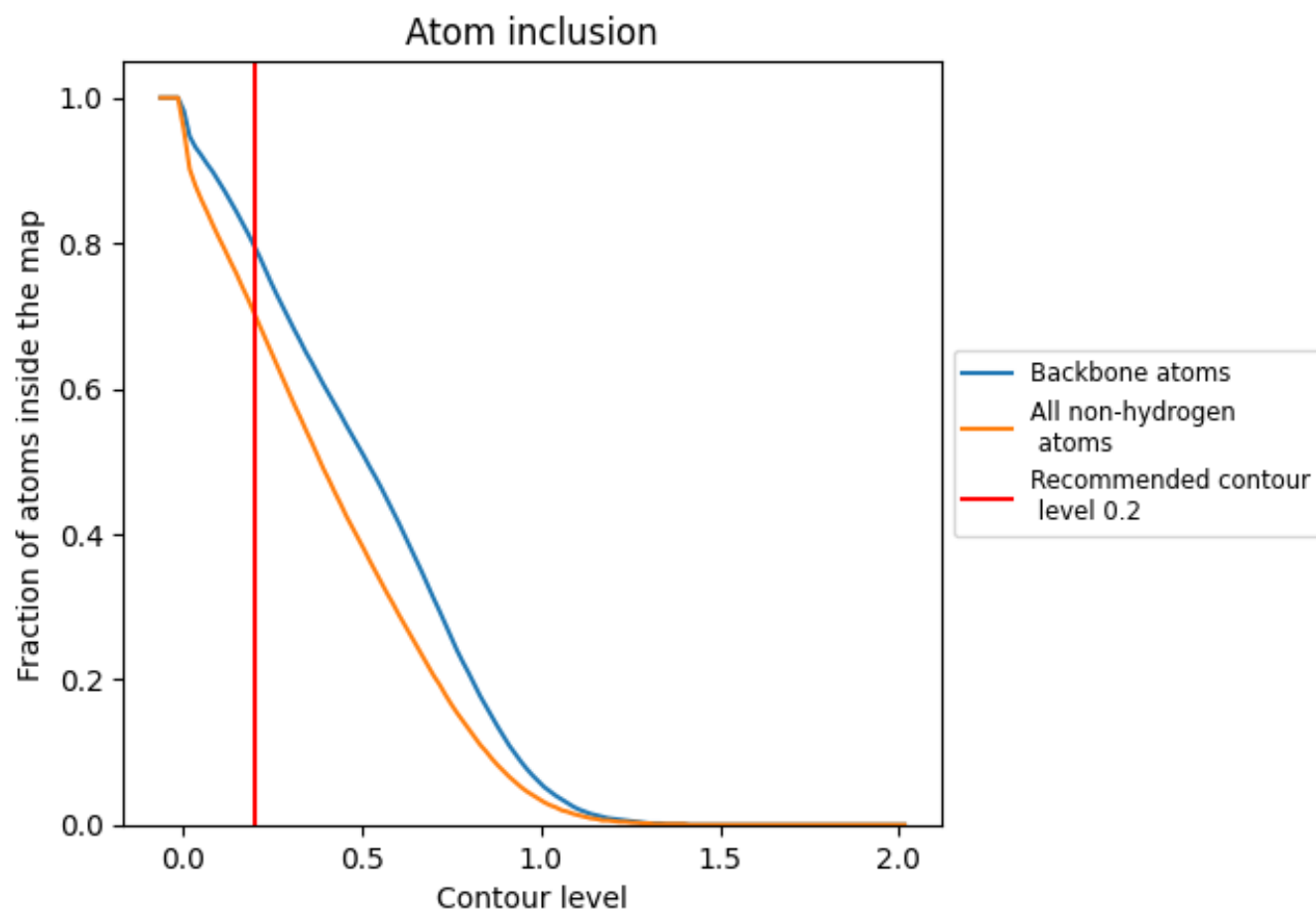


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 70% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7010	 0.5540
A	 0.7420	 0.5850
AA	 0.6940	 0.5500
AB	 0.7470	 0.5820
AC	 0.7240	 0.5610
AD	 0.7070	 0.5500
B	 0.7880	 0.6090
BA	 0.7140	 0.5480
BB	 0.6120	 0.4980
BC	 0.7200	 0.5610
BD	 0.5860	 0.4930
C	 0.7480	 0.5880
CA	 0.7330	 0.5610
CB	 0.6880	 0.5450
CC	 0.7480	 0.5810
CD	 0.6940	 0.5550
D	 0.6160	 0.5140
DA	 0.7320	 0.5650
DB	 0.6040	 0.4890
DC	 0.7750	 0.5940
DD	 0.7090	 0.5530
E	 0.7060	 0.5570
EA	 0.7320	 0.5800
EB	 0.6850	 0.5520
EC	 0.7490	 0.5780
ED	 0.7180	 0.5550
F	 0.6190	 0.5070
FA	 0.7910	 0.6010
FB	 0.7070	 0.5540
FC	 0.6270	 0.4990
FD	 0.7130	 0.5650
G	 0.7090	 0.5690
GA	 0.7580	 0.5840
GB	 0.7150	 0.5580
GC	 0.7100	 0.5460



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Chain	Atom inclusion	Q-score
GD	 0.7400	 0.5720
H	 0.7170	 0.5670
HA	 0.6210	 0.5030
HB	 0.7260	 0.5700
HC	 0.5770	 0.4810
HD	 0.7720	 0.5980
I	 0.7340	 0.5780
IA	 0.6960	 0.5510
IB	 0.7410	 0.5800
IC	 0.6790	 0.5480
ID	 0.7300	 0.5840
J	 0.7390	 0.5880
JA	 0.5770	 0.4980
JB	 0.7800	 0.6030
JC	 0.7020	 0.5480
JD	 0.6120	 0.5000
K	 0.7350	 0.5730
KA	 0.6710	 0.5590
KB	 0.7370	 0.5850
KC	 0.7040	 0.5530
KD	 0.7060	 0.5540
L	 0.7500	 0.5940
LA	 0.6990	 0.5580
LB	 0.6030	 0.5010
LC	 0.7140	 0.5560
LD	 0.6020	 0.4970
M	 0.7260	 0.5810
MA	 0.7080	 0.5640
MB	 0.6930	 0.5470
MC	 0.7410	 0.5780
MD	 0.6950	 0.5580
N	 0.6070	 0.5080
NA	 0.7060	 0.5680
NB	 0.6120	 0.4940
NC	 0.7940	 0.6100
ND	 0.7160	 0.5560
O	 0.6880	 0.5510
OA	 0.7370	 0.5710
OB	 0.6980	 0.5530
OC	 0.7600	 0.5880
OD	 0.7280	 0.5680
P	 0.6040	 0.4830

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Chain	Atom inclusion	Q-score
PA	 0.7670	 0.6010
PB	 0.7100	 0.5560
PC	 0.6200	 0.5020
PD	 0.7240	 0.5740
Q	 0.6870	 0.5490
QA	 0.7290	 0.5880
QB	 0.7250	 0.5690
QC	 0.6900	 0.5420
R	 0.7170	 0.5530
RA	 0.6140	 0.5060
RB	 0.7210	 0.5710
RC	 0.5940	 0.4880
S	 0.7320	 0.5620
SA	 0.6960	 0.5450
SB	 0.7480	 0.5840
SC	 0.6820	 0.5500
T	 0.7190	 0.5710
TA	 0.5920	 0.4880
TB	 0.7750	 0.6000
TC	 0.6930	 0.5490
U	 0.7510	 0.5820
UA	 0.6740	 0.5510
UB	 0.7470	 0.5790
UC	 0.7090	 0.5580
V	 0.7840	 0.5990
VA	 0.7020	 0.5560
VB	 0.6170	 0.5040
VC	 0.7220	 0.5660
W	 0.7450	 0.5760
WA	 0.7150	 0.5600
WB	 0.7080	 0.5500
WC	 0.7520	 0.5810
X	 0.6240	 0.5000
XA	 0.7140	 0.5660
XB	 0.5910	 0.4860
XC	 0.7850	 0.6010
Y	 0.7120	 0.5460
YA	 0.7450	 0.5770
YB	 0.6850	 0.5530
YC	 0.7330	 0.5830
Z	 0.6000	 0.4780
ZA	 0.7760	 0.6030

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Chain	Atom inclusion	Q-score
ZB	 0.7190	 0.5530
ZC	 0.6280	 0.5060